

Dataset S1. Supplementary sequence information. Virome components of banana and non-banana leaf samples from SEA (ALYU-25 to ALYU-56).

ALYU-25 - *Musa itinerans* - **Vietnam**

Virome

- 1. **BBTV** six components
- 2. **BBTA5** - new alphasatellite named here Banana bunchy top alphasatellite 5, genus *Banaphisatellite*
- 3. **BBTA2** - Banana bunchy top alphasatellite 2, genus *Muscarsatellite*
- 4. **Badnavirus** new species - named here Banana streak *Musa itinerans* virus

BBTA5

Best matches to MF510475 MF510474 73% coverage 66.6% identity Faba bean necrotic yellows virus associated alphasatellite 2; AJ132187 AJ005966 74% coverage 66.6-66.4% identity Faba bean necrotic yellows C9 alphasatellite; MK291270 72% coverage 67.1% identity Sophora yellow stunt alphasatellite 3

Rep protein best matches to QBF29185 99% coverage 63% identities 80% positives Sophora yellow stunt alphasatellite 3; ATU31571 99% coverage 62% identities 80% positive Faba bean necrotic yellows virus associated alphasatellite 2; NP_19574 100% coverage 62% identities 77% positives Faba bean necrotic yellows C9 alphasatellite

>BBTA5_alyu25
TATTACCGACCTTGGCTCACTGGCTCACTATATAAGGCGGAGATGTCGCAGCAGCGAAATTTGGGTATTACGCGTAACCTTCCGGCGACCCGCGAAATTTAAAGTTTCGCCGGAGAAAC
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CGAAGCCATGAGAGGAACAATCGACGAAGCAATAAGGTACGTGACGAAAGAGAGACAGGATAGCAGGTCGGTGGGAATTCGGAGAATTACTACGAAAAGGATCTCATAAGAGGAAAT
GATGGAATTTGCTCGACGATTCGAGAACGAAATAATGGAACCCCAAAATATTCGACGCCCATTAATAACAAGCAATGGACGCGTCAAGGAAGAGGGCGAAATAGGGTTTCTCTACGA
CTTAAAGGATGGCAAAAGATGGTTATTGAGTTAATCGAAGAACCAACCCGACACAGAACTATTATCTGGGTCTATGGACCTAATGGTGGAAGAGGTAAACCGCAGTTCGCAAGGATTA
TGGATTACTCAAGGATGGACATATCTACCTGGTGGTGAACCTGAAAGACATGATGATCTGTGGCAAAAGAAATTAATAATAACGTTATTATTGATTTCCCGGATGTACAAGGATTT
CATATCCTATAAGTTTATTGAGATGGTAAAGAACCGATGCATATTTAGTTATAAATATGAACCAATCGGGGCTATTGTAAGTAATGAAGTCCATGTAAATGTGCAATGAGCTTCC
AGATTATTCAAAATTTCCGGAAGACAGAATAAAATTAATTTACATAACGCACACTATGACCAAAAGGGCAAAATGCAAAATCGGGGGTTGATTTGCTATATTACGAATAAGGGCCG
CAGGCCGTACACAATCGCGGGGAAATTCAAATCGGACGCCAAATATTATTAATACAATACACCGCCTTTTAGAAATCCGTGGACGAGAAGATGCCACGTAGCAAAACACTGTACTCC
TTGGCTCACTATAAATACCTGAGCCAGGTGCGGCATAG

BBTA2

Best matches to EU437030 100% coverage 98% identity; MG545616 100% coverage 96% identity; NC_038953 100% coverage 96% identity

Rep protein best matches to AZL93963 100% coverage 99% identities (1 aa) 100% positives; ACB86656 100% coverage 99% identities (2 aa) 99% positives; YP_009508281 100% coverage 94% identities (11 gaps in middle) 94% positives

>BBTA2_alyu25
TATTACCCACCTTCGCGCACCACTCCGCGCACCTATAAAATGTCTGCCTCCCGATGGACATTTACGCTTCATTATTCCGACGCAACGGAGCGAGGCAAAATTCCTCGCGACTTTGAAGGA
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TATATAGCGGAGGTGGGCTAG

DNA-C

41 SNPs to MF039864 KY427060 (**Thailand**). **44 SNPs** to MF039876 (**Thailand**). **49 SNPs** to MF039870 (**Thailand**) KM607098 (**China**)

C protein (161 aa): 4 aa to KM607098 KM607099 (**China**) MF039864 KY427060 (**Thailand**)

>C_alyu25
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCATCTAACAAATGCACGTGATATAGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCAAAAAAGTAAGAGGAATATTCGTGTC
TAGGGACTAAGCAACGGGTATAGATATTTGTCGAGAAGCGACATTTGGAGGCTAATTTAAACCTGTGGTTTTGTGATTTCCGGAATCACTATCGGAGCAGCAAAATGGAGTTCTGGGAAT
CGCTCTCAATGCCAGACGATGTCAAGAGAGTGATCAAGGAAATATATTGGGAGCATCGAAACAACTTCTGTTTTGTCAAGAGTTGAAGGCTGTGTAAGAGGATTTCTGAGCATCGAG
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ATGAAGAAGTAAATACAGGAATGTTATCATGGCATCGACGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTAACTTACTGTAAATGTAATACCC
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TGGCAACGTAGGGTCCATGTCCCGAGTTAGTGCGCCACGTGAGCGCTGGGGCTTAT

DNA-M

23-27 SNPs to MF039871 KY427061 MF039865 MF039876 (**Thailand**). **56 SNPs** to KM607239 (**China**)

M protein (117 aa): 0 aa to KC581796 (**Thailand**) **1 aa** to MF039871 MF039865 MF039877 (**Thailand**)

>M_alyu25
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCAACTAAGAAATGCACGTGACTGATATATTCTACATAACGGTTTATTGAACCGTTATATATTGTTGTAACGTAAAGTCACGTGCTGTG
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TGTAAATATGTAATGTATACGAGTGGTGATTATTAGAACATACAACACGCTATTGACAAACAGGGGAAAAATGAAGAAATCGGGGGTTGATTGGTCTATCGTATCCGTTAAAGGGCCGAG
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ATATTTGTGAAGGATAAGGATCAACACCACCACTTTAGTGGTGGTGCATATGTCCGAGTTAGTGCGCCACGTAGCGCTGGGGCTTAT

DNA-N

19-20 SNPs to MF039872 MF039878 (**Thailand**). **22 SNPs** to KM607387 KM607385 (**China**). **23 SNPs** to MF039866 KY427062 (**Thailand**). **32 SNPs** to KM607386 (**China**)

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (**Thailand**) KM607387 KM607385 (**China**) **1 aa** to MF039866 (**Thailand**)

>N_alyu25
TATTACCCCCCGTCTTGGGACGATGACGTGACATAGATTATAATGGGCCAACTAAAGGCCCATTTAATAGAATAGCGGGGCTTTGACATATTTCAAGGCCCGACCGTGGAAAT
GGATAATGTACAGTGCCTAATAAGAGGTTGCTTCGCCCGAAGCAATCCGAATAAATGTTGCGTATTCAATACGCAACTGAAGTCTATTAAATATGATGTCTCTCGCGCAATAAATCAGAG
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CGACGCTGGCAGCGGAAGAAGTCACTCGCAAGGTACTGCTAAGATCTATTGAAGCTGTGTTAATGGAAGCTTCAAGGAATAACAGGAATGTTCTGTGGGTTTATATACGATATCAAT

TGGTATCAGACGAAGTTCTCTCTAGTAATAATGTCGCTTT**TATGGGGTAA**AAACCCTTAGATAGGAGCCCTGAGGGCTCTGCTATGCTTTATTTTGGAAATAGCTGTGTAAGTACTGTAAT
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CCACTGCAAGCTTACTTCTGAGAAAGATTAAAGCAATAAAATTCCAATTTCCCTTTACATTAGTGTCTTTGAAAGGTCGATTGAATCGAGCGAGTAGAGAGCAAGATCTTTTGGGATTT
CCGCACCTACA

ALYU-26 - *Musa sp.* - **Vietnam**

Virome

1. **BBTV** six components
2. **BBTA6** *alyu26=27=38v2* - new alphasatellite named here Banana bunchy top alphasatellite 6, genus *Banaphisatellite*
3. **BBTA2** *alyu26=27* - Banana bunchy top alphasatellite 2, genus *Muscarsatellite*
4. **BBTA3** *alyu26=27=38* - Banana bunchy top alphasatellite 3, genus *Muscarsatellite*

BBTA6

Best matches to MF510475 MF510474 75% coverage 66.6% identity Faba bean necrotic yellows virus associated alphasatellite
2; AJ005966 AJ132187 74% coverage 66.6-66.3% identity Faba bean necrotic yellows C9 alphasatellite; KX534406 75% coverage 63.9% identity Sophora alopecuroides yellow stunt alphasatellite 3 isolate

Rep protein best matches to ARI50297 100% coverage 61% identities 77% positives Sophora alopecuroides yellow stunt alphasatellite 3; P0CKR1 100% coverage 60% identities 77% positives Faba bean necrotic yellows C9 alphasatellite; ATU31571 100% coverage 59% identities 77% positives Faba bean necrotic yellows virus associated alphasatellite 2

>BBTA6_alyu26

TATTACCCGACTTTGGCGCAGGGCGCACTATAAAAGATGTCTGTGAGAAATTTGGTCTTTCACAGCAAAATTTGAAAGGCGAAAGACCAGAGCTCTGTTTCGGCGCGGAACTCAATACGCC
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CACTATATATAGGTGCGCCAAAGTCGCCCATAG

BBTA2

Best match to EU430730 100% coverage 98% identity; MG545616 100% coverage 97% identity; NC_038953 100% coverage 96% identity

Rep protein best matches to AZL93963 100% coverage 99% identities (1 aa) 100% positives; ACB86656 100% coverage 99% identities (2 aa) 99% positives; YP_009508281 100% coverage 94% identities (11 gaps in middle) 94% positives Banana bunchy top alphasatellite 2

>BBTA2_alyu26

TATTACCCACCTTCGCGCACCACTCCGCGCACCTATAAAATGTCTGCCTCTCGATGGACATTTACGCTTCATTATTCCGACGCAACGGAGCGAGGCAAATTCCTCGCGACTTTGAAGGA
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10/13 SNPs to AB113661/AB113662 (Viet Nam). 17 SNPs to MF039874 (Thailand). 19-20 SNPs to KM607535 KM607534 (China). 23 SNPs to KY427064 (Thailand)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) 1 aa to several isolates

>S_alyu26
TATTACCCCGAGCGCTCGGACGGGACATGGGCTTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTTAGATGGGTTTGGGCTTATGGGCTCTATCCAGAAGACAAAAACAGCGGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCCGCAAGCAAACTAAAAGTCTATATATACCAGTGTAGACATATTGTTCCAGAGAACAAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGGCGGGTTGGGCGACGGAAGTATGGAAGCAAGGCGGCAACCAAGTACGAGCTACTCGTCGTTAGGTTCAATATTGGTTCTGAAAAACCGCTCAAGGTATTAGGAATTGAGCCTAC
TGATAAAACATTACCCAGATATTTTATCTGGAAAAATGTTTATGCTTTTGGTGTGCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAAAAAGTTTCATGGGAAATCAACAGCC
GACTACATGTCGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAAACTGGTATGCAGTGGGGAACCTGAAGCCGGAGTCGCAACAGGGACATCAGATGTTGAATG
TCTTTAAGGAAGACACACCGTGTGGAGGAAGATGTAACAGAGGTGGATTCTTGATTGGCATTTTATTGTAGTCTGGAGTTAGTATTAACTACCAGAACAGAAATTACATATCATGT
ATGATATGTTTATGTAACATAAACCTTTGTATGGAATAATGACCAATAACATACAGACGCTATGAAATACAAACGCTATGACAAACAGGGAAAAATGAAGAATCGGGGGTTGATTG
GTCATATCGTATCGCTTAAGGCCCGCAGGCCCGTTGAAATGATTCTTTATAAAACAATATACATGATACCGGATTGTTGAAATATATCAACGATGTATAAATACAAACAGAAATTGTTAA
ACTAATTAATAAAATGAGAAGAAAAAATATTTGTGAAGGATAAGCATCAGAACACCACCTTTAGTGGTGGGTATATGTCCCGAGTTAGTGCCACAGTAAAGCGCTGGGGCTTAT

DNA-U3
46-48 SNPs to KY427065 MF039869 (Thailand)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alyu26
TATTACCCCGAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAA
TCTGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATTCTGGCTTCGGGAGCAAGCAACAAGAAATTAATATTAAATTCGTATGACACGTGGACGGACCGAAATACCTCGCATCT
CTATAAATAGCTAAAACCTGGCATGGATAATTGCTCTCGCTCTTCTGTCAAAGCTATTGTGTTGAGCGCGAAGATCGCCATCGCGCATCATCGGACGAAAAAGTCCGAAGAGAGACGGATA
ACCATGCTCGGAAGCGCTATATCGGTTATTATAGACTCTAGCGCAGCTAGAAGTTTCCTGTATTTGATATTGATTTTGTAAATTCGAGAAGAAATTCGTACATGTAATAATAAA
ATCTGGGATTGTTAATGTTTACATTAAACAGTATTAATAATGTACAATAACAAATATTGTATGAGGAACGAATACAATAATTAATAATATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGTAAATTAATTAATTAATGCAATGTAATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAATAACCCCAATTATATTATTATAATACATACAAC
ACGCTATGACAAACCGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCTAACGATTAAAGGCCCGAGGCCCGCTCAAGATGGATGAACGGTTAGATTGATTGCTAGCACGACGAAGA
AAGGAATCGTTTTGGGACCACAGACAAGACAGCTGTCACTACTTTAAAAAATAATATAATAACCAATTGACGATAGTACCCCTCCCAAGATGACGATAGGGGTGTCCCGAGGTAAAT
TAACATAGCTTGACAAAGAGATAGTGACGTTGGATGGCCAGCATCGGACGATCGTGGTTTGTATGAACCAATGATGACGTAGGGGTGGGGCTTAT

ALYU-27 - *Commelina sp.* - Vietnam

Neighbour of Musa ALYU-26

Virome
1. **BBTV** six components - consensus alyu27 = consensus alyu26. However, many SNPs distinguish alyu27 from alyu26, while only some SNPs are shared between alyu26 and alyu27
2. **BBTA6** alyu27=26=38v2 - new alphasatellite named here Banana bunchy top alphasatellite 6, genus *Banaphisatellite*
3. **BBTA2** alyu27=26 - Banana bunchy top alphasatellite 2, genus *Muscarsatellite*
4. **BBTA3** alyu27=26=38 - Banana bunchy top alphasatellite 3, genus *Muscarsatellite*

BBTA6 (alyu27 = alyu26)

>BBTA6_alyu27
TATTACCCGACTTTGGCGCAGGGCGCACTATAAAAGATGTCTGTGAGAAATGGGTCTTCACACGCAATTCGAAGCGGAAAGACCAGAGCTCCTGTTGCGCGCGGAACTCAATACGCC
GCTTGGCAACATGAAGAAGAAATCACAGCACCTACAGGGTGTGATTTCAGTTGAAGAAGAAAGACCCGACTGAACGCAGTGAAGAGCATAATCGGTGGAAATCCACATCTGCAACCCCATG
CGAGCGTCTTTCCGACATGCCCTAGCATACGTATGAAAGACGAAACCCGAATCGATGGTCCATGGGAATTCGGTATTGCAATCCGTCAGGGTTCGAATAAACGAAAGCTGTTAGAAATA
CTGAGGATTTCGGACACCAAGTCTTCAACCCCAAAATACAGACGAGCCATGGCCAAACAGGCCATGAGTGAGTCTAAGAAGAAAGCTGCAGAAGAAGGATTAGTTATGAATCGCA
GAGTGGCAAGTCCAATTACGCAAGTTCTTGAAGAACAACCCGATAACAGAACAAATAATTTCCGTATATTGACCAAAAGGCTCGAGAAGTAAACACAGCTTCCTTAACATTAGGGTTA
AAGGATGGTTGGACATATTTGCCCGGTGGTGAACCTCAAAGATATGATGTACCTGTTATCAAAGGACATGAAAAATAATGTTGTAATTGATTTCGCCCGTTGACCAAGGAATTTATTTCA
TATAAATCTTGTAGATGGTTAAGAATAGAACATATATAGTTATAAGTATGAACACAGTTGGTTCATCGTATGTAATAAGGTTCAATGATGTTGTTAGTGGTCTTCAGTAATGAGGAGCGAGATTAT
GTAAATATTCAGTGGATCGAATAAAGTTGATTCTTGTCTGAACACGCTATGAAATACAAACACATATGAAATACTGTACGGGTATCTGTATGGTTATCTTTAACGCTATTGGGCGGAAG
GCCCAAGCCCAAGCCATGCCCCCAAAATGAACGGTCAAGATTGATTGCTTCGCACGAGCAACAAATAATCGCTGGTGGAGAATTTCGCACGCTCATTTGGGTACTGTTATCTCTGGCG
CACTATATATAGGTGCGCAAGTCGCCCATAG

BBTA2 (alyu27 = alyu26)

>BBTA2_alyu27
TATTACCCACCTTCGCGCACCACTCCGCGCACCTATAAAATGTCTGCCTTCGATGGACATTTACGCTTCATTATTCCGAGCGCAACGGAGCGAGGCCAAATTCCTCGCGACTTTGAAGGA
GGAAGATGTGCACTACGCCGCTCGTCGGCGACGAACTGCTCCGAATACTGGTCGAAAAACATCTTCAAGGATATCTTCTTGAAGAAACGTTTTTCGTATTAGCGGGATAAAGAAGAAATA
TCTGTCGAGAGCGCATTTGGGAGAAGCTCGAGGATCAGATTACGACAACAAGGCGTATTGTTCCAAAGAAGCCCTAATTCTCGAATTAGGGGTTCCTTGCCAAACAGGTTTCGAATAAGCG
TAAATTAGCAGATATGTTTACAGATCTCCGGAACGAATGAAATTTGAACAGCCAGAGATATTTCAACCGATACGAATCGGTGAAGAAGATGAAAGAAATTCAAAGAAGGATGTCTATCC
TATCCTCGATAGGCCATCGCAGGTACAATTAACGGAGTTAATTGAAGCAGAACCTGATGATCGAACGATCATCTGGGTATTTCGGACAAAGGGAATGAAGGCAATCAACGATATGCGAA
GTCATTAAATCAAAGGATTGGTTCTACACAGGGAGGAAGAAGCAACATCTGTTCCGCTACGTAGATGAAGGTTTCGACCAAAACGTTGTTATGTTGATCTTCCGCTCAGCTACAGTACA
AGAATTTATTAATTATGATGTAATTCGAGGCACTGAAGGATAGAGTAATCGAGAGTACAAAAACAGGCTGTGAAGTATTTAGAATTGAATACTGTACATGTAATAGTTATGGCTAAATTT
TCTTCTGATATGTGTAATAATATCTGAAGATCGAATAAAAAATAGTTGCTTGTCTGAACACGCTATGCAAAACGCGCATGACAAAAGGGGAAAAAAGAAAAATCGGGGGTTGATTGGCG
TATCCTAACGATTAAAGGGCCGACGGCCCGTCAAGATGGATCCAATAACCCGATAAGAAGGTAACGGGCTAAACCGATTCTTTCGCCCGCAAGCAACCACTTTAACTCTGCGCACCTA
TATATAGCGGAGGTGGGCTAG

BBTA3 (alyu27 = alyu26)

>BBTA3_alyu27
TATTACCCGCTTCTCGCCCCCTCTTCTCGCCCCAGTGCAAAGCACGTGATGCTCTCCTTTAAATGGTGCTTCACGCTGAATTACTCCAACGCAACAGAGAGAGAAGACTTTCTCTCTCT
TTTGAAGGAGGAGGACTTGCCTACGCAAGTGGGAGACGAAGTCGCCCGTCAACTGGTCAGAAGCACCTACAGGGATATATATCCCTAAGGAAGAGATGAAACTGGGTGGTTTGAA
GAAAAAATCTCGCGGAAGGCACACTGGGAGAAGGCGAAAGGATCAGATGAAGATAATACAAAGTATTGTTCCAAAGAAACCCCTAATTCTTGAATTAGGGGTTCCTACATCCGAGGGTTC
AAACAAGCGTAAAGTTTACAGATGGTTACAGATCACCGGAACGATGAGGATAGAACAGCCAGAGATATACAGATATCAATCTGTGAATAAGTTAAAACATTTCAAAGAGGAATT
CGTACATCCTTGCTCGATAGACCATGGCAGATACAATTGACGGAGGCAATTGAAGAGGAACAGATGATCGAAGTATCATCTGGGTCTATGGAACGCAATGGCAATGAGGGGAAATCAAC
ATATGCGAAGTCTCTGATAAACAATGATTGGTTCTATACAAGGGGAGGCAAGAAGGAGAACTATCTGTTCTCCTACGTAGACGAAGGGCTACCAAGCATGTTGTGTTGCGCATACCAAG
ATGTCATCAAGAATATCTAAATTAATGATGTAATCGAGGCATTGAAGGATAGGGTGATCGAGAGCACTAAGTATAAGCCGATTAAATTAATCGAGTTCAATACGGTACATGTAATTTGTAAT
GGCTAACTTCATGCCAGAGTACTGTAAGATCTCTGAGGATCGAATAAAATTAATATTTGCATAGCGCACGCTATGACAAAAGGGCAAAAAATGCAAAATCGGGGGTTGATTGGGCTATCCT
AACGAATAAGGGCCGACGGCCCGTCAAGATGGATCGCTTAACCCGTTATCAGATTACTTCGGGACGAAGGAATCACTTTAAGTTCTCTGCCCTATATATAGTTTGGCCCGAGGAAGCGG
CCTAG

DNA-C

>C_alyu27
TATTACCCCGCTGCTCGGGACGGGACATCACGTGCATCAAAACAAATGCACGTGACAAAGTAGTAGCTTGTAGCGAAAGATAACCATCCTATCACAAAAGTGAGAGGAATATTCGTTGCT
TAGGCACTAAGCAACGAGGACAGATAATTGTTGAGAAGCGCAATGAGAGCTATTTAAACCTGATGGTTTTGTGATTCCGAAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAAT
CGCTCGCCATGCCAGAGATGTCGAAGAGATGATCAAGGAAATATATTGGGAGCATCGAAACAACTTCTGTTCTGTCAAGAAGTTGAAAGGCTGTGTGAAGAAGGATTCTGGAGATGGAA
ATCAAGATGATGCTGTAGACGCAAGTGAAGGAGATGAAGACTTCTATTATTTCGATGTAGCGAATTTGAAGAAACCTGTGTGGTATTGTGTTTGTAGTAATAATAAATCTATTGCAATATA
GGTTAAACCAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTGATCGGTATATCAAGATCTGTTTGTGATGAGGAACCTTCCTTATTCGTGCAGAGAAGAAGAG
ATGAAGAATAATAACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGAACATTAAGTGTGTTGAATGAATATCCA
TATCATATAATAAATAATGAATGATGATTATGTATCTAGTATAAATACATAATGGTATACGTATACGATAAAATACATATACCTACATACAAACACATGACAAACAGGGAAAAAT
GAAGAATCGGGGGTTGATTGGCTATCTTAACGATTAAAGGCCGAGGCCGCTTTAAATATGTGGTGGACGAAGTCCCAACACATATAAAAGTGAGCAGAACAATGGAATATAATGAGCT
GGCAATGTAGGACCATGTCCCGAGTTAGTGCCGCCAGTGAGCAGGGGGCTTAT

DNA-M

M_alu2022

TATTACCCGACGCGTCAGGACGGGCACATCAGTGCACCTAACAAATGCAGCTGACTGATATATATCTACATCAACGGTTTATTGAACCGTTATATATTTCTTGTAACGTAAAGTCAGCTGTG
ATAATGAAATGCAGCTGACCAAGTCAAATGATTGAATAAACATTTGACGTCGGATGCTTCTTACGGAAGCCATGATTGCTTCGTGGCGAAGCAAAACATTTATATATTGGCTTGGACT
TCGCGCTATAAATAGGCACAGCGGAAATGGCATTAACAACAGGAGCGTGAACATCTTCTTGAATGTGTTCTTGTTATGGCGCAATATTTATTTGCAATAACAATATATACATATTG
TTGGCGTTGCTCTTTAGAGTCGCCAAAGTATATTAAGGATTTGTGAGGATATCTTGTAAGATCTGACAGACAGCGTGTATGCGTGCAGAGAAGCCAGTTGACGAGGCGACAGAGAT
CAGAACTGACGAGAGGATTTGTGGAAGACAGACGGGATCAACAACCTCGGCTGTATACACATACGACACAGCGTTATCCCTTCGCATCAACCTGACAGAGGATGACAGGAAGACAGGAGA
ACCGCGGACCGAATGTTTAAATCACCGTATTTGTAATATCAAGAAATGGAATGGTATAGTATAGTATTTGTAACAAATTTATTTGTAACCAATATATATATGTTTGATTAATTTACATAT
ATAATATGTGAATTTGTATACAGAGTGTGTAATTTATAGAACATACAACACGCTATGACAAACAGGAAAAATGAAGAACTCGGGGTGTTGATTGGTCTATCGTATCGCTTAAGGGCCGCGGC
CGTTGGAAGTATGTTCTTTATAAACAACATATACATGATCGGGTGTGAAATATAATCAACAGTGATATATATACACAGCAAGTTTGTGTACTAATTAAAAATGAGAAGATAAGTAT
ATTTGTGAATGATAAGATCAACACCAACCTTTAGTGTGGGTGATGTCGCCAGTGTATGCGCCACGTGTAAGCCGCTGGGGCTTAT

DNA-N

N_N_alu27

TATTACC25CCCGTGCTTGGGACGGGACATGAGCTCAGCATAGATTATAATGGGCCCACTAAAGGCCCACTTTAATAGAAATAGCGGGGCTTTTGACATATTTCAAAGGCCAGGCTTGAAGTGGATAATCTGCAGTGCCTAATAAGAGGTGCTTGCCTCGGAAGCAATCGGAATAAATGTTCGCTATTCAATACGCAACTGAAGTCTTATTAATATGATGTCTCTCGGCAATAAATCAGAGCTGAAGCGAAGCTGAAGCAGTGGATTGGGACAGATCACAATTCAAGACATGTACTCATGGTGCAGTTGGAAGACGATATCATCGGATCTCCGGAAGTCGCAATATGTACCTTGCCTGCAGCGCTGCGAGCGAGGAAGTCACTCGAAGGTACTGCTAGAGTCTATTGAAGCTGTATTGAATGGAAGCTCTCAAGGAAALAACAGGAATGTCTCGTGCGTTTATATACGATATCATAGACGACGATGATGGAGAAGTACGCTCGAGTACTCATATAACCATTCGAGGAGATGGATATCGTTATTTCTATTATTTTCGAAGGAGAGGGGAAAGTGAATGTGATATATCAAGATATGTAGCGCGAGGATGCGATTGGAGCAGCACTGGAAGTGTAGTATTGATGACCAACCACTGATCAATGAATATGTGATCTGGAAGTGTATGTTGTTCTGTCGTAAGAATAAAGGAATAACAGCATGTGCTGTAATGATTATATAAAACATATTTTCATGTAATTGATAGTTGTATAAAACATGAACACCGCTATGACAAACCGGGAAATAAGAAATCGGGGGTTGATTGTGCTATCGTATTAATCTTAAAGGCGCGAGGCCCGTTGAAAAATAATCTCGAATTTAAACGTTTGTATATAATTCAGAGATGATGATGAAGCATCTTAAACATACGAGGAAGTATATTCGCTGTATATAATATGGAAGCATATAATAAAATATGTAACCTCTGATTGGTTTGAAGTGAACCCCAACCACTTTATGTGTGGGAAGTCCCGGTACGCTAGCAGTGAAGCAGGGGACAT

DNA-R

RA_alu27

TATTACCCGCCAGCGCTCGGGACGGGACATTTCGATCTATAAATAGACCTCCCCCCCCCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGCGATATGTGGTATGCTGGATGTTTAC
CATCAACAATCCCCCTTCACTACACGATGATCTCGGGATGAGCTTTAAATATATGTGATATCAAGTCGGAGGGGACAGAGGGTACTCTGTATCTCAGGGATACCTCGAGATCAAGAGAC
AAGTTCTCTGAAGCAGATGAGAGTCTTCTTCCTGGCGCACACTTTGAGAAGCAAGGGAAGCAAGAGCAGGGCATCTCTGATTAAGGAAGAGACACCAAGATCGAAGTCCGAGTCCCTT
CGAGTTTGGTGCCCTTTAAATTTGTCATGTAATGATAATTTATTGATGTGATACAGGATATCGGTGAAACGCACAAACCGGCTTGGAGTATTTATATGAGTGTCAAATACCTTCGATAG
AAGTAAGAATACATATTCACAGAGTTCAAGCAGAGTTGATAAAACAGAGGCGATGAATAGTCTGGAAACATCTCTCAGTTTCGTGGACATCGGAAGTTGAAAATATTTATGGCGGCGCATG
TCACCGAAGGATAATTTGGGTCTATTCGGCCAGTTGGAGGAGGAGGAAGCAACATTTGCAAAATTTTAAATGAAGCAGGAATCGGTTTTTTTCGCTGGGAGAAAATACCTGGGATAT
ATGTAGATTTGTAATATGAGAAATAGTTATTTTGTATTTCCGAGATCAAGGAGGAATTTAAACATCTGTTTATTTAGAAGATTTAAAAATGGAATATTTGAGACCGGGAATA
TGAACCGGCTTTGAAAATTTGAGAATTTGGAAGTCATTTGATGCTCAATCTTCCTCCGAAAGGAGGAATCTTTCAAGAATCGAATAAGGCTAGTTGCTGTCAACCGCTATGGA
CAATCGTCAGCTATGACAAAGGGGAGAAACAAAGAAATCGGGGGTGATTGGGCTATCCTACAGATTAAAGGGCGCAGGCGCGCTCAAGATGGACGGTTTGTATCAGATGTCCCGAGTTAGT
CGGCGCATAGCGCTGGGCGCTAT

DNA-S

TS_alyu22

TATTACC20CCAGCGCTCGGGACGGGAACATGGGCTAATGGATCATGTGAATAAAGGGCCCATCGGGCCGGTTTAGATGGGTTTTGGGCTTATGGGCTCTATCCAGAAGCAAAAAACAGCGCGG
GAACCGCTCCCAATTTCAAATTTAGATAGCTTGCCCGCAAGCAAACTAAAAGTGCTATATATACAGGTGTAGACATATCTGTGCAGAGAACAATGGCGGAGGTTTCCGAAGAACTCGTACAA
GAAGGCGGCTTTGGGCGCGGAAGTATGAAGACAGGCGGCAACAGCTACGACTACTCGTGTAGTTGTCATATTTGGTTCGAAAAATACCGTCAAGGTAATTTAGGATTGAGCGCTAC
TGATAAAAAATCTACCGAGATATTTTATCTGGAAAATGTTTATGCTTTTGGTGTGCAAGGTGAAGCCGGGAAGATATCTTCACTGGGCTATGATTTAAAGTTTCTGGGAAAATCAACACGCC
GACTACATCTGTGGAAGCCACAGGTTTATTATTA AAAACCTGAACATAGCCATTGTGTGAAACCTGGTATAGCTGGGGAAGTTGAAGCGGGAGTCGCAACAGGGAACATCAGATGTGTAATG
TCTCTAAGGAAGACCAACCGGTGTGAGGAAGAAGTGAACAGAGGTGGATTATCTGTATTTGGCATTTTAAATGTAGTGTGGAGTTAGTATTAATCAACAGAACGAATTAATACATCATGT
ATGATATGTTTATGAATAAAACCTTTTGTATGGAATATGACCAAAATACATACAAGACCGTATGAATAACAAACAGCTATGAACAAGGAAAAATGAAGATCGGGGGTGATTG
CTCTATCTGTATCGCTTAAAGGGCCGAGGCGCGGTGAGGATGATTTCTTTAAAAACAAATATACATGTACGAGTATTTGAAAATATATCAACGATATGATTAATACAAAGACGATTTGTGTA
ACTAATTA AAAAAATGAGAAGAAAAGAAATTTTGTGAAGGATAGCAATCAGAACCCACTTTAGTGGTGGGTCAATGTCGCGGATGTAGTGGCCGCAATGAGCGCTGGGGCTTAT

DNA-U3

[illegible]

ALYU-28 - Ipomoea aquatica - Vietnam

Neighbour of Musa ALYU-26

Virome

"Virus-free": Reads representing BBTV genome components and alphasatellites are at a cross-contamination level (see Supplementary Figure S3B).

ALYU-29 - Musa AA sucrier Pisang mas ? - Vietnam

Virome

1. **BBTV** six components
2. **BbTA5** *alyu29* - new alphasatellite named here Banana bunchy top alphasatellite 5, genus *Banaphisatellite*
3. **BbTA2** *alyu29* - Banana bunchy top alphasatellite 2, genus *Muscarsatellite*
4. **BbTA3** *alyu29v2* - Banana bunchy top alphasatellite 3, genus *Muscarsatellite*
5. **BbTA5** *defective alyu29*
6. **BbTA2** *defective alyu29*
7. **BBTV DNA-R defective alyu29** 532 nt circular (deletion within Rep ORF)

alphasatellite 2; NP_619574 98% coverage 62% identities 80% positives Faba bean necrotic yellows C9 alphasatellite; QB055993 98% coverage 61% identities 79% positives Faba bean necrotic yellows alphasatellite 2

>BBTA5_alyu29
TATTACCCGACCTTGCTCTACTGGCTCACTATAAAGGGGGAGATGTCgCaGCAGCGAAATTTGGGTATTACGCGTAACCTTCTCCGGCGACCTGCCGATTTTAAAGTTTCGCCGGAGAAAC
TCAATACCGGTGTTGGCAACATGAGAGGAAGAAATCAGCACCATTCTCAGGGAGTGATTCAATTGAAGAAGAAGCTCCGGATGAACGCAGTGAAGACGTTTAATTTGGGGGAAATCCACACCT
CGAAGCCATGAGAGGAACAATCGCAGGAACAATAAGGTACGTGACGAAAGAAGAGACACGAGTAGCAGGTCCTGGGAATTTCGGAGAATTACTACGAAAGGATCTCATAAGAGGAAAT
GATGGAATTGCTCGACGATCCAGATAACGAAATATGGAACCTCAAAATATCGACGCCCATTAATAACAAGCAATGGACGCGTCAAAGAAGAGCGGAATTAGGGTTTCCTTACGA
CTTAAGGAGTGGCAAAAGATGTTTATTGATTAATCGAAGAACAACCCGACAACAGAACTATTATCTGGGTGATGACCTAATGGTGGAGAAGGTAAACGCAGTTCGCAAGGATTA
TGGATTACTCAAAGGATGACATATCTCCAGGTGGTGAACCTGAAGACATGATGATCTGTGGCAAAAGAAATTAACAATAACGTTAATTATTGATTTCGCCGATGTACAAGGATTT
CATATCTCTAAGTTTATTGAGATGGTAAGAACCGATGCATATTTAGTTATAAATATGAACCAATCGGGGCGATTCTAAGTAATGAAGTCCATGTAATTGTAATGTCGAATGAGCTTC
AGATTATTTCAAAATATCGGAAGACAGAATAAAATTAATATTTGCATAGCGCACACTATGACAAAAGGGCAAAATGCAAAATCGGGGTTGATTGTCTATATTTACGATTAAAGGCCG
AAGGCCGTACACATTGCGCGGGAATTTCAAAATCGGACGCCAAATATTATTAATAACAATACACCGCTTTTAGAAATCCGTGGACGAGAAGATGCCACGTAGCAAAACACTGTACTCC
TTGGCTCACTATAAATCACTGAGCCAAAGTCGGGCATAG

BBTA5def
Defective derivative of BBTA5_alyu29 (87% non-gap nt identity), **non-autonomous satellite**
Two big regions are derived from BBTA5_alyu29: 886-1119/1-265 and 617-876 (with several SNPs)
Two short regions (140 and 80 nt) share 80% identity with BBTv DNA-N

no Rep protein coding capacity, only short ORFs but two of them matching to alphasatellite Rep (due to BBTA5-derived regions)

>BBTA5def_alyu29
TATTACCCGACCTTGCTCTACTGGCTCACTATAAAGGGGGAGATGTCCTCCGACGCGAAATTTGGGTATTACGCGTAACCTTCTCCGGCGACCGAGCGGATTTTAAAGTTTCGCCGGAGAACT
TAATACCGGTGTTGGTAATATGAGATGAAGAAATCAGCACCATTCTCAGGGAGTGATTCAATTGAAGAAGAAGCTCCGGATGAACGCAGTGAAGACGTTTAATTTGGGGGAAATCCACTCCTC
GAAGCCATGAGAGGAAGAATCAGCACCATTGTTACGGGAGTGATTCAATTGAAGAAGAAGCTCCGAATGAACGCAGTGAAGGTGTTAATTTGGGGATTATCCACAATAATTAATTTATAAAT
TAGATAATAATCAGAGATAGATGATTAGCATCTAAAAACATAGACGAAGTATATGCTGTATAAATAAAGAGATATACATAAACAAAAAATAAAGTGAACCTAATCTCGATTG
GACATATCTACCAAGTGGATGAACCTGAAAGCCCTGATGATCTGTTGGTAAAGAAATTAATAATAATGTAATCATTGATTTCGCCCGATGTACAGAGGATTTTCATATCTCTAAGTTTAT
GGGATGGTAAGAAGAACCGATGTCATATTTAGTTATAAATATGAATCAATCTCGGGCGATCGTAAGTAATGAATCCATGTAATTGTAATGTTCAACGAGCTTCAGATTAATCAAAAAATTTTC
GGAAGACATAATAAAATTTTAGTAACATAATGCACACTATGACAAAAGGCCACTAGTTCGCTGCTGAACACGCTATGTCAATCTGACGTTACGACAGATGGCAAAATGTAATAATCGCA
CACTATGACAAAAGGGCAAAATGCAAAATCGGGGTTGATTGTCTATATTACGATTAAAGGCCGAAGGCCGTACACATTGCGCGGGAATTTCAAAATCGGACGCCAAAAATTTATTA
AATAACAATACCCGCTTTTAGAAATCCGTGGACGAGAAGATGCCACGTAGCAAAACACTGTACTCTTGGCTCACTATAAATACCTGAGCCAAGGTTCGGGCATAG

BBTA2
Best match to EU430730 100% coverage 98% identity; MG545616 100% coverage 97% identity; NC_038953 100% coverage 96% identity

Rep protein best matches to AZL93963 100% coverage, 99% identities (1 aa) 100% positives; YP_009508281 100% coverage 94% identities (11 gaps in middle), 94% positives

>BBTA2_alyu29
TATTACCCACCTTCGCGCACCACTCCGCGCACCTATAAAATGTCTGCCTCTCGTGGACATTTACGCTTCATTATTCCGACGCAACCGGAGCGAGGCAAAATTCCTCGCAGCTTTGAAGGA
GGAAGATGTGCACTACGCGCTGCTCGCGGACGAACTGCTCCGAATACTGGTCGAAACATCTTCAAGGATATCTTCTCTGAAGAAACGTTTTCGTATTAGCGGAATAAAGAAGAAATA
TCTGTCGAGAGCGCATTTGGGAGAAGCTCGAGGATCAGACTACGACAACAAGGCGTACTGTTTCCAAGAAGCCCTAATCTTGAATTAGGGGTTCTTGCACAACAGGTTTCGAATAAGCG
TAAATTAGCAGATATGGTTACAAGATCGCCGGAACGAATGAAATTTGAACAGCCAGAGATATTTACCCGATACGAATCGGTGAAGAAGATGAAGAATTCAAAGAAAGGTATGCTTATCC
TATCCTCGATAGGCCATGGCAGGTACAATTAACGGAGTTAATTGAAGCAGAACCTGATGATCGAAGCATCATCTGGGTATTCCGACCAAAAGGGGAATGAAGGCAATCAACGTACGCGAA
GTCATTAATCAAAAGGATGGTTCTTACACCAGGGGAGGAAGAAAGGAGAACAATCTGTTCCGCTACGTAGATGAAGGTTTCGACAAAACACGTTGTTATTGATCTTCGCGCTACAGTACA
AGAATTTTAAATATGATGTTATCGAAGCACTGAAGCATAGACATAATCGACAGTACAAAATACAAAGCTGTGAAGTATTGAAGATTAATCTGTACATGTAATAGTTATCGCTAATTT
TCTTCTGATATGTTAAAAATATCTGAAGATCGAATAAAAAATAGTTGCTTGCTGAACACGCTATGAAATACAAACGCTATGACAAACGGGGAAAAATGAAGAATCGGGGGTTGATTGGG
CTATCTAACGATTAAAGGGCCGACGGCCGTCGAAGATGGATCCAATAACCCGATAAGAAGTTAAACGGGTCTAAAACGATTTCTTCGCCCGCAAGCAACACTTTAACCCTCTGCGCACCT
ATATATAGCGGAGGTGGGCTAG

BBTA2def
Defective no-Rep variant of BBTA2, best match to EU430730 89% identity; MG545616 89% identity; NC_038953 89% identity
Defective muscarsatellite BBTA2 - **no Rep protein** (Rep ORF is lost through several short and long indels and multiple SNPs; CRM and CR-SL are highly similar to those of BBTA2_alyu29)

>BBTA2def_alyu29
TATTACCCACCTTCGCGCACCACTCTGCGCACCTATAAAGGATTGTCTCGATGAAAATTTGCGCTTCATCATTCGACGCAACGGAGCGAGGCATATTCCTCGCAGCTTCGAAGGAG
GAAGATGTGGACGACGCCGTGCTCGCGGACGAATCTGCTCCGACCACTGGTCGGAACATCTTCAAGGATATCTTCTCTGAAGACCGGATCAGATTACGACAACAAGGCGGTTCTGCTCCA
AAGAAAGCCCTAATCTTGAATTAGGGCTTTTATGCCAAACAGGATCGAAAAGCCAAATTTATCAGATATGGATACAAGATCGCCGGAACGAATGAAATTTGAACAGCCAGAGATTATCA
CCGATGCAATCCGGTGAAGAAAGTATTCAAAGAAAGGTATGCTTACTCTTCACTAGGTCATGGCAGGTACAATTAACCGAGTTAATTGAAGCAGAACCTGATGATCGAACG
ATCATCTGGGTATTCCGGATCAAAAGGAATGAAGGCAATCAACGTATGGAAGGCAATAATCCAAAAGGATTGGATCTACACCAGGGGAGGAAAGAGGAGAACATATTTGTTGCCTACG
AAGATGAAGGATCAATCAAAACGTTGTATTTGATCTTCCGCGTATTGTACACGAATTAATTAATAATGATATATCGAGGCGATTGAAGGATAGTGTAAATCGAGAATATAAAATACAAAC
CTGTGAAGTATTGGAGATGAATACTGTACATGTAATAGTTATGGCCAAATTTCTTCTTGATATGTTGAATAATCTGAAGATCGAATAACATGTTGTTGCTTCGAGAACCGCATGAA
ATACAACGCGCTATGACAAAAGGGGAAAAATGAAGAATCGGGGGTTGATTGGGCTATCCTAACGATTAAAGGCCGCGAGGCCGCTTAAGATGGATCCGATAACCCGATAAGAGGATCCGAT
AACCTAATAAGCGGTGAACCGGGTCTAAAACGATTGCTTCCGCCGCAAGCAACAACCTTTAACCTCTGCGCACTATATATAGCGGAGGTGGGCTAG

BBTA3
Best match to BBU12586 ca 100% coverage ca. 83% identity; NC_038955 ca 100% coverage 82% identity; GU074392 ca 100% coverage 82% identity; AF216221 ca 100% coverage 79% identity

Rep protein best matches to ADV18492 100% coverage 87% identities 96% positives; YP_009508283 100% coverage 86% identities 96% positives, ACJ36781 100% coverage 85% identities 94% positives

>BBTA3_alyu29
TATTACCCGCTTCCTCGCCCTCTTCTCGCCCGATGCAAGACGATGATCTTCTCTTAAATGGTGCTTACGCTGAATTACTCAAACGCAACAGAGAGAGAAGACTTTCTCTCTCT
TTTGAAGGAGGAGGACCTCGCTACGAGTAGTGGGAGACGAAGTCGCCCCGCTCAACTGGACAGAAGCACCTACAGGGATATATATCCCTAAGGAAGAGATGAAACTGGGTGGTTTGA
AAAAAATACTACGCGAAGGCACACTGGGAGAAGGCGAAAGGATCAGATGAAGATAATAACAAAGTATTGTTCTAAGGAAACCCCTAATCTAGAATTAGGGGTTCTTACATCCCAAGGTTTC
AAACAGCGCTAAGCTTTCAGAGATGGTTACTAGATCACCGGAAACGATGAGGATAGAACAGCCAGAGATATATCAGATATCAATCTGTGAATAGTTAAACATATTCAAAGAGGAAT
CGTTCTATCTTCGCTCGATAGACCTTGACCGAGGCAATTGAAGGAACAGATGATCGAAGCATCATCTGGGTCTATGGACGGAATGGCAATGAGGGGAAATCAAC
ATATGCGAAGTCTCTGATAAAACATGATTGGTTCTATACAAGGGGAGGCAAGAGGAGAACTACTGTTCTCTTCACTGACGCAAGGAGGACTACGAAGCATGTTGTGTCGACATACCAAG
ATGTCATCAAGAATATCTAAATATGATGTAATCGAGGCATTGAAGGATAGGGGTGATCGAGAGCACTAAGTATAAGCCGATTAAAAATATCGAGTTGAATAGGGTACATGTAATTGTAAT
GGCTTACTTCTAGCCAGTACTGTAAGATCTCTGAGGATCGAATAAAATTAATATTGTCATAGCCGCACTATGACAAAAGCGGCAAAATGCAAAATCGGGGGTTGATTGGGCTATCCT
ACCGATTAAAGGCCGCGAGGCCCGTTAAGATGAATAAATCCAAACCCGTTAAACCCGTTATCCGATTACTTCCGGACGAAGGAATCACTTTAAGTTCTCGCCCTATATATAGTTTGGCC
GAGGAAGCGGCTAG

DNA-C
21-25 SNPs to KY427060 MF039864 MF039876 MF039870 (Thailand). **27 SNPs** to KM607098 KM607099 (China)

C protein (161 aa): 1 aa to KY427060 (Thailand) **2 aa** to KM607098 KM607099 (China) MF039864 (Thailand)

>C_alyu29

TATTACCCCCCTGCTCGGGACGGGACATCACGTGCATCTAACAAATGCACGTGACAAAGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCACAAAAGTGAGAGGAATATTCGTTGC
TTAGCGAATAGCAACGTGGACAGATATTGTTGAGAGCGGACAAATGGAGGCTATTAAACCTGATGGTTTTGTGATTTCGAAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAAT
CGTCTGCCATGCCAGACGATGTCAAGAGAGTGATCAAGGAAATATATTGGGAGCATCGAAACAACTCTGTCTGTGAGAGTTGAAAGGCTGTGTAAAGAGGATCTTGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCACTGAAGGAGATGAAGACTTCTATTATTCGCTATAGCGAATATTGGAAGAAACCTTGTGTGGTATTGTGTTTACTACTAATTAATCTTATGCATATA
GGTTAAACCAATGGTATTCTTTTATCATGAATATATTGAGGACCTAGGAGGAGACTACTCGGTATATCAAGATCTGTTCTGTGATGAGGAACTTCCTTATTCGTCGACAGAGAAGAAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAGAGAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTACATATTACTGTAATGAAATCCA
TTATCATAAATAAAATAATGGAATGATGATTCTAGTATAAAATACATAATGGTTATACGTTATAGCATATAAAATACATATACCAACATACAAACACCGCTATGACAAACAGGGGAAAAAT
GAAGAATCGGGGGTGTATGGGCTATCTTAACGATTAGGGCCGAAGGCCGCTTAAATATGTGGTGGACGAAGTCCACAACACATAAAAAGTGATCAGAAATGGAATAATGAGCT
GGCAAGGTAGGACCATGTCCCGAGTTAGTGCGCCACGTGAGCAGGGGGCTTAT

DNA-M

14-18 SNPs to MF039865 KY427061 MF039871 MF039876 (Thailand). **53 SNPs** to KM07239 (China)

M protein (117 aa): 1 aa to KC581796 (Thailand) **2 aa** to MF039871 MF039865 MF039877 KY427061 (Thailand)

>M_alyu29
TATTACCCCAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACGGTTTATGAACCGTTATATATTGTTGTAACGCAAAGTCACGTGTG
ATAGCGAATGCACGTGACTAAGTCAAATGTTATTGAATAAACATTTGACGTCCGGATGCTTCCTACGGAAGCCATGGTTGCTTCGTGGCGAAGCAAAACATTTATATATTGGCATGGACT
GCTGCCTATAAATAGGCACGCAGGAAATGGCATTAAACAACGAGCGAGTGAACATATCTCTTGAATCGTTTTCTGTTTATTCTGCTCAATATTTATTCGCATAAACATATTATACATATTG
TTGGTGTTCCTTTGAGGTCCCCAAGTATATTAAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACCAGACGACGTGTATGGATGCAGAGAACCGAGTTGACGGAGGCAACAGGAGAT
GTAGAATCTGGCAGAGGATAGTTGGGAAGCAGACGGGATCAACAACCGGCTGCATACCATCATGCAACACAGGTTATCCCTTCGCATCAACCTGAGAGGGATGAGCAAGGAAGCAGGA
AACCCGCGACCGATGTTTTAATACACGGTATTGTAATATACGAAATATAAATGGATAAGTATTGTGAACATATAATATGTGAACATATAATATGTTGTATTAATTACATATT
TAAATATGTAATTGTATACGAGTGTGTTATTTATAAAACATACAACACGCTATGACAAACAGGGAATAATGCAGAAATCGGGGGTGTATTGGCTATCGTATCGGTTAAGGGCCGACGG
CCGTTGAAATGATTCTGTATAAAACAAATATACATGATACGGATTGTGAAATATAATCAACTATGTATAAATACAACAGAAATGTTGTATACTAATTAATAATGAGAAGATAAGTAT
ATTGTGAGGATAAGGATCAACAACCACTTTAGTGTGGGTCATATGTCCCGAGTTAGTGCCCCACGTAAGCGCTGGGGCTTAT

DNA-N

22-26 SNPs to MF039872 MF039878 MF039866 KY427062 (Thailand). **27 SNPs** to KM07387 KM07385 (China)

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (Thailand) KM07387 KM07385 (China) **1 aa** to MF039866 (Thailand:)

>N_alyu29
TATTACCCCCTGCTTGGGACGGGACATGACGTGACATAGATTATAATGGGCCAACTAAAGGCCCATTTAATAGAATAGGCGGGCTTTTGACATATTTCAAAGGCCAGACTGGATGT
GGATAATGTCACGTGCCCTAATAAGAGGTTGCTTCGCCCTCGAAGCAATCCGATTAAATGTTTCGCTGATTCAATACGCAACTGAAGTCTATTAAATGATGCTCTCTGCCGAATAAATCAGAG
CGAAAGCGAAGCAGAAGCGATGGATTGGGCAGAATCACAATTCAGACATGTACTCATGGGTGCGATTGGAAGACGATATCATCGGATTTCATCCGAGAATCGACAATATGTACCGTGCCT
CGACGCTGGCAGCGGGAAGAGTCACTCGCAAGGTACTGCTAAGATCTATTGAAGCTGTGTTTAATGGAAGCTTCAAAGGAAATAACAGGAATGTTCTGGGGTTTATATACGTATCAAT
ACGAGACGATGATGGAGAAATGCGTCCAGTACTATAATACCATTCGGAGGATATGGATATCATAATGATTCTTATATTATTTCGAAGGGAAGGGGAAAGTTGAATGTGATATATCATCAGA
TTATGTAGCGCCAGGAGTGCATGGAGCAGAGACATGGAAGTTAGTATTAGTAACAGCAACAACCTGTAATGAATATGTGATCTGAAGTGTATGTTGTTGTTCCGTTAAGAAATAAAGGA
ATAACAGATGTGCTGTAATGATTATTATAAAACATATTTTCATGTAATTGATAGTTGTATAAAACATACAACACGCTATGACAAACAGGGAATAATGAAATAATCGGGGGTGTATTGGTC
TATCGTATCGCTTAAGGGCCGACGGCCCTTGAAATAATAATCGAATTATAAACGTTTGATATAATCAGAGATAGATGATAAGCATCCAAAACATAGACCAAGTATATGCTGTAT
AATATAAAGACATATAAATAAATATGTAACATACTCTGATTGGTTAGAAATGAAACCCACCACTTTATGTTGGTGAAATGTCCCGATGACGTAAGCAGCGGGGACTAT

DNA-R

10 SNPs to MF039879 (Thailand). **12 SNPs** to MF039873 (Thailand) KM07678 (China). **13 SNPs** to MF039867 (Thailand) KM07677 (China)

R protein (286 aa): 0 aa to KM07676 KM07677 KM07679 (China) **1 aa** to MF039879 (Thailand) AF146464 AB113660 (Vietnam)...

>R_alyu29
TATTACCCCAGCGCTCGGGACGGGACATTTGCGATCTATAAATAGACCTCCCCCCCCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAAC
ATCAACAATCCCGCTTCACTACCGATGATGCGGGATGAGTTCAAATATATGTGATATCAAGTGGAGAGGGGACAGGAGGCTACTCGTCATGTGCGAGGATACGTCGAGATGAAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAGAAGAAGACACGGGCATCTGTATGAAGGAAGACACAAGATCGAAGGTCCCTTC
GAGTTTGGTGCCCTTAAATTTGTCATGTAATGATAATTTATTGATGTCATACAGGATATGCGGTGAACGCACAAACCGGCTTTGGAGTATTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAGCAAGGCGATGAATAGCTGGAACACATCCTTCAGTTCTCGGACATCGGAAGTTGAAATATATTGGCGGAGCCATGT
CATCGAAGGATAAATTTGGGCTCTATGGCCCAATGGAGGAGAGGAAGACAACTTATGCAAAATATTTAATGAAGACGAAGAATGCGTTTATTTCGCGAGGAGGAAATCATTTGGATATA
TGTAGATTGTATAATATGAGGAATAGTTATATTGATATTCTAGATGCAAAAGAGGAATATTTAAACTATGTTTATTAGAAGATTAAAAATGGAATTATTCAAAGCCGGAAATAT
GAACCCGTTTTGAAATTTGATAATATGTTGAAGTCATTGTAATGGCAAACTTCCTCCGAGGAAGGAATCTTTTCTGAAGATCGAATAAAGCTAGTTGCTTGTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAGCAAGAATCGGGGGTTGATTGGGCTATCCTAACGATTAAGGGCCGACGGCCCTCAAGATGGACGGTTTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

DNA-Rdef

Defective derivative of DNA-R: deletion in Rep ORF (nts ca. 250-750), followed by SNP mutations.

Protein 57 aa: a truncated Rep/mutated N-terminal part of Rep protein

>Rdef_alyu29
TATTACCCCAGCGCTCGGGACGGGACATTTGGGCTATAAATAGACATCCCCCTCTCCAATACAAGATCAACATCGTCGACAGAAATGGCGGATGCGGGAATGCTGGATCGTCAAC
ATCAACAATCCCGCTTCTCACTACAGTGATGCGGGATGAGATCAAGGATATGGTATATCAAGAGGAGAGGGGAAAGGATGGAAGTCTGATCTCCAAGGATACATCGAGATGAAGACGA
AGTTCTCTGAAATCTCTGTAATGCCTAACTTCCTCCGAAGGAAGACGAAGTTCTCTGAGTATGCTAGTATGCTTCTCCTCCGAAGGAAGGAATCTTTCTGAAAAACGAATAAA
GCTAGTTGCTTGTGAACACGCTATGACAATCTGACGCTATGACAAAAGGGGAAAGCAAGATTGCGGGGTTGATTGCTATCTCAACGATTAAAGGCCGACGCGCTCAGATGGA
CGGCTTGATCAAAATGTCCCGAGTTAGTGCCACGTAAGCGCTGGGGCTTAT

DNA-S

16 SNPs to AB113662, AB113661 (Viet Nam). **17 SNPs** to MF039874 (Thailand). **19-20 SNPs** to KM07535 KM07534 (China). **23 SNPs** to KY427064 (Thailand)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) **1 aa** to several isolates

>S_alyu29
TATTACCCCAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTTGGGCTTATGGGCTCTATCCAGAAGACCAAAAAACAGCGGG
GAAACGTCGCAAAATCAAATTTAGATAGCTTGCCCGCGAAGCAAACTAAAAGTCTATATATACGAGTGTAGACATATTGTTAGATAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGGCGGGTTGGGCGACGGAAGTATGGAAGCAAGGCGGCAACAGTCACGACTACTCGTCTGTTAGTTCAATATTGGTTCTGAAAATACCGTCAAGGTATTTAGGATTGAGCCATC
TGATAAAACATTATCCCAATATTTTATCTGGAAATGTTTATGCTTTTGGTGTCAAGGTGAAGCCCGGAAGAATACTTCATTGGGCTATGATTAAAGTTTCATGGGAATCAACACGCG
GACTCATGCTCGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAATGGGGAAGTGAAGCCGGAGTGCACACAGGAGCATCAGATGTTGAATG
TCTCTTAAGAAAGACACCGTGTGAGGAAGAATGTAACAGAGGTGGATTACTGTTTGGCATTTTATTTAGTGTAGTGTGAGATTAGTATTAACTACCGACAGACAGATATACATATCATGT
ATGATATGTTTATGATAAACATAAACCTTTGTATGGAATAATGACCAATAACATACACACGCTATGAAATACAAACACGCTATGACAAACAGGGAATAATGAAGATCGGGGGTGTATTG
GCTCATCGTATCGCTTAAGGGCCGACGCGCTTGAATGATTCTTTATTAACAAATATACATGATACGGATTGTTGAAAATATAATCAACGATGTATAAATACAACAGAAATGTTGAT
ACTAATTAATAAATGAGAAGAAAGAATTTTGTGAAGGATAAGCATCAGAACCACACTTTAGTGTGGGTGATATGTCGCGAGTTAGTGCCCACTGAAGCGCTGGGGCTTAT

DNA-U3

34-42 SNPs to MF039881 MF039875 KY427065 MF039869 (Thailand)

U3 protein (39 aa): 1 aa to KY427065 (Thailand)

>U3_alyu29

TATTACCCCGAGCCCCAGGACGGGACATGGGCTTTTAAATGGGCGGAGAGTTTGAACAGTTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAAAA
TCTGGGTGAGACCAAGGTCAGGTAGACGGTCAACAATATTCTGGCTTGGGAGCAAGCAACGAATTAATATCTAATTCGTAAGACACGTGGACGGACCGAAATACTCCTGTATCT
CTATAAATAGCTTAAATCTGGCTTGGATAAATCTCTCGCTCTCTGTCAAAGTGTGTGTGAGGCGGAAGATCGCCATCGGGATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGGAAGCGTATATCGGGTATTATAGACTTCTAGCGCAGCTAGAAGTTTCTCTGACTTGTATTGTTGTAATACGAAGAATTCGTACATTGATAATAATAAAC
ATCTGGGATTGTTAATGTTTACATTAAACAGTATTAATAATGTACAATAACAATATTGTATGAGGAACGAATACAATAATTAATAATATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGTATAATTAATTAATGCAATGTCATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAATAACCAATTATATTATTATAATACATACAAC
ACGCTATGACAAAAGGGGAAAAAGAAAAATCGGGGGTTGATTGTTCTATCTCAACGATTAAAGGCGCAGGCGCTCAAGATGGATGAACGGTTAGATTGATTGCTTAGCCACGAAGA
AAGGAATCTTTGTGGGACACAGACAGACAGCTGTCACTACTTTTAAATAATATAATAACCAATGGACGATACTACCCCTCCCAAGATGACGTATAGGGGTGTCGCCAGGTAATT
TAACATAGTCTTGACAAAGAGATAGTGGACGTTGGATGCCACGATCGGACGATCTGTGTTTGTATGAACATAATGATGACGTAGGGGTGGGGCTTAT

ALYU-30 - *Phyllanthus* sp. - Vietnam

Neighbor to *Musa* ALYU-29

Virome

"Virus free": however, low titre infection with BBTV and alphasatellites cannot be ruled out 100%, because of somewhat higher coverage with viral reads of a concatenated reference virome genome, compared to other "virus free" samples (see Supplementary Figure S3C)

ALYU-31 - *Arachis hypogaea* - Vietnam

Neighbor to ALYU-29

Virome

"Virus free": Reads representing BBTV genome components and alphasatellites are at a cross-contamination level (see Supplementary Figure S3D).

ALYU-32 - *Musa sweet banana* - Vietnam

Virome

1. **BBTV** six components
2. **BETA5** *alyu32* - new alphasatellite named here Banana bunchy top alphasatellite 5, genus *Banaphisatellite*
3. **BETA2** *alyu32* - Banana bunchy top alphasatellite 2, genus *Muscarsatellite*
4. **Babu2def** *alyu32* 164 nt circle (CR-SL)

BETA5

Best matches to MF510475 MF510474 73% coverage 66.5% identity Faba bean necrotic yellows virus associated alphasatellite 2; MK291270 72% coverage 67.2% identity Sophora yellow stunt alphasatellite 3; AJ132187 AJ005966 74% coverage, 66.3-65.8% identity Faba bean necrotic yellows C9 alphasatellite

Rep protein best matches to QBF29185 100% coverage 63% identities 80% positives Sophora yellow stunt alphasatellite 3; ATU31571 100% coverage 62% identities 80% positives Faba bean necrotic yellows virus associated alphasatellite 2; ARI50297 100% coverage 62% identities 80% positives Sophora alopecuroides yellow stunt alphasatellite 3; NP_619574 100% coverage 62% identities 80% positives Faba bean necrotic yellows C9 alphasatellite

>BETA5_alyu32

TATTACCGACTTGGCTCACTGCTCTACTATAAAGGGGAAATGTCGAGCAGCGAAATGGGTATTACGCGTAACTTCTCCGCGACCCCGCGGATTTTAAAGTTCGCGGAGAAAC
TCAATACGCGTGTGGCAACATGAGAAGAAGAAATCAGCACCATTCTCAGGGAGTGATTCAATTGAAGAGAAGCTCCGGATGAACGAGTGAAGACGTTAATGGGGGAAATCCACACCT
CGAAGCCATGAGAGGAACAATCGACGAAGCAATAAGGTACGTGACGAAAGAGAGACACGAGTAGCAGGTCCGTGGGAATTCGGAGAATTACTACGAAAAGGATCTCATAAGAGGAAAT
GATGGAAATGCTCGACGATCCAGATAACGAAATTAATGGAACCTCAAAAATATCGACGCGCCATTACTAAACAAGCAATGGACGCGTCAAAGAAGAGCGGAATTAGGGTTTCCTTACGA
CTTAAGGGAGTGGCAAAAGATGGTTATTGAGTTAATCGAAGAACACACGACAGCAACTATTATCTGGGTCTATGGACCTAATGGTGGAGAAGGTAACACGCAATTCGCAAGCATT
TGGATTACTCAAAGGATGGACATATCTACCAGTGGTGAACGAAAGACATGATGTATCTGTGGCAAAAGAAATTAATAATAACGTTATTATTGATTTCGCCGATGTACAAAGGATT
CATATCCTATAAGTTTATGAGATGGTAAAGAACCGATGCATATTAGTTATAAATATGAACCAATCGGGCGATTGTAAGTAATGAAGTCCATGTAATTGTAATGTCGAATGAGCTTCC
AGATTATTCAAAATTTCCGGAAGACAGAAATAAATTAATTTGCATAACGCACACTATGACAAAAGGGCAAAATGCAAAATCGGGGGTTGATTGTTCTATATTACGAATAAGGGCGC
CAGGCCGTACAAATTCGCGGGGAATTCAAATTCGGACGCCAAATATTATTAATACATAACACCGCCTTTTAGAAATCCGTGGACGAGAAGATGCCACGTAGCAAAACACTGTACTCC
TTGGCTCACTATAAATACCTGAGCCAAAGGTGGGCGATAG

BETA2

Best match to EU430730 100% coverage 97% identity; MG545616 100% coverage 97% identity; NC_038953 100% coverage 95% identity

Rep protein best matches to AZL93963 100% coverage 99% identities (2 aa) 99% positives; ACB86656 100% coverage 99% identities (4 aa) 99% positives; YP_009508281 100% coverage 93% identities (11 gaps in middle) 94% positives *Banana bunchy top alphasatellite 2*

>BETA2_alyu32

TATTACCCACCTTCGGCGCACACCTTCGGCACCTTATAAATGTCTGCCTCTCGTGGACATTTACGCTTCATTATTCGACGCAACGGAGCGAGGCAAAATCTCTCGGACTTTGAAGGA
GGAAGATGTGCACTACGCGCTCGTTCGGCGACGAACTGCTCCGAATACAGGTGCAAAACATCTTCAAGGATATCTTTCCTTGAAGAACGTTTTCGTATTAGCGGAATAAAGAAGAAATA
TTCGTGAGAGCGGATGGGAGAAAGCTCGAGGATCAGATTACGACAAACAGGCGTACTGTTCCAAAGAAGCCCTAATCTTGAAATTAGGGGTTCTTCCCAACAGGTTCAAGTAAGGG
TAAATTAGCAGATATGGTTACAAGATCTCCGGAACGAATGAAAATTTGAACAGCCACAGATATTTACCCGATACCAATCGGTGAAGAAGATGAAAGAAATTCAAAGAAAGGATGTCTATCC
TAACCTCGATAGGCCATGGCAGGTACAATTAACGGAGTTAATTGAAGCAGAACCTGATGATCGAACGATCATCTGGGTATTTCGGACCAAAAGGGAATGAAGGCAATCAACGTATGCGAA
GTCATTAAATCCAAAAGGATGGTTCTACACAAGGGGAGGAAAGAGGAGAACATACTGTTCCGCTACGTAGATGAAGGTTTCGACCAAAACGTTGTATTTGATCTCCGCGTACAGTACA
AGAAATTTATTAATATGATGTTATCGAAGCATTGAAGGATAGAGTAATCGAGAGTACAAAATACAAGCCTGTGAAGTATTAGAATTGAATTCGTACATGTAATAGTTATGGCTAATTT
TCTTCCTGATGTGTAATAATCTGAAGATCGAATAAAAAATAGTTGCTTGTCTGAACACGCTATGAAATAACAACGCTATGACAAACGGGGAAAAATGAAGAATCGGGGGTTGATTGGG
CTATCCTAACGATTAAAGCGCCGAGGCCCTCAAGATGGATCCAATAACCCGATAAGAAGTTAAACGGGTTTAAATGATTCCCTTCGCCCGCAAGCAACACCTTTAACCTCTGCGCACCT
ATATATACGGAGGTGGGCTAG

Babu2def

Defective derivative of **BETA2_alyu32 CR-SL** + non-viral DNA

>BETA2def_alyu32

TATTACCCACCTTCGGCGCACACCTTCGGCACCTGACGTCACACACATACAACACACTATGACAAAAGGGCAAAAAATCATTTCATTATAGGACCCACCAAAACACTTTAACCTT
CGCGCACTCCTCTCAACAACAGCGACGCGCGGAGGGTGGGCTAG

DNA-C

30-36 SNPs to KY427060 MF039864 MF039876 MF039870 (Thailand). **35 SNPs** to KM607098 (China)

C protein (161 aa): **2 aa** to KY427060 (Thailand) **3 aa** to KM607098 KM607099 (China) MF039864 (Thailand)

>C_alyu32

DNA-M

M protein (117 aa): 0 aa to KC581796 (Thailand) 1 aa to MF039871 MF039865 MF039877 KY427061 (Thailand)

ATTATCCCCAGCGCTGAGCAGGGGACATATGTGCAACTACAAATGCACGTGATATATATCTATACCAATCGGTTTAAACGACCGTTATATATGTTATACAGTATAGTCGAGTTGT
ATAGACATCTGCAGCTGACATGCTCAATGTATTGATAAAATCAATTGACGTCGGATGCTCCGACGGAAGCTTAGGTTACTCTGGTGGGACGAAACCAATTATAAAATTCGTCGTT
GCTGCTATATAATAGGCAACGAAGAAATGGCATTAACACACGCGAGTGAACATCTTCTTGAATGGTTCTCTGTCTGCTGCTGCTCAATATTTATTCGACACCAATATTATATATATG
TTGGCGTTGCTCTTGTAGGTCGCCAGATATTAAGGATGTGTGTGAGGATCTCTGTAAGTAACTCTGACGAGAAGACGCTGTGATGACGAGACCGCATGTGACGGAGGCACAGGAT
GTAGAGCTCGGACAGGTTGTGGGAAGACAGCGGGATCAACAACCGGCTGTCATACACATGCAACACAGGATTTCCCTTCGCATTAACCTAGAAGGATGAGCAAGGAAGACAGGA
AACCGCGGCACCGATGTTTATACACGGTATTTGTAATATACGAATATAAAATGGATATGATGTATGTGAAACATAATATATGTAACATAATATATGTTGTAATATTTACATATT
GTAATTTGTAAATGTATACAGTGTGTGTTATTTAGAACATACAAACGCTATGACAAACAGGGAAGAAATGAAGATCGGGGGTGTAGTTGGTCTATCGCTATCGCTTATAGGCGCGACGGC
CGTTGGTAATGTATATATAGACAAATATACATGATCGGATATGTAATTAATAAATCAAGGATTAATACACAGCAATGTTGTATCTAATATAAAATATGAGAAGATAAGTAT
ATTTGTGAGGATGATGATCAACACCCACACTTTTAGTGTGCGGTCTATATGTCGCGAGTATGTCGCGACGCTAAGCTCGCTGGGGCTTAT

DNA-N

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (Thailand) KM607387 KM607385 (China) 1 aa to MF039866 (Thailand)

ATATACCCCGCGGTGTGGGACGGGACATCTGCAGCATAGATTTAATGGGCCCAATAGGAGCCCAATTTAATAGAAATAGCGGGGCTTTGGACATATTTCAAGGCGGACCGTGGAAAT
 GGATATGCTCAGGTGCCTTAATAAGAGTGTGCTTCGGCTCGAAGCAATCCGAATAAATGTTGCGTATTCAATACGCACTAAGCTCATTAATATGTGATGTCTCTGCGCCAGTAATCAGAG
 CGTAAGCGAAGCAGCAAGCATGGATTGGGCAGAAATCACAATTCAGACATGTACTCATGGTCCGATTGGAAGCACTATCATCGGATTCATCCGAGAAATCAGCAAAATGTACCTTGGCT
 CGACGCTGGGACGGAGAAGTCACTCGAAGGTACTGCGTAAGTCTATTGAAGCTGTGTTTAAATGGAAGCTTCAAGGAAAATACAGGAATTTCTCGGTTTATATACGCTATCATTA
 ACAGCAGCATGATGGAGAAGTCCCTCGAGTACTCATATAACCATTCGGAGGATATGATATCAATTAAGTTCTTATTATTTTCGAAGGGAAGGGGAAATTTGAAATGTGATATATCATCA
 TATGTATGCGCCAGAGTCGATTGGAGCAGACAGATCGGAAGTTGATATTAGTAAACCAACCACTGTAATGAATTAATTTGTGATCTGGAAGTGTGTATGTTGTTGTTCTTGAAGATAAAGGA
 ATACAGCATGTCTGTAATGATTTTATAAATAACATTTTTCATGTAATGTAGTTGTATATAAACATCAACCGCTATGACAAACAGGAAAAATGAAAAATTTGGGGGTTGATGGTCT
 TATCGTATCTTTTGAAGGCGCGAGGCGCGTTGAAAAATTAATCATGAAATTTAAACGTTTGATATATATCATCAGATAGATGATAGCAATCCAAAAATCAGACGAAGTATATGTGCTGTAT
 AATATATAAAGAGCATATAAATAAATATGAAACATCTCTGATTTGGTTTGATGAATGAACCCCAACCAATTTATGTTGGTGGAAGTCCCGCATGACGTAGCAACCGGGGACATAT

DNA-R

R protein (286 aa): 0 aa to KM607676 KM607677 KM607679 (China) 1 aa to MF039879 (Thailand) AF416464 AB113660 (Vietnam)...

ATATATCCACCCAGCGCTCGGGAGCGGGACATTTATCTATAATGACCTTCGGCTATCTCCATCACAAGATCATCATCGTGCAGACAAATGGCGGCATATGTGGTATGCTGGTATGTTCCAC
 ATCAACAATCCCGCTTACCTACCAAGTATGCGGGATGAGTTCAAATATATCTGTTATCATAGTTGGAAGGCGCGGAGGAGGATCTCGTATGTGTCAGGAGTATCGTCAGATGAAGACGAAG
 GTTCTCTGAAGCAGATGAGAGGCTTTCTCCCTCGGGCCACCATCTGTAGAAACGAAAGGAAGACCGCAAGGAAGCAGCGGCTCATGTGTATGAAGGAAGACACAAGAATCGAAGGCTCCCTTC
 GAGTTTGGTGCGCTTTAAATTTCTGTATGATTAATTTTGTGTCATACAGGATATGCGTGTAAGCAACCAAGCGCCTTTGGGATATTTATGAGTGTCCAAATACCTTCGACAGA
 AGTAAAGATACATATTCACAGAGTTCAACGAGGCTGTAATAAAACGAAGGCGCATGAATAGTGGCAAAACCTCTCTTCGATCTTGGCATCGGAAGTGGAAATAATCATGCGGCGGACCATGT
 ACCCGAAGATATATTTGGGCTTATGCGGCCAAATGGGAGGGAAGGAAGACAACCTATGCAAAATTTTAAATGAAGCAGAAGATGTGCGTTTATTTCCGCGGAGGAAGAAATCTTGGTATAT
 GTGATGTTGTTAATATATGAGGAATATGTTATTTTATGATATCCCGATGCAAGAGGAATATTTAAACTACGGTTTGTATGAAGAAATTTAAATAAGGATTTGGAATATTCAGCGCGGAAATAT
 CAACCGCTTTGAAATTTAGAAATGTGTTGGAAGTCATGTGTAATGGCTAATCTCTTCGGAAGGAAGGAATCTTTTCAAGAAGTCGAAATAAAGCTAGTGTGCTGTCAACCGCTATGTAC
 AATCTGCAGCTGATGACAAAAGGGGGAAGAAAGCAAGATTGCGGGGTGATTGTGCTATCTTAAGCATTAAAGGGCGCAGGCCGCTCAAGATGGACGGCTTGTACAGATGTCCGAGGTTAGTG
 CGCCACGTAAACGGCTGGGGCTTAT

DNA-S

S protein (170 aa): 0 aa to AY337715 AY494786 H0378191 (China) FJ787433 FJ787434 (Philippines) 1 aa to several isolates

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>S alvu32
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TATTATCCCCACGCGCTCGGGACGGGACATCTAATGGATCATGGAAATAGGGCCCATCGGGCCGCTTAAGATGGGTTTGGGCTTATGGGCTTATCCAGAAAGCAAAAACAGCGGCC
 GAACCGTCCCAATTTCAAATAGTAGTACGTGCCCGCAGCAACAACTAAAGTCTATATATACACGTAGACATATCTTCAGAAACAAATGGCGAGGTTTCCGAGAAATCGATCAAG
 AAGCGGCGGGTTGGCGCAGCGAAGTATGGAAGCAAGCGGCGCAACGACTCAGCATCTCGTGCTAGGTTTCAATATGTGGTCCCTGAGAAATACCGCTCAAGGTATTTAGAGATTGAGCC
 TACTATACATATCCACAGATATTTTATCTGGAAAAATGTTTATCTTTGGTGTGCAAGGTGAAGCCCGGGAAGAAATCTCACTGGGTATGTTAAATCTCTATGGGAAATCAACCGCGC
 ACTACATCTCTGGAAGCAGACAGGTTTATTTATAAACCTGACATAGCCATCTGTGGAAATGGTATGATCGTGGGAATCTGAAGCGGAGTCGACACAGGACATCAGATGTGAATGT
 TCTTATGAAGAAAGCAACCGGTGTGAGGAAGAATTACACGAGGTGGATTACTTGTTATGGCAATTTATGTAGTCTCGGAGTTAGTATTAATCAACGACAGAAATTCGATTCATGTAT
 TGATATGTTTATGTAAACATAAACCCTTTGTATGGAAATATGACAAAATAACATACACAGACCGCTATGAATATACACAGCTATGACAAACCGGGAAAAATGAAGAAATCGCGGGTGTAGTGG
 TCTATCGTCTGCGTTATAGGGCGCAGAGCGCCGTGGAATGATCTTTTATAAACAAATATACATGATACCGGTTGTGTGAAATATTAATCAACGAGTGTATTAATACACAGAAATGTGTAT
 CTAAATAAAAATATGAGAAAGAAAAAATTTTGTGGAAGTAAAGCATCAAGCAACACCACTTTATGGTGGGCGTATATGTCTCGCGAGTTAGTCGCCCAATCAAGCGCTGGGGCTTAT

DNA-U3

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3 a1yu32

ATATACCCCAGCCGCCAGGAGGGACATATTTTAAATGGCGGACAGAGTGTGAACAGTTCAGTATCTCGTTATTTGGGCGCATCTGGCCCAAAATTAATGAGAACGCTGTTTCAAAT
 TCTGGGTTTGACCGAAGTCAAGGTACAGCGGTCAACAATATCTTGGCTTGGCGACGAGCAACACAGATAAATAATTTAAATCTGTATGACAGCTTGACGGCCGCGAAATATCTTCGATCT
 CTATAAAATAGCTTAAATCTGGCTTGGATAATTTGCTCTCGCTCTTCTGTCAAAAGATTTGTGTTGAGCGGGAAGATCGCCATCGGCGATCATCAGACGAAAAGCTGCAAGAGAGACGGAGA
 ACCATCTCGCGGACGGGTATATCTGGGTATTTATAGACTCTAGCCGCACTAGAGTTTCTTGTCATGTTTGTATTGTTATTTGAAATACGAGAAGAAATTCGTATATTTGTAATAATAAAAT
 ATCTGGGATTTGTTATTTTACATTAACCAAGTATAATAATGTACATAACAATAATTTGTATGAGGAACGAATACATAATAATTAATAATGAGGAGCGTGAGCGTGATAAACAGGTTGGTT
 AAGGTAATAAAATTAATTAATGCAATTCGTATGATATACGGTATAAGTTTGAAGTATGAGGTTGAAAGGAGGATATAGAATTAATAAACCCCAATATATTTATTTAATAACATACAAAC
 ACGCTATGACAAAAGGGGAAAAAGAAATCGGGGGTTAGTTGTCATAGTATCGCTTATAGGCCGACGAGCCGCTGAGATAGGATGGAATGAAAGCGTTAGATTGATTCCTAGCCACGAAGA
 AAGGAATCTTTTGGGACACAGATAGACAGCTGTCACTACTTTTAAAAATAATAATAACCAAAAGACGATGATACCCCTCCCAAGATGACGATATAGGGGTGTGCCGAGGTAATTT
 AACTAGCTCTGACAGAGATAGTTGGACGCTTGGATGCCACGCTGGCAGCTCGTGCTTTTATGAACCAATGATACGATGAGGCGTGGGGCTTAT

ALYU-33 - Musa ABB Chuoi Ngop - Vietnam

Virome

1. **BBTV** six components
2. **BbTA5** *alyu33*- new alphasatellite named here Banana bunchy top alphasatellite 5, genus *Banaphisatellite*
3. **BbTA2** *alyu33* - Banana bunchy top alphasatellite 2, genus *Muscarsatellite*
4. **BSNVV** *alyu33* new isolate of Banana streak VN virus (*Badnavirus*, *Caulimoviridae*)

BBTA5

Best matches to MK2912170 72% coverage 67.2% identity Sophora yellow stunt alphasatellite 3; MF510475 MF510474 73% coverage 66.2% identity Faba bean necrotic yellows virus associated alphasatellite 2; AJ132187 AJ005966 73% coverage 66.1-65.6% identity Faba bean necrotic yellows C9 alphasatellite

Rep protein best matches to QBF29185 98% coverage, 63% identities 80% positives Sophora yellow stunt alphasatellite 3;
 ATU31571 99% coverage 62% identities 80% positives Faba bean necrotic yellows virus associated alphasatellite 2;
 ARI50297 98% coverage 61% identities 81% positives Sophora alopecuroides yellow stunt alphasatellite 3

ABETA5_alyu33

TATTACCCGACTTGGCTCACTGGCTCAATATAAAAGGGGGAGATGTCGCAGCAGCAAGAAATTGGGTATTACGCGGTAACCTTCTCCGGCAGCTGCCGATTTTAAATTCGCGGGAGAAAC
TCAATTACCGGTTGGCAAGTACGAGGAAGACTCAGCACATCTCTCAGGAGAGTGATTCAATTGAAGAAGAAAGTCTGGATGAACAGCAAGTAAAGCGGTATTATGGGGGAAATACCAACCT
CAGCCATCAGAGAGCAATCGACGAGCAAAAGTAGCTGCAGAAAGAGACAGCAAGTACAGGTCGCGGTAATTCGGAAATCTAGACAGAAAGATCTCTAAGAGGAAAT
GTGGAATTGCTCAGACATTCAGATAACGAAATATGGAACCTCAAAAATTTCGACCGGCCATTACTAAACAAGCAATTGGACCGCTCAAAGAAGAGCGGAATTAGGGTTTCTCTACGA
CATTAAGGAGTGGCCAAAGATGATTGTGAGTTAATCGAAGAACCCCGCAACGAACTATTATTCTGGGTGTATGGACCTAATGGTGGAGAAGTAAACCGCATTCGCAAAAGCATT
TGGATTCTCAAAGAGTGACATATCTACCGGTGGTGAACCTAAGACGATGATGATCTGTTGGCAAGAAATTAACATAACGTAATTATTGATTTCCCCGATGTCAAGAGATT
CATATCTCTAAGATTTATGAGATGGTAAAGAACCGATGCATTAATTTAGTTATAAATATGACCAACTCGGGCGCATGTGAAGTAATGAAGTCGATGTGTAATGTGTAATCGATGAGCTTC
AGATTATTCAAAGTTTTCGGAAGACAGATAAAATTAATTTGCATACGCACATGACCAAAAGGGCAAAATGCAAATCGGGGTGTGTTGGTCTAATTACGAAATAGAGGGCG
AAGGCCGTCACATTTGCGCGGGAATTTCAAATCGCGGACGCGAAATATTATTAAATACAATACCGCCTTTTGAAGATCCGTGACGACGAAGATGCCACGTAGCAAAACACTGTACTC
TCTGGCTCATATAAATACCTGACCAAGTCGGGCGATG

BBTA2

Best match to EU430730 100% coverage 97% identity; MG545616 100% coverage 97% identity; NC_038953 100% coverage 96% identity

Rep protein best matches to ACB86656 100% coverage 99% identities (4 aa) 99% positives; YP_009508281 100% coverage 93% identities (11 gaps in middle) 94% positives Banana bunchy top alphasatellite 2

BBTA2_alyu31
 TATTACCCACCTCCGCGCACCACTCTCCGCGCACTATAAAATGTCTGCCTCTCGCTGGACATTTACGCTTCATTATTCGACGCAACGAGGAGCGAGGCAAAATCTCTCGCAGCTTTGAAGGA
 GGAAGATGTGCATCAGCCGCTGTCGCGCAAGCAAACTGTCTCGCAATACAGGTCGAAAACATCTCTCAAGGATATCTTCTCTTGAAGAAACCTGTTCTGATATAGCGGAATTAAGAGAAGATA
 TCTCTCGAAGAGCTATTCGGAGAAGCTCAGGATCAGATACGACAAACGGGCTACTGTTCCAAAGAGCCCTAATCTTGAATATAGGGGTTCTGCCCAACAGCTTGCATATAGCG
 TAAATTAGCAGATATTGTTTACAAGATCGCCGGAACGAATGAAATTTGAACAGCCAGATAGATATCTTACCCGATATCTGAATCTGGTGAAGAAGATGAAGAATTTAAGCAAGGATATCTCTCA
 TAACCTCGATAGGCCATGGCAGGTACAATTAACGGAGTTAAATGAAGCAAGCCATGATGATCGAACGATCATCTCGGTTATCTCGGACCAAAAGGGAATGAAGGCAATACAGCTATGTCGAA
 GCTTAAATCCAAAAGGATGTGTTCTACACAGAGGGAAGAAGAAGGAGCAATATGTTGCGCTACGTAGATGAAGGTTGCAGCAAAAACGTTGTATTGTCATCTCCGCTACAGTACA
 AGAATTTATTAATATATGCTGATTCGAGACCTCAAGGATAGAGATATCTCGAGATGACCAAAATACAGCCCTGTGAAGTATTTAGAATTTGAATTTCTGCATCATGTAATGTTATGCTTAATTT
 TCTCTCGTATGTGTAATAATCTCTGAAGATCGAATAAAAATAGTGTCTTCTGCAACAGCGTATGAAAATCAACACGCTATGTGCAACAAAGGGGAAAAATGAAGAATCGGGGTGTTATGGG
 CATCTCTAACGATTAAGGGCCGACGCGCCGTCAAGATGGATCCAATAACCCGATAAGAAGCTAAACGGGTCTAAACAGTATCTCTCGCCCCGAAGCAACCTTTAACTCTCGCGCACT
 ATATATAGCGAGGTGGCTAG

DNA-C

18-22 SNPs to KM607098 KM607099 (China). **24-30 SNPs** to KY427060 MF039864 MF039876 MF039870 (Thailand)

C protein (161 aa): 1 aa to KY427060 (Thailand) 2 aa to KM607098 KM607099 (China) MF039864 (Thailand)

NC_012133.1
TACTACCCCGCTGCTCGGGACGGGACATCAGTGCATCAAAACAAATGCAAGTGCACAAAGCAGTAGCTTGTAGCGAAAGATAAACCATCACTATCAAAAAGTGAGAGGAATATTCTGTTC
TAGGAGCATGAAGCAACGAGGACAGATATTTGTTCGAGAGAGGACAAATGAGGCGTATTAAACCTGTAGTGTGTTGTGATTTCGCGAAATCACTCATCGGAGCAGAGGATGGAGTTCTCGGAAAT
CGTCTGCATCGCCAGACAGTCTCAAGAGAGTGATCAAGAAATAATTTGGGAGATCGAAATTAACCTCTGTTCTGCAAGAGTTGAAAGCGTGCTGAAGAGGATTTCTGGAGCATGGAA
ATCAAGATGATCTCTAGACCGCTGAAGGAGATGAGAAGCTCTTATTATTCGCTATAGCGAATATTGAAGAACCACTGATGGTGTATGTGTTTATGACTATAATTAATCTTGTCATATA
GGTTAAATCAACTGGTGTCTTTTATCATGAATATATTAGGACCTAGGAGGTGACTACTCGGTATACAAGATGTCTTCTGTGTAGGAGAACTCCCTATTCTGTCGCAGAGAAGAAAG
ATGAAGAAGTAAATATACAGGAAGTGTATCATGCGATCGCAGAGAAGAGAACTCTGTGAGTGAATGCACAAAGATGTTTATTCAGATTATGATGATGAACATCTCTGTAATGAATATCCA
TTATCATAAATAAAATATGAAGTAGGATGATTGTATTCTGATATAGATACATACATGGTATAGCTATAGCATATAAATACATAAAACCAATCAACACCGCTATGACAAACGGGAAAAAT
GAAGAATCTGGGGGCTGATTGGGCTATCTTAACGATTAAAGGCGCAAGGCGCGTTTAAATATTCTGGTGGACGAAGTCCACAACACAAAAAGTGATCAGAACAAATGGAAATATCTGAGCTG
GCACCGTAGGGACCATGCCCGAGTTTGCGCCGCACTGACAGCGGGGGCTTAT

DNA-M

19-22 SNPs to KY427061 MF039865 MF039871 MF039876 (**Thailand**). **55 SNPs** to KM607239 (**China**)

M protein (117 aa): 0 aa to KC581796 (Thailand) 1 aa to MF039871 MF039865 MF039877 KY427061 (Thailand)

TM_aluY33
TATTACCCGACGCGTCAGGACGGGACATCAGTGCACCTAACAAATGCAGTGACTGATATATACATATAAACGGTTTATGAAGCCGTTATATATTGTTGTGAACGCAAGTCACTGTG
AAAGCGAAATGACGCGTAATFAGTCAARTGATTTGAATAAACTTTGAGCTCCGATGTCTCTTCAAGGAACGAGTGGCTGCTCGTGGGCAAGCAAACTATATATATGGCCCTGGACT
CTGCCTCTAATAATAGCTGACGGGAAATGGCAATTAACACAGAGGACGTAAGAACTATCTTTGAATGGTTCTGTGTTATTTGGTGAATTAATTTTGGCATTAACATATATACATATTG
TTGGCGTTGCTCTTTGAGGTGCCCAAGTATTAAGGATTTGTGGAGTATCTCGTAGAATCACTGACAGCAGCTGTATGGATGTGAGAGAACGAGGTGACGAGGACACAGAGAT
GTAGAATCTGGGACAGAGTGTGGGAAGACAGCGGGATCAACACACCGCTGTCTGACATACCTGCAACACGCAACAGGTTTATCCCTTGCATCAACCTAGAAGAGTGAAGCAAGGAGGAGGA
ACCGCCGGACGGAATTTTAAATACCGGTTATTTGAATATACGAAATATAAAATGTAATTAATGTAAGTATTTGTAAGAAAAATATATTTGTAACATATAATATTTGTAATATTTACATATT
CAATATGTGAAATTTGATACAGGTGTGTTATTTATAAAACATACACACCGTATACACAAACGAGGAAATAAGAAGATCGGGGGTTGTGTGGTCTGTCTGTATCGCTTAGGGCGCGAGGCC
CTGTGAAATGATTTCTTATAAAACAAATATACATGATACGGAATTTGAAATATATAATCAACGATGTATAATCAACAGAACTTTGTATCTAAATTTAAATTAATGAGAAGATAAGATATA
TTTGTGAAGGATAAGGATACACCAACCAACTTAGTGGTGGGTCATATGTCGGAGTTAGTCGGCCACGTAAGGCTCGTGGGGCTTAT

DNA-N

20-24 SNPs to MF039872 MF039878 MF039866 KY427062 (Thailand). **25 SNPs** to KM607387 KM607385 (China)

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (Thailand) KM607387 KM607385 (China) 1 aa to MF039866 (Thailand)

TN_alu3p3
 TATTACCCCCCGTCTGGGACGGGACATGAGCTGACGATAGATTATAATGGGCCAACTAAAGGCCCACTTTAATAGAAATAGCGGGGCTTTTGACATATTTCAAAAGGCCGCGCTGGAAGG
 GGATATGCTCAGCTGCTCTAATAAGAGGTGCTTTGCGCTCGAAGCAATCCGAAATAAATGTGCGGTATTCATTAACGCCAATCGAAGTCTATTATATATGGATGCTCTCGGCAATAAATCAGAG
 CTAAGCGAAGACGACGAAGCATGATTGGGACAGATACAAATTCAAGACATGTACTCATGGTCGGATTGGGAACGATATCATCGGATTCTCCGGAACATCGCAATATGTACCTTGCTGCGT
 CGACGCTGCGCAGCGAGGAAGAACTCACTCGAAGGTACCTGTAAAGTCTATTGAAGCTGTATTGAAGCTTTTAATGGAAGCTTCAAAAGAAATACGAGGAATGCTGCTGGGTTTATATACGATTCAAT
 ACGACGACGACATGGAGAAGATCGCTGCGAGTACATATAACCTTCGGAGGATATGGATATCATAAATGTTCTATTATTTTCGAAGGAGGAGGGAAGTGAATGTTGATATCATCAATCA
 TTAATGTAGCCGCGAGGATGATTGGACGAGACAGATCGGAAGTTAGTATTGTAACACCAACCAATGTAATGAATATGTTGATCTGAAGTGTATTGTTGTTCTGAAGAATAAAGGA
 ATAAACGATCTGCTGATGATGATTAATAAAAAATATTTTCATGTAATGTAGTGTGTTATAAAACATACAAACAGCTATACAAACAGGAAAAATGAAAAATCGGGGGTTGATTGTC
 TATCGTATTAATGTTTAAGGCGCGAGCCCGCTGAAAAATATGTAATCGAAATTTAAACGTTGATATAATAAATCAGAGATAGATACGAAGCATCCCAAAACATACAGGAGATATATGCTGTAT
 AATATACCAAGAGCATATAAAATAAAATGTAAACATCAATCTCTGATGGTTTGAAGTTTAAACCCCAACAACTTTATGTGTGGGAATGTCGGAAGTACGACGATGACGTAAGCAGCGGGGACAT

DNA-R

11-15 SNPs to MF039879 MF039873 MF039867 KY427063 (Thailand). **15 SNPs** to AB113659 (Viet Nam: Hanoi). **17-19 SNPs** to KM607678 KM60767 KM607676 KM607679 (China)

R protein (286 aa): 0 aa to KM607676 KM607677 KM607679 (China) **1 aa** to MF039879 (Thailand) AF416464 AB113660 (Vietnam)

>R_alyu33

TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCCCCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGCGATATGTGGTATGTGGATGTTCCAC
CATCAACAATCCCGCTTCACTACCAGTGTATCGGGATGAGTTTAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCAGGGATACGTCGAGATGAAGAGACG
AAGTTCCTCTGAAGCAGATGAGAGGCTTCTTCCTTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAAGAAAGCACGCGCATACTGTATGAAGGAAGACACAAGATCGAAGGTCCTT
CGAGTTTGGTGCCCTTTAAATTTGTCATGTAAATGATAATTTATTTGATGTCATACAGGATATGCGTGAACGCACAAACGCGCTTTGGAGTATTTATATGAGTGTCCAAATACCTTCGATAG
AAGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAACGAAGCGCATGAATAGCTGGAAAAATCCTTCAGTTCATGGACATCGGAAGTTGAAAAATATTATGGCGAGCCATG
TCACCGAAGGATAATTTGGGTCTATGGCCCAAATGGAGGAGAAAGGAAAGACAACCTTATGCAAAATATTTAATGAAGACGAAGAATGCGTTTTATTTCGCCAGGAGGAAAAATCATTGGATAT
ATGTAGATTGTATAAATTATGAGGAAATAGTTATATTTGATATTCCTAGATGCAAGAGGAATATTTAAACTATGGTCTATTAGAAGAAATTTAAAAATGGAATATTCAAAGCGGGAATA
TGAACCCGTTTGAATAATTGTAAGATATGTAGAAGTCATTGTAATGGCTAACTTCTCCGAAGGAAGGAATCTTCTGGAAGATCGAATAAAGCTAGTTGCTTGGCTGAACACGCTATGA
CAATCGTACGCTATGACAAAGGGGAAAGCAAGAAATCGGGGGTGTATTGGGCTATCTTAACGATTAAAGGCGTAGGCCCGTCAAGATGGACGGTTTGATCAGATGTCCCGAGTTAGT
GCGCCACGTAAAGCGCTGGGCTTAT

DNA-S

15/16 SNPs to AB113661 AB113662 (Viet Nam). **16 SNPs** to MF039874 (Thailand). **17-20 SNPs** to KM607535 KM607534 KM607536 KM607533 (China). **22 SNPs** to KY427064 (Thailand)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) **1 aa** to several isolates

>S_alyu33

TATTACCCCGAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTTGGGCTTCTGGGCTTTATCCGAAGACCAAAAAACAGCGGG
GAACCGTCCCAATTTCAAAATTTAGATAGCTTGCCTCGCAAGCAAACTAAAAGTCTATATATACAGCTGTAGACATATTGTTCCAGATAACAAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAGAGGCGGGTGGGCGACGGAAGTATGGAAGCAAGGCGGCAACCAAGTCACGACTACTCGTCGTTAGGTTCAATATTGGTTCCTGAAATACCGCTCAAGGTTATTAGGATTTGAGCGCTAC
TGATAAAACATTACCCAGATATTTTATCTGGAAAAATGTTTATGCTTTTGGTGTGCAAGGTGAAGCCGGAAGAATACTTCATTGGGCTATGATTAAAAATTCATGGGAAATCAACCAAGC
GACTACATGTCGGAAGCACCAAGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAAGTGGGAACTTGAAGCCGGAGTAGCAACAGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGCACAAACGCTGTTGAGGAAGAATGTAACAGAGGTGGATTACTTGTATTGGCATTATTTAGTGTGCTGGAGTTAGTATTAACTACCAGACAGCAATACATATCATGT
ATGATATGTTTATGTAACATAAACCTTGTATGGAATAATGCCCAAATAACATACAACTCTATGAAATACAAACGCTATGACAAACAGGGAAAAATGAAGAATCGGGGGTGTATTG
GCTCATGCTATGCTTAAAGGCCGAGCGCGCTTGAATGATTCTTTATAAAACAAATATACATGATACGGAATGTTGAAAAATATAATCAAGTGTATATAATACACAGAAATGTTGTAT
ACTAATTAATAATGAGAAGAAATAATTTTGTGAAGGATAAGCATCAGAACCCACTTTAGTGGTGGGTATATGTCGCCAGTTAGTGCGCCACGTAAAGCGCTGGGGCTTAT

DNA-U3

25-32 SNPs to KY427065 MF039869 MF039881 MF039875 (Thailand)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alyu33

TATTACCCCGAGCGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAAGCTGTTCAAAA
TCGGGGTTTGACCCGAAGGTCGAAGTAGACGGTCAACAATATTCTGGCTTCGGGAGCAAGCAACAGCAATTAATATTAAATTTGATAGACAGCTGGACGGACCGAAATCTCTGATATCTC
TATAAATAGCTTAAATCTGGCTTGGATATTGCTCTCGCTCTCTGTCGAAAGCTGTTGTTGTTGAGGCGGAAGATCGCCATCGGCGATCATCAGACGAAAGCTGCAAGAGAGACGGAGAA
CATAGCTCGGAAGGTGATATCCGGTATTTATAGACTCTAGCGCAGCTAGAAGTTCCCTGTACTTGTATTTGATTTGTTAAATACGAAGAAATTCGTACATTGATAATAATAAAACA
TCTGGGTTTGTAAATGTTTACATTAAACAGTATCAATAATGTACAATAACAAATATTGTATGAGGAACGAATACAAATAATTTAAATATGAGGAGCGTAGCGTGATAAACAGGTGTTTA
AGGTATAAATTAATTAATGATGCAATGTCAATGATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAATAAACCCCAATATATATTTATTAATACATACAC
ACGCTATGACAAAGGGGAAAAATGAAGAATCGGGGCTGATTGGTCTATCTTAACGATTAAAGGCCCGAGGCCCTCAAGATGGATGAACGGTTAGATTGATTGCTTAGCCAAAGAA
AAGGAATCTTTTTGGGACCAGATGAAGCAGCTGTACTACCTTTAAAAATAATATAATATCAATTTGACGATAGTACCCCTCCCAAGATGACGTATAGGGGTGTCCCGAGGTAATTT
AACATAGCTCTGACAAGAGATAGTTGACGCTTGGATGCCACATCGGACGATGGCTTTTGATGATAATGATGACGTAGGGGTGGGGCTTAT

BSNVN

Best match to KJ013510 **Banana streak VN virus** Banana streak virus Acuminata Yunnan 100% coverage 90.4% Identity Gaps: 46/7738; AY750155 Banana streak virus Acuminata Vietnam 100% coverage 88% Identity 1% Gaps: 74/7516

ORF I protein (CTG start codon) best match to YP_605809 Banana streak virus Acuminata Yunnan 96% identity 99% positives

ORF II protein best match to YP_233109 Banana streak virus Acuminata Vietnam 89% identity, 94% positives

ORF III polyprotein best match to YP_605811 Banana streak virus Acuminata Yunnan 96% Identity 98% Positives

>BSNVN_alyu33

TGGTATCAGAGCTAGATTTGTAAATATTTATGGCTTTTATGGGGTAAACCCTTAGATAGGAGCCTAAGGGCTCTGCTATGTTCTGCTTATGAAAATAGTTGTTCAAGTAGAAAAATGCA
TGATAAATCGAGTAGGTTCTTACAAATGGTCCTGAAATATGAAATATACCTTTTATACCTTTGAGGGAACCTCTGTGCTCCAAAGTTCTACTGAGATGATACCTATCCAAAGAAAGGTAG
TAGGCTGGTGAAGGGGAAGAAAAATGAGTTGAGTTGGGAGTAGAATTTCTTAAGGGCTAGGGGCAAAAGAACCGGAACCTTACCAGTAGAAGTGAAGACCCCGGGAAGGGCAGTAGAGCTGGA
GAAOCCCGGTGTAGCTCTCTTTACCTTGAAAAAATATACTCTAGTATCCTCAAAACTCGCTGAAGTAAATTTCCCAAAACCATGTTACTAATTTTATAGGATATTTTACAGATCACAATCAA
ACTTGAGTTGTACAGGGTAGAATCTTGGTATGACTGGATAACTAATGATTAAAGACCTTCACTAAGAACTTAGTAAGAAGTAAGTGATAGACTACCTCTGGAAGTACATCAATCATGA
GCAAAACATATGCATCCGAAGGTTACTCTATCTGCTTAAGACCATAAAGAACTTCTCCTTAAAAACTCTGGAATCCTATTTGGGATCTTGAATTTGAAAAATATAAAAAATTTCACTCC
AAATCTGTCTGTATCTTTCTTATCTAGACTTAGTACTGCTGAAAAGGTCTCTAATAAAGACCTAGCACATAATTTGATATAAAACCTATCGTAGTGATCTTGGCTTTAAAGTTGCA
ATTCATTCTTTATCAAAATCTGGTGCTACTAATCCAGAACGAAAGCTCTTGGAGGAGCAAAAGCAACAGCTTTCTGAATCAGCAACCTATCTAAGGTTGTGGCTCTCAACGCGCT
GACTTAAAGGAGACCTTAAAGCAGCAGGACGTCCTTGCAGAGGAGCTTCAAGCTTCTGCTAAAGACTATCTGGAGAGGCGTCCCTCAGCAAAAAGGACGTAGAAGAACTGGTTGTCGGA
ATCTCAGAAACACGAAGTTCATTGAAAAACAACTGAGGCTCTCACTATAGAGCTCACAAGAAAGTCAATTAAGTCCATCATCAAGACTTTGAGCAAAAGGCTCCTGGGATGA
GCTTAGCTGGAAGCAAGGCAACAGCTGCATATCAAGAAAGCTTGCATCCACTACTGCTGGCTGGGAAGATCTCGGCATCGGATTCACTGACAAAGGGAATATCAGCAACAACTTGT
CAAGGCAAGCTTAATCGCTGTTATTTTGGTGGTTAAGCAAAACAGCAAAATACCAACCATCACTGAAGAGCTGACCCAACCTCCACAACCGGGTCAAAAACCTTGAAGGGAAGACAGGGG
TATCCGCAAGTCCCTGAACAAATCTGAATTTGAATCCATCAACGACAAGCTTAGAAGGATTCAAGAAATCCAGGGGAGTCAACCAACCAAGAGACCCCTCCGAGCTATCAAGGTTT
TTGAGGATCCCTATAACATCCTCAGAAAAATATAATGGCATCAAGCGCGAGGGTTTCCGGAAGCACCAACCGCAACCATGGTGGCAGAACCAAGGGGTTCCCTGGTTGATGATCAGATCCG
GGAATACCGGAATGCGGCCGAGGCCCATATGAAGCGCAAGGATTTGCTCAGCAGCAGGGCAATATTTTGGAAAGATTGTTGGCGCAACCAAGGGAACATACCTTGAATGGTTCGT
AGACCCCAACAGCTGAGCTGGAAGCTCTACTAGCTCACCGCTGCAGAACGATACCCGCTGAAGCTCCTCATATGACCCAGCGCGTGAGCTTCAAATCGGGTCTACCCGGAACCGAAGTGA
AGAAAGGATGCTCGTGACTCATGAGCAACAGACAGGACCTTCATCCTGCTGAGTCATATGAAGAAGCTCAGAGAAGCTGGATTTCGAGTACATCCATCTAGGAGTACTCCAGGTGGCGAT
CCAAATTTAGCACCGTTTCAACGCTGGTATAGCTATGGCGCTAATAGTTTTCAGAGACACAGGTGGAGCAGCAAGAAACCAAGGACAGATCCATTATAGCAACCATGGAGGCTGACCTTTC
ACAAGGGCATCAGCTTATTTATGCTATCCAGATATAATGATGACAATCAGGATTTTACCAGCACATCCAGATCAGATCCTTCAACAAAGGATATGAGGGCTTTCAAGGAGGAAGCAAA
TCTCCTTTATACAGAAGCTGCGGGTGAGATTAAAGCAAGCTTCTTAACGTTGGCTTCAGATATAATTTCAAACAGCTCGTGGAAATTCCTAAAAATCAAAAGGCTTAAACCG
GATGAAATTAAGCAACAGGAGTTTCAAGGAGGATGAATGGAACATCCGACCATCAGAAGTGGTGGTCCCTATGAGGCAACCAACATGATAGTACGAGTTAATATGACTCGCTCAAGAG
CAGCAATTTGGGGATATTGAAGCCAGACATCATCAGCCCCAAAGTACGAAACAGAGCGTATGAAATTAAGCAATGAAGCACTTGGTGAATCCCAAGTAAATATGATCACAATATTGA
AGATGATGCAGAAATGACTACCCAGGTTATCAGCTTTAGAGCGAATAATCGCTCCAGAAAGCATGGTGGGAGAGGAGCACAATTGCCGAATTTTATAGGCAATCTGCTCCTTAGATTG
CTCCACTGATGAGGAATTCATAGCGCTGACAATATGCTTTTCGAGGAAGAAGATATGATGGAGATATGATTTCTGAAGTCAGCACACCAAGGAGCAAAATACAAATATTTGTCATAGA
GTTAGTAGTACCAAGGCTTCAACAGCTGGAAGGCTAGTACTTCCACAAACAGAGTCTGCCATCAGCGCGTTAGAGCTGCAGACACAGACATGATCGCATAGGGCCCGGCTATGCAAC
AGCAACCGGAACAGCTGGCTACATCTGGAGCCAGTTTCATCTGATTTCCCTTACCCAGAAAGGCCAAGAAAGTGGGCAACAACTCAGAATGGTTTAACTCGCCACTGCTAATGCCAGGCA
AGCATCAATATTCTGTCACTGCTCAGAGCTTCGACACAAGGCTTTTGAAGATGGGAAGCTCTGTTTCTCTCCATATGCTGATAAGGTTTTCGATGATCCACAAGATGAAGCTTACCTTA
TGTGGAAAAATCTGCTAGGAGAAATCAGAGAAAAAGATGTTTATCACTTGGAGAGTATGTTTACAGCGCAATATGAAGAAATGAAGAACACCGCCCTCGGCTCAAATGGAACAGCAACAT
CCTGAACAGATAGCTGATGATATTTCTTTCTGGAGAACTCCCAAGTCGGAACACATATGCTCAGGACGCTGCATACAAAACGCTCAACCACTGGTGTGCAACAGAAATCTCCGAGCTGC
AATCTACAGGTTACCTCAAGATTACTTCCATTAGCTGTAATCTGGAAGAGCATGGGCTATCTGATGAGCTGTCCAAAGGTTCTTTACTAATTAACCAAGGATTTGGGGATAGAGT
GAAAAGCAATTTCAAGAAAGATACCCCAACCACTATTGGAGTGCCACCAAGTAATCTTCAAGAAATATATGAAGCAAAATATGCCAAGAGCCGATTTCCAAAGGATCTGAAAGCTGAA
GAAGCTGGACTTCTGCAAGGAACACCTGTCCATGGCTTATACGGAAGAAAGATAAGGTATATGGGAGGAAATACGGAGTCAGAAAGAGTACTTCTGACAAAGGAAGCCCTCACAAGTCACA

TATTACCCCTGCTCGGGACGGGACATCACTGTCATCAACCAATGCAGCTGACAAAGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCACAAAHGTGAGAGGAATATTCTGTGC
TAGGAGCATAGCAACGAGGACAGATATTGTTGCGAAGGCGCATATGAGGCTATTAAACCTGTAGTGGTTTGTGATTTCGGAATCACTCATCGGAGGAGGAATGGAGTTCTGGGAAT
CGTCTGCATCGCCAGAGATGTTCAAGAGATGATCAAGAAATATATTGGGAGATTTGAACTTAACCTTGTTCTGTCAGAAGTTGAAAGCGCTGTGAAGAGGAATTCTGGAGCATGGA
ATCAAGATGATCACTGACGCCAGTGAAGGAGATGAAGACTTCTATTATTCCGTATAGCCGAATATTTGAAGAACTCTGTTGTGATGCTGTTTATACGAATAAACTCTGATATTA
GGTTAAGCAAGCTGGTGTCTTTTATCGATGAATATGTTGAAGACCTAGGTGTGACCTCGGTATCATCAAGATCTGTTGATGAGGAATCTCCTTATTCGTGCGACGAAAGGAAG
ATGAAGAAGTAATATACAGAAGTGTATCATCGCATCGACGAAAGAGATCTCTTGGAGTGAATCGAAAGATAGTTATATACAGATTATGATGATAACATCTGTTAATGAATATCC

TTATCATAAATAAAATAATGGAATGATGATTATGTATTCTAGTATAAAACATAATGGTATACGTATAGCATATAAAATACATAAACCAACATACAACACGCTATGACAAACAGGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAAACGATTAAAGGCCGAAGGCCGTTTAAATATGTGGTGGACGAAGTCCACAACACATAAAAGTAATCAGAACAATGGAATATAATGAGCT
GGCAACGTAGGGACCATGTCCCGAGTTAGTGCGCCAGTGAGCAGGGGGCTTAT

SNPs in C (all minor - ca. 15% reads): C42A T81C GAl05AC G140T C164A T190G G461T G516A G577A G584A A807T G819A AA934GT

DNA-M

16-21 SNPs to KM607239, KM607240 (China). **49-50 SNPs** to KY427061 MF039871 MF039865 (Thailand: Chonburi)

M protein (117 aa): v1 **1 aa** to KC581796 (Thailand) **2 aa** to MF039871 (Thailand) KM607240 (China)
v2 **0 aa** to KC581796 (Thailand) **1 aa** to MF039865 (Thailand) **4 aa** to KM607240 (China)

>M_alyu34_v1
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACGGTTTAAACGAACCGTTATATAATGTTATAACGAAGTCACGTGTG
ATAGAGACATGCACGTGACATAGTCAAATGTATTGAATAAACATTTGACGTCCGGATGCTTCCGACGGAAGCTTAGGTTACTTCGTGGCGAAGCAAAACATTTATAAATGGGCTGGAGT
GCTGCCATAAATAGGCAAGCAAGGAAATGGCATTAAACAACAGAGCGAGTGAAATATTCTTTTGAATGGTTTCTGTTTCATCGGTGCAATATTTATTGCGGATAACAATATTATATATTG
TTGGCGTTGCTTTTGGAGTCCCCAAGTATATTAAAGGATGTTGTGAGGTATCTCTGAGAATACCTGACCAGAAGACGCTGTATGGATGCAGAGAACCGCAGTTGACGGGAGGCAACAGGAGAT
GTAGAGCTCGGCAGAGGTAGTTGGGAAGACAGACGGGATCAACAACCGGCTGTCATACCACATCAACACAGGTTATCCCTTCGCATCAACCTAGAAAGGGATGATCAAGGAAGACGAGGA
AACGCCGAGCCATGTTTTTAATACACGGTATTGTAATATACGAAATATAAATGGATATGATATGTTGTGAACATAATATACTGTAACATAATATATGTTGATATTTACATATT
ATAATATGTAAATGTATACGAGTGTGTTGATTATATACAACATACAACACCGCTATGACAAACAGGGAATAATGAAGATCGGCGGTTGATTGCTCTATCGTATCGCTTAAGGCCCGCAGGCG
CCGTTGAAATGATTCTTAATAAAACAAATATACATGATACGGATAATTGAATATATAAACACGAAGTATAAATACAACAGAATGGTGATACTAATTAATAATGAGAAGATAAGTAT
ATTTGTGAGGGATGATGATCACAAACCACCATTTAGTGTGGGTTCATATGTCCCGAGTTAGTGGCCACGTAAGCGCTGGGGCTTAT

T/C (16364/81303) **A/T** (16346/81967) **A/T** (16783/80754) **C/T** (100085/21127) **C/T** (81691/20307) **C/T** (80026/17034) **T/A** (97135/20874) **A/C** (90266/19352)
A/G (88699/19010) **T/A** (32213/7550) **C/T** (23115/7191) **A/G** (23455/5601) **T/A** (27080/7060) **G/A** (34811/6758) **A/T** (33006/6267) **A/T** (45174/9845)

>M_alyu34_v2
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACGGTTTAAACGAACCGTTATATAATGTTATAACGAAGTCACGTGTG
ATAGAGACATGCACGTGACATAGTCAAATGTATTGAATAAACATTTGACGTCCGGATGCTTCCGACGGAAGCTTAGGTTACTTCGTGGCGAAGCAAAACATTTATAAATGGGCTGGAGT
GCTGCCATAAATAGGCAAGCAAGGAAATGGCATTAAACAACAGAGCGAGTGAAATATTCTTTTGAATGGTTTCTGTTTCATCGGTGCAATATTTATTGCGGATAACAATATTATATATTG
TTGGCGTTGCTTTTGGAGTCCCCAAGTATATTAAAGGATGTTGTGAGGTATCTCTGAGAATACCTGACCAGAAGACGCTGTATGGATGCAGAGAACCGCAGTTGACGGGAGGCAACAGGAGAT
GTAGAGCTCGGCAGAGGTAGTTGGAAGACAGACGGGATCAACAACCGGCTGTCATACCACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGATCAAGGAAGACGAGGA
AACGCCGAGCCATGTTTTTAATACACGGTATTGTAATATACGAAATATAAATGGATATGATATGTTGTGAACATAATATACTGTAACATAATATATGTTGATATTTACATATT
TAATATGTAAATGTATACGAGTGTGTTGATTATATAGAACATACAACACCGCTATGACAAACAGGGAATAATGAAGATCGGCGGTTGATTGCTCTATCGTATCGCTTAAGGCCCGCAGGCG
CCGTTGAAATGATTCTTAATAAAACAAATATACATGATACGGATAATTGAATATATAAACACGAAGTATAAATACAACAGAATGGTGATACTAATTAATAATGAGAAGATAAGTAT
ATTTGTGAGGGATGATGATCACAAACCACCATTAGTGTGGGTTCATATGTCCCGAGTTAGTGGCCACGTAAGCGCTGGGGCTTAT

DNA-N

23 SNPs to KM607387 KM607385 (China). **29-31 SNPs** to MF039872 MF039878 MF039866 (Thailand). **32 SNPs** to KM607386 (China)

N protein (154 aa): **0 aa** to MF039872 MF039878 KY427062 (Thailand) KM607387 KM607385 (China) **1 aa** to MF039866 (Thailand)

>N_alyu34_v1
TATTACCCCCCGTGCTCGGGACGGGACATGACGTGACATAGATTATAATGGGCCAACTAAAGGCCCTTTAATAGAATAGGCGGGCTTTTGACATATTTCAAAGGCCAGCCTGGAAGT
GATTAAATGTCACGTGCGCATGAATGAAGGTTGCTTCGCTCGAAGCAATCGAATAAATGTTCGCTATTCAATACGCAACTGAAGTCTATTAATATGATGTCTCTCGCGCAATAAATCAGAG
CTCAAGCGAAGCAGAACCGATGGATTGGGCAGAAATCACAAATCAAGACATGTACTCATGGTTGGGATGGGAAGCAGATATCATCGATTTCATCCGAGAAATCGACAATATGTACCTTCGCT
CGACCGCGCACGGGAAGAACTCTCCTCGCAAGTACTGCTTAGATCTATTGAAGCTGTGTTTATGGAAGCTTCAAAGGAACACACAGGAATGTTCTGCGGTTTATATACGTATCAAT
ACGAGACGATGATGGAGAAATGCGTCCAGTACTCATAATACCATTCCGAGGATATGGATATCATAATGATTCTTATTATTTCGAAGGGAAGGGGAAAGTTGAATGTGATATATCATCAGA
TTATGTAGCGCCAGGAGTGCATTGGAGCAGAGACATGGAAGTTAGTATTAGCAACAGCAACAACCTGTAAATGAATTATGTGATCTGAAGTGTATGTTGTTGTTGCTTGAAGATAAAGGA
ATAACAGATGTGCTTAATGATCATTAATAAAACCTTATTTTCATGAAATGTAGATTGTATAAACAATCAACACACGCTATGACAAACAGGGAATAATGAAAAATCAGGGGTTGATTGGTC
TATCGTATCGCTTAAGGGCCGAGGCCCTTGAAAAATAAATTCGAATTATAACGATGATATAAATCAGAGATAGATGATAAGCATCCAAAAACATAAACGAAGTATATGGCTGTAT
AATATAAAGAACATATAAATAAATAAATCTCTGATTGGTTCAGAACGTAACCCCAACCTTTTATGTTGGTGGAAATGTCCCGATGACGTAAAGCACGGGGACTAT

G/A (54977/218448) **C/G** (59319/220772) **C/T** (61780/233524) **T/C** (62781/236903), + several other SNPs

DNA-R

5/6/7 SNPs to KM607677 KM607676 KM607679 KM607678 (China). **8 SNPs** to AB113660 (Viet Nam). **14-19 SNPs** to MF039879
MF039873 MF039867 (Thailand)

R protein (286 aa): v1=v2 **0 aa** to KM607676 KM607677 KM607679 (China) **1 aa** to MF039879 (Thailand) AF416464 AB113660
(Vietnam)

>R_alyu34_v1
TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCTCCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCCACC
ATCAACAATCCCGCTTCACTACCAGTGATCGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCAAGGATAAGTGCAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAGGAAGAGCACGGGCATCTGTATGAAGGAAGACACAAGAAATCGAAGTCCCTTC
GAGTTTGGTGCCCTTAAATTTGTCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGGTGAACGCACAAACCGGCCCTCGGAGTATTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCCATGAATAGCTGGAAACATCCTTCAGTTTCATGGACATCGGAAGTTGAAAAATATATGGCGGAGCCATGT
CATCGAAGGATAAATTTGGGCTATGCGCCAAATGGAGGAGAAGGAAGACAACCTTATGCAAAATATTTAATGAAGACGAAGAATGCGGTTTATTCACGAGGAGGAAAAATCATGTGATATA
TGTAGATTGTATAATTACGAGGAAATAGTTATATTGATATTTCCAGATGCAAAAGAGGAATATTTAACTATGGTTTATTAGAAGAAATTAATAATGGAATTTATCAAGCGGGAATAT
GAACCCGTTTCAAATTTAGCAATATGTGGAAGTCATTGTAATGGCTAACTCCTTCGGAAGGAAGGAATCTTTTCAAGATCGAATAAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAGCAAGATTCGGGGGTGATTGGCTATCTCTAACGATTAAGGGCCGAGGCCCTCAAGATGGACGGCTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

SNPs close to 50% reads supporting R_v2

>R_alyu34_v2
TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCTCCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCCACC
ATCAACAATCCCGCTTCACTACCAGTGATCGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCAAGGATAAGTGCAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAGGAAGAGCACGGGCATCTGTATGAAGGAAGACACAAGAAATCGAAGTCCCTTC
GAGTTTGGTGCCCTTAAATTTGTCATGTAATGATAATTTATTTGATGTCTATACAGGATATGCGGTGAACGCACAAACCGGCCCTCGGAGTATTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCCATGAATAGCTGGAAACATCCTTCAGTTTCATGGACATCGGAAGTTGAAAAATATATGGCGGAGCCATGT
CATCGAAGGATAAATTTGGGCTATGCGCCAAATGGAGGAGAAGGAAGACAACCTTATGCAAAATATTTAATGAAGACGAAGAATGCGGTTTATTCACGAGGAGGAAAAATCATGTGATATA
TGTAGATTGTATAATTACGAGGAAATAGTTATATTGATATTTCCAGATGCAAAAGAGGAATATTTAACTATGGTTTATTAGAAGAAATTAATAATGGAATTTATCAAGCGGGAATAT
GAACCCGTTTCAAATTTAGCAATATGTGGAAGTCATTGTAATGGCTAACTCCTTCGGAAGGAAGGAATCTTTTCAAGATCGAATAAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAGCAAGATTCGGGGGTGATTGGCTATCTCTAACGATTAAGGGCCGAGGCCCTCAAGATGGACGGCTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

DNA-S

6/16 SNPs to AB113662, AB113661 (Viet Nam). **16-19 SNPs** to KM607535 KM607534 KM607536 KM607533 (China). **20-26 SNPs** to
MF039874 KY427064 (Thailand)

S protein (170 aa): **0 aa** to U97526 AF246122 FJ463044 KX779467 (China) **1 aa** to several isolates

>S_alyu34_v1

TATTACCCCCAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTTAAGATGGGTTTTGGGCTTATGGGCTTATCCAGAAGACCAAAAAACAGCGGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTTGCCCGCAAGCAAACCTAAAAGCTCTATATATACCAAGTGTAGACATATTTGTTACAGAGAACAATGGCAGGATCCGAAGaaATCGATCAA
GAAGAGGCGGGTTGGGCGAAGGAATATGGAAGCAAGGCGGCAACAGCTACGACTACTCTGCTGTTAGGTTCAATATTTGGTTCTTGAAATACCGCTCAAGGTATTTAGGATTGAGCCTAC
TGATTAACAACATTACCAGATATTTTATCTGGAAATGTTTATGCTTTTGGTGTCAAGGTGAACGGTGAACGAATACTTCACTGGGCTATGATTAAAGTTCTATGGGAAATCAACACGCC
GACTACATGTCTGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAGTGGGAACTTGAAGCAGGAGTGCACACAGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACAACCGTGTGGAGGAAGATGTAACAGAGGTGGATTACTTGTATTTGGCATTTTATTTGTAGTGTGGAGTTAGTATTAACTACCAGAACAGAATTACATATCATGT
ATGATATGTTTATGTAACAATAAAACCTTTGTATGGAATAATGACCAAAATAACATACAAGACGCTATGAAATACAAACACGCTATGACAAACAGGGAAAAATGAAGAATCGGGGGTTGATTG
GTCTATCGTATCGTTAAGGGCCGAGGCCGCTTGAATGATTCTTAATAAAACAATAACATGATACGATACGGATAGTTGAATATATAAAACAACGATGTATAAATACACAGAAATGTTGTAT
ACTAATTAATAATAGAGAAGAAAGAAATTTTGTGAAGGATAAGCATCAGAACCCACTTTTAGTGGTGGGTATATGTCCCGAGTTAGTCGCCACGTAAGCGCTGGGGCTTAT

SNPs (all minor – ca. 15–20% reads)

DNA-U3

37–44 SNPs to KY427065 MF039869 MF039875 MF039881 (Thailand)

U3 protein (39 aa): v1=v2 0 aa to KY427065 (Thailand)

>U3_alyu34_v1
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTTATGGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAAAA
TCGGGGTTTGACCGAAGGTCGAAGTGACCGGTCAACAATATTCTGGCTTGGCGAGCAACAAACAAGAAATTAATTTAATTCATATGACACGTGGACGGACCGAAATACTCCTGTATCT
CTATAAATAGCTAAATCTGGCTTGGATAATGTCTCTCGCTCTTCTGTCAAAGTGTTGTGTTGAGGCGGAAGATCGCCATCGGCGATCATCGGACGAAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGAAGCGTATATCGGGTATTATAGACTCTAGCGCAGCTAGAAGTTTCCCTGTACTTGTATTGATTTTGTAAATTCGAAAGAAATTCGTATTTGATAATAATAAAAC
ATCTGGGATTGTTAATGTTTACATTAACTAGTATTAATAATGTACAATAACAATAATTTGTATGAGGAACGAATACAAGAAATATTAATAATGAGGAGCGGTAGCGGTGATAAACAGGTGTTT
AAGGTATAATTAATAATATGCAAGTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATAGAATATTAATAAACCCAAATATATATTATTTATAATACATACAAC
ACGCTATGACAAACCGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCTTAACGATTAAGGCCCGCAGGCCCGTCAAGATGGATGAACGGTTAGATTGATTGCTTAGCCACGAAGA
AAGGATCCTTTTGGGACCACAGACAGACAGCTGTCTACTACTTTTAAAAATAATAATAAACCAATTGACGATAGTACCCCTCCCAAAGATGACGTATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGACAAGAGATAGTGACCTTGGATCCACGATCGGACGATCGTGGTTTGTATGAACCAATGATGACGTAGGGGCTGGGGCTTAT

A6125C (59313/127758) **T/G** (50157/109485) **T/C** (45228/94445) **G/C** (54292/77699) **G/A** (46608/101167) **A/T** (31236/63372) **T/C** (20182/42722) **T/A** (26100/4720) **T/A** (27311/49528) **T/A** (27243/47228) **C/A** (26625/48191) **A/T** (77680/18847) **T/A** (61736/33152) **G/C** (152398/44365) **T/C** (69631/143453)

>U3_alyu34_v2
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTTATGGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAAAA
TCGGGGTTTGACCGAAGGTCGAAGTGACCGGTCAACAATATTCTGGCTTGGCGAGCAACAAACAAGAAATTAATTTAATTCATATGACACGTGGACGGACCGAAATACTCCTGTATCT
CTATAAATAGCTAAATCTGGCTTGGATAATGTCTCTCGCTCTTCTGTCAAAGTGTTGTGTTGAGGCGGAAGATCGCCATCGGCGATCATCGGACGAAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGAAGCGTATATCGGGTATTATAGACTCTAGCGCAGCTAGAAGTTTCCCTGTACTTGTATTGATTTTGTAAATTCGAAAGAAATTCGTATTTGATAATAATAAAAC
ATCTGGGATTGTTAATGTTTACATTAACTAGTATTAATAATGTACAATAACAATAATTTGTATGAGGAACGAATACAAGAAATATTAATAATGAGGAGCGGTAGCGGTGATAAACAGGTGTTTA
AGGTATAATTAATAATATGCAAGTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATAGAATATTAATAAACCCAAATATATATTATTTATAATACATACAACA
CGCTATGACAAACCGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCTTAACGATTAAGGGCCCGCAGGCCCGTCAAGATGGATGAACGGTTAGATTGATTGCTTAGCCACGAAGAA
AGGATCCTTTTGGGACCACAGACAGACAGCTGTCTACTACTTTTAAAAATAATAATAAACCAATGACGATAGTACCCCTCCCAAAGATGACGTATAGGGGTGTCCCGAGGTAATTT
AACATAGCTCTGACAAGAGATAGTGACCTTGGATCCACGATCGGACGATCGTGGTTTGTATGAACCAATGATGACGTAGGGGCTGGGGCTTAT

ALYU-35 – *Musa sp.* – *Vietnam*

Virome

- 1. **BBTV** six components
- 2. **BBTA6** *alyu35* – new alphasatellite named here Banana bunchy top alphasatellite 6, genus *Banaphisatellite*

BBTA6

Best matches to MF510475 MF510474 75% coverage 66.6% identity Faba bean necrotic yellows virus associated alphasatellite 2; AJ132187 AJ005966 74% coverage 66.3–66.6% identity Faba bean necrotic yellows C9 alphasatellite; MK291270 68% coverage 64.6% identity Sophora yellow stunt alphasatellite 3

Rep protein best matches to ARI50297 100% coverage 61% identities 77% positives Sophora alopecuroides yellow stunt alphasatellite; P0CK6 100% coverage 60% identities 77% positives Faba bean necrotic yellows C9 alphasatellite; ATU31571 100% coverage 60% identities 77% positives Faba bean necrotic yellows virus associated alphasatellite 2

>BBTA6_alyu35
TATTACCCGACTTTGGCGCAGGGCGCACTATAAAAGATGCTGTGAGAAATTGGGTTTCCACAGCAATTTGGAAGCGGAAAGACCAGAGCTCCTGTTTCGGCGCGGAAACTCAATACGCC
CTTGGCAACATGAAGCAAAGAAATCAGCACCACTACAGGGCGTATTTCAGTTGAAGCAAGAACCCGACTGAACGCAGTGAAGAGCATATCCGTTGGAAATCCCAATGCTCGAACCCATG
CGAGCGTCTTTCGACGATGCCCTAGCATACGTCATGAAGAAGCAAAACCCGAAATCGATGGTCCATGGGAATTCGGTATTCGAAATCCGTAAGGGTTCAAAATTAACAGAGCTGTTAGAAATA
CTGGAGGATTTCGGACAAACGAAGTCCTTCAACCCCAAAAATACAGACGAGCCATGGCCAAACAGGCCATGAGTGAGTCTAAGAAAGAAAGCTGCTGAAGAGGATTAGTTATGAACCTGCGA
GAGTGGCAAGTGCAAGTTGACGAGCTTGTGGGAAGAAACCCGATAACAGAACTAATTTTGGGATTTGGACCAAGAGGTGGAGAAAGTAAACAGGATTCGCTAAACATTTAGGTTTA
AAGGATGGTTGGACATATTTGCCCGGTGGTGAACCTCAAAGATATGATGTAACCTGTTATCAAAGGACATGAAAAATAATGTTGTAATGATTTCGCCCGTTGACCAAGGAATTTATTTCA
TATAAATTCCTTGAAGTTGAAGATGAAGCTATATATAGTTATAAGTATGAACCAAGTGGTTCAATCGTATGTAATAAGGTTTCATGTAGTGGTCTTCAGTAATGAGGAGCGAGATTAT
GTAAATTTATCATTTGGATCGAATAAGTGTGATTCTTGCTGAACACGCTATGAAATACAAACACATGAAATACTACACGGGTAGAGTTGTGTATATTAACGATATTTGGGCCGAAGGCC
CAAGCCCAAGCCCATGCCCCAAATGAACGGTCAGAATTGATTGCTTCCCAAGCAAGCAACAAAAATGCGTGGTGAAGAAATTCGCCACGTCATTGGTTACTGTTATCTTTGGCGCAC
TATATATAGGTGCGCCAAAGTCGCCCATAG

DNA-C

24–29 SNPs to KM607098 KM607099 (China) . **26–32 SNPs** to KY427060 MF039864 MF039876 MF039870 (Thailand)

C protein (161 aa): 1 aa to KY427060 (Thailand) **2 aa** to KM607098 KM607099 (China) MF039864 (Thailand)

>C_alyu35
TATTACCCCCCTGCTCGGGACGGGACATCAGTGCATCAAAACAAATGCACGTGACAAAGCAGTAGCTTGTAGCGAAAGACAAACCATCCTATCACAAAAGTGAACGGAATATTCGTTGC
TTAGGGAATGAAGCAACGATACAGATATTTGTTGAGAAAGCGAAATGGAGGCTATTTAAACCTGATGGTATTGTGATTTCCGAAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAAT
CGTCTGCCATGCCAGCAGATGTCAAGAGAGTGATCAAGGAATATATTTGGGAGCATCGAAATAAATCTCTGTTCTGTCAGAAGTTGAAAGGCTGTGTAAGAGAGGATTCTGGAGCATGGAA
ATCAAGATGATGGCCCTAGACGCGAGTGAAGGAGATGAAGACTTCTATATTTCGCTATAGCGGAATATTGAAGAAACCTTGTGTGGTATTGTGTTTGTAGTACTAATAAATCTATTGTCATATA
GGTTAAACCAATGGTGTCTTTTATCATGAATATATTTGAAGACCTAGGTGGTGACTACTCGGTATATCAAGATCTATTCTGTGATGAGGAACCTTCTTATTTCATCGACAGAAGAGAAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATTAACATTTACTGTAATGAATATCCA
TTATCATAAATAAAATAATGGAATGATGATTATGATTCTAGTATATATACATAATGGTATACGTATACGATAAAATACATAAAACCAACATACACACACTATGACAAACCGGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGCCCGCAGGCCGCTTTAAATATGTGGTGGACGAAGTCCACAAACACAAAAAAGTGATCAGAACAATGGAATATAATGAGCT
GGCAACGTAGGAGCCATGTCGGAGTTAGTGGCCACGTGAGCAGGGGGCTTAT

DNA-M

26–31 SNPs to KM607239 KM607240 (China) . **49–52 SNPs** to KY427061 MF039865 MF039876 MF039871 (Thailand)

M protein (117 aa): 1 aa to KC581796 (Thailand) **2 aa** to MF039871 MF039865 MF039877 KY427061 (Thailand)

>M_alyu35
TATTACCCCCAGCGCTCAGGACGGGACATCAGTGCACCTAACAAATGCACGTGACATATATACTACATAACCGGTTTAAACGAACCGTTATATAAGTGTATAACGATAAGTCACGTGTG
ATAGAGACATGCACGTGACATAGTCAAATGATTGAATAAACATTTGACGTCCGGATGTTCCGACGGAAGCTTAGGTTACTTCTGGCGAAGCAAAACATTTATAAAATGGCCTGGATT
GCTGCCATATAATAGGCAAGCAAGGAATGGCATTAAACACAGAGCGAGTGAACATATCTTCTTGAATGGTTCTGTTTCATCGGTGCAATATTTATTGCGGATAACAATATTATATATATTG

TTGGCGTTGCTCTTTGAGGTCCCCAAGTATATTAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACCAGAAGACGTGTATGGATGCAGAGAACGCAGTTGACGGAGGCAACAGGAGATGTAGAGCTCGGCAGAGGTAGTTGTGGAAGACAGACGGGATCAACAACCGGCTGTCATTCCACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGATCAAGGAAGACGAGGAACCCGGGACCGGATGTTTTAATACACGGTATTGTAATATACGAAATATAAATGGATGAATGATGTTGTTGAAACATAATATACGTGAAACATAATATATGTTTGATATTTACATATACTAATATGTAAATGTTATACGAGTGTGTTATTATAGAACATACAACCGCTATGACAAACAGGGAATAAGAAATCGGGGTTGATTGGCTATCGTCATCGTTAAGGGCCGAGCCCGTTGAAATGATTCTTAATAAAAAAATATACATGATACGGATAATTGAAATATAAAACAACGAAGTATAAATACACAGAAATGTTGTATACTAATTAATAATGAGAAGATAAGTATATTTGTGAGGGATGATGATCACAACCACCACCTTTAGTGGTGGGTATATGTCGGAGTTAGTGGCCACGTAAGCGCTGGGGCTTAT

DNA-N

34 SNPs to KM607387 KM607385 (China) . **37-41 SNPs** to MF039872 MF039878 KY427062 MF039866 (Thailand)

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (Thailand) KM607387 KM607385 (China) **1 aa** to MF039866 (Thailand)

>N_alu35
TATTACCCCCGCTGCTCGGGACGGGACATGACGTCAGCATAGATTATAATGGGCCAACTAAAGGCCCATTTAATAGAATAGCGGGGCTTTTGACATATTTCAAAGGCCAGCCTGGAAAGTGGATAATGTCACGTGCCGAATAAGAGGTTGCTTCGCCTCGAAGCAATCCGAATAAATGTTGCGTATTCAATACGCAACTGAAGTCTATTAAATATGGATGTCCTCGCCGAATAAATCAGAGCTAAGCGAAGCAGAAGCGATGGATTGGGCAGAATCACAATTCAGACATGTACTCATGGTTGCGATTGGAAGACGATATCATCGGATTCATCCGAGAATCGACAATATGTACCTTGCGTCGACGCTGGCAGTGGAGAAGTCTCCTCGCAAGGTACTGCTTAGATCTATTGAAGCTGTGTTAAATGGAAGCTTCAAAGGAATAACAGGAATGTTTCGTGGGTTTATATACGTATCAATACGAGACGATGATGGAGAATGCGTCCAGTACTCATAATACCATTGCGAGGATATGGATATCATAATGATTCTCTATTATTTCGAAGGGAAGGGGAAGTTGAATGTGATATATCATCAGATTATGTAGCCCGAGACTCGATTGGACGAGACATCGAAGTTAGTATTAGCAACACCAACAACCTGTAATGAATTATCTGATCTGAAGTGTATTGTCTTCTTCTCGTTAAGAATAAAGGAATAACAGATGTGCTGTAATGATTATTAATAAAAAATATTTTCATGTAAATGATAGTTGTATAAAACATACAAACACTATGAAATACAAACAGCTATGACAAACAGGGAAAAATGAAAAATCGGGGGTTGATTGGTCTATCGTAAAGGCCGTGAAAAATATAATCGAATATATAAACGTTTGATAATAATCAGAGAAAGATGATAAGCATCCAAAAACATAGACGAAGTATATGGCTGTATAATATAAAGAAGCATATAAATAAAATATGTGAATCTCTGATTGGTTGAGAAGTAAACCCCAACTTTATGTTGGTGGAATGTCCCGATGACGTAAAGCAGGGGACTAT

17 nt insert downstream of ORF identical to that in alu32_Gabon

DNA-R

12 SNPs to AF416475 AB113660 (Viet Nam) . **14 SNPs** to MF039879 (Thailand) . **14-16 SNPs** to KM607677 KM607678 KM607676 KM607679 (China) . **15 SNPs** to AB113659 (Viet Nam) . **16-17 SNPs** to MF039873 MF039867 (Thailand)

R protein (286 aa): 1 aa to AF416464 (Vietnam) **2 aa** to KM607676 KM607677 KM607679 (China) **3 aa** to AB113660 (Vietnam) MF039879 (Thailand)...

>R_alu35
TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCCCCTCCACTCCAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAACATCAACAATCCCCGTTCACTACCAAGTATGCGGGGAAGATATAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCTATGTGCAAGGATACGTCGAGATGAAGAGACGAAGTTCTCTGAAGCAGATGAGAGGCTTCTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAAGAAGACACGGGCATACTGTATGAAGGAAGACACAAGAAATCGAAGTCCCTTCGAGTTTGGTGCTTTAAATTTGCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGGTGAACGCAACAAACGGCCTTTGGAGTATTTATATGAGTGTCCAATACCTTCGACAGAGTAAGGATACATTATACAGAGTTCAAGCAGAGTTAAATAAAACGAAAGGCGATGAATAGCTGAAACATCCTTCAGTTCTTGACATCGGAAGTTGAAAAATATTATGGCGGAGCCATGTCTCAGAGGATATAATTTGGTCTATGGCCCAATGGAGGAGAAGGAAGACAACTATGCAAAATATTTAATGAAGACGAAGATGCGGTTTATTCGCCAGGAGGAAAAATCATTTGGATATACTAGATTTGATAAATATGAGGAATATGTTATTTGATATTTCCAGATGCAAAAGAGAAATATTAAACTATGGTTTATTAGAAGAAATTTAAAAATGGAATTTATCAAAGCGGGAATATGAACCCGTTTTGAAAAATGTAGAATATGTGGAAGTCATTGTAATGGCTAACTTCTTCCGAAGGAAGAACTTTTTCAGAAGATCGAATAAAGCTAGTTGCTTGCTGAACACGCTATGCAATCGTACGCTATGACAAAGGGGAAAAAGCAAGATTTCGGGGGTTGATTGGGCTATCCTTAACGATTAAAGGGCCGAGGCCGCTCAAGATGGACGGGTAGATCAGATGTCCCGAGTTAGTGGCACGTAAGCGCTGGGGCTTAT

DNA-S

15 SNPs to AF148945 (Viet Nam) . **16-18 SNPs** to KM607534 KM607535 KM607536 KM607533 (China) . **17-20 SNPs** to AB113662 AB113661 (Viet Nam) . **21-27 SNPs** to MF039874 KY427064 (Thailand)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) . **1 aa** to several isolates

>S_alu35
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTTGGGCTTATGGGCTTTATCCATAAGACAAAAACAGCGCGGGAACCGTCCCAATTTCAAATTTAGATAGCTTGCTCGCAAGCAAACTAAAGTCTATATATACCAAGTGTAGACATATTGTTGAGATAACAAATGGCGAGGTTCCGAAGAAATCGATCAAGAGCGGGTTGGCGAGCGGAAGTATGGAAGCAAGGCGGCAACCACTGACGACTACTCGTCTAGGTTCAATATTGGTTCTGAAAAATACCGTCAAGGTATTAGGATTGAGCCTACCGATTAACCAATTACCCAGATATTTTATCTGGAATAATGTTATGCTTTTGGTGCAAGGTAAGCCCGGAGCAATACTTCACTGGGCTATGATTAAAGTTTCATGGGAAATCAACAGCCGACACTAGCTGCTGGAAGCACCAGGTTTATTATATAAACCTGAACATAGCCATCTCGTGAACTGGTATGCACTGGGGAAGTTGAAGCCGGAGTCCGAACAGGGACATCAGATGTTGAATGTCTTCTAAGGAAGACAACCGTGTGAGGAAGAATGTAACAGAGGTGGATTACTGTTATTTGGCATTTTATTGTAGTGTGGAGTTAGTATTAACTACCAGACAGAAATACATATCATGTATGATATGTTTATGTAACATAAACCTTTGTATGGAATAATGACCAAAATACATATCAACACACTATGAAATACAAACGCTATGACAAACGGGGAAAAATGAAGAATCGGGGGTTGATTGCTATCGTATCGCTTAAGGGCCGAGGCCCGTTGAAATGATTCTTTATAAAAAAATAATATACAGGATACGGATAGTTGAAATATAAAACAACATGTATAAATACAAACAGAAATGTTGTATACTAATTAAAAAATGAGAAGAAAAGGATATTTGTGAAGGATAAGCATCAGAACCACTTTAGTGGTGGGTATATGTCCCGAGTTAGTGCCGACAGTAAGCGCTGGGGCTTAT

DNA-U3

37-45 SNPs to KY427065 MF039881 MF039875 MF039869 (Thailand)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alu35
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTAAATGGGCGAGAGAGTTGAACAGTTAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAAGCGTGTCAAATTCGGGGTTTGACCGAAGGTTCAAGGTAGACGGTCAACAATATTTCTGGCTTGCGGAGCAAGCAACACGAATTAATATTTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTATCTCTATAAATAGCTTAAATCTGGCTTGGATAATTGCTCTCGCTTCTGCTCAAAAGCTGTTGTGTTGAGGCCGAAGATCGCCATCGGCGATCATCGGACGAAAGCTGCAAGAGAGACGGGAACCATGCCCAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTTCTTGTACTTGATATTGTTATTTTGAATTTACGAAGAAATTCGTATATTGATAATAATAAAACATCTGGGATGTTAATGTTTACATTAAACAGTATTAATATGTACAATAACAAATATTTGATAGGGAACGAATACAAAAATATTAATAATGAGGAGCGTAGCATGATAAACAGGTTGTTAAGGTATAATTAATTAATTTATGCAATGTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATAAGAATATTAATAACCAATTTATTTATTTATAGGACATACAACACGCTATGACAAAAGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCTAACGATTAAAGGCCGAGGCCCTCAAGATGGATGAACGGTTAGATTGATTGCTTAGCTACGGAAGAAGGAATCCTTTGGGACCACAGACAGACAGCTGTCACTACTTTTAAAAAATAATATAAACAACAAATGACGATAGTACCCCTCCCAAGATGACGCTATAGGGGTGCCGAGGTAATTAAACATAGCTCTGCAAGAGATAGTGGACGTGGATGCCAGCATCGGACGATCGTGTTTGTATGAACTAATGATGACGTAGGGGCTGGGGCTTAT

ALYU-36 - *Musa sp.* - Vietnam

Virome

1. **BBTV** six components
3. **BBTA2** alyu36 isolate of Banana bunchy top alphasatellite 2, genus *Muscarsatellite*

BBTA2

best match to EU430730 100% coverage 99% identity; NC_038953 100% coverage 97% identity; MG545616 (100% coverage, 97% identity

Rep protein best matches to ACB86656 100% coverage 99% identities (1 aa), 100% positives; AZL93963 100% coverage 99% identities (2 aa) 99% positives; YP_009508281 100% coverage, 94% identities (11 gaps in middle) 95% positives

>BBTA2_alu36
TATTACCACTCGCGCACTACCTCCGCGCACTATAAAATGTCGCTCTCGTTGGACATTTACGCTTCACTATTCCGACGCAACGAGCGAGGCAAAATTCCTCGGACTTTGAAGGAAGAAGATGTGCACTACCGCGTCGTCGGCGACGAACTGCTCCGAATACTGGTCGGAACATCTTCAAGGATATCTTTCTTGAAGAAAGCTTTTCTGATTAGCGGAATAAAGAAGAATA

DNA-C

C protein (161 aa): 2 aa to KY427060 (Thailand) 3 aa to KM607098 KM607099 (China) MF039864 (Thailand)

>C alvu36

DNA-M

34-38 SNPs to MF039865 KY427061 MF039876 MF039871 (**Thailand**)

M protein (117 aa): 2 aa MF039865 MF039877 KY427061 (Thailand) 3 aa to KC581796 (Thailand)

>M alvu36

DNA-N

16-23 SNPs to MF039872 MF039878 MF039866 KY427062 (Thailand). **23 SNPs** to KM607387 KM607385 (China)

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (Thailand) KM607387 KM607385 (China) 1 aa to MF039866 (Thailand)

>N alvu36

ATATACCCCGCTGTGGGACGGGACATCTTCAGCATAGATTTAAATGGGCCAATGAAGGCCCACTTAATAGAAATAGCGGGGCTTTGGACATATTTCAAGGCGCCAGCGTGGAAAT
 GGATATGCTACGCTGCTCTATAAGAGTGTGCTTCGCCCTCGAAGCAACCGGAATAAATGTTCGCTATTCATACGCACTGAAGCTCTATTAATATGATGTCTCTGCGCGAATAAATCAGAG
 CGTAAGCGAAGCAGAAGCATGGATTGGCGAAGTACAATTCAGACATGTACTCATGGTTCGATTGGAAGCACTATCATCGGATTCATCCGAGAACTCAGCAAAATATGTACCTTGGCT
 CAGCGCTGGGACGGAGAAAGCTCACTTCGCAAGTGCTCGTAAGTCTATTTGAAGCTGTGTTTAAATGGAAGCTTCAAGGAAATAACAGGAATTTCTCGGGTTTATATACGCTATCAAT
 ACAGCAAGCATGTAGGAGAAATCGCTCGAGTACTCATATAACCATTCGGAGGATATGATATCATTAATGTTCTTATTATTTTCAAGAGGGAAGGGGAAATTTGAATGTGATATATCATCAAG
 TATGTAGCGCCAGGATCGATTGGACAGACAGACATGGAAGTTGATATAGTAAACCAACCACTGTAATGAATCTATGTGATTTGAAATGTGTTATGTTTGTCTTGAAGATAAAGGA
 ATAACAGATGTGCTGTAATGATTTAATAAAAAATATTTTCATGTAATGTAGTTGTGTATAAACATCAACACGCTATGACAAACAGGGAATAATGAAAAATCGGGGGTTGATGGTCT
 TATCGTATGTGTTTGAAGGCGCGAGCCGGTTGAAAAATATATCATGAAATTTAAACGTTGTGATATAATCATCAGATAGATGATGAAGATCTCAAAAAATCAGACGAAGTATATGTGCTGTAT
 AATATAAAGGAGCATATAAATAAATATGTAACATCTCTGATTTGGTTTGATGAATGAACCCCAACCACTTTATGTTGGTGGAAGTCCCGCATAGCAGTAAGCACCGGGGACATAT

DNA-R

10-12 SNPs to MF039879 MF039873 (Thailand). 12-14 SNPs to KM607677 KM607678 KM607676 KM607679 (China). 13-14 SNPs to MF039867 KY427063 (Thailand). 20 SNPs to AF416475 AB113660 (Viet Nam)

R protein (286 aa): 0 aa to KM607676 KM607677 KM607679 (China) 1 aa to MF039879 (Thailand) AF41646 AB113660 (Vietnam)...

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>R alvu36
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TATTACCCCCAGCGCTCGGGACGGGACATTGCACTCATATAAATAGACCTCCCCCCCCCTCACTACAAGATCATCATCGTCGACAGAAATGGCGCGATATGTGGTATGCTGGATGTTCACTACAACAATCCCGGTTCACTACAGTGTACGCGGGATGAGTTTAAATATATGTGATATCAAGTGGAGGGAGGACAGGGGATCTCGTATCTGTCGAGGAGTATCGTCGAGATGAAGAGACAGTTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCCACACCTTGAGAAAGCAAGGAAGGCCAAGAAGACAGCGGCATATGTATGAAGGAACACAAGAATCTGAAGGTCCTCTCGAGTTTGGTGGCTTTAAATTTGTCATGTAATGATATTTATTTGATGTCATACAGATATGCTGGTGAAGCAGCAACCGGCTTTGGGATATTTATATGATGTCGAAATACCTTCGATAGATGAAGTAACATATACAGAGTCAACAGAGCTTGATAAAGCAAGGCGATGAATAGCTGGAATACTCTTCAGTTCTTGGCATCGGAAGTAAAAATATTTGGCGGACGATAGTCAATCGAAGGATATTTGGGCTTATGAGGCCAATGAGGAGAGAAGGAAGACAACCTATGCAAAATATTTAATGAAGACGAAGAATGCGGTTTTATTCGCCAGGAGGAAATTAATTCGGATATATGTAGATTTGATAAATTTAGGAAATAGTTATATTTGATATTTCTGATCGCAAGAGGAACTATTTAACTATGTTTATATGAAGAATTTAAAAATGGAATTTAAACGCGGAAATATGAACCGGTTTTGAAATTTGAGAAATGTAGAAATCATATGATGGCTAATCTCTTCCGAAGGAAGGAATCTTTCAAGAGTCGAAATAAGCTAGTTGCTTGCTGAACACGCTATGACAACTGATCGCTATGACAAAGAGGGGAAAGCAAGATTCGGGGGTTGATTGCTATCCTTAACGATTAAAGGCCCGCAGGCCGTCAGATGGACGGTTTGATCAGATGCTCCGAGTTATGTCGCCACCTGATAGCGCTGAT

DNA-S

9/12 SNPs to AB113661 AB113662 (Viet Nam). 16 SNPs to MF039874 (Thailand). 18-22 SNPs to KM607535 KM607534 KM607536 KM607533 KY427064 (China). 22 SNPs to AF148945 (Viet Nam)

S protein (170 aa): 0 aa to AY33771 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) 1 aa to several isolates

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>S alyu36
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TAT TAT CCCC CAGCT CGGG CAG GGC AAT CTA TGA TGA TCA TGA TTA AAG GGC CCA TCG GGC CCG TTA AAG AT GGG TTT TGG CCG TAT TGG CCG TAT TCC CAGA AAG CAAAA AAG CAG GGC
GAAC CGT CCG CAA TT TCA AAT TTAG ATAG CT TGC CC CAG ACAA GAA TAA AAG CT TAT ATA CCA GGT TAG CAA TAT TTG TCA GAG ACAA AAT GGC GAG GTT TCC GAA CAA AAT CGT CAA
GAAG AGG CCG GGT TGG CGC AGG AAG TAT GGA AGC AAG GCG GGC AAC CAG TCA CTA TCT CGT CGT TAG GTT CAA AT TTT GGT ACT GAAA ATAC CGT CAAG GTT ATT TAG GAT TAG GCCT AC
TG ATAAAA ATAC CAG GAT ATT TTAT CT GAAA AT GTT AT CT TTT TGG TGT GTC AAG GT GAAG CCG GAA GAA TCA TCT CCG GGT ATG TTT AAAAG GT TCT GGG AAA AT CCAAC CGC
GACT ACAT TCT GGA GAA CAG CAG GGT TTAT TATA AAA CCT GAAC AT CAG GACT CTT GGT GAA C TGTA GAT CAG TCG GGG AAT CT GAAG CCG GGT CGCA AAG CAG GGA CT CAT GAT TT GAA GT
TCT TCA AGA GAA CCA CCG GTT GGA GGA AAG AT TAA CAG AGG GT GATT AT CTG TAT TTG GCA TCT TAT CTT AGT CCG TGG AAT TGAT TAA TCA CAG AAG AAT TACA TAT CAT GT
ATG AT TAT TTG TAA CAA TAAA CTT TTG TGA TGA AT TACA CAA TAA CTA CAA GAC AGT TCA GAA TCA CAA CAG CCA TCA GCA ACAA GGG AAAA ATG AAG AAT CCG GGG GTT TAT GT
GCT CTA CTG TAT CGCT TAA GGA GGG CAG GCG CTT GAA AT GAT TCT TTATA AAA CAA TATAC ATG TCA GCG TAT TTG TAAA AAT TAA TCA AAG TAT TAA TAA TCA CAA GAA CTT GTG AT
ACT AAT TAAAAA ATGAGG AAAAAA AAT TTG TGA AGG ATA GCA TCA CAA CACC ACT TTAG TGG TGG GTG CAT GT TCCG GAT TATG CCGGC CAG TAC GCG CTT AGC GTGGG CTT AT

DNA-U3

37-43 SNPs to MF039881 MF039875 KY427065 MF039869 (**Thailand**)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alyu36
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTTGAAACAGTTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAAGCTGTTCAAAA
TCGGGGTTTGACCCGAAGGTCAGGTAGACGGTCAACAATATCTTGGCTTGGCGAGCAAGCAACACGAATTTAAATATTTAATTCGTAAGACACGTGGACGGACCGAAATACCTCTGAATCT
CTATAAATAGCTTAAATCTGGCTTGGATAATTGCTCTCGCTCTTCTGTCAAAGCTGTGTGTTGAGCGGAAGATCGCCATCGGCGATCATCGGACGAAAAAGCTGCAAGAGAGACGGAGA
ACCATGCTACGAAGCGTATATCGGGTATTTATAGACTCTAGCGCAGCTAGAAGTTCCCTGTACTTGATATTGTAATTTGTAAATACGAAGAAATTCGTATATTGATAATAATAAAAC
ATCTGGGACTGTTAATGTTTACATTAAACAGTATTAAATAATGTATAATAACAAATATGTATGAGGAACGAATACAGAATATTTAAATATGAGGAGCGTAGCGGTGATAAACAGGTGTTT
AAGGTATAATTAATTAATTATGCAATGTCATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTTAAAAACCAATTTATATTATTATATAACATACAC
ACGCTATGACAAACGGGAAAAAAGAAAAATCGGGGTTGATTGGTCTATCTTAACGATTAAAGGCCCGCAGGCCCGTCAAGATGGATGAACGGTTAGATTGTTGCTTAGCCACGAAAGA
AAGGAATCGTTTTGGGACCCTGACAAGACAGCTGTCACTACTTTAAAAATAATATAATAACCAATTGACGATAGTACCCCTCCCAAGATGACGTATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGACAAGAGATAGTGGACGTTGGATGCCAGATCGGACGATCGTGGTTGATGAACATATGATGACGTAGGGGTGGGGCTTAT

ALYU-37 - Musa ABB bluggoe type rosé - Vietnam

Virome

1. **BBTV** six components
2. **BBTA2** *alyu37* isolate of Banana bunchy top alphasatellite 2, genus *Muscarsatellite*
3. **BBTA5** *partial*: 275 nt *contig* to *alyu32_38_40*; above cross-contamination threshold -> low titre infection?

Minor genetic variants in M, N, U and Babu2

BBTA2

Best match to EU430730 100% coverage 98% identity; MG545616 100% coverage 97.5% identity; NC_038953 100% coverage 96% identity

Rep protein best matches to AZL93963 100% coverage 99% identities (2 aa) 100% positives; ACB86656 100% coverage 99% identities (1 aa) 99% positives; YP_009508281 100% coverage 94% identities (11 gaps in middle) 95% positives

>Babu2_alyu37
TATTACCCACCTCGCGCACTACCTCCGCGCACCTATAAATGTCTGCCTCTCGATGGACATTTACGGTTCACCTATTCGAGCGCAACGGAGCGAGGCAAATTCCTCGCGACTTTGAAGGA
GGAAGATGTGCACTACGCCGTCTCGCGGACGAAACCTGCTCCGAATACTGGTCGAAAGCATCTTCAAGGATATCTTCCCTTGAAGAAACGTTTTCGTATTACCGGAATAAAGAAAGAAATTA
TTCGTCGAGAGCGCATTTGGGAGAAAGCTCGAGGATCAGACTACGACAACAAGGCGTACTGTTCCAAAGAAAGCCCTAATTCTTGAATTAGGGGTTCCTTGCCAAACAGGTTTCAATAAGCG
TAAATTAGCAGATATGGTTACAAGATCGCCGGAACGAATGAAAATTTGAACAGCCAGAGATATTTACCCGATACGAATCGGTGAAGAAAGATGAAAGAAATTCAAAGAAAGGTATGCTTATCC
TATCCTCGATAGGCCATGGCAGGTACAATTAAACGGAGTTAATTGAAGCAGAACCTGATGATCGAACGATCATCTGGGTATTCGGACCAAAGGGAATGAAGGCAATCAACGTATCGCAA
GTCATTAATCCAAAGAGTATGGTTCTACACAAAGGGGAGGAAGAGAGAAACATATTTGTTCCGCTACGTAGATGAAGGTTTCGACCAAAAACGTTGTATTGATCTTCCGCGTACAGTACA
AGAATTTTATTAATTATGATGTTATCGAAGCATTTGAAGGATAGAGTAATCGAGAGTACAAAATACAAGCCTGTGAAGTATTTAGAATTGAATACTGTACATGTACTAGTTATGGCTAATTT
TCTTCCGTATATGTTGTAATAATCTGAAGATCGAATAAAAATAGTTGCTTGTGTAACACGCTATGAAATACAACACGCTATGACAAACGGGAAAAATGAAGAAATCGGGGTTGATTGGG
CTATCCTAACGATTAAAGGCCCGCAGGCCCGTCAAGATGATCCATAACCCGTTAAGAAGTTAAACGGGTCTAAAACGATAAATCTCGCCCGCAAGCAACACCTTTAACTCTCGGCACCT
ATATATAGCGGAGTGGGCTAG

BBTA5 partial

>BBTA5_partial
ACTTAAAGAGTGGCAAAAGATGGTTATTGAGTTAATCGAAGAACACACGACACAGAATATTATCTGGTCTATGGACCTAATGGTGGAAGAGTAAAACGAGTTTCGCAAGCAAT
ATGGATTACTCAAGGATGGACATATCTACAGGTGGTGAATGAAAGACATGATGATCTGTGGCAAAGAAATTAATAATAACGTTATTATTGATTTCGCCCGATGTACAAAGGATT
TCATATCCTATAAGTTTATTGAGATGGTAAGAAC

DNA-C

23/26 SNPs to KM607098 KM607099 (China) . **29-35 SNPs** to KY427060 MF039876 MF039864 to MF039870 (Thailand)

C protein (161 aa): 1 aa to KY427060 (Thailand) 2 aa to KM607098 KM607099 (China) MF039864 (Thailand)

>C_alyu37
TATTACCCCCCTGCTCGGACGGGACATCACGTGCATCAACAATGCAAGTACGAGTGGTGTAGCGAAAGATAAACCATCACTATCAGAAAAGTGAGAGGAATATTCGTTGC
TTAGGAGCTAAGCAACGAGGACAGATATATGTTGAGAAGCGCAATGGAGGCTATTTAAACCTGATGGTTTTGTGATTCCGAAATCACTCATCGGACGAGAAATGGAGTTTTGGGAAT
CGCTCGCCATGCCAGATGTCAAAGAGAGTATCAAGGAAATATATTGGAGAGCTCGAAATAAATCTGTTCTGTCAGAAAGTTGAAAGGCTGTGAAGAGGATTCTGGAGCATGGAA
ATAAGATGATGCTCTAGACGCAAGTGAAGAGATGAAGACTTCTATTTATTCGCTATAGCGAATATTTGAAGAAACCTTGTGTGGTATTGTTTTAGTACTAATAAATCTATTGCTTATA
GGTTAAACACAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTACTCGGTATATCAAGATCTGTTTTGTGATGAGGAACCTCCTTATTCGTCGACAGAAAGAAAG
ATGAAGAAATATATACAGGAATGTTATCATGGCATCGACAGAGAGAAGATCTCTGGAGTGAAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATCTACTGTAATGAATATCCA
TGTATCATATAAATAATGGAATGATGATTCTAGATATAAATACATATAACATATACGATACGATAAATAACACATACAAACGCTGATCAACACCGGTAATGAAGGCGGAAAAAT
GAATATCTGGGGGTTGATTGGGCTATCTTAACGATTAAAGGCCGAAGGCCGTTTAAATATGTGGTGGACGAAGTCCACAACACAAAAAAGTGATCAGAACAATGGAATATATGAGCT
GGCAACGTAGGGACCATGTCGCCGAGTTAGTGCGCCACGTGAGCAGGGGGGACTAT

DNA-M

28-33 SNPs to KM607239 KM607240 (China) . **51-52 SNPs** to MF039871 KY427061 MF039865 MF039876 (Thailand)

M protein (117 aa): 1 aa to KC581796 (Thailand) 2 aa to MF039871 MF039865 MF039877 KY427061 (Thailand)

>M_alyu37
TATTACCCCCAGCGCTCAGGACGGGACATCAGTGCATCAACATATGCAAGTACGATGATATATACTACATACAGGTTTAAATGAACCGTTATATAATGTTATAACGAAAAGTCACGTGTG
ATAGAGACCTGCACGTTGACATAGTCAAAATGTTTGAATAAACATTTGACGTCCGGATGCTTCCGACGGAAGCTTATGTTACTTCTGTTGGCGAAGCAAAACATTATATATTTGCCCTGGAGCT
GCTGCCATATAAATAGGCAAGCAAGGAAATGGCATTAAACAACAGAGCGAGTGAATCTTCTTTGAATGGTTTCTGTTTCATCGGTGCAATATTTATTGCGGATAACAATATATATATATTG
TTGGCGTGTCTCTTTGAGGTCCCCAAGTATATTAAGGATGTTGTGAGGTAATCTCGTAGAATACCTGACCAGAAGACGCTGTATGGATGACAGAGAACGCGTTTACGGAGGCAACAGGAGAT
GTAGAGCTCGGCAGAGGTAGTTGGGAAGACAGACGGGATCAACAACCGGCTGTCATACCATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGAGCAAGGAAGACGAGGA
AACGCCGGAACCAATGTTTAAATACACGGTATTGTAATATACGAAATATAAATTTGGTAATGATATCTATTGTTGAACATATAATACGTGAACATATAATATGTTTGATAATTTACATATT
GTAATATGTAATATGATATACGAGTGTGTTATTTATAGAACATACAACACGCTATGACAAACAGGGAATAAGAAATCGGGGGTTGATTGCTCTATCGTATCGCTTAAGGCCGCGAGCG
CCGTTGAATGATTCTTAAATAAAACAAATATACATGATACGGATAGTTGAATATATAAACAACGAAGTATAAATACAACAAATGTTGTATACTAATTAATAATGAGAAGATAAGTAT
ATTTGTGAGGGATGATGATCACAACCAACCACTTTAGTGGTGGGTCATATGTCGCCGAGTTAGTGGGCCAGTAAGCGCTGGGGCTTAT

DNA-N

11-13 SNPs to MF039872 MF039878 MF039866 (Thailand) . **14 SNPs** to KM607387 KM607385 (China) . **15 SNPs** to KY427062 (Thailand)

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (Thailand) KM607387 KM607385 (China) 1 aa to MF039866 (Thailand)

>N_alyu37
TATTACCCCCCGTGTGGGACGGGACATGACGTGACATAGATTATAATGGGCCAACTAAAGGCCCATTTAAATAGAATAGCGGGGCTTTTGACATATTTCAAAGGCCAGCCTGGAAAGT
GGATAATGTACAGTGCCTAATAAGAGGTTGCTTCGCCTCGAAGCAATCCGAATAAATGTTGCGTATTCAATACGCAACTGAAGTCTATTAAATATGGATGTCTCTGCCGAATAAATCAGAG
CTGAAGCGAAGCAGAAGCGATGGATTGGGCAGAAATCACAATTCAGACATGTACTCATGGTGGCATTTGGAAGACGATATCATCGGATTCATCCGAGAATCGACAATATGTACCTTGCCT
CGACGCTGGCAGCGGAAGAAAGTCACTCGCAAGGTACTGCTAAGATCTATTGAAGCTGTGTTAATGGAAGCTTCAAAGGAATAACAGGAATGTTCGTGGGTTTATATACGTATCAAT
ACGAGACGATGATGGAGAAATGCGTCCAGTACTCATAATACCTTCGGAGGATATGGATATCATATGATTTCTATTATTTCGAAGGGAAGGGGAAGTTGAATGTGATATATCATCAGA
TTATGTAGCGCCAGGATCGATTGGACGACAGACATCGAAGTTAGTATTAGTAACAGCAACACTGTAATGAATTATGTGATCTGAAGTGTATTGTTGTTCTGTTTGAAGAAATAAGGA
ATAACAGATGTGCTGAATGATTATTAATAAATCTTATTTTCATGTAAATGATAGTTGTATAAAACATACAACACGCTATGACAAACAGGGAATAAATGAAAAATCAGGGGTTGATTGGTC

TATCGTATCGCTTAAGGGCCGAGGCCCGTTGAAAAATAATAATCGAATTATAAAGCTTTGATAATAATCAGAGATAGATGATAAGCATCCAAAAACATAGACGAAGTATATGGATGTAT
AATATAAACCAAGCATATAATAAAATATGTGAACATACTCTGATTGGTGCAGAACGTAGCCCCACTAACCTTTAAGTTAGTGGAATGTCCCGATGACGTAAAGCAGCGGGGACTAT

DNA-R

10 SNPs to AF416475 AB113660 (**Viet Nam**) . **10-12 SNPs** to KM607678 KM607677 KM607676 KM607679 (**China**) . **18 SNPs** to AB113659 (**Viet Nam**) . **18-21 SNPs** to MF039873 MF039879 KY427063 MF039867 (**Thailand: Chonburi**)

R protein (286 aa) : 1 aa to AB113660 (**Vietnam**) KM607676 KM607677 KM607679 (**China**) **2 aa** to several isolates ...

>R_alyu37
TATTACCCCGAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCTCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAACC
ATCAACAATCCCGCTTCACTACCACTGATCGGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCGGGATACGTCGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCAGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAAGAAAGCAGGGGCATCTGTATGAAGGAAGACACAAGAAATCGAAGGTCCTCTC
GAGTTTGGTGCCCTTTAAATTTGTCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGTGAAACGCACAAACGGCCTTTGGAGTATTTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCGATGAATAGCTGGAAGACATCCTTCAGTGCATGGACATCGGAAGTTGAAAAATATATGGCGGAGCCATGT
CATCGAAGGATAAATTTGGGCTCTATGGCCCAATGGAGGAGAAGGAAAGACAACCTATGCAAGTATTTAATGAAGACGAAGAATGCGCTTTTATTCTCCAGGAGGAAATCATTTGGATATA
TGTAGATTGTATAATTACGAGAAATAGTTATATTTGATATTTCCAGATGCAAAAGAGGAATATTAAACTATGGTTTATTAGAAGAATTTAAAAATGGAATTTATCAAAGCGGGAATAT
GAACCCGTTTGAATAATTGTAGAATATGTCGAAGTCATTGTAATGGCTAACTCTCTCCGAGGAAGAAATCTTTCTGAAGATCGAATAAAGCTAGTGTGCTGCTGAACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAGCAAGATTCGGGGGTTGATTGGGCTATCCTAACGATTAAAGGCCGAGGCCCTCAAGATGGACGGCTTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

DNA-S

14/15 SNPs to AB113661 AB113662 (**Viet Nam**) . **19 SNPs** to MF039874 (**Thailand**) . **19-22 SNPs** to KM607535 KM607534 KM607536 KM607533 (**China**) . **25 SNPs** to KY427064 (**Thailand**) . **25 SNPs** to AF148945 (**Viet Nam**)

S protein (170 aa) : 0 aa to AF148068 (**Philippines**) **1-2 aa** to several isolates

>S_alyu37
TATTACCCCGAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAAAGCGCGG
GAACCGGTCCCAATTTCAAATTTAGATAGCTTGCCCGCAAGCAAACTAAAAAGTCTATATAACCACTGTAGACATATTGTTCCAGAGAAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGGCGGGTTGGCGCAGGAATATGCAAGCAAGGCGGCAACTAGTCACGACTACTCGTCGTTAGGTTCAATATTGGTTCCTGAAAAATACCGTCAAGGTATTTAGGATTGAGCCTAC
TGATAAAACATTCCAGATATTTTATCTGGAAATGTTTATGCTTTTGGTGTGCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAAAAGTTTCATGGGAAATCAACACGCC
GACTACATCTCTGGAAGCACCAGGTTTATTTATTAACCTGAACATAGCCATCTGGTGAACCTGGTATCGAGTGGGGAACTTGAAGCCGGAGTCGCAACAGGCGACATCAGATGTTGAATG
TCTCTCAAGGAAGCAACCGTTGTTGAGGAAGAATGTAACAGAGGTGAGTACTTGTATTGGCATTTTATTGTAGTCTGGAGTACTGATTAACTACCAGAACGAATTCATCATCATGT
ATGATATGTTTATGTAACATAAACCATTTGTATGGAATATGACCAATAACATACACACGCTATGAAATACACACGCTATGACAAACAGGAAAAATGAAGAATCGGGGGTTGATTG
GTCTATCGTATCGCTTAAGGGCCGAGGCCCGCTGAAATGATTCTTTATAAAACAAATATACATGATACGGATTGTTGAAAAATATAATCAACGATGTATAAATACACAGAAATGATGTAT
ACTAATTAATAATAGAGAAGAAAGAATATTTGTGAAGGATAAGCATCAGAACCCACTTTAGTGGTGGGTCATATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3

36-43 SNPs to MF039881 MF039875 KY427065 MF039869 (**Thailand**)

U3 protein (39 aa) : 0 aa to KY427065 (**Thailand**)

>U3_alyu37
TATTACCCCGAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGGTTTGAACAGTTCAAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAAGCTGTTCAAAA
TCGGGGTTTGACCGAAGGTTCAAGGTAGAGCGGTCAACAATATCTGGGCTTGCGAAGCAAGCAACACGAATTAATATTTAATTCGTATGACAGCTGGACGGACCGAAATCTCCTGTATCT
CTATAAATAGCTTAAATCTGGCTTGGATAATTTGCTCTCGCTCTTCTGTCAAAGCTGTGTGTGAGGCGGAAGATCGCCATCGGCGATCATCGGACGAAAGCTGCAAGAGAGACGGAGA
ACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTTGAAGTTTCCCTGTGACTTGATATTGTTTGTAAATTCGAGAAGAAATTCGTATATTGATAATAATAAAC
ATCTGGGATTGTTAATCTTTACATTAACCACTATTAATATCTCAATAAACAAATATTGTATGAGGAACGAATACAAGAATATTAAAAATAGCAGACCGTACCGTGATAAACAGGCTGTT
AAGGTATAATTAATTAATTTATGCAATGTCATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAACCAACCAATATATTTATTTATAATACATACAAC
ACGCTATGACAAACGGGGAAAAAGAAAAATTCGGGGTTGATTGGTCTATCTCAACGATTAAAGGCCCGAGGCCGTCGAAGATGGATGAACGGTTAGATTGTTGCTTAGCCACGAAGA
AAGGAATCGTTTTGGGACACAGACAGACAGCTGTCTATTCTTTAAAAAATAATATAATAACCAATTGACGATAGTACCCCTCCCAAAGATACGATATAGGGGTGTCCCGAGGTAAT
TAACATAGCTCTGACAAGAGATAGTGGACGTGGATGGCACGATCGGACGATCGTGGTTTGTATGAACCAATGATGACGTAGGGGTGGGGCTTAT

ALYU-38 - *Bidens pilosa* - **Vietnam**

Neighbour to Musa ALYU-37 (Musa ABB infected with BBTV + one satellite BBT2)

Virome

1. **BBTV** six components - identical to BBTV components in alyu37 (the Musa neighbour)
2. **BBTA5** alyu38=40 - identical to **BBTA5** alyu40 (Musa ALYU-40 at another location)
3. **BBTA6** alyu38=26=27 - identical to **BBTA6** alyu26 (Musa ALYU-26 at another location) and its *Commelina* neighbour alyu27
4. **BBTA2** alyu38=37 - identical to **Babu2** alyu37 in the Musa neighbour
5. **BBTA3** alyu38=26=27 - identical to **BBTA2** alyu26 (Musa ALYU-26 at another location) and its *Commelina* neighbour alyu27
6. **Bidens microvirus** - a new Rep-encoding ssDNA virus, 5051 nt circle
7. **Bidens circovirus** - a new Rep-encoding ssDNA virus, 2164 nt circle

BBTA5 = alyu40 (Musa)

>BBTA5_alyu38
TATTACCCGACCTTGCTCACTGGCTCACTATAAAGGGGGAAATGTGCGAGCAGCGAAATTTGGGTATTCACGCGTAACCTTCCGGCGACCCGCGGATTTTAAAGTTCCGCGGAGAAAC
TCAATACGGGTCTGGCAACATGAGAAGAAGAAATCACGACCATCTTCAGGAGTGATTCAATTGAAGAAGAAGCTCCGGATGAACGCAGTGAAGACGTTAATTTGGGGAAATCCACACCT
CGAAGCCATGAGAGGAACAATCGACGAAGCAATAAAGGTACGTGACGAAGAAGAAACACGAGTAGCAGGTCCTGGGAATTTCGGAGAATTACTACGAAAGGATCTCATAAGAGGAAAT
GATGGAATTGCTCGACGATCCAGATAACGAATAATGGAACCTCAAAAATATCGACGCGCCATTACTAAACAAGCAATGGACGCGTCAAAGAAGAGGCGGAATTAGGTTTCTCTACGA
CTTAAAGGAGTGGCAAAAGATGGTTATTGAGTTAATCGAAGAACAACCGACACAACAGAACTATTATCTGGGTCTATGGACCTAATGGTGGAGAAGGTAAAAACGAGTTCGCAAAAGCATTA
TGGATTACTCAAAGGATGGACATATCTACCAAGTGGTGAACCTGAAAGACATGATGATCTGTGGCAAAAGAAATTAATAATAACGTTATTATTGATTTCGCCCGATGTACAAAGGATT
CATATCCTATAAGTTATTGGAGATGGTAAAGAACCGATGCATATTAGCTATAAATATGAACCAATCGGGCGATTGTAAGTAAATGAAGTTCATGTAGTGGTCTTCAGTAATGAGGACGAGATT
AGATTATTCAAATAATTTCCGAAGACGAATAAAATTAATATTACATAACGCACACTATGACAAACGGCGAAATAATGCAAAATCGGGGTTGATTGTCTATATTTACGAATAAGGGCCG
CAGGCCCGTACACATTGCGCGGGAAATTCAAATTCGGAGCGCAAAATATTATTAATAACAATACACGCGCTTTTAGAAATCCGTGGACGAGAAGATGCCACGTAGCAAAACACTGTACTCC
TTGGCTCACTATAAATACCTGAGCCAGGTGCGGCATAG

BBTA6 = alyu26 (Musa) = alyu27 (*Commelina*)

>BBTA6_alyu38
TATTACCCGACTTTGGCGCAGGGCGCACTATAAAGATGTCTGTGAGAAATTTGGGTCTTCACACGCAATTTCAAGAGCGAAAGACCAGAGCTCCTGTTCCGCGGCGAAACTCAATACGCC
GCTTGGCAACATGAAGAAAGAAATCACGACCCACTACAGGGTGTGATTCAAGTTGAAGAAGAAGCCGACTGAACGCAGTGAAGAGCATAATCCGTGGAAATCCACATGTCGAACCCATG
CGAGCGTCTTTCGACCATGCCATAGCTACGTCATGAAAGACGAAACCGAATCGATGGTCTTCGGAATTCGGTATTCGAATCCGTGAGGTTTCGAATAAACGAAAGCTGTTAGAAATA
CTGGAGGATTTCGACAAACGAGTCTTCAACCCCAAAAATACAGACGAGCCATGGCCAAACAGCCATGAGTGAGTCTAAGAAGAAGCTGCAGAAGAAGGATTAGTTATGGAACCTGCGA
GAGTGGCAAGTGTACCAAGTTGTTGGAGAAGAAGCCGATACAGAACCAATAATTTGGGTATTTGGACCAAGAGGTGGAGAAGGTAAAAACAGAGTTCGCTAAACATTTAGGGTTA
AAGGATGGTTGGACATATTTCCCGCGTGGTGAACCTCAAAGATATGATGTAAGTCTGTTATCAAGAGCAATGAAAAATTAATGTTGAATGATTTCGCCCGTTGACCAAGGAATTTATTTCA
TATAAATCTTGGATGGTTAAGAATAGAACTATATAGTTATAAGTATGAACCAATCGGGCGATTGTAAGTAAATGAAGTTTCATGTAGTGGTCTTCAGTAATGAGGACGAGATTAT
GTAAATATCAGTGGATCGAATAAGTTGATTCTTGTGTGAACGCTATGAAATACAAACACATATGAATACTGTACGGGTATCTGTATGGTTTATCTTAAACGCTATTGGGCGGAAG
GCCACGCCCAAGCCATGCCCAAGGTGAGGCTGCAAGTTGATTGCTTCGCCACGAAGCAACAAAAATCGTGGTGGAGAATTGCCACGTCATTGGGTACTGTTATCTTGGCG
CACTATATATAGGTGCGCCAAAGTCGCCCATAG

BBTA2 = alyu37 (Musa neighbour)

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>BBTA2_alyu38_v1
TATTACCCACCTCGCGCACTACCTCCGCGCACCTATAAAATGTCCTGCCTCTCGATGGACATTTACGCTTCACTATTCCGACGCAACGGAGCGAGGCAAATTCCTCGCGACTTTGAAGGA
GGAAGATGTGCACTACGCCGTCTGTCGGCGACGAAACTGCTCCGAATACTGGTCGAAACATCTTCAAGGATATCTTCCCTTGAAGAAACGTTTTTCGTATTAGCGGAATAAAGAAGAAATA
TTCGTGCGAGAGCGCATTGGGAGAAAGCTCGAGGATCAGACTACGACAACAAGGCGTACTGTTCCAAAGAAAGCCCTAATTCTTGAATTAGGGGTTCCCTTGCCAAACAGGTTCGAATAAGCG
TAAATTAGCAGATATGGTTACAAGATCGCCGGAACGAATGAAAATTGAACAGCCAGAGATATTTCAACCGATACGAATCGGTGAAGAAAGATGAAAGAAATTCAAAGAAAGGTATGCTATCC
TATCCTCGATGGCCATGGCAGGTACAATTAACGGAGTTAATTGAAGCAGAACCTGATGATCGAACGATCATCTGGGTATTCGGACCAAAGGGAATGAAGGCAATCAACGATTCGCGAA
GTCATTAATCCAAAGGATGGTTCTACACAGGGGAGGAAAGAGGAGAACATATTGTCGCCATCGTAGATGAAGGTTTCGACCAAAACCGTTGTATTGATCTTCCGCGTACAGTACA
AGAATTTTATTAAATTGATGTTTCTGAAGCATTGAAGCATAGAGTAATCGAGAGTACAAAATACAAGCCTGTGAAGTATTAGAAATTGAATCTGTACATGTACTAGTTATGGCTAATTT
TCTTCCATGATATGTGTAATAATATCTGAAGATCGAATAAAAAATAGTTGCTTGTCTGAACACGCTATGAAATACAACACGCTATGACAAACGGGGAAAAATGAAGAAATCGGGGGTTGATTGGG
CTATCTTAACGATTAAAGGCGCCAGGCCCGCTCAAGATGGATCCAAATAACCCGTTAAGAAGTTAAACGGGTCTAAACAGATAACTTCGCCCGCAAGCAACACCTTTAACTCTGCGCACCT
ATATATAGCGGAGGTGGGCTAG
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C/T (7275/8316)

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>BBTA2_alyu38_v2
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GGAAGATGTGCACTACGCCGTCTGTCGGCGACGAAACTGCTCCGAATACTGGTCGAAACATCTTCAAGGATATCTTTCCTTGAAGAAACGTTTTTCGTATTAGCGGAATAAAGAAGAAATA
TTCGTGCGAGAGCGCATTGGGAGAAAGCTCGAGGATCAGACTACGACAACAAGGCGTACTGTTCCAAAGAAAGCCCTAATTCTTGAATTAGGGGTTCCCTTGCCAAACAGGTTCGAATAAGCG
TAAATTAGCAGATATGGTTACAAGATCGCCGGAACGAATGAAAATTGAACAGCCAGAGATATTTCAACCGATACGAATCGGTGAAGAAAGATGAAAGAAATTCAAAGAAAGGTATGCTATCC
TATCCTCGATGGCCATGGCAGGTACAATTAACGGAGTTAATTGAAGCAGAACCTGATGATCGAACGATCATCTGGGTATTCGGACCAAAGGGAATGAAGGCAATCAACGATTCGCGAA
GTCATTAATCCAAAGGATGGTTCTACACAGGGGAGGAAAGAGGAGAACATATTGTCGCCATCGTAGATGAAGGTTTCGACCAAAACCGTTGTATTGATCTTCCGCGTACAGTACA
AGAATTTTATTAAATTGATGTTTCTGAAGCATTGAAGCATAGAGTAATCGAGAGTACAAAATACAAGCCTGTGAAGTATTAGAAATTGAATCTGTACATGTACTAGTTATGGCTAATTT
TCTTCCATGATATGTGTAATAATATCTGAAGATCGAATAAAAAATAGTTGCTTGTCTGAACACGCTATGAAATACAACACGCTATGACAAACGGGGAAAAATGAAGAAATCGGGGGTTGATTGGG
CTATCTTAACGATTAAAGGCGCCAGGCCCGCTCAAGATGGATCCAAATAACCCGTTAAGAAGTTAAACGGGTCTAAACAGATAACTTCGCCCGCAAGCAACACCTTTAACTCTGCGCACCT
ATATATAGCGGAGGTGGGCTAG
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BBTA3 = alyu26 (Musa) = alyu27 (Commelina)

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>BBTA3_alyu38
TATTACCCGCTTCTCGCCCTCTTCTCGCCCCAGTGAAGACAGCTGATGCTTCTCCTTTAAATGGTGCTTACGCTGAATTACTCCAACGCAACAGAGAGAGAAGACTTCTCTCTCT
TTTGAAGGAGGAGGACTTGCCTACGCAGTAGTGGGAGACGAAGTCGCCCCGCTCAACTGGTCAGAAGCACCTACAGGGATATATATCCCTAAGGAAGATGTAAGAACTGGGTGGTTTGAA
GAAAAAATACTCGCGGACGAGCAGCTGGGAGAAAGGCAAGGATCAGATGAGATATAATCAAAAGTATTGTTCCAAAGGAAACCCCTAATTCTTGAATTAGGGGTTCTTACATCCAGGGGTT
AAAACAGGCTAAGGTTTACAGAGTTTACAGATCACCAGCAAGCGATGAGGATAGAGATAGACAGCCAGGATATATCAGAGATATCAATCTGTGAATTAAGGTTTAAAGTTCAAAGAGGAAT
CGTACATCCTTGCCTCGATAGACCATGGCAGATACAATTGACGAGGCAATTGAAGAGGAACAGATGATCGAAGTATCATCTGGGTCTATGGACCGGAATGGCAATGAGGGGAAATCAAC
ATATCGCAAGTCTCTGATACCAACATGATTGGTTCTATACAAGGGGAGGCAAGGAGACATCTTCTCCTACGTAGACGAAGGCTTACGAAGCATGTGTGTTTCGCATCGACATACCGAA
ATGTCATCAAGAAATATCAAAATGATGATTAATCGAGGCATTGAAGGATAGGGTGATCGAGAGCACTAAGTATAAGCCGATTAAATATAATCGAGTTGAATAGGGTACATGTAATGTAAT
GGCTAACTTCTATGCCAGACTACTGTAAGATCTCTGAGGATCGAATAAAATTAATTTTGCATACGCCACGCTATGACAAACGGGCAAAAATGCAAAATCGGGGGTTGATTGGGCTATCCT
AACGAATAAGGGCGCAGGCCCGCTCAAGATGGATCCGTTAACCCCGTATCAGATTACTTGGGACGAAGGAATCACTTTAAGTTCTCGCCCTATATATAGTTTGGCCGAGGAAGCGG
CCTAG
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DNA-C = alyu37

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>C_alyu38
TATTACCCCCCTGCTCGGACGGGACATCAGCTGCATCAAAACAAATGCACGTGACAAGAGGTAGCTTGTAGCGAAAGATAAACCATCACTATCACAAAAGTGAGAGGAATATTCGTTGC
TTAGGGAATTAAGCAACGAGGACAGATATATGTTGCAAGAGCCACAATTGAGGCTATTAAACCTGATGCTTTTGTGATTCCGAAATCACTCATCGGACGCAAAATCGAGTTTGGGAAT
CGCTCGCCATGCCAGACGATGTCAAGAGAGTGATCAAGGAAATATATTGGGAGATCGGAAATAAATCTGTTCTGTCAAGAGTTGAAAGGCTGTGAAGAAGGATTCGTGAGCATGGAA
ATCAAGATGATGCTCTAGACGCACTGACATAGTCAAATGTATTGAATAAACATTTGACGTCGGGATTTCCGACGGAAGCTTATGTTACTTCGTGGCGAAGCAAAACATTATATATTGCCCCGGACT
GCTGCCATTAAGATAGGCAAGCAAGAAATGGCATTAAACAACAGGCGAGTGAACATTTCTTTGAATGGTTTCTGTTTCATCGGTGCAATATTTATTCGATATCAATATATATATATTG
TTGCGGTGCTCTTTAGAGTCCCAAGATATTAAGGATGTTGTGAGTATCTCGTAGAATACCTGACCAGAAGACGCTGTATGGATCGAGACAAGCAGCTTTTACGAGGCAACAGGAGAT
GTAGAGCTCGGCAGAGGTAGTGTGGAAAGACAGACGGGATCAACAACCCGGCTGTATACCCACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGAGCAAGGAAGACGAGGA
AACGCCGGAACCAATGTTTTAATACAGCGTATTGTAATATACGAAATATAAATTTGGTAATGATATCTATTGTAACATATAATATACGTGAAACATAATATATGTTTGAATATTTACATATT
GTAATATGTAATATGATACAGGTGTTGTATTATAGAACATACAACACGCTATGACAAACAGGAAAAATGAAGAAATCGGGGGTTGATTGGCTATCGTATCGCTTAAGGCCCGCAGG
CCGTTGAAATGATTCTTAATAAAACAAATATACATGATACGGATAGTTGAATATAAACAACGAAGTATAAATACAACAAATGTTGTATCACTAATTAATAATGAGAAGTAAGTAT
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DNA-M = alyu37

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>M_alyu38
TATTACCCCCAGCGCTCAGGACGGGACATCAGCTGCAACTAACATATGCACGTGACTGATATATACTACATAACGGTTTAATGAACCGTTATATAATGTTATAACGAAAAGTCACGTGTG
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GCTGCCATTAAGATAGGCAAGCAAGAAATGGCATTAAACAACAGGCGAGTGAACATTTCTTTGAATGGTTTCTGTTTCATCGGTGCAATATTTATTCGATATCAATATATATATATTG
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CCGTTGAAATGATTCTTAATAAAACAAATATACATGATACGGATAGTTGAATATAAACAACGAAGTATAAATACAACAAATGTTGTATCACTAATTAATAATGAGAAGTAAGTAT
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DNA-N = alyu37

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>N_alyu38
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AATATAAAACAAGCATATAAATAAATATGTGAACATACTCTGATTGGTGACAGCTAGCCCCCTAATCTTAAGTTAGTGGAAATGTCCTGATGACGTAAAGCAGCGGGGACTAT
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DNA-R = alyu37

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>R_alyu38
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AGTTCTCTGAAGCAGATAGAGGGTCTTCTCCAGGCGCACACCTTGAGAAACAGAAAGGAGACGCAAGAGAGACAGGGCATACTGTATGAAGGAAGACACAAGATCGAAGGTCCTCT
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CATGAAGGATACATTTACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCGATGAATAGCTGGAAGACATCTTCAGTGCATGGACATCGGAAGTTGAAAAATATATTGGCGGAGCCATGT
GTGCAAGGATAAATTTGGGCTATGCGGCTAATGGAGGAAGGAAAGACCACTGTCGAAAGTATTAAATGAAGACGAAGATGCGGTTTATTTCTCGAGGAGAAAAATCATTTGGATATA
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GAACCCGTTTGGAAAAATTGAGAATATGTCGAAGTCATTGTAATGGCTAACTTCTTCCGAAGGAAGGAATCTTTCTGAAGATCGAATAAAGCTAGTTGCTTGTGAACACGCTATGAC
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AATCGTACGCTATGACAAAAGGGGAAAAAGCAAAGATTCGGGGGTTGATTGGGCTATCCTAACGATTAAAGGCCGCGAGGCCCTCAAGATGGACGGCTTGATCAGATGTCCCAGGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

DNA-S = alyu37

>S_alyu38
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GAAGAGCGGGTTGGCGCGCGGAAGTATGCAAGCAAGGCGGCAACTAGTCACGACTACTCGTCTGTTAGGTTCAATATTGGTTCTGAAAAATACCGTCAAGGATTATTAGGATTGAGCCCTAC
TGATAAAACATTACCAGATATTTTATCTGGAAGATGTTTATGCTTTTGGTGTGCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAAGATTTCATGGGAAATCAACGACGC
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ATGATATGTTTATGTAACATAAACCAATTGTATGGAATAATGACCAAAATAACATACAAACCGCTATGAAATACAAACCGCTATGACAAACAGGGAAAAATGAAGAAATCGGGGGTTGATTG
GTCTATCGTATCGCTTAAGGGCCGAGGCCCGTTGAAATGATTCTTTATAAAACAATATACATGATACGGATTGTTGAAATATATAAACACGATGTATAAATACAAAGAATGATGAT
ACTAATTAATAATGAGAAGAAAGAAATTTTGTGAAGGATAAGCATCAGAACCCACCTTTAGTGGTGGGTCATATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3 = alyu37

>U3_alyu38
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CTATAAATAGTCTAAATCTGGCTGGATAATTGCTCTCGCTCTTCTGTCAAAGCTGTGTGTTTGGGCGGAAGATCGCCATCGCGCATCATCGGAAGAAAAAGCTGCAAGAGAGACGGGAGA
ACCATGCTACGAAGCGCTATTCGGGTATTATAGACTTCTAGCGCAGCTTGAAGTTTCCTGTATCTTGATATTGATTTTGTAAATTCAGAGAAGAAATTCGTATGTATAATAAAAC
ATCTGGGATTGTTAATGTTTACATTAAACAGTATTAATAATGTACAATAACAAATATTGTATGAGGAACGAATACAGAATATTAATAATGAGGAGCGTAGCGTGATAAACAGGTTGTT
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ACGCTATGACAAACCGGGAAAAAGAAAATCGGGGTTGATTGGTCTATCTAACGATTAAAGGCCGAGGCCGCTCAAGATGGATGAACGGTTAGATTGATTGCTTAGCCACGAAGA
AAGGAATCGTTTTGGGACCACAGACAAGCAGCTGTCAATTCTTTAAAAAATATATATAATACCAATTGACGATAGTACCCCTCCCAAGATGACGATATAGGGGTGTCCCAGGTAATT
TAACATAGCTTGCACAGAGATAGTGCAGCTTGCAGGACGATCTGGTTGATGAACCAATGATGACGTAGGGGCTGGGGCTTAT

Bidens microvirus

Major capsid protein most related to:
QCS37406 Tortoise microvirus 100 source: Turtle Gopherus morafkai feces 100% coverage 45% identity, 59% positives; 13% gaps; AXH74625 Microviridae sp. source: Macaque stool 67% coverage, 64% identity, 78% positives; 13% gaps
DNA pilot protein most related to:
QCS37408 Tortoise microvirus 100 source: Turtle Gopherus morafkai feces 49% coverage, 35% identity, 50% positives; AXH73738 Microviridae sp. source: Macaque stool 86% coverage, 43% identity, 55% positives
Replication initiator protein most related to:
AXH74235 Microviridae sp. source: Mouse vaginal tissue 86% coverage, 40% identity, 55% positives, 11% gaps; AXH74625 Microviridae sp. source: Mouse vaginal tissue 98% coverage, 37% identity, 50% positives, 12% gaps; QCS37407 Tortoise microvirus 100 source: Turtle Gopherus morafkai feces 78% coverage, 38% identity, 55% positives, 12% gaps

>Bidens_microvirus_alyu38
ATGAAAAAAGCAAATTCAACTAACACACCTACACAGCACACGCTTGACCCCGGCTATCTCGTTCCTTTCTGCTTAATCCCTACGCTCCCAACAGCACTCTTTTAGGCTTGGTCTCTCA
ACATTTCATTTCGAGCGCCAGCAATGCTCGCCCCCTTGATGCATGAAGTTCGCTCTTTACGCAATCTGGTTTGTACCGAATCGTATATTCTGGGAAGAATGGGAAGACTTCATCACCGGT
GGTAATGACCTCTCGCTAACGCCCCCGGTTTCTACAGTCAAACCTCACAGCTGACGATTGCAAGTAGGTTCTCTCACCGCACTATTTGGTTCCTCGCTGGTTCAAGATTGGAGGTCCTCA
GCTCTACCATATCGCGCTATGGCTGAAATCTGGAATACAGCTATCGCGATGAGGATTGCAAGATGAGCTACCCATAGATTACGGCAGTAGTGAAGACACAACGACATCTCGTAAGCTT
CTCTCTCAAAGTTTTCGCCAAGACTCTTCACGACTGCTAGACCTTTTACGCAACGAGGCGGTGACGTGGTTGTTCTCTGTTGTTTCAGCTCCATACTGGCTCCCAATCTGGTAAAAAG
GTTTCCTTTTTCGCTATTATCGGAACAGCTACAAAATCTACTACTGGTGGTTCTGAGCACTTGTTCAGGCTGCACAAAATTTAGCTCTTCACTCTGTTCTGCTATTATTCAAAATTGG
ATTACTGCACGTATTGAAGATGGAACCTATAGACCAACTATTGTTTCACTGATTTTAGGATTGCCATTTGAGGTTGCGAATTCGACTTCTATTGAGACTAATAATTCAACCCCTGACGAT
TGGTCTTTCAGCTTTCGAGGAGGAGTTGGTTCTAGCCAGTATGCAACTGGAATAGTGGTGCACTTTAAAGCTTTTTCCTTTGAGTGTGAAAAATATGAACAACCTGACGCTCTTT
GCTAGTAAGGTCGATTTTCCGATTTTCGCCCAATTTTACTGCCCCGGGTGTTGGTTTCGCTCCATCTAAATGTCGGCTATGGCGCTTTTGGCACTGGTGAAGGACATTTATTATTCGTTTGGT
GACCTTCAAGATCATGACAGTCTTTGACGCACTTATTAAGCTCACAGCTCTTTTTCAGCTTATAGAGTATTTGGTACTGCTATTTATTTGCTGAAACTACTTCTGCTCTGCTTTT
TCAATTTCGAGACTTCGTAGGTGACGGGCTTTCAACGCTACGAGAGAGGAGTTTGAATATGGAATCGATATGAGGAATTCATTACGCGAGAATTTGGTATTAAAGCCTCGAGACTAT
CGAATTCAGCGCCCGAGTATCTTGGAGGTGGTAGTGGTATATCTCAATATCTCTGAAGTCTTGAAGCTGCAAGTCACTGATACGGGAGTTGGCACTATGCGTGGTATGGGCTGTGCT
TCGATATCTCAAAGACCAATTAGGTTTTCGTTGCTCCAGAGCAGCGCATCATCTTGAAGTCTCTCAATTAGACCAAAATCGGTTTATATCTCAAGCGCTCGATAGAGATTTGGCTCAAAGC
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CAAGAATATCGCTATCAGAAGCGAGCTCACAGGTGAATTCAGAGTACTTTGAAATTTTGAAGATATGGCTCGTTTGTGTTGCTAATTCTCAAATTTGAATGGTGAAGTTTATTAATATG
GGTAATGCTGTTGATGACTTCAAGCGTCCATTCCAAATTCAGACAAATTCGGCTCACGCTTTTGTATGTATGCTTAAAAATCATATTTCGAGCATATAGCGCGATTCCAAAACGCGCAAAA
GATATTCCTCAAGTAAGGATTAAACATGAAAAACAAGAAATCGATTACAGAGAGCGCTCGAGCTTAAAGGAGCTTAAAGGATGAGTAGAATTGGCAATCTGATTAAAAAGGCACAAGTTACA
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ATGACTACGGAGTAGAAGATATCCCAAGTGCACCAAGGAACAGAAGTTGTTCAGTCAAGCTTGGCAAGCAACAAACGAAGTTTGTTCAGCAGCTAGTACCGATACACCTCGAGAG
CAACAGATGACCGGGCTTGCAATTTGAGTTTGAAGGCACAATTCGAGCAAGAAATCTAGCTTAAAGGGCACTTACGGGCGCTTCAGGCCCAATTCAGCCCGGCTTCGCGGCTTCGCGCT
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GAGGTTTTCCTCAACACTCGTAATTTGACATAGATTTACAGCCTACGGTGTGTCAAAAACGGCAACAGCGAAGACGCTCTATTTCGCTTTAGGTTTGACTGGTAAGGGCGCTAGAAGCC
CTAAAAAACACACGCCAAGATCCAAAATAAGGTGTTTCGTGATGATAGGTTCAATTTTGGTGGAGCAGCTCAGGCTGCTTCTGGTATTGCGGGTTGATTGGTGGTTCGCAAAAGATAAAAA
GAATGCTGAAGCTGCTGCTGAGCGCTCTTGGCAACGCAATTTATGAAGCTCAGAAAGAGTTTGCACAAAACAGCATACAATGGCGCGTTCAAGACGCTAAGAACGCTGGTATTAAATCCCTA
TGCTGTAGTATCAGGTCAGTCTGAGGTTTATACACCGCAAGACACGAGCTATCAGACTAATCTAACAGGCGAGCTAGTCAAATGATGAATGGCTTTTCTGACGCGATGGGCAACTTAA
TCTCGCTTTCGACGCTGAGGATTTGAAGGGCAAAAAGCTTGACAATGATGCAAAAGCTTCTGAGCTGGTCAACAGACGATAGTAAACGAGCTAGGCGAGTTATCGGCAACTCTTAAGCA
ACCTAGTTTACGCACTCAAAATTAAGGAAGTCTGATGGTAAGAGCTTACTCAGTGTGACGCTCTCAATGGTTCAAGTCGACATCGGATGATATGGATCTCATGGAATATTCAG
GGCTGTGAGAGACGTTTTTACAGCTCTTTATGACCAGAGCAATACAAAGCGCTACAAAAGCCAATAAAGGTAAGGTTGAGCAGGCGCTTTATGTACTTGGACGCGGCTATCATCTCTAA
AAAAGGCACAGCTCCAGCTCCCAATGTTGAAGCTGCTAAGCTTGCCGATAGAGCTGGAACACTTGCAGGTTGGCTGAGTTTGCCTTCGCAGTGGGCTCAAAACAGGCGATATATTCTCTGA
CGCTGCTTTTCTAGTAGGTCGCTAAATTTAAGAGGAGGTAGACCAAAATGGCATTTAGATGGTATCGAAGACGGCGGAAGACGTGGTTTGAAGAGACGTGGTTTACGCGGTAGACGACGT
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CCCTGCGGCAATGCCCGCTTGGCTTCAAAGCGAGCTTAACGAATGGTCTCTGCTATCTCTTTGGAATCCCGTATGATGACGATTGGCAATTTGTTACGCTTACTTACTACCCGAA
GCTTTGTATAGCAATGAGTTAATCCCTCTCATCTTTTCGAGCTTTATCAAACGCTTTTCGCACTTATCTCTGAGCGTCTCGGTTTCACTGGTAAGATTCGTTTCTATGGTGTGGAGATAT
GGAGAAAAACGCGGTCGCCCCCACTTTCACGTTGTTTTGTTTGAAGTCTCCCAAGGTTTGGTCTTGTATCAAAGACGCTTTCGCGCGGTTCAATTCGATATTTCAAGACCCAGCCACC
TTCATGCTGTAGCAAGCTATGTGCTGGTTATGTTGTTAAGAAGCTTTATACGACATCGAAGGTTATTTATGCGTCAATCTCAGGGGCTTGGTAAAAATTTGTGCAAGTATTCAGCAT
GTACGCAACAATCGTTTATGAATGGCAAAACGCGCTACATTTGAGCGTATTTGGCAATAGACTAGCTAAACGACTTGGTGTCTTTGAGCATTTGAAGAGCAAGGATGCGTGGCCCTC
GAACAGCAATTTTCTGTTCTCATCCCTTATCACATACCACTGCTTCTCAAGGAAGACGAGAAATCTTCTGTTAGGAATGGCAACGATTTACAAAGGGCAAAATAGACTATGTGCAATCT
CTGCAACAACCTTAAATTTTGAAGGTTTTCATATGAACAGCTTCTTCTGTCAGGCAATTTTGGTCTTGTATTGTTTGAAGTGTGACGCTTCTAGCTTGAAGTGTGAGGAGTGA
TTTATCATCAGCTTGGCAATAGCCTGATACATACATAAGGAGTTCAAATGAGACCGGATTCAGAGAGCGGCTCGAGCTTAAAGAAATCTGACCCCTATCGATGCTATCTGTTGA
GTGATTGACAGCTTTGTTGAAGCTTCGTATGAAGATAGCGAGGTTACAGACGTTGAGTTACGATAGCTAAGAAACGCTTTTCGTTCTGCTTTACAATATATCATATACAAACAGTGGA
GGATTACTTCT

Bidens circovirus

BlastN best hit: KM392285 Swine cyclovirus (3% coverage; 75% identity)

Rep protein best match to AUM61980 uncultured virus from wastewater 91% coverage, 41% identity, 57% positives, 9% gaps;
YP_009551384 False black widow spider associated circular virus 1 92% coverage, 35% identity, 52% positives, 10% gaps

>Bidens_circovirus_alyu38

TAGTATTACCCCTTCAACCTCTGTACACCTCTGTACACCTATTCTCATTTTTTATGAGTGAACGAAACATTTGGCTGTTTACGCTCAACAACTTCACCGTAGATGAATTCAACAACTTGC
GAAGCCACCAGGAATGGGTGCTTTATCTCGTGTTCACACATGAGCGCGCAATGAAGGAAGTATGATCATTTGCAAGGGTATCTCGAACTTGTGGACGATATAGGATGTCGGGATTACGGC
ATTTTCCTCCACGGCCCACTGGGAGCCACGACGTGGATCTCAAGCTCAAGCTATTGCTTACTGCTCCAAAGCCGACACTCGAGTCGACGGACCATGGACAGTGGGGATTTTGAAGAAA
CCCGGGCTGGACAAGGAAGATCTGGACGAACCTTGCTCTACGAGCTACTCCGGACAGACCCCTCCATTCTCTGCAAGAGGCTTACCCTGGACACTGCTCCGATACAGAAAGTCCA
TCAAGAGGCACTGCTCGACCACAGACGAAAGCTTGCCAAAACCATCCAAGTGACCTGGAGGTGCTCATCTATGGGCGACCCCGGCACTGGTAAGACAAGGAGCGTATACGAATCTG
AGGGAATGTCCAATGTTTACACCCCTTAACACCGCCCAATGGAACCCCTTTGGTTCGATGGATACGATGGGAGTCCGTCTACTTATCGACGATTTTCGAGGATGGATTTCGATTCAATG
AGGTTCTAAAGATCTCGCAGCGTTATCCCTACCGTCTCGCGTCAAGGGTCTTTTGATTATGCAAGCTGGACGAAAGTCTACTTCACATCTAATCACAATCTGAAACGTGGTGGAGTG
AAGACTCTGGCCATTGCTTTAGCGCTTTTCGACAGCGTGTGCTGCTGTGGAGCATTTTTCATCCGACACCCATGGGTACCTTCCGTGCGCCACTCCGACGACGCGCGTCTGACCGCG
ACTAACCACGACGAACTCTTTTCGCGGTGCTACTAACCGTAAAGACGCGTGTCTCGAGTCTGTTAAAACTACCGCGCAAGAACATGACCGCCTTATCACTAAAGGCACCTTCAACTG
GGAAACCAATGATGATTACAGGCTCGCTTGGAGTCAACCAACAGGTATTCCCAACGCTACCGACGTACAACATGGTGTATCTGCATCGAAGATAACGCTGGCACCATTGCAACAGCT
ATCCTTTGCTGGAGTCAACGCTTCTACGACGACCTTTACGCTGCTAACCAACGAGCTTCTCTCAATCGCGCTATTGCTTGGGTCAAGATGACCTTCTCCCTGTGATTACGAAATCCC
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CCTTACGGGAGTCAAAACAGAGTCCATGCTGAAACAATTCAAGGTCTTCAGGAAGTCCCGAAAGTTCGCCCGCATTTTCAGAAATGATGCTGCGTCCCCAAGCTGGTACCGTAGACAACAT
GTCTACTCCATCGGGAGCCTGGCCTACGCTACGACCTCTCTATTCTGGGCTCTACATTCGCACATACATCAATGCTCTTGGATCTCGACGCCACTCACTGGGAGGGCGGAGATGTGTT
CACTGTGTTTTTGAATCAAATATCAATGGTGCAGTAGACGTGAGTAAATCTTTTAATGGAGTTTAAACAACCTTGATCAACCACTTTTCTCGAATTCACACGCTGGACCATCAGGGCA
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ATTAACCTGTCTTGGCCCGCTTCTCCATGCATCTTTCGATCCCGAAGCTCATCAACCTTGGACGGCTGCTTCTTATGGACCAATAGCCCTTTGGGTCTTTCGTGTAAACCCCTACT
CTCCATGTGTAAGAATAACAGAATACCCGACAGATTCTGAGAAAATTCGAGAAATTCGCCATAATTATGGGCATGGGCAAAAAACATCATATTTGCGCTCGCTGTACCAAGGTTGA
AGGC

Host plant contigs

Bidens aristosa voucher Steele 1224 **plastid sequence**
Sequence ID: KP126872.1
5x contigs 35, 36, 70, 73, 94, 98 (ca. 98-99% identity)

ALYU-39 - *Musa sp.* - **Vietnam**

Virome

- 1. **BBTV** six components
- 2. **BbTA6** alyu39
- 3. **BbTA2** alyu39

BbTA6

Best matches to AJ005966 AJ132187 82% coverage 66.9-66.5% identity *Faba bean necrotic yellows C9 alphasatellite isolates*; MF510475 MF510474 83% coverage 66.7% identity *Faba bean necrotic yellows virus associated alphasatellite 2*

Rep protein best matches to ARI50297 100% coverage 62% identities, 77% positives *Sophora alopecuroides* yellow stunt alphasatellite 3; P0CK61 100% coverage 60% identities 76% positives *Faba bean necrotic yellows C9 alphasatellite*; ATU31571 100% coverage 59% identities 77% positives *Faba bean necrotic yellows virus associated alphasatellite 2*

>BbTA6_alyu39
TATTACCCGACCTTGGCGCAGTGGCGCACTATAAAGATGTCTCTGAGAAATTTGGGTCTTACACGCAATTTTCGAAGGCGAAAGACCAGAGCTCCTGTTCCGGCGCGAAACTCAATACGC
CGCTTGGCAACATGAAGAAGAAGATCAGCACCACTACAGGGCGTGATTTCAGTTGAAGAAGAAGACCCGACTGAACGCACTGAAGAGCATATTCGGTGGAAATCCACATGTCGAGCCCAT
GCGAGCGTCTTTCGAGCATGCCCTAGCATACGTCATGAAAGACGAAACCCGAATCCGATGGTCCATGGGAATTCGGTATTTCGAATCCGTAAGGGTTTCGAATAAACGAAAGCTGTTTGAAT
ACTGGAGGATTCGGAACAACGAAGTCCCTCAACCCCAAAAATACAGACGAGCCATGGCCAAACAGGCCATGAGTGAGTCTAAGAAGAAAGCTCGAAGAAGAGGATTAGTTATGAATCGCG
AGAGTGGCAAGTGCATTTGACGAAGTTGTTGGAAGAAGAACCCGATAACAGATCAATATTTGGGTATATGGACCAAGGGTGGAGAAGGTAAGAACAGAGTTTCGCTAAACATTTAGGGTT
AAAGGATGTTGCGCATATTTCCCTGCTGGTCAACTCAAAGATATGATGTACCTGTTATCAAAAGACATGAAAAAATATGTTGTAATTGATTTCCCCCGTTTACCAAGGAATTTATTTTC
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TGAAAAATTATCATTTGGATTCGAATAAAGTTGATTTCTTGCTGAACCGCTATGAAATACACACGCTATGACAAAAAGGGGAAAAATGAAGAAATCGGGGTTGATTGGGCTATCCTAACGCA
ATAAGGCCGACGGCCCGTCAAGATGGATGAACGGTCGAATGATTGCTTCGCCACGAAGCAAAACAAAAATGCGTGGACGAGAACGTCGCCAGTAGCAAAACACTGTACTCCTTGGCG
CACTATATATAGGTGGCCCAAGGTTCGCCCATAG

BbTA2

Best match to EU430730 100% coverage 98% identity; MG545616 100% coverage 97% identity; NC_038953 100% coverage 96% identity, 26 SNPs (98%) to BbTA2_alyu29

Rep protein best matches to AZL93963 100% coverage 99% identities (2 aa) 99% positives (1 aa); YP_009508281 100% coverage 94% identities (11 gaps in middle) 94% positives *Banana bunchy top alphasatellite 2*; YP_009508283.1 100% coverage 73% identities 88% positives *Banana bunchy top alphasatellite 3*

>BbTA2_alyu39
TATTACCCACCTTCGCGCACTACCTCCGCGCACTATAAATGTCTGCCTCAGCATGGACATTTACGCTTCACTATTCCGACGCAACGGAGCGAGGCAAAATTCCTCGCGACTTTGAAGGA
GGAAGATGTGCACTACCGCGTCTGCGCGACGAAACTGCTCCGAACACCGGTTCGGAACACTCTTCAAGGATATCTTTCCTTGAAGAAACGTTTTCGTATTAGCGGCATAAAGAAAGAAATA
TTCGTCGAGAGCGCATTTGGGAGAAAGCTCGAGGATCAGATTACGACAACAGGGGTACTGTTCCAAAGAAGCCCTAATTTCTGTAATTAGGGGTTCTTGCCAAACAGGTTTCGAATAAGCG
TAAATTAGCAGATATGGTTACAAGATCTCCGGAACGAATGAAATTTGAACAGCCAGAGATATTTACCGGATACGAATCGGTGAAGAAGATGAAAGAAATTCAAAGAAAGGATGTCTATCC
TATCCTCGATAGGCCATGCGAGGTACAATTAAACGGAGTTAATTGAAGCAGAACCTGATGATCGAACGATCATCTGGGTATTTCGGACCAAAAGGGAATGAAGGCAAAATCAACGTATGCGAA
GTCAATTAATCCAAAGGATTTGGTTCTACACAGGGGAGGAAAGGAGAACATATTTGTCGCTACGATGATGAAGTTTCGACCAAAACGTTGTATTGTATCTTCCGCGTACAGTACA
AGAATTTAATTAACATCAGATGTTATCGAGGCACTGAAGGATAGAGTATCGAGAGTACAAAAATCAAGCCTGTGAAGTATTAGAATTTGAATCTGTACATGTAAATGTTATGGCTAATTT
TCTTCCTGATATGTGTAAATATCTGAAGATCGAATAAATATAGTTGCTTGCTGAACCGCTATGACAAACGCAACGCTATGACAAAAAGGGAAGAAAGAAATTCGGGGGTTGATTGGGG
TATCCTAACGATTAAGGGCCGACGGCCCTCAAGATGGATCCAATAACCCGATAAGAAGGTAACGGGTCTAAAACGATTCTTCGCCCCGAAGCAACACCTTTAACTCTGCGCACCTA
TATATAGCGAGGTTGGGATAG

DNA-C

24 SNPs to KY427060 (**Thailand**). **23-28 SNPs** to KM607098 KM607099 (**China**). **27-29 SNPs** to MF039864 MF039876 MF039870 (**Thailand**)

C protein (161 aa): 1 aa to KY427060 (**Thailand**) **2 aa** to KM607098 KM607099 (**China**) MF039864 (**Thailand**)

>C_alyu39
TATTATCCCCCTGCTCGGGACGGGACATCAAGTGCATCAAAACAAATGCACGTGACAAAGCAGTAGCTTGTAGCGAAAAGATAACCATCACTATCAGAAAAGTGAACGGAATATTCTGTGTC
TTAGGCACTAAGCAACGTGGACAGATATTGTTTCGAGAAGCGACAATGGAGGCTATTAAACCTGATGGTTTTGTGATTTCCGAATCACTCATCGGAGCAGAAATGGAGTTTGGGAAT
CGTCTGCCATGCCAGCATGTCAAGAGAGTGATCAAGGAAATATATTGGGAGCATCGAAATAAATCTCTGTTCTGTCAGAAAGTGAAGGCTGTGAAGAGGATCTCGAGCATGGAA
ATCAAGATGATGCTCTAGACGCACTGAAGGAGATGAAGACTTCTATTATTTCGCTATAGCGAATATTTGAAGAAACCTTGTGTGTTATGTTTGTATCTTCCGCGTACAGTACA
GGTTAAACCAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTACTCGGTATATCAAGATCTGTTCTGTGATGAGGAACCTCTCTATTCTGCGCAGAAAGAG
ATGAAGAAGTAAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGAACATTACTGTAATGAATATCCA
TTATCATAAATAAAAAATATGGAATGATGATTATGTTTCTAGTATAAAATACATAATGATATAGCATAGCAATAAATACATAAACCAACATACACACGCTATGACAAACGGGGAAAA
TGAAGAAATCGGGGTTGATTGGGCTATCTTAAACGATTAAGGGCCGAAGGCCGTTTAAATATGTTGGTGGACGAAGTCCACACACACAAAAAGTGAAGCAGAACACGGAATATAATGAGC
TGGCAACGTAGGGTCCATGTCCAGGATTAGTCGCCCACTGAGCAGGGGGCTTAT

DNA-M

23-28 SNPs to KM607239 KM607240 (**China**). **53-54 SNPs** to KY427061 MF039871 MF039865 (**Thailand**)

M protein (117 aa): 0 aa to KC581796 (**Thailand**) **1 aa** to MF039871 MF039865 MF039877 KY427061 (**Thailand**)

>M_alyu39
TATTACCCCGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACGGTTTAAACGAACCGTTATATAATGTTATAACGATAAGTCACGTGTG
ATAGAGACATGCACGTGACATAGTCAAAATGTATTGAATAAACATTTCAGCTCCGGATGCTTCCGACGGAGCTTAGGTTACTTCGCGCGGAAGCAAAACATTATATATTGGCCAGGACT
CCTGCCTATAAATAGGCAAGCAAGGAAATGGCATTAAACAACAGAGCGAGTGAACATATCTTTTGAATGGTTCCTGTTCATCGGAGCAATATTTATTGCGATAACAATATATATATATTG
TTGGCGTTGCTCTTTGAGTCCCCAAGTATATTAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACCAGAAAGACGTGTATGGATGCAGAGAACGCAGTTGACGGAGGCAACAGGAGAT
GTAGAGCTCGGCAGAGGTAGTGTGGAGACAGACGGGATCAACAACCGGCTGTACACACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAAGGGATGAGCAAGGAAGACGAGGA
AACGCTGGACCAATGTTTTAATACACAGTATTGTAATATACGAAATATAAATGGATAATGATATGATTGTGAAACATAATATACGTGAAACATAATATATGTTTGATAATTTACATATT
TTAATATGTAAATTTGATACGAGTGTGTTATTTATAGAACATACAACACGCTATGACAAACAGGGAAAAATGAAGAAATCGGGGGTTGATTGGTCTATCGTATCGCTTAAGGCCCGCAGGC
CCGTTGAATGATTCTTAATAAAACAATATACATGATACGGTAGTTGAATATATAAACACAGTAGTATAAATACAACAAATGTTGTATCTAATTAAAATATGAGAAGATAAGTAT
ATTTGTGAGGGATGATGATCACACCACCATTTCAGTGGTGGGTCATATGTCCTCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-N

24-28 SNPs to MF039872 MF039878 MF039866 KY427062 (Thailand). **27-38 SNPs** to KM607387 KM607385 KM607386 (China)

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (Thailand) KM607387 KM607385 (China) **1 aa** to MF039866 (Thailand)

>N_alyu39
TATTACCCCGCTGCTTGGACGGGACATGACGTCAACATAGATTATAATGGCCAACTAAAGGCCCATTTAATAGAATAGCGGGCTTTTGCATATTTCAAAGGCCAGCCTGGAAGT
GGATAATGTCACGTGCCTAATAAGAGTTGCTTGCCTCGAAGCAATCCGAATAAAGTTGCGTATTCAATACGCAACTGAAGTCTATTAAATATGGATGCTCTCGCGCAATAAATCAGAG
CGTATGCGAAGCAAGAGCGATGGATTGGGCAGAAATCAAGACATGTACTCATGGTGGGATTTGGAGACGATATCATCGGATTCAATCGAGAAATCGAACAATATGACCTTGGCG
CGAGCTCGGCAGCGGAAGAAAGTCACCTCGCAAGGTACTGCTAAGATCTATTGAAGCTGTGTTAATGGAAGCTTCAAAGGAAATAACAGGAATGTTTCGTGGGTTTATATACGTATCAAT
ACGAGACGATGATGGAGAAATGCGTCCAGTACTATAATACCATTTCGGAGGATATGGATATCATAAATGATTCTTATATTTCGAAGGGAAGGGGAAAGTTGAATGTGATATATCATCAGA
TATGTAGCGCCAGGAGTCGATTGGAGCAGAGACATGGAAGTTAGTATTAGTAACAGCAACAACCTGTAATGAATTATGTGATCTGAAGTGTATGTTGTTGTTTCGTTAAGAAATAAAGGA
ATAACAGATGTCGTGTAATGATTATTAATAAACTTATTTTCATGAAATTGATAGTTGTATAAAACATACACACGCTATGACAAACAGGGAAAAATGAAAAATCAGGGGTTGATTGGTC
TATCGTATCGCTTAAGGCCCGCAGGCCCTTGAAATAATAATCGAATTATAACCGTTGATATAATACAGAGATAGATGATAAGCATCCCTAAACATAGACCAAGTATATGGATGTAT
AATATAAAACAAGCATATAAATAAATATGTGAACATATCTCTGATTGGTGCAGAACGTAGCCCCACTAACCTTTAAGTTAGTGGAAATGTCCCGATGACGTAAGCAGCGGGGACTAT

DNA-R

6 SNPs to AB113660 (Viet Nam). **10-12 SNPs** to KM607677 KM607678 KM607676 KM607679 (China). **16-20 SNPs** to MF039879 MF039873 MF039867 KY427063 (Thailand)

R protein (286 aa): 0 aa to KM607676 KM607677 KM607679 (China) **1 aa** to AB113660 (Vietnam) MF039879 (Thailand)...

>R_alyu39
TATTACCCCGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCTCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAACC
ATCAACAATCCCGCTTCACTACCAAGTATGCGGGATGAGTTCAAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCTATGTGACGGGATACGTCGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCTCGGCACACCTTGAGAAACGAAGGGAAGCCAAAGGAAGACACGGGCATCTGTATGAAGGAAGACACAAGAAATCGAAGGTCCCTTC
GAGTTTGGTGGCTTTAAATTGTCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGTGAAACGCACAAACGGCCTTGGAGTATTTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCGATGAATAGCTGGAACACATCCTTCAGTTCTTGACATCGGAAGTTGAAATATATTGCGGAGGCCATGT
CATCGAAGATAAATTTGGGCTCTATGGCCCAATGGAGCAGAAGGAAGACAACTATGCAAAATATTTAATGAAGACGAAGAATGCGCTTTATTTCTCAGGAGGAAATCACTTGGATATA
TGTAAGATTGTATAATTACGAGGAAATAGTTATATTTGATATTTCCAGATGCAAGAGGAATATTTAACTATGTTTACTAGAGAATTTAAAAATGGAATTATTTCAAAGCGGGAATAT
GAACCCGTTTGAATAATTGAGAATATGTGAAGTCATTTGAATGGCTAATCTCCTTCGAGGAGGAAGGAATCTTTTCAGAAAGTCAAGTAAGAGTGTGCTGCTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAAAGCAAAGATTCGGGGGTTGATTGTGCTATCCTAACGATTAAAGGGCCGACGGCCGCTCAAGATGGACGGCTTGATCAGATGTCGCGAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

DNA-S

11 SNPs to AB113662 (Viet Nam). **15/16 SNPs** to KM607535 KM607534 (China). **19 SNPs** to MF039874 (Thailand)

S protein (170 aa): 0 aa to AY33771 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) **1 aa** to several isolates

>S_alyu39
TATTACCCCGCGCTCGGGACGGGACATGGGCTTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAAACAGCCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCCGCAAGCAAACTAAAAGTCTATATATACAGGTGTAGACATATTGTTTCAGAGAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGCGGGTTGGGCGCGGAAGTATGGAAGCAAGGCGGCAACCACTCAGCTACTCGTCTAGGTTCAATATTGGTTCTGAAAAACCGCTCAAGGTATTTAGGATTGAGCCTCA
TGATTAACACATTACCCAGGTATTTATCTGGAATAATGTTATGCTTTTGGTGCAAGGTGAAGCCCGGAAGAATACCTTCACCTGGGCTATGATTAAAGTTTCATGGGAAATCAACAGCC
GACTACATGCTCGGAAGCCAGGTTTATTTATTAACCTGAACATAGCCATCTCGTGAACTGGTATGCAGTGGGAACTTGAAGCCGGAGTCGAACAGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACAAACCGTGTGGAGGAAGAATGAACAGAGGTGGATTACTTGATTGTCGATTTTATTTGGCATTTTATTTGATGCTGGAGTTAGTATTAACACAGACAGAATTACATATCATGT
ATGATATGTTTATGTAACATAAACCTTTGTATGGAATAATGACCAAAATACATACAAACACACTATGAAATACAAACACGCTATGACAAACAGGGAAAAATGAAGATCGGGGGTTGATTG
CTTATCGTATCGCTTAAGGCGCCGAGGCCCTTGAATGATTCTTAATAAAACAATATACATGATACGGATAGTTGAATATATAAAACAACGATGTATAAATACACAGAAATGTTGAT
ACCAATTAATAAATATGAGAAGAAAAGATATTTGTGAAGGATAAGCATCAGAACCACCATTTCAGTGGTGGGTCATATGTCCTCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3

42-46 SNPs to KY427065 MF039869 (Thailand)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alyu39
TATTACCCCGCGCTCGGGACGGGACATGGGCTTTTAAATGGGCGAGAGAGTTGAACAGTTAGTATCTTCTGTTATTGGGCCATCTGGCCCAATAATTAAGAGAAGCTGTTCAAAA
TCGGGGTTTGACCGAAGGTCAAGGTAGACGGTCAACAATATTTCTGGCTTGGCGGACAGCAACAGCAATTAATATTTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAACT
CTATAAATAGCTTAAATCTGGCTTGGATAATTGCTCTCGCTTCTGTCGAAAGCTGTTGTGTTGAGCGCGAAGATCGCCATCGGCATCATCGGACGAAAAGCTGCAAGAGAGACGGAGA
ACCATGCTACGAAGCGTATATCGGGTATTTATAGACTCTAGCGCAGCTAGAAGTTTCTCTTGACTTGATATTGTTATTTGTAATACGAAGAAATTCGTATATTGATAATAATAAAC
ATCTGGGATGTTAATGTTTACATTAACTAGTATTAAATATGTACAATAACAATAATGTTATGAGGAACGAATACAAGAATAATAAAATATGAGGAGCGTAGCGTGATAAACAGTTGTTT
AAGGTATATAATTAATTAATTATGCAATGCTGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAATAACCAATTTATATTATTTATAATACATACAAAC
ACGCTATGACAAACGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCCTAACGATTAAAGGCCGAGGCCCTCAAGATGGATGAACGGTTAGATTGATTGCTTAGCCACCAAGA
AAGGAATCGTTTGGGACCAACAGACAGAGCTGTCACCTATTTAAAAAATAATATAAACAATTAAGCAATGACGATAGTACCCCTCCAAAGATGACGATATAGGGGTGTCGCCGAGTAATT
TAACATAGCTCTGACAGAGATAGTGGACGTGGATGCCAGATCGGACGATCGTGGTTTGTATGAACCAATGATGACGTAGGGGCTGGGGCTTAT

ALYU-40 - Musa AAA red - Vietnam

Virome

1. **BBTV** six components
2. **BbTA5** alyu40=38

BbTA5

Best matches to MF510475 MF510474 33% coverage 66.5% identity Faba bean necrotic yellows virus associated alphasatellite
2 isolates; MK291270 72% coverage 66.9% identity Sophora yellow stunt alphasatellite 3; AJ132187 AJ005966 73% coverage
66.3-65.8% identity Faba bean necrotic yellows C9 alphasatellite

Rep protein best matches to QBF29185 100% coverage 59% identities 77% positives Sophora yellow stunt alphasatellite 3;
ATU31571 100% coverage 62% identities 80% positives Faba bean necrotic yellows virus associated alphasatellite 2;
ARI50297 100% coverage 62% identities 80% positives Sophora alopecuroides yellow stunt alphasatellite 3

>BbTA5_alyu40

TATTATCCCGACCTTGGCTCACTGGCTCACTATAAAAGGGGAAATGTCGCAGCAGCGAAATTGGGTATTACGCGTAACCTTCTCCGCGACCCGCCGATTTTAAAGTTCGCGGGAGAAAC
TCAATACGGCTGCTGGCAACATGAGAAGAAGAAATCACGACCATCTTCAGGAGTGATTCAATTGAAGAAGAAGCTCCGGATGAACGCAGTGAAGACGTTAAATTGGGGAAATCCACACCT
CGAAGCCATGAGAGGAAACAATCGACGAAGCAATAAGGTACGTGACGAAGAGAAACACGAGTAGCAGGTCCGTGGGAATTCCGGAGAATTACTACGAAAGGATCTCATAAGAGGAAAT
GATGGAATTGCTCGACGATCCAGATAACGAATAATGGAACCTCAAAATATGACACCGCCCACTTACTAAACAAGCAATGGACCGCTCAAAAGAAGCGGGAATTAGCGTTTCCTTACGA
CTTAAAGGAGTGGCAAAAGATGGTTATTGAGTTAATCGAAGAACAACACAGAACTATTATCTGGGTCTATTGGACCTAATGGTGGAGAAGGTAAACGCAGTTTCGCAAAAGCATT
TGGATTACTCAAAGGATGGACATATCTACCAGGTGGTGAACGTGAAAGACATGATGATCTGTTGGCAAAAGAAATTAATAATAACGTTATTATTGATTTCGCCGATGTACAAAGGATTT
CATATCCTATAAGTTTATTGAGATGGTAAAGAACCGATGCATATTAGCTATAAAATGAACCAATCGGGGCGATTGTAAGTAATGAAGTCCATGTAATTGTAATGTCGAATGAGCTTCC
AGATTATTCAAATAATTCGGAAGACAGAATAAAATTAATATTACATAACGCACATATGACAAAAGGGCAAAATGCAAAATCGGGGGTTGATTGTCTATATTACGAATAAGGGCCG
CAGGCCGTACACATTGCGCGGGAATTCAAATTTCGACGCGCAAAATATTATTAAATACAATACACCGCTTTTAGAAATCCGTGGACGAGAAGATGCCAGTAGCAAAACACTGTACTCC
TTGGCTCACTATAAATACCTGAGCCAAGTCGGGCATG

DNA-C

23 SNPs to KY427060 (Thailand). **25-28 SNPs** to KM607098 KM607099 (China). **26-28 SNPs** to MF039864 MF039876 MF039870 (Thailand)

C protein (161 aa): 1 aa to KY427060 (Thailand) **2 aa** to KM607098 KM607099 (China) MF039864 (Thailand)

>C_alyu40
TATTATCCCCCTGCTCGGACGGGACATCACGTGCATCAACCAATGCACGTGACAAAGGAGTAGCTTGTAGCGAAAGATAACCATCACTATCACAAAAGTGAGAAGAATATTCGTTGC
TTAGGAGCTAAGCAACGTTGGTCAGATATTGTTTCGAGAAGCGAAAATGGAGGCTATTTAAACCTGATGGTCTTGTGATTTCGGAATCACTCATCTGGAGCAGAAAATGGAGTTCTGGGAAT
CTGCTGCTATGCCAGCAGATGTCAAGAGAGTGATCAAGGAAATATATTGGGAGCATCGAAATAAACTTCTGTTCTGCAGAAGTTGAAAGGCTGTGTAAGAGGATTTCCGAGCATGGAA
ATCAAGATGACGCTCTAGACGCAGTGAAGGAGATGAAGACTTCTATTATTCGCTATAGCGAATATTGAAGAAACCTTGTGTGTTATTGTTTGTAGTACTAATAAATCTATTGCATATA
GGTTAAACCAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTACTCGGTATATCAAGATCTGTTCTGTGATGAGGAACTTCCTTATCGTCGACAGAAGAAGAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATTAAGTGAATGAATATCCA
TTATCATAAATAAAATAATGGAATGATGATTATGATTCTAGTATAAATACATAATGGTATACGTATAGCATAAAATACATAAACCAACATACACATGACAAACAGGGAAAAAT
GAAGATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGCCGAAGGCCCGCTTTAAATATGTGGTGGACGAAGTCCACAACACATAAAAAGTGATCAGAACAATGGAATATAATGAGCT
GGCAACGTAGGGACCATGTCCCGAGTTAGTGCGCCACGTGAGCAGGGGGCTTAT

DNA-M

16-21 SNPs to KM607239 KM607240 (China). **55-56 SNPs** to KY427061 MF039871 MF039865 MF039876 (Thailand)

M protein (117 aa): 1 aa to KC581796 (Thailand) **2 aa** to MF039871 MF039865 MF039877 KY427061 (Thailand)

>M_alyu40
TATTATCCCCAGCGCTCAGGACGGGACATCACGTGCAACTAACCAATGCACGTGACTGATATATACTACATACAACGGTTTAAACGAACCGTTATATAATGTTATAACGAAAAGTCACGTGTG
ATGACAGCTGCAACGTTGACATAGTCAAAATGAATGAATAAACATTTGACGTCGCGGATGCTTCCGACGGGAAGCTTAGGTTACTTCGTGGCGAAGCAAAACATTATATATTGGCCTGGGACT
CTGCTCATTAATAATGGCAAGTCAGGAAATGGCATTAAACAACAGAGCGGGTGAACATATTCTTTGAATGGTTTCTGTTCATCGGTGCAATATTATTTCGCATAAACAATATTATATATTG
TTGGCGTGTCTCTTTGAAGTCCCAAGTATATAAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACCAAGACGCTGTATGGATGCAGAGAACCGCAGTTGACGGAGGCAACAGGAGAC
GTAGAGCTCGGCAGAGCAGTGTGGAAGACAGACGGGATCAACAACCGGCTGTCATACCATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGATCAAGGAAGACGAGGA
AACCGAGGCAACATGTTTAAATACCGGTAATTGTAATATACGAAATATAAATGGATATGATATGTAATGTAAGTGAACATATAATACGTGAACATATAATATGTTGTAATTTACATATT
ATAATATGTAATATGTAATACAGTGTGTTGATTATATAGAACATACAACCGCTATTGACAAACAGGAAATAAGAAATCGGGGGTTGATTGCTCTATCCGTATCCGCTTAAGGCCCGAAGC
CCGTTGAAATGATTCTTAATAAAACAATATACATGATACGGATAGTTGAATATATAAACCAACGAAGTATAAATACACAGAATGGTGATATACTAATTAATAATGAGAAGATAAGTAT
ATTTGTGAGGGATGATGATCACAACCACCACTTTAGTGGTGGGTATATGTCGCGAGTTAGTGCGCCACGTAAGCGCTGGGCTTAT

DNA-N

21-25 SNPs to MF039872 MF039878 KY427062 MF039866 (Thailand). **26 SNPs** to KM607387 KM607385 (China)

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (Thailand) KM607387 KM607385 (China) **1 aa** to MF039866 (Thailand)

>N_alyu40
TATTATCCCCCGCTTGGGACGGGACATGACGTGACGAAAGATTATAATGGGCCAACTAAAGGCCCATTTAATAGAATAGCGGGCTTTTGACATATTCAAAGGCCAGCCTGGAAGT
GGATAATGTCACGTGCCATAAAGAGGTTGCTTCGCCCTGAAGCAATCCGAATATGTTGCGTATTCAATACGCAACTGAAGTCTATTAAATGAGATGCTCTCGCGCAATAAATCAGAG
CTAAGCGAAGCAGAAGCAGATGGATTGGGCAGAATCACAAATCAAGACATGTACTCATGGTGGCATTTGGGAAGCAGATATCTTCGGATTCAATCGGAAATCGCAATATTGACCTTGCCT
CGACGCTGGCAGCGGAAGAAAGTCTCTCGCAAGGTACTGCTAAGATCTATTGAAGCTGTGTTAATGGAAGCTTCAAAGGAAATAACAGGAATGTTTCGTGGGTTTATATACGTATCAAT
ACGAGACGATGATGAGGATGATGCGTCAGTACTATAATCCATTTCGAGGATATGGATATCATAAATGATTCTATTATTTCGAAGGGAAGGGGAAGTTGAATGTGATATATCATCAGA
TTATGTAGCGCCAGGAGTCGATTGGACGAGACATCGAAGTTAGTATTAGTAACACCAACAACCTGTAATGAATTATGTGATCTGAAGTGTATTGTTGTTCTGTTTGAAGTAATAAGGA
ATAACAGATGCTGCTGAATGATTATTAATAAAACATATTTTCATGTAAATTGATAGTTGTATAAACAATACACACGCTATGACAAACAGGGAAAAATGAAATATCGGGGGTTGATTGGTC
TATCGTATCGCTTAAAGGCCCGGACCGGTTGAAAAATAATAACGAATTCGAATTTGATAAATAACAGAGAAGATGATAAGCATCCAAAACATGACGAAGATATATGCTGTAT
AATATAAAGAAGCATATAAATAAATATGTAACATACTCTGATTGGTTTGAAGTGAACCCCAACAACTTTATGTTGGTGAAGATGTCCCGATGACGTAAGCAGCGGGGACAT

DNA-R

7 SNPs to AB113660 (Viet Nam). **8-10 SNPs** to KM607677 KM607678 KM607676 KM607679 (China). **16-19 SNPs** to MF039879 MF039873 KY427063 MF039867 (Thailand: Chonburi)

R protein (286 aa): 0 aa to KM607676 KM607677 KM607679 (China) **1 aa** to AB113660 (Vietnam) MF039879 (Thailand)...

>R_alyu40
TATTATCCCCAGCGCTCGGACGGGACATTTGCATCTATAAATAGACCTCCCCCTCTCCAATACAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAAC
ATCAACAATCCCGCTTCACTACCGATGATCGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCAGGGATACGTCAGATGAAGACGA
AGCTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCGCACACTTGAAGAAACGAAGGGAAGCCGAAGAAGACACGGGCATCTGTATGAAGGAAGACACAAGAAATCGAAGGTCCTCTC
GAGTTGGTGGCTTTAAATTTGTCATGTAATGATAATTTATTTGATGTATACAGGATATGCGTGAACACGACAAACCGCCTCTGGAGTATTTATATGAGTGTCCAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGCGCATGAATAGCTGGAAAACATCCTTCAGTTCTTGACATCGGAAGTTGAAAATATTATGCGGGAGCCATGT
CATCGAAGGATAATTTGGGTCTATGGCCCAATGGAGGAGAAGGAAGACAACCTTATGCAAAATATTAAATGAAGACGAAGAATGCGTTTATTCTCCAGGAGGAAAAATCAATGGATATA
TGTAGATTGTATAATTACGAGGAATAGTTATATTGATATTCCAGATGCAAGAGGAATATTTAAACTATGGTTTACTAGAAGAAATTTAAAAATGGAATTTATTCAAAGCGGGAATAT
GAACCCGTTTTGAAATTGTAGAATATGTGGAAGTCATTGTAATGGCTAACTCCTTCCGAAGGAAGGAATCTTTTTCAGAAGATCGAATAAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAAGCAAGATTCGGGGGTTGATTGTGCTATCCTAACGATTAAAGGCCGACGGCCGTCAGATGGACGGCTTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAGCGCTGGGCTTAT

DNA-S

18 SNPs to AB113662 (Viet Nam). **18/19/21 SNPs** to KM607535 KM607534 KM607536 (China). **20 SNPs** to MF039874 (Thailand)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) **1 aa** to several isolates

>S_alyu40
TATTATCCCCAGCGCTCGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTTGGGCTTTATGGGCTTTATCCAGAAGACCAAAAAAGGCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCCGAAGCAAACTAAAGCTCTATATATACCAAGTGTAGACATATTGTTTCAGATAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGCGGGTTGGGCGACGGAAGTATGGAAGCAAGGCGGCAACCGACTACGACTCTGCTGTAGGTTCAATATTGGTTCCTGAAAATACCGTCAAGGTATTTAGGATTGAGCCTAC
CGATAAAACATTACCCAGATATTTATCTGGAAAATGTTTATGCTTTTGGTGTGCAAGTGGAAGCCGGAAGAATACTCTACTGGGCTATGATTAAAGGTTCTAGGAAATCAACACGCC
GACTACCTGTCTGGAAGCACCAGGTTTATTATAAAACCTGAACATAGCCACTTGGTGAACCTGGTATCGATGGGGAACTTGAAGCCGGAGTCGCAACAGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACAAACCGTGTGTGAGGAAGAATGTAACAGAGGTGGATTCTGTTGTTTGGCATTTTATTGTAAGTGTGGAGTTAGTATTAACTACCAAGACAGAAATACATCATGT
ATGATATGTTTATGTAAACATAAACCTTTGTATGGAATAATGACCAAAATACATACACACATATGAAATACAAACACGCTATGACAAACAGGGGAAAAATGAAGAATCGGGGGTTGATTG
TGCTATCGTATCGCTTAAAGGCCGCGAGGCCGTTGAAATGATTCTTTATAAAACAATATACAGGATACGGATAGTTGAATATATAACAACATGTGTAATAACACAGAAATGTTGAT
ACCAATTAATAAAATGAAAGAAAAGATATTGTGAAGGATAAGCATCAGAACCCACTTTAGTGGTGGGTATATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGACTAT

DNA-U3

28-38 SNPs to MF039881 MF039875 KY427065 MF039869 (**Thailand: Chonburi**)

U3 protein (34 aa): a **truncated** version of a 39 aa protein encoded by KY427065 (**Thailand**)

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>U3_alyu40
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGCGGCCGAGAGAGTTTGAACAGTTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAAAA
TCGGGAATTGAACCGAAGGTCAAGGTAGACGGTCAACAATATTTCTGGCTTTCGGGAGCAAGCAACACGAATTAAATATTTAATTCGTATGACACGTGGACGGACCGAAATCTCCTGTACC
TCTATAAATAGCTTAAACATGGCTTGGATAATTGCTCTCGCTCTTCTGTCAAAGCTGTTGTGTTGAGGCGGAAGATCGCCATCGGCGATCATCAGACGAAAGCTGCAAGAGAGACGGAG
AACCATGCTGCGAAGCGTATATCGGGTATTATAGACTTCTAGCGCAGCTAGAAGTTTCCTTGTACTTGTATTTGTTAAATTACGAAGAAATTCGTAGATTGATAATAAAAA
CATCTGGGTTTGTTAATGTTTACATTAAACCAATTAATAATGTACAATAACAAAAATTTGATGAGGAACGAATACAATAATATTAATAATGAGGAGCGGTAGCGTGATAAACAGGTGTT
TAAGGTATAAATTAATTAATTCGAAAGTCATGATAATACGGTATAAGTTGAAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAACCAACCAATTATATTTTATAATACATACAA
CACGCTATGACAAAAGGGGAAAAAAGAAAAATCGGGGGTTGATTGGTCTATCCTAACGATTAAGGGCCGAGGCCCCGTCAAGATGGATGAACGGTCAGATTTTATTGCTTAGCCACGAAG
AAAGGAATCTTTTGGGACCCACAGATAAGACAGCTGTCACTACTTTTTAAAAATATATAATAACCAATTGACGATAGTACCCCTCCCAAGATGACGTATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGACAAGAGATAGTGAGCTTGGATGCCACGATCGGACGATCGTGGTTTGTATGAACATAATGATGACGTAGGGGTGGGGCTTAT
```

The insA in U (truncating ORF1) is confirmed by most reads (no minor SNP).

ALYU-41 - *Chromolaena odorata* - Laos

Neighbour to Musa ALYU-42

Virome:

1. **BBTV** 5 core components (distinct genetic variants) **DNA-N is at a cross-contamination level**
2. **BBTA5** *alyu41* isolate: **1 SNP compared to BBTA5_alyu42** (*Musa* neighbour is invariant at this position)
3. **Cucumber mosaic virus** (detected by IC-PCR)

At 5x - BBTA5, incomplete C, partial M

1. BBTA5 1 SNP to *alyu42*

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>BBTA5_alyu41
TATTACCCGACCTTGGCTCACTTGTCTACTATAAAAGGGGAGATGTCGCAGCAGCGAAATTGGGTATTACGCGTAACTTCTCCGCGACCCGCCGATTTTAAAGTTCGCCGGAGAAAA
TCAATACGGGTCTGGCAACATGAGAAGAAGAAATCACGACCATTCTCAGGGAGTGATTCAATTGAAGAAGAAGCTTCGGATGAACGCGAGTGAAGACGTTAATTGGGGGAAATCCACACCT
CGAAGCCATGAGAGGAACAATCGACGAAGCAATAAGGTACGTGACGAAAGAGAGACAGAGTAGCAGGTCGCTGGGAATTTCGGGAATTACTACGAAAAGGATCTCATAGAGGAAAT
GATCGAATTGCTCCAGCATCCAGATAACGAAATAATGGAACCTCAAAAATATCGACGCCCATTACTAAACAAGCAATGGACGCGTCAAGGAAGAGGCGGAATTAGGGTTTCCCTACGA
CTTAAAGGAGTGGCAAAAGATGGTTATTGAGTTAATCGAAGAACCAACCCGACACAGAACTATTATCTGGGTGTATGGTCCTAATGGTGGAGAAGGTAAACCGCAGTTCGCAAAAGCATT
TGGATTACTCAAAGGATGGACATATCTACCAGGTGGTGAACGTGAAGAGACATGATGATCTCTTGGCAAAAGAAATTAATAATAACGTTATTATTGATTTCCCCCGATGTACAAGGATT
CATATCTCTAATAGTTTATTGAGATGGTAAAGAACCGATGCATATTTAGTTATAAATTAAGCAACATCGGGCGATTGTAAGTAATGAAGTCCATGTAATTTGATATTCGAATGAGCTCC
AGATTATTCAAAATTTTCGGAAGACAGAATAAAATTAATTTTACATAACGCACACTATGACAAACAGGCAAAAATGAAAATCGGGGGTTGATTGTCGTATATTACGATTAAAGGGCC
CAGGCCGTACACTTTGCGCGGGAAATTCAAAATCCGGACGCCAAATTTTATTAATAACAATACACCGCTTTTAGAAATCCGTGGACGAGAAGATGCCCGTATCAAAACACTGTACTC
CTTGGCTCACTATAAATACCTGAGCCAAGGTGGGCGATAG
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A-to-G

DNA-C = ALYU-42

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>C_alyu41
TATTACCCCCCTGCTCGGGACGGGACATCACGTGCATCTAACAAATGCACGTGACAATGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCATAAAAGTGAAGGAATATTTCGTTGC
TAGGAGCATTAAGCAACGTGAACAGATATTGTTTCGAGAAGCGCAATGGAGGCTATTTAAACCTGATGGTTTGTGATTTCGGAATCACTCATCGGAGAAGAAATGGAGTTCTGGGAAT
CGTCTGCCATCGCAGACGATGTCGAAGAGATGATCAAGGAATATATTGGGAGATCGAAACAACTTCTGTTTGAATGGTTTCTGTTTATGGTGCAATATTATTGCGATATAACATATTATACATATTG
ATCAAGATGATGCTCTAGACGCGAGTGAAGGAGATGAAGACTTCTATTATTTCGCTATAGCGAATATTGAAGAAACCTTGTGTGGTATTGTTTGTAGTACTAATAAATCTATTGCATATA
GTTTAAACCAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTACTCGGTATATCAAGATTGTTTGTGATGAGGAACCTCCCTATTCTGTCGACAGAGAAGAAG
ATGAAGAAGTAAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA
TTATGATAAATAAAATAATGGAATGATGATTATGTATTCTAGTATAAATACATAATGGTATACGTATAGCATAAAAATACATATACCTACATACAACACACTATAACAACAGGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGCCGAGGCCGTTTAAATATGTGGTGGACGAAGTCCACAACACATAAAAAGGTATCAGAACAATGGAATATAATGAGCT
GGCAACGTAGGACCATGTCCCGAGTTATGCGCCACGTGAGCAGGGGGCTTAT
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DNA-M 6 SNPs to ALYU-42

MP protein: identical to ALYU-42

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>M_alyu41
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATACAACGGTTTATTGAACCGTTATATATTGTTGAACGAAAGTCACGTGTG
ATAGCGAAATGCACGTGACCAAGTCAAATGTATTGAATAAACATTTGACGTCGCGATGCTTCCTACGGAAGCCATGGTGTCTCGTGGCGAAGCAAAACATTATATATTGGCTTGGATT
GCTGCTCTATAAATAGGCACGACGGGAAATGGCATTAAACAACAGAGCGAGTGAACATTATCTGTTGAATGGTTTCTGTTTATGGTGCAATATTATTGCGATATAACAAATATTATACATATTG
TTGGCGTGTCTCTTGTAGTCCCAAGTATATTAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACCAGACGACGTGTATGGATGCAGAGAACGCGATTGACGGAGGCAACAGGAGAT
GTAGAATCTGGCAGAGTAGTGTGGAAGACAGACGGGATCAACAACCGGCTGTCAATCCATCAATGCAACACAGGTTATCCCTTCACATCAACCTGAAGAGGATGAGCAAGGAAGCAGGAGA
AACGCCGGACCGATGTTTAAATACACGGTATTGTAATATACGAAATATAAATGGATAATGATAAGTATTGTGAAACAAAATATATGTGAACATATAATATGTTTGAATTTACATATT
GTAATATGTGAATTGTATACGAGTGTGTATTATTAACACATACAACACGCTATGACAAACAGGGGAAAAATGAAGATCGGGGGTTGATTGCTCTATCGTATCCGTTAAGGCCGACAGC
CCGTTGAATGATTCTTTATAAAACAAATATACATGATACGGATTGTTGAAAATATAATCAACGATGTATAAATACAACAGAATGTTGTATACCAATTAATAAAGAGAGAAGATAAGTAT
ATTTGTGAAGGATATGGATACACACCACCACTTTAGTGGTGGGTATATGTCGCGAGTTAGTGGCCACGTAAGCGCTGGGGCTTAT
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DNA-N missing or at a very low level = ALYU-42

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>N_alyu41
tattacccccgctgctcggaacgggacatgacgtcagcatagattataatgggccaaactaaaggccaccttaataagaataggcgggcttttgacatatttcaaaggcccgagcctggaagt
ggataatgtcacgtgcggaataagaggttgcttgcctcgaagcaaccgcgaacaaatgttgcgtattcaatacgcgaactgaagctctattaatatggatgtctctgcggaataaaatcacag
cgtaagcggaagcagaagcgatggattgggcagaatcacaaattcaagacatgtactcatgggtgcgattgggaagcagatcatcggtatcccgagaatcgacaatatgtacctgtgcgt
cgacgcgcagcggaagaaaggtcacctcgcaaggtcatctgtaagctgtgttttaatgggaagcttcaaaggaaataaacaggaatgttctcgtgggtttatatatcgttatcaat
acgagacgatgatggagaatgcgtccagtactcataatcaccattcggaggatattggatcatcataatgatcttctattatttcgaagggaaggggaaagtgaattgtgatataatcatcaga
ttatgtagccgaggaagtcgatttggagcagagacatggaagttagtattagtaaacagcaaacctgtaataatgatgtgatctgaagtggttatgtgtgttgcgttaagaataaaggga
ataacagatgtgctgaatgaatataataaaatatatttctcatgtaattgtatagttgtataaaacatacaacacgctatgacaaacaggggaaaaatgaaaaatcaggggttgattgtgtc
tatcgtatcgcttaaggcccgccggttgaaaaataataatcgaattataacgcttggataataatcagagatagatgataagcatccaaaaaacatagacgaagtatatggcgtga
taataaaaaacagcatataataaaatatgtgaactaatctctgattggtttacaacgtagccccaccaactttatgttggtggaagtgtcccgatgacgtaagcagcgggggaactat
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DNA-R 2 SNPs to ALYU-42

Rep protein: identical to ALYU-42

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>R_alyu41
TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCCCCTCCACTACAAGATCATCATCGTCACAGAAATGGCGCGATATGTGGTATGCTGGATGTTCAAC
ATCAACAATCCCGCTTCACTACAGTGTACGCGGATGAGTTTAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCGAGGATACGTGCGATGAAGAGACGA
AGTTCTTGACGACAGATGAGAGCGTTCTTCCCTGGCCACAGCTTGAGAAACCAAGGAGGCCACAAGAAGACACGGCGATCTGTATGAAGGAGACACAGAATCCGAAGGTCCTCTC
GAGTTTGGTGCTTTAAATTTGTCATGTAATGATAATTTATTGTATGTCATACAGGATATCGGTGAAACGCACAAACGGCCCTTTGGAGTATTATATGAGTGTCCAAATACCTTCGATAGA
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AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCGATGAATAGCTGGAAAACATCCTTCAGTTCTTGGACATCGGAAGTTGAAAAATTATTATGGCGGAGCCATGT
CATCGAAGGATAAATTTGGGTCTATGGCCCAATGGAGGAGAAGGAAGCAACTATGCAAAATATTTAATGAAGACGAAGAATGCGTTTTATTTCGCCAGGAGGAAAACTTTTGGATATA
TGATAGTTGTATATATGAAGAAATAGTTATATTTGGATATTTCCAGATGCAAGAGGAATATTTAAACTATGGTTTATTAGAAGATTAAAAATGGAATTATTCAAAGCGGGAATAT
GAACCCGTTTTCGAAAATGTGAAATATGTGGAAGTCATTGTAATGGCTAACTTCCTTCGAAGGAAGGAATCTTCTCTGAAGATCGAATAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAAGCAAGAtCGGGGGTTGATTGtGCTATCCTAACGATTAAGGGCCGAGGCCCGTCAAGATGGACGGTTTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

DNA-S 12 SNPs to ALYU-42

CP protein: identical to ALYU-42

>S_alyu41
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAAACAGGCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCCGCAAGCAAACTAAAAGCCTATATATACCAAGTGTAGACATATTGTTCAAGATAACAAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGCGGCGGTTGGGCGACGGAATATGGAAGCAAGGCGGCAACCACTCAGCTACTCGTCTTAGGTTCAATATTGGTTCTGAAAAATACCGTCAAGGTATTAGGATTGAGCCTAC
TGATAAAACATTACCCAGATATTTTATCTGGAAAAATGTTTATGCTTTTGGTGTGCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAAGAGTTCTATGGGAAATCAACCAGCC
GACTACATGCTCGGAAGCACCAGGTTTATTATATAAAACCTGAACATAGCCATCTGGTGAACTGGTATCAGTGGGGAACCTGAAGCCGGAGTCGCAACAGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACAACCGTGTGGAGGAAGATGTAAACAGAGGTGGATTACTTGTATTGGCATTTTATTGTAGTGCTGGAGTTAGTATTAACACCAGAACAGAATTACATATCATGT
ATGATATGTTTATGTATAACATAAAACCTTTGTTATGGAATAATGACCAATAACATACACACaCTATGAAATACAAACACGCTATGACAAACAGGGAAAAATGAAGATCGGGGTTGATTG
GTCTATCGTaaCCCTTAAGGGCCGACGCCCTTGAATGATTTCTTTATAAAACAATATACATGATACGGAATaGTTGAaCATATAaaCAACGATCTATAAATACAACGAATGTTCTAT
ACTAATTAATAAATAAGAGAAGAAAGAAATATTGTAAGGATTAAGCATCAGAACCAACCTTTAGTGGTGGGTCAAGTGTCCCGAGTTAGTGGCCACGTAAGCGCTGGGGCTTAT

DNA-U3

Aligned sequences: 2
1: U3_alyu41
2: U3_alyu42
Length: 1079
Identity: 988/1079 (91.6%)
Similarity: 988/1079 (91.6%)
Gaps: 49/1079 (4.5%)

39 aa protein-encoding ORF is preserved

>U3_alyu41
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCATTCGGCCCAATAAATTAAGAGAACGTGTTCAAAA
TctGGGTTTGACCCGAAGGTCAAGGTAGACGGTCAACAATATTCGCTTTCGGGAGCAAGCAACAAGAAATTAATATTTAATTCGTATGACACGTGGACGGACCGGAAATACTCCTGTATCT
CTATAAATAGCCTAAATCTGGCATGGATAAATGCTCTCGCTCTCTGTCAAAGCTGTGTTGTGTTGAGGCGGAAGATCGCCATCGGGCATCATCAGACGAAAAGCTGCAAGAGAGACGGGAGA
ACCATGCTGCGGAAGCGTATATCGGGTATTATAGACTTCTAGCGCAGCTAGAAGTTTCCTGTACTTGTATTGTTATTTGTAAATACGAAGAAATTCGTACATTGATAATAATAAAAC
ATCTGGGATTGTTAATGTTTACATTAACTAGTATTAATAATGTACAATAACAACCATTTGATGAGGAACGAATACAAGAAATATTAATAATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGAATAATTAATAATTAATGCAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAATAAACCCCAATTATATTATTATTAATACATACAAC
ACGCTATCAAAAGGGGAAAAAGAAAAATCGGGGTTGATTGGTCTATCTCAACGATTAAGGGCCGAGGCCCTCAAGATGGATCCAATACCCCGTTAAGAGGTAAACGGGTCTAA
AACGATTTCTTCGCCCGCAAGCAACACCTTTAACTCTCGGCACCTATATATATAATAATAACCAATGACCATAGTGCCCTCCCAAGATGACGTATAGGGGTGTCCCGAGGTAAT
TTAACATAGCTCTGATAAGAGATAGTGGACGTTGGATTCCACGATCGGACGATCGTGGTTTGATGAACCTTATGATGACGTAGGGGCTGGGGCTTAT

ALYU-42 - Musa AAA Cavendish - Laos

Virome

1. **BBTV** six components
2. **BBTA5** alyu42

BBTA5

Best matches to MF510475, MF510474 73% coverage 66.4% identity Faba bean necrotic yellows virus associated
alphasatellite 2; AJ132187 AJ005966 73% coverage 66.2-65.7% identity Faba bean necrotic yellows C9 alphasatellite;
MK291270 72% coverage 67.0% identity Sophora yellow stunt alphasatellite 3

Rep protein best matches to QBF29185 100% coverage 63% identities 80% positives Sophora yellow stunt alphasatellite 3;
ATU31571 100% coverage 620% identities 80% positives Faba bean necrotic yellows virus associated alphasatellite 2;
ARI50297 100% coverage 62% identities, 80% positives Sophora alopecuroides yellow stunt alphasatellite 3

>BBTA5_alyu42
TATTACCCGACCTTGGCTCACTTGTCTACTATAAAAGGGGGAGATGTCGAGCAGCGAAATTTGGGTATTACGCGTAACTTCTCCGCGACCCCGGATTTTAAAGTTTCGCCGGGAAAAAC
TCAATACGCGTCTGGCAACATGAGAGAAGAAATCACGACCATCTTCAGGAGTGATTCATTTGAAGAAGAGCTTCGGATGAACGCGTGAAGAGCTTAATTTGGGGGAAATCCACACCT
CGAAGCCATGAGAGGAACAATCGACGAAGCAATAAGGTACGTGACGAAGAAGAGACACGAGTACGAGTCCGTGGGAATTCGAGAAATTAACGAAAGAGGCTCTAAGAGGAATTT
GATGGAATTTGCTCGACGATCCAGATAACGAAATATGGAACCTCAAAAATATCGACGCGCCATTACTAAACAAGCAATGGACGCGTCAAAGAAGAAGGCGGAATTAGGGTTTCCCTACGA
CTTAAAGGATGGCCAAAGATGGTTATTGAGTTAATCGAAGAACACCCGACACAGAACTATTATCTGGGTGTATGGTCTTAATGGTGGAGAAGGTAAACCGCAGTTTCGAAAGCATTAT
TGGATTACTCAAAGGATGGACATATCTACAGGTGGTGAACGTGAAGACATGATGTATCTGTGGCAAAAGAAATTAATAATAACGTTATTATTGATTTCGCCGATGTACAAAGGATTT
CATATCCTATAAGTTTATTGAGATGGTAAAGAACCGATGCATATTTAGTTATAAATATGAACCAATCGGGGCGATTGTAAGTAATGAAGTCCATGTAATTGTAATTCGAATGAGCTCC
AGATTATTCAAAGATTTTCGGAAGACAGAATAAAATTAATATTACATAACGCACACTATGACAAAAGGGCAAAAATGAAAAATCGGGGTTGATTGTCTATATTACGATTAAAGGGCC
CAGGCCGTACACTTTGCGCGGGAAATCAAAATCCGGACGCCAAATTTTATTAAATACAATACACGCCCTTTAGAAATCCGTGGACGAGAAGATGCCACGTATCAAACACTGTACTC
CTTGGCTCACTATAAATACCTGACCAAGTCGGGCATAG

DNA-C

7-15 SNPs to KY427060 MF039864 MF039876 MF039870 (Thailand). **31 SNPs** to KM607098 KM607099 (China)

C protein (161 aa): 1 aa to KY427060 (Thailand) **2 aa** to KM607098 KM607099 (China) MF039864 (Thailand)

>C_alyu42
TATTACCCCCCTGCTCGGACGGGACATCACGTGCATCTAACAAATGCACGTGACAATGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCATAAAAGTGAAGGAATATTCGTTGC
TTAGGACATAAGCAACGTGAACAGATATTTGTTGAGAGAAGCGACAATGGAGGCTATTTAAACCTGATGGTTTTGTGATTTCCGAAATCACTCATCGGAGAAGAAATGGAGTTCTGGGAAT
CGCTCGCCATGCCAGACGATGTCAAGAGAGTGATCAAGGAATATATTGGGAGCATCGAAACAACTTCTGTTTTGCAGAAGTTGAAAGGCTGTGTAAGAGGATTCTGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCGAGTGAAGGAGATGAAGACTTCTATTATTCGCTATAGCGAATATTGAAGAAACCTTGTTGGTATTGTTTTAGTACTAATAAATCTATTGCATATA
GGTTAAACCAATGGTGTCTTTTATCATGAATATATTGAAGACCTTAGGTGGTGACTACTCGGTATATCAAGATTTGTTTTGTGATGAGGAACTTCCTTATTCGTGCACAGAAGAAGAG
ATGAAGAAGTAAATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGCTCAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA
TTATGATAAATAAAATAATGGAATGATGATTATGTTCTAGTATAAATACATAATGGTATACGTATAGCATAAAAATACATATACCTACATACACACACTATAACAACAGGGGAAAAAT
GAAGATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGGCCGACGCCCTTTAAATATGTGGTGGACGAAGTCCACAACACATAAAAGGTATCAGAACAATGGAATATAATGAGCT
GGCAACGTAGGGACCATGTCCCGAGTTAGTGCGCCACGTGAGCAGGGGGCTTAT

DNA-M

6-10 SNPs to MF039865 KY427061 MF039871 MF039876 (Thailand). **52-59 SNPs** to KM607239 KM607240 (China)

M protein (117 aa): 0 aa to KC581796 (Thailand) **1 aa** to MF039871 MF039865 MF039877 KY427061 (Thailand)

>M_alyu42

TATTACCCCGAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACGGTTTATGAACCGTTATATATGTGTGAACGCAAAGTCACGTGTG
ATAGCGAAATGCACGTGACCAAGTCAAATGTATTGAATAAACATTTGACGTCCGGATGCTTCCTACGGAAGCCATGGTTGCTTCGTGGCGAAGCAAAACATTTATATATTGGCTTGGATT
GCTGCCATTAAATAGGCACGACGGAATGGCATTAAACAACAGAGCGAGTGAACATATTCCTTTGAATGGTTTCGTGTTATTGGTGCAATATTTATTGGCATAACAATATTATACATATTG
TTCGGCGTTCCTTTAGGTCCTCCCAAGTATATTAAAGGATGTTTGTAGGTATCTCGTAGAATACCTGACCAGACGACGTGTATGGATCGAGAGAACCAGCATTCGCGAGGACACAGGAGAT
GTAGAAGTCGCGAGAGGTAGTGTGGAAGACAGACGGGATCAACAACCGGCTGTATACCACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGAGCAAGGAAGACGAGGA
AACGCCGACCGATGTTTAAATACACGGTATTGTAATATACGAAATATAAATGGATAATGATAAGTATTGTGAAACAAAATATATGTGAAACATAATATATGTTGATAATTTACATATT
GTAATATGTGAATGTATACGAGTGTGTATTATTAATAACATACAACACGCTATGACAAACAGGGGAAAAATGAAGAAATCGGGGGTTGATTGGCTCATCGTATCCGTTAAGGCCCGCAGGC
CCGTTGAAATGATTCTTTATAAAACAAATATACATGATACGGATTGTTGAAAATATAATCAACGATGTATAAATACAACAGAAATGTTGTATAAATATAAATAATGAGAAGATAAGTAT
ATTTGTGAAGGATATGGATCACAAACCACCATTTAGTGGTGGGTGCATATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-N

2-6 SNPs to MF039878 MF039866 KY427062 MF039866 (Thailand). **24-34 SNPs** to KM607387 KM607385 KM607386 (China)

N protein (154 aa): 0 aa to MF039872 MF039878 KY427062 (Thailand) KM607387 KM607385 (China) **1 aa** to MF039866 (Thailand)

>N_alyu42
TATTACCCCGCTGCTCGGGACGGGACATGACGTGACGATAGATTATAATGGGCCAACTAAAGGCCCATTTAATAGAATAGCGGGCTTTTGACATATTTCAAAGGCCAGCCTGGAAGT
GATTAATGTACGTGCGCAATAAGAGTTGCTTCGCCCTCGAAGCAACCCGACAAATGTTCGGTATTCAATACGCAACTGAAGTCTATTAATATGGATGTCTCTGCCGAATAAATCAGAG
CCTAAGCGAAGCAGAACCAGATCGATTCCGCACAATCACAAATTCAGACATGTACTCATGGTTCGATTTGGAAGACATATCATCGGATTCATCCGACAATCCACAATATGTACCTTCGCT
CGACGACGGCAGCGGAAGAAAGTCACTCGCAAGGTACTGCTAAGATCTATTGAAGCTGTGTTTAAATGGAAGCTTCAAAGGAAATAACAGGAATGTTCTGGGTTTATATACGTATCAAT
ACGAGACGATGATGGAGAAATGGCTCCAGTACTATAATACCATTTCGGAGGATATGGATATCATAATGATTTCTATTATTTCGAAGGGAAGGGGAAAGTTGAATGTGATATATCATCAGA
TATGTAGCGCCAGGAGTGCATTGGAGCAGAGACATGGAAGTTAGTATTAGTAACAGCAACAACCTGTAATGAATTATGTGATCTGAAGTGTATGTTGTTGTTTCGTTAAGAAATAAAGGA
ATAACAGATGTGCTGTAATGAATATAATAAAATATATTTTCATGTAATTGATAGTTGTATAAAACATACACACGCTATGACAAACAGGGAaAATGAAAAATCAGGGGTTGATTGGTC
TATCGTATCGCTTAAGGGCCGACGGCCGTTGAAAAATAATAATCGAATTATTACGTTTGATAATAATCAGAGATAGATGATAAGCATCCAAAAACATAGACGAGATATATGGCTGTA
ATAATAAACCAAGCATATAATAAAATATGTGAACATACTCTGATTGTTTACACGATAGCCCCACCACCTTATGTTGGTGGAAATGTCCCGATGACGTAAGCAGCGGGGACAT

DNA-R

3-6 SNPs to MF039879 MF039873 MF039867 KY427063 (Thailand). **10 SNPs** to AF416475 (Viet Nam). **14-16 SNPs** to KM607677
KM607678 KM607676 KM607679 (China)

R protein (286 aa): 0 aa to KM60767 KM607677 KM607679 (China) **1 aa** to AB113660 (Vietnam) MF039879 (Thailand) KM607678
(China) ...

>R_alyu42
TATTACCCCGAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCCCCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAAC
ATCAACAATCCCGCTTCACTACCAAGTATGCGGGATGAGTTTAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCAAGGATACGTCGAGATGAAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCCTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAAGAAGACACGGGCATACTGTATGAAGGAAGACACAAGAATCGAAGGTCCCTTC
GAGTTTGGTGCTTTAAATTTGCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGTGAAACGCACAAACCGCCCTTGGAGTATTTATATGAGTGTCCAATACCTTCGATAGA
AGTAAGGATACATTATACAGATTTCAAGCAGAGTTGAATAAAACGAAGGGCATGAATAGCTGAAAACATCCTTCAGTTCTTGACATCGGAAGTTGAAAAATATTATGGCGGAGCCATGT
CATCGAAGATATAATTTGGTCTATGCGCCAAATGGAGGAGAAGGAAGACAACTTATGCAAAATATTTAATGAAGACGAAGATGCGGTTTATTCGCGAGGAGAAATCTTTGGATATA
TGTAGATTTGTATAATTATGAACAAATATGTTATTTGATATTTCCAGATGCAAAAGGAAATATTTAACTATGGTTTATTAGAAGAAATTTAAATATGAAATTTCAAAGCGGAAATAT
GAACCCGTTTTGAAATTTGAGAATATGTGGAAGTCATTGTAATGGCTAACTTCTTCCGAAGGAAGAAATCTTCTGAAGATCGAATAAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAGCAAAAGATCGGGGGTGTATTGGGCTATCCTAACGATTAAAGGGCCGAGGCCCTCAAGATGGACGGTTTATCAGATGTCCCGAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

DNA-S

6-20 SNPs to MF039874 KY427064 MF039880 (Thailand). **24-27 SNPs** to AB113661 AB113662 (Viet Nam). **27-29 SNPs** to KM60753
KM607534 KM607536 KM607533 (China)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines), **1 aa** to several isolates

>S_alyu42
TATTACCCCGAGCGCTCGGGACGGGACATGGGCTTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAAACAGCGCG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCCCGCAAGCAAACATAAAAGCTATATATACCAAGTGTAGACATATTGTTTCAGATAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGCGGGTTGGCGACGGAAGTATGGAAGCAAGCGCGCAACAGTCACGACTACTCGTCTTAGGTTCAATATTGGTTCCTGAAAAATACCGTCAAGGTATTAGGATTAGCCTAC
TGATTAACCAATTACCCAGATATTTTATCTGGAATAATGTTATGCTTTTGGTGCAAGGTGAACCTGGAAGCAATACTTCATTGGGCTATGATTAAAGTTCTATGGGAAATCAACAGCC
GACTACATGCTCGGAAGCACCAGGTTTATTCATAAAACCTGAACATAGCCATCTCGTGAAACTGGTATGCAGTGGGAACTTGAAGCCGGAGTCGAACAGGGACATCAGATGTAGAATG
TCTTCTAAGGAAGACAAACCGTGTGGGAAGAATGTAAACAGAGTGGATTACTTGTATTGGGCATTTATTGTAGTGTGGAGTTAGTATTAACTACCAGACAGAAATACATATCATGT
ATGATCTGTTTATGTAAACATAAACCAATTGTATGGATTAAATGACCAAAATACATACAACACGCTATGAAATACAACACGCTATGACAAACGGGGAAAAATGAAGAAATCGGGGGTTGATTG
CTCTATCGTATCGCTTAAGGGCCGACGGCCGTTGAAATGATTCTTTATAAAACAAATATACATGATACGGATTgTTGAAATATAATCAACGATGTATAAATACAACAGAAATGTTGTAT
ACAAATTAATAAAAAAAGAGAAGATAAGTATATTGTGAAGGATAAGCATCAGAACCACCACCTTTAGTGGTGGGTGAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3

11-21 SNPs to MF039881 MF039875 KY427065 MF039869 (Thailand)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alyu42
TATTACCCCGACCCCGAGGACGGGACATGGGCTTTTAAATGGCCGAGAGAGTTTGAACAGTTAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAAGCTGTTCAAAA
TCGGGGTTTGACCGAAGGTCAAGGTAGACGGTCAACAATATTTCTGGCTTGCGGAGCAAGCAACACGAATTAATATTTAATTCGTATGACACGTGGACGGACGAAATACTCTGTAAAT
CTATAAATAGCCTAAATCTGGCGGTGATAAATGTCTCTTCGCTTCTGTCAAAGCTGTGTGTGAGGCCGAAGATCGCCATCGGCGATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
AACATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTTCGTTGTATTGATATTGTAATTTGTAATTTACGAAGAATTCGTACATTGATAATAATAAAACA
TCTGGGATTGTTAATGTTTACATTAAACGATTAATTAATGTACAATAAAAAAATTTGATGAGGATCGAATACAATAATATTAATAATGAGGAGCGTAGCATGATAAACAGGTGTTTA
AGGTATAAATTAATAAATTTATGCAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAATAACCAATTTATATTATTATAATACATAACA
CGCTATGACAAAAGGGGAAAAATGAAGAAATCGGGGTTGATTGGTCTATCGTATCGCTTAAGGGCCGACGCGCCGCAAGATGGATGAACGGTCAGATTGATTGGCTTAGCCACGAGAA
AGGAATCTTTTGGGACCACAGATAAGACAGCTGTCAATACCTTTTAAAAATAATAATAAACCAATTGACGATAGTACCCCTCCCAAAGATGACGTATAGGGGTGTCCCGAGGTAATTTA
ACATAGCTCTGACAAGAGATAGTGGACGTTGGATGCCACGATCGGACGATCGTGGTTGATGAACCTTATGATACGTAGGGGCTGGGGCTTAT

ALYU-43 - Musa AAA Cavendish - Laos

Virome

- 1. **BBTV** six components (all except N are represented with 2 genetic variants)
- 2. **BBTA5** alyu43

BBTA5 v1 - 1 SNP to alyu42 / v2 - 2 SNPs to alyu42

In both variants, Rep protein is identical to alyu42

>BBTA5_alyu43_v1
TATTACCCGACCTTGGCTCACTTGTCTACTATAAAGGCGGAGATGTCGACGACGCAAAATGGGTATTACGCGTAACTTCTCCGGCAGCCCGCGGATTTAAAGTTCGCGGAGAAAC
TCAATAGCCGTGCTGGCAACATGAGAAGAAGAAATCACGACCATCTTCAGGAGTGATTCAATTGAAGAAGAAGCTTCGGATGAACGCAGTGAAGACGTTAATGGGGGAAATCCACACCT
CGAAGCCATTGAGAGGAACAATCGACGAAGCAATAAGGTACGTGACGAAGAGAGACACGAGTACGAGTCCGTTGGGAATTCGGAAGAAATCTACGAAAAGAGTCTCATAGAGGAAAT
GATGAAATCTTTTGGGACCACAGATAAGACAGCTGTCAATACCTTTTAAAAATAATAATAAACCAATTGACGATAGTACCCCTCCCAAAGATGACGTATAGGGGTGTCCCGAGGTAATTTA
CTTAAAGGATGGCAAAAGATGGTTATTGAGTTAATCGAAGAACAACCCGACAACAGAATATTTATCTGGGTGATGGTCTAATGGTGGAAGAGTAAACGCAGTTCGAAAGCATTA

TGGATTACTCAAAGGATGGACATATCTACCAGGTGGTGAACCTGAAAGACATGATGTATCTGTGGCAAAAGAAATTAATAATAACGTTATTATTGATTTCCCCCGATGTACAAAGGATTT
CATATCCCTAAAGTTTATTGGAGTGGTAAAGAACCAGTGCATATTTAGTTATAAAATGAACCAATCGGGGCGATTGTAAGTAATGAAGTCCATGTAATTGTAATGTCGAATGAGCTTCC
AGATTATTCAAAGATTTCGGGAAGACAGAATAAAATTAATATTTACATAACGCACACTATGACAAAGGGCAAAAATGAAAATCGGGGGTTGATTGTCTATATTTACGATTAAAGGGCCG
CAGGCCCGTACACATTTCCGCGGGAAATTCAAAATTCGGACGCCAAATTTTATTAATAACAATACACCGCTTTTAGAAATCCGTGGACGAGAAGATGCCACGTATCAAAACACTGTACTC
CTTGGCTCACTATAAATACCTGAGCCAAAGGTCGGGCATAG

G/C (64895/29398) A/G (111791/14216) T/C (99589/70722)

>BBTA5_alyu43_v2
TATTACCCGACCTTGGCTCACTTGTCTACTATAAAAGGCGGAGATGTCGACGACGCAAAATTGGGTATTACGCGTAACTTCTCCGGCGACCCGCCGATTTTAAAGTTCGCGGAGAAAC
TCAATACGCGTGTCTGGCAACATGAGAAGAAGAACACGACCATCTTCAGGAGTGATTCAATTAAGAAGAAGCTTCGGATGAACGCGAGTGAAGACGTTAATTTGGGGAAATCCACACCT
CGAAGCCATGAGAGGAACAATCGACGAAGCAATAAGGTACGTGACGAAAGAGAGACACGATGACAGGTCCGTGGGAATTCGGAGAATTACTACGAAAAGGATCTCATAGAGGAAAT
GATGGAATTGCTCGACGATCCAGATAACGAAATAATGGAACCTCAAAAATATCGACCGGCCATTACTATAACAAGCAATGGACCGTCAAAAGAAGCGCGGAATTAGGTTTCTCTAACGA
CTTAAAGGAGTGGCAAAAGATGGTTATTGAGTTAATCGAAGAACAACCCGACACAGAACTATTATCTGGGTGTATGGTCTAATGGTGGAGAAGGTAAACGCGAGTTCGCAAGCATTAT
TGGATTACTCAAAGGATGGACATATCTACCAGGTGGTGAACCTGAAAGACATGATGTATCTGTGGCAAAAGAAATTAATAATAACGTTATTATTGATTTCCCCCGATGTACAAAGGATTT
CATATCCTATAAGTTTATTGGAGTGGTAAAGAACCGATGCATATTTAGTTATAAATGAACCAATCGGGGCGATTGTAAGTAATGAAGTCCATGTAATTGTAATGTCGAATGAGCTTCC
AGATTATTCAAAGATTTCGGGAAGACAGAATAAAATTAATATTTACATAACGCACACTATGACAAAGGGCAAAAATGAAAATCGGGGGTTGATTGTCTATATTTACGATTAAAGGGCCG
CAGGCCCGTACACATTTCCGCGGGAAATTCAAAATTCGGACGCCAAATTTTATTAATAACAATACACCGCTTTTAGAAATCCGTGGACGAGAAGATGCCACGTATCAAAACACTGTACTC
CTTGGCTCACTATAAATACCTGAGCCAAAGTTCGGGCATAG

DNA-C v1 = alyu42

Link protein is identical in v1 and v2

>C_alyu43_v1
TATTACCCCCCTGCTCGGGACGGGACATCACGTGCATCTAACAAATGCACGTGACAATGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCATAAAAGTGAAAGGAATATTCTGTTGC
TAGGGACTAAGCAACGTGACACAGATATTTGTCGAGAAGCGACAATGGAGGCTATTTAAACCTGAAGGTTTTGTGATTTCCGAAATCACTCATCGGAGAAGAAATGGAGTCTCGGGAAT
CGTCTGCCATGCCAGACGATCTCAAGAGAGTGATCAAGGAATATATTTGGAGCATCGAAACAACTCTGTTTTGTCAGAAGTTGAAAGGCTGTGTAAGAAGGATTCTGGAGCATCGAA
ATCAAGATGATGCTCTAGACCGAGTGAAGGAGATGAAGACTTCTATTATTCGCTATAGCGAATATTGGAAGAAACCTTGTGTGGTATTGTGTTTGTAGTACTAATAAATCTATTGCATATA
GGTTAAACACAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTACTCGGTATATCAAGATTGTTTGTGTGATGAGGAACCTCTTATTCGTCGACAGAAGAAGAAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA
TTATGATAAATAAAATAATGGAATGATGATTATGTTCTAGTATAAATACATAATGGTATACGTATAGCATATAAATACATATACCTACATACAAACACACTATAACCAACAGGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGGCCGAGGCCCGGTTTAAATATGTGGTGGACGAAGTCCACAACACATAAAAAGGTATCAGAACAATGGAATATAATGAGCT
GGCAACGTAGGGACCATGTCCCGAGTTAGTGCGCCACGTGAGCAGGGGGGCTTAT

>C_alyu43_v2
TATTACCCCCCTGCTCGGGACGGGACATCACGTGCATCTAACAAATGCACGTGACAATGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCATAAAAGTGAAAGGAATATTCTGTTGC
TAGGGACTAAGCAACGTGACACAGATATTTGTCGAGAAGCGACAATGGAGGCTATTTAAACCTGAAGGTTTTGTGATTTCCGAAATCACTCATCGGAGAAGAAATGGAGTCTCGGGAAT
CGTCTGCCATGCCAGACGATCTCAAGAGAGTGATCAAGGAATATATTTGGAGCATCGAAACAACTCTGTTTTGTCAGAAGTTGAAAGGCTGTGTAAGAAGGATTCTGGAGCATGGAA
ATCAAGATGATGCTCTAGACCGAGTGAAGGAGATGAAGACTTCTATTATTCGCTATAGCGAATATTGGAAGAAACCTTGTGTGGTATTGTGTTTGTAGTACTAATAAATCTATTGCATATA
GGTTAAACACAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTACTCGGTATATCAAGATTGTTTGTGTGATGAGGAACCTCTTATTCGTCGACAGAAGAAGAAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA
TTATGATAAATAAAATAATGGAATGATGATTATGTTCTAGTATAAATACATAATGGTATACGTATAGCATATAAATACATATACCTACATACAAACACACTATAACCAACAGGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGGCCGAGGCCCGGTTTAAATATGTGGTGGACGAAGTCCACAACACATAAAAAGTATCAGACAACAATGGAATATAATGAGCT
GGCAACGTAGGGACCATGTCCCGAGTTAGTGCGCCACGTGAGCAGGGGGGCTTAT

DNA-M v1 = alyu42

MP v1=v2

>M_alyu43_v1
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACGGTTTATTGAACCGTTATATATTGTTGAACGAAAGTCACGTGTG
ATAGCGAAATGCACGTGACCAAGTCAAATGTATTGAATAAACATTTGACGTCGGGAAGCTTCCTACGGAAGCCATGGTTGCTTCGTGGCGAAGCAAAACATTATATATTGGCTTGGATT
GCTGCCATATAAATAGGCACGACGGGAAATGGCATTAAACAACAGAGCGAGTGAACATATCTTTTGAATGGTTTCTGTTTATTGGTCAATATTTATTGCCGATAACAATATTTATACATATTG
TTGGCGTTGCTCTTTGAGTCCCAAGTATTTAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACAGACGACGTGTATGGATGACAGAAACCGAGTTGACGAGGCAACAGGAGAT
GTAGAACTCGGCAGAGGTAGTGTGGAAGACAGACGGGATCAACACCGGCTGTCTCCACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGAGCAAGGAAGACGAGGA
AACGCCGACCGATGTTTAAATACACGGTATTGTAATATACGAAATATAAATGGATATGATAAGTATTGTGAAACAAAATATATGTGAAACATAATATATGTTTATGATAATTTACATATT
GTAATATGTGAATGTTATACGAGTGTCTTATTATAAAACATACACACGCTATGACAAACAGGGAATAATCAAGAATCGGCGGTTGATTGCTCTATCGTATCGCTTAAGGGCCCGAGGC
CCGTTGAAATGATCTTTTATAAAACAAATATACATGATACCGGATTGTTGAAATATAATCAACGATGTATAAATACACAGAATGTTGTATAGTAATTTAAATCAACGAAGATGAGAAG
ATAAGTATATTGTTGAAGGATATGGATCAACACCACGTTTATGTGGTGGTCTATGTGCCGAGTTAGTGGCCACGTAAAGCGCTGGGGCTTAT

>M_alyu43_v2
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACGGTTTATTGAACCGTTATATATTGTTGAACGAAAGTCACGTGTG
ATAGCGAAATGCACGTGACCAAGTCAAATGTATTGAATAAACATTTGACGTCGGGAAGCTTCCTACGGAAGCCATGGTTGCTTCGTGGCGAAGCAAAACATTATATATTGGCTTGGATT
GCTGCCATATAAATAGGCACGACGGGAAATGGCATTAAACAACAGAGCGAGTGAACATATCTTTTGAATGGTTTCTGTTTATTGGTCAATATTTATTGCCGATAACAATATTTATACATATTG
TTGGCGTTGCTCTTTGAGTCCCCAAGTATATTAAAGATGTTGTGAGGTATCTCGTAGAATACCTGACCAAGACGACGTGTATGGATGACAGAAACCGAGTTGACGAGGCAACAGGAGAT
GTGAACTCGGCAGAGGTAGTGTGGAAGACAGACGGGATCAACACCGGCTGTCTCCACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGAGCAAGGAAGACGAGGA
AACGCCGACCGATGTTTAAATACACGGTATTGTAATATACGAAATATAAATGGATATGATAAGTATTGTGAAACAAAATATATGTGAAACATAATATATGTTTATGATAATTTACATATT
GTAATATGTGAATGTTATACGAGTGTCTTATTATAAAACATACACACGCTATGACAAACAGGGAATAATCAAGAATCGGCGGTTGATTGCTCTATCGTATCGCTTAAGGGCCCGAGGC
CCGTTGAAATGATCTTTTATAAAACAAATATACATGATACCGGATTGTTGAAATATAATCAACGATGTATAAATACACAGAATGTTGTATAGTAATTTAAATCAACGAAGATGAGAAG
ATAAGTATATTGTTGAAGGATATGGATCAACACCACGTTTATGTGGTGGTCTATGTGCCGAGTTAGTGGCCACGTAAAGCGCTGGGGCTTAT

DNA-N = alyu42

>N_alyu43
TATTACCCCCGCTGCTCGGACGGGACATGACGTGACGATAGATTATAATGGGCCAACTAAAGGCCCATTTAATAGAATAGCGGGGCTTTTGACATATTTCAAAGGCCAGCCTGGAAGT
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CGTAAGCGAAGCAGAAGCGATGGATTGGGCAGAAATCACAAATTCAGACATGTACTCATGGTGGGATTGGAAGACGATATCATCGGATTTCGCGAGAATCGACAATATGTACCTTGGCT
CGACGACGAGCAGCGAAGAAAGTCACCTCGCAAGGTACTGCTAAGATCTATTGAAGCTGTGTTTAAATGGAAGCTTCAAAGGAATAACAGGAATGTTCTGGGGTTATATACGATATCAAT
ACGAGCATGATGGAGAATCGCTCCAGTACTATAATACCATTCCGAGGATATGGATATCTAATGATTCTTATTATTTCGAAGCGAAGGGGAAAGTTGAATGTTGATATATCATCAGA
TTATGTAGCGCCAGGAGTCGATTGGAGCAGAGACATGGAAGTTAGTATTAGTAACAGCAACAACCTGTAATGAATTATGTGATCTGAAGTGTATTGTGTTTGTCTGTTAAGAATAAAGGA
ATAACAGATGTGCTGTAATGAATATTAATAAAATATATTTTCATGTAAATGATAGTTGTATAAAACATACACACGCTATGACAAACAGGGGAAAAATGAAAAATCAGGGGTTGATTGGTC
TATCGTATCGCTTAAGGGCCGACGGCCGTTGAAAAATAAATCGAATATTAACTGTTGATAAATAACAGAGATAGATGATAAGCATCCAAAAACATAGACGGAAGTATATGGCTGT
TAATAAAACAAAGCATATAAATAAAATATGTGAACATACTCTGATTGGTTTAAACGTAGCCCCCAACTTTATGTTGGTGAAATGTCCCGATGACGTAAACGACGGGGACTAT

DNA-R v2 - 1 SNPs to alyu42

Rep protein is identical

>R_alyu43_v1
TATTACCCCCAGCGCTCGGACGGGACATTTGTCATCTATAAATAGACCTCCCCCCCCCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCCACC
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AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAAGAAGACGACGGGCATCTGTATGAAGGAAGCACAGAATCGAAGGTCCCTTC
GAGTTTGGTGCATTAAATTTGTCATGTGAATGATAATTTATTGATGTATACAGGATATGCGTGAAACGCACAAACGCCCTTTGGAGTATTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTCAAGCAGAGTTGAATAAAACGAAGCGATGAATAGCTGGAAACATCTCTCAGTCTTGGACATCGGAAGTTGAAAATATTATGCGGAGCCATGT

CATCGAAGGATAATTTGGGCTCTATGGCCCAATGGAGGAGAAGGAAAGACAACCTTATGCAAAATATTTAATGAAGACGAAGAATGCGTTTTATTCGCCAGGAGGAAAACTCTTTGGATATA
TGATAGATTGTATAATTATGAAGaaatagTTATATTTGATATTCCAGATGCAAAAGAGGAATATTAACTATGGTTTATTAGAAGAAATTTAAAAATGGAATTATTCAAAGCGGGAATAT
GAACCCGTTTGGAAATTGTAGAATATGTGGAAGTCATTGTAATGGCTAACTCCTTCGGAAGGAAGGAATCTTCTCTGAAGATCGAATAAAGCTAGTTGCTTCTGCTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAGCAAAGATTCGGGGGTGATTG**T**GCTATCCTAACGATTAAAGGCCCGAGGCCCTCAAGATGGACGGTTTGATCAGATGTCCCAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

A/C (9857/8782) **A/G** (10726/8560) **T/G** (7640/5914)

>R_alyu43_v2
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ATCAACATCCCGCTTCACTACCAGTATGCGGGATGAGTTTAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCTATGTGCAGGGATACGTCGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAGAAGACACGCGGCATCTGTATGAAGGAAGACACAAGAATCGAAGGTCCTCTC
GAGTTTGGTGC**T**TTAAATTGTCTATGTAATGATAATTTATTTGATGTCATACAGGATATGCGTGAACGCACAAACG**G**CTTTGGAGTATTTATATGATGTGCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCGATGAATAGCTGGAACACATCCTTCAGTTCTTTGGACATCGGAAGTTGAAAAATATTATGGCGGAGCCATGT
CATCGAAGGATAATTTGGGCTCTATGGCCCAATGGAGGAGAAGGAAGACAACCTTATGCAAAATATTTAATGAAGACGAAGAATGCGTTTTATTCGCCAGGAGGAAAACTCTTTGGATATA
TGATAGATTGTATAATTATGAAGAAATGATTATTTGATATTCCAGATGCAAAAGAGGAATATTAACTATGGTTTATTAGAAGAAATTTAAAAATGGAATTATTCAAAGCGGGAATAT
GAACCCGTTTGGAAATTGTAGAATATGTGGAAGTCATTGTAATGGCTAACTCCTTCGGAAGGAAGGAATCTTCTCTGAAGATCGAATAAAGCTAGTTGCTTCTGCTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAGCAAAGATTCGGGGGTGATTG**G**GCTATCCTAACGATTAAAGGCCCGAGGCCCTCAAGATGGACGGTTTGATCAGATGTCCCAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

DNA-S v2 4 SNPs to alyu42

CP protein is identical

>S_alyu43_v1
TATTACCCCGAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAAACAGGCGG
GAACCGTCC**T**AAATTTCAAATTTAGATAGCTTGCCCCGCAAGCAAACTAAAAGTCTATATATACCAAGTGTAGACATATTGTTTCAGATAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGCGCGGTTGGGCGACGGAAGTATGGAAGCAAGCGCGCAACCACTACGACTACTCTGCTCTAGGTTCAATATTGGTTCTGAAATACCGCTCAAGGTATTATTAGGATTGAGCCTAC
TGATAAAACATTACCCAGATATTTATCTGGAATAATGTTTATGCTTTTGGTGTGCAAGGTGA**A**CTTGGGAAGAATACTTCATTGGGCTATGATTAAAGTTTCATGGGAATCAACACGCG
GACTACATCTGTCCGAGCACCAAGGTTTATTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAGTGGGGAACCTGAAGCCGGAGTCGCAACAGGGACATCAGATGTAGAATT
TCTTCTAAGGAAGACAAACCGTGTGAGGAAGAATGTAAACAGAGGTGGATTACTTGTATTGGCATTTTATTGTAGTCTGGAGTTAGTATTAACTACCAGAACAGAAATACATATCATGT
ATGATCTGTTTATGTAACATACAAAC**T**TTGATGG**T**TAATGACCAATAACATACACACGCTATGAAATACAAACACGCTATGACAAACGGGGAAAAATGAAGAATCGGGGGTTGATTG
GTCATCGTATCGCTTAAGGGCCGACGGCCCGTTGAAATGATTCCTTTATAAAACAAATATACATGATACGGATTGTTGAAAATATAATCAACGATGTATAAATACACAGAAATGTTGTAT
ACCAATTAACAAAA**A**GAGAAGATAAGTATATTTGTGAAGGATA**E**G**A**TC**A**ACCACCACCTTTAGTGGTGGGTCATATGTCCCAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

C/T (1903/495) A/G (1352/1225) T/A (1165/923) C/A (1092/945) ins-G5723AG (3220/710) A/T (1654/2258) C/G (1253/2610) G/C (1282/2111)

>S_alyu43_v2
TATTACCCCGAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAAACAGGCGG
GAACCGTCC**T**AAATTTCAAATTTAGATAGCTTGCCCCGCAAGCAAACTAAAAGTCTATATATACCAAGTGTAGACATATTGTTTCAGATAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGCGCGGTTGGGCGACGGAAGTATGGAAGCAAGCGCGCAACCACTACGACTACTCTGCTCTAGGTTCAATATTGGTTCTGAAATACCGCTCAAGGTATTATTAGGATTGAGCCTAC
TGATAAAACATTACCCAGATATTTATCTGGAATAATGTTTATGCTTTTGGTGTGCAAGGTGA**A**CTTGGGAAGAATACTTCATTGGGCTATGATTAAAGTTTCATGGGAAATCAACACGCG
GACTACATCTGTGGAAGCACCAAGGTTTATTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAGTGGGGAACCTGAAGCCGGAGTCGCAACAGGGACATCAGATGTAGAATT
TCTTCTAAGGAAGACAAACCGTGTGAGGAAGAATGTAAACAGAGGTGGATTACTTGTATTGGCATTTTATTGTAGTCTGGAGTTAGTATTAACTACCAGAACAGAAATACATATCATGT
ATGATCTGTTTATGTAACATACAAAC**T**TTGATGG**T**TAATGACCAATAACATACACACGCTATGAAATACAAACACGCTATGACAAACGGGGAAAAATGAAGAATCGGGGGTTGATTG
GTCATCGTATCGCTTAAGGGCCGACGGCCCGTTGAAATGATTCCTTTATAAAACAAATATACATGATACGGATTGTTGAAAATATAATCAACGATGTATAAATACACAGAAATGTTGTAT
ACCAATTAACAAAA**A**GAGAAGATAAGTATATTTGTGAAGGATA**E**G**A**TC**A**ACCACCACCTTTAGTGGTGGGTCATATGTCCCAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3 v1 = alyu42

ORF1 (39 aa) v1=v2

>U3_alyu43_v1
TATTACCCCGAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCGAGAGAGTTTGAACAGTTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAA
TCGGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATTCTGGCTTGCAGGACGAAGCAACACGAATTAATATTTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAAAT
CTATAAATAG**C**TAAATCTGGC**T**GGATAATTGCTCTCGCTCTTCTGTCAAAG**T**GTGTGTGTAGGCGGAAGATCGCCATCGGGCATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
AACATGCTCGGAAGCGTATATCGGGTATTATAGACTTCTAGCGCAGCTAGAAGTTTC**E**TTGTA**T**TTGATATTGTATTTTGTAAATTACGAAGAA**T**TCGTACATTGATAATAATAAAACA
TCTGGGATTGTTAATGTTTACATTAAACAGTATTAATAATGTACAATAAAAAAATTGTATGAGG**T**CGAATAACAATAATATTAATAATGAGGAGCGTAGCATGATAAACACAGTGTTTA
AGGTATAATTAACAAAAATTATGCAATGTTATGATAATACGGTATAAGTTCAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAACAAACCAATTATATATTATTATAATACATACAACA
CGCTATGACAAAGGGGAAAAATGAAGAATCGGGGGTTGATTGGTCTATCGTATCGCTTAAGGGCCGACGGCCCGTCAAGATGGATGAACGGTCAGATTGATTGCTTAGCCAGCAAGAA
AGGAATCTTTTGGGACCAAGATAGACAGCTGTCAATTACCTTTTAAAAATAATAATAACCAATTGACATAGTACCCCTCCAAAGATGACGTATAGGGGTGTCCCGAGGTAAATTTA
ACATAGCTCTGACAAAGAGATAGTGGACGTGGATGCCACGATCGGACGATCGTGGTTTGATGAACCTTATGATGACGTAGGGGCTGGGGCTTAT

T/C (5206/18054) T/C (5922/19995) G/C (6323/21286) G/T (14217/4390) T/C (13764/4364) T/A (10443/3360) A/T (5860/1868) T/A (5939/2125)

>U3_alyu43_v2
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TCGGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATTCTGGCTTGCAGGACGAAGCAACACGAATTAATATTTAATTCGTATGACACGTGGACGGACCGGAAATACTCCTGTAAAT
CTATAAATAG**C**TAAATCTGGC**T**GGATAATTGCTCTCGCTCTTCTGTCAAAG**T**GTGTGTGTAGGCGGAAGATCGCCATCGGGCATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
AACATGCTCGGAAGCGTATATCGGGTATTATAGACTTCTAGCGCAGCTAGAAGTTTC**E**TTGTA**T**TTGATATTGTATTTTGTAAATTACGAAGAA**T**TCGTACATTGATAATAATAAAACA
TCTGGGATTGTTAATGTTTACATTAAACAGTATTAATAATGTACAATAAAAA**A**ATTGTATGAGGA**T**CGAATAACAATAATATTAATAATGAGGAGCGTAGCATGATAAACAGGTGTTA
AGGTATAATTAACAAAAATTATGCAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAACAAACCAATTATATATTATTATAATACATACAACA
CGCTATGACAAAGGGGAAAAATGAAGAATCGGGGGTTGATTGGTCTATCGTATCGCTTAAGGGCCGACGGCCCGTCAAGATGGATGAACGGTCAGATTGATTGCTTAGCCAGCAAGAA
AGGAATCTTTTGGGACCAAGATAGACAGCTGTCAATTACCTTTTAAAAATAATAATAACCAATTGACATAGTACCCCTCCAAAGATGACGTATAGGGGTGTCCCGAGGTAAATTTA
ACATAGCTCTGACAAAGAGATAGTGGACGTGGATGCCACGATCGGACGATCGTGGTTTGATGAACCTTATGATGACGTAGGGGCTGGGGCTTAT

ALYU-44 - *Musa ornata* - Laos

Virome

1. **BBTV** six components

DNA-C

4-12 SNPs to KY427060 MF039864 MF039876 MF039870 (Thailand) . 30 SNPs to KM607099 KM607098 (China)

C protein (161 aa) : 1 aa to KY427060 (Thailand) 2 aa to KM607098 KM607099 (China) MF039864 (Thailand)

>C_alyu44
TATTACCCCGCTGCTCGGACGGGACATCACGTGCATCTAACAAATGCACGTGACAATGCAGTAGCTTGTAGCGAAAGATAACCATCACATCATATAAAAGTGAAAGGAATATTCGTTGC
TTAGGCAATTAAGCAAGCTGGATAGATATTGTTTCGAGAAGCGCAATGGAGGCTATTAAACCTGATGGTTTTGTGATTTCCGAAATCACTCATCGGAAGAAATCGAGTTCTGGGAAT
CGTCTGCCATGCCAGACGATGTCAGAGAGTGATCAAGGAAATATATTGGGAGCATCGAAACAACTCTGTTTTGTGCAAGAGTTGAAAGGCTGTGTAAGAAGGATTCTGGAGCATGGAA
ATCAAGATGATGCTTAGACGCGAGTGAAGAGATGAAGACTTCTATTATTTCGCTATAGCGGAATATTGAAGAAACCTTGTTGGTATTGTTTGTAGTACTAATAAATCTATTGCATATA
GGTTAAACCAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTACTCGGTATATCAAGATTTGTTCTGTGTATGAGGAACCTCTTATTCTGTGCAGAGAAGGAAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA

DNA-M

M protein (117 aa): 0 aa to KC581796 (Thailand) 1 aa to MF039871 MF039865 MF039877 KY427061 (Thailand)

TATTATCCCCACCGCGCTGACGACGGGACATCTGTGCAACTACAAAAATGCAGGTGATGATATATACATCAACGGTTTATTGAACCGTTTATATATGTTTGAATCCGAAAGTCAGGTGTG
ATACGGAAGAAGCAATCTGACCAAGACAATGATTGATAAAACATTGACGTCGGATGCTCTCCACGGAAGCAATCGTGTCTCGTGGCGAAGCAAAACATTATATATTGGCTGGATTT
CTTGCGTCTATTAATAGGCACGCGAGGAATGGCACTAACACAGACAGAGGTGAAACATTCTTTGATAGTGTGTTCTGTTTATTCGTTGCAATTTATTCGCGATAACAATATTATACATAT
TTGGCGTGTCTCTTTGAGGTCCTAAAGTATATTAAAGATGTGTGTGAGGTATCTCGTAGAATACCTGACCAGACGACGTGTATGATGCGAGAGAACGCGATTGACGGAGGCCACAGGAGAT
GTAGAACTCGGCAGAGGTGTGTGGAAGACAGACGGGATCAACAACCGGCTGTATACACATCAACAACAGGTTTATCCCTTCGCATCAACCTAGAAGGATGACGAAGGAACAGGAGA
AAGCCGGGACCGAGCTGTTTAAATACACGGTATTTGTAATATACGAATATAAAATGTAATGATAGTATTTGTAACAACAAAATATATGTGAACAAATATATATGTTTGCTTAATTTACATAT
TGTAATATGTGGAATTGATACAGGTGTGTGTTATATAAAACATCAACAACGATGTAGCAAAACAGGAAAAAGAGAATCGGGGTGTGTGGTCTCTGATCGTATCGGTAATGAAGGCCAGCGC
CGGTTGAAATGATCTTTATAAAACAATATACATGATCGGATGTGTGAAATATAATCAAGTATGATAAAATCAACAAGATTTGTTGATAGCAATTAAAAATAATGAGAAGATAAGTAT
ATTGTTGAGGATATGGAATCAACAACCACCTTTAGTGTGGGTCGATATGTCOCAGGATGTCAGTGGCCAGCTGATGAGCTCGGCTGGGGGCTTAT

1-5 SNPs to MF039878 MF039866 KY427062 MF039866 (**Thailand**). **23-33 SNPs** to KM607387 KM607385 KM607386 (**China**)

TATTACCCCGCTCGTCGGGACGGACATATCTGCAGCATAGATTAAATGGGCCAACTAAAGGCCCATTA²TGAGAATAGCGGGGCTTTGCACATATTTCAAAGGCCCGCAGCTGGGAATGGTAATGCTCAGTCGCCGATAAAGAGTTGCTTGCCTCGAGGAAACCCGACAAATTTGGTCGTTTCAATACAGCAATGAAGTCTATTAAATGTAGTCTCTTCGCCGATAAATACAGAGCGACCGGAACGAGCAATGGATTGGCCGAGAATCACAATCAAGACATGTACTCATGGTGGCATTTGGGAAGACGATATCATCGGAATTATCCGGAATCGCACATATGTACCTTGGCTCGACCGAGGCAGCGGAAGAAGTCACTCTCGAAGTGTACTGCTAAGTCTATTGAAGCTGTGTTTAAATGGAAGCTTCAAAGGAATAACAGGAATTTCTCTGGTTCATCGTATCAATACGAGACGATGATGAGAAATCGCTCGAGTACTATAATACCATTCGGAGGATATGGATATCATAAATGATTTCTATTATTTCGAAGGGAAGGGGAAAGTTGAATGTGATATATCATCAGATTAATGTAGGCCAGGAGCTGATTTGGAGCAGACGATCGGAAGTTGATATGATGACCAACACCTGATGAATTAATGTGATCTGAAGTGTGTTTGTGTTCTGTTGCTGTAAGAATAAAGGAATAACAGCATGTCTGATGAATTAATAAATAATATTTTATCGATTAATGTATGTTTATAAACAATGTAACACGCTATGACAAACGGGAAATAAGAAATCGGGGGTTGATTGGTCTATCTGCTATCGCTTTAAGGCGCGAGCCGCTTGAAAAATATCATCGAATTAATTAAGCTTGTATATAATCATCAGAGATAGATGAATGACATCCATAAAAAACATAGACGAAGTATATGGCTGTAATAAAAAACAGCATATAATAAATAATGTGAACATATCTCTGATTGGTTTACAACGTTAGCCCCCAACTTTATGTGGTGAAGATCCCGGATGACGTACGACGACGGGGGATAT

R protein (286 aa): 0 aa to KM607676 KM607677 KM607679 (China) 1 aa to AB113660 (Vietnam) MF039879 (Thailand) KM607678 (China) ...

ATTATCCCCAGCGCTGGGAGCGGACATTTGCATCTATAAATAGACCTCCCCCCCCCATCAAGATCATCATCGTGCACGAAATGGCGGCATATGTGGTATGCTGGATGTTCCAC
ATAACAATCCCGCTTCCATCAACAGTGATCGGGATGAGTTTAAATATATGTTATATCAAGTGGAGAGGGGACAGGAGGCTACTCTGCATATGTCAGGAGTAAAGACGCG
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CATCGAAGGATATTTGGGCTATAGGCCAAATGGAGGAGGAAGGAAGAACATATGCAAAATTTTAAATGAAGACGAAGATGCGTTTATTCCGCAAGGAGGAAAAATCTTTGGATATA
TGAGATGTATAAATATGAGAAATAGTTATATTTGATATCCGAGTCAAGAGGAAATATTTAACTATGTTTATTAGAAGATTTAAATAGTAAATTTCAAAGCGGAAATAT
GAACCCGTTTGGAAATTTGAAATTTGTTGGAAGTCACTGTAATGGCTCACTCTCTCGAAGGAAGGAATCTCTCTGAAGATCGAATAACAGTGTGCTGCTGAACCGCTATGAC
AATCTGACGCTATGACAAAGGGGGAAGAAGCAAGAACTCGGGGGTTGATTGGGCTATCTCAAGGATTAAAGGCGCCAGGCGCGTCAAGATGACGGTTTGATCAGATGTCCTCGAGTTATGT
CGCCACGTAAAGCGCTGGGGCTTAT

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) 1 aa to several isolates

TATTACCTCCGAGCTCGGGACGAGTCTAATGTGATATGGAATGAAGGCCCATTCGGGCCGTTAAGATGGGTTTGGGGCTTTATGGGCTTTATCCAGAAGCAAAAACAGCGGGC
CAAGCTGCCCAATTTCAAATTTAGATAGATTTCGCCCGCAAGCAAACTAAAAGCTCTATATACCGGTAGTACATATTTGTCAGTAAACAAATGGCGAGGTTTCCGAGAAATCATCAAC
GAAGAGGGCGGGTTGGGCGACGGAAGTATGGAAGCAAGGCGGCAACCACTGACGACTACTCGTCGTTAGGTTCATATTTGGTTGCTGAAAAACCGCTGAAGGTATTTAGGATTGAGCCTA
TGATAAACAATCCACAGGATATTTATCTGGAAATGTTTATGCTTTGGGTCGCAAGGTGAAGCCTCGAAGAATACCTTATCTGGGCTATGATTAAGGTTATCGGAAATCAACCAAGC
GACTACATCTCTGGAAGCAGCAGGTTTATTCTATAAAACCTGAATACAGGATCTTGCTTTAACTCGGTATCGAGTGGGGAAGTTGAAGCGGGAGTCGCAACAGGGAACATCAGATGTGAAGTT
TCTTCTGAAGGAAGCAACCGTGTCTGAGGAAGAATGTAAACGAAGTGATTACTTGTTATTTGGCATTTATTCTAGTGTCTGAGTATAGTATTAATCAACGAAGCAAGATTAATCATATCATGT
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GCTATCTGATATCGGTTAAGGCCGAGAGCCCGCTGGAATGATCTTTTATGAACAAATATACATGATACAGGATTTGTGAAAATATATAACCAAGTATGATATAATACACAGAATATGTTGATA
GCAATTAATAAAAAAAGGAGAGAAAGAATATTTGTGAAGATAGATCAATCAGAACACCACCTTTAGTGGTGGGTCGATAGTCCCGAGTGTATGGCGGCACGTAAGCGCTGGGGGCTAT

U3 protein (39 aa): 0 aa to (Thailand)

TATTACCCACCAGCCAGCAGGACGATCTTTTAAATGGGGCAGAGAGATTGAACACGTCAGTATCTCGTTATGGGCGCATCGGCCCAATAAATGAAGAACGCTTCTCAAAATCGGGGTTTGACCGAAGCTCAGGTAGACGGTCAACAATATTCTGGCTTCGGGACGACACACAGAAATAAATTAATTAATCTGTATGACAGCTGGAGCGGACGAAATCTCTGTAACTCTATAAATAGCTTAAATCTGGCTTGGATAATTGCTCTCGCTCTTCTGCTCAAAAGGTTGTGTGTGAGGCGGAAGATCGCCATCGCGCATCATCAGACGAAAAGCTCAAGAGAGACGGGAGAACATGCTGCGGAAGCGTATACCGGTTATTTATAGACTCTAGCCGACAGTAAGGTTCTGTGATCTGTATTTGATTTGTAATTCAGGAAGAACTGTACATGTGTAATAATAAACATCTCGGTTGTTGTAATTTTACATTACCACTGATTAATAATGTACAGATAAAAAATTTGTATGAGGAACGAATACATAATAATAATAATAGGAGGCGTGACATGTGATATAAACAGGTGTTTAAAGCTATAAAAAATTTATGTAATGTATGATATCAATACGGTATTAAGTTGAAGTATGAGGTGAAGAAGAGATATAGAATATTAATAAACCAATATATTATTTATTAATACATCAACAACGTATACAAAAGGGGAAAAATGAAGAATCGGGGGTTGATGTTCTATCTCGCTTAAAGGCGCGAGCCCGCTGACAGATGATGATGACGCGAGCTTGATTGTTGTTATGCCACGAAGAAGAAATCTTTTGGGACACAGATAGAAGACAGCTGTCATTACCTTTTAAAAATATAATAAACCAATTGACATGATGACCTCCCGAAGATGACGATATAGGGGTGTCGCCAGGATTAATTAACATAGCTCTGCACAGAGATATGAGCACTGTGATGCGCAGCATCGGACGATCTGGTTTGTGATGAACCTATGATGACATGGGGGTGGGGCTTAT

Virome

1. **BBTV** six components (near identical to ALYU-44 in *Musa ornata* at the same location: 1 SNP in M and 1 nt del in S, both in non-coding sequence)

DNA-C = alyu44

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>C_alyu45
TATTACCCCCCTGCTCGGGACGGGACATCAGCTGCATCTCAACAAATGCACGTGACAAATGCAGTAGCTTGTAGCGAAAGATAACCATCCTATCATAAAAGTGAAAGGAATATTCGTTGC
TTAGGACTAAGCAACGTGGATAGATATTTGTTGAGAAAGCGCAAAATGGAGGCTATTTAAACCTGATGGTTTGTGATTTCGGAATCAGTCTATCGGAGAAAGAAATGGAGTTCTGGGAAT
CGTCTGCCATGCCAGCGATGTCAAGAGAGTGATCAAGGAAATATATTTGGGAGCATCGAAACAACTCTGTTTGTGAGAGTTGAAAGGCTGTGAAGAGGAAATTCGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCGAGTGAAGGAGATGAAGACTTCTATTATTCGCTATAGCGGAATTTTGAAGAAACCTTGTGTGGTATTGTGTTTAGTACTATAAATATCTATTGCATATA
GCTTAAACACAAATGGTCTTCTTTATCATGAATATATTGAAGACCTAGGTGGTGACTACTCGGTATATCAAGATTTCCTCTGTGATGAGGAACTTCCTTATTCGTCGACAGAAGAAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAAGAATCTCTTGGAGTGAATGTCAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA
TTATGATAAATAAAATAATGGAATGATGATTATGATTCTAGATATAAATACATAATGGTATACGTATAGCATATAAATACATATACCTACATACAAACACACTATAACAAACAGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAACGATTAAGGGCCGAGGCCGCTTAAATATGTGGTGGACGAATCCACAACACATAAAAGTGATCAGAACAATGGAATATATATGAGCT
GGCAACGTAGGGACCATGTCCCGAGTTAGTGCGCCACGTGAGCAGGGGGCTTAT
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DNA-M 1 SNP to alyu44

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>M_alyu45
TATTACCCCAGCGCTCAGGACGGGACATCAGTGCACACTAACAAATGCACGTGACTGATATATACACATACCGGTTTATTGAACCGTTATATATTGTTGAACGAAAGTCACGTGTG
ATAGCGAAAGGCACGTCAGCAAGACAAATGTATTGAATAAACATTTGACGTCCGGATGCTTCCTACGGAAGCCATGGTTGCTTCGTGGCGAAGCAAAACATTATATATTGGCTTGGATT
GCTGCTCTATAAATAGGCACGACGAGGAAATGGCATTAAACACAGAGCGGATGAAACTATTCTTTTGAATGGTTTCTGTTTATTGGTGCAATATTTATTGCGATAACAAATATTATACATATTG
TTGGCGTTGCTCTTTGAAGTCCCAAAGTATATTAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACCAGACGACGTGTATGGATGCAGAGAACGCGAGTTGACGGAGGCAACAGGAGAT
GTAGAATCGGCAGAGTAGTGTGGAAGACAGACGGGATCAACAACCGGCTGTATACACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGATGAGCAAGGAGACGAGGA
AACCGCGGACCGATGTTTAAATACACGGTATTGTAATATACGAAATATAAATGGATTAATGAATGATTGTGAAACAAATATATGTGAAACATATATATGTTTGTATAATTTACATATT
GTAATATGTGAATGTAACGAGTGTGTTATTATAAAACATACACACGCTATGACAAACAGGGAAAAATGAAGATCGGGGTTGATTGCTCTATCGGTATCGCTTAAGGGCCGACGGC
CCGTTGAAATGATTCTTTATAAAACAAATATACATGATACGGATTGTTGAAATATAATCAACGATGTATAAATACACAGAATGTTGTATAGCAATTAATAATGAGAAGATAAGTAT
ATTTGTGAAGGATATGGATGACACACCACTTTAGTGTGGGTATATGTCOCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT
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A - T in alyu44

DNA-N = alyu44

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>N_alyu45
TATTACCCCCTGCTCGGGACGGGACATGACGTGACATAGATTATAATGGGCCAACTAAAGGCCCATTTAATAGAATAGCGGGCTTTTGACATATTTCAAAGGCCAGCCTGGAAGT
GGATAATGTACAGTCCCGAATAAGAGGTTGCTTCGCTCGAAGCAACCGCAACAAATGTTGCGTATTCAATACGCAACTGAAGTCTATTAAATATGGATGCTCTCGCGCAATAAATCAGAG
CTAAGCGAAGCAGCAAGCGATGGATTGGGCAGAAATCACAAATCAAGACATGTACTCATGGGTGCGATTGGGAAGACGATATCATCGGATTCATCCGAGAATCGACAATATGTACCTTGGCT
CGACGACGACGCGGGAAGAAAGTCACCTCGCAAGGTACTGCTAAGATCTATTGAAGCTGTGTTAATGGAAGCTTCAAAGGAAATACAGGAAATGTTTCGTGGGTTTATATACGTATCAAT
ACGAGACGATGATGGAGAAATCGCTCAGTATCTATAACCATTCGGAGGATGTGATATCATATAATGATTCTTCTATTATTTCGAAGGGAAGGGGAAAGTTGAATGTATATATCATCAGA
TATGTAGCGCCAGGAGTCGATGGAGCAGACATGGAAGTTAGTATTAGTAACGCAACAACCTGTATGAATATGTGATCTGAAGTGTATGTTGTTGTTGCTTGAAGATAAAGGA
ATAACAGATGTGCTGTAAATGAATATTAATAAATATATTTTCATGTAATTGATAGTTGTATAAAACATACACACGCTATGACAAACAGGGAAAAATGAAAAATCGGGGGTTGATTGGTC
TATCGTATCGCTTAAGGGCCGAGGCCCTTGAAAAATAAATCGAATTATTAACGTTTGTATAAATACAGAGATAGATGATAAGCATCCAAAAACATAGACGAAGTATATGGCTGTA
TAATAAAACAAAGCATATAAATAAATATGTGAACATATCTCTGATTGGTTTACAACGTAGCCCCACCACTTTATGTTGGTGGAAATGTCCCGATGACGTAAAGCAGGGGGACTAT
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DNA-R = alyu44

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>R_alyu45
TATTACCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCCCCTCCATACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAAC
ATCAACAACTCCCCTTCACTACCACTGATGCGGGATCAGTTTAAATATATGCTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCTATGTGACGGGTACCTCGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAGAAGAAGCACGGGCATCTGTATGAAGGAAGACACAAGAATCGAAGGTCCTCT
GATTTGGTGCTTTAAATTTGTCATGTAATGATAATTTATTGATGTCATACAGGATATTCGCTGAACCCGACAAACCGGCTTTGGAGTATTTATGAGAGTGTCCGAATACCTCTGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCGATGAATAGCTGGAAACATCCTTCAGTTCTTGACATCGGAAGTTGAAATATTTATGGCGGAGCCATGT
CATCGAAGGATAAATTTGGGCTCTATGGCCCAAATGGAGGAGAAGCAAGCAACTTATGCAAAATATTTAATGAAGACGAAGAATGCGGTTTATTTCGCGGACGAGAAATTTGGATATA
TGATATTGTATAATATGAAGAAATAGTTATATTTGATATTCCAGATGCAAAAGAGGAATATTTAAACATATGGTTTATTAGAAGAATTTAAAAATGGAATTTATCAAAGCGGGAAATAT
GAACCCGTTTGAATAATGTAGAATATGTGGAAGTCATTGTAATGGCTAECTTCCTTCGGAAGGAAGGAATCTTCTCTGAAGATCGAATAAAGCTAGTTGCTTGTCTGAACCGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAACAAAGAATCGGGGGTTGATTGGGCTATCTCAACGATTAAAGGGCCGAGGCCGCTCAAGATGGACGGTTTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT
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DNA-S 1 nt indel to alyu44

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>S_alyu45
TATTACCCCAGCGCTCGGGACGGGACATGGGCTTTTAAATGGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTTTCAAAA
TCGGGCTTTGACCGAAGGTCAGGTAGACGGTCAACAATATCTGGCTTCGGGAGCAAGCAACGAACTAAAAGTCTATATATACCACTGTAGACATATTGTTTCAGATAACAAATGGCGAGGTTCCGAAGAAATCGATCAA
GAAAGGCGGGTTGGGCGACGGAAGTATGGAAGCAGCGCGCAACCACTACGACTACTCTGCTTAGGTTCAATATTGGTTCTGAAATACCGTGAAGGTTATTAGGATTAGGCTCAC
TGATAAAACATTACCCAGATATTTTATCTGGAAATGTTTATGCTTTTGGTGTGCAAGGTGAAGCTTGAAGAATACCTTCATTGGGCTATGATTAAGGTTTATGGGAATCAACACAGCC
GACTACATGCTGGAAGCAGCAGGTTTATTCATAAAACCTGAACATAGCCATCTGGTTAAACTGGTATGAGTGGGGAACCTTGAAGCCGGAGTCGCAACAGGGACATCAGATGTAGAATG
TCTTCTAAAGGAAGCAACCGTGTGGAGGAAGAATGTAACAGAGGTGGATTACTTGTATTGGCATTTTATTGTAGTGTGGAGTTAGTATTAACATCCAGAACAGCATATACATATCATGT
ATGATCTGTTTATGTAAACATAAACCTTTGTATGGATTAAATGACCAAAATACATACACACGCTATGAAATACAAACGCTATGACAAAAGGGGAAAAATGAAGAATCGGGGGTTGATTG
GCTCTATCGTATCGCTTAAGGGCCGAGGCCGCTTGAATGATTCTTTATAAACAAATATACATGATACGGATTGTTGAAAAATAAATCAACGATGTATAAATACACAGCAAGATTTGTGATA
GCAATTAATAAAAAAAAGAGAAGAAAGAAATATTGTGAAGGATAGCATCAGAACCACTTTAGTGTGGGTGAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT
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A - AA in_alyu44

DNA-U3 = alyu44

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>U3_alyu45
TATTACCCCAGCCCCAGGACGGGACATGGGCTTTTAAATGGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTTTCAAAA
TCGGGCTTTGACCGAAGGTCAGGTAGACGGTCAACAATATCTGGCTTCGGGAGCAAGCAACGAAATTAATAATTTAATTTCGTATGACACGTGAGCGACCGGAAATATCTCTGTAAC
CTATAAATAGCTTAAATCTGGCTTGATAAATGCTCTCGCTTCTCTCTCAAAGTGTGTTGCTGTGAGCGGAAGATCCGCATCGCGCATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
AACATGCTCGCAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTTCGTTGTACTTGATATTGATTTTGTAAATACGAAAGAAATCGTACATTGATATAATAAAAA
TCTGGAGTTGTTAATGTTTACATTAACAGTATTAATAATGTACAATAAAAAATATTGTATGAGGAACGAATACAATAATATTAATAATGAGGAGCGTAGCATGATAAACCGAGTGTGTTA
AGGTATAATTAATAAAATATGTAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTTGAAAGAGGAGATATAGAAATATTAATAAACCAATATATATTATTTATAATACATACAACA
CGGTATGACAAAAGGGGAAAAATGAAGAATCGGGGGTTGATTGGCTATTCGTTAAAGGCCGAGGCCGCTCAAGATGGATGAACGGCCAGATTGCTTGTAGGAAATATAATCAACGATGTATAAATACACAGCAATTTGTGATA
AGGAATCTTTTGGGACCCAGATAGACAGCTGTCAATTACCTTTTAAATAATATAATTAACCAATTTGACGATAGTACCCCTCCCAAAGATGACGTATAGGGGGTGTCCCGAGGTAATTTA
ACATAGCTCTGACAGAGATAGTGGACGTTGGATGCCAGATCGGACGATCGTGGTTTATGATGAACCTATGATGACGTAGGGGCTGGGGCTTAT
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ALYU-46 S22 La5 V7-Laos - *Musa* ABB Klue Tiparot - Laos

Virome (-)

"Virus-free": Reads representing BBTV genome components are at a cross-contamination level (see Supplementary Figure S3H). BBTA5: 96 reads; BBTA6: 21 reads; BBTA2: 44 reads + spot 30 reads; BBTA3: 17 reads

ALYU-47 - *Musa yunnanensis* - Laos

Virome

1. **BSTV** six components

DNA-C

28-36 SNPs to KM607098 KM607099 (China) . **31-36 SNPs** to KY427060 MF039864 MF039876 MF039870 (Thailand)

C protein (161 aa): 1 aa to KY427060 (Thailand) **2 aa** to KM607098 KM607099 (China) MF039864 (Thailand)

>C_alu47
TATTACCCCGAGCGCTCAGGACGGGACATCACGTGCATCTAACAAATGCACGTGACAAAGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCACAAAAGTGAGAGGAATATTCGTTGC
TTAGGGACTAAGCAACGTGAACAGATATTTGTTTCGAGAAGCGAAAATGGAGGCTATTTAAACCTGATGGTGTGTTGATTCCGAAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAAT
CGTCTGCCATGCCAGACGATGTCAAGAGAGTGATCAAGGAAATATATTTGGGAGCATCGAAATAAACTTCTGTTCTGTCAGAAAGTTGAAAGGCTGTGTAAGAGAGGATTCTGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCGAGTGAAGAGATGAAGACTTCTATTATTCGCTATAGCGAATATTTGAAGAAACCTTGTGTGGTATTGTGTTTGTAGTACTAATAAATCTATTGCATATA
GGTTAAACCAATGGTGTCTTTTATCATGAATATATTTGAAGACCTAGGTGGTGACTATTCGGTATATCAAGATCTGTTCTGTGATGAGGAACCTCCTTATTCGTGCAGAGAAGAAGAAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA
TATCATATAAATAAAATGAATGATGATTATGATTCTAGTATATACATAAATGGTATACGTATAGCATATAAATACATAAACCACATACAACACGCTATGACAAACGGGGGAAAAAT
GAAATATCGGGGGTTGATGGGCTATCTTAACGATTAAAGGCCGAAGGCCGCTTAAATATGTGGTGGACGAAGTCCACAACACATAAAAAGTGCTCAGAACAGGGAATATATGAGCT
GGCAACGTAGGGACCATGTCCCGAGTTAGTGCCGCCACGTAAAGCGCTGGGCTTAT

DNA-M

13-18 SNPs to KM607239 KM607240 (China) . **55-57 SNPs** to MF039865 KY427061 MF039871 MF039876 (Thailand)

M protein (117 aa): 2 aa MF039865 MF039877 (Thailand) **3 aa** to KC581796 (Thailand) **4 aa** to MF039871 KY427061 (Thailand)

>M_alu47
TATTACCCCGAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAAAGGTTTAAACGAACCGTTATATAATGTTATAACGAAAAGTCACGTGTG
ATAGAGACCTGCACGTGACATAGTCAAATGTATTGAATAAACATTTGACGTCGGGATGCTTCCGACGGGAAGCTTAGGTACTTCTGTGGCGAAGCAAAACATTATATATTTGGCCTGGGACT
CGTCCCTATAAATAGGCAAGCTAGGAAATGGCATTAAACACAGAGCGGGTGAACACTATTTCTTGAATGGTTCCTGTTTCATCGGTGCAATATTTATTTCGCATAAACAATATTTATATATTTG
TTGGTGTTCCTCTTTGAGGTCCCAAGTATATTAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACACAGAAGACGCTGATGGATGCAGAGAAGCGAGATGTACGGAGGCAACAGGAGAT
GTAGAGCTCGGCAGAGGTATTGTGGAAGACAGACGGGATCAACAACCGGCTGTATACCAATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGATGATCAAGGAAGACGAGGA
AACCGAGGACCAATGTTTTTAATACACGGTATTGTAATATACAAAATATAAATGGATGAATGATGTTGTTGAAACATAATATACGTGAAACATAATATGTTGTAATTTACATATT
ATAATATGTAATTTGATACGAGTGGTGTATTATAGAACATACAACACGCTATGACAAACAGGGAATAAGGAATCGGGGGTTGATTGGCTCTATCGTATCCGTTAAAGGCCGACGAGC
CCGTTGAATGATTCTTTAATAAAACAATATACATGATACGGATAGTTGAATATAAACAACGAAGCTATAAATACACAGAATGGTGTATATACTAATTAATAAATATGTGAAGATAAGTAT
ATTTGTGCGGGATGATGATCACAACCAACCACTTTAGTGGTGGGTATATGTCGCCGAGTTAGTGCCGACCGTAAGCGCTGGGCTTAT

DNA-N

26-29 SNPs to KX787074 EF470243 AF238879 KX787071 KX787072 (China)

N protein (154 aa): 1 aa to AF238879 KX787070 KX787071 KX787072 KX787074 (China) **3 aa** to AY494787 KX787073 (China)
KM607304 KM607313 KM607314 (Philippines) KM607316 KM607319 (Taiwan)

>N_alu47
TATTACCCCGGCTGCTCGGAGCGGACATGACGTGACATATATTATAATGGGCTTTTTAAAGCCCATATAAGTGAAGTGGGCCGGGTTTGAGACATATTTTCGAAAGCCCGACCCGGAAA
AGGATAAAGTCACGTGCCGAATAATAGTTGCTTCGCCCTCGAAGCAAACTAATAAAAGTTGCGTATTCAATACGCAACTAAGTCTATTAAATAGGGTTGTCTCTGCCGAATAAATCAGAG
CGTATCGGAAGCAGAAGCGATGGATTGGGCAGAAATCACAAATCAAGACATGTACCCATGGCTGTGATTGGGAAGACGATATCATCGGATTTCATCAGAAAATCGGCAATATGTACCTTCGCT
GACTCTCGGAGCTGGGAAGAGACTCCTCGCAAGGTACTTCTTAGATCTATTGAAGCTGTGTTTAATGGAGCTTCAAAGGGAATAATAGGAATGTTTCGTGGCTTCTTATACGTATCAAT
CCGAGACGATGATGGAGCAATGCGTCCAGTACTTATAGTACCATTGGAGGATATGGATATCATATGATTCTTATATTATTCGAAGGGAAGGGGAAGTTGAATGTGATATATCATCAGA
TTATGTTGCCGCAGAACTCGATTGGACGAGACATCGAAGTTAGTATTAGTAACACCAACCACTGTAATGAATCATGTGATCTGAAGTGTTATGTCTTTCTTCGTTAAGAATAAAGGA
ATAACAGATGTGCTGTAATGATTATTAATAAAACATATTTTTCATGCAATTGATGTTGTAATAAACAATACAACACGCTATGACAAACGGGGAAAAATGAAAATCAGGGGTTGATTGTT
CTATAGTATTCGCTTAAGGGCCGAGGCCCGTTGAAAATTAATAATCGAATTATATACGATTATATACGATCAGAGATAGATGAAGGATATATAAACATATATAACATATATGGCGGTA
TAATTAACAGAAACATATAATATAAAATATGTAACCTAATCTCTGATTGGTGCAGAGTGTAGGTCCACTAAGTTAAGTTAGTGAAATGTCCCGATGACGTGAAGCAGGGGGACTAT

DNA-R

4-6 SNPs to KM607677 KM607678 KM607676 KM607679 (China) . **9-14 SNPs** to AB113660 AB113659 (Viet Nam) . **14-18 SNPs** to
MF039879 MF039873 MF039867 KY427063 (Thailand) . **14 SNPs** to AF416475 (Viet Nam)

R protein (286 aa): 0 aa to KM607676 KM607677 KM607679 (China) **1 aa** to AB113660 (Vietnam) MF039879 (Thailand)
KM607678 (China)...

>R_alu47
TATTACCCCGAGCGCTCGGAGCGGACATTTGCATCTATAAATAGACCTCCCCCCCCCTCCAATACAAGATCATCATCGTCGACAGAAATGGCGCGATATGTGGTATGCTGGATGTTCAACC
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AGTTCTCTGAGCAGATGAGAGGCTTCTTCCTGCCGCACACCTTGAGAAACGAAGCGGAAGCACAAGACACGGGCATCTGTATGAAGGAAGACACAAGAATCGAAGTCCCTTC
GAGTTTGGTGCCCTTTAAATGTGCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGTGAACGCAACACCGGCCCTCGGAGTATTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAACGAAGGCGATGAATAGCTGGAAACATCCTTCAGTTTCATGGACATCGGAAGTTGAAAATATATTATGGCGGAGCCATGT
CATCGAAGGATAAATTTGGGTCTATGGCCCAATGGAGGAGAAGGAAGACAACTTATGCAAAATATTTAATGAAGACGAAGAATGCGTTTTATTTCOCAGGAGGAAAAATCATTTGGATATA
TGTAAGATTGTATAATTACGAGGAAATAGTTATATTTGATATTCACAGATGCAAGAGGAAATTTTAAACTATGGTTTATAGAAGAATTTAAAAATGGAATATATCAAGCGGGAAATAT
GAACCCGTTTTGAAAATTTAGAAATATGTGGAAGTCATTGTAATGGCTAACTTCTTCCGAGGAAGGAATCTTTTCAGAAGATCGAATAAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAACAAAGATTCCGGGGTTGATTGGGCTATCCTAACGATTAAAGGCCGAGGCCGCTCAAGATGGACGGCTTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAAGCGCTGGGCTTAT

DNA-S

5-8 SNPs to KM607535 KM607534 KM607536 KM607533 (China) . **15-19 SNPs** to AB113662 AB113661 (Viet Nam) . **19 SNPs** to
AF148945 (Viet Nam) . **20-32 SNPs** to MF039874 KY427064 MF039880 (Thailand)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) **1 aa** to several isolates

>S_alu47
TATTACCCCGAGCGCTCGGAGCGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAAACAGCGGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCCGCGAAGCAAACTAAAAGCTATATATACAGCTGTGAGACATATTGTTACAGATAACAAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGCGCGGGTTGGCGCAGGAAGTATGGAAGCAAGGCGGCAACCAAGTCACGACTACTCTGCTGTTAGGTTCATATTGGTTCCTGAAAATACCGCTCAAGGTATTAGGATTGAGCCTAC
TGATAAAACATTACCAAGATATTTTATCTGGAAATGTTTATGCTTTTGGTGTGCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAAAGAGTTCTGGGAAATCAACAGCC
GACTACATGCTGGAAGACACAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCACTGGGGAACTTGAAGCCGGAGTCGCAACAGGAGACATCAGATGTTGAATG
TCTTCTAAGGAAGACACCGTGTGTGAGGAAGAATGTAACAGAGGTGGATTACTTGTATTGGCATTTTGTAGTGTGGAGTTAGTATTAACTACCAAGACAGAGATTACATATCATGT
ATGATATGTTTATGTAACATATAACCTTTGTATGGAATAATGACCAATAACATACACACACATATGAAATACAAACACGCTATGACAAACAGGGAAAAATGAAGAATCGGGGGTTGATTG
GCTCATCGTAACGCTTAAGGGCCGAGGCCCGTTGAATGATTCTTTATAAAACAATATACATGATACGGATAGTTGAACATATAAACACAGATGTATAAATACACAGAATGTTGTAT
ACTAATTAATAAATAGAGAAGAAAAGAATTTTGTGAAGGATAAGCATCAGAACCACCACTTTAGTGGTGGGTGAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3

35-48 SNPs to KY427065 MF039869 MF039875 MF039881 (Thailand)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alu47

TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTGAACAGTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAAAA
TCTGGGTTTGACCAAGGCTCAAGGTAGACGGTCAACAATATTCCTGGCTTCGGGAGCAAGCAACAAGATTAATATTTAATTCGTATGACACGTGGACGGACCCGAAATACTCCTGTATCT
CTATAAATAGCCTAATCTCGGCATGGATAATTTGCTCTCGCTCTCTGTCAAAGCTTCTGTGTGAGGCGGAAGATCGCCATCGCGCATCATCAGACGAAAAGCTGCAAGAGAGACGGGA
ACCATGCTCGCAAGCGTATATCGGGTATTATAGACTTCTAGCCGACGTAGAAGTTTCTCTGACTTGTATTGTTATTTGTAATTCGAAGAAATTCGTACATTGATAATAAAG
ATCTGGGATTGTTAATGTTTACATTAACTAGTATTAAATAGTACAATAACAACATTGTATGAGGAACGAATACAGAATATTTAAATATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGAATAATTAATAATATGCAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTTAAACCCAAATATATTATTATATACATACAAC
ACGCTATGACAAAAGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCTTAACGATTAAGGGCCGACGGCCCTCAAGATGGATGAACGGTTAGATTGATTGCTTAGACACGAAGA
AAGGAATCTTTTGGGACCACAGATAAGACAGCTGTCACTACTTTTAAAAATAATATAAACAACATGACCATAGTGCCCTCCCAAAGATGACGTATAGGGGTGTCGCCGAGGTAAT
TAACATAGCTCTGACAAGAGATAGTGGACGTTGGATTCCACGATCGGACGATCGTGTTTATGATGAACCTTATGATGACGTAGGGGCTGGGGCTTAT

ALYU-48 - *Musa sp.* - Laos

Virome

1. **BTV** six components (2 dominant genetic variants for DNA-C and DNA-U3 but not other components)

Close to ALYU-47 in *M. yunnanensis* at a nearby location

DNA-C v1 - 1 SNP to alyu47

CP is identical in v2 and alyu47

>C_alyu48_v1
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCATCTAACAAATGCACGTGACAAAGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCACAAAAGTGAGAGGAATATTCGTTGC
TATAGGACTAAGCAACGTGAACAGATATTGTTTCGAGAAGCGAAAAATGGAGGCTATTTAAACCTGATGGTTTTGTGATTTCCGAAATCACTCATCGGAGCAGAAATGGAGTCTGGGAAT
CGTCTGCCATGCCAGACGATGTCAAGAGAGTGATCAAGGAAATATATTGGGAGCATCGAAATAAACCCTTCTGTTCTGTCAAGAGTTGAAAGGCTGTGTAAGAAAGGATTCTGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCGAGTGAAGGAGATGAAGACTTCTATTATTTCGCTATAGCGAATATTGGAAGAAACCTTGTGTGGTATTGTGTTTGTAGTACTAATAAATCTATTGCATATA
GGTTAAACACAATGGGTCTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTATTCCGTTATCAAGATCTGTTCTGTGATGAGGAACCTCCTTATTCTCGTCGACAGAAGAAGAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGTATATCCA
TTATCATATAAATAAATAATGGAATGATGATTATGTATTCTAGTATATATACATAATGGTATACGTATAGCATATAAATACATAAACCACATACAAACACGCTATGACAAACGGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGCCGAAGGCCCGCTTTAAATATGTGTTGGACGAAGTCCACAACACATAAAAAGTGCTCAGAACAAAGGAATATAATGAGCT
GGCAACGTAGGACCATGTCCCGAGTTAGTGCGCCACGTAAAGCCTGGGGCTTAT

C to T in alyu47

>C_alyu48_v2
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TATAGGACTAAGCAACGTGAACAGATATTGTTTCGAGAAGCGAAAAATGGAGGCTATTTAAACCTGATGGTTTTGTGATTTCCGAAATCACTCATCGGAGCAGAAATGGAGTCTGGGAAT
CGTCTGCCATGCCAGACGATGTCAAGAGAGTGATCAAGGAAATATATTGGGAGCATCGAAATAAACCCTCTGTTCTGTCAAGAGTTGAAAGGCTGTGTAAGAAGGATTCTGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCGAGTGAAGGAGATGAAGACTTCTATTATTTCGCTATAGCGAATATTGGAAGAAACCTTGTGTGGTATTGTGTTTGTAGTACTAATAAATCTATTGCATATA
GGTTAAACACAATGGGTCTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTATTCCGTTATCAAGATCTGTTCTGTGATGAGGAACCTCCTTATTCTCGTCGACAGAAGAAGAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGTATATCCA
TTATCATATAAATAAATAATGGAATGATGATTATGTATTCTAGTATATATACATAATGGTATACGTATAGCATATAAATACATAAACCACATACAAACACGCTATGACAAACGGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGCCGAAGGCCCGCTTTAAATATGTGTTGGACGAAGTCCACAACACATAAAAAGTGCTCAGAACAAAGGAATATAATGAGCT
GGCAACGTAGGACCATGTCCCGAGTTAGTGCGCCACGTAAAGCCTGGGGCTTAT

DNA-M 2 SNPs to alyu47

1 aa substitution in MP

>M_alyu48
TATTACCCCCAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACCGGTTTAACGAACCGTTATATAATGTTATAACGAAAAGTCACGTGTG
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GCTGCCCTTAATAAGGCAAGCTAGGAAATGGCATTAAACACAGAGCGGGTGAACCTATTCTTTGAATGGTTTTCTGTTCATCGGTGCAATATTTATTGCGATAACAATATTTATATATATTG
TTGGTGTGCTCTTTGAGGTCCCAAGTATATTAAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACCAGAAGACGCTGTATGGATGCAGAGTACCGAGTTGACGGAGGCAACAGGAGAT
GTAGAGCTCGGCAGAGGTATTGTGGAAGACAGACGGGATCAACAACCGGCTGTATACACACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGATCAAGGAAGACGAGGA
AACCGAGGACCAATGTTTTAATACACGGTATTGTAATATACAAAAATATAAATGGATAATGATATGTAATTGTGAACATAATATACGTGAACATAATATATGTTGATAATTTACATATT
ATAATATGTAATTTGATACAGAGTTGTGTTATTATAGAACATACAAACCGCTATGACAAACAGGGAATAAGAAATCGGGGTTGATTGGCTCTATCGTATCGCTTCAACCGGGCCAGCG
CCGTTGAATGATTCTTAATAAAACAAATATACATGATACGGATAGTTGAATATATAAACAACAGGATATAAATCAACAAGAAATGGTGTATACATAATTAATAATATGTAAGATAAGTAT
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DNA-N = alyu47

>N_alyu48
TATTACCCCCCGTGCTCGGACGGGACATGACGTGACATATATTATAATGGGCTTTTTAAAGCCCATATAAGTGAAGTGGGCCGGGTTTGAGACATATTTCGAAAGCCCGACCCGGAAA
AGGATAAAGTCACGTGCCGAATAATAGTTGCTTCGCCTCGAAGCAAACTAATAAAAAGTTGCGTATTCAATACGCAACTAAGTCTATTAAATAGGGTTGCTCTCGCGCAATAAATCAGAG
CGTATGCGAAGCAGCAAGCGATGGATTGGGCAGAAATCACAAATCAAGACATGTACCCATGGCTGTGATTGGAAGACGATATCATCGGATTCAACAGAAAATCGGCAATATGTACCTTGCGT
CGACTCTGGAGCTGGAAGAAAGACTCCTCGCAAGGTACTTCTTAGATCTATTGAAGCTGTGTTAATGGAAGCTTCAAGGGAATAATAGGAATGTTCTGGGCTTCTTATACGTATCAAT
CCGAGACGATGATGGAGCAATGCGTCCAGTACTTATAGTACCATTGAGGAGTATGGATATCATAATGATTCTTATATTATTCGAAGGGAAGGGGAAAGTGAATGTGATATATCATCAGA
TTATGTTGCGCCAGAAGTGATTGGAGCAGAGCATGGAAGTTAGTATTAGTAACAGCAACAACCTGTAATGAATCATGTGATCTGAAGTGTTATGTTGTTGTTGTCGTGAAGATAAAGGA
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TAATTAACAGAGAATATAATATAAAATATGTAAACTAATCTCTGATTGGTGCAGAGTGTAGGTCCTACTAACCCTTAAGTTAGTGAAATGTCCCGATGACGTAAAGCAGGGGGACTAT

DNA-R 2 SNPs to alyu47

1 aa substitution in Rep

>R_alyu48
TATTACCCCCAGCGCTCGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCCCCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAAC
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AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCAAGAGAAGACGCGGCATCTGTATGAAGGAAGACACAAGAAATCGAAGGTCCTCTC
GAGTTTGGTGCTCTTAAATTTGTCATGTAATGATAATTTATTGATGTCATACAGGATATGCGGTGAACCGCACAAACCGGCTCTCGAGTATTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAGCAAGGCGCATGAATAGCTGGAACACATCCTTCAGTTCTATGGACATCGGAAGTTGAAACTATATTGGCGGAGCCATGT
CATCGAAGGATAAATTTGGGCTCTATGGCCCAATGGAGGAGAGGAAGACACTTATGCAAAATATTTAATGAAGACGAAGAATGCGGTTTATTTCTCCAGGAGGAAAAATCATTTGGATATA
TGTAGATTGTAATAATACGAGGAAATAGTTATATTGTATTTCCAGATGCAAAAGAGCAATATTTAAACTATGGTTTATTAGAAGAAATTAATAATCGAATTTATCAAGCGCGGAAATAT
GAACCCGTTTTGAAATTTGAGAATATGTGGAAGTCATTGTAATGGCTAACCCTCCTCCGAGGAAGGAATCTTTTCAGAAGATCGAATAAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAAAGCAAGATTGCGGGGTTGATTGGGCTATCCTTAACGATTAAAGGCCGACGGCCGTCAAGATGGACGGCTTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAAGCGCTGGGGCTTAT

DNA-S = alyu47

>S_alyu48
TATTACCCCCAGCGCTCGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGCGCCGTTAAGATGGGTTTGGGCTTATGGGCTTATCCAGAAGACCAAAAAACGGCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCCCGAAGCAAACTAAAAGCCTATATATACCAGTGTAGACATATTGTTCCAGATAACAATGGCAGGTTTTCCGAAGAAATCGATCAA

GAAGCGCGGGTTGGGCGACGGAAGTATGGAAGCAAGGCGGCAACCAGTCACGACTACTCGTCGTTAGGTTCAATATTGGTTCCTGAAAAATACCGTCAAGGTATTTAGGATTGAGCCTAC
TGATAAAACATTACCAGCATATTTATCTGGAAAAATGTTTATGCTTTTGGTGTGCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAAAGAGTTTCATGGGAAATCAACCAGCC
GACTACATGTCCTGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATCGAGTGGGGAACCTGAAGCCGGAGTCGCAACAGGACCATCAGATGTTGAATG
TCTCTTAAGGAAGACAACCGTGTGAGGGAAGAATGTAACAGAGGTGGATTACTTGTTTGGCATTTTATTGTAGTCTGGAAGTTAGTATTAACACCAGAACAGAATTACATATCATGT
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GTCTATCGTAACGCTTAAGGGCCGAGGCCCGTTGAAATGATTCTTTATAAAACAAATATACATGATACGGATAGTTGAACATATAAACCAACGATGTATAAATACAACAGAATGTTGTAT
ACTAATTAATAATGAGAAGAAAAAATATTTGTGAAGGATAAGCATCAGAACCCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3 v1 - 1 SNP to alyu47 / v2 - 2 SNPs to alyu47

ORF1 is identical in all

>U3_alyu48_v1
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTGAACAGTTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTTGTTCAAAA
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CTATAAATAGCCTAAATCTGGCATGGATAAATTGCTCTCGCTCTTCGTCAAAGCTGTGTGTTGAGGCGGAAGATCGCCATCGGCATCATCAGACGAAAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGGAAGCGTATATCGGGTATTTATAGACTCTAGCGCAGCTAGAAGTTTCCTTGACTTGTATTGTTGTTTAAATTCGAGAAGAAATTCGTACATTTGATAAATAAATAAC
ATCTGGGATTCTTAATCTTTACATTAACTAGTATTAAATATCTCAATAAACAACATTGTATGAGGAACGAATACAAGAATATTAAATATCAGGACCGTACCGTGATAAACAGCTGTT
AAGGAATAATAAAAATATTATGCAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAACCAACCAATATATATTATTATAATACATACAAC
ACGCTATGACAAAAGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCCTAACGATTGAAGGCCCGAGGCCGTCAGATGGATGAACGGTTAGATTGTTGCTTAGACACGAAGA
AAGGAATCTTTTTAGGACCACAGATAAGACAGCTGTCACTACTTTTAAAAATAATATAATAACCAATGACCATAGTGCCCTCCCAAAGATGACGTATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGACAAGAGATAGTGGACGTGGATTCCACGATCGGACGATCGTGGTTTGATGAACCTTATGAGACGTAGGGGCTGGGGCTTAT

>U3_alyu48_v2
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CTATAAATAGCCTAAATCTGGCATGGATAAATTGCTCTCGCTCTTCGTCAAAGCTGTGTGTTGAGGCGGAAGATCGCCATCGGCATCATCAGACGAAAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGGAAGCGTATATCGGGTATTTATAGACTCTAGCGCAGCTAGAAGTTTCCTTGACTTGTATTGTTGTTTAAATTCGAGAAGAAATTCGTACATTTGATAAATAAATAAC
ATCTGGGATTCTTAATGTTTACATTAACTAGTATTAAATATGTCATAAACAACATTGTATGAGGAACGAATACAAGAATATTAAATATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGAATAATAAAAATATTATGCAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAACCAACCAATATATATTATTATAATACATACAAC
ACGCTATGACAAAAGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCCTAACGATTGAAGGCCCGAGGCCGTCAGATGGATGAACGGTTAGATTGTTGCTTAGACACGAAGA
AAGGAATCTTTTTAGGACCACAGATAAGACAGCTGTCACTACTTTTAAAAATAATATAATAACCAATGACCATAGTGCCCTCCCAAAGATGACGTATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGACAAGAGATAGTGGACGTGGATTCCACGATCGGACGATCGTGGTTTGATGAACCTTATGAGACGTAGGGGCTGGGGCTTAT

ALYU-49 - *Musa sp.* - Laos

Virome

1. **BRTV** six components (close to ALYU-47 and ALYU-48 at nearby locations)

DNA-C = alyu47 / 1 SNP to alyu48

>C_alyu49
TATTACCCCCAGCGCTCAGGACGGGACATCAGCTGCATCTCAACAAATGCAGTGACAAAGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCACAAAAGTGAGAGGAATATTCGTTGC
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CGCTCGCCATCGCAGACGATCTCAAGAGAGTGTCAAGGAAATATATTGGGAGCATCGAAATAAATCTTCTGTTCTGTCAAGAGTTGAAAGGCTGTGTAGAGAGGATTCTCGAGAGATGGAA
ATCAGTATGACAAAAGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCCTAACGATTGAAGGCCCGAGGCCGTCAGATGGATGAACGGTTAGATTGTTGCTTAGACACGAAGA
GGTAAACCAATGGTCTCTTTTATCATGAATATATTGAAGACCTAGTGGTGACTATTCCGTATATCAAGATCTCTCTCTGATCAGGAACCTTCCTTATTCTGCACAGAAAGAACG
ATGAAGAGTAAATATACAGGAATGTTATCATGGCATCGACAGAGAGAAGATCTCTGGAGTGAAATGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA
TTATCATATAAATAATGAAGATATGATTCTAGATATATACATATAGGTTATACGTATAGCATATAAATACATAAACCAACATACAGCATATGACAAACGGGGAAAAAT
GAAGATCGGGGGTTGATTGGGCTATCTTAACGATTGAAGGCCCGAAGGCCGCTTTAAATATGTGGTGGACGAAGTCCACAACACATAAAAGTGCTCAGAAACAGGGAATATAATGAGCT
GGCAACGTAGGACCATGTCCCGAGTTAGTGCGCCAGTGAAGCGTGGGGCTTAT

DNA-M 3 SNPs to alyu47 / 3 SNPs to alyu48

MP is identical to alyu47

>M_alyu49
TATTACCCCCAGCGCTCAGGACGGGACATCAGCTGCAACTAACAAATGCAGTGACTGATATATACTACATACACGGTTTAAACGAACCGTTATATAATGATATAACGAAAAGTCACGTGTG
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GCTGCCATATAAATAGGCAAGCTAGGAAATGGCATTAACAACAGAGCGGGTGAACACTATCTTTGAATGGTTTTCTGTTTCATCGGTGCAATATTTATTGGCATAACCAATATTATATATTG
TTGGTGTGCTCTTTAGGTTCCCAAGTATATTAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACCAGAGACGCTGTATGGATGCAGAGAACCGGTTGACGAGGCAACAGGAGAT
GTAGAGCTCGGACAGGATGTTGTGGAAGACAGACGGGATCAACACCGCTGCTTCCATCCACATCAACAGCTTATCCCTTCGCATCAACCTAGAAGGATGATCAAGGAAGACGAGGA
AACGACGAGCAATGTTTTAATACACGGTATTGTAATATACAAAAATATAAATGGATAATGATATGATTGTGAACATATAATACGTGAACATATAATATGTTTGATAATTTACATATT
ATAATATGTAATTTGATACAGAGTGTGATTATTAAGAACATACAAACCGCTATGACAAACAGGGAATAAGAAATCGGGGGTTGATTGGTCTATCGTATCGCTTAAGGGCCGAGGC
CCGTTGAATGATTCTTAATAAAACAAATATACATGATACGGATAGTTGAATATAAACAACAGATATAAATACAACAGATGGTGATATACTAATTAATAATATGTGAAGATAAGTAT
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DNA-N 4 SNPs to alyu47

NSP is identical to alyu47

>N_alyu49
TATTACCCCCCGTCTCGGGACGGGACATGACGTGACATATATTATAATGGGCTTTTTAAAGCCCATATAAGTGAAGTGGGCCGGGTTGAGACATATTTGAAAGCCCGACCCCGAAAA
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CGTATCGGAAGCAGAGCGATGGATTGGGCAGAAATCACAATTCAGACATGTACCCATGGCTGTGATTGGAAGACGATATCATCGGATTATCATGAAAAATCAGCAATATGTACCTTGGT
CGACTCTGGAGCTGGAGAAGAGACTCCTCGCAAGGTACTTCTTAGATCTATTGAAGCTGTGTTAATGGAAGCTTCAAAGGGAATATAGGAATGTTCTGCTGGCTCTTATACGTATCAAT
CCGAGACGATGATGGACCAATCGCTCCAGTACTTATAATACCATTTGAGGATATGGATATCATATGATTTCTATTATTTCGAAGGGAAGGGGAAGTTGAATGTGATATATCATCAGA
TTATGTTGCGCCAGAAGTCGATTGGAGCAGAGACATGGAAGTTAGTATTAGTAACAGCAACCACTGTAATGAATCATGTGATCTGAAGTGTATTGTTGTTGTTGCTTGAAGATAAAGGA
ATAACAGATGTGGCTGAATGATTATTATAAACAATATTTTCATGCAATTGATAGTTGTATAAAACATACAACACGCTATGACAAACGGGGAAAAATGAAAAATCAGGGGTTGATTGTT
CTATAGTATCGCTTAAGGGCCGAGGCCCGTTGAAAAATAATATCGAATTATATACGATTGATAAATCAGAGATAGATGTAAGGATATATATAAACATATAACGAAGTATATGGCGG
TATAATTAACAGAGCATATAATATAAAAAATATGTAACCTAATCTCTGATTGGTGCAGAGTGAAGTCCACTAATCTTAAGTTAGTGAAGATGTCCCGATGACGTGAAGCAGGGGGACT
AT

DNA-R 4 SNPs to alyu47 / 4 SNPs to alyu48

Rep is identical to alyu47

>R_alyu49
TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCTCTCCATTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAAC
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GAGTTCTCGAAGCAGATGAGAGGCTTCTCCCTGGCGCACCTTGAGAAGCAAGAGGGAAGCAGAAGAGCAGCGGCATCTGTATGAGAGAGACACAGAATCGAAGGCTCTTTC
GAGTTTGGTGCCTTTAAATGTCATGTAATGATAATTTTATGATGTCATACAGGATAGTGGCTGAAACGCACAACCGCCTCGGACTATTTATAGTGTCCCAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGCGGATGAATAGCTGGAACCACTCCTCAGTTCATGGACATCGGAAGTTGAAAAATATTATGCGGAGCCATGT

CATCGAAGGATAATTTGGGTCTATGGCCCAATGGAGGAGAAGGAAAGACAACCTTATGC AAAATATTTAATGAAGACGAAGAATGCGT TTTATCTCCAGGAGGAAAAATCATTGGATATA
TGATAGTTGTATAATTACGAGGAAATAGTTATATTTGATATTCCAGATGCAAAAGGAATATTTAACTATGGTTTATTAGAAGAATTTAAAAATGGAATTATTCAAAGCGGGAATAT
GAACCCGTTTGGAAATTTAGAAATATGTGGAAGTCATTGTAATGGCTAACTCCCTCCGAGGAAGGAATCTTTTCAGAAGATCGAATAAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCTACGCTATGACAAAAGGGGAAAGCAAGATTCGGGGGTGATTGGGCTATCCTAACGATTAAAGGCCGAGGCCGCTCAAGATGGACGGCTTGATCAGATGTCCGAGTTAGTG
CGCCACGTAAGCGCTGGGCTTAT

DNA-S = alyu47 = alyu48

>S_alyu49
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GAAGCGCGCGGTTGGGCGACGGAAGTATGGAAGCAAGSCGGAACCAAGCTACGACTACTCTGCTGTAGTTCAATATTGGTTCCTGAAAAATACCGTCAAGGTATTAGGATTGAGCCTAC
TGATAAAACATTACCCAGATATTTTATCTGGAATATGTTATGCTTTTGGTGTCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAAAGAGTTCATGGGAAATCAACCAGCC
GACTACATGTCTGGAAGCACCAGGTTTATTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAGTGGGGAACTTGAAGCCGGAGTCGCAACAGGGACATCAGATGTTGAATG
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GTCATATCGTAACGCTTAAGGGCCGAGGCCCGTTGAAATGATTCTTTATAAAACAAATATACATGATACGGAATAGTTGAACATATAAACCAACGATGTATAAATACAACAGATGTTGTAT
ACTAATTAATAATAGAGAAGAAAGAATATTTGTGAAGGATAAGCATCAGAACACCACCTTTAGTGGTGGGTGAGATGTCCCGAGTTAGTGCCACAGTAAGCGCTGGGCTTAT

DNA-U3 1 SNP to alyu48 and alyu47_v1

ORF1 is identical

>U3_alyu49
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTTGAACAGTTAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAAAA
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CTATAAATAGCCTAAATCTGGCATGGATAATGTCTCTCGCTCTTCTGTCAAAGCTGTTGTGTTGAGGCGGAAGATCGCCATCGCGGATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGCAAGCGGTATATCGGGTATTATAGACTTCTAGCGCAGCTAGAAGTTTCCTTGTACTTGATTGTTATTTGTAAATTACGAAGAAATTCGTACATTGATAATAATAAAAC
ATCTGGGATTGTTAATGTTTACATTAACTAGTATTATAATGTACAATAACAACACATTGTATGAGGAACGAATACAAGAATATTAATAATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGAATAATTAATAATAATTATGCAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAATAAACCAATTATATTATTTATAATACATACAAC
ACGCTATGACAAAAGGGGAAAAAAGAAAAATCGGGGGTTGATTGGTCTATCCTAACGATTAAAGGCCGAGGCCGCTCAAGATGGATGAACGGTTAGATTGATTGCTTAGACACGGAAGA
AAGGAATCTTTTTGGGACCACAGATAAGACAGCTGTCACTACTTTTAAAAATAATATAATAACCAAAATAGCCATAGTGCCCTCCCAAAGATACGATATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGACAAGAGATAGTGGACGTGGATTCCACGATCGGACGATCGTGGTTTGTATGACTTATGATGACGTAGGGCTGGGCTTAT

ALYU-50 - Musa AA sucrier Kouay nien mung - Laos

Virome

1. **BBTV** six components (close to ALYU-47, ALYU-48 and ALYU-49 at nearby locations)

DNA-C 2 SNPs to alyu47

Clink is identical

>C_alyu50
TATTACCCCCAGCGCTCAGGACGGGACATCAGTGCATCTAACAAATGCACGTGACAAAGCAGTAGCTTGTAGCGAAAGATAACCATCACTATCACAAAAGTGAGAGGAATATTCTGTGTC
TAGGAGCTAAGCAACGTGAACAGATATTTGTCGAGAAGCGAAATGGAGGCTATTTAAACCTGATGGTTTTGTGATTTCGGAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAAT
CGCTCGCCATGCCAGACGATGTCAAGAGAGTGATCAAGGAATATATTGGGAGCATCGAAATAAACTCTGTCTCTCAGAGATTGAAGGCTGTGAAGAGGATTCTCGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCACTGAAGCAGATGAAGACTTCTATTATTCCCTATAGCGAATATTTGAAGAAACCTTGTCTGCTATTGTGTTTACTACTAATAAATCTATTGCATATA
GGTTAAACCAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTATTCGGTATATCAAGATCTGTTCTGTGATGAGGAACCTCCCTTATTCGTGCAGAGAAGAAG
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TTATCATTAATAAAATAAGGAATGATGATTATGATTTTGTATATATACATATATGGTATACGTATAGCATATAAATACATAAAACCAACATACAACACGCTATGACAAACGGGGAAAT
GAAGAATCGGGGTTGATTGGGCTATCTTAACGATTAAAGGCCGAAGGCCCTTTAAATATGTGGTGACGAAGTCCACAACACATAAAAAGTGCTCAGAACCAAGGAATATAATGAGCT
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DNA-M 1 SNP to alyu47

MP is identical

>M_alyu50
TATTACCCCCAGCGCTCAGGACGGGACATCAGTGCACCTAACAAATGCACGTGACTGATATATACTACATAACGGTTTAAACGAACCGTTATATAATGTTATAACGAAAAGTCACGTGTG
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TGCTGCTTAAGATAGGCAAGCTAGGAAATGGCATTAAACACAGAGCGGGTGAACATTCTTTGATGGTTTTCTGTTCATCGGTGCAATATTTATTGCGATACAATATTTATATATTG
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ATTTGTGCGGGATGATGATCACAACCACCATTAGTGGTGGGCATATGTCCCGAGTTAGTGGGCCACGTAAAGCGCTGGGCTTAT

DNA-N = alyu47

>N_alyu50
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CGACTCTGGAGCTGGAAGAAAGACTCCTCGCAAGGTACTTCTAGATCTATTGAAGCTGTGTTAATGGAAGCTTCAAAGGGAATAATAGGAATGTTCTGTGGCTTCTTATACGTATCAAT
CCGAGACGATGATGGAGCAATGCGTCCAGTACTTATAGTACCATTGGAGGATATGGATATCATAATGATTCTTATTATTTCGAAGGGAAGGGGAAGTTGAATGCTGATATATCATCAGA
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CTATAGATTCCGCTTAAGGGCCGAGGCCGTTGAAAATTAATAATCGAATTATATACGATTGATAAATCAGAGATAGATGAAGGATATATAAACATAAACCAAGATGATATGGCGGTA
TAATTAACAGAGCATATTAATATAAAAATGTAAACTAATCTCTGATTGGTGCAGAGTGTAGGTCCACTAACTTAAAGTTAGTGAAATGTCCCGATGACGTAAAGCAGGGGACTAT

DNA-R 2 SNPs to alyu47

Rep is identical

>R_alyu50
TATTACCCCCAGCGCTCGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCCCCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGCGATATGTGGTATGCTGGATGTTCAACC
ATCAACAATCCCGCTTCACTACCAGTGATGCGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCTATGTGACAGGATACGTTGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAAGAAGAGCACGGGCATCTGTATGAAGGAGACACAAGAAATCGAAGGTCCCTTCT
GAGTTTGGTGCTTTAAATTTGCTATGTAATGATAATTTTATTGATGTCATACAGGATATTCGCTGAACACGCAACACAGCCCTCTCGAGTATTTATAGTGTCTGCAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAACGAAGGCGATGAATAGCTGGAATACCTTCACTGTTTATGCAATCGGAAGTTGAAATATTTATGGCGGACCATGT
CATCGAAGGATATTTCCGGTCTATGGCCAAATGGAGGAGAAGAAAGCAACTATGTCAAAATATTTAATGAAGACGAAGAAATGCGCTTTATTCTCCAGGAGAAATCATTTGGATAT
TGTAGATTGTATAATTACGAGGAAATAGTTATATTTGATATTCACAGATGCAAAAGAGGAATATTTAACTATGTTTATTAGAAGAATTTAAAAATGGAATATTCAAAGCGGGAATAT

GAACCCGTTTTGAAAAATTGTAGAATATGTGGAAGTCATTGTAATGGCTAACTCTCTCCGAAGGAAGGAATCTTTTCAGAAGATCGAATAAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAAGCAAAGATTCCGGGGTGTATTGGGCTATCCTTAACGATTAAGGGCCGACGCGCCGTCAAGATGGACGGCTTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAAGCGTGGGCTTAT

DNA-S = alyu47 = alyu48 = alyu49

>S_alyu50
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTTGGGCTTATGGGCTTATCCAGAAGACCAAAAAACAGGCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCCGCAAGCAAACATAAAAGCCTATATATACCAAGTGTAGACATATTGTTCCAGATAACAAATGGCAGGTTTCCGAAGAAATCGATCAA
GAAGCGCGGGTTGGGCGACGGAAGTATGGAAGCAAGGCGGCAACCAAGTCACTACTCGTCTAGGTTCAATATTGGTTCTGAAAAATACCGTCAAGGTATTTAGGATTGAGCCTAC
TGATAAAACATTACCCAGATATTTTATCTGGAAAAATGTTTATGCTTTTGGTGTCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAAGAGTTTCATGGGAAATCAACCAGCC
GACTACATGTCTGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAGTGGGAACTTGAAGCCGGAGTGCACACAGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACAACCGTGTGAGGAAGAATGTAACAGAGGTGGATTACTTGTATTGGCATTTTATTGTAGTGTGGAGTTAGTATTAACCTACCAGAACAGAATTACATATCATGT
ATGATAATGTTTATGTAACATAAACCTTTGTATGGAATAATGACCAAATAACATACAACACACTATGAAATACAAACACGCTATGACAAACAGGGAAAAATGAAGAATCGGGGGTTGATTG
GCTCTATCGTAACGCTTAAGGGCCGACGCGCCGTGAAATGATTCTTTATAAAACAAATATACATGATACGGATAGTTGAACATATAAACCAACGATGTATAATACAACAGAAATGTTGTAT
ACTAATTAATAAATGAGAAGAAAAAATATTGTGAGGATAAGCATCAGAACCCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGCTTAT

DNA-U3 1 SNP to alyu47

ORF1 is identical

>U3_alyu50
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGGCCGAGAGAGTTGAACAGTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATAAGAGAACGTGTTCAA
TCTGGGTTTGACCGAAGGTCAAGGTAGACGGTCAACAATATTCTGGCTTGCAGGACCAAGCAACAAAGAAATTAATATTAAATTCGTATGACACGTGGACCGGACCGAAATCTCCTGTATCT
ATGATAATGCCCTAAATCTGGCATGGATAATTGCTCTCGCTCTTCTGTCAAGAGCTGTTGTTGTAGGCGGAAGATCGCCATCGGCGATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGCAAGCGTATATCGGGTATTATAGACTTCTAGCGCAGCTAGAAGTTTCCCTTGCTACTTGTATTGTTATTGTTAAATACGAGAATTCGTACATTTGATAATAATAAAC
ATCTCGGGATTGTTAATGTTTACATTAACTAGTATTAATAATGTACAATAACAACATTGTATGAGGAACCAATACAAGAATATTAATAATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGAATAATTAATAATAATTATGCAATGTTATGATAATACGGGTATAAGTTGAAGTATGAGGTGAAAGGAGGATATTAGAATATTAATAACCAATTATATTATTATTAATACATACAAC
ACGCTATGACAAAAGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCCTAACGATTAAAGGCCGACGCGCCGTCAAGATGGATGAACGGTTAGATTGATTGCTTACACACGAAGA
AAGGAATCTTTTGGGACACAGATAAGACAGCTGTCACTACTTTTAAAAAATAATATAATAACCAATGACCATATTGCCCTCCCAAAGATGACGTATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGACAAGAGATAGTGGACGTGGATTCCACGATCGGACGATCGTGGTTTGTATGAACCTTATGATGACGTAGGGGTGGGGCTTAT

ALYU-51 - Musa ABB Pisang Awak ? - Laos

Virome

1. **BBTV** six components (close to ALYU-47, ALYU-48, ALYU-49 and ALYU-50 at nearby locations)

DNA-C 1 SNP to alyu47

Clink is identical

>C_alyu51
TATTACCCCCAGCGCTCAGGACGGGACATCAGTGCATCTAACAAATGCAGTGACAAAGCAGTAGCTTGTAGCGAAAGATAACCATCCTATCACAAAAGTGAGAGGAATATTCTGTGTC
TAGGAGCTAAGCAACGTGAACAGATATTGTTCTGAGAAGCGAAAAATGGAGGCTATTATAACCTGATGGTTTTGTGATTCCGAAATCACTCATCGGAGCAGAAAAATGGAGTTCTGGGAAT
CGTCTGCCATGCCAGCATGTCAAGAGAGTGATCAAGGAATATATTGGGAGATCGAAATAAATCTCTGTTCTGTCAGAAGTTGAAAGGCTGTGAAGAGGATCTCGAGAGATGGAA
ATAAGATGATGCTCTAGACCGAGTGAAGGAGATGAAGACTTCTATTATTTCGCTATAGCGAATATTGGAAGAAACCTGTGTGGTATTGTGTTTGTAGTACTAATAAATCTATTGCATATA
GGTTAAACACAAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGGTGGTGACTATTCGATATATCAAGATCTGTTCTGTGATGAGGAACCTCCCTATTCTCGCGACAGAAGAAG
ATGAAGAATAATATACAGGAATGTTATCATGCCATCGACAGAAGAGAAGATCTCTTGGAGTGAATCTCAAAAGATAGTTATATCAGATTATGATGTGAACATTACTGTAATGAATATCCA
TTATCATAAATAAATAATGGAATGATGATTATGATTCTAGTATATATACATAATGGTATACGTATAGCATAAAAATACATAAACCAACATACAACACGCTATGACAAACGGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATTCTAACGATTAAAGGCCGAAGGCCGTTTAAATATGTGGTGACGAAGTCCACAACACATAAAAAAGTCTAAGAACCAAGGAATATAATGAGCT
GGCAACGTAGGACCATGTCCCGAGTTAGTGCGCCACGTGAAGCGCTGGGGCTTAT

DNA-M 1 SNP to alyu47

MP is identical

>M_alyu51
TATTACCCCCAGCGCTCAGGACGGGACATCAGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACCGTTTTAACGAACCGTTATATAATGTTATAACGAAAAGTCACGTGTG
ATAGAGACCTGCAGCTGACATAGTCAAAATGTAATTGAATAAACATTTGACGTCGGATGTTCCGACGGAAGCTTAGGTTACTTCTGTGGCGAAGCAAAACATTTATATATTGGCCTGGACT
GCTGCTCTATAAATAGGCAAGCTAGGAAATGGCATTAAACAACAGAGCGGGTGAACCTATTCTTTGAATGGTTTCTGTTCATCGGTGCAATATTTATTCGATACAAATATTTATATATTG
TTGGTGTGCTCTTTAGAGTCCCAAGTATATTAAGGATGTTGTGAGGTATCTCGTAGAATACCTGACAGAAGACGTGTATGGATGCAGAGAACGAGGTGACGAGGACACAGGAGAT
GTAGAGCTCGGCAGAGGATTTGTGGAAGACAGACGGGATCAACAACCGGCTGTCATACCACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGATGATCAAGGAAGACGAGGA
AACCGACGACAAGTTGTTTATAACACGGTATTGTAATATACAAAATATAAATGGATAATGATATGTAATTGTTGAACACATAATATACGTGAACACATAATATATGTTGATAATTTACATATT
ATAATATGTAATTTGTATACGAGTGTGTTATTTATAGAACATACAACACGCTATGACAAACAGGGAATAAGAAATCGGGGGTTGATTGGTCTATCGTATCGCTTAAGGGCCGACGGC
CCGTTGAATGATTTCTAATAAAACAAATATACATGATACGGATAGTTGAATATATAAACCAACGAAGTATAAATACAAACAGAAATGGTGTATCTAATTAATAAATATGTGAAGATAAGTAT
ATTTGTGCGGGATGATGATCCACAACCACCACTTTAGTGGTGGGTCATATGTCGCGAGTTAGTGGCCACGTAAGCGCTGGGGCTTAT

DNA-N 2 SNP to alyu47

NSP is identical

>N_alyu51
TATTACCCCCGCTGCTCGGACGGGACATGACGTGACATATATTATAATGGGCTTTTTAAAGCCCATATAAGTGAAGTGGCGCGGTTTGAGACATATTTCGAAAGCCCGACCCGGAAA
AGGATAAAGTCACGTGCCGAATAATAGTTGCTTCGCCCTCGAAGCAAACTAATAAAAGTTGCGTATTCAATACGCAACTAAGTCTATTAAATAGGGTTGTCTCTGCCGAATAAATCAGAG
CGTATGCGAAGCAGAAGCGATGGATTGGGCAGAAATCACAATTCAAGACATGTACCCATGGCTGTGATTGGAAGACGATATCATCGGATTATCAGAAAAATCGGCAATATGTACCTTGGCT
CGACTCTGGAGCTGGAAGAAAGACTCCTCGCAAGGTACTTCTTAGATCTATTGAAGCTGTGTTTAATGGAAGCTTCAAAGGGAATAATAGGAATGTTCTGTGGCTTCTTATACGTATCAAT
CGGACGATGATGGAGCAATGCGTCCAGTACTTATAGTACCATTGGAGGATATGGATATCATAATGATTCTATATTATTTCGAAGGGAAGGGGAAAGTTGAATGTGATATATCATCAGA
TTATGTTGCGCCAGAAGTCGATTGGACGAGACATCGAAGTTAGTATTAGTAAACAGCAACCACTGTAATGAATCATGTGATCTGAAGTGTATTGTTCTTCTTCTGTTAAGAAATAAGGA
ATAACAGATGTGCTGTAATGATTATTAATAAAACATATTTTCATGTAATTGATAGTTGTATAAACATACAACACGCTATGACAAACGGGGAAAAATGAAAAATCAGGGGTTGATTGTT
CTATAGTATCGCTTAAGGGCCGACGCGCCGTTGAAAAATATAATCGAATTATATACGATTGATAATAATCAGAGATAGATGATAAGGATATATAAACATAAACGAAGTATATGGCGGTA
TAATTAACAGAAAGCATATAATATAAAAAATGTAACATACTCTGATTGGTGCAGAGTGTAGGTCCTACTACCTTAAAGTTAGTGAAATGTCCCGATGACGTAAAGCAGGGGGACTAT

DNA-R 1 SNP to alyu47

Rep is identical

>R_alyu51
TATTACCCCCAGCGCTCGGACGGGACATTTGCATCTATAAATAGACCTCCCCCCCCCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGCGATATGTGGTATGCTGGATGTTCAACC
ATCAAGCAATCCCGCTTCACTACCAAGTGTGCGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCTATGTGAGGGATACGTGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCGCACACCTTGAGAAACCAAGGGGAAGCAGAAGAGACACGGGCATCTGTATGAAGGAAGACACAAGAAATCGAAGGTCCCTTC
GAGTTTGGGCTTTAAATTTGATCTGATACAGGATATTCGCTGAACACGCAACACCGCCCTCTGGAGTATTATATGAGTGTCTGCAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAACGAAAGGCGATGAATAGCTGGAAATACCTTCAGTTTCATGGACATCGGAAGTTGAAATATTTATGGCGGACCATGT
CATCGAAGGATAATTTGGGCTCTATGGCCAAATGGAGGAGAAGGAAAGCAACTATGTCAAAATATTAAATGAAGACGAAGAATGCGCTTTATTCTCCAGGAGAAATCTTGGATATA
TGTAAGTTGTATAATTACGAGGAAATAGTTATATTGTATATCCAGATGCAAGAGGAATATTTAAACTATGGTTTATTAGAAGAATTTAAAAATGGAATATTCAAAGCGGGAATAT

GAACCCGTTTTGAAATTGTAGAATATGTGGAAGTCATTGTAATGGCTAACTCTCTCCGAAGGAAGGAATCTTTTCAGAAGATCGAATAAAGCTAGTTGCTTGTCTGAACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAAGCAAAGATTCCGGGGTTGATTGGGCTATCCTAACGATTAAGGGCCGACGGCCGCTCAAGATGGACGGCTTGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAAGCGCTGGGCTTAT

DNA-S = alyu47

>S_alyu51
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAAGATGGGTTTTGGGCTTATGGGCTTTATCCAGAAGACCAAAAAACAGGCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCCGCAAGCAAACATAAAGCCTATATATACCAAGTGTAGACATATTGTTTCAGATAACAAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGCGCGGGTTGGGCGACGGAAGTATGGAAGCAAGGCGGCAACCACTCAGCACTACTCGTCGTTAGGTTCAATATTGGTTCCTGAAAAATACCGTCAAGGTATTTAGGATTGAGCCTAC
TGATAAAACATTACCCAGATATTTTATCTGGAATAATGTTATGCTTTTGGTGTGCAAGGTGAAGCCGGAAGAATACTTCACTGGGCTATGATTAAAGAGTTTCATGGGAAATCAACCAGCC
GACTACATGTCTGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAGTGGGAACTTGAAGCCGGAGTGCACACGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACAACCGTGTGAGGAAGAATGTAACAGAGGTGGATTACTTGTATTGGCATTATTTGTAGTGTGGAGTTAGTATTAACACCAGAACAGAATTACATATCATGT
ATGATAATGTTTATGAAACATAAACCTTTGTATGGAATAATGACCAAATAACATACACACACTATGAAATACAAACACGCTATGACAAACAGGGAAAAATGAAGAATCGGGGGTTGATTG
GTCTATCGTAACGCTTAAGGGCCGACGGCCCTTGAATGATTCTTTATAAAACAAATATACATGATACGGATAGTTGAACATATAAACCAACGATGTATAATACACAGAAATGTTGTAT
ACTAATTAATAATGAGAAGAAAAAATATTGTGAGGATAAGCATCAGAACCCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3 1 SNP to alyu47

ORF1 is identical

>U3_alyu51
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCGAGAGAGTTGAACAGTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATAAGAGAACGTGTTCAAAA
TCTGGGTTTGACCGAAGGTCAAGGTAGACGGTCAACAATATCTGGCTTCGGAGCAAGCAACAAGAAATTAATATTTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTATCT
ATGATAATGCTTAAATCTGGCATGGATAATTGCTCTCGCTCTTCGTCAAAGCTGTGTGTTGAGGCGGAAGATCGCCATCGGCGATCATCAGACGAAAAGCTGCAAGAGAGACGGGAGA
ACCATGCTCGCAAGCGTATATCGGGTATTATAGACTTCTAGCGCAGCTAGAATTTTCCTTGTACTTGTATTGTTATTGTTAAATACGAAGAAATTCGTACATTGATAATAATAAAC
ATCTGGGATTGTTAATGTTTACATTAACTAGTATTAATAATGTACAATAACAACATTGTATGAGGAACCAATACAAGAATATTAATAATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGAATAATTAATAATAATTATGCAATGTTATGATAAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAATAAATTAATAAATTAATAAATTAATAAATTAATAA
ACGCTATGACAAAAGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCCTAACGATTAAAGGGCCGACGGCCCGTCAAGATGGATGAACGGTTAGATTGATTGCTTACACACGAAGA
AAGAAATCTTTTGGGACCAAGATAGACAGCTGTCACTACTTTTAAAAATAATATATAAACCAAAATGACCATAGTGCCCTCCCAAAGATGACGTATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGATAAGAGATAGTGGACGTGGATTCCACGATCGGACGATCGTGGTTTGTATGAACCTTATGATGACGTAGGGGCTGGGGCTTAT

ALYU-52 - *Musa acuminata* wild - China

Virome

BBTV free - all six components at a cross-contamination level (Supplementary Figure S3H); Babu2 200 reads
Badnavirus BSVNV partial sequence (mapping revealed a new isolate of BSVNV with ca. 90% identity to ALYU-33)

ALYU-53 - *Musa yunnanensis* - China

Virome

1. **BBTV** six components (two variants of DNA-C and DNA-M: v1 > v2)

DNA-C

12-13 SNPs to KM607099 KM607098 (China). **23-27 SNPs** to KY427060 MF039870 MF039864 MF039876 (Thailand)

C protein (161 aa): v1 **2 aa** to KM607098 KM607099 (China) **3 aa** to KY427060 (Thailand) **4 aa** to MF039864 (Thailand). v2: 1
aa to v1

>C_alyu53_v1
TATTACCCCCCTGCTCGGGACGGGACATCAGTGCTTCTAACAAATGCACGTGACAAAGCAGTAGCTTGTAGCGAAAGATAACCATCACTTTACAAAAGTGAAAGGAATATTCTGTTGC
TAGGGAACCTAAGCAACGAGGACAGATATTTGTCGAGAAGCGACAATGGAGGCTATTTAAACCTGATGGTTTTGTGATTCCGAAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAAT
CGTCTGCTATGCCAGACGATGTCAAGAGAGTGATCAAGGAATATATTGGGAGCATCGAAATAAATCTCTGTTTTGTCAGAAGTTGAAAGGCTGTGTAAGAGGATTCTGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCACTGAAGGAGATGAAGACTTCTATTATTCCGCTATAGCGAATATTTGAAGAAACCTTGTGTGGTATTGTGTTTACTACTAATAAATCTATTGTATATA
GGTTAAACCAATGGTGTTCTTTTATCATGAATATATTGAAGACCTAGTGGTGACTACCGGATATATCAAGATCTGTTTTGTGATGAGGAACCTCCTTCGCTCTCGACAGAAGAAGAAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTTTGGAGTGAAGTGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA
TTATCATATAATAAATAAATGAATGATGATTATGATTCTAGTATAAATACATAATGGTATACGTATAGCATATAAATACATAAACCAACATACACACACTATGACAAACAGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGCCCAAGGCCCTTTAAATATGTGGTGGACGAAGTCCACAACACAAAAAAGTGATCAGAACAAATGGAATATAATGAGCTG
GCAATGTAGGGACCATGTCCCGAGTTAGTGCGCCACGTGAGCAGGGGGCTTAT

A/T (159758/57046) T/A (80706/48469)

>C_alyu53_v2
TATTACCCCCTGCTCGGGACGGGACATCAGTGCTTCTAACAAATGCACGTGACAAAGCAGTAGCTTGTAGCGAAAGATAACCATCACTTTACAAAAGTGAAAGGAATATTCTGTTGC
TTAGGGAACCTAAGCAACGAGGACAGATATTTGTCGAGAAGCGACAATGGAGGCTATTTAAACCTGATGGTTTTGTGATTCCGAAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAAT
CGTCTGCTATGCCAGACGATGTCAAGAGAGTGATCAAGGAATATATTGGGAGCATCGAAATAAATCTCTGTTTTGTCAGAAGTTGAAAGGCTGTGTAAGAGGATTCTGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCACTGAAGGAGATGAAGACTTCTATTATTTCGCTATAGCGAATATTTGAAGAAACCTTGTGTGGTATTGTGTTTACTACTAATAAATCTATTGTATATA
GGTTAAACCAATGGTGTTCTTTTATCATGAATATATTGAAGACCTAGTGGTGACTACCGGATATATCAAGATCTGTTTTGTGATGAGGAACCTCCTTCGCTCTCGACAGAAGAAGAAG
ATGAAGAAGTAATATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAAGTGTCAAAAGATAGTTATATCAGATTATGATGTAACATTACTGTAATGAATATCCA
TTATCATATAATAAATAAATGAATGATGATTATGATTCTAGTATAAATACATAATGGTATACGTATAGCATATAAATACATAAACCAACATACACACACTATGACAAACAGGGAAAAAT
GAAGAATCGGGGGTTGATTGGGCTATCTTAACGATTAAAGGCCCAAGGCCCTTTAAATATGTGGTGGACGAAGTCCACAACACAAAAAAGTGATCAGAACAAATGGAATATAATGAGCTG
GCAATGTAGGGACCATGTCCCGAGTTAGTGCGCCACGTGAGCAGGGGGCTTAT

DNA-M

16/21 SNPs to KM607239, KM607240 (China). **53-54 SNPs** to KY427061 MF039865 MF039871 MF039876 (Thailand)

M protein (117 aa): **3 aa** to KC581796 (Thailand) **4 aa** to KM607239 (China) MF039871 MF039865 MF039877 KY427061 (Thailand)
v2: 1 aa to v1

>M_alyu53_v1
TATTACCCCCAGCGCTCAGGACGGGACATCAGTGCAACTAACAAATGCACGTGACTGATATATACTACATACAACGGTTTAAAGCAACCGTTATATAATGTTATAACGAAAAGTCACGTGAG
ATAGAGACCTGCACGTGACATAGTCAAAATGTTATGAATAAACTTTGACGCTCCGAGTGCTTCCGACGGGAAGCTTAGGTTACTTCGTGGCGAAGCAAAACATTATATATTGGCCTGGACT
GCTGCTCTATAAATAGGCAAGCTAGGTAATGGCATTAAACAACAGAGCGGGTGAACACTATCTTTGAATGGTTCTGTTTCATCGGTTCAATATTTATTCGCGATAACAATATTATATATTG
TTGGCGTGTCTCTTGAAGTCCCCAAGTATATAAGGATGTTGTGAGGATATTCGTAAGAATACCTGACCAAGACGCTGATGGATGCAGAGAACGCGAGTTGACGAGGCAACAGGAGAT
GTAGAGCTCGGCACAGGAGTAGTGTGGAGACAGACGGGATCAACAACCGGCTGTATACCATATGCACACAGGTTATCCCTTCGCATCAACCTAGAGGGAAGATCAAGGAAGACGAGGA
AACGCAGCACCATTGTTTAAATACACCGTATTGTAATATACGAATATAAATGCGATAATGATATGTTGTTGAAACATAATATACCTGAAACATAATATATCTTTGATAATTTACATATT
ATAATATGTAATTTGATACAGGTGTTGATTTTATAGAACATACACACGCTATGACAAACAGGGAAAAATGAAGAATCGGGGGTTGATTGGTCTATCGTATCGCTTAAGGGCCGACGGC
CCGTTGAATGATTTCTTATAAACAATAATACATGATACGGGATAGTTGAATATAAACAACAGAGTATAAATACACAGAATGTTGTATACTAATTAATAATGAGAAGATAAGTAT
ATTTGTGAGGGATGATGATCAACACCACCTTTAGTGGTGGGTCATATGTCCTCGAGTTAGTGGGCCACGTAAGCGCTGGGGCTTAT

C/G (62472/28164)

>M_alyu53_v2

TATTACCCCGAGCGCTCAGGACGGGACATCACGTGCAACTAACAAATGCACGTGACTGATATATACTACATAACGGTTTAACGAACCGTTATATAATGTTATAACGAAAAGTCACGTGAG
ATAGAGACCTGCACGTGACATAGTCAAATGTATTGAATAAACATTTGACGTCCGGATGCTTCCGACGGAAGCTTAGGTTACTTCGTGGCGAAGCAAAACATTTATATTGGCCTGGACT
GTCGCCCTATAAATAGGCAAGCTAGGTAATGGCATTAAACAACAGAGCGGGTGAACATATTCCTTGAATGGTTCTGTTTCATCGGTTCAATATTTATTGCGGATAACAATATATATATTG
TTGGCGGTGCTCTTTAGGTCTCCCAAGTATATTAAGGATGTTGTGAGGTATGTCGTAGAATACTTGACCAAGAAGACGCTGTATGGATCGAGAGAAGCGAGTTGACGGAGGCAACAGGAGAT
GTAGAGCTCGGCAGAGGTAGTGTGGAAGACAGACGGGATCAACAACCGGCTGTCATACCACATGCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGGAAGATCAAGGAAGACGAGGA
AACCGAGGACCAATGTTTTAATACACGGTATTGTAATATACGAAATATAAATGGGATAATGATATGTTGTGAACATAATATACGTGAACATAAATATATGTTTGATAATTTACATATT
ATAATATGTAAATGTATACGAGTGTGTATTTATAGAACATACAACACGCTATGACAAACAGGGAAGAAATGAAGAAATCGGGGTTGATTGGCTCATCGTATCCGTTAAGGCCCGCAGGC
CCGTTGAAATGATTCTTAATAAAACAAATATACATGATACGGATAGTTGAATATATAAACACAGGATATAAATACAACAGAAATGTTGTATACTAATTAATAATGAGAAGATAAGTAT
ATTTGTGAGGATGATGATCACAACCACCATTAGTGTGGGTGCATATGTCCCGAGTTAGTGCGCCACGTAAAGCGCTGGGCTTAT

DNA-N

11-13 SNPs to KM607387 KM607385 KM607386 (China). **25-18 SNPs** to MF039872 MF039878 MF039866 KY427062 (Thailand)

N protein (154 aa): 0 aa to KM607387 KM607385 (China) MF039872 MF039878 KY427062 (Thailand) **1 aa** to MF039866 (Thailand)

>N_alyu53
TATTACCCCGCTGCTCGGGACGGGACATGACGTGACGATAGATTATAATGGGCCAACTAAAGGCCCATTTAATAGAAAAGCGGGCTTTTGACATATTTCAAAGGCCAGCCTGGAAGT
GATTAATGTACAGTGCAGCAATGAAGGTTGCTTCGCCCTCGAAGCAATCCGAATAAATGTGCGTATTCAAACGCACTGAAGTCTATTAATATGTTGTCTCTGCCGAATAAATCAGAG
CCTAAGCGAAGCAGAACCAGATCGATTCCGCACAATCACAAATTCAGACCTGTACTCATGGGTGCGATTGGAAGACGATATCATCGGATTTCATCCGACAATCCACAATATGTACCTTCGCT
CGACGCGAGGAGTGGGAAGAAAGTCACTCGCAAGGTACTGCTTAGATCTATTGAAGCTGTGTTTAATGGAAGCTTCAAAGGAAATAACAGGAATGTTCTGGGTTTATATACGTATCAAT
ACGAGACGATGATGGAGAAATGCGTCCAGTACTCATAAATCCATTCCGAGGATATGGATATCATAAATGATTTCTATTATTTCGAAGGGAAGGGGAAAGTTGAATGTGATATATCATCAGA
TTATGTAGCGCCAGGAGTGCATTGGAGCAGAGACATGGAAGTTAGTATTAGCAACAGCAACAACCTGTAATGAATTATGTGATCTGAAGTGTATGTTGTTGTTGTTTCGTTAAGGAATAAAGGA
ATAACAGATGTGCTGTAATGATTATTAATAAACTTATTTTCATGTACTGTATGTTGATAAAACATACACACGCTATGACAAACAGGGAAGAAATGAAAAATCGGGGTTGATTGTTTC
TATAGTATCGCTTAAGGGCCGAGGCCCTTGAAAAATAAATATCGAATTATAAACGTTAGATAAATAACAGAGATAGATGATAAGCATCAAAAAACATAGACGAGTATATGGCTGTAT
AATATAAAGAAGCATATAAATAAATAATGTGAACATATCTCTGATTGGTTCAGAAGCTAGCCCCACCACTTTATGTTGGTGAAATGTCCCGATGACGTAGCAGACGGGGGACTAT

DNA-R

10-12 SNPs to KM607677 KM607678 KM607676 KM607679 (China). **11-17 SNPs** to AB113660 AF416475 AB113659 (Viet Nam). **16-20 SNPs** to MF039879 MF039873 MF039867 KY427063 (Thailand)

R protein (286 aa): 0 aa to KM607676 KM607677 KM607679 (China) **1 aa** to AB113660 (Vietnam) MF039879 (Thailand) KM607678 (China) ...

>R_alyu53
TATTACCCCGAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCTCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAAC
ATCAACAATCCCGCTTCACTACCAGTGTGCGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCAATGTGCAAGGATACGTCGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCCAAGAAGAAGCACGCGGCATACTGTATGAAGGAAGACACACGAATCGAAGGTCCCTTC
GAGTTTGGTGCTTTAAATTTGCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGGTGAACGCAACAAACGCGCTTTGGAGTATTTATATGAGTGTCCAATAACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAAGGCGATGAATAGCTGAAAAACATCCTTCAGTTCTTGACATCGGAAGTTGAAAAATATTATGGCGGAGCCATGT
CATCGGAGGATATAATTTGGTCTATGGCCCAATGGAGGAGAAGGAAGACAACTTATGCAAAATATTTAATGAAGACGAAGATGCGGTTTATCTCCAGGAGGAAAAATCATTTGGATATTA
TGTAGATTTGATAATTAACGAGCAAAATGTTATTTGATATTTCCAGATGCAAAAGAGTAATTTAAATTTATGTTTATTAGAAGAATTTAAAAATGCAATTTATCAAAGCGGAAATAT
GAACCCGTTTTGAAAAATTGAGAATATGTGGAAGTCATTGTAATGGCTAACTTCTTCCGAAGGAAGAACTTTTTCAGAAGATCGAATAAAGCTAGTTGCTTGCTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAAGCAAGATTCGGGGGTTGATTGGGCTATCCTAACGATTAAAGGCCCGCAGGCCCTCAAGATGGACGGCTCGATCAGATGTCCCGAGTTAGTG
CGCCACGTAAGCGCTGGGGCTTAT

DNA-S

14-16 SNPs to KM607534 KM607535 KM607536, KM607533 (China). **17-20 SNPs** to AB113662 AF148945 AB113661 (Viet Nam). **21-33 SNPs** to MF039874 KY427064 MF039880 (Thailand)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) **1 aa** to several isolates

>S_alyu53
TATTACCCCGAGCGCTCGGGACGGGACATGGGCTTAATGGATCATGGAATAAGGGCCCATCGGGCCCGTTAGGATGGGTTTGGGCTGATGGGCTTTATCCAGAAGACCAAAAAACAGCGCG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCCGCAAGCAAACTAAAAAGTCTATATACCAAGTGTAGACATATTTGTCAGATAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGCGGGTTGGCGCGGATGGAAGCAAGGCGGCAACAGTCAGCATCTGCTCGTTAGGTTCAATATTGGTTCCTGAAAAATACCGCTCAAGGTATTAGGATTAGGCTCAC
TGATAAAAATTACCCAGATATTTTATCTGGAATAATGTTATGCTTTTGGTGTCAAGGTGAACCCCGGAAGAACTACTTCACTGGGCTATGATTAAAAAGTTCATGGGAAATCAACAGCC
GACTACATGCTCGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTCGTGAAACTGGTATGCACTGGGGAAGTTGAAGCCGGAGTCCGAACAGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACAAACCGTGTGTGAGGAAGAATTGAACAGAGGTGGATTACTGTTATTTGGCATTTTATTGTAGTGCTGGAGTTAGTATTAACACAGACAGAAATACATATCATGT
ATGATATGTTTATGTAACATAAAACCTTTGTATGGAATAATGACCAAAATACATACACACACTATGAAATACAAACGCTATGACAAACAGGGAAGAAATGAAGAAATCGGGGGTTGATTG
GTCATATCGTATCGCTTAACGGCCCGAGGCCCTTGAAATGATTCTTTATAAAACAAATATACATGATACGGATAGTTGAATATATAAACCAACGATGTATAAATACACAGAAATGTTGTAT
ACTAATTAACAAATGAGAAGAAAAGGATATTTGTGAAGGATAAGCATCAGAACCAACCTTTAGTGGTGGGTGAGATGTCCCGAGTTAGTGCCACAGTAAAGCGCTGGGGCTTAT

DNA-U3

32-42SNPs to MF039875 MF039881 KY427065 MF039869 (Thailand)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alyu53
TATTACCCCGAGCGCTCGGGACGGGACATGGGCTTTTAAATGGCCGAGAGAGTTGAACAGTTAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAAGCGTGTCAA
TCTGGGTTTGACCGAAGGTCAAGGTAGACGGTCAACAATATTCCTGGCTTGCGGAGCAAGCAACGAATTAATATTTAATTCGTATGACAGCTGGACGGAGCGAAATACTCCTGTATCT
CATAAATAGCCTAAATCTGCTATGGATAATTTGCTCTCGCTTCTGTCAAAGGTGTGTGTTGAGCCGGAAGATCGCCATCGGCGATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGGAAGCGTATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTATACCTTGTTACTTGATATTTGTTAAATACGAAGAAATTCGTATTGATAAATAAATAACAT
CTGGGATGTTAATGTTTACATTAACATAGTATTAATAATGTACAATAACAAAAATTTGATGAGGAACGAATACAGAATATTAATAAGAGGAGCGGTAGCGTGATAAACAGGTGTTTAA
GGTATAATTAATAATTTATGCAAAATGTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAATAACCAATTTATATTTATTAATACATACAA
CGCTATGACAAAAGGGGAAAAATGAAGAAATCGGGGTTGATTGGTCTATCCTAACGATTAAAGGCCGCGAGGCCCTCAAGATGGATGAACGGTTAGATTGATTGCTTAGCCACGAAGAA
AGGAATCTTTTGGGACCAAGATGAAGACAGCTGTCACTACCTTTAAAAATAATAATAACCAATTGACGATAGTACCCCTCCCAAGATGACGTATAGGGGTGTCCCGAGGTAATTTA
ACATAGCTCTGACAAGAGATAGTGGACGTGGATGCCACGATCGGACGATCGTGGTTGATGAACTTATGATGACGTAGGGGCTGGGGCTTAT

ALYU-54 - Musa AAA Cavendish - China

Virome

- 1. **BBTV** six components (two variants of DNA-U3: v1 > v2)
- 2. **BBTA6** alyu54
- 3. **BBTA2** alyu54
- 4. **BBTA6def** 690 nt circle (deletion in Rep ORF)

BBTA6

BlastN preferentially finds matches to short sequences of BBTV U (including a 150 nt region upstream of the SL-CR)

>BBTA6_alyu54
TATTACCGACCTTGGCGCAGGGCGCACTATAAAGATGTCTGTGAGAAATTTGGGCTTTCACACGCAATTTGCAAGGCGAAGACCAGAGCTCTGTTTGGCGCGGAACTCAATACGCC
GCTTGGCAACATGAAGAAGAAATACAGCACCTACAGGGCGTGATTCAAGTGAAGAAGAACGCCGACTGAACGCGATGAAGAGCATAAATCGGTGGAATCCCAATCTCGAACCCTATG
CGAGCGCTCTTTCGACGATGCCCTAGCATACGTCTGAAGAAGCAAAACCGAATCGATGTGCTTCCATGGGAATTCGGTATTGGAATCCCGTAAGGGTTCGAATAAACGAAAGGTGTAGAATA
CTGGAGGATTGGGACAACGAAGTCTTCAACCCCAAAAAATACAGACGAGCCATGGCCAACACGGCCATGAGTGAAGTCTAAGAAGAAAGCTGCAGAAGAAGGATTTGTTATGAACTCGCA

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>R alyu54
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TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCTCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAACC
ATCAACAATCCCGCTTCACTACCAGTGATCGGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCAGGGATACGTCGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGGCTTCTCCCTGGCCACACCTTGAGAAACGAAAGGGAAGCCCAAGAAAGACGACGGGCATCTGTATGAAGGAAGACACAAGAATCGAAGGTCCTCTC
GAGTTTGGTGCCCTTAAATTTGCTCATGTGTAATGATAATTTATATGATGTCATACAGGATATGCGGTGAACGCACAAACGCCCTTTGGAGTATTTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCGATGAATAGCTGGAAAAACATCCTTCAGTTCTTTGGACATCGGAAGTTGAAAAATATTATGCGGGAGCCATGT
CATCGGAGGATAAATTTGGGCTATGGCCCAATGGAGGAGAAGGAAAGACAACCTTATGCAAAATATTTAATGAAGACGAAGAATGCGTGTATTTCTCCAGGAGGAAAAATCATTGGATATA
TGTAAGATTGTATAATTACGAGGAAATAGTTATATTTGATATTCCAGATGCAAAAGAGGAATATTTAAACTATGGTTTATTAGAAGAATTTAAAAATGGAAATATTCAAAGCGGGAAATAT
GAACCCGTTTTGAAATTTGAGAATATGTGGAAGTCATTGTAATGGCTAACCTCCTTCCGAGGAAGGAATCTTTTCAGAAGATCGAATAAAGCTAGTTGCTGCTGAACACGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAAAGCAAAGATTCGGGGGTTGATTGTGCTATCCTAACGATTAAGGGCCGACAGGCCCTCAAGATGGACGGCTCGATCAGATGTCCCGAGTTAGTG
CGCCACGTAGCGCTGGGCTTAT

DNA-S

4-7 SNPs to KM607535 KM607534 KM607536 KM607533 (China) . 14-19 SNPs to AB113662 AF148945 AB113661 (Viet Nam) . 20-32 SNPs to MF039874 KY427064 MF039880 (Thailand)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) 1 aa to several isolates

>S_alyu54
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTTAATGGATCATGGAATAAGGGCCCATCGGGCCCTTAAGATGGGTTTTCGGCTTATGGGCTTTATCCACAAGACAAAAACAGCCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCCGCAAGCAAACTAAAAGCCTATATATACCGATGTAGACATATTGTTCCAGATAACAAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGCGCGGGTTGGGCGCAGGAAGTATGGAAGCAAGGGCGCAACCAAGTCAGCACTACCTGCTGCTTAGGTTCAAATATTGGTTTCTGAAAAATACCGTCAAGGATTTAGGATTGAGCCTAC
TGATAAAACATTACCCAGATATTTTATCTGGAATAATGTTATGCTTTTGGTGTGCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAGAGGTTTCATGGGAAATCAACAGCC
GACTACATGCTCTGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAAGTGGGGAACCTGAAGCCGGAGTCCGAACAGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACAACCGTGTGAGGAAGAATGTAAACAGAGGTGGATTACTTGTATTGGCATTTTATTTAGTGTCTGGAGTTAGTATTAACACCAGAACAGAAATACATATCATGT
ATGATATGTTTATATAACATAAACCTTTGTATGGAATAATGACCAATAACATACACACACTATGAAATACAACACGCTATGACAAACAGGGAAAAATGAAGAAATCGGGGGTTGATTG
GTCATCGTAACGCTTAAGGGCCGACGCCCCGTGAATGATTCTTTATAAAACAAATATACATGATACGGAATAGTTGAATATATAAACACAGATGTATTAATACAACAGAAATGTTGAT
ActaattaaaaatAATGAGAAGAAAAAATATTTGTGAAGGATAAGCATCAGAACCACCCTTTAGTGGTGGGTGAGATGCCGAGTTAGTGCCACGTAAGCGCTGGGCTTAT

DNA-U3

42/42/44/49 SNPs to MF039875 MF03988 KY427065 MF039869 (Thailand)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alyu54_v1
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTGGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAAAA
TCTGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATTCGGCTTGCGGAGCAAGCAACAGAATTTAAATATTTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGCATCT
CTATAAATAGCCTAAATCTGGCATGGATAATTGCTCTCGCTCTTCTGTCAAAGGTTTGTGTTGAGCGGAAGATCGCCATCGGCGATCATCGGACGAAAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGCAAGCGTATAACGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTATCTTGTACTTGATATTGTATTTTGTAAATTACGAAGAAATTCGTACATTGATAATAATAAAAC
ATCTGGGATTGTTAAATTTTACATTAAACAGTATTAATAATGTACAATAACAAATATTTGATGAGGAACGAATACAAGAATATTAATAATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGTATAATTAATTAATTTATGCAATGTCATGATAATACGGTATAAGTTGAATGATGAGGTGAAGAGGAGATATTAGAATATTAATAACCCAAATATATTTATTTATATAATACATACAAC
ACGCTATGACAAACCGGGAAAAAAGAAAAATCGGGGGTTGATTGGCTATCTCAACGATTAAGGGCCGACGCCCCGTCAGATGGATGAACGGTTAGATTGCTTAGCCACGAAGA
AAGGAATCGTTTTGGGACCACAGACAAGACAGCTGTCACTACTTTTAAAAAATAATATAATAACCAATGACGATAGTACCCCTCCCAAGATGACGTATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGACAAGAGATAGTGGACGTTGGATGCCACGATCGGACGATCGTGGTTTGACGAACCAATGATGACGTAGGGGTGGGGCTTAT

T/G (13643/8939)

>U3_alyu54_v1
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TCTGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATTCGGCTTGCGGAGCAAGCAACAGAATTTAAATATTTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGCATCT
CTATAAATAGCCTAAATCTGGCATGGATAATTGCTCTCGCTCTTCTGTCAAAGGTTTGTGTTGAGCGGAAGATCGCCATCGGCGATCATCGGACGAAAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGCAAGCGTATAACGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTATCTTGTACTTGATATTGTATTTTGTAAATTACGAAGAAATTCGTACATTGATAATAATAAAAC
ATCTGGGATTGTTAAATTTTACATTAAACAGTATTAATAATGTACAATAACAAATATTTGATGAGGAACGAATACAAGAATATTAATAATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGTATAATTAATTAATTTATGCAATGTCATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAATAACCCAAATATATTTATTTATATAATACATACAAC
ACGCTATGACAAACCGGGAAAAAAGAAAAATCGGGGGTTGATTGGCTATCTCAACGATTAAGGGCCGACGCCCCGTCAGATGGATGAACGGTTAGATTGATTGCTTAGCCACGAAGA
AAGGAATCGTTTTGGGACCACAGACAAGACAGCTGTCACTACTTTTAAAAAATAATATAATAACCAATGACGATAGTACCCCTCCCAAGATGACGTATAGGGGTGTCCCGAGGTAATT
TAACATAGCTCTGACAAGAGATAGTGGACGTTGGATGCCACGATCGGACGATCGTGGTTTGACGAACCAATGATGACGTAGGGGTGGGGCTTAT

ALYU-55 - Musa AAA Cavendish - China

Virome

1. BBTV six components
2. BBTA6 alyu55
3. BBTA2 alyu55
4. BBTA3 alyu55
5. BBTA5-U3 chimera (2 or more variants)
6. Badnavirus BSVNV partial coverage of BSVNV_alyu33 (confirmed by PCR with YN-specific primers)

Two major variants (v1 > v2) of DNA-N, BBTA2 and BBTA3, while only minor variants of DNA-C, DNA-M, DNA-U2 and BBTA5

BBTA6

Best matches to
MF510475 MF510474 low coverage, short stretches of identity *Faba bean necrotic yellows virus associated alphasatellite 2*

Rep protein best matches to RI50297 100% coverage 61% identities 77% positives Sophora yellow stunt alphasatellite 3;
POCK61 100% coverage 60% identities 77% positives Faba bean necrotic yellows C9 alphasatellite; ATU31571 100% coverage
60% identities 77% positives Faba bean necrotic yellows virus associated alphasatellite 2

>BBTA6_alyu55
TATTACCGACTTTGGCGCAGGGCGCACTATAAAAGATGTCTGTGAGAAATTTGGCTTTCACACGCAATTTCAAGGCGGAAGACAGAGCTCTGTTCCGCGCGGAACTCAATACGCC
GCTTGGCAACATGAAGAAAGAATCACGACCACCTACAGGGCGTGATTGAGTTGAAGAAGAAGACCCGCTGAACGCGAGTGAAGAGCATATCGGTGGAATCCACATTCGAACCCCATG
CAGCGCTCTTTCGACATGCCCTAGCATACGTCATGAAAGACGAAACCGAATCGATGGTCCATGGGAATTCGGTATTCGAATCCGTAAAGGTTGCAATTAACGAAAGCTGTTAGAAATA
CTGAGGATTTCGGACACAGAGTCTTCAACCCCAAAAATACAGACGAGGACCTGGCCAAACAGGCCATGAGTGAGTCTAAGAAGAAAGCTGCAGAAAGAGGATTAGTTTATGAACTCGGA
GAGTGGCAGGTGCAATTTGACGAAGTTGTTGGAAGAAGAACCAGATACAGAGAACATAATTTGGGTATATGGACCAAGGGTGGAGAAGGTAACAGAGTTCGCTAAACATTTAGGGTTA
AAGGATGGTTGGACATATTTGCCCGGTGGTGAACCTCAAAGATATGATGTAACCTGTTATCAAAAGGACATGAAAAATAATGTTGTAATTGATTTCGCCCGTTGACCAAGGAATTTATTCA
TATAAATCCTTGAGATGGTTAAGAATAGAACTATATAGTTATAAGTATGAACAGTTGGTTCATCGTATGTAATAAGGTTTCATGATAGTGGTCTTCAGTAATGAGGAGCGAGATAT
GTAAATATCATTTGATCGAATAAGTTGATTCTTCTGCTGAACACGCTATGAAATACAACACGCTATGACAAAGGGGAAAAATGAAAAATCGGGGGTTGATTGGTCTATCCACCGA
CTAAGGGCCGACGCGCTCAAGATGGATGAACGGTTAGATTGATTGCTTCGCCACGAAGCAACAAAAATCGTGGTGGAGAATTCGCCACGTCATTGGTTACTGTTATCCTTGGCG
CACTATATATAGGTGCGCCAAAGTCGCCCATAG

BBTA2

best match to EU430730 98% coverage 97% identity; MG545616 99% coverage 97% identity; NC_038953 98% coverage, 95% identity

Rep protein best matches to AZL93963 100% coverage 99% identities (1 aa) 100% positives; ACB86656 100% coverage 99% identities (2 aa) 99% positives; YP_009508281 100% coverage 94% identities (11 gaps in middle) 94% positives Banana bunchy top alphsatellite 2

BBTA2_alyu51_v1
 TATTACCACCTTCGCGGCACACCTTCGCGGCACCTATAAAATGTCTGCCTCTCGCTGGACATTTACGCTTCATTATTCGCAAGCAACGGAGCGAGGCAAAATTCCTCGCAGCTTTGAAGGA
 GGAAGATGTGCACTACCGCGCTGTCGCGCAAGCAAACTGTCTCGCAATCTGTTGCAAAACATCTCTTCGTAAGAACTCTTCGTATAGCGGCTAATAAGGAAGAATA
 TCTGTCGAGAGCGATTGGGAGAAGCTCGAGGATCAGATTAACACAAAGCGGTACTGTTCAACAGAGGCCCTAATTCCTGAAGATCTGGGGTGCATGCCAGGCTCTCGAATACGG
 TAAATTCAGCATATGTTTACCAAGATCGCGCAAGCGATGAAATTAACACAGCCAGAGATATTTACCCAGATACCAATCGGTGAAGAAAGATGAAGAAATTCAGAAAGATATGCTCTATCC
 TATCTCCGTAGAGGCATGCGCAGCTCAATTAACGAGTATTAAGCAAGACCGGATATCGAACGATCATCTGGGTATTTGACCAAAAGGGAATGAAGCGCAATCAAGTACCGCGA
 GTCAATTAATCCAAAGGATTTGGTCTGCAACACAGGCGAGGAAGAAGGAGAACATCTGTTCCGCTACGTAGATGAAGGTTGCACAAAAGAACTGTTGATTGTATCTCCCGCTACAGCTA
 AGAATTTATTAATATGATGTTATCGAAGCATGAAGGTATAGATAGATCGAGATCAAAAATACAGCGCTGTGAAGATTTAGAAATCTGTACATGTATAGTTATGCTCAATTT
 TCTTCTGATATGTGTAAATATCTGAAGATCGAATAAAAAATGTTGCTTGTGCAACCGCTATGAATACAAACCGCTATGACCAACGGGGAAAAATGAAATACGGGGGTGATTGGG
 CATCTTACCAAGGATTAAGGGCCGACGAGCCGCTCAAGATGGATCCAAATACCCGCTAAGAAGCTAAACGGGTCTAAACAGTTCTCTCGCCCGCAAGCAACCTTTAACTCTCGCGCACT
 ATATATAGCGAGTTGGGCTAG

C/T (6278/1543) T/A (14489/22452) A/C (17821/27199) TT/AC A/T A/G T/A G/T C/T C/A 2 substitutions (similar aa) in Rep

BBTA2_alyu512
 TATTACCCACCTTCGCGGCACACCTCCGCGCACCTATAAAATGTCTGCCTTCGCTGGACATTTAGCGTTCATTATTCCGACGCAACGGAGCGAGGCAAAATCTCTCGCAGCTTTGAAGGA
 GGAAGAGTGTCATACCGCGCTGTCGCGCAGCAAACTGTCTCGCAATATCTGTTCAAGAACTCATTTCTTGAAGAAACCTTTCTGATATACGGCATATAAAGAGAATAA
 TCTCTCGAAGAGCTATGGGAGAAGCTCGAGGATCAGATACGACCAAGGGCTACTGTTCAAAGAGGCCATTAATCTTGAAGATAGGGGGTCTGCCAACAAGGCTCGAATAGCG
 TAAATACGAGATATGGTTACAAGATCCGCCGAAGCGATGAAATGAACAGCCAGAGATATTTACCCGATACCAATCGGTTGAAGAAGATGAAGAAGATTTCAAGAAAGGATATCTCTGCC
 TATCTCGATAGGCCATGGCAGGTACAAATTAACGGGATTAATTAAGCAAGCCAGGATATCGAACGATCATCTGGGTATCGGCAAAAAGGGAATGAAGGCCAAATCAAGCTACGCTACC
 GCTTAATATCCAAAAGGATGGTCTACACAGAGGGAAGAAGAAGGAGAACATCATGTTCCGCTCATAGATGAAGTTGCGCAAAAAAGCTGTGATTTAGTCTTCGCGTACAGTACA
 AGAATTTATTAATTAATGATGATTCAGAGCATCAAGGATAGAGATATCGAGATGACAAATACAAGCCCTGGAAGTTTGAAGATTTGAATTTCTGTCATAGTAAATGATTATGCTTAAT
 TCTCTCGTATATGTGTAATAATCTCGAAGCATGCAATAAAAATAGTGTCTTGCAGCAACGCTATGAATAACACAGCTATGACCAACGGGGAAAAATGAAGAAATCGGGGGTATTTGGG
 CTATCCCTAACAGATTAAAGGCCCGCAGGCCGCTCAAGATGGATCCAATAACCCCGATAAGAGATAAACGGGTTAAACAGATTCTCTCGCCCGCAAGCAACACTTTAACTCTCGCGACCT
 ATATATAGCGGAGTGGGATAG

BBTA3

best match to GU074391 ca 100% coverage 97% identity; NC_038955 ca 100% coverage 97% identity; GU074392 ca 100% coverage, 97% identity

Rep protein best matches to: YP_009508283 100% coverage 99% identities (1 aa) 100% positives Banana bunchy top alphasatellite 3; ADV18492 100% coverage 98% identities, 99% positive; ACJ36781 100% coverage 89% identities 95% positives

EBBTA3_alyu55
TATTACCACTCTCTCCGCCCTACTTCTCGCCCTGACGTCATAAGATGTCATTCATCAAAATGGTGTTTCACTCTGAATTATTCTCCCGAGCCGAGAGAGAAGCACTTCTCTCGCGTCTG
AAGGAGGATGATGTTTATTACCGCGCTGTCGGCGCAGGAAGTCGCTCGAGCTCGCGCCGAGAACCACTTCAGGAGATATCTCTCCCTGAAGAAATCGATGAAGCTAGGCGGCATGAAGAG
AGCTACTCTTCGAAGGCTCAGTCGGGAGAGCGGAGAGACAGACAGAAAGAAATTCGAAGTATGTTCTCGAAGGAATCCCTAATTCCTGAAGATAGGTTGTTCTGCTACTCAGGGTTCTAAT
AAACGAAACTCATCAGAGATGGTATCCAGATCCAGCGGACAGTCAGAAATCGAACACGCCGAGATATATACAGCATATCTCATCTGGTAGGATCCGATAAAAAAATCAAGGAAGCAATTGTTGT
TATCTCTCTCGAAGACCATGCCAAATTCAAATTACCGAGGACCAATTCGCGAGAACCCGATATCGCAGATCTATCTGGGTTTACGGTCCGAATGGCAATGAGGAAAGATCCACATAT
CGCAAGTCGCTGATTAAAGAATGATGGTTCTACACAGAGGTTGGGAAGAAGGAGAAATATCTTATTCTCTATGTGGACGAGCAAGTCCACGAAACATATAGTATTTTCATCTCCCTCGATGT
AATCAGGATATCTCAAAATATGATGTAATAGAGGCTTTAAAGGATAGAGATATAGAGAGTCAGAAATTAAGAACCCATAAAGATGTTGAATATAGATAGATTTCATGATCTCGTATGGCT
AATTTCTATCGCAGGATTTCTGTAAAATCTCTGAGGATCGACATAAATATATATATTTGTGAACCGCTGATGAATCAACCAACACATGAAGAAATCAACACAGAGTAAGATTGTGATCTTCAAC
GAATATGGGCGCCGAGGCCCAACACTATTCTGGGCGCAGCGCCAGCGGAAGCGCTTTCGGCTGAAGCTTCTCGAAGGAAGAACCACTTTAAGTCCTCTCGCCCTATAAATAGTTTTCGCC
GAGGAATGGGCTAG

A/G (26975/76754) No change in Rep aa

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>Babu3chn_alyu55_uncorrected
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AAGGATGATGATGTTTATTACCGGCGTCTCGGCGACAGATCGCTCGAGCTCTCGGCCGAGAAACCACTTCAGGATATATCTCTCGAAGAAATCGATGAAGCTAGGCCGCGATGAAGAAAG
 AGGACTCTTCGAAAGGCTCTCGGGAGAGCGAGAGGAACGACAGCAAGAAATTCGAAGTATGTCTCGAAAGAACCCCTAATTCCTCGAAATAGGGTTGTTCTGCTCATCGGGTCTTAAT
 AATCAAGAAATCATCAGAGATGGTATCCAGATCCAGCGGACGATGAGAATCGAACAGCCGAGATATATAACAGATATCTATCTGTGATGAGCACTAAAAAATTCAGGAAGCAATTGTTT
 CATCTCTCTCGAAGACCATGCGCAATTCAAATTACCGAGGCAATTCGCGAGAACCCGATATCGCAGATCTATCTGGGTTTACGCTCGCAATGCGCAATGAGGAAAGCTCAACATAT
 CGCAAGTCGCTGATTAAAGAGGATTGGTTCTACACCGAGGTTGGGAAGAAGGAAATATCTTATTCTCCTATGTGTGACGAAGGATCGACGAAACATATAGTATTTTGATATCCCTCGATGT
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 AATTTCTCCGAGGATTTCTGATAAACTCTGAGGATCGAATAAATATATATTTGTGAACCGCCTATGAAATCAACCACTATGAAATCAACACAGCTAAGATTTGTGATCTCCAA
 GAATATGGGCCGCGGCCCAACACTATTTGGGCCGACGCCCAGACGCAAGCCGCTTCGCTGTAAGCTCTTCGAAAGAAGAACCACTTTAAGTCCCTCGCCCTATAAATAGTTTTCGCC
 GAGGAAGTGGGCTAG

BBTA5-U3 chimera

830-1056/1-260 - BBTV5 (with CR-M and CR-SL)
260-914 - DNA-U3 (share CR-M)

[illegible]

BBTA5_U3_aluY5S_correction1
TATTACCGGACCTTTGGCGAGCGGCACATATAAAGATGTCGACGACGCGAAATGGGCTCTCACACGCAATTTGAAGCGGAAGACGACGAGCTCTGTTCGGCGGGCAAACTCAATAC
CGGTGGTCCGCAACATGAGAAGAGAACTACGACCATCTTCAGGAGAGTATTCAATTGAAGAAAGAGCTCCGGATTGAACGAGTGAAGACGTTAATTGGGGGAATCCACACCTCGAAGCC
ATGACGAGAACAACATCGATGAACAATATTTCTGGCTTCGGAAGACGAGCAAGAATATAATTAATTAATTCATGAGACACGCTGGAGCGCTCCGAAATCTCTCGATCTCTATATAATACCTAA
aactcTGCATGTGATAAATTTGCTCTCGGTCTTTAGCAAGACCTCGTGTAGGCGGGAAGCTCGCCGTCGGCGCTATCAGACGAATCTCGAAGATAGACGGAAGATCATGTCGGAAG
CGTATATCGGGTATTATATATATATATGACGAGCTGACGAATAACTTGTGATCATGATACGTATTTTGTGAAATAAATGAAGAATAATTCGAATATGCAAAATAATAAACAATCTGGGTTTGT
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AAATAAATATGCAATGTAACTATAATAACGGTATAAGTTGAAGTATGAGGAGAAAGAGAGATATTAGAATATTAATAAAAGCCAATTTATATTTTATATGACATACACACGCTATGACA
AAGGGGAAAAATGAAGAATCGGGGGTTTATGGGCTCTACACGATTATGGGCGCGAGCCCGCTACAAGATGCGGGGAATAATCAAATCCGACGCGCAAAATATTATTAATACAAATAC
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>BBTA5 U3 alyu55 correction2
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 CGGTGTGGCAACATGAGAAGAAGATCACGACCATCTTCAGGAGGTGATTCAATTTGAAGAAGAAGATCCCGGTGAACGCGATGAAGACGTTAAATTTGGGGGAAATCCACACCTCCGAAGC
 ATGAGAGAACCAATCATGAAACAATTTCTGCGTTCCGAAGCGAGCAACAAGATTAATAATTAATTTGCTAGACAGCGTGAGCGCTCCGAAATCTCTGcATctCTATAAATACCTta

B2BTA5 13_4_u3_alyu55_correction3

TATTACCCGACTTTGGCGAGGCGGCACATAAAAGATGTCGCAGCAGCGAAATTTGGGCTTTCACACGCAATTTTCGAAGGCGAAAGACACAGAGCTCCTGTTCCGGCGGCGAAACTCAATAC
CGGTGTTGGCAACATGAGAGAAGAAATACACGACCATCTCCAGGAGATGTTCAATTTCGAAGAAGAGCTCCGGATGAACCGATGAAGACGCTTAATTTGGGGGAAAACCCACACCTTCGAAACC
ATGAGAGAACAACATCGATGAACAATATTTCTGGCTTCGGAAGCGAGCAACAAGATTAATAATTAATTCGTAGGACACGCTGGACGGCTCGCAAAATCTCTGCATCTCTATAAATCCCTAA
AACCTCGGCATGTAATAATGCTCTCGGCTTCTTCAGCAAGCACTCTGGTGTTCGAGGCGGAAGATCGCCGTCGGGCATCATACAGACAAATGCTCGCAAGAGACGCGGAAGATCATGCTCGCGAAG
CGTATATCCGGTATTTATATACGTATACGGAAGCTAGAACTAACTGTATCAATCTGTTATCTGTTAAATATGAGAAGAAATTCGAATATGCAAAATTAACAAACATCTCGGTTTGTGT
AATGTTTACATTAACCGAGTATTAATATGTCACAAATACAAATTTGTTGATCGGAACGAATACACAAATATACAAATATGAGGACCGCTAGCGGTATTAACAGATGTTTAAGGATATATAAT
AAATAATTTGCAAGTTGATTAATATACCGGTATAAGTTGAAGTATGAGGAGAAGAGGAGATATTAGAATATTAATAAGGCAAGCTATTTTATGAGACATACACACCGCTATGACA
AACCGGGAAAAATGAAATAACCGGGTTGTTGGGCTATCTCTAACCAATGATCGGCCCGCAGGCGGCTATACAAATGACCGGGAAAAATCAAATCTCGGACGCGCAAAATTTATTAATACCAATAC
ACCGCCTTTTGAAGATCCCGTGACGAGAGGATCGCCAGCTAGCAAGAACTGTACTCTTGGCGCAGCTATATATAGGTGCGCGCAAGTCCGGCCATAG

12 SNPs to KM607099 KM607098 (China). **20-24 SNPs** to KY427060 MF039864 MF039876 MF039870 (Thailand)

NC_012811.1
 TATTACCCCCCTGCTCGGGACGGGACATCAGTGCTTCTAACAAATGCACGTGACAATGCAGTAGCTTGTAGCGAAAGATAACCTACACTTTCCAAAAGTGAAGGAATATTCGTTGCTTAGGAGCATAGCAACGAGGACAGATATTGTTTCGAGAAGCGACAAATGGAGGCTATTAAACCTGATGGTTTTGTGATTCCGAAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAATCGTCTGTGATCGCCAGCAGGTGTCAGAGAGGTGATCAAGAAATATTTGGGAGCATCGAAATAAATCTCTGTTCTCGAGAAGTGAAGAGGCTGCTGAGAGAGGATTCGAGCATGGAAATCAAGATGATCTCTAGACGCTGAGGAGGATGAAGACTCTTATTTTCGCTATGCGAATATTTGAAGAAGCTTGTGGTGATTTGTTGTAGTACATAATAAATCTATTGCATATATAGTTTAAAGTAAACAAATGGTGTCTTTTATCATGAATATATTAAGAACCTAGGTGGTCTGACTACTCGGTATATCAAGAATCTGTTTGTGATGGGAACCTCTCTCTGCTCTGCAGCAGAGAAGAAGATGAAGAAGATTAATATACAGAAGTTTATCATGGCATCGACAGAAGAAGATCTTGTGGATGTAATGATAAAGATAGTATATTCAGATTATGATGTATGATCTGATTAATGAATATCCATTTATCATAAAATAAAATAATGGAATGATGATTATGTATTCTAGTATAAATACATAATGGTATACGTATAGCATAAAATACATAAACTACATACACACATCATGACAAACAGGGAAAAATGAAGATCGGGGGTGTATTGGGCTATCTAACGATTAAAGGGCCAGAGGCCGTTTAAATATGTGGTGGACGAAGTCTTCAACACAAAAAGTATGATCAGAAATGGAAATATATGAGCTGCGAACGTAGGAGGATCTCCCGAGTTAGTGGCCGACGTGACGAGGGGGCTTAT

18-23 SNPs to KM607239 KM607240 (China). **51-52 SNPs** to KY427061 MF039871 MF039865 MF039876 (Thailand)

M_aluys5
TATTACCCCGAGCGCTCAGGACGGGACATCAGTGCAACTAACAAATGCACGTGACTGATATATACTACATAAACGGTTCAACGAACCGTTATATAATGTTTATAACGACAAGTCACGTGTG
ATAGACGATGCACTGACATAGTCAAATGATTGAATAAACATTGACGTCCGGATGCTCCGACGGAGCTTAGTGTTACTCGTGGCGAAGCAAAACATTTATATATGGCCGGAATT
GCTGGCTATAAATAGCAAGCAAGGAATGGCATTAACAACGAGGCGTGAAACATTTCTTCAATGTGTTCTTGCTGATGCGCAATATTTATGGCATACAACATATATATATATTG
TGCCGTTGCTCTTTGAGGTGCCCAAGTATATAAAGATGTGTGAGGATTCGTGAGAATCTCAGAGAAGCAGCTGTATGGTGCAGAGAACCAGTTGACGGAGGCAACAGAGAT
GTAGACTCCGCAAGAGTTGTGGAAGACAGACGGGATCTCAACACGGCTGTATACACATCAACACAGGTTATCCCTTCGCATCAACCTAGAAGGATGATCAAGGAAGACAGGAGA
CAGCAGGACCAAGTGTTTAATACACCGTATGTGAATATACGAATAATAATGGTAATGATATGTTGTAATCTTGTGAACATATAATACAGTGAACATATATATGTTTAAATTTACATAT
ATAATATGTAATTTGTATACAGAGTGTTGATTTTATAGAACATACAACACGCTATGACAACACAGGAAAAATGAAGAATCGGGGGTTGATTGGTCTATCGTATCGCTTAAGGGCCGCAAGC
CGGTGAAATGATTTATATAAAACAATATACATGATACGGATATGTTGAATATATAAACACAGCAAGTATAAATCAACCAAGTTTGTATAGATTTAAAAATAATGAGAAGATAGATAT
ATTTTGACAGGTGATGATGATCAACACCCCAATTTAGTGGTGCGATGATGTCGCCAGTATGTCGCCAGCAGTACCAAGCTCGGGGGTTAT

26 SNPs to KM607387 KM607385 (China). 26-29 SNPs to MF039872 MF039878 MF039866 KY427062 (Thailand). 36 SNPs to KM607386 (China)

N_N_aluys5_v1
TATTACCCCGCGTCTGGGACGGGCATGACGTCAGCATAGATTATAATGGGCCATTAAGAGGCCCAATTTAATAGAATAGCGGGGCTTTTGACATATTTCAAAGGCCCGAGCTGGAAGT
GGATAATGTCACGTGCGCAAAATAGAGGTGCTTTCGCGCTCGAAGCAAAACCGGATAAAATGTTCGGTATTTCATTAACGCCAATCGAAGTCATTATTAATGATGATCTTCGCGCAATAAATACAGAG
CTAAGCGAAGCTGAAGCATGCGATGGGACGATACCAATCAAGACATGACTACTCGGTGGCGATTGGAAGACGATATCATCGGATCTATCCGAGGATACGCAATATGCTCATCTTCGCT
CGACGCTGGCAGCGAAGAAAGTCTCTCGCAAGGTACTGCTAAGTACTTATGAAGTCGTGTTTATGAAGGCTTCAAAGGAAGTACAAGGAATGTCTCGTGCGTTTATATACGATATCAAT
ACGAGACGATGATGAGAANAATCGCTCAGFATCATATAATCACTCGGAGATATGGATATCAATATGTTCTTATTATTTTCGAAGGGAAGGGGAAAGTGATGTGATATATCATAGA
TTATGTAGCCGCGAGGATGATTGGACAGCAGACATGGAAGTTAGTATTAGTACCAACCAACCTGTAATGAATCTGTTGATCTGAAAGTGTGTTATGTTGTTCTGTAAGAATAAAGGA
ATAACAGATGCTGTGAATGATTTATAAATAAATTTTATTCATGTAAATGTATGTTGTATAAATAACATCAACACGCGTATGACAAACAGGGGAAATAAAAAATCAGGGGTTGATGTGTC
TATCGTATCTGTTTAAAGGCGCGAGGCCGTTGAAAAATAATCAATCGAATTTAAACAGTATGATATAATCAACAGATAGATGATGAACATTCGCAAAACATGACGGAAGTATATGCGTGTAT
AATATAAACAACGATATAATAAATAAATGGAACAATAATCTCGATGGTTCAGAAAGTACCCCACTAATCAATCTTAAGTGTAGTGCGGATCTCCCGATGACGTAAGCAGCGGGGACAT

9 SNPs to AB113660 (Viet Nam). 10-13 SNPs to KM607678 KM607677 KM607676 KM607679 (China). 17 SNPs to MF039879 (Thailand)

NR_aluY55
TATTATCC005CAGCGCTCGGGACGGGACATTTCGATCTATAAAATAGACCTCCCCCTCTCCCACTACAAGATCATCATCGTGCACAGAAATGGCGCGATATGTGGTATGCTGGATGTTCAACC
ATCAACAACCTCCCGCTTCACATGACCACTGATCGGGGATGAGTTCAAATATTATGTCATATCAAGTGGAGGGGACAGGAGGAGTACTCGTCATGTTCGAGGATATCTCGAGATGAAGACAGCA
AGTTCTCTGACGAGATGAGAGGCTTCTTCTCGGCGCACACCTTGTAGAAAGCGAAAGGGGACCAAGGACATCTGTATGGAGGAAGCACCAAGATCGAAGGTCCTTCT
GAGTTTGGTGCGCTTTAAATGTGTCATGTAATGATAATTTTATGTGTCATACAGGATATGCGTGAAACGCACAAAGGCGCTTTGGAGTATTTATATGAGTGTCGCAAAATACCTTCGATAGA
AGTAAGGATACATTATACAGAGTTCCAGCAGAGTGTAATAAAGGACAGGCGCATGAATAGCTGGAAACATCTCTTCAGTACATTTGGAATCTCGGAAGTTGAAATATTTATGGGGGAGCGATG
CATCGGAGGATTAATTTGGGTTCTATGGCCCAATGGAGGAGGAAGGAAGCAACTTTGCAAAAATTTTAAATGAAGCAGAAGATCGCTTTTATTTCTCAGAGGAGAAATCATTTGGATATA
TGTCATGTTGATAATTCAGGAAGAAATAGTTATATTTGATATTCGACGATCCAAAGGAGGAATATTTAAACTATGTTTCTATTAGAAGAAATTTAAATATGAAATTTCAAAGCGGAAATAT
GAACCGGTTTGAATATGTAGAAATGTCTGAAGTCATGTAATGGCTAACTTCTTCGAGGAAGGAATCTTTCAGGAATCGAAATAAAGCTAGTTGTGCTGGTGAACACGCTATGAC
AATCTGATCGCTATGACAAAAGGGGAAAGCAAGATTCGGGGGTTGATTGTGCTATCTCTAAGCATTAAGGCGCGCAGGCGCGTCAAGATGGACGGCTCGATCAGATGTCGCGAGTTAGTG
CGCCACATGACGCGTGGGGCTAT

13-15 SNPs to KM607534 KM607535 KM607536 KM607533 (**China**). **14-17 SNPs** to AB113662 KY427064 AB113661 (**Viet Nam**). **20 SNPs** to MF039874 (**Thailand**)

S8_aluY55
 TAATTACCCCCAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTAAGATGGGTTTGGGCTGATGGGCTTTATCCAGAAGACAAAACAGGCGG
 GATCCCTCCCAATTTCAAATTTAGATAGCTTGCCCCCAAGAAACAAATAAAGTCTATATATACACAGTGTAGACATATTGTCAGATAACAAATGGCGAGGTTCCGAAGAGATCGATCAA
 GAAAGAGGGGGTTGGCGAGCGGAAGATGGAAGAACAGTTGGGACACCTGACAGCATCGCTGCTAGGTGTCATTAATTTGGTTCTGAAAAATAGCTCAAGTAGTTTATAGGATTGAACGCTC
 TGATAAATCATTGGCCAGATATTTTATCTGGAAATGGTGGTCTTTGGTGTCAGAGTGGACCCCGGAAGATACTCTACTGGGCTATGCTTAAAGGTTCTATGGGAATTCAGCAAGC

TATAGTATCGCTTAAAGGCCGAGGCCCGTTGAAAAATAAATATCGAATTATAAACGTTAGATAAATACAGAGATAGATGATAAGCATCAAAAAACATAGACGAAGTATATGGCTGTAT
AATATAAAGAAGCATATAAATAAATAATGTGAACATACTCTGATTGGTTCAGAGCGTAGCCCCACCAACTTTATGTTGGTGAAATGTCCCGATGACGTAAGCACGGGGGACTAT

DNA-R

7-9 SNPs to KM607677 KM607678 KM607676 KM607679 (China). **8-14 SNPs** to AB113660 AF416475 AB113659 (Viet Nam). **13-17 SNPs** to MF039879 MF039873 MF039867 KY427063 (Thailand)

R protein (286 aa): 0 aa to KM607676 KM607677 KM607679 (China) **1 aa** to AB113660 (Vietnam) MF039879 (Thailand) KM607678 (China) ...

>R_alyu56
TATTACCCCCAGCGCTCGGGACGGGACATTTCATCTATAAATAGACCTCCCCCTCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCAACC
ATCAACAATCCCGCTTCACTACCAAGTATCGGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGGTACTCGTCATGTGCAGGGATACGTCGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCCAAAGAAGACACGGGCATCTGTATGAAGGAAGACAAAGAATCGAAGGTCCTTC
GAGTTTGGTGCTTTAAATTTGCATGTAATGATAATTTATTTGATGTCATACAGGATATCGGTGAAACGCACAAACGGCCTTTGGAGTATTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCCATGAATAGCTGGAACACATCCTTCAGTTCTTGACATCGGAAGTTGAAAATATTATGGCGGAGCCATGT
CATCGAAGGATAATTTGGGTCTATGGCCCAATGGAGGAGAAAGAACACCTATGCAAAATATTTAATGAAGACGAAGAATGCGTTTATTTCTCCAGGAGGAAAATCATTTGGATATA
TGATGATTGTATAATTACGAGGAATAGTTATTTGATATTCCAGATGCAAAAGAGGAATTTTAACTATGGTTTATTAGAAGAATTTAAAAATGGAAATTTTCAAAGCGGGAATAT
GAACCCGCTTTCAAATTTGACAATATCTCGAAGTCATTGTAATGGCTAACTCCTTCCGAAGGAAGCAATCTTTTCAAGATCGAATAAAGCTACTGCTTCTCAACACCGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAGCAAAGATTCCGGGGGTGATTGGGCTATCCCTAACGATTAAAGGCCGAGGCCGCTCAAGATGGACGGCTTGATCAGATGTCCCGAGTTAGTG
CGCCAGCTAAGCGCTGGGGCTTAT

DNA-S

11-13 SNPs to KM607534 KM607535 KM607536 KM607533 (China). **14-19 SNPs** to AB113662 AB113661 (Viet Nam). **16 SNPs** to AF148945 (Viet Nam). **20-30 SNPs** to MF039874 KY427064 MF039880 (Thailand)

S protein (170 aa): 0 aa to AY337715 AY494786 HQ378191 (China) FJ787433 FJ787434 (Philippines) **1 aa** to several isolates

>S_alyu56
TATTACCCCCAGCGCTCGGGACGGGACATGGGCTTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTTATGATGGTTTTGGGTGATGGGCTTTATCCAGAAGACAAAAACAGCGCG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCGCAAGCAAACTAAAGTCTATATATACCAAGTGTAGACATATTGTTTCAGATACAAAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGCGGGTTGGCGCGCGGAAGTATGGAAGCAAGGCGGCAACCAAGTCACGACTACTCGTCGTTAGGTTCAATATTGGTTCTGAAAATACCGTCAAGGTATTTAGGATTGAGCCTAC
TGATAAAACATTACCCAGATATTTTATCTGGAATAATGTTTATGCTTTTGGTGTGCAAGGTGAAGCCCGGAAGAATACTTCACTGGGCTATGATTAAGTTTCATGGGAATCAACCAAGCC
GACTACTGCTGGAAGCACCAACGCTTATTTATAAAACCTGAACATAGCCATCTGGTGAACTGGTATGCAGTGGGGAACTTGAAGCCGAGCTCGCAACAGGCAATCATGATGTTGAATG
TCTTCTAAGGAAGACAACCGTGTGAGGAAGAATGTAACAGAGGTGGATTACTTGTATTGGCATTTTTATTGTAGTGTGGAGTTAGTATTAACTACCAGAACAGAATTACATATCATGT
ATGATATGTTTATGTAACATAAACCTTTGTATGGAATAATGACCAAAATACATACAACACATATGAAATACAAACAGCTATGACAAACAGGGGAAAATGAAGAATCGGGGGTTGATTG
GCTATTCGATTCGCTTAAAGGCCGAGGCCGCTTGAAATGATTCTTTATACAACAAATATACATGATACGGATAGTTGAATATATAAAACACGATGTATAAATACAAACAGAATTTGTGAT
ACTAATTAATAATGAGAAGAAAGGATATTTGTGAAGGATAAGCATCAGAACCAACCTTTAGTGGTGGGTGAGATGTCCGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

DNA-U3

42/44/46/50 SNPs to MF039875 MF039881 KY427065 MF039869 (Thailand)

U3 protein (39 aa): 0 aa to KY427065 (Thailand)

>U3_alyu56
TATTACCCCCAGCCCCAGGACGGGACATGGGCTTTTTAAATGGGCCGAGAGAGTTTGAACAGTTTCAGTATCTTCGTTATTGGGCCAATCGGCCCAATAATTAAGAGAACGTGTTCAAAA
TCGGGGTTTGACCGAAGGTCAAGGTAGACGGTCAACATTATTTCTGGCTTGGCGAGCAAGCAACAGCAATTAATATTTAATTCGTATGACAGCTGGACGGACCGAAATACTCCTGTATCT
CTATAAATAGCCTAAATCTGGCTTGATAATTGCTCTGCTCTTCTGTCAAAGCTGCTGTGTTGAGCGGGAAGATCGCCATCGGCGATCATCGGACGAAAAGCTCGGAAGAGAGCGGAGA
ACCATGCTACGAAGCGCTATATCCGGTATTATAGACTTCTACCGCAGCTAGAAGTTTCTCTTCTACTTGTATTTGATTATTGTTGTAATTTACGAAGAAATTCGTATATTGATAATAATAAAC
ATCTGGGATTGTTAATGTTTACATTAAACAGTATTAAATAGTACAATAACAAATATTGTATGAGGAACGAATACAAGATTATTAATAATGAGGAGCGTAGCGTGATAAACAGGTGTTT
AAGGTATAATTAATTAATTTAGTAAATGTCATTATAATACGGTATAAGTTGAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAAAAACCGAATATATTATTATTAATACATACAAAC
ACGCTATGACAAACCGGGGAAAAAGAAAAATCGGGGGTTGATTGGTCTATCTCAACGATTAAAGGCCGAGGCCGCTCAAGATGGATGAACGGTTAGATTGATTGCTAGCTACGAAGA
AAGAAATCGTTTGGGACACAGACAGACAGCTGTCACTACTTTTAAAAAATAATATAAATCAACAAATTGACGATAGTACCCTACCAAAGATGACGTATAGGGGTGTCCTCGAGGTAAT
TAACATAGCTCTGACAAGAGATAGTGGACGTGGATGCCAGATCGGACGATCGTGGTTTGTATGAACCAATGATGACGTAGGGGTGGGGCTTAT

Dataset S1B. DNA-U3 components of BBTV PIO (JGF-1, ALYU-14 to ALYU-24) and SEA (ALYU-25 to ALYU-56) isolates and their multiple alignment with conserved features highlighted

Conserved **TATA-boxes** and **poly(A) signal**

miR156 family target sequence: **TGCTCTCTCTCTCTGTCAA** in PIO isolates; **TGCTCTCTCTCTCTGTCAA** in SEA isolates

>U3_jgf1_v1
TATTACCCCGCTGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCCTTGAGAGTTTGAACAGTTTCAGTATCTTCGTTATTGGGCCAATCGGCC**CAATAA**TTAAGAGAACGTGTTCAAAA
TCGTGGTATGACCGAAGGTCAAGGTAAACCGGTCAACATTATTTCTGGCTTGGCGAGCAAGATACACGAATTAATATTAATTCGTAGGACACGTGGACGGACCGGAATACTCCTGCATC
TCATATAATACCCCTAGTCTTGTAAGGATAA**TGCTCTCTCTCTCTCTGTCAA**GGTGGTTGTGCTGAGGCGGAAGATCGCCAGCGCGGATCGTCGGAACGATGTCATCTAGAGAGCGGT
GAAGCAAACACGAAGCGTATATCGGGTATTTATAGACTTATAGCGGACGTAGAAGTATACACTGTACAGATTATGATTTTGTAAATACGAAGAATTCGTATATGATAT**TAATAAA**
CACCTGGGTGTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAAAATACAGTATACGGAACGTATACTGACAAAGTAATAATGATAGGCGAAGCATGATTAAACAGGTGTT
TAGGTATAATTAAACATAATTATGAGAAGTAATAATAACGGAAAAATGAATAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAAAAACCAATTTATATTATTTTGGAAACGAATAAC
AACACGCTATGAAATACAAGACGCTATGACAAATGTACGGGTAT**T**GATTGTATATCTTAACGATCTAGGGCCGTAGGCCCGTGAGCAATGAACGGT**T**AGATTAAATCCTTAGCGACGA
AGAAAGGAATCTTAATAGGGACCAATTAAGACAGCTGTCATTGATTAATAAATAATATAATATACAAAGACTTTTGACCCCTGATAATGATGACGTATAGGGGTGTCCTCGATGTA
ATATAGCATAGCTATGTGAAGAGATAAGCATGTGCCGCAACCTTTAGTGGTGGCCAGATGTCCGAGTTAGTGCGCCACGTAGCACGGGGACTAT

>U3_jgf1_v2
TATTACCCCGCTGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCCTTGAGAGTTTGAACAGTTTCAGTATCTTCGTTATTGGGCCAATCGGCC**CAATAA**TTAAGAGAACGTGTTCAAAA
TCGTGGTATGACCGAAGGTCAAGGTAAACCGGTCAACATTATTTCTGGCTTGGCGAGCAAGATACACGAATTAATATTAATTCGTAGGACACGTGGACGGACCGGAATACTCCTGCATC
TCATATAATACCCCTAGTCTTGTAAGGATAA**TGCTCTCTCTCTCTCTGTCAA**GGTGGTTGTGCTGAGGCGGAAGATCGCCAGCGCGGATCGTCGGAACGATGTCATCTAGAGAGCGGT
GAAGCAAACACGAAGCATATATCGGGTATTTATAGACTTATAGCGGACGTAGAAGTATACACTGTACAGATTATGATTTTGTAAATACGAAGAATTCGTATATGATAT**TAATAAA**
CACCTGGGTGTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAAAATACAGTATACGGAACGTATACTGACAAAGTAATAATGATAGGCGAAGCATGATTAAACAGGTGTT
TAGGTATAATTAAACATAATTATGAGAAGTAATAATAACGGAAAAATGAATAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAAAAACCAATTTATATTATTTTGGAAACGAATAAC
AACACGCTATGAAATACAAGACGCTATGACAAATGTACGGGTAT**T**GATTGTATATCTTAACGATCTAGGGCCGTAGGCCCGTGAGCAATGAACGGT**T**AGATTAAATCCTTAGCGACGA
AGAAAGGAATCTTAATAGGGACCAATTAAGACAGCTGTCATTGATTAATAAATAATATAATATACAAAGACTTTTGACCCCTGATAATGATGACGTATAGGGGTGTCCTCGATGTA
ATATAGCATAGCTATGTGAAGAGATAAGCATGTGCCGCAACCTTTAGTGGTGGCCAGATGTCCGAGTTAGTGCGCCACGTAGCACGGGGACTAT

>U3_alyu14
TATTACCCCGcGtGCTCGGGACGGGACATGGGCTTTTTAAATGGGCCCTTGAGAGTTTGAACAGTTTCAGTATCTTCGTTATTGGGCCAATCGGCC**CAATAA**TTAAGAGAACGTGTTCAAAA
TTCGTGGTATGACCGAAGGTCAAGGTAAACCGGTCAACATTATTTCTGGCTTGGCGAGCAAGCTACACGAATTAATATTAATTCGTAGGACACGTGGACGGACCGGAATACTCCTGCATC
TCATATAATACCCCTAGTCTTGTAAGGATAA**TGCTCTCTCTCTCTCTGTCAA**GGTGGTTGTGCTGAGGCGGAAGATCGCCAGCGCGGATCGTCGGAACGATGTCATCTAGAGAGCGGT
GAAGCAAACACGAAGCATATATCGGGTATTTATAGACTTATAGCGGACGTAGAAGTATACACTGTACAGATTATGATTTTGTAAATACGAAGAATTCGTATATGATAT**TAATAAA**
ACACCTGGGTGTTTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAAAATACAGTATACGGAACGTATACTGACAAAGTAATAAATGATAGGCGAAGCATGATTAAACAGGTG
TTTAGGTATAATTAAACATAATTATGAGAAGTAATTATAATACGGAAAAATGAATAAGTATGAGGTGAAAGAGGAGATATTAGAATATTAAAAACCAATTTATTTTGGAAACGAAT

ACAAACGCGTATGAAATACAAGACGCTATGAAATACGGGTATCTGATTGTTTATCTTAACGCTTAAGGGCCGACGGCTCAGTGTGATTAACCGGTCGAGATTAAATTCCTTAGCGA
CGAAGAAAGGAATCTTAATGGGGTAAACATTAAGACAGCTGTCTGATTAAATAATAATATAATACAAAGACCTTATGTACCCCTGATTAATGACGTGTGACGTGTGAGCGGTGTCCCGAT
GTAAATATAGCATAGCTATGTGTAAGAGATAAGCATGTGGCCGACAACCTTTAGTTGTGGGCCAGATGTCCGCGATTGTGCGCCGATGATGAAGCAgGGGGACTAT

>U3_al_yu15

TATTACCCCCCGTCTGGGACGGGACATCGCTTTTAAATGGGCGCTGAGAGTTTGAACAGTTCAGTATCTCTGGTTATGGGCGCACTCGGCGCAATTAATTAAGAGAAGCTGTTCAAA
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CTATAAATAACCTCATCTGTGTGAAGATAATTTGCTGCTCTCTCTCTGCTGACGGTGTGTCGGAGGCGGAAGATCCGACCGGCGCATCTCGTGGAAACGATGTGCATCTAGAGAGCGGT
GAGGAATATACGACGAATATATCTCGGTATTTATAGACTTATAGCCGACAGTAAGATACACTTCACAGTTTGTATTTTGAATATACGAAGAATTCGTATATGATTAATTAATTA
ACACCTGGGTCTTTAATGTTTACATTAATAGTATCCTGAATGCACAAATAAAATACAGTATACGGAACTGATACTGACAAAGTATAAATGATAGCGGAAGCATGATTAACAGGTGT
TTAGGTATTAATAACATAAATTTAGGAAGATTAATAATACGAAATAATGAATAGTATGAGTGAAGAGGAGATATAGAATATTTAAACCCCAATATATATTTTTCGACGAATAA
CAACACGATTAATAACACAGCGCTATGACAAATCCGGTATCTGATTTGTTTAAACCGTTAAAGCGCGCGAGCCGCTCAAGTGAATGAACCGGTGCAGATATTTTGAATCGGAC
GAGAAAGAAATCTTGATGGAGATCACAATTAAGACGCTGTCATTTGTTAAATAAATAATATAATACAAAGAGCTATGTCAACCTGATAATGATGAGCTGTAGGGGTGTCGCCGAT
TAATATAGCATGACTATGTGAAGATAAGCATGTGGCGCAACCTTGGTTGTGGCCAGATGTCCCGAGTTAGTGGCCCACTGACCAACGAGGGGGCATG

>U3_al_yu16

TATTACACCCCCTGCTCTGGCAGGAGGACATCGCTTTTAAATGGGGCTTGAGAGTTTGAACAGTTCAGTATCTCTGGTTATGGGCCCACTCGGGCCGTAATTAATTAAGAGAACGCTTCTCAAATCTCTGGTGTATGACCAAGGTCAGGATTAACGGTCAACATTAATCTCTGGCTCTGCGCAGCAAGATACAGCAATAAATTAATTAATCTCTAGGACAGCTGAGGACCAACGAAATCTCTGCATCTCTATAATAATCCCTAGTCTCTGACGGATTAATGTCGCTCTCTCTCTCTCTGTCGCAAGGTGGTGTCTCTGAGGCCGAAGATCCGGACCGCGCATCTGTGCGGAACGATGTGCATCTAGAGAGCGGGGAGCAACGATACGGAACATATATCAAGGTAATTTATAGACTTATAGCCGAGCTAGAAGTACACTCTACAGATTTTGTATTTTGTAAATACAGAAGATTTTCGTATATGATATTAATATGACACCTCGGGTGTGTAATGTTTACATTAATAGTCTGTAAGTTGTACACATAAATAACGATACGATACGCTGATTAATGCAAAAGTAATAATGATAGGCGAAGCATGATTAACAGSGTGTAGGTTATTAATAACATTAATATGAGAAGTAATAATAATACGAAATAAATAAGTATGAGGTGAAGAGGAGATATAGGAATATTTAAACCAATTAATATATTTTGGCAAGCAAAATACAAACGCTTATGAATAACAGACGCTATGACAAATCTACGGGTATCTGTTGTATCTGAAGCTCTAAGGCGCGGACGGCCGTCAGTGTGAATCAAGCTGCGAGTAAATCTCTTAGCGCATGAAGAAAGGAATCTTAATGGAGCCCATTAATAAGACAGCTGTATTGATTAAATAATAATAATAATCTCAAAGAGACTTATGTACCTCGCTGATAATTTGTTCAGCTGTGAGGGGTGTCGCCGATGTAATATAGCATAGCTATGTGGAAGATAGACTGTGGCCGCAACTTTTAGTGTGGGCCAGATGCTCCGAGTATGTGCGCCAGCTAAGCAACGGGGACATAT

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>U3 alyu17 v1
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CLUSTAL multiple sequence alignment by MUSCLE (3.8)

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U3_aluyl22 GATACACGAATTAATTTATTAATTCGTAGCACACGTGGACGGACCGAAATACTCCTGCAAT
U3_aluyl41 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl53 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl50 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl47 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl49 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl51 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl48_v1 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl48_v2 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl42_3 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl43_v2 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl44_45 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl55 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl26 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl54_v1 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT
U3_aluyl54_v2 GCACCAAGAATTAATTTATTAATTCGTATGACACGTGGACGGACCGAAATACTCCTGTAT

U3_alyu32 GTGTTGAGCGGAAGATCGCCATCGCGATCATCAG-ACGAAAAGCTGCAAGAGAGACGG
*** ***** ** * *****

Stop codon PIO

U3_alyu14 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu15 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu19 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_jgf1_v1 TGAAGCAAACTACGAAGCGTATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_jgf1_v2 TGAAGCAAACTACGAAGCGTATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu17_v1 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu17_v2 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu21_v1 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu21_v2 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu18 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu24 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu16 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu22 TGAAGCAAACTACGAAGCATATATCGGGTATTTATAGACTTATAGCGCAGCTAGAAGTAT
U3_alyu41 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu53 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTT
U3_alyu50 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu47 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu49 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu51 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu48_v2 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu48_v1 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu42_43 AGAATCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu43_v2 AGAATCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu44_45 AGAATCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu55 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu26 ATAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu54_v1 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTT
U3_alyu54_v1 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTT
U3_alyu35 AGAACCATGCCACGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu34_v2 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu56 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu25 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTT
U3_alyu36 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu34_v1 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu39 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu37 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu33 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu40 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu29 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
U3_alyu32 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCGCAGCTAGAAGTTT
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U3_alyu14 ACACTGTAC-AGATTTTGTATTTTGTA--AATACGAAGAATTCGTATA-TGATATTA
U3_alyu15 ACACTGTAC-AGATTTTGTATTTTGTA--AATACGAAGAATTCGTATA-TGATATTA
U3_alyu19 ATACTGTAC-AGATTTTGTATTTTGTA--AAT-TACGAAGAATACTGTATA-TGATATTA
U3_jgf1_v1 ACACTGTAC-AGATTATGTATTTTGTA--AAT-TACGAAGAATTCGTATA-TGATATTA
U3_jgf1_v2 ACACTGTAC-AGATTATGTATTTTGTA--AAT-TACGAAGAATTCGTATA-TGATATTA
U3_alyu17_v1 ACACTGTAC-AGATTTTGTATTTTGTA--AAT-TACGAAGAATACTGTATA-TGATATTA
U3_alyu17_v2 ACACTGTAC-AGATTATGTATTTTGTA--AAT-TACGAAGAATACTGTATA-TGATATTA
U3_alyu21_v1 ACACTGTAC-AGATTTTGTATTTTGTA--AAT-TACGAAGAATTCGTATA-TGATATTA
U3_alyu21_v2 ACACTGTAC-AGATTTTGTATTTTGTA--AAT-TACGAAGAATTCGTATA-TGATATTA
U3_alyu18 ACACTGTAC-AGATATTGTATTTTGTAATT-TACGAAGAATTCGTATA-TGATATTA
U3_alyu24 ACACTGTAC-AGATTTTGTATTTTGTA--CAT-TACGAAGAATTCGTATA-TGATATTA
U3_alyu16 ACACTGTAC-AGATTTTGTATTTTGTA--AAT-TACGAAGAATTCGTATA-TGATATTA
U3_alyu22 ACACTGTAC-AGATTTTGTATTTTGTA--AAT-TACGAAGAATTCGTATA-TGATATTA
U3_alyu41 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAATTCGTACATTGATAATA
U3_alyu53 AC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAATTCGTAT--TGATAATA
U3_alyu50 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAATTCGTACATTGATAATA
U3_alyu47 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAATTCGTACATTGATAATA
U3_alyu49 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAATTCGTACATTGATAATA
U3_alyu51 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAATTCGTACATTGATAATA
U3_alyu48_v2 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAATTCGTACATTGATAATA
U3_alyu48_v1 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAATTCGTACATTGATAATA
U3_alyu42_43 CG-TTGATTTGATATTGTATTTTGTA--AAT-TACGAAGAAATTCGTACATTGATAATA
U3_alyu43_v2 CT-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTACATTGATAATA
U3_alyu44_45 CG-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTACATTGATAATA
U3_alyu55 CC-TTGACTTGTATTTGTATTTTGTA--AAG-TACGAAGAAATTCGTATATTGATAATA
U3_alyu26 CC-TTGATTTGATATTGTATTTTGTA--AAT-TACGAAGAAATTCGTACATTGATAATA
U3_alyu54_v1 TC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTACATTGATAATA
U3_alyu54_v1 TC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTACATTGATAATA
U3_alyu35 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu34_v2 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu56 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu25 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu36 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu34_v1 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu39 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu37 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu33 CC-CTGTACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTACATTGATAATA
U3_alyu40 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTACATTGATAATA
U3_alyu29 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTACATTGATAATA
U3_alyu32 CC-TTGACTTGTATTTGTATTTTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
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Poly(A) signal PIO (mapped by Bentham et al. 1999 and Guyot et al. 2022)

U3_alyu14 ATAAACACCTGGGTGTTTTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAA
U3_alyu15 ATAAACACCTGGGT-GTTTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAA
U3_alyu19 ATAAACACCTGGGT-GTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAA
U3_jgf1_v1 ATAAACACCTGGGT-GTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAA
U3_jgf1_v2 ATAAACACCTGGGT-GTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAA
U3_alyu17_v1 ATAAACACCTGGGT-GTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAA
U3_alyu17_v2 ATAAACACCTGGGT-GTGTTAATGTTTACATTAAATAGTATCCTGAATGTACACAATAA
U3_alyu21_v1 ATAAACACCTGGGT-GTGTTAATGTTTACATTAAATTTGTATCCTGAATGTACACAATAA

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GAAGTATGAGGTGAATGAGGAGATAT TAGAATAT AAAAACCCTATATATATAT A
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[illegible]

U3_alyu24	ATAAGCATGTGGCCGACAACTTTAGTGGTGGGCCAGATGTCCCAGTTAGTGCGCC----
U3_alyu16	ATAAGCATGTGGCCGACAACTTTAGTGGTGGGCCAGATGTCCCAGTTAGTGCGCC----
U3_alyu22	ATAAGCATGTGGCCGACAACTTTAGTGGTGGGCCAGATGTCCCAGTTAGTGCGCC----
U3_alyu41	ATA-----GTGGACGTTGGATTCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu53	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu50	ATA-----GTGGACGTTGGATTCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu47	ATA-----GTGGACGTTGGATTCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu49	ATA-----GTGGACGTTGGATTCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu51	ATA-----GTGGACGTTGGATTCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu48_v2	ATA-----GTGGACGTTGGATTCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu48_v1	ATA-----GTGGACGTTGGATTCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu42_43	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu43_v2	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu44_45	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu55	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu26	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu54_v1	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu54_v1	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu35	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu34_v2	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu56	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu25	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu36	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu34_v1	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu39	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu37	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu33	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu40	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu29	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
U3_alyu32	ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCAATG
	*** *** * * * * *
U3_alyu14	---ACGTAAAGCACGGGGGACTAT
U3_alyu15	---ACGTAAAGCACGGGGGACTAT
U3_alyu19	---ACGTAAAGCGCTGGGGCTTAT
U3_jgf1_v1	---ACGTAAAGCACGGGGGACTAT
U3_jgf1_v2	---ACGTAAAGCACGGGGGACTAT
U3_alyu17_v1	---ACGTAAAGCGCTGGGGCTTAT
U3_alyu17_v2	---ACGTAAAGCACGGGGGACTAT
U3_alyu21_v1	---ACGTAAAGCGCTGGGGACTAT
U3_alyu21_v2	---ACGTAAAGCACGGGGGACTAT
U3_alyu18	---ACGTAAAGCACGGGGGACTAT
U3_alyu24	---ACGTAAAGCACGGGGGACTAT
U3_alyu16	---ACGTAAAGCACGGGGGACTAT
U3_alyu22	---ACGTAAAGCACGGGGGACTAT
U3_alyu41	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu53	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu50	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu47	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu49	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu51	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu48_v2	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu48_v1	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu42_43	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu43_v2	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu44_45	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu55	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu26	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu54_v1	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu54_v1	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu35	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu34_v2	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu56	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu25	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu36	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu34_v1	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu39	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu37	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu33	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu40	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu29	ATGACGTAGGGGCTGGGGCTTAT
U3_alyu32	ATGACGTAGGGGCTGGGGCTTAT
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