Supplementary Material

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Tables S1-S4

Table S1 miRNAs in miRBase which are homologous to miR414 predicted from *Stevia*

Plant species	EST name	Location	Sequence	Homology
Stevia rebaudiana	gi|16948646	5’	ucaucuucaucaucaucguca	
Oryza sativa	PUT-163a-*Oryza_sativa*-35580	5’	ucaucuucaucuucaucguca	95%
Raphanus raphanistrum subsp raphanistrum	PUT-165a-*Raphanus_raphanistrum_subsp__raphanistrum*-27094	5’	caucuucaucaucaucguc	100%

Table S2. List of potential miR414 target proteins with GO terms

Targeted protein	Function	Targeted gene	GO annotations
DNA-binding storekeeper protein	Transcription regulator	At5g14280.1	Transcriptional regulator activity (GO:0030528) Molecular function unknown (GO:0003674) Integral to membrane (GO:0016021) Biological process unknown (GO:0008150)
		At4g00270.1	Transcriptional regulator activity (GO:0030528) Molecular function unknown (GO:0003674) Chloroplast (GO:0009507) Biological process unknown (GO:0008150)
Zinc finger (C2H2 type) family protein	Transcription regulator	At4g31420.1	Transcription factor activity (GO:0003700) Regulation of transcription (GO:0045449) Intracellular (GO:0005622)
		At3g48430.1	Transcription factor activity (GO:0003700) Intracellular (GO:0005622) Biological process unknown (GO:0008150)
		At5g56200.1	Nucleic acid binding (GO:0003676) Intracellular (GO:0005622) Zinc ion binding (GO:0008270) Transcription factor activity (GO:0003700)
		At3g20880.1	Intracellular (GO:0005622) Regulation of transcription (GO:0045449) Zinc ion binding (GO:0008270) Transcription factor activity (GO:0003700) Nucleic acid binding (GO:0003676)
Pentatricopeptide repeat (PPR) -containing protein	Sequence specific RNA binding, role in post-transcriptional processes	At2g40240.1	Biological process unknown (GO:0008150) Molecular function unknown (GO:0003674)
		At3g49710.1	Biological process unknown (GO:0008150) Binding (GO:0005488)

			Cellular component unknown (GO:0005575)
		At5g16860.1	Binding (GO:0005488)
		At3g59040.1	Binding (GO:0005488) Chloroplast (GO:0009507) Biological process unknown (GO:0008150)
		At5g04810.1	Nucleic acid binding (GO:0003676) Binding (GO:0005488) Nucleotide binding (GO:0000166)
		At3g18970.1	Binding (GO:0005488) Biological process unknown (GO:0008150)
		At2g34400.1	Cellular component unknown (GO:0005575) Binding (GO:0005488) Biological process unknown (GO:0008150)
		At1g56570.1	Binding (GO:0005488)
		At3g49140.1	Binding (GO:0005488)
Ubiquitin-conjugating enzyme 4 (UBC4) E2	Post-transcriptional protein modification, amino acid ligase activity	At5g41340.1	Ubiquitin dependent protein catabolic process (GO:0006511) Ubiquitin protein ligase activity (GO:0004842)
		At3g15355.1	Small conjugating protein ligase activity (GO:0019787) Protein modification process (GO:0006464) Cellular component unknown (GO:0005575) Ubiquitin cycle (GO:0006512)
SWIB complex BAF60b domain-containing protein	ATP-dependent chromatin-remodelling proteins	At5g08430.1	Nucleus (GO:0005634) Molecular function unknown (GO:0003674) Biological process unknown (GO:0008150)
Importin beta-2 subunit family protein	Intracellular protein transporter	At2g31660.1	Nucleus (GO:0005634) Cytoplasm (GO:0005737) Nuclear pore (GO:0005643) Protein import to nucleus, docking (GO:0000059)
		At4g27640.1	Protein transporter activity (GO:0008565)

			Nucleus (GO:0005634) Nuclear pore (GO:0005643) Cytoplasm (GO:0005737) Protein import into nucleus, docking (GO:0000059)
Nucleosome assembly protein (NAP)	Histone chaperones, regulate gene expression and cellular differentiation	At2g19480.1	DNA binding (GO:0003677) Nucleosome assembly (GO:0006334) Nucleus (GO:0005634)
		At3g13782.1	DNA binding (GO:0003677) Nucleosome assembly (GO:0006334) Nucleus (GO:0005634)
		At5g56950.1	DNA binding (GO:0003677) Nucleosome assembly (GO:0006334) Nucleus (GO:0005634)
Protein kinase family protein	Protein phosphorylation ability	At3g01840.1	Cell wall catabolic process (GO:0016998) Protein amino acid phosphorylation (GO:0006468) Kinase activity (GO:0016301) Endomembrane system (GO:0012505)
		At5g13530.1	Developmental growth (GO:0048589) Protein binding (GO:0005515) Protein kinase activity (GO:0004672) Ubiquitin protein ligase (GO:0004842) Abscisic acid mediated signaling (GO:0009738) Protein ubiquitination (GO:0016567)
		At5g28080.1	Kinase activity (GO:0016301)
		At1g13350.1	Cytoplasm (GO:0005737) Protein amino acid phosphorylation (GO:0006468) Nucleus (GO:0005634) Protein kinase activity (GO:0004672)
		At3g53640.1	Protein amino acid phosphorylation (GO:0006468) Nucleus (GO:0005634) Kinase activity (GO:0016301)
Expressed protein similar to 6b-interacting protein 1	Transcription factor	At5g05550.1	Regulation of transcription (GO:0045449) Cellular component unknown (GO:0005575)

			Transcription factor activity (GO:0003700)
		At3g11100.1	Cellular component unknown (GO:0005575) Transcription factor activity (GO:0003700) Regulation of transcription (GO:0045449)
Tetratricopeptide repeat (TPR)-containing protein	Structural motif, to mediate protein–protein interactions	At4g37210.1 At4g37210.2	Biological process unknown (GO:0008150) Binding (GO:0005488) Cellular component unknown (0005575)
Structural maintenance of chromosomes (SMC) family protein	Role in chromosome structural changes	At2g27170.1	ATP binding (GO:0005524) Nucleus (GO:0005634) Chromosome segregation (GO:0007059)
Myb family transcription factor	Transcription factor	At5g41020.1	Transcription factor activity (GO:0003700) DNA binding (GO:0003677) Regulation of transcription (GO:0045449) Nucleus (GO:0005634)
		At4g18770.1	Nucleus (GO:0005634) Regulation of transcription, DNA dependent (GO:0006355) DNA binding (GO:0003677)
		At3g18100.1	Regulation of transcription (GO:0045449) Transcription factor activity (GO:0003700) Nucleus (GO:0005634)
		At3g18100.2	Nucleus (GO:0005634) Transcription factor activity (GO:0003700)
		At3g10580.1	Transcription factor activity (GO:0003700) Regulation of transcription, DNA dependent (GO:0006355) DNA binding (GO:0003677) Nucleus (GO:0005634)
		At5g23000.1	Regulation of transcription, DNA dependent (GO:0006355) Transcription factor activity (GO:0003700) DNA binding (GO:0003677) Nucleus (GO:0005634)
		At2g03470.1	Regulation of transcription (GO:0045449) Nucleus (GO:0005634)

			DNA binding (GO;0003677)
Endo/excinuclease amino terminal domain-containing protein	Nuclease activity, role in DNA repair	At2g30350.1 At2g30350.2	Intracellular (GO:0005622) DNA repair (GO:0006281) Nuclease activity (GO:0004518)
WRKY family transcription factor	Transcription factor	At3g01080.1	Regulation of defense response (GO:0031347) Transcription factor activity (GO:0003700) Nucleus (GO:0005634) Regulation of transcription, DNA dependent (GO:0006355)
		At5g56270.1	Regulation of transcription, DNA dependent (GO:0006355) Nucleus (GO:0005634) Transcription factor activity (GO:0003700)
		At3g62340.1	Nucleus (GO:0005634) Transcription factor activity (GO:0003700) Regulation of transcription, DNA dependent (GO:0006355)
		At1g18860.1	Nucleus (GO:0005634) Transcription factor activity (GO:0003700) Regulation of transcription, DNA dependent (GO:0006355)
Transducin family protein	Nucleotide binding activity	At3g21060.1 At5g23730.1	Nucleotide binding (GO:0000166) Heterotrimeric G-protein complex (GO:0005834) Biological process unknown (GO:0008150)
		At4g31160.1 At5g58760.1 At2g19540.1 At4g18905.1 At4g38480.1 At5g14050.1	Nucleotide binding (GO:0000166) Cellular component unknown (GO:0005575)
		At5g11240.1	Nucleotide binding (GO:0000166) Endomembrane system (GO:0012505)
		At4g05410.1	Mitochondrial fission (GO:0000266) Nucleotide binding (GO:0000166) Anaphase promoting complex (GO:0005680) Small nucleolar ribonucleoprotein complex (GO:0005732)

			Nucleic acid binding (GO:0003676)
26S proteasome AAA-atpase subunit	ATP dependent hydrolase, post-translational modifications	At3g05530.1	ATPase activity (GO:0016887) Nucleus (GO:0005634) Ubiquitin dependent protein catabolic process (GO:0006511) Calmodulin binding (GO:0005516) Proteasome regulatory particle, base subcomplex (GO:0008540) Cytoplasm (GO:0005737)
Histone deacetylase family protein	Deacetylation in histone modification	At3g18520.1 At3g18520.2	Histone deacetylation (GO:0016575) Histone deacetylases activity (GO:0004407) Intracellular (GO:0005622)
		At3g44750.1	Polarity specification of adaxial/abaxial axis (GO:0009944) Nucleic acid binding (GO:0003676) Nucleolus (GO:0005730) Zinc ion binding (GO:0008270)
EXS family protein / ERD1/XPR1/SYG1 family protein	Cellular response to phosphate starvation	At1g69480.1	Biological process unknown (GO:0008150) Integral to membrane (GO:0016021) Molecular function unknown (GO:0003674)
Bzip transcription factor family protein	Transcription factor	At1g42990.1	Regulation of transcription, DNA dependent (GO:0006355) Transcription factor activity (GO:0003700) DNA binding (GO:0003677) Nucleus (GO:0005634) Unfolded protein response (GO:0030968)
Sas10/U3 ribonucleoprotein (Utp) family protein	Protein synthesis/modification	At2g43650.1	Biological process unknown (GO:0008150) Cellular component unknown (GO:0005575) Molecular function unknown (GO:0003674)
SUMO activating enzyme 1a (SAE1a)	Protein modification, small protein activating enzyme activity	At4g24940.1	SUMO activating enzyme activity (GO:0019948) Protein sumoylation (GO:0016925)
DNA-damage-repair/toleration protein	DNA repair	At1g30480.1	Nucleic acid binding (GO:0003676) Nucleotide binding (GO:0000166) Nucleus (GO:0005634) Cytoplasm (GO:0005737)
PWWP domain-containing protein	Cell growth and differentiation, protein-protein interactions	At5g40340.1	Cellular component unknown (GO:0005575) Molecular function unknown (GO:0003674)
		At5g23150.1	Regulation of timing of vegetative to reproductive phase (GO:0048510) Maintenance of floral organ identity

			(GO:0048497) Negative regulation of flower development (GO:0009910) Transcription factor activity (GO:0003700)
DNA mismatch repair protein	DNA repair	At4g02070.1	Damaged DNA binding (GO:0003684) Chloroplast (GO:0009507) Mismatch repair (GO:0006298)
		At4g02460.1	Mismatch repair (GO:0006298) ATP binding (GO:0005524)
SKP1 family protein	Ubiquitination of proteins involved in cell cycle progression, signal transduction and transcription	At5g59140.1	Biological process unknown (GO:0008150) Cellular component unknown (GO:0005575) Molecular function unknown (GO:0003674)
SET domain-containing protein	Histone methyltransferases (hmtases)	At1g04050.1	Chromatin modification (GO:0016568) Nucleolus (GO:0005730) Histone-lysine N-methyltransferase activity (GO:0018024) Zinc ion binding (GO:0008270)
Heat shock transcription factor	Transcription factor	At2g41690.1	Regulation of transcription, DNA dependent (GO:0006355) DNA binding (GO:0003677) Transcription factor activity (GO:0003700) Nucleus (GO:0005634)
Ulp1 protease family protein	Proteolysis, cysteine type peptidase activity	At1g10570.1 At1g60220.1 At1g10570.2 At4g33620.1	Cellular component unknown (GO:0005575) Cysteine-type peptidase activity (GO:0008234) Proteolysis (GO:0006508)
Calmodulin-binding protein	Signal transduction	At5g57580.1	Calmodulin binding (GO:0005516) Biological process unknown (GO:0008150) Cellular component unknown (GO:0005575)
Transcriptional factor B3 family protein	Transcription factor	At3g53310.1	Endomembrane system (GO:0012505) Regulation of transcription, DNA dependent (GO:0006355) DNA binding (GO:0003677)
		At4g31610.1 At5g57720.1	Transcription factor activity (GO:0003700) DNA binding (GO:0003677) Cellular component unknown (GO:0005575) Regulation of transcription, DNA dependent (GO:0006355)
Eif4-gamma/eif5/eif2-epsilon domain-containing protein	Translation initiators	At2g34970.1	Translation initiation factor (GO:0003743) Regulation of translational initiation (GO:0006446)

ABC transporter protein	Translocation of various substrates across membranes and non-transport-related processes such as translation of RNA and DNA repair	At3g30842.1	ATP binding (GO:0005524) Nucleotide binding (GO:0000166) Multidrug transport (GO:0006855) ATPase activity (GO:0016887) Nucleoside triphosphatase activity (GO:0017111)
RNA recognition motif (RRM)-containing protein	Play important roles in the processing of RNA and regulation of protein synthesis	At4g00830.1	RNA binding (GO:0003723)
		At1g70200.1	Chloroplast (GO:0009507) Nucleic acid binding (GO:0003676)
		At5g09880.1	mRNA processing (GO:0006397)
		At2g16940.1	Nucleic acid binding (GO:0003676) Nucleus (GO:0005634)
AAA-type atpase family protein	Cell cycle regulation, protein proteolysis, disaggregration, organelle biogenesis, intracellular transport, as molecular chaperons, DNA helicase and transcription factors.	At1g43910.1	Endomembrane system (GO:0012505) ATP binding (GO:0005524) ATPase activity (GO:0016887)
		At5g22010.1	DNA replication (GO:0006260) Defense response (GO:0006952) ATP binding (GO:0005524) Intracellular (GO;0005622)
Met-10+ like family protein	Methyltransferase activity and transferase activity	At4g04670.1	Cellular component unknown (GO:0005575) Wybutosine biosynthestic process (GO:0031591)
TCP family transcription factor	Transcription factor	At3g18550.1	Nucleus (GO:0005634) Transcription factor activity (GO:0003700) Secondary shoot formation (GO:0010223) Regulation of transcription (GO:0045449)
Scarecrow transcription factor family protein	Transcription factor	At3g46600.1 At3g46600.2	Cellular component unknown (GO:0005575) Transcription factor activity (GO:0003700) Regulation of transcription (GO:0045449)
SNF2 domain-containing protein	Transcriptional regulation, maintenance of chromosome	At1g50410.1	Protein binding (GO:0005515) DNA binding (GO:0003677)

	stability during mitosis and various aspects of processing of DNA damage and post-replication daughter strand gap repair		Zinc ion binding (GO:0008270) Helicase activity (GO:0004386) ATP binding (GO:0005524)
		At5g63950.1	DNA binding (GO:0003677) ATP binding (GO:0005524) Helicase activity (GO:0004386)
		At2g16390.1	DNA methylation (GO:0006306) Nucleic acid binding (GO:0003676) ATP binding (GO:0005524) Helicase activity (0004386) DNA binding (GO:0003677)
		At3g42670.1	DNA binding (GO:0003677) Helicase activity (GO:0004386) ATP binding (GO:0005524)
		At2g02090.1	ATP binding (GO:0005524) Chloroplast (GO:0009507) DNA binding (GO:0003677) Helicase activity (GO:0004386)
No apical meristem (NAM) family protein	DNA binding, regulation of transcription.	At4g28530.1 At1g34190.1 At1g32870.1	Cellular component unknown (GO:0005575) Transcription factor activity (GO:0003700) Multicellular organismal development (GO:0007275)
KH domain-containing protein single-stranded nucleic acid-binding protein CBP	Post-transcriptional regulations, inducer of cell cycle arrest and apoptosis.	At4g26000.1	Nucleic acid binding (GO:0003676) Shoot development (GO:0048367) Cellular component unknown (GO:0005575) Gynoecium development (GO:0048467)
F-box family protein	Ubiquitination of proteins, signal transduction and regulation of the cell cycle, microrna-mediated gene silencing via RNA interference	At1g67390.1 At3g10430.1 At3g24760.1 At3g27290.1 At1g33020.1 At3g58960.1 At1g48400.1 At5g41840.1 At1g47340.1 At3g13820.1	Cellular component unknown (GO:0005575) Molecular function unknown (GO:0003674) Biological process unknown (GO:0008150)

DNA (cytosine-5-)-methyltransferase (METII)	Methylation, DNA binding, DNA (cytosine-5-)-methyltransferase activity	At4g14140.1	DNA methylation (GO:0006306) Cellular component unknown (GO:0005575) DNA (cytosine-5-)-methyltransferase activity (GO:0003886)
PHD finger family protein	igenetic response, involved in chromatin-mediated gene regulation.	At3g05670.1	DNA binding (GO:0003677)
		At1g14510.1	Regulation of transcription, DNA dependent (GO:0006355)
		At3g42790.1	
			DNA binding (GO:0003677)
		At3g11200.1	Regulation of transcription, DNA dependent (GO:0006355)
		At3g11200.2	Endomembrane system (GO:0012505)
DNA cross-link repair protein	A interstrand cross-link (ICL) repair	At1g19025.1	Cellular component unknown (GO:0005575) Molecular function unknown (GO:0003674) Biological process unknown (GO:0008150)
High mobility group (HMG1/2) family protein	A binding, architectural role in assembly of nucleoprotein complexes in a variety of biological processes	At5g23405.1	DNA binding (GO:0003677)
			Regulation of transcription, DNA dependent (GO:0006355)
		At3g51880.1	Nucleus (GO:0005634)
		At3g51880.2	Chromatin (GO:0000785)
			Transcription factor activity (GO:0003700)
		At5g23420.1	Transcription factor activity (GO:0003700)
		At5g23405.2	Regulation of transcription, DNA dependent (GO:0006355)

Note: The proteins with transcription factor activity or transcriptional regulator activity and proteins involved in DNA dependent regulation of transcription were classified into the same group with roles in transcriptional regulation. Likewise, proteins having ubiquitin-protein ligase activity, small conjugating protein ligase activity, protein transporter activity and protein phopshorylation activity were categorized as members of a group regulating protein modifications. The proteins with DNA methylation activity or histone deacetylase activity were categorized in chromatin modification. Similarly, proteins having nucleic acid and nucleotide binding ability or mismatch repair activity were grouped into DNA repair family proteins.

Table S3 GO enrichment analysis on target proteins

Process	Gene numbers	%
Transcriptional regulation	40	34.18
Regulation of translation	1	0.85
Protein modification	16	13.67
DNA repair	10	8.54
Chromatin modification	9	7.69
Unknown	41	35.04
Total	117	

Table S4 miRNA and primer sequences

miR408	miRNA sequence	AUGCACUGCCUCUUCCCUGGC
	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGCCAGG
	Forward primer	CTGCGTTATGCACTGCCTCTTC
miR399	miRNA sequence	UGCCAAAGGAGAUUUGCCCUG
	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCAGGGC
	Forward primer	CTGCGTTTGCCAAAGGAGATTT
miR398	miRNA sequence	UGUGUUCUCAGGUCACCCCUU
	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCAGGGG
	Forward primer	CTGCGTTTGTGTTCTCAGGTCA
miR397	miRNA sequence	UCAUUGAGUGCAGCGUUGAUG
	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCATCAA
	Forward primer	CTGCGTTTCATTGAGTGCAGCG
miR395	miRNA sequence	GUGAAGUGUUUGGGGGAACUC
	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGAGTTC
	Forward primer	CTGCGTTGTGAAGTGTTTGGGG
miR319	miRNA sequence	UUGGACUGAAGGGAGCUCCCU
	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGGGAGC
	Forward primer	CTGCGTTTTGGACTGAAGGGA
miR169	miRNA sequence	CAGCCAAGGAUGACUUGCCGA
	RT primer	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCCGGCA
	Forward primer	CTGCGTTCAGCCAAGGATGACT
miR167	miRNA sequence	UGAAGCUGCCAGCAUGAUCUA