

S15 File. The gene model for *RcWRKY35*. 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 blacked and the misannotated sequences are boxed.

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1 ttgagatggagtctccccatccactaacatTTTTATGAGAATTATCATCTGAATTGCAAG
61 ggaaagggctacgtcaaattatgtaagacatTTTCAAGAACCTAATGCATGAAATCTGA
121 gaatgttaccagtaaatatcatgccctaaaaacttcaggcggccaaaaaaaaaagcagt
181 cgcaggatctacatgaaattctgagaatgttaccattgaggtaacggcggctatttaa
241 tttgaccaagcattggctgtttacacatatatgaatcttgaacatgactactggttcaag
301 gTTTTCTCTTTCTACATGCACAAACGTTGAAATTGAGCATTCTTTCTTACTTTTAA
361 caaaTTTTCTTTCTCAGAACCTCAATTAaaaaaaaaaattcaataagaaatgatgacct
421 tctctctttggagtatatgtgtttgacatTTCTCAACGAGAGTAACATGCATAATAGATA
481 agtactcgagtttgaatatctatTTTCTTTCTTTTAAAGTATAAAAGTCAGAACTGGA
1
M A N K
541 ggctctattatgtgtatataatgaccagcctagctactaaatgggcatATGGCAAATAA
5 R I S S I S M E T D K S G S L E K P D H
601 AAGAATAAGCTCAATATCTATGGAGACCGACAAGAGTGGTAGCTTGAGAAGCCTGATCA
25 C A N T A A V Q E E K K M K S S G D D E
661 TTGTGCAAATACTGCTGCAGTACAGGAAGAGAAGAAAATGAAATCAAGCGGTGATGATGA
45 E V V V A E I N K
721 GGAGTTGTTGTTGCAGAAATCAACAAGgtgattatgtcttttagttaattagacctgag
781 tgcattggaagatTTTAGATATGTTTATATGCTATGTGTTCTTTCTTGGGAAGTTTT
841 tcttgtcttgttgattagctttccatgcataggaatccacaaaggaactaaaagattta
901 tccattaaaaagaagaagaaaaatctccaaatgaaatcttcttttcttccacttaaat
961 tcttggaaatacacatagcgaatgatttgtctTTTTTGGATTAATTAATCTGGTATCAT
1021 atacttatagTTTTCTCCATGACAAGATCCACTTTCTAGAAAATTAGTTTTCAAGTTCA
1081 tccattaatgactcttccatgTTTTGACTCTTTGCTTGAATATTGATTTTTCTAATTTCT
1141 ttttcagtaatacacaaaaatgcttttgaagcttatgtatattgaaatgaaatcattat
1201 tcacgttatttcagaaatatttatcttatcaagcaatattcatgtTTTTTTTCTCTTT
54 E E G D V N H V I N I K Q E E
1261 ggtgtatgccatcttagGAAGAAGGAGATGTGAATCATGTGATAAAATATTAACAAGAAG
69 N I R K R P S S T M N K D L T S I N H
1321 AGAATATCAGAAAGCGGCCTTCTCCACGATGAATAAAGATCTTACTTCTATCAATCATg
1381 taagaatTTTcatatacttgttttgTTTTATATGTAACACCTTAATTTTTCTTTTCACT
1441 attattactTTGGTTGTTGGCAAAGACTTGTATGTAAGAAAAATGTGTTCTTCCACTC
1501 atatgtgcaagttgatctataacatattaatagTTTGATTATTCTTATAATAATTAAGT
1561 tcaacttaatTTTGAAGAATTTATTTGATAAGTTTTCTTAAACTATTGAGTTGTTCAAC
1621 caaatgatggtagaccaattctgtaaatcctaattgaatattaattattgaggagtt
1681 ttgctttcaaaagatgatcactgcattattaattgatctattctaaacatTTTGTGCTA
1741 taccgagtcaaacattgttcacaaatccaccatgaagatcagatctcctcttaattagt
1801 catttgcagaaattgactgagatctattgttattattttatcttcattatatatattcta
1861 gttagtacctTTTCTTTTCAAAAAGAAAATCATAAAAGCACTCAGACTGCATAAATTTG

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1921 aattccttaaatataaagtagtattgggtttattggttatggtcttaatttctagtcttga
1981 ttcccttgcttggttttacaatttttagtttgattttgattattgtagtctgctattttgt
2041 ttctcattttcaatgtgaaattttgctgcccatattttacaagtagccacttcatgatta
2101 gaatattatctcaataataattattcgatgccatattatgtaactaaacctatagaattc
2161 agatgttacatttttctgaagctcttagttaagtcgtgtagtctggagatggactaactc
2221 aatgcaagaactttcccaaagattactattattattattttttattttttagaagtctt
88 E D Q L R S T K A K
2281 aatcatttagttcacttcttttgacaccagGAGGATCAGCTGAGGTCCACAAAAGCTAA
98 I G E V K E E N E R L K Q L L S K I L N
2341 AATTGGTGAGGTAAAGAAGAGAACGAAAGATTAACAGTTACTATCCAAAATTTTGAA
118 D Y Q S L Q K H F C K V V Q E E E E K K
2401 CGATTACCAATCTCTACAGAAACATTTCTGTAAAGTTGTTTCAGGAGGAAGAAGAAAAAA
138 P A K L T T A H Q K N Q E P E L V S L S
2461 ACCCGCCAAACTAACGACTGCCATCAAAAAAATCAGGAACCAGAGCTCGTCTCTCTCAG
158 L G R S S S S E P K K E E K K S S N L S
2521 CCTTGGTAGAAGTAGTTCAGTGAACCCAAAAAGGAAGAGAAAAAGAGCAGCAATCTAAG
178 D G N E D D E L N N K G L S L G L D C K
2581 TGATGGGAATGAAGATGATGAAGTGAATAATAAAGGACTTTCTCTTGGTTTGGACTGCAA
198 F E P D S S V T V K N N A S S E N S F D
2641 GTTCGAGCCAGATTCATCTGTAAGTGAAGAATAATGCAAGTCCGAAAATAGCTTTGA
218 E D P K E E E P T E T W S P N K I R K T
2701 TGAAGATCCAAAGGAAGAGAACCTACTGAGACATGGTCACCAAAACAAAATCAGGAAGAC
238 T I T P D D E A M Q Q N Q I K K T R V S
2761 AACCATAACTCCAGATGATGAAGCGATGCAACAAAATCAGATCAAGAAAATAGGGTTTC
258 V R A R C D T P T
2821 AGTCAGAGCCAGATGTGATACTCCAACGgtagcatctaactttttatttattatataatca
2881 tgcactggaatgcatgcatgtgcgcatcaaaaaatactgtttaagggttaactcagttg
2941 gtacttcttattttacgtgattgttttcaaattctgagattggatcattattagagatta
3001 attttcttacttgtggtctcaatgtaaatgatttgactaattggtaaattaaaaaaaaa
3061 agtaataggaatattttcatattaagaaaaaaagtaatgaattgttttttcaatgaatt
267 M N D G C Q W R K Y G Q K I A K G
3121 ataatacagATGAATGATGGATGTCAATGGAGAAAATATGGACAAAAGATAGCGAAAGGA
284 N P C P R A Y Y R C T A S P T C P V R K
3181 AATCCGTGCCCTAGGGCTTACTATCGTTGCACAGCCTCACCAACTGTCCAGTGAGAAAA
304 Q
3241 CAGgtatgttttctgcatgccattgttgacatttcaatgattaaaatattttgtttggttt
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3541 attacttgacatttgatataagataaaagattatattttccaaaatctagttaagttgct
3601 ccaatgtaaatttgatttttatctcgtactatttgaatcaacacatgtaaaatgatttac
3661 ctggtacaaatgataatttaattatacgaactccgactttggattcagtttctcatg
305 V Q R C A K D M S V L I T

3721 cagctttttcttgaatttcagGTGCAAAGATGTGCTAAAGATATGTCAGTCTTGATCACC
318 T Y E G T H N H P L P L S A T A M A S T
3781 ACATATGAAGGAACCCACAACCATCCACTTCCACTTTCAGCAACGGCAATGGCTTCCACA
338 T S A A A S M I Q S R S S T S A Q P G S
3841 ACATCTGCAGCTGCATCCATGATACAGTCAGTTCATCAACATCAGCACAGCCAGGCTCA
358 S I S A P S S I S T S N G L N F S L S Q
3901 TCGATCTCTGCACCAAGTCAATCTCAACTTCAAATGGACTAAACTTCAGTCTCTCCCAA
378 N S R P Q Q I Y F P N S S I S T S N S H
3961 AACTCAAGACCCCAACAAATCTATTTCCGAACTCTCAATCTCAACTTCCAATTCGCAC
398 P T V T L D L T T A P S T T T A Q Y F N
4021 CCCACTGTTACTCTTGACCTCACTACTGCACCATCCACAACACTACTGCCAATATTTCAAC
418 R F S S A P R C L N F S S S P S S T S L
4081 AGATTTTCTTCTGCTCCAAGATGTCTCAACTTTTCTTCTTCCACATCATCTACTTCTCTA
438 D Q S N I N T L Q S L W N P S S Y S T Y
4141 GATCAATCCAACATTAATACTCTGCAATCACTATGGAACCCTCAAGCTACTCCACTTAT
458 G T V P L N R N Y V E K Q P T P G N H H
4201 GGAACAGTACCTCTAAACAGAACTACGTAGAAAAGCAACCAACTCCAGGTAATCATCAT
478 V Y Q P Y M H I I N S E T T P P P N Q Q
4261 GTTACCAGCCATACATGCATATAATTAACAGCGAGACTACTCCTCCTCCTAATCAACAA
498 S L T E S I A A A T K M I T S N P N F R
4321 TCTTTGACAGAGAGCATTGCAGCTGCAACAAAGATGATTACTTCAAATCCCAATTTCAGG
518 S A L A A A I T S F V G N N G G S T T T
4381 TCAGCCTTGGCAGCTGCAATAACATCATTTGTTGGTAATAATGGAGGGAGTACTACTACT
538 T T T T T N S N N S N N P G A G E H Y S
4441 ACTACTACTACTACTAATAGTAATAATAGTAATAATCCTGGTGCTGGAGAGCATTATTCT
558 G L N L K L G D H H Q S L A F N T L Y P
4501 GGCCTGAACTGAAGTTGGGTGATCATCATCAGTCATTAGCATTAAACACACTTTATCCA
578 S S N S N G I G C A S S Y L N K S A T S
4561 AGCAGCAATAGTAATGGAATAGGGTGTGCTTCAAGCTACCTGAATAAATCGGCTACCAGT
598 L S S Q Q G S L V L F P G S L P F S S A
4621 TTAAGCTCTCAACAAGGGAGCTTGGTTTTGTTTCCAGGTTCAATGCCATTTTCTTCTGCT
618 T R S A S E S P A N S R D H N K G *
4681 ACCAGGAGTGCTTCTGAATCTCCTGCTAATAGTAGGGACCATAACAAGGGTTAAaggatag
4741 tacagagaaattaatatgtaaatTTTgctgcactttgTTtagctagatcgattgatattt
4801 tctgtgtaaaattgtagagatgTTTccatattgtatttctgctacaaattgtacattgatt
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