Supplemental Table S1 :Summary of predicted and identified novel miRNAs targeting nicotine pathway genes

MiRNA accession	Mature sequences (5'-3')	Mature length	Precursor length	MFE/ kcal/ mol	Predicted target	Expression abundance (RPM*)		RT-qPCR analysis
						root	leaf	Root
nta-miRX13	AGTGTATAGCTATAAATAGGGACC	24	167	-90.8	PMT2	0.3	0.2	No
nta-miRX17	CCCCACTTGTGGGATTATACTGGG	24	153	-75.2	QPT1	0.5	2.5	Yes
nta-miRX19	CGGATCTCTTGGCGGAAAGAC	21	85	-40.6	NAC_148	4.5	5.6	Yes
nta-miRX20	CGTTGAAGTGGCAAGGATGAC	21	169	-76.4	CYP82E4	1.0	0.3	Yes
nta-miRX27	TATTTTTGGAGAGTTCGAGCA	21	131	-65.5	QPT2	0.5	22.0	Yes

Supplemental Table S1.Summary of predicted and identified novel miRNAs targeting nicotine pathway genes.*RPM: Repeat normalized reaSummary of predictSummary of predicted and identified novel miRNAs targeting nicotine pathway geneed and identified novel miRNAs