

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

TATTACCCGACCTGGCTCAGTGGCTCAGTATAAAAGGGGGAGATGTCyCaGCAGCGAAATTTGGGTATTACGCGTAACCTTCCGGCGACCTGCCGATTTTAAAGTTCCGGCGGAGAACTCAATACCGGTTGGCAACATGAGAGGAAGAAATCAGCACCATTCTCAGGGAGTGATCAATTGAAGAAGAAGCTCCGGATGACCGAGTGAAGCGTTAAATGGGGAAATCCACACCTCGAAGCCATGAGAGGAACAATCGCAAGCAATAAGGTACCTGACGAAAGAGAGACACGATGACAGTCCGTGGGAATTCGGAGAATTACTCGAAAGGGATCTCATAAGAGGAAATGATGGAATTCGACGATCCAGATAACGAATAATGGAACCTCAAAAATATCGACGCGCCATTACTAAACAAGCAATGGACCGCTCAAAGAAGAGCGGAATTAGGGTTTCCTACGACTTAAAGGAGTGGCAAAAGATGTTTATTGATTAATCGAAGAACAACCCGACAACAGAACTATTATCTGGGTGATGGACCTAATGGTGGAGAAGGTAAACCGCAGTTCGCAAAAGATTA TGGATTACTCAAGGATGACATATCTCAGCGTGTGAACGAAAGACATGATGATCTGTGGCAAAAGAAATTAACAATAACGTTAATTTGATTTCCCCCGATGTACAAGGATTCATATCTCTAATAGTTTATTGAGTGGTAAAGAACCGATGCATATTTAGTTATAAATATGAACCAATCGGGCGATTGTAAGTAATGAAGTCAATGTAATTTGTAATGTCGAATGAGCTTCAGATTATTCAAAATATCGGAAGACAGAATAAAAATTAATATTTGCATAGCCACACTATGACAAAAGGGCAAAAATGCAAAATCGGGGTTGATTTGCTATATTTACGATTAAAGGCCG AAGGCCGTACACATTTGGCGGGAAATCAAATCGGAAGCCAAATATTTATAATACAATACACCGCTTTTAGAAATCCGTGGACGAGAAGATGCCAGTAGCAAAACACTGTACTCTTGGCTCCTATAAATACCTGAGCCAGGTCCGGCATG

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

TATTACCCGACCTGGCTCAGTGGCTCAGTATAAAAGGGGGAGATGTCyCaGCAGCGAAATTTGGGTATTACGCGTAACCTTCCGGCGACCGAGCGATTTTAAAGTTCCGGCGGAGAACTCAATACCGGTTGGTAAATGATGATGAAGATCAGCACCATTCTCAGGGAGTGAATCAATTGAAGAAGAAGCTCCGGATGACCGCAGTGAAGACGGAAATTTGGGGAAATCCACTCTCCGGAAGCCATGAGAGGAAGAATCAGCACCATTCTCAGGGAGTGAATCAATTGAAGAAGAAGCTCCGAATGAACCGCAGTGAAGGTGAATTTGGGGTATCCCAATAAATAAATATAAATGATAGATAAATAATCAGACGAGTATAGCTGTATAAATAAAGAATATACATAAACAACAAAAAATAAAGTGAACATAATCTCGATTGACATATCTCAGCGTGGTGAACGAAAGCCCTGATGATCTGTGGTAAAGAAATTAATAAATGTAATCATTGATTTCCCCCGATGTACAGAGGATTTCCATATCTCTAATAGTTTATTTGGATGGTAAAGAGTGGCAAAAGATGTTTATTGATTAATAAATGAAATCAATCTCCGGCATCTGAAGTAATGAAATCCATGTAATTTGTAATGTTCAACCGAGCTCCAGATTAATCAAAAAATTTCCGGAAGACATAAATAAATTTAGTAAACATAATGCACACTATGACAAAAGGCCACTAGTTGCTGTGTAACAGCTATGCAATCGTACGTTACGACAGATGGCAAAAATGTAATAATCGCAACTATGACAAAAGGGCAAAAATGCAAAATCGGGGTTGATTTGCTATATTTACGATTAAAGGCCGAGGCGGTACACATTCGGCGGGAAATCAAATCGGACGCAAAAATTTATTAATAACAATACACCGCTTTTAGAAATCCGTGGACGAGAAGATGCCAGTAGCAAAACACTGTACTCTTGGCTCCTATAAATACCTGAGCCAGGTCCGGCATG

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

TATTACCCACCTCCGGCGACCCACTCCGGCGACCTATAAAAATGTCGCTCTCGTGGACATTTACGCTTCATTATTCGACGCAACCGGAGCGAGGCAAAATTCCTCGCGACTTTGAAGGAGAGATGTCGACTACGCGCTCGTCCGGCAGCAAACTGCTCCGAATACTGGTTCGAAAACATCTCAAGGATATCTTCTTGAAGAAACGTTTTCGTTATAGCGGAATAAAGAGAAATA TCTGTCGAGAGCGGATTTGGAGAAGCTCGAGGATCAGACTACGCAACAAGGCGTACTGTTTCAAGAAGCCCTAATCTTGAATTTAGGGGTTCTTCCCAACAGGTTTCGAATAGGCTAAATTAGCAGATATGGTTACAAGATCGCCGCAACGAATGAAAATTTGAACCGCAGAGATATTTCCAGGATACGAATTCGGTGAAGAAGATGAAGAATTCAAAGAAAGGATGATGTTATCC TATCCTCGATAGGCCATGGCAGGTACAATTAACGGAGTTAATGAAGCAGAACCTGATGATCGAAGCATCATCTGGGTATTCGGCAAAAAGGGAATGAAGGCAAAATCAACGTCACGCAAGCATTAATTAACAAAGGATTTGGTTCTACACCGGGGAGAAAGAGGAGCAACTACTGTTCCGCTACGATGATGAAGGTTCGACAAAACCGTTGATTTGATTTCTCCGCTACAGTACA AGAATTTAATAATGATGTTTATCGAACACTGAAGCAGTACGATTAATCGAGTACAAAATACACCGCTCTGAAGTATTTAGAAATGAATACTGATACATGTAATCTATCGCTAATTTCTTCTGATATGTTAAAATCTGAAGATCGAATAAAAATAGTTGCTTGGTGAACACGCTATGAAATCAACACCGCTATGACAAAAGGGGAAATGAAGAATCGGGGTTGATTTGGTCTTCTAACGATTAAGGGCCGAGGCGGTCAAGATGGATCCAATAACCCGATAAGAAGTTAAACGGGTTTAAAAGATTTCTGCCCGCAAGCAACACTTTAACTCTGGCGACCT ATATAAGCGGAGGTGGGCTAG

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

TATTACCCACCTCCGGCGACCCACTCCGGCGACCTATAAAAAGGATTTGTCGATGAAAATTTGCGCTTCATCATTCGACGCAACCGGAGCGAGGCATATTCCTCGCGACTTCGAAGGAGAGATGTCGACTACGCGCTCGTCCGGCAGCAAACTGCTCCGACCACTGGTTCGAAAACATCTCAAGGATATCTTCTTGAAGACCGGATCAGATTACGACAAACAGGGCGTTCTGCTCCAANGAACCTAATCTTGAATTTAGGGGTTCTTCCCAACAGGTTTCGAATAGGCTAAATTAGCAGATATGGTTACAAGATCGCCGCAACGAATGAAAATTTGAACCGCAGAGATATTTCCAGGATACGAATTCGGTGAAGAAGATGAAGAATTCAAAGAAAGGATGATGTTATCC TATCCTCGATAGGCCATGGCAGGTACAATTAACGGAGTTAATGAAGCAGAACCTGATGATCGAAGCATCATCTGGGTATTCGGCAAAAAGGGAATGAAGGCAAAATCAACGTCACGCAAGCATTAATTAACAAAGGATTTGGTTCTACACCGGGGAGAAAGAGGAGCAACTACTGTTCCGCTACGATGATGAAGGTTCGACAAAACCGTTGATTTGATTTCTCCGCTACAGTACAAG AATTTAATAATGATGTTTATCGAACACTGAAGCAGTACGATTAATCGAGTACAAAATACACCGCTCTGAAGTATTTAGAAATGAATACTGATACATGTAATCTATCGCTAATTTCTTCTGATATGTTAAAATCTGAAGATCGAATAAAAATAGTTGCTTGGTGAACACGCTATGAAATCAACACCGCTATGACAAAAGGGGAAATGAAGAATCGGGGTTGATTTGGTCTTCTAACGATTAAGGGCCGAGGCGGTAAAGATGGATGCCGATAAAGGATCCGAT AACCTAATAAGCGTGTGAACCGGTTTAAAACGATTTGCTTCCGGCAGCAACAACTTTAACTCTGGCGACTATATATAGCGGAGGTGGGCTAG

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

TATTACCCGCTTCTCCGCCCTCTCTCCGCCCGATGCAAAAGCAGTATGTCCTCTTAAATGTTGCTTCCAGCTGAATTAATCAACCGCAACAGAGAGAGAAGCACTTTCTCTCTCTTTTGAAGGAGGAGGACCTCGCTACGAGTGGGAGACGAAGTCCGCCCTCAACTGGACAGAACCACTCAGGGATATATATCCCTAAGGAAGATGATGAACTGGGTGGTTGAA GAAAAAATACTCAGCGAAGGCACACTGGGAGAGGGCAAGGATCAGATGAAGATAATAACAAGTATTGTTCTAAGGAACCCCTAATCTAGAATTTAGGGGTTCTACATCCAGGGGTTCAAACAGCGTAAGCTTTCAGAGATGGTTACTAGATCACCAGCAACGATGAGGATAGAACAGCCAGAGATATATACAGATATCAATCTGTAATAGTTAAAACATATTAAGAGGAAATCGTTCACTCTCGCTCGATGCAAGCTTGGCAGATACAAATGACCGAGGCAATTTGAAGAGCAACCGATGATCGAAGCATCATCTGGGTTCTATGGCAAGGCAATGGAAGGAAATCAAC ATATGGCAAGTCTGATAAAAACATGATTTGTTCTATACAAGGGGAGGCAAGAGGAGAACTACTGTTCTCTACGACGCAAGGCACTCAAGGATGTTGTTGTCGACATACCAAG ATGTCATCAAGAAATCTAAATATGATGATTAATCGAGGCAATGAAGGATAGGGTGTCTGAGAGCACTAAGTATAAGCCGATTAATAAATAATCGAGTTGAATAGGGTACATGTAATGTAAT GCCTACTCTATGCCAGACTACTGATGATCTCTGAGGATCGAATAAATTAATATTTGCATACGCCCACTATGACAAAAGGGCAAAAATGCAAAATCGGGGTTGATTTGGGCTATCCT ACCGATTAAGGGCCGAGGCGGTTAAGATGAATAAATCAAACCCGTTAAACCCGTTATCCGATTACTTCCGGCAGGAGGATCACTTTAAGTTCTCCGCCCTATATATAGTTTGGCC 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

TATTACCCCGACCCAGGACGGGACATGGGCTTTTAAATGGGCCGAGAGAGTTTGAACAGTTTCTTCGTTATTGGCCATCTGGCCCAATAATTAAGAGAACGGTTCAAAA
TCTGGGTGACCCGAAGGTCAGGTAGACGGTCAACAATTTCTGGCTTGGGAGCAAGCAACGAATTAATATCTAATTCGTAGACACGTGGACGGACCGAAATACTCCTGTATCT
CTATAAATAGCTTAATCTGGCTGGATAATTAATCTCTGCTCTCTGTCARAGCTGTGTGTGAGGGGAGATCGCCATCGGCGATCATCAGACGAAAGCTGCAAGAGAGCGGAGA
ACCATGCTCGGAAGCGTATATCCGGTATTATAGACTTCTAGCCGAGCTAGAAGTTTCTCTGACTTGTATTTGTAATCAGAAAGAAATTCGTACATTGATAATAA
ATCTGGGATGTTAATGTTTACATTAAACAGTATTAATAATGTACAATAACAAATATTGTATGAGGAACGAATACAAATAATTAATAATGAGGACCGTAGCGTGATAAACAGGTGTT
AAGGTATAATTAATAATGCAATGTCATGATAATACGGTAAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATTAATAACCAATTAATATTATTAATACATACAA
ACGCTATGACAAAAGGGGAAAAAAGAAAAATCGGGGTTGATTGGTCTATCCTAACGATTAAGGGCCGAGGCCCGTCAAGATGGATGAACGGTTAGATTGATTGCTTAGCCAGGA
AAGGAATCTTTGTGGGACACAGACAGACAGCTGTACTACTTTTAAATAATAATAAACCATGGACGATACTACCCTCCCAAGATGACGTATAGGGGTGCCGAGGTAAT
TAACATAGCTCTGACAAGAGATAGTGGACGTTGGATGCCAGATCGGACGATCTGTGTTTATGAACTAATGATGACGTAGGGGTGGGGCTTAT

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. **BBTA5** *alyu32* - new alphasatellite named here Banana bunchy top alphasatellite 5, genus *Banaphisatellite*
3. **BBTA2** *alyu32* - Banana bunchy top alphasatellite 2, genus *Muscarsatellite*
4. **Babu2def** *alyu32* 164 nt circle (CR-SL)

BBTA5

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

>BBTA5_alyu32

TATTACCGACCTTGGCTCACTGGCTACTATAAAGGGGAAATGTCGACGAGCAAAATGGGTATTACGCGTAACTTCTCCGCGACCCCGGATTTTAAAGTTCGCGGAGAAAC
TCAATACCGGCTGGCAACATGAGAAGAAGAAATCACGACCATCTTCAGGAGTGATTCAATTGAAGAAGAAGCTCCGGATGACCGAGTGAAGACGTTAATGGGGAAATCCACACCT
CGAAGCCATGAGAGGAAACAATCGACGAAGCAATAAAGTACGTGACGAAAGAGAGACCGAGTAGCAGGTCCGTGGGAATTCGGAGAAATTAACGAAAAGGATCTCATAAGAGGAAAT
GATGGAAATGCTCGACGATCCAGATAACGAAATTAATGGAACCTCAAAAATATCGACGCGCCATTACTAAACAGCAATGGACCGCTCAAAGAAAGAGGCGGAAATAGGGTTTCCTACGA
CTAAAGGAGTGGCAAAAGATGGTTATTGAGTTAATCGAAGAACCAACAGACACGAACTATTCTGGTCTATGGACCTAATGGTGGAGAAGTTAAACCGCAGTTCGCAAGCATT
TGGATTACTCAAAGATGACATATCTCCAGGTGGTGAACGAAAGACATGATGATCTGTGGCAAAAGAAATTAATAAATACGTTATTATTGATTTCGCCGATGTACAAGGATT
CATATCCTATAAGTTTATGAGATGGTAAAGAACCGATGCATATTAGTTATAAATATGAACCAATCGGGCGATTGTAAGTAATGAAGTCCATGTAATGTAATGTCGAATGAGCTCC
AGATTATTCAAAAATTTCCGAAAGACAGAAATAAATAAATTTATGTCATAACGCACACTATGACAAAAGGGCAAAAATGCAAAATCGGGGGTTGATTGTCATATTACGAATAAGGGCG
CAGGCCGTCACAAATTCGCGGGGAAATTCAAATTCGGAAGCCAAATATTATTAATAACAATACACCGCTTTTAGAAATCCGTGGACGAGAAGATGCCAGTAGCAAAACACTGTACTCC
TTGGCTCACTATAAATACCTGAGCCAAAGTTCGGGCATG

BBTA2

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*

>BBTA2_alyu32

TATTACCCACCTTCGCGCACACCTTCGCGCACCTATAAATGTCGCTCTCGCTGGACATTTACGCTTCAATTTCCGACGCAACGAGGAGCGGCAAAATTCCTCGGACTTTGAAGGA
GGAAGATGTGCACTACGCGCTCGTTCGCGCACGAACTGCTCCGAATACAGGTCGAAAACATCTTCAAGGATATCTTTCCTTGAAGAACGTTTTCGTATTAGCGGAATAAAGAAGARATA
TTCGTGAGAGCGGATTTGGGAGAAAGCTCGAGGATCAGATTACGACAACAAGGGCTACTGTTCCAAAGAAAGCCCTAATTTCTTGAATTAGGGTTCTTCCCAACAGGTTCAAGTAAGG
TAAATTAGCAGATATGGTTACAAGATCTCCGGAACGAATGAAAATTTGAACAGCCAGAGATATTTACCAGGATACCAATCGGTGAAGAAGATGAAGAATTTCAAGAAAGGATGTCCTATCC
TAACTTCGATAGGCCATGCGAGGTACAATTAACGAGGATTAATGAAGCAGAACCTGATGATCGAAGCATCTCTGGTATTTCGCAACAAAAGGGAATGAAGGCAATCAACGTATCGCAA
GTCATTAATCCAAAAGGATGGTTTACACAAGGGGAGGAAAGAAAGGAGAACATCTGTCGCTACGTAGATGAAGTTTCGACCAAAAACGTTGTAATTTGATCTTCGCGGTACAGTACA
AGAATTTAATTAATGATGTTATCGAAGCATTGAAGGATAGAGTAATCGAAGTACAAAATACAGCCCTGTAAGTATTAGAAATGAAATCTGTACATGTAATGTTATGGCTAATTT
TCTCCCTGATATGTAATAATCTGAAGATCGAATAAATAATGTTGCTTGTCAACACGCTATGAAATAACAACCGCTATGACAAACGGGGAAAAATGAAGAATCGGGGGTTGATTGGG
CTATCCTAACGATTAACGGCCCGAGCCCGTCAAGATGATCCAATAACCCGATAAGAAGTTAAACGGGTTTAAATGATTTCTTCGCCCGCAAGCAACCTTTAACCTTCGCGCACCT
ATATATACGGAGGTGGGCTAG

Babu2def

Defective derivative of **BBTA2_alyu32 CR-SL** + non-viral DNA

>BBTA2def_alyu32

TATTACCCACCTTCGCGCACACCTTCGCGCACCTGACGTCACACACATACACACACTATGACAAAAGGGCAAAAATCTTTCTATTATAGGACCCCAAAAACACTTTAACCTT
CGCGCACTCCTTCACAACAGCGAGCGCGGAGGGTGGCTAG

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

TATTACCCCGACGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTAAGATGGGTTTTGGGCTTATGGGCTTATCCAGAAGACCAAAAAACAGCGGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCCGCAAGCAAACATAAAGTCTATATACACAGTGTAGACATATGTTTCAGAGAACAATGGCGAGGTATCCGAAGaaATCGATCAA
GAAGGGCGGTTGGCGCAAGGAATATGGAGCAAGCGCGCAACAGTACAGTACTCTGCTGATAGGTTCAATATGGTTCCTGAAAATACCGTCAAGGTATTTAGGATTTGAGCCTAC
GTATAAACCAATTTACCAGATTTTTATCTGGAAATGTTTATGCTTTTGGTGTGCAAGTGTGAAGCGGAAGAATACTTCACTGGCCTATGATTAAGAATCTTGGGAAATCAACACGCC
GACTACATGTCTGGAAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCACTGGGAACTTGAAGCAGGAGTGCACAGGGGACATCAGATGTTGAATG
TCTTCAAGGAAGCAACCGTGTGGAGGAAGATGTAACAGAGGTGGATTAATGTTTGGCATTTTATGATGCTGGAGTGTAGTATTAACACAGGACAGAAATACATATCATGT
ATGATATGTTTATGAAACATAAACCTTTGATGGAAATAGTACCAAAATAACATACAGACCGTATGAAATACAAACACCGTATGACAAAACAGGGAAAAATGAAGAATCGGGGGTGTATTG
GCTATCGTATCGTTAAGGGCCGAGGCGGCTTGAATGATCTTATAAAACAATAATACATGATCGGATAGTGAATATATAAAACAAGATGATATAAATACAAACAGATTTGTTAT
ACTAATTAATAATAGAAAGAAAGAAATTTTGTGAAGGATAAGCATCAGAACCACCACTTTAGTGGTGGGTCATATGTCGGAGTTAGTGCGCCACGTAAGCGCTGGGGCTTAT

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

TATTACCCCGACGCTCGGGACGGGACATGGGCTTTTTAAATGGGCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTTGGGCCATCTGGCCCAATAAATTAAGAGAACGTTGTTCAAAA
TCGGGGTTTGACCGAAGGTCAGGTAGACCGGTCAACAATATTTGGCTTGGCGAGCAAGCAACAAGAAATTAATTTAAATTCATGACACGCTGGACGGCCGAAATACTCCTGTATCT
CTATAAATAGCTAAATCTGGCTGGATAATGTCTCTGCTCTCTCTGTCAAAGTTGTTGTGTTGAGCGGAAAGATCGCCATCGGGCATCATCGGACGAAAAGCTGCAAGAGAGACGGGAGA
ACCATGCTCGAAGCGTATATCGGGTATTTATAGACTCTAGCGCAGCTAGAAGTTTCCCTGTACTTGTATTGTTAAATTCGAAAGAAATTCGTATATTGATAATAATAAAAC
ATCTGGGATTTGTAATGTTTACATTAACAGTATTAATAATGTACAAATAACAATATTTGATGAGGAACGAATACAGAAATATAAAATATGAGGAGCGGTAGCTGATAAACAGGTGTTT
AAGTATAAATAAATAATATGCAAGTAAATGATAAATACCGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATAGAATATAAAACCCAAATATATATTTATAATACATCAAC
ACGCTATGACAAACCGGGAAAAAAGAAAAATCGGGGTTGATTTGGTCTATCCTAACGATTAAGGGCCGAGGCCCTCAAGATGGATGAACGGTTAGATTTGATGCTTAGCCACGAAGA
AAGGATCGTTTTGGGACACAGACAGCAGCTGTCACTACTTTAAAAATAATAATAAACAATTTGACGATAGTACCCCTCCCAAGATGACGTATAGGGGTGCCCGAGGTAAT
TAACATAGCTCTGACAAGAGATAGTGGACCTGGATCCACGATCGGACGATCGTGGTTTGGATGAACCAATGATGACGTAGGGGCTGGGGCTTAT

A6125C (59313/127758) **T/A** (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

TATTACCCCGACGCTCGGGACGGGACATGGGCTTTTTAAATGGGCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTTGGGCCATCTGGCCCAATAAATTAAGAGAACGTTGTTCAAAA
TCGGGGTTTGACCGAAGGTCAGGTAGACCGGTCAACAATATTTGGCTTGGCGAGCAAGCAACAAGAAATTAATTTAAATTCATGACACGCTGGACGGCCGAAATACTCCTGTATCT
CTATAAATAGCTAAATCTGGCTGGATAATGTCTCTGCTCTCTCTGTCAAAGTTGTTGTGTTGAGCGGAAAGATCGCCATCGGGCATCATCGGACGAAAAGCTGCAAGAGAGACGGGAGA
ACCATGCTCGAAGCGTATATCGGGTATTTATAGACTCTAGCGCAGCTAGAAGTTTCCCTGTACTTGTATTGTTAAATTCGAAAGAAATTCGTATATTGATAATAATAAAAC
ATCTGGGATTTGTAATGTTTACATTAACAGTATTAATAATGTACAAATAACAATATTTGATGAGGAACGAATACAGAAATATAAAATATGAGGAGCGGTAGCTGATAAACAGGTGTTT
AGTATAAATAAATAAATATGCAAGTAAATGATAAATACCGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATAGAATATAAAACCCAAATATATATTTATAATACATCAACA
CGCTATGACAAACCGGGAAAAAAGAAAAATCGGGGTTGATTTGGTCTATCCTAACGATTAAGGGCCGAGGCCCTCAAGATGGATGAACGGTTAGATTTGATGCTTAGCCACGAAGA
AAGGATCGTTTTGGGACACAGACAGCAGCTGTCACTACTTTAAAAATAATAATAAACAATTTGACGATAGTACCCCTCCCAAGATGACGTATAGGGGTGCCCGAGGTAAT
AACATAGCTCTGACAAGAGATAGTGGACCTGGATCCACGATCGGACGATCGTGGTTTGGATGAACCAATGATGACGTAGGGGCTGGGGCTTAT

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

TATTACCCGACTTTGGCGAGGGGCACTATAAAGATGCTGTGAGAAATTTGGGCTTCCACAGCAATTCGAAGGGCGAAAGACCAGAGCTCCTGTTGGCGGGCAAACTCAATACGCC
CCTGGCAACATGAAAGCAAAATACAGCAACCCACCTACAGGGCGTATTCAGTTGAAGAAGCAACCCGACTGAACCGCTGAGAGAGCATAATCGGTGGAAATCCACATCGCAACCCATG
CGAGCGCTTTCGACGATGCCATAGCATACGTCATGAAAGACGAAACCCGATTCGATGTTCCATGGGAATTCGGTATTCGAAATCCGTAAGGGTTCGAAATAAACAGAGCTGTTAGAAATA
CTGGAGGATTCGGACAAAGGTCCTTCAACCCCAAAAATACAGACGAGCCATGGCCAAACAGCCATGAGTGAAGTCAAGAAAGGAGCTGCTGAAGAGGATTTAGTTATGAACTGCGA
GAGTGGCAAGTGAAGTTCAGCGCTGTTTGAAGAAAGAACCCGATACAGAAACATATTTGGGATATTTGGACCAAGGGTGGAGAAAGGTAACAGGATTCGCTAAACATTAAGGTTTA
AAGGATGGTTGACATATTTCCCGCGTGGTGAACCTCAAGATATGATGACCTGTTATCAAGAGCATGAAATAAATGTTGTAATGATTTCCCCCGTTGACCAAGGAATTTATTTCA
TATAAATTCCTTGAATGTTAAGAATAGAATATATAGTTAAGTATGAACAGTGGTTCATCGTATGTAATAAGTTCATGATGAGTTCAGTAAATGAGGAGCGAGATTT
GTAAATATCATTTGATGAAATAGGTTGATTTCTTGTGACACGCTATGAAATACAAACACATGAAATACTACACGGGTAGATTTGTTATATTAACGATATTTGGCCGAAGGCC
CAAGCCCAAGCCATGCCCAAAATGACGGTCGAATGATGCTTCCCACGAAGCAACAAAAATGCGTGGTGAAGAAATTCGCCACGTCATTTGTTACTGTTATCTTGGCGCAC
TATATATAGTGGCCCAAATCGCCCATAG

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

TATTACCCCGCTCGGGACGGGACATCAGTGCATCAACAAATGACGTCGACAAAGCAGTACGTTGATGCGAAAGACAAACCATCACTATCACAAGGTGAACGGAATATTCGTTGC
TTAGGACTAAGCAACGAGTACAGATATTTGTTGAGAAAGGAAATGGAGGCTATTTAAACCTGATGTTATTTGATTTCCGAAATCACTCATCGGACGAGAAATGGAGTTCTGGGAAT
CGTCTGCCATGCCAGACGATGTCAGAGAGAGTGAACAGAAATATTTGGGAGCATCGAAATAAATCTCTGTTCTGTCAGAAAGTGAAGGCTGTGAAGAGGATTTGGAGCATGGAA
ATCAAGATGATGCTGAGCAAGTTCAGCGCTGTTTGAAGAAAGAACCCGATACAGAAACATATTTGGGATATTTGGACCAAGGGTGGAGAAAGGTAACAGGATTCGCTAAACATTAAGGTTTA
GGTTAAACCAATGGTGTCTTTATCATGAATATATGAGACCTAGTGGTACTACTCGGTATATCAAGATCTATTCTGTGATGAGGAACTTCTCTATTCATCGACAGAAAGAGAG
ATGAAAGAGTAAATACAGGAATGTTATCATGGCATCGACAGAAAGAAAGTCTCTTGGAGTGAATGTCAAAGATAGTATATCAGATATGATGTAACATCTGTAATGAAATATCA
TTATCATAAATAAATAATGGAATGATGATTTATGATTTCTAGTATATATACATAATGGTATACGATATACGATAAATAACATAAACAACATACACACACTATGACAAACGGGGAAAAAT
GAAGAATCGGGGTTGATTTGGCTATCTTAACGATTAAGGGCCGAGGCCGTTTAAATATGTTGGTGGACGAAGTCCCAACACAAAAAAGTATCAGAACAATGGAATATAATGAGCT
GGCAACGTAGGACCAATGTCGAGTTAGTGGCCACGTTAGCGAGGGGGCTTAT

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

TATTACCCCGCTCGGGACGGGACATCAGTGCATCAACAAATGACGTCGACGATGATATATACTACATACAAACGGTTTAAAGCAACGGTTATATAAGTATAACGATAAGTACGTTG
ATGAGACATGCAAGTGAATGATGAAATGATTTGAATAAATGATTTGACGCTCGGATGCTCCGACGAGGAGCTTAGGTTACTCTGTCGAGGAAAGCAAAATTTATAAATGGCCGATG
GCTGCCATAAATAGGCAAGCAAGAAATGGCATTAAACAACAGAGGAGTAAACTATTTCTTGAATGTTCTGTTCATCGGTGCAATATTTATTCGATACAAATATATATATATTG

TATCGTATCGCTTAAGGGCCGAGGCCGCTTGAATAATAATCGAATTATAAACGTTTGAATAATAATCAGAGATAGATGATAAGCATCCAAAAACATAGACGAAGTATATGGATGTAT
AATAAACAACAGCATATAAATAAATAATGTGAACCTAATCTCTGATTTGGTGCAGAACGTAGCCCCACTAATCTTAAGTTAGTGGAAATGTCCCGATGACGTAAAGCAGCGGGGACTAT

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

TATTACCCCGAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCTCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTGGTATGCTGGATGTTCCACC
ATCAACAATCCCGCTTCACTACCAGTGATCGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGTACTCGTCATGTGCGGGATACGTCGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTCCAGCGCCACACCTTGAGAAACGAAAGGGAAGCCAAAGAAAGACAGGGGCATCTGTATGAAGGAAGACACAAGAAATCGAAGGTCCTCTC
GAGTTGGTGCCTTTAAATTTGCATGTAATGATAATTTTATGATGTCATACAGGATATGCGTGAACGCACAAACGGCCTTTGGAGTATTTATATGAGTGTCCAATACCTTCGATAGA
AGTAAGGATACATATACAGAGTCAAGCAGAGTTGAATAAAACGAAAGGCGATGAATAGCTGGAAGACATCCTCAGTGCATGGACATCGGAAGTTGAAAAATATATGGCGGAGCCATGT
CATCGAAGGATAATTTGGGCTATGGCCCAATGGAGGAGAAGAAAGACAACTATGCAAAAGTATTTAATGAAGACGAAGAATGCGTTTATTTCCAGGAGGAAATCATTTGGATATA
GTAGATTTGATAATACGAGAAATAGTTATATTTGATATTCACAGATGCAAAAGGAAATTTAACTATGTTTATTTAGAAATTTAAAAATGAAATTTTCAAGCGGGAAATAT
GAACCGTTTGAATAATGTGAATATGTCGAAGTCAATGTAATGGCTAATCTTCCGAAAGGAAGTCTTTTCTGAAGTCCGAATAAAGCTAGTTGCTTCTGAACAGCAGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAGCAAGATTCGGGGTGTATGGGCTATCCTAACGATTAAAGGCCGAGCCCTCAAGATGGACGGCTGTATCAGATGTCCCGAGTTAGTG
CGCCAGTAAGCGCTGGGGCTTAT

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

TATTACCCCGAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTAAGATGGGTTTTGGGCTTATGGGCTTATCCAGAAGACAAAAACAGCGGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCCGCAAGCAAACTAAAAGTCTATATAACAGTGTAGACATATTTGTCAGAGAAACAATGGCGAGGTTTTCCGAAGAATCGATCAA
GAAGAGCGGGTTGGCGCAGGAGTATGCAAGCAAGGGCGGCAACTAGTCAGACTACTCGCTGCTAGTTCAATATTTGGTCTGAAAATACCGTCAAGGTATTTAGGATTTAGCCCTCA
TGATAAAGCAATATCCAGATATTTATCTGGAAATGTTTATGCTTTTGGTGTGCAAGTGAACCCGGAAGAATACTTCACTGGGCTATGATTAAGAGTTTCATGGGAAATCAACAGCC
GCTACATGTCGGAAGCAGCTGATTTATTTAATTAACATGAACATGACCTTGGTGAACCTGGTATCGAGTGGGGAATTTGAAGCCGGATCGCAACAGGACATCAGATGTTGATGT
TCTCTAAGGAAGACAACTGTTGAGGAAGAATGTAACAGAGTGGATCTACTTGTATTTGGCAATTTTATTTGATGCTGGAGTGTATTAACACCAAGCAAGAAATACATATCATGT
ATGATATGTTTATGTAACATAAACCATTTGTATGGAATATGACCAAAATACATACAACAGCCTATGAAATACAACAGCCTATGACAAAACAGGAAATGAAGAATCGGGGTTGATTTG
GTCATCGTATCGCTTAAGGGCCGAGGCCGCTTGAATGATCTTTATAAAGCAAAATATACATGATCGGATTTGTTGAAAATATAATCAACGATGATAAATACAACAGAAATGATGTAT
ACTAATTAATAATAATGAGAAGAAAGAAATATTTGTGAAGGATAAGCATCAGAACCACCACTTTAGTGGTGGGCTATATGTCCCGAGTTAGTGGCCACGTAAGCGCTGGGGCTTAT

DNA-U3

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

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

>U3_alyu37

TATTACCCCGAGCGCTCGGGACGGGACATGGGCTTTTTAAATGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTTGGCCATCTGGCCCAATAATTAAGAGAACGTGTTCAAAA
TCGGGTTTGACCGAAGGTTCAAGTGTAGACGGTCAACAATATCTGGCTTGCAGAAAGCAAGCAACCAATTAATTTGATGATGACACGTTGACCGGACCGGAAATACCTCTGTATCT
CTATAAATAGCTTAAATCTGGCTTGGATAATTTGCTCTCGCTCTCTGTCAAAGCTGTTGTTGAGCGGGAAGATCGCCATCGGCGATCATCGGACGAAAGCTGCAAGAGAGACGGGAGA
ACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCCGACGTTGAAGTTTCTGTCCTTGTATTTGTAATTTGTAATTTACGAAAGAAATTCGATATTTGATAATAAATAAAC
ATCTGGGATGCTTAACTGTTACATTAACCACTTAAATATCTCAATAAACAATATTTGATGAGGAAGCAATACAAGAAATTAATAATGAGGACCGTACCGTGAATAACAGGTTT
AAGGTATAATTAATTAATGCAATGTCATGATAATACGTTAAGTTGAAGTATGAGGTGAAGAGGAGATTTAGAATATTAATAACCAATATATTTATTAATACATACAAC
AGCCTATGACAAACGGGGAAAAAGAAAAATCGGGGTTGATTTGGTCTATCTCAACGATTAAAGGCCGAGCCGCTCAAGATGGATGAACCGGTTAGATTGCTGCTAGCCACGAAGA
AAGGAATCGTTTTGGGACCAAGACAGCAGCTGCTATTAATTTAAAAATAATAAATAACCAATGACGATAGTACCCCTCCCAAGATGACGATATAGGGGTGTCGCGAGGTAAT
TAACATAGCTCTGACAAGAGATAGTGGACGTTGGATGGCAGCATCGGACGATCTGGTGTGATGAACCAATGATGACGTAGGGGCTGGGGCTTAT

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

TATTACCCGACTTGGCTCAGTGGCTCACTATAAAGGGGGAAATGTCGCGACGCGAAATTTGGTATTACGCGTAACTTCTCCGGCAGCCGCGGATTTAAAGTTCCCGGAGAGAAAC
TCAATACGGGTCTGGCAACATGAGAAGAAGAAATCAGCACCATCTCAGGGAGTGATTCAATTGAAGAAGAGCTCCGGATGACCGAGTGAAGCGTAAATGGGGAAATCCACACCT
CGAAGCCATGAGAGGAACAATCGACGAAGCAATAAGGTACGTGACGAAGAAGAAACACGAGTACAGGTCCTGGGAATTCGGAGAAATTTACGAAAGGATTCATAAGAGGAAAT
GATGGAATTTGCTCAGCATCCAGATAACGAATAATGGAACCTCAAAAATATCGACGCGCCATTAATAACAAGCAATGGACCGCTCAAAGAAGAGGCGGAATTTAGGTTTCTCTACGA
CTTAAAGGAGTGGCAAAAGATGGTTATTGAGTTAATCGAAGAACAACAGACAGCAAGCAATATTATCTGGGCTATGAGACCTAATGGTGGAGAAGGTAACACGAGTTCGCAAAAGATTA
TGGATTAACAAGGATGGACATATCTACAGGTTGGTGAACCTGAAGACATGATGATCTGTTGGCAAAAGAAATTAATAAATACGTTATTTGATTTCCCGGATGTAACAAGGATTT
CATATCTCTAATAGTTTATTTAGAGTGGTAAAGAACCCGATGATATTTAGCTATAAATGAAACCAATCGGGCGATTTGTAAGTAAATGAAGTCCATGTAATTTGATTTGCAATGAGCTTCC
AGATTATTAATAATTTCCGAAGACGAATAAATAAATTTTACATAACCGCACACTGACAAAAGCGCAAAATGCAAAATCGGGGTTGATTTGCTCTATATTTACGAATAAGGGCCG
CAGGCCGCTACACATTTGGCGGGAAATTCAAATTCGGAAGCCAAATATTTAATAACAATACACCGCCTTTTGAATAATCGGTGGACGAGAAGATGCCACGTGACAAAACACTGTACTCC
TTGGCTCACTATAAATACCTGAGCCAAAGGTCGGGCATG

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

>BBTA6_alyu38

TATTACCCGACTTGGCGCAGGGCGCACTATAAAGATGCTGTGAGAAATTTGGTCTTCAACAGCAATTTGAAAGGCGAAAGACAGAGCTCTGTTCCGGCGGCAAACTCAATACGCC
GCTTGGCAACATGAAAGAAAGATCAGCACCACCTACAGGGTGTGATTCAAGTGAAGAAGAGCCGACTGAACCGAGTGAAGAGCATAATCGGTGGAAATCCACATTCGCAACCCATG
CGAGCGTCTTTCAGCATGCCCTAGCATACGTCATGAAAGACAAACCCGAAATCGATGCTCCATGGGAATTCGGTATTGCAATCCGTCAGGTTTCAATAAAGCAAGGCTGTTAGAAAT
CTGGAGGATTCGGACAACGAGTCTTCAACCCCAAAAATACAGACGAGCCATGGCCAAACAGCCATGAGTGAAGTCAAGAAGAAAGCTGCAAGAAGAGGATTTAGTTATGACTGCGA
GAGTGGCAAGTCAATTTGCAAGGTTGTTGGAAGAAGAACCAGATACAGAAACAATAATTTGGGTATTTGAGGATATGGAAGAAAGGTTGGAAGAAGGTAACACAGAGTTCGCTAAAACATTTAGGGTTA
AAGATGTTTGGACATATTTCCCGGTTGGTGAACCTCAAAGATATGATGACTCTGTTATCAAAGCAATGAAATAATGTTGTAATGATTTCCCGGTTGTAACAAGGAAATTTATTTCA
TATAAATCTTGAAGTGGTTAAGAATGAACTATATATAGTTAAGTAAAGTGAACCACTGGTCTCAATCGTATGTAATAAGGTTCAATGATGTAATAAGGTTCAATGATGTTGCAATGAGCTTCC
GTAAATTTAATGAGTGAATGAAATGAGTTGATTTCTGCTGAAACGCTATGAAATACAACACACTGAAATACTGACGGGATCTGATGTTGTTATCTTAAACGCTATTGGGCGGAG
GCCAAGCCCAAGCCATGCCCAAAATGAACGGTCAAGATGATGCTTCCGACGAAGCAACAAAAATCGGTGGTGGAAATTCGCCACGCTATTGGGTACTGTTATCTTTGGCG
CACTATATATAGTTGCCCAAGTTCGGCCATG

>M_alyu39
TATTACCCCGCGCTCAGGACGGGACATCACGTCGCAACTAACAAATGCACGCTGACTGATATATACTACATAACGGTTTAAACGAAACCGTTATATAATGTTATAACGATAAGTCACGTTG
ATAGAGACATGCACGTGACATAGTCAAAATGTAATGAATAAACATTGACGCTCCGGATGCTCCGACGGAAGCTAGGTTACTTCGGGGCGAAGCAAAACATTTATATATATGGCCAGGACT
cctgcctataaattaggcaagcaaggaatggcattaacacacagcagcagtgaaactattctttgaaatgggttctgttcacgagcaatattttatggcagatacaatatttatatatattg
TTGGCGTTGCTCTTTCAGGTCCTCCCAAGTATATTAAGGATGTTGTGAGGATCTCTGTAGAAATACCTGACCAGAAAGCGGTATGGATGCAGAGAACCGAGTTGACGGAGGCAACAGGAGAT
GTAGAGCTCGGCAGAGTAGTGTGGAAGACAGACGGGATCAACAACCGGCTGTCAACACATGCACACAGGTTATCCCTTCGCATCAACCTAGAAGGGATGAGCAAGGAAGACAGGA
AACGCTGGACCAATGTTTAAATACACAGTATTGTAATATACGAAATATAAATGGATAATGATATGTTGTAACATAATACGTGAAACATAATATATGTTGATAATTTACATATT
TTAATATGTAATTTGATACGAGTGTGTTATTTATAGAACATACAAACCGCTATGACAAACAGGAAAAATGAAGAAATCGGGGTTGATGGTCTATCGTATCGCTTAAGGGCCGAGG
CCGTTGAAATGATCTTATAAACAATATACATGATACGGATAGTTGAATATATAAACACAGTATATAAACAAGAAATGTTGATACCTAATTAATAATGAGAAGATAAGTAT
ATTTGTGAGGATGATGATCAACACCACCTTTAGTGGTGGGTCATATGTCGCGAGTTAGTGCGCCACGTAAGCGCTGGGCTTAT

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

TATTACCCCGCTTGGGACGGGACATGACCTCACCATAGATTATAATGGGCCAACTAAAGGCCCATTTAATAGAATAGCCGGCTTTTGCATATTTCAAAGGCCAGCCTGGAAGT
GGATAATGTCACGTGCTAATAAGAGGTTGCTTCGCTCGAAGCAATCCGAAATAAAGTTGCGTATTCAAATACGCAACTGAAGTCTATTAATATGGATGCTCTGCCGAAATAATCAGAG
CGTATGCGAAGCAGAAAGCGATGGATTGGGCAGAAATCACAAATCAAGACATGTACTCATGTTGGGATGGGAAGACGATATCATCGGATTCACGAAATCGCAAAATATGACCTTCGCT
CGACGCTGGCAGCGGAAGAAAGTCACTCGCAAGGCTACTGCTAAGATCTATTGAAAGCTGTGTTAATGGAAGCTTCAAAGGAAATAACAGGAATGTTTCGTTGGGTTATATACGTATCAAT
ACGAGACGATGATGGAGAAATGCGTCCAGTACTATAATACCATTCCGAGGATATGGATATCATAATGATTTCTATTTTCGAAGGAAAGGGGAAAGTTGAATGTGATATATCATCAGA
TATGTAGCGCCAGGAGTGCATGGAGCAGAGACATGGAAGTTAGTATTAGTAACAGCAACAACCTGTAATGAATATGTTGATCTGAAGTGTATGTTGTTGTTGCTGTTAAGAAATAAAGGA
ATAACAGATGTCGTGTAATGATTTAATAAACTTATTTTCATGAAATGATGATTTGATAAAACATACACACGCTATGACAAACAGGAAAAATGAAATAACAGGGGTTGATGGTCT
TATCGTATCGCTTAAGGGCCGAGGCCCTTGAAATAATAATCCGAAATATAAACGTTTGAATATAATCAGAGATAGATGATAAGCATCTTAAACATAGACGAGTATATGGATGAT
AATATAAAACAAGCATATAAATAAATATGTGAATCTCTGATTTGGTGCAGAACGTCAGCCCACTAATTTAAGTTAGTGAAGTATGCCGATGACGTAGCACGGGGGACTAT

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

TATTACCCCGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCTCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTTGATGCTGGATGTTCCAC
ATCAACAATCCCGCTTCACTACAGTGTGCGGGATGAGTTCAAATATATGGTATATAAGTGGAGAGGGGACAGGAGGTTACTCGTCTATGTGACGGGATACGTCGAGATGAAGAGACGA
AGTTCCTCGAAGCAGATGAGAGGCTTCTCCCTGGCGCACACCTTGAGAAACGAAAGGGAAGCGAAGAAAGACAGGGGATCTGTATGAAGGAAGACACAAGAAATCGAAGGTCCTTC
CAGTTTGGTGGCTTAAATGTCATGTAATGATAATTTATTTGATGTCATACAGGATATGCGTGAACCGCAACAGGGCTTTGGAGTATTTATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATATACAGAGTTCAGCAGAGTGAATAAACAAGGCGCATGAATAGCTGAAACATCTCTCAGTCTTGGACATCGGAAGTTGAAATAATATGTCGGGAGCCATG
CATCGAAGCATAATTTGGCTCTATGGCCAAATGGAGGAGAAGGAAAGACAACTATGCAAAATTTAATGAAGACGAAAGAAATGCGCTTTTATCTCCAGGAGGAAATCATTTGATATA
TGATAGTTGTAATACGAGGAAATAGTTATATTTGATATTTCCAGATGCAAAAGGAAATATTTAACTATGTTTACTAGAGAATTTAAAAATGGAATTTTCAAAGCGGGAATAT
GAAACCGTTTGAATAATGAGAATATGTTGAAGTCAATGTAATGGTCACTCTCCCTCGAAGGAGGAAATCTTTTCAGAAATCGAATAAAGCTAGTGTGCTGTAACAGCTATGAC
AATCGTACGCTATGACAAAGGGGAAAAAGCAAAGATTCGGGGTTGATGTCATCTTAACGATTAAGGGCCGAGGCCCTCAAGATGGACGGCTTGATGAGATGTCGCGAGTTAGT
CGCCACGTAAGCGCTGGGCTTAT

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

TATTACCCCGCGCTCGGGACGGGACATGGGCTTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTAAGATGGGTTTGGGCTTATGGGCTTATCCAGAAGACAAAAACAGCGGG
GAAACCGTCCCAATTTCAAATTTAGATAGCTTGGCCCGAAGCAAACTAAAAGTCTATATACACAGTGTAGACATATGTTTCAGAGAACAATGGCGAGGTTCCGAAAGAAATCGATCAA
GAAGAGCGGGTTGGCGACCGAAGTATGGAAAGCAAGGGCCGCAACAGTCAAGCTACTCTCGTTCGTTAGGTTCAATATGGTTCCTGAAATAACCGCTCAAGTATTTAGGATTTAGCCCTAC
TGATAAAAACATTTCCAGATTTTATCTGGAATAATGTTATGCTTTTGGTGCAAGTGAAGCCCGGAGAAATCTCTCAGTGGCTATGATTAAGATTTCTGGAAGTCAACAGCC
GACTACATGCTGGAAGCAGCAAGTTTATTTAATTAACCTGAACATAGCCATCTGGTGAAGTGGTATGCACTGGGAACTTGAAGCCGGAGTCCGACAGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACAAACCGTGTGAGGAAGAATTAACAGAGGTTGATTTGATTTGGCATTATTTGATGCTGGAGTTAGTATTAACACAGACAGAAATACATATCATGT
ATGATATGTTTATGTAACATAAACCTTTGATGGAATAATGACCAAAATACATACAAACACACTATGAAATACAAACAGCTATGACAAACAGGAAAAATGAAGAAATCGGGGTTGATTTG
CTTATCGTATCGCTTAAGGGCCGAGGCCCTGAAATGATTTCTTAATAAAACAAATATACATGATACCGGATAGTTGAATATATAAAACAACATGTATAAATACACAGATTTGAT
ACCAATTAATAAATGAGAAGAAAAAATATTTGTGAAGATAAGCATCAGAACCACCACTTTAGTGGTGGGTCATATGTCGCGAGTTAGTGCGCCACGTAAGCGCTGGGCTTAT

DNA-U3

42-46 SNPs to KY427065 MF039869 (Thailand)

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

>U3_alyu39

TATTACCCCGCGCTCGGGACGGGACATGGGCTTTTAAATGGCCGAGAGAGTTGAACAGTTCAGTATCTTCCGTTATTTGGCCATCGGCCCAATAAATAAGAGAAGCTGTTCAA
TCGGGTTTGACCGAAGTCAAGTGTAGACGTTCAACAATATTTCTGGCTTGGCGAGCAAGCAACAGCAATTAATATTTAATTCGATGACACGTTGGACGGACCGAAATCTCTGTA
CTATAAATAGCTTAAATCTGGCTGGATAATTTGCTCTGCTCTCTGTCARAAAGCTGTTGTTGAGGGCGAAGATCGCCATCGCGCATCTCGACGAAAGCTGCAAGAGAGACGGAGA
ACCATGCTACGAAGCTATATCGGGTATTTATAGACTCTAGCGCAGCTAGAAGTTTCTTGTACTTGATATTTGTAATTTACGAAGAAATTCGATATTTGATAATAATAAAC
ATCTGGGATTTGTAATGTTTACATTAACATAGTATTAATAATGTAACAATAAATATGATGAGGAAGCAATACAAATAAATAAATATGAGGAGCGTAGCGTGATAAACAGTGTGTT
AAGGTATAAATAAATTAATGCAATGTCCTGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATTTAGAATAAATAAACAACCAATTTATTTATTAATACATACAA
ACGCTATGACAAACGGGAAAAAAGAAAAATCGGGGTTGATTTGGTCTATCCTAACGATTAAGGGCCGAGGCCCTCAAGATGATGACCGGTTAGATTTGATTTGCTAGCCACGAAGA
AAGGAATCGTTTGGGACCAACAGCAAGACAGCTGTCACTACTTTTAAAAAATAATAAATAAATGACAGATAGTACCCTCCAAAGATGACGTATAGGGGTTGTCGCGAGTAAAT
TAACATAGCTCTGACAGAGATAGTGGACGTTGGATGCCAGCATCGGACGATCGTGGTTGATGAACCAATGATGACGTAGGGCTGGGCTTAT

ALYU-40 - Musa AAA red - Vietnam

Virome

- 1. **BBTV** six components
- 2. **BETA5** alyu40=38

BETA5

Best matches to MF510475 MF510474 33% coverage 66.5% identity Faba bean necrotic yellows virus associated alphasatellite 2
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

>BETA5_alyu40

CATCGAAGGATAATTTGGGCTCTATGGCCCAATGGAGGAGAAGAAAGCAACCTTATGCAAAATTTAATGAAGACGAAGAATCGGTTTTATTCGCCAGGAGGAAAACTTTGGATATA
TGATAGTTGTATAATTTAGAGaaatagTTATATTTGGATATTCACAGATGCAAAAGGAAATTTAAACTATGGTTTTATAGAAGAAATTTAAAAATGGAATTTTCAAAGCGGGAATAT
GAACCCGTTTTGAAATTTAGAAATATGTTGAAGTCAATGTAATGGCTAATCTCCCTCCGAGGAAGGAATCTCTCTGAAGATCGAATAAAGCTAGTTGCTGCTGAACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAGCAAAAGATTCGGGGGTTGATTGGCTATCTCAACGATTAAGGGCCGAGGCCCTCAAGATGGACGGTTTTGATCAGATGCTCCGAGTTAGTG
CGCCAGTAAGCGCTGGGCTTAT

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

>R_alyu43 v2

TATTACCCCGAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCGCCCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGTTGATGCTGGATGTTCCACC
ATCAACAATCCCGCTTACTACCAGTATCGGGATGAGTTTAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGTAATCGTCTATGTCAGGGATACGTCGAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCCCTCCGCGCACCTTGAAGAACGAAAGGGAAGCCAGAGAGACAGCGGCTACTGTATGAAGAGGACACAAGAAATCGAAGGTCCTCTC
GAGTTTGGTGCCTTTAAATTTGCATGTAATGATAAATTTATTTGATGTCATACAGATATTCGCTGAAACGCACAACCGCTTTGGAGTATTTATATGAGTGTCCAAATACCTTCGATAGA
AGTAAGGATACATTAACAGATTTCAAGCAGAGTTGAATAAAACGAAGGCGATGATAGCTGGAACACATCTTCACTGCTTTGGACATCGGAAGTTGAAAAATTTATGGCGGAGCCATGT
CATCGAAGGATAATTTGGGCTATGGCCCAATGGAGGAGAAGAAAGCAACCTTATGCAAAATTTAATGAAGACGAAGAATCGGTTTTATTCGCCAGGAGGAAAACTTTGGATATA
TGATAGTTGTATAATTTAGAAATGTTATATTTGATATTTCCAGATGCAAAAGGAAATTTAAACTATGGTTTTATAGAAGAAATTTAAAAATGGAATTTTCAAAGCGGGAATAT
GAACCCGTTTTGAAATTTAGAAATATGTTGAAGTCAATGTAATGGCTAATCTCCCTCCGAGGAAGGAATCTCTCTGAAGATCGAATAAAGCTAGTTGCTGCTGAACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAGCAAAAGATTCGGGGGTTGATTGGCTATCTCAACGATTAAGGGCCGAGGCCCTCAAGATGGACGGTTTTGATCAGATGCTCCGAGTTAGTG
CGCCAGTAAGCGCTGGGCTTAT

DNA-S v2 4 SNPs to alyu42

CP protein is identical

>S_alyu43 v1

TATTACCCCGAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTAAGATGGGTTTTGGGCTTATGGGCTTTATCCAGAAGACAAAAACAGGCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCCGCAAGCAAACCTAAAAGTCTATATATACAGTGTAGACATATTTGTCAGATAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGCGGGCTTGGCGACCGAAGTATGGAAGCAAGCGGCAACCACTACGACTACTCTCTAGGTTCAATATTTGGTCTGAAAATACCGTCAAGGTTATTTAGGATTTAGCGCTAC
TGATAAATCCTACCCAGATATTTATCTGAAAATGTTTATGCTTTTGGTGTGCAAGGTGAACTCTGGAAGAATACTCATTTGGGCTATGATTAAGATTCATGGGAATCAACAGCC
GACTACATCTTGGAGCACCGAGTTTATCTATAAAACCTGAAATAGCCATCTGGTGAACCTGGTATCGATGGGGAACCTTGAAGCCGGAGTGAAGACCGGAGATCAGATGTAGAATG
TCTTCTAAGGAAGACAAACCGTTGAGGAAGAATGTAACAGAGTGGATCTGTTATTTGGCATTTTATGATGCTGGAGTTAGTATTAACACAGGACAGAAATACATATCATGT
ATGATCTGTTTATGAACATAAACCCTTTGATGGCTTAATGACCAATAACATACAACAGCTATGAAATACAACAGCTATGACAAACGGGAAAAATGAAGAATCGGGGGTTGATTG
GCTATCGTATCGCTAAGGGCCGAGGCCGCTGAAATGATCTTTATAAAACAAATATACATGATACGGATTTGAAAATATAATCAACGATGTAATAACACAGAAATGTTGAT
ACCAATTAATAAAAAAGAGAAGATAAGTATATTTGTGAAGGATAAGCATCACACCACCCTTTAGTGGTGGGTCATATGCTCCGAGTTAGTGGCCACGTAAGCGCTGGGCTTAT

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

TATTACCCCGAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTAAGATGGGTTTTGGGCTTATGGGCTTTATCCAGAAGACAAAAACAGGCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCCGCAAGCAAACCTAAAAGTCTATATATACAGTGTAGACATATTTGTCAGATAACAATGGCGAGGTTTCCGAAGAAATCGATCAA
GAAGAGCGGGCTTGGCGACCGAAGTATGGAAGCAAGCGGCAACCACTACGACTACTCTCTAGGTTCAATATTTGGTCTGAAAATACCGTCAAGGTTATTTAGGATTTAGCGCTAC
TGATAAATCCTACCCAGATATTTATCTGAAAATGTTTATGCTTTTGGTGTGCAAGGTGAACTCTGGAAGAATACTCATTTGGGCTATGATTAAGATTCATGGGAATCAACAGCC
GACTACATCTTGGAGCACCGAGTTTATCTATAAAACCTGAAATAGCCATCTGGTGAACCTGGTATCGATGGGGAACCTTGAAGCCGGAGTGAAGACCGGAGATCAGATGTAGAATG
TCTTCTAAGGAAGACAAACCGTTGAGGAAGAATGTAACAGAGTGGATCTGTTATTTGGCATTTTATGATGCTGGAGTTAGTATTAACACAGGACAGAAATACATATCATGT
ATGATCTGTTTATGAACATAAACCCTTTGATGGCTTAATGACCAATAACATACAACAGCTATGAAATACAACAGCTATGACAAACGGGAAAAATGAAGAATCGGGGGTTGATTG
GCTATCGTATCGCTAAGGGCCGAGGCCGCTGAAATGATCTTTATAAAACAAATATACATGATACGGATTTGAAAATATAATCAACGATGTAATAACACAGAAATGTTGAT
ACCAATTAATAAAAAAGAGAAGATAAGTATATTTGTGAAGGATAAGCATCACACCACCCTTTAGTGGTGGGTCATATGCTCCGAGTTAGTGGCCACGTAAGCGCTGGGCTTAT

DNA-U3 v1 = alyu42

ORF1 (39 aa) v1=v2

>U3_alyu43 v1

TATTACCCCGAGCGCCCGAGGACGGGACATGGGCTTTTTAAATGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTTGGGCGATCGGCCCAATAAATTAAGAGAAGCTGTTCAAAA
TCGGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATCTGGCTTGGCGGAGCAAGCAACCAAGTAAATTTAATTCGATGACACGTTGGACGGGCGAAATCTCCTGTAAT
CTATAAATAGCTAAATCTGGCTGGATAATTTGCTCTCGCTCTCTGCTCAAGCTGGTGTGTGAGGCGGAAGATCGCCATCGGGCATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
ACATGCTCGGAAGCGTATATCGGGTATTTATAGACTCTAGCGCAGCTAGAAGTTTCTTTGTAATTGATATTTGTAATTTACGAGAAATCTGTACATTTGATAATAAATAACA
TCTGGATTTGTTAATGTTTACATTAACAGTATTAATAATGTACAATAAATAAATTTGATGAGGATTCGAAATCAATAAATTTAATAATGAGGAGCGTACGATGATAAACAAGTGTTA
AGGTATAATTAATAAATTTATGCAATGTTATGATAAATCGGTATAAGTTGAAGTATGAGGTGAAAGAGGAGATTTAGAATTTAAAAACCAATTTATATTTATAATACATACAACA
CGCTATGACAAAAGGGGAAAAATGAAGAATCGGGGGTTGATTGGTCTATCGTATCGCTTAAGGGCCGAGGCCGCTCAAGATGGATGAACGGTCAGATTTGATTTGCTTAGCCAGGAGAA
AGGAATCTTTTGGGACCCAGAGATAAGACAGCTGTCACTACCTTTTAAAAATAATAATAAACAATTTACGATAGTACCCCTCCAAAGATGACGCTATAGGGGTGCTCCGAGGTAATTTA
ACATAGCTCTGACAAAGAGATAGTGGACGTTGGATGCCACGATCGGACGATCGTGGTTTGTGAACTTTATGATGACGTAGGGGCTGGGGCTTAT

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

TATTACCCCGAGCGCCCGAGGACGGGACATGGGCTTTTTAAATGGCCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTATTTGGGCGATCGGCCCAATAAATTAAGAGAAGCTGTTCAAAA
TCGGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATCTGGCTTGGCGGAGCAAGCAACCAAGTAAATTTAATTCGATGACACGTTGGACGGGCGAAATCTCCTGTAAT
CTATAAATAGCTAAATCTGGCTGGATAATTTGCTCTCGCTCTCTGCTCAAGCTGGTGTGTGAGGCGGAAGATCGCCATCGGGCATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
ACATGCTCGGAAGCGTATATCGGGTATTTATAGACTCTAGCGCAGCTAGAAGTTTCTTTGTAATTGATATTTGTAATTTACGAGAAATCTGTACATTTGATAATAAATAACA
TCTGGATTTGTTAATGTTTACATTAACAGTATTAATAATGTACAATAAATAAATTTGATGAGGATTCGAAATCAATAAATTTAATAATGAGGAGCGTACGATGATAAACAAGTGTTA
AGGTATAATTAATAAATTTATGCAATGTTATGATAAATCGGTATAAGTTGAAGTATGAGGTGAAAGAGGAGATTTAGAATTTAAAAACCAATTTATATTTATAATACATACAACA
CGCTATGACAAAAGGGGAAAAATGAAGAATCGGGGGTTGATTGGTCTATCGTATCGCTTAAGGGCCGAGGCCGCTCAAGATGGATGAACGGTCAGATTTGATTTGCTTAGCCAGGAGAA
AGGAATCTTTTGGGACCCAGAGATAAGACAGCTGTCACTACCTTTTAAAAATAATAATAAACAATTTACGATAGTACCCCTCCAAAGATGACGCTATAGGGGTGCTCCGAGGTAATTTA
ACATAGCTCTGACAAAGAGATAGTGGACGTTGGATGCCACGATCGGACGATCGTGGTTTGTGAACTTTATGATGACGTAGGGGCTGGGGCTTAT

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

TATTACCCCGCTCTCGGGACGGGACATCACGTCATTAACAATGACAGTGAACATGCGATAGCTTTGAGCGAAGATAAACCATCACTATCAAAAAGTGAAGGAAATTTCTGTTGC
TTAGGAACTGCTCAACCTGGATAGATTTGTTTCGAGAAGCGACATGGAGGCTTTAAACCTGATGGTTTTGTGATTTCCGAAATCACTCATCGGAAGAAGATCGAGTTCTGGGAAT
CGTCTGCCATGCCAGCAGTATGCAAGAGAGTGTATCAAGGAAATATATTTGGGAGCATCGAAACAACTCTGTTTTGTCAGAAGTTGAAAGGCTGTGTAAGAGGATTTCTGGAGCATGGAA
ATCAAGATGATGCTTAGACCGAGTGAAGGAGATGAAGACTTCTATTTATTCGCTATAGCGAATTTTGAAGAACTTGTGTGGTATTTGTTTTAGTACTAATAAATCTATGCATATA
GTTTAAACAAATGGTCTTTTATCATGAATATATTTGAAGACTAGTGGTGTGACTACTCGGTATATCAAGATTTGTTCTGTGATGAGGAACCTCTTATTCGTGACAGAGAAGGAAG
ATGAAGAAGTAAATACAGGAATGTTATCATGGATCGACAGAAGAGAATCTCTTGGAGTGAATGTCAAAGATAGTTATATCAGATTTATGATGTAACATTAAGTAAATCA

GAACCCGTTTTGAAATTTGAGAATATGTGGAAGTCATTGTAATGGCTAACTCTCTCCGAGGAAGGAATCTTTTCAGAAGATCGAATAAAGCTAGTTGCTTGTGCTGAACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAGCAAAGATTCGGGGGTTGATTTGGCTATCTTAACGATTAAGGGCCGACGGCCCTCAAGATGGACGGCTTATCAGATGTCCCGAGTTAGTG
CGCCACGTAGCGCTGGGCTTAT

DNA-S = alyu47 = alyu48 = alyu49

>S_alyu50

TATTACCCCGAGCGCTCGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTAAGATGGGTTTTGGGCTTATGGGCTTATCCAGAAGACCAAAAAACAGGCGG
GAACCCGTTCCCAATTTCAAATTTAGATAGCTTGCCTCCGCAAGCAAACATAAAAGCCTATATATACCAAGTGTAGACATATTTGTTCCAGATAACAAATGGCAGGTTTTCCGAAGAAATCGATCAA
GAAGCGCGGGTTGGCGACGGAAGTATGGAGCAAGCGCGCAACAGTCACTACTCTGCTGTTAGGTTCAATATTTGGTTCTGAAAATACCGTCAAGTATTTAGGATTTAGCGCTAC
TGATAAAAACATTCCAGATATTTTATCTGAAAATGTTTATGCTTTTGGTGTCAAGGTGAAGCCGGAAGAATACTTCACTGGGCTATGATTAAGAGTTTCATGGGAAATCAACAGCC
GACTACATGTCTGGAAGCACCAGTATTTTATAAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCAGTGGGAACTTGAAGCCGGAGTCCGACAGGGACATCAGATGTTGAATG
TCTTCAAGGAAGACACCGTGTGAGGAAGAATGTAACAGAGTGGATTACTTGTATTTGGCATTATTTGTAGTGTGGAGTTAGTATTAACCTACCAGAACAGAAATACATATCATGT
ATGATATGTTTATGTAACATAAACCTTTGATGGAATAATGACAAAATAACATACAACACTATGAAATACAACACGCTATGACAAACAGGAAAAATGAAGAAATCGGGGGTTGATTTG
GCTCTATCGTAACCGTTAAGGGCCGACGGCCGTTGAAATGATCTTTATAAAAACAAATATACATGATACGGATAGTTGAACATATAAACCAACGATGATAAATACAACAGAAATGTTGAT
ACTAATTAATAAATGAGAAGAAAAGAAATTTTGTGAGGATAAGCATCAGAACCACCACTTTAGTGGTGGGTCAGATGTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGCTTAT

DNA-U3 1 SNP to alyu47

ORF1 is identical

>U3_alyu50

TATTACCCCGAGCGCTCGGACGGGACATGGGCTTTTTAAATGGGCGAGAGAGTTGAACAGTTCAGTATCTTCGTTTATGGGCCATTCGGCCCAATAATTAAGAGAAGCTGTTCAA
TCTGGGTTTGAACGAGGTTCAAGTGTAGACGTTCAACAATATCTTGGCTTGCAGGAGCAAGCAACAAAGAAATTAATTTAATTCGTATGACAGCTGGACGGACCGAAATCTCCTGTATCT
CTATAAATGGCTAAATCTGGCATGGAATAATGCTCTGCTCTGTCGTAAGACTGTTGTGTGTCGAGGCGAAGATCGCCATCGGCGATCATCAGACGAAAATGCAAGAGACGGGAA
ACCATGCTCGCAAGCGTATATCGGGTATTTATAGACTCTAGCCGACGTAGAAGTTTCTGTTACTTGTATTTGATTTTGTAAATTCAGAAAGAAATTCGTACATGTAATAATAA
ATCTGGGATGTTAATGTTTACATTAACCTAGTATTAATAATGTACAATAACAACATTTGATGAGGAACGAATACAAGAATAATAAATATGAGGAGCGTACGCTGATAAACAGGTT
AAGGAATAATTAATAAATTAATGCAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAAGAGGAGATATTAGAATAATAAACCCTAATTAATTTAATAACATACAAC
ACGCTATGACAAAAGGGGAAAAAGAAAATCGGGGGTGTATGTTGCTATCCTAAGCAATTAAGGGCCGACGGCCCTCAAGATGATGAAAGCTGATGTTGATTTGCTTACACAGGA
AAGGAATCTTTTGGGACACAGATAAGACAGCTGTCACTACTTTTAAAAAATAATATAAACAACCAATATTGCCCTCCCAAGATATCCAGGATATGGGGTGTCCGAGGTAAT
TAACATAGCTCGACAAGAGATAGTGGACGTTGGATTCCACGATCGGACGATCGTGGTTTGTAGACTTATGATGACGTAGGGGCTGGGCTTAT

ALYU-51 - Musa ABB Pisang Awak ? - Laos

Virome

1. **BTV** 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

TATTACCCCGAGCGCTCGGACGGGACATCAAGTGCATCTAACAATGACAGTGCACAAAGCAGTACGTTGTAGCGAAAAGATAACCATCACTATCACAAGTGAGAGGAATATTCGTTGC
TTAGGACTAAGCAACGTTGAACAGATTTTGTTCGAGAAGCGAAAATGGAGGCTATTTAAACCTGATGGTTTTGTGATTTCCGAAATCACTCTCGGAGCAGAAATGGAGTTCTGGGAAT
CGCTCGCCATGCCAGAGCATGTCAAGAGAGTGTCAAGGAATAATATGGAGGATCGAAATAAATCTCTGTTCTGTCAGAAAGTTGAAAGGCTGTGAAGAGGATTTCTGGAGATGGAA
ATCAAGATGATGCTCTAGACCGCAGTGAAGGAGATGAAGACTTCTATTTATTCGCTATAGGCAATATTTGAAGAACCCTGTGTGGTATTTGTTTTAGTACTAATAAATCTATTGCATATA
GGTTAAACACAAATGGTGTCTTTATCATGAATATATGAAGACCTAGGTGGTACTATTCGGTATATCAAGATCTGTTCTGTGATGAGGAACTTCTTATTCGTCGACAGAAGAAG
ATGAAGAAATATACAGAAATGTTATCATGCCATCGACAGAAGAGAAATCTCTGGAAGTGAATCTCAAAAGATAGTTATATCAGATTTATGATGTCACATTTACTGTAATGAATATCCA
TTATCATAAATAAATAATGGAATGATGATTTATGATTTCTAGTATATATACATAAATATACGATATAGCATATAAATAACCAACATACAACACGCTATGACAAACGGGGAAAAAT
GAAGAAATCGGGGGTTGATTTGGGCTATCTTAACGATTAAGGGCCGAGGGCCGTTTTAAATATGTTGGTGGACGAAGTCCACAACACATAAAAAGTCTAAGAAACAGGGAATAATGAGCT
GGCAACGTAGGACCAATGTTCCCGAGTTAGTGCGCCACGTAAGCGCTGGGCTTAT

DNA-M 1 SNP to alyu47

MP is identical

>M_alyu51

TATTACCCCGAGCGCTCGGACGGGACATCAAGTGCATCTAACAATGACAGTGCACGATATATACTACATAACCGTTTAAAGCAACGTTATATAAATGTTATAACGAAAAGTCAAGTGTG
ATAGAGACCTCGACGTTGACATAGTCAAAATGTTAATAAACAATTTGACGTCGGATGCTCCGACGGAAGCTTAGGTTACTTCTGTGCGAAGCAAAAACATTTATATATTGGCCTGGACT
GCTCCCTATAAATAGGCAAGCTAGGAAATGGCATTAAACAAGAGCGGGTGAACCTATTTTGAATGGTTTTCTGTTCATCGGTTGCAATATTTATTGCGATACAATATATATATATTG
TTGGTGTGCTCTTTGAGTCCCGCAAGTATATTAAGGATGTTGTGAGGATCTCTGTAAGAACTCTGACAGAAAGACGCTGTATGGATGACAGAAACCGGATTTGACGAGGCAACAGGAGAT
GTAGAGCTCGGACAGGATTTGGAAGACAGACGGGATCAACAACCGGCTGTATACCACTACCAACAGGTTATCCCTTCGATCAACCTAGAAGGATGATCAGGAAGACGAGGA
AACCGAGCAATGTTTAAATCACCGTATTTGATAATACAAAATAAATAAATGATAATGATATGTTGAACATAAATAACGTAACATAATATATGTTGATAATTTACATATT
ATAAATATGTAATTTGATACAGTGTGTTATTTATAGAACATACAACACCGTATGACAACAGGAAAAATGAAGAAATCGGGGGTTGATGGTCTATCGTATCGCTTAAAGGGCCGAGGC
CCGTTGAAATGATTTAATAAACAATAATACATGATACGGATAGTTGAATATATAACAACAGGAAATATAAACAAGAAATGTTGATCTAATTAATAAATAATGTAAGATAAGTAT
ATTTGCGGGATGATGATCAACAACCAACCTTTAGTGGTGGGTCATATGCCGAGTTAGTGGCCACGTAAGCGCTGGGCTTAT

DNA-N 2 SNP to alyu47

NSP is identical

>N_alyu51

TATTACCCCGGCTCGGACGGGACATGACGTCAGCATATATATAATGGGCTTTTTAAAGCCCATATAAGTGAAGTGGCCGGGTTTGGACATATTTCCGAAAGCCGACCCGGAAA
AGGATAAAGTCACGTCGCAATAATAGTTGCTTCGCTCGAAGCAACATAAATAAAGTTGCGTATTAATACGCAACTAAGTCTATTAATAGGTTGCTCTCGCAATAAATCAGAG
CGTATGCGAAGCAGAAGCGATGGATTGGGCAAGATCAAAATCAAGACATGTACCCATGGCTGATTTGGAAGCAGATATCATCGGATTCACAGAAAATCGGCAATATGTACCTTGGCT
GACTCTGGAGCTGGAAGAAGACTCCTCGCAAGTACTTCTAGATCTATTGAAGCTGTGTTAATGGAAGCTCAAGGGAATAATAGGAATGTTCTGGCTTCTTATAGCTATCAAT
CCGACGATGATGGAGCAATGCTCCAGTACTTATAGTACCAATTTGGAGATATGGATATCATAATGATTTCTTATTTTTCGAAAGGAAAGGAAAGTTGAATGATATATCATCA
TTATGTTCCGCGAAGCTCGATGGACAGACATCGAAGTATGATTAAGTCAACCAACCACTGTAATGAATCATGTGATCTGAAGTGTATGTTCTTCTTCTTGAATAAAGGA
ATAACAGATGTCGTAATGATTTAATAAACAATAATTTTCTATGTAATTTGATGTTGATAAACAACACAGCTATGACAACCGGGAAAAATGAAAATCAGGGGTTGATTTGTT
CTATAGTATCGCTTAAAGGGCCGACGGCCGTTGAAAAATAAATAATCGAATATATACGATTTGATAAATAACAGATAGATGAAGGATATAAACAATAAACAAGAAATGATGGCGGTA
TAATTAACAAGAAATATAAATAAATAATGTAACATACTCTGATTTGGTGCAGAGTGTAGGTCACCTTAAAGTTAGTGAAATGTTCCCGATGACGTAAGCAGGGGACTAT

DNA-R 1 SNP to alyu47

Rep is identical

>R_alyu51

TATTACCCCGAGCGCTCGGACGGGACATTTGATCTATAAATAGACTCCCGCCCTCCACTACAAGATCATCATGTCGACAGAAATGGCGGATATGTTGATGCTGGATGTTCCACC
ATCAACAATCCCGCTTCACTACAGTGTGCGGGATGAGTTCAAATATATGGTATATCAAGTGGAGAGGGGACAGGAGGTTACTGTCATGTGACGGGATACGTCAGATGAAGAGACGA
AGTTCTCTGAAGCAGATGAGAGGCTTCTCCCTGGCGCACACTTGAAGAAACAGGAAAGCAAGAAAGACGAGGCACTGTATGAAGGAAGACACAAAGATTCGAAGGTTCCCTT
GAGTTTGGTGGCTTTAAATTTGATGATAATTTTATGATGTCATACAGGATATTCGTTGAACACGCAACCGCCCTCGGATTTTATATGATGTTCCAAATACCTTCGATAGA
CATGAAGGATACATATACAGGTTCCAGCAGAGTTGAATAAACAAGGCAATGATGATGCTGAAAACACTCTCTGATGATGCAATCGGAAGTTGAAAATATTTAGGGCCGACGAT
GTCAGAAGATAATTTGGGCTATTTGGGCTATTTGGCCAAATGGAGGAAAGAAAGCAATTTAGTCAAAATTTAATGAAGACGAAGAAATGCGCTTTTATTTCCAGGAGGAAATTTGGATATA
TGTAGATTGATAAATACGAGGAAATAGTTATATTTGATATTTCCAGATGCAAAAGAGAAATTTAAACATAGTGGTTTATAGAAGAAATTTAAAAATGGAATTTTCAAAGCGGAAATAT

GAACCCGTTTTGAAATTTGAGAATATGTGGAAGTCATTTGTAATGGCTAACTTCTCCGAGGAAGGAATCTTTTCAGAAGATCGAATAAAGTAGTTGCTTGTGTAACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAGCAAAAGATTCGGGGGTTGATTTGGGCTATCCTAACGATTAAGGGCCGACGGCCCTCAAGATGGACGGCTTATGATGATGTCCTCCGAGTTAGTG
CGCCACGTAGCGCTGGGCTTAT

DNA-S = alyu47

>S_alyu51

TATTACCCCGAGCGCTCGGGACGGGACATGGGCTAATGGATCATGGAATAAGGGCCCATCGGGCCGTTAAGATGGGTTTTGGGCTTATGGGCTTATCCAGAAGACCAAAAAACAGGCGG
GAACCGTCCCAATTTCAAATTTAGATAGCTTGCCTCCGCAAGCAAACATAAAGCCCTATATATACCAGTGTAGACATATTTGTTTCAGATAACAATGGCGAGGTTCCGAAAGAAATCGATCAA
GAAGCGCGGGTTGGCGACGGAAGTATGGAGCAAGGGCGCAACAGTACGACTACTCTGCTGATAGGTTCAATATGGTTCTGAAATACCGTCAAGTATTTAGGATTGAGCCTAC
TGATAAAACATTACCAGATATTTATCTGGAAATGTTTATGCTTTTGGTGTCAAGGTGAAGCCGGAAGAATCTTCACTGGGCTATGATTAAGAGTTTCATGGGAAATCAACAGCC
GACTACATGTCTGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCCATCTGGTGAACCTGGTATGCGATGGGAACTTGAAGCCGGAGTCCGACAGGGACATCAGATGTTGAATG
TCTTCTAAGGAAGACACCGTGTGAGGAAGAATGTAAACAGAGTGGATTAATTTGGCATTATTTGATGTTGAGTATTAACTACCAGACAGAAATACATATCATGT
ATGATAATGTTTATAACATAAACCTTTGATGGAATAATGACCAAATAACATACAACACACTATGAAATACAAACACCGTATGACAAACAGGAAAAATGAAGAAATCGGGGGTTGATG
GTCATCGTAACCGTTAAGGGCCGAGGCGGCTTGAATGATCTTTATAAAACAATATACATGATACGGATAGTTGAACATATAAACCAACGATGATAAATACACAGAAATGTTGAT
ACTAATTAATAATGAGAAGAAAAGATTTTGTGAGGATAAGCATCAGAACCACCTTTAGTGGTGGTCCAGATGTCGCCGAGTTAGTGCGCCACGTAAGCGCTGGGCTTAT

DNA-U3 1 SNP to alyu47

ORF1 is identical

>U3_alyu51

TATTACCCCGAGCGCCCGAGGACGGGACATGGGCTTTTTAAATGGGCGAGAGAGTTGAACAGTTCAGTATCTTCGTTTATGGGCCATTCGGCCCAATAATTAAGAGAAGCTGTTCAA
TCTGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATCTGGCTTCGGGAGCAAGCAACAAGAAATTAATTTAATTCGTATGACAGTGGACGGACCGAAATCTCCTGTATCT
ATGATAATGCTTAAATCTGGCATGGATAATGCTCTCGCTCTCTGTCGAAAGCTGTTGTTGAGGCGGAGATCGCCATCGGCATCATCAGACGAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGCAAGCGTATATCGGGTATTTATGACTCTCAGCCGACGTAGAATTTTCCTGCTACTGTTGATTTGATTTTGAATTTACGAAGAATTCGTACATGTAATAATAA
ATCTGGGATGTTAATGTTTACATTAACCTAGTATTAATAATGTACAATAACAACATTTGATGAGGAACGAATACAAGAATATAAATAATGAGGAGCGTACCGTGATAAACAGGTTGTT
ATGAATAATTAATAATTAATGCAATGTTATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATATTAGAATATAAACCCTAATTAATTTATAATACATACAAC
ACCGTATGACAAAAGGGGAAAAAAGAAAAATCGGGGGTTGATTTGGTCTATCCTAACGATTAAGGGCCGAGGCGGCTCAAGATGGATGAACGGTTAGATTTGATTTGCTAGACACGAAGA
AAGAAATCTTTTTGGGACACAGATAGACAGCTGCTACTCTTTAAATAAATAAATAAACAACATGACCATAGTGCCTCCCAAAGATACCGATAGGGGTGTCCTCCAGGTAAT
TAACATAGCTCGATAAGAGATAGTGGACGTTGGATTCCACGATCGGACGATCGTGGTTTGTGAACTTATGATGACGTAGGGGCTGGGCTTAT

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

TATTACCCCGCTGCTCGGGACGGGACATCAGCTGCTTCTAACAATGACAGTGCACAAAGCAGTACGTTGTAGCGAAAGATAACCATCACTTTACAAAAGTGAAGGAATATTCGTTGC
TTAGGACTAAGCAACGAGGACAGATATTTGTCGAGAAGCGACAATGGAGGCTATTTAAACCTGATGGTTTTGATTTCCGAAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAAT
CGTCTGCTATGCCAGACGATGTCAGAGAGTGCACAGGAATATATTTGGAGCATCGAAATAAATCTCTGTTTTCAGAGTGAAGGCTGTGAAGAGGATTTGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCACTGAAGGAGATGAAGACTTCTATTTATTCGCTATAGCGAATATTTGAAGAAACCTGTGTGGTATGTTGTTTACTACTAATAAATCTATTGTATATA
GGTTAAACAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGTGGTGTACTACCGGATATCAAGATCTGTTTTGATGAGGAATCTCCTTCGCTTCGACAGAAGAAGAAG
ATGAAGAAGTAAATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAGATAGTTATATCAGATTTATGATGAACATTAATCTGTAATGAATATCCA
TTATCATAAATAAATAATGGAATGATGATTTATGATTTCTAGTATAAATACATAATGGTATACGATATGATCAATAAATAAATAAACAACATCAACACACTATGACAAACAGGAAAAAT
GAAGAAATCGGGGGTTGATTTGGGCTATCTTAACGATTAAGGGCCGAGGCGGCTTTAAATATGTTGGTGGACGAAGTCCACAACAAAAAAGTATCAGAAACATGGAATATAATGAGCTG
GCAATGTAGGGACCATGTCGCCGAGTTAGTGCGCCAGTGCAGGGGGCTTAT

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

>C_alyu53_v2

TATTACCCCGCTGCTCGGGACGGGACATCAGCTGCTTCTAACAATGACAGTGCACAAAGCAGTACGTTGTAGCGAAAGATAACCATCACTTTACAAAAGTGAAGGAATATTCGTTGC
TTAGGACTAAGCAACGAGGACAGATATTTGTCGAGAAGCGACAATGGAGGCTATTTAAACCTGATGGTTTTGATTTCCGAAATCACTCATCGGAGCAGAAATGGAGTTCTGGGAAT
CGTCTGCTATGCCAGACGATGTCAGAGAGTGCACAGGAATATATTTGGAGCATCGAAATAAATCTCTGTTTTCAGAGTGAAGGCTGTGAAGAGGATTTGGAGCATGGAA
ATCAAGATGATGCTCTAGACGCACTGAAGGAGATGAAGACTTCTATTTATTCGCTATAGCGAATATTTGAAGAAACCTGTGTGGTATGTTGTTTACTACTAATAAATCTATTGTATATA
GGTTAAACAATGGTGTCTTTTATCATGAATATATTGAAGACCTAGTGGTGTACTACCGGATATCAAGATCTGTTTTGATGAGGAATCTCCTTCGCTTCGACAGAAGAAGAAG
ATGAAGAAGTAAATACAGGAATGTTATCATGGCATCGACAGAAGAGAAGATCTCTTGGAGTGAATGTCAAAGATAGTTATATCAGATTTATGATGAACATTAATCTGTAATGAATATCCA
TTATCATAAATAAATAATGGAATGATGATTTATGATTTCTAGTATAAATACATAATGGTATACGATATGATCAATAAATAAATAAACAACATCAACACACTATGACAAACAGGAAAAAT
GAAGAAATCGGGGGTTGATTTGGGCTATCTTAACGATTAAGGGCCGAGGCGGCTTTAAATATGTTGGTGGACGAAGTCCACAACAAAAAAGTATCAGAAACATGGAATATAATGAGCTG
GCAATGTAGGGACCATGTCGCCGAGTTAGTGCGCCAGTGCAGGGGGCTTAT

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

TATTACCCCGAGCGCTCGAGGACGGGACATCAGCTGCAACTAACAATGACAGTGCACAAAGCAGTATATATACATACAAAGGTTAAGCAACCGTTATATAATGTTATAACGAAAAGTCAAGTGCAG
ATAGAGACTGCACGCTGACATAGTCAAAATGTTAATAAACAATTTGACGCTCCGATGCTCCGACGGAAGCTTAGGTTACTTCGTGGCGAAGCAAAACATTTATATATTTGGCTGGACT
GCTGCCCTATAAATAGGCAAGCTAGGTAATGGCATTAAACAACAGAGCGGGTGAACATTTCTTGAATGGTTTTCTGTTTCATCGGTTCAATATTTATGCGATAACAATATATATATTTG
TTGGCGTTCCTTTAGGTCCTCCCAAGTATATTAAGGATGTTGTGAGGATTTGCTGATAGATACCTGACCAAGACGCTGATGATGAGAGACCGGCTTGGAGGCAACAGGAGAT
TAGAGCTCGGCAAGGATGTTGGAGACGACAGCGGATCAACAACCGGCTGATACACACACTGACACAGGTTATCCCTTCGCTACAGGAGGAAAGATCAAGGAAAGACGAGGA
AACCCAGCACAATGTTTAAATACACCGTATCTAATATACGAATATAAATGATATGATGATGTTGTAACATATAATACCTGAACATATAATATCTTTGATATTTACATATTT
ATAATATGTAATTTGATACAGGTTGTTATTTATAGAACAATACAACCGCTATGACAAACAGGAAAAATGAAGAAATCGGGGGTTGATTTGGTCTATCGTATCGCTTAAAGGGCCGAGGC
CGGTTGAATGATTTCTTAATAAACAATAATACATGATACGATGTTGAATATAAACAACAGGATATAAATAACAACAGAAATTTGTTATCTAATTAATAAATGAGAAGAAATGAT
ATTTGTTAGGGATGATGATCAACACCACCTTTAGTGGTGGTCCATGTCGCCGAGTTAGTGCGCCACGTAAGCGCTGGGCTTAT

C/G (62472/28164)

>M_alyu53_v2

TATTACCCCCAGCGCTCGGGACGGGACATTTGCATCTATAAATAGACCTCCCCCTCTCCACTACAAGATCATCATCGTCGACAGAAATGGCGGATATGGTATGCTGGATGTTACC
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AGTCTCTCGAAGCAGTGAAGGGTCTTCCCTGGCCACACCTTGAAACAGAAAGGGAAGCCAAAGAAAGACAGCGGCATCTGTATGAAGAAAGACACAAGATCGAAGGTCCTCTC
GAGTTGGTGCCTTAAATTTGCTATGTAATGATAATTTATATGATGTCATACAGGATATGCTGAAACGCAACACCGCCCTTGGAGTATTTATGATGTCCTCAATACCTTCGATAGA
AGTAAAGATACATTTACAGAGTTCAAGCAGAGTTGAATAAAACGAAGGCGATGAATAGCTGGAACACATCCTCAGTCTTGGACATCGGAAGTTGAAAAATATTTATGGCGGACCCATGT
CATCGGAGGATAATTTGGGCTATGGCCCAATGGAGGAGAAGGAAAGACAACCTTATGCAAAAATTTAATGAAGACGAAGAATGCGTTTATTTCTCCAGGAGGAAAAATCATTGGATATA
TGATGATTTGATAAATACAGGAAATAGTTATATTTGATATTTCCAGATGCAAAAGAGGAATTTAAACTATGGTTTATAGAAAGAAATTTAAAAATGGAAATTTCAAAGCGGGAAATAT
GAACCCGTTTTGAAAATGTAGAATATGGAAGTCATTGTAATGGCTAACCTCCTCCGAGGAAGGAATCTTTTCAAGAGTCAATAAAGCTAGTTGCTGCTGACACGCTATGAC
AATCGTACGCTATGACAAAAGGGGAAAAGCAAGATTCGGGGGTTGATTTGCTATCCTAACGATTAAGGGCCGACGGCCCTCAAGATGGACGGCTCGATCAGATGTCGGAGTTAGTG
CGCCAGTAAAGCGCTGGGCTTAT

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

TATTACCCCCAGCGCTCGGGACGGGACATGGGCTTAATGGATCATGGAATAAGGGCCATCGGGCCCTTAAGATGGGTTTGGGCTTATGGGCTTATCCAGAAGACAAAAACAGCCGG
GAAACCGTCCCAATTTCAAATTTAGATAGCTTCCCGCGCAAGCAAACTAAAAGCCCTATATATACCAGTGTAGACATATTGTCAGATAACAATGGCGAGGTTCCGAAGAAATCGATCAA
GAAGCCGGGGTTGGGCGCAAGAGTATGGAAAGCAAGGGCAACCAAGTCAAGCTACTCGCTGCTTAGGTTCAATATTGGTTCTGAAAAATCCGCTCAAGGTTATAGGATTTAGCCCTAC
TGATAAAAACATTACCAGATATTTTATCTGGAAAATGTTTATGCTTTTGGTGTCAAGGTGAAGCCCGGAAGAATACTCACTGGGCTATGATTAAGAGTTCCATGGGAAATCAACAGCC
GACTACATGCTCGGAAGCACCAGGTTTATTTATAAAACCTGAACATAGCAACTCTGGTGAACCTGGTATGCAAGTGGGAACTGAGTGGGAACTGAAACCGGAGTCCGAACAGGGACATCAGATGTTGAATG
TCTTCAAGGAAACACCGCTGTTGAGGAAGAATGTAACAGAGGTGGATTAATTTGGCATTTTATTTAGTGTCTGGAGTTAGTATTAACACCAGAACAGATTAACATATCATGT
ATGATATGTTTATTAACATAAACCTTTGATGGAATAATGACCAAATAACATACACACACTATGAAATACAACACGCTATGCAAAACAGGAAAAATGAAGATCGGGGGTTGATG
GTCATCGTACCGCTTAAAGGCCCGAGGCCCTGAAATGATTTCTTATAAAACAATATACATGATACGATAGTTGAATATATAAACACAGATGTAATAACACAGATGTTGAT
ActaattaaataATGAGAAGAAAAGAAATTTTGTGAGGATAAGCATCAGAACACCCTTTAGTGGTGGGTCAGATGCCCCAGTTAGTGCCACCGTAAAGCGCTGGGCTTAT

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

TATTACCCCCAGCGCTCGGGACGGGACATGGGCTTTTTAAATGGGCGAGAGAGTTTGAACAGTTCAGTATCTTCGTTTATGGGCCATTCGGCCCAATAAATTAAGAGAAGCTGTTCAA
TCTGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATTTCTGGCTTGGGAGCAAGCAACAAGAAATTAATATTTAAATTCGTATGACAGCTGGACGGACCGAAATCTCCTGCATCT
CTATAAATAGCCCTAAATCTGGCATGGATAAATGCTCTCGCTCTTCTGTCAAAAGTTTGTGTGGAGCGGAAGATCGCCATCGCCGATCATCGGACGAAAAAGCTGCAAGAGAGACGGAGA
ACCATGCTCGCAAGCGTATAACGGGATTTATAGACTTCTAGCCGAGCTAGAAGTATCTTGTACTTGATATTTGTAATTTACGAAGAAATTCGTACATGTAATAATAAAAC
ATCTGGGATTTGTAATTTTACATTAACCAAGTATTAATAATGTACAATAACAATAATTTGATGAGGAACGAATACAAGAATTTAAAAATAGGAGCGGTAGCGTGATAAACAGGTTGTT
AAGTATAATTAATTAATTTGCAATGTCATGATAATACGGTATAAGTTGAAGTATGAGGTGAAGAGGAGATTTAGAATTTAAAAACCCAAATTAATTTATTAATACATACAC
ACGCTATGACAAAACGGGAAAAAAGAAAATCGGGGGTTGATTTGGTCTATCCTAACGATTAAGGGCCGACGGCCCTCAAGATGGATGAACGGTTAGATTTGATTTGCTAGCCACGAAGA
AAGGAATCGTTTTGGGACCACAGCAAGCAGCTGTCACTACTTTAAAAAATAATAATAACCAATGACGATAGTACCCCTCCAAAGATGACGATAGGGGTGTCGGAGGTAAT
TAAATAGCTCTGACAAAGAGATAGTGGACGTTGGATGCCAGATCGGACGATCGTGGTTTACGAAACCAATGATGACGTAGGGGCTGGGCTTAT

T/G (13643/8939)

>U3_alyu54_v1

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TCTGGGTTTGACCGAAGGTCAGGTAGACGGTCAACAATATTTCTGGCTTGGGAGCAAGCAACAAGAAATTAATATTTAAATTCGTATGACAGCTGGACGGACCGAAATCTCCTGCATCT
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ACCATGCTCGCAAGCGTATAACGGGATTTATAGACTTCTAGCCGAGCTAGAAGTATCTTGTACTTGATATTTGTAATTTACGAAGAAATTCGTACATGTAATAATAAAAC
ATCTGGGATTTGTAATTTTACATTAACCAAGTATTAATAATGTACAATAACAATAATTTGATGAGGAACGAATACAAGAATTTAAAAATAGGAGCGGTAGCGTGATAAACAGGTTGTT
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ACGCTATGACAAAACGGGAAAAAAGAAAATCGGGGGTTGATTTGGTCTATCCTAACGATTAAGGGCCGACGGCCCTCAAGATGGATGAACGGTTAGATTTGATTTGCTAGCCACGAAGA
AAGGAATCGTTTTGGGACCACAGCAAGCAGCTGTCACTACTTTAAAAAATAATAATAACCAATGACGATAGTACCCCTCCAAAGATGACGATAGGGGTGTCGGAGGTAAT
TAAATAGCTCTGACAAAGAGATAGTGGACGTTGGATGCCAGATCGGACGATCGTGGTTTACGAAACCAATGATGACGTAGGGGCTGGGCTTAT

ALYU-55 - Musa AAA Cavendish - China

Virome

1. **BTV** six components
2. **BETA6** alyu55
3. **BETA2** alyu55
4. **BETA3** alyu55
5. **BETA5-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, BETA2 and BETA3, while only minor variants of DNA-C, DNA-M, DNA-U2 and BETA5

BETA6

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*; P0CK61 100% coverage 60% identities *Faba bean necrotic yellows C9 alphasatellite*; ATU31571 100% coverage 60% identities 77% positives *Faba bean necrotic yellows virus associated alphasatellite 2*

>BETA6_alyu55

TATTACCGACTTTGGCGAGGGCGCACTATAAAGATGCTGTGAGAAATTTGGTCTTACACGCAATTTCAAGGCGAAAGACAGAGCTCTGTTGGCGCGGAACTCAATACGCC
GCTTGGCAACATGAAAGAAAGATACAGCACCTACAGGGCGTATTGATGTTGAAGAAGAAGCCCGCTGAACGAGTGAAGAGCATATCGGTTGAAATCCACATGTCGAACCCATG
CGAGCGTCTTTCAGCATGCCATAGCATAGTCAAGAAAGCAAAACCGAATCGATGTTCCATGGGAATTCGGTATTCGAATCCGTAAGGTTTCAATAAACGAAAGCTGTAGAAATA
CTGGAGGATTCGGACACAGGAGCTTCAACCCCAAAAATACAGCAGGACCTGGCCAAACAGGCAATGAGTGTAGTCTAAGAAAGAAAGCTGCAAGAAAGGATTTAGTTATGAATCGCA
GAGTGGCAAGTGAATGACGAAGTTGTTGGAAGAAAGACCCGATACAGCAACAATAATTTGGTATATGGAACCAAGGGTGGAAAGGTAACAGAGTTCGCTAAACATTTAGGGTTA
AAGGATGTTGACATATTTGCCCGTGGTGAACCTCAAGATATGATGTAACCTGTTATCAAGGACATGAAAAATAATGTTGTAATGATTTCCCGCTTGTACCAAGGAATTTATTTCA
TATAAATCCTTGAATGTTAAGAAATAGAACTATATAGTTATAGTATGAAACAGTGGTCAATCGTATGTAATAGGTTCAATGATGTTGTTGCTTCCAGGAAATTTAGGATTTAT
GTAAATATCATTTGATCGAATAAGTTGATTTCTGCTGAACAGCTATGAAATACAACAGCTATGAAATACAACAGCTATGCAAAAAGGGGAAAAATGAAAAATCGGGGGTGTGTTGGCTACCTACCGA
CTAAGGGCCGACGGCCCTCAAGATGGATGAACGGTTAGATTTGATGCTTCCGACGAAGCAACAAAAATCGGTGGGAGAAATCGCCACGCTATTGGTTACTGTTATCCTTGGCG
CACTATATATAGGTTGCCCAAGTCCGCCATG

BETA2

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 alphasatellite 2

>BBTA2_alyu55_v1
TATTACCCACCTTCGGCCAC...
GGAAGATGTGCACTACGCGCTCGTCGGCGACGAACTGCTCCGAACTACTGGTCGAAACATCTTCAAGGATATCTTTCCTTGAAGAACGTTTTCGATTAGCGGCATAAAGAAGAAATA

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_alyu55_v2
TATTACCCACCTTCGGCCAC...
GGAAGATGTGCACTACGCGCTCGTCGGCGACGAACTGCTCCGAACTACTGGTCGAAACATCTTCAAGGATATCTTTCCTTGAAGAACGTTTTCGATTAGCGGCATAAAGAAGAAATA

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

>BBTA3_alyu55
TATTACCCACTTCCTCGCCCTACTTCTCGCCCTGACGCTCATAAGATGTATCATCTCAAATGGTGTTCCTACTCTGAATATTTCCTCGCAGCCGAGAGAGAAGACTTCTCTCGCGTCTG
AAGGAGGATGATGTTTATTACGCGGTCTCGCGCAGCAAGTCTGCTCCGAGCTTCGCGCCAGAAACCTTCAGGGATATCTATCCCTGAAGAAATCGATGAAGCTAGGCGGACTGAAGAAG

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

>Babu3chn_alyu55_uncorrected
TATTACCCACTTCCTCGCCCTACTTCTCGCCCTGACGCTCATAAGATGTATCATCTCAAATGGTGTTCCTACTCTGAATATTTCCTCGCAGCCGAGAGAGAAGACTTCTCTCGCGTCTG
AAGGAGGATGATGTTTATTACGCGGTCTCGCGCAGCAAGTCTGCTCCGAGCTTCGCGCCAGAAACCTTCAGGGATATCTATCCCTGAAGAAATCGATGAAGCTAGGCGGACTGAAGAAG

BBTA5-U3 chimera

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

>BBTA5_U3_alyu55_uncorrected contig
TATTACCCGACTTTGGCGCAGGGCGCACTATAAAAGATGTCGCGAGCAGGAAATGGGTCTTCACACGCAATTTCCGAAAGGCGAAAGACCAGAGCTCCTGTTGCGCGCGAAACTCAATAC
CGGTGTGGCAACATGAGAAGAAGATACGACCACTTTCAGGGAGTGATTCAAATGAAGAAGAAGCTCCGGATGAACCGAGTGAAGACGTTAATTTGGGGAAATCCACACCTCGAAGCC

>BBTA5_U3_alyu55_correction1
TATTACCCGACTTTGGCGCAGGGCGCACTATAAAAGATGTCGCGAGCAGGAAATGGGTCTTCACACGCAATTTCCGAAAGGCGAAAGACCAGAGCTCCTGTTGCGCGCGAAACTCAATAC
CGGTGTGGCAACATGAGAAGAAGATACGACCACTTTCAGGGAGTGATTCAAATGAAGAAGAAGCTCCGGATGAACCGAGTGAAGACGTTAATTTGGGGAAATCCACACCTCGAAGCC

>BBTA5_U3_alyu55_correction2
TATTACCCGACTTTGGCGCAGGGCGCACTATAAAAGATGTCGCGAGCAGGAAATGGGTCTTCACACGCAATTTCCGAAAGGCGAAAGACCAGAGCTCCTGTTGCGCGCGAAACTCAATAC
CGGTGTGGCAACATGAGAAGAAGATACGACCACTTTCAGGGAGTGATTCAAATGAAGAAGAAGCTCCGGATGAACCGAGTGAAGACGTTAATTTGGGGAAATCCACACCTCGAAGCC

U3_alyu32 TGTTGAGCGGAAGATCGCCATCGGGATCATCAG-ACGAAAAGCTGCAAGAGACGGG

Stop codon PIO
TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu14 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu15 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu19 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_jgf1_v1 TGAAGCAAACCTACGAAGCGTATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_jgf1_v2 TGAAGCAAACCTACGAAGCGTATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu17_v1 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu17_v2 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu21_v1 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu21_v2 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu18 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu24 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu16 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu22 TGAAGCAAACCTACGAAGCATATATCGGGTATTTATAGACTTATAGCCAGCTAGAAGTAT
U3_alyu41 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu53 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu50 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu47 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu49 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu51 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu48_v2 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu48_v1 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu42_43 AGAAACATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu43_v2 AGAAACATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu44_45 AGAAACATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu55 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu26 ATAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu54_v1 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu54_v1 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu35 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu34_v2 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu56 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu25 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu36 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu34_v1 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu39 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu37 AGAACCATGCTACGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu33 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu40 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu29 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT
U3_alyu32 AGAACCATGCTGCGAAGCGTATATCGGGTATTTATAGACTTCTAGCCAGCTAGAAGTTT

U3_alyu14 ACACGTGAC-AGATTTTGTATTTTGTGTA--AATAACGAAGAAATTCGTATA-TGATATTA
U3_alyu15 ACACGTGAC-AGATTTTGTATTTTGTGTA--AATAACGAAGAAATTCGTATA-TGATATTA
U3_alyu19 ATACTGTAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_jgf1_v1 ACACGTGAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_jgf1_v2 ACACGTGAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_alyu17_v1 ACACGTGAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_alyu17_v2 ACACGTGAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_alyu21_v1 ACACGTGAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_alyu21_v2 ACACGTGAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_alyu18 ACACGTGAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_alyu24 ACACGTGAC-AGATTTTGTATTTTGTGTA--CAT-TACGAAGAAATTCGTATA-TGATATTA
U3_alyu16 ACACGTGAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_alyu22 ACACGTGAC-AGATTTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATA-TGATATTA
U3_alyu41 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu53 AC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu50 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu47 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu49 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu51 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu48_v2 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu48_v1 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu42_43 CG-TTGATTTGATATTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu43_v2 CT-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu44_45 CG-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu55 CC-TTGACTTGTATTTGTATTTTGTGTA--AAG-TACGAAGAAATTCGTATATTGATAATA
U3_alyu26 CC-TTGATTTGATATTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu54_v1 TC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu54_v1 TC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu35 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu34_v2 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu56 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu25 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu36 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu34_v1 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu39 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu37 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu33 CC-CTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu40 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu29 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA
U3_alyu32 CC-TTGACTTGTATTTGTATTTTGTGTA--AAT-TACGAAGAAATTCGTATATTGATAATA

Poly(A) signal PIO (mapped by Bentham et al. 1999 and Guyot et al. 2022)

U3_alyu14 ATAAAACACCTGGGTGTTTAAATGTTTACATTAATAGTATCCTGAATGTACACAATAA
U3_alyu15 ATAAAACACCTGGGTGTTTAAATGTTTACATTAATAGTATCCTGAATGTACACAATAA
U3_alyu19 ATAAAACACCTGGGTGTTTAAATGTTTACATTAATAGTATCCTGAATGTACACAATAA
U3_jgf1_v1 ATAAAACACCTGGGTGTTTAAATGTTTACATTAATAGTATCCTGAATGTACACAATAA
U3_jgf1_v2 ATAAAACACCTGGGTGTTTAAATGTTTACATTAATAGTATCCTGAATGTACACAATAA
U3_alyu17_v1 ATAAAACACCTGGGTGTTTAAATGTTTACATTAATAGTATCCTGAATGTACACAATAA
U3_alyu17_v2 ATAAAACACCTGGGTGTTTAAATGTTTACATTAATAGTATCCTGAATGTACACAATAA
U3_alyu21_v1 ATAAAACACCTGGGTGTTTAAATGTTTACATTAATAGTATCCTGAATGTACACAATAA

U3_alyu24 ATAAAGCATGTGGCCGACAACTTTAGTGGTGGCCAGATGTCCCAGTTAGTGCGCC---
U3_alyu16 ATAAAGCATGTGGCCGACAACTTTAGTGGTGGCCAGATGTCCCAGTTAGTGCGCC---
U3_alyu22 ATAAAGCATGTGGCCGACAACTTTAGTGGTGGCCAGATGTCCCAGTTAGTGCGCC---
U3_alyu41 ATA-----GTGGACGTTGGATTCACAGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu53 ATA-----GTGGACGTTGGATGCCACGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu50 ATA-----GTGGACGTTGGATTCACAGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu47 ATA-----GTGGACGTTGGATTCACAGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu49 ATA-----GTGGACGTTGGATTCACAGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu51 ATA-----GTGGACGTTGGATTCACAGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu48_v2 ATA-----GTGGACGTTGGATTCACAGATCGGACGATCGT---GGTTTGATGAACCTATG
U3_alyu48_v1 ATA-----GTGGACGTTGGATTCACAGATCGGACGATCGT---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 ATAAAGCATGTGGCCGACAACTTTAGTGGTGGCCAGATGTCCCAGTTAGTGCGCC---
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U3_alyu14 ---ACGTAAGCACGGGGACTAT
U3_alyu15 ---ACGTAAGCACGGGGACTAT
U3_alyu19 ---ACGTAAGCGCTGGGGCTTAT
U3_jgf1_v1 ---ACGTAAGCACGGGGACTAT
U3_jgf1_v2 ---ACGTAAGCACGGGGACTAT
U3_alyu17_v1 ---ACGTAAGCGCTGGGGCTTAT
U3_alyu17_v2 ---ACGTAAGCACGGGGACTAT
U3_alyu21_v1 ---ACGTAAGCGCTGGGGACTAT
U3_alyu21_v2 ---ACGTAAGCACGGGGACTAT
U3_alyu18 ---ACGTAAGCACGGGGACTAT
U3_alyu24 ---ACGTAAGCACGGGGACTAT
U3_alyu16 ---ACGTAAGCACGGGGACTAT
U3_alyu22 ---ACGTAAGCACGGGGACTAT
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
