

Supplementary Materials

Table S1 The gene sequences and names of *RrAP2* family

Sequence	Gene name
evm.model.Chr6.4678	RrAIL1
evm.model.Chr4.20	RrAIL2
evm.model.Chr5.468	RrAIL3/4
evm.model.Chr6.2418	RrAIL6
evm.model.Chr2.276	RrANT1
evm.model.Chr6.2219	RrANT2
evm.model.Chr3.1277	RrWRI1
evm.model.Chr6.6474	RrWRIL1
evm.model.Chr1.4006	RrWRIL2
evm.model.Chr6.3660	RrWRI4
evm.model.Chr4.2960	RrWRI2
evm.model.Chr6.1996	RrAP2
evm.model.Chr5.1758	RrTOE1A
evm.model.Chr5.2157	RrTOE1B
evm.model.Chr4.1706	RrTOE3
evm.model.Chr6.1999	RrTOE4
evm.model.Chr4.2805	RrTOE5
evm.model.Chr4.2818	RrTOE6

Table S2 The primers used for amplifying the *RrANT1* by RACE

Gene name	Primer(5'-3')	Application
<i>RrANT</i>	TTCCGTGGGGTAAATGCG	1st of 3' RACE
<i>RrANT</i>	TTCAAATCCTTCGTCGCT	2nd of 3' RACE
<i>RrANT</i>	CCAAGCAGCAAATAGAGGCAAGTGAGACA	5' RACE

Table S3 The primers used for different kinds of experiment

Coding	Experiment	Gene	Forward Primer (5'-3')	Reverse primer (5'-3')
a	RT-qPCR	Alpha-tubulin <i>RrANT1</i>	TGAGGCCATTTACGACAT CTGGGGCTCTTCAACCCACA	AGATCACAGGAGCATAGGAG CCACCTCCCATGCTGGTGAT
b	pBWA(V)HS- <i>ANT1</i> - GLosgfp expression vectors	<i>RrANT1</i>	cagt <u>CGTCT</u> Cacaacatgaagccatacatgatca	cagt <u>CGTCT</u> Catacaggtgtcattccaagcagcaa
c	overexpression vector construction	<i>RrANT</i>	GGACTCTTG <u>ACCATGGT</u> TATGAAG CCCATACATGATCACAGTC	GTCAGATCTA <u>CCATGGG</u> CCCTACTTTC CTCCTCCAT
d	DNA testing of transgenic plants	<i>RrANT</i> α -tubulin	AAGGAATGGTGCCGAAC TGGAGGATGGAAGGACTTTGG	AGGGCTCATGGACAAAGTAA CAGGACGACAACAAGCAACAG
e	gene fragment amplification	Hyg resistance gene	GTCCTGCGGGTAAATAGC	GGATCGGACGATTGCGT

Table S4 Genetic transformation medium for *Petunia hybrida*

Medium type	Formula
Infection solution	30g/L Sucrose + MS+0.5mg/L MES + 30μmol/L As
Pre culture medium	30g/L Sucrose + MS+7g/L Agar + 3.0mg/L 6-BA + 0.2mg/L IAA
Co-culture medium	30g/L Sucrose + MS+7g/L Agar + 6-BA 3.0mg/L + 0.2mg/L IAA + 30μmol/L As
Selection and differentiation medium	30g/L Sucrose + MS+7g/L Agar + 3.0mg/L 6-BA + 0.2mg/L IAA + 7mg/L Hyg + 500mg/L Cb
Screening rooting medium	30g/L Sucrose + 1/2MS + 7g/L Agar + 0.1 mg/L NAA + 6mg/LHyg + 500mg/L Cb

MS: Murashige & Skoog medium; MES: 2-Morpholinoethanesulfonic Acid; As: Acetosyringone; BA: 6-Biamido purine; IAA: Indole-3-acetic acid; Hyg: Hygromycin B; Cb: Carbenicillin sodium salt; NAA: Naphthaleneacetic acid

ATGAAGCCCATACATGATCACAGTCATAACAACAATGGAAGCCATATTAACAATAACAACAACACTGGTTGGG
GTTTTCACTCTCAGCTCCCCACATGAAAATGGAGGTCACCTCTTCTTCTGACCCTCATCAACACTACAGTCA
TCAACAAGCTCAGGCCTCCTCTGCTTCAGCTCAGCTTCCAAGTAGCTTCTACAATCTGACCCCACTCTGCTA
TGAAAATGGTGGGTTTTCACTCTCCCTTGACTGTAATGCCACTCAAGTCAGATGGGTCTCTTTGCATCATGGA
AGCTCTCACTCGCTCACAAGCTGAAGGAATGGTGCCGAACCTCGTCCCCAAAACCTTGAGGACTTTCTAGGA
GGAGCAAGCATGGGAGCTCATGACTATGGAACCCATCAAAGAGAGGTGGCAATGGCTCTCAGCTTAGACA
GCTTGATTACAATGAAAATGCAGAGGCAGAGCAACAATACTACTCTGGAATCCCTTTCCCTGGAGCTTACC
AAACTCAAATGGAGGAAGAGTCCTCTAAGCAAGCCACATTGTGGGCTGTGATAGTCACCAAATGACCCA
GAACTGGGTGACTAGGCAGTACTCTGCTGCTCATCATGCTTTCAATCAACAACACATGAGTAACAACAGCT
TGGACAATGGAGGAGTTTCTGGGTCTGTAAATGGTGGAATGCAGTGTGGGGATTTACAGTCTCTTACTTTGT
CCATGAGCCCTGGATCTCAGTCCAGCTGTGTACAGCTCCAAGGCAGATCTCACCCTGAAACAGAGAG
TCTAGCCATGGAAACCAAGAAGAGAGGTTCTGGTAAAATTAGTCAAACAAAGCAGCCAGTGCACAGAAA
GTCCATTGACACATTGGGCAGAGAACTTCACAGTATAGAGGAGTCAACAAGGCATAGATGGACCGGTAGAT
ATGAAGCTCATCTATGGGACAACAGTTGCAAGAAGGAGGGGCAAACCAGAAAAGGAAGGCAAGTTTATCT
TGGGGGATATGATATGGAAGAGAAAAGCTGCAAGGGCATATGATCTTGCTGCTCTTAAGTACTGGGGCTCTTC
AACCACATAAACTTCCCATTTGGATGATTACACAACACAAATTGAAGAAATGAAGAATATGAACCGGCAAG
AGTATGTTGCGCATCTGAGGAGGAAAAGCAGTGGATTTTCAAGGGGAGCTTCAATTTACCGAGGAGTTACA
AGACATCACCAGCATGGGAGGTGGCAAGCTCGAATTGGCAGGGTTGCAGGAAACAAGGACCTTTATCTTG
GTACATTTGGCAGCCAAGAGGAAGCAGCCGAAGCTTATGACATAGCTGCAATCAAGTTCCGTGGGGTAAAT
GCGGTCACCAACTTTGACATTACCAGATATGATGTTGAGAAAATCATGGCCAGCAATACTTTGCTTGCTGGA
GAATTCGCTAGGCGTAACAAGGAGGTTGAACCTAACAAACAAGTCATTGAGTACAACCTACCAGCACAGA
ACAATGTGGAAGCCAATACACCCGAAAATAGTCATGGGAATAGTTCAGATTGGAATAATGGCTTTGTACCAA
GCTGCACAGCAACAACAAGCAACTGCTGCTACTTGTGTTCAAACACTTGATCAAAAATCAATGTCTTCAGG
GAATTACAGAAGTCCTGCATCTTTCTCAATGGCATTGCAAGACCTCATTCGCGTTGAATCAGTGAACCTCTAG
CCAGCAGTTGATGGATGAATCAGCTAAAGCCGGTGCTCATTTTTCAAATCCTTCGTCGCTGGTGACCAGTCT
GAGCAGCTCCAGAGAAGATAGCCCTGACAAATCAGGCCCCACAATGCTGTTTGCAAAACCTCCAATGGCA
TCAAAGTTCATAAGTCCAAGTACTGCTGCTGCTGTTAGCTCTTGGTTCCCATCAGCTCAGTTGAGGCCTGCA
GCTGCCATTTCCATGTCTCACTTGCTCTATTTGCTGCTTGGAATGACACCTAG

Figure S1 The fragment of *RrANT1* amplified by PCR in the subcellular localization experiment

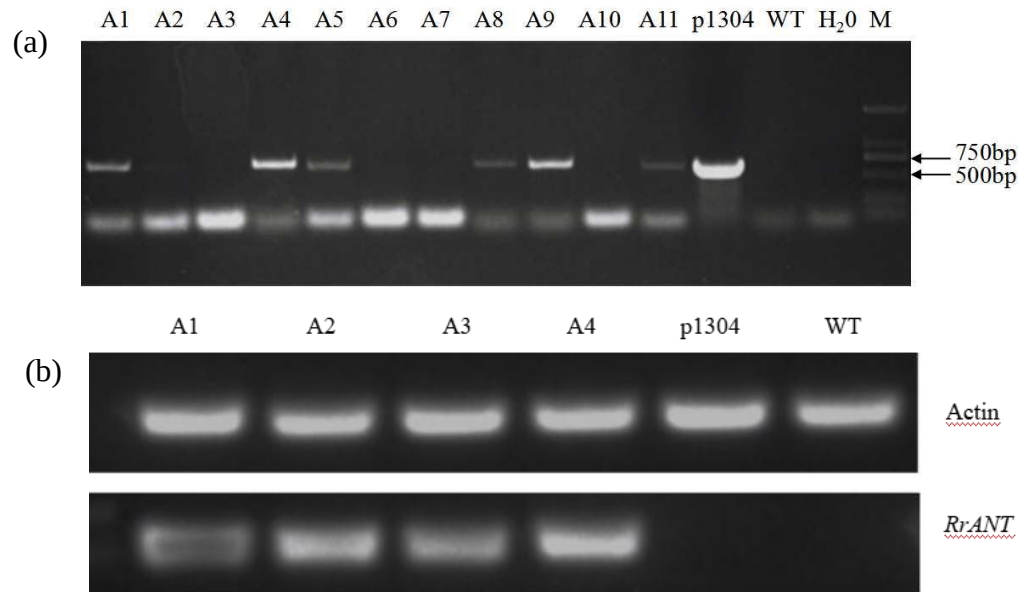


Figure S2 *RrANT1* verification and semi-quantitative analysis of transgenic petunias.

(a) six of the eleven strains can amplify a single band with a length of ~750bp, while the wild type shows no band, which shows that the *RrANT1* gene has been integrated into the petunia genome. (b) The transgenic plants showed bands with brightness, indicating *RrANT1* had been successfully transferred into petunia and could be expressed, no bands were detected in the control groups.

A1-A11: overexpression petunias; p1304: petunias transformed into pCAMBIA1304; WT: wild Type; H₂O: water; M: marker.