

File S8 The gene model for *RcDof06* 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

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1 atcggttcttatatttaaacagccattaacaggttattatatctacacagcattataata
61 tctaacagattagctcttttggtttcacataataggtgtcttttagtgggattggagctaga
121 attaataataagggaaacaaaaaagagaaactgtttaccgtgtaatacatgtatgtac
181 actgcatgcaggtcaacagaaacagtaaaaccaattggaaacacatgtactgaatcatct
241 ctgectctcagtaccaaaaatacgccactgacctacaagccacgcgtctagccgctcatt
301 aaacattgtattaccaccgcctgtgggtgtgcaggagaccaaagagcaaacgcacttcct
361 ttaaaaccatctctctattttccattcctcctccaaaatcattactcgcttctctctc
1
1 M P T
421 tttgectctccaaattccttctcttcttctcgaaaagacacccaaaatcgaaATGCCAACT
4 E S T P G Q N N T N P V S H S H P P P K
481 GAATCAACTCCAGGCCAAAACAACACCAACCCAGTCTCAGACTCGCACCCACCGCCAAAA
24 L A E P L P C P R C D S N N T K F C Y Y
541 CTGGCTGAGCCACTCCCGTGCCCAAGGTGTGATTCTAACAACACAAAATTTTGCTACTAC
44 N N Y N L S Q P R H F C K A C R R Y W T
601 AATAACTACAACCTTTCTCAGCCAGCCATTCTGCAAGGCATGTAGACGTTACTGGACC
64 H G G T L R N V P I G G G T R K N S K R
661 CATGGTGGCACTTTCGTAACGTACCTATTGGCGGTGGAACCCGCAAGAACTCGAAACGT
84 S R S Y S S S I T T S T T T T S A S A L
721 TCTCGCTCTTATTCTTCTTCGATCACCACCTCCACCACTACTACTCAGCTTCTGCTTTG
104 S S L N T P D Q P D Q S L P V L A I P E
781 TCATCTTTGAATACTCCAGATCAGCCCGATCAATCTTTGCCTGCTCTGCTATTCTCTGAG
124 S V L T A K S E N L S D N W N L N D E K
841 TCTGTTTTGACAGCCAAAAGTGAGAACTTGTAGATAATTGGAATCTAAACGATGAGAAA
144 V N L V S Q N G N F I S L L S S Q Q G Q
901 GTTAATCTTGTGAGCCAAAACGAAACTTTATCTCGCTGTTGAGCTCTCAGCAGGGACAA
164 G F M G M V G Y G P G F G Y G F C D T G
961 GGGTTCATGGGGATGGTTGGTTACGGGCCAGGTTTTGGATATGGGTTTTGTGATACGGGA
184 R E N W V Y P G M A Y V N G G D A V E D
1021 AGAGAGAATTGGGTTTATCCAGGCATGGCCTATGTTAATGGAGGTGATGCTGTAGAGGAT
204 G T S S G C N T W Q Q V E V G D A G G G
1081 GGTACTTCTTCAGGGTGCAACACATGGCAGCAAGTGGAGGTGGGTGATGCTGGTGGTGGG
224 L V D G E N N C L S W P G L A I S T P G
1141 TTAGTTGATGGAGAAAATAACTGCCTTTCTTGGCCTGGTCTTGCAATTTCCACACCAGGA
244 K G F K *
1201 AAAGGTTTCAAGTGAagaattggcttttagccattttaaaatTTTTTgttttaaaaaggg
1261 gctttcttgtaacgttttcttctcttttttggga

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