S2 File. The gene model for *RcWRKY06*. 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 sequences misannotated as the second intron are boxed.

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   1 aataatccttttattattattatttttctcttcttctattaaccttccttaaattcattt
   1       M  A  S  F  T  T  S  S  S  S  S  S  S  C  S  L  N  T
  61 cttttcATGGCATCCTTTACTACTTCTTCTTCTTCTTCTTCTTCTTGTAGCTTAAATACT
  19 S  I  N  S  Q  S  S  F  F  S  T  Q  F  L  M  T  N  P  S  S
 121 TCTATAAATTCTCAATCCTCCTTTTTCTCAACGCAGTTCCTCATGACTAATCCTTCTTCT
  39 S  S  L  S  S  F  T  D  L  L  S  S  G  N  I  N  S  K  D  N
 181 TCTTCATTATCTTCTTTCACTGATCTTCTTTCTTCTGGTAATATTAATTCTAAGGACAAT
  59 N  M  D  N  I  N  V  G  W  G  L  F  D  H  G  N  G  I  D  I
 241 AATATGGACAATATTAATGTTGGCTGGGGACTTTTTGACCATGGCAATGGTATTGATATT
  79 P  K  F  K  S  F  P  P  P  S  L  P  L  S  P  P  P  V  S  P
 301 CCAAAATTTAAGTCATTTCCTCCTCCTTCTTTACCTCTTTCTCCTCCTCCTGTTTCTCCT
  99 S  S  Y  F  A  I  P  P  A  G  L  S  P  T  D  F  L  D  S  P
 361 TCTTCTTATTTTGCTATTCCTCCTGCTGGTTTAAGCCCAACTGACTTCTTGGATTCACCT
 119 V  L  F  S  T  S  N
 421 GTTCTTTTTTCCACTTCTAATgtaagttgcattgtattttactcctgggttttagatttt
 481 aacttgttttcacatgttcttgttactaaatatctatttgtttgtttgtttgtttgtttg
 126       V  V  P  S  P  T  T  G  T  F  A  G  Q  T  F  N  W  R
 541 tttcagGTTGTTCCATCTCCAACTACTGGGACTTTTGCTGGTCAAACTTTCAACTGGAGG
 144 S  N  I  S  N  D  N  Q  R  G  F  K  G  D  E  K  T  Y  S  D
 601 AGTAATATTTCCAACGATAATCAGAGAGGTTTTAAAGGGGATGAGAAAACCTACTCTGAT
 164 F  S  F  Q  T  Q  T  R  P  L  L  A  S  S  S  S  S  S  S  L
 661 TTTTCTTTCCAAACCCAAACAAGGCCTCTTCTTGCTTCTTCTTCTTCGTCTTCATCATTA
 184 S  S  S  I  F  Q  S  S  S  S  I  I  S  G
 721 TCATCCTCTATCTTTCAATCTTCTTCAAGCATCATTTCTGGGgtatgatttatgattcaa
 781 cagacatcattctgtttcctgtatatactttacttaatttgggtgtttaattgtttattc
 841 cttcttttaaggccaattgtatataaaagaaatgctcttacctttttgtctttatgattt
 901 tgaccctgtttagttgcaaactttgaggtaatgaagtaaagtgctaactgcaaatcattg
 961 caggtcgactagaaatgaagtccacatgtttgctttaggacaaacccgtctggataaatc
1021 aaatataaaaagatactttcttgtttaacatccaaataattttcttgaaaaagaatacaa
1081 gaatcaagagagggagacaagtttcttcgtctttttatcatgctgtgatgagttggggtc
1141 actgatactagtttaaagggttgagataataaattcgaactcaaaaggagccaaattgta
1201 ttacaaagaaaagaaaaaacttctaccaaaaagaattgtataaaagaagcaaaaaatata
1261 tgtaaatcttttctacagatatagtgatgaaaagcaatatgctatctatgtctataattc
1321 attcaattgcatcctagtttgtttttgaatttgttcttgctaacctccctttcattcgac
 198   D  E  S  M  K  K  Q  Q  E  A  W  N  F  K  K  P  I  K  Q  A
1381 agGATGAATCGATGAAAAAGCAACAAGAAGCCTGGAATTTTAAGAAACCCATAAAGCAAG
 218   D  R  P  S  E  K  G  V  V  K  Q  E  F  T  P  V  Q  S  F  S
1441 CGGATAGACCGTCAGAGAAAGGAGTAGTAAAGCAAGAATTTACACCAGTGCAGAGTTTCT
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238 S E M A P L Q S S M Q T N A V A P Q P Q
1501 CTTCAGAAATGGCTCCACTTCAGTCAAGCATGCAAACTAATGCGGTTGCTCCTCAACCTC
258 P S Y N H Y S Q P A S Y M R E Q R R S D
1561 AACCGAGTTACAATCATTACAGTCAACCAGCTTCATATATGAGAGAACAGAGAAGGTCAG
278 D G Y N W R K Y G Q K Q V K G S E N P R
1621 ATGATGGGTACAATTGGAGAAAATATGGACAGAAACAGGTAAAAGGAAGTGAAAATCCGC
298 S Y Y K C T Y P N C P T K K K V E R S L
1681 GTAGCTATTACAAGTGTACTTATCCAAATTGCCCAACAAAGAAAAAGGTTGAGAGATCTT
318 D G Q I T E I V Y K G S H N H P K P Q A
1741 TGGATGGACAGATTACGGAAATAGTCTATAAAGGGAGTCATAATCATCCCAAGCCTCAGG
338 R S S S Q L I Q L A A G G T Q E I S D Q
1801 CTAGATCATCCTCCCAATTGATTCAACTTGCTGCAGGAGGCACTCAAGAAATCTCAGATC
358 S F A P V E S V T M Q E D S S L S I G D
1861 AATCTTTTGCTCCAGTGGAATCTGTCACCATGCAGGAGGACTCTTCACTTTCGATTGGAG
378 D E F D Q S S P I S N S G G N E D E N E
1921 ACGATGAATTTGATCAAAGTTCGCCAATTAGTAATTCAGGGGGAAACGAAGATGAAAATG
398 P E A K R F
1981 AACCTGAAGCTAAGAGATTgtaagttgaaaaaagatcacaagactgatgattatgcttta
404 K G Q
2041 tgttctgtatctggattatgaatttaatagtaatctttcatggctttacagCAAGGGACA
407 N E N E S I L A A G S R T V R E P R I V
2101 GAATGAGAATGAGAGTATTTTGGCCGCTGGTAGCAGGACTGTTAGAGAACCAAGAATTGT
427 V Q T T S D I D I L D D G Y R W R K Y G
2161 GGTGCAAACTACAAGTGATATTGACATACTTGACGATGGGTATAGGTGGAGGAAATATGG
447 Q K V V K G N P N P R
2221 ACAGAAAGTAGTCAAGGGAAATCCCAATCCAAGgtaaattagtgatgatattcgatttct
2281 tgctgtttccttgtttgcaagaagtttgtttcatggatttataattgttgcaaatctttt
458 S Y Y K C T S I G C P V R K H V
2341 attctctacagGAGCTACTACAAGTGTACATCTATCGGTTGTCCGGTTCGGAAACATGTT
474 E R A S H D T R A V I T T Y E G K H N H
2401 GAACGGGCATCGCATGATACAAGGGCTGTGATCACCACTTATGAAGGGAAGCACAACCAT
494 D V P A A R G S G Y A S N R L P V N A N
2461 GATGTTCCAGCTGCTCGTGGCAGCGGCTATGCTTCCAATAGACTTCCAGTCAATGCTAAC
514 S S M P I P I R P S V T A N T N Y S N S
2521 AGCAGTATGCCGATTCCTATAAGGCCCTCGGTCACAGCCAACACAAATTACTCAAATTCC
534 L N S T R S S G N Q A P F T L Q M L Q G
2581 CTTAACAGCACAAGATCATCAGGAAATCAAGCACCATTCACCCTGCAAATGTTGCAGGGT
554 T G N I G F S N F G K P S A S Y M N Q T
2641 ACAGGGAATATTGGATTCTCAAATTTTGGAAAGCCAAGTGCATCCTACATGAATCAAACA
574 Q Y T E N V F S G A K E E P K D D S F L
2701 CAGTACACAGAAAATGTGTTCTCAGGGGCAAAGGAAGAGCCAAAGGATGACTCATTTCTC
594 D S F L C *
2761 GACTCATTCCTATGC**TGA**aacgactaactccaaagtagcagttaggattcagggaaaatt
2821 tgttgtggtagatttgcttgtaatagtgtaatgtaggttatagttgcaatttttttcattt

2881 gttttgaggccttttgaagctctatagattaggcctcaatttattacagtacagaataat

2941 tcaacagaaatacaatgaacacttttcttagcaatctcatttgagtctgtagaagttaaa

3001 agaagttcctaaaatcattttcttttcctcttatcttctagattgataataggacttcta

3061 caaagcatttttctttctgatacgacaaaacatctaaatacaggaaacagaagaggatct

3121 tgtttgcatcactctgtattgaagacaagtatttacttacattgaagttaatagtttatt

3181 aattagcaatcaacacttaaaagaatctgaaaccaaaacaagccttggaattaaacataa

3241 gattgagtagataacttgtatcctgaaataagagccgatacagccgacacaaaaaatgca

3301 aagaatgccatgctaatggatgctgcggaggagtctgtaaatatgttatctgcaccttct

3361 cgcatcctgtttgtcataggaactgctgtagaagctgaggatatcaacaaataggataga

3421 agctgcaaccaaacccacaaaaaataatacaacaggaaagtaaatcaataaggcatatta

3481 tcttaaatttcaatttaactcatcatctgttaacagtatgcaataactcaaaagaatgtg

3541 atggtaaggatggaaatttttcagtgcatcctatatatgatataaaactgactcctaaga

3601 aatagcttttatgaatgaatcccatattgaatattctaattcattctggaattcttttta

3661 tatccttaaaaggattggtttctatgagaaataagtcatggttcaaaattgggtccatgt

3721 gcatgctgacacatagatgctctagaagcaaaaggaagtgggaagaacatgaggctaggg

3781 catatcaagtcatatggctcacgcaaattgtcaagtcaaaccagagacgtttcctatgtt

3841 tttcacgacagtatcatttctagaaagtgttaattgctttttctccaagaacagaaagga

3901 tttttctcattgttcaatcaaggaatctccaattccaggctctagaaaaccactaatggc

3961 acttgaatatttgcactctttttctcatccttcaaaatcaaacactttaatcattgaatt

4021 tcacagaaaacctcacatattaatcattttatagataaaactagtacttactttttttcct

4081 accggtcccagatatacatatatattgttttcaaacatacatttaatttgagaaagggtg

4141 tgaagtactgatatttataaactgcccggaccaatatttttgttactgaaataaaaagat

4201 ggcattgacatttttttgattaagcgaattcccaaggttccatgttagttaatatcaatgt

4261 cttctaaattaaaattgcagcaatgaagaattactagactgtctaactaaaaaaagatca

4321 tcttttatattaaagaaaatggaaacgaatcaataatatttcatgaccattcaagtgcca

4381 atcaataaaagtttaatcctttatcttattccaccaattcctcagcaacgtaacagaaag

4441 tttaaaaaaaaaaaaaaaaaagaaagaaagagaaggaaaaagaacaaaagaaggttataa

4501 taaaagaaagaagtctagcctgatcaccaaagaaatctaacatagcagaagtctgtcgct

4561 gaaaaataagttttcctgtagaaagctcatgaacatttcgcagcacttgtcctccagagt

4621 acaaagtcgaaagtattgatattgccaacaagtacctacacccaaatccatcaataaatc

4681 catattcaatcttacagaaaagaaaaatcttgatttgtataatcagacatgaactgacct

4741 gtactcttcatatctatcaaagtttttccaatccccatgtttattactagccatgataat

4801 aaaagcaagcaaagagaacaaaa