S13 File. The gene model for *RcWRKY29*. 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 sequence is boxed.

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   1 tgtgactttccttctcatccaattgccaattgccaattgctatctttccctcttctatat
  61 attcaacttttcttgatatgttttctttcattctcttgaccatcttctttcaaagacttg
 121 taatctaatctaaagctattacgtgagaagctaagctatactgttatatctctctccttc
   1                                M  D  S  A  S  W  V  N  T  S  L
 181 tttcccaattctcggaagagtttcagttcATGGATTCTGCTTCCTGGGTTAATACTTCTC
  12   D  L  N  V  N  S  T  F  K  H  I  D  S  V  P
 241 TCGATCTCAACGTCAATAGTACTTTCAAGCATATTGATTCAGTTCCGgtaagttgattaa
 301 tcttaatctttctattgaatgtttcaaattttcttttcttttgatctgaattgtctcac
  27                            K  R  E  L  L  A  V  D  F  S  G  L
 361 tcctgaatttcttgcacatgttcagAAGAGAGAATTGTTGGCAGTAGACTTTTCTGGGCT
  39  D  P  K  V  P  I  K  E  E  K  P  F  L  D  P  Q  T  S  V  L
 421 TGATCCGAAAGTACCAATTAAGGAAGAGAAACCTTTTCTTGATCCACAGACTAGCGTTTT
  59  V  E  E  L  T  R  I  S  T  E  N  K  K  L  T  Q  M  L  T  V
 481 GGTTGAAGAGCTTACCAGAATAAGCACCGAGAACAAGAAGCTCACTCAAATGCTAACTGT
  79  L  C  E  N  Y  N  V  L  Q  N  H  L  A  D  L  M  S  K  N  S
 541 TCTATGTGAAAATTACAATGTTTTGCAAAACCATTTGGCTGATTTGATGTCCAAGAATTC
  99  D  K  E  I  I  A  P  S  S  S  R  K  R  K  A  A  E  S  E  D
 601 TGATAAAGAAATCATCGCCCCATCATCATCAAGGAAGAGAAAGGCTGCTGAGAGCGAGGA
 119  Y  S  N  I  I  S  G  A  N  N  I  N  N  G  T  T  E  S  T  S
 661 TTATAGTAATATCATCAGTGGAGCCAATAACATTAATAATGGAACTACAGAAAGCACCTC
 139  S  D  E  L  E  S  G  T  K  R  T  K  E  I  K  T  K  I  S  S
 721 TAGCGATGAGTTAGAATCAGGTACTAAAAGGACTAAGGAAATCAAAACAAAGATTTCAAG
 159  A  Y  L  R  T  D  P  S  D  T  S  L
 781 CGCTTATCTTCGGACCGATCCATCAGACACAAGCCTGgtaagttccctcatttacccata
 841 tcttttctttcttgcgattaagtcttatttttgttagaagtagtattaacagaccaactg
 171                     V  V  K  D  G  Y  Q  W  R  K  Y  G  Q  K
 901 gtgcatatatcgtattagGTTGTGAAGGATGGATATCAATGGAGGAAGTATGGCCAAAAA
 185 V  T  R  D  N  P  S  P  R  A  Y  Y  K  C  S  F  A  P  S  C
 961 GTTACTAGAGACAACCCTTCTCCTAGGGCTTACTATAAGTGCTCATTTGCCCCAAGCTGC
 205 P  V  R  K  K
1021 CCTGTCAGAAAGAAGgtaacagcaacaatatccctcttaattattgcttgtagtcatnnn
1081 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1141 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1201 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1261 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1321 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
1381 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
 210                                V  Q  R  S  A  E  D  P  S
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1441 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnagGTGCAAAGAAGCGCTGAAGATCCATCA
219 I L V A T Y E G E H N H A R L S Q P E F
1501 ATCTTAGTAGCAACTTATGAAGGAGAGCACAACCACGCGCGCCTTTCACAACCCGAATTT
239 S L G P N R C N S N S V P V P N S T S S
1561 TCTTTAGGCCCAAACCGATGCAATTCAAATTCAGTTCCAGTTCCCAACAGTACTTCATCA
259 T P M M K V P P A S V T L D L M Q D S N
1621 ACACCTATGATGAAAGTTCCTCCAGCTTCTGTAACTCTTGACTTGATGCAAGACAGTAAT
279 A R K A I Q E S E S P A P I Q Q I L V Q
1681 GCTAGAAAGGCAATCCAAGAATCTGAATCTCCAGCTCCAATCCAACAGATTCTGGTGCAA
299 Q M A S S L T R D P N F T A A L A A A I
1741 CAAATGGCTTCCTCATTGACAAGAGATCCAAATTTCACGGCAGCACTTGCAGCTGCTATT
319 S S R F S K T P I Q K W *
1801 TCAAGCAGATTCAGCAAGACTCCGATCCAGAAATGGTGAaattaatagtagaattaagag
1861 ttttacttttgtctttgaattttttttttgaagttacttagagagtacgaagtgatgta
1921 tatagaagatggacactgattctaaatttcag