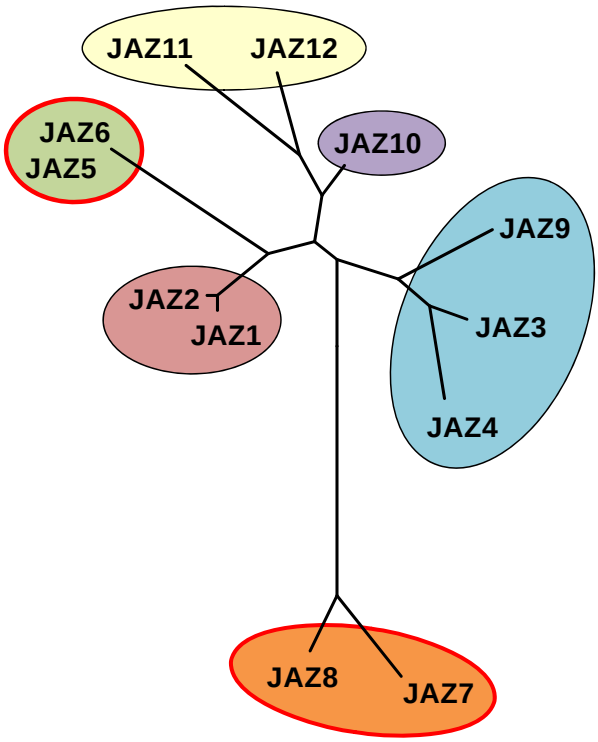
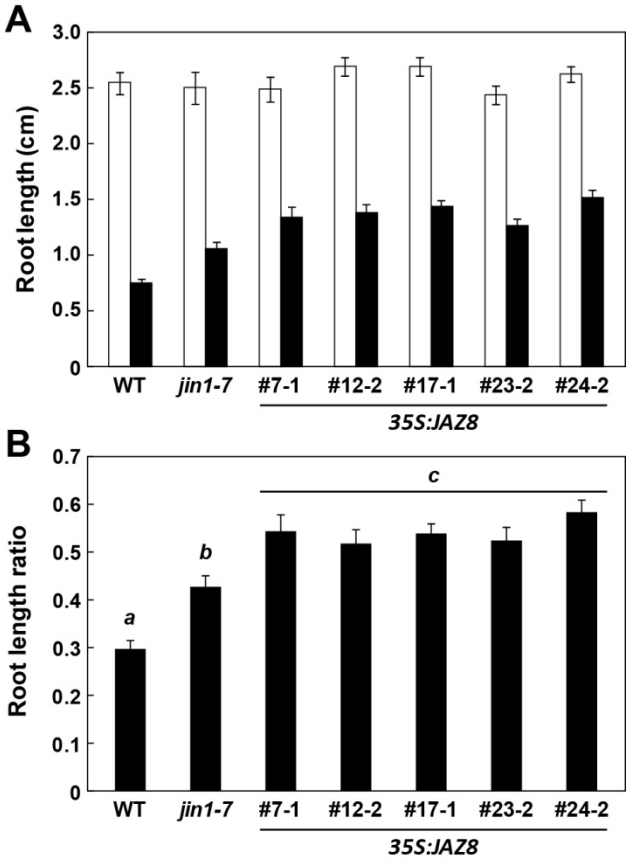


Supplemental Figure 1. Phylogenetic Tree Constructed from the Jas Motif of Arabidopsis JAZ Proteins.

The 27-amino-acid Jas motif in all 12 Arabidopsis JAZ proteins was aligned with MUSCLE (Edgar, 2004). The phylogenetic tree was generated with the Neighbor-joining method using MEGA5 software (http://www.megasoftware.net). Red circles indicate JAZ proteins that have a predicted EAR motif.

Reference

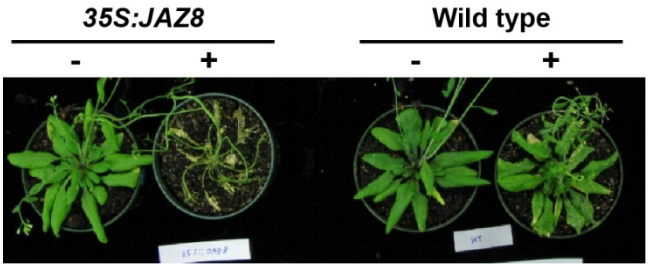
Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. **32:**1792-1797.



Supplemental Figure 2. JA-Mediated Root Growth Inhibition in Independent *35S:JAZ8* Lines.

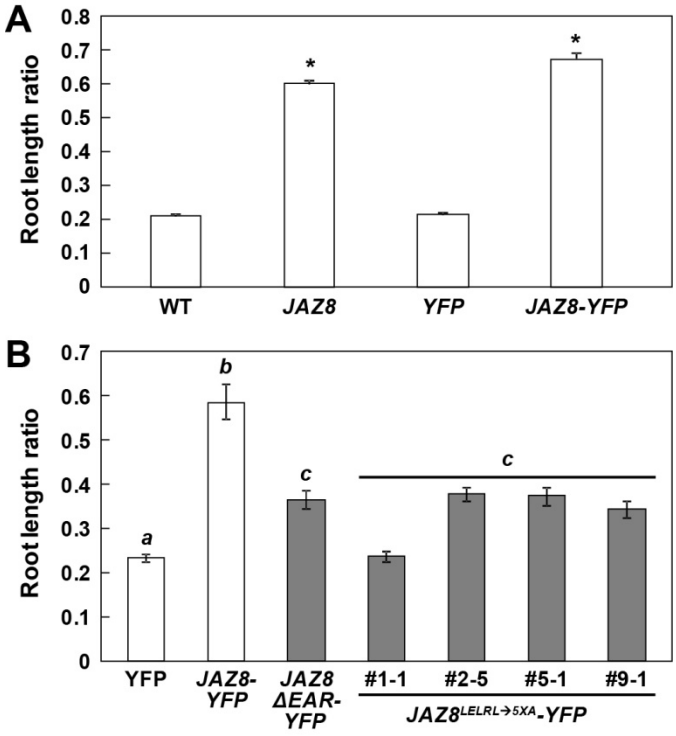
(A) Five independent homozygous *35S:JAZ8* lines, which were selected for high expression of the transgene, were grown together with WT and *jin1-7* seedlings on MS medium supplemented (filled bars) or not supplemented (open bars) with 20 μM MeJA. Plants were grown for 8 d on a 16-h light and 8-h dark cycle. Data show the mean ± SE for each genotype (n >18 seedlings per genotype). The mean root length of each *35S:JAZ8* line was significantly longer ($P<0.05$, Student's t-test) than that of the *jin1-7* mutant in the presence of MeJA.

(B) Data shown in (A) were plotted as root length ratio, which was calculated by dividing the average the root length of seedlings grown on MeJA-containing medium by the mean root length of seedlings of the same genotype grown in the absence of MeJA. Means with different italicized letters are significantly different at $P<0.05$.



Supplemental Figure 3. *35S:JAZ8* Plants are Compromised in Resistance to Herbivory by *S. exigua* Larvae.

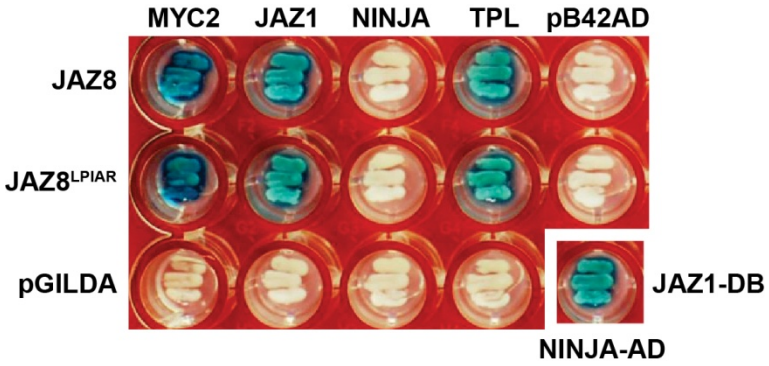
Six-week-old *35S:JAZ8* (line #24) and wild-type (WT) plants were challenged (+) for 14 d with *Spodoptera exigua* larva. A separate set of control plants grown side-by-side with the challenged plants were not infested (-) with larvae. The photograph was taken at the end of the feeding trial.



Supplemental Figure 4. JA-Mediated Root Growth Inhibition in *35S:JAZ8-YFP* Lines.

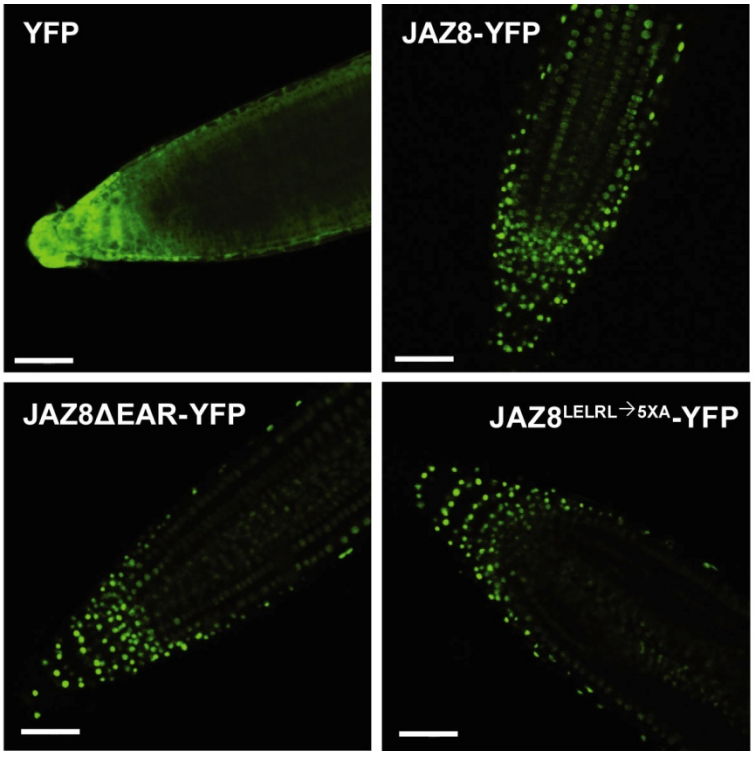
(A) *35S:JAZ8-YFP* plants are insensitive to MeJA. Wild-type (WT), *35S:JAZ8* (line #24; *JAZ8*), *35S:YFP* (*YFP*), and *35S:JAZ8-YFP* (*JAZ8-YFP*) seedlings were grown on MS medium supplemented with or without 25 μM MeJA for 8 d under continuous light. Root length ratios were calculated as described in the legend of Supplemental Figure 2B. Data show the mean ± SE for each genotype (n > 20 seedlings per genotype). Asterisks indicate significant differences ($P<0.05$, Student's t-test) in comparisons between the indicated transgenic line and WT.

(B) Mutation of the EAR motif suppresses the JA-insensitive root growth phenotype of *35S:JAZ-YFP* seedlings. Root growth inhibition assays were performed with *35S:YFP* (*YFP*), *35S:JAZ8-YFP* (*JAZ8-YFP*), *35S:JAZ8ΔEAR-YFP* (*JAZ8ΔEAR-YFP*; gray bars), and four independent *35S:JAZ8*$^{LELRL\rightarrow 5xA}$*-YFP* (*JAZ8*$^{LELRL\rightarrow 5xA}$*-YFP*; gray bars) homozygous lines (T3 generation). Seedlings were grown for 8 d on MS medium containing or lacking 20 μM MeJA. Data were plotted as root length ratio as described in panel (A). Data show the mean ± SE for each genotype (n > 23 seedlings per genotype). Means with different italicized letters are significantly different at $P<0.05$. The root length ratio of *35S:JAZ8*$^{LELRL\rightarrow 5xA}$*-YFP* seedlings was calculated as the mean of all four independent *35S:JAZ8*$^{LELRL\rightarrow 5xA}$*-YFP* lines.

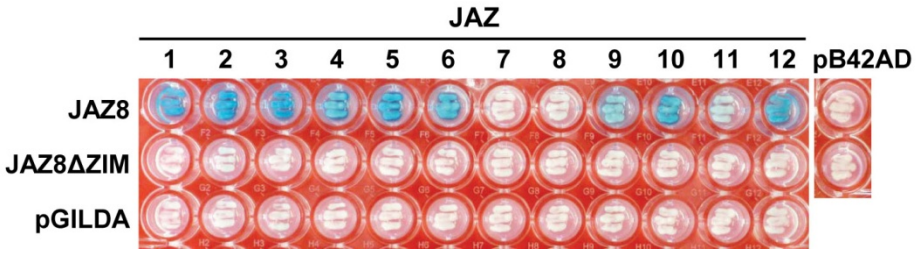


Supplemental Figure 5. Substitution of PKASM to LPIAR does not Affect the Ability of JAZ8 to Interact with MYC2, JAZ1, or TPL.

Yeast strains expressing both the bait (JAZ8 or JAZ8^{LPIAR}) and prey (MYC2, JAZ1, NINJA or TPL) were plated on SD-Gal medium containing X-gal. Blue color indicates protein-protein interaction. Photographic image was taken 48 h after incubation of yeast cells at 30°C. As a positive control for NINJA interaction, yeast cells were cotransformed with pB42AD-NINJA and pGILDA-JAZ1 (lower right).



Supplemental Figure 6. Nuclear Localization of JAZ8-YFP Fusion Proteins.
Root tips of 9-day-old seedlings expressing the indicated JAZ-YFP reporter were imaged with an Olympus Fluoview confocal microscope. Transgenic lines were *35S:YFP* (YFP), *35S:JAZ8-YFP* (JAZ8-YFP), *35S:JAZ8ΔEAR-YFP* #1-1 (JAZ8ΔEAR-YFP), and *35S:JAZ8$^{LELRL→5xA}$-YFP* #5-1 (JAZ8$^{LELRL→5xA}$-YFP). Scale bar = 50 μm.



Supplemental Figure 7. Yeast Two-hybrid Analysis of JAZ8 and JAZ8ΔZIM Interactions with other Arabidopsis JAZ proteins.

Yeast strains expressing both the bait (JAZ8 or JAZ8ΔZIM) and prey (JAZ1 – JAZ12) were plated on plates containing X-gal. Blue colors indicate protein-protein interaction. Photographic images were taken 48 h after incubation of yeast cells at 30°C.

Supplemental Table 1. List of oligonucleotide primers used in this study.

Primers in this section used for Y2H and overexpression constructs

INSERT	VECTOR	PRIMER NAME	SEQUENCE	NOTE
JAZ8	pGILDA & pB42AD	JAZ8_NcoI_FP	5'-CCATGGATGAAGCTACAGCAAAATTGTG-3'	Yeast two-hybrid vectors
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
	pBI-TONY	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	Overexpression vector
		JAZ8_KpnI_RP	5'-ATATGGTACCTTATCGTCGTGAATGGTACG-3'	
	pBI-EYFP	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	Overexpression vector tagged with EYFP
		JAZ8ns_XhoI_RP	5'-CTCGAGTCGTCGTGAATGGTACGGTG-3'	
	pENTR-TOPO	JAZ8_pENTR_FP	5'-CACCATGAAGCTACAGCAAAATTGTG-3'	Gateway construct
		JAZ8_pENTR_RP	5'-TTATCGTCGTGAATGGTACGGTG-3'	
JAZ8-Jas10	pGILDA & pB42AD	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	Used EcoRI site from pGEM -T Easy for
		JAZ10_NcoI_RP	5'-CCATGGTTAGGCCGATGTCGGATAGTAAG-3'	cloning into Y2H vectors
	pBITONY	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	
		JAZ10_KpnI_RP	5'-GGTACCTTAGGCCGATGTCGGATAGTAAG-3'	
	pBI-EYFP	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	
		JAZ10ns_KpnI_RP	5'-GGTACCGGCCGATGTCGGATAGTAAGGAG-3'	
JAZ10-Jas8	pGILDA & pB42AD	JAZ10_NcoI_FP	5'-CCATGGATGTCGAAAGCTACCATAGAAC-3'	
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
	pBITONY	JAZ10_BamHI_FP	5'-GGATCCATGTCGAAAGCTACCATAGAAC-3'	
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
	pBI-EYFP	JAZ10_BamHI_FP	5'-GGATCCATGTCGAAAGCTACCATAGAAC-3'	
		JAZ8ns_XhoI_RP	5'-CTCGAGTCGTCGTGAATGGTACGGTG-3'	
JAZ8ΔZIM	pGILDA & pB42AD	JAZ8_NcoI_FP	5'-CCATGGATGAAGCTACAGCAAAATTGTG-3'	
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
	pBI-TONY	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	
		JAZ8_KpnI_RP	5'-ATATGGTACCTTATCGTCGTGAATGGTACG-3'	
	pBI-EYFP	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	
		JAZ8ns_XhoI_RP	5'-CTCGAGTCGTCGTGAATGGTACGGTG-3'	
JAZΔEAR	pENTR-TOPO	JAZ8_pENTR_FP	5'-CACCATGAAGCTACAGCAAAATTGTG-3'	JAZΔEAR further cloned into pGILDA
		JAZ8_pENTR_RP	5'-TTATCGTCGTGAATGGTACGGTG-3'	& pB42AD via Gateway cloning
	pBI-TONY	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
	pBI-EYFP	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	
		JAZ8ns_XhoI_RP	5'-CTCGAGTCGTCGTGAATGGTACGGTG-3'	
JAZ8ΔEZ	pENTR-TOPO	JAZ8_pENTR_FP	5'-CACCATGAAGCTACAGCAAAATTGTG-3'	JAZΔEZ further cloned into pGILDA
		JAZ8_pENTR_RP	5'-TTATCGTCGTGAATGGTACGGTG-3'	& pB42AD via Gateway cloning
	pBI-TONY	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
	pBI-EYFP	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	
		JAZ8ns_XhoI_RP	5'-CTCGAGTCGTCGTGAATGGTACGGTG-3'	

Primers in this section used for MBP-JAZ-His constructs

INSERT	VECTOR	PRIMER NAME	SEQUENCE	NOTE
JAZ6	pRMG-nMAL	AtJAZ6-5'NotI	5'-GCGCGGCCGCCATGTCAACGGGACAAGCGC-3'	
		AtJAZ6-3'XhoI	5'-CGGCTCGAGAAGCTTGAGTTCAAGGTTTTTGG-3'	
JAZ7	pRMG-nMAL	NotI-C-JAZ7-FP	5'-GCGCGGCCGCCATCATCATCAAAAACTGCGACAAGCC-3'	
		JAZ7_NotI_FP	5'-GCGGCCGCATGATCATCATC-3'	
		JAZ7_XhoI_RP	5'-CTCGAGCTATCGGTAACGGTGGTAAG-3'	
JAZ8	pRMG-nMAL	JAZ8_NotI_FP	5'-GCGGCCGCATGAAGCTACAGC-3'	
		JAZ8 XhoI RP	5'-CTCGAGTTATCGTCGTGAATGGTACG	
JAZ12	pRMG-nMAL	AtJAZ12-NotI F	5'-GCGCGGCCGCCACTAAGGTGAAAGATGAG-3'	
		AtJAz12-SalI R	5'-TCGGTCGACAGCAGTTGGAAATTCCTCC-3'	
JAZ8-Jas10	pRMG-nMAL	JAZ8_NotI_FP	5'-GCGGCCGCATGAAGCTACAGC-3'	
		AtJAZ10-SalI	5'-TCGGTCGACGGCCGATGTCGGATAG-3'	
JAZ10-Jas8	pRMG-nMAL	AtJAZ10-NotI	5'-GCGCGGCCGCCTCGAAAGCTACCATAGAACTCG-3'	
		JAZ8 XhoI RP	5'-CTCGAGTTATCGTCGTGAATGGTACG	
JAZ8^{LPIAR}	pRMG-nMAL	JAZ8_NotI_FP	5'-GCGGCCGCATGAAGCTACAGC-3'	
		JAZ8 XhoI RP	5'-CTCGAGTTATCGTCGTGAATGGTACG	

Primers in this section used for chimeric proteins and deletion constructs

CONSTRUCT	TEMPLATE	PRIMER NAME	SEQUENCE	NOTE
JAZ8-Jas10	JAZ8	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	1st PCR reaction to amplify a portion of JAZ8 (1-100 aa)
		JAZ8_Jas10_RP	5'-GCGATGGGAAGATCTGGAAGCTGATTATGATGAAATG-3'	
	JAZ10.1	JAZ8_Jas10_FP	5'-CATAATCAGCTTCCAGATCTTCCCATCGCAAGGAG-3'	2nd PCR reaction to amplify a portion of JAZ10.1 (166-205 aa)
		JAZ10_KpnI_RP	5'-GGTACCTTAGGCCGATGTCGGATAGTAAG-3'	
	JAZ8 (1-100 aa) & JAZ10.1 (166-205 aa)	JAZ8_XbaI_FP	5'-ATATTCTAGAATGAAGCTACAGCAAAATTGTG-3'	3rd PCR reaction to amplify JAZ8-Jas10
		JAZ10_KpnI_RP	5'-GGTACCTTAGGCCGATGTCGGATAGTAAG-3'	
JAZ10-Jas8	JAZ10.1	JAZ10_BamHI_FP	5'-GGATCCATGTCGAAAGCTACCATAGAAC-3'	1st PCR reaction to amplify a portion of JAZ10.1 (1-165 aa)
		JAZ10_Jas8_RP	5'-GATGCTTTTGGATTTCCTTCTAGATTCTGGCCAAAG-3'	
	JAZ8	JAZ10_Jas8_FP	5'-GAATCTAGAAGGAAATCCAAAAGCATCAATGAAAAAATC-3'	2nd PCR reaction to amplify a portion of JAZ8 (101-131 aa)
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
	JAZ10.1 (1-165 aa) & JAZ8 (101-131 aa)	JAZ10_BamHI_FP	5'-GGATCCATGTCGAAAGCTACCATAGAAC-3'	3rd PCR reaction to amplify JAZ10-Jas8
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
JAZ8ΔZIM	JAZ8	JAZ8_NcoI_FP	5'-CCATGGATGAAGCTACAGCAAAATTGTG-3'	1st PCR reaction to amplify a portion of JAZ8 (1-44 aa)
		JAZ8_deltaZIM_RP	5'-GGTTTTCATTTCTCTGCTTTGAGATTCTTCATTTGG-3'	
	JAZ8	JAZ8_deltaZIM_FP	5'-CCAAATGAAGAATCTCAAAGCAGAGAAATGAAAACC-3'	2nd PCR reaction to amplify a portion of JAZ8 (72-131 aa)
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
	JAZ8 (1-44 aa) & JAZ8 (72-131 aa)	JAZ8_NcoI_FP	5'-CCATGGATGAAGCTACAGCAAAATTGTG-3'	3rd PCR reaction to amplify JAZ8ΔZIM
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	
JAZ8ΔEAR	JAZ8	JAZ8_deltaEAR_FP	5'-GCTACAGCAAAATTGTGAC TTTCCCACTTCTTATGATTC-3'	1st PCR reation to amplify a portion of JAZ8 lacking the EAR motif
		JAZ8_pENTR_RP	5'-TTATCGTCGTGAATGGTACGGTG-3'	
	JAZ8 (6-396 bp)	JAZ8_pENTR_FP	5'-CACCATGAAGCTACAGCAAAATTGTG-3'	2nd PCR reaction to amplify JAZ8ΔEAR
		JAZ8_pENTR_RP	5'-TTATCGTCGTGAATGGTACGGTG-3'	
JAZ8ΔEZ	JAZ8ΔZIM	JAZ8_deltaEAR_FP	5'-GCTACAGCAAAATTGTGAC TTTCCCACTTCTTATGATTC-3'	1st PCR reation to amplify a portion of JAZ8 lacking the EAR motif and ZIM domain
		JAZ8_pENTR_RP	5'-TTATCGTCGTGAATGGTACGGTG-3'	
	JAZ8ΔZIM (6-315 bp)	JAZ8_pENTR_FP	5'-CACCATGAAGCTACAGCAAAATTGTG-3'	2nd PCR reaction to amplify JAZ8ΔEZ
		JAZ8_pENTR_RP	5'-TTATCGTCGTGAATGGTACGGTG-3'	
JAZ8ΔJas	JAZ8	JAZ8_NcoI_FP	5'-CCATGGATGAAGCTACAGCAAAATTGTG-3'	
		JAZ8_XhoI_306R	5'-CTCGAGTTATGGATTTGGAAGCTGATTATG-3'	
JAZ8-Jas	JAZ8	JAZ8_ATG133_NcoI_FP	5'-CCATGGATGCATAATCAGCTTCCAAATCC-3'	
		JAZ8_XhoI_RP	5'-CTCGAGTTATCGTCGTGAATGGTACG-3'	

Primers in this section used for site-directed mutagenesis

CONSTRUCT	TEMPLATE	PRIMER NAME	SEQUENCE	NOTE
JAZ8$^{LPIAR\rightarrow AAAAA}$	JAZ8	JAZ8_AR_FP	5'-CCAAATCCAAAAGCAGCAAGGAAAAAATCTCTCC-3'	Forward primer to create SM ->AR mutation
		JAZ8_AR_RP	5'-GGAGAGATTTTTTCCTTGCTGCTTTTGGATTTGG-3'	Reverse primer to create SM ->AR mutation
	JAZ8$^{AR\rightarrow AA}$	JAZ8_IAR_FP	5'-CCAAATCCAAATCCAAAAATCGCAAGGAAAAAATCTCTC-3'	Forward primer to create ASM ->IAR mutation
		JAZ8_IAR_RP	5'-GAGAGATTTTTTCCTTGCGATTTTTGGATTTGGATTTGG-3'	Reverse primer to create ASM ->IAR mutation
	JAZ8$^{IAR\rightarrow AAA}$	JAZ8_PIAR_FP	5'-CTTCCAAATCCAAATCCACCCATCGCAAGGAAAAAATC-3'	Forward primer to create KASM ->PIAR mutation
		JAZ8_PIAR_RP	5'-GATTTTTTCCTTGCGATGGGTGGATTTGGATTTGGAAG-3'	Reverse primer to create KASM ->PIAR mutation
	JAZ8$^{PIAR\rightarrow AAAA}$	JAZ8_LPIAR_FP	5'-CATAATCAGCTTCCA AATCTTCCCATCGCAAGGAAAAAATC-3'	Forward primer to create PKASM ->LPIAR mutation
		JAZ8_LPIAR_RP	5'-GATTTTTTCCTTGCGATGGGAAGATTTGGAAGCTGATTATG-3'	Reverse primer to create PKASM ->LPIAR mutation
JAZ8$^{LELRL\rightarrow AAAAA}$	JAZ8	JAZ8_LEtoAA_FP	5'-GCTACAGCAAAATTGTGACGCGGCACTTCGTCTTTTTCCCAC-3'	Forward primer to create LE -> AA mutation
		JAZ8_LEtoAA_RP	5'-GTGGGAAAAAGACGAAGTGCCGCGTCACAATTTTGCTGTAGC-3'	Reverse primer to create LE ->AA mutation
	JAZ8$^{LE\rightarrow AA}$	LELRLtoAAAAA_FP	5'-GCAAAATTGTGACGCGGCAGCTGCTGCTTTTCCCACTTCTTATGATTC-3'	Forward primer to create LELRL -> AAAAA mutation
		LELRLtoAAAAA_RP	5'-GAATCATAAGAAGTGGGAAAAGCAGCAGCTGCCGCGTCACAATTTTGC-3'	Reverse primer to create LELRL -> AAAAA mutation

Primers in this section used for constructs in the carrot protoplast assay

CONSTRUCT	TEMPLATE	PRIMER NAME	SEQUENCE	NOTE
35S::GD-JAZ8	JAZ8	JAZ8-F	5´-GGGGACAAGTTTGTACAAAAAAGCAGGCTCAATGAAGCTACAGCAAAATTGTGACTTGG-3´	Effector primers used in carrot protoplasts assay
		JAZ8-R	5´-GGGGACCACTTTGTACAAGAAAGCTGGGTCTCATCGTCGTGAATGGTACGGTGAAGTAG-3´	Effector primers used in carrot protoplasts assay
35S::GD-JAZ8-N		JAZ8N-F	5´-GGGGACAAGTTTGTACAAAAAAGCAGGCTCAATGAAGCTACAGCAAAATTGTGACTTGG-3´	Effector primers used in carrot protoplasts assay
		JAZ8N-R	5´-GGGGACCACTTTGTACAAGAAAGCTGGGTCCTATTGAGATTCTTCATTTGGTTGTGGATTT-3	Effector primers used in carrot protoplasts assay
JAZ8-L9A		JAZ8-L9A-F	5´-AAGCTACAGCAAAATTGTGACGCGGAACTTCGTCTTTTTCCCAC-3´	Site-directed mutagenesis primer used in carrot protoplast assay
		JAZ8-L9A-R	5´-GTGGGAAAAAGACGAAGTTCCGCGTCACAATTTTGCTGTAGCTT-3´	Site-directed mutagenesis primer used in carrot protoplast assay
JAZ8-E10A		JAZ8-E10-F	5´-CAGCAAAATTGTGACTTGGCACTTCGTCTTTTTCCCACT-3´	Site-directed mutagenesis primer used in carrot protoplast assay
		JAZ8-E10-R	5´-AGTGGGAAAAAGACGAAGTGCCAAGTCACAATTTTGCTG-3´	Site-directed mutagenesis primer used in carrot protoplast assay
JAZ8-L11A		JAZ8-L11A-F	5´-GCTACAGCAAAATTGTGACTTGGAAGCTCGTCTTTTTCCCACT-3´	Site-directed mutagenesis primer used in carrot protoplast assay
		JAZ8-L11A-R	5´-AGTGGGAAAAAGACGAGCTTCCAAGTCACAATTTTGCTGTAGC-3´	Site-directed mutagenesis primer used in carrot protoplast assay
JAZ8-R12A		JAZ8-R12A-F	5´-CTACAGCAAAATTGTGACTTGGAACTTGCTCTTTTTCCCACTTC-3´	Site-directed mutagenesis primer used in carrot protoplast assay
		JAZ8-R12A-R	5´-GAAGTGGGAAAAAGAGCAAGTTCCAAGTCACAATTTTGCTGTAG-3´	Site-directed mutagenesis primer used in carrot protoplast assay
JAZ8-L13A		JAZ8-L13A-F	5´-CAAAATTGTGACTTGGAACTTCGTGCTTTTCCCACTTCTTATGATTCTGA-3´	Site-directed mutagenesis primer used in carrot protoplast assay
		JAZ8-L13A-R	5´-TCAGAATCATAAGAAGTGGGAAAAGCACGAAGTTCCAAGTCACAATTTTG-3´	Site-directed mutagenesis primer used in carrot protoplast assay
JAZ8-F14A		JAZ8-F14A-F	5´-ACAGCAAAATTGTGACTTGGAACTTCGTCTTGCTCCCACTTCTTATGATT-3´	Site-directed mutagenesis primer used in carrot protoplast assay
		JAZ8-F14A-R	5´-AATCATAAGAAGTGGGAGCAAGACGAAGTTCCAAGTCACAATTTTGCTGT-3´	Site-directed mutagenesis primer used in carrot protoplast assay

Primers in this section used for other Y2H constructs

INSERT	VECTOR	PRIMER NAME	SEQUENCE	NOTE
NINJA	pENTR-TOPO	NINJA_pEntr_EcoRI_FP NINJA_BglII_pB42AD_RP	5'-CACCGAATTCATGGACGATGATAATGGGCTC-3' 5'-AGATCTTCAGGTGTGAGCTGACGCTGC-3'	NINJA further cloned into pGILDA & pB42AD via Gateway cloning
TPL	pENTR-TOPO	TPL_pENTR_FP TPL_pENTR_RP	5'-CACCATGTCTTCTCTTAGTAGAGAGCTCG-3' 5'-CCCGGG TCATCTCTGAGGCTGATCAG-3'	TPL further cloned into pGILDA & pB42AD via Gateway cloning
MYC2	pGILDA & pB42AD			Described in Chung et al (2009)
JAZ3	pGILDA & pB42AD			Described in Chung et al (2009)
JAZ1	pGILDA & pB42AD			Described in Melotto et al (2008)

Supplemental Table 2.
***JAZ* genes used for construction of consensus motifs shown in Figure 6.**

JAZ8-like sequences used for consensus Jas motif shown in Figure 6A

SPECIES	GENE ID	Jas MOTIF
Arabidopsis lyrata	881314	NPKASMKKSLQSFLQKRKSRIQATSPY
Arabidopsis lyrata	333262	NQKVSMKRSLRSFLQKRNVRIQATSPY
Arabidopsis lyrata	482423	NQKVSMKRSLRSFLQKRNVRIQATSPY
Glycine max	Glyma05g27280.1	STGLSMKRSLQRFLQKRKNRVQETSPY
Glycine max	Glyma08g27280.1	GTGLSMKRSLQRFLQKRKNRVQETSPY
Glycine max	Glyma13g29070.1	GTGLSMRKSLQRFLQKRKNRVQEASPY
Glycine max	Glyma15g09980.1	GTGPSMRKSLQRFLQKRRNRVQEASPY
Carica papaya	supercontig_17.12	ANGLSMKRSLQRFLQKRKHSIRATSPY
Ricinus communis	29693.m001988	STGLSMKRSIQRFLQKRKHRAQATSPY
Ricinus communis	29693.m001989	NNGLSMKRSLQRFLQKRNHRIQATCPY
Cucumis sativus	Cucsa.047800.1	TPGLSMKKSLQRFLQKRKHRVQATSPY
Cucumis sativus	Cucsa.054580.1	EASPSMRRSLQRFLQKRKLRIQTLSPY
Cucumis sativus	Cucsa.054630.1	GSGLSMKRSLQRFLQKRKNRIQSASPY
Cucumis sativus	Cucsa.179960.1	AGFSIKKSLQKFLQRRKMRRIRTMSPY
Medicago truncatula	Medtr2g024430.1	GPGLSMKRSLQRFLQKRKNRVQEASPY
Medicago truncatula	Medtr4g154880.1	QSGLSMKRSLQRFLQKRKNRVQEASPY
Prunus persica	ppa013410m	VAGMSMKRSLQRFLQKRKHRVQATSPY
Prunus persica	ppa018461m	PPGVSMKRSLQSFLQKRKKRSQEASPY
Mimulus guttatas	mgv1a016361m	TSGLSMKRSLQRFLEKRKTRLQCTSPY
Mimulus guttatas	mgv1a016202m	SSVVSMKRSLKMFLQKRKTRSQASSPY
Vitus Vinifera	GSVIVT01021514001	ATGLSMKRSLQRFLQKRKNRMEATSPY
Vitus Vinifera	GSVIVT01021516001	PTGLSMKRSLQRFLQKRKNRMEATSPY
Vitus Vinifera	GSVIVT01021519001	PTGLSMKRSLRSFLQKRKNRIEATSPY
Manihot esculenta	cassava4.1_026855m	VYSPNMKISLQRFLEKRNHRIQTTYPY
Manihot esculenta	cassava4.1_019045m	AAGLSMKRSIQRFLQKRKHRVQENSPY
Manihot esculenta	cassava4.1_018315m	NTALSMKRSLQRFLQKRNNRMQATYPY
Citrus sinensis	orange1.1g046141m	NSGLSMKRSLQRFLQKRKHRSLATSPY
Poplus trichocarpa	POPTR_0006s02410.1	PPGLSLKRSLQRFLQKRKKRAEAISPY
Eucalyptus grandis	Egrandis_v1_0.031045m	STGLSMKRSLQRFLQKRQHRSQATSPY
Eucalyptus grandis	Egrandis_v1_0.049073m	GTGLSMKRSLQRFLQKRKLRFHATSPY
Citrus clementina	clementine0.9_025662m	NSGLSMKRSLQRFLQKRKHRSLATSPY
Arabidopsis thaliana	AT2G34600.1	YQKASMKRSLHSFLQKRSLRIQATSPY
Arabidopsis thaliana	AT1G30135.1	NPKASMKKSLQSFLQKRKIRIQATSPY

JAZ10-like sequences used for consensus Jas motif shown in Figure 6B

SPECIES	GENE ID	JAS MOTIF
Sorghum bicolor	Sb01g045180	DMPLARKVSLKRFLEKRKNRLTAADPY
Sorghum bicolor	Sb02g025720	DLPIARRNSLHRFLEKRKDRITAKAPY
Sorghum bicolor	Sb06g031060	DLPIARRHSLQRFLEKRRDRIVSKAPY
Selaginella moellendorffii	439249	DLPQARKASLHRFLEKRKDRLFAKSDK
Arabidopsis lyrata	488996	DLPIARRHSLQRFLEKRRDRLVNKNPY
Arabidopsis lyrata	936941	DVPIARRRSLQRFLEKRRDRFVHTNPY
Arabidopsis lyrata	476379	VERIARRASLHRFFAKRKDRAVARAPY
Arabidopsis lyrata	472142	ELPIARRASLHRFLEKRKDRVTSKAPY
Arabidopsis lyrata	476633	ELPIARRASLHRFLEKRKDRITSKAPY
Arabidopsis lyrata	488138	DLPIARRKSLQRFLEKRKERLVSTSPY
Glycine max	Glyma09g09100.1	EFPIARRHSLQRFLEKRRDRLGSKAPY
Glycine max	Glyma09g09100.2	EFPIARRHSLQRFLEKRRDRLGSKAPY
Glycine max	Glyma13g17180.1	DLPIARKASLHRFLSKRKDRIAAKAPY
Glycine max	Glyma13g17640.2	EFPLARRQSLQRFLEKRRNRLANKSPH
Glycine max	Glyma15g19840.4	HLPIARKASLHRFLEKRKDRIASKAPY
Glycine max	Glyma15g20670.1	EFPIARRHSLQRFLEKRRDRLGSKTPY
Glycine max	Glyma17g05540.1	ELPIARKVSLHRFLSKRKDRIASKAPY
Carica papaya	supercontig_113.51	NLPIARKISLQHFIEKRKSRVMSQSPY
Brachypodium distachyon	Bradi1g72600.1	EMPMARKASLQRFLEKRKSRLAAADPY
Brachypodium distachyon	Bradi3g10820.1	DLPIARKASLHRFLEKRKDRLHAKAPY
Brachypodium distachyon	Bradi4g31240.1	DLPIARRNSLHRFLEKRKGRVIAKAPY
Brachypodium distachyon	Bradi5g08650.1	DIPLARTKSLQQFLVKRKERLTHLGPY
Brachypodium distachyon	Bradi5g24410.2	DLPIARRHSLQRFLEKRRDRIVSKAPY
Ricinus communis	29727.m000494	DLPIARRASLHRFFEKRKDRAAAKAPY
Ricinus communis	29765.m000754	DLPIARKLSLQHFLEKRRRRRTGKSPY
Ricinus communis	30128.m009047	DLPIARRKSLQRFLEKRKERLTSASPY
Oryza sativa	Os03g08320	DMPIARKVSLQRFLEKRKNRIVVAEPL
Oryza sativa	Os04g32480	KEPLTRTKSLQRFLSKRKERLTSLGPY
Oryza sativa	Os09g26780	DLPIARRNSLHRFLEKRKGRMNANAPY
Cucumis sativus	Cucsa.141940	ALPMARKASIQRFLEKRKDRLTPRTPY
Cucumis sativus	Cucsa.149450	DLPIARRASLHRFFEKRKDRVAARGPY
Cucumis sativus	Cucsa.349280	DLPIARKKSLQRFLEKRKERLTTASPY
Medicago truncatula	Medtr5g013690	DLPMTRKASLHRFLEKRKDRIAAKAPY
Prunus persica	ppa011370m	DLPIARRASLHKFLAKRKERVAAIAPY
Prunus persica	ppa011303m	EFPIARRHSLQRFLEKRRDRLVSKNPY
Prunus persica	ppa011173m	DLPIARRKSLQRFLEKRKERLNSVSPF
Mimulus guttatas	mgv1a012664m	YLPIARKKSLARFLEKRKDRITANAPY
Mimulus guttatas	mgv1a015572m	DLPITRRISLQRFLEKRRERLIMLSPY
Mimulus guttatas	mgv1a015559m	DLPITRRISLQRFLEKRRERLIMLSPY
Vitus Vinifera	GSVIVT01000967001	DLPLARRKSLHRFLEKRKERLTSVYPY
Vitus Vinifera	GSVIVT01015042001	ELPIARKASLHRFLEKRKDRITARAPY
Vitus Vinifera	GSVIVT01023256001	DFPIARKSSLQRFLEKRRDRITSRSPY
Manihot esculenta	cassava4.1_013723m	DLPIARRASLHRFLEKRKDRITARAPY
Manihot esculenta	cassava4.1_031135m	GLPIVTRVSLHRFFEKRKERVASKAPY
Manihot esculenta	cassava4.1_016821m	DLPIARRKSLQRFLEKRKERLTSLSPY
Manihot esculenta	cassava4.1_016877m	DLPIARRKSLQRFLEKRKERLTSLSPY
Manihot esculenta	cassava4.1_015933m	ELPIARRHSLQRFFEKRRDRLYSKSPY
Manihot esculenta	cassava4.1_014096m	DLPIARRASLHRFLEKRKDRVASKAPY
Manihot esculenta	cassava4.1_017020m	DLPIARRKSLQRFLEKRKERLTLAFPH

JAZ10-like sequences used for consensus Jas motif shown in Figure 6B, continued

SPECIES	GENE ID	JAS MOTIF
Citrus sinensis	orange1.1g027340m	ELPMARRHSLQRFFEKRRDRLVSKNPY
Citrus sinensis	orange1.1g027356m	ELPMARRHSLQRFFEKRRDRLVSKNPY
Citrus sinensis	orange1.1g028845m	ELPMARRHSLQRFFEKRRDRLVSKNPY
Citrus sinensis	orange1.1g030011m	ELPMARRHSLQRFFEKRRDRLVSKNPY
Citrus sinensis	orange1.1g028982m	TVPIARRASLHRFFEKRKDRAIARAPY
Aquilegia coerulea	AcoGoldSmith_v1.011636m	DLPFARKKSLQRFLEKRKERLISVTPY
Poplus trichocarpa	POPTR_0006s23390.1	ELPIARRHSLQRFFEKRRDRLVSKSPY
Poplus trichocarpa	POPTR_0018s08300.1	ELPIARRQSLQRFFKKRRDRLVSKSPY
Poplus trichocarpa	POPTR_0003s16350.1	DLPIARRKSLQRFLEKRKERLTSATPY
Poplus trichocarpa	POPTR_0003s06670.1	DVPHARRASLHRFFSKRKDRVTARAPY
Poplus trichocarpa	POPTR_0012s04220.1	AVPQARKASLARFLEKRKERVTQTSPY
Poplus trichocarpa	POPTR_0012s04220.2	AVPQARKASLARFLEKRKERVTQTSPY
Poplus trichocarpa	POPTR_0012s04220.3	AVPQARKASLARFLEKRKERVTQTSPY
Poplus trichocarpa	POPTR_0001s13240.1	DLPIARRKSLQRFLEKRKGRLTSVSPY
Eucalyptus grandis	Eucgr.F02865.1	TLPQARRATLVRFLEKRKDRLSSDIYN
Eucalyptus grandis	Eucgr.F02865.2	TLPQARRATLVRFLEKRKDRLSSDIYN
Eucalyptus grandis	Eucgr.G01954.1	DLPLTRRKSLERFFEKRKERLTFASPY
Eucalyptus grandis	Eucgr.B03545.1	YLPIARRKSLQRFLEKRKERLTSASPY
Eucalyptus grandis	Eucgr.C00753.1	DLPIARRHSLQRFFEKRRDRLVNKAPY
Eucalyptus grandis	Eucgr.C00753.2	DLPIARRHSLQRFFEKRRDRLVNKAPY
Eucalyptus grandis	Eucgr.H00537.1	ALPQARQASLARFLEKRKERAMTTSPY
Eucalyptus grandis	Eucgr.H00537.2	ALPQARQASLARFLEKRKERAMTTSPY
Citrus clementina	clementine0.9_021045m	ELPMARRHSLQRFFEKRRDRLVSKNPY
Citrus clementina	clementine0.9_021054m	ELPMARRHSLQRFFEKRRDRLVSKNPY
Citrus clementina	clementine0.9_022268m	TVPIARRASLHRFFEKRKDRAIARAPY
Citrus clementina	clementine0.9_023056m	DLPIARRKSLQRFLEKRKERNDMESDI
Zea mays	GRMZM2G116614_T01	DLPIARRNSLHRFLEKRKDRITAKAPY
Zea mays	GRMZM2G145407_T01	DMPLTRTKSLQQFLQKRKERLSGPGPY
Zea mays	GRMZM2G086920_T02	DLPIARRHSLQRFLEKRRDRVVSKAPY
Zea mays	GRMZM2G005954_T01	DLPIARRNSLHRFLEKRKDRITAKAPY
Zea mays	GRMZM2G005954_T02	DLPIARRNSLHRFLEKRKDRITAKAPY
Zea mays	GRMZM2G024680_T01	MPPIARKLTLQNFLRKRKNRIAGTDDA
Zea mays	GRMZM2G143402_T03	DLPIARRHSLQRFLEKRRDRVVSKAPY
Zea mays	GRMZM2G143402_T01	DLPIARRHSLQRFLEKRRDRVVSKAPY
Zea mays	GRMZM2G143402_T02	DLPIARRHSLQRFLEKRRDRVVSKAPY
Arabidopsis thaliana	AT1G72450.1	VERIARRASLHRFFAKRKDRAVARAPY
Arabidopsis thaliana	AT1G70700.2	SVPQARKASLARFLEKRKERLMSAMPY
Arabidopsis thaliana	AT1G74950.1	ELPIARRASLHRFLEKRKDRITSKAPY
Arabidopsis thaliana	AT1G19180.1	ELPIARRASLHRFLEKRKDRVTSKAPY
Arabidopsis thaliana	AT1G19180.2	ELPIARRASLHRFLEKRKDRVTSKAPY
Arabidopsis thaliana	AT3G43440.1	DVPIARRRSLQRFFEKRRHRFVHTKPY
Arabidopsis thaliana	AT3G43440.2	DVPIARRRSLQRFFEKRRHRFVHTKPY
Arabidopsis thaliana	AT5G20900.1	DLPIARRHSLQRFLEKRRDRLVNKNPY
Setaria italica	Si037628m	DLPIARKASLQRFLQKRKHRINAAEPY
Setaria italica	Si023275m	DLPIARRHSLQRFLEKRRDRIVNKAPY

JAZ8-like sequences used for consensus EAR motif shown in Figure 6C

SPECIES	GENE ID	EAR MOTIF
Arabidopsis lyrata	881314	LELRL
Arabidopsis lyrata	333262	LELRL
Glycine max	Glyma05g27280.1	LELRL
Glycine max	Glyma08g27280.1	LELRL
Glycine max	Glyma13g29070.1	LELAL
Glycine max	Glyma15g09980.1	LELAL
Carica papaya	evm.model.supercontig_17.12	LELRL
Ricinus communis	29693.m001989	LELRL
Cucumis sativus	Cucsa.047800.1	LELRL
Cucumis sativus	Cucsa.054580.1	LELCL
Cucumis sativus	Cucsa.054630.1	LELRL
Cucumis sativus	Cucsa.179960.1	LELGL
Medicago truncatula	Medtr2g024430.1	LELCL
Medicago truncatula	Medtr4g154880.1	LELCL
Prunus persica	ppa013410m	LELQL
Mimulus guttatas	mgv1a016361m	LELPL
Mimulus guttatas	mgv1a016202m	LDLRL
Vitus Vinifera	GSVIVT01021514001	LELRL
Vitus Vinifera	GSVIVT01021516001	LEVRL
Manihot esculenta	cassava4.1_026855m	LELRL
Manihot esculenta	cassava4.1_019045m	LELRL
Manihot esculenta	cassava4.1_018315m	LELRL
Citrus sinensis	orange1.1g046141m	LELRL
Aquilegia coerulea	AcoGoldSmith_v1.025874m	LDLCL
Poplus trichocarpa	POPTR_0006s02410.1	LDLCL
Poplus trichocarpa	POPTR_0011s02260.1	LELRL
Eucalyptus grandis	Egrandis_v1_0.031045m	LELRL
Citrus clementina	clementine0.9_025662m	LELRL
Arabidopsis thaliana	AT2G34600.1	LELRL
Arabidopsis thaliana	AT1G30135.1	LELRL