File S2 The gene model for *JcDof6.2* The coding region is marked with uppercase letters, above which are its deduced amino acids (the DOF domain is shown in red). The transcribed untranslated regions, including 5' UTR, intron and 3' UTR sequences, are marked with lowercase letters. The start and stop codons are marked with **bold** letters

```
   1 ctttcttgctttctcctttctctctctctctctctctctctggatctttctctgcaaa
  61 tactaaaactcctcctcttgttgatttgattctccacttgtgtgtattatctcacaaaaa
 121 ttaagaaccactcaatcaacctttacaagaaaaaagaaaagagagaaagctatagctcaa
   1           M  V  F  S  S  I  P  A  Y  L  D  P  A  N  W  Q  Q
 181 gaattgaaccATGGTTTTCTCTTCTATCCCAGCTTATCTTGATCCAGCCAACTGGCAACA
  18
 241 Agtaaggatttcttgaatttttttggtccttaaggtttctttatttctttgcctaaaaa
 301 gcaaaagattgtttcaaaagataaatattcttgttacttttatttcttgtatctttattt
  18                                          Q  P  N  N  H  H  Q
 361 tgaatataccagatatttgttcttctttctattttacagCAACCAAATAATCACCACCAG
  25 P  G  G  T  S  G  A  N  T  H  Q  L  P  P  P  P  P  P  P  P
 421 CCTGGCGGAACTAGTGGTGCAAACACTCATCAGCTTCCTCCACCTCCACCTCCACCACCA
  45 L  P  Q  P  H  G  S  G  G  A  G  S  I  R  P  G  S  M  A  D
 481 CTTCCTCAACCTCATGGAAGCGGAGGTGCGGGCTCGATCCGACCTGGTTCAATGGCAGAT
  65 R  A  R  L  A  N  I  P  M  P  E  T  A  L  K  C  P  R  C  E
 541 CGAGCCCGTCTGGCTAACATACCTATGCCAGAGACAGCATTAAAATGCCCAAGATGTGAA
  85 S  T  N  T  K  F  C  Y  F  N  N  Y  S  L  T  Q  P  R  H  F
 601 TCAACAAACACAAAATTTTGCTATTTCAACAACTACAGTCTTACGCAGCCTCGACACTTC
 105 C  K  T  C  R  R  Y  W  T  R  G  G  A  L  R  N  V  P  V  G
 661 TGCAAAACCTGTAGAAGGTACTGGACAAGAGGAGGTGCTCTAAGGAATGTCCCAGTTGGT
 125 G  G  C  R  R  N  K  R  S  K  G  S  N  S  K  S  P  V  S  G
 721 GGTGGTTGTAGGAGAAACAAAAGAAGCAAAGGAAGCAACTCAAAATCTCCGGTCAGTGGT
 145 D  R  P  T  G  S  G  S  S  S  T  V  S  S  N  S  G  T  S  D
 781 GATCGCCCAACGGGTTCTGGTTCCTCAAGTACCGTATCATCTAATAGTGGAACCAGTGAT
 165 M  L  G  L  V  P  Q  V  P  P  L  R  F  M  A  P  L  H  H  L
 841 ATGCTAGGCCTTGTACCACAGGTTCCACCGTTAAGGTTCATGGCTCCTCTTCATCATCTA
 185 S  E  F  A  T  G  D  I  G  L  N  Y  G  A  L  S  G  Q  V  G
 901 TCCGAATTTGCTACTGGAGATATCGGGTTAAACTATGGTGCCCTTTCAGGTCAAGTTGGA
 205 G  P  S  D  L  N  F  Q  I  G  S  A  L  A  S  V  G  L  G  G
 961 GGACCAAGTGACTTGAATTTTCAAATAGGGAGTGCTTTAGCTAGTGTTGGTCTTGGTGGT
 225 S  G  G  G  C  G  S  G  S  G  S  G  V  G  G  S  L  L  S  V
1021 AGTGGTGGTGGTTGTGGAAGTGGCAGTGGCAGTGGCGTTGGTGGTTCACTTTTGTCAGTG
 245 G  G  L  E  Q  W  R  L  H  Q  G  P  Q  F  P  F  L  G  G  L
1081 GGTGGTCTAGAGCAGTGGAGGTTACATCAAGGGCCGCAATTTCCTTTCTTGGGTGGGTTA
 265 D  S  S  S  S  N  S  G  L  Y  P  F  E  S  S  G  G  G  E  P
1141 GATTCTTCTTCTTCTAATTCAGGGTTATACCCATTTGAAAGTAGTGGTGGTGGTGAACCA
 285 S  G  Y  G  G  G  V  G  Q  V  R  P  K  I  S  S  S  L  T  T
1201 TCTGGTTATGGTGGCGGGGTAGGTCAAGTCAGGCCAAAGATATCAAGTTCTTTAACAACC
 305 Q  F  A  S  V  K  M  E  D  N  P  E  L  N  L  S  R  Q  L  L
1261 CAGTTCGCATCAGTGAAAATGGAAGATAATCCAGAATTGAATTTGTCAAGACAGCTTCTG
 325 G  M  T  G  N  D  H  Y  W  T  G  T  A  W  T  D  L  S  S  F
1321 GGTATGACAGGGAATGATCACTATTGGACTGGAACTGCATGGACAGATCTTTCTAGTTTT
 345 S  S  S  S  T  S  N  P  L  *
1381 AGCTCTTCTTCTACTAGCAATCCATTATAAgtcttttgccatggaatgaagctcatgaag
1441 ctaagtttttttttttttttttttttcctctcctttttctgaagtaggatctcactgttt
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1501 ctcagcatcgatcttcttgtaattccatatctcaaagaacttatagttcttgtgtttaag
1561 ttatatggaagagctcagaagatgaatcaagaaatttgcttctctaaagacatatgagct
1621 agaaaaccctagaattatagcttttgcattttatt