

Supplementary File S2. The gene model for *RcRbohC*. The coding region is marked with uppercase letters, above which is its deduced amino acids. 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 ttttttctttctttacttcaatctgccacagttcaccttttaatctccgtctctttgttc
61 tgagaatcataatctcgagtggtcagattcattattccatcttcaagattcaagcttttc
1
M Q K M G R E D
121 tgttttaacttccaagaatgttgaatcaaaacccagATGCAAAAGATGGGTAGAGAAGAT
9 N S H H Q H H H S D S E L I E G D Q R V
181 AATAGCCATCACCAGCACCATCATTCTGATTCCGGAGCTGATAGAAGGTGATCAAAGGGTA
29 P Y S G P L S G P L N K R T T R K S A R
241 CCTTATAGTGGTCCTCTAAGTGGACCTCTAAACAAGAGGACGACAAGAAAGAGTGCCAGG
49 F N I P D S T S S Q D E Q Y L E V T L D
301 TTCAACATTCCTGACTCTACTTCATCCCAAGATGAACAATACTTGAAGTAACCCTTGAT
69 V R D D S V A V H S V K T A N G A E E D
361 GTTCGAGATGATTCTGTTGCTGTACACAGTGTCAAACAGCAAATGGTGCTGAAGAAGAT
89 P E L T L L A K G L E K K S N S N I V R
421 CCAGAATTAACACTGCTTGCTAAAGGACTAGAAAAGAAATCTAACTCTAACATTGTCAGG
109 N A S N R F R Q V S Q E I K R L A S F S
481 AACGCCTCTAATAGGTTTAGACAGGTTTCTCAGGAAATTAAGCGGTTAGCTTCGTTTTTCG
129 K R P P P G R L D R T K S A A A H A L K
541 AAAAGACCTCCTCCTGGTCGTCTTGACAGGACTAAATCTGCAGCTGCTCATGCTTTGAAA
149 G L K F I S K T D G G A G W A A V E K R
601 GGACTCAAGTTTATTAGCAAGACCGATGGAGGAGCTGGATGGGCTGCTGTGGAGAAACGA
169 F D D I T A S T D G L L P R S R F C E C
661 TTCGATGACATTACTGCTTCTACTGATGGATTGCTTCCTCGTTCAAGATTCTGCGAATGC
189 I G
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721 ATAGgtagttccccgtgcaagatcaacttccttgtatgagttatttaatttttggtta
191 M K E S K
781 ggactaactgatgctatctgtttgtgaacttgtgaaaataacagGTATGAAGGAGTCAAA
196 D F A G E L F N A L A R K R H I E R D S
841 AGATTTTGCAGGGGAGCTGTTTAATGCACTTGCTAGGAAGAGGCACATAGAAAAGGATTC
216 I G K D E L K E F W E Q I S N Q G F D S
901 AATCGGTAAAGACGAGCTCAAGGAATTCTGGGAACAGATTCTAACCAGGGCTTTGATTC
236 R L Q T F F D M
961 CAGGCTTCAGACTTTCTTTGACATgtaatggtatattagaaagtgtgaatcatttattat
1021 tatgatttttatttttgtgtgtaacaacaaaaaacgtgtattctgatttgattaccaa
244 V D K D A D G
1081 gcgtttaagatgtaacgtaaagatgaaaattaattgcagGGTTGATAAAGATGCAGATG
251 R I T E E E V K E
1141 GAAGAATTACAGAAGAGGAAGTAAAGGAGgtatagactttatttaataatcaaca
1201 aatgtatatgatgcacatgatataatccagaagttgactcatatctttctgtagtatcaa
1261 taatttcaatgcatcagagcatgtgcttcatatccgaagaagtttggactaattgagac
260 I I T L S A S A N K L S
1321 aaattttaccattccgatttgcagATTATTACCCTTAGTGCTTCTGCGAATAAACTATCA
272 N I Q K Q A E E Y A A L I M E E L D P E
1381 AATATTCAAAAACAAGCAGAGGAATATGCAGCCTTGATCATGGAAGAGCTGGATCCAGAG
292 N H G Y I M
1441 AATCATGGATATATCATGgtaaataaatgagaaatgctcttcgtgtgaccattctttcgc
1501 ttttttttgggtacaattttattgtgataggcattgattgtgtgaatattgtttcaaata
298 I E N L E M L L L Q G P N Q S V R V G
1561 cagATAGAGAACTTGAAAATGCTTCTATTGCAAGGACCAAACCAATCTGTAAGAGTAGGA
317 E S K N L S Q M L S Q K L K P S L D D N
1621 GAGAGCAAAAACCTGAGCCAAATGCTTAGTCAAAAGCTTAAGCCTAGTTTGGATGACAAC

337 P I R R W G R S T K Y F L F D N W K R V
1681 CCAATAAGGAGATGGGGTAGAAGCACCAAATACTTCCTTTTTGATAACTGGAAGAGAGTG
357 W V I A L W I G V M A G L F A Y K Y V Q
1741 TGGGTGATAGCTCTGTGGATTGGTGTATGGCTGGCCTGTTGCCTACAAATATGTGCAA
377 Y K R R A A Y E V M G A C V C I A K G G
1801 TATAAACGGAGAGCTGCATATGAAGTAATGGGCGCATGCGTGTGTATTGCAAAGGGAGGT
397 A E T L K L N M A L I L L P V C R N T L
1861 GCTGAGACACTCAAATTGAATATGGCTTTAATTTTACTACCAGTCTGCAGAAACACCCTC
417 T W L R N K T K L G V V V P F D D N L N
1921 ACTTGGCTTAGGAATAAGACCAAGTTAGGTGTTGTGGTTCCTTTTGATGACAATCTTAAT
437 F H K
1981 TTCCACAAGgtattagcttagttaattgccttcacttattcacgcccttttctactgaaag
440 V I A V G I T
2041 aaaacagaaagtaaataaatgggctgcgttctttttccagGTGATAGCAGTGGGAATTA
447 I G V G L H A I S H L A C D F P R L L S
2101 CAATTGGAGTTGGTCTGCATGCAATTTCTCATTTGGCTTGTGACTTCCCTCGCCTTCTTA
467 A S E E K W E L M E P F F G D Q P S S Y
2161 GTGCAAGTGAAGAGAAGTGGGAACCTTATGGAGCCATTCTTTGGGGATCAACCTTCAAGTT
487 W H F V K S V E G V T G I I M V V L M A
2221 ACTGGCATTTTGTAAAGTCAGTGAAGGAGTACTGGGATCATAATGGTGGTGTAAATGG
507 I A F T L A A P W F R R N K L N L P S F
2281 CAATAGCCTTTACTACTGGCTGCCCTTGGTTTAGGCGTAACAAGCTGAATTTGCCTTCTC
527 L K K L T G F N A F W Y S H H L F I I V
2341 TTCTTAAGAAGCTCACTGGTTTCAATGCCTTTTGGTACTCTCATCATCTCTTCATCATTG
547 Y T L L I V H G Q Y L Y L T H D W Y K K
2401 TCTACACTCTGCTCATTGTTTCATGGTCAATACCTGTACCTGACTCATGATTGGTACAAGA
567 T

2461 AAACGgtaagacacttcttaaattgaaatcaacactatattattataaatatTTTTgaact
568 T W M Y L A V P I I I Y A
2521 gatccttctctgtattggcagACATGGATGTATTGGCTGTCCATTATCATTATGCT
581 S E R L T R A L R S S I K P V T I K K
2581 AGTGAAAGATTGACAAGGGCACTAAGGTCCAGTATCAAGCCTGTTACCATTAAGAAGgtg
2641 agcagaacacaattagatgttcatttatagtttgtctgtattacattaagaagttatgga
600 V A I Y P
2701 aattagaaaagtggtgcctaaataatcttgtttttgatattgaagGTGGCTATTTATCCT
605 G N V L A L H M S K P Q G F R Y K S G Q
2761 GGAAATGTTCTGGCACTTCACATGTCAAAGCCTCAAGGATTCAGATATAAGAGTGGACAA
625 Y M F V N C A A V S P F E W
2821 TACATGTTTGTCAATTGTGCTGCTGTGTCTCCATTTGAGTGgtaggtgaatTTTTagttt
2881 agtactaaatgttgcaggtaataataactttgctattacttaaaaaagttaaaatttc
639 H P F S I T S A P G D D Y L S V
2941 acatgtcaacagGCACCCATTTCCATCACTTCAGCTCCTGGAGATGACTATCTAAGCGT
655 H I R T L G D W T R Q L K T V F S Q
3001 TCACATCAGAACTTTGGGCGATTGGACAAGGCAACTTAAAAACAGTATTCTCACAGgcatg
3061 tgtttttttatTTggaaatgagtgatttataatgcgtaactgtttccaagattcctat
3121 atactgccccctctgttggcgactcgactactgtggctaattcaatttcctcatgttct
673 V C Q P P D T G K S G L L R A D
3181 tcgatttcacagGTGTGTCAACCACCAGATACGGGAAAAGTGGACTTCTCAGAGCGGAT
689 G F Q G N N C P S
3241 GGCTTTCAAGGAAATAATTGCCCAAGtaagttctttcaacttggggaaaatgcttactc
3301 tattcacatgtatTTcatgaaataagtaatacaataaccattttcaaaggagtgcata
3361 tgtaaagaggggtacattctgttgtgcatacgtgacaagcattatatcaggtcaacttgt
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3481 catgcgcaacttagctacttgcccttagggctctcatctcactgtcatttctttgggcg

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3661 gacacctatctatagtgccacgcaatcattgtcattccatgccccacatagacaggga
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3781 ttttgaaattctgatccattgttttggttgtataaggtaacgctagtgaatttcttgaac
698 F P R V L I D G
3841 tgattacttaattgtggtattgacgatgatgaacagTTTCCAAGAGTACTGATTGATGG
706 P Y G A P A Q D Y K K Y E V V L L V G L
3901 TCCATATGGAGCACCAGCACAAGACTACAAGAAATATGAGGTGGTTCTGCTTGTGGGTTT
726 G I G A T P M I S I V K D I V N N I R A
3961 AGGAATTGGAGCAACCCCATGATCAGTATAGTTAAGGACATAGTTAACAATATCAGAGC
746 R E D E E E E N A L E N G T L P K T P S
4021 CAGGGAAGATGAAGAAGAAGAGAATGCATTAGAAAACGGTACATTGCCAAAAACACCTAG
766 P D A Q K R R E N F K T R R A Y F Y W V
4081 TCCTGATGCACAAAAAAGAAGAGAGAACTTTAAAACAAGAAGGGCGTACTTCTATTGGGT
786 T R E Q G S F D W F K G V M N E V A E L
4141 GACAAGGGAGCAAGGATCTTTTGACTGGTTTAAAGGGGTGATGAATGAGGTAGCTGAACT
806 D H N H V I E L H N Y C T S V Y E E G D
4201 GGACCATAACCATGTAATAGAGCTACACA ACTACTGCACTAGTGTATATGAAGAAGGGGA
826 A R S A L I T M L Q S L H H A K N G V D
4261 TGCAAGGTCTGCTCTAATTACCATGCTTCAGTCTCTGCATCATGCCAAGAATGGTGTGA
846 I V S G T R V K S H F A K P N W R S V Y
4321 CATTGTCTCAGGCACTCGTGTTAAGTCTCACTTTGCTAAGCCCAACTGGAGAAGTGTCTA
866 K R T A L N H P N S R V G
4381 CAAGCGCACCGCCCTAAATCACCCCTAATTCTCGAGTTGgtaagtccccattcatttttcc
4441 ttttaacaaaacatagtattcttatctttttcacctttcttttagaaaaagcatcttct
4501 gcattattgtgetctttctgtcagttagtaggaaaagtggttaaaaagaacacaaagata

4561 agtatatatattagtggtcgctgggcagtagaggtagtgcttttctctgataatatggatg
4621 cttactggtttatctaaaaattaatcaccattttctgctagggaaagctttctagttaa
879 V F Y C G A P A L T K E
4681 caattgtctcttccctgactgcagGGGTGTTTTACTGTGGGGCACCAGCGCTAACGAAAG
891 L R H L A S D F S H K T N T K F D F H K
4741 AGCTACGCCATCTAGCTTCGGATTTCTCGCATAAGACAAACACCAAATTTGATTTTCATA
911 E N F *
4801 AAGAGAACTTCTAAaactttcaatcggtgattaaggaagacagaagaaagaaagaaagag
4861 aggtcttgaattgagttccatcaacatcccactcgttactgaatattctttattggcccc
4921 cttttgttgacatttctattagcctcctttcaataatggcatagtcttattgataaatta
4981 atcagcgagcagaagatagtgcgttggttgattgcaggggcaaccacttaagacagcaa
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