

**S12 File. The gene model for *RcWRKY28*.** **A**, 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 sequence of scaffold43951 is boxed and its overlapping sequence with scaffold30131 is marked in yellow. The start and stop codons are blacked. **B**, EST mapping graphical representation of *RcWRKY28*.

**(A)**

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1 ctctatataccccacactcgccactttccacctgtttcttcaaacgagtagagcctt
61 gattctttttatcttctctctatatacgctatataatataatatactggttcttgcattt
121 tgggttcatcaggaggactagctagctacaagaattttgaaggatttactatcttcac
181 aagaaaagttttcaagagaaaagtataaagatatacatagacttgtttcttggcgctt
1
1 M D Y S S S W V
241 agttttgcttcaagattcttaagtacaagttttattATGGATTATTCTTCTTCTTGGGTG
9 D T S L D L N L N P R R V K D D V P I Q
301 GACACTTCTTGGATCTTAATCTTAATCCTCGACGTGTGAAGGATGATGTTCCATTCAA
29 E R L A M A N D V Q S N F M E L G R N I
361 GAAAGGTTAGCCATGGCTAACGACGTTCAAGCAACTTTATGGAGTTGGGAAGGAATATT
49 S V K E E
421 TCTGTTAAAGAAGAGgtagttatgtgagtcgattttcttgtttaaagtgtgtctcgataa
481 tgattgaatcaattgtttcttgaaactgagaggttttgannnnnnnnnnnnnnnnnnnn
541 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
601 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
661 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
721 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
781 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
841 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
901 nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
54 T G A L V E
961 ngttttgaagtttgattaatttgttgttttaataactttcagACTGGAGCTTGGTGG
60 E L N R V S A E N K K L T E M L T V M C
1021 AGGAATTGAACAGGGTGAGTGCAGAAAACAAGAACTGACAGAAATGCTTACTGTGATGT
80 E N Y N A L K S Q L M D Y V S K N R D K
1081 GCGAAAACATAATGCTTTGAAAAGCCAGTTGATGGATTATGTGAGCAAGAATCGGATA
100 E L S P S R K R K S E S S N N D N T I A
1141 AGGAGCTTAGCCCTTCAAGGAAAAGAAAGTCTGAAAGCAGTAATAATGATAATACCATTG
120 M N G N S E S S S T D E E S C K K P R E
1201 CAATGAATGGGAATTCAGAAAGCAGCTCAACTGATGAAGAATCTGCAAGAAACCAAGAG
140 E I V K A K I S R T Y V K T E A P D T S
1261 AAGAAATTGTCAAAGCAAAGATTTCAAGAACTTATGTTAAGACAGAAGCACCCGACAAA
160 L
1321 GCCTTgtaagtcacatcaatcaatttaactaattctgcataactttatgaggettgtttaga
161 I

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1381 tattaatgttttatatttatgggcttttacttagcaattgcataaaattggtgttcagA  
 162 V K D G Y Q W R K Y G Q K V T R D N P S  
 1441 TTGTAAAGGATGGATATCAATGGAGGAAGTATGGCCAAAAGGTCACCAGAGACAACCTT  
 182 P R A Y F K C S F A P S C P V K K K  
 1501 CTCCAAGAGCTTACTTCAAATGCTCTTTTGCTCCTAGCTGCCCTGTCAAAAAGAAGgtaa  
 1561 tgttcctgatatttatecagaatcattttaacattaatggttctttcttacataaaagcaat  
 1621 agtttaggtttcagtccttgatacattcataaaataattccgtgaaatgaaatcaaagtt  
 1681 tccatgtgcattggcatagagttctcagttcctaattggtttgtatcatctgtggttcttc  
 200 V Q R S I E D Q T I L V A T Y E G E H N  
 1741 agGTTCAAAGAAGCATTGAAGACCAAACACTATTCTAGTAGCAACATATGAAGGAGAGCACAA  
 220 H P H P S Q M E A T S G A S R S L T L G  
 1801 ATCATCCACATCCATCACAATGGAGGCAACATCAGGCGCAAGCCGAAGCCTGACTCTTG  
 240 S V P C S A S L G S S G P T I T L D L T  
 1861 GCTCAGTACCCTGCTCAGCCTCCCTTGGATCGTCCGACCGACCATTACTCTTGACCTGA  
 260 K S K S S N D A R S S K P R M E T P E V  
 1921 CCAAATCCAAGTCCAGCAATGACGCCAGAAGTTCAAAACCAAGAATGGAAACTCCTGAAG  
 280 R Q F L V E Q M A S S L T K D P N F T A  
 1981 TAAGGCAGTCTTGGTAGAACAGATGGCCTCTTCGTTGACAAAAGATCCTAATTTACAG  
 300 A L A A A I S G K M L Q Q N H K D K W \*  
 2041 CAGCATTAGCAGCAGCCATCTCAGGAAAAATGTTGCAGCAGAATCACAAAGACAAGTGGT  
 2101 GAagattttctcagtttaggccattttgaaatttggaaatgtagttgtacataacaacatc  
 2161 aggaaaaggggaaacacaattttcataaatttgctttgaattgctattttaaggaggaagt  
 2221 atattgtcattggaaatgattgatgaaaaattcatccccaattttgcaagacgcaattgg  
 2281 ggtggagttcatgccatattgaattgatcttcaacatttttttttctttttcttgatt  
 2341 tattttagttattagttccttttaattttaacattaatagtttctctagcaatat

(B)

