S7 File. The gene model for *RcWRKY18*. 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 sequences are boxed.

```
   1 cagaagtaggtgaaatatagttgcctttaacccttgggtgcaagataggtattcagactt
  61 tttttcaaaatccatatctatcaaaaaccgcctcctcttttcttctttctccatgtatg
 121 tagacatgttctcttctgtccaacctcttctcaccttccaccacttcttttgaccctata
 181 tatatatatatatatatatatatacctaatccaaaacatcttcagttcctctctgaacat
   1                     M  E  G  Q  E  T  P  Q  P  P  L  L  V  H
 241 tctatctggagccccacaaATGGAAGGACAAGAAACCCCACAACCACCATTATTAGTCCA
  15 E  L  P  P  Q  N  S  P  Y  L  F  T  P  P  H  P  L  L  P  S
 301 TGAACTGCCACCCCAAAACTCTCCCTACCTCTTTACACCACCACATCCACTACTTCCATC
  35 S  S  L  H  P  P  V  I  D  P  Q  V  V  L  P  D  I  D  W  V
 361 ATCTTCATTGCACCCTCCTGTAATTGATCCTCAAGTTGTTCTTCCTGATATCGACTGGGT
  55 A  L  L  S  S  Q  S  V  V  G  E  N  R  P  M  M  M  E  N  A
 421 TGCCCTTCTCTCCAGCCAATCAGTAGTTGGTGAGAATAGGCCAATGATGATGGAAAACGC
  75 S  L  I  G  E  T  G  A  E  E  E  K  G  N  K  D  K  L  R  K
 481 TTCTTTAATTGGTGAAACAGGAGCTGAGGAAGAAAAGGGCAATAAGGATAAGCTAAGAAA
  95 S  G  R  I  K  K  H  I  T  P  R  F  A  F  Q  T  R  S  A  D
 541 AAGTGGCAGAATCAAAAAGCACATCACGCCAAGGTTTGCTTTCCAAACCAGGAGTGCTGA
 115 D  I  L  D  D  G  Y  R  W  R  K  Y  G  Q  K  A  V  K  N  S
 601 TGACATTCTTGATGATGGATATCGATGGAGAAAATATGGGCAGAAAGCTGTCAAGAACAG
 135 S  Y  P  R
 661 CTCATATCCCAGgtgtgcacatgtaaatagttctcaaggtcatggacttaattaatacaa
 721 tgctcaaaaactcaattcataatgccgcttgagatagcaataaagattgtggatcgtctt
 781 tattacatttttcagcaggttttataaataccatgcatgctttaattatataaaaactga
 841 gttagttaaggtttattaattttaggtgagcgacaatgaaaactccaagtttctcctaga
 901 atagagacttaagaattctcatctcaactagacataatactttatatagttatagctagt
 961 tatgttaatgtttgataagaatgtctttcatttaagaattgaactgaaaactctgaacaa
1021 ttaagcaataatggagacaattaattaactaaaatagttatttgtgatttcaaaagtaaa
1081 taaaatagtagtgttgtaatgtgccgttttgatttgaaatttggtcggatatgaagctct
1141 aattgatggaaaaatatatagttatgatacagaatagacctaatgatgctatgttaaata
1201 atatgtttatgctaaaacttaaatgaaaattctggttaggaaatatttttttagtcttaa
1261 ttatataaaaaataataatctgaaattggcaaaaagaacctaaggaaaaatctcgcatta
1321 atcagaaaaaataattaaatgtagtcactaattacataaagagtgcttggcttctaaaaa
1381 cttatataaatacatctcataaaatatgttatttaattaattactataataagtcactgt
1441 atttatcattaatatagcaaacttgctgtcaaaatagtgccggacgccataatattattt
1501 agcggcaatgtattttggtcgcttatggtctgttctttttttttctttgtcgttgttga
1561 atatattatcaacctgccaccacttttgcgagctcgctcgcagaagtgattattttcgac
1621 ttcccctcgcgcgcaaataaaaaaaaataaaaaaaaaattgcaggcgagagagggttgag
1681 acaaataacgacggtaatggcagtcgttaacgcgacgccattagcgataaatatttagtc
 139                                                           S
```

1741 gtataaagttttctagtgtctgatataaatattcttctccggatttgaaaaataagGAGT

140 Y Y R C T H H T C I V K K Q V Q R L S K

1801 TACTATAGGTGCACCCATCACACATGCATCGTGAAGAAGCAAGTGCAAAGGCTATCGAAG

160 D T S I V V T T Y E G I H N H P C E K L

1861 GACACGAGTATTGTGGTGACCACGTATGAGGGAATCCATAACCATCCTTGCGAGAAGCTG

180 M E T L T P L L K Q M Q F L T R F *

1921 ATGGAAACCCTAACTCCTCTTCTCAAGCAGATGCAGTTCCTCACTAGGTTC**TAA**tttgtt

1981 taagtttaatacctagctacttacatgattatgatattggaatgtttcatcaacgacaga

2041 acccgaaaagctcagtcattttatgttgttatatacgtttctttttgtaaattgaaatgt

2101 caaattcgctgttaataccgcaagatcaataaattttatgctttttatatgtacttctcg

2161 gaaaatctgcaatcttttgtttcaccttagattctttgacgtgtattaattaatcgggaa

2221 tagaaatac