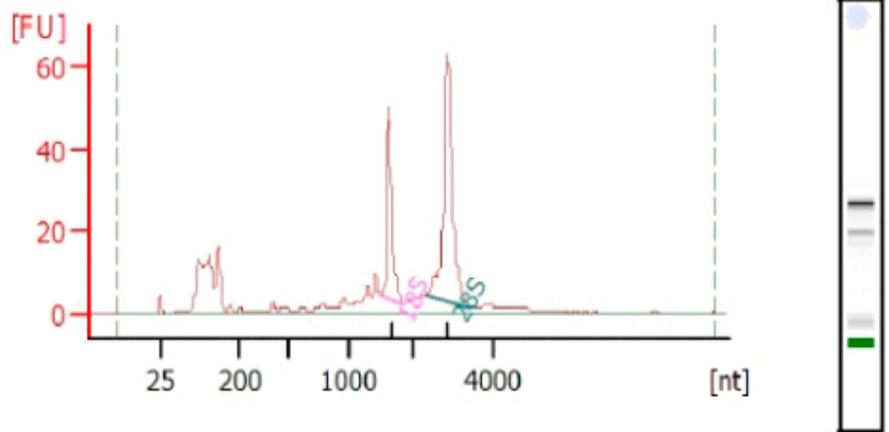


**Supplementary File S2 includes 4 subfigures**

Figure S1 A sample data for the RNA quality from the functional leaves of *R. glutinosa* at 30 days of cultivation using Agilent 2100 analyzer.



**Overall Results for sample :**

RNA Area: 400.3  
RNA Concentration: 416 ng/ $\mu$ l  
rRNA Ratio [28s / 18s]: 2.1  
RNA Integrity Number (RIN): 8.6 (B.02.07)  
Result Flagging Color:   
Result Flagging Label: RIN: 8.60

**Fragment table for sample :**

Name	Start Size [nt]	End Size [nt]	Area	% of total Area
18S	1,497	1,842	54.2	13.5
28S	2,361	3,441	111.8	27.9

Figure S2 The constructs for various RgMATE35 vectors. These include: (A) subcellular localization (CaMV35S:RgMATE35-GFP), (B) heterogeneous expression (RgMATE35-mCherry), (C) overexpression (RgMATE35-OE), and (D) RNAi repression (RgMATE35-RNAi).

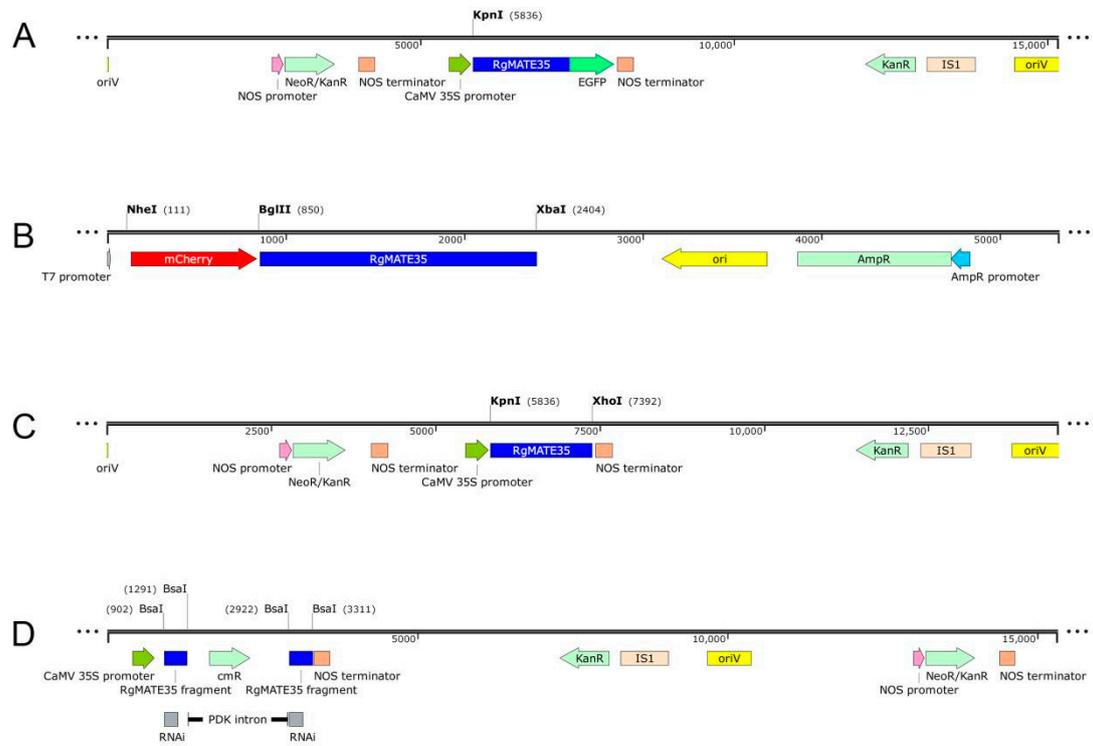


Figure S3 HPLC-Q-TOF-MS profiles of the labeled  $[^2\text{H}_3]$ -FA and  $[^2\text{H}_6]$ -pCA efflux amounts in expressing-RgMATE35 and control *X. oocytes* at the 90-minute time point. The mass (A) and HPLC (B) spectra of the labeled phenolic acid standards are presented, along with the HPLC spectra of efflux phenolic acids from expressing-RgMATE35 (C) and control (D) cells.

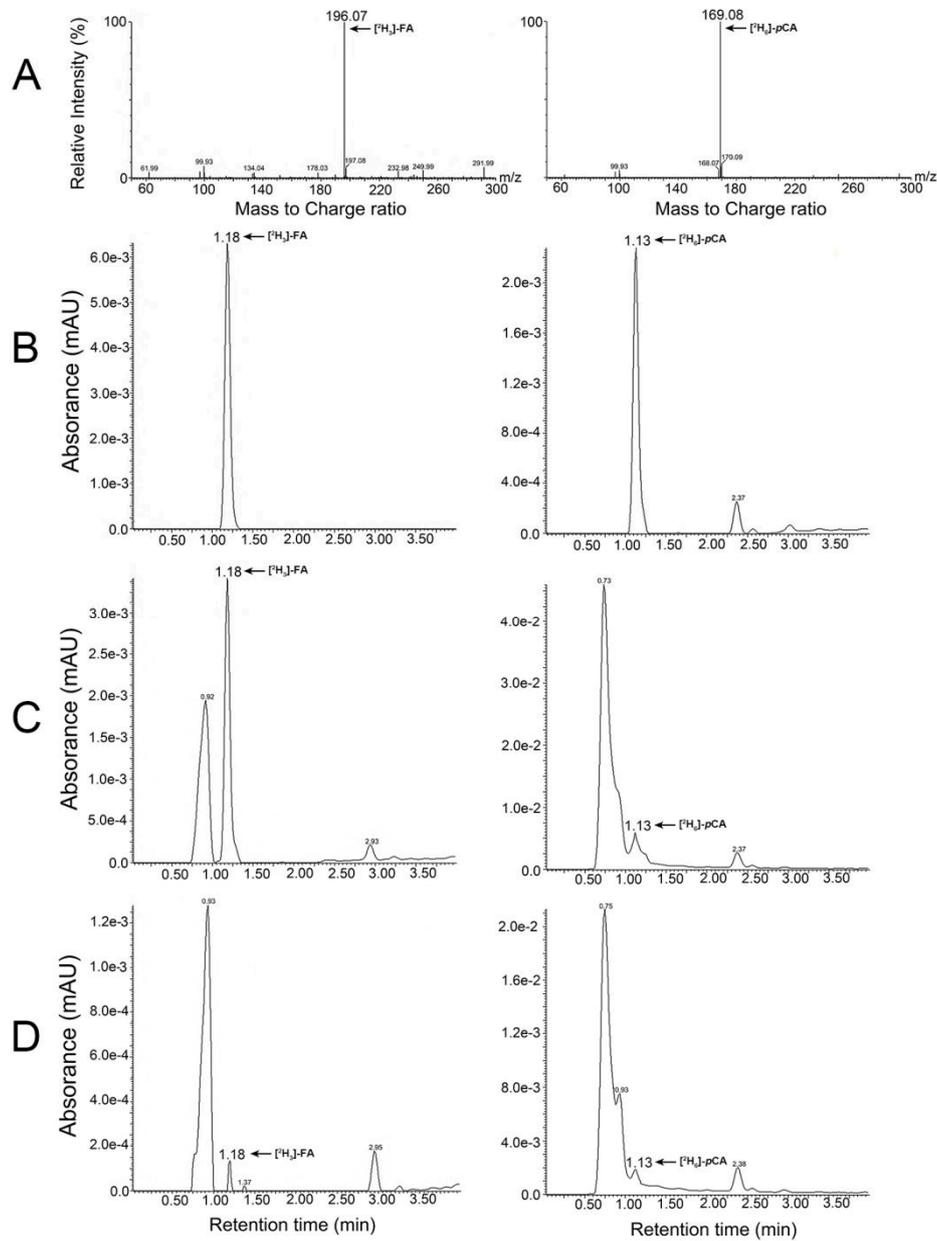


Figure S4 Generation of transgenic *RgMATE35 R. glutinosa* plants. (A) Co-cultivation of the explants and *Agrobacterium tumefaciens*; (B) and (C) the callus induction/selection medium from the explants-transferred; (D) the adventitious buds induction/selection medium from the callus; (E) and (F) the transgenic seedlings were generated in the selection medium; (G) agarose gel images of *NPTII* PCR products from the positive transgenic *RgMATE35* and wild-type (WT) plants; (H) these seedlings-transplanted to pots in organic matrix nutrition soils to facilitate adaption to soil environments; (I) these seedlings were transplanted to pots in field soils. Scale bar = 4 cm.

