

```

1      ATGTGCGGCGGTTCAATCCTCGACGAATTCATCCCTCGCAACGGTAACCACCGCGTCTCC
1      M C G G S I L D E F I P R N G N H R V S
61     GCCTCCCAACTCTGGCCCACTCCCCCTTCGTACCAAATTCAAACCCCCACAAGATCAA
21     A S Q L W P N S P F V T K F K P P Q D Q
121    AACGACGGTGATGAGCGTGTGAAAAAGAAGGCCAAGAGACAGCGCAAGAACCTGTACAGG
41     N D G D E R V E K K A K R Q R K N L Y R
181    GGAATTAGGCAGCGTCCGTGGGGAAAATGGGCAGCGGAGATCCGAGATCCGAGAAAAGGT
61     G I R Q R P W G K W A A E I R D P R K G
241    GTGAGGGTTTGGATCGGTACCTTCAACACGGCCGAAGAGGCCGCCAGAGCCTACGACAGG
81     V R V W I G T F N T A E E A A R A Y D R
301    GAAGCTCGCAAGATCCGAGGCCAACAAAGCCAAGGTTAATTTTCCCAACGAAGACGACCAT
101    E A R K I R G N K A K V N F P N E D D H
361    TCCATTCAATTTACTCCACAAACCCATCATTTACCCACCGCTATGAGTCATCCCAACGGA
121    S I Q F T P Q T H H L P T A M S H P N G
421    GGGTTTAGTGGCAATCTGAACCAAGTTGGGGCATAACAGCTCTAATGGGTTCAATAGCGTC
141    G F S G N L N Q F G A Y S S N G F N S V
481    CCCTGTTCCGACCCCTGTTTCGGTTCTTCACTTTGAAGAAATTTCTGGGTCTGGTTTAGAA
161    P C S D P V S V L H F E E I S G S G L E
541    AGTTCTTACTCTTCGATTGATTTCAAATTAGAGGTGAAGGAAGAGAGAGAAGCAAGAG
181    S S Y S S I D F K L E V K E E R E K Q E
601    GAGAGAGGAAACAGGAAGGAAGCGCGGTGATGGAAGTGGAGGAAGCAGCAGGGGAAGAG
201    E R G N R K E A A V M E V E E A A G E E
661    AGCGAAGTGGAGAAGCTGTCGGAGGAGTTGATGGCCTACGAGTCCGTCATGAAATTCAT
221    S E V E K L S E E L M A Y E S V M K F Y
721    CAGATTCCATATCTCGACGGCCAATCGACGAATGCTCCGCCAGCGGAGAACGACGTCATC
241    Q I P Y L D G Q S T N A P P A E N D V I
781    GGCTGTGGTGTGTGGAACATGGAGCTTCGACGATCTTACCCCTACGGTGGCCTGA
261    G C G A V E L W S F D D L T P T V A *

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**Figure S1.** Nucleotide sequence and deduced amino acid of *AdRAP2.3* gene from *A. deliciosa*. The AP2/ERF conserved domain is underlined, the conserved 14<sup>th</sup> alanine and 19<sup>th</sup> aspartic acid are marked with asterisks.

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AdRAP2.3      MCGSSTLIDFIPRNGNHR...VSASCLWPNSEF.....VIRKPKPQDQNDGDERV.....EKKAKRORKNLYRGIKRFWGWKAAEIRDEKGVVWVIGTENT 90
PSR94738.1   MCGSSTLAELIPRNGNHR...LSASCLWPNSEF.....VIRKPKPQDQNDGDERV.....EKKAKRORKNLYRGIKRFWGWKAAEIRDEKGVVWVIGTENT 90
HRE2         MCGSALISDFIWSKSES...EPSCLGSVS.....SRKRRKRVSVSE.....SRDGKRORKNLYRGIKRFWGWKAAEIRDEKGVVWVIGTENT 81
RAP2.3       MCGSALISDYALVITKAKGRKLTAEELASLDASAADDFWGFYSTSLHETNIVNVKLEAVKKEQATPGKRORKNLYRGIKRFWGWKAAEIRDEKGVVWVIGTENT 110
Consensus    mcgg i          l          k          e   r   kn yrgir rpwgkw eirdp kg rzw gtf t

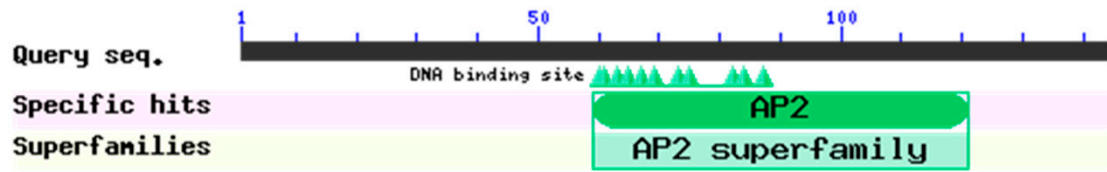
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PSR94738.1   AFEAAAYDREARKIRGNKAKNFEEDDHSIIPPCAHQCPAAMTHRNGGFRDNLIQFGAYNSDGFHSVPCSDPVSVLHSEVFGSGLESAYPSMCKLKVKEEREKKE 200
HRE2         AFEAAAYDVAALIRGKAKNFE.....TQVEEADTKP 118
RAP2.3       AFEAAAYDVAALIRGKAKNFEHLHHPPPKNYTPPPSSFRSTDF.....PAKRVCVVVSQSESE 172
Consensus    a eaa ayd a   irg kak nfp

AdRAP2.3      ERGNRKEAAVMEVEEAGESESEVKELSEELMAYESVMKFYQIPYLDGQSTNAFF...AENDVIGCGAVELTSEFLITFTV 277
PSR94738.1   ERENSKAAAVILEHTAGESELEKLESELMAYESIMKFYQIPYLDGQSPESPNTAAENDVIGCGAVELTSEFLITFTV 280
HRE2         .GNNENLIS.....ENOVESLSEDLMALEDYMRFYQIPVADGQSATDIG.....NIVSYQDSN... 171
RAP2.3       LSQPSFFVECTGFGNGLDFCNLSYGEFHYDLKQCSLESELELIGNTAEQES.....QLDESVSEVLDVWMLDVIASV 247
Consensus    d          w   d

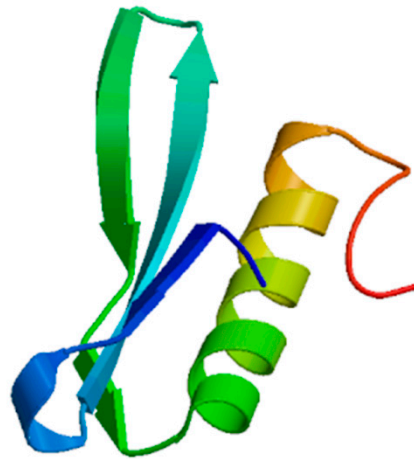
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**Figure S2.** Protein sequence alignment of AdRAP2.3 with the PSR94738.1, HRE1, RAP2.3 proteins.

A

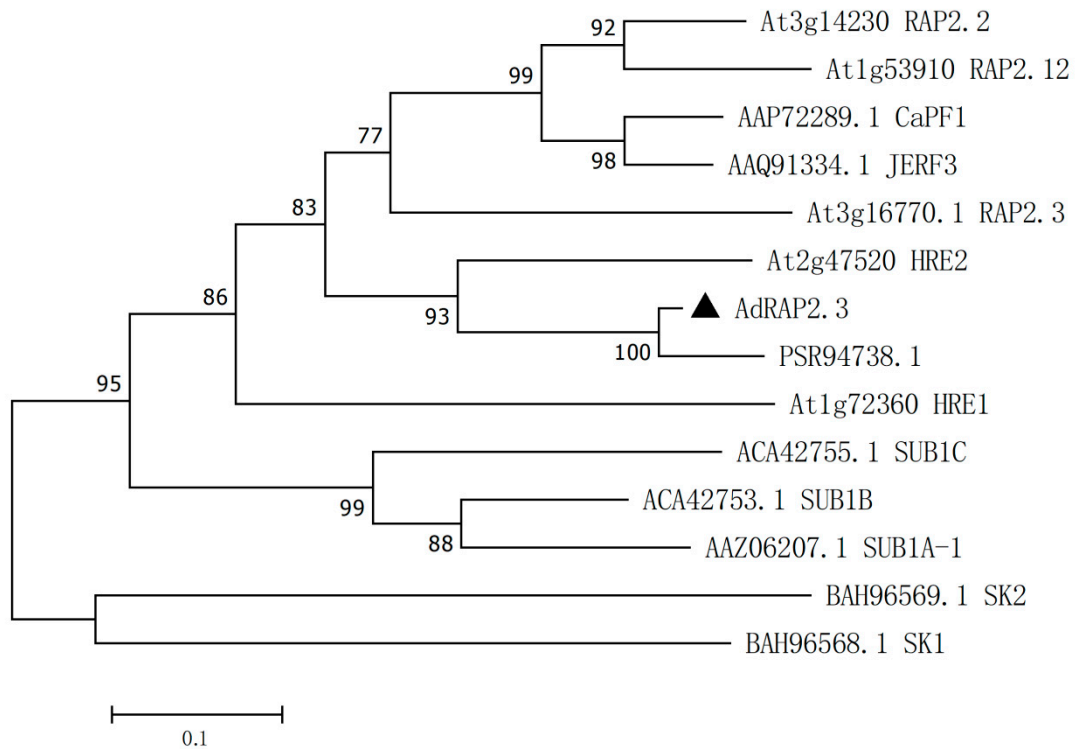


B

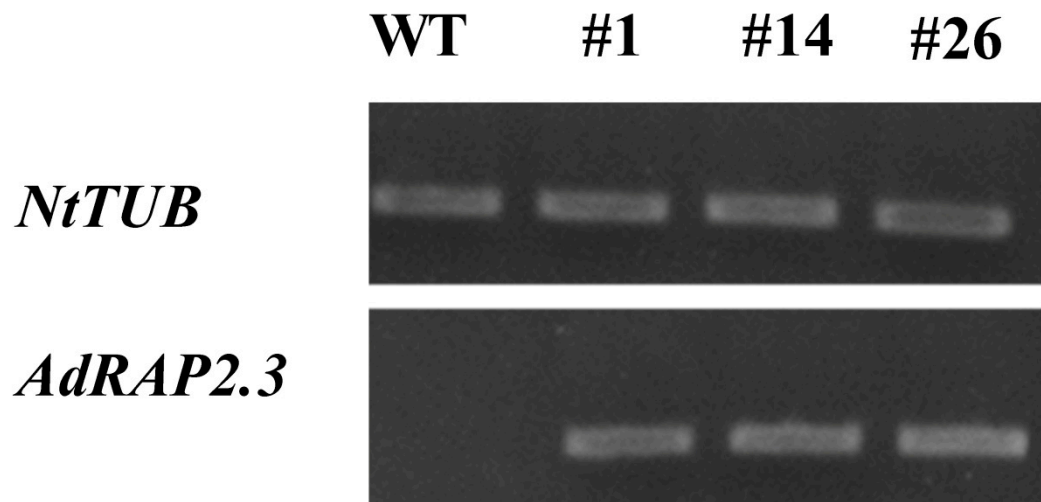
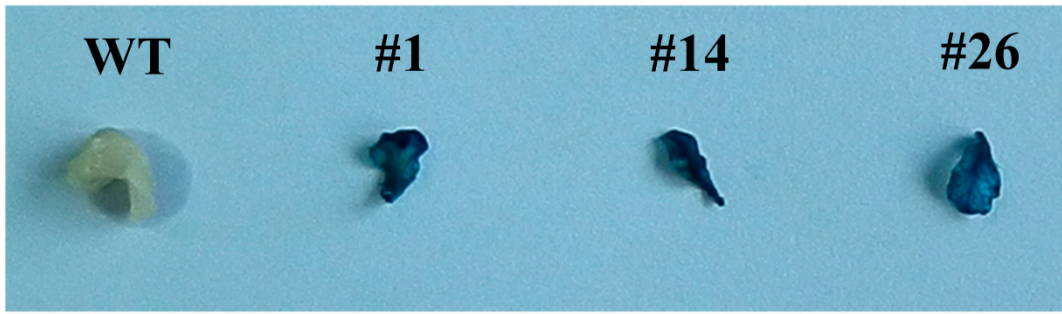


**Figure S1.** Secondary and three-dimensional structure of main part of AdRAP2.3

A: AP2 superfamily and DNA binding site; B: one  $\alpha$ -helix and three  $\beta$ -flods



**Figure S4.** Neighbor-joining phylogenetic analysis of AdRAP2.3 with other ERF VII subgroup proteins from *Arabidopsis* (RAP2.2, RAP2.12, RAP2.3, HRE2, HRE1), *Oryza* (SUB1B, SUB1A-1, SUB1C, SK1, SK2), *Capsicum* (CaPF1), *Lycopersicon* (JERF3) and *Actinidia* (PSR94738.1). Tree topology was constructed using MEGA6 programs. The numbers above or below the branches indicated the bootstrap values from 1000 replicates. AdRAP2.3 is marked with a black triangle.



**Figure S5.** GUS and PCR detection of transgenic tobacco. WT: Wild type; #1, #14, #26: Transgenic tobacco lines.

Table S1. Sequence of primers

Gene name	Primer name	Sequence 5'-3'	Gene ID
<i>AdRAP2.3</i>	F1	CCCGTTCTTCTTATCTTC	
	R1	TATCGTTCCTCAACTCGGGA	
	F2	AGGAAGCAGCAGGGGAAGAG	
	R2	CAGCACCACAGCCGATGAC	
<i>AdActin</i>	F	TGCATGAGCGATCAAGTTTCAAG	NA
	R	TGTCCCATGTCTGGTTGATGACT	
<i>NtTub</i>	F	AGATGTTCCGTCGTGTCAGTG	EF051136
	R	TGCTTCCTCTTCATCCTCATATCC	
<i>NtPDC</i>	F	GGACTACACTGGTCTTGTGAATGC	XM_016599474
	R	GTGCTTGTTGCTGTTGCTATTGC	
<i>NtADH</i>	F	CGTTCTGATCTTCCTTCTGTCGTC	NM_001325141
	R	CAATTAGTCCTCCATGTTGATGATGC	
<i>NtHB1</i>	F	TGGAGCGTTGATATGAAGAATGCG	XM_016636369
	R	ACGAAAGACATAACCCAACAGGAG	
<i>NtHB2</i>	F	GATCCGTCCATCTCCAAAAGGG	XM_016615748
	R	CGTCTTCGCTCCATTTCTCTCC	
<i>NtPCO1</i>	F	CAATGCGGCTGGGGATTCAAC	XM_016577567
	R	GCGACCTTCAGGATCACAATATGG	
<i>NtPCO2</i>	F	GGTCATCCTACAGTGAGACTAGCC	XM_016660262
	R	AAGAATATCCAGAACCGCACAAGG	

F: Forward primer, R: Reverse primer. AdRAP2.3F1, AdRAP2.3R1 the pair of primer for *AdRAP2.3* gene clone, AdRAP2.3F2, AdRAP2.3R2 the pair of primer for transgenic plant detection and RT-PCR. *AdActin* the reference gene of kiwifruit, *NtTub* the reference gene of tobacco.