Appendix 1. 111 CBSV sequences downloaded from GenBank all with the highly conserved DAG motif in the coat protein.

Consensus	110 120 130 140 154 162 170 180 190 200 210 220 230 Integrace contransistic contrans
Identity	
1. LT560315	CTTCGTGCCCCTCAAGTAGCCCGTGTGAATGAATTGCTTCAACAACTGAAAAGTGCTGGGATACAAACAA
2. LT560309	CTTCGTGCCCCTCAAGTAGCCCGTGTGAAGAATTGCTTCAACAACTGAAAGAAGGTGGGATACAAAGAGCAAAAGGCCGTGTGGAGAACCCGATGAAGGGGAAGTGCTAATCAGAGTGAAGGGAAGTGCAAGTGAAGGAGAACGA L R A P Q V A R V N E L L Q Q L K D A G I Q T S K R P C G E P D E G E V A N P E S S E D
3. LT560302	CTTCGTGCCCCCAGGTAGCTCGTGTGAAC GAACTGATTAAACAACTGAAGGAAGGCGGGGAGGCCATGTGGGAGGAGCCTGATGGGGAGAGGGGGGGG
4. LT560282	CTTCGTGCCCCTCAGGTAGCCCGTGTGAACGACTGCTGAAACAACTGAAGGAGGTGCGGGATACAAACAA
5. LT560294	CTTCGTGCCCCTCAGGTAGCTCGTGTGAACGAACTGCTGAACAACTGAACGAAGTGAAGGAGAGTACTAACAAGTAAAAAGGCCAGGGGAGGGCCTGGTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
6. LT560305	CTTCGTGCCCCCAGGTAGCTCGTGTGAACGACTGCTTAAACAACTGAAGGAAG
7. LT577538	CTTCGTGCCCCCAGGTAGCTCGTGTGGAGCAGCTGCTTAAACAACTGAAGGAAG
8. LT577537	CTTCGTGCCCCCAGGTAGCCCGTGTGAACGAACTGCTTAAACAACTGAAGGAAG
9. LT560330	CTTCGTGCTCCTCAAGTGGCCCCTGTGAACGAACTGCTCAAACAACTAAAAGAAGTGCGGGATACAAACGAGTAAGAAGGCCATGTGGAAGGAA
10. LT560329	CTTCGTGCTCCTCAAGTGGCCCGTGTGAACGACTGCTTAAACAACTAAAAG AGTGCTGGG ATACAAGAAGAAGCAAGTAAGAAGGCCATGTGGAAGGAAG
11. LT560328	CTTCGTGCTCCTCAAGTGGCCCGTGTGAACGAACTACAACTAAAAGAAGTGCGGGATACAAACAA
12. LT560327	CTTCGTGCTCCTCAAGTGGCCCGTGTGAACGAACTGCTCAAACAGCTAAAAGAAGGGGCATGTGGAGGAGCCTGGTGGAGGAAGGA
13. LT560326	CTTCGTGCTCCTCAAGTGGCCCGTGTGAACGAACTGCTCAAACAGCTAAAAGAAGGGGCATGTGGGAGAACCTGATGAAGGAAG
14. LT560325	CTTCGTGCTCCTCAAGTGGCCCCTGTGGACGACGCGCATGTGGGACGAGGAGGCAGGGCATGGGGAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA
15. LT560324	CTTCGCGCTCCTCAAGTGGCCCGTGTGGATGAATGCTTAAACAACTGAGAGAGGCTGGGATACAAACAA
16. LT560323	CTTCGCCGCCTCGTCAAGTGGCCCGTGTGGGAGAAGTGCTTAAACAACTGAGGAGAGTGCGGGGATACAAGGAAGCAAGGTAAGAGAACCATGTGGAGGAGAAGCAGGGAGAAGCTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA
17. LT560322	CTTCGCGCTCCTCAAGTGGCCCGTGTGGATGAATTGCTTAAACAACTGAGAGAGTGCTGGGATACAAACAA
18. LT560321	CTTCGCCGCAGTGGCCCGTGTGGGAGAGTGCTTAAACAACTGAGGAGAGTGCGGGATACAAACAA
19. LT560320	CTTCGCGCTCCTCAAGTGGCCCGTGTGGATGAATTGCTTAAACAACTGAGAGAGTGCTGGGATACAAACAA
20. LT560319	CTTCGTGCTCCTCAAGTGGCCCGTGTGGACGCACTGCTTAAACAACTAAAAGATGCTGGGATACAAACAA
21. LT560318	CTTCGTGCTCCTCAAGTGGCCCGTGTGAACGAACTGCTTAAACAACTAAAAGATGCTGGGATACAAACAA
22. LT560317	CTTCGTGCTCCTCAAGTGGCCCGTGTGAACGAACTGCTTAAAACAACTAAAAGATGCTGGGATACAAACAA
23. LT560316	CTTCGTGCTCCTCAAGTGGCCCGTGTGAAC GAACTGCTTAAACAACTAAAAGAGCTGGGATACAAACAAGTAAGAAGGCCATGTGGAGAAGGAAG
24. LT560313	CTTCGTGCTCCTCAAGTGGCCCGTGTGAATGAACTGCTTAAAACAACTAAAAGAAGTGTGGGATACAAACAA
25. LT560312	CTTCGTGCTCCTCAAGTGGCCCGTGTGAACGACTGCTTAAACAACTAAAAGATGCTGGGATACAAGTAAGAAGGCCATGTGGAGAAGGAAG
26. LT560311	L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E L D C G E V A S F E S S E D ICTICGTGCTCCTCAAGTGGCCCCTGTGGAAGGAAGCTAAACAACTAAAGAAGGCAAGTAAGAAGGCAAGTGGAGAAGGAAG
27. LT560310	CTTCGTGCCCCCAGGTAGCCCGTGTGAACGAACTGAACAACTGAAGGAAG
28. LT560308	L R A P Q V A R V N E L L K Q L K D A GOATGCTGGA ACAACTAACTAACTAACTAACTAACTAACTAACTAACT
29. LT560307	L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E P D C G E V A S P E S S E D ICTICGTGCCCCCAGGTAGCTCCTGTGGAGCAGCGCTGCTAAACAACTGAAGAGGAGGTGCTGGAGAGCAGCGGAGGAGCCTGGTGGAGGAGGAGGAGGAGGAGGAGGAG L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S E D
30. LT560306	L K A P V V A K V N E L L K V L K U L K U L K U L K U K F L G E P D E G E V A S P E S S E D CTTCGTGCCCCCCGTGGTGGCTCGTGTGAAGGAGCTGCTTAAACAACTGAAGGAGGTGCGGATACAACAAGTAAAAGGCCATGTGGGGAGGAGCCTGATGAAGGAGGGGCCGAGGGAGG

Consensus Interface Interface <t< th=""></t<>
31. LT560304 Introduction of an one of a construction of an one of a construction of a const
32. LT560303 Intercention of the analysis of the
33. LT560301 LT 5 & A B D A B
31. LT560290 E R P O N R P O N R P O N A F P C G F <t< th=""></t<>
36. LT560298 CTCCTGCCCCTCAGCTAGCTGAACGAACCCTGAACGAACCCTGAGCGAACGCGAACGCGAAGGAACGCCTGGAAGGAA
33. LTS60297 IF R A P 0 IV A R IV A I R I
37. LT560297 Int Condeccent Actor Actor Control Contro Control Control Contrecontrol Control Control Contrecontrol Contr
38. LT560296 CTCGTGCCCCTCAGGTAGCCCGTGTGAAC GAAC GCAC GC
39. LT560295 CTCCGTCCCCCCTAGGTACCCCGTCGAACGAACTCCTTAAACAACTGAACGAAC
40. LT560293CTTCGTGCCCTCAGGTAGCTCGTGTGAACGAACTGCTAAACAACTGAACGAAGGGTTGGGGATACTAACAGTGAAAGGCCATGTGGAGAGCCTGATGAAGGAGAGTTGCTAGCCCAGGGTCAAGTGAAGGACGAGGT41. LT560292CTTCGTGCCCTCAGGTAGCTCGTGGACGACGTGCTGAACGAAC
41. LT560292CT ICG IGCCCCTCAGG AGCTICGT GAAC GACTIGCT AAACAACTIGAA GAAC GACTIGCT GAAC GAACTIGCT GAACGAACTIGCT GGAACGAACTIGCT GGAACGAACTIGCT GAACGAACTIGCT GAACGAACTIGCT GAACGAACTIGCT GAACGAACTIGCT GAACGAACTIGCT GAACGAACTIGCT GAACGAACTIGCT GAACGAACTIGT GGAAGGAACTIGCT GGAAGGACCTIGCT GAACGAACTIGCT GAACGAACTIGCT GAACGAACTIGCT GGAACGAACTIGT GGAAGGACCTIGT GGAAGGAACGT GCCCAGACTIGCT GAACGACCAGGA44. LT560289CT ICG IGCCCCTCAGG TACCCCTIG IGCAACGAACTICCT TAAACAACTIGAAGGAATGCT GGAAACAACTIGT GAAGGAACGACTIGCT GAACGAACTIGCT GAACGAACTIGCT GGAAACAACTIGAAAGAACTIGGAAAGGACTIGCT GAAGGAAGGCT IGC TAACAACAACTIG GAAGGAACGACTIGT GAAGGAAGGCT IGC TAACAACAACTIGAAGGAAGGACTIGCT GAAGGAAGGCT IGC TAACAACAACTIG GAAGGAAGGCT IGC TAACAACAACTIG GAAGGACGAGCT IGC TAACAACAACTIG GAAGGACGAGCT IGC TAACAACAACTIG GAAGGACGAGCT IGC TAACAACAACTIG GAAGGACGAGCT IGC TAACAACTIG GAAGGACGAGCT IGC TAACAACAACTIG GAAGGACGAGCT IGC TAACAACTIG GAAGGACGAGCT IGC TAACAACTIG GAAGGACGAGGATIGC TAACAACTIG GAAGGACGAGCT IGC TAACAACTIG GAAGGACGAGGATIGC TAACAACTIG GAAGGACGAGCT IGC TAACAACTIG GAAGGACGAGCT IGC TAACAACTIG GAAGGACGAGGATIGC TAACAACTIG GAAGGACGAGCT IGC TAACAACTIG GAAGGACGAGGATIGC TAACAACTIG GAAGGACGAGGCT IGC TAACAACTIG GAAGGACGAGGATIGC TAACAACTIG GAAGGACGAGGCT IGC TAACAACTIG GAAGGACGAGGATIGC TAACAACTIG GAAGGACGAGGATIGC TAACAACTIG GAAGGACGAGGCT IGC TAACAACTIG GAAGGACGAGGATIGC TAAGAACAACTIG GAAGGACGAGGCT IGC TAACAACTIG GAAGGACGAGGATIGC TAACAACTIG GAAGGACGAGGATIGC TAAGAACAACTIG GAAGGACGAGGCT IGC TAACAACTIG GAAGGACGAGGATIGCC
42. LT560291 CTCCTGCCCCCAGGTGGGTCGTGTGAAC GAACTGCTTAAACAACTGAACGGGGTACTAACAAGTGAAAGGCCTGTGGAGAGCCTGATGAAGGAGGGGTGCTAGCCAGGGGCCGAGGGCCCAGGTGAGGCCCAGGTGCCAAGGGAAGGCGGGGCAACAAACA
43. LT560290 CTCCGTGCCCCCAGGTAGGTCGTCGAACGAACGCGACGTCGTAAACAACTGAACGAGGTAGCAAGGTAGAAGGAGGCTGGTAGCCCAGGGGAGGCCGAGGAGGGTGGTAGCCCAGGGGAGGCCGAGGAGGGTGGTAGCCCAGGGGGAGGCCGAGGAGGGTGGTAGCCCAGGGGGGGAGGCGGAGGGGAGGCGGAGGGGAGGGTGGTAGCCCAGGGGGGGG
44. LT560289 CTCCTGCCCCCCAGGTAGCCCGTGTGAACGAACTGCTTAAACAACTGAACGAGGGTAGCAACAGTGAAAGGAGAGGCTGGTGCAAGGAAGG
46. LT560287 46. LT560287 47. LT560286 48. LT560285 48. LT560285 49. LT560285 49. LT560284 49. LT560284 49. LT560284 49. LT560284 49. LT560284 49. LT560284 49. LT560284 49. LT560285 49. LT560284 49. LT560285 49. LT560285 49
46. LT560287 CTTCGTGCCCCTCAGGTAGCCCGTGTGAACGAACTGCTTAAACAACTGAAGGGGGTAGCAACAGTAAAAGGCCATGTGGAAGGAGGGCTGGTGAAGGAGGGGGCGTGGTGCAAGTGAAGGAGGGGGCGGAGGCCGGAGGAGGGTGCTAGCCCAGGTGAAGGAGGGGGGGG
47. LT560286 CTCCTCCTCCCCCCAGGTAGCCCCTGTGAACGAACTGCTTAAACAACTGAACGAGGAACGACGAGGCCAGATGCAAGGAGAGGCCTGATGAAGGAGAGGGTGCTAGCCAGAGTCAAGTGAAGGAGGAGGCCAGTGCTAGCCAGGGGAGGCCAGGTGCAAGGAGGGGGGGG
48. LT560285 CTCGTGCCCCCCAGGTAGCCCGTGTGAACGAACTGCTTAAACAACTGAAGGGGAGGCCATGTGGAGGGAG
L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S E D E E
50. LT560283
51. LT560281
52. LT560280
53. LT560279
54. KR911743
55. KR911742
56. KR911741
57. KR911740
58. KR911739
59. KR911738
60. KR911737

Consensus	110 120 130 140 154 162 170 180 190 200 210 220 230 2 CTTCGTGCCCCTCAAGTAGCCCGTGTGTGAACGAACTGCTTAAACAACTGAAGGAAG
	LRAPQVARVNELLKQLK <mark>DAG</mark> IQTSKRPCGEPDEGEVVASPESSEDEE
Identity	
61. KR911736	ICTICGIGCCCCICAGGIAGCCCGIGIGAACGAACIGCITAAACAACIGAAGGAGGGGGGGGATACAAACAAGTAAAAGGCAIGIGAGAGAGCCIGAIGAAGGAGAGGGIIGCIGAGAGAGGICAACIGAAGACGAGG L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S E D E E
62. KR108833	ICTICGIGCICCICAAGIGGCCCCIGIGAACGAACIGCITAAACAACIGAAA <mark>GAIGCIGGG</mark> ATACAAACAAGIAAGAGGGCAIGIGGGGAAACCIGAIGAGGGGAGAAGIIGCIGAGGGCAAGIGAAGGGGGGAGA I R A P Q V A R V N E L I K Q I K <mark>D A G I</mark> Q T S K R P C G E P D E G E V A S S E S S E D E E
63. KR108832	ICTTCGWGCTCCTCAAGTAGCTCGTGTGAATGAACTGCTTAAACAACTGAAAG ATGCTGGG GTGCAAACAAGTAAAAGGCCATGTGGAGARCCTGATGAAGGGGAAGTTGYYAGCCCAGAGYCAACTGAAGATGAAGATGAGGA L R A P Q V A R <mark>V N E L L K Q L K D A G M/V Q T S K R P C G E P D E G E V A/V S P E P/S S E D E E</mark>
64. KR108831	CTTCGTGCTCCTCAAGTAGCTCGTGTGAATGAACTACTAAAACAACTGAAAACAAGTGGAGAACAAGTAAAAAGGCCATGTGGAGAACCTGATGAAGGGGAGGTTGCTAGCCCAGAGTCAAGTGAAGACGAGGA L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S E D E E
65. KR108830	ICTTCGTGCCCCTCAGGTAGCTCGTGTGAACGAACTGCTTAAACAACTGAAGCGAAGGTGGGGGAGGCCTGATGAAGGAAG
66. KR108829	ICTTCGCGCTCCTCAAGTAGCTCGTGTGAACGAACTGCTTAAAAAAACTGAACTGAAGAGTGCTGGAAAAAGGCCATGTGAAGAGGCCTGATGAAGGGGAAGTTGCCAGGCCAGAGTCAAGTGAAGGAGGAAGT L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S E D E E
67. KR108828	ICTTCGTGCCCCTCAAGTAGCTCGTGTGAATGAACTGCTTAAAAAACTGCTTGAAACAACTGCAAACAAGTAAAAGGCCATGTGGAAGGCCTGATGAAGGTGAAGGTGCAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTCAAGTGAAGGTGAAGGTGAAGGTCAAGTGAAGGTCAAGTGAAGTGCAAGTGAAGTGCAAGTGAAGTGCAAGTGAAGTGCAAGTGAAGGTCAAGTGAAGTGCAAGTGAAGTGCAAGTGAAGTGCAAGTGAAGTGCAAGTGAAGTGCAAGTGAAGTGCAAGTGAAGTGCAAGTGGCCTGATGGAGTGGAGTGGAGTGGAGTGGCTGAAGTGGAGTG AGTGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGGTGGAGGTGGGAGGTGGAGGGGGG
68. KJ606250	ICTTCGTGCTCCTCAAGTGGCCCCGTGTGAATGAACTGCTTAAACAACTGAAAG ATGCTGGA ATACAAACAAGTAAGAAGGCCATGTGGAGAAGCCTGATGAAGGAGAAGTTGCTAGCCCAGAGTCAAGTGAAGATGAGGA
69. KJ606249	CITCGIGCCCCICAAGIAGCICGIGIAAAIGAACIGCTICAACAACIGAAA <mark>GAIGCIGGG</mark> ATACAAACAAGIAAAAGGCCGIGIGGGGAAGCIGAAGGGGAAG <mark>IIGCIAGCCCAGAAIC</mark> AAGIGAAGACGAGG L R A P Q V A R V N E L L Q Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S E D E E
70. KJ606247	CTTCGTGCCCTCAGGTAGCTCGTGTGAACGAACTGCTTAAACAACTGAAGCGAAGGGGTGCAAGGTAAAAGGCCATGTGGGAGGAGGGCGTGATGCAAGGGGGAGGGTGACGAGGGCGAGGTGAAGGAGGAGGGCGAGGGTGACGAGGGGGGGG
71. KJ606246	CTICGTGCCCCTCAGGTAGCTCGTGTGGACGAACTGCTTAAACAACTGAAGCGAGGGTGCAAGGTAAAAAAGCCATGTGGGAGGAGGCCTGATGAAGGAGGAGGGTGCTAGCCCAGAGTCAAGTGAAGACGAGG L R A P Q V A R V D E L L K Q L K D A G I Q T S K K P C G E P D E G E V A S P E S S E D E E
72. KJ606245	CTTCGTGCCCCTCAGGTAGCTCGTGTGGACGAACTGCTTAAACAACTGAAGCGAGGGTGCAAGGTAAAAAAGCCATGTGGGAGGAGGCCTGATGAAGGAGGAGGTGCTAGCCCAGAGTCAAGTGAAGACGAGG L R A P Q V A R V D E L L K Q L K D A G I Q T S K K P C G E P D E G E V A S P E S S E D E E
73. KJ606244	CTTCGTGCTCCTCAAGTGGCCCCGTGTGAATGAACTGCTTAAACAACTGAAAGATGCTGGGAAACAAGTAAGAGGCCATGTGGGAGAACCTGATGAAGGAGAAGTTGCTAGCCCAGAGTCAAGTGAAGATGAGA L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S E D E E
74. KJ606243	CITCGTGCCCCTCAGGTAGCTCGTGTGAACGAACTGCTTAAACAACTGAACGAAC
75. KJ606242	CITCGTGCTCCTCAAGTGGCCCGTGTGAATGAACTGCTTAAACAACTGAAAGAAG GATGCTGGGA ATACAAACAAGTAAGAGGCCATGTGGGAGAACCTGATGAAGGAGAAGTGCTAGCCCAGAGTCAAGTGAAGGAGAAGTGAAGGAGAAGTGCTAGCCCAGAGTCAAGTGAAGGAGAAGTGAAGGAGAAGTGCTAGCCCAGAGTCAAGTGAAGGAGAAGTGAAGGAGAAGTGCTAGCCAGAGTCAAGTGAAGGAGAAGTGCTAGCCAGAGTCAAGTGAAGGAGAAGTGCTAGCCAGAGTCAAGTGAAGGAGAAGTGCAAGTGAAGGAGAAGTGCTAGCCAGAGTCAAGTGAAGAGAGAG
76. KJ606241	CTTCGTGCCCCTCAGGTAGCTCGTGTGAACGAACTGCTTAAACAACTGAACGAGCGGGGATACAAACAA
77. KJ606240	CTICGTGCCCTCAGGTCGTGTGAACGAACTGCTTAAACAACTGAACGAAC
78. KJ606239	CITCGTGCCCTCAGGTAGCTCGTGTAAACAACTGCTTAAACAACTGAACAACTGGGGAACAACAAGTAAAAGACCATGTGGAAGGAGCAGGAGGAGGAGGAGGATGCTAGGCCAGAGTGACGACGACGACGACGACGACGACGACGACGACGACGACG
79. KJ606238	CITICGTOCICCTCAAGTGGCCCGTGTGAATGAACTGCTTAAACAACTGCAAACAACTGGAACAACAAGTAAGAGGCCATGTGGGAGAACGTGATGAAGGAAG
80. KJ606237	CITICG TGCCCTCAGGIAGCTCGI GTGAACGAACTAGCAACTGAACAACTGGAGGAGAGCTGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA
81. KJ606236	CITICG TOCTCCTCAAG T GAATGAATGCTAAACAACTAAACAACTGCAAACAAGTAAACAAGTAAGAGGCCATGTGGAAGAACGTGATGAAGGAAG
82. KJ606235	ICT T CG T GC T CC T CAAG T G G C C CG T G T G AAT G C T T A ACCAAC T G A A G A T G C T G G A G A G C C A T G T G G A G A G C C T G A T G A G G A G C C A G A G T G C C A G A G T C A G T G A T G A T G A G G A G C C A G A G T G A T G A G A
83. KJ606234	L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S D D E E CITICGIGCCCTCIAGGIAGCICGIGIGAAGGAACIGCITAAACAACIGAAG <mark>AGGCIGGGA</mark> TACAAACAAGIAGAAAAGCCCIGIGGAGAGGCIGCIGAAGAGGGGAGGCIGAAGIGAAGAAGAAGACGAGGA D D D D D D D D D D D D D D D D D D D
84. KJ606233	L R A P Q V A R V N E L L K Q L K D A G I Q T S K K P C G E P D E G E V A S P E S S E D E E CTTCGTGCCCCTCAGGTAGCTCGTGTGAACGAACTGCTTAAACAACTGAAG <mark>ATGCTGGG</mark> ATACAAACAAGTAAAAAGCCATGTGGAGAGGCCTGATGAAGGAGAGGGTTGCTAGCCCAGAGTCAAGTGAAGACGAGGA
85. KJ606232	L R A P Q V A R V N E L L K Q L K D A G I Q T S K K P C G E P D E G E V A S P E S S E D E E CITCGIGCCCCICAGGIAGCICGIGIGAACGAACIGCIIAACAACIGAAG <mark>AIGCIGGG</mark> AIACAAACAAGIGAAAAAGCCAIGIGGAGAGCCIGAIGAAGGAGAGGGIGCAAGIGAAGACGAGGA
86. KF878104	L R A P Q V A R V N E L L K Q L K D A G I Q T S K K P C G E P D E G E V A S P E S S E D E E CTTCGTGCCCCTCAAGTAGCTCGTGTGAATGAACTGCTTCAACAACTAAAA <mark>GATGCTGGG</mark> ATACAAACAAGTAAAAGGCCGTGTGGAGAACCTGATGAAGGGGAAGTTGCTAGCCCAGAGTCAAGTGAAGACGAGG
87. HM346960	L R A P Q V A R V N E L L Q Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S E D E E CITCGTGCTCCTCAGTGGCCCGTGTGGACTGCTTAAACAACTGAGAGAGA
88. HM346959	L R A P Q V A R V S E L L K Q L R D A G I Q T S K R P C G E P D E G E L A S P E S S E D E E CTTCGCGCCCCTCAAGTAGCTCGTGTGGACGAACTGCTCAAACAACTGAAGAGTGGAGGCAAGTAAAAGGCCATGTGGAGAGCCTGATGAAGGGGAAGTTGCTAGCCCAGAGTAAGTGAAGACGAGGA
89. HM346958	L R A P Q V A R V D E L L K Q L K D A G I Q T S K R P C G E P D E G E V A S P E L S E D E E CTTCGTGCTCCTCAAGTGGCCCCGTGTGAATGAACTGCTTAAACAACTGAAACAAGTGGAGAGCCATGTGGAGGAAGCTGATGAAGGAGAAGTTGCTAGCCCAGAGTCAAGTGAAGACGAGGA
90. HM346957	L R A P Q V A R V N E L L K Q L K D A G I Q T S K R P C G E P D E G E V A S P E S S E D E E ICTICGTGCCCCCCAAGTAGCCCGTGTGAAATGAACTGCTTCTACAACTGATGAAGAAG <mark>ATGCTGGG</mark> ATACAAACAAGCAAAAGGCCGTGTGGAGAAGCTGGTGGGAAGTTGCTAATCCAGAGTCA-GTGAAGACGAGGG
30.110307	