S8 File. The gene model for *RcWRKY20*. 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 of the first intron and the first two exons that were not annotated previously are boxed.

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   1 agccacctctcagtccatgttaaaccaaggattatttgaggagcaagagattccttctac
   1     M  G  F  F  S  L  P  Q  N  M  S  F  P  Q  L  G  S  C  H
  61 acagATGGGTTTCTTTTCTTTACCTCAAAACATGTCCTTTCCTCAATTGGGTAGTTGCCA
  20  Q  S  L  K  G  I  F  T  I  P  H  S  L  A  V  D  A  P  S  S
 121 TCAATCTCTTAAAGGCATATTCACTATACCTCATTCACTTGCAGTTGATGCACCCTCTTC
  40  T  A  N  L  T  E  I  L  L  S  S  S  S  S  T  A  T  K  Q  R
 181 TACTGCTAATCTCACCGAAATCCTACTCTCTTCATCATCATCCACTGCTACGAAGCAAAG
  60  D  D  F  T  S  N  F  G  G  P  H  L  L  S  L  Q  R  S  S  A
 241 AGACGACTTTACTTCTAATTTTGGAGGACCCCATCTTCTTTCTCTGCAAAGATCTAGTGC
  80  N  L  W
 301 AAATCTCTGgtaaagataatacactttttacaaacacaatcatgcaaaaaataccctcct
 361 ttttcagttttcatggttttatcactttttttttctttattctttctctctatttttttatc
 421 acttagtttaaatttaaactagctagattatattctaacttcgtttccccaatcaatgaa
 481 atataagtcatactagatctcttaattttaatggaattaataagatattcaatttatgaa
 541 tcttcataattttcatgcatgtaccctctccctttcactatacatataatgaagtgaata
  83                     A  W  G  D  V  N  E  C  L  S  N  K  R
 601 tttattggaattgttttcagGGCATGGGGAGACGTAAATGAATGTTTAAGCAACAAAAGA
  96 S  S  V  E  D  D  H  H  H  H  H  H  L  G  I  S  T  M  K  M
 661 AGCAGCGTAGAAGACGATCATCACCATCACCATCATCTAGGGATTTCTACAATGAAAATG
 116 K  K  I  K  A  R  R  K  V  R  E  P  R  F  C  F  K  T  M  S
 721 AAAAAGATAAAAGCAAGGAGAAAGGTAAGGGAGCCTAGGTTTTGCTTCAAGACAATGAGC
 136 D  V  D  V  L  D  D  G  Y  K  W  R  K  Y  G  Q  K  V  V  K
 781 GATGTAGATGTGCTTGATGATGGTTACAAATGGAGGAAGTACGGCCAGAAAGTGGTAAAG
 156 N  T  L  H  P  R
 841 AACACACTTCATCCCAGgttagacattcaaatctaataaaatttcaaatcctatatatgt
 901 atttgttttctagcttttcttgatcttcttgttcttgttgttgtcgtttttgtgtacccc
 961 atatacacatgctatgctcctcttccctttctctctctctctcacatttttttttttcttt
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1081 ttggtgcaggagattttgatggataaatgtgtgtatatatatgtgtgtgtgtgaatatta
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1201 gctttcaaaagacaaaatcgcaattgtgaagaaagtaaagaaaaggaaaataaaaaaagt
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1441 gccgagtttagattacttcctcatgatagttgaggttcttgtgtatgtaaaatgtgcata
1501 actagattcttgtatttaacttgaaaaatgggtataaatgttttaccaaaaaaatatgtt
1561 gaattacaatacactttcatctctccgagaacaaggaaaagagataccatttgcttgtct
1621 gcgtttatgacccaagagaaattcattgatagacaaagtctgctctaagtaatgtgacat
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1681 aataatttgacatgactcatttttattagatgtgtctatgaagaatgccaattggagaat
1741 ttctttccaatcccagaatgttataatcttaggatttataacaagagaggtggactttta
1801 gatttagcagttctttgacaatcttgtaatatagagataaaagattatttaagatatact
1861 ttagagttttccatctgaacttttgacgtgtacaccgcaacaaataagagagtgacatgt
1921 gtatatgagtattttagactttgacatttgatgattgatatatactcaatttatgctaag
1981 catatatcagtttagtgtatagacgagacacacctaaactagacaagaaatttcccaact
2041 attatttgtcttggccgggaattgcattgttcatttgtcagtacaacatagaacgtgatg
2101 aggcttattgctcataatgtccattaaaattctacagcaatgatttcagctttttgaatt
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2341 tttaactatagttttgagcaatacatgcatctaaggccacatgcatctagaaactcttgt
2401 actattatagtcaaatttgcaattaatagaagacttaattaatactgaatactattagtt
2461 aaaaaagacaaataaaggacaaaatactaaatggattagtgggtaatgctgatgtggcct
2521 tctaaacaaaagacagtaataataaggataaaattcttacactgtaatagttaaacaaac
2581 ttctaatattgacaaggttagaaagaaaggaaaaaaagaaaagaaaaaagagaagaagat
2641 tacatagaggctgctccttgcacttttcactttttcctgtttctttttcttcctccattt
2701 gtgtttgagcagctatatgctattattgaggaaattaacttttcagttatcacgctccaa
2761 aggtgttgtacgtaaagtttctttgatcattatgatttttacagtgcatggacttggtgt
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3361 ataattaaaaaggagagtcttcgattcgagacctcaacttccgatgttaagcgtctggtt
3421 tttaattcatataactttatacttggcctgtttcttaaacttttatatatataactatatag
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3601 tatcgtgtgatttaagttacagtttccatagagaattccatgcagttaattaacttcttc
 162                 S  Y  Y  R  C  T  Q  D  N  C  R  V  K  K  R
3661 tggtacaaaatccagGAGCTATTATCGCTGTACACAAGATAACTGCAGGGTAAAGAAACG
 177  V  E  R  L  A  E  D  P  R  M  V  I  T  T  Y  E  G  R  H  A
3721 AGTGGAGAGATTGGCAGAAGATCCAAGAATGGTGATAACAACGTATGAAGGGAGACATGC
 197  H  S  P  S  H  D  L  E  D  S  Q  A  Q  S  Q  L  N  N  F  F
3781 ACATTCTCCATCACATGATCTCGAAGACTCCCAAGCTCAATCCCAGCTTAACAATTTCTT
 217  F  *
3841 TTTCTAGttctctttgtgtttttttcttttctttctcttttaattaaagattacttgatt
3901 cccaatatgtttggagctttgttagtaaatttgctgcttgtgtaagagcttttccattat
3961 tatgtctttgattaatatactacttactgtgttcaaggcatgtaaaaaataaaacagtat
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