Molecular manipulation of the miR396 and miR399 Expression Modules Alters the Response of *Arabidopsis thaliana* to Phosphate Stress

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Table S1. The DNA oligonucleotide sequences of the stem-loop primers used for the reverse transcription of miR396- and miR399-specific cDNAs are provided below in the Table S1 (denoted by RTSL). Post synthesis of a miR396- and miR399-specific cDNA, miRNA-specific forward primers (denoted by RTF in the below Table) together with a generic reverse primer (denoted by SLR in the below table (underlined sequence of the RTSL primer identifies the binding site for the generic reverse primer)) were used to quantify miR396 and miR399 abundance. Also provided below in Table S1 is the sequence of the DNA oligonucleotide used as either the forward (denoted by RTF in the below Table) or reverse (denoted by RTR in the below Table) primer to quantify the expression of either miR396 or miR399 target genes, or a cohort of PO_4-related high molecular weight RNA transcripts. The snoRNA, *snoR101*, was used to normalize miRNA abundance across the different plant lines assessed in this study. The reference gene, *UBI10* (*AT4G05320*), was used to normalize the expression of each analyzed high molecular transcript.

Targeted Sequence	Primer Name	Oligonucleotide sequence (5' to 3')
DNA oligonucleotides used to quantify sRNA abundance		
miR396	**p396-RTSL**	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAAGTTC
	p396-RTF	GCGCGTTCCACAGCTTTCTTGAAC
miR399	**p399-RTSL**	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCAGGGC
	p399-RTF	GCATGCCAAAGGAGATTTGCCCTG
miRNA stem-loop oligo	**pSLR-Generic**	CCAGTGCAGGGTCCGAGGTA
snoR101	**psnoR-RTF**	CTTCACAGGTAAGTTCGCTTG
	psnoR-RTR	AGCATCAGCAGACCAGTAGTT
DNA oligonucleotides used to analyze gene transcript expression		
GRF1 (*AT2G22840*)	**pGRF1-RTF**	CGTCGCATAAACAAGCCTCG
	pGRF1-RTR	ATTTCAGCTCTTCGGGCCAA
GRF2 (*AT4G37740*)	**pGRF2-RTF**	CTTGGCCTGAAGAGCTGACA
	pGRF2-RTR	GTGTGTGGAGGAAGGGGATG
GRF3 (*AT2G36400*)	**pGRF3-RTF**	CCATACGAGTCCCACATCGG
	pGRF3-RTR	CTGAGCTCATGGGGCTTGAA
GRF7 (*AT5G53660*)	**pGRF7-RTF**	CATCCCCCACCGTTAGATCG
	pGRF7-RTR	TGCTTCCATGCTTCCGACAT

DNA oligonucleotides used to analyze gene transcript expression (continued)		
GRF8 (*AT4G24150*)	**pGRF8-RTF**	GCTGCTGTGACTGTAGCAGA
	pGRF8-RTR	CTCATGCCATTGAGCTTCGC
GRF9 (*AT2G45480*)	**pGRF9-RTF**	CTCACATGAGAATGCCGGGT
	pGRF9-RTR	ATCAGAAACTCGGGGCAGTG
MIR399A (*AT1G29265*)	**p399A-RTF**	AGGGTAAGATCTCTATTGGCAGGAAAC
	p399A-RTR	GCAGAAGAATTACAGGGCAAATCTCC
PHO2 (*AT2G33770*)	**pPHO2-RTF**	ACCGTTTCTCATCAAGGCGT
	pPHO2-RTR	GTGCCCGTCCACCATAAGAA
PHR1 (*AT4G28610*)	**pPHR1-RTF**	AAACCAACCCGGCGATTCA
	pPHR1-RTR	CAGCCCATTCATGCCAATCACTT
PHT1;4 (*AT2G38940*)	**pPHT1-4-RTF**	TGTGCCGGCCGAAATCT
	pPHT1-4-RTR	TTGCTCCTAATTTTCCTGATGCT
PHT1;8 (*AT1G20860*)	**pPHT1-8-RTF**	CCCGAAGTAAACCGTATGAGAA
	pPHT1-8-RTR	AATACGTCACCAAGATTCCAGCAA
PHT1;9 (*AT1G76430*)	**pPHT1-9-RTF**	TGGAGCTGCAGGGAAGTTTG
	pPHT1-9-RTR	ATCTGGAAAACCGTCCTCTTCAT
UBI10 (*AT4G05320*)	**pUBI10-RTF**	GGCCTTGTATAATCCCTGATGAATAAG
	pUBI10-RTR	AAAGAGATAACAGGAACGGAAACATA