2017

Evolution of antagonistic relationships in proteins: a case study of RADIALIS- and DIVIRICATA-like genes

Ao Gao

Evolution of antagonistic relationships in proteins: a case study of *RADIALIS*- and *DIVIRICATA*-like genes

A Thesis submitted in partial fulfillment of the requirements for the degree of Master of Science at Virginia Commonwealth University.

by

AO GAO
BACHELOR OF SCIENCE, TEXAS A&M UNIVERSITY-CORPUS CHRISTI, 2014
MASTER OF SCIENCE, VIRGINIA COMMONWEALTH UNIVERSITY, 2017

Director: WENHENG ZHANG, PHD
ASSISTANT PROFESSOR, DEPARTMENT OF BIOLOGY

Virginia Commonwealth University
Richmond, Virginia
July, 2017

Acknowledgements

It is a great opportunity and pleasure to express my profound gratitude to people who helped me during these two years. To my advisor Dr. Wenheng Zhang, a very special thank you for the inspiration, priceless advice, constant guidance, friendship, mentorship, and continuing gifts of wisdom. Thank you for helping me as a research scientist and in life. I am also very thankful to my committee members: Dr. Wenheng Zhang, Dr. Andrew Eckert, Dr. Maria Rivera, and Dr. Cheng Ly who gave me helpful advice during for my thesis. To my dear parents, thank you for all of the endless support and encouragement. In addition, I would like to extend my special appreciation to my labmates-Dr. Jingbo Zhang, Farahnoz Khojayori, Joon Kim, and Ghadeer Bukhari-for their friendship and support in providing assistance to complete my study. My roomates also helped me in life.

Table of Contents

List of Tables

List of Figures

List of Abbreviations

RADIALIS: *RAD*

DIVIRICATA: *DIV*

CYCLOIDEA: *CYC*

DICHOTOMA: *DICH*

DIV-and-RAD-interacting-factors: DRIFs

fruit SANT/MYB binding protein1: FSB1

fruit SANT/MYB-like: FSM1

ML: Maximum likelihood.

Abstract

Evolution of antagonization relationships in proteins: a case study of *RADIALIS*- and *DIVIRICATA*-like genes

By Ao Gao, B.S.

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science
in Biology at Virginia Commonwealth University.

Virginia Commonwealth University, 2017

Major Advisor: Wenheng Zhang
Assistant Professor, Department of Biology

The antagonistic relationship of proteins describes the opponent interactions that result in one protein suppressing the function of another. Developmental genetic studies of *Antirrhinum majus* demonstrated that two transcription factors from the MYB gene family, *RAD* and *DIV*, interact through antagonism to regulate floral dorsoventral asymmetry. Interestingly, similar antagonistic interactions were found among proteins of FSM1 (RAD-like), MYBI (DIV-like), and DRIF in *Solanum lycopersicum*, which is involved in fruit development. Here, we report on the homology of these antagonistic MYB proteins based on reconstruction of the phylogeny of I-

box-like and R-R-type clades, where *RAD*- and *DIV*-like belong, respectively. Three paralogs of *RAD-/I-box*-like genes, *RAD1*, *RAD2*, and *RAD3* are reprensent in the phylogeny, which originated in the common ancestor of the core eudicots. In contrast, R-R-type sequences fall into two major clades, *RR1* and *RR2,* which are the result of gene duplication in the common ancestor of monocots and dicots. *RR1* was divided into clades, *RR1A*, *RR1B*, and *RR1C*, while *RR2* divided into clades, *RR2A*/*DIV1*, *RR2B*/*DIV2*, and *RR2C*/*DIV3*. We demonstrate that among similar antagonistic interactions in *A. majus* and *So. lycopersicum*, *RAD*-like genes originate from the RAD2 clade, while *DIV*-like genes originate from distantly related paralogs of the R-R-type lineage.

Introduction

Antagonism is a type of competitive relationship among molecules, which is a key mechanism used for regulating development in organisms (Zimmerman, DeJesusEscobar, & Harland, 1996). When antagonist and agonist molecules compete for the target site of the receptor, the binding of the antagonist to the target site will prevent the binding of the agonist. The antagonist, therefore, blocks the biological function of the agonist and the receptor (Zimmerman et al., 1996). How the proteins involved in the antagonistic relationships evolve as a whole system still awaits to be revealed.

In plants, one such example has been found in the regulation of the development of floral symmetry in the Lamiales (!!! INVALID CITATION !!!). In the zygomorphic flowers of *Antirrhinum majus* L., the two dorsal petals are significantly enlarged compared to the lateral and ventral petals and the single dorsal stamen is aborted (Luo, Carpenter, Vincent, Copsey, & Coen, 1996). Two genes, *CYC* and *DICH*, belonging to the *CYC*/*TB1* clade of the TCP transcription factor family, were found to promote the dorsal identity of zygomorphic flowers (!!! INVALID CITATION !!!). *RAD*, a member of the MYB gene family, was found to be the downstream target of *CYC* and *DICH* (!!! INVALID CITATION !!!). Plants of the double *cyc/dich* or the single *rad* mutants produce flowers that have entirely or partially lost their dorsal identity (!!! INVALID CITATION !!!). The dorsal petals assume the ventral petal identity and the aborted dorsal stamen becomes functional (Luo et al., 1996). *DIV*, a member of a different MYB lineage, promotes ventral floral identity (Almeida, Rocheta, & Galego, 1997). A single *div* mutant causes the loss of the ventral petal identity (!!! INVALID CITATION !!!). In the *cyc/dich/div* triple mutant, where the function of both the dorsal and ventral identity genes was lost, all petals resume the lateral petal identity (!!! INVALID CITATION !!!)

Recently, antagonism involving three MYB-like proteins was found to be a mechanism regulating floral symmetry in the flowers of *Antirrhinum* (!!! INVALID CITATION !!!). Despite the role of *DIV* in controlling ventral petal identity, its mRNA is transcribed across the floral meristem (!!! INVALID CITATION !!!). RAD was found to be the dorsal factor inactivating DIV, but not at the transcriptional level (!!! INVALID CITATION !!!). Interestingly, it was found that RAD and DIV do not directly interact with each other, but instead compete for the same protein target. DRIFs is also members of MYB family (!!! INVALID CITATION !!!). In particular, DIV and DRIFs show overlapping expression patterns and can form heterodimer complexes that bind to the DNA sequence of *DIV*, suggesting regulation of its transcription. RAD inhibits the interaction between DIV and DRIFs in the dorsal regions of the flowers of *Antirrhinum* by either binding directly to a DRIF protein in the nucleus and/or by sequestering the DRIF proteins in the cytoplasm (!!! INVALID CITATION !!!). Therefore, RAD acts as the antagonist that blocks the binding of DIV, the agonist, with the DRIFs, which is required for regulating ventral symmetry in the flowers of *Antirrhinum*.

Similar antagonistic relationships involving three MYB homologs were reported in fruit development of *Solanum lycopersicum*. (!!! INVALID CITATION !!!). FSB1, a DRIF homolog, was found to form a protein complex with the transcription factor MYBI, a DIV homolog. The fruit

FSM1, a RAD homolog, competes for FSB1 with MYBI. The function of FSM1 is to reduce fruit size and preferentially restricts differential cell expansion (!!! INVALID CITATION !!!). Ectopic expression of FSM1 results in a reduction in organ size by negatively affecting cell expansion. In contrast, FSB1 positively regulates differential cell expansion through physical interaction with MYBI (!!! INVALID CITATION !!!). This is analogous with the competition between RAD and the DIV-DRIF complex in the dorsal regions of the flowers of flowers of *Antirrhinum*. The function for the FSM1-FSB1-MYBI complex in *So. lycopersicum* controls cell expansion, while RAD-DRIF-DIV similarly also controls cell expansion in regulating dorsoventral flower asymmetry in *An. majus* (!!! INVALID CITATION !!!).

Previous research indicated frequent gene duplications during the evolution of *RAD*- and *DIV*-like genes (!!! INVALID CITATION !!!). Three paralogs of the RAD lineage, RAD1, RAD2, and RAD3, and three paralogs of the DIV lineage, DIV1, DIV2, and DIV3, are recognized (!!! INVALID CITATION !!!). The gene duplications that gave rise to these paralogs were predicted to have occurred around the diversification of the Pentapetalae. There may be antagonistic relationships among the homologs of RAD-DRIF-DIV in diverse lineages of the core eudicots. DRIFs, one of the three factors involved in this antagonistic interaction, belongs to an ancient MYB-like protein family with several homologs in the moss *Physcomitrella patens* (!!! INVALID CITATION !!!). Two paralogs of DRIFs resulting from gene duplication in the common ancestor of monocots and dicots are named Group 1 and 2 (!!! INVALID CITATION !!!). The DRIF1 and DRIF2 of *An. majus* belong to Group 1, while the only DRIF-like protein

(SlFSB1) found in *So. lycopersicum* belongs to Group 2. Therefore, in the antagonized systems in *A. majus* and *So. lycopersicum*, the DRIF homologs involved belong to two paralogous clades.

Here, we report on the evolution of the I-box-like and R-R-type gene lineages where *RAD*- and *DIV*-like genes belong, respectively, and aim to (1) reconstruct the phylogeny of the two MYB lineages, (2) clarify the phylogenetic relationships of the paralogs, and (3) identify the homology of *RAD*- and *DIV*-like genes that form the antagonistic relationships in *A. majus* and *So. lycopersicum*. We also focus on *RAD*-like gene evolution in Solanaceae, where lineage specific gene duplications were identified. We demonstrate that among similar antagonistic interactions in *An. majus* and *So. lycopersicum*, *RAD*-like genes originate from the closely related ortholog, while *DIV*-like genes originate from distantly related paralogs.

Materials and Methods

Cloning RAD-like genes from species of Solanaceae and Convolvulaceae:

Primers incorporated with degenerate polymorphic sites based on the alignment of *RAD*-like sequences, especially the RAD2 clade from Solanaceae and Lamiales, were used for amplifying the genes from species of Solanaceae and representatives of Convolvulaceae. The locations of our primers were referred to the study by (!!! INVALID CITATION !!!). These primers, i.e., forward primer 5'-AACAAGGCITTTGARARGGCWTYRGC-3', and reverse primer 5'-GGRAARGGBAYIMYACCAIDITCAAT-3', successfully amplified *RAD*-like genes from both the basal and derived clades of Solanaceae (*Schizanthus pinnatus* Ruiz & Pav, *Schizanthus grahamii* Gillies, *Petunia sp.*, *Nicotiana obtusifolia* M. Martens & Galeotti, *Solanum lycopersicum* L., *Lycium ruthenicum* Murray and *Atropa belladonna* L.) and species of Convolvulaceae (*Evolvulus sp*. and *Ipomoea tricolor* Cav.) (Table 1). PCR reactions were performed using GoTaq® G2 Hot Start Polymerase (Promega, Madison, WI, USA), as follows: 95°C for 5 min, 95°C for 45 s, 55°C for 45 s, and 72°C for 1 min, 30 s, repeated for 39 cycles, with a final step at 72°C for 10 mins. PCR products were then purified through gel extraction using Wizard SV Gel and PCR Clean-Up System from Promega (Madison, WI, USA). The purified PCR products were used as a template for the second round of PCR following the same PCR program described above. The purified second round PCR products were used in ligation and transformation with pGEM-T Easy Vector System I from Promega (Madison, WI, USA). At least 50 clones were screened for each species. The sequences of the clones were determined using Sanger sequencing by GENEWIZ (115 Corporate Boulevard, South Plainfield, NJ, USA).

Gene mining:

The *RAD*- and *DIV*-like genes were obtained through blasting *RAD* and *DIV* CDS sequences of *A. majus* (GenBank accession numbers: AY954971.1 and AY077453.1, respectively) against the following databases NCBI Blastn (http://www.ncbi.nlm.nih.gov/BLAST/), Phytozome 11 (https://phytozome.jgi.doe.gov), Sol Genomics Network (https://solgenomics.net), and Rice Genome Annotation Project (http://rice.plantbiology.msu.edu).

Alignment and phylogenetic analyses:

The DNA matrices of the coding sequences were aligned using Geneious version 7.1.9 (PO Box 5677, Wellesley St, Auckland 1010, New Zealand, USA). The MUSCLE algorithm that refers to the protein sequence alignment for building nucleotide sequence alignment was applied. Each DNA matrix was analyzed by using Bayesian and ML inferences, which were implemented in RAxML_HPC2, and MrBayes version 3.2.6 on XSEDE, respectively, at the CIPRES Science Gateway V. 3.3. (!!! INVALID CITATION !!!). For ML analyses, a random seed value for rapid ML bootstrapping was estimated on each dataset. The GTRCAT model was chosen for the bootstrapping analysis based on the programs because GTRCAT shows lower computational costs and memory consumption for the ML method (Stamatakis, 2006). The models used for the Bayesian analyses were estimated using jmodeltest 2.1.10 (!!! INVALID CITATION !!!). The Akaike Information Criterion (AIC) (Akaike, 1973) was used to determine the best-fit model for each DNA sequence matrix, i.e., K80 (K2P) + G model for the *I-box-like/RAD* gene phylogeny including *Arabidopsis*, *Solanum*, and *Oryza* alone, JC + G model for the large *RAD* phylogeny, GTR + I + G model for the *R-R-type* gene phylogeny including *Arabidopsis*, *Solanum*, and *Oryza* alone, and GTR + I + G model for the large *R-R-type* gene phylogeny. We used the Metropolis-coupled Markov chain Monte Carlo method as implemented in MrBayes to run four chains. We ran five million generations for each chain, and sampled every 1000 generations with a burn-in of the first 2000 trees.

Motif analyses:

We also did the domain test for *I-box*-like and *R-R*-type genes. For *I-box*-like genes, we included six sequences of *Arabidopsis thaliana*, i.e., At4g39250 (*Arabidopsis thaliana RL1*, NM_120086.2), At2g21650 (*Arabidopsis thaliana RL2*, NM_127736.3), At4g36570 (*Arabidopsis thaliana RL3*, BT011255.1), DQ395345 (*Arabidopsis thaliana RL4*, NM_001084443.1), At1g19510 (*Arabidopsis thaliana RL5*, NM_101808.4), and At1g75250 (*Arabidopsis thaliana RL6*, NM_001084356.2); eight sequences of *Oryza sativa*, i.e., (Oryza sativa RAD1, LOC_Os01g44390.2), 9640.m03280 (Oryza sativa RAD2, LOC_Os12g33950), 9631.m01422 (Oryza sativa RAD3, LOC_Os03g14810), 9631.m06332 (Oryza sativa RAD4, LOC_Os03g63890), 9633.m03415 (Oryza sativa RAD5, LOC_Os05g37040), 9633.m03416 (Oryza sativa RAD6, LOC_Os05g37050), 9635.m02514 (Oryza sativa RAD7, LOC_Os07g26150.1), 9640.m03280 (Oryza sativa RAD8, LOC_Os12g33950); one sequence of *An. majus*, *RAD*; one sequence of *So. Lycopersicum*, i.e., *FSM1*.

For *R-R*-type genes, we included nine sequences of *Arabidopsis thaliana*, i.e., At1g49010 (AY519528.1), At2g38090 (AY519529.1), At3g11280 (AY550308.1), At5g01200 (AY519530.1), At5g05790 (AY519531.1), At5g08520 (AY519532.1), At5g58900

(AY519533.1), At5g23650 (DQ056685.1), and At5g04760 (AB493736.1); seven sequences of *Oryza sativa*, i.e., 9632.m05667 (LOC_Os04g58020), 9629.m00414 (LOC_Os01g04930), 9629.m06276 (LOC_Os01g63460), 9629.m06374 (LOC_Os01g64360), 9633.m03417 LOC_Os05g37060), 9633.m03487 (LOC_Os05g37730), and 9631.m06132 (LOC_Os03g62100); one sequence of *An. majus*, i.e., *DIV*; one sequence of *So lycopersicum*, i.e., *MYBI.*

The nucleotide sequences of these CDS were translated into amino acid sequences by Mesquite version 3.2 (build 801). These amino acid sequences were prepared in an fasta file. The MEME algorithm extends the expectation maximization (EM) algorithm for identifying motifs in unaligned biopolymer sequences, which is designed to discover novel, ungapped motifs in a set of sequences (Bailey & Elkan, 1995). To use this function, we uploaded and analyzed the *I-box*-like and *R-R*-type genes into the Multiple Em for Motif Elicitation (MEME) option at http://meme-suite.org/index.html (Bailey & Elkan, 1994). We set each sequence in the dataset contains exactly one occurrence of each motif, and set three motifs should be found.

Results

RAD-like genes from Solanaceae:

Sixteen sequences of *RAD*-like genes were discovered in this study (GenBank numbers MF398572-MF398587) (Table 1). We show that our cloning method can recover all of the RAD2 paralogs identified from the genome data of *P. hybrida* and *So. lycopersicum* (Table 1).

Table 1. Species sampled for the RAD2 clade with collection locations, voucher information, sequence name, phylogenetic placement and number of clones sequenced.

Species	Family	Location	Voucher	Sequence names	Clades	No. of clones sequenced
Petunia sp.	Solanaceae	VCU Greenhouse	Zhang_Lab_23 (VCU)	*Petunia sp RAD1* *Petunia sp RAD2* *Petunia sp RAD3*	RAD2A RAD2A RAD2B	12 20 8
Lycium ruthenicum Murray.	Solanaceae	Taxkorgan Tajik Autonomous County, Xinjiang, China	CPG13183 (PE)	*Lycium ruthenicum Murr RAD*	RAD2A	20
Atropa belladonna L.	Solanaceae	Hotel Elites, Nathia Gali, Northwest Frontier Province, Pakistan	CPG13594 (PE)	*Atropa belladonna Linn RAD*	RAD2B	20
Schizanthus pinnatus Ruiz & Pav.	Solanaceae	VCU Greenhouse	Zhang_Lab_20 (VCU)	*Schizanthus pinnatus RAD1* *Schizanthus pinnatus RAD2*	RAD2B RAD2A	21 22
Schizanthus grahamii Gillies	Solanaceae	VCU Greenhouse	Zhang_Lab_19 (VCU)	*Schizanthus grahamii RAD1* *Schizanthus grahamii RAD2*	RAD2A RAD2B	21 19
Nicotiana obtusifolia M.Martens & Galeotti.	Solanaceae	VCU Greenhouse	Zhang_Lab_11 (VCU)	*Nicotiana obtusifolia RAD1* *Nicotiana obtusifolia RAD2*	RAD2A RAD2A	14 16
Solanum lycopersicum L.	Solanaceae	VCU Greenhouse	Zhang_Lab_21 (VCU)	*Solanum lycopersicum microtom RAD1*	RAD2A	17
				Solanum lycopersicum microtom RAD2	RAD2B	13
Evolvulus sp.	Convolvulaceae	VCU Greenhouse	Zhang_Lab_18 (VCU)	*Evulupus sp RAD1* *Evulupus sp RAD2*	RAD2B RAD2A	20 17
Ipomoea tricolor Cav.	Convolvulaceae	VCU Greenhouse	Zhang_Lab_22 (VCU)	*Ipomoea tricolor RAD1*	RAD2A	20

Virginia Commonwealth University (VCU) is in Richmond, VA, USA. VCU, Virginia Commonwealth University Herbaria; PE, Institute of Botany, Chinese Academy of Sciences Herbarium, Beijing, China.

Diversity and phylogeny of I-Box-like MYB genes:

A total of 274 *RAD*-like CDSs were found in 101 species representing 28 families and 15 orders of dicots (Solanales, Vitales, Brassicales, Malvales, Malpighiales, Ranunculales, Lamiales, Saxifragales, Rosales, Fabales, Proteales, Cucurbitales, Myrtales, Dipsacales, and Sapindales) and monocots (Appendix 1). Among the sequences, 79 CDS belong to 17 species of seven genera of Solanaceae, which includes the FSM1 from *So. lycopersicum* (!!! INVALID CITATION !!!). For *Arabidopsis*, six *RAD* homologs, At4g39250 (*Arabidopsis thaliana RL1*, NM_120086.2), At2g21650 (*Arabidopsis thaliana RL2*, NM_127736.3), At4g36570 (*Arabidopsis thaliana RL3*, BT011255.1), DQ395345 (*Arabidopsis thaliana RL4*, NM_001084443.1), At1g19510 (*Arabidopsis thaliana RL5*, NM_101808.4), and At1g75250 (*Arabidopsis thaliana RL6*, NM_001084356.2) were included.

A phylogeny of *RAD*-like genes was constructed based on 53 sequences from four species of *Arabidopsis* (*A. thaliana*, *A. halleri*, *A. lyrata*, and *A. salsuginea*), six species of *Solanum* (*So. melongena So. pennellii*, *So. lycopersicum*, *So. pimpinellifolium*, and *So. peruvianum,* and *So. tuberosum*), and *Oryza sativa* (Fig. 1 and Appendix 4). The phylogeny indicated that sequences from *O. sativa* form a monophyletic clade. But the phylogenetic relationships among the three previously identified RAD1, RAD2, and RAD3 clades (!!! INVALID CITATION !!!) were not fully resolved. The RAD2 clade is likely monophyletic while the RAD1 and RAD3 are not (Fig. 1 Appendix 4, also see below). The RAD2 clade consists of *Arabidopsis thaliana RL1* and *Arabidopsis thaliana RL2* and species of *Solanum*, which were further divided into two *Solanum*-specific clades, RAD2A and RAD2B. The *FSM1* of *So. lycopersicum* was placed in the RAD2A clade. It is unclear, however, how the other sequences of *Solanum* sould be placed within the RAD1 represented by

Arabidopsis thaliana RL3 and *Arabidopsis thaliana RL4* and with the RAD3 clade represented by *Arabidopsis thaliana RL5* and *Arabidopsis thaliana RL6* (Fig. 1 and Appendix 4) (!!! INVALID CITATION !!!).

Another phylogeny of *RAD*-like genes was reconstructed based on 274 CDS, including 258 from blast results and 16 in this study (Fig. 2, Appendix 1 and 5). All eight species from seven families of monocots form a clade and were used to root the phylogeny. RAD2 formed a clade, while both RAD1 and RAD3 were not fully resolved (Figs. 1 and 2; Appendix 4 and 5). RAD2 comprised representatives from eleven orders: Vitales, Rosales, Malvales, Fabales, Cucurbitales, Sapindales, Malpighiales, Brassicales, Solanales, Lamiales, and Dipsacales (Fig. 2; Appendix 1 and 5). Most of the solanaceous and convolvulaceous *RAD*-like sequences fell into the RAD2 clade, which was further divided into two clades, RAD2A and RAD2B (Figs. 1 and 2; Appendix 2, 4, 5, and 8). The unrooted phylogeny including only RAD2 of Solanaceae and Convolvulaceae further indicated that two paralogs were likely formed at least in the common ancestor of the two families (Appendix 2 and 8). Further gene duplication and gene losses likely also occurred, which led to *Nicotiana* and *Petunia* having additional paralogs in RAD2A (Fig. 2, Appendix 2, 5, and 8). RAD2 sequences from the two species of *Schizanthus*, the first branching clade of Solanaceae (Särkinen, Bohs, Olmstead, & Knapp, 2013), were more closely related to the sequences from Convolvulaceae, which might be due to the limited sampling. The *FSM1* of *So. lycopersicum* that expresses in fruit was grouped in the RAD2A clade, while the *RAD* of *An. majus* was also in the RAD2 clade.

Figure. 1

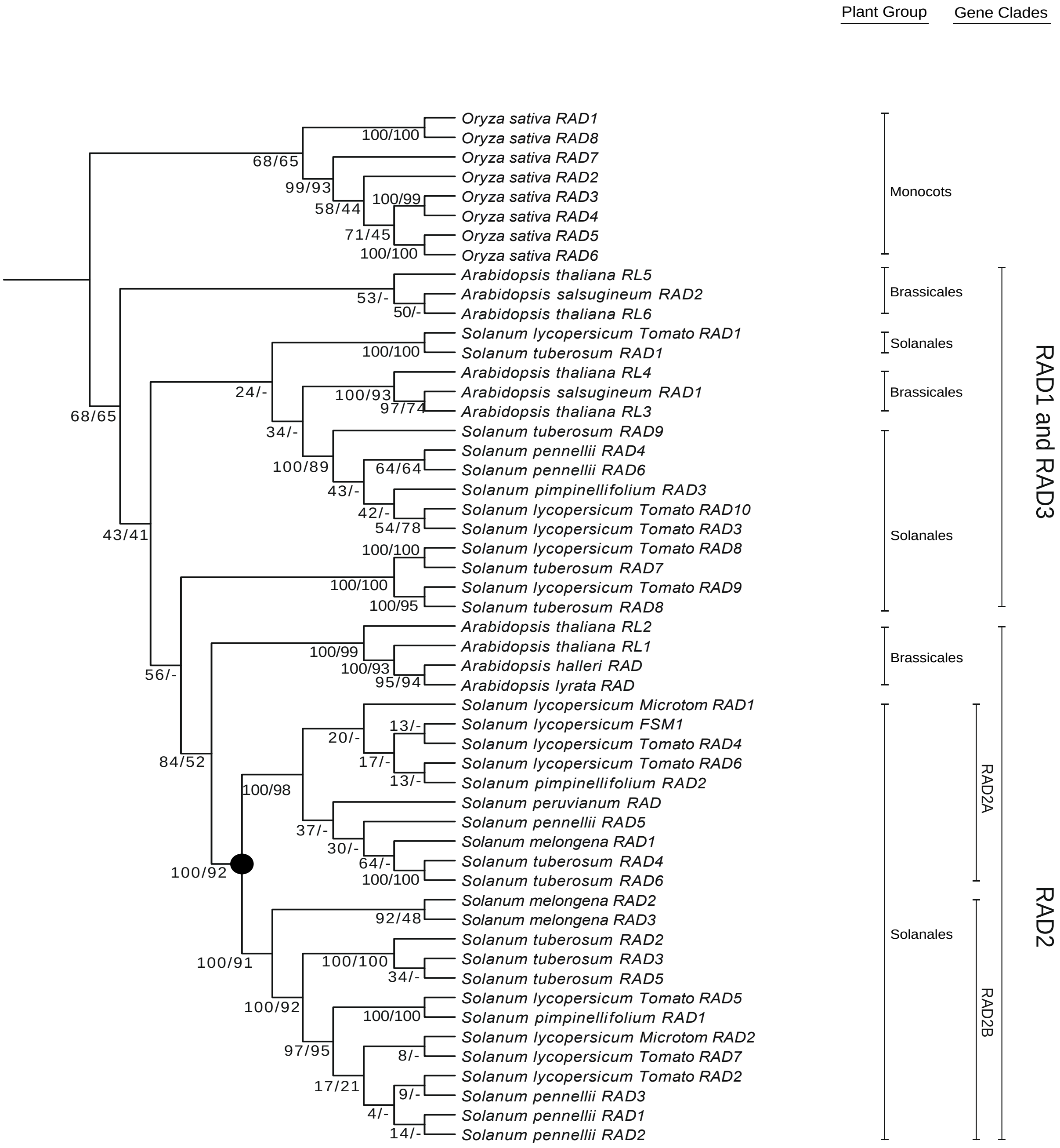

Plant Group
Gene Clades
Oryza sativa RAD1
Oryza sativa RAD8
Oryza sativa RAD7
Oryza sativa RAD2
Oryza sativa RAD3
Oryza sativa RAD4
Oryza sativa RAD5
Oryza sativa RAD6
Arabidopsis thaliana RL5
Arabidopsis salsugineum RAD2
Arabidopsis thaliana RL6
Solanum lycopersicum Tomato RAD1
Solanum tuberosum RAD1
Arabidopsis thaliana RL4
Arabidopsis salsugineum RAD1
Arabidopsis thaliana RL3
Solanum tuberosum RAD9
Solanum pennellii RAD4
Solanum pennellii RAD6
Solanum pimpinellifolium RAD3
Solanum lycopersicum Tomato RAD10
Solanum lycopersicum Tomato RAD3
Solanum lycopersicum Tomato RAD8
Solanum tuberosum RAD7
Solanum lycopersicum Tomato RAD9
Solanum tuberosum RAD8
Arabidopsis thaliana RL2
Arabidopsis thaliana RL1
Arabidopsis halleri RAD
Arabidopsis lyrata RAD
Solanum lycopersicum Microtom RAD1
Solanum lycopersicum FSM1
Solanum lycopersicum Tomato RAD4
Solanum lycopersicum Tomato RAD6
Solanum pimpinellifolium RAD2
Solanum peruvianum RAD
Solanum pennellii RAD5
Solanum melongena RAD1
Solanum tuberosum RAD4
Solanum tuberosum RAD6
Solanum melongena RAD2
Solanum melongena RAD3
Solanum tuberosum RAD2
Solanum tuberosum RAD3
Solanum tuberosum RAD5
Solanum lycopersicum Tomato RAD5
Solanum pimpinellifolium RAD1
Solanum lycopersicum Microtom RAD2
Solanum lycopersicum Tomato RAD7
Solanum lycopersicum Tomato RAD2
Solanum pennellii RAD3
Solanum pennellii RAD1
Solanum pennellii RAD2
100/100
68/65
99/93
58/44
100/99
71/45
100/100
53/-
50/-
100/100
68/65
24/-
100/93
97/74
34/-
100/89
64/64
43/-
42/-
54/78
43/41
100/100
100/100
100/95
56/-
100/99
100/93
95/94
13/-
20/-
17/-
13/-
84/52
100/98
37/-
30/-
64/-
100/92
100/100
92/48
100/91
100/100
34/-
100/92
100/100
97/95
8/-
17/21
9/-
4/-
14/-
Monocots
Brassicales
Solanales
Brassicales
Solanales
Brassicales
Solanales
RAD1 and RAD3
RAD2A
RAD2
RAD2B

Figure 1. Phylogeny of *I-box-binding/RADIALIS*-like genes of four species of *Arabidopsis*, six species of *Solanum*, and *Oryza sativa* based on Bayesian and ML inferences. All sequences from *O. sativa* form a clade, which was used to root the phylogeny. Based on the clade defined by Boyden et al. (2012), only the RAD2 clade was found to be monophyletic and contains sequences from *Arabidopsis* and *Solanum*. There are two paralogs, in RAD2 clade, RAD2A and RAD2B, of which the *Arabidopsis* does not involve in this gene duplication. RAD1 and RAD3 are paraphyletic. Bayesian posterior probabilities and bootstrap frequencies are labeled at the nodes and are separted by a slash

Figure. 2a

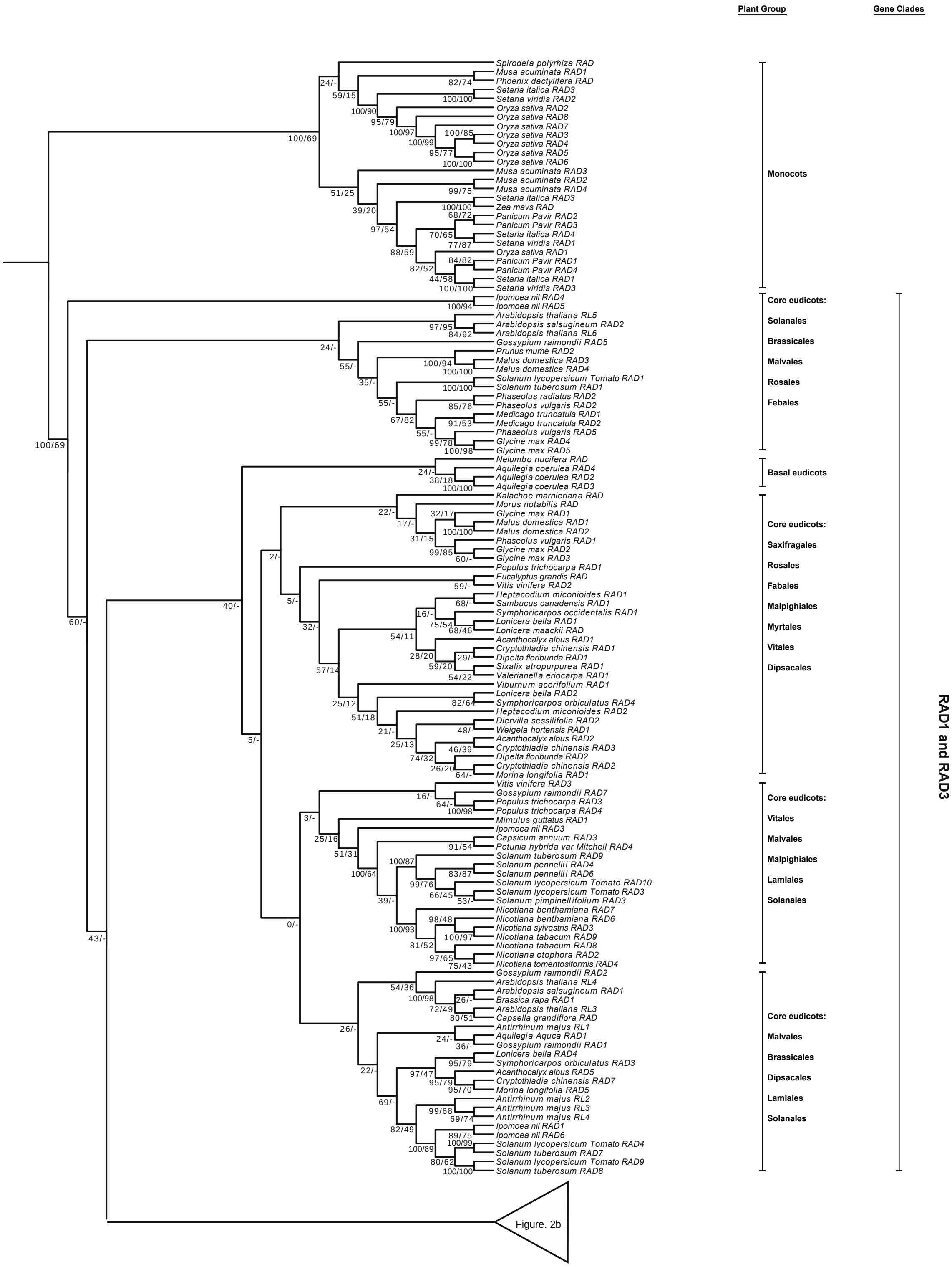

Plant Group
Gene Clades
Spirodela polyrhiza RAD
Musa acuminata RAD1
Phoenix dactylifera RAD
Setaria italica RAD3
Setaria viridis RAD2
Oryza sativa RAD2
Oryza sativa RAD8
Oryza sativa RAD7
Oryza sativa RAD3
Oryza sativa RAD4
Oryza sativa RAD5
Oryza sativa RAD6
Musa acuminata RAD3
Musa acuminata RAD2
Musa acuminata RAD4
Setaria italica RAD3
Zea mavs RAD
Panicum Pavir RAD2
Panicum Pavir RAD3
Setaria italica RAD4
Setaria viridis RAD1
Oryza sativa RAD1
Panicum Pavir RAD1
Panicum Pavir RAD4
Setaria italica RAD1
Setaria viridis RAD3
Ipomoea nil RAD4
Ipomoea nil RAD5
Arabidopsis thaliana RL5
Arabidopsis salsugineum RAD2
Arabidopsis thaliana RL6
Gossypium raimondii RAD5
Prunus mume RAD2
Malus domestica RAD3
Malus domestica RAD4
Solanum lycopersicum Tomato RAD1
Solanum tuberosum RAD1
Phaseolus radiatus RAD2
Phaseolus vulgaris RAD2
Medicago truncatula RAD1
Medicago truncatula RAD2
Phaseolus vulgaris RAD5
Glycine max RAD4
Glycine max RAD5
Nelumbo nucifera RAD
Aquilegia coerulea RAD4
Aquilegia coerulea RAD2
Aquilegia coerulea RAD3
Kalachoe marnieriana RAD
Morus notabilis RAD
Glycine max RAD1
Malus domestica RAD1
Malus domestica RAD2
Phaseolus vulgaris RAD1
Glycine max RAD2
Glycine max RAD3
Populus trichocarpa RAD1
Eucalyptus grandis RAD
Vitis vinifera RAD2
Heptacodium miconioides RAD1
Sambucus canadensis RAD1
Symphoricarpos occidentalis RAD1
Lonicera bella RAD1
Lonicera maackii RAD
Acanthocalyx albus RAD1
Cryptothladia chinensis RAD1
Dipelta floribunda RAD1
Sixalix atropurpurea RAD1
Valerianella eriocarpa RAD1
Viburnum acerifolium RAD1
Lonicera bella RAD2
Symphoricarpos orbiculatus RAD4
Heptacodium miconioides RAD2
Diervilla sessilifolia RAD2
Weigela hortensis RAD1
Acanthocalyx albus RAD2
Cryptothladia chinensis RAD3
Dipelta floribunda RAD2
Cryptothladia chinensis RAD2
Morina longifolia RAD1
Vitis vinifera RAD3
Gossypium raimondii RAD7
Populus trichocarpa RAD3
Populus trichocarpa RAD4
Mimulus guttatus RAD1
Ipomoea nil RAD3
Capsicum annuum RAD3
Petunia hybrida var Mitchell RAD4
Solanum tuberosum RAD9
Solanum pennellii RAD4
Solanum pennellii RAD6
Solanum lycopersicum Tomato RAD10
Solanum lycopersicum Tomato RAD3
Solanum pimpinellifolium RAD3
Nicotiana benthamiana RAD7
Nicotiana benthamiana RAD6
Nicotiana sylvestris RAD3
Nicotiana tabacum RAD9
Nicotiana tabacum RAD8
Nicotiana otophora RAD2
Nicotiana tomentosiformis RAD4
Gossypium raimondii RAD2
Arabidopsis thaliana RL4
Arabidopsis salsugineum RAD1
Brassica rapa RAD1
Arabidopsis thaliana RL3
Capsella grandiflora RAD
Antirrhinum majus RL1
Aquilegia Aquca RAD1
Gossypium raimondii RAD1
Lonicera bella RAD4
Symphoricarpos orbiculatus RAD3
Acanthocalyx albus RAD5
Cryptothladia chinensis RAD7
Morina longifolia RAD5
Antirrhinum majus RL2
Antirrhinum majus RL3
Antirrhinum majus RL4
Ipomoea nil RAD1
Ipomoea nil RAD6
Solanum lycopersicum Tomato RAD4
Solanum tuberosum RAD7
Solanum lycopersicum Tomato RAD9
Solanum tuberosum RAD8
Figure. 2b
24/-
59/15
82/74
100/100
100/90
95/79
100/97
100/85
100/99
95/77
100/100
100/69
51/25
99/75
39/20
100/100
68/72
97/54
70/65
77/87
88/59
84/82
82/52
44/58
100/100
100/94
97/95
84/92
24/-
55/-
100/94
100/100
35/-
100/100
55/-
85/76
67/82
91/53
55/-
99/78
100/98
100/69
24/-
38/18
100/100
22/-
32/17
17/-
100/100
31/15
99/85
60/-
2/-
59/-
5/-
68/-
40/-
16/-
75/54
32/-
68/46
54/11
60/-
28/20
29/-
59/20
57/14
54/22
25/12
82/64
51/18
21/-
48/-
25/13
46/39
74/32
26/20
64/-
5/-
16/-
64/-
100/98
3/-
25/16
51/31
91/54
100/87
100/64
83/87
99/76
66/45
39/-
53/-
43/-
0/-
98/48
100/93
100/97
81/52
97/65
75/43
54/36
100/98
26/-
72/49
80/51
26/-
24/-
36/-
95/79
22/-
97/47
95/79
95/70
69/-
99/68
69/74
82/49
89/75
100/99
100/89
80/62
100/100
Monocots
Core eudicots:
Solanales
Brassicales
Malvales
Rosales
Febales
Basal eudicots
Core eudicots:
Saxifragales
Rosales
Fabales
Malpighiales
Myrtales
Vitales
Dipsacales
Core eudicots:
Vitales
Malvales
Malpighiales
Lamiales
Solanales
Core eudicots:
Malvales
Brassicales
Dipsacales
Lamiales
Solanales
RAD1 and RAD3

Figure. 2b

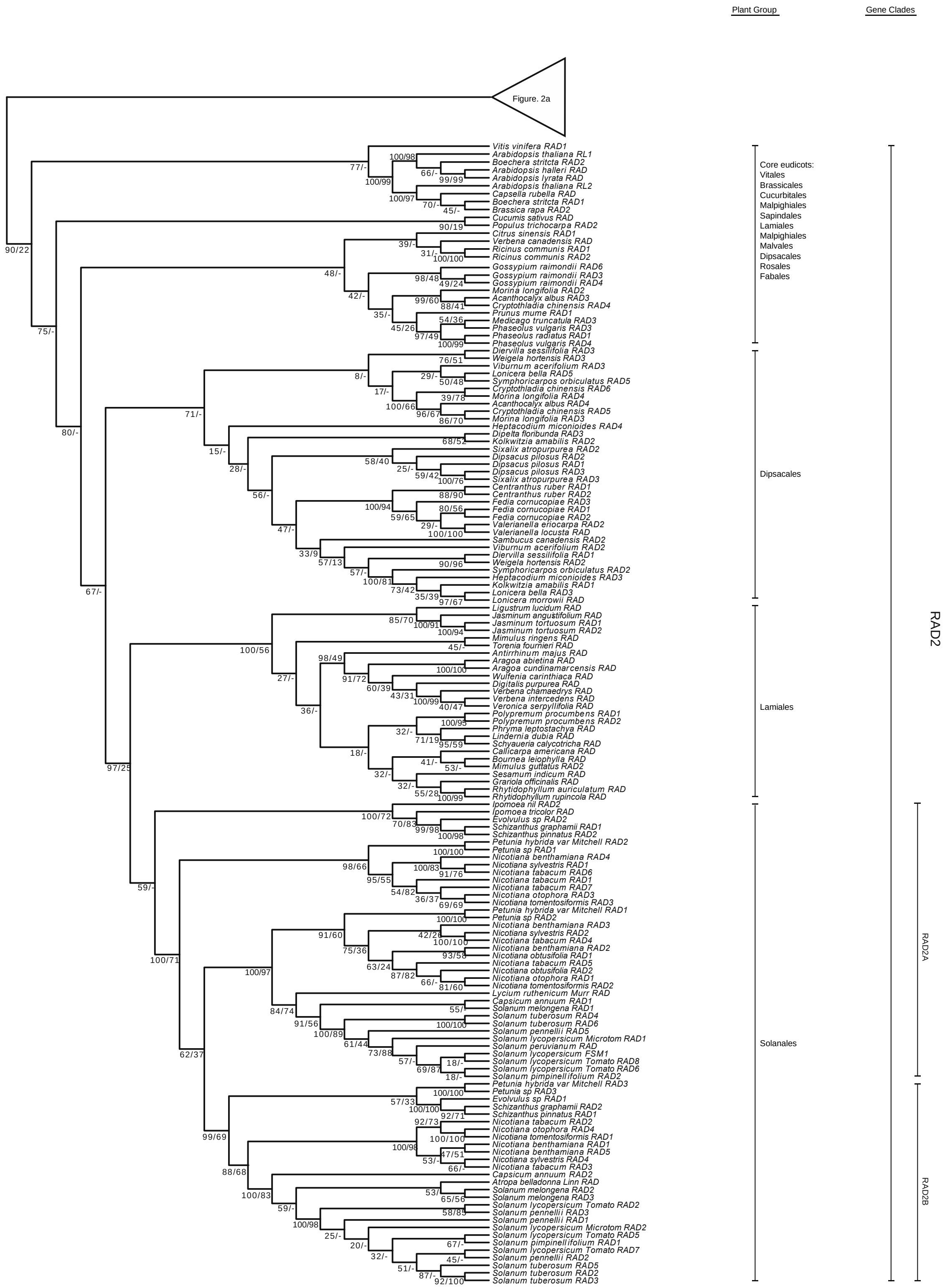

Plant Group
Gene Clades
Figure. 2a
Vitis vinifera RAD1
Arabidopsis thaliana RL1
Boechera strictca RAD2
Arabidopsis halleri RAD
Arabidopsis lyrata RAD
Arabidopsis thaliana RL2
Capsella rubella RAD
Boechera strictca RAD1
Brassica rapa RAD2
Cucumis sativus RAD
Populus trichocarpa RAD2
Citrus sinensis RAD1
Verbena canadensis RAD
Ricinus communis RAD1
Ricinus communis RAD2
Gossypium raimondii RAD6
Gossypium raimondii RAD3
Gossypium raimondii RAD4
Morina longifolia RAD2
Acanthocalyx albus RAD3
Cryptothladia chinensis RAD4
Prunus mume RAD1
Medicago truncatula RAD3
Phaseolus vulgaris RAD3
Phaseolus radiatus RAD1
Phaseolus vulgaris RAD4
Diervilla sessilifolia RAD3
Weigela hortensis RAD3
Viburnum acerifolium RAD3
Lonicera bella RAD5
Symphoricarpos orbiculatus RAD5
Cryptothladia chinensis RAD6
Morina longifolia RAD4
Acanthocalyx albus RAD4
Cryptothladia chinensis RAD5
Morina longifolia RAD3
Heptacodium miconioides RAD4
Dipelta floribunda RAD3
Kolkwitzia amabilis RAD2
Sixalix atropurpurea RAD2
Dipsacus pilosus RAD2
Dipsacus pilosus RAD1
Dipsacus pilosus RAD3
Sixalix atropurpurea RAD3
Centranthus ruber RAD1
Centranthus ruber RAD2
Fedia cornucopiae RAD3
Fedia cornucopiae RAD1
Fedia cornucopiae RAD2
Valerianella eriocarpa RAD2
Valerianella locusta RAD
Sambucus canadensis RAD2
Viburnum acerifolium RAD2
Diervilla sessilifolia RAD1
Weigela hortensis RAD2
Symphoricarpos orbiculatus RAD2
Heptacodium miconioides RAD3
Kolkwitzia amabilis RAD1
Lonicera bella RAD3
Lonicera morrowii RAD
Ligustrum lucidum RAD
Jasminum angustifolium RAD
Jasminum tortuosum RAD1
Jasminum tortuosum RAD2
Mimulus ringens RAD
Torenia fournieri RAD
Antirrhinum majus RAD
Aragoa abietina RAD
Aragoa cundinamarcensis RAD
Wulfenia carinthiaca RAD
Digitalis purpurea RAD
Verbena chamaedrys RAD
Verbena intercedens RAD
Veronica serpyllifolia RAD
Polypremum procumbens RAD1
Polypremum procumbens RAD2
Phryma leptostachya RAD
Lindernia dubia RAD
Schyaueria calycotricha RAD
Callicarpa americana RAD
Bournea leiophylla RAD
Mimulus guttatus RAD2
Sesamum indicum RAD
Gratiola officinalis RAD
Rhytidophyllum auriculatum RAD
Rhytidophyllum rupincola RAD
Ipomoea nil RAD2
Ipomoea tricolor RAD
Evolvulus sp RAD2
Schizanthus graphamii RAD1
Schizanthus pinnatus RAD2
Petunia hybrida var Mitchell RAD2
Petunia sp RAD1
Nicotiana benthamiana RAD4
Nicotiana sylvestris RAD1
Nicotiana tabacum RAD6
Nicotiana tabacum RAD1
Nicotiana tabacum RAD7
Nicotiana otophora RAD3
Nicotiana tomentosiformis RAD3
Petunia hybrida var Mitchell RAD1
Petunia sp RAD2
Nicotiana benthamiana RAD3
Nicotiana sylvestris RAD2
Nicotiana tabacum RAD4
Nicotiana benthamiana RAD2
Nicotiana obtusifolia RAD1
Nicotiana tabacum RAD5
Nicotiana obtusifolia RAD2
Nicotiana otophora RAD1
Nicotiana tomentosiformis RAD2
Lycium ruthenicum Murr RAD
Capsicum annuum RAD1
Solanum melongena RAD1
Solanum tuberosum RAD4
Solanum tuberosum RAD6
Solanum pennellii RAD5
Solanum lycopersicum Microtom RAD1
Solanum peruvianum RAD
Solanum lycopersicum FSM1
Solanum lycopersicum Tomato RAD8
Solanum lycopersicum Tomato RAD6
Solanum pimpinellifolium RAD2
Petunia hybrida var Mitchell RAD3
Petunia sp RAD3
Evolvulus sp RAD1
Schizanthus graphamii RAD2
Schizanthus pinnatus RAD1
Nicotiana tabacum RAD2
Nicotiana otophora RAD4
Nicotiana tomentosiformis RAD1
Nicotiana benthamiana RAD1
Nicotiana benthamiana RAD5
Nicotiana sylvestris RAD4
Nicotiana tabacum RAD3
Capsicum annuum RAD2
Atropa belladonna Linn RAD
Solanum melongena RAD2
Solanum melongena RAD3
Solanum lycopersicum Tomato RAD2
Solanum pennellii RAD3
Solanum pennellii RAD1
Solanum lycopersicum Microtom RAD2
Solanum lycopersicum Tomato RAD5
Solanum pimpinellifolium RAD1
Solanum lycopersicum Tomato RAD7
Solanum pennellii RAD2
Solanum tuberosum RAD5
Solanum tuberosum RAD2
Solanum tuberosum RAD3
Core eudicots:
Vitales
Brassicales
Cucurbitales
Malpighiales
Sapindales
Lamiales
Malpighiales
Malvales
Dipsacales
Rosales
Fabales
Dipsacales
Lamiales
Solanales
RAD2
RAD2A
RAD2B

Figure 2. Phylogeny of *I-box-binding/RADIALIS*-like genes based on Bayesian and ML inferences. 274 CDS of *I-box-binding/RADIALIS*-like genes from both monocots and dicots were analyzed. All sequences from monocots formed a monophyletic group, which was used to root the phylogeny. RAD2 forms a clade. At least one gene duplication was identified in the common ancestor of Solanaceae and Convolvulaceae. RAD1 and RAD3 are paraphyletic. Bayesian posterior probabilities and bootstrap frequencies are labeled at the nodes and are separted by a slash

Diversity and phylogeny of R-R-type MYB genes:

One thousand seventy five CDS that represent both *R-R-type* and *CCA1*-like genes from 109 species representing 34 different families from 22 orders of plants (16 of dicots, four of monocots, and two of mosses) were recovered (Appendix 3). For *A. thaliana*, the blast results in nine *R-R-type*, i.e., At1g49010 (AY519528.1), At2g38090 (AY519529.1), At3g11280 (AY550308.1), At5g01200 (AY519530.1), At5g05790 (AY519531.1), At5g08520 (AY519532.1), At5g58900 (AY519533.1), At5g23650 (DQ056685.1), and At5g04760 (AB493736.1) and one *CCA1*-like gene, i.e., At3g16350 (AY519512.1) (!!! INVALID CITATION !!!). For Solanaceae, we recovered 124 CDS, named *DIV*-, *MYB*- or *MYB1R1*-like genes, from the original studies of 12 species in 4 genera, including the *MYBI* of *So. lycopersicum*.

An *R-R-type* phylogeny was first reconstructed based on 52 CDS from *O. sativa japonica*, *A. thaliana*, and five species of *Solanum* (*So. melongena*, *So. lycopersicum*, *So. pennellii*, *So. peruvianum*, and *So. tuberosum*) (Fig. 3 and 6). All sequences fell into two clades, RR1 and RR2/DIV. The RR2/DIV clade was the same as the DIV clade identified by (!!! INVALID CITATION !!!). Each of those two clades contained sequences from *O. sativa*, *A. thaliana*, and *Solanum*.

The *R-R-type* gene phylogeny was also reconstructed based on 298 CDS from 75 species of 23 families (Appendix 3). The unrooted tree indicated that the RR1 and RR2/DIV clades were indeed monophyletic (Fig. 4 and Appendix 7). RR1 was further divided into three clades i.e., RR1A, RR1B, and RR1C. The RR1A clade included sequences from 12 orders of dicots

(Myrtales, Fabales, Sapindales, Vitales, Brassicales, Rosales, Malvales, Malpighiales, Ranunculales, Caryophyllales, Apiales, and Solanales). The RR1B clade had representatives from monocots and five orders of dicots (Myrtales, Brassicales, Fabales, Apiales, and Solanales). The RR1C clade had representatives from monocots and six orders of dicots (Caryophyllales, Myrtales, Brassicales, Rosales, Fabales, and Solanales). For *Arabidopsis*, AT5g04760 was placed in the RR1A clade, AT5G08520 and At5g23650 in the RR1B clade, and AT1G49010 in the RR1C clade. For the RR2/DIV clade, previously identified DIV2 and DIV3 clades formed monophyletic groups (!!! INVALID CITATION !!!). The sequences of *A. thaliana*, At2g38090, At5g01200, At5g58900 belonged to DIV1, and At3g11280 and At5g05790 belonged to DIV2. *Arabidopsis* lacked the *DIV3* gene based on previous work (!!! INVALID CITATION !!!). The *MYBI* of *So. lycopersicum* expressed in fruit was grouped in the RR1A group of the RR1 clade, while the *DIV* of *A. majus* was in RR2A/DIV1 of the RR2 clade.

Figure. 3

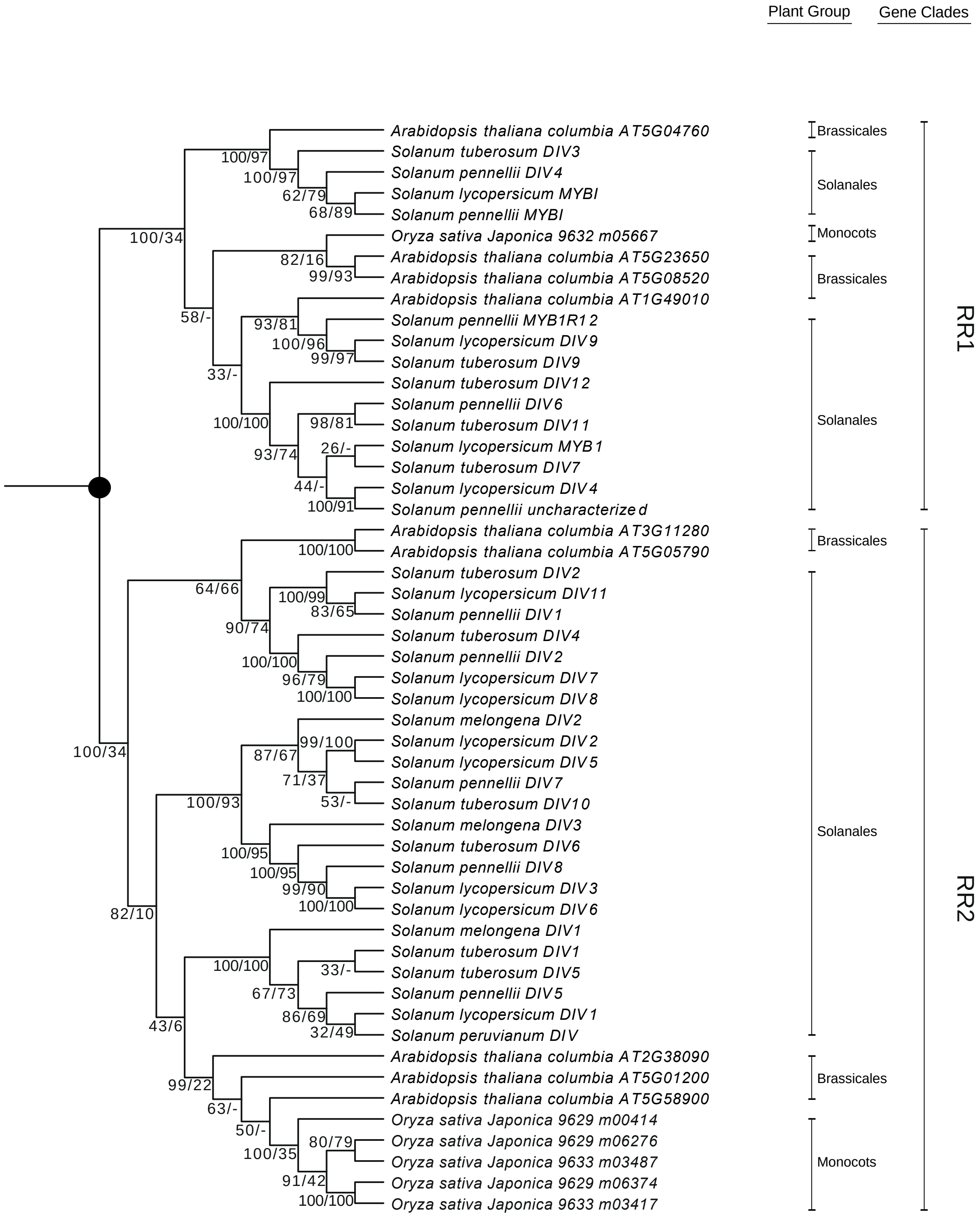

Plant Group
Gene Clades
Arabidopsis thaliana columbia AT5G04760
Solanum tuberosum DIV3
Solanum pennellii DIV4
Solanum lycopersicum MYBI
Solanum pennellii MYBI
Oryza sativa Japonica 9632 m05667
Arabidopsis thaliana columbia AT5G23650
Arabidopsis thaliana columbia AT5G08520
Arabidopsis thaliana columbia AT1G49010
Solanum pennellii MYB1R12
Solanum lycopersicum DIV9
Solanum tuberosum DIV9
Solanum tuberosum DIV12
Solanum pennellii DIV6
Solanum tuberosum DIV11
Solanum lycopersicum MYB1
Solanum tuberosum DIV7
Solanum lycopersicum DIV4
Solanum pennellii uncharacterized
Arabidopsis thaliana columbia AT3G11280
Arabidopsis thaliana columbia AT5G05790
Solanum tuberosum DIV2
Solanum lycopersicum DIV11
Solanum pennellii DIV1
Solanum tuberosum DIV4
Solanum pennellii DIV2
Solanum lycopersicum DIV7
Solanum lycopersicum DIV8
Solanum melongena DIV2
Solanum lycopersicum DIV2
Solanum lycopersicum DIV5
Solanum pennellii DIV7
Solanum tuberosum DIV10
Solanum melongena DIV3
Solanum tuberosum DIV6
Solanum pennellii DIV8
Solanum lycopersicum DIV3
Solanum lycopersicum DIV6
Solanum melongena DIV1
Solanum tuberosum DIV1
Solanum tuberosum DIV5
Solanum pennellii DIV5
Solanum lycopersicum DIV1
Solanum peruvianum DIV
Arabidopsis thaliana columbia AT2G38090
Arabidopsis thaliana columbia AT5G01200
Arabidopsis thaliana columbia AT5G58900
Oryza sativa Japonica 9629 m00414
Oryza sativa Japonica 9629 m06276
Oryza sativa Japonica 9633 m03487
Oryza sativa Japonica 9629 m06374
Oryza sativa Japonica 9633 m03417
100/97
100/97
62/79
68/89
100/34
82/16
99/93
58/-
93/81
100/96
99/97
33/-
100/100
98/81
93/74
26/-
44/-
100/91
100/100
64/66
100/99
83/65
90/74
100/100
96/79
100/100
100/34
99/100
87/67
71/37
53/-
100/93
100/95
100/95
99/90
100/100
82/10
100/100
33/-
67/73
86/69
32/49
43/6
99/22
63/-
50/-
80/79
100/35
91/42
100/100
Brassicales
Solanales
Monocots
Brassicales
Solanales
Brassicales
Solanales
Brassicales
Monocots
RR1
RR2

Figure 3. Phylogeny of *R-R-type* genes of five species of *Solanum*, *Arabidopsis thaliana,* and *Oryza sativa* based on Bayesian and ML inferences. Two major clades, RR1 and RR2 were identified, each of which includes sequences from *Arabidopsis*, *Oryza*, and *Solanaum*. Bayesian posterior probabilities and bootstrap frequencies are labeled at the nodes and are separted by a slash.

Figure. 4a

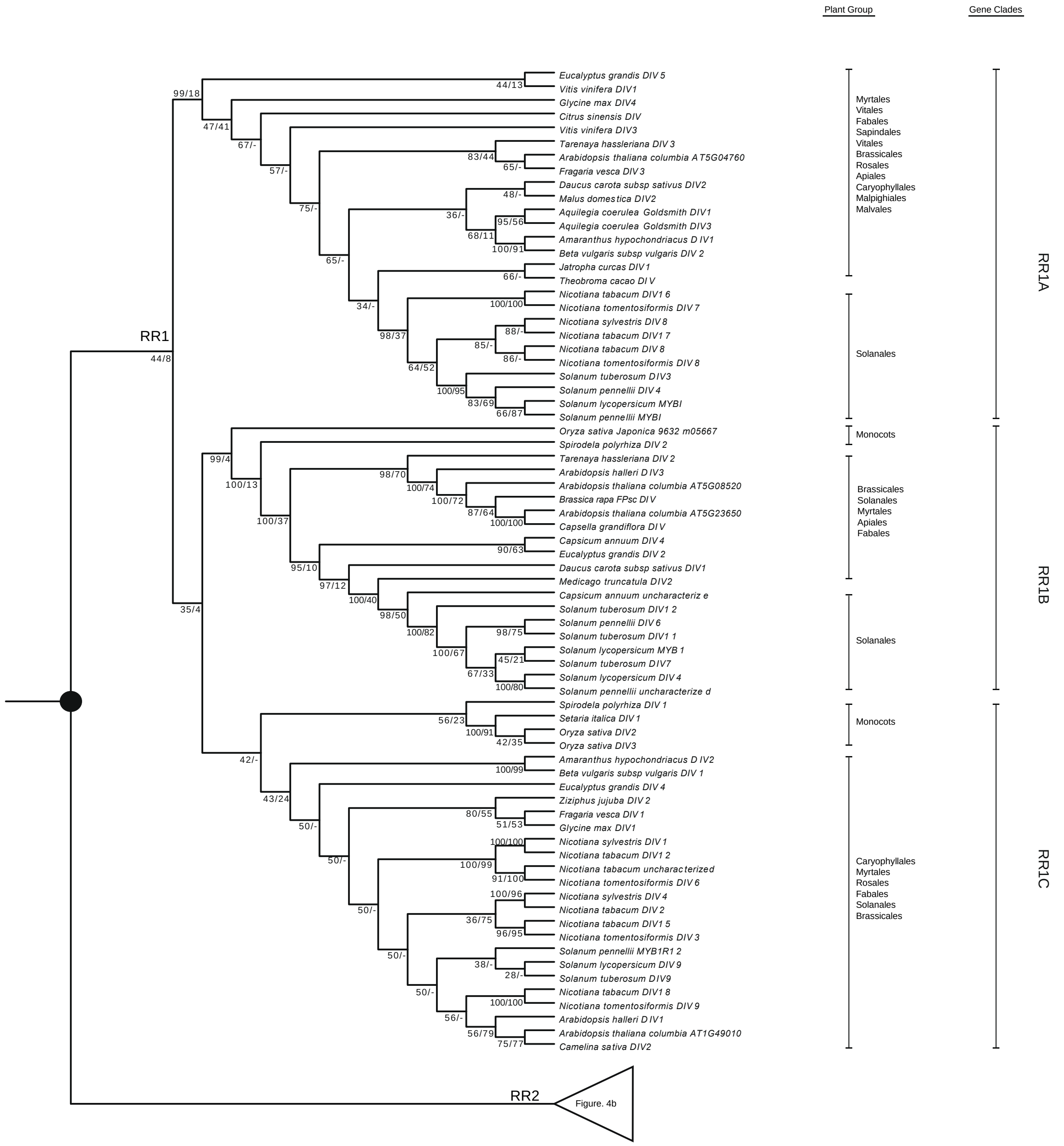

Plant Group
Gene Clades
Eucalyptus grandis DIV 5
Vitis vinifera DIV1
Glycine max DIV4
Citrus sinensis DIV
Vitis vinifera DIV3
Tarenaya hassleriana DIV 3
Arabidopsis thaliana columbia AT5G04760
Fragaria vesca DIV 3
Daucus carota subsp sativus DIV2
Malus domestica DIV2
Aquilegia coerulea Goldsmith DIV1
Aquilegia coerulea Goldsmith DIV3
Amaranthus hypochondriacus DIV1
Beta vulgaris subsp vulgaris DIV 2
Jatropha curcas DIV 1
Theobroma cacao DIV
Nicotiana tabacum DIV1 6
Nicotiana tomentosiformis DIV 7
Nicotiana sylvestris DIV 8
Nicotiana tabacum DIV1 7
Nicotiana tabacum DIV 8
Nicotiana tomentosiformis DIV 8
Solanum tuberosum DIV3
Solanum pennellii DIV 4
Solanum lycopersicum MYBI
Solanum pennellii MYBI
Oryza sativa Japonica 9632 m05667
Spirodela polyrhiza DIV 2
Tarenaya hassleriana DIV 2
Arabidopsis halleri DIV3
Arabidopsis thaliana columbia AT5G08520
Brassica rapa FPsc DIV
Arabidopsis thaliana columbia AT5G23650
Capsella grandiflora DIV
Capsicum annuum DIV 4
Eucalyptus grandis DIV 2
Daucus carota subsp sativus DIV1
Medicago truncatula DIV2
Capsicum annuum uncharacterize
Solanum tuberosum DIV1 2
Solanum pennellii DIV 6
Solanum tuberosum DIV1 1
Solanum lycopersicum MYB 1
Solanum tuberosum DIV7
Solanum lycopersicum DIV 4
Solanum pennellii uncharacterize d
Spirodela polyrhiza DIV 1
Setaria italica DIV 1
Oryza sativa DIV2
Oryza sativa DIV3
Amaranthus hypochondriacus DIV2
Beta vulgaris subsp vulgaris DIV 1
Eucalyptus grandis DIV 4
Ziziphus jujuba DIV 2
Fragaria vesca DIV 1
Glycine max DIV1
Nicotiana sylvestris DIV 1
Nicotiana tabacum DIV1 2
Nicotiana tabacum uncharacterized
Nicotiana tomentosiformis DIV 6
Nicotiana sylvestris DIV 4
Nicotiana tabacum DIV 2
Nicotiana tabacum DIV1 5
Nicotiana tomentosiformis DIV 3
Solanum pennellii MYB1R1 2
Solanum lycopersicum DIV 9
Solanum tuberosum DIV9
Nicotiana tabacum DIV1 8
Nicotiana tomentosiformis DIV 9
Arabidopsis halleri DIV1
Arabidopsis thaliana columbia AT1G49010
Camelina sativa DIV2
RR1
44/8
99/18
44/13
47/41
67/-
57/-
83/44
65/-
75/-
48/-
36/-
95/56
68/11
100/91
65/-
66/-
34/-
100/100
98/37
88/-
85/-
86/-
64/52
100/95
83/69
66/87
99/4
100/13
98/70
100/74
100/72
87/64
100/100
100/37
90/63
95/10
97/12
100/40
98/50
100/82
98/75
100/67
45/21
67/33
100/80
35/4
56/23
100/91
42/35
42/-
100/99
43/24
80/55
51/53
50/-
100/100
100/99
91/100
50/-
100/96
50/-
36/75
96/95
50/-
38/-
28/-
50/-
100/100
56/-
56/79
75/77
RR2
Figure. 4b
Myrtales
Vitales
Fabales
Sapindales
Vitales
Brassicales
Rosales
Apiales
Caryophyllales
Malpighiales
Malvales
Solanales
Monocots
Brassicales
Solanales
Myrtales
Apiales
Fabales
Solanales
Monocots
Caryophyllales
Myrtales
Rosales
Fabales
Solanales
Brassicales
RR1A
RR1B
RR1C

Figure. 4b

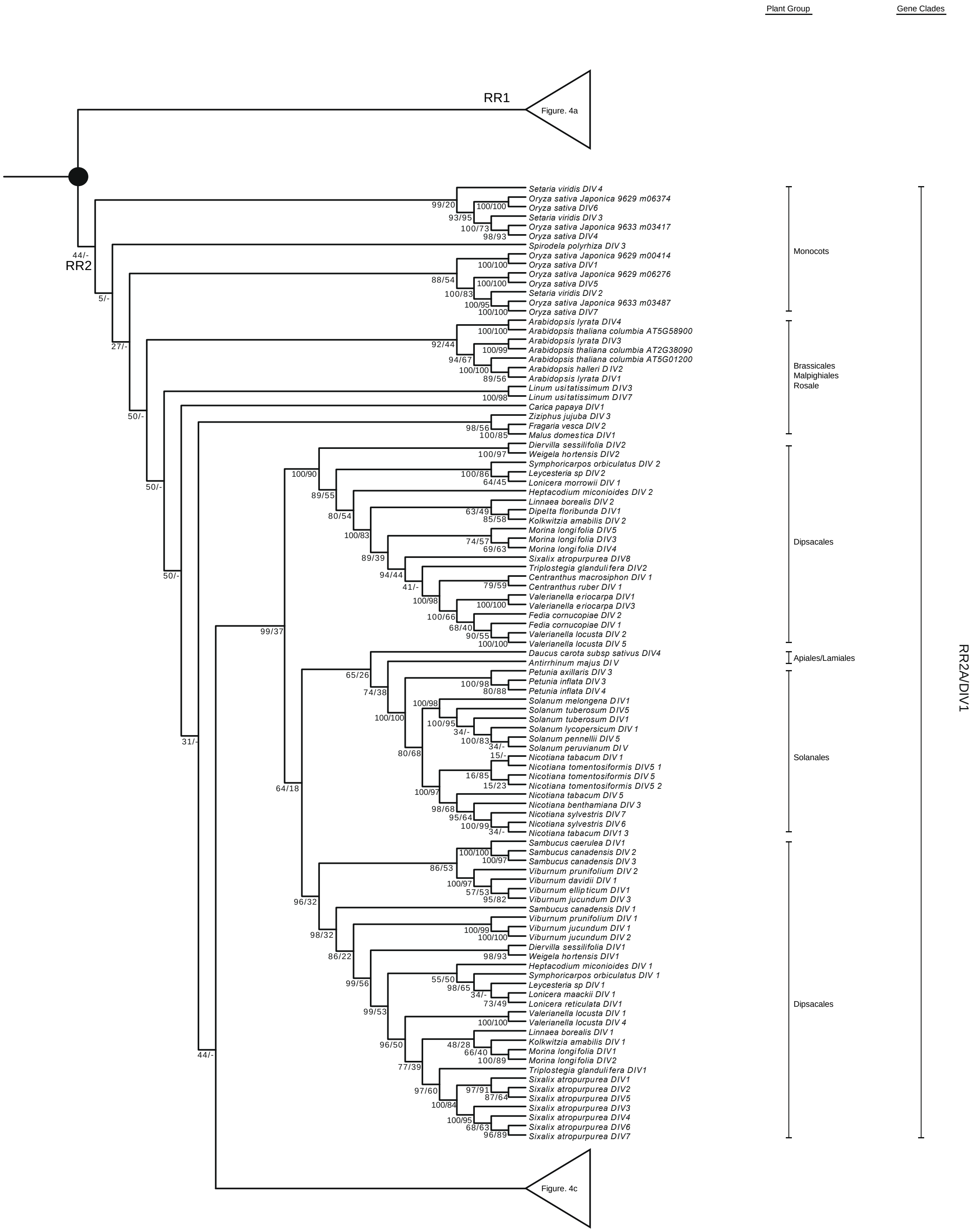

Plant Group
Gene Clades
RR1
Figure. 4a
RR2
Setaria viridis DIV 4
Oryza sativa Japonica 9629 m06374
Oryza sativa DIV6
Setaria viridis DIV 3
Oryza sativa Japonica 9633 m03417
Oryza sativa DIV4
Spirodela polyrhiza DIV 3
Oryza sativa Japonica 9629 m00414
Oryza sativa DIV1
Oryza sativa Japonica 9629 m06276
Oryza sativa DIV5
Setaria viridis DIV 2
Oryza sativa Japonica 9633 m03487
Oryza sativa DIV7
Arabidopsis lyrata DIV4
Arabidopsis thaliana columbia AT5G58900
Arabidopsis lyrata DIV3
Arabidopsis thaliana columbia AT2G38090
Arabidopsis thaliana columbia AT5G01200
Arabidopsis halleri DIV2
Arabidopsis lyrata DIV1
Linum usitatissimum DIV3
Linum usitatissimum DIV7
Carica papaya DIV1
Ziziphus jujuba DIV 3
Fragaria vesca DIV 2
Malus domestica DIV1
Diervilla sessilifolia DIV2
Weigela hortensis DIV2
Symphoricarpos orbiculatus DIV 2
Leycesteria sp DIV 2
Lonicera morrowii DIV 1
Heptacodium miconioides DIV 2
Linnaea borealis DIV 2
Dipelta floribunda DIV1
Kolkwitzia amabilis DIV 2
Morina longifolia DIV5
Morina longifolia DIV3
Morina longifolia DIV4
Sixalix atropurpurea DIV8
Triplostegia glandulifera DIV2
Centranthus macrosiphon DIV 1
Centranthus ruber DIV 1
Valerianella eriocarpa DIV1
Valerianella eriocarpa DIV3
Fedia cornucopiae DIV 2
Fedia cornucopiae DIV 1
Valerianella locusta DIV 2
Valerianella locusta DIV 5
Daucus carota subsp sativus DIV4
Antirrhinum majus DIV
Petunia axillaris DIV 3
Petunia inflata DIV 3
Petunia inflata DIV 4
Solanum melongena DIV1
Solanum tuberosum DIV5
Solanum tuberosum DIV1
Solanum lycopersicum DIV 1
Solanum pennellii DIV 5
Solanum peruvianum DIV
Nicotiana tabacum DIV 1
Nicotiana tomentosiformis DIV5 1
Nicotiana tomentosiformis DIV 5
Nicotiana tomentosiformis DIV5 2
Nicotiana tabacum DIV 5
Nicotiana benthamiana DIV 3
Nicotiana sylvestris DIV 7
Nicotiana sylvestris DIV 6
Nicotiana tabacum DIV1 3
Sambucus caerulea DIV1
Sambucus canadensis DIV 2
Sambucus canadensis DIV 3
Viburnum prunifolium DIV 2
Viburnum davidii DIV 1
Viburnum ellipticum DIV1
Viburnum jucundum DIV 3
Sambucus canadensis DIV 1
Viburnum prunifolium DIV 1
Viburnum jucundum DIV 1
Viburnum jucundum DIV 2
Diervilla sessilifolia DIV1
Weigela hortensis DIV1
Heptacodium miconioides DIV 1
Symphoricarpos orbiculatus DIV 1
Leycesteria sp DIV 1
Lonicera maackii DIV 1
Lonicera reticulata DIV1
Valerianella locusta DIV 1
Valerianella locusta DIV 4
Linnaea borealis DIV 1
Kolkwitzia amabilis DIV 1
Morina longifolia DIV1
Morina longifolia DIV2
Triplostegia glandulifera DIV1
Sixalix atropurpurea DIV1
Sixalix atropurpurea DIV2
Sixalix atropurpurea DIV5
Sixalix atropurpurea DIV3
Sixalix atropurpurea DIV4
Sixalix atropurpurea DIV6
Sixalix atropurpurea DIV7
Figure. 4c
Monocots
Brassicales
Malpighiales
Rosale
Dipsacales
Apiales/Lamiales
Solanales
Dipsacales
RR2A/DIV1

Figure. 4c

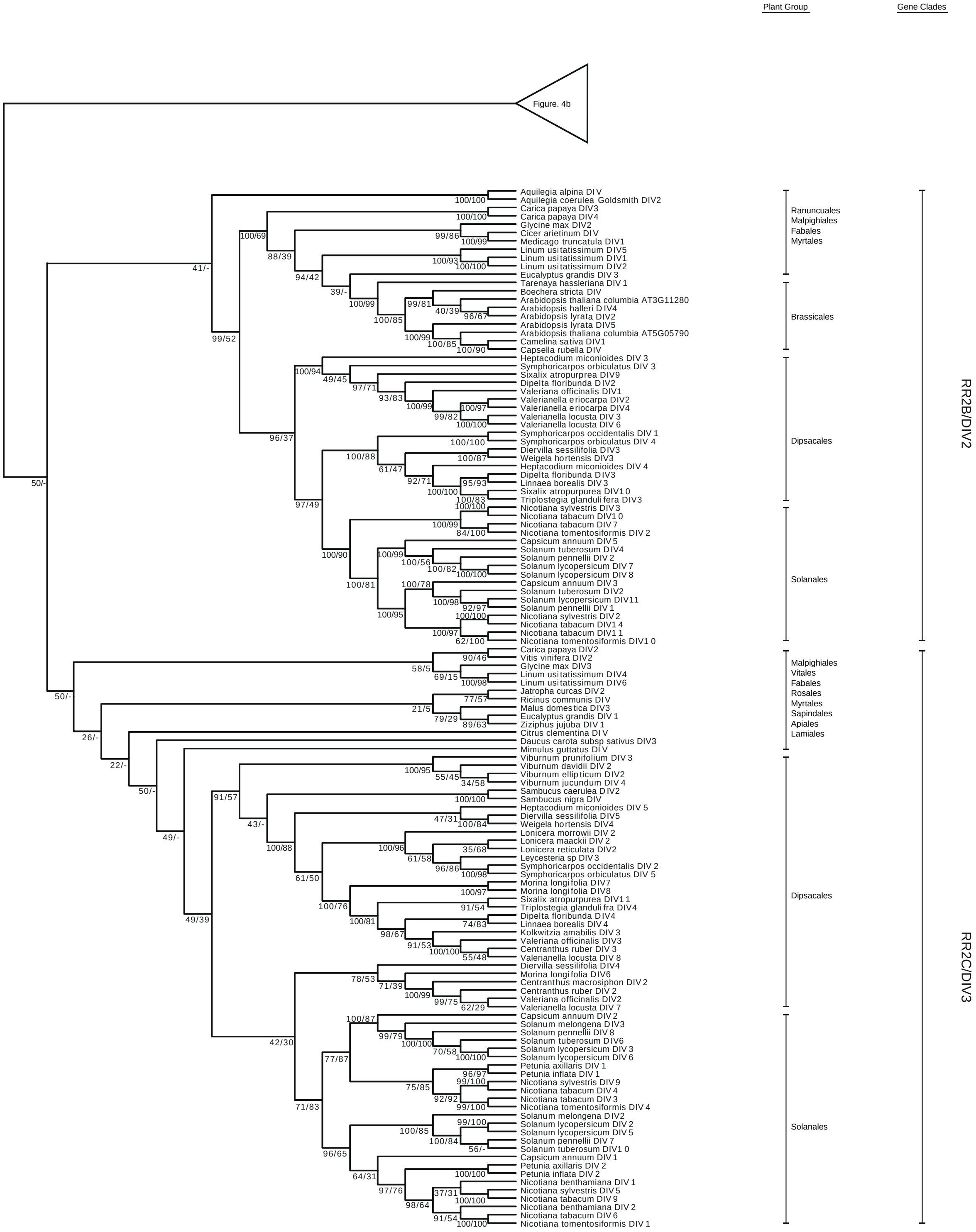

Plant Group
Gene Clades
Figure. 4b
Aquilegia alpina DIV
Aquilegia coerulea Goldsmith DIV2
Carica papaya DIV3
Carica papaya DIV4
Glycine max DIV2
Cicer arietinum DIV
Medicago truncatula DIV1
Linum usitatissimum DIV5
Linum usitatissimum DIV1
Linum usitatissimum DIV2
Eucalyptus grandis DIV 3
Tarenaya hassleriana DIV 1
Boechera stricta DIV
Arabidopsis thaliana columbia AT3G11280
Arabidopsis halleri DIV4
Arabidopsis lyrata DIV2
Arabidopsis lyrata DIV5
Arabidopsis thaliana columbia AT5G05790
Camelina sativa DIV1
Capsella rubella DIV
Heptacodium miconioides DIV 3
Symphoricarpos orbiculatus DIV 3
Sixalix atropurprea DIV9
Dipelta floribunda DIV2
Valeriana officinalis DIV1
Valerianella eriocarpa DIV2
Valerianella eriocarpa DIV4
Valerianella locusta DIV 3
Valerianella locusta DIV 6
Symphoricarpos occidentalis DIV 1
Symphoricarpos orbiculatus DIV 4
Diervilla sessilifolia DIV3
Weigela hortensis DIV3
Heptacodium miconioides DIV 4
Dipelta floribunda DIV3
Linnaea borealis DIV 3
Sixalix atropurpurea DIV10
Triplostegia glandulifera DIV3
Nicotiana sylvestris DIV 3
Nicotiana tabacum DIV10
Nicotiana tabacum DIV 7
Nicotiana tomentosiformis DIV 2
Capsicum annuum DIV 5
Solanum tuberosum DIV4
Solanum pennellii DIV 2
Solanum lycopersicum DIV 7
Solanum lycopersicum DIV 8
Capsicum annuum DIV 3
Solanum tuberosum DIV2
Solanum lycopersicum DIV11
Solanum pennellii DIV 1
Nicotiana sylvestris DIV 2
Nicotiana tabacum DIV14
Nicotiana tabacum DIV11
Nicotiana tomentosiformis DIV10
Carica papaya DIV2
Vitis vinifera DIV2
Glycine max DIV3
Linum usitatissimum DIV4
Linum usitatissimum DIV6
Jatropha curcas DIV 2
Ricinus communis DIV
Malus domestica DIV3
Eucalyptus grandis DIV 1
Ziziphus jujuba DIV 1
Citrus clementina DIV
Daucus carota subsp sativus DIV3
Mimulus guttatus DIV
Viburnum prunifolium DIV 3
Viburnum davidii DIV 2
Viburnum ellipticum DIV2
Viburnum jucundum DIV 4
Sambucus caerulea DIV2
Sambucus nigra DIV
Heptacodium miconioides DIV 5
Diervilla sessilifolia DIV5
Weigela hortensis DIV4
Lonicera morrowii DIV 2
Lonicera maackii DIV 2
Lonicera reticulata DIV2
Leycesteria sp DIV 3
Symphoricarpos occidentalis DIV 2
Symphoricarpos orbiculatus DIV 5
Morina longifolia DIV7
Morina longifolia DIV8
Sixalix atropurpurea DIV11
Triplostegia glandulifra DIV4
Dipelta floribunda DIV4
Linnaea borealis DIV 4
Kolkwitzia amabilis DIV 3
Valeriana officinalis DIV3
Centranthus ruber DIV 3
Valerianella locusta DIV 8
Diervilla sessilifolia DIV4
Morina longifolia DIV6
Centranthus macrosiphon DIV 2
Centranthus ruber DIV 2
Valeriana officinalis DIV2
Valerianella locusta DIV 7
Capsicum annuum DIV 2
Solanum melongena DIV3
Solanum pennellii DIV 8
Solanum tuberosum DIV6
Solanum lycopersicum DIV 3
Solanum lycopersicum DIV 6
Petunia axillaris DIV 1
Petunia inflata DIV 1
Nicotiana sylvestris DIV 9
Nicotiana tabacum DIV 4
Nicotiana tabacum DIV 3
Nicotiana tomentosiformis DIV 4
Solanum melongena DIV2
Solanum lycopersicum DIV 2
Solanum lycopersicum DIV 5
Solanum pennellii DIV 7
Solanum tuberosum DIV10
Capsicum annuum DIV 1
Petunia axillaris DIV 2
Petunia inflata DIV 2
Nicotiana benthamiana DIV 1
Nicotiana sylvestris DIV 5
Nicotiana tabacum DIV 9
Nicotiana benthamiana DIV 2
Nicotiana tabacum DIV 6
Nicotiana tomentosiformis DIV 1
Ranunculales
Malpighiales
Fabales
Myrtales
Brassicales
Dipsacales
Solanales
Malpighiales
Vitales
Fabales
Rosales
Myrtales
Sapindales
Apiales
Lamiales
Dipsacales
Solanales
RR2B/DIV2
RR2C/DIV3

Figure 4. Phylogeny of *R-R-type* genes based on Bayesian and ML inferences. A lot of 298 CDS of *R-R-type* genes from both monocots and dicots were analyzed, which form two major clades, RR1 and RR2/DIV. Each of these clades contains sequences from monocots and dicots. The RR1 clade was further divided into three groups, RR1A, RR1B, and RR1C. For the three RR2/DIV clades identified by Howarth and Donoghue (2009), only the DIV2 and DIV3 are monophyletic. The *Arabidopsis* sequences included AT2G38090, AT5G01200, and AT5G58900 identified as DIV1, which is not a clade in this phylogeny. Bayesian posterior probabilities and bootstrap frequencies are labeled at the nodes and are separted by a slash.

Motif analyses:

The results of motif analyses indicate that the *I-box*-like genes have only one domain, while *R-R*-type genes have two domains: R-R (A), and R-R (B). The N-terminal R-R (A) was closely related to the *I-box*-like genes (Appendix 9). These findings agree with the study of Chen et al. (2006), which tested the motifs *R-R*-type, *I-box*-like, and *CCA1*-like MYB genes.

Discussion

<u>*Phylogenetic positions of RAD- and DIV-like genes in the plant MYB lineage:*</u>

MYB proteins contain a conserved MYB domain, which usually comprises one to three imperfect repeats, namely R1, R2, and R3 (!!! INVALID CITATION !!!). Each of these repeats comprises about 52 amino acid residues that encode a helix-loop-helix structure involved in DNA binding (!!! INVALID CITATION !!!). *MYB*-like genes have been found in all eukaryotes (!!! INVALID CITATION !!!).

Phylogenetic analysis indicates that the *MYB* genes of plants, which are sister to all animal *MYB* genes, form a clade (Rosinski & Atchley, 1998). *MYB* genes in plants are structurally and functionally more variable compared to the *MYB* genes in vertebrates (!!! INVALID CITATION !!!). Based on the MYB domain structures, the MYB proteins of plants can be classified into three major groups: R1R2R3-MYB with three adjacent repeats, R2R3-MYB with two adjacent repeats, and MYB-related proteins, a heterogeneous group, often containing a single MYB repeat (!!! INVALID CITATION !!!). The R2R3-MYB group is thought to be derived from the R1R2R3-MYB group, which occurs in all major lineages of land plants (Kranz, Scholz, & Weisshaar, 2000). Based on the phylogenetic analysis and the protein domain structure, MYB-related proteins were further divided into five subfamilies: CCA1-like, CPC-like, TBP-like, I-box-binding-like (abbreviated I-box-like), and R-R-type (!!! INVALID CITATION !!!). Based on (!!! INVALID CITATION !!!), *A. thaliana* has five I-box-like genes, i.e., At1g75250, At1g19510, At2g21650, At4g39250, and At4g36570, and nine R-R-type genes, i.e., At1g49010, At2g38090, At3g11280, At5g01200, At5g05790, At5g08520, At5g58900, At5g23650, and At5g04760. Boyden, Donoghue and Howarth (2012). (2012) indicated that *RAD*-like genes belong to the *I-box*-like clade. Our analyses further indicate that the *I-box*-like lineage is synonymous with *RAD*-like genes (Figs. 1 and 2). Howarth and Donoghue (2009) focused on the evolution of *DIV*-like genes in core eudicots especially in Dipsacales, and indicated that the *DIV*-like genes belong to an *R-R-type* gene lineage. Our analysis of *R-R-type* genes showed that gene duplication occurred at least in the common ancestor of dicots and monocots giving rise to two paralogs, the RR1 and RR2 clades (Figs. 3 and 4), of which the RR2 clade is synonymous with the *DIV*-like lineage (Howarth and Donoghue, 2009).

.

<u>*Evolution of the I-box-like subfamily:*</u>

Boyden, Donoghue and Howarth (2012) indicated that *RAD*-like genes consist of three major clades: RAD1, RAD2, and RAD3, which were speculated as resulting from genome duplications associated with the origin of core eudicots. The RAD1 clade has *Arabidopsis* AT4G36570 and DQ395345 of Clade I (defined by Chen et al., 2006), and RAD2 and RAD3 have the *Arabidopsis* sequences from Clade III (AT2G21650 and AT4G39250 belong to the RAD2, and AT1G19510 and AT1G75250 belong to RAD3). Our analysis recognized *RAD2* as a clade (Fig. 1 and 2). Furthermore, there are two RAD2 paralogs involving Solanaceae and Convolvulaceae, RAD2A and RAD2B, which likely resulted from a gene duplication at least in the common ancestor of these two plant families. On the other hand, the *RAD1* and *RAD3* clades were not fully resolved based on our analyses. Our phylogenetic analyses indicated that the *RAD* of *An. majus* belongs to the RAD2 clade, while FSM1 is placed in the RAD2A clade, which belong to RAD2 clade, suggesting that RAD and FSM1 belong to the same orthologous lineage.

Evolution of the R-R-type subfamily:

The R-R-type genes have two imperfect repeats of the MYB domain, namely R-R (A) and R-R (B) (Chen et al., 2006). The N-terminal MYB repeat R-R (A) was found to be closely related to the MYB repeats of the I-box-like genes (Appendix 9), and the C-terminal MYB repeat R-R (B) was closely related to those of certain CCA1-like genes based on the positions of the introns and shared motifs (Chen et al., 2006). The phylogeny of R-R-type genes based on nine sequences of *A. thaliana* and seven of *O. sativa japonica* suggests several gene duplications in the common ancestor of the monocots and dicots, but the phylogenetic relationships of the predicted paralogs were unresolved in that study (Chen et al., 2006). The work by Howarth and Donoghue (2009), focused on the evolution of *DIV*-like genes in core eudicots especially in Dipsacales, showed duplications giving rise to three *DIV*-like clades in the core eudicots, DIV1, DIV2, and DIV3. Our blast and phylogenetic analyses indicated that most of the sequences named *DIV*-like genes belong to the R-R-type subfamily, while most of the sequences named as *MYB1R1*-like genes belong to the *CCA1*-like gene family (Appendix 3). Each of the two R-R-type subclades, RR1 and RR2, was further divided into three paralogs, which likely resulted from genome duplication in the common ancestor of core eudicots (Howarth and Donoghue, 2009). RR1 consists of RR1A, RR1B, and RR1C, while RR2/DIV is composed of RR2A/DIV1, RR2B/DIV2, and RR2C/DIV3 (Figs. 3 and 4) (Howarth and Donoghue, 2009). We find that the *DIV* of *An. majus* belongs to the *DIV1* of the *RR2/DIV* clade (also see Howarth and Donoghue, 2009), while the *MYBI* of tomato belongs to the *RR1A* of the *RR1* clade.

Evolution of the antagonism among RAD-DRIF-DIV and FSM1-FSB1-MYBI in An. majus and So. lycopersicum, respectively:

Based on an analysis of amino acid sequences, the two MYB domains of DIV had different functions with the C-terminal domain similar to known DNA binding MYB proteins, while the N-terminal domain was associated with protein-protein interactions (Galego and Almeida, 2002; Rose et al., 1999). In contrast, RAD has a single MYB domain that is predicted to act through a mechanism involving protein–protein interactions (Corley et al., 2005). As the members of MYB-related subfamilies, I-box-like and R-R-type genes, were previously placed in the same clade by Riechmann and Ratcliffe (2000), which suggests that they may be closely related paralogs. One possible hypothesis proposed for the evolution of these two MYB-related subfamilies is that I-box-like genes evolved through the loss of the MYB domain at the C-terminal end (Chen et al., 2006; Stevenson et al., 2006). RAD-DRIF-DIV and RAD-DRIF-DIV, therefore, represent the recruitment of homologous genes from similar MYB lineages in the development of floral zygomorphy in *An. majus,* and the development of fruit in *So. lycopersicum* (Raimundo et al., 2013). Our work clarified the evolution of I-box-like and R-R-type lineages and will help future inquiry into the functional studies of the paralogs that may have been involved in the evolution of molecular antagonism.

References

Akaike H 1973 Information theory and an extension of the maximum likelihood principle. Pages 267-281 *in* BN Petrov, F Csaki eds. Second International Symposium in Information Theory. Akademiai Kiado, Budapest.

Almeida J, M Rocheta, L Galego 1997 Genetic control of flower shape in *Antirrhinum majus*. Development 124: 1387-1392.

Bailey,T.L., C.Elkan, 1993 Unsupervised Learning of Multiple Motifs in Biopolymers Using Expectation Maximization. Machine Learning. 21: 51-80.

Bailey,T.L., C.Elkan, 1994 Fitting a mixture model by expectation maximization to discover motifs in biopolymers, *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology* pp: 28-36.

Baxter CEL, MMR Costa, ES Coen 2007 Diversification and co-option of RAD-like genes in the evolution of floral asymmetry. Plant J 52: 105-113.

Boyden GS, MJ Donoghue, DG Howarth 2012 Duplications and Expression of Radialis-Like Genes in Dipsacales. Int J Plant Sci 173: 971-983.

Chen YH, XY Yang, K He, MH Liu, JG Li, ZF Gao, ZQ Lin, YF Zhang, XX Wang, XM Qiu, YP Shen, L Zhang, XH Deng, JC Luo, XW Deng, ZL Chen, HY Gu, LJ Qu 2006 The MYB transcription factor superfamily of arabidopsis: Expression analysis and phylogenetic comparison with the rice MYB family. Plant Mol Biol 60: 107-124.

Corley SB, R Carpenter, L Copsey, E Coen 2005 Floral asymmetry involves an interplay between TCP and MYB transcription factors in *Antirrhinum*. Proc Natl Acad Sci U S A 102: 5068-5073.

Costa MMR, S Fox, AI Hanna, C Baxter, E Coen 2005 Evolution of regulatory interactions controlling floral asymmetry. Development 132: 5093-5101.

Cubas P, N Lauter, J Doebley , E Coen. 1999. The TCP domain: a motif found in proteins regulating plant growth and development. Plant J. 18:215–222.

Dal-Pra, S.; Fuerthauer, M.; Van-Celst, J.; Thisse, B.; Thisse, C. Noggin1 and follistatin-like2 function redundantly to chordin to antagonize bmp activity. *Dev Biol* 2006, *298*, 514-526.

Darriba D, GL Taboada, R Doallo, D Posada 2012 jModelTest 2: more models, new heuristics and parallel computing. Nat Meth 9: 772-772.

Galego L, J Almeida 2002 Role of DIVARICATA in the control of dorsoventral asymmetry in Antirrhinum flowers. Genes Dev 16: 880-891.

Guindon S, O Gascuel 2003 A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. Syst Biol 52: 696-704.

Howarth DG, MJ Donoghue 2006 Phylogenetic analysis of the "ECE" (CYC/TB1) clade reveals duplications predating the core eudicots. Proc Natl Acad Sci U S A 103: 9101-9106.

Howarth DG, MJ Donoghue 2009 Duplications and Expression of DIVARICATA-Like Genes in Dipsacales. Mol Biol Evol 26: 1245-1258.

Huelsenbeck JP, F Ronquist 2001 Mrbayes: bayesian inference of phylogenetic trees. Bioinformatics 17: 754-755.

Jin HL, C Martin 1999 Multifunctionality and diversity within the plant MYB-gene family. Plant Mol Biol 41: 577-585.

Kranz H, K Scholz, B Weisshaar 2000 c-MYB oncogene-like genes encoding three MYB repeats occur in all major plant lineages. Plant J 21: 231-235.

Kranz HD, M Denekamp, R Greco, H Jin, A Leyva, RC Meissner, K Petroni, A Urzainqui, M Bevan, C Martin, S Smeekens, C Tonelli, J Paz-Ares, B Weisshaar 1998 Towards functional characterisation of the members of the R2R3-MYB gene family from Arabidopsis thaliana. Plant J 16: 263-276.

Lipsick JS 1996 One billion years of Myb. Oncogene 13: 223-235.

Luo D, R Carpenter, L Copsey, C Vincent, J Clark, E Coen 1999 Control of organ asymmetry in flowers of *Antirrhinum*. Cell 99: 367-376.

Luo D, R Carpenter, C Vincent, L Copsey, E Coen 1996 Origin of floral asymmetry in *Antirrhinum*. Nature 383: 794-799.

Luttrell, L.M.; Maudsley, S.; Bohn, L.M. Fulfilling the promise of "biased" g protein-coupled receptor agonism. *Mol Pharmacol* 2015, *88*, 579-588.

Machemer K, O Shaiman, Y Salts, S Shabtai, I Sobolev, E Belausov, E Grotewold, R Barg 2011 Interplay of MYB factors in differential cell expansion, and consequences for tomato fruit development. Plant J 68: 337-350.

Martin C, J.Paz-Ares.1997. MYB transcription factors in plants. Trends Genet. 13:67–73.

Miller MA, W Pfeiffer, T Schwartz. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees Proceedings of the gateway computing environments workshop (GCE).

Raimundo J, R Sobral, P Bailey, H Azevedo, L Galego, J Almeida, E Coen, MMR Costa 2013 A subcellular tug of war involving three MYB-like proteins underlies a molecular antagonism in Antirrhinum flower asymmetry. Plant J 75: 527-538.

Riechmann JL, OJ Ratcliffe 2000 A genomic perspective on plant transcription factors. Curr Opin Plant Biol 3: 423-434.

Rose A, I Meier, U Wienand 1999 The tomato I-box binding factor LeMYBI is a member of a novel class of Myb-like proteins. Plant J 20: 641-652.

Rosinski JA, WR Atchley 1998 Molecular evolution of the Myb family of transcription factors: Evidence for polyphyletic origin. J Mol Evol 46: 74-83.

Särkinen T, L Bohs, RG Olmstead, S Knapp 2013 A phylogenetic framework for evolutionary study of the nightshades (Solanaceae): a dated 1000-tip tree. BMC Evol Biol 13: 214.

Stamatakis A 2006 RAxML-VI-HPC: Maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics 22: 2688-2690.

Stamatakis A, P Hoover, J Rougemont 2008 A Rapid Bootstrap Algorithm for the RAxML Web Servers. Syst Biol 57: 758-771.

Stevenson CEM, N Burton, MMR Costa, U Nath, RA Dixon, ES Coen, DM Lawson 2006 Crystal structure of the MYB domain of the RAD transcription factor from Antirrhinum majus. Proteins-Structure Function and Bioinformatics 65: 1041-1045.

Stracke R, M Werber, B Weisshaar 2001 The R2R3-MYB gene family in Arabidopsis thaliana. Curr Opin Plant Biol 4: 447-456.

Zimmerman LB, JM DeJesusEscobar, RM Harland 1996 The Spemann organizer signal noggin binds and inactivates bone morphogenetic protein 4. Cell 86: 599-606.

APPENDIX

Appendix 1. Accession information of I-box-like genes.

Taxa	Families	Sequence ID in this study	Clades on phylogeny	Accession numbers in databases	Databases	Sequence ID in databases	Orders
Acathocalyx albus	Caprifoliaceae	Acanthocalyx_albus_RAD3	*RAD2*	JX123727	Paper/Genebank	Acanthocalyx_albus_RAD2A	Dipsacales
Acathocalyx albus	Caprifoliaceae	Acanthocalyx_albus_RAD4	*RAD2*	JX123728	Paper/Genebank	Acanthocalyx_albus_RAD2B	Dipsacales
Acathocalyx albus	Caprifoliaceae	Acanthocalyx_albus_RAD1	*RAD1/RAD3*	JX123730	Paper/Genebank	Acanthocalyx_albus_RAD1A	Dipsacales
Acathocalyx albus	Caprifoliaceae	Acanthocalyx_albus_RAD2	*RAD1/RAD3*	JX123729	Paper/Genebank	Acanthocalyx_albus_RAD1B	Dipsacales
Acathocalyx albus	Caprifoliaceae	Acanthocalyx_albus_RAD5	*RAD1/RAD3*	JX123721	Paper/Genebank	Acanthocalyx_albus_RAD3	Dipsacales
Antirrhinum majus	Plantaginaceae	Antirrhinum_majus_RAD	*RAD2*	AY954971	Genebank	Antirrhinum_majus_RADIALIS_RAD	Lamiales
Antirrhinum majus	Plantaginaceae	Antirrhinum_majus_RL1	*RAD1/RAD3*	Paper	Paper	Antirrhinum_majus_RL1	Lamiales
Antirrhinum majus	Plantaginaceae	Antirrhinum_majus_RL2	*RAD1/RAD3*	DQ375230	Genebank	Antirrhinum_majus_RL2	Lamiales
Antirrhinum majus	Plantaginaceae	Antirrhinum_majus_RL3	*RAD1/RAD3*	DQ375229	Genebank	Antirrhinum_majus_RL3	Lamiales
Antirrhinum majus	Plantaginaceae	Antirrhinum_majus_RL4	*RAD1/RAD3*	DQ375228	Genebank	Antirrhinum_majus_RL4	Lamiales
Aquilegia coerulea	Ranunculaceae	Aquilegia coerulea_RAD1	*RAD1/RAD3*	Aquca_010_00499.1	Phytozome	Aquilegia_Aquca_010_00499_1	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia coerulea_RAD2	*RAD1/RAD3*	Aquca_070_00018.1	Phytozome	Aquilegia_Aquca_070_00018_1	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia coerulea_RAD3	*RAD1/RAD3*	Aquca_010_00512.1	Phytozome	Aquilegia_Aquca_010_00512_1	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia coerulea_RAD4	*RAD1/RAD3*	Aquca_007_00235.1	Phytozome	Aquilegia_Aquca_007_00235_1	Ranunculales
Arabidopsis halleri	Brassicaceae	Arabidopsis_halleri_RAD	*RAD2*	Araha.4538s0007.1	Phytozome	Arabidopsis_halleri_Scaffold4538_17905_18098	Brassicales

Arabidopsis lyrata	Brassicaceae	Arabidopsis_lyrata_RAD	*RAD2*	943897	Phytozome	Arabidopsis_lyrata_scaffold_7_465405_465598	Brassicales
Arabidopsis salsugineum	Brassicaceae	Arabidopsis_salsugineum_RAD_1	*RAD1/RAD3*	Thhalv10026710m	Phytozome	Arabidopsis_salsugineum_scaffold_1_1487751_1487903	Brassicales
Arabidopsis salsugineum	Brassicaceae	Arabidopsis_salsugineum_RAD_2	*RAD1/RAD3*	Thhalv10019367m	Phytozome	Arabidopsis_salsugineum_scaffold_9_2360114_2360299	Brassicales
Arabidopsis thaliana	Brassicaceae	Arabidopsis_thaliana_RL1	*RAD2*	NM_120086.2	Genebank	Arabidopsis_thaliana_RL1	Brassicales
Arabidopsis thaliana	Brassicaceae	Arabidopsis_thaliana_RL2	*RAD2*	NM_127736.3	Genebank	Arabidopsis_thaliana_RSM1	Brassicales
Arabidopsis thaliana	Brassicaceae	Arabidopsis_thaliana_RL3	*RAD1/RAD3*	BT011255.1	Genebank	Arabidopsis_thaliana_At4g36570	Brassicales
Arabidopsis thaliana	Brassicaceae	Arabidopsis_thaliana_RL4	*RAD1/RAD3*	NM_001084443.1	Genebank	Arabidopsis_thaliana_RL4	Brassicales
Arabidopsis thaliana	Brassicaceae	Arabidopsis_thaliana_RL5	*RAD1/RAD3*	NM_101808.4	Genebank	Arabidopsis_thaliana_RL5	Brassicales
Arabidopsis thaliana	Brassicaceae	Arabidopsis_thaliana_RL6	*RAD1/RAD3*	NM_001084356.2	Genebank	Arabidopsis_thaliana_RL6	Brassicales
Aragoa abietina	Plantaginaceae	Aragoa_abietina_RAD	*RAD2*	HQ853607.1	Genebank	Aragoa_abietina_RADIALIS_cds	Lamiales
Aragoa cundinamarcensis	Plantaginaceae	Aragoa_cundinamarcensis_RAD	*RAD2*	HQ853608.1	Genebank	Aragoa_cundinamarcensis_RADIALIS_cds	Lamiales
Atropa belladonna Linn	Solanaceae	Atropa_belladonna_Linn_RAD	*RAD2*	Lab sequcing	Lab sequcing	Atropa_belladonna_Linn_RAD_CS1 extraction*	Solanales
Boechera stricta	Brassicaceae	Boechera_stritcta_RAD1	*RAD2*	Bostr.5022s0065.1	Phytozome	Boechera_stritcta_Scaffold5022_501604_501735	Brassicales
Boechera stricta	Brassicaceae	Boechera_stritcta_RAD2	*RAD2*	Bostr.25542s0114.1	Phytozome	Boechera_stritcta_Scaffold25542_467661_467854	Brassicales
Bournea leiophylla	Gesneriaceae	Bournea_leiophylla_RAD	*RAD2*	EF207557.1	Genebank	Bournea_leiophylla_RAD	Lamiales
Brassica rapa	Brassicaceae	Brassica_rapa_RAD2	*RAD2*	Brara.C02496.1	Phytozome	Brassica_rapa_A03_12583653_12583846	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_RAD1	*RAD1/RAD3*	Brara.A00032.1	Phytozome	Brassica_rapa_A01_164306_164501	Brassicales
Callicarpa americana	Lamiaceae	Callicarpa_americana_RAD	*RAD2*	KT284321	Genebank	Callicarpa_americana	Lamiales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_RAD	*RAD1/RAD3*	Cagra.1695s0021.1	Phytozome	Capsella_grandiflora_Scaffold1695_86172_86324	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_RAD	*RAD2*	Carubv10024389m	Phytozome	Capsella_rubella_Scaffold4_256378_256576	Brassicales
Capsicum annuum	Solanaceae	Capsicum_annuum_RAD1	*RAD2*	CA00g07860	Sol Genomics Network	Capsicum_annuum_CA10g07860	Solanales
Capsicum annuum	Solanaceae	Capsicum_annuum_RAD2	*RAD2*	CA00g64330	Sol Genomics Network	Capsicum_annuum_CA00g64330	Solanales

Capsicum annuum	Solanaceae	Capsicum_annuum_RAD3	*RAD1/RAD3*	CA00g64350	Sol Genomics Network	Capsicum_annuum_CA00g64350	Solanales
Centranthus ruber	Caprifoliaceae	Centranthus_ruber_RAD1	*RAD2*	JX123699	Paper/Genebank	Centranthus_ruber_RAD2Ba	Dipsacales
Centranthus ruber	Caprifoliaceae	Centranthus_ruber_RAD2	*RAD2*	JX123692	Paper/Genebank	Centranthus_ruber_RAD2Bb	Dipsacales
Citrus sinensis	Rutaceae	Citrus_sinensis_RAD	*RAD2*	orange1.1g034615m	Phytozome	Citrus_sinensis_scaffold00250_39631_39815	Sapindales
Cryptothladia chinensis	Morinaceae	Cryptothladia_chinensis_RAD4	*RAD2*	JX123732	Paper/Genebank	Cryptothladia_chinensis_RAD2A	Dipsacales
Cryptothladia chinensis	Morinaceae	Cryptothladia_chinensis_RAD5	*RAD2*	JX123731	Paper/Genebank	Cryptothladia_chinensis_RAD2Ba	Dipsacales
Cryptothladia chinensis	Morinaceae	Cryptothladia_chinensis_RAD6	*RAD2*	JX123733	Paper/Genebank	Cryptothladia_chinensis_RAD2Bb	Dipsacales
Cryptothladia chinensis	Morinaceae	Cryptothladia_chinensis_RAD1	*RAD1/RAD3*	JX123736	Paper/Genebank	Cryptothladia_chinensis_RAD1A	Dipsacales
Cryptothladia chinensis	Morinaceae	Cryptothladia_chinensis_RAD2	*RAD1/RAD3*	JX123734	Paper/Genebank	Cryptothladia_chinensis_RAD1Ba	Dipsacales
Cryptothladia chinensis	Morinaceae	Cryptothladia_chinensis_RAD3	*RAD1/RAD3*	JX123735	Paper/Genebank	Cryptothladia_chinensis_RAD1Bb	Dipsacales
Cryptothladia chinensis	Morinaceae	Cryptothladia_chinensis_RAD7	*RAD1/RAD3*	JX123720	Paper/Genebank	Cryptothladia_chinensis_RAD3	Dipsacales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_RAD	*RAD2*	Cucsa.377650.1	Phytozome	Cucumis_sativus_scaffold03806_35501_35657	Cucurbitales
Diervilla sessilifolia	Caprifoliaceae	Diervilla_sessilifolia_RAD1	*RAD2*	JX123745	Paper/Genebank	Diervilla_sessilifolia_RAD2A	Dipsacales
Diervilla sessilifolia	Caprifoliaceae	Diervilla_sessilifolia_RAD3	*RAD2*	JX123693	Paper/Genebank	Diervilla_sessilifolia_RADIALIS_RAD2B	Dipsacales
Diervilla sessilifolia	Caprifoliaceae	Diervilla_sessilifolia_RAD2	*RAD1/RAD3*	JX123746	Paper/Genebank	Diervilla_sessilifolia_RADIALIS_RAD1B	Dipsacales
Digitalis purpurea	Plantaginaceae	Digitalis_purpurea_RAD	*RAD2*	HQ853602	Genebank	Digitalis_purpurea_RADIALIS	Lamiales
Dipelta floribunda	Caprifoliaceae	Dipelta_floribunda_RAD3	*RAD2*	JX123742	Paper/Genebank	Dipelta_floribunda_RAD2B	Dipsacales
Dipelta floribunda	Caprifoliaceae	Dipelta_floribunda_RAD1	*RAD1/RAD3*	JX123743	Paper/Genebank	Dipelta_floribunda_RAD1A	Dipsacales
Dipelta floribunda	Caprifoliaceae	Dipelta_floribunda_RAD2	*RAD1/RAD3*	JX123744	Paper/Genebank	Dipelta_floribunda_RAD1B	Dipsacales
Dipsacus pilosus	Caprifoliaceae	Dipsacus_pilosus_RAD1	*RAD2*	JX123714	Paper/Genebank	Dipsacus_pilosus_RAD2Ba	Dipsacales
Dipsacus pilosus	Caprifoliaceae	Dipsacus_pilosus_RAD2	*RAD2*	JX123715	Paper/Genebank	Dipsacus_pilosus_RAD2Bb	Dipsacales
Dipsacus pilosus	Caprifoliaceae	Dipsacus_pilosus_RAD3	*RAD2*	JX123716	Paper/Genebank	Dipsacus_pilosus_RAD2Bc	Dipsacales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_RAD	*RAD1/RAD3*	Eucgr.I02431.1	Phytozome	Eucalyptus_grandis_Chr09_34776285_34776472	Myrtales

Evolvulus sp	Convolvulaceae	Evolvulus_sp_consensus_sequence_RAD1	*RAD2*	Lab sequcing	Lab sequcing	Evolvulus_sp_consensus_sequence_1	Solanales
Evolvulus sp	Convolvulaceae	Evolvulus_sp_consensus_sequence_RAD2	*RAD2*	Lab sequcing	Lab sequcing	Evolvulus_sp_consensus_sequence_2	Solanales
Fedia cornucopiae	Caprifoliaceae	Fedia_cornucopiae_RAD1	*RAD2*	JX123689	Paper/Genebank	Fedia_cornucopiae_RAD2Ba	Dipsacales
Fedia cornucopiae	Caprifoliaceae	Fedia_cornucopiae_RAD2	*RAD2*	JX123691	Paper/Genebank	Fedia_cornucopiae_RAD2Bb	Dipsacales
Fedia cornucopiae	Caprifoliaceae	Fedia_cornucopiae_RAD3	*RAD2*	JX123690	Paper/Genebank	Fedia_cornucopiae_RAD2Bc	Dipsacales
Glycine max	Fabaceae	Glycine_max_RAD1	*RAD1/RAD3*	Glyma.14G067100.1	Phytozome	Glycine_max_Chr14_5553186_5553318	Fabales
Glycine max	Fabaceae	Glycine_max_RAD2	*RAD1/RAD3*	Glyma.12G042900.1	Phytozome	Glycine_max_Chr12_3114986_3115198	Fabales
Glycine max	Fabaceae	Glycine_max_RAD3	*RAD1/RAD3*	Glyma.11G117200.1	Phytozome	Glycine_max_Chr11_8920336_8920548	Fabales
Glycine max	Fabaceae	Glycine_max_RAD4	*RAD1/RAD3*	Glyma.06G031800.1	Phytozome	Glycine_max_Chr06_2463627_2463768	Fabales
Glycine max	Fabaceae	Glycine_max_RAD5	*RAD1/RAD3*	Glyma.04G031700.1	Phytozome	Glycine_max_Chr04_2539796_2539937	Fabales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_RAD3	*RAD2*	Gorai.002G005800.1	Phytozome	Gossypium_raimondii_Chr02_369832_370026	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_RAD4	*RAD2*	Gorai.005G244000.1	Phytozome	Gossypium_raimondii_Chr05_62441800_62442002	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_RAD6	*RAD2*	Gorai.013G036700.1	Phytozome	Gossypium_raimondii_Chr13_2868497_2868710	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_RAD2	*RAD1/RAD3*	Gorai.011G101700.1	Phytozome	Gossypium_raimondii_Chr11_11508442_11508615	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_RAD7	*RAD1/RAD3*	Gorai.009G201200.1	Phytozome	Gossypium_raimondii_Chr09_15572686_15572869	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_RAD1	*RAD1/RAD3*	Gorai.003G014600.1	Phytozome	Gossypium_raimondii_Chr03_969386_969571	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_RAD5	*RAD1/RAD3*	Gorai.009G201700.1	Phytozome	Gossypium_raimondii_Chr09_15635662_15635798	Malvales
Gratiola officinalis	Plantaginaceae	Gratiola_officinalis_RAD	*RAD2*	FJ649696	Genebank	Gratiola_officinalis_RADIALIS_RAD	Lamiales
Heptacodium miconioides	Caprifoliaceae	Heptacodium_miconioides_RAD3	*RAD2*	JX123698	Paper/Genebank	Heptacodium_miconioides_RAD2A	Dipsacales
Heptacodium miconioides	Caprifoliaceae	Heptacodium_miconioides_RAD4	*RAD2*	JX123696	Paper/Genebank	Heptacodium_miconioides_RAD2B	Dipsacales
Heptacodium miconioides	Caprifoliaceae	Heptacodium_miconioides_RAD1	*RAD1/RAD3*	JX123695	Paper/Genebank	Heptacodium_miconioides_RAD1A	Dipsacales
Heptacodium miconioides	Caprifoliaceae	Heptacodium_miconioides_RAD2	*RAD1/RAD3*	JX123697	Paper/Genebank	Heptacodium_miconioides_RAD1B	Dipsacales

Ipomoea nil	Convolvulaceae	Ipomoea_nil_RAD2	*RAD2*	XM_019310275.1	Genebank	Ipomoea_nil_protein_RADIALIS_like_2_LOC109161773	Solanales
Ipomoea nil	Convolvulaceae	Ipomoea_nil_RAD1	*RAD1/RAD3*	XM_019296980.1	Genebank	Ipomoea_nil_protein_RADIALIS_like_1_LOC109149288	Solanales
Ipomoea nil	Convolvulaceae	Ipomoea_nil_RAD6	*RAD1/RAD3*	XM_019319295.1	Genebank	Ipomoea_nil_protein_ RADIALIS_like 6_LOC109170262	Solanales
Ipomoea nil	Convolvulaceae	Ipomoea_nil_RAD3	*RAD1/RAD3*	XM_019310260.1	Genebank	Ipomoea_niL_protein_RADIALIS_like_ 4_LOC109161758	Solanales
Ipomoea nil	Convolvulaceae	Ipomoea_nil_RAD4	*RAD1/RAD3*	XM_019319660.1	Genebank	Ipomoea_nil_protein_RADIALIS_like 4_LOC109170511	Solanales
Ipomoea nil	Convolvulaceae	Ipomoea_nil_RAD5	*RAD1/RAD3*	XM_019296979.1	Genebank	Ipomoea_niL_protein_RADIALIS_like_ 4_LOC109149287	Solanales
Ipomoea tricolor	Convolvulaceae	Ipomoea_tricolor_RAD	*RAD2*	Lab sequcing	Lab sequcing	Ipomea_tricolor_consensus_sequence_1	Solanales
Jasminum angustifolium	Oleaceae	Jasminum_angustifolium_RAD	*RAD2*	KT284313	Genebank	Jasminum_angustifolium_RADIALIS	Lamiales
Jasminum tortuosum	Oleaceae	Jasminum_tortuosum_RAD1	*RAD2*	KT284318	Genebank	Jasminum_tortuosum_RADIALIS1	Lamiales
Jasminum tortuosum	Oleaceae	Jasminum_tortuosum_RAD2	*RAD2*	KT284314	Genebank	Jasminum_tortuosum_RADIALIS2	Lamiales
Kalachoe marnieriana	Crassulaceae	Kalachoe_marnieriana_RAD	*RAD1/RAD3*	Kalax.0713s0018.1	Phytozome	Kalachoe_marnieriana_scaffold_713_102609_102799	Saxifragales
Kolkwitzia amabilis	Caprifoliaceae	Kolkwitzia_amabilis_RAD1	*RAD2*	JX123707	Paper/Genebank	Kolkwitzia_amabilis_RAD2A	Dipsacales
Kolkwitzia amabilis	Caprifoliaceae	Kolkwitzia_amabilis_RAD2	*RAD2*	JX123706	Paper/Genebank	Kolkwitzia_amabilis_RAD2B	Dipsacales
Ligustrum lucidum	Oleaceae	Ligustrum_lucidum_RAD	*RAD2*	KT284323	Genebank	Ligustrum_lucidum_RADIALIS	Lamiales
Lindernia dubia	Linderniaceae	Lindernia_dubia_RAD	*RAD2*	KT284316	Genebank	Lindernia_dubia_RADIALIS	Lamiales
Lonicera bella	Caprifoliaceae	Lonicera_bella_RAD3	*RAD2*	JX123709	Paper/Genebank	Lonicera__bella_RAD2A	Dipsacales
Lonicera bella	Caprifoliaceae	Lonicera_bella_RAD5	*RAD2*	JX123694	Paper/Genebank	Lonicera_bella_RADIALIS_RAD2B	Dipsacales
Lonicera bella	Caprifoliaceae	Lonicera_bella_RAD1	*RAD1/RAD3*	JX123719	Paper/Genebank	Lonicera__bella_RAD1A	Dipsacales
Lonicera bella	Caprifoliaceae	Lonicera_bella_RAD2	*RAD1/RAD3*	JX123741	Paper/Genebank	Lonicera__bella_RAD1B	Dipsacales
Lonicera bella	Caprifoliaceae	Lonicera_bella_RAD4	*RAD1/RAD3*	JX123747	Paper/Genebank	Lonicera__bella_RAD3	Dipsacales
Lonicera maackii	Caprifoliaceae	Lonicera_maackii_RAD1	*RAD1/RAD3*	JX123705	Paper/Genebank	Lonicera_maackii_RADIALIS_RAD1A	Dipsacales
Lonicera morrowii	Caprifoliaceae	Lonicera_morrowii_RAD1	*RAD2*	JX123708	Paper/Genebank	Lonicera_morrowii_RADIALIS_RAD2A	Dipsacales
Lycium ruthenicum Murr	Solanaceae	Lycium_ruthenicum_Murr_RAD	*RAD2*	Lab sequcing	Lab sequcing	Lycium_ruthenicum_Murr_RAD_CS1 extraction*	Solanales

Malus domestica	Rosaceae	Malus_domestica_RAD1	*RAD1/RAD3*	MDP0000671095	Phytozome	Malus_domestica_MDC001494_453_6322_6513	Rosales
Malus domestica	Rosaceae	Malus_domestica_RAD2	*RAD1/RAD3*	MDP0000137765	Phytozome	Malus_domestica_MDC005436_527_3989_4108	Rosales
Malus domestica	Rosaceae	Malus_domestica_RAD3	*RAD1/RAD3*	MDC000889	Phytozome	Malus_domestica_MDC000889_407_5900_6053	Rosales
Malus domestica	Rosaceae	Malus_domestica_RAD4	*RAD1/RAD3*	MDP0000129858	Phytozome	Malus_domestica_MDC017434_201_3508_3661	Rosales
Medicago truncatula	Fabaceae	Medicago_truncatula_RAD3	*RAD2*	Medtr7g089210.1	Phytozome	Medicago_truncatula_chr7_34888188_34888371	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_RAD1	*RAD1/RAD3*	Medtr1g022290.1	Phytozome	Medicago_truncatula_chr1_7023224_7023416	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_RAD2	*RAD1/RAD3*	Medtr3g111880.1	Phytozome	Medicago_truncatula_chr3_52365364_52365485	Fabales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_RAD2	*RAD2*	XM_012975507.1	Genebank	Mimulus_guttatus_RADIALIS_like	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_RAD1	*RAD1/RAD3*	Migut.B00229.1	Phytozome	Mimulus_guttatus_scaffold_2_974316_974509	Lamiales
Mimulus ringens	Phrymaceae	Mimulus_ringens_RAD	*RAD2*	KT284322.1	Genebank	Mimulus_ringens_RADIALIS	Lamiales
Morina longifolia	Caprifoliaceae	Morina_longifolia_RAD2	*RAD2*	JX123723	Paper/Genebank	Morina_longifolia_RAD2A	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_RAD3	*RAD2*	JX123722	Paper/Genebank	Morina_longifolia_RAD2Ba	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_RAD4	*RAD2*	JX123724	Paper/Genebank	Morina_longifolia_RAD2Bb	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_RAD1	*RAD1/RAD3*	JX123726	Paper/Genebank	Morina_longifolia_RAD1B	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_RAD5	*RAD1/RAD3*	JX123725	Paper/Genebank	Morina_longifolia_RAD3	Dipsacales
Morus notabilis	Moraceae	Morus_notabilis_RAD	*RAD1/RAD3*	XM_010090622	Genebank	Morus_notabilis_hypothetical_protein_partial_mRNA	Rosales
Musa acuminata	Musaceae	Musa_acuminata_RAD1	*OUTGROUP*	GSMUA_Achr2T22930_001	Phytozome	Musa_acuminata_chr2_21835244_21835403	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_RAD2	*OUTGROUP*	GSMUA_Achr4T14930_001	Phytozome	Musa_acuminata_chr4_11228816_11228961	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_RAD3	*OUTGROUP*	GSMUA_Achr6T27230_001	Phytozome	Musa_acuminata_chr6_27804355_27804503	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_RAD4	*OUTGROUP*	GSMUA_Achr7T25590_001	Phytozome	Musa_acuminata_chr7_27171015_27171160	Zingiberales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_RAD	*RAD1/RAD3*	XM_010256523.1	Genebank	Nelumbo_nucifera_protein_RADIALIS_like3	Proteales
Nicotiana benthamian	Solanaceae	Nicotiana_benthamiana_RAD1	*RAD2*	Niben101Scf00226Ctg004	Sol Genomics Network	Nicotiana_benthamiana_101Scf00226Ctg004	Solanales

Nicotiana benthamian	Solanaceae	Nicotiana_benthamiana_RAD2	*RAD2*	Niben 101Scf03214Ctg008	Sol Genomics Network	Nicotiana_benthamiana_101Scf03214Ctg008	Solanales
Nicotiana benthamian	Solanaceae	Nicotiana_benthamiana_RAD3	*RAD2*	Niben 101Scf05279Ctg014	Sol Genomics Network	Nicotiana_benthamiana_101Scf04784Ctg004	Solanales
Nicotiana benthamian	Solanaceae	Nicotiana_benthamiana_RAD4	*RAD2*	Niben 101Scf05279Ctg014	Sol Genomics Network	Nicotiana_benthamiana_101Scf05279Ctg014	Solanales
Nicotiana benthamian	Solanaceae	Nicotiana_benthamiana_RAD5	*RAD2*	Niben 101Scf08718Ctg007	Sol Genomics Network	Nicotiana_benthamiana_101Scf08718Ctg007_reversed	Solanales
Nicotiana benthamian	Solanaceae	Nicotiana_benthamiana_RAD6	*RAD1/RAD3*	Niben 101Scf00226Ctg017	Sol Genomics Network	Nicotiana_benthamiana_101Scf00226Ctg017	Solanales
Nicotiana benthamian	Solanaceae	Nicotiana_benthamiana_RAD7	*RAD1/RAD3*	Niben 101Scf06885Ctg002	Sol Genomics Network	Nicotiana_benthamiana_101Scf06885Ctg002_Copy_reversed	Solanales
Nicotiana obtusifolia	Solanaceae	Nicotiana_obtusifolia_RAD1	*RAD2*	Lab sequcing	Lab sequcing	Nicotiana_obtusifolia_RAD_CS1 extraction*	Solanales
Nicotiana obtusifolia	Solanaceae	Nicotiana_obtusifolia_RAD2	*RAD2*	Lab sequcing	Lab sequcing	Nicotiana_obtusifolia_RAD_CS2 extraction*	Solanales
Nicotiana otophora	Solanaceae	Nicotiana_otophora_RAD1	*RAD2*	Noto_AWOL01S0001215.1	Sol Genomics Network	Nicotiana_otophora_AWOL01S0001215_1	Solanales
Nicotiana otophora	Solanaceae	Nicotiana_otophora_RAD3	*RAD2*	Noto_AWOL01S0020501.1	Sol Genomics Network	Nicotiana_otophora_AWOL01S0020501_1_reversed	Solanales
Nicotiana otophora	Solanaceae	Nicotiana_otophora_RAD4	*RAD2*	Noto_AWOL01S0353723.1	Sol Genomics Network	Nicotiana_otophora_AWOL01S0353723_1	Solanales
Nicotiana otophora	Solanaceae	Nicotiana_otophora_RAD2	*RAD1/RAD3*	Noto_AWOL01S0013838.1	Sol Genomics Network	Nicotiana_otophora_AWOL01S0013838_1_reversed	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_RAD1	*RAD2*	Nsyl_KD943156.1	Sol Genomics Network	Nicotiana_sylvestris_KD943156_1	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_RAD2	*RAD2*	Nsyl_KD947279.1	Sol Genomics Network	Nicotiana_sylvestris_KD947279_1_reversed	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_RAD4	*RAD2*	Nsyl_KD981784.1	Sol Genomics Network	Nicotiana_sylvestris_KD981784_1_34001_35200_reversed	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_RAD3	*RAD1/RAD3*	Nsyl_KD981784.1	Sol Genomics Network	Nicotiana_sylvestris_KD981784_1_12701_14000	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_RAD1	*RAD2*	Ntab-BX_AWOK_SS7714	Sol Genomics Network	Nicotiana_tabacum__BX_AWOK_SS7714_503101_504400_2	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_RAD2	*RAD2*	Ntab-BX_AWOK_SS	Sol Genomics Network	Nicotiana_tabacum_BX_AWOK_SS11549_62401_63700_reversed	Solanales

				11549			
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_RAD3	*RAD2*	Ntab-BX_AWOK_SS12565	Sol Genomics Network	Nicotiana_tabacum_BX_AWOK_SS12565_408001_409300	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_RAD4	*RAD2*	Ntab-BX_AWOK_SS20044	Sol Genomics Network	Nicotiana_tabacum_BX_AWOK_SS20044_5101_6400	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_RAD5	*RAD2*	Ntab-BX_AWOK_SS20469	Sol Genomics Network	Nicotiana_tabacum_BX_AWOK_SS20469_156401_157700	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_RAD6	*RAD2*	Ntab-BX_AWOK_SS4546	Sol Genomics Network	Nicotiana_tabacum_BX_AWOK_SS4546_28701_29900	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_RAD7	*RAD2*	Ntab-BX_AWOK_SS7714	Sol Genomics Network	Nicotiana_tabacum_BX_AWOK_SS7714_503101_504400	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_RAD8	*RAD1/RAD3*	Ntab-BX_AWOK_SS11549	Sol Genomics Network	Nicotiana_tabacum_BX_AWOK_SS11549_294401_295700	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_RAD9	*RAD1/RAD3*	Ntab-BX_AWOK_SS12565	Sol Genomics Network	Nicotiana_tabacum_BX_AWOK_SS12565_390001_391300_reversed	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_RAD1	*RAD2*	Ntom_ASAG01027075.1	Sol Genomics Network	Nicotiana_tomentosiformis_ASAG01027075_1_reversed	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_RAD2	*RAD2*	Ntom_KB957561.1	Sol Genomics Network	Nicotiana_tomentosiformis_KB957561_1__reversed	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_RAD3	*RAD1/RAD3*	Ntom_KB968946.1	Sol Genomics Network	Nicotiana_tomentosiformis_KB968946_1_reversed	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_RAD4	*RAD1/RAD3*	Ntom_KB974396.1	Sol Genomics Network	Nicotiana_tomentosiformis_mRNA_82056_gene_44214_reversed	Solanales
Oryza sativa	Poaceae	Oryza_sativa_RAD1	*OUTGROUP*	LOC_Os01g44390.2	Phytozome	Oryza_sativa_Chr1_25462123_25462290	Poales
Oryza sativa	Poaceae	Oryza_sativa_RAD2	*OUTGROUP*	LOC_Os12g33950.1	Phytozome	Oryza_sativa_Chr12_20469052_20469176	Poales
Oryza sativa	Poaceae	Oryza_sativa_RAD3	*OUTGROUP*	LOC_Os03g14810	RiceGenome	Oryza_sativa_Japonica_9631_m01422_	Poales
Oryza sativa	Poaceae	Oryza_sativa_RAD4	*OUTGROUP*	LOC_Os03g63890	RiceGenome	Oryza_sativa_Japonica_9631_m06332	Poales
Oryza sativa	Poaceae	Oryza_sativa_RAD5	*OUTGROUP*	LOC_Os05g37040	RiceGenome	Oryza_sativa_Japonica_9633_m03415	Poales
Oryza sativa	Poaceae	Oryza_sativa_RAD6	*OUTGROUP*	LOC_Os05g37050	RiceGenome	Oryza_sativa_Japonica_9633_m03416	Poales

Oryza sativa	Poaceae	Oryza_sativa_RAD7	*OUTGROUP*	LOC_Os07g26150.1	RiceGenome	Oryza_sativa_Japonica_9635_m02514	Poales
Oryza sativa	Poaceae	Oryza_sativa_RAD8	*OUTGROUP*	LOC_Os12g33950	RiceGenome	Oryza_sativa_Japonica_9640_m03280	Poales
Panicum Pavir	Poaceae	Panicum_Pavir_RAD1	*OUTGROUP*	Pavir.Eb01660.1	Phytozome	Panicum_Pavir_Eb01660_1	Poales
Panicum Pavir	Poaceae	Panicum_Pavir_RAD2	*OUTGROUP*	Pavir.Eb01777.1	Phytozome	Panicum_Pavir_Eb01777_1	Poales
Panicum Pavir	Poaceae	Panicum_Pavir_RAD3	*OUTGROUP*	Pavir.J04159.1	Phytozome	Panicum_Pavir_J04159_1	Poales
Panicum Pavir	Poaceae	Panicum_Pavir_RAD4	*OUTGROUP*	Pavir.J04509.1	Phytozome	Panicum_Pavir_J04509_1	Poales
Petunia × hybrida	Solanaceae	Petunia_hybrida_var__Mitchell_RAD1	*RAD2*	comp10497_c0_seq1	Sol Genomics Network	P_hybrida_var__Mitchell_Transcriptome_comp10497	Solanales
Petunia × hybrida	Solanaceae	Petunia_hybrida_var__Mitchell_RAD2	*RAD2*	comp30347_c0_seq1	Sol Genomics Network	P_hybrida_var__Mitchell_Transcriptome_comp30347	Solanales
Petunia × hybrida	Solanaceae	Petunia_hybrida_var__Mitchell_RAD3	*RAD2*	comp36583_c0_seq1	Sol Genomics Network	P_hybrida_var__Mitchell_Transcriptome_comp36583_reversed	Solanales
Petunia × hybrida	Solanaceae	Petunia_hybrida_var__Mitchell_RAD4	*RAD1/RAD3*	comp56155_c0_seq1	Sol Genomics Network	P_hybrida_var__Mitchell_Transcriptome_comp56155_reversed	Solanales
Petunia sp.	Solanaceae	Petunia_sp_RAD1	*RAD2*	Lab sequcing	Lab sequcing	Petinua_sp_RAD1_CS extraction*	Solanales
Petunia sp.	Solanaceae	Petunia_sp_RAD2	*RAD2*	Lab sequcing	Lab sequcing	Petinua_sp_RAD2_CS extraction*	Solanales
Petunia sp.	Solanaceae	Petunia_sp_RAD3	*RAD2*	Lab sequcing	Lab sequcing	Petinua_sp_RAD3_CS extraction*	Solanales
Phaseolus radiatus	Fabaceae	Phaseolus_radiatus_RAD1	*RAD2*	XM_007148777.1	Genebank	Phaseolus_radiatus_RADIALIS_Like1	Fabales
Phaseolus radiatus	Fabaceae	Phaseolus_radiatus_RAD2	*RAD1/RAD3*	XM_014648763.1	Genebank	Phaseolus_radiatus_RADIALIS_Like4	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_RAD3	*RAD2*	Phvul.004G002400.1	Phytozome	Phaseolus_vulgaris_Chr04_246326_246508	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_RAD4	*RAD2*	Phvul.005G018500.1	Phytozome	Phaseolus_vulgaris_Chr05_1605332_1605518	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_RAD1	*RAD1/RAD3*	Phvul.011G044900.1	Phytozome	Phaseolus_vulgaris_Chr11_3875052_3875264	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_RAD2	*RAD1/RAD3*	Phvul.001G014300.1	Phytozome	Phaseolus_vulgaris_Chr01_1192834_1193015	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_RAD5	*RAD1/RAD3*	Phvul.009G058100.1	Phytozome	Phaseolus_vulgaris_Chr09_10554350_10554529	Fabales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_RAD	*OUTGROUP*	XM_008797709.1	Genebank	Phoenix_dactylifera_protein_RADIALIS_like_3	Arecales
Phryma leptostachya	Phrymaceae	Phryma_leptostachya_RAD	*RAD2*	KT284317	Genebank	Phryma_leptostachya_RADIALIS	Lamiales
Polypremum procumbens	Tetrachondraceae	Polypremum_procumbens_RAD1	*RAD2*	KT284319	Genebank	Polypremum_procumbens_RADIALIS1	Lamiales

Polypremum procumbens	Tetrachondraceae	Polypremum_procumbens_RAD2	*RAD2*	KT284315	Genebank	Polypremum_procumbens_RADIALIS2	Lamiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_RAD2	*RAD2*	XM_002305394.2	Genebank	Populus_trichocarpa_0004s16270g	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_RAD1	*RAD1/RAD3*	XM_006383124.1	Genebank	Populus_trichocarpa_0005s12390g	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_RAD3	*RAD1/RAD3*	XM_002300730.1	Genebank	Populus_trichocarpa_0002s03640g	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_RAD4	*RAD1/RAD3*	XM_002307624.2	Genebank	Populus_trichocarpa_0005s24960g	Malpighiales
Prunus mume	Rosaceae	Prunus_mume_protein_RAD1	*RAD2*	XM_008238680.1	Genebank	Prunus_mume_protein_RADIALIS_like_1	Rosales
Prunus mume	Rosaceae	Prunus_mume_protein_RAD2	*RAD1/RAD3*	XM_008222584.1	Genebank	Prunus_mume_protein_RADIALIS_like_3	Rosales
Rhytidophyllum auriculatum	Gesneriaceae	Rhytidophyllum_auriculatum_RAD	*RAD2*	KP794060	Genebank	Rhytidophyllum_auriculatum_radialis_mRNA	Lamiales
Rhytidophyllum rupincola	Gesneriaceae	Rhytidophyllum_rupincola_RAD	*RAD2*	KP794061	Genebank	Rhytidophyllum_rupincola_radialis_mRNA	Lamiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_RAD1	*RAD2*	XM_015726876	Genebank	Ricinus_communis_transcription_factor_RADIALIS1	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_RAD2	*RAD2*	XM_015726913	Genebank	Ricinus_communis_transcription_factor_RADIALIS2	Malpighiales
Sambucus canadensis	Adoxaceae	Sambucus_canadensis_RAD2	*RAD2*	JX123704	Paper/Genebank	Sambucus_canadensis_RAD2A	Dipsacales
Sambucus canadensis	Adoxaceae	Sambucus_canadensis_RAD1	*RAD1/RAD3*	JX123700	Paper/Genebank	Sambucus_canadensis_RAD1A	Dipsacales
Schaueria calycotricha	Acanthaceae	Schaueria_calycotricha_RAD	*RAD2*	KT284324	Genebank	Schaueria_calycotricha_RADIALIS	Lamiales
Schizanthus grahamii	Solanaceae	Schizanthus_grahamii_RAD1	*RAD2*	Lab sequcing	Lab sequcing	Schizanthus_grahamii_1	Solanales
Schizanthus grahamii	Solanaceae	Schizanthus_grahamii_RAD2	*RAD2*	Lab sequcing	Lab sequcing	Schizanthus_grahamii_2	Solanales
Schizanthus Pinnatus	Solanaceae	Schizanthus_Pinnatus_RAD1	*RAD2*	Lab sequcing	Lab sequcing	Schizanthus_Pinnatus_Consensus_Sequence_1	Solanales
Schizanthus Pinnatus	Solanaceae	Schizanthus_Pinnatus_RAD2	*RAD2*	Lab sequcing	Lab sequcing	Schizanthus_Pinnatus_Consensus_Sequence_2	Solanales
Sesamum indicum	Pedaliaceae	Sesamum_indicum_RAD	*RAD2*	XM_011094498	Genebank	Sesamum_indicum_transcription_factor_RADIALIS_like	Lamiales
Setaria italica	Poaceae	Setaria_italica_RAD1	*OUTGROUP*	Seita.5G238500.1	Phytozome	Setaria_italica__Si002888m	Poales
Setaria italica	Poaceae	Setaria_italica_RAD2	*OUTGROUP*	Seita.5G238400.1	Phytozome	Setaria_italica__Si003521m	Poales

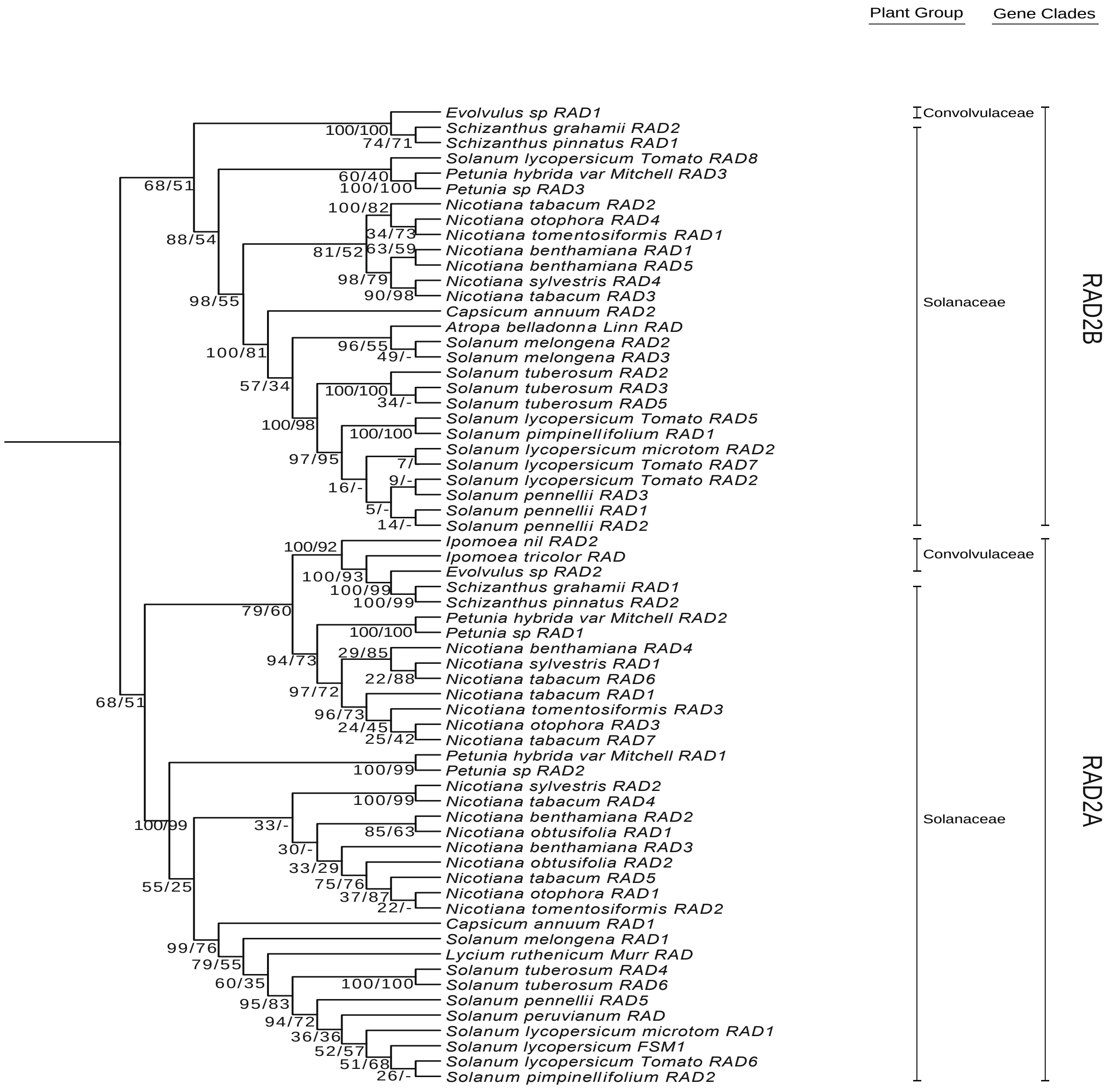
Setaria italica	Poaceae	Setaria_italica_RAD3	*OUTGROUP*	Seita.4G148800.1	Phytozome	Setaria_italica__Si008591	Poales
Setaria italica	Poaceae	Setaria_italica_RAD4	*OUTGROUP*	Seita.3G134100.1	Phytozome	Setaria_italica__Si023770m	Poales
Setaria viridis	Poaceae	Setaria_viridis_RAD1	*OUTGROUP*	Sevir.3G135700.1	Phytozome	Setaria_viridis_Chr_03_9327754_9327933	Poales
Setaria viridis	Poaceae	Setaria_viridis_RAD2	*OUTGROUP*	Sevir.4G163500.1	Phytozome	Setaria_viridis_Chr_04_22920265_22920381	Poales
Setaria viridis	Poaceae	Setaria_viridis_RAD3	*OUTGROUP*	Sevir.5G246000.1	Phytozome	Setaria_viridis_Chr_05_29550565_29550730	Poales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_RAD2	*RAD2*	JX123713	Paper/Genebank	Sixalix_atropurpurea_RAD2Ba	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_RAD3	*RAD2*	JX123711	Paper/Genebank	Sixalix_atropurpurea_RAD2Bb	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_RAD1	*RAD1/RAD3*	JX123712	Paper/Genebank	Sixalix_atropurpurea_RAD1A	Dipsacales
Solanum lycopersicum	Solanaceae	Solanum lycopersicum_FSM1	*RAD2*	AJ583670.1	Genebank	Lycopersicon_esculentum_FSM1_gi_7981379_78_344	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_microtom_RAD1	*RAD2*	Lab sequcing	Lab sequcing	Tomato_microtom_RAD2_CS*	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_Tomato_RAD6	*RAD2*	Solyc10g052470.1.1	Sol Genomics Network	Solanum_lycopersicum_Tomato_Solyc10g052470_1_1	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_Tomato_RAD8	*RAD2*	Solyc04g080500	Sol Genomics Network	Solanum_lycopersicum_Tomato_phytozome_Solyc04g080500	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_Tomato_RAD9	*RAD1/RAD3*	Solyc12g089190.1.1	Sol Genomics Network	Solanum_lycopersicum_Tomato_phytozome_Solyc12g089190_1_1	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_microtom_RAD2	*RAD1/RAD3*	Lab sequcing	Lab sequcing	Tomato_microtom_RAD1_CS*	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_Tomato_RAD2	*RAD1/RAD3*	HG975513.1	Sol Genomics Network	Solanum_lycopersicum_Ch01_gi_663680609_88338256_88338433	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_Tomato_RAD3	*RAD1/RAD3*	HG975513.1	Sol Genomics Network	Solanum_lycopersicum_ch01gi_663680609_88346974_88347103_reversed	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_Tomato_RAD4	*RAD1/RAD3*	Solyc10g052470.1.1	Phytozome	Solanum_lycopersicum_Tomato_phytozome_Solyc10g052470_1_1	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_Tomato_RAD5	*RAD1/RAD3*	Solyc01g109670.2	Sol Genomics Network	Solanum_lycopersicum_Tomato_Solyc01g109670_2_1	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_tomato_RAD7	*RAD1/RAD3*	XM_004231375	Genebank	Solanum_lycopersicum_transcription_factor_RADIALIS_LOC101244536gi723665865	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_Tomato_RAD10	*RAD1/RAD3*	Solyc01g109690.1.1	Sol Genomics Network	Solanum_lycopersicum_Tomato_Solyc01g109690_1_1	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_Tomato_RAD1	*RAD1/RAD3*	Solyc2.40.04	Phytozome	Solanum_lycopersicum_Tomato_phytozome_Solyc2_40_04	Solanales

Solanum melongena	Solanaceae	Solanum_melongena_RAD1	*RAD2*	Sme2.5_01830.1_g00008.1	Sol Genomics Network	Solanum_melongena_Eggplant_Sme2_5_01830_1_g00008_1	Solanales
Solanum melongena	Solanaceae	Solanum_melongena_RAD2	*RAD2*	Sme2.5_00311.1_g00015.1	Sol Genomics Network	Solanum_melongena_Eggplant_00311_1_g00015_1	Solanales
Solanum melongena	Solanaceae	Solanum_melongena_RAD3	*RAD2*	Sme2.5_00474.1_g00002.1	Sol Genomics Network	Solanum_melongena_Eggplant_Sme2_5_00474_1_g00002_1	Solanales
Solanum pennelli	Solanaceae	Solanum_pennellii_RAD1	*RAD2*	HG975440.1	Genebank	Solanum_pennellii_chromosome_ch01_gi_663673439_107392364_107392541	Solanales
Solanum pennelli	Solanaceae	Solanum_pennellii_RAD2	*RAD2*	XM_015206270.1	Genebank	Solanum_pennellii_transcription_factor_RADIALIS_LOC107007562gi_969996200	Solanales
Solanum pennelli	Solanaceae	Solanum_pennellii_RAD3	*RAD2*	Sopen01g051860.1	Sol Genomics Network	Wild_tomato_Sopen01g051860_1	Solanales
Solanum pennelli	Solanaceae	Solanum_pennellii_RAD5	*RAD2*	Sopen10g023180.1	Sol Genomics Network	Wild_tomato_Sopen10g023180_1	Solanales
Solanum pennelli	Solanaceae	Solanum_pennellii_RAD4	*RAD1/RAD3*	Sopen01g051880.1	Sol Genomics Network	Wild_tomato_Sopen01g051880_1	Solanales
Solanum pennelli	Solanaceae	Solanum_pennellii_RAD6	*RAD1/RAD3*	HG975440.1	Genebank	Solanum_pennellii_chromosome_ch01_gi_663673439_107405095-107405224_reversed	Solanales
Solanum peruvianum	Solanaceae	Solanum_peruvianum_RAD	*RAD2*	pSolyc10g052470.1.1	Sol Genomics Network	Solanum_peruvianum_pSolyc10g052470_1_1	Solanales
Solanum pimpinellifolium	Solanaceae	Solanum_pimpinellifolium_RAD1	*RAD2*	contig:unspecified:5570027:1:2646:1	Sol Genomics Network	Solanum_pimpinellifolium_WGS_contig_unspecified_5570027_1_2646	Solanales
Solanum pimpinellifolium	Solanaceae	Solanum_pimpinellifolium_RAD2	*RAD2*	contig:unspecified:6560171:1:6145:1	Sol Genomics Network	Solanum_pimpinellifolium_WGS_contig_unspecified_6560171_1_6145_1_reversed	Solanales
Solanum pimpinellifolium	Solanaceae	Solanum_pimpinellifolium_RAD3	*RAD1/RAD3*	contig:unspecified;6619945:1:3357:1	Sol Genomics Network	Solanum_pimpinellifolium_WGS_contig_unspecified_6619945_1_3357_1_reversed	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_RAD2	*RAD2*	XM_006365046.1	Genebank	Solanum_tuberosum_Potato_gi_565399123_refXM_006365046_1	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_RAD4	*RAD2*	PGSC0003DMT400084268	Sol Genomics Network	Solanum_tuberosum_Potato_phytozome_PGSC0003DMT400084268	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_RAD5	*RAD2*	ST4.03ch01	Sol Genomics Network	Solanum_tuberosum_Potato_ST4_03_ch01_86000634_86000811	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_RAD6	*RAD2*	ST4.03.ch10	Sol Genomics Network	Solanum_tuberosum_Potato_ST4_03_ch10_44202018_44202260	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_RAD7	*RAD2*	PGSC0003DMT400009583	Phytozome	Solanum_tuberosum_Potato_phytozome_PGSC0003DMT400009583	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_RAD8	*RAD1/RAD3*	PGSC0003DMT400039974	Phytozome	Solanum_tuberosum_Potato_phytozome_PGSC0003DMT400039974	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_RAD3	*RAD1/RAD3*	PGSC0003DMT400001883	Sol Genomics Network	Solanum_tuberosum_Potato_phytozome_PGSC0003DMT400001883	Solanales

Solanum tuberosum	Solanaceae	Solanum_tuberosum_RAD9	*RAD1/RAD3*	ST4.03ch01	Sol Genomics Network	Solanum_tuberosum_Potato_ST4_03_ch01_86016901_86018100_reversed	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_RAD1	*RAD1/RAD3*	PGSC0003DMT400009450	Phytozome	Solanum_tuberosum_Potato_phytozome_PGSC0003DMT400009450	Solanales
Spirodela polyrhiza	Araceae	Spirodela_polyrhiza_RAD	*OUTGROUP*	Spipo0G0019500	Phytozome	Spirodela_polyrhiza_pseudo0_1655509_1655697	Alismatales
Symphoricarpos occidentalis	Caprifoliaceae	Symphoricarpos_orbiculatus_RAD2	*RAD2*	JX123739	Paper/Genebank	Symphoricarpos_orbiculatus_RAD2A	Dipsacales
Symphoricarpos occidentalis	Caprifoliaceae	Symphoricarpos_orbiculatus_RAD5	*RAD2*	JX123737	Paper/Genebank	Symphoricarpos_orbiculatus_RADIALIS_2	Dipsacales
Symphoricarpos occidentalis	Caprifoliaceae	Symphoricarpos_occidentalis_RAD1	*RAD1/RAD3*	JX123710	Paper/Genebank	Symphoricarpos_occidentalis_RAD1A	Dipsacales
Symphoricarpos occidentalis	Caprifoliaceae	Symphoricarpos_orbiculatus_RAD3	*RAD1/RAD3*	JX123740	Paper/Genebank	Symphoricarpos_orbiculatus_RAD3	Dipsacales
Symphoricarpos occidentalis	Caprifoliaceae	Symphoricarpos_orbiculatus_RAD4	*RAD1/RAD3*	JX123738	Paper/Genebank	Symphoricarpos_orbiculatus_RADIALIS	Dipsacales
Torenia fournieri	Linderniaceae	Torenia_fournieri_RAD	*RAD2*	LC090634.1	Genebank	Torenia_fournieri_TfRAD1_mRNA_for_RADIALIS_like_transcription_factor	Lamiales
Valerianella eriocarpa	Caprifoliaceae	Valerianella_eriocarpa_RAD2	*RAD2*	JX123703	Paper/Genebank	Valerianella_eriocarpa_RAD2B	Dipsacales
Valerianella eriocarpa	Caprifoliaceae	Valerianella_eriocarpa_RAD1	*RAD1/RAD3*	JX123701	Paper/Genebank	Valerianella_eriocarpa_RAD1A	Dipsacales
Valerianella locusta	Caprifoliaceae	Valerianella_locusta_RAD	*RAD2*	JX123702	Paper/Genebank	Valerianella_locusta_RAD2B	Dipsacales
Verbena canadensis	Plantaginaceae	Verbena_canadensis_RAD	*RAD2*	KT284320.1	Genebank	Verbena_canadensis_RADIALIS	Lamiales
Verbena chamaedrys	Plantaginaceae	Verbena_chamaedrys_RAD	*RAD2*	HQ853605.1	Genebank	Verbena_chamaedrys_RADIALIS	Lamiales
Verbena intercedens	Plantaginaceae	Verbena_intercedens_RAD	*RAD2*	HQ853606.1	Genebank	Verbena_intercedens_RADIALIS	Lamiales
Verbena serpyllifolia	Plantaginaceae	Verbena_serpyllifolia_RAD	*RAD2*	FJ649695	Genebank	Verbena_serpyllifolia_RADIALIS	Lamiales
Viburnum acerifolium	Adoxaceae	Viburnum_acerifolium_RAD2	*RAD2*	JX123748	Paper/Genebank	Viburnum_acerifolium_RAD2A	Dipsacales
Viburnum acerifolium	Adoxaceae	Viburnum_acerifolium_RAD3	*RAD2*	JX123717	Paper/Genebank	Viburnum_acerifolium_RAD2B	Dipsacales
Viburnum acerifolium	Adoxaceae	Viburnum_acerifolium_RAD1	*RAD1/RAD3*	JX123749	Paper/Genebank	Viburnum_acerifolium_RAD1B	Dipsacales
Vitis vinifera	Vitaceae	Vitis_vinifera_RAD1	*RAD2*	XM_003631612	Genebank	Vitis_vinifera_protein_RL_1_LOC100853747	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_RAD2	*RAD1/RAD3*	XM_010650835.1	Genebank	Vitis_vinifera_RL3_LOC100246097	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_RAD3	*RAD1/RAD3*	XM_003631618.	Genebank	Vitis_vinifera_RL3LOC100853961	Vitales

				2			
Weigela hortensis	Caprifoliaceae	Weigela_hortensis_RAD2	*RAD2*	JX123750	Paper/Genebank	Weigela_hortensis_RAD2A	Dipsacales
Weigela hortensis	Caprifoliaceae	Weigela_hortensis_RAD3	*RAD2*	JX123718	Paper/Genebank	Weigela_hortensis_RAD2B	Dipsacales
Weigela hortensis	Caprifoliaceae	Weigela_hortensis_RAD1	*RAD1/RAD3*	JX123751	Paper/Genebank	Weigela_hortensis_RAD1B	Dipsacales
Wulfenia carinthiaca	Plantaginaceae	Wulfenia_carinthiaca_RAD	*RAD2*	HQ853604	Genebank	Wulfenia_carinthiaca_RADIALIS	Lamiales
Zea mavs	Poaceae	Zea_mavs_RAD	*OUTGROUP*	GRMZM2G451116_T01	Phytozome	Zea_GRMZM2G451116_T01	Poales

Appendix 2.



Appendix 2. Phylogeny of RAD2 clade of Solanaceae and Convolvulaceae based on Bayesian and ML inferences. The unrooted tree shows the two clades, each of these including both sequences from Solanaceae and Convolvulaceae. Bayesian posterior probabilities and bootstrap frequencies are labeled close to the branches, respectively.

Appendix 3. Accession information of R-R-type genes

Taxa	Families	Sequence ID in this study	Inclusion in phylogeny: Y, yes with clade names; N, no	Accession numbers in databases	Databases	Sequence ID in databases	Orders
Aegilops speltoides	Poaceae	Aegilops_speltoides_clone_TaMYB51_MYB_related_protein	N	JF951934.1	genebank	Aegilops_speltoides_clone_TaMYB51_MYB_related_protein	Poales
Aegilops speltoides	Poaceae	Aegilops_speltoides_GID2_1	N	KU857040.1	genebank	Aegilops_speltoides_GID2_protein_isoform_1_gid2	Poales
Aegilops speltoides	Poaceae	Aegilops_speltoides_GID2_2	N	U857041.1	genebank	Aegilops_speltoides_GID2_protein_isoform_2_gid2	Poales
Aegilops speltoides	Poaceae	Aegilops_speltoides_GID2_3	N	KU857042.1	genebank	Aegilops_speltoides_GID2_protein_isoform_3_gid2	Poales
Aeluropus littoralis	Poaceae	Aeluropus_littoralis_MYB	N	EF534705.1	genebank	Aeluropus_littoralis_MYB_Al_protein_gene_CDS	Poales
Amaranthus hypochondriacus	Amaranthaceae	Amaranthus_hypochondriacus_3	N	AHYPO_017018	phytozome	Amaranthus_hypochondriacus_AHYPO_017018	Caryophyllales
Amaranthus hypochondriacus	Amaranthaceae	Amaranthus_hypochondriacus_4	N	AHYPO_017235	phytozome	Amaranthus_hypochondriacus_AHYPO_017235	Caryophyllales
Amaranthus hypochondriacus	Amaranthaceae	Amaranthus_hypochondriacus_AHYPO_000402	N	AHYPO_000402	phytozome	Amaranthus_hypochondriacus_AHYPO_000402	Caryophyllales
Amaranthus hypochondriacus	Amaranthaceae	Amaranthus_hypochondriacus_AHYPO_001520	N	AHYPO_001520	phytozome	Amaranthus_hypochondriacus_AHYPO_001520	Caryophyllales
Amaranthus hypochondriacus	Amaranthaceae	Amaranthus_hypochondriacus_AHYPO_004695	N	AHYPO_004695	phytozome	Amaranthus_hypochondriacus_AHYPO_004695	Caryophyllales
Amaranthus hypochondriacus	Amaranthaceae	Amaranthus_hypochondriacus_AHYPO_006444	N	AHYPO_006444	phytozome	Amaranthus_hypochondriacus_AHYPO_006444	Caryophyllales
Amaranthus hypochondriacus	Amaranthaceae	Amaranthus_hypochondriacus_AHYPO_010419	N	AHYPO_010419	phytozome	Amaranthus_hypochondriacus_AHYPO_010419	Caryophyllales
Amaranthus hypochondriac	Amaranthaceae	Amaranthus_hypochondriacus_DIV1	Y RR1A	AHYPO_007744	phytozome	Amaranthus_hypochondriacus_AHYPO_007744	Caryophyllales

us							
Amaranthus hypochondriacus	Amaranthaceae	Amaranthus_hypochondriacus_DIV2	Y RR1C	AHYPO_013679	phytozome	Amaranthus_hypochondriacus_AHYPO_013679	Caryophyllales
Ananas comosus	Bromeliaceae	Ananas_comosus_1	N	Aco010322	phytozome	Ananas_comosus_Aco010322	Poales
Ananas comosus	Bromeliaceae	Ananas_comosus_2	N	Aco014113	phytozome	Ananas_comosus_Aco014113	Poales
Ananas comosus	Bromeliaceae	Ananas_comosus_3	N	Aco015386	phytozome	Ananas_comosus_Aco015386	Poales
Ananas comosus	Bromeliaceae	Ananas_comosus_4	N	Aco016874	phytozome	Ananas_comosus_Aco016874	Poales
Ananas comosus	Bromeliaceae	Ananas_comosus_Aco008934	N	Aco008934	phytozome	Ananas_comosus_Aco008934	Poales
Ananas comosus	Bromeliaceae	Ananas_comosus_Aco009969	N	Aco009969	phytozome	Ananas_comosus_Aco009969	Poales
Antirrhinum majus	Plantaginaceae	Antirrhinum_majus_DIV	Y RR2A/DIV1	AY077453.1	genebank	Antirrhinum_majus_DIV_cds	Lamiales
Aquilegia alpina	Ranunculaceae	Aquilegia_alpina_DIV	Y RR2B/DIV2	FJ805376.1	genebank	Aquilegia_alpina_FJ805376	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia_coerulea_Goldsmith_3	N	Aquca_004_00370	phytozome	Aquilegia_coerulea_Goldsmith_Aquca_004_00370	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia_coerulea_Goldsmith_4	N	Aquca_009_00736	phytozome	Aquilegia_coerulea_Goldsmith_Aquca_009_00736	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia_coerulea_Goldsmith_Aquca_001_00262	N	Aquca_001_00262	phytozome	Aquilegia_coerulea_Goldsmith_Aquca_001_00262	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia_coerulea_Goldsmith_Aquca_002_00032	N	Aquca_002_00032	phytozome	Aquilegia_coerulea_Goldsmith_Aquca_002_00032	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia_coerulea_Goldsmith_Aquca_002_00384	N	Aquca_002_00384	phytozome	Aquilegia_coerulea_Goldsmith_Aquca_002_00384	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia_coerulea_Goldsmith_DIV1	Y RR1A	Aquca_004_00257	phytozome	Aquilegia_coerulea_Goldsmith_Aquca_004_00257	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia_coerulea_Goldsmith_DIV3	Y RR1A	Aquca_072_00078	phytozome	Aquilegia_coerulea_Goldsmith_Aquca_072_00078	Ranunculales
Aquilegia coerulea	Ranunculaceae	Aquilegia_coerulea_Goldsmith_DIV2	Y RR2B/DIV2	Aquca_004_00289	phytozome	Aquilegia_coerulea_Goldsmith_Aquca_004_00289	Ranunculales
Arabidopsis halleri	Brassicaceae	Arabidopsis_halleri_20436s0006	N	Araha.20436s0006	phytozome	Arabidopsis_halleri_Araha_20436s0006	Brassicales
Arabidopsis halleri	Brassicaceae	Arabidopsis_halleri_4	N	Araha.17955s0001	phytozome	Arabidopsis_halleri_Araha_17955s0001	Brassicales
Arabidopsis halleri	Brassicaceae	Arabidopsis_halleri_DIV3	Y RR1B	Araha.1682s0001	phytozome	Arabidopsis_halleri_Araha_1682s0001	Brassicales

Arabidopsis halleri	Brassicaceae	Arabidopsis_halleri_DIV1	Y RR1C	Araha.0937s0001	phytozome	Arabidopsis_halleri_Araha_0937s0001	Brassicales
Arabidopsis halleri	Brassicaceae	Arabidopsis_halleri_DIV2	Y RR2A/DIV1	Araha.15560s0002	phytozome	Arabidopsis_halleri_Araha_15560s0002	Brassicales
Arabidopsis halleri	Brassicaceae	Arabidopsis_halleri_DIV4	Y RR2B/DIV2	Araha.33366s0002	phytozome	Arabidopsis_halleri_Araha_33366s0002	Brassicales
Arabidopsis lyrata	Brassicaceae	Arabidopsis_lyrata_479087	N	479087	phytozome	Arabidopsis_lyrata_479087	Brassicales
Arabidopsis lyrata	Brassicaceae	Arabidopsis_lyrata_950353	N	950353	phytozome	Arabidopsis_lyrata_950353	Brassicales
Arabidopsis lyrata	Brassicaceae	Arabidopsis_lyrata_DIV1	Y RR2A/DIV1	349486	phytozome	Arabidopsis_lyrata_349486	Brassicales
Arabidopsis lyrata	Brassicaceae	Arabidopsis_lyrata_DIV3	Y RR2A/DIV1	482816	phytozome	Arabidopsis_lyrata_482816	Brassicales
Arabidopsis lyrata	Brassicaceae	Arabidopsis_lyrata_DIV4	Y RR2A/DIV1	496013	phytozome	Arabidopsis_lyrata_496013	Brassicales
Arabidopsis lyrata	Brassicaceae	Arabidopsis_lyrata_DIV2	Y RR2B/DIV2	478469	phytozome	Arabidopsis_lyrata_478469	Brassicales
Arabidopsis lyrata	Brassicaceae	Arabidopsis_lyrata_DIV5	Y RR2B/DIV2	940007	phytozome	Arabidopsis_lyrata_940007	Brassicales
Arabidopsis thaliana columbia	Brassicaceae	Arabidopsis_thaliana_columbia_AT3G16350	N	AY519512.1	phytozome	Arabidopsis_thaliana_columbia_AT3G16350	Brassicales
Arabidopsis thaliana columbia	Brassicaceae	Arabidopsis_thaliana_columbia_AT5g04760_R_R_type	Y RR1A	AB493736.1	phytozome	Arabidopsis_thaliana_columbia_AT5g04760_R_R_type	Brassicales
Arabidopsis thaliana columbia	Brassicaceae	Arabidopsis_thaliana_columbia_AT5G08520_R_R_type	Y RR1B	AY519532.1	phytozome	Arabidopsis_thaliana_columbia_AT5G08520_R_R_type	Brassicales
Arabidopsis thaliana columbia	Brassicaceae	Arabidopsis_thaliana_columbia_AT5G23650_R_R_type	Y RR1B	DQ056685.1	phytozome	Arabidopsis_thaliana_At5g23650_extraction	Brassicales
Arabidopsis thaliana columbia	Brassicaceae	Arabidopsis_thaliana_columbia_AT1G49010_R_R_type	Y RR1C	AY519528.1	phytozome	Arabidopsis_thaliana_columbia_AT1G49010_R_R_type	Brassicales
Arabidopsis thaliana columbia	Brassicaceae	Arabidopsis_thaliana_columbia_AT2G38090_R_R_type	Y RR2A/DIV1	AY519529.1	phytozome	Arabidopsis_thaliana_columbia_AT2G38090_R_R_type	Brassicales
Arabidopsis thaliana columbia	Brassicaceae	Arabidopsis_thaliana_columbia_AT5G01200_R_R_type	Y RR2A/DIV1	AY519530.1	phytozome	Arabidopsis_thaliana_columbia_AT5G01200_R_R_type	Brassicales
Arabidopsis thaliana	Brassicaceae	Arabidopsis_thaliana_columbia_AT5G58900_R_R_type	Y RR2A/DIV1	AY519533.1	phytozome	Arabidopsis_thaliana_columbia_AT5G58900_R_R_type	Brassicales

columbia							
Arabidopsis thaliana columbia	Brassicaceae	Arabidopsis_thaliana_columbia_AT3G11280_R_R_type	Y RR2B/DIV2	AY550308.1	phytozome	Arabidopsis_thaliana_columbia_AT3G11280_R_R_type	Brassicales
Arabidopsis thaliana columbia	Brassicaceae	Arabidopsis_thaliana_columbia_AT5G05790_R_R_type	Y RR2B/DIV2	AY519531.1	phytozome	Arabidopsis_thaliana_columbia_AT5G05790_R_R_type	Brassicales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107458408	N	XM_016076613.1	genebank	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107458408	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107471987_variant1/2	N	XM_016091550.1/XM_016091549.1	genebank	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107471987_variant1/2	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107479628	N	XM_016099749.1	genebank	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107479628	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107481302_variant1/2/3	N	XM_016101556.1/XM_016101557.1/XM_016101558.1	genebank	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107481302_variant1/2/3	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107493640	N	XM_016114720.1	genebank	Arachis_duranensis_transcription_factor_DIVARICATA_like_LOC107493640	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_DIVARICATA_LOC107469352	N	XM_016088733.1	genebank	Arachis_duranensis_transcription_factor_DIVARICATA_LOC107469352	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_DIVARICATA_LOC107469352	N	XM_016088733.1	genebank	Arachis_duranensis_transcription_factor_DIVARICATA_LOC107469352	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_DIVARICATA_LOC107609503	N	XM_016311496.1	genebank	Arachis_duranensis_transcription_factor_DIVARICATA_LOC107609503	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_MYB1R1_like_LOC107487487	N	XM_016108133.1	genebank	Arachis_duranensis_transcription_factor_MYB1R1_like_LOC107487487	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_transcription_factor_MYB1R1_LOC107489059	N	XM_016109835.1	genebank	Arachis_duranensis_transcription_factor_MYB1R1_LOC107489059	Fabales
Arachis duranensis	Fabaceae	Arachis_duranensis_uncharacterized_LOC107485662	N	XM_016106193.1	genebank	Arachis_duranensis_uncharacterized_LOC107485662	Fabales

Arachis duranensis	Fabaceae	Archis_duranensis uncharacterized_LOC107490116	N	XM_016110882.1	genebank	Archis_duranensis uncharacterized_LOC107490116	Fabales
Arachis hypogaea	Fabaceae	Arachis_hypogaea_putative_MYB_related_protein_17_MYB17_gene	N	KF208671.1	genebank	Arachis_hypogaea_putative_MYB_related_protein_17_MYB17_gene	Fabales
Arachis hypogaea	Fabaceae	Arachis_hypogaea_putative_MYB_related_protein_22_MYB22_gene	N	KF208676.1	genebank	Arachis_hypogaea_putative_MYB_related_protein_22_MYB22_gene	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_myb_like_I_LOC107642150	N	XM_016345457.1	genebank	Arachis_ipaensis_myb_like_I_LOC107642150	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107467340	N	XM_016086400.1	genebank	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107467340	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107608860	N	XM_016310649.1	genebank	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107608860	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107609463_variant1/2	N	XM_016311454.1/XM_016311455.1	genebank	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107609463_variant1/2	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107623719	N	XM_016326067.1	genebank	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107623719	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107630413	N	XM_016333523.1	genebank	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107630413	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107631454_variant1/2	N	XM_016334902.1/XM_016334903.1	genebank	Arachis_ipaensis_transcription_factor_DIVARICATA_LOC107631454_variant1/2	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_transcription_factor_MYB1R1_like_LOC107634521	N	XM_016337976.1	genebank	Arachis_ipaensis_transcription_factor_MYB1R1_like_LOC107634521	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_transcription_factor_MYB1R1_like_LOC107642580	N	XM_016345975.1	genebank	Arachis_ipaensis_transcription_factor_MYB1R1_like_LOC107642580	Fabales
Arachis ipaensis	Fabaceae	Arachis_ipaensis_transcription_factor_MYB1R1_LOC107643461	N	XM_016347116.1	genebank	Arachis_ipaensis_transcription_factor_MYB1R1_LOC107643461	Fabales
Archis hypogaea	Fabaceae	hypogaea_putative_MYB_related_protein_16_MYB16_gene	N	KF208670.1	Gene bank	hypogaea_putative_MYB_related_protein_16_MYB16_gene	Fabales
Archis hypogaea	Fabaceae	hypogaea_putative_MYB_related_protein_18__MYB18_gene	N	KF208672.1	Gene bank	hypogaea_putative_MYB_related_protein_18__MYB18_gene	Fabales

Archis hypogaea	Fabaceae	hypogaea_putative_MYB_related_protein_28_MYB28_gene	N	KF208682.1	Gene bank	hypogaea_putative_MYB_related_protein_28_MYB28_gene	Fabales
Archis hypogaea	Fabaceae	hypogaea_putative_MYB_related_protein_29__MYB29_gene	N	KF208683.1	Gene bank	hypogaea_putative_MYB_related_protein_29__MYB29_gene	Fabales
Archis hypogaea	Fabaceae	hypogaea_putative_MYB_related_protein_30__MYB30_gene	N	KF208684.1	Gene bank	hypogaea_putative_MYB_related_protein_30__MYB30_gene	Fabales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104883750	N	XM_010668309.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104883750	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104886638	N	XM_010671111.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104886638	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104900000	N	XM_010687312.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104900000	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104903689	N	XM_010691783.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104903689	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104907690	N	XM_010696658.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104907690	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_transcription_factor_MYB1R1_like_LOC104883142	N	XM_010667609.2	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_MYB1R1_like_LOC104883142	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_transcription_factor_MYB1R1_like_LOC104888923	N	XM_010674037.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_MYB1R1_like_LOC104888923	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_transcription_factor_MYB1R1_like_LOC104894172	N	XM_010680348.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_MYB1R1_like_LOC104894172	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_transcription_factor_MYB1R1_like_LOC104898042	N	XM_010685047.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_MYB1R1_like_LOC104898042	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_DIV2	Y RR1A	XM_010696772.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104907781	Caryophyllales
Beta vulgaris	Amaranthaceae	Beta_vulgaris_subsp_vulgaris_DIV1	Y RR1C	XM_010682550.1	genebank	Beta_vulgaris_subsp_vulgaris_transcription_factor_DIVARICATA_like_LOC104895904	Caryophyllales

Boechera stricta	Brassicaceae	Boechera_stricta_Bostr_13129s0103	N	Bostr.13129s0103	phytozome	Boechera_stricta_Bostr_13129s0103	Brassicales
Boechera stricta	Brassicaceae	Boechera_stricta_Bostr_13129s0394	N	Bostr.13129s0394	phytozome	Boechera_stricta_Bostr_13129s0394	Brassicales
Boechera stricta	Brassicaceae	Boechera_stricta_Bostr_23794s0264	N	Bostr.23794s0264	phytozome	Boechera_stricta_Bostr_23794s0264	Brassicales
Boechera stricta	Brassicaceae	Boechera_stricta_Bostr_26833s0356	N	Bostr.26833s0356	phytozome	Boechera_stricta_Bostr_26833s0356	Brassicales
Boechera stricta	Brassicaceae	Boechera_stricta_Bostr_26833s0577	N	Bostr.26833s0577	phytozome	Boechera_stricta_Bostr_26833s0577	Brassicales
Boechera stricta	Brassicaceae	Boechera_stricta_Bostr_28625s0055	N	Bostr.28625s0055	phytozome	Boechera_stricta_Bostr_28625s0055	Brassicales
Boechera stricta	Brassicaceae	Boechera_stricta_DIV	Y RR2B/DIV2	Bostr.19424s1061	phytozome	Boechera_stricta_Bostr_19424s1061	Brassicales
Bournea leiophylla	Gesneriaceae	Bournea_leiophylla_transcription_factor_DIV1_mRNA	N	EF211118.1	genebank	Bournea_leiophylla_transcription_factor_DIV1_mRNA	Lamiales
Bournea leiophylla	Gesneriaceae	Bournea_leiophylla_transcription_factor_DIV2_mRNA	N	EF211120.1	genebank	Bournea_leiophylla_transcription_factor_DIV2_mRNA	Lamiales
Brachypodium distachyon	Poaceae	Brachypodium_distachyon_Bradi2g02810	N	Bradi2g02810	phytozome	Brachypodium_distachyon_Bradi2g02810	Poales
Brachypodium distachyon	Poaceae	Brachypodium_distachyon_Bradi2g23710	N	Bradi2g23710	phytozome	Brachypodium_distachyon_Bradi2g23710	Poales
Brachypodium distachyon	Poaceae	Brachypodium_distachyon_Bradi2g55217	N	Bradi2g55217	phytozome	Brachypodium_distachyon_Bradi2g55217	Poales
Brachypodium distachyon	Poaceae	Brachypodium_distachyon_Bradi3g14830	N	Bradi3g14830	phytozome	Brachypodium_distachyon_Bradi3g14830	Poales
Brachypodium distachyon	Poaceae	Brachypodium_distachyon_Bradi3g17170	N	Bradi3g17170	phytozome	Brachypodium_distachyon_Bradi3g17170	Poales
Brachypodium distachyon	Poaceae	Brachypodium_distachyon_Bradi3g33400	N	Bradi3g33400	phytozome	Brachypodium_distachyon_Bradi3g33400	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brasr26833s0577	N	Brast08G101100	phytozome	Brachypodium_stacei_Brasr26833s0577	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast01G080300	N	Brast01G080300	phytozome	Brachypodium_stacei_Brast01G080300	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast01G086200	N	Brast01G086200	phytozome	Brachypodium_stacei_Brast01G086200	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast01G255500	N	Brast01G255500	phytozome	Brachypodium_stacei_Brast01G255500	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast01G387300	N	Brast01G387300	phytozome	Brachypodium_stacei_Brast01G387300	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast03G011700	N	Brast03G011700	phytozome	Brachypodium_stacei_Brast03G011700	Poales

Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast03G036600	N	Brast03G036600	phytozome	Brachypodium_stacei_Brast03G036600	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast03G198600	N	Brast03G198600	phytozome	Brachypodium_stacei_Brast03G198600	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast03G199200	N	Brast03G199200	phytozome	Brachypodium_stacei_Brast03G199200	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast08G105400	N	Brast08G105400	phytozome	Brachypodium_stacei_Brast08G105400	Poales
Brachypodium stacei	Poaceae	Brachypodium_stacei_Brast09G257200	N	Brast09G257200	phytozome	Brachypodium_stacei_Brast09G257200	Poales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_A01814	N	Brara.A01814	phytozome	Brassica_rapa_FPsc_Brara_A01814	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_A03415	N	Brara.A03415	phytozome	Brassica_rapa_FPsc_Brara_A03415	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_B00032	N	Brara.B00032	phytozome	Brassica_rapa_FPsc_Brara_B00032	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_B01892	N	Brara.B01892	phytozome	Brassica_rapa_FPsc_Brara_B01892	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_B03706	N	Brara.B03706	phytozome	Brassica_rapa_FPsc_Brara_B03706	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_C00358	N	Brara.C00358	phytozome	Brassica_rapa_FPsc_Brara_C00358	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_C01111	N	Brara.C01111	phytozome	Brassica_rapa_FPsc_Brara_C01111	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_C01919	N	Brara.C01919	phytozome	Brassica_rapa_FPsc_Brara_C01919	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_C03606	N	Brara.C03606	phytozome	Brassica_rapa_FPsc_Brara_C03606	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_C04549	N	Brara.C04549	phytozome	Brassica_rapa_FPsc_Brara_C04549	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_D02327	N	Brara.D02327	phytozome	Brassica_rapa_FPsc_Brara_D02327	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_E00711	N	Brara.E00711	phytozome	Brassica_rapa_FPsc_Brara_E00711	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_E02518	N	Brara.E02518	phytozome	Brassica_rapa_FPsc_Brara_E02518	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_F00380	N	Brara.F00380	phytozome	Brassica_rapa_FPsc_Brara_F00380	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_F02600	N	Brara.F02600	phytozome	Brassica_rapa_FPsc_Brara_F02600	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_G02453	N	Brara.B03706	phytozome	Brassica_rapa_FPsc_Brara_G02453	Brassicales

Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_H00322	N	Brara.H00322	phytozome	Brassica_rapa_FPsc_Brara_H00322	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_I04759	N	Brara.I04759	phytozome	Brassica_rapa_FPsc_Brara_I04759	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_J01271	N	Brara.J01271	phytozome	Brassica_rapa_FPsc_Brara_J01271	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_J02420	N	Brara.J02420	phytozome	Brassica_rapa_FPsc_Brara_J02420	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_Brara_J02638	N	Brara.J02638	phytozome	Brassica_rapa_FPsc_Brara_J02638	Brassicales
Brassica rapa	Brassicaceae	Brassica_rapa_FPsc_DIV	Y RR1B	Brara.B00290	phytozome	Brassica_rapa_FPsc_Brara_B00290	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104704166	N	XM_010420300.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104704166	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104704175	N	XM_010420307.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104704175	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104708229	N	XM_010424765.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104708229	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104708533	N	XM_010425126.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104708533	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104734584	N	XM_010454183.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104734584	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104734881	N	XM_010454557.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104734881	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104742411	N	XM_010463413.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104742411	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104745330	N	XM_010466529.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104745330	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104748110	N	XM_010469799.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104748110	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104748112	N	XM_010469800.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104748112	Brassicales
Camelina	Brassicaceae	Camelina_sativa_transcription	N	XM_010469801.	Gene bank	Camelina_sativa_transcriptio	Brassicales

sativa		_factor_DIVARICATA_like_LOC104748113		1		n_factor_DIVARICATA_like_LOC104748113	
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104756243	N	XM_010478801.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104756243	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104756353	N	XM_010478930.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104756353	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104756353	N	XM_010478930.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104756353	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104758201	N	XM_010481029.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104758201	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104761990_variant1/2	N	XM_010485197.1/XM_010485198.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104761990_variant1/2	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104764489	N	XM_010488068.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104764489	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104764773	N	XM_010488369.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104764773	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104764879	N	XM_010488474.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104764879	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104772172	N	XM_010496816.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104772172	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104782242	N	XM_010507118.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104782242	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104785667	N	XM_010510926.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104785667	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104792604	N	XM_010518791.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104792604	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_LOC104728980	N	XM_010447886.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_LOC104728980	Brassicales

Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_DIVARICATA_LOC104785667	N	XM_010510926.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_LOC104785667	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_MYB1R1_like_LOC104705024	N	XM_010421018.1	Gene bank	Camelina_sativa_transcription_factor_MYB1R1_like_LOC104705024	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_transcription_factor_MYB1R1_like_LOC104776016_variant1/2	N	XM_010500005.1/XM_010500006.1	Gene bank	Camelina_sativa_transcription_factor_MYB1R1_like_LOC104776016_variant1/2	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_uncharacterized_LOC104726752	N	XM_010445683.1	Gene bank	Camelina_sativa_uncharacterized_LOC104726752	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_uncharacterized_LOC104745965	N	XM_010467355.1	Gene bank	Camelina_sativa_uncharacterized_LOC104745965	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_uncharacterized_LOC104765474	N	XM_010489189.1	Gene bank	Camelina_sativa_uncharacterized_LOC104765474	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_uncharacterized_LOC104781253	N	XM_010505881.2	Gene bank	Camelina_sativa_uncharacterized_LOC104781253	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_DIV2	Y RR1C	XM_010502142.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104777819	Brassicales
Camelina sativa	Brassicaceae	Camelina_sativa_DIV1	Y RR2B/DIV2	XM_010492814.1	Gene bank	Camelina_sativa_transcription_factor_DIVARICATA_like_LOC104768774	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_Carubv10001525m_g	N	Carubv10001525m.g	phytozome	Capsella_rubella_Carubv10001525m_g	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_Carubv10003231m_g	N	Carubv10003231m.g	phytozome	Capsella_rubella_Carubv10003231m_g	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_Carubv10009808m_g	N	Carubv10009808m.g	phytozome	Capsella_rubella_Carubv10009808m_g	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_Carubv10011841m_g	N	Carubv10011841m.g	phytozome	Capsella_rubella_Carubv10011841m_g	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_Carubv10013924m_g	N	Carubv10013924m.g	phytozome	Capsella_rubella_Carubv10013924m_g	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_Carubv10014411m_g	N	Carubv10014411m.g	phytozome	Capsella_rubella_Carubv10014411m_g	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_Carubv10023736m_g	N	Carubv10023736m.g	phytozome	Capsella_rubella_Carubv10023736m_g	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_Carubv10026903m_g	N	Carubv10026903m.g	phytozome	Capsella_rubella_Carubv10026903m_g	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_Carubv10027693m_g	N	Carubv10027693m.g	phytozome	Capsella_rubella_Carubv10027693m_g	Brassicales
Capsella rubella	Brassicaceae	Capsella_rubella_DIV	Y RR2B/DIV2	Carubv10001695m.g	phytozome	Capsella_rubella_Carubv10001695m_g	Brassicales

Capsella grandiflora	Brassicaceae	Capsella_grandiflora_Cagra_0090s0025	N	Cagra.0090s0025	phytozome	Capsella_grandiflora_Cagra_0090s0025	Brassicales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_Cagra_0891s0087	N	Cagra.0891s0087	phytozome	Capsella_grandiflora_Cagra_0891s0087	Brassicales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_Cagra_1365s0066	N	Cagra.1365s0066	phytozome	Capsella_grandiflora_Cagra_1365s0066	Brassicales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_Cagra_1613s0002	N	Cagra.1613s0002	phytozome	Capsella_grandiflora_Cagra_1613s0002	Brassicales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_Cagra_1655s0043	N	Cagra.1655s0043	phytozome	Capsella_grandiflora_Cagra_1655s0043	Brassicales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_Cagra_1961s0096	N	Cagra.1961s0096	phytozome	Capsella_grandiflora_Cagra_1961s0096	Brassicales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_Cagra_4850s0001	N	Cagra.4850s0001	phytozome	Capsella_grandiflora_Cagra_4850s0001	Brassicales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_Cagra_5131s0007	N	Cagra.5131s0007	phytozome	Capsella_grandiflora_Cagra_5131s0007	Brassicales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_Cagra_6624s0006	N	Cagra.6624s0006	phytozome	Capsella_grandiflora_Cagra_6624s0006	Brassicales
Capsella grandiflora	Brassicaceae	Capsella_grandiflora_DIV	Y RR1B	Cagra.25796s0001	phytozome	Capsella_grandiflora_Cagra_25796s0001	Brassicales
Capsicum annuum	Solanaceae	Capsicum_annuum_transcription_factor_MYB1R1_like_LOC107875928	N	XM_016722831.1	Gene bank	Capsicum_annuum_transcription_factor_MYB1R1_like_LOC107875928	Solanales
Capsicum annuum	Solanaceae	Capsicum_annuum_transcription_factor_MYB1R1_LOC107840959	N	XM_016684918.1	Gene bank	Capsicum_annuum_transcription_factor_MYB1R1_LOC107840959	Solanales
Capsicum annuum	Solanaceae	Capsicum_annuum_uncharacterized_LOC107850716	N	XM_016695436.1	Gene bank	Capsicum_annuum_uncharacterized_LOC107850716	Solanales
Capsicum annuum	Solanaceae	Capsicum_annuum_DIV4	Y RR1B	XM_016716914.1	Gene bank	Capsicum_annuum_transcription_factor_DIVARICATA_like_LOC107870395	Solanales
Capsicum annuum	Solanaceae	Capsicum_annuum_DIV6	Y RR1B	XM_016692228.1/XM_016692230.1/XM_016692231.1	Gene bank	Capsicum_annuum_transcription_factor_DIVARICATA_like_LOC107847759_transcript_variant1/2/3	Solanales
Capsicum annuum	Solanaceae	Capsicum_annuum_DIV3	Y RR2B/DIV2	XM_016709385.1	Gene bank	Capsicum_annuum_transcription_factor_DIVARICATA_like_LOC107863460_variant1	Solanales
Capsicum annuum	Solanaceae	Capsicum_annuum_DIV5	Y RR2B/DIV2	XM_016717901.1/XM_016717902.1	Gene bank	Capsicum_annuum_transcription_factor_DIVARICATA_like_LOC107871103_transcript_variant1/2	Solanales

Capsicum annuum	Solanaceae	Capsicum_annuum_DIV1	Y RR2C/DIV3	XM_016686800.1	Gene bank	Capsicum_annuum_transcription_factor_DIVARICATA_like_LOC107842776	Solanales
Capsicum annuum	Solanaceae	Capsicum_annuum_DIV2	Y RR2C/DIV3	XM_016689193.1	Gene bank	Capsicum_annuum_transcription_factor_DIVARICATA_like_LOC107844851	Solanales
Carica papaya	Caricaceae	Carica_papaya_evm_TU_supercontig_2092_1	N	evm.TU.supercontig_2092.1	phytozome	Carica_papaya_evm_TU_supercontig_2092_1	Brassicales
Carica papaya	Caricaceae	Carica_papaya_evm_TU_supercontig_89_70	N	evm.TU.supercontig_89.70	phytozome	Carica_papaya_evm_TU_supercontig_89_70	Brassicales
Carica papaya	Caricaceae	Carica_papaya_DIV1	Y RR2A/DIV1	evm.TU.supercontig_112.58	phytozome	Carica_papaya_evm_TU_supercontig_112_58	Brassicales
Carica papaya	Caricaceae	Carica_papaya_DIV3	Y RR2B/DIV2	evm.TU.supercontig_19.216	phytozome	Carica_papaya_evm_TU_supercontig_19_216	Brassicales
Carica papaya	Caricaceae	Carica_papaya_DIV4	Y RR2B/DIV2	evm.TU.supercontig_19.217	phytozome	Carica_papaya_evm_TU_supercontig_19_217	Brassicales
Carica papaya	Caricaceae	Carica_papaya_DIV2	Y RR2C/DIV3	evm.TU.supercontig_1130.1	phytozome	Carica_papaya_evm_TU_supercontig_1130_1	Brassicales
Centranthus macrosiphon	Caprifoliaceae	Centranthus_macrosiphon_DIV1	Y RR2A/DIV1	FJ805295.1	Gene bank	Centranthus_macrosiphon_DIV1B_FJ805295	Dipsacales
Centranthus macrosiphon	Caprifoliaceae	Centranthus_macrosiphon_DIV2	Y RR2C/DIV3	FJ805296.1	Gene bank	Centranthus_macrosiphon_DIV3A_FJ805296	Dipsacales
Centranthus ruber	Caprifoliaceae	Centranthus_ruber_DIV1	Y RR2A/DIV1	FJ805297.1	Gene bank	Centranthus_ruber_DIV1B_FJ805297	Dipsacales
Centranthus ruber	Caprifoliaceae	Centranthus_ruber_DIV2	Y RR2C/DIV3	FJ805298.1	Gene bank	Centranthus_ruber_DIV3A_FJ805298	Dipsacales
Centranthus ruber	Caprifoliaceae	Centranthus_ruber_DIV3	Y RR2C/DIV3	FJ805299.1	Gene bank	Centranthus_ruber_DIV3B_FJ805299	Dipsacales
Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_factor_DIVARICATA_like_LOC101489770	N	XM_004506202.1	Gene bank	Cicer_arietinum_transcription_factor_DIVARICATA_like_LOC101489770	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_factor_DIVARICATA_like_LOC101490415_variant1/2	N	XM_004506203.1/XM_004506204.2	Gene bank	Cicer_arietinum_transcription_factor_DIVARICATA_like_LOC101490415_variant1/2	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101494305	N	XM_004506730.2	Gene bank	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101494305	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101494332	N	XM_004490518.2	Gene bank	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101494332	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101499316	N	XM_004509798.2	Gene bank	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101499316	Fabales

Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101504133	N	XM_004492358.2	Gene bank	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101504133	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101508945_variant1/2	N	XM_004513192.2/XM_004513193.2	Gene bank	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101508945_variant1/2	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101511974	N	XM_004497078.2	Gene bank	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101511974	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_factor_MYB1R1_like_LOC101511722_variant1/2	N	XM_004489888.2/XM_012712802.1	Gene bank	Cicer_arietinum_transcription_factor_MYB1R1_like_LOC101511722_variant1/2	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_transcription_uncharacterized_LOC101505306	N	XM_004513041.2	Gene bank	Cicer_arietinum_transcription_uncharacterized_LOC101505306	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_uncharacterized_LOC101500241	N	XM_004503481.2	Gene bank	Cicer_arietinum_uncharacterized_LOC101500241	Fabales
Cicer arietinum	Fabaceae	Cicer_arietinum_DIV	Y RR2B/DIV2	XM_004490894.2	Gene bank	Cicer_arietinum_transcription_factor_DIVARICATA_LOC101492144	Fabales
Citrus clementina	Rutaceae	Citrus_clementina_hypothetical_protein_CICLE_v10028910mg	N	XM_006424954.1	Gene bank	Citrus_clementina_hypothetical_protein_CICLE_v10028910mg	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_hypothetical_protein_CICLE_v10029205mg	N	XM_006424140.1	Gene bank	Citrus_clementina_hypothetical_protein_CICLE_v10029205mg	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_Ciclev10006714m_g	N	Ciclev10006714m.g	phytozome	Citrus_clementina_Ciclev10006714m_g	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_Ciclev10009011m_g	N	Ciclev10009011m.g	phytozome	Citrus_clementina_Ciclev10009011m_g	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_Ciclev10009128m_g	N	Ciclev10009128m.g	phytozome	Citrus_clementina_Ciclev10009128m_g	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_Ciclev10016071m_g	N	Ciclev10016071m.g	phytozome	Citrus_clementina_Ciclev10016071m_g	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_Ciclev10021067m_g	N	Ciclev10021067m.g	phytozome	Citrus_clementina_Ciclev10021067m_g	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_Ciclev10021342m_g	N	Ciclev10021342m.g	phytozome	Citrus_clementina_Ciclev10021342m_g	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_Ciclev10025950m_g	N	Ciclev10025950m.g	phytozome	Citrus_clementina_Ciclev10025950m_g	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_Ciclev10028910m_g	N	Ciclev10028910m.g	phytozome	Citrus_clementina_Ciclev10028910m_g	Sapindales

Citrus clementina	Rutaceae	Citrus_clementina_Ciclev10032309m_g	N	Ciclev10032309m.g	phytozome	Citrus_clementina_Ciclev10032309m_g	Sapindales
Citrus clementina	Rutaceae	Citrus_clementina_DIV	Y RR2C/DIV3	Ciclev10012285m.g	phytozome	Citrus_clementina_Ciclev10012285m_g	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_orange1_1g019948m_g	N	orange1.1g019948m.g	phytozome	Citrus_sinensis_orange1_1g019948m_g	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_orange1_1g021756m_g	N	orange1.1g021756m.g	phytozome	Citrus_sinensis_orange1_1g021756m_g	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_orange1_1g021816m_g	N	orange1.1g021816m.g	phytozome	Citrus_sinensis_orange1_1g021816m_g	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_orange1_1g023196m_g	N	orange1.1g023196m.g	phytozome	Citrus_sinensis_orange1_1g023196m_g	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_orange1_1g032677m_g	N	orange1.1g032677m.g	phytozome	Citrus_sinensis_orange1_1g032677m_g	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_orange1_1g038601m_g	N	orange1.1g038601m.g	phytozome	Citrus_sinensis_orange1_1g038601m_g	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_orange1_1g047042m_g	N	orange1.1g047042m.g	phytozome	Citrus_sinensis_orange1_1g047042m_g	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_transcription_factor_DIVARICATA_like_LOC102606644_variant1/2	N	XM_006475882.2/XM_006475883.2	Gene bank	Citrus_sinensis_transcription_factor_DIVARICATA_like_LOC102606644_variant1/2	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_transcription_factor_DIVARICATA_like_LOC102615932	N	XM_006485691.2	Gene bank	Citrus_sinensis_transcription_factor_DIVARICATA_like_LOC102615932	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_transcription_factor_DIVARICATA_like_LOC102620659	N	XM_006486309.2	Gene bank	Citrus_sinensis_transcription_factor_DIVARICATA_like_LOC102620659	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_transcription_factor_DIVARICATA_like_LOC102626223	N	XM_006485395.2	Gene bank	Citrus_sinensis_transcription_factor_DIVARICATA_like_LOC102626223	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_transcription_factor_DIVARICATA_LOC102610732	N	XM_006488419.2	Gene bank	Citrus_sinensis_transcription_factor_DIVARICATA_LOC102610732	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_transcription_factor_DIVARICATA_LOC102614640	N	XM_006480908.2	Gene bank	Citrus_sinensis_transcription_factor_DIVARICATA_LOC102614640	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_transcription_factor_MYB1R1_LOC102609132	N	XM_006465625.1	Gene bank	Citrus_sinensis_transcription_factor_MYB1R1_LOC102609132	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_transcription_factor_MYB1R1_LOC102619396	N	XM_006477081.2	Gene bank	Citrus_sinensis_transcription_factor_MYB1R1_LOC102619396	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_transcription_	N	XM_006475356.	Gene bank	Citrus_sinensis_transcription	Sapindales

		factor_MYB1R1_LOC102624682		2		_factor_MYB1R1_LOC102624682	
Citrus sinensis	Rutaceae	Citrus_sinensis_uncharacterized_LOC107178582	N	XM_015533933.1	Gene bank	Citrus_sinensis_uncharacterized_LOC107178582	Sapindales
Citrus sinensis	Rutaceae	Citrus_sinensis_DIV	Y RR1A	XM_006487846.1	Gene bank	Citrus_sinensis_transcription_factor_DIVARICATA_like_LOC102624360	Sapindales
Cucumis melo	Cucurbitaceae	Cucumis_melo_transcription_factor_DIVARICATA_like_LOC103484855	N	XM_008442171.2	Gene bank	Cucumis_melo_transcription_factor_DIVARICATA_like_LOC103484855	Cucurbitales
Cucumis melo	Cucurbitaceae	Cucumis_melo_transcription_factor_DIVARICATA_like_LOC103486321	N	XM_008444241.2	Gene bank	Cucumis_melo_transcription_factor_DIVARICATA_like_LOC103486321	Cucurbitales
Cucumis melo	Cucurbitaceae	Cucumis_melo_transcription_factor_DIVARICATA_like_LOC103491144	N	XM_008450974.2	Gene bank	Cucumis_melo_transcription_factor_DIVARICATA_like_LOC103491144	Cucurbitales
Cucumis melo	Cucurbitaceae	Cucumis_melo_transcription_factor_DIVARICATA_LOC103496517	N	XM_008458386.2	Gene bank	Cucumis_melo_transcription_factor_DIVARICATA_LOC103496517	Cucurbitales
Cucumis melo	Cucurbitaceae	Cucumis_melo_transcription_factor_DIVARICATA_LOC103501421	N	XM_008464994.2	Gene bank	Cucumis_melo_transcription_factor_DIVARICATA_LOC103501421	Cucurbitales
Cucumis melo	Cucurbitaceae	Cucumis_melo_transcription_factor_DIVARICATA_LOC103502037	N	XM_008465835.2	Gene bank	Cucumis_melo_transcription_factor_DIVARICATA_LOC103502037	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_067080	N	Cucsa.067080	phytozome	Cucumis_sativus_Cucsa_067080	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_103200	N	Cucsa.103200	phytozome	Cucumis_sativus_Cucsa_103200	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_139090	N	Cucsa.139090	phytozome	Cucumis_sativus_Cucsa_139090	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_164580	N	Cucsa.164580	phytozome	Cucumis_sativus_Cucsa_164580	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_176140	N	Cucsa.176140	phytozome	Cucumis_sativus_Cucsa_176140	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_197320	N	Cucsa.197320	phytozome	Cucumis_sativus_Cucsa_197320	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_198920	N	Cucsa.198920	phytozome	Cucumis_sativus_Cucsa_198920	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_321060	N	Cucsa.321060	phytozome	Cucumis_sativus_Cucsa_321060	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_364590	N	Cucsa.364590	phytozome	Cucumis_sativus_Cucsa_364590	Cucurbitales

Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_395160	N	Cucsa.395160	phytozome	Cucumis_sativus_Cucsa_395160	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_Cucsa_397260	N	Cucsa.397260	phytozome	Cucumis_sativus_Cucsa_397260	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_transcription_factor_MYB1R1_like_LOC101204468	N	XM_004142991.2	phytozome	Cucumis_sativus_transcription_factor_MYB1R1_like_LOC101204468	Cucurbitales
Cucumis sativus	Cucurbitaceae	Cucumis_sativus_transcription_factor_MYB1R1_like_LOC101214626	N	XM_004138088.2	phytozome	Cucumis_sativus_transcription_factor_MYB1R1_like_LOC101214626	Cucurbitales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108192597_mRNAx1/x2/x3	N	XM_017373206.1/XM_017373207.1/XM_017373208.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108192597_mRNAx1/x2/x3	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108193653_mRNA	N	XM_017360403.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108193653_mRNA	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108198695_mRNA	N	XM_017366473.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108198695_mRNA	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108204772_mRNA x1/x2/x3/x4	N	XM_017374378.1/XM_017374379.1/XM_017374380.1/XM_017374381.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108204772_mRNA x1/x2/x3/x4	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108206843_mRNA	N	XM_017377259.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108206843_mRNA	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108210874_mRNAx1/x2	N	XM_017382323.1/XM_017382324.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108210874_mRNAx1/x2	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108220214_mRNA	N	XM_017393915.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108220214_mRNA	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108227234_mRNA	N	XM_017402279.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108227234_mRNA	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIVARICATA_like_OC108199511_mRNA x1/x2	N	XM_017367344.1/XM_017367345.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_OC108199511_mRNA x1/x2	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_myb_like_protein_J_LOC108213042	N	XM_017384773.1	Gene bank	Daucus_carota_subsp_sativus_myb_like_protein_J_LOC108213042	Apiales

Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_MYB1R1_like_LOC108193779	N	XM_017360600.1	Gene bank	Daucus_carota_subsp_sativus_MYB1R1_like_LOC108193779	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_MYB1R1_like_LOC108205942	N	XM_017376075.1	Gene bank	Daucus_carota_subsp_sativus_MYB1R1_like_LOC108205942	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_uncharacterized_LOC108211336	N	XM_017382906.1	Gene bank	Daucus_carota_subsp_sativus_uncharacterized_LOC108211336	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIV2	Y RR1A	XM_017376508.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108206263_mRNA	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIV1	Y RR1B	XM_017367914.1/XM_017367915.1/XM_017367916.1/XM_017367917.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108199895_mRNAx1/x2/x3/x4	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIV4	Y RR2A/DIV1	XM_017376150.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_LOC108205998_mRNA	Apiales
Daucus carota	Apiaceae	Daucus_carota_subsp_sativus_DIV3	Y RR2C/DIV3	XM_017389054.1	Gene bank	Daucus_carota_subsp_sativus_DIVARICATA_like_LOC108216321_mRNA	Apiales
Diervilla sessilifolia	Caprifoliaceae	Diervilla_sessilifolia_DIV1	Y RR2A/DIV1	FJ805300.1	Gene bank	Diervilla_sessilifolia_DIV1A_FJ805300	Dipsacales
Diervilla sessilifolia	Caprifoliaceae	Diervilla_sessilifolia_DIV2	Y RR2A/DIV1	FJ805301.1	Gene bank	Diervilla_sessilifolia_DIV1B_FJ805301	Dipsacales
Diervilla sessilifolia	Caprifoliaceae	Diervilla_sessilifolia_DIV3	Y RR2B/DIV2	FJ805302.1	Gene bank	Diervilla_sessilifolia_DIV2B_FJ805302	Dipsacales
Diervilla sessilifolia	Caprifoliaceae	Diervilla_sessilifolia_DIV4	Y RR2C/DIV3	FJ805303.1	Gene bank	Diervilla_sessilifolia_DIV3A_FJ805303	Dipsacales
Diervilla sessilifolia	Caprifoliaceae	Diervilla_sessilifolia_DIV5	Y RR2C/DIV3	FJ805304.1	Gene bank	Diervilla_sessilifolia_DIV3B_FJ805304	Dipsacales
Dipelta floribunda	Caprifoliaceae	Dipelta_floribunda_DIV1	Y RR2A/DIV1	FJ805305.1	Gene bank	Dipelta_floribunda_DIV1B_FJ805305	Dipsacales
Dipelta floribunda	Caprifoliaceae	Dipelta_floribunda_DIV2	Y RR2B/DIV2	FJ805306.1	Gene bank	Dipelta_floribunda_DIV2A_FJ805306	Dipsacales
Dipelta floribunda	Caprifoliaceae	Dipelta_floribunda_DIV3	Y RR2B/DIV2	FJ805307.1	Gene bank	Dipelta_floribunda_DIV2B_FJ805307	Dipsacales
Dipelta floribunda	Caprifoliaceae	Dipelta_floribunda_DIV4	Y RR2C/DIV3	FJ805308.1	Gene bank	Dipelta_floribunda_DIV3B_FJ805308	Dipsacales

Epimedium sagittatum	Berberidaceae	Epimedium_sagittatum_R2R3_MYB_transcription_factor_MYB8	N	JN426955.1	Gene bank	Epimedium_sagittatum_R2R3_MYB_transcription_factor_MYB8	Ranunculales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_Eucgr_B02575	N	Eucgr.B02575	phytozome	Eucalyptus_grandis_Eucgr_B02575	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_Eucgr_C03026	N	Eucgr.C03026	phytozome	Eucalyptus_grandis_Eucgr_C03026	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_Eucgr_D00726	N	Eucgr.D00726	phytozome	Eucalyptus_grandis_Eucgr_D00726	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_Eucgr_D02103	N	Eucgr.D02103	phytozome	Eucalyptus_grandis_Eucgr_D02103	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_Eucgr_J00349	N	Eucgr.J00349	phytozome	Eucalyptus_grandis_Eucgr_J00349	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_Eucgr_J01940	N	Eucgr.J01940	phytozome	Eucalyptus_grandis_Eucgr_J01940	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_Eucgr_J02939	N	Eucgr.J02939	phytozome	Eucalyptus_grandis_Eucgr_J02939	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_Eucgr_K00122	N	Eucgr.K00122	phytozome	Eucalyptus_grandis_Eucgr_K00122	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_Eucgr_K02897	N	Eucgr.K02897	phytozome	Eucalyptus_grandis_Eucgr_K02897	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_transcription_factor_DIVARICATA_like_LOC104424007	N	XM_010036412.1	Gene bank	Eucalyptus_grandis_transcription_factor_DIVARICATA_like_LOC104424007	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_transcription_factor_MYB1R1_LOC104426316	N	XM_010039315.1	Gene bank	Eucalyptus_grandis_transcription_factor_MYB1R1_LOC104426316	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_DIV5	Y RR1A	XM_010032992.1	Gene bank	Eucalyptus_grandis_transcription_factor_DIVARICATA_like_LOC104421142	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_DIV2	Y RR1B	Eucgr.G02591	phytozome	Eucalyptus_grandis_Eucgr_G02591	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_DIV4	Y RR1C	Eucgr.K02659	phytozome	Eucalyptus_grandis_Eucgr_K02659	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_DIV3	Y RR2B/DIV2	Eucgr.G03029	phytozome	Eucalyptus_grandis_Eucgr_G03029	Myrtales
Eucalyptus grandis	Myrtaceae	Eucalyptus_grandis_DIV1	Y RR2C/DIV3	Eucgr.B02800	phytozome	Eucalyptus_grandis_Eucgr_B02800	Myrtales
Fedia cornucopiae	Caprifoliaceae	Fedia_cornucopiae_DIV1	Y RR2A/DIV1	FJ805309	Gene bank	Fedia_cornucopiae_DIV1Ba_FJ805309	Dipsacales
Fedia cornucopiae	Caprifoliaceae	Fedia_cornucopiae_DIV2	Y RR2A/DIV1	FJ805310	Gene bank	Fedia_cornucopiae_DIV1Bb_FJ805310	Dipsacales
Fragaria vesca	Rosaceae	Fragaria_vesca_gene11419_v1	N	gene11419-v1.0-	phytozome	Fragaria_vesca_gene11419_v	Rosales

		.0_hybrid		hybrid		1.0_hybrid	
Fragaria vesca	Rosaceae	Fragaria_vesca_gene18815_v1.0_hybrid	N	gene18815-v1.0-hybrid	phytozome	Fragaria_vesca_gene18815_v1.0_hybrid	Rosales
Fragaria vesca	Rosaceae	Fragaria_vesca_gene20912_v1.0_hybrid	N	gene20912-v1.0-hybrid	phytozome	Fragaria_vesca_gene20912_v1.0_hybrid	Rosales
Fragaria vesca	Rosaceae	Fragaria_vesca_gene25733_v1.0_hybrid	N	gene25733-v1.0-hybrid	phytozome	Fragaria_vesca_gene25733_v1.0_hybrid	Rosales
Fragaria vesca	Rosaceae	Fragaria_vesca_subsp_vesca_transcription_factor_MYB1R1_LOC101305277	N	XM_004302813.2	Gene bank	Fragaria_vesca_subsp_vesca_transcription_factor_MYB1R1_LOC101305277	Rosales
Fragaria vesca	Rosaceae	Fragaria_vesca_DIV3	Y RR1A	XM_011470961.1	Gene bank	Fragaria_vesca_subsp_vesca_transcription_factor_DIVARICATA_LOC101298361	Rosales
Fragaria vesca	Rosaceae	Fragaria_vesca_DIV1	Y RR1C	gene26214-v1.0-hybrid	phytozome	Fragaria_vesca_gene26214_v1.0_hybrid	Rosales
Fragaria vesca	Rosaceae	Fragaria_vesca_DIV2	Y RR2A/DIV1	XM_004294220.2	Gene bank	Fragaria_vesca_subsp_vesca_transcription_factor_DIVARICATA_LOC101297998	Rosales
Glycine max	Fabaceae	Glycine_max_Glyma_01G003000	N	Glyma.01G003000	phytozome	Glycine_max_Glyma_01G003000	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_01G038600	N	Glyma.01G038600	phytozome	Glycine_max_Glyma_01G038600	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_01G112700	N	Glyma.01G112700	phytozome	Glycine_max_Glyma_01G112700	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_02G026300	N	Glyma.02G026300	phytozome	Glycine_max_Glyma_02G026300	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_02G224900	N	Glyma.02G224900	phytozome	Glycine_max_Glyma_02G224900	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_03G078000	N	Glyma.03G078000	phytozome	Glycine_max_Glyma_03G078000	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_05G013000	N	Glyma.05G013000	phytozome	Glycine_max_Glyma_05G013000	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_05G062300	N	Glyma.05G062300	phytozome	Glycine_max_Glyma_05G062300	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_05G222600	N	Glyma.05G222600	phytozome	Glycine_max_Glyma_05G222600	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_06G143600	N	Glyma.06G143600	phytozome	Glycine_max_Glyma_06G143600	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_07G146300	N	Glyma.07G146300	phytozome	Glycine_max_Glyma_07G146300	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_08G029400	N	Glyma.08G029400	phytozome	Glycine_max_Glyma_08G029400	Fabales

Glycine max	Fabaceae	Glycine_max_Glyma_08G290100	N	Glyma.08G290100	phytozome	Glycine_max_Glyma_08G290100	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_10G277800	N	Glyma.10G277800	phytozome	Glycine_max_Glyma_10G277800	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_11G176500	N	Glyma.11G176500	phytozome	Glycine_max_Glyma_11G176500	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_11G227200	N	Glyma.11G227200	phytozome	Glycine_max_Glyma_11G227200	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_14G191700	N	Glyma.14G191700	phytozome	Glycine_max_Glyma_14G191700	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_17G094400	N	Glyma.17G094400	phytozome	Glycine_max_Glyma_17G094400	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_17G144100	N	Glyma.17G144100	phytozome	Glycine_max_Glyma_17G144100	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_18G065200	N	Glyma.18G065200	phytozome	Glycine_max_Glyma_18G065200	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_18G075100	N	Glyma.18G075100	phytozome	Glycine_max_Glyma_18G075100	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_19G060700	N	Glyma.19G060700	phytozome	Glycine_max_Glyma_19G060700	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_20G011700	N	Glyma.20G011700	phytozome	Glycine_max_Glyma_20G011700	Fabales
Glycine max	Fabaceae	Glycine_max_Glyma_20G111800	N	Glyma.20G111800	phytozome	Glycine_max_Glyma_20G111800	Fabales
Glycine max	Fabaceae	Glycine_max_DIV4	Y RR1A	Glyma.20G097900	phytozome	Glycine_max_Glyma_20G097900	Fabales
Glycine max	Fabaceae	Glycine_max_DIV1	Y RR1C	Glyma.17G121000	phytozome	Glycine_max_Glyma_17G121000	Fabales
Glycine max	Fabaceae	Glycine_max_DIV2	Y RR2B/DIV2	Glyma.18G030300	phytozome	Glycine_max_Glyma_18G030300	Fabales
Glycine max	Fabaceae	Glycine_max_DIV3	Y RR2C/DIV3	Glyma.18G197500	phytozome	Glycine_max_Glyma_18G197500	Fabales
Glycine max	Fabaceae	Glycine_max_clone_HN_CCL_88_MYB_HD_like_transcription_factor_Glyma03g14440_1	N	KT031184.1	Gene bank	Glycine_max_clone_HN_CCL_88_MYB_HD_like_transcription_factor_Glyma03g14440_1	Fabales
Glycine max	Fabaceae	Glycine_max_clone_HN_CCL_94_MYB_HD_like_transcription_factor_Glyma17g15330_1_like1	N	KT031272.1	Gene bank	Glycine_max_clone_HN_CCL_94_MYB_HD_like_transcription_factor_Glyma17g15330_1_like1	Fabales
Glycine max	Fabaceae	Glycine_max_clone_HN_CCL_95_MYB_HD_like_transcription_factor_Glyma17g15330_	N	KT031273.1	Gene bank	Glycine_max_clone_HN_CCL_95_MYB_HD_like_transcription_factor_Glyma17g1533	Fabales

		1_like2				0_1_like2	
Glycine max	Fabaceae	Glycine_max_MYB_transcription_factor_MYB126	N	DQ822954.1	Gene bank	Glycine_max_MYB_transcription_factor_MYB126	Fabales
Glycine max	Fabaceae	Glycine_max_MYB_transcription_factor_MYB180	N	NM_001251693.1	Gene bank	Glycine_max_MYB_transcription_factor_MYB180	Fabales
Glycine max	Fabaceae	Glycine_max_MYB_transcription_factor_MYB51	N	DQ822962.1	Gene bank	Glycine_max_MYB_transcription_factor_MYB51	Fabales
Glycine max	Fabaceae	Glycine_max_MYB_transcription_factor_MYB57	N	NM_001248746.1	Gene bank	Glycine_max_MYB_transcription_factor_MYB57	Fabales
Glycine max	Fabaceae	Glycine_max_transcription_factor_DIVARICATA_like_LOC100794742	N	XM_006601430.1	Gene bank	Glycine_max_transcription_factor_DIVARICATA_like_LOC100794742	Fabales
Glycine max	Fabaceae	Glycine_max_transcription_factor_MYB1R1_like_LOC780554	N	XM_003517833.3	Gene bank	Glycine_max_transcription_factor_MYB1R1_like_LOC780554	Fabales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_factor_DIVARICATA_LOC108450805	N	XM_017748579.1	Gene bank	Gossypium_arboreum_factor_DIVARICATA_LOC108450805	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_factor_DIVARICATA_LOC108454763	N	XM_017753331.1	Gene bank	Gossypium_arboreum_factor_DIVARICATA_LOC108454763	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_factor_DIVARICATA_LOC108455839	N	XM_017754403.1	Gene bank	Gossypium_arboreum_factor_DIVARICATA_LOC108455839	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108464353	N	XM_017764619.1	Gene bank	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108464353	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108472604	N	XM_017774149.1	Gene bank	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108472604	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108480852	N	XM_017783973.1	Gene bank	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108480852	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108484696	N	XM_017788578.1	Gene bank	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108484696	Malvales

Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108485641	N	XM_017789494.1	Gene bank	Gossypium_arboreum_transcription_factor_MYB1R1_like_LOC108485641	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC105769526	N	XM_012590213.1	Gene bank	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC105769526	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108450804	N	XM_017748578.1	Gene bank	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108450804	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108456179	N	XM_017754778.1	Gene bank	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108456179	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108460379	N	XM_017759857.1	Gene bank	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108460379	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108460927_variant1	N	XM_017760633.1	Gene bank	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108460927_variant1	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108467331	N	XM_017767958.1	Gene bank	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108467331	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108470384	N	XM_017771666.1	Gene bank	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108470384	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108486922	N	XM_017791086.1	Gene bank	Gossypium_arboreum_transcription_factor_DIVARICATA_LOC108486922	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_uncharacterized_LOC108455236	N	XM_017753820.1	Gene bank	Gossypium_arboreum_uncharacterized_LOC108455236	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_uncharacterized_LOC108476665	N	XM_017778936.1	Gene bank	Gossypium_arboreum_uncharacterized_LOC108476665	Malvales
Gossypium arboreum	Malvaceae	Gossypium_arboreum_uncharacterized_LOC108477505	N	XM_017780051.1	Gene bank	Gossypium_arboreum_uncharacterized_LOC108477505	Malvales
Gossypium arboreum	Malvaceae	Gossypium_hirsutum_factor_DIVARICATA_LOC107889761	N	XM_016814311.1	Gene bank	Gossypium_hirsutum_factor_DIVARICATA_LOC107889761	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_factor_DIVARICATA_LOC107892493	N	XM_016817570.1	Gene bank	Gossypium_hirsutum_factor_DIVARICATA_LOC107892493	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_factor_DIVARICATA_LOC107906602	N	XM_016833640.1	Gene bank	Gossypium_hirsutum_factor_DIVARICATA_LOC107906602	Malvales

Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_factor_DIVARICATA_LOC107930146	N	XM_016861719.1	Gene bank	Gossypium_hirsutum_factor_DIVARICATA_LOC107930146	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_factor_DIVARICATA_LOC107941704	N	XM_016875285.1	Gene bank	Gossypium_hirsutum_factor_DIVARICATA_LOC107941704	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_factor_DIVARICATA_LOC107951473	N	XM_016886540.1	Gene bank	Gossypium_hirsutum_factor_DIVARICATA_LOC107951473	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_factor_DIVARICATA_LOC107958042	N	XM_016893695.1	Gene bank	Gossypium_hirsutum_factor_DIVARICATA_LOC107958042	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_factor_DIVARICATA_LOC107959172	N	XM_016895161.1	Gene bank	Gossypium_hirsutum_factor_DIVARICATA_LOC107959172	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_factor_DIVARICATA_LOC108467331	N	XM_017767958.1	Gene bank	Gossypium_hirsutum_factor_DIVARICATA_LOC108467331	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_myb_like_protein_J_LOC107934092	N	XM_016866442.1	Gene bank	Gossypium_hirsutum_myb_like_protein_J_LOC107934092	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_myb_like_protein_J_LOC107946923	N	XM_016881428.1	Gene bank	Gossypium_hirsutum_myb_like_protein_J_LOC107946923	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_myb_like_protein_J_LOC108470026	N	XM_017771204.1	Gene bank	Gossypium_hirsutum_myb_like_protein_J_LOC108470026	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_MYB1R1_like_LOC107889182	N	XM_016813541.1	Gene bank	Gossypium_hirsutum_transcription_factor_MYB1R1_like_LOC107889182	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_MYB1R1_like_LOC107901127	N	XM_016827007.1	Gene bank	Gossypium_hirsutum_transcription_factor_MYB1R1_like_LOC107901127	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_MYB1R1_like_LOC107907149	N	XM_016834398.1	Gene bank	Gossypium_hirsutum_transcription_factor_MYB1R1_like_LOC107907149	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_MYB1R1_like_LOC107937711	N	XM_016870666.1	Gene bank	Gossypium_hirsutum_transcription_factor_MYB1R1_like_LOC107937711	Malvales

Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_ MYB1R1_like_LOC107962763	N	XM_016899262.1	Gene bank	Gossypium_hirsutum_transcription_factor_ MYB1R1_like_LOC107962763	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_ MYB1R1_like_XM_LOC107950107	N	XM_016884855.1	Gene bank	Gossypium_hirsutum_transcription_factor_ MYB1R1_like_XM_LOC107950107	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_ MYB1R1_lLOC107887295_variant1/2	N	XM_016811486.1/XM_016811487.1	Gene bank	Gossypium_hirsutum_transcription_factor_ MYB1R1_lLOC107887295_variant1/2	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_ MYB1R1_LOC107956276	N	XM_016891985.1	Gene bank	Gossypium_hirsutum_transcription_factor_ MYB1R1_LOC107956276	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107889761	N	XM_016814311.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107889761	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107891532	N	XM_016816365.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107891532	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107891567	N	XM_016816408.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107891567	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107892493	N	XM_016817570.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107892493	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107898851	N	XM_016824415.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107898851	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107899044	N	XM_016824640.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107899044	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107901859	N	XM_016828051.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107901859	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107906602	N	XM_016833640.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107906602	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107929382	N	XM_016860785.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_ LOC107929382	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_	N	XM_016861719.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_	Malvales

		LOC107930146				LOC107930146	
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107935417	N	XM_016868024.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107935417	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107935420	N	XM_016868028.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107935420	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107939370	N	XM_016872700.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107939370	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107941704	N	XM_016875285.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107941704	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107943249	N	XM_016876996.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107943249	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107951473	N	XM_016886540.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107951473	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107951480	N	XM_016886545.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107951480	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107955159	N	XM_016890888.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107955159	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107957113	N	XM_016892553.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107957113	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107958042	N	XM_016893695.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107958042	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107959172	N	XM_016895161.1	Gene bank	Gossypium_hirsutum_transcription_factor_DIVARICATA_LOC107959172	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_uncharacterized_LOC107886060_variant2	N	XM_016809866.1	Gene bank	Gossypium_hirsutum_uncharacterized_LOC107886060_variant2	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_uncharacterized_LOC107931377	N	XM_016863256.1	Gene bank	Gossypium_hirsutum_uncharacterized_LOC107931377	Malvales
Gossypium hirsutum	Malvaceae	Gossypium_hirsutum_uncharacterized_LOC107933474	N	XM_016865688.1	Gene bank	Gossypium_hirsutum_uncharacterized_LOC107933474	Malvales

Gossypium raimondii	Malvaceae	Gossypium_raimondii_factor_DIVARICATA_LOC105761854	N	XM_012579797.1	Gene bank	Gossypium_raimondii_factor_DIVARICATA_LOC105761854	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_002G261600	N	Gorai.002G261600	phytozome	Gossypium_raimondii_Gorai_002G261600	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_003G071500	N	Gorai.003G071500	phytozome	Gossypium_raimondii_Gorai_003G071500	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_004G196500	N	Gorai.004G196500	phytozome	Gossypium_raimondii_Gorai_004G196500	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_006G113100	N	Gorai.006G113100	phytozome	Gossypium_raimondii_Gorai_006G113100	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_006G118200	N	Gorai.006G118200	phytozome	Gossypium_raimondii_Gorai_006G118200	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_006G180900	N	Gorai.006G180900	phytozome	Gossypium_raimondii_Gorai_006G180900	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_006G274300	N	Gorai.006G274300	phytozome	Gossypium_raimondii_Gorai_006G274300	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_007G371900	N	Gorai.007G371900	phytozome	Gossypium_raimondii_Gorai_007G371900	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_007G378300	N	Gorai.007G378300	phytozome	Gossypium_raimondii_Gorai_007G378300	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_008G213600	N	Gorai.008G213600	phytozome	Gossypium_raimondii_Gorai_008G213600	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_008G233500	N	Gorai.008G233500	phytozome	Gossypium_raimondii_Gorai_008G233500	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_009G030900	N	Gorai.009G030900	phytozome	Gossypium_raimondii_Gorai_009G030900	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_009G093700	N	Gorai.009G093700	phytozome	Gossypium_raimondii_Gorai_009G093700	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_010G081800	N	Gorai.010G081800	phytozome	Gossypium_raimondii_Gorai_010G081800	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_011G279800	N	Gorai.011G279800	phytozome	Gossypium_raimondii_Gorai_011G279800	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_012G075600	N	Gorai.012G075600	phytozome	Gossypium_raimondii_Gorai_012G075600	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_012G112000	N	Gorai.012G112000	phytozome	Gossypium_raimondii_Gorai_012G112000	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_Gorai_012G135600	N	Gorai.012G135600	phytozome	Gossypium_raimondii_Gorai_012G135600	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_myb_like_protein_J_LOC105765086	N	XM_012584002.1	Gene bank	Gossypium_raimondii_myb_like_protein_J_LOC105765086	Malvales
Gossypium	Malvaceae	Gossypium_raimondii_myb_li	N	XM_012620421.	Gene bank	Gossypium_raimondii_myb_l	Malvales

raimondii		ke_protein_J_LOC105792049		1		ike_protein_J_LOC105792049	
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105761789_variant1/2	N	XM_012579711.1/XM_012579713.1	Gene bank	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105761789_variant1/2	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105770100	N	XM_012591155.1	Gene bank	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105770100	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105774410	N	XM_012596902.1	Gene bank	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105774410	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105761854	N	XM_012579797.1	Gene bank	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105761854	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105775723	N	XM_012598198.1	Gene bank	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105775723	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105776640	N	XM_012599427.1	Gene bank	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105776640	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105779902_variant1	N	XM_012603883.1	Gene bank	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105779902_variant1	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105780118	N	XM_012604250.1	Gene bank	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105780118	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105780813	N	XM_012605324.1	Gene bank	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105780813	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105786539	N	XM_012613025.1	Gene bank	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105786539	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105799232	N	XM_012629670.1	Gene bank	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105799232	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105799928	N	XM_012630750.1	Gene bank	Gossypium_raimondii_transcription_factor_DIVARICATA_LOC105799928	Malvales

Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105762521	N	XM_012580284.1	Gene bank	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105762521	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105788122	N	XM_012614857.1	Gene bank	Gossypium_raimondii_transcription_factor_MYB1R1_like_LOC105788122	Malvales
Gossypium raimondii	Malvaceae	Gossypium_raimondii_uncharacterized_LOC105800854_variant1	N	XM_012632213.1	Gene bank	Gossypium_raimondii_uncharacterized_LOC105800854_variant1	Malvales
Heptacodium miconioides	Caprifoliaceae	Heptacodium_miconioides_DIV1	Y RR2A/DIV1	FJ805311	Gene bank	Heptacodium_miconioides_DIV1A_FJ805311	Dipsacales
Heptacodium miconioides	Caprifoliaceae	Heptacodium_miconioides_DIV2	Y RR2A/DIV1	FJ805312	Gene bank	Heptacodium_miconioides_DIV1B_FJ805312	Dipsacales
Heptacodium miconioides	Caprifoliaceae	Heptacodium_miconioides_DIV3	Y RR2B/DIV2	FJ805313	Gene bank	Heptacodium_miconioides_DIV2A _FJ805313	Dipsacales
Heptacodium miconioides	Caprifoliaceae	Heptacodium_miconioides_DIV4	Y RR2B/DIV2	FJ805314	Gene bank	Heptacodium_miconioides_DIV2B_FJ805314	Dipsacales
Heptacodium miconioides	Caprifoliaceae	Heptacodium_miconioides_DIV5	Y RR2C/DIV3	FJ805315	Gene bank	Heptacodium_miconioides_DIV3B_FJ805315	Dipsacales
Hevea brasiliensis	Euphorbiaceae	Hevea_brasiliensis_MYB_transcription_factor	N	AY712938.1	Gene bank	Hevea_brasiliensis_MYB_transcription_factor	Malpighiales
Hevea brasiliensis	Euphorbiaceae	Hevea_brasiliensis_MYB_transcription_factor_2	N	DQ323739.1	Gene bank	Hevea_brasiliensis_MYB_transcription_factor_2	Malpighiales
Hevea brasiliensis	Euphorbiaceae	Hevea_brasiliensis_unknown_mRNA	N	AF239956.1	Gene bank	Hevea_brasiliensis_unknown_mRNA	Malpighiales
Hordeum vulgare	Poaceae	Hordeum_vulgare_subsp_vulgare_cv_Haisa_mRNA_for_MCB1_protein	N	AJ303354.1	Gene bank	Hordeum_vulgare_subsp_vulgare_cv_Haisa_mRNA_for_MCB1_protein	Poales
Hordeum vulgare	Poaceae	Hordeum_vulgare_subsp_vulgare_mRNA_for_predicted_protein_clone_NIASHv1053H08	N	AK357435.1	Gene bank	Hordeum_vulgare_subsp_vulgare_mRNA_for_predicted_protein_clone_NIASHv1053H08	Poales
Hordeum vulgare	Poaceae	Hordeum_vulgare_subsp_vulgare_mRNA_for_predicted_protein_clone_NIASHv1069M06	N	AK358140.1	Gene bank	Hordeum_vulgare_subsp_vulgare_mRNA_for_predicted_protein_clone_NIASHv1069M06	Poales
Hordeum vulgare	Poaceae	Hordeum_vulgare_subsp_vulgare_mRNA_for_predicted_protein_clone_NIASHv2063H16	N	AK367843.1	Gene bank	Hordeum_vulgare_subsp_vulgare_mRNA_for_predicted_protein_clone_NIASHv2063H16	Poales
Jatropha curcas	Euphorbiaceae	Jatropha_curcas_myb_like_protein_J_LOC105637863	N	XM_012221513.1	Gene bank	Jatropha_curcas_myb_like_protein_J_LOC105637863	Malpighiales
Jatropha	Euphorbiaceae	Jatropha_curcas_transcription	N	XM_012212681.	Gene bank	Jatropha_curcas_transcription	Malpighiales

curcas		_factor_DIVARICATA_LOC105630744_variant1/2		1/XM_012212689.1		_factor_DIVARICATA_LOC105630744_variant1/2	
Jatropha curcas	Euphorbiaceae	Jatropha_curcas_transcription_factor_DIVARICATA_LOC105632398	N	XM_012214772.1	Gene bank	Jatropha_curcas_transcription_factor_DIVARICATA_LOC105632398	Malpighiales
Jatropha curcas	Euphorbiaceae	Jatropha_curcas_transcription_factor_DIVARICATA_LOC105649136	N	XM_012235696.1	Gene bank	Jatropha_curcas_transcription_factor_DIVARICATA_LOC105649136	Malpighiales
Jatropha curcas	Euphorbiaceae	Jatropha_curcas_transcription_factor_MYB1R1_LOC105632298	N	XM_012214642.1	Gene bank	Jatropha_curcas_transcription_factor_MYB1R1_LOC105632298	Malpighiales
Jatropha curcas	Euphorbiaceae	Jatropha_curcas_transcription_factor_MYB1R1_LOC105640456	N	XM_012224771.1	Gene bank	Jatropha_curcas_transcription_factor_MYB1R1_LOC105640456	Malpighiales
Jatropha curcas	Euphorbiaceae	Jatropha_curcas_transcription_factor_MYB1R1_LOC105649814	N	XM_012236609.1	Gene bank	Jatropha_curcas_transcription_factor_MYB1R1_LOC105649814	Malpighiales
Jatropha curcas	Euphorbiaceae	Jatropha_curcas_DIV1	Y RR1A	XM_012210078.1	Gene bank	Jatropha_curcas_transcription_factor_DIVARICATA_LOC105628634	Malpighiales
Jatropha curcas	Euphorbiaceae	Jatropha_curcas_DIV2	Y RR2C/DIV3	XM_012232513.1	Gene bank	Jatropha_curcas_transcription_factor_DIVARICATA_LOC105646628	Malpighiales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0006s0005	N	Kaladp0006s0005	phytozome	Kalanchoe_laxiflora_Kaladp0006s0005	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0032s0059	N	Kaladp0032s0059	phytozome	Kalanchoe_laxiflora_Kaladp0032s0059	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0036s0258	N	Kaladp0036s0258	phytozome	Kalanchoe_laxiflora_Kaladp0036s0258	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0043s0275	N	Kaladp0043s0275	phytozome	Kalanchoe_laxiflora_Kaladp0043s0275	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0045s0220	N	Kaladp0045s0220	phytozome	Kalanchoe_laxiflora_Kaladp0045s0220	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0048s0278	N	Kaladp0048s0278	phytozome	Kalanchoe_laxiflora_Kaladp0048s0278	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0048s0933	N	Kaladp0048s0933	phytozome	Kalanchoe_laxiflora_Kaladp0048s0933	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0050s0108	N	Kaladp0050s0108	phytozome	Kalanchoe_laxiflora_Kaladp0050s0108	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0053s0429	N	Kaladp0053s0429	phytozome	Kalanchoe_laxiflora_Kaladp0053s0429	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0059s0055	N	Kaladp0059s0055	phytozome	Kalanchoe_laxiflora_Kaladp0059s0055	Saxifragales

Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0059s0088	N	Kaladp0059s0088	phytozome	Kalanchoe_laxiflora_Kaladp0059s0088	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp0092s0168	N	Kaladp0092s0168	phytozome	Kalanchoe_laxiflora_Kaladp0092s0168	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp1246s0018	N	Kaladp1246s0018	phytozome	Kalanchoe_laxiflora_Kaladp1246s0018	Saxifragales
Kalanchoe laxiflora	Crassulaceae	Kalanchoe_laxiflora_Kaladp1295s0017	N	Kaladp1295s0017	phytozome	Kalanchoe_laxiflora_Kaladp1295s0017	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0003s0068	N	Kalax.0003s0068	phytozome	Kalanchoe_marnieriana_Kalax_0003s0068	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0003s0302	N	Kalax.0003s0302	phytozome	Kalanchoe_marnieriana_Kalax_0003s0302	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0020s0119	N	Kalax.0020s0119	phytozome	Kalanchoe_marnieriana_Kalax_0020s0119	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0029s0126	N	Kalax.0029s0126	phytozome	Kalanchoe_marnieriana_Kalax_0029s0126	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0031s0012	N	Kalax.0031s0012	phytozome	Kalanchoe_marnieriana_Kalax_0031s0012	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0047s0054	N	Kalax.0047s0054	phytozome	Kalanchoe_marnieriana_Kalax_0047s0054	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0068s0087	N	Kalax.0068s0087	phytozome	Kalanchoe_marnieriana_Kalax_0068s0087	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0079s0041	N	Kalax.0079s0041	phytozome	Kalanchoe_marnieriana_Kalax_0079s0041	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0085s0026	N	Kalax.0085s0026	phytozome	Kalanchoe_marnieriana_Kalax_0085s0026	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0086s0020	N	Kalax.0086s0020	phytozome	Kalanchoe_marnieriana_Kalax_0086s0020	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0089s0036	N	Kalax.0089s0036	phytozome	Kalanchoe_marnieriana_Kalax_0089s0036	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0091s0104	N	Kalax.0091s0104	phytozome	Kalanchoe_marnieriana_Kalax_0091s0104	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0136s0060	N	Kalax.0136s0060	phytozome	Kalanchoe_marnieriana_Kalax_0136s0060	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0248s0040	N	Kalax.0248s0040	phytozome	Kalanchoe_marnieriana_Kalax_0248s0040	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0299s0038	N	Kalax.0299s0038	phytozome	Kalanchoe_marnieriana_Kalax_0299s0038	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0329s0049	N	Kalax.0329s0049	phytozome	Kalanchoe_marnieriana_Kalax_0329s0049	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0331s0018	N	Kalax.0331s0018	phytozome	Kalanchoe_marnieriana_Kalax_0331s0018	Saxifragales

Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0367s0014	N	Kalax.0367s0014	phytozome	Kalanchoe_marnieriana_Kalax_0367s0014	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0430s0029	N	Kalax.0430s0029	phytozome	Kalanchoe_marnieriana_Kalax_0430s0029	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0431s0003	N	Kalax.0431s0003	phytozome	Kalanchoe_marnieriana_Kalax_0431s0003	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0450s0019	N	Kalax.0450s0019	phytozome	Kalanchoe_marnieriana_Kalax_0450s0019	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0493s0034	N	Kalax.0493s0034	phytozome	Kalanchoe_marnieriana_Kalax_0493s0034	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0527s0004	N	Kalax.0527s0004	phytozome	Kalanchoe_marnieriana_Kalax_0527s0004	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0544s0012	N	Kalax.0544s0012	phytozome	Kalanchoe_marnieriana_Kalax_0544s0012	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0578s0015	N	Kalax.0578s0015	phytozome	Kalanchoe_marnieriana_Kalax_0578s0015	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0698s0018	N	Kalax.0698s0018	phytozome	Kalanchoe_marnieriana_Kalax_0698s0018	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0897s0010	N	Kalax.0897s0010	phytozome	Kalanchoe_marnieriana_Kalax_0897s0010	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_0928s0006	N	Kalax.0928s0006	phytozome	Kalanchoe_marnieriana_Kalax_0928s0006	Saxifragales
Kalanchoe marnieriana	Crassulaceae	Kalanchoe_marnieriana_Kalax_2316s0001	N	Kalax.2316s0001	phytozome	Kalanchoe_marnieriana_Kalax_2316s0001	Saxifragales
Kolkwitzia amabilis	Caprifoliaceae	Kolkwitzia_amabilis_DIV1	Y RR2A/DIV1	FJ805316	Gene bank	Kolkwitzia_amabilis_DIV1A_FJ805316	Dipsacales
Kolkwitzia amabilis	Caprifoliaceae	Kolkwitzia_amabilis_DIV2	Y RR2A/DIV1	FJ805317	Gene bank	Kolkwitzia_amabilis_DIV1B_FJ805317	Dipsacales
Kolkwitzia amabilis	Caprifoliaceae	Kolkwitzia_amabilis_DIV3	Y RR2C/DIV3	FJ805318	Gene bank	Kolkwitzia_amabilis_DIV3B_FJ805318	Dipsacales
Leycesteria sp	Caprifoliaceae	Leycesteria_sp_DIV3	Y RR2C/DIV3	FJ805321	Gene bank	Leycesteria_sp_DIV3B_FJ805321	Dipsacales
Leycesteria sp	Caprifoliaceae	Leycesteria_sp_DIV1	Y RR2A/DIV1	FJ805319	Gene bank	Leycesteria_sp_DIV1A_FJ805319	Dipsacales
Leycesteria sp	Caprifoliaceae	Leycesteria_sp_DIV2	Y RR2A/DIV1	FJ805320	Gene bank	Leycesteria_sp_DIV1B_FJ805320	Dipsacales
Linnaea borealis	Caprifoliaceae	Linnaea_borealis_DIV1	Y RR2A/DIV1	FJ805323	Gene bank	Linnaea_borealis_DIV1B_FJ805323	Dipsacales
Linnaea borealis	Caprifoliaceae	Linnaea_borealis_DIV2	Y RR2A/DIV1	FJ805322	Gene bank	Linnaea_borealis_DIV1A_FJ805322	Dipsacales
Linnaea borealis	Caprifoliaceae	Linnaea_borealis_DIV3	Y RR2B/DIV2	FJ805324	Gene bank	Linnaea_borealis_DIV2B_FJ805324	Dipsacales

Linnaea borealis	Caprifoliaceae	Linnaea_borealis_DIV4	Y RR2C/DIV3	FJ805325	Gene bank	Linnaea_borealis_DIV3B_FJ805325	Dipsacales
Linum usitatissimum	Linaceae	Linum_usitatissimum_Lus10004248_g	N	Lus10004248.g	phytozome	Linum_usitatissimum_Lus10004248_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_Lus10004384_g	N	Lus10004384.g	phytozome	Linum_usitatissimum_Lus10004384_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_Lus10006826_g	N	Lus10006826.g	phytozome	Linum_usitatissimum_Lus10006826_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_Lus10025822_g	N	Lus10025822.g	phytozome	Linum_usitatissimum_Lus10025822_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_Lus10036652_g	N	Lus10036652.g	phytozome	Linum_usitatissimum_Lus10036652_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_Lus10037560_g	N	Lus10037560.g	phytozome	Linum_usitatissimum_Lus10037560_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_Lus10038279_g	N	Lus10038279.g	phytozome	Linum_usitatissimum_Lus10038279_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_Lus10040181_g	N	Lus10040181.g	phytozome	Linum_usitatissimum_Lus10040181_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_Lus10040225_g	N	Lus10040225.g	phytozome	Linum_usitatissimum_Lus10040225_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_DIV3	Y RR2A/DIV1	Lus10018209.g	phytozome	Linum_usitatissimum_Lus10018209_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_DIV7	Y RR2A/DIV1	Lus10040696.g	phytozome	Linum_usitatissimum_Lus10040696_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_DIV1	Y RR2B/DIV2	Lus10009884.g	phytozome	Linum_usitatissimum_Lus10009884_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_DIV2	Y RR2B/DIV2	Lus10014837.g	phytozome	Linum_usitatissimum_Lus10014837_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_DIV5	Y RR2B/DIV2	Lus10028264.g	phytozome	Linum_usitatissimum_Lus10028264_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_DIV4	Y RR2C/DIV3	Lus10027781.g	phytozome	Linum_usitatissimum_Lus10027781_g	Malpighiales
Linum usitatissimum	Linaceae	Linum_usitatissimum_DIV6	Y RR2C/DIV3	Lus10035518.g	phytozome	Linum_usitatissimum_Lus10035518_g	Malpighiales
Lonicera maackii	Caprifoliaceae	Lonicera_maackii_DIV1	Y RR2A/DIV1	FJ805326	Gene bank	Lonicera_maackii_DIV1A_FJ805326	Dipsacales
Lonicera maackii	Caprifoliaceae	Lonicera_maackii_DIV2	Y RR2C/DIV3	FJ805327	Gene bank	Lonicera_maackii_DIV3B_FJ805327	Dipsacales
Lonicera morrowii	Caprifoliaceae	Lonicera_morrowii_DIV1	Y RR2A/DIV1	FJ805328	Gene bank	Lonicera_morrowii_DIV1B_FJ805328	Dipsacales
Lonicera morrowii	Caprifoliaceae	Lonicera_morrowii_DIV2	Y RR2C/DIV3	FJ805329	Gene bank	Lonicera_morrowii_DIV3B_FJ805329	Dipsacales

Lonicera reticulata	Caprifoliaceae	Lonicera_reticulata_DIV1	Y RR2A/DIV1	FJ805330	Gene bank	Lonicera_reticulata_DIV1A_FJ805330	Dipsacales
Lonicera reticulata	Caprifoliaceae	Lonicera_reticulata_DIV2	Y RR2C/DIV3	FJ805331	Gene bank	Lonicera_reticulata_DIV3B_FJ805331	Dipsacales
Lotus japonicus	Fabaceae	Lotus_japonicus_clone_JCVI_FLLj_17M3_unknown	N	BT146253.1	Gene bank	Lotus_japonicus_clone_JCVI_FLLj_17M3_unknown	Fabales
Lotus japonicus	Fabaceae	Lotus_japonicus_clone_JCVI_FLLj_19I19_unknown	N	BT144481.1	Gene bank	Lotus_japonicus_clone_JCVI_FLLj_19I19_unknown	Fabales
Malus domestica	Rosaceae	Malus_domestica_clone_BE1767_MYB_transcription_factor_MYB173	N	KF569668.1	Gene bank	Malus_domestica_clone_BE1767_MYB_transcription_factor_MYB173	Rosales
Malus domestica	Rosaceae	Malus_domestica_clone_BE2334_MYB_transcription_factor	N	KF033367.1	Gene bank	Malus_domestica_clone_BE2334_MYB_transcription_factor	Rosales
Malus domestica	Rosaceae	Malus_domestica_cultivar_Jiangsu_Fuji_MYB_transcription_factor_MYB53	N	GQ246163.1	Gene bank	Malus_domestica_cultivar_Jiangsu_Fuji_MYB_transcription_factor_MYB53	Rosales
Malus domestica	Rosaceae	Malus_domestica_MDP0000136727	N	MDP0000136727	phytozome	Malus_domestica_MDP0000136727	Rosales
Malus domestica	Rosaceae	Malus_domestica_MDP0000142580	N	MDP0000142580	phytozome	Malus_domestica_MDP0000142580	Rosales
Malus domestica	Rosaceae	Malus_domestica_MDP0000209471	N	MDP0000209471	phytozome	Malus_domestica_MDP0000209471	Rosales
Malus domestica	Rosaceae	Malus_domestica_MDP0000221993	N	MDP0000221993	phytozome	Malus_domestica_MDP0000221993	Rosales
Malus domestica	Rosaceae	Malus_domestica_MDP0000243328	N	MDP0000243328	phytozome	Malus_domestica_MDP0000243328	Rosales
Malus domestica	Rosaceae	Malus_domestica_MDP0000277813	N	MDP0000277813	phytozome	Malus_domestica_MDP0000277813	Rosales
Malus domestica	Rosaceae	Malus_domestica_MDP0000292581	N	MDP0000292581	phytozome	Malus_domestica_MDP0000292581	Rosales
Malus domestica	Rosaceae	Malus_domestica_MDP0000522009	N	MDP0000522009	phytozome	Malus_domestica_MDP0000522009	Rosales
Malus domestica	Rosaceae	Malus_domestica_MDP0000809640	N	MDP0000809640	phytozome	Malus_domestica_MDP0000809640	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_DIVARICATA_hypothetical_protein_PHAVU_004G065500g	N	XM_007151600.1	Gene bank	Malus_domestica_transcription_DIVARICATA_hypothetical_protein_PHAVU_004G065500g	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_DIVARICATA_like_LOC103418999	N	XM_008357122.2	Gene bank	Malus_domestica_transcription_DIVARICATA_like_LOC103418999	Rosales

Malus domestica	Rosaceae	Malus_domestica_transcription_DIVARICATA_like_LOC103426918	N	XM_008364997.2	Gene bank	Malus_domestica_transcription_DIVARICATA_like_LOC103426918	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_DIVARICATA_like_LOC103455477	N	XM_008395062.2	Gene bank	Malus_domestica_transcription_DIVARICATA_like_LOC103455477	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_factor_DIVARICATA_like_LOC103418999	N	XM_008357122.2	Gene bank	Malus_domestica_transcription_factor_DIVARICATA_like_LOC103418999	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_factor_DIVARICATA_like_LOC103426918	N	XM_008364997.2/XM_008368741.2/XM_017331005.1	Gene bank	Malus_domestica_transcription_factor_DIVARICATA_like_LOC103426918	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_factor_DIVARICATA_like_LOC103430594_variant1/2/3	N	XM_008368741.2	Gene bank	Malus_domestica_transcription_factor_DIVARICATA_like_LOC103430594_variant1/2/3	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_factor_DIVARICATA_like_LOC103450544	N	XM_008389913.2	Gene bank	Malus_domestica_transcription_factor_DIVARICATA_like_LOC103450544	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_factor_uncharacterized_LOC103435142	N	XM_008373531.1	Gene bank	Malus_domestica_transcription_factor_uncharacterized_LOC103435142	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_hypothetical_protein_PHAVU_003G222900g	N	XM_007155628.1	Gene bank	Malus_domestica_transcription_hypothetical_protein_PHAVU_003G222900g	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_hypothetical_protein_PHAVU_006G065700g	N	XM_007146678.1	Gene bank	Malus_domestica_transcription_hypothetical_protein_PHAVU_006G065700g	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_MYBR_domain_class_transcription_factor_MYBR11	N	HM122636.1	Gene bank	Malus_domestica_transcription_MYBR_domain_class_transcription_factor_MYBR11	Rosales
Malus domestica	Rosaceae	Malus_domestica_transcription_MYBR_domain_class_transcription_factor_MYBR17	N	HM122642.1	Gene bank	Malus_domestica_transcription_MYBR_domain_class_transcription_factor_MYBR17	Rosales
Malus domestica	Rosaceae	Malus_domestica_DIV2	Y RR1A	MDP0000610242	phytozome	Malus_domestica_MDP0000610242	Rosales
Malus domestica	Rosaceae	Malus_domestica_DIV1	Y RR2A/DIV1	MDP0000255630	phytozome	Malus_domestica_MDP0000255630	Rosales
Malus domestica	Rosaceae	Malus_domestica_DIV3	Y RR2C/DIV3	XM_008389913.2	Gene bank	Malus_domestica_transcription_DIVARICATA_like_LOC103450544	Rosales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_01G083900	N	Manes.01G083900	phytozome	Manihot_esculenta_Manes_01G083900	Malpighiales

Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_01G164800	N	Manes.01G164800	phytozome	Manihot_esculenta_Manes_01G164800	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_01G194000	N	Manes.01G194000	phytozome	Manihot_esculenta_Manes_01G194000	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_02G122200	N	Manes.02G122200	phytozome	Manihot_esculenta_Manes_02G122200	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_04G134000	N	Manes.04G134000	phytozome	Manihot_esculenta_Manes_04G134000	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_05G093800	N	Manes.05G093800	phytozome	Manihot_esculenta_Manes_05G093800	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_05G139200	N	Manes.05G139200	phytozome	Manihot_esculenta_Manes_05G139200	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_06G099100	N	Manes.06G099100	phytozome	Manihot_esculenta_Manes_06G099100	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_07G125100	N	Manes.07G125100	phytozome	Manihot_esculenta_Manes_07G125100	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_08G089700	N	Manes.08G089700	phytozome	Manihot_esculenta_Manes_08G089700	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_10G018000	N	Manes.10G018000	phytozome	Manihot_esculenta_Manes_10G018000	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_11G033900	N	Manes.11G033900	phytozome	Manihot_esculenta_Manes_11G033900	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_14G039400	N	Manes.14G039400	phytozome	Manihot_esculenta_Manes_14G039400	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_14G071900	N	Manes.14G071900	phytozome	Manihot_esculenta_Manes_14G071900	Malpighiales
Manihot esculenta	Euphorbiaceae	Manihot_esculenta_Manes_16G103300	N	Manes.16G103300	phytozome	Manihot_esculenta_Manes_16G103300	Malpighiales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr1g111830	N	Medtr1g111830	phytozome	Medicago_truncatula_Medtr1g111830	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr2g100930	N	Medtr2g100930	phytozome	Medicago_truncatula_Medtr2g100930	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr3g462790	N	Medtr3g462790	phytozome	Medicago_truncatula_Medtr3g462790	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr4g107230	N	Medtr4g100630	phytozome	Medicago_truncatula_Medtr4g107230	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr4g111975	N	Medtr4g111975	phytozome	Medicago_truncatula_Medtr4g111975	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr5g027550	N	Medtr5g027550	phytozome	Medicago_truncatula_Medtr5g027550	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr5g037080	N	Medtr5g037080	phytozome	Medicago_truncatula_Medtr5g037080	Fabales

Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr5g069710	N	Medtr5g069710	phytozome	Medicago_truncatula_Medtr5g069710	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr5g088010	N	Medtr5g088010	phytozome	Medicago_truncatula_Medtr5g088010	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr5g088060	N	Medtr5g088060	phytozome	Medicago_truncatula_Medtr5g088060	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr5g488160	N	Medtr5g488160	phytozome	Medicago_truncatula_Medtr5g488160	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr6g092540	N	Medtr6g092540	phytozome	Medicago_truncatula_Medtr6g092540	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr7g067080	N	Medtr7g067080	phytozome	Medicago_truncatula_Medtr7g067080	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr8g063870	N	Medtr8g063870	phytozome	Medicago_truncatula_Medtr8g063870	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr8g073050	N	Medtr8g073050	phytozome	Medicago_truncatula_Medtr8g073050	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_Medtr8g101650	N	Medtr8g101650	phytozome	Medicago_truncatula_Medtr8g101650	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_DIV2	Y RR1B	Medtr8g063600	phytozome	Medicago_truncatula_Medtr8g063600	Fabales
Medicago truncatula	Fabaceae	Medicago_truncatula_DIV1	Y RR2B/DIV2	Medtr5g081860	phytozome	Medicago_truncatula_Medtr5g081860	Fabales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_A01139	N	Migut.A01139	phytozome	Mimulus_guttatus_Migut_A01139	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_D01891	N	Migut.D01891	phytozome	Mimulus_guttatus_Migut_D01891	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_E00676	N	Migut.E00676	phytozome	Mimulus_guttatus_Migut_E00676	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_F00707	N	Migut.F00707	phytozome	Mimulus_guttatus_Migut_F00707	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_F01593	N	Migut.F01593	phytozome	Mimulus_guttatus_Migut_F01593	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_I00074	N	Migut.I00074	phytozome	Mimulus_guttatus_Migut_I00074	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_I00388	N	Migut.I00388	phytozome	Mimulus_guttatus_Migut_I00388	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_J00595	N	Migut.J00595	phytozome	Mimulus_guttatus_Migut_J00595	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_K00589	N	Migut.K00589	phytozome	Mimulus_guttatus_Migut_K00589	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_L01371	N	Migut.L01371	phytozome	Mimulus_guttatus_Migut_L01371	Lamiales

Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_M01627	N	Migut.M01627	phytozome	Mimulus_guttatus_Migut_M01627	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_Migut_N00823	N	Migut.N00823	phytozome	Mimulus_guttatus_Migut_N00823	Lamiales
Mimulus guttatus	Phrymaceae	Mimulus_guttatus_DIV	Y RR2C/DIV3	Migut.L00854	phytozome	Mimulus_guttatus_Migut_L00854	Lamiales
Morina longifolia	Caprifoliaceae	Morina_longifolia_DIV1	Y RR2A/DIV1	FJ805332	phytozome	Morina_longifolia_DIV1Aa_FJ805332	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_DIV2	Y RR2A/DIV1	FJ805333	Gene bank	Morina_longifolia_DIV1Ab_FJ805333	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_DIV3	Y RR2A/DIV1	FJ805334	Gene bank	Morina_longifolia_DIV1Ba_FJ805334	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_DIV4	Y RR2A/DIV1	FJ805335	Gene bank	Morina_longifolia_DIV1Bb_FJ805335	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_DIV5	Y RR2A/DIV1	FJ805336	Gene bank	Morina_longifolia_DIV1Bc_FJ805336	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_DIV6	Y RR2C/DIV3	FJ805337	Gene bank	Morina_longifolia_DIV3A_FJ805337	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_DIV7	Y RR2C/DIV3	FJ805338	Gene bank	Morina_longifolia_DIV3Ba_FJ805338	Dipsacales
Morina longifolia	Caprifoliaceae	Morina_longifolia_DIV8	Y RR2C/DIV3	FJ805339	Gene bank	Morina_longifolia_DIV3Bb_FJ805339	Dipsacales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr10G00660_001	N	GSMUA_Achr10G00660_001	phytozome	Musa_acuminata_GSMUA_Achr10G00660_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr10G06880_001	N	GSMUA_Achr10G06880_001	phytozome	Musa_acuminata_GSMUA_Achr10G06880_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr10G14040_001	N	GSMUA_Achr10G14040_001	phytozome	Musa_acuminata_GSMUA_Achr10G14040_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr11G00670_001	N	GSMUA_Achr11G00670_001	phytozome	Musa_acuminata_GSMUA_Achr11G00670_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr11G09110_001	N	GSMUA_Achr11G09110_001	phytozome	Musa_acuminata_GSMUA_Achr11G09110_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr2G01080_001	N	GSMUA_Achr2G01080_001	phytozome	Musa_acuminata_GSMUA_Achr2G01080_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr5G28940_001	N	GSMUA_Achr5G28940_001	phytozome	Musa_acuminata_GSMUA_Achr5G28940_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr6G14820_001	N	GSMUA_Achr6G14820_001	phytozome	Musa_acuminata_GSMUA_Achr6G14820_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr6G33620_001	N	GSMUA_Achr6G33620_001	phytozome	Musa_acuminata_GSMUA_Achr6G33620_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr7G06880_001	N	GSMUA_Achr7G06880_001	phytozome	Musa_acuminata_GSMUA_Achr7G06880_001	Zingiberales

Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr7G14890_001	N	GSMUA_Achr7G14890_001	phytozome	Musa_acuminata_GSMUA_Achr7G14890_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr8G02260_001	N	GSMUA_Achr8G02260_001	phytozome	Musa_acuminata_GSMUA_Achr8G02260_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr8G02370_001	N	GSMUA_Achr8G02370_001	phytozome	Musa_acuminata_GSMUA_Achr8G02370_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr9G05930_001	N	GSMUA_Achr9G05930_001	phytozome	Musa_acuminata_GSMUA_Achr9G05930_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_Achr9G20620_001	N	GSMUA_Achr9G20620_001	phytozome	Musa_acuminata_GSMUA_Achr9G20620_001	Zingiberales
Musa acuminata	Musaceae	Musa_acuminata_GSMUA_AchrUn_randomG03500_001	N	GSMUA_AchrUn_randomG03500_001	phytozome	Musa_acuminata_GSMUA_AchrUn_randomG03500_001	Zingiberales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104589256	N	XM_010247513.1	Gene bank	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104589256	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104596997	N	XM_010258353.1	Gene bank	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104596997	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104601206	N	XM_010264470.1	Gene bank	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104601206	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104601275	N	XM_010264567.1	Gene bank	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104601275	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104603045	N	XM_010266970.1	Gene bank	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104603045	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104610012	N	XM_010276462.1	Gene bank	Nelumbo_nucifera_transcription_factor_DIVARICATA_like_LOC104610012	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC104591730_variant	N	XM_010250759.1	Gene bank	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC104591730_variant	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC104598416_variant	N	XM_010260459.1	Gene bank	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC104598416_variant	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC104598450	N	XM_010260516.1	Gene bank	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC104598450	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC1046044920_variant	N	XM_010268848.1	Gene bank	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC1046044920_variant	Proteales

Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC104610453	N	XM_010277068.1	Gene bank	Nelumbo_nucifera_transcription_factor_MYB1R1_like_LOC104610453	Proteales
Nelumbo nucifera	Nelumbonaceae	Nelumbo_nucifera_uncharacterized_LOC104592058	N	XM_010251204.1	Gene bank	Nelumbo_nucifera_uncharacterized_LOC104592058	Proteales
Nicotiana benthamiana	Solanaceae	Nicotiana_benthamiana_DIV3	Y RR2A/DIV1	Niben101Scf02250g00006.1	Sol Genomics Network	Nicotiana_benthamiana_Niben101Scf02250g00006_1	Solanales
Nicotiana benthamiana	Solanaceae	Nicotiana_benthamiana_DIV1	Y RR2C/DIV3	Niben101Scf00348g08003.1	Sol Genomics Network	Nicotiana_benthamiana_Niben101Scf00348g08003_1	Solanales
Nicotiana benthamiana	Solanaceae	Nicotiana_benthamiana_DIV2	Y RR2C/DIV3	Niben101Scf01738g07002.1	Sol Genomics Network	Nicotiana_benthamiana_Niben101Scf01738g07002_1	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_transcription_factor_MYB1R1_like_LOC104229719	N	XM_009782407.1	Gene bank	Nicotiana_sylvestris_transcription_factor_MYB1R1_like_LOC104229719	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_DIV8	Y RR1A	XM_009798637.1	Gene bank	Nicotiana_sylvestris_transcription_factor_DIVARICATA_like_LOC104243449	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_DIV1	Y RR1C	XM_009763701.1	Gene bank	Nicotiana_sylvestris_transcription_factor_DIVARICATA_like_LOC104214088	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_DIV4	Y RR1C	XM_009784067.1	Gene bank	Nicotiana_sylvestris_transcription_factor_DIVARICATA_like_LOC104231123	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_DIV6	Y RR2A/DIV1	XM_009796013.1	Gene bank	Nicotiana_sylvestris_transcription_factor_DIVARICATA_like_LOC104241099_Variant 1	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_DIV7	Y RR2A/DIV1	XM_009796014.1	Gene bank	Nicotiana_sylvestris_transcription_factor_DIVARICATA_like_LOC104241099_Variant 2	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_DIV2	Y RR2B/DIV2	XM_009768247.1	Gene bank	Nicotiana_sylvestris_transcription_factor_DIVARICATA_like_LOC104217904	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_DIV3	Y RR2B/DIV2	XM_009769048.1	Gene bank	Nicotiana_sylvestris_transcription_factor_DIVARICATA_like_LOC104218527	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_DIV5	Y RR2C/DIV3	XM_009788417.1	Gene bank	Nicotiana_sylvestris_transcription_factor_DIVARICATA_like_LOC104234785	Solanales
Nicotiana sylvestris	Solanaceae	Nicotiana_sylvestris_DIV9	Y RR2C/DIV3	XM_009803890.1	Gene bank	Nicotiana_sylvestris_transcription_factor_DIVARICATA_like_LOC104247788	Solanales

Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_myb_like_protein_J	N	XM_016636329.1	Gene bank	Nicotiana_tabacum_myb_like_protein_J	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_transcription_factor_MYB1R1_like_LOC107775558	N	XM_016595310.1	Gene bank	Nicotiana_tabacum_transcription_factor_MYB1R1_like_LOC107775558	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV16	Y RR1A	XM_016654978.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107827775	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV17	Y RR1A	XM_016655002.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107827800	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV8	Y RR1A	XM_016603619.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107782691	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV12	Y RR1C	XM_016640701.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107815176	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV15	Y RR1C	XM_016651310.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107824524	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV18	Y RR1C	XM_016625200.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107801809_mRNA	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV2	Y RR1C	XM_016579335.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107761153	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_uncharacterized	Y RR1C	XM_016582152.1	Gene bank	Nicotiana_tabacum_uncharacterized_LOC107763661	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV1	Y RR2A/DIV1	XM_016576992.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107759117	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV13	Y RR2A/DIV1	XM_016643402.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107817548	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV5	Y RR2A/DIV1	XM_016591792	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107772296	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV10	Y RR2B/DIV2	XM_016620056.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107797194	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV11	Y RR2B/DIV2	XM_016635586.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107810761	Solanales

Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV14	Y RR2B/DIV2	XM_016645575.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107819472	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV7	Y RR2B/DIV2	XM_016599641.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107779245	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV3	Y RR2C/DIV3	XM_016584938.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107766192	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV4	Y RR2C/DIV3	XM_016587690.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107768566	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV6	Y RR2C/DIV3	XM_016594549.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107774893	Solanales
Nicotiana tabacum	Solanaceae	Nicotiana_tabacum_DIV9	Y RR2C/DIV3	XM_016613251.1	Gene bank	Nicotiana_tabacum_transcription_factor_DIVARICATA_like_LOC107791228	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_myb_like_protein_J	N	XM_009591901.1	Gene bank	Nicotiana_tomentosiformis_myb_like_protein_J	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_myb_like_protein_J_LOC104121017	N	XM_009632913.1	Gene bank	Nicotiana_tomentosiformis_myb_like_protein_J_LOC104121017	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_myb_like_protein_J_LOC107817283	N	XM_016643082.1	Gene bank	Nicotiana_tomentosiformis_myb_like_protein_J_LOC107817283	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV7	Y RR1A	XM_009619140.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104109780	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV8	Y RR1A	XM_009620637.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104111037	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV3	Y RR1C	XM_009593942.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104089113	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV6	Y RR1C	XM_009618195.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104109017	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV9	Y RR1C	XM_009623919.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104113678	Solanales

Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV5	Y RR2A/DIV1	XM_009605089.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104098372_Variant1	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV5_1	Y RR2A/DIV1	XM_009605089.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104098372_Variant1	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV5_2	Y RR2A/DIV1	XM_009605089.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104098372_Variant1	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV10	Y RR2B/DIV2	XM_009629025.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104117894	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV2	Y RR2B/DIV2	XM_009592103.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104087587	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV1	Y RR2C/DIV3	XM_009590949.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104086633	Solanales
Nicotiana tomentosiformis	Solanaceae	Nicotiana_tomentosiformis_DIV4	Y RR2C/DIV3	XM_009604166.1	Gene bank	Nicotiana_tomentosiformis_transcription_factor_DIVARICATA_like_LOC104097582	Solanales
Oryza sativa	Poaceae	Oryza_sativa_Japonica_9631_m06132	N	LOC_Os03g62100	Rcie Genome	Oryza_sativa_Japonica_9631_m06132	Poales
Oryza sativa	Poaceae	Oryza_sativa_Japonica_9636_m00410	N	LOC_Os08g04840	Rcie Genome	Oryza_sativa_Japonica_Group_genomic_DNA_chromosome_8_9636_m00410	Poales
Oryza sativa	Poaceae	Oryza_sativa_LOC_Os01g09280	N	LOC_Os01g09280	phytozome	Oryza_sativa_LOC_Os01g09280	Poales
Oryza sativa	Poaceae	Oryza_sativa_LOC_Os08g05510	N	LOC_Os08g05510	phytozome	Oryza_sativa_LOC_Os08g05510	Poales
Oryza sativa	Poaceae	Oryza_sativa_LOC_Os10g41200	N	LOC_Os10g41200	phytozome	Oryza_sativa_LOC_Os10g41200	Poales
Oryza sativa	Poaceae	Oryza_sativa_LOC_Os10g41260	N	LOC_Os10g41260	phytozome	Oryza_sativa_LOC_Os10g41260	Poales
Oryza sativa	Poaceae	Oryza_sativa_Japonica_9632_m05667	Y RR1B	LOC_Os04g58020	Rcie Genome	Oryza_sativa_Japonica_9632_m05667	Poales
Oryza sativa	Poaceae	Oryza_sativa_DIV2	Y RR1C	LOC_Os01g34060	phytozome	Oryza_sativa_LOC_Os01g34060	Poales
Oryza sativa	Poaceae	Oryza_sativa_DIV3	Y RR1C	LOC_Os04g27410	phytozome	Oryza_sativa_LOC_Os04g27410	Poales

Oryza sativa	Poaceae	Oryza_sativa_DIV1	Y RR2A/DIV1	LOC_Os01g04930	phytozome	Oryza_sativa_LOC_Os01g04930	Poales
Oryza sativa	Poaceae	Oryza_sativa_DIV4	Y RR2A/DIV1	LOC_Os05g37050	phytozome	Oryza_sativa_LOC_Os05g37050	Poales
Oryza sativa	Poaceae	Oryza_sativa_DIV5	Y RR2A/DIV1	LOC_Os01g63460	phytozome	Oryza_sativa_LOC_Os01g63460	Poales
Oryza sativa	Poaceae	Oryza_sativa_DIV6	Y RR2A/DIV1	LOC_Os01g64360	phytozome	Oryza_sativa_LOC_Os01g64360	Poales
Oryza sativa	Poaceae	Oryza_sativa_DIV7	Y RR2A/DIV1	LOC_Os05g37730	phytozome	Oryza_sativa_LOC_Os05g37730	Poales
Oryza sativa	Poaceae	Oryza_sativa_Japonica_9629_m00414	Y RR2A/DIV1	LOC_Os01g04930	Rcie Genome	Oryza_sativa_Japonica_9629_m00414	Poales
Oryza sativa	Poaceae	Oryza_sativa_Japonica_9629_m06276	Y RR2A/DIV1	LOC_Os01g63460	Rcie Genome	Oryza_sativa_Japonica_9629_m06276	Poales
Oryza sativa	Poaceae	Oryza_sativa_Japonica_9629_m06374	Y RR2A/DIV1	LOC_Os01g64360	Rcie Genome	Oryza_sativa_Japonica_9629_m06374	Poales
Oryza sativa	Poaceae	Oryza_sativa_Japonica_9633_m03417	Y RR2A/DIV1	LOC_Os05g37060	Rcie Genome	Oryza_sativa_Japonica_9633_m03417	Poales
Oryza sativa	Poaceae	Oryza_sativa_Japonica_9633_m03487	Y RR2A/DIV1	LOC_Os05g37730	Rcie Genome	Oryza_sativa_Japonica_9633_m03487	Poales
Panicum hallii	Poaceae	Panicum_hallii_Pahal_C02785	N	Pahal.C02785	phytozome	Panicum_hallii_Pahal_C02785	Poales
Panicum hallii	Poaceae	Panicum_hallii_Pahal_C02822	N	Pahal.C02822	phytozome	Panicum_hallii_Pahal_C02822	Poales
Panicum hallii	Poaceae	Panicum_hallii_Pahal_E00907	N	Pahal.E00907	phytozome	Panicum_hallii_Pahal_E00907	Poales
Panicum hallii	Poaceae	Panicum_hallii_Pahal_E03927	N	Pahal.E03927	phytozome	Panicum_hallii_Pahal_E03927	Poales
Panicum hallii	Poaceae	Panicum_hallii_Pahal_E04275	N	Pahal.E04275	phytozome	Panicum_hallii_Pahal_E04275	Poales
Panicum hallii	Poaceae	Panicum_hallii_Pahal_F00945	N	Pahal.F00945	phytozome	Panicum_hallii_Pahal_F00945	Poales
Panicum hallii	Poaceae	Panicum_hallii_Pahal_F00959	N	Pahal.F00959	phytozome	Panicum_hallii_Pahal_F00959	Poales
Panicum hallii	Poaceae	Panicum_hallii_Pahal_H02252	N	Pahal.H02252	phytozome	Panicum_hallii_Pahal_H02252	Poales
Panicum hallii	Poaceae	Panicum_hallii_Pahal_I04006	N	Pahal.I04006	phytozome	Panicum_hallii_Pahal_I04006	Poales
Panicum virgatum	Poaceae	Panicum_hallii_Pahal_I04025	N	Pahal.I04025	phytozome	Panicum_hallii_Pahal_I04025	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Ea00264	N	Pavir.Ea00264	phytozome	Panicum_virgatum_Pavir_Ea00264	Poales

Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Ea00523	N	Pavir.Ea00523	phytozome	Panicum_virgatum_Pavir_Ea00523	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Ea01767	N	Pavir.Eb00572	phytozome	Panicum_virgatum_Pavir_Ea01767	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Ea03421	N	Pavir.Ea03421	phytozome	Panicum_virgatum_Pavir_Ea03421	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Eb00572	N	Pavir.Eb00572	phytozome	Panicum_virgatum_Pavir_Eb00572	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Eb01413	N	Pavir.Eb01413	phytozome	Panicum_virgatum_Pavir_Eb01413	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Fa01954	N	Pavir.Fa01954	phytozome	Panicum_virgatum_Pavir_Fa01954	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Fa01963	N	Pavir.Fa01963	phytozome	Panicum_virgatum_Pavir_Fa01963	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Gb00055	N	Pavir.Gb00055	phytozome	Panicum_virgatum_Pavir_Gb00055	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Hb00090	N	Pavir.Hb00090	phytozome	Panicum_virgatum_Pavir_Hb00090	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Ia02215	N	Pavir.Ia02215	phytozome	Panicum_virgatum_Pavir_Ia02215	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Ib02262	N	Pavir.Ib02262	phytozome	Panicum_virgatum_Pavir_Ib02262	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_Ib02319	N	Pavir.Ib02319	phytozome	Panicum_virgatum_Pavir_Ib02319	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_J01328	N	Pavir.J01328	phytozome	Panicum_virgatum_Pavir_J01328	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_J04337	N	Pavir.J04337	phytozome	Panicum_virgatum_Pavir_J04337	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_J08778	N	Pavir.J08778	phytozome	Panicum_virgatum_Pavir_J08778	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_J16113	N	Pavir.J16113	phytozome	Panicum_virgatum_Pavir_J16113	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_J25346	N	Pavir.J25346	phytozome	Panicum_virgatum_Pavir_J25346	Poales
Panicum virgatum	Poaceae	Panicum_virgatum_Pavir_J37988	N	Pavir.J37988	phytozome	Panicum_virgatum_Pavir_J37988	Poales
Petunia axillaris	Solanaceae	Petunia_axillaris_DIV3	Y RR2A/DIV1	Peaxi162Scf01058	Sol Genomics Network	Petunia_axillaris_Peaxi162Scf01058	Solanales
Petunia axillaris	Solanaceae	Petunia_axillaris_DIV1	Y RR2C/DIV3	Peaxi162Scf00014g00715.1	Sol Genomics Network	Petunia_axillaris_Peaxi162Scf00014g00715	Solanales
Petunia axillaris	Solanaceae	Petunia_axillaris_DIV2	Y RR2C/DIV3	Peaxi162Scf00141g00622.1	Sol Genomics Network	Petunia_axillaris_Peaxi162Scf00141g00622_1	Solanales

Petunia inflata	Solanaceae	Petunia_inflata_DIV3	Y RR2A/DIV1	Peinf101Scf02272g00040.1	Sol Genomics Network	Petunia_inflata_Peinf101Scf02272g00040_1	Solanales
Petunia inflata	Solanaceae	Petunia_inflata_DIV4	Y RR2A/DIV1	Peinf101Scf02316g00011.1	Sol Genomics Network	Petunia_inflata_Peinf101Scf02316g00011_1	Solanales
Petunia inflata	Solanaceae	Petunia_inflata_DIV1	Y RR2C/DIV3	Peinf101Scf00347g03017.1	Sol Genomics Network	Petunia_inflata_Peinf101Scf00347g03017_1	Solanales
Petunia inflata	Solanaceae	Petunia_inflata_DIV2	Y RR2C/DIV3	Peinf101Scf01078g01011.1	Sol Genomics Network	Petunia_inflata_Peinf101Scf01078g01011_1	Solanales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_001G240300	N	Phvul.001G240300	phytozome	Phaseolus_vulgaris_Phvul_001G240300	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_002G078600	N	Phvul.002G078600	phytozome	Phaseolus_vulgaris_Phvul_002G078600	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_002G304400	N	Phvul.002G304400	phytozome	Phaseolus_vulgaris_Phvul_002G304400	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_003G013600	N	Phvul.003G013600	phytozome	Phaseolus_vulgaris_Phvul_003G013600	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_003G054100	N	Phvul.003G054100	phytozome	Phaseolus_vulgaris_Phvul_003G054100	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_003G072800	N	Phvul.003G072800	phytozome	Phaseolus_vulgaris_Phvul_003G072800	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_003G176800	N	Phvul.003G176800	phytozome	Phaseolus_vulgaris_Phvul_003G176800	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_003G195700	N	Phvul.003G195700	phytozome	Phaseolus_vulgaris_Phvul_003G195700	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_003G222900	N	Phvul.003G222900	phytozome	Phaseolus_vulgaris_Phvul_003G222900	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_004G171200	N	Phvul.004G171200	phytozome	Phaseolus_vulgaris_Phvul_004G171200	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_006G065700	N	Phvul.006G065700	phytozome	Phaseolus_vulgaris_Phvul_006G065700	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_007G023600	N	Phvul.007G023600	phytozome	Phaseolus_vulgaris_Phvul_007G023600	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_008G085700	N	Phvul.008G085700	phytozome	Phaseolus_vulgaris_Phvul_008G085700	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_008G085800	N	Phvul.008G085800	phytozome	Phaseolus_vulgaris_Phvul_008G085800	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_008G107000	N	Phvul.008G107000	phytozome	Phaseolus_vulgaris_Phvul_008G107000	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_008G226600	N	Phvul.008G226600	phytozome	Phaseolus_vulgaris_Phvul_008G226600	Fabales
Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_008G262900	N	Phvul.008G262900	phytozome	Phaseolus_vulgaris_Phvul_008G262900	Fabales

Phaseolus vulgaris	Fabaceae	Phaseolus_vulgaris_Phvul_009G183300	N	Phvul.009G183300	phytozome	Phaseolus_vulgaris_Phvul_009G183300	Fabales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_like_LOC103710308	N	XM_008795974.2	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_like_LOC103710308	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_like_LOC103718882	N	XM_008807882.2	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_like_LOC103718882	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_like_LOC103718883	N	XM_008807883.2	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_like_LOC103718883	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_like_LOC103720751	N	XM_008810617.1	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_like_LOC103720751	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_LOC103695489_variant1/2	N	XM_008776835.1/XM_008776836.1	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_LOC103695489_variant1/2	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_LOC103704058_variant1/2/3	N	XM_008787197.2/XM_008787198.2/XM_008787199.2	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_LOC103704058_variant1/2/3	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_LOC103710236_variant1/2	N	XM_017843579.1/XM_008795891.1	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_LOC103710236_variant1/2	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103695599	N	XM_008776968.2	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103695599	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103713455	N	XM_008800395.2	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103713455	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103714322	N	XM_008801527.2	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103714322	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103720263	N	XM_008809880.2	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103720263	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103723983	N	XM_008815094.1	Gene bank	Phoenix_dactylifera_transcription_factor_DIVARICATA_MYB1R1_like_LOC103723983	Arecales

Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_uncharacterized_LOC103707412	N	XM_008791888.2	Gene bank	Phoenix_dactylifera_uncharacterized_LOC103707412	Arecales
Phoenix dactylifera	Arecaceae	Phoenix_dactylifera_uncharacterized_LOC103713598	N	XM_008800586.2	Gene bank	Phoenix_dactylifera_uncharacterized_LOC103713598	Arecales
Physcomitrella patens	Funariaceae	Physcomitrella_patens_Pp3c15_23090	N	Pp3c15_23090	phytozome	Physcomitrella_patens_Pp3c15_23090	Funariales
Physcomitrella patens	Funariaceae	Physcomitrella_patens_Pp3c15_23110	N	Pp3c15_23110	phytozome	Physcomitrella_patens_Pp3c15_23110	Funariales
Physcomitrella patens	Funariaceae	Physcomitrella_patens_Pp3c4_17230	N	Pp3c4_17230	phytozome	Physcomitrella_patens_Pp3c4_17230	Funariales
Physcomitrella patens	Funariaceae	Physcomitrella_patens_Pp3c4_5410	N	Pp3c4_5410	phytozome	Physcomitrella_patens_Pp3c4_5410	Funariales
Physcomitrella patens	Funariaceae	Physcomitrella_patens_Pp3c9_19080	N	Pp3c9_19080	phytozome	Physcomitrella_patens_Pp3c9_19080	Funariales
Plantago lanceolata	Plantaginaceae	Plantago_lanceolata_DIVARICATA	N	KF964142.1	Gene bank	Plantago_lanceolata_DIVARICATA	Lamiales
Plantago lanceolata	Plantaginaceae	Plantago_lanceolata_DIVARICATA_2	N	KF964145.1	Gene bank	Plantago_lanceolata_DIVARICATA_2	Lamiales
Plantago lanceolata	Plantaginaceae	Plantago_lanceolata_DIVARICATA_3	N	KF964143.1	Gene bank	Plantago_lanceolata_DIVARICATA_3	Lamiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_001G155300	N	Potri.001G155300	phytozome	Populus_trichocarpa_Potri_001G155300	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_001G189800	N	Potri.001G189800	phytozome	Populus_trichocarpa_Potri_001G189800	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_001G248800	N	Potri.001G248800	phytozome	Populus_trichocarpa_Potri_001G248800	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_003G049100	N	Potri.003G049100	phytozome	Populus_trichocarpa_Potri_003G049100	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_003G079500	N	Potri.003G079500	phytozome	Populus_trichocarpa_Potri_003G079500	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_005G087700	N	Potri.005G087700	phytozome	Populus_trichocarpa_Potri_005G087700	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_006G097300	N	Potri.006G097300	phytozome	Populus_trichocarpa_Potri_006G097300	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_006G150300	N	Potri.006G150300	phytozome	Populus_trichocarpa_Potri_006G150300	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_006G230500	N	Potri.006G230500	phytozome	Populus_trichocarpa_Potri_006G230500	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_007G076200	N	Potri.007G076200	phytozome	Populus_trichocarpa_Potri_007G076200	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_008G064200	N	Potri.008G064200	phytozome	Populus_trichocarpa_Potri_008G064200	Malpighiales

Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_008G191800	N	Potri.008G191800	phytozome	Populus_trichocarpa_Potri_008G191800	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_009G042600	N	Potri.009G042600	phytozome	Populus_trichocarpa_Potri_009G042600	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_010G039300	N	Potri.010G039300	phytozome	Populus_trichocarpa_Potri_010G039300	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_010G193000	N	Potri.010G193000	phytozome	Populus_trichocarpa_Potri_010G193000	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_012G060300	N	Potri.012G060300	phytozome	Populus_trichocarpa_Potri_012G060300	Malpighiales
Populus trichocarpa	Salicaceae	Populus_trichocarpa_Potri_016G112300	N	Potri.016G112300	phytozome	Populus_trichocarpa_Potri_016G112300	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_29610_t000025	N	29610.t000025	phytozome	Ricinus_communis_29610_t000025	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_29681_t000001	N	29681.t000001	phytozome	Ricinus_communis_29681_t000001	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_29736_t000085	N	29736.t000085	phytozome	Ricinus_communis_29736_t000085	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_29912_t000113	N	29912.t000113	phytozome	Ricinus_communis_29912_t000113	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_30055_t000059	N	30055.t000059	phytozome	Ricinus_communis_30055_t000059	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_30131_t000414	N	30131.t000414	phytozome	Ricinus_communis_30131_t000414	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_30146_t000086	N	30146.t000086	phytozome	Ricinus_communis_30146_t000086	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_30147_t000299	N	30147.t000299	phytozome	Ricinus_communis_30147_t000299	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_30147_t000608	N	30147.t000608	phytozome	Ricinus_communis_30147_t000608	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_30155_t000022	N	30155.t000022	phytozome	Ricinus_communis_30155_t000022	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_30174_t000114	N	30174.t000114	phytozome	Ricinus_communis_30174_t000114	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_transcription_factor_DIVARICATA_LOC8286480	N	XM_002525549.2	Gene bank	Ricinus_communis_transcription_factor_DIVARICATA_LOC8286480	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_transcription_factor_MYB1R1_LOC8265075_variant1	N	XM_015716307.1	Gene bank	Ricinus_communis_transcription_factor_MYB1R1_LOC8265075_variant1	Malpighiales
Ricinus communis	Euphorbiaceae	Ricinus_communis_uncharacterized_LOC8273781_variant1/2	N	XM_015717362.1/XM_002515920.2	Gene bank	Ricinus_communis_uncharacterized_LOC8273781_variant1/2	Malpighiales

Ricinus communis	Euphorbiaceae	Ricinus_communis_DIV	Y RR2C/DIV3	28288.t000001	phytozome	Ricinus_communis_28288_t000001	Malpighiales
Sambucus caerulea	Adoxaceae	Sambucus_caerulea_DIV1	Y RR2A/DIV1	FJ805277	Gene bank	Sambucus_caerulea_DIV1_FJ805277	Dipsacales
Sambucus caerulea	Adoxaceae	Sambucus_caerulea_DIV2	Y RR2C/DIV3	FJ805278	Gene bank	Sambucus_caerulea_DIV3_FJ805278	Dipsacales
Sambucus canadensis	Adoxaceae	Sambucus_canadensis_DIV1	Y RR2A/DIV1	FJ805279	Gene bank	Sambucus_canadensis_DIV1aa_FJ805279	Dipsacales
Sambucus canadensis	Adoxaceae	Sambucus_canadensis_DIV2	Y RR2A/DIV1	FJ805280	Gene bank	Sambucus_canadensis_DIV1ab_FJ805280	Dipsacales
Sambucus canadensis	Adoxaceae	Sambucus_canadensis_DIV3	Y RR2A/DIV1	FJ805281	Gene bank	Sambucus_canadensis_DIV1ac_FJ805281	Dipsacales
Sambucus nigra	Adoxaceae	Sambucus_nigra_DIV	Y RR2C/DIV3	FJ805282	Gene bank	Sambucus_nigra_DIV3_FJ805282	Dipsacales
Setaria italica	Poaceae	Setaria_italica_Seita_3G222600	N	Seita.3G222600	phytozome	Setaria_italica_Seita_3G222600	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_3G225500	N	Seita.3G225500	phytozome	Setaria_italica_Seita_3G225500	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_4G214200	N	Seita.4G214200	phytozome	Setaria_italica_Seita_4G214200	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_5G098300	N	Seita.5G098300	phytozome	Setaria_italica_Seita_5G098300	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_5G133800	N	Seita.5G133800	phytozome	Setaria_italica_Seita_5G133800	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_5G183700	N	Seita.5G183700	phytozome	Setaria_italica_Seita_5G183700	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_5G232400	N	Seita.5G232400	phytozome	Setaria_italica_Seita_5G232400	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_6G063100	N	Seita.6G063100	phytozome	Setaria_italica_Seita_6G063100	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_6G065500	N	Seita.6G065500	phytozome	Setaria_italica_Seita_6G065500	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_9G319600	N	Seita.9G319600	phytozome	Setaria_italica_Seita_9G319600	Poales
Setaria italica	Poaceae	Setaria_italica_Seita_9G321800	N	Seita.9G321800	phytozome	Setaria_italica_Seita_9G321800	Poales
Setaria italica	Poaceae	Setaria_italica_DIV1	Y RR1C	Seita.3G113700	phytozome	Setaria_italica_Seita_3G113700	Poales
Setaria viridis	Poaceae	Setaria_viridis_Sevir_5G096400	N	Sevir.5G096400	phytozome	Setaria_viridis_Sevir_5G096400	Poales
Setaria viridis	Poaceae	Setaria_viridis_Sevir_5G131800	N	Sevir.5G131800	phytozome	Setaria_viridis_Sevir_5G131800	Poales

Setaria viridis	Poaceae	Setaria_viridis_Sevir_5G185000	N	Sevir.5G185000	phytozome	Setaria_viridis_Sevir_5G185000	Poales
Setaria viridis	Poaceae	Setaria_viridis_Sevir_5G390500	N	Sevir.5G390500	phytozome	Setaria_viridis_Sevir_5G390500	Poales
Setaria viridis	Poaceae	Setaria_viridis_Sevir_6G060900	N	Sevir.6G060900	phytozome	Setaria_viridis_Sevir_6G060900	Poales
Setaria viridis	Poaceae	Setaria_viridis_Sevir_6G064000	N	Sevir.6G064000	phytozome	Setaria_viridis_Sevir_6G064000	Poales
Setaria viridis	Poaceae	Setaria_viridis_Sevir_9G325200	N	Sevir.9G325200	phytozome	Setaria_viridis_Sevir_9G325200	Poales
Setaria viridis	Poaceae	Setaria_viridis_Sevir_9G327500	N	Sevir.9G327500	phytozome	Setaria_viridis_Sevir_9G327500	Poales
Setaria viridis	Poaceae	Setaria_viridis_DIV2	Y RR2A/DIV1	Sevir.3G227500	phytozome	Setaria_viridis_Sevir_3G227500	Poales
Setaria viridis	Poaceae	Setaria_viridis_DIV3	Y RR2A/DIV1	Sevir.3G230600	phytozome	Setaria_viridis_Sevir_3G230600	Poales
Setaria viridis	Poaceae	Setaria_viridis_DIV4	Y RR2A/DIV1	Sevir.4G223800	phytozome	Setaria_viridis_Sevir_4G223800	Poales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV1	Y RR2A/DIV1	FJ805340	Gene bank	Sixalix_atropurpurea_DIV1Aa_FJ805340	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV2	Y RR2A/DIV1	FJ805344	Gene bank	Sixalix_atropurpurea_DIV1Aa_FJ805344	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV3	Y RR2A/DIV1	FJ805341	Gene bank	Sixalix_atropurpurea_DIV1Ab_FJ805341	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV4	Y RR2A/DIV1	FJ805345	Gene bank	Sixalix_atropurpurea_FJ805345	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV5	Y RR2A/DIV1	FJ805342	Gene bank	Sixalix_atropurpurea_DIV1AcFJ805342	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV6	Y RR2A/DIV1	FJ805346	Gene bank	Sixalix_atropurpurea_FJ805346	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV7	Y RR2A/DIV1	FJ805343	Gene bank	Sixalix_atropurpurea_DIV1Ad_FJ805343	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV8	Y RR2A/DIV1	FJ805347	Gene bank	Sixalix_atropurpurea_FJ805347	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV10	Y RR2B/DIV2	FJ805349	Gene bank	Sixalix_atropurpurea_FJ805349	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV9	Y RR2B/DIV2	FJ805348	Gene bank	Sixalix_atropurpurea_FJ805348	Dipsacales
Sixalix atropurpurea	Caprifoliaceae	Sixalix_atropurpurea_DIV11	Y RR2C/DIV3	FJ805350	Gene bank	Sixalix_atropurpurea_FJ805350	Dipsacales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV10	N	XM_004245060.2	Gene bank	Solanum_lycopersicum_transcription_factor_DIVARICATA_like_LOC101261941	Solanales

Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_MYB1R11	N	XM_004250798.1	Gene bank	Solanum_lycopersicum_transcription_factor_MYB1R1_like_LOC101256155	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_MYB1R12	N	XM_010329047.1	Gene bank	Solanum_lycopersicum_transcription_factor_MYB1R1_like_LOC104644286	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_MYB1R13	N	XM_004237025.2	Gene bank	Solanum_lycopersicum_transcription_factor_MYB1R1_like_LOC101257759	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_MYB1R14	N	NM_001320533.1	Gene bank	Solanum_lycopersicum_transcription_factor_MYB1R1_like_LOC101261036	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_MYB1R15	N	XM_004251616.2	Gene bank	Solanum_lycopersicum_transcription_factor_MYB1R1_like_LOC101267581	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_MYB2	N	XM_004242920.2	Gene bank	Solanum_lycopersicum_myb_like_protein_J_LOC101265743	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_MYBI	Y RR1A	AK328632.1	Gene bank	Solanum_lycopersicum_cDNA_clone_LEFL3024O07_HTC_in_root	Solanales
Solanum lycopersicum	Solanaceae	Solanum_pennellii_MYBI	Y RR1A	NM_001309875.1	Gene bank	Solanum_pennellii_transcription_factor_DIVARICATA_like_LeMYBI	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV4	Y RR1B	XM_004246872.2	Gene bank	Solanum_lycopersicum_transcription_factor_DIVARICATA_like_LOC101246465	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_MYB1	Y RR1B	LOC101245877	Gene bank	Solanum_lycopersicum_myb_like_protein_1_LOC104644286	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV9	Y RR1C	XM_004235692.2	Gene bank	Solanum_lycopersicum_transcription_factor_DIVARICATA_like_LOC101260117	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV1	Y RR2A/DIV1	Solyc06g076770.2	Sol Genomics Network	Solanum_lycopersicum_Solyc06g076770_2	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV11	Y RR2B/DIV2	XM_004235209.2	Gene bank	Solanum_lycopersicum_transcription_factor_DIVARICATA_like_LOC101265111	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV7	Y RR2B/DIV2	XM_004239892.2	Gene bank	Solanum_lycopersicum_transcription_factor_DIVARICATA_like_LOC101257376_transcript_variant_1	Solanales

Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV8	Y RR2B/DIV2	XM_004239893.2	Gene bank	Solanum_lycopersicum_transcription_factor_DIVARICATA_like_LOC101257376_transcript_variant_2	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV2	Y RR2C/DIV3	Solyc09g014250.2	Sol Genomics Network	Solanum_lycopersicum_Solyc09g014250_2	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV3	Y RR2C/DIV3	Solyc10g076820.1	Sol Genomics Network	Solanum_lycopersicum_Solyc10g076820_1	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV5	Y RR2C/DIV3	XM_004246290.2	Gene bank	Solanum_lycopersicum_transcription_factor_DIVARICATA_like_LOC101253014	Solanales
Solanum lycopersicum	Solanaceae	Solanum_lycopersicum_DIV6	Y RR2C/DIV3	XM_004249035.3	Gene bank	Solanum_lycopersicum_transcription_factor_DIVARICATA_like_LOC101251526	Solanales
Solanum melongena	Solanaceae	Solanum_melongena_DIV1	Y RR2A/DIV1	Sme2.5_00021.1_g00013.1	Sol Genomics Network	Solanum_melongena_Eggplant_Sme2.5_00021_1_g00013_1	Solanales
Solanum melongena	Solanaceae	Solanum_melongena_DIV2	Y RR2B/DIV2	Sme2.5_02906.1_g00002.1	Sol Genomics Network	Solanum_melongena_Eggplant_Sme2.5_02906_1_g00002_1	Solanales
Solanum melongena	Solanaceae	Solanum_melongena_DIV3	Y RR2B/DIV2	Sme2.5_08168.1_g00002.1	Sol Genomics Network	Solanum_melongena_Eggplant_Sme2.5_08168_1_g00002_1	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_DIV3	N	XM_015220504.1	Gene bank	Solanum_pennellii_transcription_factor_DIVARICATA_like_LOC107020212	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_MYB1R11	N	XM_015202163.1	Gene bank	Solanum_pennellii_transcription_factor_MYB1R1_like_LOC107003917	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_MYB1R13	N	XM_015216524.1	Gene bank	Solanum_pennellii_transcription_factor_MYB1R1_like_LOC107016050	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_MYB1R14	N	XM_015223660.1	Gene bank	Solanum_pennellii_transcription_factor_MYB1R1_like_LOC107023103	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_MYB1R15	N	XM_015229856.1	Gene bank	Solanum_pennellii_transcription_factor_MYB1R1_like_LOC107028690	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_MYB1R16	N	XM_015199324.1	Gene bank	Solanum_pennellii_transcription_factor_MYB1R1_like_LOC107001177	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_transcription_factor_MYB1R1_like_LOC107005205	N	XR_001454839.1	Gene bank	Solanum_pennellii_transcription_factor_MYB1R1_like_LOC107005205	Solanales

Solanum pennellii	Solanaceae	Solanum_pennellii_DIV4	Y RR1A	XM_015220587.1	Gene bank	Solanum_pennellii_transcription_factor_DIVARICATA_like_LOC107020292	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_DIV6	Y RR1B	XM_015231505.1	Gene bank	Solanum_pennellii_transcription_factor_DIVARICATA_like_LOC107030110	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_uncharacterized	Y RR1B	XM_015232605.1	Gene bank	Solanum_pennellii_uncharacterized_LOC107031291	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_MYB1R12	Y RR1C	XM_015212014.1	Gene bank	Solanum_pennellii_transcription_factor_MYB1R1_like_LOC107012232	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_DIV5	Y RR2A/DIV1	XM_015223698.1	Gene bank	Solanum_pennellii_transcription_factor_DIVARICATA_like_LOC107023125_mRNA	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_DIV1	Y RR2B/DIV2	XM_015212787.1	Gene bank	Solanum_pennellii_transcription_factor_DIVARICATA_like_LOC107012843	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_DIV2	Y RR2B/DIV2	XM_015219655.1	Gene bank	Solanum_pennellii_transcription_factor_DIVARICATA_like_LOC107019075	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_DIV7	Y RR2C/DIV3	XM_015233100	Gene bank	Solanum_pennellii_transcription_factor_DIVARICATA_like_LOC107031660	Solanales
Solanum pennellii	Solanaceae	Solanum_pennellii_DIV8	Y RR2C/DIV3	XM_015233878.1	Gene bank	Solanum_pennellii_transcription_factor_DIVARICATA_like_LOC107032289	Solanales
Solanum peruvianum	Solanaceae	Solanum_peruvianum_DIV	Y RR2A/DIV1	a78521	Sol Genomics Network	Solanum_peruvianum_de_novo_transcriptome_a78521	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV8	N	XM_015315076.1	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102600540	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_MYB	N	XM_006345272.2	Gene bank	Solanum_tuberosum_myb_like_protein_J_LOC102594971	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_MYB1R11	N	XM_006353466.2	Gene bank	Solanum_tuberosum_MYB1R1_like_LOC102587181	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_MYB1R12	N	XM_006363481.2	Gene bank	Solanum_tuberosum_transcription_factor_MYB1R1_LOC102595084	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_MYB1R13	N	XM_015304213.1	Gene bank	Solanum_tuberosum_transcription_MYB1R1_LIKE	Solanales

Solanum tuberosum	Solanaceae	Solanum_tuberosum_putative_DNA binding_protein_like_LOC102577613	N	NM_001288417.1	Gene bank	Solanum_tuberosum_putative_DNA binding_protein_like_LOC102577613	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102583764_transcript_variant_2	N	XM_015312461.1	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102583764_transcript_variant_2	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102583764_transcript_variant_3	N	XM_015312462.1	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102583764_transcript_variant_3	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV3	Y RR1A	XM_006345809.1	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102582848	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV11	Y RR1B	XM_015309619.1	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC107060978	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV12	Y RR1B	XM_015312861.1	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC107062329	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV7	Y RR1B	XM_006361758.1	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102595824	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV9	Y RR1C	XM_006341575.2	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102604472	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV1	Y RR2A/DIV1	ST4.03ch10	Sol Genomics Network	Solanum_tuberosum_4_03ch06	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV5	Y RR2A/DIV1	XM_006350761.2	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102584517	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV2	Y RR2B/DIV2	XM_006362924.2	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102581033	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV4	Y RR2B/DIV2	XM_006355593.2	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102583764_transcript_variant_1	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV10	Y RR2C/DIV3	XM_006362989.2	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_like_LOC102605598	Solanales
Solanum tuberosum	Solanaceae	Solanum_tuberosum_DIV6	Y RR2C/DIV3	XM_006349407.	Gene bank	Solanum_tuberosum_transcription_factor_DIVARICATA_	Solanales

				2		like_LOC102588148	
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_001G297500	N	Sobic.001G297500	phytozome	Sorghum_bicolor_Sobic_001G297500	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_003G034800	N	Sobic.003G034800	phytozome	Sorghum_bicolor_Sobic_003G034800	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_003G076500	N	Sobic.003G076500	phytozome	Sorghum_bicolor_Sobic_003G076500	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_003G076600	N	Sobic.003G076600	phytozome	Sorghum_bicolor_Sobic_003G076600	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_003G132300	N	Sobic.003G132300	phytozome	Sorghum_bicolor_Sobic_003G132300	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_006G040700	N	Sobic.006G040700	phytozome	Sorghum_bicolor_Sobic_006G040700	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_006G266600	N	Sobic.006G266600	phytozome	Sorghum_bicolor_Sobic_006G266600	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_007G037100	N	Sobic.007G037100	phytozome	Sorghum_bicolor_Sobic_007G037100	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_009G024700	N	Sobic.009G024700	phytozome	Sorghum_bicolor_Sobic_009G024700	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_009G154200	N	Sobic.009G154200	phytozome	Sorghum_bicolor_Sobic_009G154200	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_009G157500	N	Sobic.009G157500	phytozome	Sorghum_bicolor_Sobic_009G157500	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_010G109700	N	Sobic.010G109700	phytozome	Sorghum_bicolor_Sobic_010G109700	Poales
Sorghum bicolor	Poaceae	Sorghum_bicolor_Sobic_010G111400	N	Sobic.010G111400	phytozome	Sorghum_bicolor_Sobic_010G111400	Poales
Sphagnum fallax	Sphagnaceae	Sphagnum_fallax_Sphfalx0002s0133	N	Sphfalx0002s0133	phytozome	Sphagnum_fallax_Sphfalx0002s0133	Sphagnales
Sphagnum fallax	Sphagnaceae	Sphagnum_fallax_Sphfalx0058s0056	N	Sphfalx0058s0056	phytozome	Sphagnum_fallax_Sphfalx0058s0056	Sphagnales
Sphagnum fallax	Sphagnaceae	Sphagnum_fallax_Sphfalx0098s0034	N	Sphfalx0098s0034	phytozome	Sphagnum_fallax_Sphfalx0098s0034	Sphagnales
Sphagnum fallax	Sphagnaceae	Sphagnum_fallax_Sphfalx0140s0008	N	Sphfalx0140s0008	phytozome	Sphagnum_fallax_Sphfalx0140s0008	Sphagnales
Spirodela polyrhiza	Araceae	Spirodela_polyrhiza_Spipo17G0012800	N	Spipo17G0012800	phytozome	Spirodela_polyrhiza_Spipo17G0012800	Alismatales
Spirodela polyrhiza	Araceae	Spirodela_polyrhiza_Spipo1G0106700	N	Spipo1G0106700	phytozome	Spirodela_polyrhiza_Spipo1G0106700	Alismatales
Spirodela polyrhiza	Araceae	Spirodela_polyrhiza_Spipo21G0031200	N	Spipo21G0031200	phytozome	Spirodela_polyrhiza_Spipo21G0031200	Alismatales

Spirodela polyrhiza	Araceae	Spirodela_polyrhiza_Spipo21G0035200	N	Spipo21G0035200	phytozome	Spirodela_polyrhiza_Spipo21G0035200	Alismatales
Spirodela polyrhiza	Araceae	Spirodela_polyrhiza_Spipo5G0049900	N	Spipo5G0049900	phytozome	Spirodela_polyrhiza_Spipo5G0049900	Alismatales
Spirodela polyrhiza	Araceae	Spirodela_polyrhiza_DIV2	Y RR1B	Spipo1G0043100	phytozome	Spirodela_polyrhiza_Spipo1G0043100	Alismatales
Spirodela polyrhiza	Araceae	Spirodela_polyrhiza_DIV1	Y RR1C	Spipo19G0030400	phytozome	Spirodela_polyrhiza_Spipo19G0030400	Alismatales
Spirodela polyrhiza	Araceae	Spirodela_polyrhiza_DIV3	Y RR2A/DIV1	Spipo23G0005800	phytozome	Spirodela_polyrhiza_Spipo23G0005800	Alismatales
Symphoricarpos occidentalis	Caprifoliaceae	Symphoricarpos_occidentalis_DIV1	Y RR2A/DIV1	FJ805351	Gene bank	Symphoricarpos_occidentalis_FJ805351	Dipsacales
Symphoricarpos occidentalis	Caprifoliaceae	Symphoricarpos_occidentalis_DIV2	Y RR2C/DIV3	FJ805352	Gene bank	Symphoricarpos_occidentalis_FJ805352	Dipsacales
Symphoricarpos orbiculatus	Caprifoliaceae	Symphoricarpos_orbiculatus_DIV2	Y RR2A/DIV1	FJ805354	Gene bank	Symphoricarpos_orbiculatus_FJ805354	Dipsacales
Symphoricarpos orbiculatus	Caprifoliaceae	Symphoricarpos_orbiculatus_DIV1	Y RR2B/DIV2	FJ805353	Gene bank	Symphoricarpos_orbiculatus_FJ805353	Dipsacales
Symphoricarpos orbiculatus	Caprifoliaceae	Symphoricarpos_orbiculatus_DIV3	Y RR2B/DIV2	FJ805355	Gene bank	Symphoricarpos_orbiculatus_FJ805355	Dipsacales
Symphoricarpos orbiculatus	Caprifoliaceae	Symphoricarpos_orbiculatus_DIV4	Y RR2B/DIV2	FJ805356	Gene bank	Symphoricarpos_orbiculatus_FJ805356	Dipsacales
Symphoricarpos orbiculatus	Caprifoliaceae	Symphoricarpos_orbiculatus_DIV5	Y RR2C/DIV3	FJ805357	Gene bank	Symphoricarpos_orbiculatus_FJ805357	Dipsacales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_protein_REVEILLE_8_like_LOC104806673	N	XM_010531674.1	Gene bank	Tarenaya_hassleriana_protein_REVEILLE_8_like_LOC104806673	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104799395	N	XM_010521901.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104799395	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104800405	N	XM_010523203.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104800405	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104810728_variant2	N	XM_010537113.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104810728_variant2	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104814904_variant1	N	XM_010543138.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104814904_variant1	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_DIVARICATA_l	N	XM_010544925.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA	Brassicales

		ike_LOC104816216				_like_LOC104816216	
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104819364_variant1	N	XM_010549397.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104819364_variant1	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104820405_variant1	N	XM_010550840.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104820405_variant1	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104823141_variant1	N	XM_010554566.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104823141_variant1	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104823386	N	XM_010554950.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104823386	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_MYB1R1_like_LOC104808319	N	XM_010533996.1	Gene bank	Tarenaya_hassleriana_transcription_factor_MYB1R1_like_LOC104808319	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_MYB1R1_like_LOC104809231	N	XM_010535133.1	Gene bank	Tarenaya_hassleriana_transcription_factor_MYB1R1_like_LOC104809231	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_MYB1R1_like_LOC104813861_variant1	N	XM_010541644.1	Gene bank	Tarenaya_hassleriana_transcription_factor_MYB1R1_like_LOC104813861_variant1	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_transcription_factor_MYB1R1_like_LOC104822074_variant1	N	XM_010553167.1	Gene bank	Tarenaya_hassleriana_transcription_factor_MYB1R1_like_LOC104822074_variant1	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_uncharacterized_LOC104798365	N	XM_010520416.1	Gene bank	Tarenaya_hassleriana_uncharacterized_LOC104798365	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_DIV3	Y RR1A	XM_010554579.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104823151	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_DIV2	Y RR1B	XM_010547974.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104818399	Brassicales
Tarenaya hassleriana	Cleomaceae	Tarenaya_hassleriana_DIV1	Y RR2B/DIV2	XM_010545445.1	Gene bank	Tarenaya_hassleriana_transcription_factor_DIVARICATA_like_LOC104816560	Brassicales
Theobroma cacao	Malvaceae	Theobroma_cacao_Duplicated_homeodomain_like_superfamily_protein_isoform_2_TCM_015926	N	XM_007039713.1	Gene bank	Theobroma_cacao_Duplicated_homeodomain_like_superfamily_protein_isoform_2_TCM_015926	Malvales

Theobroma cacao	Malvaceae	Theobroma_cacao_Duplicated_homeodomain_like_superfamily_protein_TCM_012262	N	XM_007036376.1	Gene bank	Theobroma_cacao_Duplicated_homeodomain_like_superfamily_protein_TCM_012262	Malvales
Theobroma cacao	Malvaceae	Theobroma_cacao_Thecc1EG014838	N	Thecc1EG014838	phytozome	Theobroma_cacao_Thecc1EG014838	Malvales
Theobroma cacao	Malvaceae	Theobroma_cacao_Thecc1EG015926	N	Thecc1EG015926	phytozome	Theobroma_cacao_Thecc1EG015926	Malvales
Theobroma cacao	Malvaceae	Theobroma_cacao_Thecc1EG021750	N	Thecc1EG021750	phytozome	Theobroma_cacao_Thecc1EG021750	Malvales
Theobroma cacao	Malvaceae	Theobroma_cacao_Thecc1EG037276	N	Thecc1EG037276	phytozome	Theobroma_cacao_Thecc1EG037276	Malvales
Theobroma cacao	Malvaceae	Theobroma_cacao_Thecc1EG037687	N	Thecc1EG037687	phytozome	Theobroma_cacao_Thecc1EG037687	Malvales
Theobroma cacao	Malvaceae	Theobroma_cacao_Thecc1EG041362	N	Thecc1EG041362	phytozome	Theobroma_cacao_Thecc1EG041362	Malvales
Theobroma cacao	Malvaceae	Theobroma_cacao_Thecc1EG041672	N	Thecc1EG041672	phytozome	Theobroma_cacao_Thecc1EG041672	Malvales
Theobroma cacao	Malvaceae	Theobroma_cacao_Thecc1EG042604	N	Thecc1EG042604	phytozome	Theobroma_cacao_Thecc1EG042604	Malvales
Theobroma cacao	Malvaceae	Theobroma_cacao_DIV	Y RR1A	Thecc1EG041160	Gene bank	Theobroma_cacao_Thecc1EG041160	Malvales
Torenia fournieri	Linderniaceae	Torenia_fournieri_TfDIV2_mRNA_for_DIVARICATA_like_transcription_factor	N	LC090632.1	Gene bank	Torenia_fournieri_TfDIV2_mRNA_for_DIVARICATA_like_transcription_factor	Lamiales
Torenia fournieri	Linderniaceae	Torenia_fournieri_TfDIV3_mRNA_for_MYB_like_transcription_factor	N	LC102289.1	Gene bank	Torenia_fournieri_TfDIV3_mRNA_for_MYB_like_transcription_factor	Lamiales
Torenia fournieri	Linderniaceae	Torenia_fournieri_TfDIV5_mRNA_for_MYB_like_transcription_factor	N	LC102291.1	Gene bank	Torenia_fournieri_TfDIV5_mRNA_for_MYB_like_transcription_factor	Lamiales
Torenia fournieri	Linderniaceae	Torenia_fournieri_TTfDIV1_mRNA_for_DIVARICATA_like_transcription_factor	N	LC090631.1	Gene bank	Torenia_fournieri_TTfDIV1_mRNA_for_DIVARICATA_like_transcription_factor	Lamiales
Triplostegia glandulifera	Dipsacaceae	Triplostegia_glandulifera_DIV1	Y RR2A/DIV1	FJ805358	Gene bank	Triplostegia_glandulifera_FJ805358	Dipsacales
Triplostegia glandulifera	Dipsacaceae	Triplostegia_glandulifera_DIV2	Y RR2A/DIV1	FJ805359	Gene bank	Triplostegia_glandulifera_FJ805359	Dipsacales
Triplostegia glandulifera	Dipsacaceae	Triplostegia_glandulifera_DIV3	Y RR2B/DIV2	FJ805360	Gene bank	Triplostegia_glandulifera_FJ805360	Dipsacales
Triplostegia glandulifera	Dipsacaceae	Triplostegia_glandulifera_DIV4	Y RR2C/DIV3	FJ805361	Gene bank	Triplostegia_glandulifera_FJ805361	Dipsacales
Valerianella eriocarpa	Caprifoliaceae	Valerianella_eriocarpa_DIV1	Y RR2A/DIV1	FJ805362	Gene bank	Valerianella_eriocarpa_FJ805362	Dipsacales

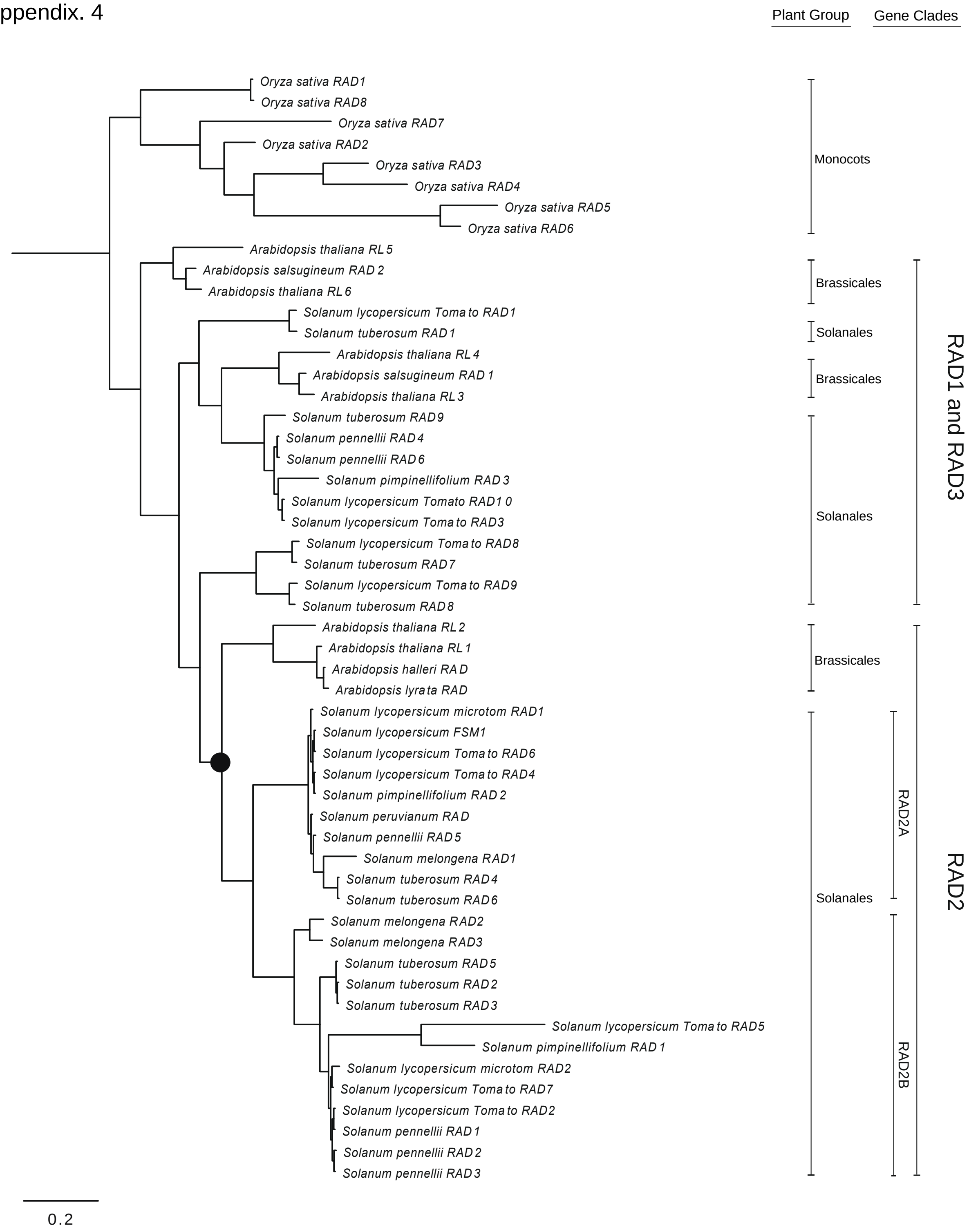
Valerianella eriocarpa	Caprifoliaceae	Valerianella_eriocarpa_DIV3	Y RR2A/DIV1	FJ805362	Gene bank	Valerianella_eriocarpa_FJ805362	Dipsacales
Valerianella eriocarpa	Caprifoliaceae	Valerianella_eriocarpa_DIV2	Y RR2B/DIV2	FJ805363	Gene bank	Valerianella_eriocarpa_FJ805363	Dipsacales
Valerianella eriocarpa	Caprifoliaceae	Valerianella_eriocarpa_DIV4	Y RR2B/DIV2	FJ805363	Gene bank	Valerianella_eriocarpa_FJ805362	Dipsacales
Valerianella locusta	Caprifoliaceae	Valerianella_locusta_DIV1	Y RR2A/DIV1	FJ805364	Gene bank	Valerianella_locusta_FJ805364	Dipsacales
Valerianella locusta	Caprifoliaceae	Valerianella_locusta_DIV2	Y RR2A/DIV1	FJ805365	Gene bank	Valerianella_locusta_FJ805365	Dipsacales
Valerianella locusta	Caprifoliaceae	Valerianella_locusta_DIV4	Y RR2A/DIV1	FJ805364	Gene bank	Valerianella_locusta_FJ805364	Dipsacales
Valerianella locusta	Caprifoliaceae	Valerianella_locusta_DIV5	Y RR2A/DIV1	FJ805366	Gene bank	Valerianella_locusta_FJ805366	Dipsacales
Valerianella locusta	Caprifoliaceae	Valerianella_locusta_DIV6	Y RR2B/DIV2	FJ805366.1	Gene bank	Valerianella_locusta_DIV2A_protein	Dipsacales
Valerianella locusta	Caprifoliaceae	Valerianella_locusta_DIV6	Y RR2B/DIV2	FJ805366.1	Gene bank	Valerianella_locusta_DIV2A_protein	Dipsacales
Valerianella locusta	Caprifoliaceae	Valerianella_locusta_DIV7	Y RR2C/DIV3	FJ805367	Gene bank	Valerianella_locusta_FJ805367	Dipsacales
Valerianella locusta	Caprifoliaceae	Valerianella_locusta_DIV8	Y RR2C/DIV3	FJ805368	Gene bank	Valerianella_locusta_FJ805368	Dipsacales
Valerianella officinalis	Caprifoliaceae	Valeriana_officinalis_DIV1	Y RR2B/DIV2	FJ805369	Gene bank	Valeriana_officinalis_FJ805369	Dipsacales
Valerianella officinalis	Caprifoliaceae	Valeriana_officinalis_DIV2	Y RR2C/DIV3	FJ805370	Gene bank	Valeriana_officinalis_FJ805370	Dipsacales
Valerianella officinalis	Caprifoliaceae	Valeriana_officinalis_DIV3	Y RR2C/DIV3	FJ805371	Gene bank	Valeriana_officinalis_FJ805371	Dipsacales
Viburnum davidiI	Adoxaceae	Viburnum_davidii_DIV1	Y RR2A/DIV1	FJ805283	Gene bank	Viburnum_davidii_FJ805283	Dipsacales
Viburnum davidiI	Adoxaceae	Viburnum_davidii_DIV2	Y RR2C/DIV3	FJ805284	Gene bank	Viburnum_davidii_FJ805284	Dipsacales
Viburnum ellipticum	Adoxaceae	Viburnum_ellipticum_DIV1	Y RR2A/DIV1	FJ805286	Gene bank	Viburnum_ellipticum_FJ805286	Dipsacales
Viburnum ellipticum	Adoxaceae	Viburnum_ellipticum_DIV2	Y RR2C/DIV3	FJ805287	Gene bank	Viburnum_ellipticum_FJ805287	Dipsacales
Viburnum jucundum	Adoxaceae	Viburnum_jucundum_DIV1	Y RR2A/DIV1	FJ805288	Gene bank	Viburnum_jucundum_FJ805288	Dipsacales
Viburnum jucundum	Adoxaceae	Viburnum_jucundum_DIV2	Y RR2A/DIV1	FJ805289	Gene bank	Viburnum_jucundum_FJ805289	Dipsacales
Viburnum jucundum	Adoxaceae	Viburnum_jucundum_DIV3	Y RR2A/DIV1	FJ805290	Gene bank	Viburnum_jucundum_FJ805290	Dipsacales

Viburnum jucundum	Adoxaceae	Viburnum_jucundum_DIV4	Y RR2C/DIV3	FJ805291	Gene bank	Viburnum_jucundum_FJ805291	Dipsacales
Viburnum prunifolium	Adoxaceae	Viburnum_prunifolium_DIV1	Y RR2A/DIV1	FJ805292	Gene bank	Viburnum_prunifolium_FJ805292	Dipsacales
Viburnum prunifolium	Adoxaceae	Viburnum_prunifolium_DIV2	Y RR2A/DIV1	FJ805293	Gene bank	Viburnum_prunifolium_FJ805293	Dipsacales
Viburnum prunifolium	Adoxaceae	Viburnum_prunifolium_DIV3	Y RR2C/DIV3	FJ805294	Gene bank	Viburnum_prunifolium_FJ805294	Dipsacales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_myb_like protein_J_LOC106769840	N	XM_014655620.1	Gene bank	Vigna_radiata_var_radiata_myb_like protein_J_LOC106769840	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_myb_like protein_J_LOC106774767	N	XM_014661805.1	Gene bank	Vigna_radiata_var_radiata_myb_like protein_J_LOC106774767	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_like_LOC106777663_varian1	N	XM_014665342.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_like_LOC106777663_varian1	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106757231	N	XM_014639857.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106757231	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106765297_variant	N	XM_014649871.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106765297_variant	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106765299	N	XM_014649873.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106765299	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106766855	N	XM_014651624.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106766855	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106776090	N	XM_014663412.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_DIVARICATA_LOC106776090	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_MYB1R1_LOC106753262	N	XM_014635051.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_MYB1R1_LOC106753262	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_MYB1R1_LOC106759549_variant1	N	XM_014642767.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_MYB1R1_LOC106759549_variant1	Fabales
Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_MYB1R1_LOC106767245_variant1	N	XM_014652093.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_MYB1R1_LOC106767245_variant1	Fabales

Vigna radiata	Fabaceae	Vigna_radiata_var_radiata_transcription_factor_MYB1R1_LOC106767808	N	XM_014652758.1	Gene bank	Vigna_radiata_var_radiata_transcription_factor_MYB1R1_LOC106767808	Fabales
Vitis vinifera	Vitaceae	Vitis_vinifera_GSVIVG01005816001	N	GSVIVG01005816001	phytozome	Vitis_vinifera_GSVIVG01005816001	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_GSVIVG01007843001	N	GSVIVG01007843001	phytozome	Vitis_vinifera_GSVIVG01007843001	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_GSVIVG01008241001	N	GSVIVG01008241001	phytozome	Vitis_vinifera_GSVIVG01008241001	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_GSVIVG01016370001	N	GSVIVG01016370001	phytozome	Vitis_vinifera_GSVIVG01016370001	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_GSVIVG01016996001	N	GSVIVG01016996001	phytozome	Vitis_vinifera_GSVIVG01016996001	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_GSVIVG01024794001	N	GSVIVG01024794001	phytozome	Vitis_vinifera_GSVIVG01024794001	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_DIV1	Y RR1A	GSVIVG01014756001	phytozome	Vitis_vinifera_GSVIVG01014756001	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_DIV3	Y RR1A	GSVIVG01036090001	phytozome	Vitis_vinifera_GSVIVG01036090001	Vitales
Vitis vinifera	Vitaceae	Vitis_vinifera_DIV2	Y RR2C/DIV3	GSVIVG01034001001	phytozome	Vitis_vinifera_GSVIVG01034001001	Vitales
Weigela hortensis	Caprifoliaceae	Weigela_hortensis_DIV1	Y RR2A/DIV1	FJ805372	Gene bank	Weigela_hortensis_FJ805372	Dipsacales
Weigela hortensis	Caprifoliaceae	Weigela_hortensis_DIV2	Y RR2A/DIV1	FJ805373	Gene bank	Weigela_hortensis_FJ805373	Dipsacales
Weigela hortensis	Caprifoliaceae	Weigela_hortensis_DIV3	Y RR2B/DIV2	FJ805374	Gene bank	Weigela_hortensis_FJ805374	Dipsacales
Weigela hortensis	Caprifoliaceae	Weigela_hortensis_DIV4	Y RR2C/DIV3	FJ805375	Gene bank	Weigela_hortensis_FJ805375	Dipsacales
Ziziphus jujuba	Rhamnaceae	Ziziphus_jujuba_transcription_factor_DIVARICATA_LOC107421964_variant1	N	XM_016031332.1	Gene bank	Ziziphus_jujuba_transcription_factor_DIVARICATA_LOC107421964_variant1	Rosales
Ziziphus jujuba	Rhamnaceae	Ziziphus_jujuba_uncharacterized_LOC107414100	N	XM_016022197.1	Gene bank	Ziziphus_jujuba_uncharacterized_LOC107414100	Rosales
Ziziphus jujuba	Rhamnaceae	Ziziphus_jujuba_uncharacterized_LOC107420077	N	XM_016028942.1	Gene bank	Ziziphus_jujuba_uncharacterized_LOC107420077	Rosales
Ziziphus jujuba	Rhamnaceae	Ziziphus_jujuba_uncharacterized_LOC107435329	N	XM_016046912.1	Gene bank	Ziziphus_jujuba_uncharacterized_LOC107435329	Rosales
Ziziphus jujuba	Rhamnaceae	Ziziphus_jujuba_uncharacterized_LOC107435334	N	XM_016046918.1	Gene bank	Ziziphus_jujuba_uncharacterized_LOC107435334	Rosales
Ziziphus jujuba	Rhamnaceae	Ziziphus_jujuba_DIV2	Y RR1C	XM_016027544.1	Gene bank	Ziziphus_jujuba_transcription_factor_DIVARICATA_LOC107418859	Rosales

Ziziphus jujuba	Rhamnaceae	Ziziphus_jujuba_DIV3	Y RR2A/DIV1	XM_016041463.1	Gene bank	Ziziphus_jujuba_transcription_factor_DIVARICATA_LOC107430601	Rosales
Ziziphus jujuba	Rhamnaceae	Ziziphus_jujuba_DIV1	Y RR2C/DIV3	XM_016015195.1	Gene bank	Ziziphus_jujuba_transcription_factor_DIVARICATA_like_LOC107407869	Rosales

Appendix. 4

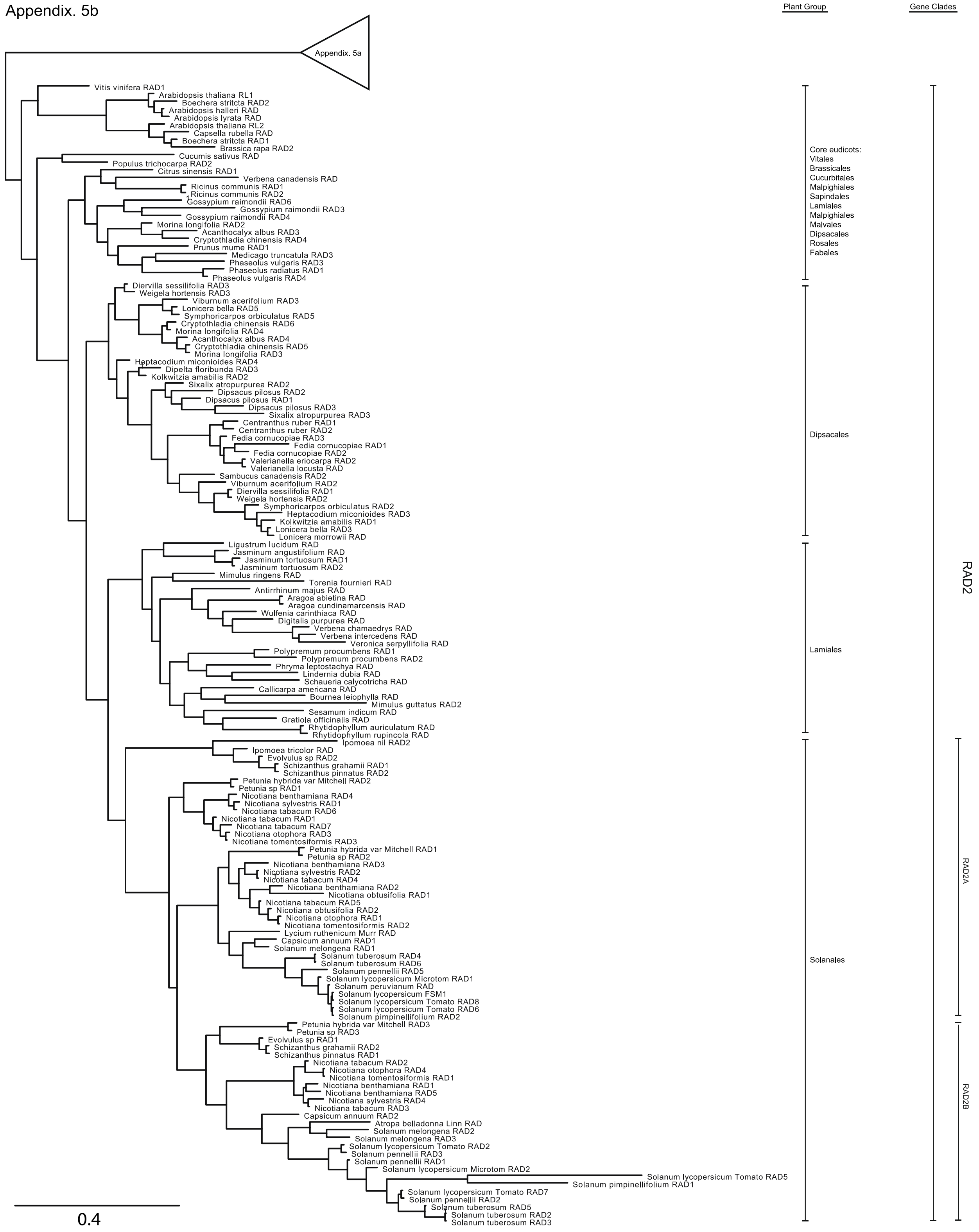

Plant Group
Gene Clades
Oryza sativa RAD1
Oryza sativa RAD8
Oryza sativa RAD7
Oryza sativa RAD2
Oryza sativa RAD3
Oryza sativa RAD4
Oryza sativa RAD5
Oryza sativa RAD6
Arabidopsis thaliana RL5
Arabidopsis salsugineum RAD2
Arabidopsis thaliana RL6
Solanum lycopersicum Tomato RAD1
Solanum tuberosum RAD1
Arabidopsis thaliana RL4
Arabidopsis salsugineum RAD1
Arabidopsis thaliana RL3
Solanum tuberosum RAD9
Solanum pennellii RAD4
Solanum pennellii RAD6
Solanum pimpinellifolium RAD3
Solanum lycopersicum Tomato RAD10
Solanum lycopersicum Tomato RAD3
Solanum lycopersicum Tomato RAD8
Solanum tuberosum RAD7
Solanum lycopersicum Tomato RAD9
Solanum tuberosum RAD8
Arabidopsis thaliana RL2
Arabidopsis thaliana RL1
Arabidopsis halleri RAD
Arabidopsis lyrata RAD
Solanum lycopersicum microtom RAD1
Solanum lycopersicum FSM1
Solanum lycopersicum Tomato RAD6
Solanum lycopersicum Tomato RAD4
Solanum pimpinellifolium RAD2
Solanum peruvianum RAD
Solanum pennellii RAD5
Solanum melongena RAD1
Solanum tuberosum RAD4
Solanum tuberosum RAD6
Solanum melongena RAD2
Solanum melongena RAD3
Solanum tuberosum RAD5
Solanum tuberosum RAD2
Solanum tuberosum RAD3
Solanum lycopersicum Tomato RAD5
Solanum pimpinellifolium RAD1
Solanum lycopersicum microtom RAD2
Solanum lycopersicum Tomato RAD7
Solanum lycopersicum Tomato RAD2
Solanum pennellii RAD1
Solanum pennellii RAD2
Solanum pennellii RAD3
Monocots
Brassicales
Solanales
Brassicales
Solanales
Brassicales
Solanales
RAD1 and RAD3
RAD2A
RAD2B
RAD2
0.2

Appendix 4. Phylogeny of *I-box-binding/RADIALIS*-like genes of four species of *Arabidopsis*, six species of *Solanum*, and *Oryza sativa* based on Bayesian inferences with branch length. All sequences from *O. sativa* form a clade, which was used to root the phylogeny. Based on the clade defined by Boyden et al. (2012), only the RAD2 clade was found to be monophyletic and contains sequences from *Arabidopsis* and *Solanum*. There are two paralogs, in RAD2 clade, RAD2A and RAD2B, of which the *Arabidopsis* does not involve in this gene duplication. RAD1 and RAD3 are paraphyletic. Index of brach length of phylogeny isat left bottom.

Appendix. 5a

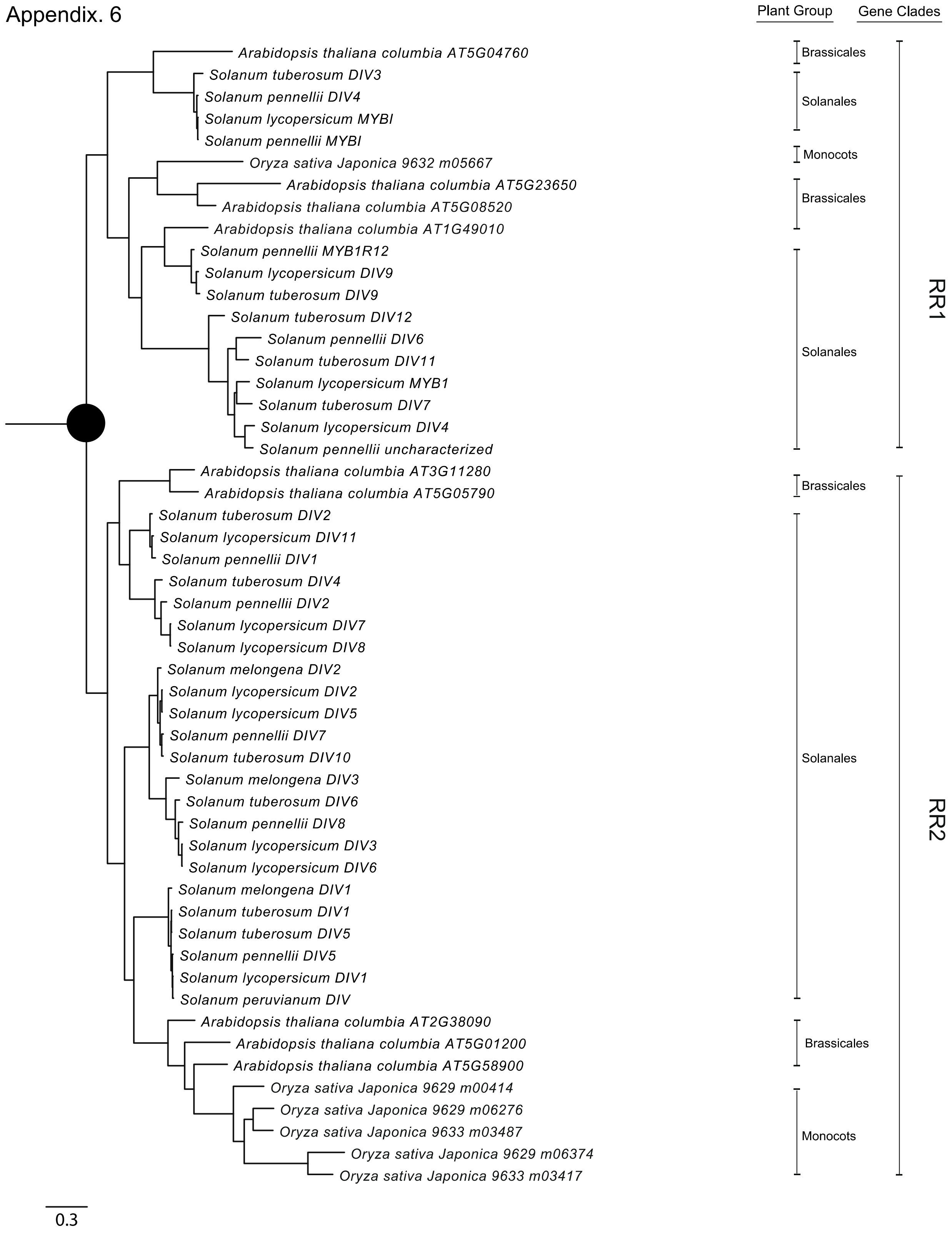

Plant Group
Gene Clades
Spirodela polyrhiza RAD
Musa acuminata RAD1
Phoenix dactylifera RAD
Setaria italica RAD3
Setaria viridis RAD2
Oryza sativa RAD2
Oryza sativa RAD8
Oryza sativa RAD7
Oryza sativa RAD3
Oryza sativ RAD4
Oryza sativa RAD5
Oryza sativa RAD6
Musa acuminata RAD3
Musa acuminata RAD2
Musa acuminata RAD4
Setaria italica RAD2
Zea mavs RAD
Panicum Pavir RAD2
Panicum Pavir_RAD3
Setaria italica RAD4
Setaria viridis RAD1
Oryza sativa RAD1
Panicum Pavir RAD1
Panicum Pavir RAD4
Setaria italica RAD1
Setaria viridis RAD3
Ipomoea nil RAD4
Ipomoea nil RAD5
Arabidopsis thaliana RL5
Arabidopsis salsugineum RAD2
Arabidopsis thaliana RL6
Gossypium raimondii RAD5
Prunus mume protein RAD2
Malus domestica RAD3
Malus domestica RAD4
Solanum lycopersicum Tomato RAD1
Solanum tuberosum RAD1
Phaseolus radiatus RAD2
Phaseolus vulgaris_RAD2
Medicago truncatula RAD1
Medicago truncatula RAD2
Phaseolus vulgaris RAD5
Glycine max RAD4
Glycine max RAD5
Nelumbo nucifera RAD
Aquilegia Aquca RAD4
Aquilegia Aquca RAD2
Aquilegia Aquca RAD3
Kalachoe marnieriana RAD
Morus notabilis RAD
Glycine max RAD1
Malus domestica RAD1
Malus domestica RAD2
Phaseolus vulgaris RAD1
Glycine max RAD2
Glycine max_RAD3
Populus trichocarpa RAD1
Eucalyptus grandis RAD
Vitis vinifera RAD2
Heptacodium miconioides RAD1
Sambucus canadensis RAD1
Symphoricarpos occidentalis RAD1
Lonicera bella RAD1
Lonicera maackii RAD
Acanthocalyx albus RAD1
Cryptothladia chinensis RAD1
Dipelta floribunda RAD1
Sixalix atropurpurea RAD1
Valerianella eriocarpa RAD1
Viburnum acerifolium RAD1
Lonicera bella RAD2
Symphoricarpos orbiculatus RAD4
Heptacodium miconioides RAD2
Diervilla sessilifolia RAD2
Weigela hortensis RAD1
Acanthocalyx albus RAD2
Cryptothladia chinensis RAD3
Dipelta floribunda RAD2
Cryptothladia chinensis RAD2
Morina longifolia RAD1
Vitis vinifera RAD3
Gossypium raimondii RAD7
Populus trichocarpa RAD3
Populus trichocarpa RAD4
Mimulus guttatus RAD1
Ipomoea nil RAD3
Capsicum annuum RAD3
Petunia hybrida var Mitchell RAD4
Solanum tuberosum RAD9
Solanum pennellii RAD4
Solanum pennellii RAD6
Solanum lycopersicum Tomato RAD10
Solanum lycopersicum Tomato RAD3
Solanum_pimpinellifolium RAD3
Nicotiana benthamiana RAD7
Nicotiana benthamiana RAD6
Nicotiana sylvestris RAD3
Nicotiana tabacum RAD9
Nicotiana tabacum RAD8
Nicotiana otophora RAD2
Nicotiana tomentosiformis RAD4
Gossypium raimondii RAD2
Arabidopsis thaliana RL4
Arabidopsis salsugineum RAD1
Brassica rapa RAD1
Arabidopsis thaliana RL3
Capsella grandiflora RAD
Antirrhinum majus RL1
Aquilegia Aquca RAD1
Gossypium raimondii RAD1
Lonicera bella RAD4
Symphoricarpos orbiculatus RAD3
Acanthocalyx albus RAD5
Cryptothladia chinensis RAD7
Morina_longifolia RAD5
Antirrhinum majus RL2
Antirrhinum majus RL3
Antirrhinum majus RL4
Ipomoea nil RAD1
Ipomoea nil RAD6
Solanum lycopersicum Tomato RAD4
Solanum tuberosum RAD7
Solanum lycopersicum Tomato RAD9
Solanum tuberosum RAD8
Appendix. 5b
0.4
Monocots
Core eudicots:
Solanales
Brassicales
Malvales
Rosales
Febales
Basal eudicots
Core eudicots:
Saxifragales
Rosales
Fabales
Malpighiales
Myrtales
Vitales
Dipsacales
Core eudicots:
Vitales
Malvales
Malpighiales
Lamiales
Solanales
Core eudicots:
Malvales
Brassicales
Dipsacales
Lamiales
Solanales
RAD1 and RAD3

Appendix. 5b


Plant Group
Gene Clades
Appendix. 5a
Vitis vinifera RAD1
Arabidopsis thaliana RL1
Boechera stritcta RAD2
Arabidopsis halleri RAD
Arabidopsis lyrata RAD
Arabidopsis thaliana RL2
Capsella rubella RAD
Boechera stritcta RAD1
Brassica rapa RAD2
Cucumis sativus RAD
Populus trichocarpa RAD2
Citrus sinensis RAD1
Verbena canadensis RAD
Ricinus communis RAD1
Ricinus communis RAD2
Gossypium raimondii RAD6
Gossypium raimondii RAD3
Gossypium raimondii RAD4
Morina longifolia RAD2
Acanthocalyx albus RAD3
Cryptothladia chinensis RAD4
Prunus mume RAD1
Medicago truncatula RAD3
Phaseolus vulgaris RAD3
Phaseolus radiatus RAD1
Phaseolus vulgaris RAD4
Diervilla sessilifolia RAD3
Weigela hortensis RAD3
Viburnum acerifolium RAD3
Lonicera bella RAD5
Symphoricarpos orbiculatus RAD5
Cryptothladia chinensis RAD6
Morina longifolia RAD4
Acanthocalyx albus RAD4
Cryptothladia chinensis RAD5
Morina longifolia RAD3
Heptacodium miconioides RAD4
Dipelta floribunda RAD3
Kolkwitzia amabilis RAD2
Sixalix atropurpurea RAD2
Dipsacus pilosus RAD2
Dipsacus pilosus RAD1
Dipsacus pilosus RAD3
Sixalix atropurpurea RAD3
Centranthus ruber RAD1
Centranthus ruber RAD2
Fedia cornucopiae RAD3
Fedia cornucopiae RAD1
Fedia cornucopiae RAD2
Valerianella eriocarpa RAD2
Valerianella locusta RAD
Sambucus canadensis RAD2
Viburnum acerifolium RAD2
Diervilla sessilifolia RAD1
Weigela hortensis RAD2
Symphoricarpos orbiculatus RAD2
Heptacodium miconioides RAD3
Kolkwitzia amabilis RAD1
Lonicera bella RAD3
Lonicera morrowii RAD
Ligustrum lucidum RAD
Jasminum angustifolium RAD
Jasminum tortuosum RAD1
Jasminum tortuosum RAD2
Mimulus ringens RAD
Torenia fournieri RAD
Antirrhinum majus RAD
Aragoa abietina RAD
Aragoa cundinamarcensis RAD
Wulfenia carinthiaca RAD
Digitalis purpurea RAD
Verbena chamaedrys RAD
Verbena intercedens RAD
Veronica serpyllifolia RAD
Polypremum procumbens RAD1
Polypremum procumbens RAD2
Phryma leptostachya RAD
Lindernia dubia RAD
Schaueria calycotricha RAD
Callicarpa americana RAD
Bournea leiophylla RAD
Mimulus guttatus RAD2
Sesamum indicum RAD
Gratiola officinalis RAD
Rhytidophyllum auriculatum RAD
Rhytidophyllum rupincola RAD
Ipomoea nil RAD2
Ipomoea tricolor RAD
Evolvulus sp RAD2
Schizanthus grahamii RAD1
Schizanthus pinnatus RAD2
Petunia hybrida var Mitchell RAD2
Petunia sp RAD1
Nicotiana benthamiana RAD4
Nicotiana sylvestris RAD1
Nicotiana tabacum RAD6
Nicotiana tabacum RAD1
Nicotiana tabacum RAD7
Nicotiana otophora RAD3
Nicotiana tomentosiformis RAD3
Petunia hybrida var Mitchell RAD1
Petunia sp RAD2
Nicotiana benthamiana RAD3
Nicotiana sylvestris RAD2
Nicotiana tabacum RAD4
Nicotiana benthamiana RAD2
Nicotiana obtusifolia RAD1
Nicotiana tabacum RAD5
Nicotiana obtusifolia RAD2
Nicotiana otophora RAD1
Nicotiana tomentosiformis RAD2
Lycium ruthenicum Murr RAD
Capsicum annuum RAD1
Solanum melongena RAD1
Solanum tuberosum RAD4
Solanum tuberosum RAD6
Solanum pennellii RAD5
Solanum lycopersicum Microtom RAD1
Solanum peruvianum RAD
Solanum lycopersicum FSM1
Solanum lycopersicum Tomato RAD8
Solanum lycopersicum Tomato RAD6
Solanum pimpinellifolium RAD2
Petunia hybrida var Mitchell RAD3
Petunia sp RAD3
Evolvulus sp RAD1
Schizanthus grahamii RAD2
Schizanthus pinnatus RAD1
Nicotiana tabacum RAD2
Nicotiana otophora RAD4
Nicotiana tomentosiformis RAD1
Nicotiana benthamiana RAD1
Nicotiana benthamiana RAD5
Nicotiana sylvestris RAD4
Nicotiana tabacum RAD3
Capsicum annuum RAD2
Atropa belladonna Linn RAD
Solanum melongena RAD2
Solanum melongena RAD3
Solanum lycopersicum Tomato RAD2
Solanum pennellii RAD3
Solanum pennellii RAD1
Solanum lycopersicum Microtom RAD2
Solanum lycopersicum Tomato RAD5
Solanum pimpinellifolium RAD1
Solanum lycopersicum Tomato RAD7
Solanum pennellii RAD2
Solanum tuberosum RAD5
Solanum tuberosum RAD2
Solanum tuberosum RAD3
0.4
Core eudicots:
Vitales
Brassicales
Cucurbitales
Malpighiales
Sapindales
Lamiales
Malpighiales
Malvales
Dipsacales
Rosales
Fabales
Dipsacales
Lamiales
Solanales
RAD2
RAD2A
RAD2B

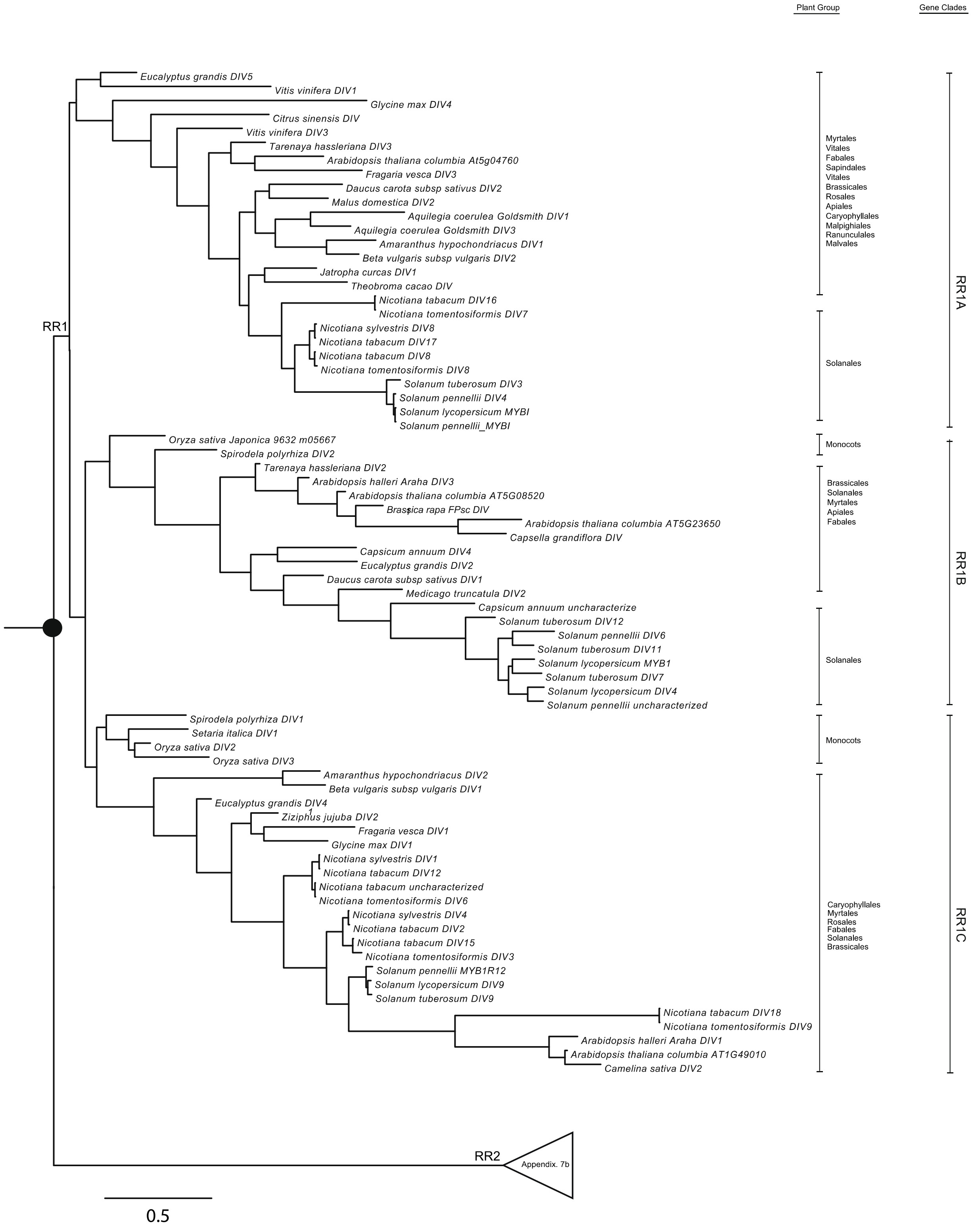
Appendix 5. Phylogeny of *I-box-binding/RADIALIS*-like genes based on Bayesian inferences with branch length. 274 CDS of *I-box-binding/RADIALIS*-like genes from both monocots and dicots were analyzed. All sequences from monocots formed a monophyletic group, which was used to root the phylogeny. RAD2 forms a clade. At least one gene duplication was identified in the common ancestor of Solanaceae and Convolvulaceae. RAD1 and RAD3 are paraphyletic. Index of brach length of phylogeny isat left bottom.

Appendix. 6


Plant Group
Gene Clades
Arabidopsis thaliana columbia AT5G04760
Solanum tuberosum DIV3
Solanum pennellii DIV4
Solanum lycopersicum MYBI
Solanum pennellii MYBI
Oryza sativa Japonica 9632 m05667
Arabidopsis thaliana columbia AT5G23650
Arabidopsis thaliana columbia AT5G08520
Arabidopsis thaliana columbia AT1G49010
Solanum pennellii MYB1R12
Solanum lycopersicum DIV9
Solanum tuberosum DIV9
Solanum tuberosum DIV12
Solanum pennellii DIV6
Solanum tuberosum DIV11
Solanum lycopersicum MYB1
Solanum tuberosum DIV7
Solanum lycopersicum DIV4
Solanum pennellii uncharacterized
Arabidopsis thaliana columbia AT3G11280
Arabidopsis thaliana columbia AT5G05790
Solanum tuberosum DIV2
Solanum lycopersicum DIV11
Solanum pennellii DIV1
Solanum tuberosum DIV4
Solanum pennellii DIV2
Solanum lycopersicum DIV7
Solanum lycopersicum DIV8
Solanum melongena DIV2
Solanum lycopersicum DIV2
Solanum lycopersicum DIV5
Solanum pennellii DIV7
Solanum tuberosum DIV10
Solanum melongena DIV3
Solanum tuberosum DIV6
Solanum pennellii DIV8
Solanum lycopersicum DIV3
Solanum lycopersicum DIV6
Solanum melongena DIV1
Solanum tuberosum DIV1
Solanum tuberosum DIV5
Solanum pennellii DIV5
Solanum lycopersicum DIV1
Solanum peruvianum DIV
Arabidopsis thaliana columbia AT2G38090
Arabidopsis thaliana columbia AT5G01200
Arabidopsis thaliana columbia AT5G58900
Oryza sativa Japonica 9629 m00414
Oryza sativa Japonica 9629 m06276
Oryza sativa Japonica 9633 m03487
Oryza sativa Japonica 9629 m06374
Oryza sativa Japonica 9633 m03417
Brassicales
Solanales
Monocots
Brassicales
Solanales
RR1
Brassicales
Solanales
RR2
Brassicales
Monocots
0.3

Appendix 6. Phylogeny of *R-R-type* genes of five species of *Solanum*, *Arabidopsis thaliana*, and *Oryza sativa* based on Bayesian inferences with branch length. Two major clades, RR1 and RR2 were identified, each of which includes sequences from *Arabidopsis*, *Oryza*, and *Solanaum*. Index of brach length of phylogeny is at left bottom.

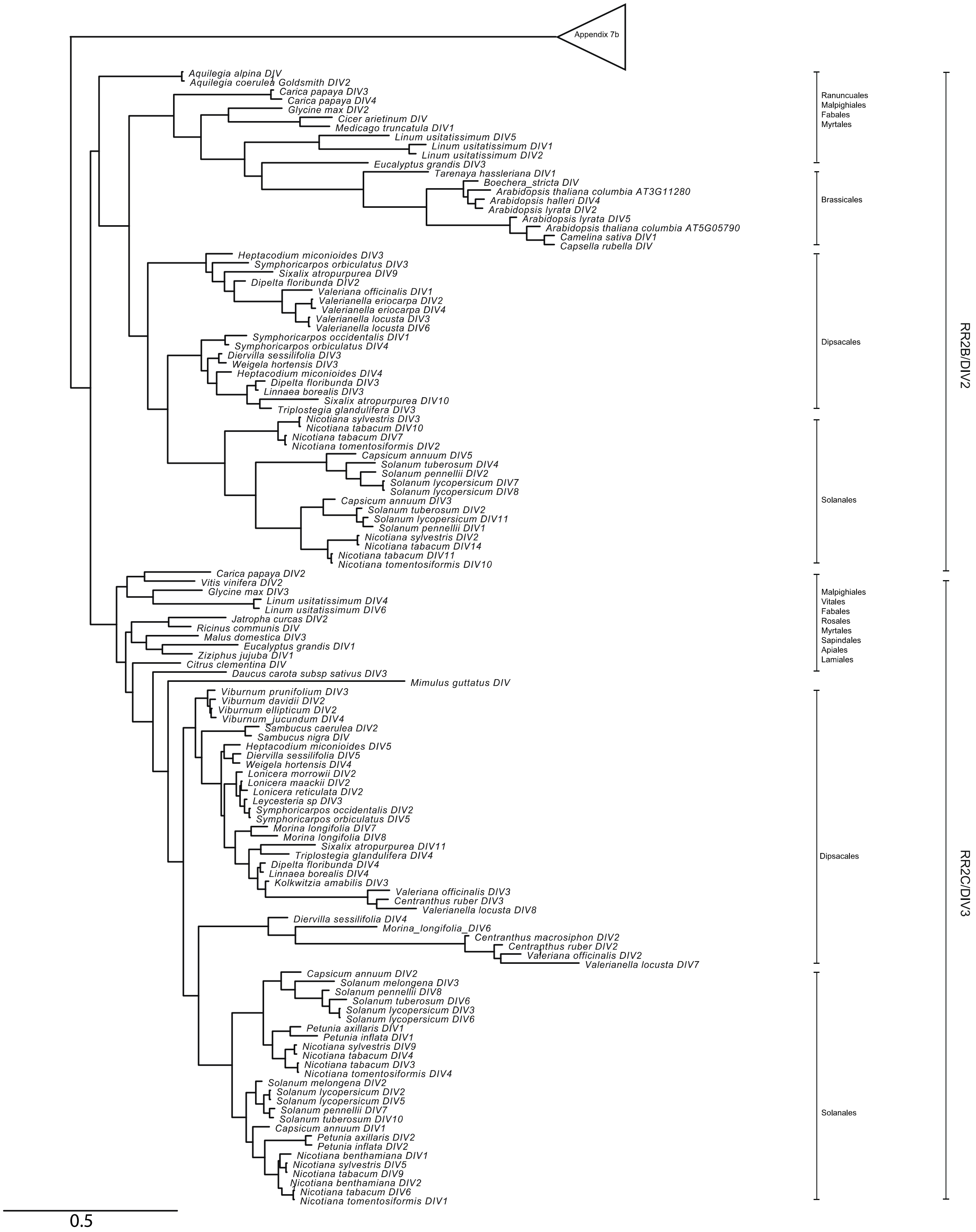
Appendix. 7a


Plant Group
Gene Clades
Eucalyptus grandis DIV5
Vitis vinifera DIV1
Glycine max DIV4
Citrus sinensis DIV
Vitis vinifera DIV3
Tarenaya hassleriana DIV3
Arabidopsis thaliana columbia At5g04760
Fragaria vesca DIV3
Daucus carota subsp sativus DIV2
Malus domestica DIV2
Aquilegia coerulea Goldsmith DIV1
Aquilegia coerulea Goldsmith DIV3
Amaranthus hypochondriacus DIV1
Beta vulgaris subsp vulgaris DIV2
Jatropha curcas DIV1
Theobroma cacao DIV
Nicotiana tabacum DIV16
Nicotiana tomentosiformis DIV7
Nicotiana sylvestris DIV8
Nicotiana tabacum DIV17
Nicotiana tabacum DIV8
Nicotiana tomentosiformis DIV8
Solanum tuberosum DIV3
Solanum pennellii DIV4
Solanum lycopersicum MYBI
Solanum pennellii_MYBI
Myrtales
Vitales
Fabales
Sapindales
Vitales
Brassicales
Rosales
Apiales
Caryophyllales
Malpighiales
Ranunculales
Malvales
Solanales
RR1A
RR1
Oryza sativa Japonica 9632 m05667
Spirodela polyrhiza DIV2
Tarenaya hassleriana DIV2
Arabidopsis halleri Araha DIV3
Arabidopsis thaliana columbia AT5G08520
Brassica rapa FPsc DIV
Arabidopsis thaliana columbia AT5G23650
Capsella grandiflora DIV
Capsicum annuum DIV4
Eucalyptus grandis DIV2
Daucus carota subsp sativus DIV1
Medicago truncatula DIV2
Capsicum annuum uncharacterize
Solanum tuberosum DIV12
Solanum pennellii DIV6
Solanum tuberosum DIV11
Solanum lycopersicum MYB1
Solanum tuberosum DIV7
Solanum lycopersicum DIV4
Solanum pennellii uncharacterized
Monocots
Brassicales
Solanales
Myrtales
Apiales
Fabales
Solanales
RR1B
Spirodela polyrhiza DIV1
Setaria italica DIV1
Oryza sativa DIV2
Oryza sativa DIV3
Amaranthus hypochondriacus DIV2
Beta vulgaris subsp vulgaris DIV1
Eucalyptus grandis DIV4
1
Ziziphus jujuba DIV2
Fragaria vesca DIV1
Glycine max DIV1
Nicotiana sylvestris DIV1
Nicotiana tabacum DIV12
Nicotiana tabacum uncharacterized
Nicotiana tomentosiformis DIV6
Nicotiana sylvestris DIV4
Nicotiana tabacum DIV2
Nicotiana tabacum DIV15
Nicotiana tomentosiformis DIV3
Solanum pennellii MYB1R12
Solanum lycopersicum DIV9
Solanum tuberosum DIV9
Nicotiana tabacum DIV18
Nicotiana tomentosiformis DIV9
Arabidopsis halleri Araha DIV1
Arabidopsis thaliana columbia AT1G49010
Camelina sativa DIV2
Monocots
Caryophyllales
Myrtales
Rosales
Fabales
Solanales
Brassicales
RR1C
RR2
Appendix. 7b
0.5

Appendix. 7b


Plant Group
Gene Clades
RR1
Appendix. 7a
RR2
Setaria viridis DIV4
Oryza sativa Japonica 9629 m06374
Oryza sativa DIV6
Setaria viridis DIV3
Oryza sativa Japonica 9633 m03417
Oryza sativa DIV4
Spirodela polyrhiza DIV3
Oryza sativa Japonica 9629 m00414
Oryza sativa DIV1
Oryza sativa Japonica 9629 m06276
Oryza sativa DIV5
Setaria viridis DIV2
Oryza sativa Japonica 9633 m03487
Oryza sativa DIV7
Arabidopsis lyrata DIV4
Arabidopsis thaliana columbia AT5G58900
Arabidopsis lyrata DIV3
Arabidopsis thaliana columbia AT2G38090
Arabidopsis thaliana columbia AT5G01200
Arabidopsis halleri DIV2
Arabidopsis lyrata DIV1
Linum usitatissimum DIV3
Linum usitatissimum DIV7
Carica papaya DIV1
Ziziphus jujuba DIV3
Fragaria vesca DIV2
Malus domestica DIV1
Diervilla sessilifolia DIV2
Weigela hortensis DIV2
Symphoricarpos orbiculatus DIV2
Leycesteria sp DIV2
Lonicera morrowii DIV1
Heptacodium miconioides DIV2
Linnaea borealis DIV2
Dipelta floribunda DIV1
Kolkwitzia amabilis DIV2
Morina longifolia DIV5
Morina longifolia DIV3
Morina longifolia DIV4
Sixalix atropurpurea DIV8
Triplostegia glandulifera DIV2
Centranthus macrosiphon DIV1
Centranthus ruber DIV1
Valerianella eriocarpa DIV1
Valerianella eriocarpa DIV3
Fedia cornucopiae DIV2
Fedia cornucopiae DIV1
Valerianella locusta DIV2
Valerianella locusta DIV5
Daucus carota subsp sativus DIV4
Antirrhinum majus DIV
Petunia axillaris DIV3
Petunia inflata DIV3
Petunia inflata DIV4
Solanum melongena DIV1
Solanum tuberosum DIV5
Solanum tuberosum DIV1
Solanum lycopersicum DIV1
Solanum pennellii DIV5
Solanum peruvianum DIV
Nicotiana tabacum DIV1
Nicotiana tomentosiformis DIV5 1
Nicotiana tomentosiformis DIV5
Nicotiana tomentosiformis DIV5 2
Nicotiana tabacum DIV5
Nicotiana benthamiana DIV3
Nicotiana sylvestris DIV7
Nicotiana sylvestris DIV6
Nicotiana tabacum DIV13
Sambucus caerulea DIV1
Sambucus canadensis DIV2
Sambucus canadensis DIV3
Viburnum prunifolium DIV2
Viburnum davidii DIV1
Viburnum ellipticum DIV1
Viburnum jucundum DIV3
Sambucus canadensis DIV1
Viburnum prunifolium DIV1
Viburnum jucundum DIV1
Viburnum jucundum DIV2
Diervilla sessilifolia DIV1
Weigela hortensis DIV1
Heptacodium miconioides DIV1
Symphoricarpos orbiculatus DIV1
Leycesteria sp DIV1
Lonicera maackii DIV1
Lonicera reticulata DIV1
Valerianella locusta DIV1
Valerianella locusta DIV4
Linnaea borealis DIV1
Kolkwitzia amabilis DIV1
Morina longifolia DIV1
Morina longifolia DIV2
Triplostegia glandulifera DIV1
Sixalix atropurpurea DIV1
Sixalix atropurpurea DIV2
Sixalix atropurpurea DIV5
Sixalix atropurpurea DIV3
Sixalix atropurpurea DIV4
Sixalix atropurpurea DIV6
Sixalix atropurpurea DIV7
Appendix. 7c
Monocots
Brassicales
Malpighiales
Rosale
Dipsacales
Apiales/Lamiales
Solanales
Dipsacales
RR2A/DIV1
0.5

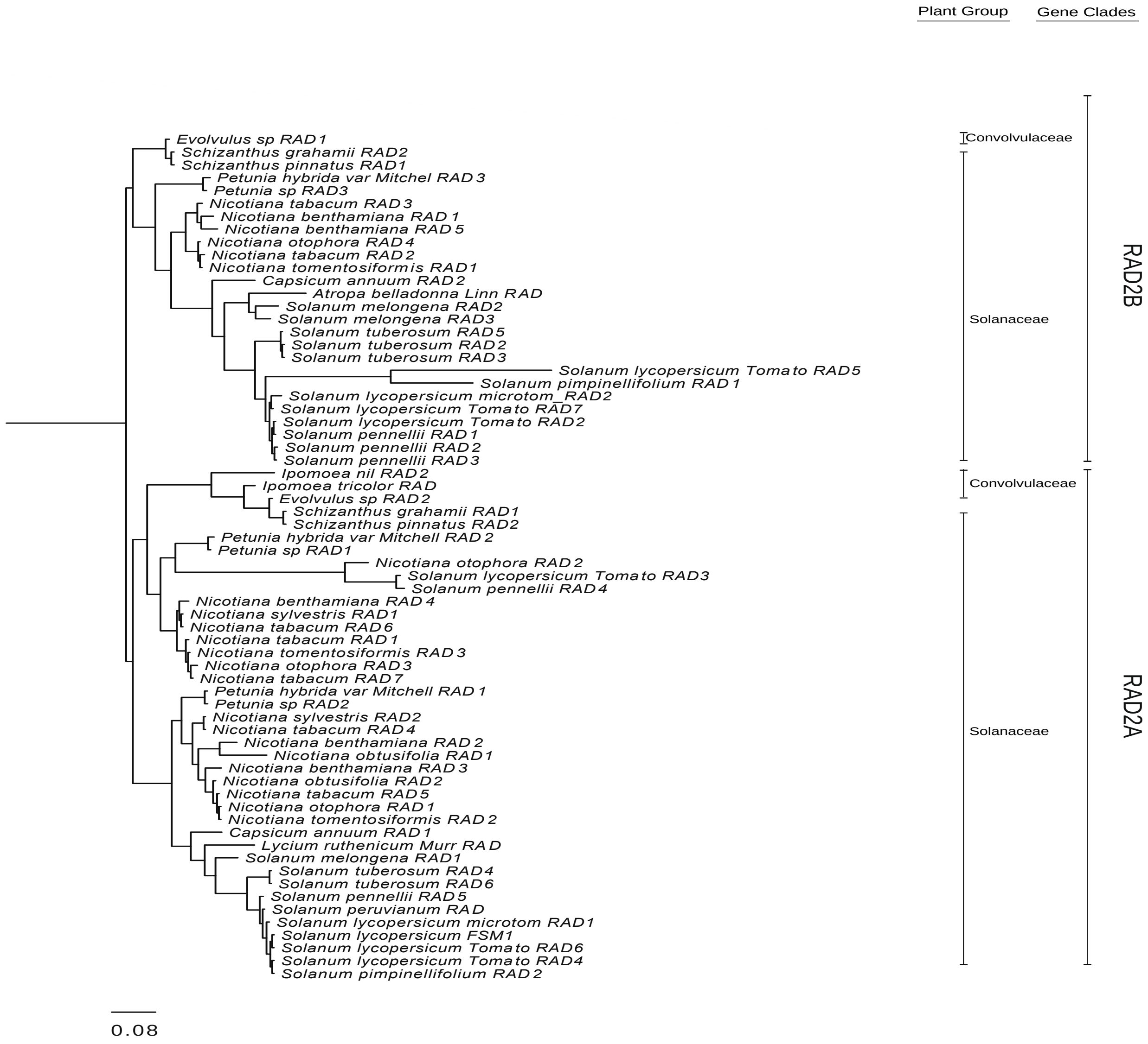
Appendix. 7c


Plant Group
Gene Clades
Appendix 7b
Aquilegia alpina DIV
Aquilegia coerulea Goldsmith DIV2
Carica papaya DIV3
Carica papaya DIV4
Glycine max DIV2
Cicer arietinum DIV
Medicago truncatula DIV1
Linum usitatissimum DIV5
Linum usitatissimum DIV1
Linum usitatissimum DIV2
Eucalyptus grandis DIV3
Tarenaya hassleriana DIV1
Boechera_stricta DIV
Arabidopsis thaliana columbia AT3G11280
Arabidopsis halleri DIV4
Arabidopsis lyrata DIV2
Arabidopsis lyrata DIV5
Arabidopsis thaliana columbia AT5G05790
Camelina sativa DIV1
Capsella rubella DIV
Heptacodium miconioides DIV3
Symphoricarpos orbiculatus DIV3
Sixalix atropurpurea DIV9
Dipelta floribunda DIV2
Valeriana officinalis DIV1
Valerianella eriocarpa DIV2
Valerianella eriocarpa DIV4
Valerianella locusta DIV3
Valerianella locusta DIV6
Symphoricarpos occidentalis DIV1
Symphoricarpos orbiculatus DIV4
Diervilla sessilifolia DIV3
Weigela hortensis DIV3
Heptacodium miconioides DIV4
Dipelta floribunda DIV3
Linnaea borealis DIV3
Sixalix atropurpurea DIV10
Triplostegia glandulifera DIV3
Nicotiana sylvestris DIV3
Nicotiana tabacum DIV10
Nicotiana tabacum DIV7
Nicotiana tomentosiformis DIV2
Capsicum annuum DIV5
Solanum tuberosum DIV4
Solanum pennellii DIV2
Solanum lycopersicum DIV7
Solanum lycopersicum DIV8
Capsicum annuum DIV3
Solanum tuberosum DIV2
Solanum lycopersicum DIV11
Solanum pennellii DIV1
Nicotiana sylvestris DIV2
Nicotiana tabacum DIV14
Nicotiana tabacum DIV11
Nicotiana tomentosiformis DIV10
Carica papaya DIV2
Vitis vinifera DIV2
Glycine max DIV3
Linum usitatissimum DIV4
Linum usitatissimum DIV6
Jatropha curcas DIV2
Ricinus communis DIV
Malus domestica DIV3
Eucalyptus grandis DIV1
Ziziphus jujuba DIV1
Citrus clementina DIV
Daucus carota subsp sativus DIV3
Mimulus guttatus DIV
Viburnum prunifolium DIV3
Viburnum davidii DIV2
Viburnum ellipticum DIV2
Viburnum_jucundum DIV4
Sambucus caerulea DIV2
Sambucus nigra DIV
Heptacodium miconioides DIV5
Diervilla sessilifolia DIV5
Weigela hortensis DIV4
Lonicera morrowii DIV2
Lonicera maackii DIV2
Lonicera reticulata DIV2
Leycesteria sp DIV3
Symphoricarpos occidentalis DIV2
Symphoricarpos orbiculatus DIV5
Morina longifolia DIV7
Morina longifolia DIV8
Sixalix atropurpurea DIV11
Triplostegia glandulifera DIV4
Dipelta floribunda DIV4
Linnaea borealis DIV4
Kolkwitzia amabilis DIV3
Valeriana officinalis DIV3
Centranthus ruber DIV3
Valerianella locusta DIV8
Diervilla sessilifolia DIV4
Morina_longifolia_DIV6
Centranthus macrosiphon DIV2
Centranthus ruber DIV2
Valeriana officinalis DIV2
Valerianella locusta DIV7
Capsicum annuum DIV2
Solanum melongena DIV3
Solanum pennellii DIV8
Solanum tuberosum DIV6
Solanum lycopersicum DIV3
Solanum lycopersicum DIV6
Petunia axillaris DIV1
Petunia inflata DIV1
Nicotiana sylvestris DIV9
Nicotiana tabacum DIV4
Nicotiana tabacum DIV3
Nicotiana tomentosiformis DIV4
Solanum melongena DIV2
Solanum lycopersicum DIV2
Solanum lycopersicum DIV5
Solanum pennellii DIV7
Solanum tuberosum DIV10
Capsicum annuum DIV1
Petunia axillaris DIV2
Petunia inflata DIV2
Nicotiana benthamiana DIV1
Nicotiana sylvestris DIV5
Nicotiana tabacum DIV9
Nicotiana benthamiana DIV2
Nicotiana tabacum DIV6
Nicotiana tomentosiformis DIV1
Ranuncuales
Malpighiales
Fabales
Myrtales
Brassicales
Dipsacales
Solanales
Malpighiales
Vitales
Fabales
Rosales
Myrtales
Sapindales
Apiales
Lamiales
Dipsacales
Solanales
RR2B/DIV2
RR2C/DIV3
0.5

Appendix 7. Phylogeny of *R-R-type* genes based on Bayesian inferences with branch length.

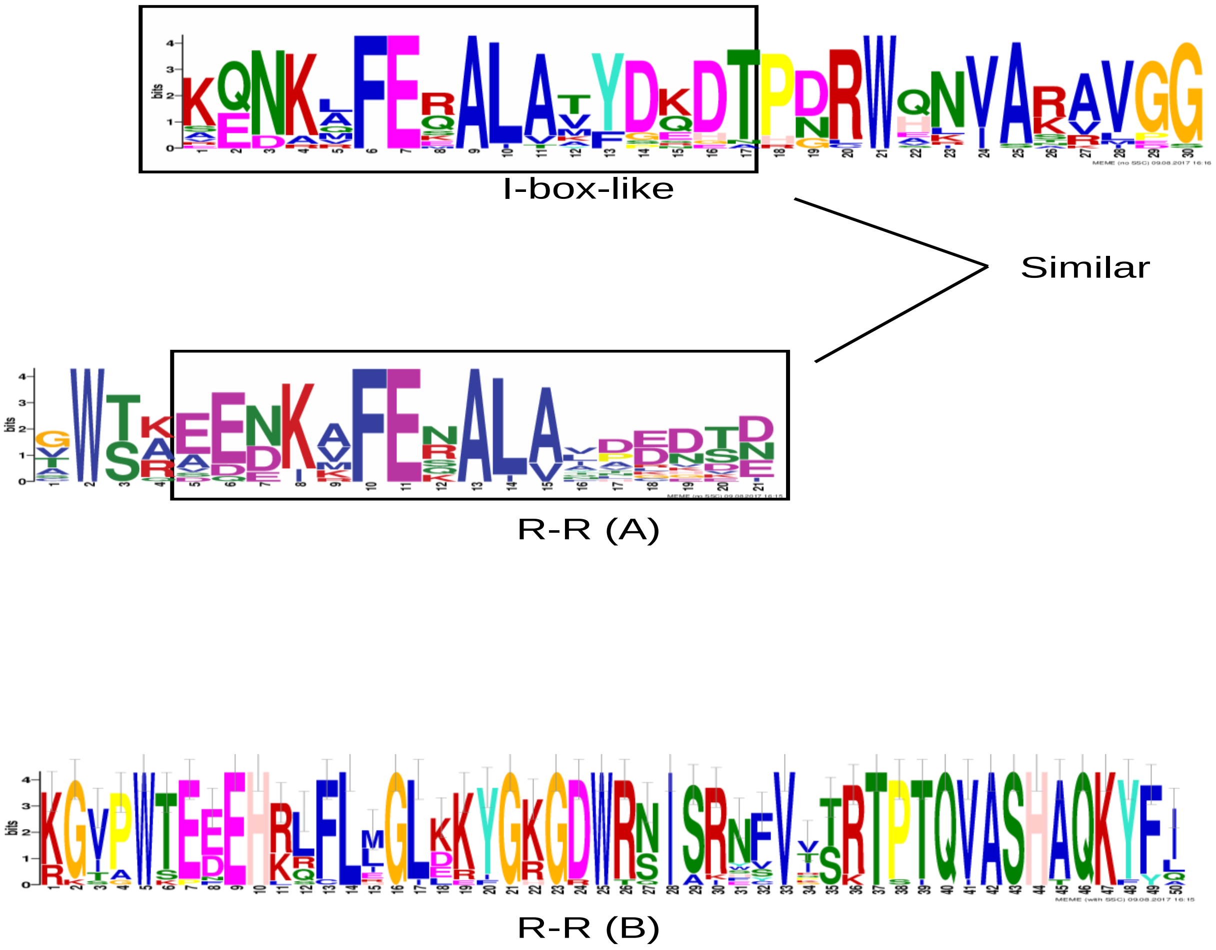
A lot of 298 CDS of *R-R-type* genes from both monocots and dicots were analyzed, which form two major clades, RR1 and RR2/DIV. Each of these clades contains sequences from monocots and dicots. The RR1 clade was further divided into three groups, RR1A, RR1B, and RR1C. For the three RR2/DIV clades identified by Howarth and Donoghue (2009), only the DIV2 and DIV3 are monophyletic. The *Arabidopsis* sequences included AT2G38090, AT5G01200, and AT5G58900 identified as DIV1, which is not a clade in this phylogeny. Index of brach length of phylogeny is at left bottom.

Appendix. 8



Appendix 8. Phylogeny of RAD2 clade of Solanaceae and Convolvulaceae based on Bayesian inferences with branch length. The unrooted tree shows the two clades, each of these including both sequences from Solanaceae and Convolvulaceae. Index of brach length of phylogeny is at left bottom.

Appendix. 9



Appendix 9. Motifs of I-box-like and R-R-type myb gene subfamilies. The motifs of I-box-like subfamily (One domain), and R-R-type subfamily (two domains: R-R (A) and R-R (B)).

Apppentix 10. Manuscript submitted for publication at IJMS.

International Journal of
Molecular Sciences

Article

Evolution of antagonistic relationships in proteins: a case study of *RAD*- and *DIV*-like genes in plants

Ao Gao[1], and Wenheng Zhang[1,*]

[1] Department of Biology, Virginia Commonwealth University, 1000 West Cary Street, Richmond, Virginia 23284, USA; gaoa2@mymail.vcu.edu; wzhang5@vcu.edu

* Correspondence: wzhang5@vcu.edu; Tel.: +1-804-828-0798

Received: date; Accepted: date; Published: date

Abstract: The antagonistic relationship of proteins describes the hostile interactions that result in one protein suppressing the function of another. Developmental genetic studies of *Antirrhinum majus* demonstrated that two transcription factors from the MYB gene family, *RADIALIS* (*RAD*) and *DIVIRICATA* (*DIV*), interact through antagonism to regulate floral dorsoventral asymmetry. Interestingly, similar antagonistic interactions were found among proteins of FSM1 (RAD-like), MYBI (DIV-like) in *Solanum lycopersicum*, which is involved in fruit development. Here, we report on the homology of these antagonistic MYB proteins based on reconstruction of the phylogeny of I-box-like and R-R-type clades, where *RAD*- and *DIV*-like belong, respectively. The results show that there are likely three paralogs of *RAD-I/I-box*-like genes, *RAD1, RAD2,* and *RAD3*, which originated in the common ancestor of the core eudicots. In contrast, R-R-type sequences fall into two major clades, *RR1* and *RR2,* the result of gene duplication in the common ancestor of both monocots and dicots. *RR1* was divided into clades, *RR1A*, *RR1B*, and *RR1C*, while *RR2* into clades, *RR2A/DIV1*, *RR2B/DIV2*, and *RR2C/DIV3*. We demonstrate that among similar antagonistic interactions in *A. majus* and *So. lycopersicum*, *RAD*-like genes originate from the RAD2 clade, while *DIV*-like genes originate from distantly related paralogs of the R-R-type lineage.

Keywords: *RADIALIS*-like genes; *DIVIRICATA*-like genes; gene duplication; angiosperms; phylogeny; antagonism of proteins; MYB gene family

---

1. Introduction

Antagonism is a type of competitive relationship among molecules, which is a key mechanism used for regulating development in organisms [1-3]. When antagonist and agonist molecules compete for the target site of the receptor, the binding of the antagonist to the site will prevent the binding of the agonist. The antagonist, therefore, blocks the biological function of the agonist and the receptor [1-3]. How the proteins involved in the antagonistic relationships evolve as a whole system still awaits to be revealed.

In plants, one such example has been found in the regulation of the development of floral symmetry in the Lamiales [4]. In the zygomorphic flowers of *Antirrhinum majus* L. the two dorsal petals are significantly enlarged compared to the lateral and ventral petals and the single dorsal stamen is aborted [5]. Two genes, *CYCLOIDEA* (*CYC*) and *DICHOTOMA* (*DICH*), belonging to the *CYC/TB1* clade of the TCP transcription factor family, were found to promote the dorsal identity of zygomorphic flowers [5-8]. *RADIALIS* (*RAD*), a member of the MYB gene family, was found to be the downstream target of *CYC* and *DICH* [9-11]. Plants of the double *cyc/dich* or the single *rad* mutants produce flowers that have entirely or partially lost their dorsal identity [5,10]. The dorsal petals assume the ventral petal identity and the aborted dorsal stamen becomes functional [5]. *DIVARICATA* (*DIV*), a member of a different MYB lineage, promotes ventral floral identity [12]. A single *div* mutant causes the loss of the ventral petal identity [12,13]. In the *cyc/dich/div* triple mutant, where the function of both the dorsal and ventral identity genes was lost, all petals resume the lateral petal identity [12,13].

Recently, antagonism involving three MYB-like proteins was found to be a mechanism regulating floral symmetry in the flowers of *Antirrhinum* [4]. Despite the role of *DIV* in controlling ventral petal identity, its mRNA is transcribed across the floral meristem [12,13]. RAD was found to be the dorsal factor inactivating DIV, but not at the transcriptional level [4,13]. Interestingly, it was found that RAD and DIV do not directly interact with each other, but compete for their protein target, DIV-and-RAD-interacting-factors (DRIFs), also members of MYB family [4]. In particular, DIV and DRIFs show overlapping expression patterns and can form heterodimer complexes that bind to DNA of *DIV*, suggesting regulation of its transcription. RAD inhibits the interaction between DIV and DRIFs in the dorsal regions of the flowers of *Antirrhinum* by either binding directly to a DRIF protein in the nucleus or/and by sequestering the DRIF proteins in the cytoplasm [4]. Therefore, RAD acts as the antagonist that blocks the binding of DIV, the agonist, with the DRIFs, which is required for regulating ventral symmetry in the flowers of *Antirrhinum*.

Similar antagonistic relationships involving three MYB homologs were reported in fruit development of *Solanum lycopersicum* L. [14]. The fruit SANT/MYB binding protein1 (FSB1), a DRIF homolog, was found to form a protein complex with the transcription factor MYBI, a DIV homolog. The fruit SANT/MYB-like (FSM1) protein, a RAD homolog, competes for FSB1 with MYBI. The function of FSM1 is to reduce fruit size and preferentially restricts differential cell expansion [14]. Ectopic expression of FSM1 results in a reduction in organ size by negatively affecting cell expansion. In contrast, FSB1 positively regulates differential cell expansion through physical interaction with MYBI [14]. This is analogous with the competition between RAD and the DIV-DRIF complex in the dorsal regions of the flowers of *Antirrhinum*. The function for the FSM1-FSB1-MYBI complex in tomato controls cell expansion, while RAD-DRIF-DIV similarly also controls cell expansion in regulating dorsoventral flower asymmetry in snapdragon [4,14].

Previous works indicated frequent gene duplications during the evolution of *RAD*- and *DIV*-like genes [15,16]. Three paralogs of the RAD lineage, RAD1, RAD2, and RAD3, and three paralogs of the DIV lineage, DIV1, DIV2, and DIV3, are recognized [15,16]. The gene duplications that gave rise to these paralogs were predicted to have occurred around the diversification of the Pentapetalae. There, therefore, may exist antagonistic relationships among the homologs of RAD-DRIF-DIV in diverse lineages of the core eudicots. DRIFs, one of the three factors involved in this antagonistic interaction, belong to an ancient MYB-like protein family with several homologs also found in the moss *Physcomitrella patens* [4]. Two paralogs of DRIFs resulting from gene duplication at least in the common ancestor of monocots and dicots are named Group 1 and 2 [4]. The DRIF1 and DRIF2 of *A. majus* belong to Group 1, while the only DRIF-like protein (SlFSB1) found in *So. lycopersicum* belongs to Group 2. Therefore, in the antagonized systems in *An. majus* and *So. lycopersicum*, the DRIF homologs involved belong to two paralogous clades.

Here, we report on the evolution of the I-box-like and R-R-type gene lineages where *RAD*- and *DIV*-like genes belong, respectively, and aim to (1) reconstruct the phylogeny of the two MYB lineages, (2) clarify the phylogenetic relationships of the paralogs, and (3) identify the homology of *RAD*- and *DIV*-like genes that form the antagonistic relationships in *A. majus* and *So. lycopersicum*. We also focus on *RAD*-like gene evolution in Solanaceae, where lineage specific gene duplications were identified. We demonstrate that among similar antagonistic interactions in *A. majus* and *So. lycopersicum*, *RAD*-like genes originate from the closely related ortholog, while *DIV*-like genes originate from distantly related paralogs.

2. Results

2.1. RAD-like genes from Solanaceae

Sixteen sequences of *RAD*-like genes were discovered in this study (GenBank numbers MF398572-MF398587) (Table 1). We show that our cloning method can recover all of the RAD2 paralogs identified from the genome data of *P. hybrida* and *So. lycopersicum* (Table 1).

Table 1. Species sampled for the RAD2 clade with collection locations, voucher information, sequence name, phylogenetic placement and number of clones sequenced.

Species	Family	Location	Voucher	Sequence names	Clades	# of clones sequenced
Petunia sp.	Solanaceae	VCU Greenhouse	Zhang_Lab_23 (VCU)	*Petunia sp RAD1*	RAD2A	12
				Petunia sp RAD2	RAD2A	20
				Petunia sp RAD3	RAD2B	8
Lycium ruthenicum Murray.	Solanaceae	Taxkorgan Tajik Autonomous County, Xinjiang, China	CPG13183 (PE)	*Lycium ruthenicum Murr RAD*	RAD2A	20
Atropa belladonna L.	Solanaceae	Hotel Elites, Nathia Gali, Northwest Frontier Province, Pakistan	CPG13594 (PE)	*Atropa belladonna Linn RAD*	RAD2B	20
Schizanthus pinnatus Ruiz & Pav.	Solanaceae	VCU Greenhouse	Zhang_Lab_20 (VCU)	*Schizanthus pinnatus RAD1*	RAD2B	21
				Schizanthus pinnatus RAD2	RAD2A	22
Schizanthus grahamii Gillies	Solanaceae	VCU Greenhouse	Zhang_Lab_19 (VCU)	*Schizanthus grahamii RAD1*	RAD2A	21
				Schizanthus grahamii RAD2	RAD2B	19
Nicotiana obtusifolia M.Martens & Galeotti.	Solanaceae	VCU Greenhouse	Zhang_Lab_11 (VCU)	*Nicotiana obtusifolia RAD1*	RAD2A	14
				Nicotiana obtusifolia RAD2	RAD2A	16
Solanum lycopersicum L.	Solanaceae	VCU Greenhouse	Zhang_Lab_21 (VCU)	*Solanum lycopersicum microtom RAD1*	RAD2A	17
				Solanum lycopersicum microtom RAD2	RAD2B	13
Evolvulus sp.	Convolvulaceae	VCU Greenhouse	Zhang_Lab_18 (VCU)	*Evulupus sp RAD1*	RAD2B	20
				Evulupus sp RAD2	RAD2A	17
Ipomoea tricolor Cav.	Convolvulaceae	VCU Greenhouse	Zhang_Lab_22 (VCU)	*Ipomoea tricolor RAD1*	RAD2A	20

Virginia Commonwealth University (VCU) is in Richmond, VA, USA. VCU, Virginia Commonwealth University Herbaria; PE, Institute of Botany, Chinese Academy of Sciences Herbarium, Beijing, China.

2.2. Diversity and phylogeny of I-box-like MYB genes

A total of 274 *RAD*-like CDSs were found in 101 species representing 28 families and 15 orders of dicots (Solanales, Vitales, Brassicales, Malvales, Malpighiales, Ranunculales, Lamiales, Saxifragales, Rosales, Fabales, Proteales, Cucurbitales, Myrtales, Dipsacales, and Sapindales) and monocots (Appendix 1). Among these sequences, 79 CDS belong to 17 species of seven genera of Solanaceae, which includes the FSM1 from *So. lycopersicum* [14]. For *Arabidopsis*, six *RAD* homologs, At4g39250 (*Arabidopsis_thaliana_RL1*, NM_120086.2), At2g21650 (*Arabidopsis_thaliana_RL2*, NM_127736.3), At4g36570 (*Arabidopsis_thaliana_RL3*, BT011255.1), DQ395345 (*Arabidopsis_thaliana_RL4*, NM_001084443.1), At1g19510 (*Arabidopsis_thaliana_RL5*, NM_101808.4), and At1g75250 (*Arabidopsis_thaliana_RL6*, NM_001084356.2) were included.

A phylogeny of RAD-like genes was constructed based on 53 sequences from four species of Arabidopsis (A. thaliana, A. halleri, A. lyrata, and A. salsuginea), six species of Solanum (S. melongena S. pennellii, S. lycopersicum, S. pimpinellifolium, and S. peruvianum, and S.

tuberosum), and Oryza sativa (Fig. 1). The phylogeny indicated that sequences from O. sativa form a monophyletic clade. But the phylogenetic relationships among the three previously identified RAD1, RAD2, and RAD3 clades [15] were not fully resolved. The RAD2 clade is likely monophyletic while the RAD1 and RAD3 clades are not (Fig. 1, also see below). The RAD2 clade consists of Arabidopsis_thaliana_RL1 and Arabidopsis_thaliana_RL2 and species of Solanum, which were further divided into two Solanum-specific clades, RAD2A and RAD2B. The FSM1 of S. lycopersicum was placed in the RAD2A clade. It is unclear, however, how the other sequences of Solanum should be placed within the RAD1 clade represented by Arabidopsis_thaliana_RL3 and Arabidopsis_thaliana_RL4 and with the RAD3 clade represented by Arabidopsis_thaliana_RL5 and Arabidopsis_thaliana_RL6 (Fig. 1)[15].

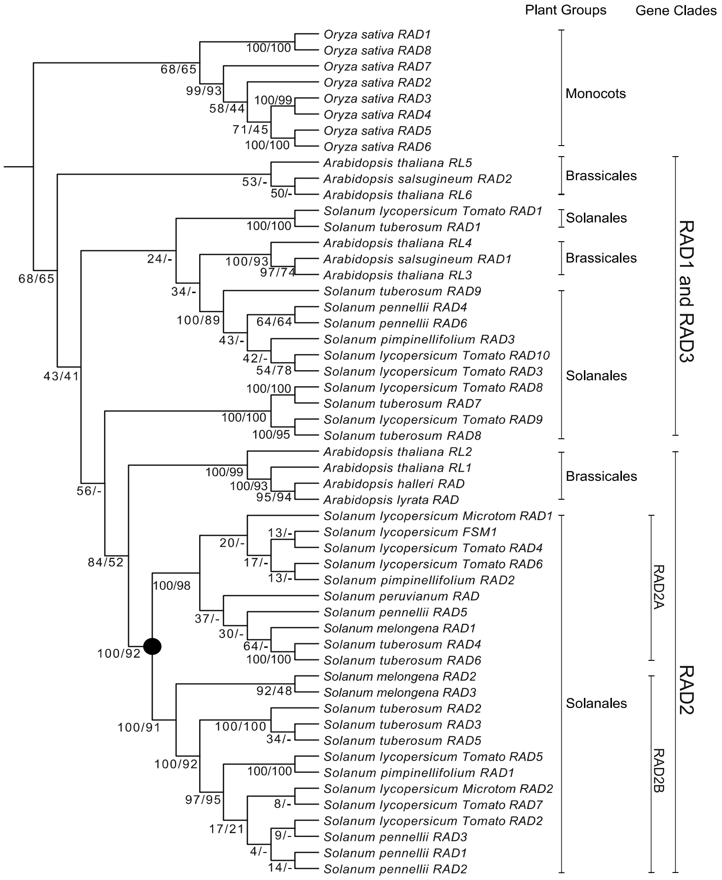
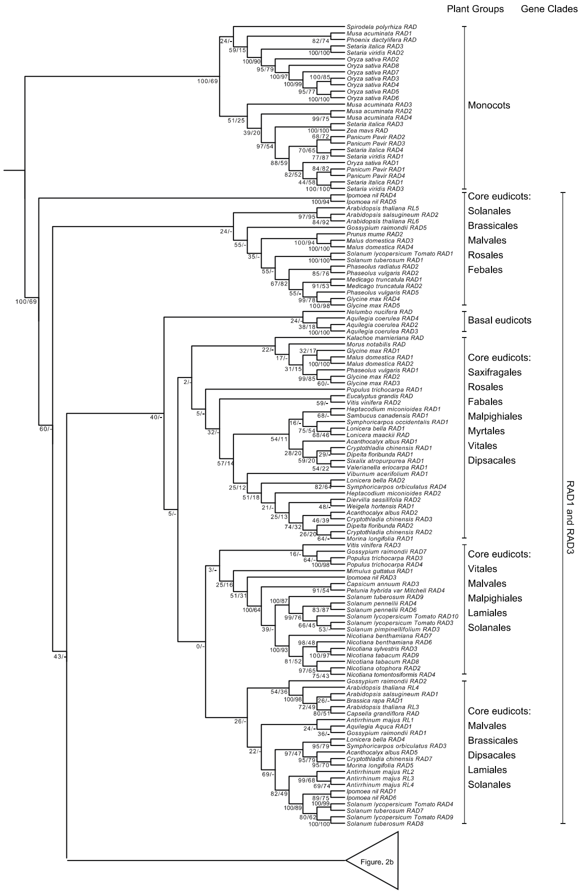


Figure 1. Phylogeny of *I-box-binding/RADIALIS*-like genes of four species of *Arabidopsis*, six species of *Solanum*, and *Oryza sativa* based on Bayesian and maximum likelihood (ML) inferences. All sequences from *O. sativa* form a monophyletic clade that was used to root the phylogeny. Based on the clade defined by Boyden et al. (2012), only the RAD2 clade was found to be monophyletic and contained sequences from *Arabidopsis* and *Solanum*. There are two paralogs in the RAD2 clade, RAD2A and RAD2B, of which *Arabidopsis* was not involved in gene duplication. RAD1 and RAD3

are paraphyletic. Bayesian posterior probabilities and bootstrap frequencies are labeled close to the branches.

Another phylogeny of *RAD*-like genes was reconstructed based on 274 CDS, including 258 from blast results and 16 in this study (Fig. 2, Appendix 1). All eight species from seven families of monocots form a monophyletic clade and were used to root the phylogeny. RAD2 forms a monophyletic clade, while both RAD1 and RAD3 were not fully resolved (Figs. 1 and 2). RAD2 comprises representatives from eleven orders: Vitales, Rosales, Malvales, Fabales, Cucurbitales, Sapindales, Malpighiales, Brassicales, Solanales, Lamiales, and Dipsacales (Fig. 2 and Appendix 1). Most of the solanaceous and convolvulaceous *RAD*-like sequences fell into the RAD2 clade, which is further divided into two clades, RAD2A and RAD2B (Figs. 1 and 2; Appendix 2). The unrooted phylogeny including only RAD2 of Solanaceae and Convolvulaceae further indicates that two paralogs have been likely formed at least in the common ancestor of the two families (Appendix 2). Further gene duplication and gene losses likely also occurred, which led to *Nicotiana* and *Petunia* having additional paralogs in RAD2A (Fig. 2, Appendix 2). RAD2 sequences from the two species of *Schizanthus,* the first branching clade of Solanaceae [24], are more closely related to the sequences from Convolvulaceae, which might be due to the limited sampling. The *FSM1* of *So. lycopersicum* that expresses in fruit is grouped in the RAD2A clade, while the *RAD* of *A. majus* is also in the RAD2 clade.



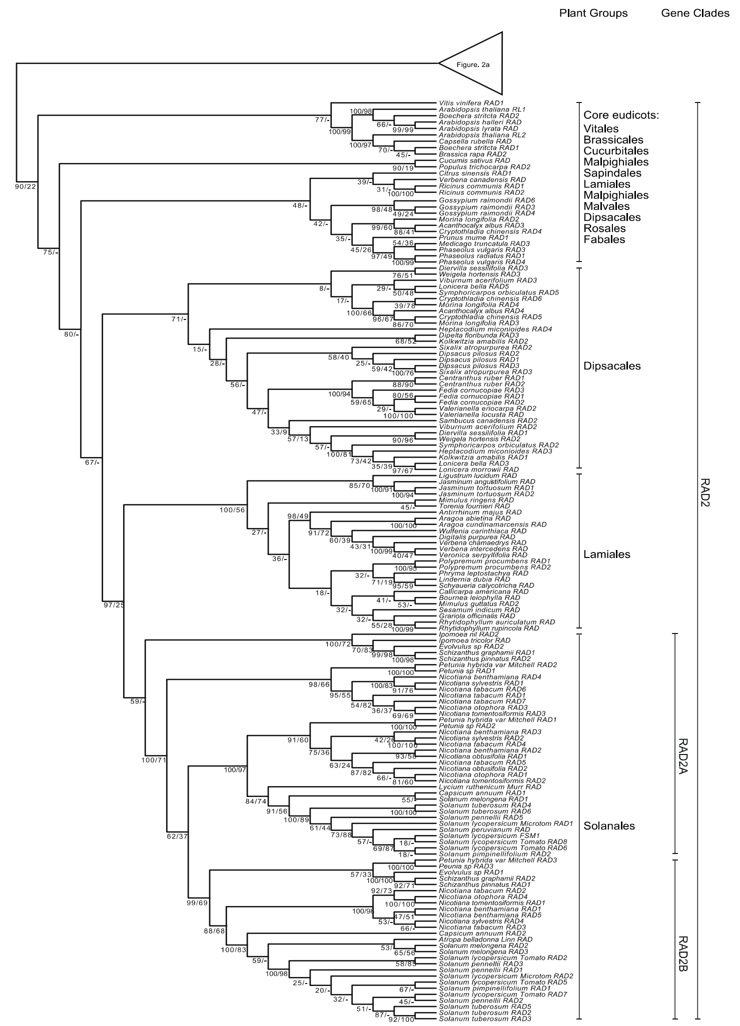


Figure 2. Phylogeny of *I-box-binding/RADIALIS*-like genes based on Bayesian and maximum likelihood (ML) inferences. 274 CDS of *I-box-binding/RADIALIS*-like genes from both monocots and dicots were analyzed. All sequences from monocots formed a monophyletic group that was used to root the phylogeny. RAD2 formed a monophyletic clade. At least one gene duplication was identified in the common ancestor of Solanaceae and Convolvulaceae. RAD1 and RAD3 clades are paraphyletic. Bayesian posterior probabilities and bootstrap frequencies are labeled close to the branches, respectively.

2.3 Diversity and phylogeny of R-R-type MYB genes

One thousand seventy five CDS that represent both *R-R-type* and *CCA1*-like genes from 109 species representing 34 different families from 22 orders of plants (16 of dicots, four of monocots, and two of mosses) were recovered (Appendix 3). For *A. thaliana*, the blast results nine *R-R-type,* i.e., At1g49010 (AY519528.1), At2g38090 (AY519529.1), At3g11280 (AY550308.1), At5g01200 (AY519530.1), At5g05790 (AY519531.1), At5g08520 (AY519532.1), At5g58900 (AY519533.1), At5g23650 (DQ056685.1), and At5g04760 (AB493736.1) and one *CCA1*-like gene, i.e., At3g16350 (AY519512.1) [25]. For Solanaceae, we recovered 124 CDS, named *DIV-*, *MYB-* or *MYB1R1*-like genes, from 12 species in four genera, including the *MYBI* of *So. lycopersicum*.

An *R-R-type* phylogeny was first reconstructed based on 53 CDS from *O. sativa japonica*, *A. thaliana*, and five species of *Solanum* (*S. melongena, S. lycopersicum, S. pennellii, S. peruvianum,* and *S. tuberosum*). All sequences fell into two clades, RR1 and RR2/DIV. RR2/DIV clade represented the DIV clade identified by Howarth and Donoghue [16]. Each of these two clades contained sequences from *O. sativa*, *A. thaliana,* and *Solanum*.

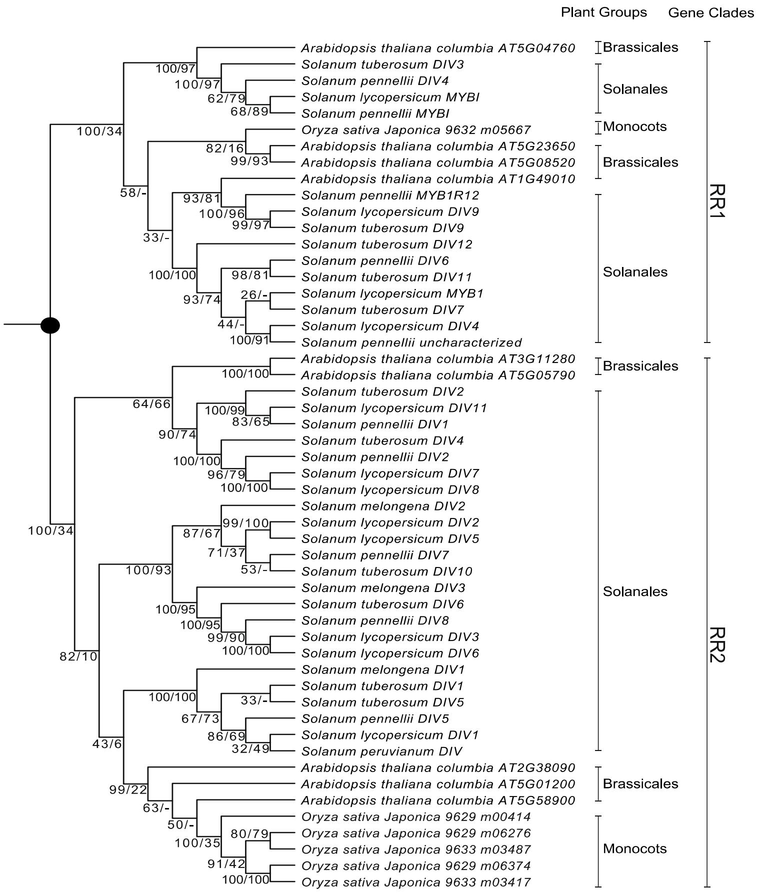
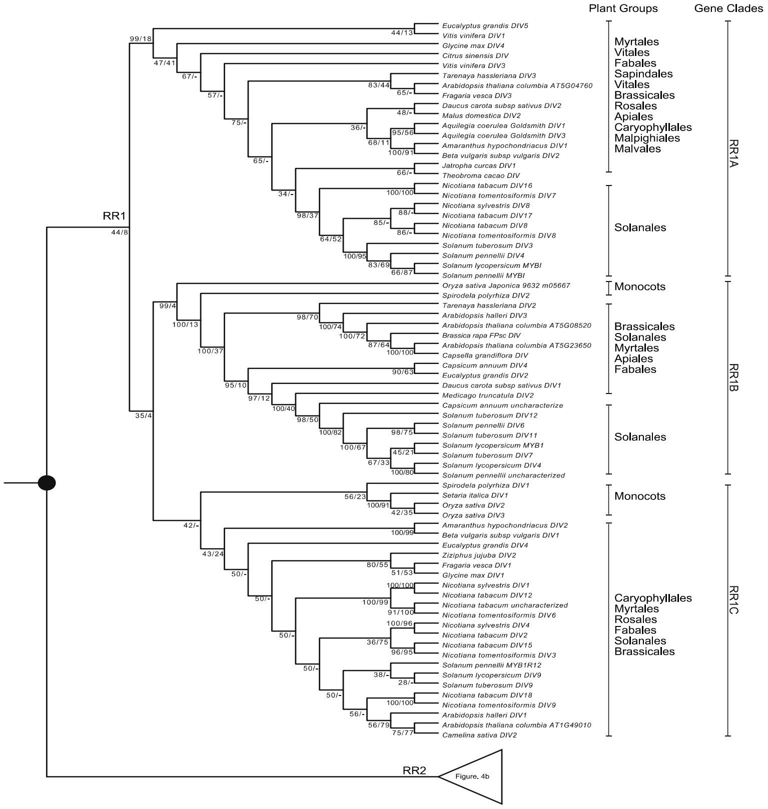
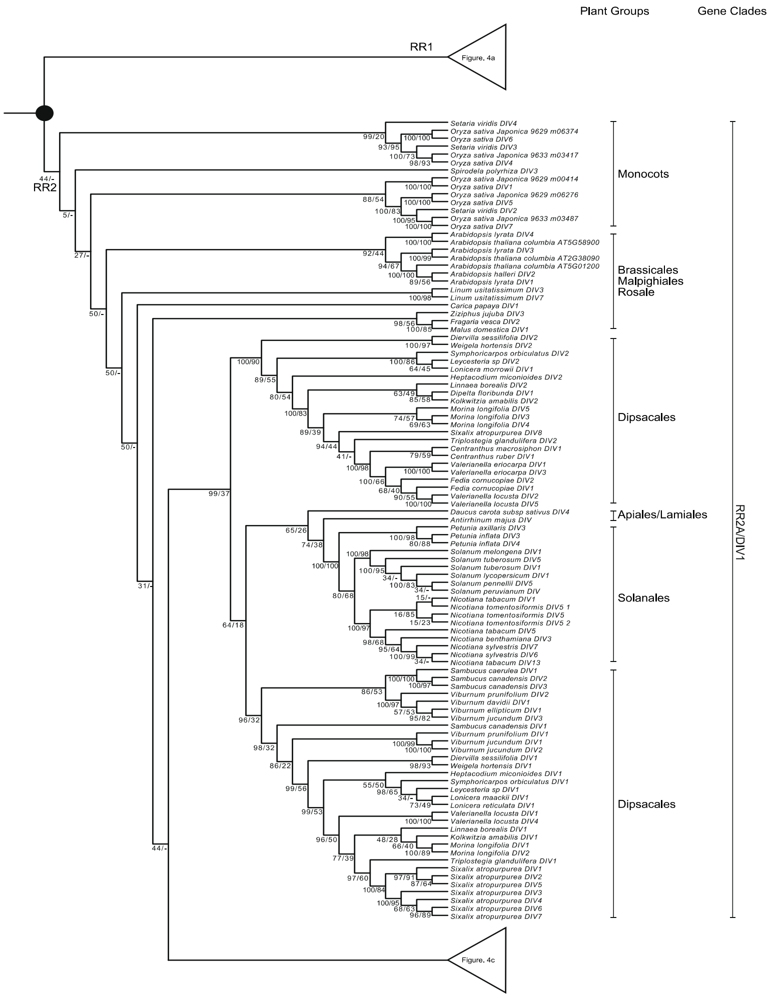


Figure 3. Phylogeny of *R-R-type* genes of five species of *Solanum*, *Arabidopsis thaliana,* and *Oryza sativa* based on Bayesian and maximum likelihood (ML) inferences. Two major clades, RR1 and RR2

were identified, each of which includes sequences from *Arabidopsis*, *Oryza*, and *Solanum*. Bayesian posterior probabilities and bootstrap frequencies are labeled close to the branches.

The *R-R-type* gene phylogeny was also reconstructed based on 298 CDS from 75 species of 23 families (Fig. 4, Appendix 3). The unrooted tree indicated that the RR1 and RR2/DIV clades were monophyletic (Fig. 4). RR1 was further divided into three clades i.e., RR1A, RR1B, and RR1C. The RR1A clade included sequences from 12 orders of dicots (Myrtales, Fabales, Sapindales, Vitales, Brassicales, Rosales, Malvales, Malpighiales, Ranunculales, Caryophyllales, Apiales, and Solanales). RR1B clade had representatives from monocots and five orders of dicots (Myrtales, Brassicales, Fabales, Apiales, and Solanales). RR1C clade had representatives from monocots and six orders of dicots (Caryophyllales, Myrtales, Brassicales, Rosales, Fabales, and Solanales). For *Arabidopsis*, AT5g04760 was placed in RR1A clade, AT5G08520 and At5g23650 in RR1B clade, and AT1G49010 in RR1C clade. For the RR2/DIV clade, previously identified DIV2 and DIV3 clades formed monophyletic clades [16]. The sequences of *A. thaliana,* At2g38090, At5g01200, At5g58900 belonged to DIV1, and At3g11280 and At5g05790 belonged to DIV2. *Arabidopsis* lacked the *DIV3* copy based on previous work [16]. The *MYBI* of *So. lycopersicum* expressed in fruit was grouped in the RR1A of RR1 clade, while the *DIV* of *A. majus* was likely in RR2A/DIV1 of the RR2 clade.


Plant Groups
Gene Clades
Eucalyptus grandis DIV5
Vitis vinifera DIV1
Glycine max DIV4
Citrus sinensis DIV
Vitis vinifera DIV3
Tarenaya hassleriana DIV3
Arabidopsis thaliana columbia AT5G04760
Fragaria vesca DIV3
Daucus carota subsp sativus DIV2
Malus domestica DIV2
Aquilegia coerulea Goldsmith DIV1
Aquilegia coerulea Goldsmith DIV3
Amaranthus hypochondriacus DIV1
Beta vulgaris subsp vulgaris DIV2
Jatropha curcas DIV1
Theobroma cacao DIV
Nicotiana tabacum DIV16
Nicotiana tomentosiformis DIV7
Nicotiana sylvestris DIV8
Nicotiana tabacum DIV17
Nicotiana tabacum DIV8
Nicotiana tomentosiformis DIV8
Solanum tuberosum DIV3
Solanum pennellii DIV4
Solanum lycopersicum MYBI
Solanum pennellii MYBI
Oryza sativa Japonica 9632 m05667
Spirodela polyrhiza DIV2
Tarenaya hassleriana DIV2
Arabidopsis halleri DIV3
Arabidopsis thaliana columbia AT5G08520
Brassica rapa FPsc DIV
Arabidopsis thaliana columbia AT5G23650
Capsella grandiflora DIV
Capsicum annuum DIV4
Eucalyptus grandis DIV2
Daucus carota subsp sativus DIV1
Medicago truncatula DIV2
Capsicum annuum uncharacterize
Solanum tuberosum DIV12
Solanum pennellii DIV6
Solanum tuberosum DIV11
Solanum lycopersicum MYB1
Solanum tuberosum DIV7
Solanum lycopersicum DIV4
Solanum pennellii uncharacterized
Spirodela polyrhiza DIV1
Setaria italica DIV1
Oryza sativa DIV2
Oryza sativa DIV3
Amaranthus hypochondriacus DIV2
Beta vulgaris subsp vulgaris DIV1
Eucalyptus grandis DIV4
Ziziphus jujuba DIV2
Fragaria vesca DIV1
Glycine max DIV1
Nicotiana sylvestris DIV1
Nicotiana tabacum DIV12
Nicotiana tabacum uncharacterized
Nicotiana tomentosiformis DIV6
Nicotiana sylvestris DIV4
Nicotiana tabacum DIV2
Nicotiana tabacum DIV15
Nicotiana tomentosiformis DIV3
Solanum pennellii MYB1R12
Solanum lycopersicum DIV9
Solanum tuberosum DIV9
Nicotiana tabacum DIV18
Nicotiana tomentosiformis DIV9
Arabidopsis halleri DIV1
Arabidopsis thaliana columbia AT1G49010
Camelina sativa DIV2
Myrtales
Vitales
Fabales
Sapindales
Vitales
Brassicales
Rosales
Apiales
Caryophyllales
Malpighiales
Malvales
Solanales
Monocots
Brassicales
Solanales
Myrtales
Apiales
Fabales
Solanales
Monocots
Caryophyllales
Myrtales
Rosales
Fabales
Solanales
Brassicales
RR1A
RR1B
RR1C
RR1
44/8
RR2
Figure. 4b
99/18
44/13
47/41
67/-
83/44
57/-
65/-
75/-
48/-
36/-
95/56
68/11
100/91
65/-
66/-
34/-
100/100
98/37
88/-
85/-
86/-
64/52
100/95
83/69
66/87
99/4
100/13
98/70
100/74
100/72
87/64
100/100
100/37
90/63
95/10
97/12
100/40
98/50
98/75
100/82
100/67
45/21
67/33
100/80
35/4
56/23
100/91
42/35
42/-
100/99
43/24
80/55
50/-
51/53
100/100
50/-
100/99
91/100
100/96
50/-
36/75
96/95
50/-
38/-
28/-
50/-
100/100
56/-
56/79
75/77


Plant Groups
Gene Clades
RR1
Figure. 4a
44/-
RR2
5/-
27/-
50/-
50/-
50/-
31/-
44/-
Setaria viridis DIV4
99/20
Oryza sativa Japonica 9629 m06374
100/100
Oryza sativa DIV6
93/95
Setaria viridis DIV3
100/73
Oryza sativa Japonica 9633 m03417
98/93
Oryza sativa DIV4
Spirodela polyrhiza DIV3
Oryza sativa Japonica 9629 m00414
100/100
Oryza sativa DIV1
88/54
Oryza sativa Japonica 9629 m06276
100/100
Oryza sativa DIV5
100/83
Setaria viridis DIV2
100/95
Oryza sativa Japonica 9633 m03487
100/100
Oryza sativa DIV7
Monocots
Arabidopsis lyrata DIV4
100/100
Arabidopsis thaliana columbia AT5G58900
92/44
Arabidopsis lyrata DIV3
100/99
Arabidopsis thaliana columbia AT2G38090
94/67
Arabidopsis thaliana columbia AT5G01200
100/100
Arabidopsis halleri DIV2
89/56
Arabidopsis lyrata DIV1
Linum usitatissimum DIV3
100/98
Linum usitatissimum DIV7
Carica papaya DIV1
Ziziphus jujuba DIV3
98/56
Fragaria vesca DIV2
100/85
Malus domestica DIV1
Brassicales
Malpighiales
Rosale
Diervilla sessilifolia DIV2
100/97
Weigela hortensis DIV2
100/90
Symphoricarpos orbiculatus DIV2
100/86
Leycesteria sp DIV2
89/55
64/45
Lonicera morrowii DIV1
80/54
Heptacodium miconioides DIV2
Linnaea borealis DIV2
63/49
Dipelta floribunda DIV1
100/83
85/58
Kolkwitzia amabilis DIV2
Morina longifolia DIV5
74/57
Morina longifolia DIV3
89/39
69/63
Morina longifolia DIV4
Sixalix atropurpurea DIV8
94/44
Triplostegia glandulifera DIV2
41/-
Centranthus macrosiphon DIV1
79/59
Centranthus ruber DIV1
100/98
Valerianella eriocarpa DIV1
100/100
Valerianella eriocarpa DIV3
100/66
Fedia cornucopiae DIV2
68/40
Fedia cornucopiae DIV1
90/55
Valerianella locusta DIV2
100/100
Valerianella locusta DIV5
Dipsacales
99/37
Daucus carota subsp sativus DIV4
Antirrhinum majus DIV
Apiales/Lamiales
65/26
Petunia axillaris DIV3
74/38
100/98
Petunia inflata DIV3
80/88
Petunia inflata DIV4
100/98
Solanum melongena DIV1
100/100
Solanum tuberosum DIV5
100/95
Solanum tuberosum DIV1
34/-
Solanum lycopersicum DIV1
100/83
Solanum pennellii DIV5
80/68
34/-
Solanum peruvianum DIV
15/-
Nicotiana tabacum DIV1
Nicotiana tomentosiformis DIV5 1
16/85
Nicotiana tomentosiformis DIV5
15/23
Nicotiana tomentosiformis DIV5 2
100/97
Nicotiana tabacum DIV5
64/18
98/68
Nicotiana benthamiana DIV3
95/64
Nicotiana sylvestris DIV7
100/99
Nicotiana sylvestris DIV6
34/-
Nicotiana tabacum DIV13
Solanales
Sambucus caerulea DIV1
100/100
Sambucus canadensis DIV2
100/97
Sambucus canadensis DIV3
86/53
Viburnum prunifolium DIV2
100/97
Viburnum davidii DIV1
57/53
Viburnum ellipticum DIV1
96/32
95/82
Viburnum jucundum DIV3
Sambucus canadensis DIV1
Viburnum prunifolium DIV1
98/32
100/99
Viburnum jucundum DIV1
100/100
Viburnum jucundum DIV2
86/22
Diervilla sessilifolia DIV1
98/93
Weigela hortensis DIV1
Heptacodium miconioides DIV1
99/56
55/50
Symphoricarpos orbiculatus DIV1
98/65
Leycesteria sp DIV1
34/-
Lonicera maackii DIV1
73/49
Lonicera reticulata DIV1
99/53
Valerianella locusta DIV1
100/100
Valerianella locusta DIV4
96/50
Linnaea borealis DIV1
48/28
Kolkwitzia amabilis DIV1
66/40
Morina longifolia DIV1
77/39
100/89
Morina longifolia DIV2
Triplostegia glandulifera DIV1
97/60
Sixalix atropurpurea DIV1
97/91
Sixalix atropurpurea DIV2
87/64
Sixalix atropurpurea DIV5
100/84
Sixalix atropurpurea DIV3
100/95
Sixalix atropurpurea DIV4
68/63
Sixalix atropurpurea DIV6
96/89
Sixalix atropurpurea DIV7
Dipsacales
RR2A/DIV1
Figure. 4c

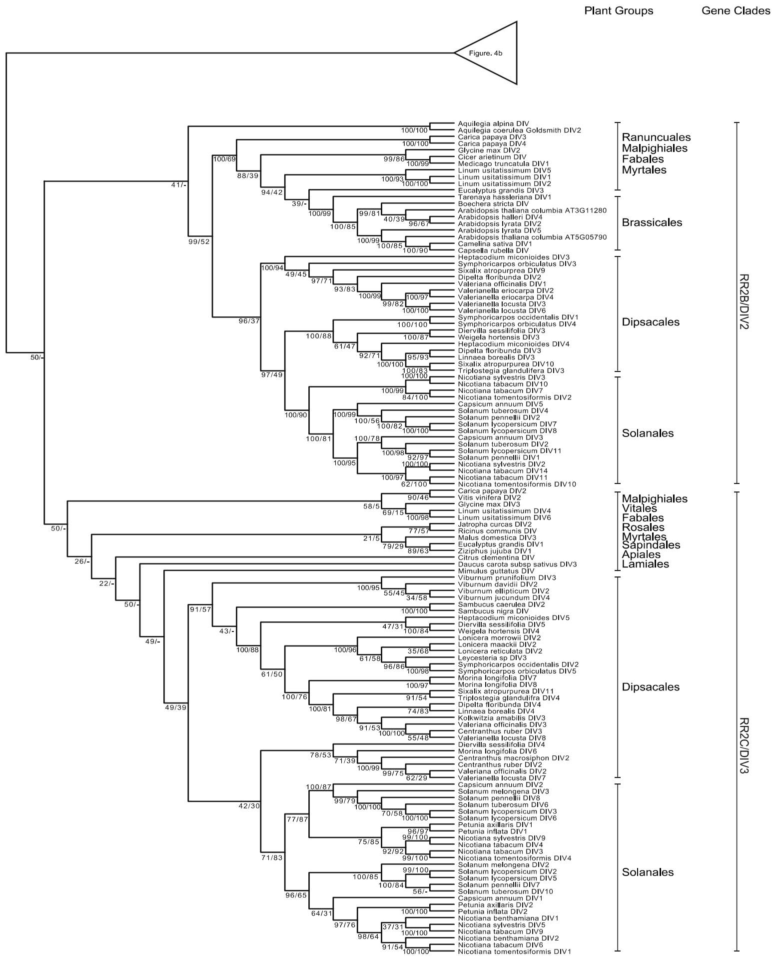


Figure 4. Phylogeny of *R-R-type* genes based on Bayesian and maximum likelihood (ML) inferences. 298 CDS of *R-R-type* genes from both monocots and dicots were analyzed. They formed two major clades, RR1 and RR2/DIV, each of which contained sequences from monocots and dicots. The RR1 clade was further divided into three groups, RR1A, RR1B, and RR1C. For the three RR2/DIV clades identified by Howarth and Donoghue (2009), only the DIV2 and DIV3 are monophyletic. The *Arabidopsis* sequences include AT2G38090, AT5G01200, and AT5G58900 identified as DIV1, which is not a clade in this phylogeny. Bayesian posterior probabilities and bootstrap frequencies are labeled close to the branches.

3. Discussion

Phylogenetic positions of *RAD*- and *DIV*-like genes in the plant MYB lineage. MYB proteins contain a conserved MYB domain, which usually comprises one to three imperfect repeats, namely R1, R2, R3 [25,26]. Each of these repeats comprises about 52 amino acid residues that encode a helix-loop-helix structure involved in DNA binding [26,27]. *MYB*-like genes have been found in all eukaryotes [26,28].

Phylogenetic analysis indicates that the *MYB* genes of plants, which is sister to all animal *MYB* genes, form a monophyletic clade [27]. *MYB* genes in plants are structurally and functionally more variable compared to the *MYB* genes in vertebrates [27,29]. Based on the MYB domain structures, the MYB proteins of plants can be classified into three major groups: R1R2R3-MYB with three adjacent repeats, R2R3-MYB with two adjacent repeats, and MYB-related proteins, a heterogeneous group, often containing a single MYB repeat [25,27,30-33]. The R2R3-MYB group is thought to be derived from the R1R2R3-MYB group, which occurs in all major lineages of land plants [29]. Based on the phylogenetic analysis and the protein domain structure, MYB-related proteins were further divided into five subfamilies: CCA1-like, CPC-like, TBP-like, I-box-binding-like (abbreviated I-box-like), and R-R-type [25,32]. Based on Chen et al. [25], *A. thaliana* has five I-box-like genes, i.e., At1g75250, At1g19510, At2g21650, At4g39250, and At4g36570, and nine R-R-type genes, i.e., At1g49010, At2g38090, At3g11280, At5g01200, At5g05790, At5g08520, At5g58900, At5g23650, and At5g04760. Boyden, Donoghue and Howarth [15] indicated that *RAD*-like genes belong to the *I-box*-like clade. Our analyses further indicate that the *I-box*-like lineage is synonymous with *RAD*-like genes (Figs. 1 and 2). Furthermore, Howarth and Donoghue [16] focused on the evolution of *DIV*-like genes in core eudicots especially in Dipsacales, and indicated that the *DIV*-like genes belong to an *R-R-type* gene lineage. Our analysis of *R-R-type* genes showed that gene duplication occurred at least in the common ancestor of dicots and monocots giving rise to two paralogs, the RR1 and RR2 clades (Figs. 3 and 4), of which the RR2 clade is synonymous with the *DIV*-like lineage [16].

Evolution of the I-box-like subfamily Boyden, Donoghue and Howarth [15] indicated that *RAD*-like genes consist of three major clades: RAD1, RAD2, and RAD3, which were speculated as resulting from genome duplications associated with the origin of core eudicots. The RAD1 clade has *Arabidopsis* AT4G36570 and DQ395345 of Clade I [defined by 25], and RAD2 and RAD3 have the *Arabidopsis* sequences from Clade III (AT2G21650 and AT4G39250 belong to the RAD2, and AT1G19510 and AT1G75250 belong to RAD3). Our analysis recognized *RAD2* as a monophyletic clade (Fig. 1 and 2). Furthermore, there are two RAD2 paralogs involving Solanaceae and Convolvulaceae, RAD2A and RAD2B, which likely resulted from a gene duplication at least in the common ancestor of these two plant families. On the other hand, the *RAD1* and *RAD3* clades were not fully resolved based on our analyses. Our phylogenetic analyses indicated that the *RAD* of *A. majus* belongs to the RAD2 clade, while FSM1 is placed in the RAD2A clade, suggesting that RAD and FSM1 belong to the same orthologous lineage.

Evolution of the R-R-type subfamily. The R-R-type genes have two imperfect repeats of the MYB domain, namely R-R (A) and R-R (B) [25]. The N-terminal MYB repeat R-R (A) was found to be closely related to the MYB repeats of the I-box-like genes, and the C-terminal MYB repeat R-R (B) was closely related to those of certain CCA1-like genes based on the positions of the introns and shared motifs [25]. The phylogeny of R-R-type genes based on nine sequences of *A. thaliana* and seven of *O. sativa japonica* suggests several gene duplications in the common ancestor of the monocots and dicots, but the phylogenetic relationships of the predicted paralogs were unresolved in that study [25]. The work by Howarth and Donoghue [16], focused on the evolution of *DIV*-like genes in core eudicots especially in Dipsacales, showed duplications giving rise to three *DIV*-like clades in the core eudicots, DIV1, DIV2, and DIV3. Our blast and phylogenetic analyses indicated that most of the sequences named *DIV*-like genes belong to the R-R-type subfamily, while most of the sequences named as *MYB1R1*-like genes belong to the *CCA1*-like gene family (Appendix 3). Each of the two R-R-type subclades, RR1 and RR2, was further divided into three paralogs, which likely resulted from genome duplication in the common ancestor of core eudicots [16]. RR1 consists of RR1A, RR1B, and RR1C, while RR2/DIV is composed of RR2A/DIV1, RR2B/DIV2, and RR2C/DIV3 (Figs. 3 and 4) [16]. We find that the *DIV* of *An. majus* belongs to the *DIV1* of the *RR2/DIV* clade [also see 16], while the *MYBI* of tomato belongs to the *RR1A* of the *RR1* clade.

Evolution of the antagonism among RAD-DRIF-DIV and FSM1-FSB1-MYBI in *An. majus* and *So. lycopersicum*, respectively. Based on an analysis of amino acid sequences, the two MYB domains of DIV had different functions with the C-terminal domain similar to known DNA binding MYB proteins, while the N-terminal domain was associated with protein-protein interactions [13,34]. In contrast, RAD has a single MYB domain that is predicted to act through a mechanism involving protein–protein interactions [10]. As the members of MYB-related subfamilies, I-box-like and R-R-type genes, were previously placed in the same clade by Riechmann and Ratcliffe [32], which suggests that they may be closely related paralogs. One possible hypothesis proposed for the evolution of these two MYB-related subfamilies is that I-box-like genes evolved through the loss of the MYB domain at the C-terminal end [25,35]. RAD-DRIF-DIV and RAD-DRIF-DIV, therefore, represent the recruitment of homologous genes from similar MYB lineages in the development of floral zygomorphy in *An. majus,* and the development of fruit in *So. lycopersicum* [4]. Our work clarified the evolution of I-box-like and R-R-type lineages and will help future inquiry into the functional studies of the paralogs that may have been involved in the evolution of molecular antagonism.

4. Materials and Methods

Cloning *RAD*-like genes from species of Solanaceae and Convolvulaceae - Primers incorporated with degenerate polymorphic sites based on the alignment of *RAD*-like sequences, especially the RAD2 clade from Solanaceae and Lamiales, were used for amplifying the genes from species of Solanaceae and representatives of Convolvulaceae. The locations of our primers were referred to the study by Boyden, Donoghue and Howarth [15]. These primers, i.e., forward primer 5′-AACAAGGCITTGARARGGCWTYRGC-3′, and reverse primer 5′-GGRAARGGBAYIMYACCAIDITCAAT-3′, successfully amplified *RAD*-like genes from both the basal and derived clades of Solanaceae (*Schizanthus pinnatus* Ruiz & Pav, *Schizanthus grahamii* Gillies, *Petunia sp*., *Nicotiana obtusifolia* M. Martens & Galeotti, *Solanum lycopersicum* L., *Lycium ruthenicum* Murray and *Atropa belladonna* L.) and species of Convolvulaceae (*Evolvulus sp*. and *Ipomoea tricolor* Cav.) (Table 1). PCR reactions were performed using GoTaq® G2 Hot Start Polymerase (Promega, Madison, WI, USA), as follows: 95°C for 5 min, 95°C for 45 s, 55°C for 45 s, and 72°C for 1 min, 30 s, repeated for 39 cycles, with a final step at 72°C for 10 mins. PCR products were then purified through gel extraction using Wizard SV Gel and PCR Clean-Up System from Promega (Madison, WI, USA). The purified PCR products were used as a template for the second round of PCR following the same PCR program described above. The purified second round PCR products were used in ligation and transformation with pGEM-T Easy Vector System I from Promega (Madison, WI, USA). At least 50 clones were screened for each species. The sequences of the clones were determined using Sanger sequencing by GENEWIZ (115 Corporate Boulevard, South Plainfield, NJ, USA).

Gene mining - The *RAD-* and *DIV*-like genes were obtained through blasting *RAD* and *DIV* CDS sequences of *A. majus* (GenBank accession numbers: AY954971.1 and AY077453.1, respectively) against the databases, including NCBI Blastn (http://www.ncbi.nlm.nih.gov/ BLAST/), Phytozome 11 (https://phytozome.jgi.doe.gov), Sol Genomics Network (https://solgenomics.net), and Rice Genome Annotation Project (http://rice.plantbiology.msu.edu).

Alignment and phylogenetic analyses - The DNA matrices of the coding sequences were aligned using Geneious version 7.1.9 (PO Box 5677, Wellesley St, Auckland 1010, New Zealand, USA). The MUSCLE algorism that refers to the protein sequence alignment for building nucleotide sequence alignment was applied. Each DNA matrix was analyzed by using the Bayesian and maximum likelihood (ML) inferences, which were implemented in RAxML_HPC2, and MrBayes version 3.2.6 on XSEDE, respectively, at the CIPRES Science Gateway V. 3.3. [17-20]. For ML analyses, a random seed value for rapid ML bootstrapping was estimated on each dataset. The

GTRCAT model was chosen for the bootstrapping analysis based on the program recommendation because GTRCAT shows lower computational costs and memory consumption for the ML method [18]. The models used for the Bayesian analyses were estimated using jmodeltest 2.1.10 [21,22]. The Akaike Information Criterion (AIC) [23] was used to determine the best-fit model for each DNA sequence matrix, i.e., K80 (K2P) + g model for the *I-box-like/RAD* gene phylogeny including *Arabidopsis, Solanum*, and *Oryza* alone, JC + g model for the large *RAD* phylogeny, GTR + i + g model for the *R-R-type* gene phylogeny including *Arabidopsis, Solanum*, and *Oryza* alone, and GTR + i + g model for the large *R-R-type* gene phylogeny. We used the Metropolis-coupled Markov chain Monte Carlo method as implemented in MrBayes to run four chains. We ran five million generations for each chain, and sampled every 1000 generations with a burn-in of the first 2000 trees.

Supplementary Materials: Supplementary materials can be found at www.mdpi.com/link.

Acknowledgments: We thank J. Zhang, F. Khojayori, and D. Boufford. This work was funded by Virginia Commonwealth University and National Science Foundation Grant DEB-1355109.

Author Contributions: A.G. and W.Z. conceived and designed the experiments; A.G. performed the experiments; A.G. and W.Z. analyzed the data; A.G. and W.Z. wrote the paper.

Conflicts of Interest: The authors declare no conflict of interest.

Appendix 1

Accession information of I-box-like genes.

Appendix 2

Phylogeny of RAD2 clade of Solanaceae and Convolvulaceae based on Bayesian and maximum likelihood (ML) inferences. The unrooted tree shows the two clades, each of which includes sequences from both Solanaceae and Convolvulaceae. Bayesian posterior probabilities and bootstrap frequencies are labeled close to the branches, respectively.

Appendix 3

Accession information of R-R-type genes.

References

1. Zimmerman, L.B.; DeJesusEscobar, J.M.; Harland, R.M. The spemann organizer signal noggin binds and inactivates bone morphogenetic protein 4. *Cell* **1996**, *86*, 599-606.
2. Dal-Pra, S.; Fuerthauer, M.; Van-Celst, J.; Thisse, B.; Thisse, C. Noggin1 and follistatin-like2 function redundantly to chordin to antagonize bmp activity. *Dev Biol* **2006**, *298*, 514-526.
3. Luttrell, L.M.; Maudsley, S.; Bohn, L.M. Fulfilling the promise of "biased" g protein-coupled receptor agonism. *Mol Pharmacol* **2015**, *88*, 579-588.
4. Raimundo, J.; Sobral, R.; Bailey, P.; Azevedo, H.; Galego, L.; Almeida, J.; Coen, E.; Costa, M.M.R. A subcellular tug of war involving three myb-like proteins underlies a molecular antagonism in *antirrhinum* flower asymmetry. *Plant J* **2013**, *75*, 527-538.
5. Luo, D.; Carpenter, R.; Vincent, C.; Copsey, L.; Coen, E. Origin of floral asymmetry in *antirrhinum*. *Nature* **1996**, *383*, 794-799.
6. Luo, D.; Carpenter, R.; Copsey, L.; Vincent, C.; Clark, J.; Coen, E. Control of organ asymmetry in flowers of *antirrhinum*. *Cell* **1999**, *99*, 367-376.
7. Howarth, D.G.; Donoghue, M.J. Phylogenetic analysis of the "ece" (cyc/tb1) clade reveals duplications predating the core eudicots. *Proc Natl Acad Sci U S A* **2006**, *103*, 9101-9106.
8. Cubas, P.; Lauter, N.; Doebley, J.; Coen, E. The tcp domain: A motif found in proteins regulating plant growth and development. *Plant J* **1999**, *18*, 215-222.
9. Baxter, C.E.L.; Costa, M.M.R.; Coen, E.S. Diversification and co-option of rad-like genes in the evolution of floral asymmetry. *Plant J* **2007**, *52*, 105-113.
10. Corley, S.B.; Carpenter, R.; Copsey, L.; Coen, E. Floral asymmetry involves an interplay between tcp and myb transcription factors in *antirrhinum*. *Proc Natl Acad Sci U S A* **2005**, *102*, 5068-5073.
11. Costa, M.M.R.; Fox, S.; Hanna, A.I.; Baxter, C.; Coen, E. Evolution of regulatory interactions controlling floral asymmetry. *Development* **2005**, *132*, 5093-5101.
12. Almeida, J.; Rocheta, M.; Galego, L. Genetic control of flower shape in *antirrhinum majus*. *Development* **1997**, *124*, 1387-1392.
13. Galego, L.; Almeida, J. Role of divaricata in the control of dorsoventral asymmetry in *antirrhinum* flowers. *Genes Dev* **2002**, *16*, 880-891.
14. Machemer, K.; Shaiman, O.; Salts, Y.; Shabtai, S.; Sobolev, I.; Belausov, E.; Grotewold, E.; Barg, R. Interplay of myb factors in differential cell expansion, and consequences for tomato fruit development. *Plant J* **2011**, *68*, 337-350.
15. Boyden, G.S.; Donoghue, M.J.; Howarth, D.G. Duplications and expression of radialis-like genes in dipsacales. *Int J Plant Sci* **2012**, *173*, 971-983.
16. Howarth, D.G.; Donoghue, M.J. Duplications and expression of divaricata-like genes in dipsacales. *Mol Biol Evol* **2009**, *26*, 1245-1258.
17. Huelsenbeck, J.P.; Ronquist, F. Mrbayes: Bayesian inference of phylogenetic trees. *Bioinformatics* **2001**, *17*, 754-755.
18. Stamatakis, A. Raxml-vi-hpc: Maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* **2006**, *22*, 2688-2690.

19. Stamatakis, A.; Hoover, P.; Rougemont, J. A rapid bootstrap algorithm for the raxml web servers. *Syst Biol* **2008**, *57*, 758-771.
20. Miller, M.A.; Pfeiffer, W.; Schwartz, T. In *Creating the cipres science gateway for inference of large phylogenetic trees*, Proceedings of the gateway computing environments workshop (GCE), 14 Nov. 2010, New Orleans, LA, 2010; pp 1 - 8.
21. Darriba, D.; Taboada, G.L.; Doallo, R.; Posada, D. Jmodeltest 2: More models, new heuristics and parallel computing. *Nat Meth* **2012**, *9*, 772-772.
22. Guindon, S.; Gascuel, O. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Syst Biol* **2003**, *52*, 696-704.
23. Akaike, H. Information theory and an extension of the maximum likelihood principle. In *Second international symposium in information theory*, Petrov, B.N.; Csaki, F., Eds. Akademiai Kiado, Budapest: 1973; pp 267-281.
24. Särkinen, T.; Bohs, L.; Olmstead, R.G.; Knapp, S. A phylogenetic framework for evolutionary study of the nightshades (solanaceae): A dated 1000-tip tree. *BMC Evol Biol* **2013**, *13*, 214.
25. Chen, Y.H.; Yang, X.Y.; He, K.; Liu, M.H.; Li, J.G.; Gao, Z.F.; Lin, Z.Q.; Zhang, Y.F.; Wang, X.X.; Qiu, X.M., *et al*. The myb transcription factor superfamily of arabidopsis: Expression analysis and phylogenetic comparison with the rice myb family. *Plant Mol Biol* **2006**, *60*, 107-124.
26. Lipsick, J.S. One billion years of myb. *Oncogene* **1996**, *13*, 223-235.
27. Rosinski, J.A.; Atchley, W.R. Molecular evolution of the myb family of transcription factors: Evidence for polyphyletic origin. *J Mol Evol* **1998**, *46*, 74-83.
28. Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Leyva, A.; Meissner, R.C.; Petroni, K.; Urzainqui, A.; Bevan, M.; Martin, C., *et al.* Towards functional characterisation of the members of the r2r3-myb gene family from arabidopsis thaliana. *Plant J* **1998**, *16*, 263-276.
29. Kranz, H.; Scholz, K.; Weisshaar, B. C-myb oncogene-like genes encoding three myb repeats occur in all major plant lineages. *Plant J* **2000**, *21*, 231-235.
30. Jin, H.L.; Martin, C. Multifunctionality and diversity within the plant myb-gene family. *Plant Mol Biol* **1999**, *41*, 577-585.
31. Stracke, R.; Werber, M.; Weisshaar, B. The r2r3-myb gene family in arabidopsis thaliana. *Curr Opin Plant Biol* **2001**, *4*, 447-456.
32. Riechmann, J.L.; Ratcliffe, O.J. A genomic perspective on plant transcription factors. *Curr Opin Plant Biol* **2000**, *3*, 423-434.
33. Martin, C.; PazAres, J. Myb transcription factors in plants. *Trends Genet* **1997**, *13*, 67-73.
34. Rose, A.; Meier, I.; Wienand, U. The tomato i-box binding factor lemybi is a member of a novel class of myb-like proteins. *Plant J* **1999**, *20*, 641-652.
35. Stevenson, C.E.M.; Burton, N.; Costa, M.M.R.; Nath, U.; Dixon, R.A.; Coen, E.S.; Lawson, D.M. Crystal structure of the myb domain of the rad transcription factor from *antirrhinum majus*. *Proteins-Structure Function and Bioinformatics* **2006**, *65*, 1041-1045.

VITA

Ao Gao was born on June 2nd, 1990 in Zhengzhou, Henan, China. Ao received his Bachelor of Science in Biology from the Biology Department with a Minor in Education from Texas A&M University-Corpus Christi, Corpus Christi, Texas, the United States in 2014. Ao matriculated in the Master of Science graduate program in the Department of Biology at Virginia Commonwealth University (VCU) in 2015, and graduate in 2017