

S6 File. The gene model for *RcWRKY11*. 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  caaaggcataaaaattaacaaaagccctaaaacattgaaaaaaaaagaagaaaaaccctc
61  gaaagaattaaatagtttgatgatgatgatgtagatggtcaaaggcaacaaaaact
121 gcccggtaataataagcaaaaagacagcaaaaagggtcccataatataccattccctct
181 ctgtttcgggtgtctcttaatcacctttctttgtttctcaaacttctcttctctctctc
241 cataaccgaacagaggacaggacttccaattcaacaaaccaacagctttttgcacta
301 aatactcgcaataaacactctttgtaccctctctcttttctctctgttaagcctgaagg
1   M C D S S M A D S A S F S S L L K S V
361 ggtc ATGTGTGACTCATCAATGGCCGATTCAGCTTCCTTCTCCAGCTACTCAAAGCGT
20  L T N N S S T V R F Q
421 TTTGACTAACAACTCTTCAACTGTTAGATTCCAGgttcctttctgctttttgttttatgc
481 ttgttttgatatatTTTTTTTaaTTatcttatttgaatgggactttacttcgctttcg
541 ctttgttgttgtctcatgaatTTTctctttctcaatttggtttcttgagttgatcttttc
601 tgaatttgttacttatgcagttcgagttttttctttgctatttggtagacttttagccac
661 tgaatcacaacaagttcactgggatctTTTTTTTTctttctttcccactatcgtagga
721 aatgaatgagcttagTTTTTatactatgtcctgtaccgTTTTTgtctaaattactcatt
781 ttttggaagatcaggtaatcagtttccataaaattcAAatacttttaaaattttataat
841 ggatcattttaatttgacgttataatttgcTTtatgagtatgcagccacgatttgttttag
901 ttaattattttgaaaagaatttcaaagtataggaattcgcaagaaactgaaaacatgct
961 gctttcatgaataatcaaatggcctgatatagattattcttcttggttggcaaggtatcc
31  G
1021 ttctgccttgaacttcttttagagttgttttatgagaattatgtgatatctatgatgtagG
32  Q Y N T S Q Q E I M V S T K P R V S E A
1081 GGCAATACAATACATCCCAACAAGAAATTATGGTGTCAACAAAGCCTAGAGTGTCTGAGG
52  Q F E L P A E C T N P S T N I S S L A P
1141 CACAGTTCGAACTTCCGGCTGAATGTACGAACCCTTCTACCAATATATCATCTCTTGCTC
72  A T I S I S H S A P V I Q K H L L T E N
1201 CAGCTACAATATCAATCTCCATTCCAGCACCTGTAATACAAAAACATTTGTTGACGGAAA
92  I D R I T S H P R I V M E S P A T D G Y
1261 ACATTGACCGCATTACTAGCCATCCCCGATTGTTATGGAGTCACCTGCCACTGATGGGT
112  S W R K Y G Q K Q V K S S R S F R S Y Y
1321 ATAGCTGGAGGAAGTATGGCCAGAAGCAGGTGAAGAGTTCTAGAAGTTTTAGAAGCTACT
132  R C S H S N C H A K K K V Q R C D Q S G
1381 ATAGGTGCTCACATTCTAATTGCCATGCGAAGAAGAAGTTCAACGCTGTGATCAATCTG
152  Q V I D T V Y I G Q H N H D L S Q N K C
1441 GTCAGGTTATCGATACTGTTTATATAGGTCAACATAATCATGATCTCTCGAAAATAAAT
172  N I S R G S A S S A K L T A S S H I V D
1501 GCAACATCTCAAGAGGGTCTGCATCATCTGCTAAGCTTACTGCAAGCAGTCATATTGTTG
192  S D N K V D N A D V S I C W E D G R Q S

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3361 tcccttcgtttctaggtgacagaaaaccaacatttacatttactgctggcctgctacca
3421 catctaagtctagcaaaatcttatacaagcacatcctcgtgtcaaaaatatgccaatgaa
3481 tgagaaaaacagcattttagctattacagcatattgcgttgggaagtgattacagaaaat
3541 ttgaatggetcaattgccacctagccatagaatgtgagctagcagcactctccctatfff
3601 agactcttaattgatccttctcacatataagattctcgtattgctgtgggcagctctagc
3661 tcagattcaagctcgcttagcggagagaaatggcagtcaccatgtcttcacttacttct
3721 cttaaactaggaggatc