S4 File. The gene model for *RcWRKY08*. 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 sequence of the first exon that was not annotated previously is boxed.

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   1                              M  S  E  N  E  T  H  H  S  P  P
   1 catagagggacaaaacatattatctttaATGTCCGAAAACGAAACCCACCACTCTCCTCC
  12  P  A  P  S  P  A  S  T  T  S  A  S  S  A  S  A  K  S  S  T
  61 TCCAGCGCCGTCGCCGGCATCCACCACCTCCGCGTCTTCAGCATCAGCAAAATCCTCCAC
  32  S  S  R  P  T  T  I  T  L  P  P  R  S  F  N  E  T  F  F  S
 121 GTCCTCACGCCCAACCACAATTACTCTCCCGCCACGCTCCTTCAACGAAACATTCTTCTC
  52  T  P  T  P  N  M  G  L  G  L  G  F  S  P  G  P  M  T  L  V
 181 CACTCCTACTCCAAATATGGGTTTGGGCTTGGGCTTTAGTCCTGGGCCCATGACTCTTGT
  72  S  S  F  F  S  D  S  D  D  F  K  S  F  S  Q  L  L  A  G  A
 241 CTCCAGCTTCTTCTCTGATTCCGATGACTTCAAATCCTTCTCTCAGCTTCTCGCCGGCGC
  92  M  A  S  P  A  A  V  K  A  P  P  F  P  P  A  Q  E  D  K  I
 301 TATGGCTTCGCCGGCAGCTGTCAAAGCTCCTCCCTTTCCTCCTGCTCAAGAAGATAAAAT
 112  S  A  I  G  V  T  R  T  P  A  N  L  S  I  V  P  P  P  P  T
 361 CTCCGCCATAGGGGTCACTAGGACGCCGGCGAATTTGTCGATCGTTCCGCCGCCGCCGAC
 132  F  S  P  V  A  L  L  D  S  P  G  F  G  F  F  S  P  Q
 421 GTTCTCTCCGGTGGCTCTTCTTGATTCACCTGGGTTTGGGTTCTTTTCTCCTCAGgtagt
 481 tgataaattgaaaagggttgcctggtgttgttaatagtttttgttttgtttagttcatta
 541 aatttctgaaagttcttttttttatatttttccaaaaagtttttaagcaatttaaataaa
 601 acctactttttcttttctttaatgcaattaaggtagatggaggatgattttgatgaacaa
 661 atgattgaacttaatgcccataagtccagctgcttaagagtggagtaataagagagaaat
 721 tttacagtaattttgagtatattaatggaagagtattttagtcattttaagttatttttc
 781 actgtaattgagtctatttagaatggaggcagtaagactttgaccaggtatacgtctgtt
 841 tcatgcttttagttttagagaataaatcacgaaccagttccatttgttaagttttggcaa
 901 aatgcctaaatggtccagccatgttgctccaatgccttgatttttgtttttttgtttttt
 961 accaaaatgtccaatgaagggctgtgcttggaacttgacatttccattttgttacatgct
1021 tatgtttttgagattaagccattgggctagtagctattttcctcattgatataatattag
1081 gaagttgaaccccttgcattacccttccctttgatatagagaaaatgttgggacattgtt
1141 ctgcctagatgtatatcaataacgagaaatgaacagcttgatttattcttcctttatatc
1201 tcttgtttgtcatcacataacatatgaaccctttttgtttttctagaatcgtgtggctgc
1261 atttgtctttctgaatgttcccacatggtcttctctgtgctatgcttatcaaccttataa
1321 gagcactctgttctcactgataattggcaccattttgtttcataaaggccaatgtttggt
1381 ctcctttatagtgattactgaaaggcgtgtaggagaacagtgcaagtatgtgaagagtag
1441 ctatattagcagctcataaatgcaccatctttgtgcttattgtttgaaccaaatacattt
1501 taagcttatagatatataacagatttggagctgttattaatgttctcgtgatatgtcact
1561 aatgtgtctttattcacaatcattttcttttaaacttattttaatcatctgtgaggtctg
 150     G  P  F  G  M  T  H  Q  Q  A  L  A  Q  V  T  A  Q  A  A
1621 tagGGGCCTTTTGGAATGACACACCAGCAAGCCCTAGCCCAGGTTACTGCTCAGGCTGCA
 169 E  A  N  S  H  I  H  I  Q  A  Q  Y  S  S  A  P  A  T  S  S
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1681 GAAGCCAATTCCCATATACATATTCAAGCACAATATTCATCAGCACCAGCAACATCTTCG
 189 T  Q  F  S  S  I  S  T  N  S  T  I  H  Q  Q  M  P  S  S  I
1741 ACCCAATTTTCATCCATCAGCACTAATTCAACCATTCACCAGCAGATGCCTTCATCAATA
 209 P  D  T  N  A  S  E  K  E  L  S  D  F  S  F  P  D  Q  R  A
1801 CCAGACACTAATGCATCTGAGAAGGAATTGTCAGACTTCTCGTTTCCTGATCAGAGAGCA
 229 Q  A  S  S  V  T  V  D  K  P  A  D  D  G  Y  N  W  R  K  Y
1861 CAAGCTTCTTCAGTCACTGTTGATAAACCTGCTGATGATGGCTACAATTGGCGAAAATAT
 249 G  Q  K  Q  V  K  G  S  E  F  P  R  S  Y  Y  K  C  T  H  P
1921 GGGCAGAAGCAAGTGAAGGGCAGTGAATTTCCTCGAAGTTATTACAAATGTACACATCCT
 269 S  C  P  V  K  K  K  V  E  R  S  L  D  G  Q  V  T  E  I  I
1981 AGTTGTCCTGTCAAGAAAAAGGTTGAGCGATCTCTTGATGGTCAAGTAACCGAAATTATC
 289 Y  K  G  Q  H  N  H  H  P  P  L  P  N  K  R  G  K  D  A  G
2041 TATAAAGGACAGCACAACCATCATCCTCCTCTACCCAATAAGCGTGGGAAGGATGCTGGA
 309 N  M  N  G  N  Q  N  N  Q  T  D  S  G  L  A  S  Q  F  Q  I
2101 AATATGAATGGAAATCAGAATAATCAAACTGATTCAGGACTAGCTTCCCAATTTCAAATT
 329 G  N  V  N  K  L  K  D  R  K  D  Q  E  S  S  Q  A  M  P  E
2161 GGAAATGTGAACAAATTGAAAGATAGGAAGGATCAAGAATCAAGCCAGGCTATGCCTGAA
 349 H  L  S  G  T  S  D  S  E  E  V  G  D  T  E  T  G  I  D  E
2221 CATTTATCTGGGACAAGCGACAGCGAGGAAGTCGGTGATACTGAAACTGGTATAGATGAA
 369 N  D  E  D  E  P  E  A  K  R  R
2281 AATGATGAAGATGAACCCGAGGCTAAGAGAAGgtacttttgcaactaagttcttatttga
2341 tcatacttaaatgatctgtattttaaatatattacatgtctaacaaaatctgtgttttgc
 380    N  T  E  V  R  V  T  E  P  V  S  S  H  R  T  V  T  E  P
2401 agAAATACAGAAGTCAGGGTAACAGAGCCAGTTTCTTCACATAGGACTGTTACAGAGCCT
 399 R  I  I  V  Q  T  T  S  E  V  D  L  L  D  D  G  Y  R  W  R
2461 AGAATCATTGTACAGACGACCAGTGAGGTTGATCTTTTGGATGATGGCTATAGATGGCGC
 419 K  Y  G  Q  K  I  V  K  G  N  P  Y  P  R
2521 AAATATGGACAGAAGATTGTCAAAGGCAATCCTTATCCAAGgtggttactatcagcctat
2581 ctgattatgacttggagcagtcattataataaaacaaacattgttcttaggttctgataa
2641 cattcattatcaatttaaaattccttcttgtagtctatctagctcaaattgataggagtt
2701 cttcagttcttagatatttatgcattttgctttgcagaggccaagggcctcttactctct
2761 ctgccatgggggatgcgggtggagttataaaattaaagaagatgaatatattatgccatc
2821 agcaacaattattccttttaggcatagaattattgtctggaactgtttgttaaattaggt
2881 acacagaaatgttaacccatatatatatttgtagtgtgaccattgtggtcattataatct
2941 caaatgcaaaatggtttgaaatcctgtcctcttattgtagtgccaaaatagcctgcatta
3001 agaaaaaacatttgatagaaagttggtcttaagaacttcagtgggagaaaacattgtggt
3061 taaagttgggacatatccttcctcttgctcttggtgctctttgataatcttttgcaggat
3121 ttttaagttcatatttttgctctctcagtctttctttcctctgcttttagaaaacgtcga
3181 tgcttttgctgatatttgattatttattgtgttttgctagtcaatagtgaaaattaaact
3241 attcttttgttgaacttttaatatcttttctacatgtctaattatttattatttcctttg
3301 gtggaggctttctcatcattgccatttctcatcaattcatgtattcatagagaaaaggtc
3361 aatggtgacatctctaacactttgctagtattatctcgaatgcttgggttctcattgctt
3421 attctattgatagaatgtatacatgttgcaatacctagttttatcaaaacaaatctagga
3481 cccatgcatatcgattttccattctgttcagtctcccaaacatgcatgcttgctctatgg
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 433                                                 S  Y  Y  K
3541 atttgatgttgacgtttaatttgaggtttccttcaatgatctacagGAGCTACTATAAA
 437 C  T  T  V  G  C  K  V  R  K  H  V  E  R  A  A  T  D  P  R
3601 TGCACAACTGTAGGCTGCAAAGTCCGTAAACATGTTGAGAGAGCTGCAACAGATCCAAGA
 457 A  V  V  T  T  Y  E  G  K  H  N  H  D  V  P  A  A  K  G  S
3661 GCAGTTGTAACAACATATGAAGGAAAACATAATCATGATGTACCAGCGGCAAAAGGGAGC
 477 S  H  N  I  A  H  S  N  S  S  E  L  K  Q  Q  N  V  E  K  N
3721 AGCCATAATATAGCCCATAGTAATTCATCTGAGCTAAAACAACAAAATGTGGAGAAGAAT
 497 A  V  N  N  R  R  R  D  S  S  T  N  N  R  P  P  I  A  R  L
3781 GCTGTAAATAACAGAAGAAGGGACTCGAGCACCAATAATCGGCCACCTATAGCGCGGTTG
 517 R  L  K  E  E  Q  I  T  *
3841 CGATTAAAGGAAGAGCAGATAACTTAGtttctttaagttatcacaaaaagtaggatgccg
3901 cagacatttactatgaatcaggaaaagctgtaagatatcttcgctgaaatctgtttttca
3961 tgctctttgaggccattgttttcgtcaaggcccatgtcacaaactgccatattcaaaagg
4021 aagaaaaaatcataaccacaagatagaaggaagtcaatctgaggcaaactttctcagatt
4081 gatctacagggcatgcgatattgttgtatttacacagtttagtaaatatatttcatttgg
4141 aaatctgttcttgtgcattcttttgtacattatctggaagaaatgttgcaaatagctgtt
4201 atacagttgttacatttggattttatgtttgaaagtgcagatatttttctactaa
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