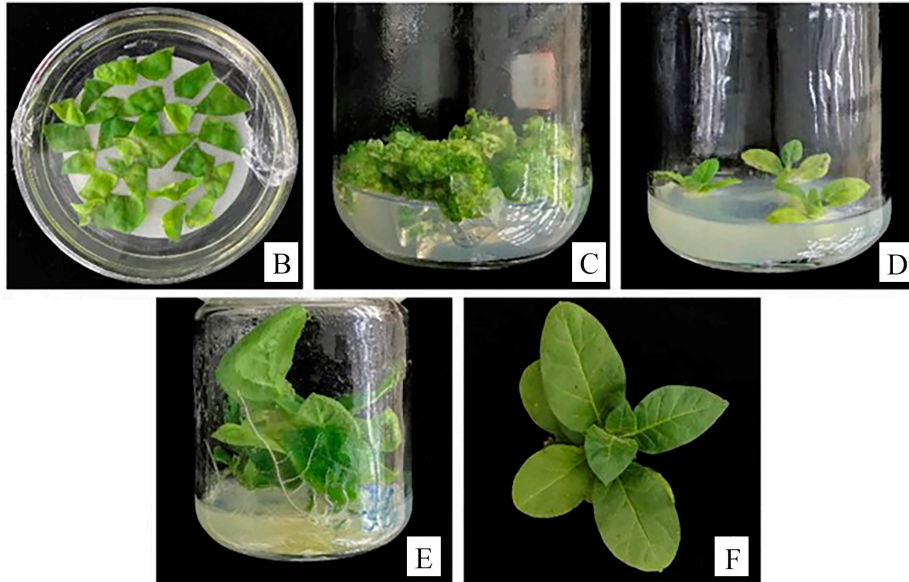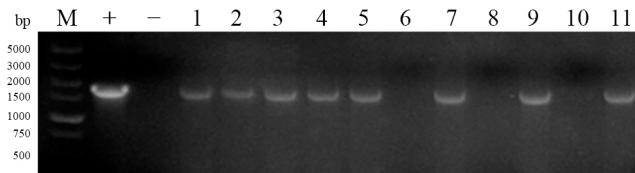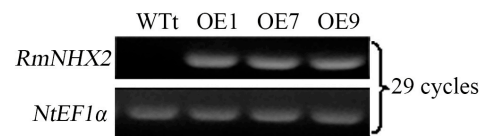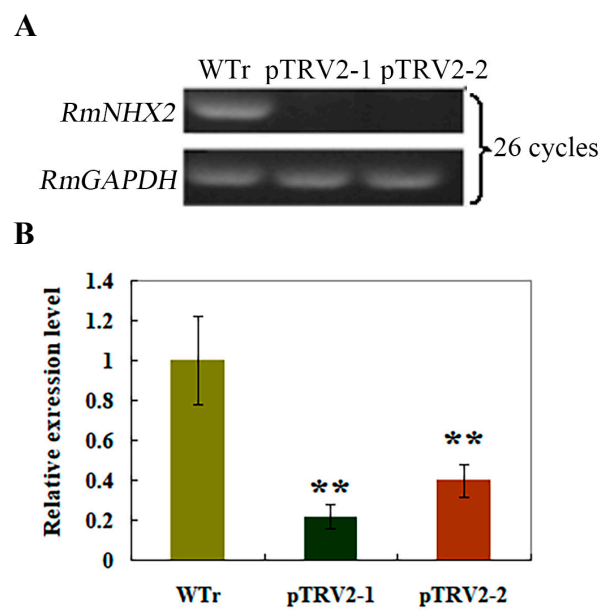**Supplementary Figure S1.** Predicted cis-acting elements in *RmNHXs* promoters. The cis-acting elements are indicated in different colored boxes.

Supplementary Figure S2. Phylogenetic tree of *RmNHX2* protein with its homologous proteins from other plant species. MEGA 7 was used to construct the phylogenetic tree with the NJ method.

A

Supplementary Figure S3. Generation and molecular identification of transgenic tobacco plants overexpressing *RmNHX2*. (A) Schematic diagram of the *RmNHX2* overexpression construct used for tobacco transformation. 35S, cauliflower mosaic virus 35S promoter. (B–F) Transformation of *RmNHX2* into tobacco. (G) PCR confirmation of the kanamycin-resistant plants using CaMV35- *RmNHX2* primers. M, molecular marker; +, plasmid DNA (used as a positive control); -, wild type; the numbers indicate different transgenic lines (lines 1, 7, and 9 are designated as OE1, OE7, and OE9, respectively). (H) Expression analysis of *RmNHX2* in three transgenic lines using RT-PCR. NtEF1*a* gene was used as an internal control.

A

B

Supplementary Figure S4. Analysis of the transcript levels of *RmNHX2* in *Rosa multiflora* silenced plants and wild type (WTr). (A) Expression analysis of *RmNHX2* in two VIGS lines using RT-PCR. *RmGAPDH* gene was used as an internal control. (B) qRT-PCR analysis of *RmNHX2* in two VIGS lines. *RmGAPDH* gene was used as an internal control.

Table S1. Summary of *NHXs* genes in *Rosa multiflora*

Gene Name	Gene ID	CDS length (bp)	Protein length (aa)	MW (kD)	Theoretical pI	GRAVY
RmNHX1	Rmu_sc0002006.1_g000006.1	1629	542	60.08	8.67	0.487
RmNHX2	Rmu_ssc0000156.1_g000005.1	1632	543	60.20	8.90	0.532
RmNHX3	Rmu_sc0000515.1_g000011.1	1314	437	49.54	9.03	0.467
RmNHX4	Rmu_sc0019265.1_g000004.1	1617	538	59.64	6.56	0.527
RmNHX5	Rmu_sc0001085.1_g000001.1	807	268	29.47	5.12	0.960
RmNHX6	Rmu_ssc0000243.1_g000029.1	1587	528	57.81	5.13	0.447
RmNHX7	Rmu_sc0006865.1_g000007.1	2088	695	74.68	5.83	0.529
RmNHX8	Rmu_sc0001509.1_g000010.1	993	330	35.45	5.03	0.738
RmNHX9	Rmu_sc0000554.1_g000036.1	1731	576	62.51	6.64	0.569
RmNHX10	Rmu_sc0021613.1_g000001.1	1647	548	59.13	5.39	0.664
RmNHX11	Rmu_sc0004688.1_g000028.1	1590	529	57.11	5.33	0.410

Table S2.   Primer sequences used in this study

Primer name		Sequence(5'-3')
For isolation of *RmNHX2* in wild rose		
RmNHX2-ORF-F	Forward	TGCATATTGGTTGTGTTGAAGAC
RmNHX2-ORF-R	Reverse	ATTTTGCTTGACTCATTGCCA
For vectors construction in tobacco		
RmNHX2-OE-F	Forward	ATGGCTTCTCATTTGGCCATGTT
RmNHX2-OE-R	Reverse	TCATTGCCATTGAGTGTTGTTC
For vectors construction in wild rose		
RmNHX2-VIGS-F	Forward	AGAATCGCCTTGAAGTTTATGGG
RmNHX2-VIGS-R	Reverse	GCCACTGACGTTCCAGGACTATC
For transgenic confirmation in tobacco		
35S-F	Forward	ACGCACAATCCCACTATCCTTC
RmNHX2-TC-R	Reverse	TCATTGCCATTGAGTGTTGTTC
For qRT-PCR analysis		
RmNHX1-qF	Forward	TTCTTTTCAGCACAGTGGTGTTTGG
RmNHX1-qR	Reverse	ATAATGGTGGACAGTGTGAGACGGA
RmNHX2-qF	Forward	TCCTCTGTTGTCTCGTTGAACCTTT
RmNHX2-qR	Reverse	GATGCGAACTTTTTCCTCCACTG
RmNHX3-qF	Forward	TCTCTTCACTAATGTGGTGTGCGGA
RmNHX3-qR	Reverse	TTGTCAAGAGCATACGCAGATTAGG
RmNHX4-qF	Forward	CACTTGTATTAATCGGAAGGGCAGC
RmNHX4-qR	Reverse	CGAACCAAATACCACTGTGCTGAAT
RmNHX5-qF	Forward	GATGACACTCCCTTTCTCTACAGTG
RmNHX5-qR	Reverse	ACCAGCTGCTATACCAAGAAGAGTG
RmNHX6-qF	Forward	TGGAGTAGCAAGGGCAGTTAATGTT
RmNHX6-qR	Reverse	CAGCATTGTACCCGTTGAACCTCCA
RmNHX7-qF	Forward	CCCTTCTTGTTGGAATGTCTTTGGC
RmNHX7-qR	Reverse	GCCAATCTCACTTAGGCTATCAGGG
RmNHX8-qF	Forward	GCTGTAGGTATTGGTCTTGCTTTTG
RmNHX8-qR	Reverse	ATCGCAGCATAAAACATTCCTAAAG
RmNHX9-qF	Forward	TTAAGCCGGGCCTCAAATCTTCATC
RmNHX9-qR	Reverse	TCAATCATCGCAACTTTCTCCTCGT
RmNHX10-qF	Forward	CAAGGGATTCGGATACAACAACAAA
RmNHX10-qR	Reverse	AAGGAGTGGTCACCAGACTAAGTGC
RmNHX11-qF	Forward	AAGTCGTGCCTCTAATCTCCATCTA
RmNHX11-qR	Reverse	TAAATCCAATCTCAACAGCACCGTC
RmGAPDH -qF	Forward	TGAAGGGTGGTGCCAAGAA
RmGAPDH -qR	Reverse	AAGGGGAGCAAGACAGTTGG
NtPOD-qF	Forward	CAAATGTAAGAGGAAACTCAGAGG
NtPOD-qR	Reverse	AGCAACAACTCCAGCTAATTGATAG
NtSOD-qF	Forward	AGCTACATGACGCCATTTCC

NtSOD-qR	Reverse	CCCTGTAAAGCAGCACCTTC
NtCAT-qF	Forward	AGGTACCGCTCATTCACACC
NtCAT-qR	Reverse	AAGCAAGCTTTTGACCCAGA
RmPOD-qF	Forward	GTGGAGGCTTCATGTCCTGGTGT
RmPOD-qR	Reverse	TGGTGCTGGTAATTGTCTGGTTT
RmSOD-qF	Forward	CATATTCACGCTCTTGGTGATACCT
RmSOD-qR	Reverse	CTGCCAGTCGTCAACAGAAACCT
RmCAT-qF	Forward	CTTGGGTAGCATGGCTGTGA
RmCAT-qR	Reverse	GGGAAGGCACACTACGTGAA