Supplemental Table 1. Quantitative PCR thermal cycle conditions and efficiency.

Gene Name	AGI number	Thermal Cycle Condition	Mean Efficiency
AtNOS1	At3g47450	A	0.930
AtCP1	At4g36880	B	1.000
AtGA3ox1	At1g15550	A	1.041
AtGA3ox2	At1g80340	C	1.002
ICL	At3g21720	D	0.911
MS	At5g03860	A	0.928
AtEPR1	At2g27380	A	0.903
AtPER	At1g48130	A	0.943
TIP4	At4g34270	B	0.903
YLS8	AT5G08290	B	0.968
ACT2	At3g18780	E	1.011

Thermal cycle condition A.	**Tm (˚C)**	**Duration (s)**	**Cycle #**
Initial denaturation	95	5:00	1
Amplification	95	0:05	40
segment	60	0:45	
Dissociation	95	1:00	1 cycle data point every 0.5 ˚C between 55˚C – 95˚C
segment	55	0:30	
	95	0:30	

Thermal cycle condition B			
Initial denaturation	95	5:00	1
Amplification	95	0:05	40
segment	60	1:00	
Dissociation	95	1:00	1 cycle data point every 0.5 ˚C between 55˚C – 95˚C
segment	55	0:30	
	95	0:30	

Thermal cycle condition C			
Initial denaturation	95	5:00	1
Amplification	95	0:05	40
segment	60	0:35	
Dissociation	95	1:00	1 cycle data point every 0.5 ˚C between 55˚C – 95˚C
segment	55	0:30	
	95	0:30	

Thermal cycle condition D			
Initial denaturation	95	5:00	1
Amplification	95	0:05	40
segment	60	0:45	
Dissociation	95	1:00	1 cycle data point every 0.5 ˚C between 55˚C – 95˚C
segment	55	0:30	
	95	0:30	

Thermal cycle condition E			
Initial denaturation	95	10:00	1
Amplification	95	0:30	40
segment	55	1:00	
	72	0:30	
Dissociation	95	1:00	1 cycle data point every 0.5 ˚C between 55˚C – 95˚C
segment	55	0:30	
	95	0:30	

Supplemental Table 2. Primer sequences, amplicon length and measured amplicon melting temperature.

Gene Name	AGI Number	5'⇒3' Primer Sequences (F/R)	Amplicon Length (bp)	Amplicon Tm (˚C)
AtNOS1	At3g47450	CCTGGAACCACCTTGGG/ GCTCTCACCCTTGGGACTAC	213	82.35
AtCP1	At4g36880	AGCCTCCAAATCCGGTAAGT CCCAAATGTTTATCGAGCGT	126	81.1
AtGA3ox1	At1g15550	ACGTTGGTGACCTCTTCCAC TATAGAGGCGATTCAACGGG	175	82.35
AtGA3ox2	At1g80340	GTTTCACCGTTATTGGCTCTCC TCACAGTATTTGAGGTGGTGGC	73	79.6
ICL	At3g21720	GGGAAAAGGTGTCACTGAAGAACAG CGCACCGCCGTAATGAACATA	132	81.85
MS	At5g03860	TTATAACTCCGGTGCCGTTCCT ACAAAGCGTCCTCGAAATCAGC	196	84
AtEPR1	At2g27380	GTCCCACTAATAGATTTCTTGAGATTCTT GCGTGACCACTATCAGTCTCATACTT	122	77.7
AtPER	At1g48130	ACGGGACGTAACATGGACGAAGTA ACGCAGATAGCCTTTCTTTGACGG	207	83.35
TIP4	At4g34270	AGTTGACTTAGCAGTCTGGAGCGA ATGGTGGGAACAAGGTAGGGAACA	297	79.85
YLS8	AT5G08290	CCGTTACTAATCGAGCTTCCCAAC GGAGAACAACCGAAACAGTAAGCA	158	77.85
ACT2	At3g18780	CTT ACA ATT TCC CGC TCT GC GTT GGG ATG AAC CAG AAG GA	477	83.2