Identification and characterization of the *Pvul-GASA* gene family in the *Phaseolus vulgaris* and expression patterns under salt stress

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Abstract: GASA (Gibberellic acid stimulated in Arabidopsis) is an important gene family that has important roles in both the developmental and physiological processes. In this study, 23 GASA genes in common bean were identified and detailed bioinformatics analyzes were conducted at both gene and protein levels. *Pvul-GASA* proteins were categorized into three clusters, and a total of 13 duplication events (12 segmental and one tandem) were shown to play a role in the expansion of the GASA gene family in *Phaseolus vulgaris* L. The identified *Pvul-GASAs* have been shown to be linked to stress and hormone signaling pathways. In addition, some of the stress-related miRNAs, such as miR164 and miR396, have been identified as targeting *Pvul-GASA* genes, which have also been shown to play a role in salt stress response based on expression data. The alterations in the expressions of *Pvul-GASA*-1, *Pvul-GASA*-12, *Pvul-GASA*-16, *Pvul-GASA*-18 and *Pvul-GASA*-23 genes between control and salt-stressed common bean cultivars have indicated their possible role in the stress response. This research is the first research on the in-silico detection and characterization of *Pvul-GASA* genes in common bean, in which the levels of gene expression were also analyzed.

Key words: GASA, bioinformatics, common bean, qRT-PCR, RNAseq

1. Introduction

Plants sometimes live under unfavorable conditions and face different stressors during their lifetime. These stress factors, which may be of biotic and abiotic origin, may cause physiological and biochemical harm and negatively affect the quantity and quality of agricultural products (Büyük et al., 2012). Although their origin is different, both biotic and abiotic stress factors induce stress in plants with similar pathways and mechanisms (Büyük et al., 2016). There are still several stress-related genes that have not been explained yet, and the discovery of these genes is extremely important for the clarification of stress mechanisms in plants (Chen and Rajewsky, 2007).

GASA (Gibberellic acid stimulated in Arabidopsis) is a CRP (cysteine-rich peptide) protein, which has low-molecular-weight and spreads widely in the plant kingdom (Aubert et al., 1998; Kaikai et al., 2021). These proteins, which comprise GASA protein family, play important roles in plant growth and physiological processes such as lateral root production, leaf spread, flower induction, fruit size control, seed development and germination in monocot and dicot plants (Trapalis et al., 2017). Apart from these,

most GASA genes are involved in hormone (gibberellic acid, abscisic acid and naphthalene acetic acid) signaling pathways and have various roles in response to abiotic stress (Furukawa et al., 2006). In addition, the GASA gene family has also been reported to have important roles in disease resistance against some pathogens (Wang et al., 2009). There are three distinct domains for GASA proteins (80–270 amino acids): (1) a peptide of 18–29 amino acids with an N-terminal signal, (2) a highly variable region (7–31 amino acids) showing a discrepancy between members of the family in terms of both the structure of the amino acid and the length of the sequence, (3) a C-terminal region consisting of 60 amino acids and 12 retained cysteine residues contributing to the molecular biochemical stability (Su et al., 2020).

The GAST1 gene was discovered in the gib1 tomato mutant and was the first member of the GASA gene family (Shi et al., 1992). After that, eight GASA genes have been identified in *Arabidopsis thaliana* by Herzog et al. (1995), and then Roxrud et al. (2007) have identified six new *GASA* genes, bringing the total number of *GASA* gene family members to 14 in *A. thaliana* (Herzog et al.,

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1995; Roxrud et al., 2007). Followingly, GASA genes have been studied on several plant species including *Solanum tuberosum* (Nahirňak et al., 2016), *Malus domestica* (Fan et al., 2017), *Phyllostachys edulis* (Hou et al., 2018), *Glycine max* (Ahmad et al., 2019), *Oryza sativa* (Muhammad et al., 2019), *Triticum aestivum* L. (Cheng et al., 2019), *Vitis vinifera* L. (Ahmad et al., 2020), *Sorghum bicolor* (Filiz and Kurt, 2020), *Theobroma cacao* (Faraji et al., 2021) and cotton (Kaikai et al., 2021) up to date. However, there is limited knowledge regarding the GASA genes in *P. vulgaris* genome.

According to FAO data (Food and Agriculture Organization of the United Nations), beans are the most cultivated crop in the world and are grown in 126 different countries despite their production being affected by abiotic stress. Common bean development is mainly restricted by drought, salinity and subzero temperatures, and a great deal of effort has recently been made in developing resistant cultivars to severe abiotic stress using molecular breeding and gene editing techniques. Targeting the required gene(s) is the most important aspect of such studies, and, thus, scientific studies on the detection of stress-related genes have gained significance in the last decade(s) (Bolat et al., 2017).

For this reason, a wide variety of bioinformatics methods were used to classify and in-depth characterize members of the *GASA* gene family in *P. vulgaris*. In addition, the functions of the identified GASA genes in response to salt stress were examined via RNAseq data and qRT-PCR analyzes. Two common bean genomes, one tolerant to stress (Yakutiye cv.) and the other susceptible to stress (Zulbiye cv.) were comparatively assessed in the qRT-PCR analyzes. This research is the first to analyze the GASA gene family in *P. vulgaris* genome in depth based on these deficiencies in the literature.

2. Materials and methods

2.1. Identification of GASA proteins in *Phaseolus vulgaris* genome

P. vulgaris GASA family sequences were obtained from Phytozome v12.1 (http:// www.phytozomes.net) and Pfam databases (Goodstein et al., 2012). Putative *P. vulgaris* GASA proteins were used for query in blastp (NCBI) for characterization of hypothetical proteins. The physicochemical properties of GASA proteins were calculated using ProtParam Tool (http:web.expasy.org/ protparam) and detection of domains was performed using HMMER (http:www.ebi.ac.uk/Tools/hmmer/).

2.2. Structure and physical locations of *GASA* genes and conserved motifs

Exon – intron structure of *Pvul-GASA* genes was represented using 'Gene Structure Display Server v2.0' (GSDS, http:// gsds.gao-lab.org) (Guo et al., 2007). The

Pvul-GASA genes have been mapped with MapChart tool on *P. vulgaris* chromosomes (Voorrips, 2002). Multiple expectation maximizations for motif elicitation tool (EM) was used (MEME 4.11.1; http:/meme-suite.org/) to classify additional conserved motifs for Pvul-GASA proteins (Bailey et al., 2006).

2.3. Phylogenetic analysis and sequence alignment

The ClustalW has been used to perform the multiple sequence alignment of Pvul-GASA proteins (Tamura et al., 2011). The neighbor-joining (NJ) was used for the construction of phylogenetic trees with a bootstrap value of 1000 replicates (MEGA7), and the tree was drawn using an Interactive Life Tree (iTOL; http://itol.embl.de/index. shtml) (Letunic and Bork, 2011).

2.4. Promoter analysis of *Pvul-GASA* genes

Applying Phytozome database v11, the 5′ upstream regions (2 kb of DNA sequence from each *Pvul–GASA* gene) were analyzed with the PlantCARE database (http:// bioinformatics.psb.ugent.be/webtools/plantcare/ html/) for a cis element scan.

2.5. In-silico prediction of miRNA targets in *Pvul-GASA* genes

All known sequences of miRNA plants have been downloaded from miRBase v21.0. (http://www.mirbase. org). psRNA Target Server was used accordingly with default miRNA prediction parameters (http://plantgrn. noble.org/psRNATarget) (Zhang, 2005). In-silico predicted miRNA targets were searched by BLASTX with ≤1e^{-10} against common bean Expressed Sequenced Tags (ESTs) in the NCBI database.

2.6. Detection of gene duplication events and prediction of synonymous and nonsynonymous substitution rates

Duplicated gene pairs were analyzed on the plant genome duplication database server (http://chibba.agtec.uga.edu/ duplication/index/locus) with a display range of 100 kb. CLUSTALW software was used to predict amino acid sequences of duplicated *Pvul-GASA* genes.

The PAML (PAL2NAL) CODEML software (http:// www.bork.embl.de/pal2nal) was used to estimate synonymous (Ks) and non-synonymous (Ka) substitution rates (Suyama et al., 2006). Duplication period (million years ago, Mya) and divergence of each *Pvul-GASA* gene was calculated using the following formula: T = Ks/2λ (λ=6.56E^{-9}) (Yang and Nielsen, 2000).

2.7. In-silico mRNA levels of *Pvul-GASA* genes in different tissues

Expression levels of *Pvul-GASA* genes in special tissue libraries of plants at different stages of development, including root 10, nodules, root 19, young buds, stem 10, stem 19, green mature buds, leaves, young triloliates, flower buds and flowers, were obtained from Phytozome database v12.1. FPKM (expected number of fragments per kilobase

of transcript sequence per million base pairs sequenced) was used for in-silico expression levels and FPKM values have been transformed into log2. Then a heatmap has been drawn with the CIMMiner algorithm (http://discover.nci.nih.gov/cimminer).

2.8. Identified expression level of *Pvul-GASA* genes through transcriptome data

Illumina RNA-seq data was collected from the sequence read archive (SRA) to measure the *Pvul-GASA* gene expression levels. For this reason, the accession numbers SRR957667 (control leaf), SRR958472 (salt-treated root), SRR958469 (control root) and SRR957668 (salt-treated leaf) were used as defined by Buyuk et al. (2016) (Büyük et al., 2016). The heat maps of hierarchical clustering were eventually built using the CIMminer (https://discover.nci.nih.gov/cimminer/home.do).

2.9. Homology modeling of GASA proteins

All Pvul-GASA proteins were searched against Protein Data Bank (PDB) by BLASTP (with default parameters) to classify the best template(s) with identical sequence and three-dimensional structure (Berman et al., 2000). Data were fed in Phyre2 (Protein Homology/AnalogY Recognition Engine; (http://www.sbg.bio.ic.ac.uk/phyre2) to predict protein structure by homology modeling in 'intensive' mode (Kelley and Sternberg, 2009).

2.10. Plant materials and growth conditions

Two nationally registered common bean cultivars, 'Yakutiye' and 'Zulbiye', were obtained from the 'Transitional Zone Agricultural Research Institute, Eskişehir, Turkey.' According to previous findings and the literature, 'Yakutiye cv.' is a salt-tolerant whereas 'Zulbiye cv.' is a salt-susceptible common bean cultivar (Büyük et al., 2016; Büyük et al., 2019). The seeds of both cultivars were germinated, following the surface sterilization in a solution containing 5 % (v/v) hypochlorite for 5 min, and were grown hydroponically in pots containing 0.2L of modified 1/10 Hoagland's solution. Hoagland solution includes macronutrients (K_2SO_4, KH_2PO_4, $MgSO_4.7H_2O$, Ca $(NO_3)_2.4H_2O$ and KCl) and micronutrients (H_3BO_3, $MnSO_4$, $CuSO_4.5H_2O$, NH_4Mo, $ZnSO_4.7H_2O$) with a final concentration of ions as 2 mM Ca, 10^{-6} M Mn, 4 mM NO_3, 2.10^{-7}M Cu, 1 mM Mg, 10^{-8} M NH_4, 2 mM K, 10^{-6} M Zn, 0.2 mM P, 10^{-4} M Fe and 10^{-6} M B. Common bean seedlings were incubated in a controlled environmental growth chamber in the light with 250 mmol $m^{-2}\,s^{-1}$ photosynthetic photon flux at 25 °C, 70 % relative humidity. Salt stress was then applied with Hoagland solution including 150 mM NaCl (for moderate salinity stress) for 9 days after common bean seedlings reached the first trifoliate stage in growth chamber. Following the 9th day of stress application, leaf tissues of two different common bean cultivars were sampled and stored at –86 °C to be used for qRT-PCR analysis.

2.11. RNA extraction, complementary DNA (cDNA) synthesis and qRT-PCR analyses

NucleoSpin RNA Kit (Macherey – Nagel, Germany) was used for RNA extraction as defined by the manufacturer, and the RNA quality control was performed using both NanoDrop spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA) and 1.5% agarose gel electrophoresis. The high fidelity cDNA synthesis kit (Roche, USA) was used for complementary DNA synthesis according to the kit protocol. Based on the RNAseq data, five *Pvul-GASA* genes (*Pvul-GASA-1, Pvul-GASA-12, Pvul-GASA-16, Pvul-GASA-18* and *Pvul-GASA-23),* which showed different expression levels then control levels in response to salt stresses according to the RNAseq data, have been selected to be used for qRT-PCR experiments. The primers were then designed using Primer3 based on sequences of five selected *Pvul-GASA* genes and shown in Supplementary Table 1. For qRT-PCR reactions, iTaq Universal SYBR Green Supermix (Biorad, USA) was used, and the reaction conditions as defined by Buyuk et al. (2019) were applied (Büyük et al., 2019). qRT-PCR reactions have been tested using Light Cycler Nano Device (Roche). Three separate biological and technological repetitions have been used and the Actin (ACT) gene has been selected for the normalization of qRT-PCR data according to the $2^{-\Delta CT}$ method (Livak and Schmittgen, 2001). Statistical analyzes were carried out using GraphPad Prism 7 software based on the two-way ANOVA method, and the least significant difference test of Fisher at 0.05 significant levels was considered.

3. Results and discussion

3.1. Identification and analysis of *Pvul-GASA* genes in *P. vulgaris* genome

In this study, 23 GASA genes were identified in the *P. vulgaris* genome using in-silico bioinformatics methods, and these genes were named from *Pvul-GASA-1* to *Pvul-GASA-23* according to their chromosomal positions (Table 1). The number of *GASA* genes in the genome of *P. vulgaris* was found to be higher than the number identified in *Oryza sativa* (n = 10) (Muhammad et al., 2019), *Sorghum bicolor* (n = 12) (Filiz and Kurt, 2020), *Arabidopsis thaliana* (n = 14) (Roxrud et al., 2007), *Vitis vinifera* L. (n = 14) (Ahmad et al., 2020), *Solanum tuberosum* (n = 16) (Nahirñak et al., 2016), *Theobroma cacao* (n = 17) (Faraji et al., 2021), *Gossypium arboreum* (n = 17) (Kaikai et al., 2021) and *Gossypium herbaceum* (n = 19) (Kaikai et al., 2021). However, it was found to be less than the number identified in *G. arboreum* (n = 25) (Kaikai et al., 2021), *Malus domestica* (n = 26) (Fan et al., 2017), *G. barbadense* (n = 33) (Kaikai et al., 2021), *Glycine max* (n = 37) (Ahmad et al., 2019), *Triticum aestivum* L. (n = 37) (Cheng et al., 2019) and *G. hirsutum* (n = 38) (Kaikai et al., 2021).

Table 1. Information regarding *P. vulgaris* L. GASA family members. pI: The isoelectric point; MW: molecular weight; I. Index: Instability index; S. Loc.: Subcellular localization; chlo: chloroplast; extr: Extracellular space , cyt: Cytoplasmic.

ID	Phytozome ID	NCBI Accession No	Chr. No.	Length (aa)	pI	MW (kDa)	I. index	S. Loc	GRAVY	Aliphatic index
Pvul-GASA-1	Phvul.001G006300	XP_007160662.1	1	99	9.07	10.49	42.58	extr	−0.006	84.85
Pvul-GASA-2	Phvul.001G006400	XP_007160663.1	1	99	8.50	10.78	42.83	extr	−0.064	73.84
Pvul-GASA-3	Phvul.001G006600	XP_007160665.1	1	99	8.30	10.67	40.75	extr	0.039	89.70
Pvul-GASA-4	Phvul.001G006700	XP_007160666.1	1	106	7.47	11.43	78.72	extr	−0.156	68.96
Pvul-GASA-5	Phvul.001G025800	XP_007160892.1	1	88	9.30	9.40	23.13	chlo	−0.024	55.57
Pvul-GASA-6	Phvul.001G127700	XP_007162142.1	1	144	9.25	15.87	40.13	extr	−0.540	60.21
Pvul-GASA-7	Phvul.001G247600	XP_007163594.1	1	92	8.61	10.23	41.42	extr	−0.105	53.04
Pvul-GASA-8	Phvul.001G268100	XP_007163834.1	1	92	8.87	10.35	38.42	extr	−0.160	60.33
Pvul-GASA-9	Phvul.001G268150	XP_007163897.1	1	92	8.26	10.14	51.04	extr	−0.049	62.50
Pvul-GASA-10	Phvul.003G055500	XP_007153677.1	3	117	9.03	12.88	38.42	extr	−0.033	78.29
Pvul-GASA-11	Phvul.003G197400	XP_007155392.1	3	114	8.25	12.54	45.48	extr	−0.176	78.60
Pvul-GASA-12	Phvul.004G019900	XP_007151125.1	4	179	9.19	19.15	70.14	extr	−0.287	66.87
Pvul-GASA-13	Phvul.004G028800	XP_007151230.1	4	110	9.52	12.25	44.17	extr	−0.260	54.09
Pvul-GASA-14	Phvul.007G042400	XP_007143086.1	7	90	8.69	9.86	36.79	extr	−0.146	65.11
Pvul-GASA-15	Phvul.007G089800	XP_007143651.1	7	96	8.94	10.53	38.69	extr	−0.080	65.10
Pvul-GASA-16	Phvul.007G243400	XP_007145489.1	7	113	9.59	12.71	58.34	cyto	−0.404	70.88
Pvul-GASA-17	Phvul.007G248900	XP_007145559.1	7	145	9.25	15.01	53.55	extr	−0.364	54.07
Pvul-GASA-18	Phvul.008G041200	XP_007139576.1	8	109	9.32	12.10	41.00	extr	−0.264	50.18
Pvul-GASA-19	Phvul.008G235300	XP_007141900.1	8	97	9.36	10.73	39.40	extr	−0.190	56.39
Pvul-GASA-20	Phvul.009G016800	XP_007136089.1	9	99	9.10	10.83	54.16	extr	−0.115	75.96
Pvul-GASA-21	Phvul.009G069900	XP_007136735.1	9	89	8.93	9.64	37.19	extr	0.038	67.98
Pvul-GASA-22	Phvul.009G181500	XP_007138116.1	9	116	8.45	12.69	50.01	extr	−0.191	73.02
Pvul-GASA-23	Phvul.009G187400	XP_007138184.1	9	112	9.22	12.38	60.04	extr	−0.293	60.09

The identified GASA proteins were found to be between 88 to 179 amino acids in length, and the molecular weights of these proteins were between 9.40 to 19.15 kDa. These findings were in agreement with the previous studies, which have revealed that *GASA* genes mostly had low molecular weights as reported for rice (Rezaee et al., 2020), *V. vinifera* L. (Ahmad et al., 2020), *A. thaliana* (Fan et al., 2017), *L. esculentum* L. (Rezaee et al., 2020) and *T. cacao* L. (Faraji et al., 2021).

The instability index values were found to be higher than '40' in 16 out 23 *Pvul-GASAs* indicating that they were unstable proteins. On the other hand, the stable proteins were as follows: *Pvul-GASA-5*, *Pvul-GASA-8*, *Pvul-GASA-10*, *Pvul-GASA-14*, *Pvul-GASA-15*, *Pvul-GASA-19* and *Pvul-GASA-21* (Table 1).

Grand average of hydropathicity index (GRAVY) is used to represent the hydrophobicity value of a peptide. Positive and negative GRAVY values indicate hydrophobic and hydrophilic proteins, respectively (Kyte and Doolittle,

1982). In the current study, Pvul-GASA proteins were found to be hydrophilic except for *Pvul-GASA-3* and *Pvul-GASA-21* proteins according to the GRAVY values, which ranged between −0.006 (*Pvul-GASA-1*) and 0.039 (*Pvul-GASA-3*). These findings were in agreement with the previous studies in which hydrophilic nature of most GASA proteins were reported for *M. domestica* (Fan et al., 2017), *V. vinifera* L. (Ahmad et al., 2020) and *T. cacao* L. (Faraji et al., 2021).

The determination of the subcellular position offers essential clues as to the function of proteins. For this reason, the subcellular localizations of Pvul-GASAs have been identified using protein subcellular localization prediction tool (WoLF PSORT) (Horton et al., 2006). Accordingly, we predicted extracellular localization of Pvul-GASA proteins, except for *Pvul-GASA-5* and *Pvul-GASA-16*, which localized in the chloroplast and cytosol, respectively (Table 1). Previously, GASA protein extracellular localization has also been reported in several plant species

similar to our findings (Zhang et al., 2009; Ahmad et al., 2019; Rezaee et al., 2020; Faraji et al., 2021). Moreover, the location in plasma membrane, cytoplasm, and nucleus of GASA proteins has also been described (Wang et al., 2009). Different factors such as the protein-protein interaction and the post-translation modifications may cause changes in the subcellular localization (Nahirñak et al., 2016). Post-translational modifications are the processes involving chemical protein modifications that produce structural and functional diversity, including subcellular location, protein-protein interaction, and allosteric enzyme activity regulation (Webster and Thomas, 2012; Duan and Walther, 2015; Nahirñak et al., 2016).

The aliphatic index value, known as the relative volume of the aliphatic side chains (alanine, valine, isoleucine and leucine), can be considered as a positive factor in increasing the thermostability of spherical proteins. In this study, the aliphatic index value of Pvul-GASA proteins ranged from 53.04 to 89.70, suggesting that these proteins were thermally stable (Gasteiger et al., 2005). In terms of amino acid content, cysteine (Cys) (56%), leucine (Leu) (17%) and proline (Pro) (13%) were found to be the most abundant amino acids in Pvul-GASA proteins. Similarly, Fan et al., (2017) have already shown a dominant presence of Cys and Leu amino acids in GASA proteins of *Malus domestica* in their study (Fan et al., 2017).

3.2. Chromosomal localization and duplication analysis of *GASA* genes in *P. vulgaris*

According to chromosome analyses, most *Pvul-GASA* genes have been found to be distributed over Chr-1, 3, 4, 7, 8 and 9. The highest number of *Pvul-GASA* genes (9 genes) were found to be located on Chr-1, and no GASA genes were found on Chr-2, 5 and 6 (Table 1; Figure 1). Similarly,

a study on *G. max* by Ahmad et al. (2019) showed that 37 *GmGASA* genes were distributed across 15 chromosomes and no *GASA* genes were found in 1, 7, 11, 12, and 15th chromosomes of *G. max* (Ahmad et al., 2019). In a study on apple, 26 *MdGASA* genes were found to be distributed on 11 chromosomes, but there was no *GASA* gene on 1, 2, 6, 10 and 11th chromosomes of *M. domestica* (Fan et al., 2017). In paralel to these findings obtained from different plant species, an uneven distribution of *Pvul-GASA* genes were also observed on *P. vulgaris* chromosomes in the current study (Figure 1).

Gene duplications are of considerable importance for the expansion and development of gene families (Mehan et al., 2004). The gene duplication analysis was therefore conducted in the current study to determine the tandem and segmental duplication events between *Pvul-GASA* genes. As a result, 12 segmentally and one tandemly duplicated gene pairs across 23 *Pvul-GASAs* have been identified (Table 2). The identified duplication events between *Pvul-GASA* genes have been estimated to be occurred from 4.4 to 445.9 million years ago (Table 2). The number of duplication events (a total of segmental and tandem duplications) of *Pvul-GASAs* was higher than the number identified in apple (2 pairs in 26 *MdGASAs*), (Fan et al., 2017) soybean (5 pairs in 37 *GmGASAs*) (Ahmad et al., 2019), grape (6 pairs in 14 *VvGASAs*) (Ahmad et al., 2020) and cacao (6 pairs in 17 *tcGASAs*) (Faraji et al., 2021); however, it was less than the number identified in *G. hirsitum* (22 pairs in 25 *GhGASAs*) (Table 2).

Gene duplication events, primarily tandem duplication, segmental duplication, and transposition are critical for gene family expansion (Kong et al., 2007). In this study, compared with tandem duplication, segmental
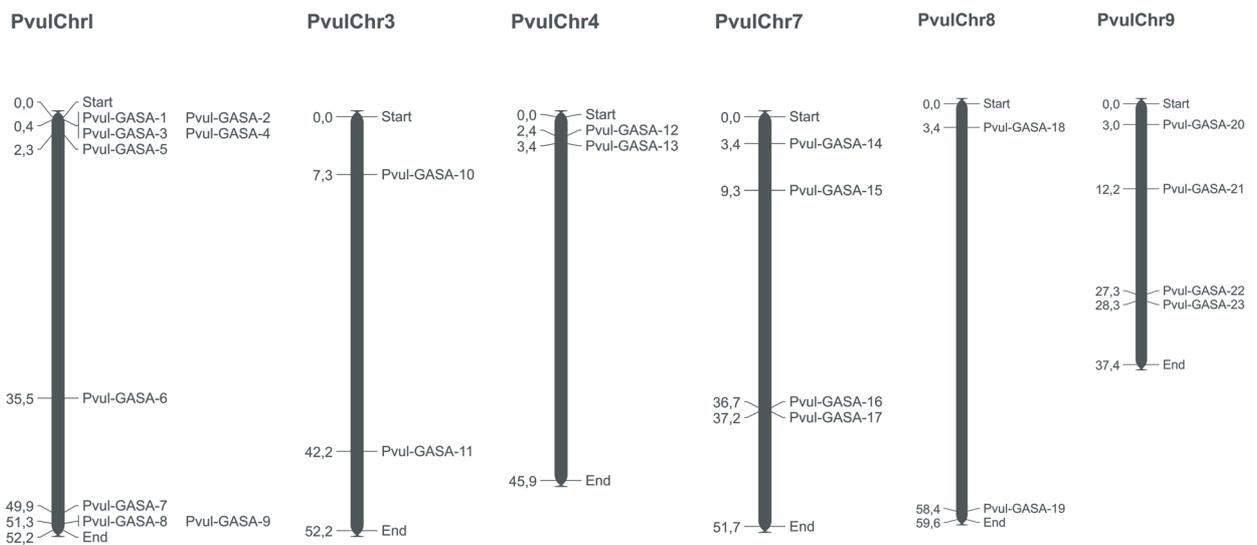

Figure 1. Chromosomal location of *P. vulgaris* GASA genes.

Table 2. The Ka/Ks ratios and date of segmental duplication for GASA genes in *P. vulgaris*.

Gene 1	Gene 2	Ks	Ka	Ka/Ks	MYA	Duplication Type
Pvul-GASA-1	*Pvul-GASA-20*	0.9469	0.1284	0.1356	7.28	Segmental
Pvul-GASA-5	*Pvul-GASA-14*	1.5125	0.2256	0.1491	11.63	Segmental
Pvul-GASA-5	*Pvul-GASA-21*	0.8666	0.1296	0.1495	6.66	Segmental
Pvul-GASA-6	*Pvul-GASA-17*	1.105	0.3041	0.2752	8.5	Segmental
Pvul-GASA-10	*Pvul-GASA-12*	53.8198	0.4795	0.0089	413.9	Segmental
Pvul-GASA-10	*Pvul-GASA-22*	2.1597	0.3558	0.1648	16.6	Segmental
Pvul-GASA-11	*Pvul-GASA-12*	57.967	0.4437	0.0077	445.9	Segmental
Pvul-GASA-11	*Pvul-GASA-22*	0.5781	0.1131	0.1957	4.44	Segmental
Pvul-GASA-13	*Pvul-GASA-18*	0.7278	0.1221	0.1677	5.59	Segmental
Pvul-GASA-13	*Pvul-GASA-23*	1.5229	0.231	0.1517	11.71	Segmental
Pvul-GASA-14	*Pvul-GASA-21*	1.8702	0.214	0.1144	14.38	Segmental
Pvul-GASA-18	*Pvul-GASA-23*	1.816	0.2359	0.1299	13.96	Segmental
Pvul-GASA-10	*Pvul-GASA-11*	1.6402	0.3748	0.2285	12.61	Tandem

duplications have been found to play a dominant role in the evolution of *GASA* gene family in *P. vulgaris*. To get more insights into the evolution of these duplicated genes, non-synonymous divergence (Ka), synonymous divergence (Ks) and their ratio (Ka/Ks) values were calculated to examine the selective pressure and duplication time of *GASA* segmentally and tandemly duplicated genes in *P. vulgaris*. The Ka/Ks ratio for *P. vulgaris GASA* duplicated genes ranged from 0.0077 to 0.2752; thus, Ka/Ks < 1 for both duplicated gene pairs (Table 2). In general, a Ka/Ks > 1 means positive selection, Ka/Ks < 1 indicates purifying selection, and Ka/Ks = 1 stands for neutral selection (Nekrutenko et al., 2002). These results suggested that the duplicated *Pvul-GASA* genes were under strong purifying selection pressure. Similarly, the duplicated *GASA* genes in *G. max* (Ahmad et al., 2019), *V. vinifera* L. (Ahmad et al., 2020) and *T. cacao* L. (Faraji et al., 2021) were also found to be under strong purifying selection pressure because their Ka/Ks ratio was less than 1.

Pvul-GASA* genes that underwent tandem and segmental duplication were also compared with *A. thaliana* and *G. max* genomes to explore the orthologous relationships between them. Seven and 45 orthologous gene pairs were therefore identified between *P. vulgaris* L. - *A. thaliana* and *P. vulgaris* L. - *G. max* genomes, respectively. These orthologous relationships have been estimated to be occurred 16 million years ago for *P. vulgaris* L. – *G. max* and 118 million years ago for *P. vulgaris* L. - *A. thaliana* (Supplementary Table 1; Figure 2). This high number of *GASA*s orthologous relationships between common bean and soybean genomes supported the hypothesis that soybean underwent a whole genome duplication event

after diverging from common bean (Shoemaker et al., 1996; Schlueter et al., 2004; McClean et al., 2010).

3.3. Gene structure, motif analysis, homology modelling and phylogenetic analysis of *GASA* members in *P. vulgaris*

The exon-intron structures of the *Pvul-GASA* genes have been determined in *P. vulgaris* genome and the exon numbers ranged from 2 to 4 (Figure 3). In a study conducted by Ahmad et al. (2020), it was also found that the exon number of *VvGASA* genes ranged from 1 to 4, with only *Vv-GASA-5* having more than five exons (Ahmad et al., 2020). In another study conducted by Ahmad et al. (2019), it was reported that the exon number of *GmGASA* genes ranged from 2 to 4 similar to our findings (Fan et al., 2017; Ahmad et al., 2020). Additionaly, it was also seen that all *Pvul-GASA* genes contained at least one intron, consistent with the results of the studies on potato (Nahirñak et al., 2016), apple (Fan et al., 2017), common wheat (Cheng et al., 2019), grapevine (Ahmad et al., 2020) and cotton (Kaikai et al., 2021). However, the analyses of GASA genomic sequences showed the absence of intron in one gene in both *T. cacao* and *G. max* genomes (Ahmad et al., 2019; Faraji et al., 2021).

The motif compositions of the Pvul-GASA proteins were examined. A total of 20 different conserved *Pvul-GASA* protein motifs have been identified, and amino acid sequences and motif lengths were shown in Figure 4. When the motif content was analyzed, it was established that the completely same motifs (Motif-1, -2, -3, -4 and -5) were found in *Pvul-GASA*-1, -2, -3 and -20 proteins. Moreover, *Pvul-GASA*-5, -14 and -21 proteins were found to commonly share the Motif-1, -2, -3 and -4 while *Pvul-*
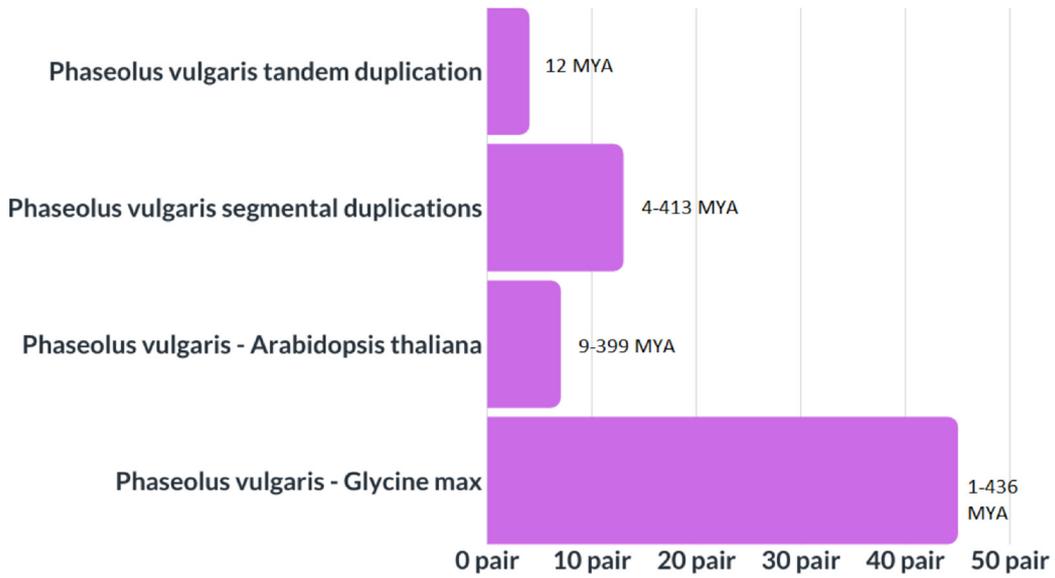
Figure 2. The mean evolutionary divergence times and the number of orthologous genes between queries.
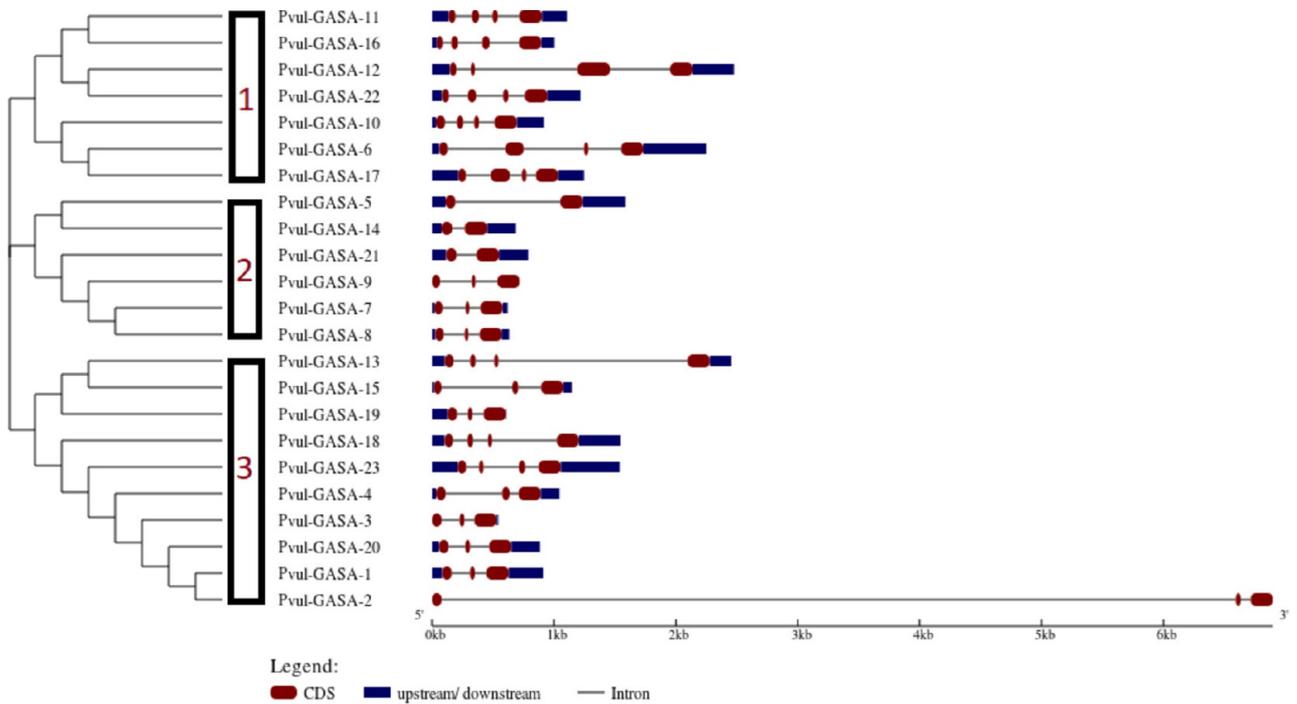

Figure 3. Gene structures of GASA family members from *P. vulgaris* with clustering based on NJ based phylogenetic tree. Introns are presented by lines. UTR and CDS are indicated by filled dark-blue and red boxes, respectively.

GASA-8 and -9 contained only Motif-1, -2, -3, -4 and -11 (Figure 4).

Additionaly, the InterPro and InterProScan databases were screened, and it was clearly demonstrated that all identified Pvul-GASA proteins were gibberellin regulated proteins as expected (Supplementary Table 2). Similar motif compositions facilitated the determination of structural similarities between Pvul-GASA proteins. According to this, Motif 1 and Motif 2 were found to be present in all Pvul-GASA proteins. It was determined that Motif 3 was absent only in *Pvul-GASA*-12. While Motif 13 was only detected in *Pvul-GASA*-18 and *Pvul-GASA*-23, these proteins were also located at the same clade in group B in the phylogenetic tree. However, it was understood that
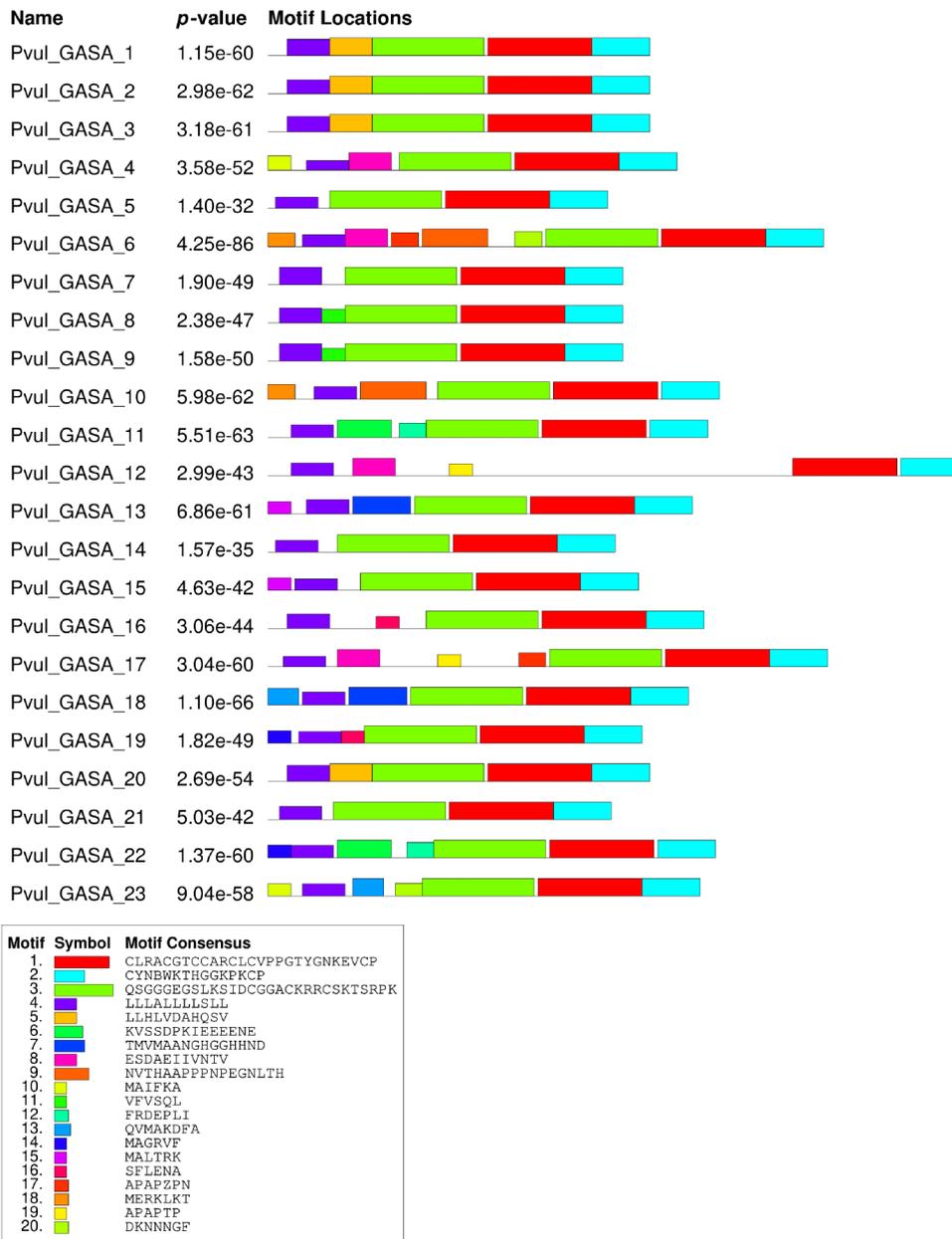
Figure 4. Conserved motifs of *Pvul-GASA* proteins from *P. vulgaris*. Schematic depiction of 20 conserved motifs in *Pvul-GASA* proteins. The MEME online tool was used to identify motifs. Each motif type is denoted using different-colored blocks, and the numbers in the boxes (1–20) signify motifs 1–20. The length and position of each colored box is scaled to size and motif consensus were provided.

the genes encoding *Pvul-GASA*-18 and *Pvul-GASA*-23 proteins acted opposite to each other in both leaf and root tissues in response to salt stress according to the RNAseq data. Moreover, Motif 19 was found to be present only in *Pvul-GASA*-12 and *Pvul-GASA*-17 proteins, and the genes encoding these proteins showed no response to salt stress based on RNAseq data (Figure 4).

Additionally, three-dimensional structure prediction and homology modeling were performed for a total of 23 Pvul-GASA proteins. It has been determined that a

total of 12 *Pvul-GASA*s had three-dimensional structure with a similarity ratio of approximately 60% to 90% with 90% confidence. All GASA proteins were found to have a flexible structure due to the presence of coils (Figure 5). The secondary structures of Pvul-GASA proteins had approximately equal amounts of α-helix and β-layer structure. Similarly, in the studies conducted in *M. domestica* and *V. vinifera* L., it was found that GASA proteins consisted of the α-helix and antiparalel β-layer (Fan et al., 2017; Ahmad et al., 2020).
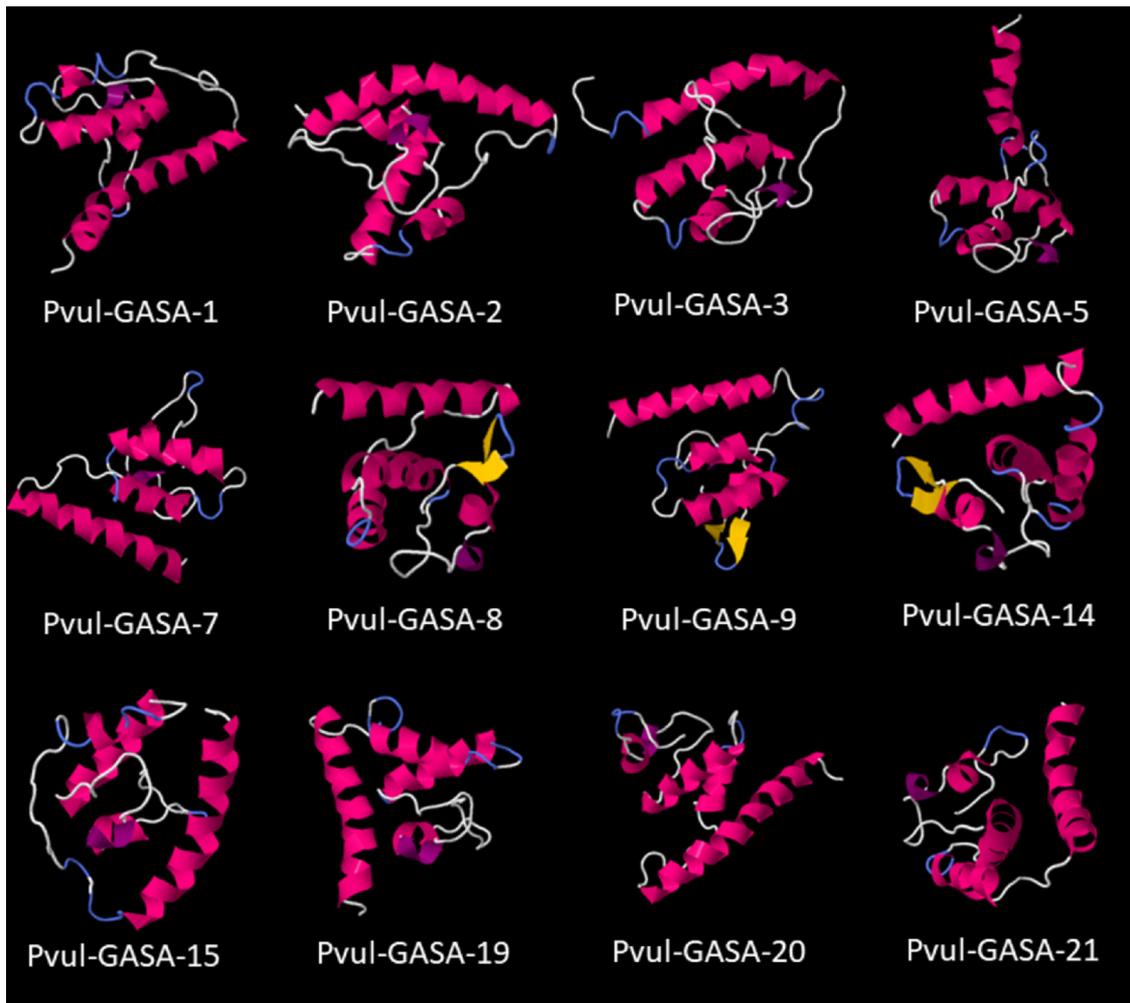
Figure 5. Predicted 3D models of common bean GASA proteins. Models were generated by using Phyr2 server. The secondary structure elements: **α**-helices (pink), β-sheets (yellow), and coils (blue-white) are indicated for the predicted 3D structures of *Pvul-GASA*s.

To better understand the evolutionary relationship between Pvul-GASA proteins and GASA proteins from *A. thaliana* and *G. max*, phylogenetic analysis was carried out, and, thus, three cluster groups (Group A, B and C) were obtained. Accordingly, the largest group was 'Group C' with 36 GASA proteins, while the smallest group was 'Group A' with 5 GASA proteins (Figure 6).

'Group A' comprised only the GmGASA and AtGASA members and had no GASA proteins from *P. vulgaris* (Figures 3, 6). Approximately 70% of Group B contained *Pvul-GASA* genes with three exons, while the remainder were found to have four exons, which were usually located under the same node of the phylogenetic tree. In Group C, in addition to the presence of two and four exon genes, 50% of the group members were found to have four exons and to be clustered under the same tree node (Figures 3, 6).

3.4. Promoter and miRNAs analysis of Pvul-GASA genes
Several environmental stresses, such as drought, salinity and low temperatures, have detrimental effects on plant growth and productivity of crops (Büyük et al., 2012). Cis-acting regulatory elements play a crucial role in the regulation of genetic networks in the presence of stress conditions and in many developmental-related processes. Therefore, understanding the complex structure of the genome is only possible with a successful study of regulator's roles in the gene network (Yamaguchi-Shinozaki and Shinozaki, 2005). For this reason, the identified *Pvul-GASA* genes were analyzed using an in-silico promoter analysis tool, and it was determined that the functions of the detected cis-acting elements were grouped under 8 headings: development, environmental stress, hormone, light, promoter, site binding, biotic stress and other (Supplementary Table 3). It was determined

Figure 6. Phylogenetic analyses of GASA proteins from three plant species. The phylogenetic tree was constructed using the NJ method. The identifier names of GASA proteins of *Phaseolus vulgaris*, *Arabidopsis thaliana* and *Glycine max* start with 'Pvul', 'AT' and 'Glyma', respectively.

that CAAT-box and TATA-box, which are core promoter elements, and light sensitive BOX4 were present in all *Pvul-GASA* genes similar to the previous studies in potato (Nahirñak et al., 2016) and cotton (Kaikai et al., 2021). Moreover, several plant hormone (ERE, CGTCA, ABRE, TGA-element, TCA-element)-related cis-elements have been identified in the promoter region of *Pvul-GASA* genes (Supplementary Table 3). Similar to our findings, these plant hormone related cis-elements have also been detected in the promoter regions of *GASA* genes in potato (Nahirñak et al., 2016), apple (Fan et al., 2017), grapes (Ahmad et al., 2020), cotton (Kaikai et al., 2021) and cacao (Faraji et al., 2021). Apart from these, cis-elements such as MBS, TC-rich repeats, ARE elements and G-BOX, involved in various stress response, were identified in the

promoters of some *Pvul-GASA* genes, and these were the cis-elements, which were also detected in *GASA* genes of cotton (Kaikai et al., 2021) and grapes (Ahmad et al., 2020) (Supplementary Table 3). The abundance of stress related motifs may show the possible roles of *Pvul-GASAs* in stress response.

It is important to determine the roles of miRNAs and the genes they target in response to plant stress. Biotic and abiotic stresses cause certain miRNAs to make tissue-specific arrangements at the same time. A total of 64 *Pvul-GASA*-associated miRNAs were identified in this study as a result of miRNA analysis (Supplementary Table 4). According to the results, the most targeted gene by these 64 miRNAs was *Pvul-GASA-3* and miR164 was the most targeting microRNA (Supplementary Table 4).

The function of miR164 in suppressing the transcripts of development associated and stress responsive NAC transcription factors has received a lot of attention (Hernández and Sanan-Mishra, 2017; Hernandez et al., 2020). Evidence suggests that miR164 target many families of TFs, including bZIP (basic leucine zipper), MYB, SPL (SQUAMOSA promoter binding protein like), AP2/ERF (apetala 2/ethylene responsive element binding factor), MADS box, and NAC (Jeong et al., 2009). These regulatory nodes were found to be responsible for increasing plant abiotic tolerance (Zhou et al., 2013; Fahad et al., 2015; Cao et al., 2017; Yu et al., 2018). This known role of miR164 in suppressing the transcripts of the stress-responsive transcription factors may also indicate that GASA genes in *P. vulgaris* may play roles in response to abiotic stress.

The gene most targeted by the identified miRNAs after *Pvul-GASA-3* was *Pvul-GASA-2* which was most frequently targeted by miR396. This is an important miRNA, which is known to be salt stress related according to findings obtained from genome-wide studies in *A. thaliana*, corn, soybean, maize (*Zea mays* L.) and *Populus* species (Sunkar

and Zhu, 2004; Liu et al., 2008; Ding et al., 2009; Gao et al., 2011; Li et al., 2011). The second miRNA that frequently targeted *Pvul-GASA-2* after miR396 was miR827 with 26% targeting rate (Supplementary Table 4). There are studies in the literature stating that this miRNA is used to regulate the transport and storage of phosphate (Pi) in *A. thaliana* and *O. sativa*, respectively. Additionaly, miR827 was also found to be drought tolerance related microRNA in barley (Ferdous et al., 2017).

3.5. Tissue-spesific mRNA levels of *Pvul-GASA* genes

Heat map revealed that *Pvul-GASA* genes offer variable levels of expression in different tissues such as flower buds, flowers, leaves, stem 10, young pods, stem 19, young trifoliates, root 10, root 19, green mature pods and nodules (Figure 7). In particular, *Pvul-GASA*-12, 18, 22 and 23 were much more expressed than other genes in most of the tissues. These genes (*Pvul-GASA*-12, 18, 22 and 23) have been also found to be in orthologous relationships with *G. max* genome, and this may explain that why they showed similar high expression levels in most of the tissues (Supplementary Table 1). Besides that, *Pvul-GASA-12, -18*
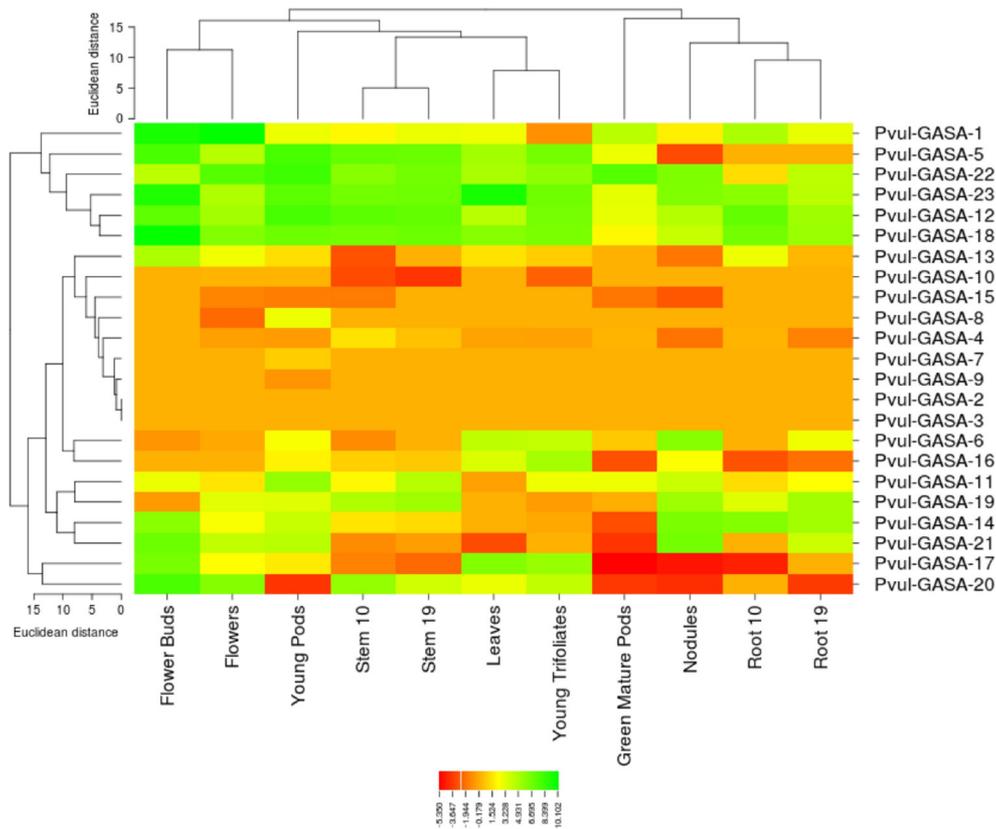
Figure 7. Tempo-spatial expression patterns of *Pvul-GASA* genes in different organs in *P. vulgaris*. The log2-transformation of the average of expression values were used to generate the heat map with PermutMatrix software. Green and red in the color scale indicate high and low transcript expression, respectively. Root 19: 19 days after planting; Root 10: 10 days after planting; Stem 19: 19 days after planting; Stem 10: 10 days after planting.

and *-23* showed almost similar expression pattern under salt stress conditions according to the qRT-PCR analyzes.

On the other hand, the expression levels of other *Pvul-GASA* genes were found to be relatively low. *Pvul-GASA-2, 3, 7* and *9* genes were found to be very close to each other in all plant tissues in terms of expression level (Figure 7).

3.6. Roles of Pvul-GASA genes in response to salt stress via RNAseq analysis

In this study, RNAseq analysis of *Pvul-GASA* genes was performed using SRA data created by Hiz et al. (Hiz et al., 2014; Büyük et al., 2016). It was determined that *Pvul-GASA* genes showed different expression levels in leaf and root tissues under salt stress conditions. When the obtained results were evaluated, it was also observed that the expression levels of *Pvul-GASA-1, Pvul-GASA-12, Pvul-GASA-16, Pvul-GASA-18* and *Pvul-GASA-23* genes have differed depending on root-leaf and control-stress conditions. In this context, it was seen that the expression levels of *Pvul-GASA-16* and *-23* genes have decreased under salt stress conditions compared to the non-treated control, while the expression levels of *Pvul-GASA-1* and *Pvul-GASA-18* have increased. In the root, while the expression level of *Pvul-GASA-1* gene has decreased under salt stress conditions compared to the non-treated control, it was observed that the expression level of *Pvul-GASA-18* has increased. The fact that the *Pvul-GASA-18* gene showed a similar response in the leaf may indicate

that this gene play a role in response to stress in both root and leaf tissue. On the other hand, *Pvul-GASA-12* gene was found to be highly expressed independent of stress in the root (Figure 8). Moreover, a model which showed the regulation of *Pvul-GASA* genes under salt stress conditions based on RNAseq data was also presented in Figure 9.

3.7. Roles of Pvul-GASA genes in response to salt stress via qRT-PCR analysis

Based on the RNAseq data, five *Pvul-GASA* genes (*Pvul-GASA-1, Pvul-GASA-12, Pvul-GASA-16, Pvul-GASA-18* and *Pvul-GASA-23)* have been selected to be used for qRT-PCR experiments as decribed in materials and methods section. For this aim, the expression levels of these genes have been analyzed under salt stress conditions in 'Zulbiye cv.' and 'Yakutiye cv.' since they are common bean cultivars, which have different responses against salt stress. According to the previous findings in the literature, 'Zulbiye cv.' and 'Yakutiye cv.' are known to be 'salt-resistant' and 'salt-susceptible' cultivars, respectively (Büyük et al., 2019). In correlation with the phenotypes of these cultivars, gene expression levels of the studied *Pvul-GASA* genes have differed. Only the *Pvul-GASA-1* gene led to increase in mRNA levels under salt stress conditions in both cultivars compared to their own controls while the rest have revealed decreases in mRNA levels. This increase in *Pvul-GASA-1* gene was also confirmed by RNAseq analysis for leaf tissue (Figure 9 and 10). However, the
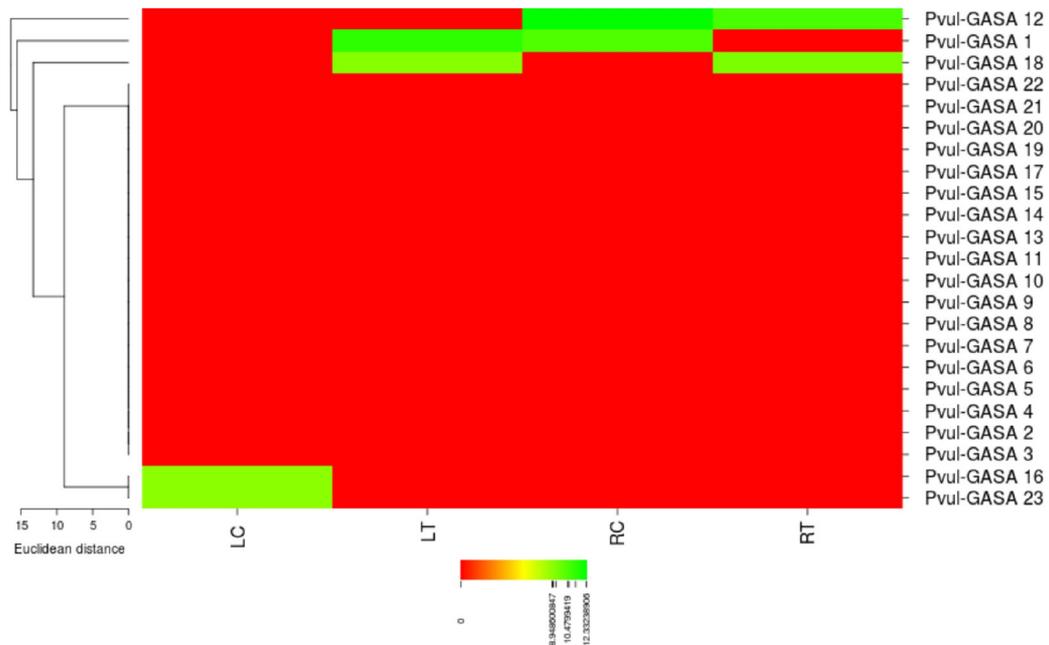
Figure 8. Heatmap of *Pvul-GASA* genes differentially expressed under control/salt stress conditions derived from RNAseq analysis. The log2-transformation of the average of expression values were used to generate the heat map with PermutMatrix software. Green and red in the color scale indicate high and low transcript expression, respectively.
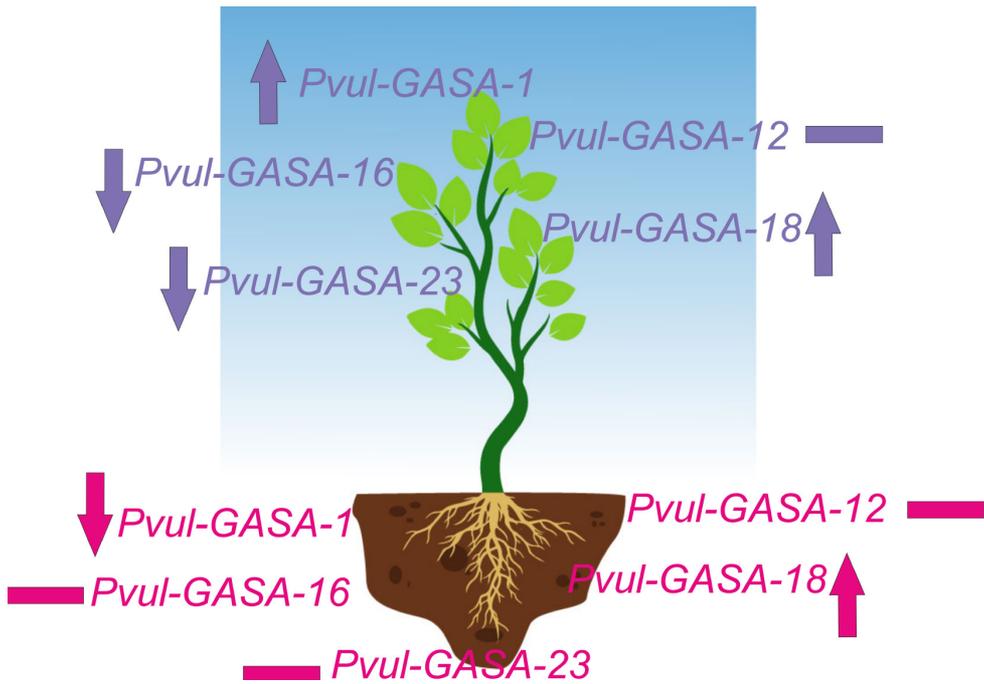
Figure 9. Representation of *Pvul-GASA* gene expressions on plant model under salt stress conditions based on RNAseq data.
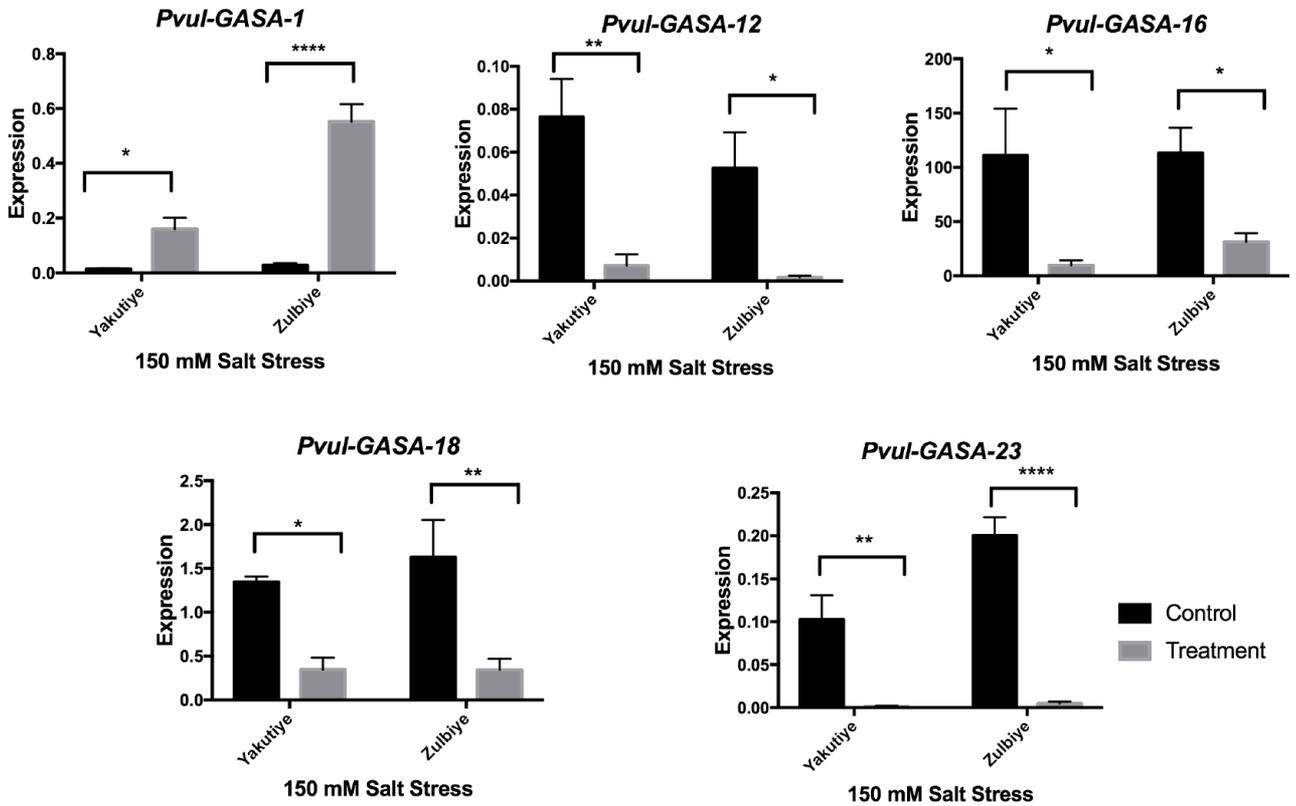
Figure 10. Five *Pvul-GASA* were selected and their expression assessed by qRT-PCR. The x-axis indicates cultivar type (Zulbiye cv.' and 'Yakutiye cv.'), and the y-axis indicates relative gene expression with error bars representing the standart error of the mean (SEM). The black box represents 'control' and the gray box represents 'salt stress'. Asterisks above bars indicate significant differences between the treatments.

changes in mRNA levels of *Pvul-GASA*-1 gene compared to the control was observed to be different between 'Zulbiye cv.' and 'Yakutiye cv.', and the increments in 'Zulbiye cv.' was statistically more pronounced according to the qRT-PCR data (Figure 10). In paralel to this, *Pvul-GASA*-1 was observed to be targeted by miR396, which is a well known miRNA that plays roles in salt stress response in many plant species according to the literature findings (Xie et al., 2015). This might support the role of *Pvul-GASA*-1 gene in response to salt stress in common bean (Figure 10).

Moreover, miRNA164 is another well known miRNA that plays role in stress response, and it was also found to target *Pvul-GASA*-18, which showed a stress related pattern according to the qRT-PCR and RNAseq data (Woo et al., 2009; Li et al., 2012). The mRNA levels of *Pvul-GASA*-12, *Pvul-GASA*-16, *Pvul-GASA*-18 and *Pvul-GASA*-23 genes were found to be decreased under salt stress conditions in both cultivars compared to their own controls. These decreases were found to be statistically more pronounced in 'Zulbiye cv.' for *Pvul-GASA*-18 and *Pvul-GASA*-23 genes while more pronounced in 'Yakutiye cv.' for *Pvul-GASA*-12 and *Pvul-GASA*-16 genes (Figure 10). On the other hand, *Pvul-GASA*-16 gene was shown to be the highest expressed gene in both cultivars under both control and salt stress conditions (Figure 10). In overall, it was seen that GASA genes may play a role in salt response in P. vulgaris, but in order to clearly distinguish the exact role of each *Pvul-GASA* genes, more detailed analyses are required in the future.

4. Conclusion

To sum up, the study herein reports a comprehensive genome-wide identification of GASA genes in P. vulgaris. A total of 23 GASA genes were identified, and were given the names; *Pvul-GASA*-1 to *Pvul-GASA*-23. To get insight into their biological functions in the genome of P. vulgaris, several analyses were conducted using many bioinformatic tools and genome databases as well. Besides that, the expression levels of *Pvul-GASA* were also evaluated using both RNAseq and qRT-PCR data under salt stress conditions and the importance of *Pvul-GASA* genes in salt stress response was also highlighted. Due to this study being the first in the identification of GASA genes in P. vulgaris, this study could be considered as a useful source for the future studies concerning GASA genes either in P. vulgaris or comparative different plant species.

Contributions

IB conceived, planned and oversaw the experiments. IB, AO, EI and MG carried out the experiments on the bioinformatic analysis, IB and AO carried out experiments on qRT-PCR analysis. IB, AO and EI analyzed and integrated the datasets and drafted the manuscript. SA critically read and contributed to improve the MS.

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Gene Names	Forward primer	Reverse primer
GASA-1	TCGCTTCTTCTGCTTCATCTC	CCACATGCTCCGTTACAATCTA
GASA-12	GTGTACCCTCCTCCTCTATCTC	TGCCCTCAAGCACAGTTT
GASA-16	GACTCTTTATTCTTGCCATTCTTCTAC	GCCACATTCTTAGTTCCTCCA
GASA-18	GAGATGTAGCAGGACCCAATAC	AGGGCACACAGCCTTATTAC
GASA-23	GGCAAACGATGCTGCTTATC	CTGTGTCTGGCTACATCTTCTT

ACCESSION	Name	Integrated Signature(s)	Go Terms BP / MF/ CC
IPR000048	IQ motif, EF-hand binding site	SM00015 PF00612 PS50096	protein binding
IPR000222	PPM-type phosphatase, divalent cation binding	PS01032	cation binding
IPR000634	Serine/threonine dehydratase, pyridoxal-phosphate-binding site	PS00165	pyridoxal phosphate binding cellular amino acid metabolic process
IPR001216	Cysteine synthase/cystathionine beta-synthase, pyridoxal-phosphate attachment site	PS00901	cysteine biosynthetic process from serine
IPR001431	Peptidase M16, zinc-binding site	PS00143	proteolysis metalloendopeptidase activity
IPR001505	Copper centre Cu(A)	PS00078	copper ion binding
IPR001882	Biotin-binding site	PS00188	
IPR001917	Aminotransferase, class-II, pyridoxal-phosphate binding site	PS00599	transferase activity
IPR002226	Catalase haem-binding site	PS00437	heme binding
IPR002355	Multicopper oxidase, copper-binding site	PS00080	copper ion binding
IPR003016	2-oxo acid dehydrogenase, lipoyl-binding site	PS00189	
IPR003952	Fumarate reductase/succinate dehydrogenase, FAD-binding site	PS00504	oxidoreductase activity oxidation-reduction process
IPR004035	Endonuclease III, iron-sulphur binding site	PS00764	
IPR004163	Coenzyme A transferase binding site	PS01273	CoA-transferase activity
IPR004838	Aminotransferases, class-I, pyridoxal-phosphate-binding site	PS00105	pyridoxal phosphate binding catalytic activity biosynthetic process
IPR006058	2Fe-2S ferredoxin, iron-sulphur binding site	PS00197	2 iron, 2 sulfur cluster binding
IPR006066	Nitrite/sulphite reductase iron-sulphur/ sirohaem-binding site	PR00397 PS00365	heme binding oxidoreductase activity oxidation-reduction process iron-sulfur cluster binding
IPR006093	Oxygen oxidoreductase covalent FAD-binding site	PS00862	oxidoreductase activity oxidation-reduction process
IPR006184	6-phosphogluconate-binding site	PS00461	pentose-phosphate shunt phosphogluconate dehydrogenase (decarboxylating) activity oxidation-reduction process
IPR013516	Phytochrome chromophore binding site	PS00245	protein-chromophore linkage

ID	Development					
Pvul-GASA-1	AAGAA-motif			O2-site		
Pvul-GASA-2		HD-Zip 1		O2-site	GCN4_motif	
Pvul-GASA-3		HD-Zip 1				
Pvul-GASA-4		HD-Zip 3				
Pvul-GASA-5	AAGAA-motif					
Pvul-GASA-6	AAGAA-motif		CAT-box	O2-site	GCN4_motif	circadian
Pvul-GASA-7	AAGAA-motif					
Pvul-GASA-8	AAGAA-motif				GCN4_motif	
Pvul-GASA-9	AAGAA-motif			O2-site		
Pvul-GASA-10			CAT-box	O2-site		circadian
Pvul-GASA-11	AAGAA-motif			O2-site		
Pvul-GASA-12	AAGAA-motif			O2-site	GCN4_motif	
Pvul-GASA-13					GCN4_motif	
Pvul-GASA-14	AAGAA-motif	HD-Zip 1				
Pvul-GASA-15	AAGAA-motif				GCN4_motif	
Pvul-GASA-16	AAGAA-motif					
Pvul-GASA-17	AAGAA-motif	HD-Zip 1	CAT-box			
Pvul-GASA-18	AAGAA-motif	HD-Zip 1	CAT-box			
Pvul-GASA-19	AAGAA-motif					circadian
Pvul-GASA-20	AAGAA-motif		CAT-box			
Pvul-GASA-21	AAGAA-motif		CAT-box	O2-site		
Pvul-GASA-22	AAGAA-motif	HD-Zip 1				circadian
Pvul-GASA-23	AAGAA-motif		CAT-box	O2-site		

ID	Environmental Stress						
Pvul-GASA-1	ARE			MYC	W box	WUN-motif	
Pvul-GASA-2	ARE	LTR					TC-rich repeats
Pvul-GASA-3	ARE	LTR		MYC			TC-rich repeats
Pvul-GASA-4				MYC		WUN-motif	TC-rich repeats
Pvul-GASA-5	ARE	LTR	MBS	MYC		WUN-motif	TC-rich repeats
Pvul-GASA-6	ARE	LTR	MBS	MYC		WUN-motif	
Pvul-GASA-7	ARE			MYC		WUN-motif	
Pvul-GASA-8							TC-rich repeats
Pvul-GASA-9	ARE	LTR	MBS	MYC	W box		TC-rich repeats
Pvul-GASA-10	ARE			MYC	W box		
Pvul-GASA-11	ARE		MBS	MYC	W box	WUN-motif	
Pvul-GASA-12	ARE	LTR	MBS	MYC			TC-rich repeats
Pvul-GASA-13	ARE			MYC	W box		TC-rich repeats
Pvul-GASA-14	ARE	LTR	MBS	MYC	W box	WUN-motif	
Pvul-GASA-15	ARE		MBS	MYC	W box		TC-rich repeats
Pvul-GASA-16				MYC			
Pvul-GASA-17	ARE			MYC			
Pvul-GASA-18	ARE			MYC			
Pvul-GASA-19	ARE		MBS	MYC		WUN-motif	
Pvul-GASA-20	ARE	LTR		MYC			TC-rich repeats
Pvul-GASA-21	ARE		MBS	MYC	W box		TC-rich repeats
Pvul-GASA-22	ARE			MYC	W box		
Pvul-GASA-23	ARE		MBS	MYC		WUN-motif	TC-rich repeats

ID	Hormone							
Pvul-GASA-1	ABRE		ERE					
Pvul-GASA-2	ABRE		ERE					
Pvul-GASA-3		P-box	ERE					
Pvul-GASA-4	ABRE	P-box	ERE	CGTCA-motif			TGACG-motif	
Pvul-GASA-5	ABRE	P-box	ERE					
Pvul-GASA-6	ABRE							
Pvul-GASA-7		P-box	ERE		TATC-box	TCA-element		
Pvul-GASA-8	ABRE		ERE	CGTCA-motif			TGACG-motif	
Pvul-GASA-9	ABRE		ERE					TGA-element
Pvul-GASA-10	ABRE	P-box	ERE	CGTCA-motif	TATC-box		TGACG-motif	
Pvul-GASA-11	ABRE		ERE	CGTCA-motif	TATC-box	TCA-element	TGACG-motif	TGA-element
Pvul-GASA-12	ABRE		ERE	CGTCA-motif	TATC-box	TCA-element	TGACG-motif	
Pvul-GASA-13	ABRE		ERE	CGTCA-motif		TGA-element	TGACG-motif	
Pvul-GASA-14		P-box	ERE			TCA-element		
Pvul-GASA-15	TGA-box			CGTCA-motif			TGACG-motif	
Pvul-GASA-16			ERE	CGTCA-motif		TCA-element	TGACG-motif	
Pvul-GASA-17	ABRE		ERE			TCA-element		
Pvul-GASA-18	ABRE		ERE			TCA-element		
Pvul-GASA-19		P-box	ERE		TATC-box			
Pvul-GASA-20	ABRE		ERE	CGTCA-motif	TATC-box	TCA-element	TGACG-motif	
Pvul-GASA-21	ABRE		ERE		TATC-box	TCA-element		
Pvul-GASA-22	ABRE	P-box	ERE					
Pvul-GASA-23	ABRE		ERE	CGTCA-motif		TCA-element	TGACG-motif	TGA-element

ID	Light													
Pvul-GASA-1		AE-box		Box 4		G-box	GATA-motif							LAMP-element
Pvul-GASA-2			ACE	Box 4	AT1-motif	G-box		GA-motif	GT1-motif					
Pvul-GASA-3		AE-box		Box 4	AT1-motif				GT1-motif					
Pvul-GASA-4	3-AF1 binding site			Box 4	AT1-motif	G-box			GT1-motif		TCT-motif		Box II	
Pvul-GASA-5		AE-box		Box 4	AT1-motif	G-box			GT1-motif		TCT-motif			
Pvul-GASA-6		AE-box		Box 4		G-Box	GATA-motif	GT1-motif		Gap-box	TCT-motif	chs-CMA1a		
Pvul-GASA-7	TCT-motif			Box 4					GT1-motif			chs-CMA1a		
Pvul-GASA-8		AE-box		Box 4	AT1-motif	G-box								
Pvul-GASA-9	AT1-motif			Box 4								chs-CMA1a		
Pvul-GASA-10				Box 4	AT1-motif	G-box	GATA-motif		GT1-motif		TCT-motif		TCCC-motif	
Pvul-GASA-11		AE-box		Box 4		G-Box	GATA-motif	GA-motif		Gap-box	TCT-motif			
Pvul-GASA-12				Box 4		G-Box	GATA-motif	GA-motif	GT1-motif				Box II	
Pvul-GASA-13				Box 4	AT1-motif	G-box		GA-motif	GT1-motif		TCT-motif			
Pvul-GASA-14	3-AF1 binding site			Box 4					GT1-motif					
Pvul-GASA-15			ACE	Box 4					GT1-motif		TCT-motif	chs-CMA1a		
Pvul-GASA-16				Box 4		G-box	GATA-motif	GA-motif	GT1-motif		TCT-motif			
Pvul-GASA-17	3-AF1 binding site	AE-box		Box 4		G-box			GT1-motif					
Pvul-GASA-18	3-AF1 binding site	AE-box		Box 4		G-box			GT1-motif					
Pvul-GASA-19	3-AF1 binding site			Box 4	AT1-motif				GT1-motif			chs-CMA1a		
Pvul-GASA-20			ACE	Box 4		G-Box	GATA-motif	GA-motif	LAMP-element					
Pvul-GASA-21				Box 4		G-Box			GT1-motif					
Pvul-GASA-22				Box 4	AT1-motif	G-box						chs-CMA1a		
Pvul-GASA-23	3-AF1 binding site			Box 4		G-Box			GT1-motif				Box II	

ID	Other			Promoter		Site binding related			Biotic stress	
Pvul-GASA-1	CTAG-motif		Unnamed__4	CAAT-box	TATA-box	AT-rich sequence	Unnamed__1	Unnamed__6	MYB	
Pvul-GASA-2		ATCT-motif	Unnamed__4	CAAT-box	TATA-box		Unnamed__1	Unnamed__6	MYB	STRE
Pvul-GASA-3	CTAG-motif		Unnamed__4	CAAT-box	TATA-box			Unnamed__6	MYB	
Pvul-GASA-4			Unnamed__4	CAAT-box	TATA-box		Unnamed__1		MYB	STRE
Pvul-GASA-5			Unnamed__4	CAAT-box	TATA-box		Unnamed__1	Unnamed__6	MYB	STRE
Pvul-GASA-6	CTAG-motif		Unnamed__4	CAAT-box	TATA-box	AT-rich element	Unnamed__1	Unnamed__6	MYB	STRE
Pvul-GASA-7			Unnamed__4	CAAT-box	TATA-box		Unnamed__1		MYB	STRE
Pvul-GASA-8			Unnamed__4	CAAT-box	TATA-box					
Pvul-GASA-9			Unnamed__4	CAAT-box	TATA-box	AT-rich element			MYB	STRE
Pvul-GASA-10			Unnamed__4	CAAT-box	TATA-box	AT-rich element			MYB	STRE
Pvul-GASA-11		ATCT-motif	Unnamed__4	CAAT-box	TATA-box	AT-rich sequence			MYB	
Pvul-GASA-12			Unnamed__4	CAAT-box	TATA-box	AT-rich element	Unnamed__1		MYB	
Pvul-GASA-13			Unnamed__4	CAAT-box	TATA-box	AT-rich sequence	Unnamed__1	Unnamed__6	MYB	
Pvul-GASA-14				CAAT-box	TATA-box			Unnamed__6	MYB	
Pvul-GASA-15		ATCT-motif	Unnamed__4	CAAT-box	TATA-box		Unnamed__1	Unnamed__6	MYB	
Pvul-GASA-16			Unnamed__4	CAAT-box	TATA-box		Unnamed__1		MYB	STRE
Pvul-GASA-17			Unnamed__4	CAAT-box	TATA-box			Unnamed__6	Myb	
Pvul-GASA-18			Unnamed__4	CAAT-box	TATA-box			Unnamed__6	Myb	
Pvul-GASA-19	TCT-motif		Unnamed__4	CAAT-box	TATA-box				MYB	STRE
Pvul-GASA-20	TCT-motif		Unnamed__4	CAAT-box	TATA-box				MYB	STRE
Pvul-GASA-21			Unnamed__4	CAAT-box	TATA-box		Unnamed__1	Unnamed__6	MYB	STRE
Pvul-GASA-22		ATCT-motif	Unnamed__4	CAAT-box	TATA-box					STRE
Pvul-GASA-23		ATCT-motif	Unnamed__4	CAAT-box	TATA-box	AT-rich element	Unnamed__1	Unnamed__6	MYB	

miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_aligned_fragment	Target_aligned_fragment
Arachis hypogaea					
ahy-miR3520-3p	Pvul-GASA14	5.0	−1.0	AAGGGAGACGUUUGAAUUAUC	CAGAGUGCAAAUGUGUUCCUU
aly-miR164a-5p	Pvul-GASA3	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
aly-miR164b-5p	Pvul-GASA3	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
aly-miR164c-5p	Pvul-GASA3	4.5	−1.0	UGGAGAAGCAGGGCACGUGCG	CCUUCUUGCCUUGCUUCUCCU
aly-miR169m-3p	Pvul-GASA9	5.0	−1.0	GGCAGUCUUCUUGGCUAUC	GGUAACAAAGAAGAAUGUC
aly-miR169m-3p	Pvul-GASA20	5.0	−1.0	GGCAGUCUUCUUGGCUAUC	GGUAACCAAGAAGUGUGUC
aly-miR172d-5p	Pvul-GASA22	4.5	−1.0	GCAACAUCUUCAAGAUUCAGA	UUCUUGUCUUGGGGAUGUUGC
aly-miR3433-3p	Pvul-GASA20	5.0	−1.0	UCACAGUUCUUGAUUACCCAC	UCCGGUAACCAAGAAGUGUGU
aly-miR397b-3p	Pvul-GASA20	5.0	−1.0	UCAGCGUUGCAUUCAAUUAUG	GCAGAUAGAUUGCAACGCUGC
aly-miR4221	Pvul-GASA14	4.5	−1.0	AAGAGUUCAAAAGUAGUGAAGA	UGUUCUCUUCUUCUGAGUUCUU
aly-miR4231	Pvul-GASA17	4.5	−1.0	UAGACCUUUGUGUUGCCAUCG	CUAUGGCAACAAGGAGGUGUG
aly-miR4231	Pvul-GASA6	4.5	−1.0	UAGACCUUUGUGUUGCCAUCG	UUAUGGCAACAAGCAGGUUUG
aly-miR4231	Pvul-GASA10	4.5	−1.0	UAGACCUUUGUGUUGCCAUCG	UUAUGGUAACAGAGAGGUGUG
aly-miR4237	Pvul-GASA8	5.0	−1.0	AAACGUAAACAUAUAUAAUCGA	GCUGUGAUAAAUGUUUAUGUGU
aly-miR4237	Pvul-GASA9	5.0	−1.0	AAACGUAAACAUAUAUAAUCGA	GUUGUGAUAAAUGUUUAUGUGU
aly-miR4237	Pvul-GASA7	5.0	−1.0	AAACGUAAACAUAUAUAAUCGA	GUUGUGAUAAAUGUUUAUGUGU
aly-miR827-3p	Pvul-GASA2	5.0	−1.0	UUAGAUGACCAUCAACAAACG	AUCUUGUUGAUGCUCAUCAAU
aly-miR831-5p	Pvul-GASA8	4.0	−1.0	AGAAGAGGUACAAGGAGAUGAGA	AAAUUUGUGUUUGUACUUCUUCU
aly-miR831-5p	Pvul-GASA21	5.0	−1.0	AGAAGAGGUACAAGGAGAUGAGA	AAUGCUCUCCUUGUGUGCCUUCU
aly-miR834-3p	Pvul-GASA10	4.5	−1.0	UGGUAGCAGUAGCGGUGGUAA	UUACUGUUGCUGCUGCUGCUC
aly-miR834-3p	Pvul-GASA17	5.0	−1.0	UGGUAGCAGUAGCGGUGGUAA	CUAUGGUUGCUGUUGCUACCU
aly-miR835-5p	Pvul-GASA2	5.0	−1.0	UUCUUGCAUAUGUUCUUUAUC	GUGCAAGAACAAAUGCAAGGU
aly-miR837-5p	Pvul-GASA13	5.0	−1.0	CAUUGUUUCUUGUUUUUUUCA	CUACAAUGACAAGAAAAAAUA
aly-miR838-5p	Pvul-GASA6	5.0	−1.0	UGCAAGAAUGAGAAGCAAAGC	CAAAUGCUGCUUGUUCUUGUA
aly-miR838-5p	Pvul-GASA1	5.0	−1.0	UGCAAGAAUGAGAAGCAAAGC	UACUUGCUUCUC-UUCUUGCC
aly-miR841	Pvul-GASA22	4.5	−1.0	UACGACCCACUGGAAACUAAA	CAUAGAUUGUGGUGGGUUGUG
aly-miR859-3p	Pvul-GASA4	5.0	−1.0	UGAUUUUACAAUAGAUAGAUA	AUUGUGAUUCUUGUAGAAUCA
aly-miR869-5p	Pvul-GASA9	5.0	−1.0	CACUUAUCUCAACCCUAGUGA	UAACUUGUGUUGUGAUAAAUG
Aegilops tauschii					
ata-miR164a-5p	Pvul-GASA3	4.5	−1.0	UGGAGAAGCAGGGCACGUGCU	CCUUCUUGCCUUGCUUCUCCU
ata-miR164b-5p	Pvul-GASA3	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ata-miR164c-5p	Pvul-GASA3	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ata-miR393-5p	Pvul-GASA14	5.0	−1.0	UUCCAAAGGGAUCGCAUUGAU	GCAAAUGUGUUCCUUCUCGGAA
ata-miR396a-5p	Pvul-GASA1	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGA
ata-miR396a-5p	Pvul-GASA4	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGA
ata-miR396a-5p	Pvul-GASA2	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGA
ata-miR396a-5p	Pvul-GASA3	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGA
ata-miR396a-5p	Pvul-GASA20	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGA
ata-miR396b-5p	Pvul-GASA1	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGA
ata-miR396b-5p	Pvul-GASA4	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGA
ata-miR396b-5p	Pvul-GASA2	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGA
ata-miR396b-5p	Pvul-GASA3	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGA
ata-miR396b-5p	Pvul-GASA20	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGA
ata-miR396d-5p	Pvul-GASA1	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGA
ata-miR396d-5p	Pvul-GASA4	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGA

ata-miR396d-5p	*Pvul-GASA2*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGA
ata-miR396d-5p	*Pvul-GASA3*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGA
ata-miR396d-5p	*Pvul-GASA20*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGA
ata-miR408-5p	*Pvul-GASA1*	5.0	−1.0	CAGGGAUGGAGCAGAGCAAGG	GCUUCUUCUGCUUCAUCUCGU
ata-miR408-5p	*Pvul-GASA15*	4.5	−1.0	CAGGGAUGGAGCAGAGCAAGG	CUAUUUUCUGCUUCAUCCUUA
Arabidopsis thaliana					
ath-miR160c-3p	*Pvul-GASA19*	5.0	−1.0	CGUACAAGGAGUCAAGCAUGA	CUAUGCGUGCCUCCUGGUACC
ath-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ath-miR164b-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ath-miR164c-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCG	CCUUCUUGCCUUGCUUCUCCU
ath-miR172d-5p	*Pvul-GASA22*	4.5	−1.0	GCAACAUCUUCAAGAUUCAGA	UUCUUGUCUUGGGGAUGUUGC
ath-miR1886.1	*Pvul-GASA7*	3.5	−1.0	UGAGAGAAGUGAGAUGAAAUC	CAUUUCUUCUCAUCUUUCUCA
ath-miR1886.1	*Pvul-GASA8*	4.0	−1.0	UGAGAGAAGUGAGAUGAAAUC	UACUUCUUCUCAUCUCUCUCA
ath-miR1886.1	*Pvul-GASA9*	5.0	−1.0	UGAGAGAAGUGAGAUGAAAUC	CCUUUCUUCUCCUCUUUCUCA
ath-miR1886.2	*Pvul-GASA12*	4.5	−1.0	UGAGAUGAAAUCUUUGAUUGG	UACCUCAAAGGUUUUUUCUCA
ath-miR3440b-3p	*Pvul-GASA14*	5.0	−1.0	UGGAUUGGUCAAGGGAAGCGU	AAGCUUCUCUUUGCUACUCUA
ath-miR3440b-3p	*Pvul-GASA23*	5.0	−1.0	UGGAUUGGUCAAGGGAAGCGU	UGGCUCUCCUUGGCCUCUCCA
ath-miR398a-5p	*Pvul-GASA6*	4.5	−1.0	AAGGAGUGGCAUGUGAACACA	CUUGUUCAAAUGCUGCUUGUU
ath-miR398a-5p	*Pvul-GASA5*	4.5	−1.0	AAGGAGUGGCAUGUGAACACA	UUUGCUGCUAUGCUACUUCUU
ath-miR4221	*Pvul-GASA22*	5.0	−1.0	UUUUCCUCUGUUGAAUUCUUGC	AAGAGGAAACAGCAGAAGAAGA
ath-miR426	*Pvul-GASA14*	4.5	−1.0	UUUUGGAAAUUUGUCCUUACG	GUUAAGGAUAGGUGUCUGAAG
ath-miR5014a-5p	*Pvul-GASA11*	3.5	−1.0	ACACUUAGUUUUGUACAACAU	GGAUUGUGCAAAACAAGGUGU
ath-miR5014a-5p	*Pvul-GASA11*	5.0	−1.0	ACACUUAGUUUUGUACAACAU	CAUGGCAACAAAACUAAGUGU
ath-miR5019	*Pvul-GASA2*	5.0	−1.0	UGUUGGGAAAGAAAAACUCUU	GCAAGGUUCUCUUUUUCAGCA
ath-miR5021	*Pvul-GASA9*	3.5	−1.0	UGAGAAGAAGAAGAAGAAAA	CUUUCUUCUCCUCUUUCUCA
ath-miR5021	*Pvul-GASA1*	4.5	−1.0	UGAGAAGAAGAAGAAGAAAA	GCUUCUUCUGCUUCAUCUCG
ath-miR5629	*Pvul-GASA14*	5.0	−1.0	UUAGGGUAGUUAACGGAAGUUA	AAGCUUCUCUUUGCUACUCUAC
ath-miR5636	*Pvul-GASA2*	4.0	−1.0	CGUAGUUGCAGAGCUUGACGG	UUGUCAA-CGCUGCAACUGCG
ath-miR5636	*Pvul-GASA3*	4.0	−1.0	CGUAGUUGCAGAGCUUGACGG	UUGUCAA-CGCUGCAACUGCG
ath-miR5636	*Pvul-GASA1*	5.0	−1.0	CGUAGUUGCAGAGCUUGACGG	CUGUCAA-CGUUGCAACUGUG
ath-miR5639-5p	*Pvul-GASA22*	5.0	−1.0	UAGUCCACUGUGGUCUAAGGC	GACAUAGAUUGUGGUGGGUUG
ath-miR5641	*Pvul-GASA14*	5.0	−1.0	UGGAAGAAGAUGAUAGAAUUA	CUACUUUGUUCUCUUCUUCUG
ath-miR5666	*Pvul-GASA21*	5.0	−1.0	AUGGGACAUCGAGCAUUUAAU	GACAGAUGCUUGAAGUUCUGU
ath-miR5998a	*Pvul-GASA22*	3.5	−1.0	ACAGUUUGUGUUUUGUUUUGU	CUAAUGCAAGACAUAGAUUGU
ath-miR5998a	*Pvul-GASA11*	3.5	−1.0	ACAGUUUGUGUUUUGUUUUGU	CUAAUGCAAGACAUAGAUUGU
ath-miR5998b	*Pvul-GASA11*	3.5	−1.0	ACAGUUUGUGUUUUGUUUUGU	CUAAUGCAAGACAUAGAUUGU
ath-miR5998b	*Pvul-GASA22*	3.5	−1.0	ACAGUUUGUGUUUUGUUUUGU	CUAAUGCAAGACAUAGAUUGU
ath-miR8165	*Pvul-GASA2*	3.5	−1.0	AAUGGAGGCAAGUGUGAAGGA	AAGUUCAUACUUGCUUCCCUU
ath-miR8165	*Pvul-GASA3*	4.5	−1.0	AAUGGAGGCAAGUGUGAAGGA	AAGCUCAUACUUGCUUCCCUU
ath-miR8165	*Pvul-GASA1*	5.0	−1.0	AAUGGAGGCAAGUGUGAAGGA	AAACUCAUACUUGCUUCUCUU
ath-miR822-5p	*Pvul-GASA6*	5.0	−1.0	UGCGGGAAGCAUUUGCACAUG	CUUGUUCAAAUGCUGCUUGUU
ath-miR827	*Pvul-GASA2*	5.0	−1.0	UUAGAUGACCAUCAACAAACU	AUCUUGUUGAUGCUCAUCAAU
ath-miR832-3p	*Pvul-GASA15*	5.0	−1.0	UUGAUUCCCAAUCCAAGCAAG	UAUGCAUGAGUUGGGGAUCCA
ath-miR833a-5p	*Pvul-GASA13*	5.0	−1.0	UGUUUGUUGUACUCGGUCUAGU	GCAGGACCCAGUAUCACAAGCC

ath-miR833a-5p	*Pvul-GASA23*	5.0	−1.0	UGUUUGUUGUACUCGGUCUAGU	GCCAGACACAGUACCACAAGCC
ath-miR833b	*Pvul-GASA12*	4.5	−1.0	UGUUUGUUGACAUCGGUCUAG	GUUGACUCAUGGCAACAAAUA
ath-miR834	*Pvul-GASA10*	4.5	−1.0	UGGUAGCAGUAGCGGUGGUAA	UUACUGUUGCUGCUGCUGCUC
ath-miR834	*Pvul-GASA17*	5.0	−1.0	UGGUAGCAGUAGCGGUGGUAA	CUAUGGUUGCUGUUGCUACCU
ath-miR835-3p	*Pvul-GASA21*	4.5	−1.0	UGGAGAAGAUACGCAAGAAAG	UCUCCUUGUGUGCCUUCUCCU
ath-miR835-5p	*Pvul-GASA2*	5.0	−1.0	UUCUUGCAUAUGUUCUUUAUC	GUGCAAGAACAAAUGCAAGGU
ath-miR851-5p	*Pvul-GASA10*	5.0	−1.0	UCUCGGUUCGCGAUCCACAAG	UUUGUGGAUUGUGGAGAGAGG
ath-miR862-5p	*Pvul-GASA12*	5.0	−1.0	UCCAAUAGGUCGAGCAUGUGC	GGGCAUGCACGACCUGUUGUU
Amborella trichopoda					
atr-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
atr-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
atr-miR396a	*Pvul-GASA20*	4.5	−1.0	UCCACAGGCUUUCUUGAACAU	AUGUGUCACAGAGCCUGUGGA
atr-miR396a	*Pvul-GASA1*	4.5	−1.0	UCCACAGGCUUUCUUGAACAU	CUCUGCAAAAGAGCUUGUGGA
atr-miR396a	*Pvul-GASA4*	4.5	−1.0	UCCACAGGCUUUCUUGAACAU	CUAUGCAAGAGGGCAUGUGGA
atr-miR396a	*Pvul-GASA2*	5.0	−1.0	UCCACAGGCUUUCUUGAACAU	CUAUGCGAAAGAGCUUGUGGA
atr-miR396a	*Pvul-GASA3*	5.0	−1.0	UCCACAGGCUUUCUUGAACAU	CUCUGCGAAAGAGCUUGUGGA
Bruguiera cylindrica					
bcy-miR529	*Pvul-GASA12*	5.0	−1.0	GAAGAAGAGAGAUGG-UAGAG	UUCUAGCCAUCUUUCUUCUGG
bcy-miR529	*Pvul-GASA20*	5.0	−1.0	GAAGAAGAGAGAUGGUAGAG	UGCUAUCCUUUCUCCUCUUC
Brachypodium distachyon					
bdi-miR164a-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
bdi-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
bdi-miR164c-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCU	CCUUCUUGCCUUGCUUCUCCU
bdi-miR164e	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
bdi-miR164f	*Pvul-GASA9*	3.5	−1.0	UGGAGAAGAAGGGCACAUGCA	UGUGUGGGCCUUUCUUCUCCU
bdi-miR319a	*Pvul-GASA5*	5.0	−1.0	UGAGGGAGCUUUCUUCUGUCC	GGGCAAGGGAAAGUGCCCUUA
bdi-miR395j-5p	*Pvul-GASA10*	5.0	−1.0	GUUUCCCGCAAGCACUUCACG	GCACAAGAGCUUGCGGGACAU
bdi-miR395p-5p	*Pvul-GASA18*	4.5	−1.0	GUUUCCUGCAAGCACUUCACG	UCAGAAGUGCU-GCAGGAAAU
bdi-miR396a-5p	*Pvul-GASA4*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGA
bdi-miR396a-5p	*Pvul-GASA1*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGA
bdi-miR396a-5p	*Pvul-GASA2*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGA
bdi-miR396a-5p	*Pvul-GASA3*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGA
bdi-miR396a-5p	*Pvul-GASA20*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGA
bdi-miR396b-5p	*Pvul-GASA4*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGA
bdi-miR396b-5p	*Pvul-GASA1*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGA
bdi-miR396b-5p	*Pvul-GASA2*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGA
bdi-miR396b-5p	*Pvul-GASA3*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGA
bdi-miR396b-5p	*Pvul-GASA20*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGA
bdi-miR408-5p	*Pvul-GASA15*	3.5	−1.0	CAGGGAUGGAGCAGAGCAUGG	CUAUUUUCUGCUUCAUCCUUA
bdi-miR437	*Pvul-GASA23*	5.0	−1.0	GAACUUAGAGAAGUUUGACUU	UCUCUAAGCUUCUCUGCGUUC
bdi-miR444c	*Pvul-GASA18*	5.0	−1.0	UGCAGUUGUUGUCUCAAGCUU	GCCCUUGCUACAACAACUGGA
bdi-miR444d	*Pvul-GASA18*	5.0	−1.0	UGCAGUUGUUGUCUCAAGCUU	GCCCUUGCUACAACAACUGGA
bdi-miR5058	*Pvul-GASA8*	5.0	−1.0	AACAGUUGAGGGAUGAAAAACA	UGGUUUUCGUCUCUCAACUUGC
bdi-miR530a	*Pvul-GASA22*	5.0	−1.0	UGCAUUUGCACCUGCACCUAC	CUGUGUG-AGGUGCAAGUGUG

bdi-miR530a	*Pvul-GASA11*	5.0	−1.0	UGCAUUUGCACCUGCACCUAC	CUGUGUG-AGGUGCAAGUGUG
bdi-miR530b	*Pvul-GASA22*	5.0	−1.0	UGCAUUUGCACCUGCACCUAC	CUGUGUG-AGGUGCAAGUGUG
bdi-miR530b	*Pvul-GASA11*	5.0	−1.0	UGCAUUUGCACCUGCACCUAC	CUGUGUG-AGGUGCAAGUGUG
bdi-miR7729a-5p	*Pvul-GASA14*	5.0	−1.0	UGUUUUCAUAGGCCAUGUAGAGC	GUCAGCCAUGGCCUAUGAAGAAU
bdi-miR7729b-5p	*Pvul-GASA14*	5.0	−1.0	UGUUUUCAUAGGCCAUGUAGAGC	GUCAGCCAUGGCCUAUGAAGAAU
bdi-miR7736-3p	*Pvul-GASA13*	5.0	−1.0	UGACAUAUCUGAUGGUAAAGG	GUUUUUCUGUCAGAAGUGUUG
bdi-miR7736-3p	*Pvul-GASA19*	5.0	−1.0	UGACAUAUCUGAUGGUAAAGG	GUUUUUCUGUCAGAAGUGUUG
bdi-miR7753-3p	*Pvul-GASA6*	5.0	−1.0	UGAGCAAGGGAGAAGAC-AUGG	CCAUUGUGCUCUUCCUUGUUCA
bdi-miR7754-5p	*Pvul-GASA8*	4.5	−1.0	AUGUUCUCUCGGCUGAGGAAC	UCUCUUAAGCCUGGAGAAUGU
bdi-miR7769-3p	*Pvul-GASA15*	5.0	−1.0	UGUCAUGUUGGCACUGAUGGG	AUGGUCGCUGCCAACAAGAUA
Bruguiera gymnorhiza					
bgy-miR529	*Pvul-GASA12*	5.0	−1.0	GAAGAAGAGAGAUGG-UAGAG	UUCUAGCCAUCUUUCUUCUGG
bgy-miR529	*Pvul-GASA20*	5.0	−1.0	GAAGAAGAGAGAUGGUAGAG	UGCUAUCCUUUCUCCUCUUC
Brassica napus					
bna-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
bna-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCG	CCUUCUUGCCUUGCUUCUCCU
bna-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCG	CCUUCUUGCCUUGCUUCUCCU
bna-miR164d	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCG	CCUUCUUGCCUUGCUUCUCCU
Brassica oleracea					
bol-miR9408	*Pvul-GASA16*	4.5	−1.0	GUUUCAUCUUAGAGAAUGUUGUC	AUGAAUGUUCUCGAAGAUGCAGC
Brassica rapa					
bra-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
bra-miR164b-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCG	CCUUCUUGCCUUGCUUCUCCU
bra-miR164c-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCG	CCUUCUUGCCUUGCUUCUCCU
bra-miR164d-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCG	CCUUCUUGCCUUGCUUCUCCU
bra-miR164e-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCAA	CCCUUCUUGCCUUGCUUCUCCU
bra-miR2111b-3p	*Pvul-GASA22*	5.0	−1.0	AUCCUCGGGAUACGGAUUACC	CGUAUUUCUUGUCUUGGGGAU
bra-miR408-5p	*Pvul-GASA5*	5.0	−1.0	GGGAGCCAGGGAAGAGGCAGU	UAUGCUACUUCUUUGCCUUCU
bra-miR5713	*Pvul-GASA8*	5.0	−1.0	AGGCUUAGAAGAACGUUUGUU	GGCGAAGGAUCUCUUAAGCCU
bra-miR6032-5p	*Pvul-GASA22*	5.0	−1.0	AACAUGGAGCAUCAACAGAUC	UUGCUGUUGGUGUGCCUUGUU
bra-miR9408-3p	*Pvul-GASA16*	4.5	−1.0	UUUCAUCUUAGAGAAUGUUGUU	AUGAAUGUUCUCGAAGAUGCAG
bra-miR9408-5p	*Pvul-GASA9*	5.0	−1.0	CAACAGUCUCAGGAUGGAAAA	UGUUCCAUC-UGGGACUGUCG
Cynara cardunculus					
cca-miR164	*Pvul-GASA3*	5.0	−1.0	UGGAGAAGCAGGGUACGUGCA	CCUUCUUGCCUUGCUUCUCCU
cca-miR393	*Pvul-GASA4*	5.0	−1.0	UCCAAAGGAAUCGCAUUGAUCC	AAGUCAUUGUGAUUCUUGUAGA
cca-miR6108a	*Pvul-GASA7*	5.0	−1.0	UGAGAAGCGUAAGAAGGGAUC	CAUUUCUUCUCAUCUUUCUCA
cca-miR6108b	*Pvul-GASA7*	5.0	−1.0	UGAGAAGCGUAAGAAGGGAUC	CAUUUCUUCUCAUCUUUCUCA
cca-miR6108g	*Pvul-GASA7*	5.0	−1.0	UGAGAAGCGUAAGAAGGGAUC	CAUUUCUUCUCAUCUUUCUCA
Cunninghamia lanceolata					
cln-miR164	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCG	CCUUCUUGCCUUGCUUCUCCU
Cucumis melo					
cme-miR156j	*Pvul-GASA23*	5.0	−1.0	GUUGACAGAAGAGAGUGAGCAC	CCAUGCAUGUUCUUCUGUCAAA
cme-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCU	CCUUCUUGCCUUGCUUCUCCU
cme-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU

cme-miR164d	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
cme-miR7130	*Pvul-GASA10*	4.5	−1.0	GUUUGGAAUGUGCGAGAUGUGUGC	AAGGCCAUCUCACCCAUUCUGAGC
cme-miR854	*Pvul-GASA17*	4.5	−1.0	GAUGAGGAUAGUGAGGAGGAG	UGCCUCCUUGCAAUCCUUCUC
cme-miR854	*Pvul-GASA13*	5.0	−1.0	GAUGAGGAUAGUGAGGAGGAG	GCUUUCAUCAUUGCCCUCAUU
Carica papaya					
cpa-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
cpa-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
cpa-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
cpa-miR164d	*Pvul-GASA3*	5.0	−1.0	UGGAGAAGGGGAGCACGUGCA	CAUACUUGCUUCCCUUCUUGC
cpa-miR164e	*Pvul-GASA3*	5.0	−1.0	UGGAGAAGGGGAGCACGUGCA	CAUACUUGCUUCCCUUCUUGC
cpa-miR8142	*Pvul-GASA13*	4.5	−1.0	UGAGGUAAGUAGACAGUAAAGGUU	CUAAGUUACUUUCUGCUUUCAUCA
cpa-miR8146	*Pvul-GASA12*	5.0	−1.0	AGGAAGACGGUGAGUAGAAGCCAA	CAUUCUUCUUCUAGCCAUCUUUCU
cpa-miR8154	*Pvul-GASA19*	4.0	−1.0	CAGAGGAGGAGAUGAAGAGGGA	CUUCUUUUGGUCUCAUUCUCUG
cpa-miR8154	*Pvul-GASA5*	5.0	−1.0	CAGAGGAGGAGAUGAAGAGGGA	UACUUCUUUGCCUUCUCCUCAG
Chlamydomonas reinhardtii					
cre-miR1144b	*Pvul-GASA5*	5.0	−1.0	UGGGUAGUGUGGCGGCAGGCAG	UCAUUUGCUGCUAUGCUACUUC
cre-miR1157-3p	*Pvul-GASA20*	5.0	−1.0	UUCAGGUAGCGGGACCAGGUG	CUCCUCUUCCAUCUACCUGAA
cre-miR1158	*Pvul-GASA10*	5.0	−1.0	ACUUGGAGGAGGCCACUGGC	GCAAGUGUGUUCCUCCAGGU
cre-miR1159.1	*Pvul-GASA22*	5.0	−1.0	UGCCACAGUGCCCGAUUGCCG	GUGCACUAGGGCA-UGUGGCA
cre-miR1171	*Pvul-GASA6*	4.5	−1.0	UGGAGUGGAGUGGAGUGGAGUGG	AAACUCCAC-CCACUUAGCUCCA
cre-miR906-5p	*Pvul-GASA2*	4.0	−1.0	CGGUUGGUGGGCGUGAUCAGC	CUUGUUGAUGCUCAUCAAUCG
cre-miR906-5p	*Pvul-GASA1*	5.0	−1.0	CGGUUGGUGGGCGUGAUCAGC	CUCGUUGAUGCUCAUCAAUCG
cre-miR906-5p	*Pvul-GASA3*	5.0	−1.0	CGGUUGGUGGGCGUGAUCAGC	CUCGUUGAUGCUCAUCAAUCG
Citrus sinensis					
csi-miR1515	*Pvul-GASA17*	4.5	−1.0	UCAUUUUUGCGUGCAAUGAUCC	ACCUCGUUGUGCGCAUAGAUGC
csi-miR164	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
csi-miR172a-5p	*Pvul-GASA22*	5.0	−1.0	GCAGCGUCCUCAAGAUUCACA	UUCUUGUCUUGGGGAUGUUGC
csi-miR3950	*Pvul-GASA16*	5.0	−1.0	UUUUUCGGCAACAUGAUUUCU	GCAAGUCAUGUUGCCACAGAU
csi-miR482a-5p	*Pvul-GASA20*	5.0	−1.0	AGUGGGAGCGUGGGGUAAGAAG	UGCCUCUCUCCAAGCUUCUACU
csi-miR535	*Pvul-GASA9*	4.5	−1.0	UGACAAUGAGAGAGAGCACAC	GCGUG-UCUCUUUUAUUGUAA
csi-miR827	*Pvul-GASA2*	5.0	−1.0	UUAGAUGACCAUCAACAAACA	AUCUUGUUGAUGCUCAUCAAU
Citrus trifoliata					
ctr-miR164	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
Digitalis purpurea					
dpr-miR160	*Pvul-GASA19*	5.0	−1.0	UGCCUGGCUCCUUGUAUGCCA	CUUCACACAAGAAGCCAUGCA
Festuca arundinacea					
far-miR396	*Pvul-GASA1*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGA
far-miR396	*Pvul-GASA4*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGA
far-miR396	*Pvul-GASA2*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGA
far-miR396	*Pvul-GASA3*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGA
far-miR396	*Pvul-GASA20*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGA
Gossypium hirsutum					
ghr-miR164	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ghr-miR7507	*Pvul-GASA14*	4.5	−1.0	AAGGUAGUGAAGUAGGCAAUUGGG	UUCUCUUUGCUACUCUACUACUUU

ghr-miR827a	*Pvul-GASA2*	5.0	−1.0	UUAGAUGACCAUCAACAAACA	AUCUUGUUGAUGCUCAUCAAU
ghr-miR827b	*Pvul-GASA2*	5.0	−1.0	UUAGAUGACCAUCAACAAACA	AUCUUGUUGAUGCUCAUCAAU
ghr-miR827c	*Pvul-GASA2*	5.0	−1.0	UUAGAUGACCAUCAACAAACA	AUCUUGUUGAUGCUCAUCAAU
Glycine max					
gma-miR1516a-5p	*Pvul-GASA2*	4.75	−1.0	CAAGUU--AUAAGCUCUUUUGAGAG	UAUGCGAAAGAGCUUGUGGAACUUG
gma-miR1520p	*Pvul-GASA11*	5.0	−1.0	AUGUUGUUAUUGGAUGAUGACGGU	CAAGGUUUCAUCCGAUGUUAACAU
gma-miR1526	*Pvul-GASA14*	5.0	−1.0	CCGGAAGAGGAAAAUUAAGCAA	CUACUUUGUUCUCUUCUUCUGA
gma-miR159b-3p	*Pvul-GASA4*	4.0	−1.0	AUUGGAGUGAAGGGAGCUCCA	CAAAGCUCUCUUAGCUUCAAU
gma-miR159b-5p	*Pvul-GASA23*	5.0	−1.0	GAGUUCCCUGCACUCCAAGUC	UCCUGGGAGUCUAAGGAGCUC
gma-miR159c	*Pvul-GASA4*	4.0	−1.0	AUUGGAGUGAAGGGAGCUCCG	CAAAGCUCUCUUAGCUUCAAU
gma-miR159f-3p	*Pvul-GASA4*	4.0	−1.0	AUUGGAGUGAAGGGAGCUCCA	CAAAGCUCUCUUAGCUUCAAU
gma-miR159f-5p	*Pvul-GASA23*	5.0	−1.0	GAGUUCCCUGCACUCCAAGUC	UCCUGGGAGUCUAAGGAGCUC
gma-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
gma-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGC	CUUCUUGCCUUGCUUCUCCU
gma-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGC	CUUCUUGCCUUGCUUCUCCU
gma-miR164d	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGC	CUUCUUGCCUUGCUUCUCCU
gma-miR164e	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
gma-miR164f	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
gma-miR164g	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
gma-miR164h	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
gma-miR164i	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
gma-miR164j	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
gma-miR164k	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
gma-miR172h-5p	*Pvul-GASA10*	4.5	−1.0	GCAGCAGCAUCAAGAUUCACA	CUUUACUGUUGCUGCUGCUGC
gma-miR172i-5p	*Pvul-GASA10*	4.5	−1.0	GCAGCAGCAUCAAGAUUCACA	CUUUACUGUUGCUGCUGCUGC
gma-miR172j	*Pvul-GASA10*	4.5	−1.0	GCAGCAGCAUCAAGAUUCACA	CUUUACUGUUGCUGCUGCUGC
gma-miR393h	*Pvul-GASA14*	5.0	−1.0	UUCCAAAGGGAUCGCAUUGAUC	UGCAAAUGUGUUCCUUCUGGAA
gma-miR393i	*Pvul-GASA14*	5.0	−1.0	UUCCAAAGGGAUCGCAUUGAUC	UGCAAAUGUGUUCCUUCUGGAA
gma-miR393j	*Pvul-GASA14*	5.0	−1.0	UUCCAAAGGGAUCGCAUUGAUC	UGCAAAUGUGUUCCUUCUGGAA
gma-miR393k	*Pvul-GASA14*	5.0	−1.0	UUCCAAAGGGAUCGCAUUGAUC	UGCAAAUGUGUUCCUUCUGGAA
gma-miR408a-5p	*Pvul-GASA17*	5.0	−1.0	CAGGGGAACAGGCAGAGCAUG	GAAGCCAUGUUUGUUCUUCUG
gma-miR408c-5p	*Pvul-GASA17*	5.0	−1.0	CAGGGGAACAGGCAGAGCAUG	GAAGCCAUGUUUGUUCUUCUG
gma-miR4340	*Pvul-GASA1*	5.0	−1.0	UGCAGAGAUAGGGACGCGCUUA	UCAUCUCGUCCAAAUCUCUGCA
gma-miR4350	*Pvul-GASA16*	4.5	−1.0	UCAAAUGAUUUUGUGUCGUUGG	CCAGCAGCACAAAAUCAAUUGC
gma-miR4402	*Pvul-GASA21*	5.0	−1.0	ACAUAUUAUGGGUCUCAGACGGAC	UGGUUUCUGUGACUCAAAGUGUGC
gma-miR4407	*Pvul-GASA6*	5.0	−1.0	CAGAGGAAGCAGCACUUGUACC	UGUUCAAAUGCUGCUUGUUCUU
gma-miR4416c	*Pvul-GASA20*	5.0	−1.0	CUGGGUGAGAGAAACACGUAU	ACUCGGGAUUCUCUUGUUCAG
gma-miR530a	*Pvul-GASA21*	5.0	−1.0	UGCAUUUGCACCUGCACUUU	CAAGGGCAAGGGCAAAUGCC
gma-miR530b	*Pvul-GASA21*	5.0	−1.0	UGCAUUUGCACCUGCACUUUA	CCAAGGGCAAGGGCAAAUGCC
gma-miR530c	*Pvul-GASA21*	5.0	−1.0	UGCAUUUGCACCUGCACUUUA	CCAAGGGCAAGGGCAAAUGCC
gma-miR530d	*Pvul-GASA21*	5.0	−1.0	UGCAUUUGCACCUGCACUUUA	CCAAGGGCAAGGGCAAAUGCC
gma-miR530e	*Pvul-GASA21*	5.0	−1.0	UGCAUUUGCACCUGCACUUUA	CCAAGGGCAAGGGCAAAUGCC
gma-miR5368	*Pvul-GASA9*	5.0	−1.0	GGACAGUCUCAGGUAGACA	GUUCCAUCUGGGACUGUCG
gma-miR5380c	*Pvul-GASA16*	5.0	−1.0	AUGAAUGGUGAAGAUGAAGAG	CUCUUUAUUCUUGCCAUUCUU

gma-miR5675	*Pvul-GASA8*	5.0	−1.0	UAGAGACGACAACAAUGGAAA	CUCUCAUGGUUUUCGUCUCUC
gma-miR5775	*Pvul-GASA1*	4.5	−1.0	AUAAGCUCUUUUG-AGAGCUUC	AAAUCUCUGCAAAAGAGCUUGU
gma-miR5775	*Pvul-GASA3*	5.0	−1.0	AUAAGCUCUUUUG-AGAGCUUC	AAAUCUCUGCGAAAGAGCUUGU
gma-miR862a	*Pvul-GASA16*	4.5	−1.0	UGCUGGAUGUCUUUGAAGGAAU	UCAAUAACAAAGAUAUCCAGCA
gma-miR9730	*Pvul-GASA18*	5.0	−1.0	CGAUUGCUGUCAUAACUGCUGC	ACAGUGGUUAUGGCUGCAAAUG
gma-miR9737	*Pvul-GASA18*	4.0	−1.0	UUGUGGCUGAAAUCACUGUUGC	CAGACAGUGGUUAUGGCUGCAA
gma-miR9740	*Pvul-GASA12*	5.0	−1.0	UGUAGGUUCCAGUGAGGGAAA	UGUUCCUC-CUGGAACUUAUG
gma-miR9740	*Pvul-GASA17*	5.0	−1.0	UGUAGGUUCCAGUGAGGGAAA	UGUGCCUC-CUGGAACCUAUG
Gossypium raimondii					
gra-miR167c	*Pvul-GASA5*	5.0	−1.0	UCAGAUGAAGCUGCCAGCAUGA	CCUUGUUCCAAGCUUCAUCUGC
gra-miR530a	*Pvul-GASA12*	2.5	−1.0	AGGUGCAGAUGCAGUUGCAGG	CCUGCACCUGUAUCUGCACCA
gra-miR530a	*Pvul-GASA2*	5.0	−1.0	AGGUGCAGAUGCAGUUGCAGG	GCUGCAACUGCGUCC-CACCU
gra-miR530b	*Pvul-GASA12*	3.0	−1.0	AGGUGCAGGUGCAGGCGCAGC	CCUGCACCUGUAUCUGCACCA
gra-miR7494b	*Pvul-GASA21*	5.0	−1.0	AGAGGGAGAAGCAGAAGAGAAUA	CCUUCUCCUCAGCUCCUCUUUCU
gra-miR7494b	*Pvul-GASA15*	5.0	−1.0	AGAGGGAGAAGCAGAAGAGAAUA	GGCUAUUUUCUGCUUCAUCCUUA
gra-miR7504h	*Pvul-GASA1*	5.0	−1.0	AGGAGGAAUAAGUCUGAUUUGUCA	UCUAAACUCAUACUUGCUUCUCUU
gra-miR8691	*Pvul-GASA7*	4.5	−1.0	AGAUGAUGAGAAAGGAAAGU-CAAG	UUUGUAUUUGCAUUUCUUCUCAUCU
gra-miR8691	*Pvul-GASA20*	5.0	−1.0	AGAUGAUGAGAAAGGAAAGUCAAG	UUCUGCUAUCCUUUCUCCUCUUCC
gra-miR8737	*Pvul-GASA2*	4.0	−1.0	GUGUAUCUCCUGAAAACGACGACA	GGUUCUCUUUUUCAGCAGAUAGAC
gra-miR8737	*Pvul-GASA3*	5.0	−1.0	GUGUAUCUCCUGAAAACGACGACA	GGUUCUCUUCUUCAGCAGAUAGAC
gra-miR8764	*Pvul-GASA10*	4.5	−1.0	UUAGAUUGCAUUUUACCCCUU	GCAAGGUGAGAUGCAGUUUAG
gra-miR8764	*Pvul-GASA3*	5.0	−1.0	UUAGAUUGCAUUUUACCCCUU	GUGGGUGUGAGGUGUAGUUUAU
gra-miR8773	*Pvul-GASA11*	5.0	−1.0	UUGGAUGAACGGUGCGUUUACUU	AACAAGGUGUGGUGUUCAUUCAA
gra-miR8773	*Pvul-GASA22*	5.0	−1.0	UUGGAUGAACGGUGCGUUUACUU	AUCAAGAUGCAGUGCUCAUUCAA
Hevea brasiliensis					
hbr-miR6485	*Pvul-GASA23*	5.0	−1.0	UAGGAUGUAGAAGAGCAUAA	CUAAGCUUCUCUGCGUUCUG
Helianthus ciliaris					
hci-miR156a	*Pvul-GASA23*	5.0	−1.0	UGACAGAAGAGAGUGAGUAC	CCAUGCAUGUUCUUCUGUCA
hci-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGAA	CCUUCUUGCCUUGCUUCUCCU
Hordeum vulgare					
hvu-miR5048a	*Pvul-GASA7*	5.0	−1.0	UAUUUGCAGGUUUUAGGUCUAA	AAUGUCCAAAAGCAUGCGAGUA
hvu-miR5048b	*Pvul-GASA7*	5.0	−1.0	UAUUUGCAGGUUUUAGGUCUAA	AAUGUCCAAAAGCAUGCGAGUA
hvu-miR6183	*Pvul-GASA9*	5.0	−1.0	UGAGCGAGUUGGCUG-CAAGUUC	ACUUUUGUCACUCAACUCGCUUA
hvu-miR6192	*Pvul-GASA9*	4.5	−1.0	UAGGAGAGGGGGGAAGGGAUCU	GCCUUUCUUCUCCUCUUUCUCA
hvu-miR6196	*Pvul-GASA21*	5.0	−1.0	AGGACGAGGAGAUGGAGAGGA	UUCUCCUCAGCUCCUCUUUCU
hvu-miR6212	*Pvul-GASA9*	5.0	−1.0	AUACAGUUUACAAUGCACGAU	CUCUUUUAUUGUAACUUGUGU
Lotus japonicus					
lja-miR408	*Pvul-GASA15*	5.0	−1.0	CAGGGAAGAGGCAGAGCAUGG	CUAUUUUCUGCUUCAUCCUUA
lja-miR408	*Pvul-GASA5*	5.0	−1.0	CAGGGAAGAGGCAGAGCAUGG	UGCUGCUAUGCUACUUCUUUG
lja-miR7537	*Pvul-GASA22*	5.0	−1.0	UAGGAAAUACGCCUGCGGUUCC	AUGGCGUCACGCGUAUUUCUUG
lja-miR7540a	*Pvul-GASA2*	4.5	−1.0	UGAUAUGAUAAGUGAUGUGA	AGGUGUCAUUUAUCAUCUCA
lja-miR7540b	*Pvul-GASA2*	4.5	−1.0	UGAUAUGAUAAGUGAUGUGA	AGGUGUCAUUUAUCAUCUCA
lja-miR7541	*Pvul-GASA15*	5.0	−1.0	UGCAUUCUCUUUUGGUGGCCC	CUGCCAACAAGAUAGACUGCG
Linum usitatissimum					

lus-miR159a	*Pvul-GASA4*	4.0	−1.0	AUUGGAGUGAAGGGAGCUCGA	CAAAGCUCUCUUAGCUUCAAU
lus-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
lus-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
lus-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
lus-miR164d	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
lus-miR164e	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
Malus domestica					
mdm-miR164a	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCC	UGUGUGGGCCUUUCUUCUCCU
mdm-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mdm-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mdm-miR164d	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mdm-miR164e	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mdm-miR164f	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mdm-miR482d	*Pvul-GASA20*	4.5	−1.0	AAUGGAAGGGUAGGAAAGAAG	UAUCCUUUCUCCUCUUCCAUC
mdm-miR482d	*Pvul-GASA14*	5.0	−1.0	AAUGGAAGGGUAGGAAAGAAG	UCUCUUUGCUACUCUACUACU
mdm-miR827	*Pvul-GASA1*	5.0	−1.0	UUAGAUGACCAUCAACGAACA	AUCUCGUUGAUGCUCAUCAAU
mdm-miR827	*Pvul-GASA3*	5.0	−1.0	UUAGAUGACCAUCAACGAACA	AUCUCGUUGAUGCUCAUCAAU
Manihot esculenta					
mes-miR159c	*Pvul-GASA4*	4.0	−1.0	AUUGGAGUGAAGGGAGCUCUG	CAAAGCUCUCUUAGCUUCAAU
mes-miR159d	*Pvul-GASA4*	4.0	−1.0	AUUGGAGUGAAGGGAGCUCUG	CAAAGCUCUCUUAGCUUCAAU
mes-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mes-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mes-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mes-miR164d	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCU	UGUGUGGGCCUUUCUUCUCCU
mes-miR827	*Pvul-GASA2*	5.0	−1.0	UUAGAUGACCAUCAACAAACA	AUCUUGUUGAUGCUCAUCAAU
Medicago truncatula					
mtr-miR1509a-5p	*Pvul-GASA3*	5.0	−1.0	UUAAUCUAGGAAAAUACGGUG	GUCCAUGUUAUGCUAGGUUAA
mtr-miR156d-3p	*Pvul-GASA10*	4.5	−1.0	UGCUCACUCAUCUUUCUGUCAAA	GGUAACAGAGAGGUGUGUGGGAA
mtr-miR159b	*Pvul-GASA4*	4.0	−1.0	AUUGGAGUGAAGGGAGCUCCA	CAAAGCUCUCUUAGCUUCAAU
mtr-miR160f	*Pvul-GASA3*	5.0	−1.0	GCGUGAAGGGAGUCAAGCAGG	CAUACUUGCUUCCCUUCUUGC
mtr-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mtr-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mtr-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
mtr-miR164d	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCU	UGUGUGGGCCUUUCUUCUCCU
mtr-miR2088-3p	*Pvul-GASA22*	4.5	−1.0	UCCAAUGUAAUCUAGGUCUA	AAGACAUAGAUUGUGGUGGG
mtr-miR2589	*Pvul-GASA11*	5.0	−1.0	GGCAUCCACGUGUGCUUCACCG	GUGUGAGGUGCAAGUGUGUGCC
mtr-miR2592bm-3p	*Pvul-GASA13*	5.0	−1.0	GGAAAACAUGAAUGUCGGGUG	CACAAGCCAUGCAUGUUUUUC
mtr-miR2592bn-3p	*Pvul-GASA13*	5.0	−1.0	GGAAAACAUGAAUGUCGGGUG	CACAAGCCAUGCAUGUUUUUC
mtr-miR2595	*Pvul-GASA11*	3.5	−1.0	UACAUUUUCUUCUUUAUGUCU	AUAGAAAAAGAAGAAAAUGAA
mtr-miR2595	*Pvul-GASA12*	4.5	−1.0	UACAUUUUCUUCUUUAUGUCU	GCACUCAAGGAAGAAACUGUG
mtr-miR2602a	*Pvul-GASA18*	5.0	−1.0	UGGCAGUGAUUGCCACG-UCAU	AUGAUCUUGGCACUCAUUGCCA
mtr-miR2602b	*Pvul-GASA18*	5.0	−1.0	UGGCAGUGAUUGCCACG-UCAU	AUGAUCUUGGCACUCAUUGCCA
mtr-miR2631	*Pvul-GASA22*	4.5	−1.0	UGACACGCCACGUGGCACACU	CAUGUGGCACGUGCUGUGUGA
mtr-miR5221	*Pvul-GASA12*	5.0	−1.0	AGGAGAGAUGGUGUUUUGACUU	CUGUGAAAUCACCAUCUUACCC

mtr-miR5273	*Pvul-GASA12*	5.0	−1.0	UAGGGGCUGUAGUUUGAGAAGAGG	CACCAAGUCCAACUACACCCCCUG
mtr-miR5286a	*Pvul-GASA11*	4.0	−1.0	CAGGACAAACUGGAGGCAAGGGAC	GGAUAUUCCUGCUGGUUUGUCUUG
mtr-miR5293	*Pvul-GASA3*	4.5	−1.0	GAUGAAGAAGUGGAAGGAAG--AAGA	UCUUGCCUUGCUUCUCCUGCUUCAUC
mtr-miR530	*Pvul-GASA21*	5.0	−1.0	UGCAUUUGCACCUGCACUUUC	CCAAGGGCAAGGGCAAAUGCC
mtr-miR5561-5p	*Pvul-GASA5*	5.0	−1.0	CAUUUGGAGAGACAUAGACAA	UGGUUUCUGUGCCUCCAAGUG
mtr-miR5744	*Pvul-GASA19*	5.0	−1.0	UAGGUAUUUUAAGGAGCACGUU	GAAGUGUUGCGCAAAAUGCCUA
Nicotiana tabacum					
nta-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
nta-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
nta-miR164c	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCU	UGUGUGGGCCUUUCUUCUCCU
nta-miR479b	*Pvul-GASA17*	4.5	−1.0	CGUGAUAUUUGUUUGGCUCAUC	CCUGAGUCAAACAAGAAUAAUG
nta-miR482b-5p	*Pvul-GASA9*	4.0	−1.0	AGUGGGUGGAGUGGUAAGAUA	ACUUUUGUCACUCAACUCGCU
nta-miR6144	*Pvul-GASA23*	4.5	−1.0	UGGCAACUUCUUCAUCAUGCC	AAAAUGCUGCAGAAGUUGCCU
nta-miR6148b	*Pvul-GASA11*	5.0	−1.0	UGUGUUAAUCGUUUGUUCUCA	UGGGAACAGAAGACUAAUGCA
nta-miR827	*Pvul-GASA2*	5.0	−1.0	UUAGAUGAACAUCAACAAACA	AUCUUGUUGAUGCUCAUCAAU
Oryza sativa					
osa-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
osa-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
osa-miR164c	*Pvul-GASA3*	5.0	−1.0	UGGAGAAGCAGGGUACGUGCA	CCUUCUUGCCUUGCUUCUCCU
osa-miR164d	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCU	CCUUCUUGCCUUGCUUCUCCU
osa-miR164e	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGAG	CCUUCUUGCCUUGCUUCUCCU
osa-miR164f	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
osa-miR169p	*Pvul-GASA6*	5.0	−1.0	UAGCCAAGGACAAACUUGCCGG	CAAGCAGGUUUGCCCUUG-CUA
osa-miR1855	*Pvul-GASA14*	4.5	−1.0	AGCACUGGAGUAGCCAAGAGA	UCUCUUUGCUACUCUACUACU
osa-miR1858a	*Pvul-GASA14*	4.0	−1.0	GAGAGGAGGACGGAGUGGGGC	CUACUACUUUGUUCUCUUCUU
osa-miR1858b	*Pvul-GASA14*	4.0	−1.0	GAGAGGAGGACGGAGUGGGGC	CUACUACUUUGUUCUCUUCUU
osa-miR1868	*Pvul-GASA2*	5.0	−1.0	UCACGGAAAACGAGGGAGCAGCCA	CCCUUGUUGUCUCGUUUCUCGUGC
osa-miR1880	*Pvul-GASA8*	5.0	−1.0	UUCCAAGCGGGCCACUUAAGCAUU	AAUGUUUAUGUGUUCCGUCUGGAA
osa-miR1882e-3p	*Pvul-GASA12*	5.0	−1.0	GAAAUGAUCUUGGACGUAAUCUAG	UCUGGUUACCUCAAAGGUUUUUUC
osa-miR2097-5p	*Pvul-GASA2*	4.5	−1.0	AGAGAUGGGACGGGCAGGGAAG	CUUCCCUUGUUGUCUCGUUUCU
osa-miR2867-3p	*Pvul-GASA10*	5.0	−1.0	CCAGGACGUGUGGGAUGGCA	GGCCAUCUCACCCAUUCUGA
osa-miR2868	*Pvul-GASA16*	5.0	−1.0	UUGGUUUUGUGUAGUAGAAA	AUCCAGCAGCACAAAAUCAA
osa-miR396d	*Pvul-GASA4*	4.5	−1.0	UCCACAGGCUUUCUUGAACGG	CUAUGCAAGAGGGCAUGUGGA
osa-miR396d	*Pvul-GASA1*	4.5	−1.0	UCCACAGGCUUUCUUGAACGG	CUCUGCAAAAGAGCUUGUGGA
osa-miR396d	*Pvul-GASA2*	5.0	−1.0	UCCACAGGCUUUCUUGAACGG	CUAUGCGAAAGAGCUUGUGGA
osa-miR396d	*Pvul-GASA3*	5.0	−1.0	UCCACAGGCUUUCUUGAACGG	CUCUGCGAAAGAGCUUGUGGA
osa-miR396d	*Pvul-GASA20*	4.5	−1.0	UCCACAGGCUUUCUUGAACGG	AUGUGUCACAGAGCCUGUGGA
osa-miR396e-5p	*Pvul-GASA1*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGA
osa-miR396e-5p	*Pvul-GASA4*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGA
osa-miR396e-5p	*Pvul-GASA2*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGA
osa-miR396e-5p	*Pvul-GASA3*	5.0	−1.0	UCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGA
osa-miR396e-5p	*Pvul-GASA20*	4.5	−1.0	UCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGA
osa-miR396g	*Pvul-GASA4*	4.5	−1.0	UCCACAGGCUUUCUUGAACGG	CUAUGCAAGAGGGCAUGUGGA
osa-miR396g	*Pvul-GASA1*	4.5	−1.0	UCCACAGGCUUUCUUGAACGG	CUCUGCAAAAGAGCUUGUGGA

osa-miR396g	*Pvul-GASA2*	5.0	−1.0	UCCACAGGCUUUCUUGAACGG	CUAUGCGAAAGAGCUUGUGGA
osa-miR396g	*Pvul-GASA3*	5.0	−1.0	UCCACAGGCUUUCUUGAACGG	CUCUGCGAAAGAGCUUGUGGA
osa-miR396g	*Pvul-GASA20*	4.5	−1.0	UCCACAGGCUUUCUUGAACGG	AUGUGUCACAGAGCCUGUGGA
osa-miR396h	*Pvul-GASA4*	4.5	−1.0	UCCACAGGCUUUCUUGAACGG	CUAUGCAAGAGGGCAUGUGGA
osa-miR396h	*Pvul-GASA1*	4.5	−1.0	UCCACAGGCUUUCUUGAACGG	CUCUGCAAAAGAGCUUGUGGA
osa-miR396h	*Pvul-GASA2*	5.0	−1.0	UCCACAGGCUUUCUUGAACGG	CUAUGCGAAAGAGCUUGUGGA
osa-miR396h	*Pvul-GASA3*	5.0	−1.0	UCCACAGGCUUUCUUGAACGG	CUCUGCGAAAGAGCUUGUGGA
osa-miR396h	*Pvul-GASA20*	4.5	−1.0	UCCACAGGCUUUCUUGAACGG	AUGUGUCACAGAGCCUGUGGA
osa-miR408-5p	*Pvul-GASA15*	3.5	−1.0	CAGGGAUGAGGCAGAGCAUGG	CUAUUUUCUGCUUCAUCCUUA
osa-miR426	*Pvul-GASA14*	5.0	−1.0	UUUUGGAAGUUUGUCCUUACG	GUUAAGGAUAGGUGUCUGAAG
osa-miR444a-5p	*Pvul-GASA17*	4.0	−1.0	GCUAGAGGUGGCAACUGCAUA	GUUGCUGUUGCUACCUCUAAG
osa-miR444b.2	*Pvul-GASA18*	5.0	−1.0	UGCAGUUGUUGUCUCAAGCUU	GCCCUUGCUACAACAACUGGA
osa-miR444c.2	*Pvul-GASA18*	5.0	−1.0	UGCAGUUGUUGUCUCAAGCUU	GCCCUUGCUACAACAACUGGA
osa-miR5076	*Pvul-GASA21*	5.0	−1.0	GAAAUGGGAGCAGAGCAGGUUU	CCUUCUCCUCAGCUCCUCUUUC
osa-miR530-3p	*Pvul-GASA12*	4.0	−1.0	AGGUGCAGAGGCAGAUGCAAC	CCUGCACCUGUAUCUGCACCA
osa-miR530-5p	*Pvul-GASA11*	5.0	−1.0	UGCAUUUGCACCUGCACCUA	UGUGUG-AGGUGCAAGUGUG
osa-miR530-5p	*Pvul-GASA22*	5.0	−1.0	UGCAUUUGCACCUGCACCUA	UGUGUG-AGGUGCAAGUGUG
osa-miR5492	*Pvul-GASA17*	4.5	−1.0	AGAAGGAGAAUAGAUAUGGUU	AGCCAUGUUUGUUCUUCUGCA
osa-miR5492	*Pvul-GASA6*	5.0	−1.0	AGAAGGAGAAUAGAUAUGGUU	AACCGUGUCUGUUUUUCUGCC
osa-miR5492	*Pvul-GASA8*	5.0	−1.0	AGAAGGAGAAUAGAUAUGGUU	AUUUGUGUUUGUACUUCUUCU
osa-miR5492	*Pvul-GASA12*	4.0	−1.0	AGAAGGAGAAUAGAUAUGGUU	UUCCAAUUCCAUUCUUCUUCU
osa-miR5494	*Pvul-GASA17*	4.5	−1.0	UUAUAGGAGGUAUAGACGGUA	GCCUGUGUGUGCCUCCUGGAA
osa-miR5494	*Pvul-GASA6*	5.0	−1.0	UUAUAGGAGGUAUAGACGGUA	GCUUGUGUGUGCCUCCUGGAA
osa-miR5523	*Pvul-GASA12*	4.5	−1.0	UGAGGAGGAACAUAUUUACUAG	GUUGCAAGUGUGUUCCUCCUGG
osa-miR5523	*Pvul-GASA14*	4.5	−1.0	UGAGGAGGAACAUAUUUACUAG	AGUGCAAAUGUGUUCCUUCUGG
osa-miR5539a	*Pvul-GASA22*	4.5	−1.0	AAGAAAACGGAUGCGCGUGCUA	CGUCACGCGUAUUUCUUGUCUU
osa-miR5539b	*Pvul-GASA22*	4.5	−1.0	AAGAAAACGGAUGCGCGUGCUA	CGUCACGCGUAUUUCUUGUCUU
osa-miR5829	*Pvul-GASA5*	4.0	−1.0	AUCAGGACCAGUAGGCGAUGGUAA	CAAGCUUCAUCUGCUGGUUCGGU
osa-miR812n-5p	*Pvul-GASA8*	5.0	−1.0	AAGUGCAGCCAUGAGUUUCCGUGC	AUGACUAAAUUUGUGUUUGUACUU
osa-miR812q	*Pvul-GASA6*	5.0	−1.0	ACGUUGGGUACGAAUAUCUACGGC	UGCAGAGAUUGUUGUGUCCACCGU
Picea abies					
pab-miR3708	*Pvul-GASA17*	3.5	−1.0	UCACACAACAUUUCUCGUACA	UCUGCAAGAAGUGUUGUGCGA
pab-miR3708	*Pvul-GASA13*	4.0	−1.0	UCACACAACAUUUCUCGUACA	UCUGUCAGAAGUGUUGUAUGA
pab-miR3708	*Pvul-GASA11*	5.0	−1.0	UCACACAACAUUUCUCGUACA	CAUGUGGGACGUGCUGUGUGA
Populus euphratica					
peu-miR2913	*Pvul-GASA17*	4.0	−1.0	GAGGUCGGGGAUUGCAAGGAG	CUCCUUGCAAUCCUUCUCCUC
Prunus persica					
ppe-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ppe-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ppe-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ppe-miR164d	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCU	UGUGUGGGCCUUUCUUCUCCU
ppe-miR530	*Pvul-GASA3*	4.5	−1.0	UCUGCAUUUGCACCUGCACCU	CGGUGCAAGAACAAAUGCAGG
ppe-miR6269	*Pvul-GASA13*	5.0	−1.0	UGUGAAUAGUGAUUGCCAUGG	CAAUGCCCAUCACAAUGCACA
ppe-miR6272	*Pvul-GASA5*	4.5	−1.0	UAGCUGUAAAUGAGUGUUUUU	UGAAGCUGUCAUUUGCUGCUA

ppe-miR6275	*Pvul-GASA14*	4.5	−1.0	AGUGGAAGUAGCAAGGGGAAGC	GCUUCUCUUUGCUACU-CUACU
ppe-miR6276	*Pvul-GASA9*	3.0	−1.0	AAAGGCUCAUACAAAUAUUCC	GCUAAAUUUGUGUGGGCCUUU
ppe-miR8122-5p	*Pvul-GASA21*	5.0	−1.0	UUCCACAGAUCUUUCCUCAUU	GAUGCUUGAAGUUCUGUGGAA
ppe-miR8123-5p	*Pvul-GASA18*	4.0	−1.0	UGAGCAAUGGCACACAGCCCU	AAGGCUGUGUGCCCUUGCUAC
ppe-miR8130-5p	*Pvul-GASA11*	5.0	−1.0	GGGUUCCUUGUUGGAAGGACU	ACUUCGGUAAUAGGGAGCUC
ppe-miR827	*Pvul-GASA2*	5.0	−1.0	UUAGAUGACCAUCAACAAACA	AUCUUGUUGAUGCUCAUCAAU
Physcomitrella patens					
ppt-miR1023a-3p	*Pvul-GASA19*	4.5	−1.0	AGAGAAUUGGAGAGAGUGCAU	UUGCCCUCUCUUUGCUUCUUU
ppt-miR1023b-3p	*Pvul-GASA19*	4.0	−1.0	AGAGAAUUGAAGAGAGUGCAU	UUGCCCUCUCUUUGCUUCUUU
ppt-miR1029	*Pvul-GASA10*	5.0	−1.0	UCUCUCUCAACCAACCAUAC	UUGUGGAUUGUGGAGAGAGG
ppt-miR1055	*Pvul-GASA5*	4.0	−1.0	UUAGGGGUGUUUUCCAGUGACU	GGGCAAGGGAAAGUGCCCUUAA
ppt-miR1066	*Pvul-GASA8*	5.0	−1.0	ACAUGUUGCAGAGCGGGGUAC	GUCUCCACUUUUGUAACAUGU
ppt-miR1066	*Pvul-GASA7*	5.0	−1.0	ACAUGUUGCAGAGCGGGGUAC	GUCUCCACUUUUGUAACAUGU
ppt-miR1074	*Pvul-GASA22*	5.0	−1.0	AGGGUUGUUAGUUGUGUUGAU	GGCAACAAGACUAAGUGCCCU
ppt-miR1074	*Pvul-GASA11*	5.0	−1.0	AGGGUUGUUAGUUGUGUUGAU	GGCAACAAAACUAAGUGUCCU
ppt-miR1214	*Pvul-GASA10*	5.0	−1.0	UACUAUGAGAAUCUCGCGGCC	UUCCUCCAGGUCCUUAUGGUA
ppt-miR1215	*Pvul-GASA22*	5.0	−1.0	UCAUUGCAAAACUGUAUACGA	AGAACUGCAGUUUCGCAAUGA
ppt-miR1219a	*Pvul-GASA11*	4.5	−1.0	CUUCCUGCCUCUCACUAGCUU	CUGAUAGUGAGAGAUGGGAAC
ppt-miR1219b	*Pvul-GASA11*	4.5	−1.0	CUUCCUGCCUCUCACUAGCUU	CUGAUAGUGAGAGAUGGGAAC
ppt-miR1219c	*Pvul-GASA11*	4.5	−1.0	CUUCCUGCCUCUCACUAGCUU	CUGAUAGUGAGAGAUGGGAAC
ppt-miR1219d	*Pvul-GASA11*	4.5	−1.0	UUUCCUGCCUCUCACUAGCUU	CUGAUAGUGAGAGAUGGGAAC
ppt-miR1221-5p	*Pvul-GASA21*	5.0	−1.0	UGGAUGGUGUGCAGGGUCAAA	AGUGCCACUGUGUGCCAUCUG
ppt-miR160g	*Pvul-GASA19*	5.0	−1.0	UGCCUGGCUCCUUGUAUGCCA	CUUCACACAAGAAGCCAUGCA
Populus trichocarpa					
ptc-miR1447	*Pvul-GASA4*	3.5	−1.0	CAGAAUUGCAGUGCCUUGAUU	UCUCAAGUCAUUGUGAUUCUU
ptc-miR159c	*Pvul-GASA4*	4.0	−1.0	AUUGGAGUGAAGGGAGCUCGA	CAAAGCUCUCUUAGCUUCAAU
ptc-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ptc-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ptc-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ptc-miR164d	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ptc-miR164e	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ptc-miR164f	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCU	UGUGUGGGCCUUUCUUCUCCU
ptc-miR482c-5p	*Pvul-GASA8*	5.0	−1.0	UAUGGGAGAGGCGGGAAUGACU	ACUUCUUCUCAUCUCUCUCAUG
ptc-miR6421-5p	*Pvul-GASA1*	4.5	−1.0	UCCCUUACAAUCUACUCUUUC	AGCAGA-UAGAUUGUAACGGA
ptc-miR6439b	*Pvul-GASA10*	4.0	−1.0	AGCAGAAGCCAUCACUAGCGC	CUGCUGCUCAUGGCUUCUGCA
ptc-miR6454	*Pvul-GASA23*	5.0	−1.0	CUUGUAACCUGAGUAGAGGCA	GAUCACAACUCAGGUUAUGGC
ptc-miR6469	*Pvul-GASA19*	5.0	−1.0	UGGCAGAAAAGGAUUCGUUUA	GCCAUGCAUGUUUUUCUGUCA
ptc-miR6469	*Pvul-GASA13*	5.0	−1.0	UGGCAGAAAAGGAUUCGUUUA	GCCAUGCAUGUUUUUCUGUCA
ptc-miR7813	*Pvul-GASA22*	5.0	−1.0	UGGUAAUGCAAGUGUUGCUAA	CUUGCUACACUGGCAUGACCA
ptc-miR7817a	*Pvul-GASA12*	2.5	−1.0	UUUGGUUAUUGUCUCGAGACA	GAUCUCGAGAUAAUGGCCAAC
ptc-miR7821	*Pvul-GASA2*	5.0	−1.0	AGAUGGGCAUCGGCAUUGUGA	UCAUCUUGUUGAUGCUCAUCA
ptc-miR827	*Pvul-GASA1*	5.0	−1.0	UUAGAUGACCAUCAACGAAAA	AUCUCGUUGAUGCUCAUCAAU
ptc-miR827	*Pvul-GASA3*	5.0	−1.0	UUAGAUGACCAUCAACGAAAA	AUCUCGUUGAUGCUCAUCAAU
Ricinus communis					

rco-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
rco-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
rco-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
rco-miR164d	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCU	UGUGUGGGCCUUUCUUCUCCU
Sorghum bicolor					
sbi-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
sbi-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCU	CCUUCUUGCCUUGCUUCUCCU
sbi-miR164d	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
sbi-miR164e	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
sbi-miR2118-5p	*Pvul-GASA18*	5.0	−1.0	GGCAUGGGAACAUGUAGGAAGG	AAACCCUGCAUGUUUUUCUGUC
sbi-miR396d	*Pvul-GASA1*	4.0	−1.0	CUCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGAA
sbi-miR396d	*Pvul-GASA4*	4.5	−1.0	CUCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGAA
sbi-miR396d	*Pvul-GASA2*	4.5	−1.0	CUCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGAA
sbi-miR396d	*Pvul-GASA3*	4.5	−1.0	CUCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGAA
sbi-miR396d	*Pvul-GASA20*	5.0	−1.0	CUCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGAA
sbi-miR396e	*Pvul-GASA1*	3.0	−1.0	UUCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGAA
sbi-miR396e	*Pvul-GASA4*	3.5	−1.0	UUCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGAA
sbi-miR396e	*Pvul-GASA2*	3.5	−1.0	UUCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGAA
sbi-miR396e	*Pvul-GASA3*	3.5	−1.0	UUCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGAA
sbi-miR396e	*Pvul-GASA20*	4.0	−1.0	UUCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGAA
sbi-miR5568b-5p	*Pvul-GASA13*	4.5	−1.0	UUUCUAGGUACAUAGCUUUUG	GAAAAAAUAUGGACCUGGAAG
sbi-miR5570	*Pvul-GASA11*	5.0	−1.0	AAAAGACAAAUCAGCAUGUCA	AUUCCUGCUGGUUUGUCUUGC
sbi-miR6218-3p	*Pvul-GASA2*	5.0	−1.0	ACAAGUUUCGUGAUUUUUGGA	GAAAGAGCUUGUGGAACUUGU
sbi-miR6218-3p	*Pvul-GASA3*	5.0	−1.0	ACAAGUUUCGUGAUUUUUGGA	GAAAGAGCUUGUGGAACUUGU
sbi-miR6233-3p	*Pvul-GASA11*	5.0	−1.0	CAAGUUUGGUUUUGGUAAUUAAUG	UGUUCAUU--CAAGGCCAAACUUG
sbi-miR6233-3p	*Pvul-GASA4*	5.0	−1.0	CAAGUUUGGUUUUGGUAAUUAAUG	GAAUUAUCAUCAAGACCAAAUCUA
Solanum lycopersicum					
sly-miR164a-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
sly-miR164b-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
sly-miR1918	*Pvul-GASA16*	5.0	−1.0	UGUUGGUGAGAGUUCGAUUCUC	AAGAAUGUGGCUCUCAAUAACA
sly-miR482d-5p	*Pvul-GASA10*	4.5	−1.0	GGAGUGGGUGGGAUGGAAAAA	GAAGGCCAUCUCACCCAUUCU
sly-miR6023	*Pvul-GASA21*	5.0	−1.0	UUCCAUGAAAGAGUUUUUGGAU	CCUCAGCUCCUCUUUCUUGGAA
sly-miR9474-5p	*Pvul-GASA10*	4.5	−1.0	UGUAGAAGUCAUGAAUAAAAUG	GCUGCUGCUCAUGGCUUCUGCA
sly-miR9475-5p	*Pvul-GASA6*	5.0	−1.0	AACGAUCUCUACAUUGUAGGC	GAAAACCAUGCAGAGAUUGUU
Selaginella moellendorffii					
smo-miR1092	*Pvul-GASA13*	5.0	−1.0	UGACAGGAAUGCAUUGGUGUU	GCCAUGCAUGUUUUUCUGUCA
smo-miR1092	*Pvul-GASA19*	5.0	−1.0	UGACAGGAAUGCAUUGGUGUU	GCCAUGCAUGUUUUUCUGUCA
smo-miR1104	*Pvul-GASA5*	5.0	−1.0	CGCAGCUGUUCUUUUUCCUUC	CAGGGAUGAAGGACAGGUGCU
Salvia sclarea					
ssl-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ssl-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
ssl-miR395	*Pvul-GASA12*	5.0	−1.0	GGGAAAUGUUUGGGGAAACUU	UGGUUACCUCAAAGGUUUUUU
Saccharum sp.					
ssp-miR444c-3p	*Pvul-GASA18*	5.0	−1.0	UGCAGUUGUUGUCUCAAGCUU	GCCCUUGCUACAACAACUGGA

Solanum tuberosum					
stu-miR164-5p	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCU	UGUGUGGGCCUUUCUUCUCCU
stu-miR408a-3p	*Pvul-GASA14*	5.0	−1.0	UGCACAGCCUCUUCCCUGGUU	UACUGUGGAAUAUGCUGUGCA
stu-miR530	*Pvul-GASA3*	4.5	−1.0	UCUGCAUUUGCACCUGCACCU	CGGUGCAAGAACAAAUGCAGG
stu-miR7992-5p	*Pvul-GASA22*	5.0	−1.0	UUUGACAAUGCACAUCUAGACACU	UUGCUGUUGGUGUGCCUUGUUAAG
stu-miR8012	*Pvul-GASA10*	4.5	−1.0	AUGACUUUAAGUCGCGUCUGGCCC	AGGUGAGAUGCAGUUUAGAGUCAA
stu-miR8029	*Pvul-GASA9*	4.5	−1.0	AGCCAUUUUUCUUUGUUUUGGAGC	UGUCGGUAACAAAGAAGAAUGUCC
stu-miR8030-5p	*Pvul-GASA4*	5.0	−1.0	UUGGGUUGGUUUGGUCUCGGGUU	UCAUCAAGACCAAAUCUAUGCAA
stu-miR8037	*Pvul-GASA14*	5.0	−1.0	AUAAUUUGGAGGAAUAGGAACC	UUGUUCUCUUCUUCUGAGUUCU
stu-miR827-3p	*Pvul-GASA2*	5.0	−1.0	UUAGAUGAACAUCAACAAACA	AUCUUGUUGAUGCUCAUCAAU
Triticum aestivum					
tae-miR1122b-3p	*Pvul-GASA17*	4.5	−1.0	AGACUUAUAUGUAGGAACGGA	GCUGUUGCUACCUCUAAGUCU
tae-miR1134	*Pvul-GASA2*	5.0	−1.0	CAACAACAACAAGAAGAAGAAGAU	UCGUGCUUCAUCUUGUUGAUGCUC
tae-miR164	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
tae-miR5085	*Pvul-GASA5*	5.0	−1.0	AAGGACAUUUUUUGUGGCCUG	AGGGCAAGGGAAAGUGCCCUU
tae-miR9655-3p	*Pvul-GASA5*	5.0	−1.0	CAAGGGAAGGAAGUAGCCAAC	CUAUGCUACUUCUUUGCCUUC
tae-miR9656-3p	*Pvul-GASA7*	5.0	−1.0	CUUCGAGACUCUGAACAGCGG	UCGUUGUUCAAAGGCUCGGAU
tae-miR9670-3p	*Pvul-GASA9*	5.0	−1.0	AGGUGGAAUACUUGAAGAAGA	AAAUGUUUAUGUGUUCCAUCU
Theobroma cacao					
tcc-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
tcc-miR164b	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
tcc-miR164c	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCU	UGUGUGGGCCUUUCUUCUCCU
tcc-miR827	*Pvul-GASA2*	5.0	−1.0	UUAGAUGACCAUCAACAAACA	AUCUUGUUGAUGCUCAUCAAU
Vitis vinifera					
vvi-miR159a	*Pvul-GASA4*	5.0	−1.0	CUUGGAGUGAAGGGAGCUCUC	CAAAGCUCUCUUAGCUUCAAU
vvi-miR159b	*Pvul-GASA4*	5.0	−1.0	CUUGGAGUGAAGGGAGCUCUC	CAAAGCUCUCUUAGCUUCAAU
vvi-miR164a	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
vvi-miR164b	*Pvul-GASA9*	5.0	−1.0	UGGAGAAGCAGGGCACAUGCU	UGUGUGGGCCUUUCUUCUCCU
vvi-miR164c	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
vvi-miR164d	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
vvi-miR3630-5p	*Pvul-GASA9*	5.0	−1.0	UGCAAGUGACGAUAUCAGACA	UCUCUUUUAUUGUAACUUGUG
vvi-miR3633a-5p	*Pvul-GASA12*	5.0	−1.0	GGAAUGGAUGGUUAGGAGAG	UUCUUCUAGCCAUCU-UUCU
Zea mays					
zma-miR159e-5p	*Pvul-GASA23*	4.0	−1.0	CAGCUCCUGCAGCAUCUGUUC	UCAAAAAUGCUGCAGAAGUUG
zma-miR159h-3p	*Pvul-GASA4*	5.0	−1.0	UUUGGAGUGAAGGGAGCUCUG	CAAAGCUCUCUUAGCUUCAAU
zma-miR159i-3p	*Pvul-GASA4*	5.0	−1.0	UUUGGAGUGAAGGGAGCUCUG	CAAAGCUCUCUUAGCUUCAAU
zma-miR164a-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
zma-miR164b-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
zma-miR164c-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
zma-miR164d-3p	*Pvul-GASA18*	4.5	−1.0	CACGUGGUCUCCUUCUCCAU	AUGGGCAUGGAGACCACCUG
zma-miR164d-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
zma-miR164f-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCU	CCUUCUUGCCUUGCUUCUCCU
zma-miR164g-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGCA	CCUUCUUGCCUUGCUUCUCCU
zma-miR164h-5p	*Pvul-GASA3*	4.5	−1.0	UGGAGAAGCAGGGCACGUGUG	CCUUCUUGCCUUGCUUCUCCU

zma-miR396c	*Pvul-GASA4*	3.5	−1.0	UUCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGAA
zma-miR396c	*Pvul-GASA1*	3.0	−1.0	UUCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGAA
zma-miR396c	*Pvul-GASA2*	3.5	−1.0	UUCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGAA
zma-miR396c	*Pvul-GASA3*	3.5	−1.0	UUCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGAA
zma-miR396c	*Pvul-GASA20*	4.0	−1.0	UUCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGAA
zma-miR396d	*Pvul-GASA1*	3.0	−1.0	UUCCACAGGCUUUCUUGAACUG	CUCUGCAAAAGAGCUUGUGGAA
zma-miR396d	*Pvul-GASA4*	3.5	−1.0	UUCCACAGGCUUUCUUGAACUG	CUAUGCAAGAGGGCAUGUGGAA
zma-miR396d	*Pvul-GASA2*	3.5	−1.0	UUCCACAGGCUUUCUUGAACUG	CUAUGCGAAAGAGCUUGUGGAA
zma-miR396d	*Pvul-GASA3*	3.5	−1.0	UUCCACAGGCUUUCUUGAACUG	CUCUGCGAAAGAGCUUGUGGAA
zma-miR396d	*Pvul-GASA20*	4.0	−1.0	UUCCACAGGCUUUCUUGAACUG	AUGUGUCACAGAGCCUGUGGAA
zma-miR399c-5p	*Pvul-GASA18*	5.0	−1.0	GGGUACGUCUCCUUUGGCACA	AAUGCUCGAGGAGAUGUAGCA
zma-miR399d-5p	*Pvul-GASA17*	4.5	−1.0	GUGUGGCUCUCCUCUGGCAUG	CCUCCUCAAGGAGAGCCAUGC
zma-miR408b-5p	*Pvul-GASA15*	5.0	−1.0	CAGGGACGAGGCAGAGCAUGG	CUAUUUUCUGCUUCAUCCUUA
zma-miR444a	*Pvul-GASA18*	5.0	−1.0	UGCAGUUGUUGUCUCAAGCUU	GCCCUUGCUACAACAACUGGA
zma-miR444b	*Pvul-GASA18*	5.0	−1.0	UGCAGUUGUUGUCUCAAGCUU	GCCCUUGCUACAACAACUGGA