

**File S14** The gene model for *RcDof24* 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 atctttcccccttcccccttctctccctttaattctttctctctctttttctctcttttgcttt
61 gctttcttgccctctggtattctcacttagtgattctccaccatattttctttctctaaa
121 gaccatcaaactttacaaaagaatagaaaagaaaaggagaaaaagatcaaaaaagaaa
1 M V F S S V P I Y L D P P
181 aagaagaaaaagaattaaaaccATGGTTTTCTCTTCAGTCCAATCTATTTAGATCCTC
14 N W Q Q
241 CCAACTGGCAGCAGgtaagattttctcttcatcgatttccatccacaacatatagagtt
301 tcttttcttttatctctctccgaaaaagaaaggaaaacaacaagagcatatatcataaa
361 gattattattcctattccttctgtaatctttttcttgaatatactacatataatttcctc
18 Q P N
421 tctaagtactaaattcttgaatttttcttatttttttggctttacagcagCAACCAA
21 Q Q Q G F T N E T P H F P S L P P P P P
481 ATCAACAACAAGGATTTACCAATGAAACTCCCCATTTCCATCTCTCTCCTCCTCCTC
41 Q V G G S G G S S G S G S I R P G S M A
541 CTCAAGTTGGGGTAGCGGGCAGCAGTGGCAGTGGCTCGATTAGACCTGGTTCGATGG
61 D R A R L A K I P Q P E A S L K C P R C
601 CAGATCGAGCCAGGTTAGCAAAGATACCACAGCCAGAAGCATCTTTAAAGTGTCCGAGGT
81 E S T N T K F C Y F N N Y S L S Q P R H
661 GTGAATCAACAACCAAGTTTGTACTTCAATAATTATAGCCTTTCTCAACCTCGTC
101 F C K T C R R Y W T R G G A L R N V P V
721 ACTTTTGCAAGACTTGCCGGGATACTGGACTAGAGGGGTGCTCTTAGAAATGTTCCAG
121 G G G C R R N K K S K S Q S N S K T P V
781 TAGGAGGTGGATGCAGGAGAAACAAGAAAAGCAAAGCAAAGTAACTCAAAGACTCCAG
141 S N T N E R R M G S N S S S T S A V P S
841 TTTCTAATACTAATGAAAGGCGAATGGGTCAAATTCAAGCTCAACAAGTGCAGTTCCTT
161 D I I S H L P P Q S S H Q L P F F S S L
901 CAGATATTATAAGCCATTTGCCTCCACAATCGAGTCATCAGTTACCTTTCTTTCTTCTT
181 H N L T Q F G V G N I G L N F G G I Q T
961 TGCATAACCTTACTCAATTTGGTGTAGGCAATATTGGGTAAACTTTGGAGGAATTCAAAA
201 S G A N G Q A D M G L F Q I G S N N N S
1021 CAAGTGGTGCTAATGGACAAGCTGACATGGGATTATTTCAAATAGGAAGTAATAAATT
221 G M T S S A M L S N G G M Q Q F P F F E
1081 CAGGCATGACTAGTAGTGTATGTTATCAAATGGAGGAATGCAACAATTCCTTTCTTTG
241 P P P A T G L Y P F H Q S D Q G I E A S
1141 AGCCACCGCCAGCTACTGGGTATATCCATTTTCATCAAAGTGATCAAGGTATAGAAGCAT
261 P S S M L G D N S Q L I P S M T S S S S
1201 CACCATCTCCATGCTAGGTGATAATAGTCAGCTTATTCATCAATGACTTCTTCAAGCT
281 R V S Q S P P V K M E D S N Q Q G L N L
1261 CTAGGGTTTCTCAGTCACCTCCAGTGAAGATGGAAGATAGTAACCAACAAGGGTAAACT
301 P V V S W Y L R D Q *
1321 TACCGTAGTTTCTTGGTATCTCAGAGATCAATAAtccagcactggagaggaaacagattt
1381 ttcaggtcccaactcttcttccacttagccatctcttataatttacacttgatcgatcgt
1441 ttctgattgaagaacgttctaagctcaaaactctatccctatagagcatttgctactta
1501 gcgataatttgacgtaaaattaagttgcattgcatatacgaacgcagatctactgaaa
1561 acccagcttaacttgccagttccaacctcaaaaaacggtgacattgcgcgcttgagttc

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1621 aatgaggagctgcctctcttgatcatacgatccgagggaaagatggcagcaaaaaatggt  
1681 agaattaatgtttactttaattgtttcctgctttgtttgtttcagtcgtgtttctggt  
1741 ctgtattatattatggcttggttgagagttgtgtaacgagagagatgatggtgtttgtt  
1801 atacctgacatggcatgctgaactattatatcaagataaacgcatctt