

1 aggaagtaaacacagctcttgtcaagattaaaagctgcgccacaaacctctgccgtatgttcgagtgtaacacttgctagtgttcagttta
 91 ctgactaatccagctttttacgcgcagatcggagcagaATGTCGGTGACAGTGAAGGCCTACCTGCTGGGGAAGGACGAGGTGGTCAAGGA
 1 M S V T V K A Y L L G K D E V V K E
 181 GGTCGGGAGGTTTTCGGTGGACCAGGACGTCTCATCCAGCTTTGAGTACCTCTGCCGGAAGACCGCAGAGATCTTTAACAACTGAAAAA
 19 V R R F A V D Q D V S S S F E Y L C R K T A E I F N N L K N
 271 CAGCGGATTTAACATGTTCTACAAAGATGAAGATGGAGACCTGGTTGCATTTTCCTCTGACGATGAACCTCTGATGGGACTGGCCTGCAT
 49 S G F N M F Y K D E D G D L V A F S S D D E L L M G L A C M
 361 GAAGGACTCCACCTTCCGCATCTTTATCAAAGAGAAGAAGGAGCACCCTCGAGACTTCCCTCTTCATGCCTTCCCTCCTTTCGGGTTTGG
 79 K D S T F R I F I K E K K E H R R D F P L H A F P P F G F G
 451 CCACCTCCTCCCCACCCGAGCTCATCATACTCTGCCGCACCAATGGCCCTCCCCAGGTGCTGCACCTAATGTACCTGTGACGG
 109 H P P P P P G A H H T L P H P M A P P Q V L H P N V T C D G
 541 CTGCGAGGGGCTGTTGTTGAACTCGTTCAAGTGTTCAGTCTGTCCAACTACGATCTTTGCTCTGCCTGCCAGGCTAGAGGGATGCA
 139 C E G P V V G T R F K C S V C P N Y D L C S A C Q A R G M H
 631 CACTGAGCAGTTTCTGCTGCCTATCTGGCACCCGCTGCAGTGGTTTCCACGTGGGAAGTGGATGAAGTGGATGAGACACTGCATGTGGAA
 169 T E H V L L P I W H P L Q W F P R G K W M K W M R H C M W N
 721 TCAGAACCACTCTCAGAATGTGAGCCAGAGCCAGAGCCAGAGCCAGGCCCTGATCAGCCTCCAGCTTCTACACCTGCTGCTGAGAGCAG
 199 Q N Q S Q N V S Q S Q S Q S Q A P D Q P P A S T P A A E S S
 811 TCTCCCTCTGACTCCCAGGCTAATGTGGATTTCCTGAAGAATATTGGTGAGGGCGTGGCAGCCATGCTGAGTCCACTGGGTATTGATGT
 229 L P S D S Q A N V D F L K N I G E G V A A M L S P L G I D V
 901 GGACATCGATGTGGAACACAGGGCCAGCGGGCTAAGGTGGTACCACCCCTTCAGAATGAGAGGGGTGAGGAAGACCTGGGGGTGGAGC
 259 D I D V E H E G Q R A K V V P P L Q N E R G E E D L G G G A
 991 CAATGATGGGGGTGGAGTCAAGACTGACTGTAGCACCAGTGTGGGAACACAAGGAAACAGGACTCTGATGAGGAGTGGACCCACCTGAG
 289 N D G G G V K T D C S T S V G T Q G N R D S D E E W T H L S
 1081 CCCCCAAGAGGTTGATCCTTCTACTGGAGAGCTGCAGTCACTGCAGGCCAGAGTCTGCCTTCAGGTGGACAGCAACATCCAACAGGTCT
 319 P K E V D P S T G E L Q S L Q A Q S L P S G G Q Q H P T G L
 1171 AAAGGAGGACGCTTTATACCCACCTTCCAGACGAGGCAGATCCTCGTCTAGTAGAGTCTTTGGCTCAGATGCTGTCAATGGGCTTCAC
 349 K E A A L Y P H L P D E A D P R L V E S L A Q M L S M G F T
 1261 AGATGAAGGCGGTTGGTTGACGCGTCTTCTGCAAGCCAAAACTATGACATTGGCGCCGCCCTTGATGCCATCCAGTACGCCAGACAACC
 379 D E G G W L T R L L Q A K N Y D I G A A L D A I Q Y A R Q P
 1351 TAACCCCAACAGCCCAGagctgtcacgggtgcaaccatgttgccttctgtcgtctggttcattcagtgatcattagtaataacctgacg
 409 N P Q Q P *
 1441 tgattacatgtttatgggaacaattaaaatgtacacttccaaaaaaaaaaaaaaaaaaaaaaaaa

Figure S3 Nucleotide and amino acid sequences of P62 of *T. fasciatus*. Note: The predicted PB1 domain is marked with straight line in black and Znf box is marked wavy line in red and UBA domain is marked with double wave line in blue. The start codon and end codon are in blue.