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Characterization of circular RNAs and their role in wilt stress tolerance in soybean

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Abstract

Soybean (*Glycine max*) is an important oil seed crop and widely grown legume in India as well as in the world. The yield of soybean is severely affected by Wilt disease caused by a fungus *Fusarium oxysporum*. Several coding and non-coding RNAs in plant cells may directly or indirectly play a role in exhibiting stress tolerance to wilt. Here, an attempt has been made to identify the role of circular RNAs (circRNAs), a type of non-coding RNAs, in wilt stress tolerance mechanism. The study also aims at identification of circRNAs that act as endogenous target mimics (eTMs) or as sponges to miRNAs that may regulate the genes involved in wilt stress tolerance. The study reveals the presence of 24 differentially expressed circRNAs (DEcircRNAs) between the transcriptomes of wilt affected and control samples out of which 18 were acted as eTMs for 10 microRNAs (miRNAs). These miRNAs in turn found to regulate 275 genes that fall under 14 Gene Ontology (GO) based functional categories. The GO analysis further shown the annotation term 'stimulus response' for most of the DEcircRNAs, which were found in various vital activities like polygalacturonase activity, carbohydrate metabolic process. Hence, it is predicted that the identified miRNAs got absorbed by the circRNAs that acted as sponges or eTMs and the miRNA regulated genes are likely to be freed up in cell to exhibit wilt stress tolerance mechanism in soybean.

Keywords: Circular RNAs, wilt stress, soybean, miRNAs, eTMs

Introduction

Soybean is one of the largest grown legume crops worldwide (Singh *et al.* 1992)^[17] and is also important for oil extraction. The crop contains about 23% oil and is also rich in protein content to an extent of 42% (Dornbos *et al.* 1992)^[5]. However, the productivity of the crop has been found to drastically reduce due to the effect of Fusarium blight or wilt. Studies on the regulatory roles of non-coding RNAs on wilt stress tolerance have been made in the past in various leguminous crops. Kohli *et al.* (2014)^[8] identified and characterized wilt stress responsive miRNAs in chickpea and found that a number of miRNAs were highly up-regulated in response to fungal infection. It has also been observed that lncRNAs are important components of the antifungal networks in *A. thaliana* (Zhu *et al.* 2014)^[21]. Several studies have been made in the recent past on the function of non-coding RNAs for a variety of stresses in soybean. Panda *et al.* (2018)^[14] reported that circular RNAs might have played significant roles in regulating genes responsible for different stress tolerance mechanisms in plants. These circRNAs are a class of non-coding RNAs formed by a covalent linkage between the 5' and 3' ends of an RNA molecule. Ebbesen *et al.* (2016)^[6] reported that circRNAs might have originated from exons, introns or intergenic regions. Chu *et al.* (2018)^[3] found that the circRNAs may have a variable length ranging from 100 nucleotides to several kilobases and may act as sponges to miRNAs. This may prevent the miRNAs from regulating the mRNAs. Differentially expressed circRNAs may act as functional regulators to biological processes specific to stress responses in plants (Li *et al.* 2018)^[12]. Zhao *et al.* (2017)^[20] identified 5,367 circRNAs associated with resistance to defoliating insects in soybean leaves. However, studies are yet to be fully explored on characterization of circRNAs in soybean for wilt stress tolerance. Hence, in this study, the circRNAs were identified from wilt affected soybean crop using RNA-Seq data and their role as eTMs in regulating genes responsible for wilt stress tolerance was studied *in silico* through bioinformatic approaches.

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Materials and Methods

RNA-seq data for wilt under control and wilt affected soybean were downloaded from <https://www.ncbi.nlm.nih.gov/> having accession numbers: SRR4095539 (control), SRR4095541 (wilt affected)

Soybean whole genome data and miRNAs present in soybean were downloaded from <http://plants.ensembl.org/index.html> and <http://www.mirbase.org/> respectively.

Data preparation

FastQC (Andrews, 2010) [1] was used for processing the raw data to get quality reads and Trimmomatic tool (Bolger *et al.* 2014) [2] was used to trim the poor quality segments of the reads. Finally quality reads were subjected to further downstream analysis.

Circular RNAs identification and differential expression pattern analysis

Mapping of the trimmed reads onto the reference genome was done using BWA-MEM (Li, 2013) [9] and the resulted SAM file and reference genome were used for identifying circRNAs by using CircRNA Identifier (CIRI) (Gao *et al.* 2015) [7]. For the analysis of differential expression pattern of the identified circRNAs, expression levels were initially calculated using RSEM (Li and Dewey, 2011) [10] and finally the differentially

expressed circRNAs were detected using the R package DESeq2 (Love *et al.* 2014) [13].

CircRNA-miRNA-mRNA interaction

Initially, prediction of miRNAs that target the differentially expressed circRNAs was done by Target Finder (<http://www.bioit.org.cn/ao/targetfinder.htm>). Subsequently, these miRNAs were subjected to psRNA Target (<http://plantgrn.noble.org/psRNATarget/>) (Dai and Zhao 2018) [4] to identify their target genes or mRNA targets. These two steps indicate that miRNAs instead of targeting the mRNAs might target the circRNAs that may mimic the mRNAs and hence may not target the genes or mRNAs. Finally, annotation of the targeted mRNAs was done using BLAST2GO (<https://www.blast2go.com/>).

Results and Discussion

Identification of circular RNAs under wilt stress condition

A total of 48 circular RNAs were identified under control condition (CT), out of which 31 (64%), 15 (32%) and 2 (4%) were of intergenic type, exonic type and intronic type respectively (Fig 1a). Whereas, 75 circular RNAs were identified under wilt stress condition, out of which 53 (71%), 18 (24%) and 3 (4%) were found to be of intergenic, exonic and intronic types respectively (Fig 1b).

Fig 1: Distribution of different types of circular RNAs (a) under control and (b) under wilt stress conditions

It can be observed that in both the conditions intergenic type of circRNAs are highest in numbers followed by circRNAs formed from the exonic regions. Previously the roles of circRNAs have been reported in several crops both at genome level and transcriptome level. Ye *et al.* (2015) [19] identified 12,037 and 6012 circRNAs at genome level from *Oryza sativa* and *Arabidopsis thaliana*, respectively. In soybean, 5372 circRNAs were identified by Zhao *et al.* (2017) [20] at whole genome level. In the present study, 75 circRNAs were found to be present in wilt affected soybean plant. Besides, in 2017 Wang *et al.* reported 60.2% intergenic circRNAs, 6.8% exonic circRNAs, and 2.3% intronic circRNAs in wheat,

which shows results similar to our findings.

Expression pattern of circular RNAs under wilt stress condition

The expression patterns of circRNAs between control and wilt affected plants were compared in order to investigate whether they are expressed in specific manner under wilt stress condition. A total of 24 differentially expressed circular RNAs were detected between wilt stress and control conditions. Among them 12 were found to be downregulated ($\log_2FC < 0$) (Table 1), and 12 were found to be upregulated ($\log_2FoldChange > 0$) (Table 2).

Table 1: List of downregulated circRNAs

circRNA ID	Base Mean	log2FC	SE(log2FC)	Wald Statistic
11_dna:chromosome_chromosome: Glycine_max_v2.1:11:1:34766867:1	2636.467	-0.26914	0.354095	-0.76009
7_dna:chromosome_chromosome: Glycine_max_v2.1:7:1:44630646:1	709.3314	-2.29063	1.350556	-1.69606
KZ847214_dna:supercontig_supercontig: Glycine_max_v2.1:KZ847214:1:64745:1	38.78359	-1.34509	1.109218	-1.21264
11_dna:chromosome_chromosome: Glycine_max_v2.1:11:1:34766867:1	356.1966	-0.87585	0.757436	-1.15633
2_dna:chromosome_chromosome: Glycine_max_v2.1:2:1:48577505:1	710.5561	-0.7436	0.670172	-1.10956
9_dna:chromosome_chromosome: Glycine_max_v2.1:9:1:50189764:1	319.6584	-0.57223	1.067934	-0.53583
16_dna:chromosome_chromosome: Glycine_max_v2.1:16:1:37887014:1	130.0271	-0.44501	0.531682	-0.83699
18_dna:chromosome_chromosome: Glycine_max_v2.1:18:1:58018742:1	145.7446	-0.40209	0.499557	-0.8049
8_dna:chromosome_chromosome: Glycine_max_v2.1:8:1:47837940:1	52.86815	-0.37559	0.580686	-0.6468
7_dna:chromosome_chromosome: Glycine_max_v2.1:7:1:44630646:1	58.78775	-0.23315	0.510527	-0.45668
13_dna:chromosome_chromosome: Glycine_max_v2.1:13:1:45874162:1	42.2537	-0.2012	0.559047	-0.3599
2_dna:chromosome_chromosome: Glycine_max_v2.1:2:1:48577505:1	234.5386	-0.0819	0.312221	-0.26232

Table 2: List of upregulated circRNAs

circRNA_ID	Base Mean	log2FC	SE (log2FC)	Wald Statistic
12_dna:chromosome_chromosome: Glycine_max_v2.1:12:1:40091314:1	41.64133	5.29E-08	0.540154	9.79E-08
6_dna:chromosome_chromosome: Glycine_max_v2.1:6:1:51416486:1	48.37742	0.035332	0.511035	0.069138
4_dna:chromosome_chromosome: Glycine_max_v2.1:4:1:52389146:1	1509.702	0.071321	0.233514	0.305426
3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	34.49698	0.114331	0.588745	0.194195
14_dna:chromosome_chromosome: Glycine_max_v2.1:14:1:49042192:1	9.185587	0.167549	0.966981	0.173271
12_dna:chromosome_chromosome: Glycine_max_v2.1:12:1:40091314:1	445.8071	0.281126	0.382938	0.73413
14_dna:chromosome_chromosome: Glycine_max_v2.1:14:1:49042192:1	433.5597	0.368008	0.440086	0.836218
3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	82.46615	0.387959	0.536982	0.72248
6_dna:chromosome_chromosome: Glycine_max_v2.1:6:1:51416486:1	2620.342	0.511998	0.518077	0.988266
3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	740.1542	0.586751	0.573614	1.022902
8_dna:chromosome_chromosome: Glycine_max_v2.1:8:1:47837940:1	1722.604	0.866811	0.736806	1.176443
9_dna:chromosome_chromosome: Glycine_max_v2.1:9:1:50189764:1	1900.396	1.843349	1.436851	1.282908

In our present study the expression patterns were found to be significantly different for 24 circRNAs suggesting that they might play a role in responding to the stress condition. Interestingly we found one down-regulated circRNAs “7_dna:chromosome_chromosome:

Glycine_max_v2.1:7:1:44630646:1” with significant p-value (<0.09). Thus to understand the potential roles of the predicted differentially expressed circRNAs, their probable binding with the miRNAs and their regulatory functions were detected.

Circ RNAs-miRNAs-mRNAs interactions for wilt stress tolerance

The miRNAs targeting the differentially expressed circRNAs are given in Supplementary Table1, which shows that there are in total 10 unique miRNAs targeting 18 differentially expressed circRNAs. It was found that majority of the circular RNAs have more than one miRNA binding sites. The mRNAs that are regulated by the identified miRNAs are presented in Supplementary Table2 which shows that there are 275 genes regulated by the miRNAs. It was also found that the interaction between miRNA and mRNA are of types: translation inhibition and cleavage inhibition. The targeted mRNAs were subjected to BLAST2GO and the gene ontology (GO) functional categorization generated 14 annotations which are presented in Fig 2, Fig 3, Fig 4 and Fig 5.

Circ RNAs-miRNAs-mRNAs interactions for wilt stress tolerance

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Fig 2: Differentially expressed circRNAs of soybean under wilt stress condition in GO terms of biological processes, cellular components and molecular functions

Fig 3: Classification of biological processes for mRNAs

Fig 4: Classification of molecular functions for mRNAs

Fig 5: Classification of cellular components for mRNAs

Prediction of eTMs

The circRNAs identified in this study have been found to be targeted by miRNAs of families like MIR1533, MIR166a-5p, MIR4415, etc (Supplementary Table1). Among these families MIR4415 (Kulcheski *et al.* 2013) ^[11] and MIR166-5p (Ramesh *et al.* 2019) ^[15] had been reported earlier to be involved in fungal infection in soybean indicating their chance of involvement in Fusarium wilt infection. It has also been found that MIR1533 is one of the largest miRNA families that are involved in plant stress responses (Ren *et al.* 2014) ^[16]. It was reported that MIR4415 remains downregulated in fungus affected soybean crops (Ramesh *et al.* 2019) ^[15], i.e., the mRNAs regulated by these miRNAs remain free which increase the tolerance of the crop against the fungus. Thus, when these miRNAs get bound to the

circRNAs, they become unavailable to regulate the mRNAs which leaves the mRNAs free. This may be a possible reason for inducing the disease tolerance to the crop. Moreover, when the functions of the mRNAs were observed, it was found that they are mainly involved in structural constituent of cell wall, in polygalacturonase activity, carbohydrate metabolic process, MAP kinase activity, carbonate dehydratase activity etc. Thus, when the eTM circRNAs are targeted by the miRNAs, probably the genes mentioned above may help the plant in tolerating the stress condition due to their non-regulation by miRNAs. Hence, due to such interaction, the differentially expressed circRNAs may be indirectly involved in regulating the genes responsible for wilt stress tolerance in soybean and thus can be considered as probable eTMs of mRNAs with regard to miRNAs.

Table 1: Supplementary

miRNA_ID	circRNA_ID	Target_start	Target_end	miRNA_aligned_fragment	circRNA_aligned_fragment
gma-miR4415a-3p	11_dna:chromosome_chromosome:Glycine_max_v2.1:11:1:34766867:1	11402	11422	UUGAUUCUCAUCACAACAU GG	UGAUGUUCUGAUGAGAAUU AA
gma-miR4415b-3p	11_dna:chromosome_chromosome:Glycine_max_v2.1:11:1:34766867:1	11402	11422	UUGAUUCUCAUCACAACAU GG	UGAUGUUCUGAUGAGAAUU AA
gma-miR10196	8_dna:chromosome_chromosome:Glycine_max_v2.1:8:1:47837940:1	12408	12429	UGAUUGUGGGAGAGCAUUU CAU	UCAAAGUGCUCUCUACAA UUA
gma-miR10407a	3_dna:chromosome_chromosome:Glycine_max_v2.1:3:1:45779781:1	16858	16881	AGUUAACGGAUGAAUGAAU UUGUC	GAUAAAUUUUUUUAUCUGU UAAUU

gma-miR10407a	3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	93765	93788	AGUUAACGGAUGAAUGAAU UUGUC	GAUAAAUUUAUUUAUCUGU UAAUU
gma-miR10407b	3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	16858	16881	AGUUAACGGAUGAAUGAAU UUGUC	GAUAAAUUUAUUUAUCUGU UAAUU
gma-miR10407b	3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	93765	93788	AGUUAACGGAUGAAUGAAU UUGUC	GAUAAAUUUAUUUAUCUGU UAAUU
gma-miR1513a-5p	7_dna:chromosome_chromosome: Glycine_max_v2.1:7:1:44630646:1	4198	4218	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUUACA CA
gma-miR1513b	7_dna:chromosome_chromosome: Glycine_max_v2.1:7:1:44630646:1	4198	4218	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUUACA CA
gma-miR1533	8_dna:chromosome_chromosome: Glycine_max_v2.1:8:1:47837940:1	14453	14471	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	8_dna:chromosome_chromosome: Glycine_max_v2.1:8:1:47837940:1	14474	14492	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	14_dna:chromosome_chromosome: Glycine_max_v2.1:14:1:49042192:1	32864	32882	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	14_dna:chromosome_chromosome: Glycine_max_v2.1:14:1:49042192:1	32885	32903	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	54784	54802	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	54805	54823	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	88405	88423	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	115094	115112	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	116797	116815	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	11_dna:chromosome_chromosome: Glycine_max_v2.1:11:1:34766867:1	4628	4646	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR1533	11_dna:chromosome_chromosome: Glycine_max_v2.1:11:1:34766867:1	13078	13096	AUAAUAAAAAUAUUAUG A	UUAUUUUUAUUUAUUUA U
gma-miR4405	11_dna:chromosome_chromosome: Glycine_max_v2.1:11:1:34766867:1	17099	17122	AUUCUAAGACGGUUAUCUG GGACC	GGUUAUACGUAACCGUCUU AGAAU
gma-miR6299	3_dna:chromosome_chromosome: Glycine_max_v2.1:3:1:45779781:1	1979	2000	AUUUAAAAUUAUUGAUUU GUCA	UAUCAAAUUAAUUUUUA AAU

Table 2: Supplementary

miRNA_ID	mRNA_ID	UPE	miRNA_st	miRNA_e	Target_st	Target_e	miRNA_aligned_fragment	Target_aligned_fragment	Inhibiti
gma-miR10407a	Glyma.11G18070.0.3	-1	1	24	2605	2628	AGUUAACGGAUGAAUGAAU UUGUC	GACAAAUUCAUUCAUCCGU UAACU	Cleavag e
gma-miR10407a	Glyma.11G18070.0.2	-1	1	24	2624	2647	AGUUAACGGAUGAAUGAAU UUGUC	GACAAAUUCAUUCAUCCGU UAACU	Cleavag e
gma-miR10407a	Glyma.11G18070.0.1	-1	1	24	2669	2692	AGUUAACGGAUGAAUGAAU UUGUC	GACAAAUUCAUUCAUCCGU UAACU	Cleavag e
gma-miR10407a	Glyma.11G18070.0.4	-1	1	24	3258	3281	AGUUAACGGAUGAAUGAAU UUGUC	GACAAAUUCAUUCAUCCGU UAACU	Cleavag e
gma-miR10407b	Glyma.11G18070.0.3	-1	1	24	2605	2628	AGUUAACGGAUGAAUGAAU UUGUC	GACAAAUUCAUUCAUCCGU UAACU	Cleavag e
gma-miR10407b	Glyma.11G18070.0.2	-1	1	24	2624	2647	AGUUAACGGAUGAAUGAAU UUGUC	GACAAAUUCAUUCAUCCGU UAACU	Cleavag e
gma-miR10407b	Glyma.11G18070.0.1	-1	1	24	2669	2692	AGUUAACGGAUGAAUGAAU UUGUC	GACAAAUUCAUUCAUCCGU UAACU	Cleavag e
gma-miR10407b	Glyma.11G18070.0.4	-1	1	24	3258	3281	AGUUAACGGAUGAAUGAAU UUGUC	GACAAAUUCAUUCAUCCGU UAACU	Cleavag e
gma-miR1533	Glyma.14G01660.0.1	-1	1	19	267	285	AUAAUAAAAAUAUUAUGA	UCAUUUUUUUUUUUAUUUAU	Cleavag e
gma-miR1533	Glyma.14G01660.0.2	-1	1	19	267	285	AUAAUAAAAAUAUUAUGA	UCAUUUUUUUUUUUAUUUAU	Cleavag e
gma-miR1533	Glyma.14G01660.0.4	-1	1	19	267	285	AUAAUAAAAAUAUUAUGA	UCAUUUUUUUUUUUAUUUAU	Cleavag e
gma-miR1533	Glyma.14G01660.0.3	-1	1	19	267	285	AUAAUAAAAAUAUUAUGA	UCAUUUUUUUUUUUAUUUAU	Cleavag e
gma-miR1533	Glyma.14G01660.0.5	-1	1	19	267	285	AUAAUAAAAAUAUUAUGA	UCAUUUUUUUUUUUAUUUAU	Cleavag e
gma-miR1513a-5p	Glyma.07G18720.0.1	-1	1	21	104	124	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUUCUCU CA	Cleavag e
gma-miR1513a-5p	Glyma.07G14830.0.1	-1	1	21	89	109	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUCUCU CA	Cleavag e
gma-miR1513b	Glyma.07G18720.0.1	-1	1	21	104	124	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUUCUCU CA	Cleavag e
gma-miR1513b	Glyma.07G14830.0.1	-1	1	21	89	109	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUCUCU CA	Cleavag e
gma-miR1533	Glyma.05G10340.0.2	-1	1	19	2164	2182	AUAAUAAAAAUAUUAUGA	UUAUUUUUUUUUUUAUUUAU	Cleavag e
gma-miR1513a-5p	Glyma.06G19700.0.1	-1	1	21	113	133	UGAGAGAAAGCCAUGACUU AC	GUAAGUCGUGGCUUUUCUCU UA	Cleavag e

gma-miR1513a-5p	Glyma.01G23270 0.1	-1	1	21	107	127	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGUUUUCUCU UA	Cleavage
gma-miR1513a-5p	Glyma.16G20260 0.1	-1	1	21	107	127	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGUUUUCUCU UA	Cleavage
gma-miR1513b	Glyma.16G20260 0.1	-1	1	21	107	127	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGUUUUCUCU UA	Cleavage
gma-miR1513b	Glyma.01G23270 0.1	-1	1	21	107	127	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGUUUUCUCU UA	Cleavage
gma-miR1513b	Glyma.06G19700 0.1	-1	1	21	113	133	UGAGAGAAAGCCAUGACUU AC	GUAAGUCGUGGCUUUCUCU UA	Cleavage
gma-miR1533	Glyma.08G28740 0.1	-1	1	19	19	37	AUAAUAAAAUAAUAAUGA	UUGUUAUUUUUUUAUUAU	Cleavage
gma-miR1533	Glyma.08G28740 0.2	-1	1	19	19	37	AUAAUAAAAUAAUAAUGA	UUGUUAUUUUUUUAUUAU	Cleavage
gma-miR1533	Glyma.13G08330 0.4	-1	1	19	2756	2774	AUAAUAAAAUAAUAAUGA	UCAUCAUUUUUUUAUUAU	Cleavage
gma-miR1533	Glyma.13G08330 0.1	-1	1	19	2754	2772	AUAAUAAAAUAAUAAUGA	UCAUCAUUUUUUUAUUAU	Cleavage
gma-miR1533	Glyma.13G16170 0.1	-1	1	19	162	180	AUAAUAAAAUAAUAAUGA	UAAUUUUUUUUUAUUAU	Cleavage
gma-miR1513a-5p	Glyma.17G01830 0.1	-1	1	21	125	145	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCA CA	Cleavage
gma-miR1513a-5p	Glyma.06G19710 0.1	-1	1	21	92	112	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCU AA	Cleavage
gma-miR1513a-5p	Glyma.16G20280 0.1	-1	1	21	65	85	UGAGAGAAAGCCAUGACUU AC	GUAAGUUAUGGUUUUCUCU UA	Cleavage
gma-miR1513a-5p	Glyma.16G20300 0.1	-1	1	21	98	118	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGUUUUUUCU UA	Cleavage
gma-miR1513a-5p	Glyma.16G20290 0.1	-1	1	21	107	127	UGAGAGAAAGCCAUGACUU AC	GUAAGUUAUGGUUUUCUCU UA	Cleavage
gma-miR1513a-5p	Glyma.06G19720 0.1	-1	1	21	86	106	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCCU CA	Cleavage
gma-miR1513a-5p	Glyma.08G25180 0.1	-1	1	21	89	109	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUAU CA	Cleavage
gma-miR1513a-5p	Glyma.17G01760 0.1	-1	1	21	254	274	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCA CA	Cleavage
gma-miR1513a-5p	Glyma.08G25230 0.3	-1	1	21	179	199	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCU GA	Cleavage
gma-miR1513a-5p	Glyma.08G25230 0.2	-1	1	21	179	199	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCU GA	Cleavage
gma-miR1513a-5p	Glyma.08G25230 0.1	-1	1	21	183	203	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCU GA	Cleavage
gma-miR1513a-5p	Glyma.08G25220 0.1	-1	1	21	161	181	UGAGAGAAAGCCAUGACUU AC	GUAAGGCAUGGCUUUCUCU UA	Cleavage
gma-miR1513a-5p	Glyma.08G25160 0.1	-1	1	21	121	141	UGAGAGAAAGCCAUGACUU AC	GUAAGACAUGGCUUUCUCU UA	Cleavage
gma-miR1513a-5p	Glyma.07G25560 0.1	-1	1	21	231	251	UGAGAGAAAGCCAUGACUU AC	CUAAGUCAUGGCUUUCUCA CA	Cleavage
gma-miR1513b	Glyma.08G25230 0.1	-1	1	21	183	203	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCU GA	Cleavage
gma-miR1513b	Glyma.08G25230 0.2	-1	1	21	179	199	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCU GA	Cleavage
gma-miR1513b	Glyma.08G25230 0.3	-1	1	21	179	199	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCU GA	Cleavage
gma-miR1513b	Glyma.17G01760 0.1	-1	1	21	254	274	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCA CA	Cleavage
gma-miR1513b	Glyma.08G25180 0.1	-1	1	21	89	109	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUAU CA	Cleavage
gma-miR1513b	Glyma.06G19720 0.1	-1	1	21	86	106	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCCU CA	Cleavage
gma-miR1513b	Glyma.16G20290 0.1	-1	1	21	107	127	UGAGAGAAAGCCAUGACUU AC	GUAAGUUAUGGUUUUCUCU UA	Cleavage
gma-miR1513b	Glyma.16G20300 0.1	-1	1	21	98	118	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGUUUUUUCU UA	Cleavage
gma-miR1513b	Glyma.16G20280 0.1	-1	1	21	65	85	UGAGAGAAAGCCAUGACUU AC	GUAAGUUAUGGUUUUCUCU UA	Cleavage
gma-miR1513b	Glyma.06G19710 0.1	-1	1	21	92	112	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCU AA	Cleavage
gma-miR1513b	Glyma.17G01830 0.1	-1	1	21	125	145	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUCA CA	Cleavage
gma-miR1513b	Glyma.08G25160 0.1	-1	1	21	121	141	UGAGAGAAAGCCAUGACUU AC	GUAAGACAUGGCUUUCUCU UA	Cleavage
gma-miR1513b	Glyma.08G25220 0.1	-1	1	21	161	181	UGAGAGAAAGCCAUGACUU AC	GUAAGGCAUGGCUUUCUCU UA	Cleavage
gma-miR1513b	Glyma.07G25560 0.1	-1	1	21	231	251	UGAGAGAAAGCCAUGACUU AC	CUAAGUCAUGGCUUUCUCA CA	Cleavage
gma-miR1533	Glyma.09G16800 0.1	-1	1	19	84	102	AUAAUAAAAUAAUAAUGA	AUAUUUUUUUUUAUUAU	Cleavage
gma-miR1533	Glyma.09G16800	-1	1	19	84	102	AUAAUAAAAUAAUAAUGA	AUAUUUUUUUUUAUUAU	Cleavage

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gma-miR1533	Glyma.14G12890 0.1	-1	1	19	248	266	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUAA	Cleavage
gma-miR1533	Glyma.U038900. 2	-1	1	19	1348	1366	AUAAUAAAAUAAUAAUGA	ACAUGUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.U038900. 1	-1	1	19	1326	1344	AUAAUAAAAUAAUAAUGA	ACAUGUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.04G23170 0.3	-1	1	19	1413	1431	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.04G00320 0.1	-1	1	19	1076	1094	AUAAUAAAAUAAUAAUGA	ACAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.09G07430 0.2	-1	1	19	3683	3701	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.09G07430 0.1	-1	1	19	2969	2987	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.11G21270 0.1	-1	1	19	153	171	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.U016300. 4	-1	1	19	923	941	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.02G12910 0.1	-1	1	19	31	49	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.03G06960 0.1	-1	1	19	1388	1406	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.U019900. 1	-1	1	19	46	64	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.03G16690 0.1	-1	1	19	1355	1373	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.03G06960 0.2	-1	1	19	1163	1181	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.16G15370 0.1	-1	1	19	1312	1330	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.01G01710 0.1	-1	1	19	1209	1227	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.17G13250 0.1	-1	1	19	1051	1069	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.19G10640 0.1	-1	1	19	187	205	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.15G19200 0.1	-1	1	19	41	59	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.13G12480 0.1	-1	1	19	2485	2503	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.13G12480 0.6	-1	1	19	2355	2373	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR1533	Glyma.02G28000 0.1	-1	1	19	1071	1089	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUAAU	Cleavage
gma-miR4405	Glyma.07G15900 0.1	-1	1	24	1809	1832	AUUCUAAGACGGUUAUCUG GGACC	GGUUAUUUUUUUUUUUUAAU AGAAU	Cleavage
gma-miR4415a-3p	Glyma.08G25680 0.1	-1	1	21	70	90	UUGAUUCUACACAACA GG	UCAAGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415a-3p	Glyma.20G05160 0.1	-1	1	21	27	47	UUGAUUCUACACAACA GG	ACACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415a-3p	Glyma.20G05190 0.2	-1	1	21	133	153	UUGAUUCUACACAACA GG	ACACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415a-3p	Glyma.08G32610 0.1	-1	1	21	1778	1798	UUGAUUCUACACAACA GG	AUAUGUUGUGAUGAGAAUU GG	Cleavage
gma-miR4415a-3p	Glyma.20G05190 0.1	-1	1	21	247	267	UUGAUUCUACACAACA GG	ACACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415a-3p	Glyma.14G04130 0.1	-1	1	21	233	253	UUGAUUCUACACAACA GG	GCACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415a-3p	Glyma.13G07690 0.1	-1	1	21	305	325	UUGAUUCUACACAACA GG	ACACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415b-3p	Glyma.08G25680 0.1	-1	1	21	70	90	UUGAUUCUACACAACA GG	UCAAGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415b-3p	Glyma.20G05160 0.1	-1	1	21	27	47	UUGAUUCUACACAACA GG	ACACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415b-3p	Glyma.20G05190 0.2	-1	1	21	133	153	UUGAUUCUACACAACA GG	ACACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415b-3p	Glyma.08G32610 0.1	-1	1	21	1778	1798	UUGAUUCUACACAACA GG	AUAUGUUGUGAUGAGAAUU GG	Cleavage
gma-miR4415b-3p	Glyma.20G05190 0.1	-1	1	21	247	267	UUGAUUCUACACAACA GG	ACACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415b-3p	Glyma.14G04130 0.1	-1	1	21	233	253	UUGAUUCUACACAACA GG	GCACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR4415b-3p	Glyma.13G07690 0.1	-1	1	21	305	325	UUGAUUCUACACAACA GG	ACACGUUGUGAUGGGAAUC AA	Cleavage
gma-miR6299	Glyma.06G08560 0.1	-1	1	22	274	295	AUUUUUUUUUUUUUUUUUG UCA	UAAAAUUUUUUUUUUUUAAU AAU	Cleavage
gma-miR6299	Glyma.06G20190 0.1	-1	1	22	76	97	AUUUUUUUUUUUUUUUUUG UCA	GCCCCAAUCAAUUUUUUAAU GAU	Cleavage

gma-miR10196	Glyma.04G06150 0.1	-1	1	22	161	182	UGAUUGUGGGAGAGCAUUU CAU	ACAAAAUGUUCUCCACAA UCC	Cleavage
gma-miR10196	Glyma.20G24470 0.1	-1	1	22	410	431	UGAUUGUGGGAGAGCAUUU CAU	CUCAGAUGCUCUCGCACAA UCA	Cleavage
gma-miR10196	Glyma.10G29490 0.1	-1	1	22	406	427	UGAUUGUGGGAGAGCAUUU CAU	CUCAGAUGCUCUCGCACAA UCA	Cleavage
gma-miR10196	Glyma.10G29490 0.2	-1	1	22	406	427	UGAUUGUGGGAGAGCAUUU CAU	CUCAGAUGCUCUCGCACAA UCA	Cleavage
gma-miR10196	Glyma.10G29490 0.3	-1	1	22	406	427	UGAUUGUGGGAGAGCAUUU CAU	CUCAGAUGCUCUCGCACAA UCA	Cleavage
gma-miR10196	Glyma.08G10710 0.2	-1	1	22	1634	1655	UGAUUGUGGGAGAGCAUUU CAU	CCAAAAUCCUUUCCUACAA UCA	Cleavage
gma-miR10196	Glyma.08G10710 0.3	-1	1	22	1634	1655	UGAUUGUGGGAGAGCAUUU CAU	CCAAAAUCCUUUCCUACAA UCA	Cleavage
gma-miR10196	Glyma.08G10710 0.1	-1	1	22	1634	1655	UGAUUGUGGGAGAGCAUUU CAU	CCAAAAUCCUUUCCUACAA UCA	Cleavage
gma-miR10196	Glyma.05G15020 0.2	-1	1	22	1598	1619	UGAUUGUGGGAGAGCAUUU CAU	CCAAAAUCCUUUCCUACAA UCA	Cleavage
gma-miR10196	Glyma.05G15020 0.1	-1	1	22	1604	1625	UGAUUGUGGGAGAGCAUUU CAU	CCAAAAUCCUUUCCUACAA UCA	Cleavage
gma-miR10407a	Glyma.05G20250 0.1	-1	1	24	63	86	AGUUAACGGAUGAAUGAAU UUGUC	CAUUGAUUCAUUCUUCGU UAAUC	Cleavage
gma-miR10407a	Glyma.04G11990 0.1	-1	1	24	398	421	AGUUAACGGAUGAAUGAAU UUGUC	UUUUUAUUCUUCUUCGU UAAUC	Cleavage
gma-miR10407b	Glyma.05G20250 0.1	-1	1	24	63	86	AGUUAACGGAUGAAUGAAU UUGUC	CAUUGAUUCAUUCUUCGU UAAUC	Cleavage
gma-miR10407b	Glyma.04G11990 0.1	-1	1	24	398	421	AGUUAACGGAUGAAUGAAU UUGUC	UUUUUAUUCUUCUUCGU UAAUC	Cleavage
gma-miR1513a-5p	Glyma.17G02130 0.1	-1	1	21	664	684	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUCCUU CA	Cleavage
gma-miR1513a-5p	Glyma.06G01630 0.1	-1	1	21	98	118	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUU AA	Cleavage
gma-miR1513a-5p	Glyma.17G16220 0.1	-1	1	21	86	106	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUUUCU AA	Cleavage
gma-miR1513a-5p	Glyma.18G27490 0.1	-1	1	21	134	154	UGAGAGAAAGCCAUGACUU AC	GUAUUUCAUGGUUUUCUCU UA	Cleavage
gma-miR1513a-5p	Glyma.10G13210 0.1	-1	1	21	92	112	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUUCU AA	Cleavage
gma-miR1513a-5p	Glyma.08G09800 0.3	-1	1	21	186	206	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUUCU GA	Cleavage
gma-miR1513a-5p	Glyma.08G09800 0.2	-1	1	21	216	236	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUUCU GA	Cleavage
gma-miR1513a-5p	Glyma.08G09800 0.1	-1	1	21	186	206	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUUCU GA	Cleavage
gma-miR1513b	Glyma.17G16220 0.1	-1	1	21	86	106	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUUUCU AA	Cleavage
gma-miR1513b	Glyma.06G01630 0.1	-1	1	21	98	118	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUUCUU AA	Cleavage
gma-miR1513b	Glyma.17G02130 0.1	-1	1	21	664	684	UGAGAGAAAGCCAUGACUU AC	GUAAGUCAUGGCUUCCUU CA	Cleavage
gma-miR1513b	Glyma.18G27490 0.1	-1	1	21	134	154	UGAGAGAAAGCCAUGACUU AC	GUAUUUCAUGGUUUUCUCU UA	Cleavage
gma-miR1513b	Glyma.08G09800 0.1	-1	1	21	186	206	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUUCU GA	Cleavage
gma-miR1513b	Glyma.08G09800 0.2	-1	1	21	216	236	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUUCU GA	Cleavage
gma-miR1513b	Glyma.08G09800 0.3	-1	1	21	186	206	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUUCU GA	Cleavage
gma-miR1513b	Glyma.10G13210 0.1	-1	1	21	92	112	UGAGAGAAAGCCAUGACUU AC	GCAAGUCAUGGCUUUUUCU AA	Cleavage
gma-miR1533	Glyma.09G07430 0.2	-1	1	19	3704	3722	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G07430 0.1	-1	1	19	2990	3008	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.U016300. 4	-1	1	19	944	962	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.U016300. 4	-1	1	19	965	983	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.05G14810 0.1	-1	1	19	579	597	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.01G21600 0.1	-1	1	19	7796	7814	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.01G21600 0.1	-1	1	19	7817	7835	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.19G03720 0.1	-1	1	19	138	156	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.19G03720 0.2	-1	1	19	122	140	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G10980	-1	1	19	262	280	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage

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gma-miR1533	Glyma.11G10980 0.4	-1	1	19	262	280	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G10980 0.3	-1	1	19	262	280	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G26890 0.1	-1	1	19	368	386	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G22810 0.1	-1	1	19	182	200	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G10110 0.1	-1	1	19	4585	4603	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G10110 0.1	-1	1	19	4606	4624	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G10110 0.1	-1	1	19	4627	4645	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G10110 0.1	-1	1	19	4648	4666	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G22810 0.2	-1	1	19	182	200	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.17G19730 0.1	-1	1	19	3839	3857	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.17G19730 0.1	-1	1	19	3860	3878	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G25150 0.1	-1	1	19	1892	1910	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.17G19730 0.2	-1	1	19	3714	3732	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.17G19730 0.2	-1	1	19	3735	3753	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.07G23350 0.1	-1	1	19	3542	3560	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G07350 0.6	-1	1	19	37	55	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G07350 0.6	-1	1	19	58	76	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G28700 0.2	-1	1	19	3979	3997	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G25150 0.8	-1	1	19	1709	1727	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.06G26700 0.1	-1	1	19	234	252	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G25150 0.5	-1	1	19	1709	1727	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G25150 0.11	-1	1	19	1709	1727	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.12G13600 0.1	-1	1	19	236	254	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G25150 0.9	-1	1	19	1709	1727	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G25150 0.6	-1	1	19	1709	1727	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G28700 0.1	-1	1	19	3806	3824	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G25150 0.16	-1	1	19	1892	1910	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G11460 0.3	-1	1	19	3524	3542	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G11460 0.2	-1	1	19	3521	3539	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G11460 0.1	-1	1	19	3533	3551	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G11460 0.4	-1	1	19	3530	3548	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G21780 0.1	-1	1	19	3652	3670	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.06G05640 0.1	-1	1	19	329	347	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.06G05640 0.3	-1	1	19	329	347	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.04G12550 0.1	-1	1	19	2785	2803	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.04G12550 0.1	-1	1	19	2806	2824	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.04G12550 0.1	-1	1	19	2827	2845	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.18G22580 0.1	-1	1	19	2881	2899	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.20G01430 0.1	-1	1	19	2935	2953	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage

gma-miR1533	Glyma.20G01430 0.1	-1	1	19	2956	2974	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.3	-1	1	19	214	232	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.3	-1	1	19	235	253	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.2	-1	1	19	214	232	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.2	-1	1	19	235	253	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.20G01430 0.2	-1	1	19	2929	2947	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.20G01430 0.2	-1	1	19	2950	2968	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.5	-1	1	19	214	232	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.5	-1	1	19	235	253	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.4	-1	1	19	214	232	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.4	-1	1	19	235	253	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.1	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.06G05640 0.2	-1	1	19	329	347	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.12G01940 0.1	-1	1	19	2793	2811	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.10G24390 0.2	-1	1	19	2519	2537	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.18G22580 0.2	-1	1	19	2821	2839	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.1	-1	1	19	146	164	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.1	-1	1	19	167	185	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.8	-1	1	19	146	164	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.8	-1	1	19	167	185	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.8	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.6	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G11600 0.1	-1	1	19	261	279	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G11600 0.1	-1	1	19	282	300	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.2	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G17990 0.1	-1	1	19	2721	2739	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.10	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.18G22580 0.3	-1	1	19	2751	2769	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.7	-1	1	19	169	187	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.7	-1	1	19	190	208	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.6	-1	1	19	169	187	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G03250 0.6	-1	1	19	190	208	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.9	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.5	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.7	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.4	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G18340 0.3	-1	1	19	178	196	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G19510 0.2	-1	1	19	193	211	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.06G23040 0.1	-1	1	19	2998	3016	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G08520	-1	1	19	70	88	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUUU	Cleavage

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gma-miR1533	Glyma.08G16730 0.1	-1	1	19	2114	2132	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.09G19510 0.1	-1	1	19	193	211	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUUUUACUAU	Cleavag e
gma-miR1533	Glyma.07G13050 0.1	-1	1	19	206	224	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUUAUUAU	Cleavag e
gma-miR1533	Glyma.04G17310 0.1	-1	1	19	194	212	AUAAUAAAAAUAAUAAUGA	UUGUUGUUGUUUUUAUUAU	Cleavag e
gma-miR1533	Glyma.13G27450 0.1	-1	1	19	2797	2815	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.13G27450 0.1	-1	1	19	2818	2836	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.12G10390 0.2	-1	1	19	25	43	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.17G05130 0.1	-1	1	19	2815	2833	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.20G04780 0.5	-1	1	19	112	130	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.15G26960 0.2	-1	1	19	2618	2636	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.15G14520 0.1	-1	1	19	130	148	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.15G14520 0.1	-1	1	19	151	169	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.12G16650 0.1	-1	1	19	411	429	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.15G14520 0.3	-1	1	19	130	148	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.15G14520 0.3	-1	1	19	151	169	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.15G21360 0.1	-1	1	19	2876	2894	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.16G21780 0.2	-1	1	19	2887	2905	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.08G29990 0.1	-1	1	19	217	235	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.04G17310 0.2	-1	1	19	194	212	AUAAUAAAAAUAAUAAUGA	UUGUUGUUGUUUUUAUUAU	Cleavag e
gma-miR1533	Glyma.09G13470 0.1	-1	1	19	2523	2541	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.09G13470 0.1	-1	1	19	2555	2573	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.15G26960 0.1	-1	1	19	2517	2535	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.09G09270 0.1	-1	1	19	52	70	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.09G09270 0.1	-1	1	19	73	91	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.09G09270 0.1	-1	1	19	94	112	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.10G15880 0.1	-1	1	19	554	572	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.02G03940 0.1	-1	1	19	118	136	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.15G21360 0.2	-1	1	19	2696	2714	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.02G23700 0.1	-1	1	19	30	48	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.08G04400 0.2	-1	1	19	1730	1748	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.08G31650 0.1	-1	1	19	503	521	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.04G11740 0.1	-1	1	19	2611	2629	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.13G27450 0.2	-1	1	19	2441	2459	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.13G27450 0.2	-1	1	19	2462	2480	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.16G01710 0.1	-1	1	19	2601	2619	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.02G29700 0.1	-1	1	19	194	212	AUAAUAAAAAUAAUAAUGA	UUAUUAUUCUUUUUAUUAU	Translati on
gma-miR1533	Glyma.04G11740 0.4	-1	1	19	2578	2596	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.04G11740 0.3	-1	1	19	2575	2593	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e
gma-miR1533	Glyma.16G00570 0.3	-1	1	19	2375	2393	AUAAUAAAAAUAAUAAUGA	UUAUUAUUAUUAUUAUUAU	Cleavag e

gma-miR1533	Glyma.16G00570 0.3	-1	1	19	2396	2414	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.07G10770 0.1	-1	1	19	2531	2549	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.04G11740 0.5	-1	1	19	2543	2561	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.2	-1	1	19	2363	2381	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.2	-1	1	19	2384	2402	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.04G11740 0.2	-1	1	19	2542	2560	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.10G29480 0.2	-1	1	19	1160	1178	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.8	-1	1	19	2360	2378	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.8	-1	1	19	2381	2399	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.7	-1	1	19	2359	2377	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.7	-1	1	19	2380	2398	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.15G14520 0.2	-1	1	19	130	148	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.15G14520 0.2	-1	1	19	151	169	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.6	-1	1	19	2348	2366	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.6	-1	1	19	2369	2387	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.19G09860 0.2	-1	1	19	192	210	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.14G18910 0.1	-1	1	19	2394	2412	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.11G25150 0.19	-1	1	19	172	190	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.06G13420 0.1	-1	1	19	2084	2102	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.06G13420 0.1	-1	1	19	2114	2132	AUAAUAAAAUAAUAAUGA	UCGUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.10G29480 0.6	-1	1	19	1160	1178	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.5	-1	1	19	2272	2290	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.5	-1	1	19	2293	2311	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.4	-1	1	19	2260	2278	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.4	-1	1	19	2281	2299	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.15G14520 0.4	-1	1	19	130	148	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.15G14520 0.4	-1	1	19	151	169	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.19G09860 0.1	-1	1	19	192	210	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G11140 0.1	-1	1	19	257	275	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.03G15330 0.1	-1	1	19	104	122	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.1	-1	1	19	2210	2228	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G00570 0.1	-1	1	19	2231	2249	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G15110 0.1	-1	1	19	2391	2409	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.05G11570 0.1	-1	1	19	162	180	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.05G11570 0.1	-1	1	19	183	201	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.05G11570 0.1	-1	1	19	204	222	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G15110 0.2	-1	1	19	2377	2395	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G13500 0.1	-1	1	19	25	43	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G01710 0.3	-1	1	19	2367	2385	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.10G29480	-1	1	19	1160	1178	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage

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gma-miR1533	Glyma.16G01710 0.2	-1	1	19	2361	2379	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.14G05920 0.2	-1	1	19	2117	2135	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.18G06520 0.1	-1	1	19	2035	2053	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.U019600. 2	-1	1	19	2159	2177	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.17G01680 0.1	-1	1	19	2209	2227	AUAAUAAAAUAAUAAUGA	UCAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G15110 0.3	-1	1	19	2349	2367	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.17G05130 0.2	-1	1	19	2182	2200	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G21870 0.1	-1	1	19	466	484	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.20G02350 0.1	-1	1	19	2222	2240	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G21870 0.2	-1	1	19	466	484	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.01G11190 0.1	-1	1	19	2232	2250	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.14G05920 0.1	-1	1	19	2034	2052	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G01950 0.1	-1	1	19	1601	1619	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G13500 0.6	-1	1	19	25	43	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G18450 0.1	-1	1	19	255	273	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G11140 0.2	-1	1	19	257	275	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.01G05360 0.1	-1	1	19	2131	2149	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.10G20660 0.1	-1	1	19	249	267	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.10G20660 0.2	-1	1	19	249	267	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.20G02350 0.3	-1	1	19	2167	2185	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.14G11600 0.1	-1	1	19	1181	1199	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.14G05990 0.1	-1	1	19	1873	1891	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.18G07750 0.1	-1	1	19	1643	1661	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.04G22870 0.1	-1	1	19	427	445	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.20G02350 0.2	-1	1	19	2140	2158	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.U021800. 3	-1	1	19	1854	1872	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.13G18450 0.2	-1	1	19	255	273	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G04660 0.2	-1	1	19	55	73	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.12G21200 0.3	-1	1	19	13	31	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.03G00910 0.8	-1	1	19	68	86	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G19790 0.1	-1	1	19	239	257	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G01710 0.4	-1	1	19	2160	2178	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.03G26060 0.1	-1	1	19	2033	2051	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.05G16820 0.1	-1	1	19	168	186	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.14G05990 0.2	-1	1	19	1758	1776	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G04660 0.3	-1	1	19	10	28	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.09G09830 0.1	-1	1	19	1990	2008	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.08G03530 0.3	-1	1	19	90	108	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.U021800. 1	-1	1	19	1714	1732	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage

gma-miR1533	Glyma.11G22300 0.1	-1	1	19	40	58	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR1533	Glyma.16G02090 0.1	-1	1	19	1024	1042	AUAAUAAAAUAAUAAUGA	UUAUUUUUUUUUUUUUUU	Cleavage
gma-miR4405	Glyma.17G01490 0.2	-1	1	24	4158	4181	AUUCUAAGACGGUUAUCUG GGACC	CUGUUCAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.17G01490 0.3	-1	1	24	4365	4388	AUUCUAAGACGGUUAUCUG GGACC	CUGUUCAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.17G01490 0.4	-1	1	24	4410	4433	AUUCUAAGACGGUUAUCUG GGACC	CUGUUCAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.17G01490 0.1	-1	1	24	4461	4484	AUUCUAAGACGGUUAUCUG GGACC	CUGUUCAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.07G25940 0.9	-1	1	24	3074	3097	AUUCUAAGACGGUUAUCUG GGACC	CUGUACAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.07G25940 0.2	-1	1	24	4127	4150	AUUCUAAGACGGUUAUCUG GGACC	CUGUACAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.07G25940 0.3	-1	1	24	4223	4246	AUUCUAAGACGGUUAUCUG GGACC	CUGUACAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.07G25940 0.4	-1	1	24	4250	4273	AUUCUAAGACGGUUAUCUG GGACC	CUGUACAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.07G25940 0.5	-1	1	24	4259	4282	AUUCUAAGACGGUUAUCUG GGACC	CUGUACAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.07G25940 0.6	-1	1	24	4346	4369	AUUCUAAGACGGUUAUCUG GGACC	CUGUACAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.07G25940 0.7	-1	1	24	4355	4378	AUUCUAAGACGGUUAUCUG GGACC	CUGUACAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.07G25940 0.8	-1	1	24	4382	4405	AUUCUAAGACGGUUAUCUG GGACC	CUGUACAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4405	Glyma.07G25940 0.1	-1	1	24	4478	4501	AUUCUAAGACGGUUAUCUG GGACC	CUGUACAGAUAAUUGUCUU GGAGU	Cleavage
gma-miR4415a-3p	Glyma.10G15350 0.1	-1	1	21	510	530	UUGAUUCUACAACAACAU GG	GCAUGUUGUGAUGAGCAUC GA	Cleavage
gma-miR4415a-3p	Glyma.01G06850 0.1	-1	1	21	123	143	UUGAUUCUACAACAACAU GG	ACAUGUUGUGGAGGGGUC GA	Cleavage
gma-miR4415a-3p	Glyma.07G08080 0.3	-1	1	21	90	110	UUGAUUCUACAACAACAU GG	UUAUGUUGUGAUGGGAAUC GU	Cleavage
gma-miR4415a-3p	Glyma.07G08080 0.2	-1	1	21	165	185	UUGAUUCUACAACAACAU GG	UUAUGUUGUGAUGGGAAUC GU	Cleavage
gma-miR4415b-3p	Glyma.10G15350 0.1	-1	1	21	510	530	UUGAUUCUACAACAACAU GG	GCAUGUUGUGAUGAGCAUC GA	Cleavage
gma-miR4415b-3p	Glyma.01G06850 0.1	-1	1	21	123	143	UUGAUUCUACAACAACAU GG	ACAUGUUGUGGAGGGGUC GA	Cleavage
gma-miR4415b-3p	Glyma.07G08080 0.3	-1	1	21	90	110	UUGAUUCUACAACAACAU GG	UUAUGUUGUGAUGGGAAUC GU	Cleavage
gma-miR4415b-3p	Glyma.07G08080 0.2	-1	1	21	165	185	UUGAUUCUACAACAACAU GG	UUAUGUUGUGAUGGGAAUC GU	Cleavage
gma-miR6299	Glyma.14G07790 0.1	-1	1	22	31	52	AUUUAAAAUUUAUUGAUUUUG AAA	AACCAGGUCAAUAAUUUUUA UAU	Cleavage
gma-miR6299	Glyma.06G11630 0.2	-1	1	22	1270	1291	AUUUAAAAUUUAUUGAUUUUG UCA	UAUUAAAUCAAUAAUUUUUA UAU	Cleavage
gma-miR6299	Glyma.06G11630 0.1	-1	1	22	1338	1359	AUUUAAAAUUUAUUGAUUUUG UCA	UAUUAAAUCAAUAAUUUUUA UAU	Cleavage
gma-miR6299	Glyma.18G14020 0.1	-1	1	22	706	727	AUUUAAAAUUUAUUGAUUUUG UCA	CACAAAACCAUAAUUUUUA AAU	Cleavage

Conclusion

The analysis carried out in the present paper on RNA Seq data of soybean under control and wilt stress conditions resulted in the prediction of circRNAs and their wilt stress specific expression patterns. Functional enrichment analysis of the circRNA-host genes also revealed the indirect involvement of the circRNAs in regulating stress condition by acting as sponges for miRNAs, which may fail to regulate the genes associated with wilt stress tolerance mechanism in soybean.

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