

A.

GRF1 5' - UCGUUCAAGAAAGCCUGUGGAA - 3'
 : **x** | | | | | | | | | | | | | | | | **x** | | | | | | | |
miR396a 3' - GUCAAGUUCUUUCG-ACACCUU - 5'

B.

GRF2 5' - UCGUUCAAGAAAGCCUGUGGAA - 3'
 : **x** | | | | | | | | | | | | | | | | **x** | | | | | | | |
miR396a 3' - GUCAAGUUCUUUCG-ACACCUU - 5'

C.

GRF3 5' - CCGUUCAAGAAAGCCUGUGGAA - 3'
 | **x** | | | | | | | | | | | | | | | | **x** | | | | | | | |
miR396a 3' - GUCAAGUUCUUUCG-ACACCUU - 5'

D.

GRF7 5' - UCGUUCAAGAAAGCAUGUGGAA - 3'
 : **x** | | | | | | | | | | | | | | | | **x** | | | | | | | |
miR396a 3' - GUCAAGUUCUUUCG-ACACCUU - 5'

E.

GRF8 5' - UCGUUCAAGAAAGCAUGUGGAA - 3'
 : **x** | | | | | | | | | | | | | | | | **x** | | | | | | | |
miR396a 3' - GUCAAGUUCUUUCG-ACACCUU - 5'

F.

GRF9 5' - ACGUUCAAGAAAGCUUGUGGAA - 3'
 xx | | | | | | | | | | | | | | | | **x** | | | | | | | |
miR396a 3' - GUCAAGUUCUUUCG-ACACCUU - 5'

Figure S1. Schematic representation of the base pairing between the miR396a sRNA and its six target genes belonging to the *GRF* transcription factor gene family. The duplex which forms between the miR396a sRNA and its target gene transcripts (**A**) *GRF1* (*AT2G22840*), (**B**) *GRF2* (*AT4G37740*), (**D**) *GRF7* (*AT5G53660*), and (**E**) *GRF8* (*AT4G24150*) harbors 2.5 mismatched base pairings at nucleotide positions 8, 20 and 21 (G:U wobble pairing) with respect to the 5' terminus of the miR396a sRNA. The duplex which forms between the miR396a sRNA and its target gene transcripts (**C**) *GRF3* (*AT2G36400*), and (**F**) *GRF9* (*AT2G45480*) harbors 2 (nucleotide positions 8 and 20) and 3 (nucleotide positions 8, 20 and 21) mismatched base pairings respectively. (**A-E**) A mismatched base pair is represented by a cross symbol (**x**), a G:U wobble pairing is represented by a colon symbol (:), and a base pairing is depicted by an upright solid line (|).

Supplementary Table S1: DNA oligonucleotides used in this study for cDNA synthesis and RT-qPCR analysis.

Transcript	Gene ID	Oligonucleotide sequence (5' to 3')
P5CS1	AT2G39800	FP: GTTTTTGAATCCCGACCTGA
		RP: TTACCCCCAACAGTCTCTGG
GRF1	AT2G22840	FP: CGTCGCATAAACAAGCCTCG
		RP: ATTTTCAGCTCTTCGGGCCAA
GRF2	AT4G37740	FP: CTTGGCCTGAAGAGCTGACA
		RP: GTGTGTGGAGGAAGGGGATG
GRF3	AT2G36400	FP: CCATACGAGTCCCACATCGG
		RP: CTGAGCTCATGGGGCTTGAA
GRF7	AT5G53660	FP: CATCCCCACCGTTAGATCG
		RP: TGCTTCCATGCTTCCGACAT
GRF8	AT4G24150	FP: GCTGCTGTGACTGTAGCAGA
		RP: CTCATGCCATTGAGCTTCGC
GRF9	AT2G45480	FP: CTCACATGAGAATGCCGGGT
		RP: ATCAGAAACTCGGGGCAGTG
NCER1	AT5G58980	FP: GACCAGGCTACCCTGATGAA
		RP: TGCATGACGATAGTCAACTTTCC
NCER2	AT1G07380	FP: TGAGATGTGCTATGGGCGTG
		RP: TGGCGGTAATCAACCTTCCC
NCER3	AT2G38010	FP: TCCGGGCTACCCTGATGAAT
		RP: CCCCTGCAGCTTCTCTGTAG
UBI10	AT4G05320	FP: GGCCTTGTATAATCCCTGATGAATAAG
		RP: AAAGAGATAACAGGAACGAAACATA
Universal-SLR		RP: CCAGTGCAGGGTCCGAGGTA
snoR101		FP: CTTACAGGTAAGTTCGCTTG
		RP: AGCATCAGCAGACCAGTAGTT
miR396		FP: GCGCGTTCCACAGCTTTCTTGAAC RTSL: GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACAAGTTC