SUPPLEMENTARY DATA

Supplementary Table 1: Conserved miRNA families in *Arabidopsis*, poplar and rice.

Supplementary Table 2: List of species used in this study

Supplementary Table 3: Validated targets in *Arabidopsis thaliana*

Supplementary Table 4: Potential targets identified in this study

Supplementary Table 5: Potential targets present in at least 10 species

Supplementary Table 6: Potential targets present in at least three *Solanaceae* species

Supplementary Table 7: Oligonucleotide primers used for RT-qPCR

Supplementary Table 8: Oligonucleotide primers used for 5´RACE

Supplementary Figure 1: Transcript levels of miR396 targets in transgenic plants overexpressing the miRNA

Supplementary Figure 2: Transcript levels of *NOZZLE* and *MYB33* in transgenic plants overexpressing miR159

Supplementary Figure 3: Presence of GU interactions in the new miRNA targets pairs

miRNA	TAG	Species	AVG_ΔG[1]	Short_description	Status in *Arabidopsis*
miR156	AT5G50570	24	-32,0	squamosa promoter-binding protein, putative	Validated
miR156	AT2G42200	23	-32,6	SPL9 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9); transcription factor	Validated
miR156	AT5G43270	22	-32,6	SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2); DNA binding / transcription factor	Validated
miR156	AT1G53160	21	-32,0	SPL4 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 4); DNA binding / transcription factor	Validated
miR156	AT2G33810	20	-30,4	SPL3 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3); DNA binding / transcription factor	Validated
miR156	AT1G69170	14	-32,4	squamosa promoter-binding protein-like 6 (SPL6)	Validated
miR156	AT1G19910	13	-28,1	AVA-P2; ATPase/ proton-transporting ATPase, rotational mechanism	New potential target
miR156	AT3G15270	12	-32,0	SPL5 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 5); DNA binding / transcription factor	Validated
miR156	AT4G34720	11	-26,8	AVA-P1; ATPase/ proton-transporting ATPase, rotational mechanism	Not present
miR156	AT1G27370	10	-32,5	squamosa promoter-binding protein-like 10 (SPL10)	Validated
miR156	AT1G24120	7	-26,0	ARL1 (ARG1-LIKE 1); heat shock protein binding / unfolded protein binding	Not present
miR156	AT1G27360	6	-32,6	squamosa promoter-binding protein-like 11 (SPL11)	Validated
miR156	AT1G18650	6	-24,7	PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding	Not present
miR156	AT1G17720	5	-25,1	ATB BETA; nucleotide binding / protein phosphatase type 2A regulator	Not present
miR156	AT1G44760	5	-25,2	universal stress protein (USP) family protein	Not present
miR156	AT3G07565	5	-22,0	DNA binding	Not present
miR156	AT3G21510	5	-25,5	AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 1); histidine phosphotransfer kinase	Not present
miR156	AT3G26935	5	-22,1	zinc finger (DHHC type) family protein	Not present
miR156	AT4G08980	5	-23,2	F-box family protein (FBW2)	Not present
miR156	AT1G75630	4	-28,8	AVA-P4; ATPase	New potential target
miR156	AT3G57920	4	-32,8	SPL15 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 15); DNA binding / transcription factor	Validated
miR156	AT1G20330	4	-29,0	SMT2 (STEROL METHYLTRANSFERASE 2); S-adenosylmethionine-dependent methyltransferase	Not present
miR156	AT1G44191	4	-26,7		Not present
miR156	AT1G64090	4	-25,9	reticulon family protein (RTNLB3)	Not present
miR156	AT1G68690	4	-25,5	ATP binding / protein kinase/ protein serine/threonine kinase	Not present
miR156	AT2G18540	4	-24,5	cupin family protein	Not present
miR156	AT3G24550	4	-24,6	ATPERK1 (PROLINE EXTENSIN-LIKE RECEPTOR KINASE 1); ATP binding / protein kinase	Not present

miR156	AT3G28770	4	-28,2	unknown protein	Not present
miR156	AT4G22505	4	-24,5		Not present
miR156	AT4G23160	4	-24,9	protein kinase family protein	Not present
miR156	AT4G23630	4	-27,0	BTI1 (VIRB2-INTERACTING PROTEIN 1)	Not present
miR156	AT4G34350	4	-23,8	HDR (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE REDUCTASE); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase/ 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Not present
miR156	AT5G11750	4	-26,2	ribosomal protein L19 family protein	Not present
miR156	AT5G54160	4	-27,6	ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3"-O-methyltransferase/ quercetin 3-O-methyltransferase	Not present
miR159	AT5G06100	11	-32,5	MYB33 (MYB DOMAIN PROTEIN 33); DNA binding / transcription factor	Validated
miR159	AT3G11440	8	-33,2	MYB65 (MYB DOMAIN PROTEIN 65); DNA binding / transcription factor	Validated
miR159	AT4G27330	6	-27,8	SPL (SPOROCYTELESS); protein binding / transcription factor	New potential target: validated
miR159	AT4G04885	6	-26,9	PCFS4 (PCF11P-SIMILAR PROTEIN 4); zinc ion binding	Not present
miR159	AT2G32460	5	-31,6	MYB101; DNA binding / transcription factor	Validated
miR159	AT1G10370	5	-26,4	ERD9 (EARLY-RESPONSIVE TO DEHYDRATION 9); glutathione transferase	Not present
miR159	AT1G13950	5	-24,0	ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor	Not present
miR159	AT1G78700	5	-25,7	brassinosteroid signalling positive regulator-related	Not present
miR159	AT3G04090	5	-25,5	SIP1A (SMALL AND BASIC INTRINSIC PROTEIN 1A); water channel	Not present
miR159	AT3G19960	5	-26,3	ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor	Not present
miR159	AT3G24170	5	-26,9	ATGR1 (glutathione-disulfide reductase); FAD binding / NADP or NADPH binding / glutathione-disulfide reductase/ oxidoreductase	Not present
miR159	AT4G08170	5	-29,3	inositol 1,3,4-trisphosphate 5/6-kinase family protein	Not present
miR159	AT3G60460	4	-30,5	DUO1 (DUO POLLEN 1); DNA binding / transcription factor	Validated
miR159	AT1G09020	4	-25,8	SNF4 (HOMOLOG OF YEAST SUCROSE NONFERMENTING 4); protein kinase activator	Not present
miR159	AT2G19810	4	-27,7	zinc finger (CCCH-type) family protein	Not present
miR159	AT3G07565	4	-33,5	DNA binding	Not present
miR159	AT3G12110	4	-26,0	ACT11 (actin-11); structural constituent of cytoskeleton	Not present
miR159	AT3G54210	4	-27,2	ribosomal protein L17 family protein	Not present
miR159	AT5G09810	4	-26,5	ACT7 (ACTIN 7); structural constituent of cytoskeleton	Not present
miR159	AT5G62000	4	-28,3	ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Not present
miR160	AT2G28350	23	-41,9	ARF10 (AUXIN RESPONSE FACTOR 10); miRNA binding / transcription factor	Validated

miR160	AT4G30080	20	-42,0	ARF16 (AUXIN RESPONSE FACTOR 16); miRNA binding / transcription factor	Validated
miR160	AT1G77850	11	-41,8	ARF17 (AUXIN RESPONSE FACTOR 17); transcription factor	Validated
miR160	AT4G28530	4	-28,9	anac074 (Arabidopsis NAC domain containing protein 74); transcription factor	Not present
miR160	AT5G09300	4	-36,7	2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative	Not present
miR162	AT1G01040	8	-31,7	DCL1 (DICER-LIKE 1); ATP-dependent helicase/ double-stranded RNA binding / protein binding / ribonuclease III	Validated
miR162	AT3G11240	8	-24,8	ATE2 (ARGININE-TRNA PROTEIN TRANSFERASE 2); arginyltransferase	Not present
miR162	AT3G11560	6	-25,8	unknown protein	Not present
miR162	AT5G46840	6	-22,4	RNA recognition motif (RRM)-containing protein	Not present
miR162	AT1G51560	5	-25,0	FMN binding	Not present
miR162	AT1G71310	5	-22,6	unknown protein	Not present
miR162	AT3G25520	5	-23,3	ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); 5S rRNA binding / structural constituent of ribosome	Not present
miR162	AT4G17090	5	-20,6	CT-BMY (CHLOROPLAST BETA-AMYLASE); beta-amylase	Not present
miR162	AT4G23160	5	-23,1	protein kinase family protein	Not present
miR162	AT5G47870	5	-24,8	unknown protein	Not present
miR162	AT5G58230	5	-24,7	MSI1 (MULTICOPY SUPRESSOR OF IRA1); protein binding	Not present
miR162	AT1G63430	4	-25,8	leucine-rich repeat transmembrane protein kinase, putative	Not present
miR162	AT2G25300	4	-25,2	transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Not present
miR162	AT2G40100	4	-26,1	LHCB4.3 (light harvesting complex PSII); chlorophyll binding	Not present
miR162	AT4G02080	4	-26,4	ATSAR2 (ARABIDOPSIS THALIANA SECRETION-ASSOCIATED RAS SUPER FAMILY 2); GTP binding	Not present
miR162	AT5G01530	4	-26,3	chlorophyll A-B binding protein CP29 (LHCB4)	Not present
miR162	AT5G37710	4	-23,9	lipase class 3 family protein / calmodulin-binding heat-shock protein, putative	Not present
miR162	AT5G39740	4	-25,3	60S ribosomal protein L5 (RPL5B)	Not present
miR164	AT5G61430	24	-36,5	ANAC100 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 100); transcription factor	Validated
miR164	AT1G56010	22	-36,3	NAC1; transcription factor	Validated
miR164	AT3G62830	14	-33,5	AUD1; UDP-glucuronate decarboxylase/ catalytic/ dTDP-glucose 4,6-dehydratase	New potential target
miR164	AT5G07680	10	-36,8	ANAC080 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 80); transcription factor	Validated
miR164	AT2G28760	9	-34,5	NAD-dependent epimerase/dehydratase family protein	Not present
miR164	AT2G01080	8	-31,1		Not present
miR164	AT2G39940	8	-29,2	COI1 (CORONATINE INSENSITIVE 1);	Not present

				protein binding / ubiquitin-protein ligase	
miR164	AT4G34490	8	-29,5	ATCAP1 (ARABIDOPSIS THALIANA CYCLASE ASSOCIATED PROTEIN 1); actin binding	Not present
miR164	AT2G47650	7	-34,3	UXS4 (UDP-XYLOSE SYNTHASE 4); UDP-glucuronate decarboxylase/ catalytic	New potential target
miR164	AT5G53950	7	-37,5	CUC2 (CUP-SHAPED COTYLEDON 2); transcription factor	Validated
miR164	AT3G46440	7	-35,4	UXS5; UDP-glucuronate decarboxylase/ catalytic	Not present
miR164	AT3G62580	7	-27,7		Not present
miR164	AT3G18170	6	-27,1	transferase, transferring glycosyl groups	Not present
miR164	AT1G01630	5	-28,2	SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative	Not present
miR164	AT1G05260	5	-29,7	RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase	Not present
miR164	AT2G29630	5	-30,4	THIC (ThiaminC); ADP-ribose pyrophosphohydrolase/ catalytic/ iron-sulfur cluster binding	Not present
miR164	AT3G22142	5	-27,4	structural constituent of cell wall	Not present
miR164	AT3G52140	5	-32,7	tetratricopeptide repeat (TPR)-containing protein	Not present
miR164	AT3G53520	5	-35,8	UXS1 (UDP-GLUCURONIC ACID DECARBOXYLASE 1); UDP-glucuronate decarboxylase/ catalytic	Not present
miR164	AT5G25610	4	-28,8	RD22; nutrient reservoir	New potential target
miR164	AT5G39610	4	-34,8	ATNAC6 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 6); protein heterodimerization/ protein homodimerization/ transcription factor	Validated
miR164	AT1G04110	4	-30,5	SDD1 (STOMATAL DENSITY AND DISTRIBUTION); serine-type endopeptidase	Not present
miR164	AT1G04240	4	-29,6	SHY2 (SHORT HYPOCOTYL 2); transcription factor	Not present
miR164	AT1G27480	4	-28,0	lecithin:cholesterol acyltransferase family protein / LACT family protein	Not present
miR164	AT1G52760	4	-28,3	esterase/lipase/thioesterase family protein	Not present
miR164	AT1G67410	4	-31,6	exostosin family protein	Not present
miR164	AT2G29570	4	-30,0	PCNA2 (PROLIFERATING CELL NUCLEAR ANTIGEN 2); DNA binding / DNA polymerase processivity factor	Not present
miR164	AT2G30530	4	-26,0	unknown protein	Not present
miR164	AT3G13220	4	-31,5	ABC transporter family protein	Not present
miR164	AT3G16570	4	-32,5	RALFL23 (ralf-like 23); signal transducer	Not present
miR164	AT3G18830	4	-29,1	ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann	Not present
miR164	AT3G21770	4	-29,8	peroxidase 30 (PER30) (P30) (PRXR9)	Not present
miR164	AT3G44340	4	-29,7	CEF (clone eighty-four); protein binding / transporter/ zinc ion binding	Not present
miR164	AT3G44735	4	-31,2	PSK1; growth factor	Not present

miR164	AT3G55646	4	-31,5	unknown protein	Not present
miR164	AT4G15800	4	-31,8	RALFL33 (ralf-like 33); signal transducer	Not present
miR164	AT4G19170	4	-31,2	NCED4 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 4)	Not present
miR164	AT5G15410	4	-31,8	DND1 (DEFENSE NO DEATH 1); calcium channel/ calmodulin binding / cation channel/ cyclic nucleotide binding / intracellular cAMP activated cation channel/ intracellular cyclic nucleotide activated cation channel/ inward rectifier potassium channel	Not present
miR164	AT5G43100	4	-35,3	aspartyl protease family protein	Not present
miR166	AT5G60690	20	-38,4	REV (REVOLUTA); DNA binding / lipid binding / transcription factor	Validated
miR166	AT2G34710	17	-38,7	PHB (PHABULOSA); DNA binding / transcription factor	Validated
miR166	AT1G52150	14	-38,8	ATHB-15; DNA binding / transcription factor	Validated
miR166	AT4G32880	9	-38,8	ATHB-8 (HOMEOBOX GENE 8); DNA binding / transcription factor	Validated
miR166	AT1G42440	9	-32,2		Not present
miR166	AT1G30490	7	-39,3	PHV (PHAVOLUTA); DNA binding / protein binding / transcription factor	Validated
miR166	AT1G49760	6	-32,6	PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor	Not present
miR166	AT4G34110	6	-32,4	PAB2 (POLY(A) BINDING 2); RNA binding / translation initiation factor	Not present
miR166	AT3G13750	5	-29,1	BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Not present
miR166	AT3G24090	5	-26,4	glutamine-fructose-6-phosphate transaminase (isomerizing)/ sugar binding / transaminase	Not present
miR166	AT4G17650	5	-30,6	aromatic-rich family protein	Not present
miR166	AT3G02230	4	-24,7	RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1); cellulose synthase (UDP-forming)	Not present
miR166	AT3G12390	4	-30,4	nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative	Not present
miR166	AT4G20330	4	-27,1	transcription initiation factor-related	Not present
miR166	AT4G34200	4	-28,1	EDA9 (embryo sac development arrest 9); ATP binding	Not present
miR166	AT5G52380	4	-32,4	zinc knuckle (CCHC-type) family protein	Not present
miR167	AT1G30330	32	-32,8	ARF6 (AUXIN RESPONSE FACTOR 6); transcription factor	Validated
miR167	AT5G37020	27	-32,9	ARF8 (AUXIN RESPONSE FACTOR 8); transcription factor	Validated
miR167	AT5G11800	8	-27,7	KEA6; potassium ion transmembrane transporter/ potassium:hydrogen antiporter	Not present
miR167	AT4G30210	6	-18,5	ATR2 (ARABIDOPSIS P450 REDUCTASE 2); NADPH-hemoprotein reductase	Not present
miR167	AT2G02760	5	-27,9	ATUBC2 (UBIQUITING-CONJUGATING ENZYME 2); ubiquitin-protein ligase	Not present
miR167	AT2G15240	5	-29,2	UNC-50 family protein	Not present
miR167	AT2G17880	5	-29,9	DNAJ heat shock protein, putative	Not present

miR167	AT3G02420	5	-22,3	unknown protein	Not present
miR167	AT3G52500	5	-25,8	aspartyl protease family protein	Not present
miR167	AT5G23860	5	-25,2	TUB8; structural constituent of cytoskeleton	Not present
miR167	AT5G05140	4	-29,5	transcription elongation factor-related	New potential target
miR167	AT1G30510	4	-23,4	ATRFNR2 (ROOT FNR 2); FAD binding / NADP or NADPH binding / electron carrier/ ferredoxin-NADP+ reductase/ oxidoreductase	Not present
miR167	AT1G32120	4	-25,5	unknown protein	Not present
miR167	AT1G52570	4	-24,7	PLDALPHA2 (phosphlipase d alpha 2); phospholipase D	Not present
miR167	AT1G78900	4	-20,7	VHA-A (VACUOLAR ATP SYNTHASE SUBUNIT A); ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism / hydrolase, acting on acid anhydrides, catalyzing transmembrane movement of substances / proton-transporting ATPase, rotational mechanism	Not present
miR167	AT2G21960	4	-27,7	unknown protein	Not present
miR167	AT3G10690	4	-24,2	DNA gyrase subunit A family protein	Not present
miR167	AT3G10910	4	-24,7	zinc finger (C3HC4-type RING finger) family protein	Not present
miR167	AT3G15730	4	-25,9	PLDALPHA1 (PHOSPHOLIPASE D ALPHA 1); phospholipase D	Not present
miR167	AT3G24430	4	-28,2	HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101); ATP binding	Not present
miR167	AT4G31410	4	-29,1	unknown protein	Not present
miR167	AT5G65470	4	-31,4	unknown protein	Not present
miR168	AT1G48410	26	-37,2	AGO1 (ARGONAUTE 1); endoribonuclease/ miRNA binding / protein binding / siRNA binding	Validated
miR168	AT3G06680	5	-27,0	60S ribosomal protein L29 (RPL29B)	Not present
miR168	AT1G65980	4	-31,5	TPX1 (thioredoxin-dependent peroxidase 1); antioxidant/ oxidoreductase	Not present
miR168	AT5G09760	4	-33,3	pectinesterase family protein	Not present
miR168	AT5G13160	4	-34,4	PBS1 (avrPphB susceptible 1); kinase/ protein serine/threonine kinase	Not present
miR168	AT5G43310	4	-35,2	COP1-interacting protein-related	Not present
miR169	AT1G72830	20	-33,6	NF-YA3 (NUCLEAR FACTOR Y, SUBUNIT A3); transcription factor	Validated
miR169	AT3G20910	18	-30,2	NF-YA9 (NUCLEAR FACTOR Y, SUBUNIT A9); specific transcriptional repressor/ transcription factor	Validated
miR169	AT5G12840	17	-30,1	NF-YA1 (NUCLEAR FACTOR Y, SUBUNIT A1); transcription factor	Validated
miR169	AT1G54160	13	-32,5	NF-YA5 (NUCLEAR FACTOR Y, SUBUNIT A5); specific transcriptional repressor/ transcription factor	Validated
miR169	AT5G06510	11	-31,1	NF-YA10 (NUCLEAR FACTOR Y, SUBUNIT A10); transcription factor	Validated
miR169	AT3G17860	11	-27,4	JAZ3 (JASMONATE-ZIM-DOMAIN PROTEIN 3)	Not present
miR169	AT1G17590	9	-33,3	NF-YA8 (NUCLEAR FACTOR Y, SUBUNIT A8); transcription factor	Validated
miR169	AT3G05690	9	-32,7	NF-YA2 (NUCLEAR FACTOR Y, SUBUNIT A2); transcription factor	Validated
miR169	AT1G17370	9	-27,9	UBP1B (oligouridylate binding protein	Not present

				1B); mRNA 3"-UTR binding	
miR169	AT3G54480	9	-26,3	SKIP5 (SKP1/ASK-INTERACTING PROTEIN 5)	Not present
miR169	AT4G28880	8	-30,2	ckl3 (Casein Kinase I-like 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Not present
miR169	AT5G47040	8	-26,2	LON2 (LON PROTEASE 2); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase	Not present
miR169	AT1G23740	7	-24,0	oxidoreductase, zinc-binding dehydrogenase family protein	Not present
miR169	AT1G30500	7	-30,3	NF-YA7 (NUCLEAR FACTOR Y, SUBUNIT A7); specific transcriptional repressor/ transcription factor	Not present
miR169	AT2G27600	7	-26,7	SKD1 (SUPPRESSOR OF K+ TRANSPORT GROWTH DEFECT1); ATP binding / nucleoside-triphosphatase/ nucleotide binding	Not present
miR169	AT3G14020	7	-32,6	NF-YA6 (NUCLEAR FACTOR Y, SUBUNIT A6); transcription factor	Not present
miR169	AT1G80770	6	-29,2	PDE318 (pigment defective 318); GTP binding	New potential target
miR169	AT1G53570	6	-29,7	MAP3KA; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Not present
miR169	AT1G77940	6	-27,0	60S ribosomal protein L30 (RPL30B)	Not present
miR169	AT3G14470	6	-26,1	disease resistance protein (NBS-LRR class), putative	Not present
miR169	AT2G44830	5	-27,8	protein kinase, putative	Not present
miR169	AT5G40670	5	-28,3	PQ-loop repeat family protein / transmembrane family protein	Not present
miR169	AT1G02130	4	-25,2	ARA-5 (ARABIDOPSIS RAS 5); GTP binding	Not present
miR169	AT1G50430	4	-26,8	DWF5 (DWARF 5); sterol delta7 reductase	Not present
miR169	AT4G23160	4	-26,8	protein kinase family protein	Not present
miR169	AT5G62360	4	-24,4	invertase/pectin methylesterase inhibitor family protein	Not present
miR171	AT4G00150	28	-35,9	scarecrow-like transcription factor 6 (SCL6)	Validated
miR171	AT4G36710	14	-27,6	transcription factor	Not present
miR171	AT4G08250	8	-29,5	scarecrow transcription factor family protein	Not present
miR171	AT1G69420	5	-26,5	zinc finger (DHHC type) family protein	Not present
miR171	AT1G14390	4	-26,5	leucine-rich repeat transmembrane protein kinase, putative	Not present
miR171	AT2G19860	4	-27,3	HXK2 (HEXOKINASE 2); ATP binding / fructokinase/ glucokinase/ hexokinase	Not present
miR171	AT4G16760	4	-26,9	ACX1 (ACYL-COA OXIDASE 1); acyl-CoA oxidase	Not present
miR172	AT4G36920	33	-33,2	AP2 (APETALA 2); transcription factor	Validated
miR172	AT2G28550	25	-33,6	RAP2.7 (RELATED TO AP2.7); DNA binding / transcription factor	Validated
miR172	AT3G25800	21	-22,7	PP2AA2 (PROTEIN PHOSPHATASE 2A SUBUNIT A2); protein phosphatase type 2A regulator	Not present
miR172	AT4G27720	10	-21,8		New potential target
miR172	AT2G42280	9	-26,1	basic helix-loop-helix (bHLH) family protein	Not present

miR172	AT5G67380	8	-23,0	CKA1 (CASEIN KINASE ALPHA 1); kinase	Not present
miR172	AT1G07900	7	-21,9	LBD1 (LOB DOMAIN-CONTAINING PROTEIN 1)	Not present
miR172	AT1G73720	6	-27,5	transducin family protein / WD-40 repeat family protein	Not present
miR172	AT2G37150	6	-27,6	zinc finger (C3HC4-type RING finger) family protein	Not present
miR172	AT5G07020	6	-22,1	proline-rich family protein	Not present
miR172	AT5G60120	5	-33,8	TOE2; DNA binding / transcription factor	Validated
miR172	AT1G69830	5	-25,9	AMY3 (ALPHA-AMYLASE-LIKE 3); alpha-amylase	Not present
miR172	AT1G77930	5	-23,3	DNAJ heat shock N-terminal domain-containing protein	Not present
miR172	AT2G47940	5	-23,4	DEGP2; serine-type endopeptidase/ serine-type peptidase	Not present
miR172	AT3G15030	5	-25,0	TCP4 (TCP family transcription factor 4); transcription factor	Not present
miR172	AT4G36960	5	-24,6	RNA recognition motif (RRM)-containing protein	Not present
miR172	AT1G17680	4	-26,0	transcription factor-related	Not present
miR172	AT2G06520	4	-22,7	PSBX (photosystem II subunit X)	Not present
miR172	AT2G20420	4	-29,6	succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative	Not present
miR172	AT2G22360	4	-23,4	DNAJ heat shock family protein	Not present
miR172	AT2G30350	4	-24,6	endo/excinuclease amino terminal domain-containing protein	Not present
miR172	AT2G30950	4	-25,5	VAR2 (VARIEGATED 2); ATP-dependent peptidase/ ATPase/ metallopeptidase/ zinc ion binding	Not present
miR172	AT2G45200	4	-24,1	GOS12 (GOLGI SNARE 12); SNARE binding	Not present
miR172	AT2G45260	4	-29,1	unknown protein	Not present
miR172	AT3G05545	4	-22,3	transcription factor, putative / zinc finger (C3HC4 type RING finger) family protein	Not present
miR172	AT3G09720	4	-26,8	DEAD/DEAH box helicase, putative	Not present
miR172	AT3G13300	4	-23,6	VCS (VARICOSE); nucleotide binding / protein homodimerization	Not present
miR172	AT4G03110	4	-22,7	RNA-binding protein, putative	Not present
miR172	AT4G26540	4	-23,2	kinase	Not present
miR172	AT4G27300	4	-21,4	S-locus protein kinase, putative	Not present
miR172	AT4G36910	4	-27,7	LEJ2 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 2)	Not present
miR172	AT5G13010	4	-20,3	EMB3011 (embryo defective 3011); ATP binding / RNA helicase/ helicase/ nucleic acid binding	Not present
miR172	AT5G16760	4	-25,4	inositol 1,3,4-trisphosphate 5/6-kinase	Not present
miR172	AT5G42390	4	-23,8	metalloendopeptidase	Not present
miR319	AT3G15030	25	-32,9	TCP4 (TCP family transcription factor 4); transcription factor	Validated
miR319	AT4G18390	22	-34,8	TCP family transcription factor, putative	Validated
miR319	AT5G06100	11	-34,2	MYB33 (MYB DOMAIN PROTEIN 33); DNA binding / transcription factor	Validated
miR319	AT1G53230	8	-32,7	TCP3; transcription factor	Validated
miR319	AT3G11440	8	-34,9	MYB65 (MYB DOMAIN PROTEIN 65); DNA binding / transcription factor	Validated
miR319	AT5G04420	7	-27,1	kelch repeat-containing protein	Not present

miR319	AT1G30210	6	-33,5	TCP24 (TEOSINTE BRANCHED1, CYCLOIDEA, AND PCF FAMILY 24); transcription factor	Validated
miR319	AT2G36530	6	-32,7	LOS2; copper ion binding / phosphopyruvate hydratase	Not present
miR319	AT4G23160	6	-32,2	protein kinase family protein	Not present
miR319	AT3G60460	4	-28,7	DUO1 (DUO POLLEN 1); DNA binding / transcription factor	Validated
miR319	AT1G13950	4	-28,1	ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor	Not present
miR319	AT1G54610	4	-28,5	protein kinase family protein	Not present
miR319	AT2G05830	4	-29,3	eukaryotic translation initiation factor 2B family protein / eIF-2B family protein	Not present
miR319	AT3G07310	4	-30,4	unknown protein	Not present
miR319	AT3G07565	4	-36,6	DNA binding	Not present
miR319	AT4G33010	4	-29,6	AtGLDP1 (Arabidopsis thaliana glycine decarboxylase P-protein 1); catalytic/ glycine dehydrogenase (decarboxylating)/ pyridoxal phosphate binding	Not present
miR319	AT4G34260	4	-29,1	FUC95A; 1,2-alpha-L-fucosidase	Not present
miR319	AT5G62000	4	-30,7	ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Not present
miR390	AT3G25230	11	-29,2	ROF1 (ROTAMASE FKBP 1); FK506 binding / calmodulin binding / peptidyl-prolyl cis-trans isomerase	Not present
miR390	AT5G48570	7	-28,6	peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative	New potential target
miR390	AT1G63430	5	-34,7	leucine-rich repeat transmembrane protein kinase, putative	Not present
miR390	AT2G33730	5	-32,8	DEAD box RNA helicase, putative	Not present
miR390	AT2G36350	4	-27,7	protein kinase, putative	New potential target
miR390	AT1G47380	4	-30,1	protein phosphatase 2C-related / PP2C-related	Not present
miR390	AT2G30950	4	-33,8	VAR2 (VARIEGATED 2); ATP-dependent peptidase/ ATPase/ metallopeptidase/ zinc ion binding	Not present
miR390	AT5G47750	4	-29,8	D6PKL2 (D6 PROTEIN KINASE LIKE 2); kinase	Not present
miR393	AT3G62980	30	-33,3	TIR1 (TRANSPORT INHIBITOR RESPONSE 1); auxin binding / protein binding / ubiquitin-protein ligase	Validated
miR393	AT3G26810	23	-34,1	AFB2 (AUXIN SIGNALING F-BOX 2); auxin binding / ubiquitin-protein ligase	Validated
miR393	AT1G12820	18	-33,7	AFB3 (AUXIN SIGNALING F-BOX 3); auxin binding / ubiquitin-protein ligase	Validated
miR393	AT4G35630	10	-24,8	PSAT; O-phospho-L-serine:2-oxoglutarate aminotransferase	New potential target
miR393	AT2G07690	8	-28,0	minichromosome maintenance family protein / MCM family protein	Not present
miR393	AT3G50845	8	-26,5		Not present
miR393	AT1G16740	7	-29,2	ribosomal protein L20 family protein	Not present
miR393	AT2G17630	5	-25,8	phosphoserine aminotransferase, putative	New potential target
miR393	AT1G53210	5	-23,4	sodium/calcium exchanger family protein / calcium-binding EF hand family protein	Not present
miR393	AT3G51860	5	-21,6	CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/	Not present

				calcium:hydrogen antiporter/ cation:cation antiporter	
miR393	AT4G03190	4	-29,7	GRH1 (GRR1-LIKE PROTEIN 1); auxin binding / protein binding / ubiquitin-protein ligase	New potential target
miR393	AT1G47240	4	-22,3	NRAMP2; inorganic anion transmembrane transporter/ metal ion transmembrane transporter	Not present
miR393	AT5G48560	4	-29,7	basic helix-loop-helix (bHLH) family protein	Not present [1]
miR393	AT5G52640	4	-25,6	ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Not present
miR394	AT1G27340	28	-35,4	F-box family protein	Validated
miR394	AT5G64550	12	-30,4	loricrin-related	New potential target
miR394	AT4G16780	8	-23,1	ATHB-2 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 2); DNA binding / protein homodimerization/ sequence-specific DNA binding / transcription factor	Not present
miR394	AT4G33430	8	-30,5	BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE); kinase/ protein binding / protein heterodimerization/ protein serine/threonine kinase	Not present
miR394	AT1G75660	7	-27,2	XRN3; 5"-3" exoribonuclease	Not present
miR394	AT2G46280	6	-33,0	TRIP-1 (TGF-BETA RECEPTOR INTERACTING PROTEIN 1); nucleotide binding / protein binding	Not present
miR394	AT3G06483	6	-28,6	PDK (PYRUVATE DEHYDROGENASE KINASE); ATP binding / histidine phosphotransfer kinase/ pyruvate dehydrogenase (acetyl-transferring) kinase	Not present
miR394	AT5G45140	6	-27,5	NRPC2; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding	Not present
miR394	AT5G64030	6	-25,1	dehydration-responsive protein-related	Not present
miR394	AT2G27110	5	-28,4	FRS3 (FAR1-related sequence 3); zinc ion binding	New potential target
miR394	AT1G64760	5	-27,9	glycosyl hydrolase family 17 protein	Not present
miR394	AT3G01280	5	-28,6	VDAC1 (VOLTAGE DEPENDENT ANION CHANNEL 1); voltage-gated anion channel	Not present
miR394	AT4G02480	5	-31,6	AAA-type ATPase family protein	Not present
miR394	AT4G02930	5	-24,5	elongation factor Tu, putative / EF-Tu, putative	Not present
miR394	AT4G30310	5	-33,8	ribitol kinase, putative	Not present
miR394	AT5G10290	5	-27,6	leucine-rich repeat family protein / protein kinase family protein	Not present
miR394	AT5G52060	5	-23,1	ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1); protein binding	Not present
miR394	AT5G52640	5	-24,0	ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Not present
miR394	AT5G09670	4	-30,7	loricrin-related	New potential target
miR394	AT1G04400	4	-24,7	CRY2 (CRYPTOCHROME 2); blue light photoreceptor/ protein homodimerization	Not present
miR394	AT1G60900	4	-26,0	U2 snRNP auxiliary factor large subunit, putative	Not present
miR394	AT2G23390	4	-30,5		Not present

miR394	AT2G34590	4	-23,2	transketolase family protein	Not present
miR394	AT2G39420	4	-28,5	esterase/lipase/thioesterase family protein	Not present
miR394	AT3G26580	4	-22,4		Not present
miR394	AT5G22300	4	-31,2	NIT4 (NITRILASE 4); 3-cyanoalanine hydratase/ cyanoalanine nitrilase/ indole-3-acetonitrile nitrilase/ nitrilase/ nitrile hydratase	Not present
miR395	AT3G22890	32	-30,0	APS1 (ATP SULFURYLASE 1); sulfate adenylyltransferase (ATP)	Validated
miR395	AT4G14680	19	-30,9	APS3; sulfate adenylyltransferase (ATP)	Validated
miR395	AT1G10290	14	-26,8	ADL6 (DYNAMIN-LIKE PROTEIN 6); GTPase	Not present
miR395	AT5G10180	11	-31,7	AST68; sulfate transmembrane transporter	Validated
miR395	AT1G77990	9	-29,5	AST56; sulfate transmembrane transporter	Not present
miR395	AT5G43780	7	-32,9	APS4; sulfate adenylyltransferase (ATP)	Validated
miR395	AT1G10390	5	-26,2	nucleoporin family protein	Not present
miR395	AT2G28100	4	-28,2	ATFUC1 (alpha-L-fucosidase 1); alpha-L-fucosidase	Not present
miR395	AT2G37250	4	-24,6	ADK (ADENOSINE KINASE); adenylate kinase/ nucleotide kinase	Not present
miR395	AT5G05580	4	-29,0	FAD8 (FATTY ACID DESATURASE 8); omega-3 fatty acid desaturase	Not present
miR395	AT5G66880	4	-26,1	SNRK2.3 (SUCROSE NONFERMENTING 1(SNF1)-RELATED PROTEIN KINASE 2.3); kinase/ protein kinase	Not present
miR396	AT2G22540	29	-25,1	SVP (SHORT VEGETATIVE PHASE); transcription factor/ translation repressor, nucleic acid binding	New potential target
miR396	AT3G13960	27	-30,5	AtGRF5 (GROWTH-REGULATING FACTOR 5); transcription activator	Not present
miR396	AT2G36400	24	-30,2	AtGRF3 (GROWTH-REGULATING FACTOR 3); transcription activator	Validated
miR396	AT2G22840	23	-30,6	AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Validated
miR396	AT4G37740	21	-30,7	AtGRF2 (GROWTHREGULATING FACTOR 2); transcription activator	Validated
miR396	AT1G71350	19	-24,2	eukaryotic translation initiation factor SUI1 family protein	New potential target
miR396	AT5G43060	14	-30,3	cysteine proteinase, putative / thiol protease, putative	New potential target: validated
miR396	AT3G52910	12	-30,3	AtGRF4 (GROWTH-REGULATING FACTOR 4); transcription activator	Validated
miR396	AT2G31880	9	-24,7	leucine-rich repeat transmembrane protein kinase, putative	New potential target
miR396	AT5G53660	9	-30,7	AtGRF7 (GROWTH-REGULATING FACTOR 7); transcription activator	Validated
miR396	AT1G06950	9	-20,1	TIC110 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 110)	Not present
miR396	AT1G12000	9	-21,9	pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative	Not present
miR396	AT1G47128	9	-30,2	RD21 (responsive to dehydration 21); cysteine-type endopeptidase/ cysteine-type peptidase	Not present
miR396	AT5G22580	9	-27,2		Not present

miR396	AT5G56030	9	-29,7	HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Not present
miR396	AT1G04950	8	-29,2	TAF6 (TBP-ASSOCIATED FACTOR 6); DNA binding / RNA polymerase II transcription factor/ transcription initiation factor	Not present
miR396	AT3G48000	8	-21,9	ALDH2B4 (ALDEHYDE DEHYDROGENASE 2B4); 3-chloroallyl aldehyde dehydrogenase/ ATP binding / aldehyde dehydrogenase (NAD)	Not present
miR396	AT3G59040	8	-24,0	pentatricopeptide (PPR) repeat-containing protein	Not present
miR396	AT2G45480	7	-28,3	AtGRF9 (GROWTH-REGULATING FACTOR 9); transcription activator	Validated
miR396	AT3G14110	7	-24,4	FLU (FLUORESCENT IN BLUE LIGHT); binding	New potential target: validated
miR396	AT4G24150	7	-29,5	AtGRF8 (GROWTH-REGULATING FACTOR 8); transcription activator	Validated
miR396	AT2G12550	7	-28,7	ubiquitin-associated (UBA)/TS-N domain-containing protein	Not present
miR396	AT3G10220	7	-22,5	tubulin folding cofactor B	Not present
miR396	AT3G43190	7	-26,5	SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups	Not present
miR396	AT3G52120	7	-19,3	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein	Not present
miR396	AT5G13700	7	-25,4	ATPAO1 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 1); FAD binding / polyamine oxidase	Not present
miR396	AT5G52640	7	-27,1	ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Not present
miR396	AT5G56000	7	-29,5	heat shock protein 81-4 (HSP81-4)	Not present
miR396	AT5G65700	7	-24,8	BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Not present
miR396	AT1G23220	6	-25,1	dynein light chain type 1 family protein	Not present
miR396	AT1G59640	6	-25,9	ZCW32; DNA binding / transcription factor	Not present
miR396	AT1G71430	6	-25,2	unknown protein	Not present
miR396	AT1G77180	6	-28,2	chromatin protein family	Not present
miR396	AT1G80050	6	-25,4	APT2 (ADENINE PHOSPHORIBOSYL TRANSFERASE 2); adenine phosphoribosyltransferase/ phosphate transmembrane transporter	Not present
miR396	AT2G44200	6	-22,5	unknown protein	Not present
miR396	AT3G15390	6	-26,1	SDE5 (silencing defective 5)	Not present
miR396	AT4G24540	6	-25,6	AGL24 (AGAMOUS-LIKE 24); protein binding / protein heterodimerization/ protein homodimerization/ sequence-specific DNA binding / transcription factor	Not present
miR396	AT4G25650	6	-23,2	ACD1-LIKE (ACD1-LIKE); 2 iron, 2 sulfur cluster binding / electron carrier/ oxidoreductase	Not present
miR396	AT5G56010	6	-30,0	HSP81-3; ATP binding / unfolded protein binding	Not present
miR396	AT5G57655	6	-24,8	xylose isomerase family protein	Not present
miR396	AT1G07380	5	-25,9	ceramidase family protein	Not present

miR396	AT1G08520	5	-25,8	CHLD; ATP binding / magnesium chelatase/ nucleoside-triphosphatase/ nucleotide binding	Not present
miR396	AT1G79050	5	-23,7	DNA repair protein recA	Not present
miR396	AT2G15790	5	-25,3	SQN (SQUINT); peptidyl-prolyl cis-trans isomerase	Not present
miR396	AT2G44310	5	-25,5	calcium-binding EF hand family protein	Not present
miR396	AT3G09650	5	-26,4	HCF152 (HIGH CHLOROPHYLL FLUORESCENCE 152); mRNA binding	Not present
miR396	AT3G15030	5	-23,5	TCP4 (TCP family transcription factor 4); transcription factor	Not present
miR396	AT3G26935	5	-22,8	zinc finger (DHHC type) family protein	Not present
miR396	AT3G42170	5	-25,5	DNA binding	Not present
miR396	AT3G56940	5	-25,9	CRD1 (COPPER RESPONSE DEFECT 1); DNA binding / magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	Not present
miR396	AT3G57990	5	-26,7	unknown protein	Not present
miR396	AT4G02570	5	-27,1	ATCUL1 (ARABIDOPSIS THALIANA CULLIN 1); protein binding	Not present
miR396	AT4G27410	5	-24,8	RD26 (RESPONSIVE TO DESICCATION 26); transcription activator/ transcription factor	Not present
miR396	AT4G32600	5	-23,8	zinc finger (C3HC4-type RING finger) family protein	Not present
miR396	AT4G39490	5	-26,1	CYP96A10; electron carrier/ heme binding / iron ion binding / monooxygenase	Not present
miR396	AT5G14620	5	-29,3	DRM2 (DOMAINS REARRANGED METHYLTRANSFERASE 2); N-methyltransferase	Not present
miR396	AT5G40770	5	-27,5	ATPHB3 (PROHIBITIN 3)	Not present
miR396	AT5G63160	5	-25,5	BT1 (BTB AND TAZ DOMAIN PROTEIN 1); protein binding / transcription regulator	Not present
miR396	AT1G03350	4	-23,3	BSD domain-containing protein	New potential target
miR396	AT1G80260	4	-27,8	emb1427 (embryo defective 1427); tubulin binding	New potential target
miR396	AT3G15500	4	-24,8	ANAC055 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 55); transcription factor	New potential target
miR396	AT3G18080	4	-23,5	BGLU44 (B-S GLUCOSIDASE 44); (R)-amygdalin beta-glucosidase/ 4-methylumbelliferyl-beta-D-glucopyranoside beta-glucosidase/ beta-gentiobiose beta-glucosidase/ cellobiose glucosidase/ esculin beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds	New potential target
miR396	AT3G59660	4	-22,6	C2 domain-containing protein / GRAM domain-containing protein	New potential target
miR396	AT5G58980	4	-26,1	ceramidase family protein	New potential target
miR396	AT1G07040	4	-19,7	unknown protein	Not present
miR396	AT1G08630	4	-26,0	THA1 (Threonine Aldolase 1); aldehyde-lyase/ threonine aldolase	Not present
miR396	AT1G10950	4	-22,8	endomembrane protein 70, putative	Not present
miR396	AT1G23800	4	-23,4	ALDH2B7; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	Not present
miR396	AT1G36160	4	-24,3	ACC1 (ACETYL-COENZYME A	Not present

				CARBOXYLASE 1); acetyl-CoA carboxylase	
miR396	AT1G60770	4	-23,0	pentatricopeptide (PPR) repeat-containing protein	Not present
miR396	AT1G75510	4	-20,2	transcription initiation factor IIF beta subunit (TFIIF-beta) family protein	Not present
miR396	AT1G79920	4	-24,5	ATP binding	Not present
miR396	AT2G30110	4	-25,2	ATUBA1; ubiquitin activating enzyme/ ubiquitin-protein ligase	Not present
miR396	AT2G37230	4	-23,9	pentatricopeptide (PPR) repeat-containing protein	Not present
miR396	AT2G38010	4	-23,6	ceramidase family protein	Not present
miR396	AT2G45320	4	-22,2	unknown protein	Not present
miR396	AT3G04520	4	-26,3	THA2 (Threonine Aldolase 2); threonine aldolase	Not present
miR396	AT3G04710	4	-27,2	ankyrin repeat family protein	Not present
miR396	AT3G25800	4	-21,2	PP2AA2 (PROTEIN PHOSPHATASE 2A SUBUNIT A2); protein phosphatase type 2A regulator	Not present
miR396	AT3G51800	4	-30,7	ATG2; aminopeptidase/ metalloexopeptidase	Not present
miR396	AT3G54340	4	-24,1	AP3 (APETALA 3); DNA binding / transcription factor	Not present
miR396	AT3G57410	4	-20,5	VLN3 (VILLIN 3); actin binding	Not present
miR396	AT4G22290	4	-25,1	ubiquitin thiolesterase	Not present
miR396	AT4G34270	4	-28,8	TIP41-like family protein	Not present
miR396	AT4G38810	4	-25,5	calcium-binding EF hand family protein	Not present
miR396	AT5G03540	4	-24,3	ATEXO70A1 (exocyst subunit EXO70 family protein A1); protein binding	Not present
miR396	AT5G22620	4	-23,1	phosphoglycerate/bisphosphoglycerate mutase family protein	Not present
miR396	AT5G23550	4	-19,9		Not present
miR396	AT5G26360	4	-19,9	chaperonin, putative	Not present
miR396	AT5G47650	4	-22,5	ATNUDT2 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 2); ADP-ribose diphosphatase/ NAD or NADH binding / hydrolase	Not present
miR396	AT5G62670	4	-24,3	AHA11 (Arabidopsis H(+)-ATPase 11); ATPase	Not present
miR396	ATMG00860	4	-23,5		Not present
miR397	AT5G60020	24	-31,0	LAC17 (laccase 17); laccase	Validated
miR397	AT2G38080	16	-32,8	IRX12 (IRREGULAR XYLEM 12); laccase	Validated
miR397	AT3G09220	16	-33,0	LAC7 (laccase 7); laccase	Not present
miR397	AT4G34480	12	-26,3	catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Not present
miR397	AT3G04120	11	-24,3	GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Not present
miR397	AT5G03260	11	-29,2	LAC11 (laccase 11); laccase	Not present
miR397	AT2G29130	10	-33,0	LAC2 (laccase 2); laccase	Validated
miR397	AT1G54100	7	-28,1	ALDH7B4 (Aldehyde Dehydrogenase 7B4); 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Not present
miR397	AT5G05390	7	-31,8	LAC12 (laccase 12); laccase	Not present

miR397	AT2G30210	6	-30,4	LAC3 (laccase 3); laccase	Not present
miR397	AT4G35335	6	-26,1	nucleotide-sugar transmembrane transporter/ sugar:hydrogen symporter	Not present
miR397	AT1G13440	5	-25,1	GAPC2 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Not present
miR397	AT1G60550	5	-24,3	ECHID (ENOYL-COA HYDRATASE/ISOMERASE D); catalytic/ naphthoate synthase	Not present
miR397	AT4G00730	5	-22,8	ANL2 (ANTHOCYANINLESS 2); transcription factor/ transcription regulator	Not present
miR397	AT5G59850	5	-25,2	40S ribosomal protein S15A (RPS15aF)	Not present
miR397	AT2G39800	4	-24,9	P5CS1 (DELTA1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1); delta1-pyrroline-5-carboxylate synthetase	New potential target
miR397	AT5G11550	4	-22,8	binding	New potential target
miR397	AT1G63850	4	-25,6	PRLI-interacting factor-related	Not present
miR397	AT1G64680	4	-28,7	unknown protein	Not present
miR397	AT1G68060	4	-26,4	ATMAP70-1 (microtubule-associated proteins 70-1); microtubule binding	Not present
miR397	AT2G40370	4	-32,3	LAC5 (laccase 5); laccase	Not present
miR397	AT3G16980	4	-29,1	NRPB9A; DNA binding / DNA-directed RNA polymerase/ nucleic acid binding / transcription regulator/ zinc ion binding	Not present
miR397	AT5G02500	4	-23,4	HSC70-1 (HEAT SHOCK COGNATE PROTEIN 70-1); ATP binding	Not present
miR397	AT5G47030	4	-26,6	ATP synthase delta" chain, mitochondrial	Not present
miR397	AT5G48100	4	-28,4	TT10 (TRANSPARENT TESTA 10); copper ion binding / laccase	Not present
miR397	AT5G50850	4	-25,5	MAB1 (MACCI-BOU); catalytic/ pyruvate dehydrogenase (acetyl-transferring)	Not present
miR398	AT1G08830	42	-30,1	CSD1 (COPPER/ZINC SUPEROXIDE DISMUTASE 1); superoxide dismutase	Validated
miR398	AT1G12520	18	-33,4	ATCCS (COPPER CHAPERONE FOR SOD1); superoxide dismutase/ superoxide dismutase copper chaperone	Validated
miR398	AT3G15640	16	-31,2	cytochrome c oxidase family protein	Validated
miR398	AT5G20230	10	-27,6	ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier	Not present
miR398	AT2G28190	6	-33,1	CSD2 (COPPER/ZINC SUPEROXIDE DISMUTASE 2); superoxide dismutase	Not present
miR398	AT3G09390	6	-31,3	MT2A (METALLOTHIONEIN 2A); copper ion binding	Not present
miR398	AT3G47420	5	-30,9	glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative	Not present
miR398	AT4G14030	5	-30,0	SBP1 (selenium-binding protein 1); selenium binding	Not present
miR398	AT5G02380	5	-31,8	MT2B (METALLOTHIONEIN 2B); copper ion binding	Not present
miR398	AT5G47900	5	-27,6	unknown protein	Not present
miR398	AT1G80230	4	-31,0	cytochrome c oxidase family protein	Not present
miR399	AT2G33770	5	-36,2	PHO2 (PHOSPHATE 2); ubiquitin-	Validated

				protein ligase	
miR399	AT5G60760	5	-22,8	2-phosphoglycerate kinase-related	Not present
miR399	AT3G45090	4	-22,8	2-phosphoglycerate kinase-related	Not present
miR399	AT4G23160	4	-25,9	protein kinase family protein	Not present
miR399	AT4G36250	4	-23,0	ALDH3F1 (Aldehyde Dehydrogenase 3F1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	Not present
miR408	AT2G02850	33	-38,3	ARPN (PLANTACYANIN); copper ion binding / electron carrier	Validated
miR408	AT1G72230	23	-33,8	plastocyanin-like domain-containing protein	Validated
miR408	AT5G21930	22	-34,7	PAA2 (P-TYPE ATPASE OF ARABIDOPSIS 2); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / copper ion transmembrane transporter	New potential target: validated
miR408	AT3G22110	20	-28,5	PAC1; endopeptidase/ peptidase/ threonine-type endopeptidase	New potential target: validated
miR408	AT5G05390	16	-30,3	LAC12 (laccase 12); laccase	Validated
miR408	AT1G22480	15	-32,0	plastocyanin-like domain-containing protein	Not present
miR408	AT5G40200	13	-26,6	DegP9 (DegP protease 9); catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase	Not present
miR408	AT2G40370	11	-30,5	LAC5 (laccase 5); laccase	Not present
miR408	AT1G19440	10	-29,8	KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Not present
miR408	AT3G60270	10	-33,2	uclacyanin, putative	Not present
miR408	AT5G43130	9	-28,3	TAF4 (TBP-ASSOCIATED FACTOR 4); transcription initiation factor	New potential target
miR408	AT3G60280	9	-37,4	UCC3 (UCLACYANIN 3); copper ion binding / electron carrier	Not present
miR408	AT3G62600	8	-26,3	ATERDJ3B; heat shock protein binding / unfolded protein binding	Not present
miR408	AT4G04340	8	-28,4	early-responsive to dehydration protein-related / ERD protein-related	Not present
miR408	AT2G32300	7	-32,7	UCC1 (UCLACYANIN 1); copper ion binding / electron carrier	Not present
miR408	AT4G20070	7	-29,3	ATAAH (Arabidopsis thaliana Allantoate Amidohydrolase); allantoate deiminase/ metallopeptidase	Not present
miR408	AT4G22120	7	-26,6	early-responsive to dehydration protein-related / ERD protein-related	Not present
miR408	AT5G11480	7	-26,5	GTP binding	Not present
miR408	AT1G23380	6	-27,6	KNAT6; DNA binding / transcription activator/ transcription factor	Not present
miR408	AT2G42070	6	-31,6	ATNUDX23 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 23); FAD diphosphatase/ hydrolase	Not present
miR408	AT3G01180	6	-28,0	AtSS2 (starch synthase 2); transferase, transferring glycosyl groups	Not present
miR408	AT5G19350	6	-27,1	RNA-binding protein 45 (RBP45), putative	Not present
miR408	AT2G30210	5	-30,3	LAC3 (laccase 3); laccase	Validated
miR408	AT1G01090	5	-28,7	PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-	Not present

				transferring)	
miR408	AT1G68560	5	-29,0	XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Not present
miR408	AT1G78680	5	-22,8	ATGGH2 (gamma-glutamyl hydrolase 2); omega peptidase	Not present
miR408	AT2G19130	5	-27,9	S-locus lectin protein kinase family protein	Not present
miR408	AT2G20580	5	-21,5	RPN1A (26S PROTEASOME REGULATORY SUBUNIT S2 1A); binding / enzyme regulator	Not present
miR408	AT3G02360	5	-30,7	6-phosphogluconate dehydrogenase family protein	Not present
miR408	AT3G49080	5	-23,4	ribosomal protein S9 family protein	Not present
miR408	AT3G56370	5	-29,9	leucine-rich repeat transmembrane protein kinase, putative	Not present
miR408	AT4G24330	5	-24,8	unknown protein	Not present
miR408	AT5G26330	5	-37,9	plastocyanin-like domain-containing protein / mavicyanin, putative	Not present
miR408	AT5G52520	5	-25,6	OVA6 (OVULE ABORTION 6); ATP binding / aminoacyl-tRNA ligase/ nucleotide binding / proline-tRNA ligase	Not present
miR408	AT1G26690	4	-28,9	emp24/gp25L/p24 family protein	Not present
miR408	AT1G78060	4	-25,6	glycosyl hydrolase family 3 protein	Not present
miR408	AT2G16440	4	-29,3	DNA replication licensing factor, putative	Not present
miR408	AT2G27510	4	-28,2	ATFD3 (ferredoxin 3); 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding	Not present
miR408	AT2G38130	4	-28,9	ATMAK3; N-acetyltransferase	Not present
miR408	AT3G06880	4	-26,6	nucleotide binding	Not present
miR408	AT3G21620	4	-25,1	early-responsive to dehydration protein-related / ERD protein-related	Not present
miR408	AT3G22330	4	-33,7	PMH2 (putative mitochondrial RNA helicase 2); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Not present
miR408	AT3G52120	4	-28,7	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein	Not present
miR408	AT4G02590	4	-30,9	UNE12 (unfertilized embryo sac 12); DNA binding / transcription factor	Not present
miR408	AT4G08150	4	-27,6	KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor	Not present
miR408	AT4G11740	4	-26,7	SAY1	Not present
miR408	AT4G23160	4	-28,9	protein kinase family protein	Not present
miR408	AT5G03530	4	-30,4	RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding	Not present
miR408	AT5G22460	4	-29,5	esterase/lipase/thioesterase family protein	Not present
miR408	AT5G59950	4	-31,6	RNA and export factor-binding protein, putative	Not present
miR408	AT5G65220	4	-32,7	ribosomal protein L29 family protein	Not present
miR827	AT1G71790	9	-29,8	F-actin capping protein beta subunit family protein	Not present
miR827	AT5G22850	8	-27,5	aspartyl protease family protein	New potential target
miR827	AT1G07140	7	-24,7	SIRANBP; Ran GTPase binding	New potential target

miR827	AT2G44530	7	-24,5	ribose-phosphate pyrophosphokinase, putative / phosphoribosyl diphosphate synthetase, putative	New potential target
miR827	AT1G02130	7	-22,4	ARA-5 (ARABIDOPSIS RAS 5); GTP binding	Not present
miR827	AT1G24490	7	-23,7	ALB4 (ALBINA 4)	Not present
miR827	AT4G22990	7	-27,4	SPX (SYG1/Pho81/XPR1) domain-containing protein	Not present
miR827	AT2G39840	6	-22,1	TOPP4; protein serine/threonine phosphatase	Not present
miR827	AT3G22750	6	-25,4	protein kinase, putative	Not present
miR827	AT4G23160	6	-24,9	protein kinase family protein	Not present
miR827	AT5G58590	6	-24,1	RANBP1 (RAN BINDING PROTEIN 1); protein binding	Not present
miR827	AT5G59240	6	-27,6	40S ribosomal protein S8 (RPS8B)	Not present
miR827	AT1G11720	5	-25,2	ATSS3 (starch synthase 3); starch synthase/ transferase, transferring glycosyl groups	New potential target
miR827	AT1G12780	5	-24,4	UGE1 (UDP-D-glucose/UDP-D-galactose 4-epimerase 1); UDP-glucose 4-epimerase/ protein dimerization	Not present
miR827	AT2G45300	5	-25,7	3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate / EPSP synthase	Not present
miR827	AT2G46090	5	-24,5	diacylglycerol kinase family protein	Not present
miR827	AT3G55580	5	-24,9	regulator of chromosome condensation (RCC1) family protein	Not present
miR827	AT4G11810	5	-29,6	SPX (SYG1/Pho81/XPR1) domain-containing protein	Not present
miR827	AT4G14000	5	-27,0	unknown protein	Not present
miR827	AT5G17190	5	-24,2	unknown protein	Not present
miR827	AT5G48970	5	-23,3	mitochondrial substrate carrier family protein	Not present
miR827	AT5G51070	5	-23,0	ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding	Not present
miR827	AT5G51230	5	-26,2	EMF2 (EMBRYONIC FLOWER 2); DNA binding / transcription factor	Not present
miR827	AT1G63010	4	-28,8	SPX (SYG1/Pho81/XPR1) domain-containing protein	Validated
miR827	AT2G36670	4	-28,2	aspartyl protease family protein	New potential target
miR827	AT1G30910	4	-23,0	molybdenum cofactor sulfurase family protein	Not present
miR827	AT1G43670	4	-26,0	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	Not present
miR827	AT2G02560	4	-23,7	CAND1 (CULLIN-ASSOCIATED AND NEDDYLATION DISSOCIATED); binding	Not present
miR827	AT2G34250	4	-21,3	protein transport protein sec61, putative	Not present
miR827	AT3G08720	4	-29,5	S6K2 (ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 2); kinase/ protein kinase	Not present
miR827	AT3G17810	4	-25,3	dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family protein	Not present
miR827	AT3G47810	4	-26,7	MAG1 (MAIGO 1); hydrolase/ protein	Not present

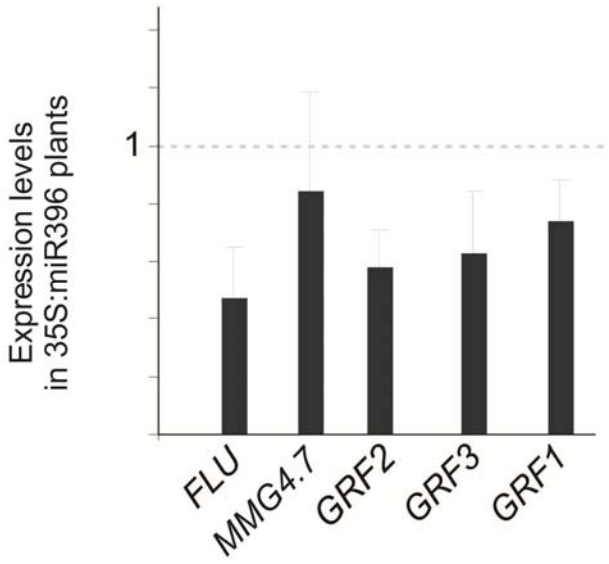
				serine/threonine phosphatase	
miR827	AT3G52260	4	-26,0	pseudouridine synthase family protein	Not present
miR827	AT3G52750	4	-21,5	FTSZ2-2; GTP binding / GTPase/ structural molecule	Not present
miR827	AT4G15545	4	-23,0	unknown protein	Not present
miR827	AT4G33410	4	-22,9	signal peptide peptidase family protein	Not present
miR827	AT5G01960	4	-21,6	zinc finger (C3HC4-type RING finger) family protein	Not present
miR827	AT5G03900	4	-23,1		Not present
miR827	AT5G13030	4	-27,1	unknown protein	Not present
miR827	AT5G25560	4	-17,5	zinc finger (C3HC4-type RING finger) family protein	Not present
miR827	AT5G28050	4	-19,4	cytidine/deoxycytidylate deaminase family protein	Not present
miR827	AT5G40990	4	-23,0	GLIP1 (GDSL LIPASE1); carboxylesterase/ lipase	Not present
miR827	AT5G51340	4	-21,3	unknown protein	Not present
miR827	AT5G53350	4	-25,1	CLPX; ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding	Not present

Supplementary table 7. Oligonucleotide primers used for RT-qPCR.

Gene	Locus ID	Forward primer	Reverse Primer
PAA2	At5g21930	GTCCTCTTATCAGGGGACAGG	CATAGTTGCTTGTGCAAGACTCAG
MYB33	At5g06100	CTATGGAAACCGACATTCACCTG	CTTGGCTTCCAGAAGCAACATATCG
NZZ	At4g27330	TCGGGTCAGGTTATGATCGA	AGGGTTTCCTTCCATGTAGCTCC
PP2A	At1g13320	CCTGCGGTAATAACTGCATCT	CTTCACTTAGCTCCACCAAGCA
tMT2A	tobacco	TACCCAGATTTGAGCTACAACGAG	GCAGGAGATTCACCCATTTCCATA
tMT2B	tobacco	TACCCAGATTTGAGCTACAACGAA	AGGGGATTCACCCATTTCCATT

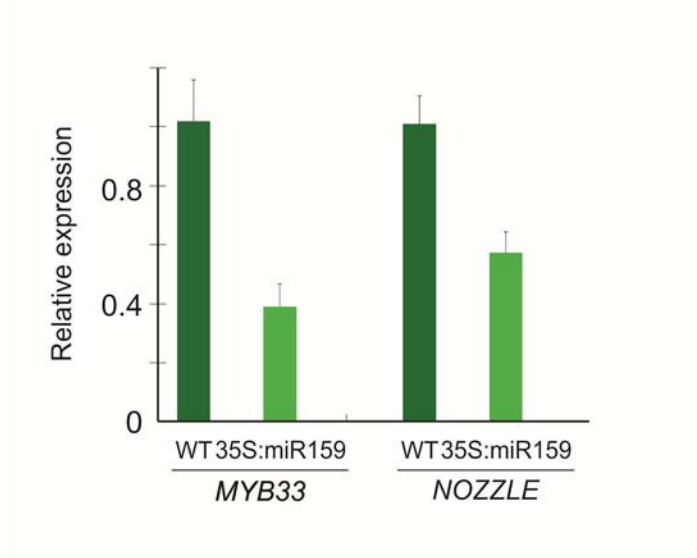
Supplementary table 8. Oligonucleotide primers used for 5´RACE.

Gene	Locus ID	5´ race	5´ race nested
General		CGACTGGAGCACGAGGACACTGA	GGACACTGACATGGACTGAAGGAGTA
PAA2	At5g21930	GACTTATGGAGCTGCAGAAGTAATG	CATAGTTGCTTGTGCAAGACTCAG
IAR3	At1g51760	ATCTTCTGATCCCATTAATGGTTGCATCTCG	CATATTCACGCTCGCTTGCCTTGTGATAACC
NZZ	At4g27330	CATTTAAAGCTTCAAGGACAAATCAATGGTATTAGG	AGGGTTTCCTTCCATGTAGCTCC
MMG4.7	At5g43060	ATGGTAACAACCTTAGCATTTTTCC	CTTCGGTATCAATACCWCCATT
UDP	At2g47650	AATGGGCCGACATGTTCTCC	CCTCGGTGATAGTCCATGGT
SVP	At2g22540	GCAACTTTCCTTCATTCATC	TTTCATCTGCCTCAGCTCAC
loricrin-related	AT5g64550	ACCATGAGCTTTGCAGTAGT	CCTCAGCACTTCGTGTACAG
	At3g14110	CGGAAGGATCAGTCAGTCTC	CCCAGCTCGGTATAACAGTC
	At3g22110	GTTTCATCGCCAAAGGTAAC	CCAGGCGAATAAGACTAGAG
AVA-P2	At1g19910	CTCTAGACTGACCAGCTCGA	GGATGATACCAACAATGAGA

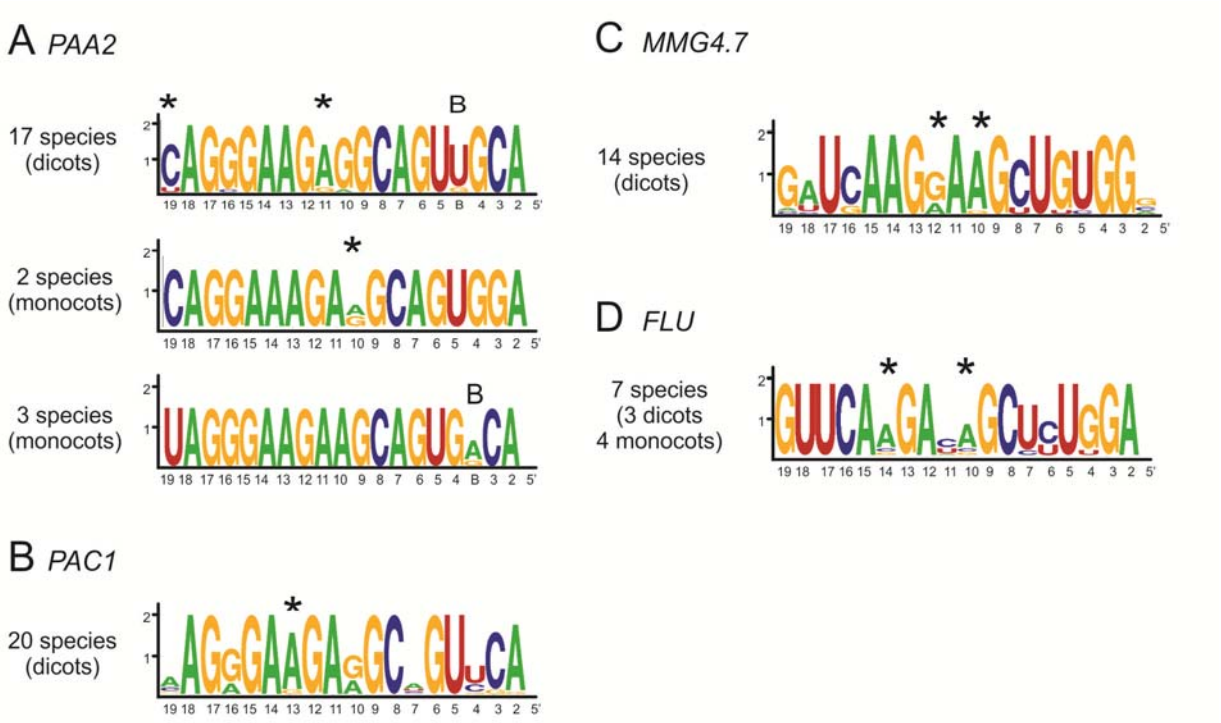


Supplementary Figure 1: Transcript levels of miR396 targets in transgenic plants overexpressing the miRNA.

The RNA levels were determined by RT-qPCR (ten days old seedlings) and are relative to transgenic plants harboring an empty vector (dashed line). Data shown are mean ± SEM of 3 biological replicates.



Supplementary Figure 2: Transcript levels of *MYB33* and *NOZZLE* in transgenic plants overexpressing miR159. The RNA levels were determined by RT-qPCR (inflorescences). Data shown are mean ± SEM of 3 biological replicates.



Supplementary Figure 3: Presence of GU interactions in the new miRNA targets pairs. Weblogo of the sequences from different species. The asterisk represents the position where C/U and A/G alternates generating a C/U-G or A/G-U interaction respectively with the miRNA. B represents a bulge. In the case of *PAA2* the position of the bulge nucleotide varies between dicot and monocot species and the alignments are presented separately.