Supplementary Information

Analysis of DNAs associated with coconut foliar decay disease implicates a unique single-stranded DNA virus representing a new taxon

Bruno Gronenborn[1], John W. Randles[2], Dennis Knierim[3], Quentin Barrière[1], H. Josef Vetten[4], Norman Warthmann[5], David Cornu[1], Tiata Sileye[6], Stephan Winter[3], Tatiana Timchenko[1,*]

[1]Institute for Integrative Biology of the Cell, UMR9198, CNRS, Université Paris-Sud, CEA, Avenue de la Terrasse, 91198 Gif sur Yvette, France.
Phone: (+33) 16982 3468
Email: tania.timtchenko@i2bc.paris-saclay.fr
Email: bgronenborn@gmail.com
Email: quentin.barriere@i2bc.paris-saclay.fr
Email: David.CORNU@i2bc.paris-saclay.fr

[2]School of Agriculture Food and Wine, University of Adelaide, Glen Osmond, South Australia 5064.
Email: john.randles@adelaide.edu.au

[3]Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ) Messeweg 11/12,
38104 Braunschweig
Germany
Email: dek13@dsmz.de
stephan.winter@dsmz.de

[4]Im Spargelfeld 1
38162 Cremlingen
Germany
Email: rvetten@gmx.de

[5]Norman Warthmann
Research School of Biology
The Australian National University
Linnaeus Way, Canberra, ACT 2601, Australia
Email: norman.warthmann@anu.edu.au
norman@warthmann.com

[6]Vanuatu Agricultural Research and Technical Centre, Santo, Vanuatu
Email: tiatas@vanuatu.com.vu
sileye.tiata@gmail.com

[*]***Corresponding author***.

Figures S1, S2, S3, S4; Tables S1, S2, S3, S4, S5, S6, S7

Figure S1

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                                           ---MAS--SRRWCFTLNFS-AXEP---LSPLSENE-VSYAVWQDEXAPTTGQRHLQGYLQLK-KRT-LGGXKKLFGG--AHLEKARGTD-EEARDYCMKEETRVSGPWEFGEPCPSGSHKR----KLMERVIRSPEEMXXEDPSTYRRCKAKL--AEEEFXK---EEIWPXXLKPWQLEL
                                                   10        20        30        40        50        60        70        80        90       100       110       120       130       140       150       160       170       180
CFDV-[VU;89]_alphasat_R_Rep                ---MGGR-ARRWCFTLNYSAEEEAASLVRRIESLN-TVYAIVGDEVAPTTGQRHLQGFLHLKGAGRTLQGLKTFLQNDKIHLERAKGSD-EQNRGYCSKE-QVRF---EHGVATRPGVRRG-----VRQRYVEDPDELRLEDPGGYRRCVASG--SSLEWARWALEHPFPHAYHDWQREL 163
CFDV-[VU;89]_alphasat_1_Rep                ---MGSS-IRRWCFTLNYETEEEAANVVRRIESLN-LVYAIVGDEVAPSTGQRHLQGFIHLK-TGRRLQGLKTVLGNDRIHLEPTRGSD-EQNRDYCSKE-RVLL---EHGVPTRPGVKRP----RLAQRFAEEPDELRLEDPGGYRRCVVHG--ASVEWTRWAAENPFPFPYHNWQLEV 163
CFDV-[VU;89]_alphasat_2_Rep                ---MAAR-VRRWCLTLNYSTEEEAARFVERVKSLT-TTYCIVGDEVAPTTGQHHLQGFIHLK-SARCLQGLKTFLQNDKVHLEAAKGSD-EQNRVYCSKE-QIRY---EHGVATRPGSKRR-----LEQRFDEDPADLRLEEPGGYRRVVAHR--ASVEWYGWALEHPFPHPYHDWQLEL 162
CFDV-[VU;89]_alphasat_4_Rep                ---MTQR-CRRWCFTLNYDSDEEAAALVRRVQSLS-LTYAIVGKETAPTTGQKHLQGFLHLKGGGRVLQGLKTVLQNDRIHLEQAHGSD-EQNRVYCSKE-ETIF---EHGIPTRPGVKRR-----LVDRFDDEPDELRLEDPGGYRRCVALR--AAVEWAGWASENPFPFPYHHWQLEL 163
CFDV-[VU;15]_alphasat_8_Rep                ---MAQR-XRRWCFTLNFNSEEEAAAVVRRLQSLS-LTYCIVGKETAPTTGQQHLQGFLHLKSGGRTVQGLKTVLQNDRIHLEQAHGSD-EQNKIYCSKD-EVIF---EHGIPTRPGVKRR-----LADRFDDDPDEVRLEDPGGYRRCVALR--SSVEWAGWAAENPFPFPYHHWQLEL 163
CFDV-[VU;89]_alphasat_5_Rep                ---MSSR-ARRWCFTLNYRSEEEAAQLVQRIESLD-PTYAIVGDETAPTTGQRHLQGFIHLKGAGKSLQALKTALRNDTVHLERAQGSD-LQNRDYCSKE-QVRF---EHGIATRAGCKRR-----LLERFAEDPDDLLLEDPGGYRRCVAHR--HAVEWREWATARDFPYPLHDWQHEV 163
CFDV-[VU;89]_alphasat_3_Rep                -MAMVS---RRWCFTLNYSEEDERTRLLSLFSEEE-LHYAIVGDEVAPSTGQKHLQGYLNFR-KVLRLGALKKKY-SDKAHWEIAKGTD-EENRVYCSKE-HKVF---ELGSPVVVGSNKR----KLAEAIERSPERMRLEQPEIFHRYASAK--KMIQFK---EQYDHPVFDRTWQIKL 159
CFDV-[VU;89]_alphasat_6_Rep                -MALQS---RRWCFTLNYSEEEERTRLLSLFSEEE-FHYAIVGDEVAPSTGQKHLQGYLNFR-KVLRLGALKKKY-SDKAHWEIAKGTD-EENRVYCSKE-HKLL---ELGSPVLVGSNKR----KLAEAIERSPERMRLEQPEIFHRYASAK--KMIQFK---EQYDHPVFDRTWQIKL 159
CFDV-[VU;89]_alphasat_7_Rep                ---MASQ-VRRWVLTFNYSDESAASDLVRRIESLK-LIYGIIGDEIAPTTGQRHLQGFLHLAGRGRTLEGLKKTLENNTVHLEPAKGSD-QQNKIYCSKE-NVLF---EHGVPTRPGSKRK-----LYERYEEDAEELRIEEPGAYRRCKQSME--KQKKWNYWVLNNPFPYDLYQWQEEL 163
BBTV_alphasat_Y_Rep_ACJ36781               ---MSS---FKWCFTLNYSSAAEREDFLSLLKEED-VHYAVVGDEVAPSTGQKHLQGYLSLK-KSIKLGGLKKRY-SSKAHWERARGTG-EDNSKYCSKE-TLIL---ELGFPVVNGSNKR----KISEMVARSPDRMKIEQPEMFHRYQSVN--CMKKFK---EEFVHPCLDRPWQIQL 157
BBTV_alphasat_HaiKou2_Rep_AEF97834         ---MSS---FKWCFTLNYSSAAEREDFLSRLKEDD-VYYAVVGDEVAPSSGQKHLQGYLSLK-KSMKLGGLKKRY-SSKAHWEKARGSD-KENSKYCSKE-TLIL---EIGFPATQGSNKR----KLSEMVSRSPERMRIEQPEIYHRYLSVS--KLKKFK---EEFVHPCLERPWQIQL 157
BBTV_alphasat_S1_Rep_AAG44003              ---MSS---FKWCFTLNYSSAAEREDFLALLKEEE-LNYAVVGDEVAPSSGQKHLQGYLSLK-KSIKLGGLKKKY-SSRAHWERARGSD-EDNAKYCSKE-TLIL---ELGFPASQGSNRR----KLSEMVSRSPERMRIEQPEIYHRYTSVK--KLKKFK---EEFVHPCLDRPWQIQL 157
CBDV_alphasat_Tung1_Rep_BAS02103           ---MAS---NKWCFTLNYSDAAERDIFLATLKEEE-LRYAVVGDEVAPTTGQKHLQGYLSLR-KLIRLGGLKKRF-SPKAHWEMAKGSD-EDNARYCSKE-TLIL---QLGIPTSQGSN-----------TRSPERMRIEQPEIFHRYESVK--KATIFK---DEYQHPSLDRQWQIQL 149
CBDV_alphasat_Fr_X7_Rep_YP_008854133       ---MAS---FKWCFTLNYSDAAERDIFLATLKKED-VHYAVVGDEVAPTTGQKHLQGYLSLR-RRIRLGGLKKKY-SPRAHWEVARGTD-GENMRYCSKE-TLIL---ELGLPATPGSNKR----KYAEMYTRSPERMKIEEPEIYHRYDSVN--CMKQFK---QEFVYPCLDRPWQIQL 157
BBTV_alphasat_4_Rep_ACB86656               ---MSA---SRWTFTLNYSDATERGKFLATLKEED-VHYAVVGDEVAPTNGTRKHLQGYLSLK-KRFRISGIKKKY-SSRAHWEKARGSD-YDNKAYCSKE-ALIL---ELGVPCQTGSNKR----KLADMVTRSPERMKIEQPEIFHRYASVK--KMKEFK---ERYVYPILDRPWQVQL 157
BBTV_alphasat_TW3S2_Rep_ACJ36782           ---MSS---FKWCFTLNYSSAAEREDFLALLKEED-VHYSVVGDEVAPATGQKHLQGYLSLK-KSIRLGGLKKKY-GSRAHWEIAKGTD-EQNRRYCSKE-TLVL---ELGTPVVPGSKKR----KLLDRFRESPEELKMDDPSKYRRCLAVE--SIKDAR---NNSEWVHELKEWQNKL 157
MDV_alphasat_C2_Rep_BAA33981               ---MAS---KRWCFTLNYKTALERETFISLFSRDE-LNYFVCGDEIAPTTGQKHLQGYVSMK-KLIRLGGLKKKF-GSIAHWEIAKGDD-FQNRDYCTKE-TLIA---EIGAPVKKGSNRR----KIMEIYEEDPEEMKLRDPDTALRCKAKK--LREEYC----SEVSVFSLRPWQIEL 156
FBNYV_alphasat_C1_Rep_CAA06791             ---MAS---KRWCFTLNYKTAVERESFISLFSRDE-LNYFVCGDEVAPTTNQKHLQGYVSLK-KMIRLGGLKKKF-GYRAHWEIAKGDD-FQNRDYCTKE-TLIS---EIGAPVKKGSNQR----KIMDLYLQDPEEMQLKDPDTALRCNAKR--LRIEYC----SSFAVISLRPWQSEL 156
SCSV_alphasat_C2_Rep_AAA68018              ----MA---RRYCFTLNYATEIERETFLSLFSQDE-LNYFVVGDETA-TTGQKHLQGYVSFK-NKIRLGGLKKKF-GNRAHWEIAKGSD-SQNRDYCCKE-TLIS---EIGIPVMKGSNKR----KTMEIYEEDPEEMQLKDPDTALRCKAKK--LKEEYC----SCYDFQKLRPWQIEL 154
FBNSV_alphasat_1_Rep_AHC72219              ---MAC---ANWVFTRNFQGALP------SLSFDERVQYAVWQHERG---THDHIQGVIQLK-KKARFSTVKEII-GGNPHVEKMKGTI-EEASAYVQKEETRVAGPWSYGDLLKRGSHRR----KTMERYLEDPEEMKLKDPDVALRCNAKR--LKEDYC----SCFSSFKLRPWQIEL 152
BMLRV_alphasat_1_Rep_AHC72176              ---MAC---ANWVFTRNFQGALP------ILSFDERVQYAVWQHERG---THDHIQGVIQLN-KKARFSTVKEII-GGNPXLEKMKGTI-EEASAYVQKEKTRVAGPWSYGELVKKGSHKR----KTMERYLEDPEEMRLKDPDTALRCNAKR--LKEDYC----LSFACIQLRSWQIEL 152
FBNYV_alphasat_C7_EG93_Rep_CAB44025        ---MPSIRATHWCFTLNFS-GSIPE--IN---WTADVQYSIWQHERVG---HDHLQGYIQMNKHVT-LKKMKELLPG--AHLEMAKAP--KKAIEYCQKKESAIAGPWEYGTWISSGSHKR----KLMERFEDGPEEMKLEDPGLYRRCLSRV--CTWNFD-LRPWQDEL 154
MDV_alphasat_C10_Rep_BAA34048              ---MPSIRAIHWCFTLNFS-GKIPE--IV---WTADVQYSIWQHERVN---HDHLQGYIQMKKQTT-LKKMKELLPG--AHLEMARAP--KKAIDYCQKKETAIDGPWEYGTWISTGSHKR----KLMERFDEDPEEMKLEDPGLYRRCLSRV--QMTKVREK--NSWDYD-LRPWQDEL 154
MDV_alphasat_C3_Rep_BAA33982               ---MPTVQSTCWVFTLNFK-GEIPI--LP---FNERVQYACWQHERVG---HDHLQGFIQMKAQQS-LGQMKAIIPG--AHFEKMRALNSDQAKAYAMKEDTRIEGPWEYGKYIKKGSHKR----KIMERFEDDPEEMKIEDPSLYRRCLSRK--MTEEQRST--AEWNYD-MKPWQDQV 156
PNYDV_alphasat_3_Rep_AHC72280              ---MPSQKSTYWVFTLNFK-GEIPI--LS---LDTRVQYALWQHEYVS---HHHLQGFIQMKAQST-LGQMKALIPG--AHFEVMKALDSDQARSYAMKEDSRLEGPWEYGLYIKKGSHKR----KVMERFDSEPEEMKVEDPSLYRRCLSRK--MTEEQRSS--STWDYD-LRPWQDSI 156
SCSV_alphasat_C6_Rep_AAA68022              ---MPTRQSTSWVFTLNFE-GEIPI--LP---FNESVQYACWQHERVG---HDHLQGFIQFKSRNTTLRQAKYIFNG--LNPHLEIARDVEKAQLYAMKEDSRVAGPWEYGLFIKRGSHKR----KLMERFEEDPEEMKIADPSLYRRCLSRK--MAEEQRCS--SEWNYD-LRPWQEEV 157
BMLRV_alphasat_2_Rep_AHC72185              ---MPTLQGTFWCFTLNFS-GDVPA--LS---FDETVQYAVWQHECVS---HDHLQGFVQMKKRST-MKMMKILLPG--AHLEVAKGT-PEQASSYAMKESSRVAGPWFYGELLKKGSNKR----KLLDRYRDSPEDMELEDPAKARRCRARI--DKEKFVSD--FKVEDD-EQEWKRLV 155
MDV_alphasat_C1_Rep_BAA33980               ---MPTLQGTFWCFTLNFS-GDAPS--LS---FNERVQYACWQHERVS---HDHLQGYIQMKKRST-LKMMKELLPG--AHLEVSKGT-PEEASDYAMKEETRVAGPWTYGELLKKGSNKR----KLLDRYKENPEDMELEDPAKARRCRAKI--DKEKFIAE--FKVEDD-EQEWKKIL 155
FBNSV_alphasat_2_Rep_AHC72218              ------MQSVSWVFTLNFS-GEVPL--LS---FDERVQYAVWQHERVN---HDHLQGVIQMKRKTR-MNTVKSLIGGN-PHLEPMRSR-IEEASAYAMKEESRVAGPWFHGELLKKGSNKR----SLMEKYKEDPVSMELEDPGKARRCRARL--DKEKFVAA--FKVEDD-EQEWKRLL 153
PNYDV_alphasat_1_Rep_AHC72279              ------MASCNWVFTRNFS-GDTPL--LS---FDERVQYACWQHEKVA---HDHLQGVIQLKKRAR-MNTVKALIGGN-PHVEMMKA-IEEASAYVQKEESRVAGPWIYGEMLKKGSHKR----SLMERYKEDPEEMELEDPGKARRCRARL--DKEKFVSE--FKVEDD-EQEWKSLL 153
PaLCuV_IN__alphasat_Rep_AFG29502           ---MPAVQSFWWCFTIFFTSAAPPD--LVSLFENTSVSYACWQEEESPTTKRRHLQGYLQLKTKKS-LSTVKSLFGDLNPHLEKQRARKTDDARDYCMKEETRVSGPFEFGDYCPSGSHKR----RQRESVIRSPVRMAEENPSVFRRVKAKI--AEEEFQKTA-HEIQISNLKSWQLRL 167
CLCuV_alphasat_Rep_AIH07616                ---MPAAQSFWWCFTIFFTTAAPPD--LVPLFENTSVSYACWQEEESPTTKRRHLQGYLQLKTKKS-LSAVKSLFGDLNPHLEKQRARRTDEARDYCMKEETRVSGPFEFGDYCPSGPHKR----RQRESVIRSPVRMAEENPSVFRRVKAKI--AEEEFQKTA-HEIQISNLKSWQLRL 167
GDS_alphasat_Rep_ALB26259                  ---MPSAQSVFWCFTIFFTSASPPD--LVPLFENTSVSYACWQEEESPTTRRRHLQGYLQLKTKKS-LSAVKSLFGDLNPHLEKQRARRTDEARDYCMKEETRVSGPFEFGDYCPSGSHKR----RQRESVIRSPVRMAEENPSLFRRVKAKI--AEEEFQKTA-REIQILNLKSWQSRL 167
SiLCuV_alphasat_Rep_CBY89002               ---MPTIQSQWWCFTVFFLSAAAPD--LVPLFENTHVSYACWQEEESPTTRRRHLQGYLQLKGKRT-LAQVKSLFGDLNPHLEKQRARKTDEARDYCMKEETRVSGPFEFGDYCPSGSHKR----RQRESVIRSPVRMAEENPSLFRRVKAKI--AEEDFQKTA-REIEILNLKSWQLRL 167
CLCuDaV_alphasat_Rep_CAD56270              ---MPALKAQWWCFTIFFVSAAAPD--LVPLFENTHVSYACWQEEESPTTRRRHLQGYLQLKGQRT-LNQVKVIFGELKPHLEKQRARRTDEARDYCMKEETRVSGPFEFGDYCPGGSHKR----RLRESVIRSPVRMAEENPSVFRRVKAKL--AEEEFQKSA-HEIQISNLKSWQTRL 167
ToLCV_alphasat_Rep_CDH98084                ---MAAIKSNWWCFTVFFLSATAPD--LVPLFENTHVSYACWQEEESPTTRRRHLQGYLQLKGQRT-LNQVKSIFGDLKPHLEKQRARKTDDARDYCMKPETRVSGPFEFVEGEYCPAGSHKR----RQRELVIRSPVRMAEENPSVFRRVKAKI--AEEEFQKSA-PEIQISNLKSWQSRL 167
TbCSV_alphasat_Rep_CBK44088                ---MAALKAQWWCFTVFFLSATAPD--LVPLFENTHVSYACWQEEESPTTRRRHLQGYLQLKGQRT-LNQVKAIFGDLKPHLEKQRARKTDEACDYCMKEETRVSGPFEFGEYCPAGSHKR----RQRELVIRSPVRMAEENPSVFRRVKAKI--AEEEFQKSA-HEIQISDLKSWQLRL 167
AEV-IN_alphasat_Rep_CEE15328               ---MAALKGQWWCFTVFFLTATAPD--LVPLFENTHVSYACWQEEESPTTKRRHLQGYLQLKGQRT-LNQVKAIFGDLKPHLEKQRARKTDEARDYCMKEETRVSGPFEFGEYCPAGSHKR----RQREIVNRSPVRMAEENPSVFRRVKAKI--AEEEFQKSA-HEIQISNLKSWQLRL 167
AYVV_alphasat_Rep_CAB59911                 ---MPALKGQWWCFTVFFLSSTAPD--LVPLFENTHVSYACWQEEEAPTSKRRHLQGYLQLKGQRT-LNQVKALFGELKPHLEKQRARKSDEARDYCMKEETRVSGPYEFGDYCPSGSHRR----RQRELVIRSPVRMAEENPSVFRRVKAKI--AEEEFQATV-AEIQISNLKSWQLRL 167
TbCSV_alphasat_Y290_Rep_CAI59924           ---MPSITSVFWCFTIFFTSASAPD--LVPLFENTHVSYACWQEEESPTTRRRHLQGYLQLKGKRT-LNQVKAIFGDLKPHLEKQRARKTDEACDYCMKEETRVSGPFEFGDYCPSGSHKR----RQRESVIRSPVRMAEENPSVFRRVKAKL--AEEEFQATV-AEIQISNLKSWQLRL 167
AYVIV_alphasat_Rep_CDH98093                ---MPTIQSQWWCFTVFFLSATAPD--LVPLFENTHVSYACWQEEESPTTRRRHLQGYLQLKGKRS-LAQVKALFGDLNPHLEKQRARKTDDARDYCMKEETRVTGPFEFGEYCPAGSHKR----RQRESVIRSPVRMAEENPSVFRRVKAKI--AEEEFQKSA-SGIQISNLKSWQLRL 167
CYMV_alphasat_Rep_CBJ19303                 ---MPTIQSQWWCFTVFYLSATAPD--LVPLFENTHVSYACWQEEESPTTGRRHLQGYLQLKGKRS-FAQVKALFGDLNPHLEKQRARKTDEARDYCMKEETRVSGPFEFGDYCPSGSHRR----RQRESVIRSPVRMAEENPSVFRRVKAKI--AEEDFQKTA-KEIQISNLKSWQLRL 167
VEM_alphasat_2_Rep_ALK03648                ---MKTPQSIWWCFTIFFASAGAPE--LFPLFENTSVSYACWQEEESPTTHRRHLQGYLQLKSKKT-LNQVKALFGDLNPHLEKQRARNSDDARDYCLKEASRVSGPWEFGEYCPSGSHKR----RQREQVQKSPERMMEENPSVFRRVKAKI--SIEAHQLSL-SELPFL-LKPWQFEI 166
Dragonfly_ass_alphasat_Rep_AFV91336        MGSFSSPRSRWWCFTLNFS-GDPPE--LAWWLARDEIKYACWQHEKG---THDHMQGYLQLKKPSR-LTAVRKLFGNFRPHLEVQKARRAEDARDYCMKDESRVAGPWIEGFIPQGSHKG----RMRDLVRRSPERMAEENPSVYRRVLAAQ--SVERFRSDP-SLLPDP-LRDWQICL 165
EuYMV_alphasat_Rep_CBA18108                ---MSGR-SRNWCFTL-FEYTLPL-----FLSLPDWAVYLVFQEEVSPSTTRKHIQGYCTLK-KPQRLSFLKTKLG-NGAHLEIAKGSA-SSNRDYCRKDDSRASGPWEFGILAEQGSHKR----KTMERFQEDPDEVRLADPKLYRRCLATK--INKEFS----CLVLPAFDRPWQLLV 157
CLCuGeV_alphasat_Rep_CDI44972              ---MAPQ-GKRWCFTS-FEEREP------FTSLPDGCSYVVXQREKCPETGREHWQGFVTFS-AARRLNSVKSFAGGNNWHWEVARGTN-SECRSYCTKEDTRVAPPVEYGVFCELGSKKR----KVMEQFEEDPEELKLADPSKYRRCLAIV--TNKRFN----NVELPLFDRPWQEEL 157
SCSV-[AU;F]_M_Rep_CAB96405                 ---MAR-QVICWCFTLNNP---L-----APLSLHESMKYLVYQTEAGDN-GTIHYQGYVEMK-KRTSLVQMKKLLPG--AHLEKRRGSQ-GEARAYAMKEDSRVEGPWEFGEFKEVLEDKLRSVMEDMKSTGKRPVEYIEDCCNTYDKSSATLREFRGELKKKQAIEEWQLQRQPWMDEV 163
FBNYV-[EG;1_93]_M_Rep_NP_619567            ---MAR-QVICWCFTLNNP---L-----SPLSLHDSMKYLVYQTEQGEA-GNIHFQGYIEMK-KRTSLAGMKKLIPG--AHFEKRRGTQ-GEARAYSMKEDPRLEGPWEYEEFVPTIEDKLREVMNDMKITGKRPIEYIEECCNTYDKSASTLREFRGELKKKAISSWELQRKPWMDEV 163
MDV-[JP;1]_M_Rep_NP_619769                 ---MAR-QVICWCFTLNNP---L-----SPLSLHELMKYLVYQREQGEA-GNIHFQGYIEMK-KRTSLAGMKKLIPG--AHFEKRRGTQ-GEARAYAMKEDTRLEGPWEYGEFIPTIEDKLREVMNDMKITGKRPIEYIEECCNTYDKSASTLREFRGELKKKAIISWELQRKPWMDEV 163
FBYLV-[ET;231]_M_Rep_CCF74113              ---MAR-QVICWCFTLNNP---L-----SPLSLHESMKYLVYQTEQGDS-GNIHFQGYIEMK-KRTSLAGMKKLIPG--AHFEKKKGTQ-GQARAYAMKEDTRVEGPWEYGEFIPTIEDKLRDVMQDMKNTGKRPIEYIEECCDTYDKSASTLREYRGELKKKQAIASWELQRKPWMDEV 163
FBNSV-[ET;Hol_97]_M_Rep_ADJ00306           ---MAR-QVICWCFTLNNP---L-----SPIFLHESMKYLVYQTEQGES-GNIHFQGYVEMK-KRTSLAGMKRLIPG--AHFEKRRGTQ-GEARAYAMKEESRIEGPWEFGEFIASVEDKLREVMNDMKNTGKRPIEYIEECCNTYDKSASTLREFRGELKKKAIATWELQRKPWMDEV 163
PNYDV-[DE;15]_M_Rep_ADE87486               ---MSR-QVICWCFTLNNP---L-----SLLSLHESMKYLVYQREQGES-GNIHFQGYVEMK-KRTSLAGMKRLIPG--AHFEKRRGTQ-GEARAYAMKEDSRLEGPWEEGEFHLTVEDKLREVMEDMKNTGKRPIEYIEECCNTYDKSSGTLREYQGELRKKRAINGWQLQRKPWMDEV 163
PYSV-[AT;15]_M_Rep_AHC72281                ---MSR-QVICWCFTLNNP---L-----SPLSLHESMKYLVYQREQGES-GNIHFQGYIEMK-KRTSLAGMKRLIPG--AHFEKRRGTQ-GEARAYAMKESSRLEGPWEEGEFHLTVEDKLREVMEDMKNTGKRPIEYIEECCNTYDKSSGTLREYQGELRKKRAISEWELQRKPWMDEV 163
BBTV-[Au]_M_Rep_AAB25544                   ---MAR-YVVCWMFTINNP---T-----TLPVMRDEIKYMVYQVERGQE-GTRHVQGYVEMK-RSSLKQMRGFFPG--AHLEKRKGSQ-EEARSYCMKEDTRIEGPFEFGSFKLSCNDNLFDVIQDMRETHKRPLEYLYDCPNTFDRSKDTLYRVQAEMNKTKAMNSWRTSFSAWTSEV 163
BBTV-[TW]_M_Rep_ABH03036                   ---MAR-YVVCWMFTINNP---A-----SLPVMRDEFKYMVYQVERGQE-GTRHVQGYVEMK-RSSLKQMRGFFPG--AHLEKRKGSQ-EEARAYCMKEDTRIEGPFEFGAFKLSCNDNLFDVIQDMRETHKRPLEYLYECPNTFDRSKDTLYRVQAEMNKTKAMNSWKTSFNAWTSEV 163
CBDV-[IN]_M_Rep_AGG38934                   ---MAR-YVVCWMFTINNP---S-----SLPVMRDEIKYMVYQVERGQE-GTRHVQGYVEMK-RSSLKQMRMFFPG--AHLEKRKGTQ-EEARTYCMKEDTRIEGPFEFGVFKLACNDSLYDVIQDMRLTNKRPLEYLYDCPNTFDRSKDTLYRVQAEMNKTKAMESWGKSYGSWTEQV 163
ABTV-[MY]_M_Rep_ABP96965                   ---MAR-YVVCWMFTINNP---E-----ALPEMREEYKYLVYQVERGES-GTRHVQGYVEMK-RSSLKQMRALIPG--AHLEKRRGTQ-EEARAYCMKADTRVEGPFEFGLFKVSCNDNLFDVIQDMRETHKRPIEYLYDCPNTFDRSKDTLYRVQAEMNKMQAMMSWSETYGCWTKEV 163
ABTV-[PH]_M_Rep_ABP96960                   ---MAR-YVICWMFTINNP---E-----TLPPMRDEYKYMVYQVERGES-GTRHVQGYVEMK-RRTSLKQMRALIPG--AHLEKRKGTQ-EEARSYCMKADTRIEGPFEYGMFKISCNDNLYDVIQDMRETNKRPIEYLYDCPNTFDRSRDTLYRVQAELNKMQAMKSWSESYGCWTKEV 163
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A

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                                              EELLEEEPDDRTIIWVYGPXGGEGKSTFAKHL-IKRDWFYTRGGKTDDVLYQYIGE-PGRNVVFDIPRCK-EDYLNYSLIEMLKNRXIVSXKYEPVMXPLINX--VHVIVMANFLPDF------------GKISEDRIKIIYC--------------------
                                                        190       200       210       220       230       240       250       260       270       280       290       300       310       320       330       340
CFDV-[VU;89]_alphasat_R_Rep                    LSAIEQPADDRTIFWVCGREGGDGKSVFAKYLGLKPDWFYTCGGTRKDVLYQYIED-PKRNLILDVPRCN-LDYLNYALLECVKNRAFSSDKYEPLSYLGFDH--VHVIVFANVLPDY------------LKISRDRIKLWNV                        290
CFDV-[VU;89]_alphasat_1_Rep                    LSAIGEPADDRTILWICGRDGGDGKSVFAKYLGLKPDWFYTCGGTRKDVLYQYIED-PKRNLILDVPRCN-LEYLNYALLECVKNRAFSSDKYEPLSYLGFDH--VHVLVFANVLPDY------------LKISRDRIKLWNI                        290
CFDV-[VU;89]_alphasat_2_Rep                    LSAIDQPADDRTIIWICGRDGGDGKSVFAKYLGLKPDWFYTCGGTRKDVLYQYIED-PKRHMILDVPRCS-VEHLNYALLECVKNRAFSSDKYEPLSYLGFDH--VHVLVFANVLPDY------------MKISEDRIKLFDI                        289
CFDV-[VU;89]_alphasat_4_Rep                    LSEIQEQADDRTILWVCGRTGGEGKSVFAKFLGLKPDWFYTCGGTRKDVLYQYIEE-PKRNVILDVPRCN-LEHLNYALLECIKNRAFSSDKYEPISYVGFDN--VHVIVFANILPDY------------LKISRDRIKLWDI                        290
CFDV-[VU;15]_alphasat_8_Rep                    LSQIDGQADDRTILWVCGRTGGEGKSVFAKYLGLKPDWFYTCGGTRKDVLYQYIED-PKRNVILDVPRCN-LEHLNYALLECIKNRAFSSDKYEPLSYLGFDN--VHVIVFANVLPDY------------LKISRDRIKLWDI                        290
CFDV-[VU;89]_alphasat_5_Rep                    LAAIEEPPDDRTIIWVCGRSGGEGKSVFGKFLGLKPDWFYTCGGSKKDILYQYIEN-PKRHVIMDFPRCT-DTYMNYAVLECMKNRAFSSDKYEPLSYLGFDN--IHVIVLSNVLPDY------------FKISEDRIKLINI                        290
CFDV-[VU;89]_alphasat_3_Rep                    REAISEAPDDRSIIWVYGPDGNEGKSTFAKSL-IKQDWFYTRGGKKENILFSYIDEGSEKNIVFDIPRCN-QDYLNYDVIEALKDRVIESTKYKPVKIIELCN--IHVVVMANFLPDY------------MKISEDRIKIIRCY                       287
CFDV-[VU;89]_alphasat_6_Rep                    GEAISEAPDDRSIIWVYGPDGNEGKSTFAKSL-IKQDWFYTRGGKKENILFSYIDEGSEKNIVFDIPRCN-QDYLNYDVIEALKDRVIESTKYKPVKIIELCN--IHVVVMANFLPDY------------MKISEDRIKIIRCY                       287
CFDV-[VU;89]_alphasat_7_Rep                    MEVLQEPADNRTILWICGRDGGDGKTEFGKYLGLNEKWFYSCGGKTRDVLYQYIEE-PERNFILDVPRCN-DQYMNYALIECIKNRAFSSDKYEPLQYLGFDK--VHVIVLCNFLPDY------------LKISEDRIKLWNI                        290
BBTV_alphasat_Y_Rep_ACJ36781                   TEAIDEEPDDRSIIWVYGPYGNEGKSTYAKSL-IKKDWFYTRGGKKENILFSYVDEGSDKHIVFDIPRCN-QDYLNYDVIEALKDRVIESTKYKPIKIVELGK--IHVIVMANFMPDF------------CKISEDRIKIIYC                        284
BBTV_alphasat_HaiKou2_Rep_AEF97834             TEAIAEEPDDRSIIWVYGPNGNEGKSTYAKSL-IKKDWFYTRGGKKENILFSYVDEGSEKHIVFDIPRCN-QDYLNYDVIEALKDRVIESTKYKPIKIVELDR--IHVIVMANFMPDF------------CKISEDRINIIYC                        284
BBTV_alphasat_S1_Rep_AAG44003                  TEAIDEEPDDRSIIWVYGPNGNEGKSTYAKSL-MKKDWFYTRGGKKENILFSYVDEGSEKHIVFDIPRCN-QDYLNYDVIEALKDRVIESTKYKPIKLVELIN--IHVIVMANFMPEF------------CKISEDRIKIIYC                        284
CBDV_alphasat_Tung1_Rep_BAS02103               TEAIAEEADDRTIIWVYGPNGNEGKSTYAKSL-MKKDWFYTRGGKKENILFSYVDEGSTKHVVFDIPRCH-QEYLNYDVIEAIKDRVIESTKYKPIKIIEVNR--VHVIVMANFMPDY------------CKISEDRIKTINC                        276
CBDV_alphasat_Fr_X7_Rep_YP_008854133           TEAINEEPDDRSIIWVYGSNGNEGKSTYAKSL-IKKDWFYTRGGKKENTLFSYIDEGDEKNVVFDIPRCN-QDYLNYDVIEALKDRVIESTKYKPVKKVRMNR--IHVIVMANFMPDY------------CKISEDRIKIIYC                        284
BBTV_alphasat_4_Rep_ACB86656                   TELIEAEPDDRTIIWVFGPKGNEGKSTYAKSL-IQKDWFYTRGGKKENILFAYVDEGSTKHIVFDLPRTV-QEFINYDVIEALKDRVIESTKYKPVKYLELNT--IHVIVMANFLPDM------------CKISEDRIKIVAC                        284
BBTV_alphasat_TW3S2_Rep_ACJ36782               IQHIEGVPDDRSIIWVYGPNGGEGKSTFARYLSLKPGWGYINGGKTSDMMH-IITMDPDNNWIIDIPRSN-SEYLNYGVIEQIKNRVLINTKYEPCVIRKDGQN-VHVIVLANVLPDY------------CKISEDRIKIINC                        285
MDV_alphasat_C2_Rep_BAA33981                   HRALMEVPDDRTIIWAYGPDGGEGKSTFAKEL-IKYGWFYTAGGKTQDILYMYAQD-PERNIAFDVPRCS-SEMMNYQAMEMMKNRVFASTKYRPVDLCIRKK--VHLIVFANVAPDP------------TKLSEDRIVIINC                        282
FBNYV_alphasat_C1_Rep_CAA06791                 HRVLMAEPDDRTIIWVYGSDGGEGKSTFAKEL-IKYGWFYTAGGKTQDILYMYAQD-PERNIAFDVPRCS-SEMMNYQAMEMLKNRVFASTKYRPVDLCVRKK--VHLIVFANVSPDP------------TKISEDRIVIINC                        282
SCSV_alphasat_C2_Rep_AAA68018                  HAALMAEPDDRTIIWVYGSDGGEGKTSFAKEL-IRYGWFYTAGGKTQDVLYMYAQD-PERNIAFDVPRCS-SEMMNYQAMEMLKNRVFASTKYRPVDLCIRKL--VHLIVFANVAPDP------------TRISEDRLVIINC                        280
FBNSV_alphasat_1_Rep_AHC72219                  HRVLMNEPDDRSIIWVYGPDGGEGKSTFAKEL-IKYGWFYTAGGKTQDVLYMYAQD-PERNIAFDVPRCS-SEMMNYQAMEMMKNRCFASTKYRSIDLCVRKN--VFLVVFANVEPDP------------TKISGDRIVIINC                        278
BMLRV_alphasat_1_Rep_AHC72176                  HTALMEEPEDRTIIWVVGSDGGEGKSTFAKEL-IKYGWFYTAGGKTQDILYMYAQD-PERNIAFDVPRCS-SDMMNYQAMEMMKNRCFASTKYRSVDLCVKKK--IHLVVFANVSPDP------------TKISEDRIVIINC                        278
FBNYV_alphasat_C7_EG93_Rep_CAB44025            LKTIEQEPDDRTIIWVYGPHGGEGKSAFAKYLTLKEGWWYTAGGKATDMLYSYSLD-PTCHVCIDIPRCTREEYINYSVIEQIKNRVIINTKYEPCTIRDDGHN-VHVIVFCNFLPDV------------TRISEDRIKIINC                        283
MDV_alphasat_C10_Rep_BAA34048                  LKTIEQEPDDRTIIWVYGPHGGEGKSVFAKYLTLKEGWWYTAGGKATDMLYSYSLD-PTCHVCIDIPRCTKEEYINYAVIEQIKNRIIINTKYEPCTIRDDGHN-VHVIVFANYLPDV------------TRISEDRIKIIYC                        283
MDV_alphasat_C3_Rep_BAA33982                   IQEIEETPDYRKIIWVYGPKGGEGKSTFARYLSLKQGWGYLPGGPTHDMLHIISGE-PKNNWVFDIPRVA-SEYVNYGVLEQVKNRVMVNTKYEPIVIRDDNHP-VHVIVFANCMPDP------------TKISEDRMKIVHC                        284
PNYDV_alphasat_3_Rep_AHC72280                  LEAIQLPPNYRDVLWVYGPNGGEGKSTFARHLSLKDGWGYLPGGKTQDMMHLITAE-PKNNWVFDIPRVS-SDYINYGVIEQVKNRVMVNTKYEPVIMRDDNNP-VHVIVFANCLPDV------------TKLSEDRIKMIYC                        284
SCSV_alphasat_C6_Rep_AAA68022                  MHLLEEEPDYRTIIWVYGPAGNEGKSTFARHLSLKDGWGYLPGGKTQDMMHLVTAE-PKNNWVFDIPRVS-SEYVNYGVIEQVKNRVMVNTKYEPCVMRDDNHP-VHVIVFANVLPDL------------GKLSEDRIKLIRC                        285
BMLRV_alphasat_2_Rep_AHC72185                  EEELNIEASPRSIIWVYGPQGGEGKTTKAKEL-ITRGWFYTRGGKKDDVAYSYVED-PTRHVVFDIPRDM-QDYCNYSLIEMLKDRIIISNKYEPITNCQVAN--IHVIVMANFLPDV------------TKISNDRLKIIYC                        281
MDV_alphasat_C1_Rep_BAA33980                   EKEIEKIASPRSILWVYGPQGGEGKTSKAKEL-ITRGWFYTRGGKKDDVAYSYVED-PTRHVVFDIPRDM-QEYCNYSLIEMLKDRIIISNKYEPITNCQVYN--IHVIVMANFLPDV------------TKISEDRIKIIYC                        281
FBNSV_alphasat_2_Rep_AHC72218                  EEELEKVPSPRSILWVYGPTGGEGKTTKAKEL-ITRGWFYTRGGRKDDVAYSYIED-PTRHVVFDIPRDM-KDYCNYSLIEMLKDRIIISNKYEPVTNCQLSN--IHVIVMANFLPDY------------CKISEDRINIIYC                        279
PNYDV_alphasat_1_Rep_AHC72279                  EEDLKKEASPRSIMWVYGPHGGEGKTTKAKEL-ITRGFFYTRGGKKDDVAYSYIED-PTRHVVFDIPRDM-QEYCNYSLIEMLKDRIIISNKYEPITNCQLDN--IHVIVMANFLPDV------------TKISNDRIKIIYC                        279
PaLCuV-IN__alphasat_Rep_AFG29502               KTLLERAPDDRTIFWVYGPDGGEGKSTFARDLYRSGTWFYTRGGSADNVAYQYIGQ-LGNNIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFLPDF------------EKISQDRVHVIPCIPCGVCRKQHHVGEKCDEYVE    315
CLCuV_alphasat_Rep_AIH07616                    KTLLDRPDDDRTIFWVYGPTGGEGKSTFARDLYRSGTWFYTRGGSADNVSYQYIGQ-LGNNIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFMPDF------------EKISQDRVHVIPCRPCGVCLKHHNINDNCEDYID    315
GDS_alphasat_Rep_ALB26259                      QTLLERDPDDRTIFWVYGPTGGEGKSTFARDLYRSGTWFYTRGGSADNVSYQYIGQ-LGNNIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFMPDF------------EKISQDRVHVIPCRPCGVCLKHHIIEMKCEEYVD    315
SiLCuV_alphasat_Rep_CBY89002                   QTLLERAPDDRTIFWVYGPTGGEGKSTFARDLYRSGTWFYTRGGSADNVSYQYIGQ-LGNNIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFMPDF------------EKISQDRVHVIPCRPCGVCLKHHIIEMKCEEYVD    315
CLCuDaV_alphasat_Rep_CAD56270                  KTLLERAPDDRTIFWVYGPNGGEGKSTFARDLYRSGTWFYTRGGSADNVAYQYIGC-LGNNIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFMPDF------------EKISQDRVHVIPCRPCGVCLKHHIIEMKCDDYMD    315
ToLCV_alphasat_Rep_CDH98084                    KTLLDRDPDDRTIFWVYGPYGGEGKSTFARDLYRSGSWFYTRGGSADNVAYQYIGC-LGNNIVFDIPRDK-KDYLQYSLIEMFKDRLVVSNKYEPLMAPLLKC--IHVVVMSNFLPDF------------EKISVDRVHVIPCIPCGVCLKHHVDDVMCGEYME    315
TbCSV_alphasat_Rep_CBK44088                    KTLLDRDPDDRTIIWVYGPTGGEGKSTFARDLYKSGSWFYTRGGSADNVSYQYIGQ-LGNNIVFDIPRDK-KDYLQYNLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFMPDF------------EKISSDRVHVIPCIPCGVCLKHHIDEIRCSEYFD    315
AEV-IN_alphasat_Rep_CEE15328                   KTLLDRDPDDRTIIWVYGPIGGEGKSTFARDLYRSGSWFYTRGGSADNVSYQYIGQ-LGNNIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFLPDF------------EKISNDRVHVIPCIPCGVCLKHHIHEIKCDEYLD    315
AYVV_alphasat_Rep_CAB59911                     KTLLDRDPDDRTIFWVYGPIGGEGKSTFARDLYRSGSWFYTRGGSADNVSYQYIGC-LGANIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFLPDF------------DKISEDRVHVIPCIPCGACLKHHIGLIKCDEYLD    315
TbCSV_alphasat_Y290_Rep_CAI59924               RTLLDRDPDDRTIIWVYGPTGGEGKSTFARDLYRSGSWFYTRGGSADNVSYQYIGQ-LGNNIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLVNC--IHVVVMSNFLPDF------------EKISSDRVHVIPCIPCGVCLKHHIGEIKCDEYLD    315
AYVIV_alphasat_Rep_CDH98093                    KTLLDRDPDDRTIIWVYGPTGGEGKSTFARDLYRSGSWFYTRGGSADNVAYQYIGC-LGNNIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFLPDF------------EKISSDRVHVIPCIPCGVCLKHHIHEIKCDEYLD    315
CYMV_alphasat_Rep_CBJ19303                     KTLLDRDPDDRTIIWVYGPTGGEGKSTFARDLYRSGSWFYTRGGSADNVSYQYIGC-LGHNIVFDIPRDK-KDYLQYSLIEMFKDRLIVSNKYEPLMAPLINC--IHVVVMSNFLPDF------------EKISMDRVHVIPCIPCGVCLK                  302
VEM_alphasat_2_Rep_ALK03648                    ERVISRPASTRDIIWVYGSTGGEGKSTYARELLRRG-WFYTRGGSVDNVAYQYLDN-VDRDVVFDIPRDK-KDYLQYSLIEMIKDGVIISNKYEPVTAVCSRP--RHVVVMSNFLPDF------------SKISVDRVSVIPCIPCGLCLNCHSSDVFCLEFNNE   314
Dragonfly_ass_alphasat_Rep_AFV91336            LELLEEVPDNRSIIWIYGPAGAEGKTMMAKELFRRG-WFYTSGGTADNVKYQYAVE-VESHVVFDIPRDK-KDYIQYSLIEELKNGMIVSNKYEPIRVVRISGREVHVVVMCNFMPDY------------SKISPDRIVIVYCRKCPSCETCLCIGC          307
EuYMV_alphasat_Rep_CBA18108                    EKVLDEGPDDRTIIWVYGSQGNEGKTTWAKSK-IQSGWFYSRGGKGENIKYSYAEH--LGHCIFDLPRQV-EDVLQYTVLEEIKDRLIRSSKYEPIDFNCSDK--VHVVVLSNFLPQIDLEYDSKGNLVKKQLLSKDRLCIINIDESVIVRNDQTVTFDEYIE  314
CLCuGeV_alphasat_Rep_CDI44972                  TSLLNLEPDDRTIIWVYGSQGNEGKTTYVKSL-IQKGWFNSRGGKSDDIMFQYIIH--GGNAVFDFPRDK-EDYVNYNVLEAIKDRTCISNKYEPLSINYPNL--VHVVVMANFKPQLEDEFDDKGRIVKKQMLSVDRIKLIEC                    295
SCSV-[AU;F]_M_Rep_CAB96405                     ERLMET-KDCRRIIWVYGPQGGEGKTSYAKHLVKTRDAFYSTGGKTADIAFAWDHQ---ELVLFDFPRSF-EEYVNYGVIEQLKNGIVQSGKYQSIVKYCNY---VEVIVFANFIPRS------------GMFSEDRIVIVYA                        286
FBNYV-[EG;1_93]_M_Rep_NP_619567                DALLQE-RDGRRIIWVYGPQGGEGKTSYAKHLVKTRDAFYSTGGKTADIAFAWDHQ---ELVLFDFPRSF-EEYVNYGVIEQLKNGIIQSGKYQSVIKYSDY---VEVIVFANFTPRS------------GMFSEDRIVYVYA                        286
MDV-[JP;1]_M_Rep_NP_619769                     DTLLQE-RDGRRIIWVYGPQGGEGKTSYAKHLVKTRDAFYSTGGKTADIAFAWDHQ---ELVLFDFPRSF-EEYVNYGVIEQLKNGIIQSGKYQSVIKYSDY---VEVIVFANFTPRS------------GMFSDDRIVYVYA                        286
FBYLV-[ET;231]_M_Rep_CCF74113                  DAMLEE-RDGRRIIWVYGPLGGEGKTSYAKHLVKTRDAFYSTGGNTADIAFAWDHQ---ELVLFDFPRSF-EEYVNYGAIEQLKNGIIQSGKYQSVIKYTDY---VEVIVFANFTPRS------------GMFSDDRIVFVYA                        286
FBNSV-[ET;Hol_97]_M_Rep_ADJ00306               DALLQE-RDGRRIIWVYGPQGGEGKTSYAKHLVKTRDAFYSTGGKTADIAFAWDHQ---ELVLFDFPRSF-EEYVNYGVIEQLKNGIIQSGKYQSVIKYSDY---VEVIVFANFTPRS------------GMFSDDRIVFVYA                        286
PNYDV-[DE;15]_M_Rep_ADE87486                   ESLLET-RDGRRIIWVYGPQGGEGKTSFAKHLVKTRDAFYSTGGKTADIAFAWDHQ---PIVLFDFPRSF-EEYVNYGVMEQLKNGIIQSGKYQSVIKYAEY---VEVIAFANFTPRS------------GMFSEDRIIIVNV                        286
PYSV-[AT;15]_M_Rep_AHC72281                    ERLMET-KDCRRIIWVYGPQGGEGKTSYAKHLVKTRDAFYTTGGKTADIAFAWDHQ---PIVLFDYPRSF-EEYVNYGVMEQLKNGIIQSGKYQSVIKYCNY---VEVIAFANFTPRS------------GMFSEDRIIIVNA                        286
BBTV-[Au]_M_Rep_AAB25544                       ENIMAQ-PCHRRIIWVYGPNGGEGKTTYAKHLMKTRNAFYSPGGKSLDICRLYNYE---DIVIFDIPRCK-EDYLNYGLLEEFKNGIIQSGKYEPVLKIVEY---VEVIVMANFLPKE------------GIFSEDRIKLVSC                        286
BBTV-[TW]_M_Rep_ABH03036                       ENIMAE-PCYRRIIWVYGPNGGEGKTTFAKHLMKTKNAFYSPGGKSLDICRLYNYE---DIVIFDIPRCK-EEYLNYGLLEEFKNGIIQSGKYEPVLKIVEY---VEVIVMANFLPKE------------GIFSEDRIKLVAC                        286
CBDV-[IN]_M_Rep_AGG38934                       EELMAQ-PCHRRIIWVYGPNGGEGKTTYAKHLMKTRNAFYTPGGKALDICRLYNYE---EIVIFDIPRCK-EEYINYGIIEEFKNGIVQSGKYEPVLKIVEY---VEVIVMANFLPKE------------GIFSEDRIKVVAC                        286
ABTV-[MY]_M_Rep_ABP96965                       EELMAE-PCHRRIIWVYGPNGGEGKTTYAKHLIKTRNAFYTPGGKTLDICRLYNYE---GIVIFDIPRCK-EDYLNYGILEEFKNGIIQSGKYEPVLKIVEY---VEVIVMANFLPKE------------GIFSEDRIKLVTC                        286
ABTV-[PH]_M_Rep_ABP96960                       EEIMAE-PCHRRIIWVYGPNGGEGKTTYAKHLIKTRNAFYTPGGKSLDICRLYNYE---SIVIFDIPRCK-EEYLNYGIVEEFKNGIIQSGKYEPVLKVVQY---VEVIVMANFLPKE------------GIFSEDRIKLVTC                        286
                                                                                                                                 B
```

Figure S1. Comparison of the master Rep protein sequences of nano- and babuviruses with the Rep protein sequences of selected alphasatellites associated with nanovirids, geminiviruses and CFDV as well as two alphasatellites isolated from insects.

Alignments were done using ClustalW in MegAlign of DNASTAR. Blue and green boxes A and B indicate the supposed M-Rep signature, i.e. two perfectly conserved sequence signatures characteristic of the M-Rep proteins of nanovirids. Names and accession numbers of the proteins are indicated on the left.

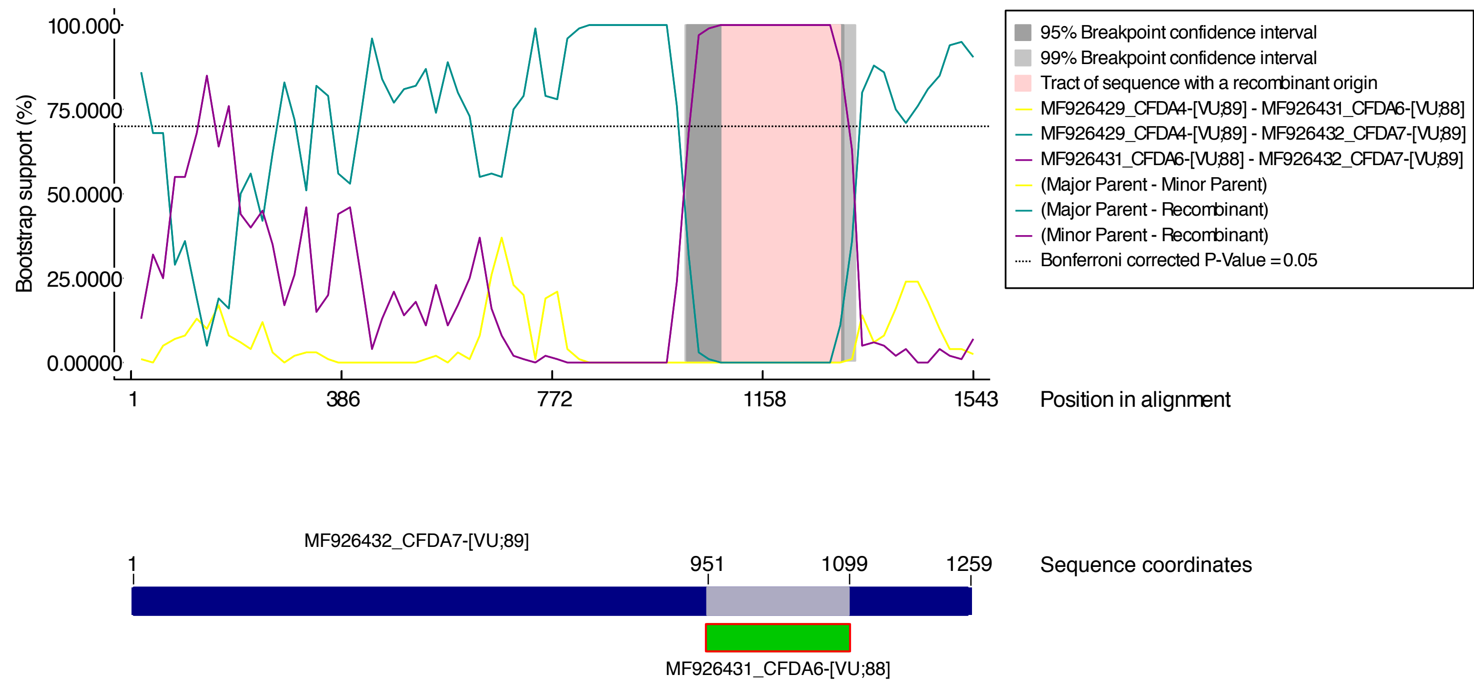


Figure S2. Recombination analysis

Sequences of CFD alphasatellites were aligned with sequences of ten banana bunchy top and two cardamom bushy dwarf alphasatellites using Muscle (UPGMB clustering, 8 iterations). A recombination analysis by RDP 4[26] identified CFDA7 as a potential recombinant. The recombination event was supported by RDP (*P* value 7.35×10^{-11}), GENECONV (*P* 1.3×10^{-10}), BootScan (*P* 1.09×10^{-12}), MaxChi (*P* 2.77×10^{-9}), Chimaera (*P* 3.51×10^{-9}), SiScan (*P* 3.0×10^{-11}) and 3Seq (*P* 1.54×10^{-5}). Top panel: Bootscan plot as implemented in RDP 4 showing the recombinant region flanked by potential recombination breakpoint regions.

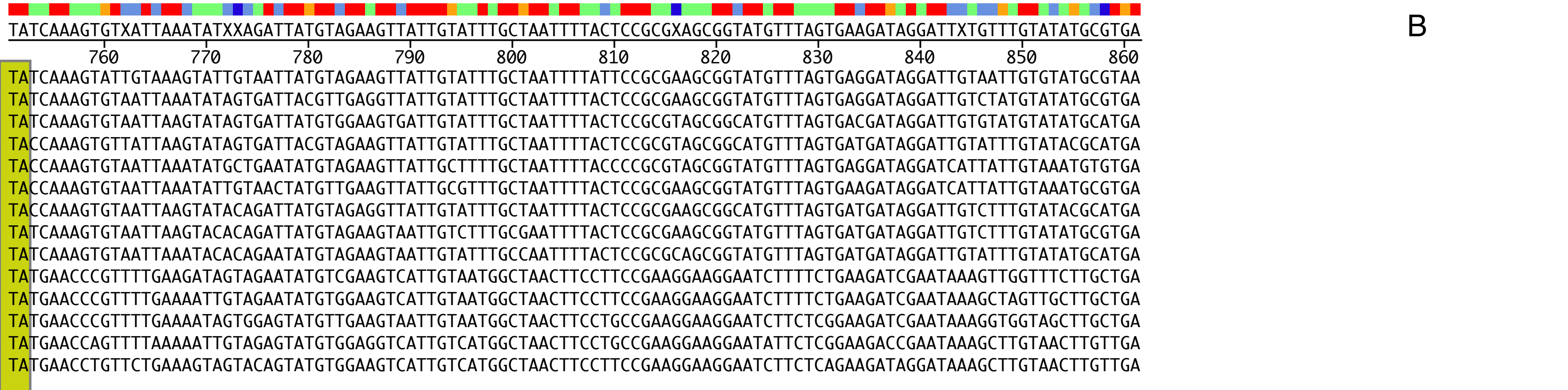
A graphic representation of CFDA7 with the recombinant region (position 951 to 1099) possibly derived from CFDA6 (minor parent) is shown below the plot.

Figure S3

A

460 470 480 490 500 510 520 530 540 550 560 570 580 590 600
SCSV-[AU;F]_DNA-R_AJ290434
FBNYV-[EG;1-93]_DNA-R_NC_003560
MDV-[JP;1]_DNA-R_NC_003648
FBNSV-[ET;Hol-97]_DNA-R_GU983866
PNYDV-[DE;15]_DNA-R_GU553134
PYSV-[AT;15]_DNA-R_KC979054
FBYLV-[ET;231]_DNA-R_HE654123
BMLRV-[AT;3]_DNA-R_KC978939
BMLRV-[AZ;47]_DNA-R_KC978949
BBTV-[AU]_DNA-R_S56276
BBTV-[TW]_DNA-R_DQ826390
CBDV-[IN]_DNA-R_JX867550
ABTV-[MY]_DNA-R_EF546813
ABTV-[PH]_DNA-R_EF546807

610 620 630 640 650 660 670 680 690 700 710 720 730 740 750
SCSV-[AU;F]_DNA-R_AJ290434
FBNYV-[EG;1-93]_DNA-R_NC_003560
MDV-[JP;1]_DNA-R_NC_003648
FBNSV-[ET;Hol-97]_DNA-R_GU983866
PNYDV-[DE;15]_DNA-R_GU553134
PYSV-[AT;15]_DNA-R_KC979054
FBYLV-[ET;231]_DNA-R_HE654123
BMLRV-[AT;3]_DNA-R_KC978939
BMLRV-[AZ;47]_DNA-R_KC978949
BBTV-[AU]_DNA-R_S56276
BBTV-[TW]_DNA-R_DQ826390
CBDV-[IN]_DNA-R_JX867550
ABTV-[MY]_DNA-R_EF546813
ABTV-[PH]_DNA-R_EF546807
B



760 770 780 790 800 810 820 830 840 850 860
SCSV-[AU;F]_DNA-R_AJ290434
FBNYV-[EG;1-93]_DNA-R_NC_003560
MDV-[JP;1]_DNA-R_NC_003648
FBNSV-[ET;Hol-97]_DNA-R_GU983866
PNYDV-[DE;15]_DNA-R_GU553134
PYSV-[AT;15]_DNA-R_KC979054
FBYLV-[ET;231]_DNA-R_HE654123
BMLRV-[AT;3]_DNA-R_KC978939
BMLRV-[AZ;47]_DNA-R_KC978949
BBTV-[AU]_DNA-R_S56276
BBTV-[TW]_DNA-R_DQ826390
CBDV-[IN]_DNA-R_JX867550
ABTV-[MY]_DNA-R_EF546813
ABTV-[PH]_DNA-R_EF546807

Figure S3. Alignment of coding sequences of nanovirus DNA-R components.
Alignments were done using ClustalW in MegAlign of DNASTAR. Coloured boxes indicate regions corresponding to the M-Rep amino acid signature regions identified in Fig. S1, boxes A and -B, respectively. These sequences were used to design degenerate oligonucleotide primers (1 to 6, Table S3). Green boxes: fully complementary primers designed for the corresponding region, yellow and blue boxes: overlapping reverse and direct primer, respectively. Names and accession numbers of the respective nano- and babuvirus DNA-R components are indicated on the left

Figure S4

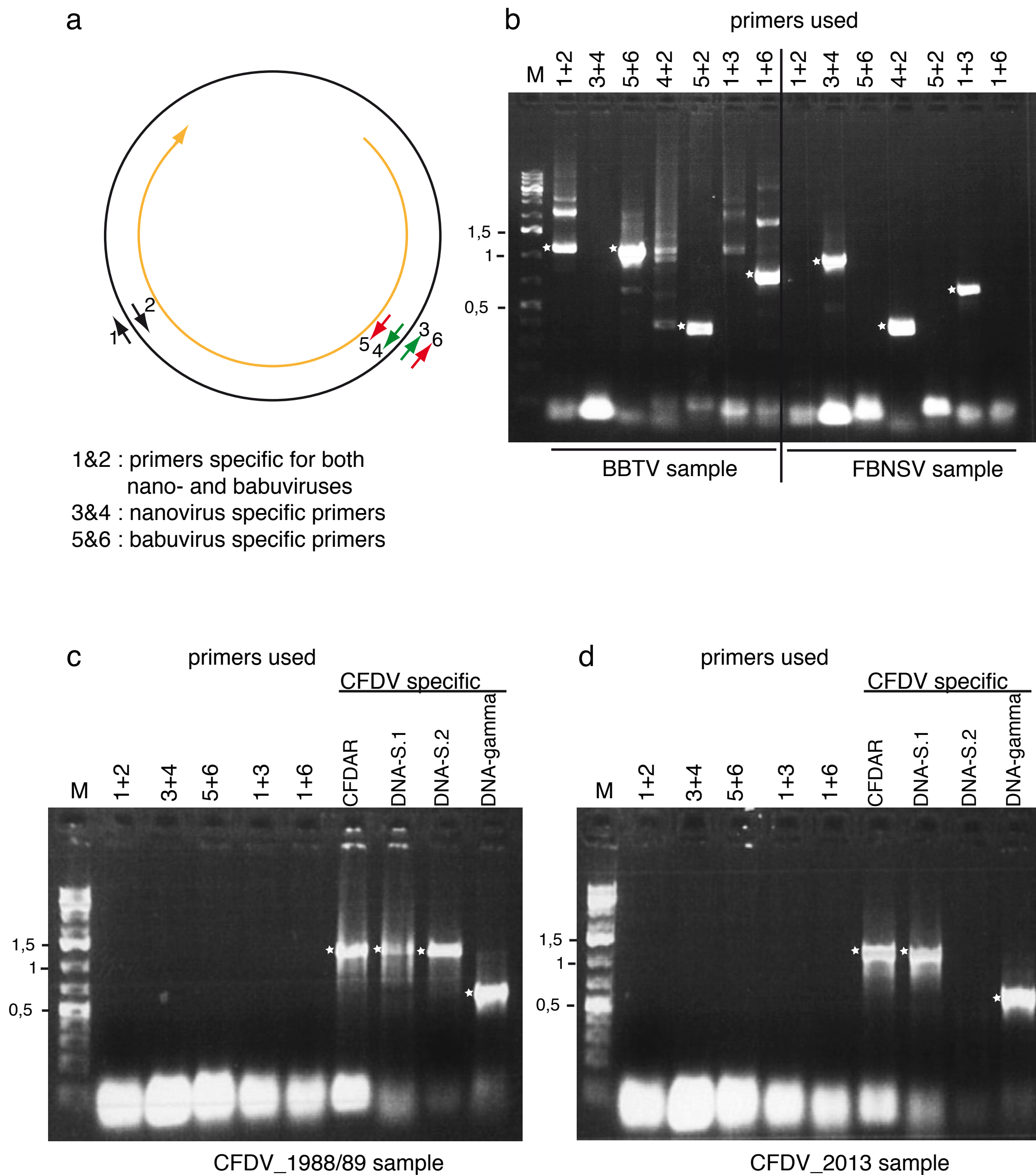


Figure S4. PCR amplification of nanovirus DNA-R components.
Degenerate primers (1 to 6, see Table S3) were designed based on the alignments of several babu- and nanovirus DNA-R sequences (see Fig. S3).
a - position and orientation of the primers in relation to nanovirus DNA-R.
b - control amplifications using total DNA extract of BBTV infected banana leaves (Hawaii-2013 sample, this work) or using the plasmid carrying a dimer of FBNSV DNA-R[30].
c - and d - PCR amplifications using CFDV samples. PCRs were performed on 1:10 diluted RCA products from a mixture of 23 different virion preparations of the CFDV_88/89 sample pool (c) or from a mixture of total DNA extracts from eleven different leaves of one symptomatic coconut palm for CFDV_2013 sample (d). CFDV specific primers were designed based on the cloned CFDV DNAs (the primer pairs used amplify a full-length DNA component as indicated, see Table S3).
M- 1 kb plus DNA ladder, the size (K bp) of several bands is indicated on the left of the marker, amplified DNA fragments of expected size are indicated by an asterisk.

Table S1. CFD samples prepared from symptomatic leaves of coconut palms showing date sampled at VARTC, palm identity, virus preparation date, and characteristics of the buoyant density zone (g/ml) in a Nycodenz® isopycnic density gradient from which the sample was collected

Sample No (CFD)	Sampling date	Palm ID (Number of palms)	Prep Date	Gradient density	DNA by PAGE	Virions by EM
1	11.1988	cfd2 (1)	28.02.89	1.23	+	+
2		cfd2 (1)	28.02.89	1.24	+	+
3[a,b]		cfd2 + cfd3 (2)	06.03.89	1.24	+	+
4		cfd2 + cfd3 (2)	06.03.89	1.24	+	+
5		cfd3 (1)	04.04.89	1.24	+	n.t.
6		cfd3 (1)	10.04.89	1.24-1.28	+	n.t.
7[b]	11.1988	cfd4 (1)	18.04.89	1.23	+	n.t.
8	04.1989	MRD25-21A (1)	13.06.89	1.24-1.29	+	n.t.
9[a,b]	09.1989	MRD19 + MRD20 (2)	16.10.89	1.25	+	+
29		MRD19 + MRD20 (2)	16.10.89	1.26	+	n.t.
30		MRD19 + MRD20 (2)	16.10.89	1.24	+	+
31		MRD19 + MRD20 (2)	16.10.89	1.28	-	-
32		MRD19 + MRD20 (2)	16.10.89	1.23	+	+
10	09.1989	MRD37.14 (1)	30.10.89	1.27	+	n.t.
11[b]		MRD37.14 (1)	30.10.89	1.26	+	n.t.
21[c]	07.1988	MRD caged (unknown)	16.08.88	1.21-1.29	+	n.t.
22[b,c]		MRD caged (unknown)	23.08.88	1.27-1.29	+	n.t.
23[c]		MRD caged (unknown)	23.08.88	1.23	+	n.t.
24	09.1988	TT17-7 + 12-86-14 + 12-86-15 (3)	07.11.88	1.27-1.29	+	n.t.
25		TT17-7 + 12-86-14 + 12-86-15 (3)	07.11.88	1.21-1.23	+	n.t.
26[b]		TT17-7 + 12-86-14 + 12-86-15 (3)	14.11.88	1.23-1.27	+	+
27		TT17-7 + 12-86-14 + 12-86-15 (3)	14.11.88	1.29	+	+
28		TT17-7 + 12-86-14 + 12-86-15 (3)	14.11.88	1.23	+	+

Samples in which DNA or virions were detected by polyacrylamide gel electrophoresis (PAGE) or electron microscopy (EM), respectively, are indicated by (+), or (-) if not detected); n.t. = not tested. MRD, Malayan Red Dwarf; cfd and other identifiers indicate that variety or hybrid source was not recorded

a – CFD samples from which RCA-DNA was used for cloning;
b – CFD samples from which RCA-DNA was pooled for deep sequencing;
c – CFD samples from caged MRD plants inoculated with viruliferous *Myndus taffini.*

Table S2. Viral DNAs identified in two CFD samples on the basis of similar RFLP patterns and sequencing

Sample	DNA	Size nt	Enzyme [a]					
			*Aat*I	*Eco*RI	*Bam*HI	*Kpn*I	*Age*I	*Sal*I
CFD9	DNA-S.1	1286	12 [b]	7				
	DNA-S.2	1263	3	3				
	DNA-gamma	641				22		
	CFDAR	1271			6			
	CFDA2	1277			14			
	CFDA3	1252			3			
	CFDA4	1276			2	6		
	CFDA7	1259	3					
CFD3	CFDA1	1291					3	
	CFDA6	1264						3

a – DNA fragment obtained upon digestion of RCA DNA by a given enzyme was cloned into Litmus28 (for *Aat*I and *Age*I fragments) or pBluescript KSII (+)
b - number of clones showing similar RFLP pattern: insert DNAs of recombinant plasmids were amplified by PCR using M13 direct and reverse primers, and the PCR products were digested by *Hae*III or *Sau*3A enzymes.

Table S3. Oligonucleotides used

DNA	Primer name (direction)	Sequence (5'-3')	Tm, C°	Use [a]
CFDV DNA-S.1	CFDV_S1-HindIII-dir	CCCATTAAGCTTAAAGCCCATTAAGCGATGAC	66.9	1
	CFDV_S1-HindIII-rev	GGCTTTAAGCTTAATGGGCCTTCACGCAATTAC	68.2	1
	CFDV_S1-590_dir	CATTGGCGTTTGTGCTCGATAGAG	62.7	2
	CFDV_S1-1160-rev	CTGCTCATCCTATGCCCGCCA	63.7	2
CFDV DNA-S.2	CFDV_S2-810-BspEI-dir	TTCCGGAGATACTGCCG	55.2	1, 2
	CFDV_S2-810-BspEI-rev	TATCTCCGGAATACTTCA	49.1	1, 2
	CFDV_S2-590-dir	CATTGGCCTTGGTGTTTGGACAAAAT	61.0	2
	CFDV_S2-1160-rev	TCTGCTCAAGCTCTGCTCATCC	62.1	2
CFDV DNA-S.1 & DNA-S.2	CFDV-CP1&2-dir	CCGGAGGAATAATGTACACGAAGAAG	63.2	
	CFDV-CP1&2-dir	CCTCCGGCATATAAAGCCGGTCTTC	66.3	
DNA-S.1 related [b]	CFDV_STL1-dir	CGGCCTAGTATTACCCGCCCACGCTC	71.1	1
	CFDV_STL1-rev	ACTAGGCCGCCCACGCTTATATACAGAGC	69.5	1
DNA-S.2 related [c]	CFDV_STL2-dir	TGCTCCCTACCTCTGCTCATCCTG	66.1	1
	CFDV_STL2-rev	CAGAGCAGAGGTAGTGAGC	58.8	1
CFDV DNA-gamma	CFDV-gamma-dir	TGGCGCTGCTCGCCCGCTTCGTCCTGGAGC	75	1, 2
	CFDV-gamma-rev	GCAGCGCCATTAGCTTCTTCCAATTTCACCTC	69.5	1, 2
CFDAR	CFDAR-BamHI-dir	CATAGAGGATCCGAAAAGAAATTTGATTCTCG	64.4	1, 2
	CFDAR-BamHI-rev	CTTTTCGGATCCTCTATGTACTGATACAGGAC	66.9	1, 2
CFDA1	CFDA1-dir	CTTGGCTATAAATGGGTTCCTCC	60.6	2
	CFDA1-rev	CTTCTCCAGCAAGCTACTCACC	62.1	2
CFDA2	CFDA2-392-SstI-dir	TGCTGAGCTCCGCTTGGAAGAACCTGG	69.5	3
	CFDA2-696-BamHI-rev	CTTCGGATCCTCTATGTACTGGTACAGTAC	66.8	3
	CFDA2-510-dir	ATTGGCAACTTGAGTTGCTCAG	58.4	2
	CFDA2-930-rev	ACAAATGCTAATTGATTATTCAAATATCAA	55.8	2
CFDA3	CFDA3-398-SstI-dir	ATTTGAGCTCGGTTCCCCGGTTGTAGTTG	68.1	2, 3
	CFDA3-789-BamHI-rev	TTTCGGATCCTTCATCGATATAGGAAAATA	61.3	2, 3
CFDA4	CFDA4-262-BamHI-dir	GACAGGATCCACCTCGAACAGGCACAC	69.5	2, 3
	CFDA4-563-BamHI-rev	TCGTCAGCTTGCTCTTGGATTTGAGACAGC	68.1	2, 3
CFDA5	CFDA5-dir	AGCAGCCGTGCTCGACGA	60.5	1, 2
	CFDA5-rev	CCGATGAGCAGGGGTATG	58.2	1, 2
CFDA6	CFDA6-dir	GTGGGTCCCACTTGTGGACTTTGTGGG	69.5	1
	CFDA6-rev	TGGGACCCACAAGGAGCGTCTGTCGAC	71.0	1
	CFDA6-KpnI-1159-dir	TGTGGGTACCACTTGTGGACTTTGTGGGTA	68.1	1,3
	CFDA6-KpnI-1172-rev	AAGTGGTACCCACAAGGAGCGTCTGTCGA	69.5	1, 2,3
	CFDA6-402-SstI-dir	ATTGGAGCTCGGTTCCCCGGTTCTTGTT	68.0	2, 3
	CFDA6-789-BamHI-rev	TTTCGGATCCTTCATCGATATAGGAAAATA	61.3	3
CFDA7	CFDA7-319-SstI-dir	CATGGAGCTCCGACGCGTCCTGGTT	69.5	2, 3
	CFDA7-523-rev	ACCACAGCTGTAAAACCACTTTTCATTAAG	62.7	2, 3
CFDA8	CFDA8-210-rev	TTGTACTGTCCGGCCACCGGAC	65.8	2
	CFDA8-540-dir	CTTGAATTGCTGTCTCAAATCGACGGA	63.4	2
	CFDA8-200-dir	AAGTCCGGTGGCCGGACAGTACAA	66.1	1
	CFDA8-200-rev	CCACCGGACTTCAGATGGAGGAAC	66.1	1
nanovirid DNA-R [d]	1 - b-KNG-dir	AArAATGGnATnaTnCArAGCGGrAArTA	61.7	1
	2 - b-KNG-rev	TAyTTyCCGCTyTGnAtnATnCCATTyTT	61.7	1
	3 - nanoEYIE-rev	GAyTTrTCrTAnGTGTTACAACACTCmTCdATrTAyTC	67.1	1
	4 - nanoEYIE-dir	GArTAyAThGAkGAGTGTTGTAACACnTAyGAyAArTC	67.1	1
	5 - babu-EYL-dir	AATACCTTCGAyAGAAGTArAGATACATTATACAG	63.6	1
	6 - babuEYL-rev	rTCGAAGGTATThGGACArTCrTATAAATACTC	64.3	1

a – a pair of primers indicated by the same number was used for PCR amplification of the corresponding DNA for the following purposes: (1) full-length cloning, (2) component-specific detection by PCR, (3) amplification of the fragment for construction of redundant copies of the component;
b – primers designed based on the DNA sequence in the region with potential stem-loop structure (STL) of CFDV DNA-S.1;
c – primers designed on the basis of the DNA sequence of STL region of CFDV_DNA-S.2;
d – primers designed on the basis of the alignment of the nanovirid DNA-R sequences.

Table S4. Mapping of primary reads from deep sequencing data of three BBTV samples

Sample / DNA	BBTV-Hawaii_2013 (26,758,442 total reads)			BBTV-Nigeria_2013 (25,761,084 total reads)			BBTV-Vietnam_2013 (34,536,988 total reads)		
	Reads	% of reads	Cov. Mean	Reads	% of reads	Cov. Mean	Reads	% of reads	Cov. Mean
DNA-R	1,671,973	6.3	149,484	562,089	2.2	50,015	731,405	2.1	65,039
DNA-S	571,790	2.1	50,314	67,470	0.3	5,952	3,042,114	8.8	271,294
DNA-M	1,306,112	4.9	122,536	264,262	1	24,898	1,302,658	3.8	124,545
DNA-N	7,240,846	27.1	657,758	6,323,995	24.6	565,927	5,100,799	14.8	460,561
DNA-C	5,137,818	19.2	502,970	893,580	3.5	87,631	850,602	2.5	82,171
DNA-U3	8,579,130	32.1	797,873	5,282,003	20.5	487,589	3,922,111	11.4	363,683
BBTA2[a]							3,161,344	9.2	279,229
total	24,507,669	91.6		13,393,399	52		18,111,033	52.4	

Geneious mapping of total reads against all identified (*de novo* assembled) BBTV DNAs, performed with the settings allowing 10% mismatch per read. Cov. Mean – average coverage.
a - a variant of the proposed alphasatellite species BBTA2[25]

Table S5. CFDV mutant spectra

DNA	Year	Type of base changes																
		Total	A C	A G	A T	C A	C G	C T	G A	G C	G T	T A	T C	T G	transitions	transversions	deletions	insertions
DNA-R	1989														0	0		
	2013	2								1					0	1		1 (+1)
DNA-S.1	1989																	
	2013	1												1				
	2015	0													0	0		
DNA-S.2	1989							1					1	1	2	1		
	2015	3													0	0		
CFDA1	1985														0	0		
	1988	2						1	1						2	0		
	1989	1											1		1	0		
	2013	20	1	1			2	3	3	2	3		1	2	7	11	1 (-3)	1 (+1)

Number and type of changes between the most recent and respective previous sampling dates are shown. For calculation of the nucleotide substitution rates per site per year the deletion of three nucleotides is counted as one event.

Table S6. Cloning of redundant copies of CFD associated DNAs used for replication assays

DNA	Primers used for PCR amplification of monomer [a]	Monomer [b]	Primers used for PCR amplification of 0,2 mer [c]	Redundant copy in pBin19
CFDV DNA-S.1	CFDV_S1-HindIII-dir CFDV_S1-HindIII-rev	pBluescriptIIKS(+)-HindIII-S1-5		Dimer first obtained by cloning a monomer into pBluescriptIIKS(+) HindIII site and then transferred into pBin19 as BamHI-KpnI fragment
CFDV DNA-S.2	CFDV_S2-810-BspEI-dir CFDV_S2-810-BspEI-rev	pBluescriptIIKS(+)-BspEI-S2-4		Dimer first obtained by cloning a monomer into pBluescriptIIKS(+) BspEI site and then transferred into pBin19 as BamHI-KpnI fragment
CFDV DNA-gamma		pBluescriptIIKS(+)-KpnI-mini-6		Direct cloning of a monomer into KpnI site of pBin19 with selection of dimer insertion
CFDAR	CFDAR-BamHI-dir CFDAR-BamHI-rev	pBluescriptIIKS(+)-BamHI-AR-1		Direct cloning of a monomer into BamHI site of pBin19 with selection of dimer insertion
CFDA1		Litmus28-AgeI-A1-6 [d]		Dimer first obtained by cloning a monomer into Litmus28 AgeI site and then transferred into pBin19 as BamHI-KpnI fragment
CFDA2		pBluescriptIIKS(+)-BamHI-A2-2	CFDA2-392-SstI-dir CFDA2-696-BamHI-rev	302 bp fragment was PCR amplified using indicated primers, digested by SstI and inserted into pBin19-(SstI-HindIIIblunt) [e] plasmid. CFDA2 monomer was consequently inserted into BamHI site of this plasmid thus giving rise to CFDA2 1,2 mer.
CFDA3		pBluescriptIIKS(+)-BamHI-A3-24	CFDA3-398-SstI-dir CFDA3-789-BamHI-rev	390 bp fragment was PCR amplified using indicated primers, digested by SstI and inserted into pBin19-(SstI-HindIIIblunt) plasmid. CFDA3 monomer was subsequently inserted into BamHI site of this plasmid thus giving rise to CFDA3 1,2 mer.
CFDA4		pBluescriptIIKS(+)-BamHI-A4-14	CFDA4-262-BamHI-dir CFDA4-563-BamHI-rev	300 bp fragment was PCR amplified using indicated primers, digested by BamHI and inserted into pBin19-(BamHI-HindIIIblunt) [f] plasmid. CFDA4 monomer was consequently inserted into BamHI site of this plasmid thus giving rise to CFDA2 1,2 mer.
CFDA6	CFDA6-KpnI-1159-dir CFDA6-KpnI-1172-rev	pBluescriptIIKS(+)-HincII-A6-7	CFDA6-402-SstI-dir CFDA6-789-BamHI-rev	360 bp fragment was PCR amplified using indicated primers, digested by SstI and inserted into pBin19-(SstI-HindIIIblunt) plasmid. CFDA6 monomer, liberated as KpnI fragment, was ligated, ligation product digested by BamHI and inserted into BamHII site of the plasmid with cloned 360 fragment, thus giving rise to CFDA6 1,2 mer.

CFDA7	Litmus28-AatII-A7-15	CFDA7-319-SstI-dir CFDA7-523-rev	320 bp fragment was PCR amplified using indicated primers, digested by SstI and inserted into pBin19-(SstI-HindIIIblunt) plasmid. CFDA7 monomer, liberated as AatI fragment, was ligated, ligation product digested by HindIII and inserted into HindIII site of the plasmid with cloned 320 fragment, thus giving rise to CFDA7 1,2 mer

a - PCR performed on RCA DNA of sample CFD_88/89
b - plasmids used to clone a given DNA in the restriction site indicated, numbers at the end identify the recombinant plasmids
c - viral DNA from the plasmid shown under "Monomer" was used for PCR amplification
d - if primers are not indicated in the second column, viral DNA was cloned as monomer after restriction of RCA DNA into the corresponding plasmid, see Table S2 for enzymes used.
e - pBluescriptIIKS(+) plasmid was digested by *Hind*III, the ssDNA ends resulting after digestion were filled using dNTPs and Klenow polymerase. After purification by phenol extraction and ethanol precipitation the plasmid DNA was digested by *Sst*I.
f - pBluescriptIIKS(+) plasmid was digested by *Hind*III, the ssDNA ends resulting after digestion were filled using dNTPs and Klenow polymerase. After purification by phenol extraction and ethanol precipitation the plasmid DNA was digested by *Bam*HI.

Table S7. GenBank accession numbers of CFD associated DNAs

DNA \ Year	1985	1988	1989	2013	2015
DNA-S.1			MF926436	MF926437	MF926438
DNA-S.2			MF926439		MF926440
DNA-gamma			MF926441	MF926442	MF926443
CFDAR			MF926434	MF926435	
CFDA1	M29963	MF926423	MF926424	MF926425	
CFDA2			MF926426		
CFDA3			MF926427		
CFDA4			MF926429	MF926444	
CFDA5			MF926430		
CFDA6		MF926431			
CFDA7			MF926432		
CFDA8					MF926433