

1 tgaggggtgagggcgggcggggagctcggctcgtagtcgggcgcgcgagccggggccgtttttgaggggtggtgactgtgtgtcctccca
91 ttataggtagctatccatccaccacagttacgATGAGGTGTCCAAATCATCGAGCACAAACATGCAGGTCAGCTTCGTGTGCAGCGGT
1 M E V S K S S S T T M Q V S F V C Q R
181 GCTGTACGCGCTCAAGCTGGACACGTCTTTAATGTCTCGACCGGTCACAGTCCATGAACCTACAGCACCGGTTAGTCACAGTGACAC
20 C C Q P L K L D T S F N V L D R V T V H E L T A P L V T V T
271 CGAGTAAACAGCGGAGAGCTCCGAGGGGAGACGGCACCAGAGGAGGCATTGTAGAAAAACAAAGATGGCGGTCAAGAAAGTACA
50 P S K Q A E S S E G E T A P E E A F V E N K Q D G V S R K Y
361 TCCACACGACGCGATGATGTCAACGGAGAGCGCCAACAGCTTCACGCTGATTGGAGAAGCATCTGATTGTGGCAACATGGAACATCTCA
80 I P P A R M M S T E S A N S F T L I G E A S D C G N M E H L
451 GTCGTAGGCTGAAGGTACCACTGACCTGTTTGACATCATGTGAGGCCAGACAGCTGGACACCCGCTCTGTGAGGAGTGTACCGACA
110 S R R L K V T S D L F D I M S G Q T D V D H P L C E E C T D
541 CACTGTGGACACCTCGACACAGCTCAATATCACAGAGAACGAATGCCAGAATTACAAGCAATGTCTGGAGCTGTGTCAAATCTGC
140 T L L D H L D T Q L N I T E N E C Q N Y K Q C L E L L S N L
631 AGGTGGAGGACGAGAACTCTGCTGGCCGAGCTGCAGCAGCTGAAGGAGGAGGAGGACGCGCTGGTGGAGAACTGGAGACGGTGGAGG
170 Q V E D E E T L L A E L Q Q L K E E E A A L V E E L E T V E
721 AGCAGAGGGCTGTGTGGCCGACGACCTGGCCAGTGCAGGTCCTCCCAACAGCTCGACACAGAGGAGCTCCAGTATCAGAAAGAGT
200 E Q R A A V A D D L A Q C R V H S Q Q L D T E E L Q Y Q K E
811 ACAGCGAGTTCAAACGGCAGCAGCTGGAGCTGGACGACGAGCTGAAGAGTGTGACAACCAGATGCGCTACTGCCAGATTAGCTGGATC
230 Y S E F K R Q Q L E L D D E L K S V D N Q M R Y C Q I Q L D
901 GTTTAAAAAGACCAATGTCTTTAATGCCACTTTTCACATCTGGCACAGTGGCCAGTTTGGCACAATCAACAACCTCCGCTGGGTGCGAC
260 R L K K T N V F N A T F H I W H S G Q F G T I N N F R L G R
991 TCCCCAGCGTCCCCGTGGAGTGAACGAGATCAATGCAGCCTGGGGCCAGACGGTGTGCTACTGCACGCTCTGGCCAATAAGATGGGGC
290 L G R L P S V P V E W N E I N A A W G Q T V L L L H A L A N
1081 TGGCCTTCAAAGATATCGTCTTGTTCATATGGAACCACTCATACTGGAGTCACTGACAGATAAGTCAAAGAACTGCCTCTGTACT
320 K M G L R F K R Y R L V P Y G N H S Y L E S L T D K S K E L
1171 GTTCAGGAGGCTTGAAGTCTTCTGGGACAATAAATTCGACCACGCCATGGTGGCTTTTCTGGACTGTGTCCAGCAGTTCAAAGAGGAGG
350 P L Y C S G G L R F F W D N K F D H A M V A F L D C V Q Q F
126 TGGAGAAAGGAGACACTGGATTCTGCCTCCCGTACAGGATGGATGTGGAGAAAGGAAGATCGAGGACACTGGCGGCAGCGCGGCTCGT
380 K E E V E K G D T G F C L P Y R M D V E K G K I E D T G G S
1351 ACTCCATCAAAACCCAGTTCAACTCGGAGGAGCAGTGGACCAAGCGCTCAAGTTCATGCTACTAACCTGAAGTGGGGACTGGCTGGG
410 Y S I K T Q F N S E E Q W T K A L K F M L T N L K W G L A W
1441 TCACCTCGCAGTTCTACAACAGATAGgctggcagactcctcctggccatttcaattaggtttcacatgaatatagatgataaagaacta
440 V T S Q F Y N R *
1531 ttggatcatttttggattttcagtactaacggcacaggactcatatcgatcttcaagaagggtgttacaaggcgactttgaaagtag
1621 aataactactactcacacagttttatcacaaataactaattttacttcgacactcttcaatgtagttgaaaaaattcttctctagtctgtt
1711 ggacgcacagcacagcccagtttccagtaggtggatgtcaagtggttctgtgtacgttaagtcattacgataaaatgttacatttttaag
1801 caaaccacagtgaaactgcttcagacacatttgaatttgttctgtatgttcaagtcatttccactgattaaacatccactactggta
1891 ataaaaaggcatcacgtgtatcctggtaatacctaactgttactgtctgtcctaattccccctaataaagcatcagaggacgtttgtg
1981 ccacaagaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Figure S2 Nucleotide and amino acid sequences of Beclin-1 of *T. fasciatus*. Note: The predicted APG6 domain is marked with straight line in black and BH3 box is marked with wavy line in red. The start codon and end codon are in blue.