S1 File. The gene model for *RcWRKY03*. 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 misassembled “TTNNNTTGAC” sequence is boxed.

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   1 ttcaaagacagtgtcttctctgattatctcagtaattttaatttgcaatctttaatctgc
  61 aattagtttcattctcatctccaaaaacgggaactgaaaaacttcattaccaagtccccg
 121 taaacgcacgctctctccatccattttcaaaaattttaaatgacggtcaggtgactctta
   1                                  M  M  D  P  N  P  P  P  P
 181 tacttccctcctctaaatccaccgtctccgccaATGATGGACCCCAATCCACCACCACCG
  10 S  P  P  R  Q  Q  P  S  F  A  D  S  E  T  L  E  M  A  S  I
 241 TCACCGCCGCGGCAACAGCCTTCCTTCGCCGACTCCGAAACCCTAGAAATGGCCTCCATT
  30 N  D  A  L  N  D  T  S  T  S  Q  N  E  S  S  R  G  S  I  A
 301 AATGATGCTCTAAACGACACCTCCACTAGCCAAAACGAGAGTAGCAGAGGAAGCATAGCG
  50 E  R  R  A  A  K  C  G  F  K  A  D  R  I  N  T  A  R  F  R
 361 GAGCGAAGAGCCGCCAAATGCGGTTTTAAAGCAGATAGAATTAATACGGCGCGATTCCGT
  70 T  I  T  P  L  T           S  P  A  A  A  V  R  S  P  C  I
 421 ACAATCACTCCCTTGACTTNNNTTGACTTCGCCGGCCGCGGCTGTCCGCTCGCCGTGTAT
  87  T  I  P  P  G  I  S  P  T  A  L  L  D  S  P  I  M  L  P  N
 481 AACTATTCCGCCTGGTATTAGCCCCACCGCGCTTCTCGATTCACCGATTATGCTGCCAAA
 107  C  Q
 541 TTGTCAGgtcaatttcatttatttattttcatttccgtttcttagctttgcaattttctt
 601 ttaatttttactaattaaaatttttaatgtaacatgtcgattgcaaatttagaaaaaaa
 661 acatttaatatgcatgttagcttagtaaaacgacaaatgatttcgtgtttgatgtttta
 109                                                           P
 721 atgtgttttattatatattaatttttctcttttattttattttactttttgggtgcagCC
 110  S  P  T  T  G  S  F  P  F  P  L  M  N  C  G  S  S  A  T  P
 781 TTCTCCAACTACAGGAAGTTTCCCGTTTCCGCTTATGAATTGTGGAAGTTCAGCGACTCC
 130  A  D  V  E  N  S  S  N  G  G  S  Y  T  L  K  P  Q  N  G  F
 841 TGCTGACGTGGAGAATAGTAGTAATGGCGGTTCCTACACATTGAAGCCTCAAAATGGCTT
 150  A  A  L  E  A  E
 901 TGCTGCCTTAGAAGCTGAGgtacttgtttaagtaatgatatttacgcaagaagcagcagc
 961 tatgtaacctcttttaattgttcatacgggtcttggttcggtacaatctgatttttctg
1021 cattaaatagcatcgtctacttgatagcactatatgaattgtgtaattttatcaatgttt
 156                                             R  S  N  A  G  D
1081 caactgagacttatatgccttctgcatttttactcttgggtagAGAAGTAATGCTGGTG
 162   F  Q  E  V  G  S  L  M  E  F  E  F  P  V  E  F  L  K  Q  A
1141 ACTTTCAAGAAGTTGGCTCGTTAATGGAATTTGAATTCCCAGTGGAGTTCTTAAAGCAAG
 182   I  T  E  S  Y  A  E  N  S  A  T  D  I  K  V  L  N  S  M  V
1201 CTATCACAGAGAGTTATGCTGAAAATTCGGCAACTGACATCAAAGTCTTAAATAGCATGG
 202   T  D  A  N  L  S  D  V  Q  M  D  S  I  P  E  E  N  V  G  T
1261 TTACAGATGCCAACTTGAGTGATGTGCAAATGGACTCCATCCCGGAAGAAAATGTTGGGA
 222   C  H  P  E  E  E  E  K  G  R  L  S  A  T  G  I  A  R  N  S
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1321 CATGCCATCCTGAGGAAGAAGAGAAAGGGAGACTCTCTGCAACAGGGATTGCAAGGAATT
 242   E  D  G  Y  N  W  R  K  Y  G  Q  K  Q  V  K  G  S  E  F  P
1381 CAGAAGATGGATACAATTGGAGAAAGTATGGACAGAAGCAAGTCAAAGGGAGTGAATTCC
 262   R  S  Y  Y  K  C  T  H  P  N  C  Q  V  K  K  K  I  E  R  S
1441 CAAGGAGCTACTATAAGTGTACCCACCCAAATTGTCAGGTAAAGAAAAAAATAGAGCGTT
 282   H  D  G  Q  I  T  E  I  I  Y  K  G  T  H  N  H  P  K  P  Q
1501 CTCATGATGGTCAGATAACAGAAATCATCTATAAAGGTACCCATAATCACCCTAAACCTC
 302   P  S  R  R  A  H  V  G  S  T  S  S  F  D  E  V  P  E  I  D
1561 AGCCTAGTCGCCGAGCACATGTTGGATCGACTTCTTCATTTGATGAGGTGCCAGAGATTG
 322   E  G  N  A  T  C  F  K  V  E  I  G  S  A  W  K  N  P  Q  P
1621 ATGAAGGGAATGCAACCTGTTTCAAAGTAGAAATTGGGTCTGCTTGGAAAAATCCGCAAC
 342   G  S  N  G  G  L  E  R  T  S  S  A  S  V  V  T  E  L  S  D
1681 CAGGGTCCAATGGGGGTCTGGAAAGGACGTCTTCAGCATCTGTTGTGACAGAGCTTTCTG
 362   P  L  S  T  T  Q  G  K  S  I  G  T  F  E  S  A  G  T  P  E
1741 ATCCTCTATCAACCACTCAAGGAAAATCTATTGGTACATTTGAATCAGCAGGAACACCAG
 382   L  S  S  T  L  V  S  N  D  D  D  D  D  G  A  T  Q  G  S  I
1801 AGCTTTCTTCCACACTTGTTAGTAATGATGACGATGACGACGGGGCCACTCAGGGAAGCA
 402   S  L  G  V  D  A  D  I  E  E  S  E  S  K  R  R
1861 TATCACTTGGAGTGGATGCTGATATTGAGGAATCCGAGTCAAAAAGAAGgtatttatctc
1921 tgttctttgctgtgtatctgcatagcagaagaacatgataagttgtttctatttctttct
 418                                  K  I  E  S  C  L  V  E  T
1981 ttttttttaattttatttctcacgttcagGAAAATAGAAAGCTGCTTGGTTGAAACA
 427 S  L  S  S  R  A  V  R  E  P  R  V  V  V  Q  I  E  S  E  I
2041 AGTCTGTCATCCAGAGCTGTTCGCGAACCAAGAGTTGTTGTCCAAATAGAGAGTGAAATT
 447 D  I  L  D  D  G  Y  R  W  R  K  Y  G  Q  K  V  V  K  G  N
2101 GACATACTTGATGATGGATACCGCTGGAGGAAGTATGGTCAAAAAGTTGTGAAGGGTAAT
 467 P  N  P  R
2161 CCAAACCCTAGgtactgacattttatactgttttaactaaacttcatcttcctatgaatt
2221 tttttcttatttaaaatggatagcactggggtacacatttgatgtttcggagtaaaataa
2281 agtgatatatttgcttttaggatttcagttatctgttttagttttatttactctcttggt
2341 gatacatatttgcatctcaggtacattggagatggtcaaagttggcttgattgatgcaat
 471                                                    S  Y  Y
2401 taaaatgcattctttttttgaatatctctctgacttctttttcttcgacagGAGTTATTAC
 474 K  C  T  S  A  G  C  S  V  R  K  H  V  E  R  A  S  H  N  L
2461 AAATGCACGAGTGCTGGATGTTCAGTGAGAAAACATGTGGAAAGAGCCTCCCACAACTTG
 494 K  F  V  I  T  T  Y  E  G  K  H  N  H  E  V  P  A  A  K  N
2521 AAATTTGTCATTACAACATATGAGGGAAAACACAATCATGAAGTGCCTGCAGCCAAAAAC
 514 S  N  N  L  S  S  G  G  T  S  L  P  Q  V  T  T  N  A  Q  P
2581 AGCAATAATCTGAGCTCAGGTGGTACCAGTTTACCTCAGGTTACTACCAATGCACAGCCT
 534 A  L  T  L  A  R  N  T  N  R  T  K  P  E  T  Q  M  Q  D  Y
2641 GCCCTGACATTAGCCAGAAACACCAACAGGACAAAACCTGAAACACAAATGCAAGATTAT
 554 A  P  G  F  D  R  K  P  V  F  N  N  D  Y  S  R  L  S  F  P
2701 GCACCTGGCTTTGATAGAAAACCAGTATTTAACAATGACTATTCGAGACTTAGTTTTCCT
 574 G  H  F  S  N  E  M  K  L  G  A  S  S  I  Y  P  L  K  F  P
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2761 GGACATTTCAGTAATGAGATGAAGCTCGGGGCTTCCTCCATCTATCCATTGAAGTTCCCA
594 P L Q H T M P Y S S L E F N R G A T H H
2821 CCCCTTCAACATACCATGCCTTACAGCTCTCTGGAATTCAATCGCGGTGCTACCCATCAC
614 S S S M A P V V P D F Q I S L P S S L H
2881 TCTAGCTCTATGGCTCCAGTTGTTCCAGATTTTCAAATTTCGCTGCCATCAAGTCTGCAT
634 T S A N L S M P G A D F N Y N G R P I S
2941 ACATCTGCAAATCTTTCTATGCCTGGTGCTGACTTTAATTATAATGGGAGACCTATTAGT
654 Q G Q P F L S G Q P F L S G Q Q L V L P
3001 CAAGGTCAGCCTTTTCTGTCAGGCCAGCCTTTCCTGTCAGGCCAGCAGTTGGTCTTGCCC
674 K Q E Q R D D D H F D A G Q A T F E H V
3061 AAGCAAGAACAAAGAGATGATGATCACTTTGATGCTGGCCAGGCCACCTTTGAGCATGTA
694 N G S L S S S V Y Q R I M G N F P S *
3121 AATGGGTCTCTGTCATCATCAGTATATCAACGCATCATGGGAAACTTTCCATCA**TAA**aag
3181 aaggaactttgcttttgaaatactgtcaggttaaaaacaaatggaaaaggaaaaagaaaa
3241 agaaaaga