S1 Dataset. Complete nucleotide sequences of the alphasatellite-BBTV isolates DRC-2016 (viruliferous aphids from Bas Congo province collected in 2016) and DRC-2012 (a leaf sample of BBTD-infected banana plant in Bas Congo province in 2012) from Democratic Republic of Congo (DRC).

(A) Nucleotide sequences of the aphid-borne alphasatellite-BBTV isolate DRC-2016 and its genetic variants in evolving quasispecies population in the *Musa acuminata* Cavendish recipient plants and in the progenies of the DRC and GAB aphids having transmitted the disease to the infected recipient plants (samples JGF-1-11; see Supplementary Figures S2-S4)

(B) Nucleotide sequences of the alphasatellite-BBTV isolate DRC-2012 from a leaf sample collected from BBTD-infected AAB banana plant in Bas Congo province in 2012

(C) Pairwise comparison of the DRC-2016 and DRC-2012 alphasatellite nucleotide sequences and encoded Rep proteins

(D) Protein and nucleotide sequence Blast analyses of DRC alphasatellite isolates

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Dataset S1A. Nucleotide sequences of the aphid-borne alphasatellite-BBTV isolate DRC-2016 and its genetic variants in evolving quasispecies population in the *Musa acuminata* Cavendish recipient plants and in the progenies of the DRC and GAB aphids having transmitted the disease to the infected recipient plants (samples JGF-1-11; see Supplementary Figures S4-S5).

DRC-alpha

>alphaDRC2016_jgf
TATTACCCCTCCTTGGCACACTGGCACAGCTGACGTACAGATGACGTGTCATCAGCGAAATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATCCTTTCCTTTGGAGAGGAAAC
ACAATATGCGTGTTGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGATCCAATTGAAGAAGAAGACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACACCT
CGAACCCATGCGAGGTTCGATTACAGAGGCGAAAGCCTACTGTACGAAAGAACAATCACGGATCGCAGGTCCGTGGGAATTCGGAGAAATTCTGCTGAAGGGGTCGAACAGACGGAAGCT
CGCAGAGCTTCTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGACGAGCGATGGCTAAGTCCGCCATGGATGAATCTCGGAAGCTTGCTGAAGAGTATGATTTCCCTCA
CGAACTACGTTCGTGGCAAAAAACCCTAATTTCATGCCTCGAAGAGGAACCGGATGATCGTACTATTTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGTAAACA
CCTAGGATTAAAAAAAGGATGGACCTATTTACCCGGAGGGGAACTGAAAGACATGATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGGTGTACGAAAGA
CTTTGTAAGTTATAAATTCCTAGAGATGGTAAAAAACAGAACTGTATATAGTTATAAATACGAACCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTCTTATGTAATTTTAT
GCCGGAAGAAGAAAAAATCTCCGGAGACAGATTAATAATAATAAATTGCTAAACACGCATTTACAAAAATACCCTCGAACAATCAATATTCCTATTATACCCCCGAAGCTCACTTCGGAA
CAACAGCTGTCGTTATCAATGACAGCTGTCATGTGGTCCCAACATAGCGTATGTAATACGCGGACTTGAAAGGATTATTAAATCCGCTTTGCTGCTACAGTGAAGCTTGGCACACTATAA
ATACCTGTGCCAAGGAGAGGGCTAG

DNA-C

8 SNPs to KM607057 (**Congo-DRC,** Stainton et al. 2015); **9 SNPs** to JQ820457 (**Malawi;** James et al. 2012). **9 SNPs** to JQ820469 (**Rwanda;** James et al. 2012). **10 SNPs** to JF957676 (**Tonga;** Stainton et al. 2015). **12 SNPs** to KM607023 (**Congo-Brazza;** Stainton et al. 2015). **12 SNPs** to KM607094 (**Samoa;** Stainton et al. 2015); **12 SNPs** to KM607080 (**Hawaii;** Stainton et al. 2015). **12 SNPs** to KM607074 (**Australia;** Stainton et al. 2015). **15 SNPs** to KM607022 (**Burundi;** Stainton et al. 2015). **15 SNPs** to KM607029 (**India;** Stainton et al. 2015).

C protein (161 aa): 99.4% identity (**1 aa**) to 5 isolates: JQ820457 (**Malawi;** James et al. 2012) KM607005 KM607008 KM607043 (**Australia;** Stainton et al. 2015). JN250597 (**Sri Lanka**)

>C_jgf
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCGACTAACAGACGCACGTGAGAATGCAGTAGCTTGCAGCGAAAGATAGACGTCAACATCAATAAAGAAGAAGGAATATTCTTTGC
TTCGGCACGAAGCAAAGGGTATAGATATTTGTTCGAGATGCGAAAATGGAGGCTATTTAAACCTGATGGTTTTGTGATTTCCGAAATCACTCGACGGAAGAGAAATGGAGTTCTGGGAAT
CGTCTGCCATGCCTGACGATGTCAAGAGAGAGATTAAGGAAATATATTGGGAAGATCGGAAGAAACTTCTGTTCTGTCAGAAGTTGAAGAGCTATGTCAGAAGGATTCTTGTTTATGGAG
ATCAAGAGGATGCCCTTGCCGGAGTGAAGGATATGAAGACTTCTATTATTCGCTATAGCGAATACTTGAAGAAACCATGTGTGGTAATCTGTTGTGTTAGCAATAAATCAATTGTGTATA
GGTTAAACAGCATGGTGTTCTTTTATCATGAATACCTTGAAGAACTAGGTGGTGATTACTCAGTATATCAAGATCTCTATTGTGATGAGGTTCTCTCTTCTTCATCGACAGAGGAAGAAG
ATGTAGGAGTAATATATAGGAATGTTATCATGGCATCGACAGAAGAGAAGTTCTCTTGGAGTGATTGTCAGAAGATAGTTATATCAGACTATGATGTAACATTACTCTAATGTAATATCC
ATTATCATCAATAAAATAATGGAATGTTGATTATGTATTTATCATAAATACATAATGGTATACGTATAGCATAAAATACATTAACCAACATACAACACACTATAAAATACAACACACTAT
GACAAAAGTACGGGTATCTGATTGGGCTATATTAACCCCTTAAGGGCCGAAGGCCCGTTTAAATATGTGTTGGACGAAGTCCAAGCACAAAAAAGTAAGCAGAACAACGGAATAATATGA
GCTGGCAACGTAGGGTCCATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-M

7 SNPs to KU759878 (**Congo-DRC,** Mukwa et al. 2016). **10 SNPs** to KM607167 (**Congo-Brazza,** Stainton et al. 2015). **11 SNPs** to JQ820462 (**Rwanda;** James et al. 2012). **13 SNPs** to JQ820456 (**Malawi;** James et al. 2012). **13 SNPs** to KM607237 (**India;** Stainton et al. 2015). **13 SNPs** to KM607241 (**Sri Lanka;** Stainton et al. 2015). **13 SNPs** to KM607222 (**Hawaii;** Stainton et al. 2015). **15 SNPs** to KM607236 (**Samoa;** Stainton et al. 2015). **17 SNPs** to KM607161 (**Burundi;** Stainton et al. 2015). **17 SNPs** to KM607220 (**Australia;** Stainton et al. 2015). **18 SNPs** to JF957669 (**Tonga;** Stainton et al. 2015).

M protein (117 aa) 2 aa to v2: **1 aa** to 5 isolates: JQ820462 JQ820468 (**Rwanda;** James et al. 2012) JQ820456 (**Malawi;** James et al. 2012) FJ609642 EF153738 (**India**) **2 aa** to AF102783 (**Egypt**)

>M_jgf_v1
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCTTCGACAAATGCACGTGAGTGATATAAGGGACATAACGGGTTCAGATAACGGTATCTTTGGTTTAGAATATAACGTCACGTGTG
AAAGTGATAGGCACGTGACTAAGTCAAATGTATTGAATAAACATTTGACGTCCGGTAGCTTCCGAAGGAAGTAAGGATTGCTTCGTGGCGAAGCAAACCATTTATATATTGCCTAGGCTT
GCGGCCTATAAATAGGACCCTGCTAAATGGCATTAACAACAGAGCGGGTTAAACTATTCTTTGAATGGTTTTTGTTCTTTGCAGCAATATTTATTGCGATTACAATATTATATATATTGT
TGGTTTTGCTCTTTGATGTACCGAAGTATATTAAGCAGCTCGTGAGGTATTTGGTAGAATACCTGACCAGAAGACGTGTATGGATGCAGAGAACGCAGTTATCGGAGGCAACTGGAGACG
TAGAGTTCGGCAGAGGTATTGTGGAAGACAGACGGGATCAACAACCGGCTGTCATACCACAGGCATCTCAGGTTAACCCTTCTCAACAAATTAGAAGGGATGATCAAGGAAGACGAGGAA
ACGTCGGACCTATGTTTTAATACACGGTATTGTAATATATGAAATATAAATGGGGATTGATGTATAAGGTCATACATACTATATGTATGTTAATGAAACATATTGTAATATGTGAATTGT
AAACGAGTGTTGAATGTATACAACATACAACACACTATGAAATACAAGACGCTATGACAAAAGTACGGGTATCTGATTAGGTATCCTAACGATCTAGGGCCGAAGGCCCGTGAGCAATAT
GCGTCGAAATAATGTTTAACAAACAAATATACATGATACGGATAGTTGAATACATAAACAACTAGGTTTACAATACAACAAACTGTTGTAAAGAAATAAAAAATAAGAAGGGAGAGTATA
TTTGTGTCGGATAAGCTTGGCAACCACCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

M protein (117 aa) 2 aa to v1: **1 aa** to 5 isolates: JQ820462 JQ820468 (**Rwanda;** James et al. 2012) JQ820456 (**Malawi;** James et al. 2012) FJ609642 EF153738 (**India**) **2 aa** to AF102783 (**Egypt**)

>M_jgf_v2
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCTTCGACAAATGCACGTGAGTGATATAAGGGACATAACGGGTTCAGATAACGGTATCTTTGGTTTAGAATATAACGTCACGTGTG
AAAGTGATAGGCACGTGACTAAGTCAAATGTATTGAATAAACATTTGACGTCCGGTAGCTTCCGAAGGAAGTAAGGATTGCTTCGTGGCGAAGCAAACCATTTATATATTGCCTAGGCTT
GCGGCCTATAAATAGGACCCTGCTAAATGGCATTAACAACAGAGCGGGTTAAACTATTCTTTGAATGGTTTTTGTTCTTTGCAGCAATATTTATTGCGATTACAATATTATATATATTGT
TGGTTTTGCTCTTTGAGGTACCGAAGTATATTAAGCAGCTCGTGAGGTATTCGGTAGAATACCTGACAAGAAGACGTGTATGGATGCAGAGAACGCAGTTATCGGAGGCAACTGGAGACG

TAGAGTTCGGCAGAGGTATTGTGGAAGACAGACGGGATCAACAACCGGCTGTCATACCACAGGCATCTCAGGTTAACCCTTCTCAACAAATTAGAAGGGATGATCAAGGAAGACGAGGAA
ACGTCGGACCTATGTTTTAATACACGGTATTGTAATATATGAAATATAAATGGGGATTGATGTATAAGGTCATACATACTATATGTATGTTAATGAAACATATTGTAATATGTGAATTGT
AAACGAGTGTTGAATGTATACAACATACAACACACTATGAAATACAAGACGCTATGACAAAAGTACGGGTATCTGATTAGGTATCCTAACGATCTAGGGCCGAAGGCCCGTGAGCAATAT
GCGTCGAAATAATGTTTAACAAACAAATATACATGATACGGATAGTTGAATACATAAACAACTAGGTTTACAATACAACAAACTGTTGTAAAGAAATAAAAAATAAGAAGGGAGAGTATA
TTTGTGTCGGATAAGCTTGGCAACCACCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-N

6 SNPs to KU759888 (**Congo-DRC,** Mukwa et al. 2016); **10 SNPs** to KM607312 (**Congo-Brazza**; Stainton et al. 2015); **10 SNPs** to KX592200 (**India**; Baldodiya et al. 2015); **11 SNPs** to KM607324 (**Egypt**; Stainton et al. 2015). **11/11/11 SNPs** to KM607352, KM607349, KM607343 (**Congo-DRC**; Stainton et al. 2015);

N protein (154 aa): identical 0 aa to 7 isolates: NC_003476 NP_604479 L41577 (?, **Australia** , ? Burns et al 1995 JGV) AY273170 AY948438 (**India**) EF529519 (**Pakistan**) JF957688 (? Stainton et al. 2012) **1 aa** to KU759884 (**Congo-DRC**), KM607364 (**Sri Lanka**), JF957695 KM607409 (**Tonga**), KM607336 (**Australia**)

>N_jgf
TATTACCCCCCGTGCTCGGGACGGGACATGACGTCAGCAATGATTATAATGGGCTTTTTATTAGCCCATCTATTGAATTGGGCCGGGTTTTGTCATTTTACAAAAGCCCGGTCCAGGATA
AGTATAATGTCACGTGCCGAATAAAAGGTTGCTTCGCCTCGAAGAAACCTAATTTGAGGTTGCGTATTCAATACGCTACCGAGTATCTATTAATATGTGAGTCTCTGCCGAAACAATCAG
AGCGAAAGCAAAGCAGAAGCGATGGATTGGGCGGAATCACAATTCAAGACTTGTACTCATGGATGCGATTGGAAGAAGATATCATCGGATTCAGCCGATAATCGACAATATGTGCCATGC
GTCGATTCTGGAGCTGGAAGAAAGTCGCCTCGCAAGGTACTTCTTAGATCTATTGAAGCTGTGTTTAACGGAAGCTTCAGCGGAAATAATAGGAACGTTCGTGGATTTCTCTACGTATCG
ATCAGAGACGATGACGGAGAAATGCGTCCAGTACTCATAGTACCATTCGGTGGATATGGATATCATAATGATTTCTATTATTTCGAAGGAAAGGGGAAAGTTGAATGTGATATATCATCA
GATTATGTTGCGCCAGGAATAGATTGGAGCAGAGACATGGAAGTTAGTATTAGTAACAGCAACAACTGTAATGAATTATGTGATCTGAAGTGTTATGTTGTTTGTTCTTTAAGAATCAAG
GAATAAAAGTTGTGCTGTAATGTTTATTAATAAAACGTATATTTGGGAAATTGATAGTTGTATAAAACATACAACACGCTATGAAATACAAGACGCTATGACAAATGTACGGGTATCTGA
ATGAGTTTTAGTATCGCTTAAGGGCCGCAGGCCCGTTGAAAAATAATAATCGAATTATAAACGTTAGATAATAATCAGAGATAGGTGATCAGATAACATAAACATAAACGAAGTATATGG
CGGTACAATAATAAAATAAGTTAAAAAAAAAAAACATAATGAATACTAATCTCTGATTGGTTCAGAAGAAAGCCCCACCAACTAAAAGGTGGGGAGAATGTCCCGATGACGTAAGCACGG
GGGACTAT

DNA-R

2 SNPs to KU687087 (**Congo-DRC,** Mukwa et al. 2016); **6 SNPs** to JQ820459 (**Rwanda**; James et al. 2012). **6 SNPs** to KM607674 (**India**; Stainton et al. 2015); **7 SNPs** to KM607598 (**Burundi**; Stainton et al. 2015); **8 SNPs** to JQ820453 (**Malawi**; James et al. 2012). **8 SNPs** to KM607658 (**Australia**; Stainton et al. 2015), **9 SNPs** to KM607603 (**Congo-Brazza**; Stainton et al. 2015). **11 SNPs** to KM607680 (**Sri Lanka**; Stainton et al. 2015)

R protein (286 aa): identical 0 aa to 5 isolates: JQ820453 JQ820465 (**Rwanda**) DQ640742 EF584545 GU085264 (**India**) **1 aa** to multiple isolates

>R_jgf
TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCTCTCCATTACAAGATCATCATCGACGACAGAATGGCGCGATATGTGGTATGCTGGATGTTCACCA
TCAACAATCCCACAACACTACCAGTGATGAGGGATGAGATCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCAAGGTTATGTTGAGATGAAGAGACGAA
GCTCTCTGAAGCAGATGAGAGGCTTCTTCCCAGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAGAAGAAGCGCGGTCATACTGTATGAAGGAAGATACAAGAATCGAAGGTCCCTTCG
AGTTTGGTGCATTTAAATTGTCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGTGAAACGCACAAAAGGCCTTTGGAGTATTTATATGATTGTCCTAACACCTTCGATAGAA
GTAAGGATACATTATACAGAGTACAAGCAGAGATGAATAAAACGAAGGCGATGAATAGCTGGAGAACGTCTTTCAGCGCATGGACATCAGAGGTGGAGAATATCATGGCGCAGCCATGTC
ATCGGAGAATAATTTGGGTCTATGGACCAAATGGAGGAGAAGGAAAGACAACGTATGCAAAACATCTAATGAAGACGAGAAATGCGTTTTATTCTCCAGGAGGAAAATCATTGGATATAT
GTAGACTGTATAATTACGAGGATATTGTTATATTTGATATTCCAAGATGCAAAGAGGATTATTTAAATTATGGGTTATTAGAGGAATTTAAGAATGGAATAATTCAAAGCGGGAAATATG
AACCCGTTTTGAAGATAGTAGAATATGTCGAAGTCATTGTAATGGCTAACTTCCTTCCGAAGGAAGGAATCTTTTCTGAAGATCGAATAAAGTTGGTTTCTTGCTGAACAAGTAATGACT
TTACAGCGCACGCTCCGACAAAAGCACACTATGACAAAAGTACGGGTATCTGATTGGTTTATCTTAACGATCTAGGGCCGTAGGCCCGTGAGCAATGAACGGCGAGATCAGATGTCCCGA
GTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-S

5 SNPs to KU759877 (**Congo-DRC,** Mukwa et al. 2016); **5/6 SNPs** to JQ820461/JQ820467 (**Rwanda**; James et al. 2012). **6 SNPs** to KM607632 (**India**; Stainton et al. 2015). **6 SNPs** to KM607503 (**Congo-DRC**; Stainton et al. 2015); **7 SNPs** to KM607537 (**Sri Lanka**; Stainton et al. 2015). **8 SNPs** to JQ820456 (**Malawi**; James et al. 2012).

S protein (175 aa) v1=v2: **identical 0 aa** to 5 isolates: EF095164 (**Taiwan**) EF593169 FJ859735 FJ859736 FJ859737 (**Pakistan**) **1 aa** to several isolates incl. JF755985 (**Congo-DRC**)

>S_jgf_v1
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTAATGGATTGTGGATATAGGGCCCAAAGGGCCCGTTTAGATGGGTTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAACAGGCGG
GAACCGTCCCAAATTCAAACTTCGATTGCTTGCCCTGCAAGCCATCTAGAAGTCTATAAATACCAGTGTGTAGATAGATGTTCAGACAACAAATGGCTAGGTATCCGAAGAAATCCATCA
AGAAGAGGCGGGTTGGGCGCCGGAAGTATGGCAGCAAGGCGGCAACGAGCCACGACTACTCGTCGTTAGGGTCAATATTGGTTCCTGAAAACACCGTCAAGGTATTTCGGATTGAGCCTA
CTGATAAAACATTACCCAGATATTTTATCTGGAAAATGTTTATGCTTCTTGTGTGCAAGGTGAAGCCCGGAAGAATACTTCATTGGGCTATGATCAAGAGTTCTTGGGAAATCAACCAGC
CGACAACCTGTCTGGAAGCTCCAGGTTTATTTATTAAACCTGAACATAGCCATCTGGTTAAACTGGTATGTAGTGGGGAACTTGAAGCAGGAGTCGCAACAGGGACATCAGATGTTGAAT
GTCTTTTGAGGAAGACAACCGTGTTGAGGAAGAATGTAACAGAGGTGGATTATTTATATTTGGCATTCTATTGTAGTTCTGGAGTAAGTATAAACTACCAGAACAGAATTACATATCATG
TTTGATATGTTTATGTAAACATAAACTATTGTATGGAATGAAATCCAAATAACATACAACACGCTATGAAATACAAGACGCTATGACAAA**A**GTACGGGTAT**C**TGATT**A**GGTATC**C**TAACG
ATCTAGGGCCG**A**AGGCCCGTGAGCAATATGCGTCGAAATAATGTTTAACAAACAAATATACATGATACGGATAGTTGAATACATAAACAACGAGGTATACAATACAACAAACTGTTGTAA
AGAAATAAAAAATAAGAAGAGAGAGTATATTTGTGTCGGATAAGCATGAAACCCACCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

>S_v2
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTAATGGATTGTGGATATAGGGCCCAAAGGGCCCGTTTAGATGGGTTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAACAGGCGG
GAACCGTCCCAAATTCAAACTTCGATTGCTTGCCCTGCAAGCCATCTAGAAGTCTATAAATACCAGTGTGTAGATAGATGTTCAGACAACAAATGGCTAGGTATCCGAAGAAATCCATCA
AGAAGAGGCGGGTTGGGCGCCGGAAGTATGGCAGCAAGGCGGCAACGAGCCACGACTACTCGTCGTTAGGGTCAATATTGGTTCCTGAAAACACCGTCAAGGTATTTCGGATTGAGCCTA
CTGATAAAACATTACCCAGATATTTTATCTGGAAAATGTTTATGCTTCTTGTGTGCAAGGTGAAGCCCGGAAGAATACTTCATTGGGCTATGATCAAGAGTTCTTGGGAAATCAACCAGC
CGACAACCTGTCTGGAAGCTCCAGGTTTATTTATTAAACCTGAACATAGCCATCTGGTTAAACTGGTATGTAGTGGGGAACTTGAAGCAGGAGTCGCAACAGGGACATCAGATGTTGAAT
GTCTTTTGAGGAAGACAACCGTGTTGAGGAAGAATGTAACAGAGGTGGATTATTTATATTTGGCATTCTATTGTAGTTCTGGAGTAAGTATAAACTACCAGAACAGAATTACATATCATG
TTTGATATGTTTATGTAAACATAAACTATTGTATGGAATGAAATCCAAATAACATACAACACGCTATGAAATACAAGACGCTATGACAAA**T**GTACGGGTAT**T**TGATT**G**TGTATC**T**TAACG
ATCTAGGGCCG**T**AGGCCCGTGAGCAATATGCGTCGAAATAATGTTTAACAAACAAATATACATGATACGGATAGTTGAATACATAAACAACGAGGTATACAATACAACAAACTGTTGTAA
AGAAATAAAAAATAAGAAGAGAGAGTATATTTGTGTCGGATAAGCATGAAACCCACCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3

12 SNPs to KU759869 (**Congo-DRC,** Mukwa et al. 2016); **21 SNPs** to KM607738 (**Congo-Brazza**; Stainton et al. 2015); **22 SNPs** to KM607732 (**Burundi**; Stainton et al. 2015). **22 SNPs** to JQ820454 (**Malawi**; James et al. 2012). **25 SNPs** to JQ820460 (**Rwanda**; James et al. 2012). **25 SNPs** to KM607809 (**Sri Lanka**; Stainton et al. 2015). **29 SNPs** to KM607731 (**India**; Stainton et al. 2015). **33 SNPs** to GQ214699 (**Pakistan**; Hyder et al. 2011); **>50 SNPs** to KM607808 (**China**; Stainton et al. 2015)

U3 protein (77 aa) v1=v2=v3=v4: **identical (0 aa)** to FJ009239 MT109277 (**India**) **1 aa** to several isolates

>U3_jgf_v1

TATTACCCCCCGTGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCTTGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCAACTCGGCCCAATAATTAAGAGAACGTGTTCAAA
TTCGTGGTATGACCGAAGGTCAAGGTAACCGGTCAACATTATTCTGGCTTGCGCAGCAAGATACACGAATTAAATTATTAATTCGTAGGACACGTGGACGGACCGAAATACTCCTGCATC
TCTATAAATACCCTAGTCCTGTGAAGGATAATTGCTCTCTCTCTTCTGTCAAGGTGGTTGTGCTGAGGCGGAAGATCGCCAGCGGCGATCGTCGGAACGATGTGCATCTAGAGAGGCGGT
GAAGCAAACTACGAAGCGTATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTATACACTGTACAGATTATGTATTTTGTAAATTACGAAGAATTTCGTATATGATATTAATAAAA
CACCTGGGTGTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAAAATACAGTATACGGAACGTATACTGACAAAGTAATAAATGATAGGCGAAGCATGATTAACAGGTGTT
TAGGTATAATTAACATAATTATGAGAAGTAATAATAATACGGAAAATGAATAAGTATGAGGTGAAAGAGGAGATATTAGAATATTTAAAAACCCAATTATATTATTTTGGAACGAAATAC
AACACGCTATGAAATACAAGACGCTATGACAAATGTACGGGTATCTGATTGTATATCTTAACGATCTAGGGCCGTAGGCCCGTGAGCAATGAACGGTATAGATTAATTCCTTAGCGACGA
AGAAAGGAATCTTAATAGGGACCACATTAAAGACAGCTGTCATTGATTAAATAAATAATATAATATACAAAAGACTTTTGTACCCCTGATAATGATGACGTGTAGGGGTGTCCCGATGTA
ATATAGCATAGCTATGTGAAGAGATAAGCATGTGGCCGACAACTTTAGTGGTGGGCCAGATGTCCCGAGTTAGTGCGCCACGTAAGCACGGGGGACTAT

>U3_jgf_v2
TATTACCCCCCGTGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCTTGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCAACTCGGCCCAATAATTAAGAGAACGTGTTCAAA
TTCGTGGTATGACCGAAGGTCAAGGTAACCGGTCAACATTATTCTGGCTTGCGCAGCAAGATACACGAATTAAATTATTAATTCGTAGGACACGTGGACGGACCGAAATACTCCTGCATC
TCTATAAATACCCTAGTCCTGTGAAGGATAATTGCTCTCTCTCTTCTGTCAAGGTGGTTGTGCTGAGGCGGAAGATCGCCAGCGGCGATCGTCGGAACGATGTGCATCTAGAGAGGCGGT
GAAGCAAACTACGAAGCGTATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTATACACTGTACAGATTATGTATTTTGTAAATTACGAAGAATTTCGTATATGATATTAATAAAA
CACCTGGGTGTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAAAATACAGTATACGGAACGTATACTGACAAAGTAATAAATGATAGGCGAAGCATGATTAACAGGTGTT
TAGGTATAATTAACATAATTATGAGAAGTAATAATAATACGGAAAATGAATAAGTATGAGGTGAAAGAGGAGATATTAGAATATTTAAAAACCCAATTATATTATTTTGGAACGAAATAC
AACACGCTATGAAATACAAGACGCTATGACAAATGTACGGGTATCTGATTGTATATCTTAACGATCTAGGGCCGTAGGCCCGTGAGCAATGAACGGTATAGATTAATTCCTTAGCGACGA
AGAAAGGAATCTTAATAGGGACCACATTAAAGACAGCTGTCATTGATTAAATAAATAATATAATATACAAAAGACTTTTGTACCCCTGATAATGATGACGTGTAGGGGTGTCCCGATGTA
ATATAGCATAGCTATGTGAAGAGATAAGCATTTGGCCGACAACTTTAGTGGTGGGCCAGATGTCCCGAGTTAGTGCGCCACGTAAGCACGGGGGACTAT

>U3_jgf_v3
TATTACCCCCAGCGCTCAGGACGGGACATGGGCTTTTTAAATGGGCCTTGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCAACTCGGCCCAATAATTAAGAGAACGTGTTCAAA
TTCGTGGTATGACCGAAGGTCAAGGTAACCGGTCAACATTATTCTGGCTTGCGCAGCAAGATACACGAATTAAATTATTAATTCGTAGGACACGTGGACGGACCGAAATACTCCTGCATC
TCTATAAATACCCTAGTCCTGTGAAGGATAATTGCTCTCTCTCTTCTGTCAAGGTGGTTGTGCTGAGGCGGAAGATCGCCAGCGGCGATCGTCGGAACGATGTGCATCTAGAGAGGCGGT
GAAGCAAACTACGAAGCGTATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTATACACTGTACAGATTATGTATTTTGTAAATTACGAAGAATTTCGTATATGATATTAATAAAA
CACCTGGGTGTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAAAATACAGTATACGGAACGTATACTGACAAAGTAATAAATGATAGGCGAAGCATGATTAACAGGTGTT
TAGGTATAATTAACATAATTATGAGAAGTAATAATAATACGGAAAATGAATAAGTATGAGGTGAAAGAGGAGATATTAGAATATTTAAAAACCCAATTATATTATTTTGGAACGAAATAC
AACACGCTATGAAATACAAGACGCTATGACAAATGTACGGGTATCTGATTGTATATCTTAACGATCTAGGGCCGTAGGCCCGTGAGCAATGAACGGTCCAGATTAATTCCTTAGCGACGA
AGAAAGGAATCTTAATAGGGACCACATTAAAGACAGCTGTCATTGATTAAATAAATAATATAATATACAAAAGACTTTTGTACCCCTGATAATGATGACGTGTAGGGGTGTCCCGATGTA
ATATAGCATAGCTATGTGAAGAGATAAGCATTTGGCCGACAACTTTAGTGGTGGGCCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

>U3_jgf_v4
TATTACCCCCCGTGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCTTGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCAACCCGGCCCAATAATTAAGAGAACGTGTTCAAA
TTCGTGGTATGACCGAAGGTCAAGGTAACCGGTCAACATTATTCTGGCTTGCGCAGCAAGATACACGAATTAAATTATTAATTCGTAGGACACGTGGACGGACCGAAATACTCCTGCATC
TCTATAAATACCCTAGTCCTGTGAAGGATAATTGCTCTCTCTCTTCTGTCAAGGTGGTTGTGCTGAGGCGGAAGATCGCCAGCGGCGATCGTCGGAACGATGTGCATCTAGAGAGGCGGT
GAAGCAAACTACGAAGCGTATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTATACACTGTACAGATTATGTATTTTGTAAATTACGAAGAATTTCGTATATGATATTAATAAAA
CACCTGGGTGTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAAAATACAGTATACGGAACGTATACTGACAAAGTAATAAATGATAGGCGAAGCATGATTAACAGGTGTT
TAGGTATAATTAACATAATTATGAGAAGTAATAATAATACGGAAAATGAATAAGTATGAGGTGAAAGAGGAGATATTAGAATATTTAAAAACCCAATTATATTATTTTGGAACGAAATAC
AACACGCTATGAAATACAAGACGCTATGACAAATGTACGGGTATTTGATTGTGTATCTTAACGATCTAGGGCCGTAGGCCCGTGAGCAATGAACGGTATAGATTAATTCCTTAGCGACGA
AGAAAGGAATCTTAATAGGGACCACATTAAAGACAGCTGTCATTGATTAAATAAATAATATAATATACAAAAGACGTTTGTACCCCTGATAATGATGACGTGTAGGGGTGTCCCGATGTA
ATATAGCATAGCTATGTGAAGAGATAAGCATGTGGCCGACAACTTTAGTGGTGGGCCAGATGTCCCGAGTTAGTGCGCCACGTAAGCACGGGGGACTAT

Dataset S1B. Nucleotide sequences of the alphasatellite-BBTV isolate DRC-2012 from a leaf sample collected from BBTD-infected AAB banana plant in village Kimpoko (Bas Congo province) in 2012 (sample ALYU-21 and its technical replicate ALYU-20).

DNA-alpha

>alphaDRC2012_alyu21
TATTACCCCTCCTTGGCACACTGGCACAGATGACGTGTCATCAGCGAAATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATCCTTTCCTTTGGAGAGGAAACACAATATGCGT
GTTGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGATCCAATTGAAGAAGAAGACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACACCTCGAACCCATGC
GAGGTTCAATTACAGAGGCGAAAGCCTACTGTACGAAAGAACAATCACGGATCGCAGGTCCGTGGGAATTCGGAGAAATGCTGCTGAAGGGGTCGAACAGACGGAAGCTCGCAGAGCTTC
TGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGACGAGCGATGGCTAAGTCCGCCATGGATGAATCTCGGAAGCTTGCTGAAGAGTATGATTTCCCTCACGAACTACGCT
CGTGGCAAAAAACCCTAATCTCATTCCTCGAAGAGGAACCGGATGATCGTACTATTTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGTAAACACCTGGGATTAA
AAAAAGGATGGACCTATTTACCCGGAGGGGAACTGAAAGACATGATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGATGTACGAAAGACTTTGTAAGTT
ATAAATTCCTAGAGATGGTAAAAAATAGAACTGTATATAGTTATAAATACGAACCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTATTATGTAATTTCCTGCCGGAAGAAG
AAAAAATCTCCGGAGACAGATTAATAATAATAAATTGCTAAACACGCATTTACAAATAACACCCTCGAACAATCAATATTTCTATTATACCCCCGAAGCTCACTTCGGAACAACAGCGAC
AGCTGTCAACATCAGCGTTAGCTGTCATGTGGGCCCAACATAGCGTATGTAATACGCGGACTTGAAAGGATTATTAAATCCGCTTTGCTGCTACAGTGAAGCTTGGCACACTATAAATAC
CTGTGCCAAGGAGAGGGCTAG

DNA-C

7 SNPs to KU759879 (**Congo-DRC**, Mukwa et al. 2015); **9 SNPs** to JQ820469 (**Rwanda**; James et al. 2012). **9 SNPs** to JQ820457 (**Malawi**; James et al. 2012), **10 SNPs** to KM607029 (**India**; Stainton et al. 2015). **12 SNPs** to KM607090 (**Tonga**; Stainton et al. 2015). **11 SNPs** to KM607023 (**Congo-Brazza**; Stainton et al. 2015). **13 SNPs** to KM607020 (**Burundi**; Stainton et al. 2015). **14 SNPs** to KM607074 (**Australia**; Stainton et al. 2015). **16 SNPs** to KM607094 (**Samoa**; Stainton et al. 2015); **16 SNPs** to KM607080 (**Hawaii**; Stainton et al. 2015)

C protein (161 aa): 100% identity (**0 aa**) to 5 isolates: JQ820457 (**Malawi**; James et al. 2012), KM607005, KM607008, KM607043 (**Australia**; Stainton et al. 2015), JN250597 (**Sri Lanka**)

>C_alyu21
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCGACTAACAGACGCACGTGAGAATGCAGTAGCTTGCAGCGAAAGATAGACGTCAACATCAATAAAGAAGGAGGAATATTCTTTGC
TTCGGCACGAAGCAAAGGGTATAGATATTTGTTCGAGATGCGAAAATGGAGGCTATTTAAACCTGATGGTATTGTGATTTCCGAAATCACTCGACGGAAGAGAAATGGAGTTCTGGGAAT
CGTCTGCCATGCCTGACGATGTCAAGAGAGAGATTAAGGAAATATATTGGGAAGATCGGAAGAAACTTCTGTTCTGTCAGAAGTTGAAGAGCTATGTCAGAAGGATTCTTGTTTATGGAG
ATCAAGAGGATGCCCTTGCCGGAGTGAAGGATATGAAGACTTCTATTATTCGCTATAGCGAATACTTGAAGAAACCATGTGTGGTAATTTGTTGTGTTAGCAATAAATCAATTGTGTATA
GGTTAAACAGCATGGTGTTCTTTTATCATGAATACCTTGAAGAACTAGGTGGTGATTACTCAGTATATCAAGATCTCTATTGTGATGAGGTTCTTTCTTCTTCATCGACAGAGGAAGAAG
ATGTAGGAGTAATATATAGGAATGTTATCATGGCATCGACACAAGAGAAGTTCTCTTGGAGTGATTGTCAGAAGATAGTTATATCAGACTATGATGTAACATTACTCTAATGTAATATCC
ATTATCATCAATAAAATAATGGAATGTTGATTATGTATTTATCATAAATACATAATGGTATACGTATAGCATAAAATACATTATCCAACATACAACACACTATAAAATACAACACACTAT
AACAAATGTAAGGGTATTTGATTGGTTTATATTAACCCCTTAAGGGCCGAAGGCCCGTTTAAATATGTGTTGGACGAAGTCCAAGCACAAAAAAGTAAGCAGAACAACGGAATAATATGA
GCTGGCAACGTAGGGTCCATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-M

7 SNPs to JQ820462 (**Rwanda**; James et al. 2012), **8 SNPs** to KM607205 (**Congo-DRC**, Stainton et al. 2015); **8 SNPs** to KM607167 (**Congo-Brazza**; Stainton et al. 2015); **9 SNPs** to JQ820456 (**Malawi**; James et al. 2012), **9 SNPs** to KM607241 (**Sri Lanka**; Stainton et al. 2015); **9 SNPs** to KM607222 (**Hawaii**; Stainton et al. 2015). **11 SNPs** to KM607237 (**India**; Stainton et al. 2015). **11 SNPs** to KM607236 (**Samoa**; Stainton et al. 2015). **13 SNPs** to KM607220 (**Australia**; Stainton et al. 2015). **13 SNPs** to KM607161 (**Burundi**; Stainton et al. 2015). **14 SNPs** to JF957669 (**Tonga**; Stainton et al. 2015)

M protein (117 aa): identical 0 aa to 5 isolates: JQ820462 JQ820468 (**Rwanda**; James et al. 2012) JQ820456 (**Malawi**; James et al. 2012) FJ609642 EF153738 (**India**) **1 aa** to AF102783 (**Egypt**)

>M_alyu21
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCTTCGACAAATGCACGTGAGTGATATAAGGGACATAACGGGTTCAGATAACGGTATCTTTGGTTTAGAATATAACGTCACGTGTG
AAAGTGATAGGCACGTGACTAAGTCAAATGTATTGAATAAACATTTGACGTCCGGTAGCTTCCGAAGGAAGTAAGGATTGCTTCGTGGCGAAGCAAACCATTTATATATTGCCTAGGCTT
GCGGCCTATAAATAGGACCCTGCTAAATGGCATTAACAACAGAGCGGGTTAAACTATTCTTTGAATGGTTTTTGTTCTTTGCAGCAATATTTATTGCGATTACAATATTATATATATTGT
TGGTTTTGCTCTTTGAGGTACCGAAGTATATTAAGCAGCTCGTGAGGTATTTGGTAGAATACCTGACCAGAAGACGTGTATGGATGCAGAGAACGCAGTTATCGGAGGCAACTGGAGACG
TAGAGTTCGGCAGAGGTATTGTGGAAGACAGACGGGATCAACAACCGGCTGTCATACCACAGGCATCTCAGGTTAACCCTTCTCAACAAATTAGAAGGGATGATCAAGGAAGACGAGGAA
ACGTCGGACCTATGTTTTAATACACGGTATTGTAATATATGAAATATAAATGGGGATTGATGTATAAGGTCATACATACTATATGTATGATAATGAAACATATTGTAATATGTGAATTGT
AAACGAGTGTTGAATGTATACAACATACAACACACTATGAAATACAAGACGCTATGACAAATGTATGGGTATCTGATTAGGTATCCTAACGATCTAGGGCCGAAGGCCCGTGAGCAATAT
GCGTCGAAATAATGTTTAACAAACAAATATACATGATACGGATAGTTGAATACATAAACAAcTAGGTATACAATACAACAAACTGTTGTAAAGAAATTAAAAATAAGAAGAGAGAGTATA
TTTGTGTCGGATAAGCTTGGCAACCACCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-N

9 SNPs to KU759880 (**Congo-DRC,** Mukwa et al. 2016); **10 SNPs** to KM607312 (**Congo-Brazza**; Stainton et al. 2015); **10 SNPs** to JQ820470 (**Rwanda**; James et al. 2012). **11 SNPs** to JQ820458 (**Malawi**; James et al. 2012), **11 SNPs** to KM607311 (**Burundi**; Stainton et al. 2015). **12 SNPs** to KX592200 (**India**; Baldodiya et al. 2017); **12 SNPs** to KM607324 (**Egypt**; Stainton et al. 2015). **14 SNPs** to KM607388 (**Sri Lanka**; Stainton et al. 2015); **18 SNPs** to JX170761 (**Pakistan**; Ali et al. 2012); **27 SNPs** to KM607359 (**Australia**; Stainton et al. 2015)

N protein (154 aa): identical 0 aa to 7 isolates: NC_003476 NP_604479 L41577 (?, **Australia** , ? Burns et al 1995 JGV) AY273170 AY948438 (**India**) EF529519 (**Pakistan**) JF957688 (? Stainton et al. 2012) **1 aa** to KU759884 (**Congo-DRC**) KM607364 (**Sri Lanka**) JF957695 KM607409 (**Tonga**) KM607336 (**Australia**)

>N_alyu21
TATTACCCCCCGTGCTCGGGACGGGACATGACGTCAGCAAGGAATATAATGGGCTTTTTATTAGCCCATGTATTGAATTGGGCCGGGTTTTGTCATTTTACAAAAGCCCGGTCCAGGATA
TGTATAATGTCACGTGCCGAATAAAAGGTTGCTTCGCCTCGAAGAAACCTAATTTGAGGTTGCGTATTCAATACGCTACCGAGTATCTATTAATATGTGAGTCTCTGCCGAAACAATCAG
AGCGAAAGCAAAGCAGAAGCGATGGATTGGGCGGAATCACAATTCAAGACTTGTACTCATGGATGCGATTGGAAGAAGATATCATCGGATTCAGCCGATAATCGACAATATGTGCCATGC
GTCGATTCTGGAGCTGGAAGAAAGTCGCCTCGCAAGGTACTTCTTAGATCTATTGAAGCTGTGTTTAACGGAAGCTTCAGCGGAAATAATAGGAACGTTCGTGGATTTCTCTACGTATCG
ATCAGAGACGATGACGGAGAAATGCGTCCAGTACTCATAGTACCATTCGGAGGATATGGATATCATAATGATTTCTATTATTTCGAAGGAAAGGGGAAAGTTGAATGTGATATATCATCA
GATTATGTTGCGCCAGGAATAGATTGGAGCAGAGACATGGAAGTTAGTATTAGTAACAGCAACAACTGTAATGAATTATGTGATCTGAAGTGTTATGTTGTTTGTTCTTTAAGAATCAAG
GAATAAAAGTTGTGCTGTAATGTTTATTAATAAAACGTATATTTGGGAAATTGATAGTTGTATAAAACATACAACACGCTATGAAATACAAGACGCTATGACAAATGTACGGGTATCTGA
ATGAGTTTTAGTATCGCTTAAGGGCCGCAGGCCCGTTGAAAAATAATAATCGAATTATAAACGTTAGATAATAATCAGAGATAGGTGATCAGATAACATAAACATAAACGAAGTATATGG
CGGTACAATAATATAATAAGTTAAAAATAAAAAACATAATGAATACTAATCTCTGATTGGTTCAGAAGAAAGGCCCACCAACTAAAAGGTGGGGAGAATGTCCCGATGACGTAAGCACGG
GGGACTAT

DNA-R

3 SNPs to KU687068 (**Congo-DRC,** Mukwa et al. 2016); **4 SNPs** to KM607674 (**India**; Stainton et al. 2015); **5 SNPs** to KM607598 (**Burundi**; Stainton et al. 2015); **6 SNPs** to JQ820459 (**Rwanda**; James et al. 2012). **6 SNPs** to KM607658 (**Australia**; Stainton et al. 2015), **7 SNPs** to KM607603 (**Congo-Brazza**; Stainton et al. 2015). **9 SNPs** to KM607680 (**Sri Lanka**; Stainton et al. 2015);

R protein (286 aa): identical 0 aa to 5 isolates JQ820453 JQ820465 (**Rwanda**) DQ640742 EF584545 GU085264 (**India**) **1 aa** to KU687088 KU687089 (**Congo-DRC**) JQ820459 (**Rwanda**) KP876489 KP876490 KP876491 GU125417 DQ656118 DQ656119 (**India**) …

>R_alyu21
TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCTCTCCATTACAAGATCATCATCGACGACAGAATGGCGCGATATGTGGTATGCTGGATGTTCACCA
TCAACAATCCCACAACACTACCAGTGATGAGGGATGAGATCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCAAGGTTATGTCGAGATGAAGAGACGAA
GCTCTCTGAAGCAGATGAGAGGCTTCTTCCCAGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAGAAGAAGCGCGGTCATACTGTATGAAGGAAGATACAAGAATCGAAGGTCCCTTCG
AGTTTGGTGCATTTAAATTGTCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGTGAAACGCACAAAAGGCCTTTGGAGTATTTATATGATTGTCCTAACACCTTCGATAGAA
GTAAGGATACATTATACAGAGTACAAGCAGAGATGAATAAAACGAAGGCGATGAATAGCTGGAGAACTTCTTTCAGTGCATGGACATCAGAGGTGGAGAATATCATGGCGCAGCCATGTC
ATCGGAGAATAATTTGGGTCTATGGACCAAATGGAGGAGAAGGAAAGACGACGTATGCAAAACATCTAATGAAGACGAGAAATGCGTTTTATTCTCCAGGAGGAAAATCATTGGATATAT
GTAGACTGTATAATTACGAGGATATTGTTATATTTGATATTCCAAGATGCAAAGAGGATTATTTAAATTATGGGTTATTAGAGGAATTTAAGAATGGAATAATTCAAAGCGGGAAATATG
AACCCGTTTTGAAGATAGTAGAATATGTCGAAGTCATTGTAATGGCTAACTTCCTTCCGAAGGAAGGAATCTTTTCTGAAGATCGAATAAAGTTGGTTTCTTGCTGAACAAGTAATGACT
TTACAGCGCACGCTCCGACAAAAGCACACTATGACAAAAGTAGGGGTATCTGATTGGGTTATCTTAACGATCTAGGGCCGTAGGCCCGTGAGCAATGAACGGCGAGATCAGATGTCCCGA
GTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-S

6 SNPs to KU759889 (**Congo-DRC,** Mukwa et al. 2016); **6 SNPs** to JQ820461 (**Rwanda**; James et al. 2012). **7 SNPs** to JQ820455 (**Malawi**; James et al. 2012). **7 SNPs** to KM607532 (**India**; Stainton et al. 2015). **8 SNPs** to KM607514 (**Hawaii**; Stainton et al. 2015); **10 SNPs** to KM607451 (**Burundi**; Stainton et al. 2015). **10 SNPs** to KM607537 (**Sri Lanka**; Stainton et al. 2015). **10 SNPs** to KM607528 (**Samoa**; Stainton et al. 2015); **12 SNPs** to KM607510 (**Australia**; Stainton et al. 2015); **12 SNPs** to KM607471 (**Egypt**; Stainton et al. 2015). **14 SNPs** to KM607573 (**Tonga**; Stainton et al. 2015);

S protein (175 aa): identical 0 aa to 5 isolates: EF095164 (**Taiwan**) EF593169 FJ859735 FJ859736 FJ859737 (**Pakistan**), **1 aa** to several isolates

>S_alyu20_v1
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTAATGGATTGTGGATATAGGGCCCAAAGGGCCCGTTTAGATGGGTTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAACAGGCGG
GAACCGTCCCAAATTCAAACTTCGATTGCTTGCCCTGCAAGCCATCTAGAAGTCTATAAATACCAGTGTCTAGATAGATGTTCAGACAACAAATGGCTAGGTATCCGAAGAAATCCATCA
AGAAGAGGCGGGTTGGGCGCCGGAAGTATGGCAGCAAGGCGGCAACGAGCCACGACTACTCGTCGTTAGGGTCAATATTGGTTCCTGAAAACACCGTCAAGGTATTTCGGATTGAGCCTA
CTGATAAAACATTACCCAGATATTTTATCTGGAAAATGTTTATGCTTCTTGTGTGCAAGGTGAAGCCCGGAAGAATACTTCATTGGGCTATGATCAAGAGTTCTTGGGAAATCAACCAGC
CGACAACCTGTCTGGAAGCCCCAGGTTTATTTATTAAACCTGAACATAGCCATCTGGTTAAACTGGTATGTAGTGGGGAACTTGAAGCAGGAGTCGCAACAGGGACATCAGATGTTGAAT
GTCTTTTGAGGAAGACAACCGTGTTGAGGAAGAATGTAACAGAGGTGGATTATTTATATTTGGCATTCTATTGTAGTTCTGGAGTAAGTATAAACTACCAGAACAGAATTACATATCATG
TTTGATATGTTTATGTAAACATAAACTATTGTATGGAATGAAATCCAAATAACATACAACACGCTATGAAATACAAGACGCTATGACAAAAGTACGGGTATCTGATTAGGTATCCTAACG
ATCTAGGGCCGAAGGCCCGTGAGCAATATGCGTCGAAATAATGTTTAACAAACAAATATACATGATACGGATAGTTGAATACATAAACAACGAGGTATACAATACAACAAACTGTTGTAA
AGAAATAAAAAACAAGAAGAGAGAGTATATTTGTGTCGGATAAGCATGAAACCCACCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGACTAT

DNA-U3

29 SNPs to KM607738 (**Congo-Brazza**; Stainton et al. 2015); **30 SNPs** to KM607773 (**Congo-DRC,** Stainton et al. 2015); **30 SNPs** to JQ820454 (**Malawi**; James et al. 2012). **31 SNPs** to KM607732 (**Burundi**; Stainton et al. 2015). **32 SNPs** to KM607809 (**Sri Lanka**; Stainton et al. 2015). **37 SNPs** to KM607731 (**India**; Stainton et al. 2015). **36 SNPs** to JQ820466 (**Rwanda**; James et al. 2012). **45 SNPs** to FJ859750 (**Pakistan**; Hyder et al. 2011); **>60 SNPs** to KM607808 (**China**; Stainton et al. 2015)

U3 protein (77 aa): 1 aa to FJ009239 MT109277 (**India**) **2 aa** to several isolates

>U3_alyu21
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCTTGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCAACTCGGCCCAATAATTAAGAGAACGTGTTCAAA
TTCGTGGTATGACCGAAGGTCAAGGTAACCGGTCAACATTATTCTGGCTTGCGCAGCAAGATACACGAATTAAATTATTAATTCGTAGGACACGTGGACGGACCGAAATACTCCTGCATC
TCTATAAATACCCTAGTCATGTGAAGGATAATTGCTCTCTCTCTTCTGTCAAGGTGGTTGTGCTGAGGCGGAAGATCGCCAGCGGCGATCGTCGGAACGATGTGCATCTAGAGAGGCGGT

GAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTATACACTGTACAGATTTTGTATTTTGTAAATTACGAAGAATTTCGTATATGATATTAATAAAA
CACCTGGGTGTGTTAATGTTTACATTAAATTGTATCCTGAATGTACACAATAAAATACAGTATACGGAACGTATACTGACAAAGTAATAAATGATAGGCGAAGCATGATTAACAGGTGTT
TAGGTATAATTAACATAATTATGAGAAGTAATAATAATACGGAAAATGAATAAGTATGAGGTGAAAGAGGAGATATTAGAATATTTAAAAACCCAATTATATTATTTTGGAACGAAATAC
AACACACTATGAAATACAAGGCGCTATGACAAATGTACGGGTATTTGATTGTGTATCTTAACGCTTAAGGGCCGCAGGCCCGTCAAGTTGAATGAACGGTCTAGATTAATTCCTTAGCGA
CGAAGAAAGGAATCTTAGTGGGGACCATATTAAAGACAGCTGTCATTGATTAAATAAATAATATAATATaCAAAAGACTATTGTACCCCTGATAATGATGACGTGTAGGGGTGTCCCGAT
GTAATATAGCATAGCTATGTGAAGAGATAAGCATGTGGCCGACAACTTTAGTGGTGGGCCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGACTAT

Acinetobacter plasmid-like

Rep protein (423 aa) best match to 421 aa rep of Acinetobacter soli plasmid-like

>Acinetobacter plasmid-like_alyu21
TTACTTGATACTATTAATTAACTCGGGACAAAATTTGATGCAAAAAGACATTAAAAAACCCCTGTTATCTCACAGTTTGGCGACCAGCGATAACAAGGGTTTGGAATCTGCTAAGGCAG
ATCAACATAGGGATAGAATAACACGTTTTGGCATTTTGAAACATAGATCGAAGCAACAAGAAAATTATCTATGGACACTAGCCAAATACAAGGAAAACTATCAAAACGATAAGCCAAACA
ACGAGTCCATTAGGGCCACTAAAGCAGCTCATAAATTGCAGTCCTGCGGCAATTTTCTTTTGTTCAAAAATTTTTACACAATTGACCAAGTCAAGCTCGCAAAATTTCATGTTTGTGGTC
AGCACTTACTTTGCCCATTTTGTGCGGGTATTCGCGCATCTAAAGCAATTCAAAAATATACTGAACGAGTTAATGAGGTTCTTTCTAAAAATCGTAAACTCAAGCCTGTTTTAATCACTT
TCACAGTAAAAAATGGTTCCGATCTCGATGAGCGATCATCTCATTTAATGAAGTCATTCAGAACTCTTCTCGATCGACGTAGGGATTTTTTAAAAAAAGGTCGTGGTTTTAATGAGTTCT
GCAAAATTAATGGTGCTATGTATTCGTATGAAAATACTTTTAATCCAGATACCAAAGAATGGCATCCACATGTTCACATGTTTGCCCTTTTAGATTCTTGGATTGATCAAGATGAGCTAT
CACAGTATTGGCATTCTATTACTGGCGATTCAATGATTGTCGATATACGACGAGTTAAAAAACAAAAAGATGTTGGTTATGCAAAAGCTGCCGCTGAAGTTTGTAAATACGCCCTTAAGT
TCGGCGATTTATCTGTTGAAAATACTTGGGAAGCATTCAAGGTACTCAAAGGCAAGCGTTTAAGCGGTGCATTTGGATCTCTATACGGTGTAAAAATTCCTGACAATCTTGCTGACGAAA
TGCCAGATGAAAACGATCTGCCATATTTAGAAATGCTCTACAAATTTGTTTTTGGAAAACAGTCCTACTATGACTTAACCATGACACGACACGTAGAGCCGCAATGCAAGGACATGCATG
ACGAGGATGGAGTAGGAGGCACGACGCCCGACCGACGAGTTGTGCATGGGCGAAGCAGTGAGGCGATAGAGGACGATGCGAGGACGTTGCCGGTGCGAGGGCCCGCAGTCACGGAACGAC
CACAGCGAGTCCGCAAAAAGCAACATTGGCAACTACCACCAACAACCCGTGTGAGGGTTCGGCAACGAATCCGAAGATGGGACGGTTATTTGTGTGTTATACACATGTGATTTTAAAAAC
GTATGTTAAAATTTAGTCGCTGAATAGCAGGACGGCCATCCTACTACCCAGCTAACCAAAACGATCTATTAAGGAGATCATCATGGCTGTACCGAATACTAATGCTTTAGATTATTTAGG
CAAGTATGTTTCATTTAATCACGACGATATTTTTGAAATATACGGAGTTATTTCCAATGTAATTTTTAATATGGATGGCTCTGTTGAAATGTCAACTGGTTGGGATAATTTTTACGAGCT
CTCTAAAATGAGCAATTTAAAAATTTTGGGCGAAATTAGACTCTATTGATTTTATTGAGCCGCACATAAGTACTGCACATAATAGCTGTTATGTGCAGTATTTTTTGCCCGTTTCTGGA
GAAACGCGTAAGCGTGCATTCTGACAAAAATTGCCGAACGAGTGTCTACGAGTGACGACTCCAGAATAAAAATTTCAAACCTTCCTTTCCCTGATTACAAGCTCCCATTTGCATTTGACG
GCAAGTACAGAGCCATCCCGCATGGGTGGCGAAGTAATGATATTGATTTAATATCATTAGTGATATATAAATATAAAACCAATTATGTCTATGAACATATCAATTTAATATTAGGTGATA
AAATGGAACCAACTAATTTACAAATCTTCGTTGCTGAAGTTAAAGGCACTGGTGAATCGGAATATATCGGCGTTTATAAGCAAGTGCCTTTGCGTCTTCGTGCAGGTGTTTTTGCTGAAG
TTGAAGCACTTCAGGAAATGATGGCTCGAACTCAGAAGGTATCTCGAAATAAGGTTATCAATGATCTCCTTCAAATCGCTATTGATCAGGTTAAAGTCTCACTGGATGAGAAATCTCTAG
AAGATTTCAATATGTTTGCTTCCCATCACTACAGTGATTTCACTGGCTCAGGTGACTTGTCAGATGAATCGTAAAATTGAAGTTTTAGGCGGTGGTCCAATGGAATCTCTTGAAGAAGCT
GCTGCTTACTTCAAGAAGGTTCTCCAGGAACATTTGGATAATAAAAGAGACATAACACTCTTTGCGATTGCCGTTGTAGGCGGTCGCTTAAAAGTAGTTGAGGGATTACCGAAATGATTA
AATTGGAAGGCACAATTATTAATGTTTTCACCCAACAGGGTGGTAAAGATAAAAAGACTGGAGAGGCATTTGCCGATCGAGACAAAATTCAACTTTTAGGTGAGCTTGACTTGCCGAATG
GAGATAAAAAACACGAGTTGATTGATCTTACTGTCGAAGACGGTAAGCATTATGAGAGCTTAAAAAATAAACGAGTTAGTATTCCATGCGGTGCTTTGGCATCTGGAAGAAATGTCATTT
TTTATGTTGCAAAAGGCGCAACTCCAAAACTACTGAGTTCAGCATGATACTCGATAAAAAACAGCAACTTACGAAGTAAGTTCGCTGTTTTTTCTT

Dataset S1C. Pairwise comparison of the DRC-2016 and DRC-2012 alphasatellite nucleotide sequences and encoded Rep proteins.

EMBOSS Needle

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# Aligned_nucleotide_sequences: 2
# 1: alphaDRC2016
# 2: alphaDRC2012
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
# Length: 1112
# Identity:    1073/1112 (96.5%)
# Similarity:  1073/1112 (96.5%)
# Gaps:          18/1112 ( 1.6%)
# Score: 5243.5

alphaDRC2016       1 TATTACCCCTCCTTGGCACACTGGCACAGCTGACGTACAGATGACGTGTC     50   Rep ORF start codon
                     |||||||||||||||||||||||||||||           |||||||||||||
alphaDRC2012       1 TATTACCCCTCCTTGGCACACTGGC------------ACAGATGACGTGTC     39   Rep ORF start codon

alphaDRC2016      51 ATCAGCGAAATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATC    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012      40 ATCAGCGAAATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATC     89

alphaDRC2016     101 CTTTCCTTTGGAGAGGAAACACAATATGCGTGTTGGCAACACGAGAAGGT    150
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012      90 CTTTCCTTTGGAGAGGAAACACAATATGCGTGTTGGCAACACGAGAAGGT    139

alphaDRC2016     151 GGATCACGACCACCTACAGGGAGTGATCCAATTGAAGAAGAAGACCCGAT    200
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     140 GGATCACGACCACCTACAGGGAGTGATCCAATTGAAGAAGAAGACCCGAT    189

alphaDRC2016     201 TAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACACCTCGAACCCATG    250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     190 TAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACACCTCGAACCCATG    239

alphaDRC2016     251 CGAGGTTCGATTACAGAGGCGAAAGCCTACTGTACGAAAGAACAATCACG    300
                     ||||||||.||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     240 CGAGGTTCAATTACAGAGGCGAAAGCCTACTGTACGAAAGAACAATCACG    289

alphaDRC2016     301 GATCGCAGGTCCGTGGGAATTCGGAGAAATTCTGCTGAAGGGGTCGAACA    350
                     ||||||||||||||||||||||||||||||||.||||||||||||||||||
alphaDRC2012     290 GATCGCAGGTCCGTGGGAATTCGGAGAAATGCTGCTGAAGGGGTCGAACA    339

alphaDRC2016     351 GACGGAAGCTCGCAGAGCTTCTGGATGATCCCGATAACGAAATAAATGAA    400
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     340 GACGGAAGCTCGCAGAGCTTCTGGATGATCCCGATAACGAAATAAATGAA    389

alphaDRC2016     401 CCTCAAAAATATAGACGAGCGATGGCTAAGTCCGCCATGGATGAATCTCG    450
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     390 CCTCAAAAATATAGACGAGCGATGGCTAAGTCCGCCATGGATGAATCTCG    439

alphaDRC2016     451 GAAGCTTGCTGAAGAGTATGATTTCCCTCACGAACTACGTTCGTGGCAAA    500
                     ||||||||||||||||||||||||||||||||||||||.||||||||||||
alphaDRC2012     440 GAAGCTTGCTGAAGAGTATGATTTCCCTCACGAACTACGCTCGTGGCAAA    489
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alphaDRC2016     501 AAACCCTAATTTCATGCCTCGAAGAGGAACCGGATGATCGTACTATTTAC    550
                     ||||||||||.|||||.||||||||||||||||||||||||||||||||||
alphaDRC2012     490 AAACCCTAATCTCATTCCTCGAAGAGGAACCGGATGATCGTACTATTTAC    539

alphaDRC2016     551 TGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGTAAACA    600
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     540 TGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGTAAACA    589

alphaDRC2016     601 CCTAGGATTAAAAAAAGGATGGACCTATTTACCCGGAGGGGAACTGAAAG    650
                     |||.||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     590 CCTGGGATTAAAAAAAGGATGGACCTATTTACCCGGAGGGGAACTGAAAG    639

alphaDRC2016     651 ACATGATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGAT    700
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     640 ACATGATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGAT    689

alphaDRC2016     701 TTCCCCAGGTGTACGAAAGACTTTGTAAGTTATAAATTCCTAGAGATGGT    750
                     ||||||||.||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     690 TTCCCCAGATGTACGAAAGACTTTGTAAGTTATAAATTCCTAGAGATGGT    739

alphaDRC2016     751 AAAAAACAGAACTGTATATAGTTATAAATACGAACCGATAGGTTCTATAG    800
                     ||||||.||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     740 AAAAAATAGAACTGTATATAGTTATAAATACGAACCGATAGGTTCTATAG    789

alphaDRC2016     801 TCAGTAACAAAGTTCATGTAGTGGTCTTATGTAATTTTATGCCGGAAGAA    850
                     |||||||||||||||||||||||||||.||||||||||..||||||||||||
alphaDRC2012     790 TCAGTAACAAAGTTCATGTAGTGGTATTATGTAATTTCCTGCCGGAAGAA    839

alphaDRC2016     851 GAAAAAATCTCCGGAGACAGATTAATAATAATAAATTGCTAAACACGCAT    900   Rep ORF stop codon
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     840 GAAAAAATCTCCGGAGACAGATTAATAATAATAAATTGCTAAACACGCAT    889   Rep ORF stop codon

alphaDRC2016     901 TTACAAA-AATACCCTCGAACAATCAATATTCCTATTATACCCCCGAAGC    949
                     ||||||| |||.||||||||||||||||||||.||||||||||||||||||
alphaDRC2012     890 TTACAAATAACACCCTCGAACAATCAATATTTCTATTATACCCCCGAAGC    939

alphaDRC2016     950 TCACTTCGGAACA------ACAGCTGTCGTTATCAATGACAGCTGTCATG    993
                     |||||||||||||       |||||||||...|||||..||..||||||||||
alphaDRC2012     940 TCACTTCGGAACAACAGCGACAGCTGTCAACATCAGCGTTAGCTGTCATG    989

alphaDRC2016     994 TGGTCCCAACATAGCGTATGTAATACGCGGACTTGAAAGGATTATTAAAT   1043
                     |||.||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012     990 TGGGCCCAACATAGCGTATGTAATACGCGGACTTGAAAGGATTATTAAAT   1039

alphaDRC2016    1044 CCGCTTTGCTGCTACAGTGAAGCTTGGCACACTATAAATACCTGTGCCAA   1093    TATA-box
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
alphaDRC2012    1040 CCGCTTTGCTGCTACAGTGAAGCTTGGCACACTATAAATACCTGTGCCAA   1089    TATA-box

alphaDRC2016    1094 GGAGAGGGCTAG   1105
                     ||||||||||||
alphaDRC2012    1090 GGAGAGGGCTAG   1101


# Aligned_protein_sequences: 2
# 1: Rep_alphaDRC2016
# 2: Rep_alphaDRC2012
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 283
# Identity:     280/283 (98.9%)
# Similarity:   282/283 (99.6%)
# Gaps:           0/283 ( 0.0%)

Rep_alphaDRC2      1 MTCHQRNWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKK     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Rep_alphaDRC2      1 MTCHQRNWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKK     50

Rep_alphaDRC2     51 KTRLNGAKRLIGGNPHLEPMRGSITEAKAYCTKEQSRIAGPWEFGEILLK    100
                     ||||||||||||||||||||||||||||||||||||||||||||||:|||
Rep_alphaDRC2     51 KTRLNGAKRLIGGNPHLEPMRGSITEAKAYCTKEQSRIAGPWEFGEMLLK    100

Rep_alphaDRC2    101 GSNRRKLAELLDDPDNEINEPQKYRRAMAKSAMDESRKLAEEYDFPHELR    150
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Rep_alphaDRC2    101 GSNRRKLAELLDDPDNEINEPQKYRRAMAKSAMDESRKLAEEYDFPHELR    150

Rep_alphaDRC2    151 SWQKTLISCLEEEPDDRTIYWVYGPNGGEGKTQFGKHLGLKKGWTYLPGG    200
                     ||||||||.||||||||||||||||||||||||||||||||||||||||||
Rep_alphaDRC2    151 SWQKTLISFLEEEPDDRTIYWVYGPNGGEGKTQFGKHLGLKKGWTYLPGG    200

Rep_alphaDRC2    201 ELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYKYEPI    250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Rep_alphaDRC2    201 ELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYKYEPI    250

Rep_alphaDRC2    251 GSIVSNKVHVVVLCNFMPEEEKISGDRLIIINC    283
                     |||||||||||||||||:||||||||||||||||
Rep_alphaDRC2    251 GSIVSNKVHVVVLCNFLPEEEKISGDRLIIINC    283


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Supplementary Dataset S1D. Protein and Nucleotide sequence Blast analyses of DRC alphasatellite isolates.

Protein BLAST Rep_alphaDRC2016

Replication-associated protein of non-essential DNA C9 [**Faba bean necrotic yellows virus (isolate SV292-88)**]
Sequence ID: P0CK61.1 Length: 281 Number of Matches: 1

Identities	**Positives**	**Gaps**
180/277(**65%**)	227/277(**81%**)	0/277(**0%**)

```
Query  7    NWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKKKTRLNGAKRLIGGNPH  66
            NWVFTLNF GE P+LSF E  QYA WQHE+V+HDH+QGVIQLKKK ++N  K +IGGNPH
Sbjct  5    NWVFTLNFAGEVPVLSFDERVQYAVWQHERVNHDHIQGVIQLKKKAKMNTVKNIIGGNPH  64

Query  67   LEPMRGSITEAKAYCTKEQSRIAGPWEFGEILLKGSNRRKLAELLDDPDNEINEPQKYRR  126
            LE M+GSI EA AY  KE+SR+AGPW +GE+L KGS++RK+ EL+ DP+NE+ EPQKYRR
Sbjct  65   LEKMKGSIEEASAYAQKEESRVAGPWSYGELLKKGSHKRKIMELIKDPENELEEPQKYRR  124

Query  127  AMAKSAMDESRKLAEEYDFPHELRSWQKTLISCLEEEPDDRTIYWVYGPNGGEGKTQFGK  186
            AMA SAMDESRKLAEE  FP+   SWQ+T++  LEEEP+DRTI WVYGPNG EGK+QFGK
Sbjct  125  AMAWSAMDESRKLAEEEGFPYMFYSWQETVLGLLEEEPNDRTIIWVYGPNGNEGKSQFGK  184

Query  187  HLGLKKGWTYLPGGELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYK  246
             LGLKK + YLPGG+ +DM Y+  K  K +VV+D PRC  ++++Y+F+E++KNRT+YSYK
Sbjct  185  FLGLKKDYLYLPGGKTQDMTYMLMKNPKANVVMDIPRCNSEYLNYQFMELIKNRTIYSYK  244

Query  247  YEPIGSIVSNKVHVVVLCNFMPEEEKISGDRLIIINC  283
            YEP+G I++NK+HV+VL N +P+ EKIS DR+ II C
Sbjct  245  YEPVGCIINNKIHVIVLANVLPDYEKISQDRIKIIYC  281
```

Replication-associated protein [**Faba bean necrotic yellows virus associated alphasatellite 2**]
Sequence ID: ATU31571.1 Length: 281 Number of Matches: 1

Identities	Positives	Gaps
179/277(**65%**)	228/277(**82%**)	0/277(0%)

```
Query  7    NWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKKKTRLNGAKRLIGGNPH  66
            NWVFTLNF GE P+LSF E  QYA WQHE+V+HDH+QGVIQLKKK ++N  K +IGGNPH
Sbjct  5    NWVFTLNFAGEVPVLSFDERVQYAVWQHERVNHDHIQGVIQLKKKAKMNTVKNIIGGNPH  64

Query  67   LEPMRGSITEAKAYCTKEQSRIAGPWEFGEILLKGSNRRKLAELLDDPDNEINEPQKYRR  126
            LE M+GSI EA AY  KE+SR+AGPW +GE+L KGS++RK+ EL+ DP+NE+ EPQKYRR
Sbjct  65   LEKMKGSIEEASAYAQKEESRVAGPWSYGELLKKGSHKRKIMELIKDPENELEEPQKYRR  124

Query  127  AMAKSAMDESRKLAEEYDFPHELRSWQKTLISCLEEEPDDRTIYWVYGPNGGEGKTQFGK  186
            AMA SAMDESRKLAEE  FP+ L SWQ+T++  L+EEP+DRTI WVYGPNG EGK+QFGK
Sbjct  125  AMAWSAMDESRKLAEEEGFPYSLYSWQETVLGLLDEEPNDRTIIWVYGPNGNEGKSQFGK  184

Query  187  HLGLKKGWTYLPGGELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYK  246
             LGLKK + YLPGG+ +DM Y+  K  K +VV+D PRC  ++++Y+F+E++KNRT++SYK
Sbjct  185  FLGLKKDYLYLPGGKTQDMTYMLMKNPKANVVMDIPRCNSEYLNYQFMELIKNRTIFSYK  244

Query  247  YEPIGSIVSNKVHVVVLCNFMPEEEKISGDRLIIINC  283
            YEP+G I++NK+HV+VL N +P+ EKIS DR+ II C
Sbjct  245  YEPVGCIINNKIHVIVLANVLPDYEKISQDRIKIIYC  281
```

Rep protein [**Faba bean necrotic yellows C9 alphasatellite**]
Sequence ID: NP_619574.1 Length: 281 Number of Matches: 1

Identities	Positives	Gaps
179/277(65%)	227/277(81%)	0/277(0%)

```
Query  7    NWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKKKTRLNGAKRLIGGNPH  66
            NWVFTLNF GE P+LSF E  QYA WQHE+V+HDH+QGVIQLKKK ++N  K +IGGNPH
Sbjct  5    NWVFTLNFAGEVPVLSFDERVQYAVWQHERVNHDHIQGVIQLKKKAKMNTVKNIIGGNPH  64

Query  67   LEPMRGSITEAKAYCTKEQSRIAGPWEFGEILLKGSNRRKLAELLDDPDNEINEPQKYRR  126
            LE M+GSI EA AY  KE+SR+AGPW +GE+L KGS++RK+ EL+ DP+NE+ EPQKYRR
Sbjct  65   LEKMKGSIEEASAYAQKEESRVAGPWSYGELLKKGSHKRKIMELIKDPENELEEPQKYRR  124

Query  127  AMAKSAMDESRKLAEEYDFPHELRSWQKTLISCLEEEPDDRTIYWVYGPNGGEGKTQFGK  186
            AMA SAMDESRKLAEE  FP+ L SWQ+T++  LEEEP+DR I WVYGPNG EGK+QFGK
Sbjct  125  AMAWSAMDESRKLAEEGGFPYTLYSWQETVLGLLEEEPNDRIIIWVYGPNGNEGKSQFGK  184

Query  187  HLGLKKGWTYLPGGELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYK  246
             LGLKK + YLPGG+ +DM Y+  K  K +VV+D PRC  ++++Y+F+E++KNRT++SYK
Sbjct  185  FLGLKKDYLYLPGGKTQDMTYMLMKNPKANVVMDIPRCNSEYLNYQFMELIKNRTIFSYK  244

Query  247  YEPIGSIVSNKVHVVVLCNFMPEEEKISGDRLIIINC  283
            YEP+G I++NK+HV+VL N +P+ EKIS DR+ II C
Sbjct  245  YEPVGCIINNKIHVIVLANVLPDYEKISQDRIKIIYC  281
```

Satellite replication initiator protein [**Sophora alopecuroides yellow stunt alphasatellite 3**]
Sequence ID: ARI50297.1 Length: 281 Number of Matches: 1

Identities	Positives	Gaps
181/277(65%)	222/277(80%)	0/277(0%)

```
Query  7    NWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKKKTRLNGAKRLIGGNPH  66
            NWVFT NF GE PILSF E  QYA WQHE+V HDHLQGVIQLKKK RLN  K +IGGNPH
Sbjct  5    NWVFTRNFAGEVPILSFDERVQYAVWQHERVTHDHLQGVIQLKKKARLNTVKAMIGGNPH  64
```

```
Query  67   LEPMRGSITEAKAYCTKEQSRIAGPWEFGEILLKGSNRRKLAELLDDPDNEINEPQKYRR  126
            LE MR +I EA  YC K  SR++GPWEFG +L KGS++RK+ ELL+DPDNEI EPQKYRR
Sbjct  65   LEKMRATIEEAAEYCRKPDSRVSGPWEFGTMLKKGSHKRKILELLEDPDNEIEEPQKYRR  124

Query  127  AMAKSAMDESRKLAEEYDFPHELRSWQKTLISCLEEEPDDRTIYWVYGPNGGEGKTQFGK  186
            AMA SAM+ SR++A    FPH L SWQ+T++   LEEEP+DRTI WVYGPNG EGK+QFGK
Sbjct  125  AMAFSAMEASREIASREGFPHSLYSWQETVLGLLEEEPNDRTIIWVYGPNGNEGKSQFGK  184

Query  187  HLGLKKGWTYLPGGELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYK  246
            HLGLKK + YLPGG+ +DM Y+  K  ++HVV+D PRC  ++++Y+F+E++KNRT+YSYK
Sbjct  185  HLGLKKDYLYLPGGKTQDMTYMLMKCPESHVVLDIPRCNSEYLNYQFMELIKNRTIYSYK  244

Query  247  YEPIGSIVSNKVHVVVLCNFMPEEEKISGDRLIIINC  283
            YEP+G+I+ NK+HVVVL N +P  EKIS DR+ +I C
Sbjct  245  YEPLGAIIKNKIHVVVLANILPNYEKISQDRIKLIYC  281
```

…

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Protein Blast Rep alphaDRC2012

Replication-associated protein of non-essential DNA C9 [**Faba bean necrotic yellows virus (isolate SV292-88)**]
Sequence ID: P0CK61.1 Length: 281 Number of Matches: 1

```
Identities   Positives    Gaps
181/277(65%)              227/277(81%)              0/277(0%)

Query  7    NWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKKKTRLNGAKRLIGGNPH  66
            NWVFTLNF GE P+LSF E  QYA WQHE+V+HDH+QGVIQLKKK ++N  K +IGGNPH
Sbjct  5    NWVFTLNFAGEVPVLSFDERVQYAVWQHERVNHDHIQGVIQLKKKAKMNTVKNIIGGNPH  64

Query  67   LEPMRGSITEAKAYCTKEQSRIAGPWEFGEMLLKGSNRRKLAELLDDPDNEINEPQKYRR  126
            LE M+GSI EA AY  KE+SR+AGPW +GE+L KGS++RK+ EL+ DP+NE+ EPQKYRR
Sbjct  65   LEKMKGSIEEASAYAQKEESRVAGPWSYGELLKKGSHKRKIMELIKDPENELEEPQKYRR  124

Query  127  AMAKSAMDESRKLAEEYDFPHELRSWQKTLISFLEEEPDDRTIYWVYGPNGGEGKTQFGK  186
            AMA SAMDESRKLAEE  FP+   SWQ+T++  LEEEP+DRTI WVYGPNG EGK+QFGK
Sbjct  125  AMAWSAMDESRKLAEEEGFPYMFYSWQETVLGLLEEEPNDRTIIWVYGPNGNEGKSQFGK  184

Query  187  HLGLKKGWTYLPGGELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYK  246
             LGLKK + YLPGG+ +DM Y+  K  K +VV+D PRC  ++++Y+F+E++KNRT+YSYK
Sbjct  185  FLGLKKDYLYLPGGKTQDMTYMLMKNPKANVVMDIPRCNSEYLNYQFMELIKNRTIYSYK  244

Query  247  YEPIGSIVSNKVHVVVLCNFLPEEEKISGDRLIIINC  283
            YEP+G I++NK+HV+VL N LP+ EKIS DR+ II C
Sbjct  245  YEPVGCIINNKIHVIVLANVLPDYEKISQDRIKIIYC  281
```

Satellite replication initiator protein [Sophora alopecuroides yellow stunt alphasatellite 3]
Sequence ID: ARI50297.1 Length: 281 Number of Matches: 1

```
Identities                Positives                 Gaps
183/277(66%)              222/277(80%)              0/277(0%)

Query  7    NWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKKKTRLNGAKRLIGGNPH  66
            NWVFT NF GE PILSF E  QYA WQHE+V HDHLQGVIQLKKK RLN  K +IGGNPH
Sbjct  5    NWVFTRNFAGEVPILSFDERVQYAVWQHERVTHDHLQGVIQLKKKARLNTVKAMIGGNPH  64

Query  67   LEPMRGSITEAKAYCTKEQSRIAGPWEFGEMLLKGSNRRKLAELLDDPDNEINEPQKYRR  126
            LE MR +I EA  YC K  SR++GPWEFG ML KGS++RK+ ELL+DPDNEI EPQKYRR
Sbjct  65   LEKMRATIEEAAEYCRKPDSRVSGPWEFGTMLKKGSHKRKILELLEDPDNEIEEPQKYRR  124

Query  127  AMAKSAMDESRKLAEEYDFPHELRSWQKTLISFLEEEPDDRTIYWVYGPNGGEGKTQFGK  186
            AMA SAM+ SR++A    FPH L SWQ+T++  LEEEP+DRTI WVYGPNG EGK+QFGK
Sbjct  125  AMAFSAMEASREIASREGFPHSLYSWQETVLGLLEEEPNDRTIIWVYGPNGNEGKSQFGK  184

Query  187  HLGLKKGWTYLPGGELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYK  246
            HLGLKK + YLPGG+ +DM Y+  K  ++HVV+D PRC  ++++Y+F+E++KNRT+YSYK
Sbjct  185  HLGLKKDYLYLPGGKTQDMTYMLMKCPESHVVLDIPRCNSEYLNYQFMELIKNRTIYSYK  244

Query  247  YEPIGSIVSNKVHVVVLCNFLPEEEKISGDRLIIINC  283
            YEP+G+I+ NK+HVVVL N LP  EKIS DR+ +I C
Sbjct  245  YEPLGAIIKNKIHVVVLANILPNYEKISQDRIKLIYC  281
```

Replication-associated protein [**Faba bean necrotic yellows virus associated alphasatellite 2]**
Sequence ID: ATU31571.1 Length: 281 Number of Matches: 1

```
Identities                Positives                 Gaps
180/277(65%)              228/277(82%)              0/277(0%)

Query  7    NWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKKKTRLNGAKRLIGGNPH  66
            NWVFTLNF GE P+LSF E  QYA WQHE+V+HDH+QGVIQLKKK ++N  K +IGGNPH
Sbjct  5    NWVFTLNFAGEVPVLSFDERVQYAVWQHERVNHDHIQGVIQLKKKAKMNTVKNIIGGNPH  64

Query  67   LEPMRGSITEAKAYCTKEQSRIAGPWEFGEMLLKGSNRRKLAELLDDPDNEINEPQKYRR  126
            LE M+GSI EA AY  KE+SR+AGPW +GE+L KGS++RK+ EL+ DP+NE+ EPQKYRR
Sbjct  65   LEKMKGSIEEASAYAQKEESRVAGPWSYGELLKKGSHKRKIMELIKDPENELEEPQKYRR  124

Query  127  AMAKSAMDESRKLAEEYDFPHELRSWQKTLISFLEEEPDDRTIYWVYGPNGGEGKTQFGK  186
            AMA SAMDESRKLAEE  FP+ L SWQ+T++  L+EEP+DRTI WVYGPNG EGK+QFGK
```

```
Sbjct  125  AMAWSAMDESRKLAEEEGFPYSLYSWQETVLGLLDEEPNDRTIIWVYGPNGNEGKSQFGK  184

Query  187  HLGLKKGWTYLPGGELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYK  246
             LGLKK + YLPGG+ +DM Y+  K  K +VV+D PRC  ++++Y+F+E++KNRT++SYK
Sbjct  185  FLGLKKDYLYLPGGKTQDMTYMLMKNPKANVVMDIPRCNSEYLNYQFMELIKNRTIFSYK  244

Query  247  YEPIGSIVSNKVHVVVLCNFLPEEEKISGDRLIIINC  283
            YEP+G I++NK+HV+VL N LP+ EKIS DR+ II C
Sbjct  245  YEPVGCIINNKIHVIVLANVLPDYEKISQDRIKIIYC  281
```

Rep protein [Faba bean necrotic yellows C9 alphasatellite]
Sequence ID: NP_619574.1 Length: 281 Number of Matches: 1

```
Identities                Positives                 Gaps
180/277(65%)              227/277(81%)              0/277(0%)

Query  7    NWVFTLNFTGETPILSFGEETQYACWQHEKVDHDHLQGVIQLKKKTRLNGAKRLIGGNPH  66
            NWVFTLNF GE P+LSF E  QYA WQHE+V+HDH+QGVIQLKKK ++N  K +IGGNPH
Sbjct  5    NWVFTLNFAGEVPVLSFDERVQYAVWQHERVNHDHIQGVIQLKKKAKMNTVKNIIGGNPH  64

Query  67   LEPMRGSITEAKAYCTKEQSRIAGPWEFGEMLLKGSNRRKLAELLDDPDNEINEPQKYRR  126
            LE M+GSI EA AY  KE+SR+AGPW +GE+L KGS++RK+ EL+ DP+NE+ EPQKYRR
Sbjct  65   LEKMKGSIEEASAYAQKEESRVAGPWSYGELLKKGSHKRKIMELIKDPENELEEPQKYRR  124

Query  127  AMAKSAMDESRKLAEEYDFPHELRSWQKTLISFLEEEPDDRTIYWVYGPNGGEGKTQFGK  186
            AMA SAMDESRKLAEE  FP+ L SWQ+T++  LEEEP+DR I WVYGPNG EGK+QFGK
Sbjct  125  AMAWSAMDESRKLAEEGGFPYTLYSWQETVLGLLEEEPNDRIIIWVYGPNGNEGKSQFGK  184

Query  187  HLGLKKGWTYLPGGELKDMMYLYSKELKNHVVIDFPRCTKDFVSYKFLEMVKNRTVYSYK  246
             LGLKK + YLPGG+ +DM Y+  K  K +VV+D PRC  ++++Y+F+E++KNRT++SYK
Sbjct  185  FLGLKKDYLYLPGGKTQDMTYMLMKNPKANVVMDIPRCNSEYLNYQFMELIKNRTIFSYK  244

Query  247  YEPIGSIVSNKVHVVVLCNFLPEEEKISGDRLIIINC  283
            YEP+G I++NK+HV+VL N LP+ EKIS DR+ II C
Sbjct  245  YEPVGCIINNKIHVIVLANVLPDYEKISQDRIKIIYC  281
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BlastN analysis of aphaDRC2016 alpfasatellite nucleotide sequence

Faba bean necrotic yellows virus associated alphasatellite 2 isolate TN-Tuf9_2-2015, complete sequence
Sequence ID: MF510475.1 Length: 1005 Number of Matches: 1
Range: 136 to 898

```
#1 Score                  Expect       Identities                Gaps         Strand
267 bits(295)             4e-66        532/774(69%)              22/774(2%)   Plus/Plus

Query  134  TGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGATCCAATTGAAGAAGAAG  193
            ||||||||||| |  ||  ||||||||||  | ||||||||||| ||||||||||||||||
Sbjct  136  TGGCAACACGAAAGAGTAAATCACGACCATATTCAGGGAGTGATTCAATTGAAGAAGAAG  195

Query  194  ACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACACCTCGAACCCATGCGA  253
             |     | |||  || ||||    | ||||| |||||||| || || ||    |||
Sbjct  196  GCAAAGATGAACACAGTGAAGAACATAATCGGAGGAAATCCTCATCTGGAGAAGATGAAG  255

Query  254  GGTTCGATTACAGAGGCGAAAGCCTACTGTAC-GAAAGAACAATCACGGATCGCAGGTCC  312
            ||||||||   ||| ||    || || ||  | ||||||| ||||| |  |||| || ||
Sbjct  256  GGTTCGATAGAAGAAGCTTCTGCGTA-TGCCCAGAAAGAAGAATCAAGAGTCGCCGGACC  314

Query  313  GTGGGAATTCGGAGAAATTCTGCTGAAGGG--GTCGAACAGACGGAAGCTCGCAGAGCTT  370
             |||   | ||| ||| | |||  ||| ||  |||  ||| ||||||| |    ||| |
Sbjct  315  CTGGAGTTACGGTGAATTACTGAAGAAAGGTAGTC--ACAAACGGAAGATTATGGAGTTA  372

Query  371  CTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGACGAGCGATGGCTAAG  430
             |  | ||||| || |||||| |  | ||||| || ||||| ||| |||||||||||  |
Sbjct  373  ATTAAAGATCCGGAGAACGAATTGGAAGAACCCCAGAAATACAGAAGAGCGATGGCTTGG  432

Query  431  TCCGCCATGGATGAATCTCGGAAGCTTGCTGAAG-AGTATGATTTCCCTCACGAACTACG  489
            ||||||||||| |||||||||||||||||||||| || | | ||||||| |   |||
Sbjct  433  TCCGCCATGGACGAATCTCGGAAGCTTGCTGAAGAAGAAGGGTTTCCCT-ATTCACTTTA  491

Query  490  TTCGTGGCAAAAAACCCTAATTTCATGCC---TCGAAGAGGAACCGGATGATCGTACTAT  546
                ||||||| ||||   | | |   |||   | || || || ||  |||| ||||||||
Sbjct  492  CAGCTGGCAAGAAAC---AGTGTTGGGCCTATTAGATGAAGAGCCCAATGACCGTACTAT  548

Query  547  TTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGTAAACACCTAGG  606
            |   |||||||| || || |||||    ||||| ||| | ||||| ||||||  | | ||
Sbjct  549  TATTTGGGTCTACGGCCCAAATGGTAATGAAGGAAAATCACAGTTTGGTAAATTCTTGGG  608

Query  607  ATTaaaaaaaGGATGGACC--TATTTACCCGGAGGGGAACTGAAAGACATGATGTATCTA  664
            |||||||||| |||  |||  |||||||| |||||  ||    |||| ||||  ||| |
Sbjct  609  ATTAAAAAAA-GAT-TACCTTTATTTACCTGGAGGTAAAACCCAAGATATGACATATATG  666

Query  665  TACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGGTGTACGAAAGACTTT  724
            |  |  ||  |   |||     |||| || || ||| | ||  ||||||    ||| | |
Sbjct  667  TTAATGAAAAATCCAAAGGCAAATGTTGTGATGGATATTCCTCGGTGTAATTCAGAATAT  726

Query  725  GTAAGTTATAAATTCCTAGAGATGGTAAAAAACAGAACTGTATATAGTTATAAATACGAA  784
             ||| |||  ||||  | ||  |  | ||||| |||||  ||| |||||||||||| |||
Sbjct  727  TTAAATTACCAATTTATGGAATTAATTAAAAATAGAACAATATTTAGTTATAAATATGAA  786
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Query  785  CCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTCTTATGTAATTTTATGCCG  844
            ||  | |||| |||  | | ||| ||| | |||||| | || |||  |||| |  ||||
Sbjct  787  CCAGTTGGTTGTATTATAAATAATAAAATACATGTAATTGTATTAGCTAATGTATTGCCT  846

Query  845  GAAGAAGAAAAAAT--CTCCGGAGACAGATTAATAATAATAAATTGCTAAACAC  896
            ||  | ||||||||   || |  |||||| ||| ||||||  |||| |||| ||
Sbjct  847  GATTATGAAAAAATTAGTCAG--GACAGAATAAAAATAATTTATTGTTAAATAC  898
```

Faba bean necrotic yellows virus associated alphasatellite 2 isolate TN-Tuf10_2-2015, complete sequence
Sequence ID: MF510474.1 Length: 1005 Number of Matches: 1
Range 1: 136 to 898

#1 Score	Expect	Identities	Gaps	Strand
267 bits(295)	4e-66	532/774(69%)	22/774(2%)	Plus/Plus

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Query  134  TGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGATCCAATTGAAGAAGAAG  193
            ||||||||||| |  ||  ||||||||||  | ||||||||||| |||||||||||||||
Sbjct  136  TGGCAACACGAAAGAGTAAATCACGACCATATTCAGGGAGTGATTCAATTGAAGAAGAAG  195

Query  194  ACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACACCTCGAACCCATGCGA  253
             |     | |||  || ||||    | ||||| |||||||| || || ||    |||
Sbjct  196  GCAAAGATGAACACAGTGAAGAACATAATCGGAGGAAATCCTCATCTGGAGAAGATGAAG  255

Query  254  GGTTCGATTACAGAGGCGAAAGCCTACTGTAC-GAAAGAACAATCACGGATCGCAGGTCC  312
            ||||||||   ||| ||    || || ||  | ||||||| ||||| |  |||| || ||
Sbjct  256  GGTTCGATAGAAGAAGCTTCTGCGTA-TGCCCAGAAAGAAGAATCAAGAGTCGCCGGACC  314

Query  313  GTGGGAATTCGGAGAAATTCTGCTGAAGGG--GTCGAACAGACGGAAGCTCGCAGAGCTT  370
             |||   | ||| ||| | |||  ||| ||  |||  ||| ||||||| |    ||| |
Sbjct  315  CTGGAGTTACGGTGAATTACTGAAGAAAGGTAGTC--ACAAACGGAAGATTATGGAGTTA  372

Query  371  CTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGACGAGCGATGGCTAAG  430
             |  | ||||| || |||||| |  | ||||| || ||||| ||| |||||||||||  |
Sbjct  373  ATTAAAGATCCGGAGAACGAATTGGAAGAACCCCAGAAATACAGAAGAGCGATGGCTTGG  432

Query  431  TCCGCCATGGATGAATCTCGGAAGCTTGCTGAAG-AGTATGATTTCCCTCACGAACTACG  489
            ||||||||||| |||||||||||||||||||||| || | | ||||||| |   |||
Sbjct  433  TCCGCCATGGACGAATCTCGGAAGCTTGCTGAAGAAGAAGGGTTTCCCT-ATTCACTTTA  491

Query  490  TTCGTGGCAAAAAACCCTAATTTCATGCC---TCGAAGAGGAACCGGATGATCGTACTAT  546
                ||||||||||   | | |   |||   | || || || ||  |||| ||||||||
Sbjct  492  CAGCTGGCAAGAAAC---AGTGTTGGGCCTATTAGATGAAGAGCCCAATGACCGTACTAT  548

Query  547  TTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGTAAACACCTAGG  606
            |   |||||||| || || |||||    ||||| ||| | ||||| ||||||  | | ||
Sbjct  549  TATTTGGGTCTACGGCCCAAATGGTAATGAAGGAAAATCACAGTTTGGTAAATTCTTGGG  608

Query  607  ATTaaaaaaaGGATGGACC--TATTTACCCGGAGGGGAACTGAAAGACATGATGTATCTA  664
            |||||||||| |||  |||  |||||||| |||||  ||    |||| ||||  ||| |
Sbjct  609  ATTAAAAAAA-GAT-TACCTTTATTTACCTGGAGGTAAAACCCAAGATATGACATATATG  666

Query  665  TACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGGTGTACGAAAGACTTT  724
            |  |  ||  |   |||     |||| || || ||| | ||  ||||||    ||| | |
Sbjct  667  TTAATGAAAAATCCAAAGGCAAATGTTGTGATGGATATTCCTCGGTGTAATTCAGAATAT  726

Query  725  GTAAGTTATAAATTCCTAGAGATGGTAAAAAACAGAACTGTATATAGTTATAAATACGAA  784
             ||| |||  ||||  | ||  |  | ||||| |||||  ||| |||||||||||| |||
Sbjct  727  TTAAATTACCAATTTATGGAATTAATTAAAAATAGAACAATATTTAGTTATAAATATGAA  786

Query  785  CCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTCTTATGTAATTTTATGCCG  844
            ||  | |||| |||  | | ||| ||| | |||||| | || |||  |||| |  ||||
Sbjct  787  CCAGTTGGTTGTATTATAAATAATAAAATACATGTAATTGTATTAGCTAATGTATTGCCT  846

Query  845  GAAGAAGAAAAAAT--CTCCGGAGACAGATTAATAATAATAAATTGCTAAACAC  896
            ||  | ||||||||   || |  |||||| ||| ||||||  |||| |||| ||
Sbjct  847  GATTATGAAAAAATTAGTCAG--GACAGAATAAAAATAATTTATTGTTAAATAC  898
```

Faba bean necrotic yellows C9 alphasatellite C9-Eg gene, isolate Egyptian EV1-93
Sequence ID: AJ132187.1 Length: 1007 Number of Matches: 1
Range 1: 85 to 918

#1 Score	Expect	Identities	Gaps	Strand
245 bits(271)	1e-59	571/846(67%)	24/846(2%)	Plus/Plus

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Query  59   AATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATCCTTTCCTTTGGAGAGGAA  118
            || ||||| |||||  | || ||| | || ||   |||| | || || || |  |||  |
Sbjct  85   AACTGGGTTTTCACGTTGAACTTCGCCGGCGAAGTTCCTGTTCTCTCGTTCGACGAGAGA  144

Query  119  ACACAATATGCGTGTTGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGATC  178
               ||||| ||    |||||||||| |  ||  ||||||||||  | |||||||||||
Sbjct  145  GTTCAATACGCCGTCTGGCAACACGAAAGAGTAAATCACGACCATATTCAGGGAGTGATT  204

Query  179  CAATTGAAGAAGAAGACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACAC  238
            ||||| ||||||||| |     | |||  || ||||    | || || |||||||| ||
Sbjct  205  CAATTAAAGAAGAAGGCAAAGATGAACACAGTGAAGAACATCATTGGTGGAAATCCTCAT  264

Query  239  CTCGAACCCATGCGAGGTTCGATTACAGAGGCGAAAGCCTACTGTAC-GAAAGAACAATC  297
            || ||    |||   ||||||||   ||| ||    || || ||  | ||||||| ||||
Sbjct  265  CTGGAGAAGATGAAGGGTTCGATAGAAGAAGCTTCTGCGTA-TGCCCAGAAAGAAGAATC  323

Query  298  ACGGATCGCAGGTCCGTGGGAATTCGGAGAAATTCTGCTGAAGGG--GTCGAACAGACGG  355
            | |  |||| || || |||   | ||| ||| |  ||  ||| ||  |||  | | ||||
Sbjct  324  AAGAGTCGCCGGACCCTGGAGTTACGGTGAATTATTGAAGAAAGGTAGTC--ATAAACGG  381

Query  356  AAGCTCGCAGAGCTTCTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGA  415
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            ||| |    ||| |  |  | ||||| || |||||| |  | ||||| || ||||| |||
Sbjct  382  AAGATTATGGAGTTAATTAAAGATCCGGAGAACGAATTGGAAGAACCCCAGAAATACAGA  441

Query  416  CGAGCGATGGCTAAGTCCGCCATGGATGAATCTCGGAAGCTTGCTGAAG-AGTATGATTT  474
             |||||||||||  ||||||||||||| ||||||||||||||||||||||| || | | |||
Sbjct  442  AGAGCGATGGCTTGGTCCGCCATGGACGAATCTCGGAAGCTTGCTGAAGAAGGAGGCTTT  501

Query  475  CCCT-CACGAACTACGTTCGTGGCAAAAAACCCTAATTTCATGCC---TCGAAGAGGAAC  530
            ||||  |||   |||     |||||| ||||   | | |   |||   | ||||| || |
Sbjct  502  CCCTATACGCTTTAC--AGCTGGCAAGAAAC---AGTGTTGGGCCTATTAGAAGAAGAGC  556

Query  531  CGGATGATCGTACTATTTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGT  590
            |  |||| |||| ||||   |||||||| || || |||||    ||||| ||| | ||||
Sbjct  557  CCAATGACCGTATTATTATTTGGGTCTACGGCCCAAATGGTAACGAAGGAAAATCACAGT  616

Query  591  TCGGTAAACACCTAGGATTaaaaaaaGGATGGACC--TATTTACCCGGAGGGGAACTGAA  648
            | ||||||  ||| ||||||||||||| |||  |||  |||||||| |||||  ||    |
Sbjct  617  TTGGTAAATTCCTGGGATTAAAAAAA-GAT-TACCTTTATTTACCTGGAGGTAAAACCCA  674

Query  649  AGACATGATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAG  708
            ||| ||||  ||| | |  |  ||  |   |||     |||| || || ||| | ||  |
Sbjct  675  AGATATGACATATATGTTAATGAAAAATCCAAAGGCAAATGTTGTGATGGATATTCCTCG  734

Query  709  GTGTACGAAAGACTTTGTAAGTTATAAATTCCTAGAGATGGTAAAAAACAGAACTGTATA  768
             ||||     || | | ||| |||| ||||  | ||  |  | ||||| |||||  |||
Sbjct  735  TTGTAATTCTGAATATTTAAATTATCAATTTATGGAATTAATTAAAAATAGAACCATATT  794

Query  769  TAGTTATAAATACGAACCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTCTT  828
            ||||||||||| |||||  | || | |||  | | ||| ||| | |||||| | || ||
Sbjct  795  TAGTTATAAATATGAACCAGTTGGATGTATTATAAATAATAAAATACATGTAATTGTATT  854

Query  829  ATGTAATTTTATGCCGGAAGAAGAAAAAAT--CTCCGGAGACAGATTAATAATAATAAAT  886
            |  |||| |  |||| ||  | ||||||||   || |  |||||| | | ||||||  ||
Sbjct  855  AGCTAATGTATTGCCTGATTATGAAAAAATTAGTCAG--GACAGAATTAAAATAATTTAT  912

Query  887  TGCTAA  892
            || |||
Sbjct  913  TGTTAA  918


Faba bean necrotic yellows C9 alphasatellite C9 gene
Sequence ID: AJ005966.1  Length: 1004 Number of Matches: 1
Range 1: 85 to 918
#1 Score                 Expect       Identities               Gaps         Strand
236 bits(261)            6e-57        570/846(67%)             24/846(2%)   Plus/Plus

Query  59   AATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATCCTTTCCTTTGGAGAGGAA  118
            || ||||| |||||  | || ||| | || ||   |||| | || || || |  |||  |
Sbjct  85   AACTGGGTTTTCACGTTGAACTTCGCCGGCGAAGTTCCTGTTCTCTCGTTCGACGAGAGA  144

Query  119  ACACAATATGCGTGTTGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGATC  178
               ||||| ||    |||||||||| |  ||  ||||||||||  | |||||||||||
Sbjct  145  GTTCAATACGCCGTCTGGCAACACGAAAGAGTAAATCACGACCATATTCAGGGAGTGATT  204

Query  179  CAATTGAAGAAGAAGACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACAC  238
            ||||| ||||||||| |     | |||  || ||||    | ||||| |||||||| ||
Sbjct  205  CAATTAAAGAAGAAGGCAAAGATGAACACAGTGAAGAATATCATCGGTGGAAATCCTCAT  264

Query  239  CTCGAACCCATGCGAGGTTCGATTACAGAGGCGAAAGCCTACTGTAC-GAAAGAACAATC  297
            || ||    |||   ||||||||   ||| ||    || || ||  | ||||||| ||||
Sbjct  265  CTGGAGAAGATGAAGGGTTCGATAGAAGAAGCTTCTGCGTA-TGCCCAGAAAGAAGAATC  323

Query  298  ACGGATCGCAGGTCCGTGGGAATTCGGAGAAATTCTGCTGAAGGG--GTCGAACAGACGG  355
            | |  |||| || || |||   | ||| ||| |  ||  ||| ||  |||  | | |||
Sbjct  324  AAGAGTCGCCGGACCCTGGAGTTACGGTGAATTATTGAAGAAAGGTAGTC--ATAAACGA  381

Query  356  AAGCTCGCAGAGCTTCTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGA  415
            ||| |    ||| |  |  | ||||| || |||||| |  | ||||| || ||||| |||
Sbjct  382  AAGATTATGGAGTTAATTAAAGATCCGGAGAACGAATTGGAAGAACCCCAGAAATACAGA  441

Query  416  CGAGCGATGGCTAAGTCCGCCATGGATGAATCTCGGAAGCTTGCTGAAG-AGTATGATTT  474
             |||| ||||||  ||||||||||| |||||||||||||||| |||| || | | |||
Sbjct  442  AGAGCTATGGCTTGGTCCGCCATGGACGAATCTCGGAAGCTTGCGGAAGAAGAAGGCTTT  501

Query  475  CCCT-CACGAACTACGTTCGTGGCAAAAAACCCTAATTTCATGCC---TCGAAGAGGAAC  530
            ||||  | |   |||     |||||| ||||   | | |   |||   | ||||| || |
Sbjct  502  CCCTATATGTTTTAC--AGCTGGCAAGAAAC---AGTGTTGGGCCTATTAGAAGAAGAGC  556

Query  531  CGGATGATCGTACTATTTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGT  590
            |  |||| |||||||||   |||||||| || || |||||    ||||| ||| | ||||
Sbjct  557  CCAATGACCGTACTATTATTTGGGTCTACGGCCCAAATGGTAATGAAGGAAAATCACAGT  616

Query  591  TCGGTAAACACCTAGGATTaaaaaaaGGATGGACC--TATTTACCCGGAGGGGAACTGAA  648
            | ||||||  ||| ||||||||||| |||  |||  |||||||| |||||  ||    |
Sbjct  617  TTGGTAAATTCCTGGGATTAAAAAAA-GAT-TACCTTTATTTACCTGGAGGTAAAACCCA  674

Query  649  AGACATGATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAG  708
            ||| ||||  ||| | |  |  ||  |   |||     |||| || || ||| | ||  |
Sbjct  675  AGATATGACATATATGTTAATGAAAAATCCAAAGGCAAATGTTGTGATGGATATTCCTCG  734

Query  709  GTGTACGAAAGACTTTGTAAGTTATAAATTCCTAGAGATGGTAAAAAACAGAACTGTATA  768
             ||||     || | | ||| |||  ||||  | ||  |  | ||||| |||||  ||||
Sbjct  735  TTGTAATTCTGAATATTTAAATTACCAATTTATGGAATTAATTAAAAATAGAACCATATA  794

Query  769  TAGTTATAAATACGAACCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTCTT  828
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            |||||||||||| |||||  | || | |||  | | ||| ||| | |||||| | || ||
Sbjct  795  TAGTTATAAATATGAACCAGTTGGATGTATTATAAATAATAAAATACATGTAATTGTATT  854

Query  829  ATGTAATTTTATGCCGGAAGAAGAAAAAAT--CTCCGGAGACAGATTAATAATAATAAAT  886
            |  |||| |  |||| ||  | ||||||||   || ||| | | ||||| ||||||  ||
Sbjct  855  AGCTAATGTATTGCCTGATTATGAAAAAATTAGTCAGGATAGA-ATTAA-AATAATTTAT  912

Query  887  TGCTAA  892
            || |||
Sbjct  913  TGTTAA  918
```

Milk vetch chlorotic dwarf virus alphasatellite 1 isolate G53, complete sequence
Sequence ID: MN273340.1 Length: 999 Number of Matches: 1
Range 1: 62 to 885

#1 Score	Expect	Identities	Gaps	Strand
231 bits(255)	3e-55	550/827(67%)	6/827(0%)	Plus/Plus

```
Query  59   AATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATC-CTTTCCTTTGGAGAGGA  117
            |||||||| || || || |||||||||||  |   ||||  || || || || |  |||
Sbjct  62   AATTGGGTTTTTACGCTGAATTTCACAGGCGCT-CTCCCTTCTCTCTCGTTCGACGAGAG  120

Query  118  AACACAATATGCGTGTTGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGAT  177
            |   ||||||||   ||||||||| ||||  ||  | || ||||| || |||||||| ||
Sbjct  121  AGTTCAATATGCAGCTTGGCAACATGAGAGAGTTAACCATGACCATCTCCAGGGAGTAAT  180

Query  178  CCAATTGAAGAAGAAGACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACA  237
             |||||||||||  ||  | ||  | |||   |  |||    |||| |||||||||||  ||
Sbjct  181  TCAATTGAAGAATAAAGCTCGCCTTAACACTGTTAAGGCTATGATTGGGGGAAATCCCCA  240

Query  238  CCTCGAACCCATGCGAGGTTCGATTACAGAGGCGAAAGCCTACTGTACGAAAGAACAATC  297
             || ||    ||| ||||    |||  ||| ||   ||  |||   | ||||||  | ||
Sbjct  241  TCTGGAGAAGATGAGAGGGAAAATTGAAGAAGCATCAGAATACGCCATGAAAGAGGAGTC  300

Query  298  ACGGATCGCAGGTCCGTGGGAATTCGGAGAAATTCTGCTGAAGGG--GTCGAACAGACGG  355
              |  | ||||| || |||   |  || || ||  ||  ||| ||  |||  ||| |||
Sbjct  301  GAGAGTTGCAGGACCTTGGATTTATGGCGAGATGTTGAAGAAAGGAAGTC--ACAAACGT  358

Query  356  AAGCTCGCAGAGCTTCTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGA  415
            ||| |    ||| |  | || ||||| || |||||| |  | ||||| |||||||  |||
Sbjct  359  AAGATTATGGAGTTAATTGAAGATCCTGAGAACGAATTGGAAGAACCCCAAAAATTCAGA  418

Query  416  CGAGCGATGGCTAAGTCCGCCATGGATGAATCTCGGAAGCTTGCTGAAGAGTATGATTTC  475
             |||||||||||  ||||||||||| |||||||||||||||||  |||| | |  ||
Sbjct  419  AGAGCGATGGCTTGGTCCGCCATGGAAGAATCTCGGAAGCTTGCTTCAGAGGAAGGGTTT  478

Query  476  CCTCACGAACTACGTTCGTGGCAAAAAACCCTAATTTCATGCCTCGAAGAGGAACCGGAT  535
            |||||   |||       |||||| ||| |    | |||    | ||| | || || |||
Sbjct  479  CCTCATACACTTTACAGCTGGCAAGAAAACGCGTTGTCACTGTTGGAAAACGACCCTGAT  538

Query  536  GATCGTACTATTTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGT  595
            |||||||| ||   |||||| ||||| ||  | ||    ||||| ||| | ||||| |||
Sbjct  539  GATCGTACAATCATCTGGGTGTATGGGCCCCACGGTAATGAAGGAAAATCACAGTTTGGT  598

Query  596  AAACACCTAGGATTaaaaaaaGGATGGACCTATTTACCCGGAGGGGAACTGAAAGACATG  655
            |||  ||| || |||||||||  |    ||||||||| || ||  ||    |||| |||
Sbjct  599  AAATTCCTGGGGTTAAAAAAAGATTACCTCTATTTACCAGGGGGTAAAACACAAGATATG  658

Query  656  ATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGGTGTACG  715
            | |||  |    |  ||| |   ||||    |||| || |||||| | ||  | ||||
Sbjct  659  ACGTACATGCTGATGAAGAACCCAAAAGCTAATGTTGTAATTGATATTCCACGCTGTAAT  718

Query  716  AAAGACTTTGTAAGTTATAAATTCCTAGAGATGGTAAAAAACAGAACTGTATATAGTTAT  775
              ||| | | | | |||| ||||  | ||  |  ||||||| |||||  | | |||||||
Sbjct  719  TCAGAATATCTGAATTATCAATTTATGGAATTAATAAAAAATAGAACAATTTTTAGTTAT  778

Query  776  AAATACGAACCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTCTTATGTAAT  835
            ||||| || ||  | |||| ||| || | ||| ||| | |||||| | || ||    |||
Sbjct  779  AAATATGAGCCAGTTGGTTGTATTGTAAATAATAAAATACATGTAATTGTATTGGCCAAT  838

Query  836  TTTATGCCGGAAGAAGAAAAAATCTCCGGAGACAGATTAATAATAAT  882
             |  |||| ||  | ||||||||      ||||||| ||| ||| ||
Sbjct  839  GTATTGCCAGATTATGAAAAAATAAGTCAAGACAGAATAAAAATGAT  885
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BlastN analysis of aphaDRC2012 alpfasatellite nucleotide sequence

Faba bean necrotic yellows virus associated alphasatellite 2 isolate TN-Tuf9_2-2015, complete sequence
Sequence ID: MF510475.1 Length: 1005 Number of Matches: 1
Range 1: 136 to 898

#1 Score	Expect	Identities	Gaps	Strand
274 bits(303)	3e-68	531/771(69%)	16/771(2%)	Plus/Plus

```
Query  123  TGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGATCCAATTGAAGAAGAAG  182
            |||||||||||  |  ||  |||||||||  | ||||||||||| |||||||||||||||
Sbjct  136  TGGCAACACGAAAGAGTAAATCACGACCATATTCAGGGAGTGATTCAATTGAAGAAGAAG  195

Query  183  ACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACACCTCGAACCCATGCGA  242
             |     | |||  || ||||    | ||||| |||||||| || || ||    |||
Sbjct  196  GCAAAGATGAACACAGTGAAGAACATAATCGGAGGAAATCCTCATCTGGAGAAGATGAAG  255

Query  243  GGTTCAATTACAGAGGCGAAAGCCTACTGTAC-GAAAGAACAATCACGGATCGCAGGTCC  301
            ||||| ||   ||| ||    || || ||  | ||||||| ||||| |  |||| || ||
Sbjct  256  GGTTCGATAGAAGAAGCTTCTGCGTA-TGCCCAGAAAGAAGAATCAAGAGTCGCCGGACC  314
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Query  302  GTGGGAATTCGGAGAAATGCTGCTGAAGGG--GTCGAACAGACGGAAGCTCGCAGAGCTT  359
            |||   | ||| ||| | |||  ||| ||  |||  ||| ||||||| |    ||| |
Sbjct  315  CTGGAGTTACGGTGAATTACTGAAGAAAGGTAGTC--ACAAACGGAAGATTATGGAGTTA  372

Query  360  CTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGACGAGCGATGGCTAAG  419
            |  | ||||| || |||||| |  | ||||| || ||||| ||| |||||||||||  |
Sbjct  373  ATTAAAGATCCGGAGAACGAATTGGAAGAACCCCAGAAATACAGAAGAGCGATGGCTTGG  432

Query  420  TCCGCCATGGATGAATCTCGGAAGCTTGCTGAAG-AGTATGATTTCCCTCACGAACTACG  478
            ||||||||||| |||||||||||||||||||||| || | | ||||||| |   |||
Sbjct  433  TCCGCCATGGACGAATCTCGGAAGCTTGCTGAAGAAGAAGGGTTTCCCT-ATTCACTTTA  491

Query  479  CTCGTGGCAAAAAACCCTAATCTCATTCCTCGAAGAGGAACCGGATGATCGTACTATTTA  538
            |   |||||| ||||  |  |      |  | || || || ||  |||| |||||||||
Sbjct  492  CAGCTGGCAAGAAACAGTGTTGGGCCTATTAGATGAAGAGCCCAATGACCGTACTATTAT  551

Query  539  CTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGTAAACACCTGGGATT  598
            ||||||||  || || |||||    ||||| ||| | ||||| ||||||  | |||||||
Sbjct  552  TTGGGTCTACGGCCCAAATGGTAATGAAGGAAAATCACAGTTTGGTAAATTCTTGGGATT  611

Query  599  aaaaaaaGGATGGACC--TATTTACCCGGAGGGGAACTGAAAGACATGATGTATCTATAC  656
            ||||||| |||  |||  |||||||| |||||  ||    |||| ||||  ||| | |
Sbjct  612  AAAAAAA-GAT-TACCTTTATTTACCTGGAGGTAAAACCCAAGATATGACATATATGTTA  669

Query  657  AGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGATGTACGAAAGACTTTGTA  716
            |  ||  |   |||     |||| || || ||| | ||  | ||||    ||| | | ||
Sbjct  670  ATGAAAAATCCAAAGGCAAATGTTGTGATGGATATTCCTCGGTGTAATTCAGAATATTTA  729

Query  717  AGTTATAAATTCCTAGAGATGGTAAAAAATAGAACTGTATATAGTTATAAATACGAACCG  776
            | |||  ||||  | ||  |  | |||||||||||  ||| |||||||||||| |||||
Sbjct  730  AATTACCAATTTATGGAATTAATTAAAAATAGAACAATATTTAGTTATAAATATGAACCA  789

Query  777  ATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTATTATGTAATTTCCTGCCGGAA  836
             | |||| |||  | | ||| ||| | |||||| | ||||||  |||| |  |||| ||
Sbjct  790  GTTGGTTGTATTATAAATAATAAAATACATGTAATTGTATTAGCTAATGTATTGCCTGAT  849

Query  837  GAAGAAAAAAT--CTCCGGAGACAGATTAATAATAATAAATTGCTAAACAC  885
             | ||||||||   || |  |||||| ||| ||||||  |||| |||| ||
Sbjct  850  TATGAAAAAATTAGTCAG--GACAGAATAAAAATAATTTATTGTTAAATAC  898
```

Faba bean necrotic yellows virus associated alphasatellite 2 isolate TN-Tuf10_2-2015, complete sequence
Sequence ID: MF510474.1 Length: 1005 Number of Matches: 1
Range 1: 136 to 898

#1 Score	Expect	Identities	Gaps	Strand
274 bits(303)	3e-68	531/771(69%)	16/771(2%)	Plus/Plus

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Query  123  TGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGATCCAATTGAAGAAGAAG  182
            |||||||||||  |  ||  |||||||||||  | ||||||||||| |||||||||||||||
Sbjct  136  TGGCAACACGAAAGAGTAAATCACGACCATATTCAGGGAGTGATTCAATTGAAGAAGAAG  195

Query  183  ACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACACCTCGAACCCATGCGA  242
            |     | |||  || ||||    | ||||| |||||||| || || ||    |||
Sbjct  196  GCAAAGATGAACACAGTGAAGAACATAATCGGAGGAAATCCTCATCTGGAGAAGATGAAG  255

Query  243  GGTTCAATTACAGAGGCGAAAGCCTACTGTAC-GAAAGAACAATCACGGATCGCAGGTCC  301
            ||||| ||   ||| ||    || || ||  | ||||||| ||||| |  |||| || ||
Sbjct  256  GGTTCGATAGAAGAAGCTTCTGCGTA-TGCCCAGAAAGAAGAATCAAGAGTCGCCGGACC  314

Query  302  GTGGGAATTCGGAGAAATGCTGCTGAAGGG--GTCGAACAGACGGAAGCTCGCAGAGCTT  359
            |||   | ||| ||| | |||  ||| ||  |||  ||| ||||||| |    ||| |
Sbjct  315  CTGGAGTTACGGTGAATTACTGAAGAAAGGTAGTC--ACAAACGGAAGATTATGGAGTTA  372

Query  360  CTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGACGAGCGATGGCTAAG  419
            |  | ||||| || |||||| |  | ||||| || ||||| ||| |||||||||||  |
Sbjct  373  ATTAAAGATCCGGAGAACGAATTGGAAGAACCCCAGAAATACAGAAGAGCGATGGCTTGG  432

Query  420  TCCGCCATGGATGAATCTCGGAAGCTTGCTGAAG-AGTATGATTTCCCTCACGAACTACG  478
            ||||||||||| |||||||||||||||||||||| || | | ||||||| |   |||
Sbjct  433  TCCGCCATGGACGAATCTCGGAAGCTTGCTGAAGAAGAAGGGTTTCCCT-ATTCACTTTA  491

Query  479  CTCGTGGCAAAAAACCCTAATCTCATTCCTCGAAGAGGAACCGGATGATCGTACTATTTA  538
            |   |||||| ||||  |  |      |  | || || || ||  |||| |||||||||
Sbjct  492  CAGCTGGCAAGAAACAGTGTTGGGCCTATTAGATGAAGAGCCCAATGACCGTACTATTAT  551

Query  539  CTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGTAAACACCTGGGATT  598
            ||||||||  || || |||||    ||||| ||| | ||||| ||||||  | |||||||
Sbjct  552  TTGGGTCTACGGCCCAAATGGTAATGAAGGAAAATCACAGTTTGGTAAATTCTTGGGATT  611

Query  599  aaaaaaaGGATGGACC--TATTTACCCGGAGGGGAACTGAAAGACATGATGTATCTATAC  656
            ||||||| |||  |||  |||||||| |||||  ||    |||| ||||  ||| | |
Sbjct  612  AAAAAAA-GAT-TACCTTTATTTACCTGGAGGTAAAACCCAAGATATGACATATATGTTA  669

Query  657  AGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGATGTACGAAAGACTTTGTA  716
            |  ||  |   |||     |||| || || ||| | ||  | ||||    ||| | | ||
Sbjct  670  ATGAAAAATCCAAAGGCAAATGTTGTGATGGATATTCCTCGGTGTAATTCAGAATATTTA  729

Query  717  AGTTATAAATTCCTAGAGATGGTAAAAAATAGAACTGTATATAGTTATAAATACGAACCG  776
            | |||  ||||  | ||  |  | |||||||||||  ||| |||||||||||| |||||
Sbjct  730  AATTACCAATTTATGGAATTAATTAAAAATAGAACAATATTTAGTTATAAATATGAACCA  789

Query  777  ATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTATTATGTAATTTCCTGCCGGAA  836
             | |||| |||  | | ||| ||| | |||||||| | ||||||  |||| |  |||| ||
Sbjct  790  GTTGGTTGTATTATAAATAATAAAATACATGTAATTGTATTAGCTAATGTATTGCCTGAT  849
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Query  837  GAAGAAAAAAT--CTCCGGAGACAGATTAATAATAATAAATTGCTAAACAC  885
             | ||||||||   || |  |||||| ||| ||||||  |||| |||| ||
Sbjct  850  TATGAAAAAATTAGTCAG--GACAGAATAAAAATAATTTATTGTTAAATAC  898
```

Milk vetch chlorotic dwarf virus alphasatellite 1 isolate G53, complete sequence
Sequence ID: MN273340.1 Length: 999 Number of Matches: 1
Range 1: 62 to 885

#1 Score	Expect	Identities	Gaps	Strand
262 bits(290)	5e-65	557/827(67%)	6/827(0%)	Plus/Plus

```
Query  48   AATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATC-CTTTCCTTTGGAGAGGA  106
            |||||||| || || || ||||||||||| |   ||||  || || || || |  |||
Sbjct  62   AATTGGGTTTTTACGCTGAATTTCACAGGCGCT-CTCCCTTCTCTCTCGTTCGACGAGAG  120

Query  107  AACACAATATGCGTGTTGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGAT  166
            |   ||||||||   ||||||||| ||||  ||  | || ||||| || |||||||| ||
Sbjct  121  AGTTCAATATGCAGCTTGGCAACATGAGAGAGTTAACCATGACCATCTCCAGGGAGTAAT  180

Query  167  CCAATTGAAGAAGAAGACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACA  226
             |||||||||||  ||  | ||  | |||   |  |||    |||| ||||||||||| ||
Sbjct  181  TCAATTGAAGAATAAAGCTCGCCTTAACACTGTTAAGGCTATGATTGGGGGAAATCCCCA  240

Query  227  CCTCGAACCCATGCGAGGTTCAATTACAGAGGCGAAAGCCTACTGTACGAAAGAACAATC  286
             || ||    ||| ||||   ||||  ||| ||   ||  |||   | ||||||  | ||
Sbjct  241  TCTGGAGAAGATGAGAGGGAAAATTGAAGAAGCATCAGAATACGCCATGAAAGAGGAGTC  300

Query  287  ACGGATCGCAGGTCCGTGGGAATTCGGAGAAATGCTGCTGAAGGG--GTCGAACAGACGG  344
              |  | ||||| || |||   |  || || ||| ||  ||| ||  |||  ||| |||
Sbjct  301  GAGAGTTGCAGGACCTTGGATTTATGGCGAGATGTTGAAGAAAGGAAGTC--ACAAACGT  358

Query  345  AAGCTCGCAGAGCTTCTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGA  404
            ||| |    ||| |  | || ||||| || |||||| |  | ||||| |||||||  |||
Sbjct  359  AAGATTATGGAGTTAATTGAAGATCCTGAGAACGAATTGGAAGAACCCCAAAAATTCAGA  418

Query  405  CGAGCGATGGCTAAGTCCGCCATGGATGAATCTCGGAAGCTTGCTGAAGAGTATGATTTC  464
             |||||||||||  ||||||||||| |||||||||||||||||  |||| | |  ||
Sbjct  419  AGAGCGATGGCTTGGTCCGCCATGGAAGAATCTCGGAAGCTTGCTTCAGAGGAAGGGTTT  478

Query  465  CCTCACGAACTACGCTCGTGGCAAAAAACCCTAATCTCATTCCTCGAAGAGGAACCGGAT  524
            |||||   |||   |   |||||| ||| |    | ||| |  | ||| | || || |||
Sbjct  479  CCTCATACACTTTACAGCTGGCAAGAAAACGCGTTGTCACTGTTGGAAAACGACCCTGAT  538

Query  525  GATCGTACTATTTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGT  584
            |||||||| ||   |||||| ||||| ||  | ||    ||||| ||| | ||||| |||
Sbjct  539  GATCGTACAATCATCTGGGTGTATGGGCCCCACGGTAATGAAGGAAAATCACAGTTTGGT  598

Query  585  AAACACCTGGGATTaaaaaaaGGATGGACCTATTTACCCGGAGGGGAACTGAAAGACATG  644
            |||  |||||| |||||||||||  |    ||||||||| || ||  ||    |||| |||
Sbjct  599  AAATTCCTGGGGTTAAAAAAAGATTACCTCTATTTACCAGGGGGTAAAACACAAGATATG  658

Query  645  ATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGATGTACG  704
            | |||  |    |  ||| |   ||||    |||| || |||||| | ||  | ||||
Sbjct  659  ACGTACATGCTGATGAAGAACCCAAAAGCTAATGTTGTAATTGATATTCCACGCTGTAAT  718

Query  705  AAAGACTTTGTAAGTTATAAATTCCTAGAGATGGTAAAAAATAGAACTGTATATAGTTAT  764
              ||| | | | | |||| ||||  | ||  |  |||||||||||||  | | |||||||
Sbjct  719  TCAGAATATCTGAATTATCAATTTATGGAATTAATAAAAAATAGAACAATTTTTAGTTAT  778

Query  765  AAATACGAACCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTATTATGTAAT  824
            ||||| || ||  | |||| ||| || | ||| ||| | |||||| | |||||    |||
Sbjct  779  AAATATGAGCCAGTTGGTTGTATTGTAAATAATAAAATACATGTAATTGTATTGGCCAAT  838

Query  825  TTCCTGCCGGAAGAAGAAAAAATCTCCGGAGACAGATTAATAATAAT  871
             |  |||| ||  | ||||||||      ||||||| ||| ||| ||
Sbjct  839  GTATTGCCAGATTATGAAAAAATAAGTCAAGACAGAATAAAAATGAT  885
```

Milk vetch chlorotic dwarf virus alphasatellite 1 isolate G50, complete sequence
Sequence ID: MN273330.1 Length: 999 Number of Matches: 1
Range 1: 62 to 885

#1 Score	Expect	Identities	Gaps	Strand
262 bits(290)	5e-65	557/827(67%)	6/827(0%)	Plus/Plus

```
Query  48   AATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATC-CTTTCCTTTGGAGAGGA  106
            |||||||| || || || ||||||||||| |   ||||  || || || || |  |||
Sbjct  62   AATTGGGTTTTTACGCTGAATTTCACAGGCGCT-CTCCCTTCTCTCTCGTTCGACGAGAG  120

Query  107  AACACAATATGCGTGTTGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGAT  166
            |   ||||||||   ||||||||| ||||  ||  | || ||||| || |||||||| ||
Sbjct  121  AGTTCAATATGCAGCTTGGCAACATGAGAGAGTTAACCATGACCATCTCCAGGGAGTAAT  180

Query  167  CCAATTGAAGAAGAAGACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACA  226
             |||||||||||  ||  | ||  | |||   |  |||    |||| ||||||||||| ||
Sbjct  181  TCAATTGAAGAATAAAGCTCGCCTTAACACTGTTAAGGCTATGATTGGGGGAAATCCCCA  240

Query  227  CCTCGAACCCATGCGAGGTTCAATTACAGAGGCGAAAGCCTACTGTACGAAAGAACAATC  286
             || ||    ||| ||||   ||||  ||| ||   ||  |||   | ||||||  | ||
Sbjct  241  TCTGGAGAAGATGAGAGGGAAAATTGAAGAAGCATCAGAATACGCCATGAAAGAGGAGTC  300

Query  287  ACGGATCGCAGGTCCGTGGGAATTCGGAGAAATGCTGCTGAAGGG--GTCGAACAGACGG  344
              |  | ||||| || |||   |  || || ||| ||  ||| ||  |||  ||| |||
Sbjct  301  GAGAGTTGCAGGACCTTGGATTTATGGCGAGATGTTGAAGAAAGGAAGTC--ACAAACGT  358
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Query  345  AAGCTCGCAGAGCTTCTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGA  404
            ||| |    ||| |  | || ||||| || |||||| |  | ||||| |||||||  |||
Sbjct  359  AAGATTATGGAGTTAATTGAAGATCCTGAGAACGAATTGGAAGAACCCCAAAAATTCAGA  418

Query  405  CGAGCGATGGCTAAGTCCGCCATGGATGAATCTCGGAAGCTTGCTGAAGAGTATGATTTC  464
             ||||||||||  ||||||||||| ||||||||||||||||||  |||| | |  ||
Sbjct  419  AGAGCGATGGCTTGGTCCGCCATGGAAGAATCTCGGAAGCTTGCTTCAGAGGAAGGGTTT  478

Query  465  CCTCACGAACTACGCTCGTGGCAAAAAACCCTAATCTCATTCCTCGAAGAGGAACCGGAT  524
            |||||   |||   |   |||||| ||| |    | ||| |  | ||| | || || |||
Sbjct  479  CCTCATACACTTTACAGCTGGCAAGAAAACGCGTTGTCACTGTTGGAAAACGACCCTGAT  538

Query  525  GATCGTACTATTTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTCGGT  584
            |||||||| ||   |||||| ||||| ||  | ||    ||||| ||| | ||||| |||
Sbjct  539  GATCGTACAATCATCTGGGTGTATGGGCCCCACGGTAATGAAGGAAAATCACAGTTTGGT  598

Query  585  AAACACCTGGGATTaaaaaaaGGATGGACCTATTTACCCGGAGGGGAACTGAAAGACATG  644
            |||  |||||| |||||||||  |    ||||||||| || ||  ||    |||| |||
Sbjct  599  AAATTCCTGGGGTTAAAAAAAGATTACCTCTATTTACCAGGGGGTAAAACACAAGATATG  658

Query  645  ATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGATGTACG  704
            | |||  |    |  ||| |   ||||    |||| || |||||| | ||  | ||||
Sbjct  659  ACGTACATGCTGATGAAGAACCCAAAAGCTAATGTTGTAATTGATATTCCACGCTGTAAT  718

Query  705  AAAGACTTTGTAAGTTATAAATTCCTAGAGATGGTAAAAAATAGAACTGTATATAGTTAT  764
              ||| | | | | |||| ||||  | ||  |  |||||||||||||  | | |||||||
Sbjct  719  TCAGAATATCTGAATTATCAATTTATGGAATTAATAAAAAATAGAACAATTTTTAGTTAT  778

Query  765  AAATACGAACCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTATTATGTAAT  824
            ||||| || ||  | |||| ||| || | ||| ||| | |||||| | |||||    |||
Sbjct  779  AAATATGAGCCAGTTGGTTGTATTGTAAATAATAAAATACATGTAATTGTATTGGCCAAT  838

Query  825  TTCCTGCCGGAAGAAGAAAAAATCTCCGGAGACAGATTAATAATAAT  871
             |  |||| ||  | ||||||||      ||||||| ||| ||| ||
Sbjct  839  GTATTGCCAGATTATGAAAAAATAAGTCAAGACAGAATAAAAATGAT  885
```

Faba bean necrotic yellows C9 alphasatellite C9-Eg gene, isolate Egyptian EV1-93
Sequence ID: AJ132187.1 Length: 1007 Number of Matches: 1
Range 1: 85 to 918

#1 Score	Expect	Identities	Gaps	Strand
256 bits(283)	7e-63	572/844(68%)	20/844(2%)	Plus/Plus

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Query  48   AATTGGGTGTTCACACTCAATTTCACAGGAGAGACTCCTATCCTTTCCTTTGGAGAGGAA  107
            || ||||| |||||  | || ||| | || ||   |||| | || || || |  |||  |
Sbjct  85   AACTGGGTTTTCACGTTGAACTTCGCCGGCGAAGTTCCTGTTCTCTCGTTCGACGAGAGA  144

Query  108  ACACAATATGCGTGTTGGCAACACGAGAAGGTGGATCACGACCACCTACAGGGAGTGATC  167
               ||||| ||    |||||||||||  |  ||  ||||||||||  | |||||||||||
Sbjct  145  GTTCAATACGCCGTCTGGCAACACGAAAGAGTAAATCACGACCATATTCAGGGAGTGATT  204

Query  168  CAATTGAAGAAGAAGACCCGATTAAACGGAGCGAAGCGACTGATCGGGGGAAATCCACAC  227
            ||||| ||||||||| |     | |||  || ||||    | || || |||||||| ||
Sbjct  205  CAATTAAAGAAGAAGGCAAAGATGAACACAGTGAAGAACATCATTGGTGGAAATCCTCAT  264

Query  228  CTCGAACCCATGCGAGGTTCAATTACAGAGGCGAAAGCCTACTGTAC-GAAAGAACAATC  286
            || ||    |||   ||||| ||   ||| ||    || || ||  | ||||||| ||||
Sbjct  265  CTGGAGAAGATGAAGGGTTCGATAGAAGAAGCTTCTGCGTA-TGCCCAGAAAGAAGAATC  323

Query  287  ACGGATCGCAGGTCCGTGGGAATTCGGAGAAATGCTGCTGAAGGG--GTCGAACAGACGG  344
            | |  |||| || || |||   | ||| ||| |  ||  ||| ||  |||  | | ||||
Sbjct  324  AAGAGTCGCCGGACCCTGGAGTTACGGTGAATTATTGAAGAAAGGTAGTC--ATAAACGG  381

Query  345  AAGCTCGCAGAGCTTCTGGATGATCCCGATAACGAAATAAATGAACCTCAAAAATATAGA  404
            ||| |    ||| |  |  | ||||| || |||||| |  | ||||| || ||||| |||
Sbjct  382  AAGATTATGGAGTTAATTAAAGATCCGGAGAACGAATTGGAAGAACCCCAGAAATACAGA  441

Query  405  CGAGCGATGGCTAAGTCCGCCATGGATGAATCTCGGAAGCTTGCTGAAG-AGTATGATTT  463
             ||||||||||  ||||||||||| |||||||||||||||||||||| || | | |||
Sbjct  442  AGAGCGATGGCTTGGTCCGCCATGGACGAATCTCGGAAGCTTGCTGAAGAAGGAGGCTTT  501

Query  464  CCCT-CACGAACTAC-GCTCGTGGCAAAAAACCCTAATCTCATTCCTCGAAGAGGAACCG  521
            ||||  |||   ||| ||   |||||| ||||  |  |      |  | ||||| || ||
Sbjct  502  CCCTATACGCTTTACAGC---TGGCAAGAAACAGTGTTGGGCCTATTAGAAGAAGAGCCC  558

Query  522  GATGATCGTACTATTTACTGGGTCTATGGTCCTAATGGAGGAGAAGGTAAAACCCAGTTC  581
             |||| |||| ||||   |||||||| || || |||||    ||||| ||| | |||||
Sbjct  559  AATGACCGTATTATTATTTGGGTCTACGGCCCAAATGGTAACGAAGGAAAATCACAGTTT  618

Query  582  GGTAAACACCTGGGATTaaaaaaaGGATGGACC--TATTTACCCGGAGGGGAACTGAAAG  639
            ||||||  |||||||||||||||| |||  |||  |||||||| |||||  ||    |||
Sbjct  619  GGTAAATTCCTGGGATTAAAAAAA-GAT-TACCTTTATTTACCTGGAGGTAAAACCCAAG  676

Query  640  ACATGATGTATCTATACAGTAAGGAGTTAAAAAACCATGTGGTTATTGATTTCCCCAGAT  699
            | ||||  ||| | |  |  ||  |   |||     |||| || || ||| | ||  | |
Sbjct  677  ATATGACATATATGTTAATGAAAAATCCAAAGGCAAATGTTGTGATGGATATTCCTCGTT  736

Query  700  GTACGAAAGACTTTGTAAGTTATAAATTCCTAGAGATGGTAAAAAATAGAACTGTATATA  759
            |||     || | | ||| |||| ||||  | ||  |  | |||||||||||  ||| ||
Sbjct  737  GTAATTCTGAATATTTAAATTATCAATTTATGGAATTAATTAAAAATAGAACCATATTTA  796

Query  760  GTTATAAATACGAACCGATAGGTTCTATAGTCAGTAACAAAGTTCATGTAGTGGTATTAT  819
            |||||||||| |||||  | || | |||  | | ||| ||| | |||||| | ||||||
Sbjct  797  GTTATAAATATGAACCAGTTGGATGTATTATAAATAATAAAATACATGTAATTGTATTAG  856
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Query  820  GTAATTTCCTGCCGGAAGAAGAAAAAAT--CTCCGGAGACAGATTAATAATAATAAATTG  877
            |||| |  |||| ||  | ||||||||   || |  |||||| | | ||||||  ||||
Sbjct  857  CTAATGTATTGCCTGATTATGAAAAAATTAGTCAG--GACAGAATTAAAATAATTTATTG  914

Query  878  CTAA  881
            |||
Sbjct  915  TTAA  918
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