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Note

Transcriptomic profiles of nodule senescence in *Lotus japonicus* and *Mesorhizobium loti* symbiosis

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Abstract Nodule senescence is a complex developmental process during which essential nutrients are recycled. In order to understand the regulatory mechanism, transcript-profiling analysis during nodule senescence was performed in the *Lotus japonicus-Mesorhizobium loti* symbiosis. Microarray data showed significantly up-regulated expressions in 641 genes out of a total of 20,165 genes during nodule senescence, and down-regulated expressions were observed in 416 genes. These up-regulated genes during senescence were related to cell wall/membrane/envelope biogenesis and extracellular structures. Down-regulated genes were mainly responsible for defense mechanisms. We classified senescence up-regulated genes in two clusters. Genes in cluster 1 were induced at senescence specific stage and those in cluster 2 were induced from nitrogen fixation stage and expressed until nodule senescence. The genes in cluster 1 included typical marker for senescence like gene for heat shock protein. Four hundred sixteen down-regulated genes during nodule senescence were also classified in two clusters, cluster 3 and cluster 4. These genes corresponded to metabolisms for amino acid and plant hormones which are necessary for growth and cell division during nodule development and nitrogen fixation. These results provide the comprehensive data source for investigation of molecular mechanisms underlying nodule senescence in *Lotus japonicus-Mesorhizobium loti* symbiosis.

Key words: *Lotus japonicus*, *Mesorhizobium loti*, nodule senescence, symbiosis, transcriptome.

The symbiotic nitrogen-fixing nodules are established and decayed by complex interactions between legume plants and Rhizobia. The nitrogen fixing activity of the nodule increased from 12 days post inoculation in *Lotus japonicus* (Kouchi et al. 2004) and the nitrogen fixing capacity of the nodules peaked early in its life when the nodule is 3 to 5 weeks post inoculation (wpi, Puppo et al. 2005). Such nodule senescence has been reported to be triggered by various types of stress. The activity of enzymes used in the hydrolysis process associating with programmed cell death increased, especially cysteine proteases and H_2O_2 generating enzymes (Alesandrini et al. 2003; Muller et al. 2001). During nodule senescence, pink color of nodules turns to green because hemes of leghemoglobin are nitrated (Navascuésa et al. 2012). However, the regulatory mechanisms that govern nodule senescence still remain elusive.

Nodules can be developmentally classified into two main groups. Indeterminate nodules, as observed in *Medicago truncatula*, form cylindrical nodules that consist of a gradient of developmental zones with a persistent apical meristem; an infection zone, a fixation zone, and a senescence zone. Aged nodules with those three zones of *M. truncatula* were monitored by microarray (Van de Velde et al. 2006). In the case of *Lotus japonicus*, determinate nodules which are round organs with a central fixation zone were formed. A large-scale gene expression profile was reported using a cDNA array during the early stages of the *L. japonicus* nodulation process (Colebatch et al. 2002; Kouchi et al. 2004). They described the nodule-induced genes, which are involved in the symbiotic nitrogen fixation. However, there is no microarray report of senescence nodule in *L. japonicus*.

In this paper, we present a detailed analysis of nodule senescence in *L. japonicus*.

L. japonicus plants inoculated with *M. loti* were grown in a growth cabinet (EYELA FLI-2000) at 24°C and exposed to 16-h/light and 8-h/dark cycles. Total RNA was isolated from nodules at 2, 4 and 8 wpi using an RNeasy Plant mini kit (Qiagen), respectively.

Abbreviations: KOGs, euKaryotic Orthologous Groups; Wpi, Weeks post inoculation; qRT-PCR, quantitative reverse transcription PCR

This article can be found at http://www.jspcmb.jp/

The acetylene reduction activity of the nodules was surveyed at 2, 4, 8 wpi in *L. japonicus*, and values were 12.28 ±3.27, 54.83±13.17, 15.04±2.60 nmol h^{-1} $plant^{-1}$, respectively. The nodules at 2 wpi, 4 wpi and 8 wpi represent early nitrogen fixation stage, mature nitrogen fixation stage and senescence stage, respectively. Extracted total RNA was quantified using a NanoDrop ND-1000 spectrophotometer (NanoDrop) and checked for quality using an Agilent 2100 Bioanalyzer (Agilent Technologies (CA, USA)). Labeling was performed using a Quick Amp labeling kit, One-color Cy3-CTP (Agilent Technologies) according to the manufacturer's protocol.

The Agilent 4×44 microarray chip was designed for *Lotus* nodule transcript sequences. We selected 20,165 genes which were expressed in nodulated roots at 12 days post inoculation by RNA-seq analysis (Handa et al. unpublished data). Two probes per target gene were designed by the eArray (Agilent Technologies). Each probe was a 60-mer oligonucleotide and the 4×44 K format Agilent microarray consisted of 40,330 probes. The Agilent microarray probes and gene ID are available from GEO (Platform Approval, GPL18811).

For microarray hybridization, 1,650 ng of Cy3-labeled cRNAs of nodules at 2, 4 and 8 wpi were fragmented and hybridized on a slide of *Lotus* 4×44 K microarray at 65°C for 17 h. Hybridization and washing of the hybridized slides were performed according to the manufacturer's instructions. Slides were scanned on the Agilent microarray scanner. The processed raw signal intensity of all probes (40,330) was subjected to 75 percentile normalization with GeneSpring for inter-array comparison (Agilent Technologies) and transformed to log 2 scale.

To isolate genes that are differentially expressed during nodule senescence, the transcriptome data of young nodules at 2 wpi was compared with that of senescence nodule at 8 wpi. The significant intensity differences of more than two-fold and less than 1/2 fold compared to nodules at 2 wpi were listed as up-regulated and down-regulated genes, respectively. The microarray data showed that 641 out of a total of 20,165 genes were up-regulated genes and 416 genes were down-regulated. To investigate the functional distribution, the identified genes were classified into 25 major functional categories according to the euKaryotic Orthologous Groups (KOGs) of NCBI (Figure 1). Among a total of 641 up-regulated genes, 55.4% of the genes displayed similarity to the sequences with known or putative functions. We classified total 20165 genes by KOG database of NCBI. Based on the classification, Figure 1 shows the percentage of each classified up- or down- regulated genes. Significantly up-regulated genes during senescence were related to cell wall/membrane/envelope biogenesis (4.45%) or extracellular structures (6.02%) were identified. These up-regulated genes were divided into two clusters, cluster 1 and cluster 2 (Figure 2, Supplemental Tables 1 and 2). Their expression profile of cluster 1 was significantly induced at 8 wpi. The genes of cluster 2 were induced from 4 wpi and continuously expressed until 8 wpi.

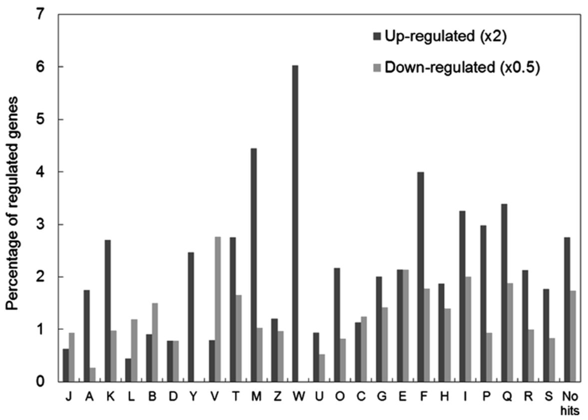
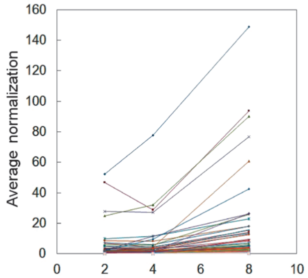


Figure 1. Functional classification according to euKaryotic Orthologous Groups (KOGs) database. Relative frequency of genes belonging to a category is given for 2 data sets: The expression of up-regulated genes (■) and down-regulated genes (▨) were more than two-fold and less than 1/2-fold nodules at 8 wpi compared to nodules at 2 wpi, respectively. J: translation, ribosomal structure and biogenesis, A: RNA processing and modification, K: transcription, L: replication, recombination and repair, B: chromatin structure and dynamics, D: cell cycle control, cell division, chromosome partitioning, Y: nuclear structure, V: defense mechanisms, T: signal transduction mechanisms, M: cell wall/membrane/envelope biogenesis, Z: cytoskeleton, W: extracellular structures, U: intracellular trafficking, secretion, and vesicular transport, O: posttranslational modification, protein turnover, chaperones. C: energy production and conversion, G: carbohydrate transport and metabolism, E: amino acid transport and metabolism, F: nucleotide transport and metabolism, H: coenzyme transport and metabolism, I: lipid transport and metabolism, P: inorganic ion transport and metabolism, Q: secondary metabolites biosynthesis, transport and catabolism, R: general function prediction only, S: function unknown, No hits. The data represents percentage of number of up- or down regulated genes in each KOGs per number of genes in each classified KOGs.

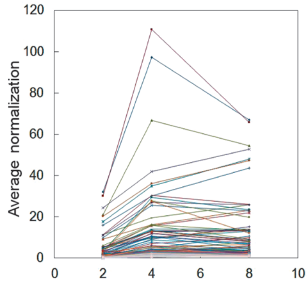
Genes classified in cluster 1 and cluster 2 were 217 and 424, respectively (Supplemental Tables 1 and 2). Cluster 1 had noticeable genes for the Kunitz-type trypsin inhibitor (LjSGA_059392.1) and NAC domain-containing proteins (chr3.CM0460.20.r2.d, Figure 2, Supplemental Table 1). The protease inhibitor of the Kunitz family is important in strictly controlling the synthesis of protease (Habib and Fazili 2007). NAC domain-containing protein, GmNAC6, is synergistically activated by a combination of endoplasmic reticulum (ER) stress and osmotic stress signals and induces a senescence-like response and cell death in soybean (Faria et al. 2011). The NAC domain-containing protein in cluster 1 of *L. japonicus* may also induce rapid cell death. The genes in cluster 1 also contained a typical marker for the senescence like a heat shock protein (chr4.CM0432.1970.r2.m).

The serine acetyltransferase gene (chr6.CM0245.580.



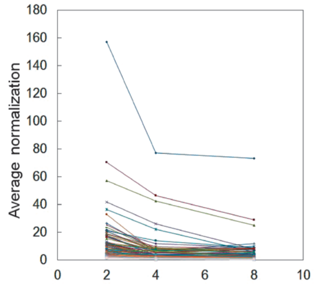
Cluster1 (217)

ID number	Annotation	2Wpi Average normalized	2Wpi SD normalized	2Wpi %CV	4Wpi Average normalized	4Wpi SD normalized	4Wpi %CV	8Wpi Average normalized	8Wpi SD normalized	8Wpi %CV
chr2.CM0191.580.r2.m	Nlj21 [Lotus japonicus]	52.30	5.42	10.36	77.67	16.04	20.64	148.91	14.81	9.95
chr1.CM0012.2130.r2.m	tonoplast intrinsic protein	46.64	1.88	4.03	28.84	0.74	2.56	93.89	2.64	2.81
chr5.CM0456.170.r2.d	acidic chitinase	27.98	2.53	9.04	27.09	4.31	15.91	76.86	7.26	9.45
LjSGA_096088.1	pathogenesis-related protein PR10	24.91	2.36	9.48	32.13	1.73	5.39	90.15	6.29	6.98
LjSGA_043683.1	U-box domain-containing protein 20-like	9.80	0.33	3.38	11.51	0.25	2.17	23.09	0.18	0.78
chr5.CM0071.800.r2.m	CBL-interacting protein kinase 4	8.50	0.79	9.34	8.42	0.07	0.82	17.99	1.25	6.93
LjSGA_025506.1	bon1-associated protein 2-like	7.17	0.81	11.27	5.94	0.37	6.25	18.25	1.43	7.83
chr2.CM0608.1150.r2.m	uncharacterized protein	6.86	0.40	5.85	4.38	0.43	9.77	15.33	0.93	6.08
LjSGA_057224.1	trypsin inhibitor	6.01	0.19	3.14	5.67	0.50	8.87	25.85	1.45	5.62
chr1.CM0433.130.r2.d	BURP domain-containing protein	5.21	0.36	7.00	2.04	0.38	18.69	13.03	0.51	3.87
chr1.LjT14M06.150.r2.d	uncharacterized protein	5.08	0.16	3.11	4.64	0.11	2.35	13.66	0.41	3.00
chr3.LjT36L22.160.r2.a	nicotianamine synthase	3.82	0.37	9.73	4.40	0.65	14.84	60.67	5.33	8.78
chr3.CM0213.540.r2.m	ATP-binding cassette	3.41	0.04	1.16	3.86	0.24	6.16	6.83	0.31	4.53
chr4.CM0432.2980.r2.d	S-adenosyl-L-methionine: 2,7,4-trihydroxyisoflavano	3.19	0.10	3.00	2.93	0.01	0.22	8.83	0.12	1.32
chr1.CM0320.110.r2.d	probable wrky transcription factor 70-like	2.57	0.06	2.27	1.96	0.01	0.51	6.76	0.17	2.51
chr2.CM0610.140.r2.m	ethylene-responsive transciptional coactivator-like pı	2.35	0.87	37.03	11.41	4.06	35.57	26.40	9.51	36.04
chr4.CM0026.1220.r2.a	cytochrome P450	2.29	0.04	1.61	2.66	0.19	7.00	15.81	1.00	6.35
chr5.CM0180.30.r2.d	aspartic proteinase nepenthesin-1-like	2.19	0.09	4.08	2.52	0.03	1.00	5.16	0.18	3.55
LjSGA_059392.1	kunitz-type trypsin inhibitor-like 2 protein	2.18	0.03	1.21	9.57	0.85	8.89	42.65	1.61	3.77
chr2.CM0249.1390.r2.m	isoflavone reductase	2.15	0.16	7.44	3.86	0.46	11.84	14.02	0.29	2.04



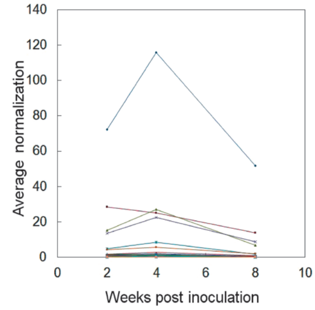
Cluster2 (424)

ID number	Annotation	2Wpi Average normalized	2Wpi SD normalized	2Wpi %CV	4Wpi Average normalized	4Wpi SD normalized	4Wpi %CV	8Wpi Average normalized	8Wpi SD normalized	8Wpi %CV
chr1.CM0195.250.r2.m	cysteine proteinase 15A-like	32.06	1.32	4.12	97.33	2.52	2.59	66.84	2.98	4.45
chr1.CM0295.970.r2.m	peptide transporter PTR3-a	30.02	3.19	10.63	110.70	8.46	7.64	65.69	5.05	7.69
chr2.CM0065.600.r2.d	uncharacterized protein	21.03	0.03	0.14	66.63	0.77	1.16	54.48	1.05	1.93
chr3.CM0135.890.r2.a	cyclophilin	24.45	1.17	4.80	41.99	0.19	0.46	52.82	1.25	2.37
LjSGA_015484.1	cysteine protease	17.53	0.63	3.59	34.97	0.85	2.44	47.98	1.24	2.59
chr4.CM0126.510.r2.m	subtilisin-like protease SDD1-like	20.26	0.90	4.46	36.20	3.61	9.98	47.11	2.20	4.66
LjSGA_062791.1	no hit	15.81	1.52	9.64	30.23	1.53	5.05	43.71	2.98	6.83
chr1.CM2079.120.r2.a	UNC93-like protein	11.24	0.66	5.88	30.39	1.73	5.70	25.93	1.66	6.39
chr1.CM0017.470.r2.a	transaldolase	11.31	1.22	10.74	19.46	2.52	12.93	25.81	2.44	9.44
LjT42E21.90.r2.m	wound-induced protein	11.07	0.61	5.48	26.92	1.85	6.87	25.75	1.17	4.54
chr4.CM0432.790.r2.m	carboxypeptidase C	2.88	0.04	1.33	29.32	1.49	5.07	23.29	0.42	1.80
LjSGA_051679.1	cysteine synthase	9.10	0.16	1.74	16.16	0.49	3.04	23.16	0.12	0.51
chr4.LjT13G24.170.r2.a	cytochrome p450 like TBP	9.95	0.12	1.18	25.66	0.95	3.71	23.02	0.52	2.24
LjSGA_019294.2	type 2 metallothionein	5.13	0.10	2.00	15.76	0.06	0.38	21.90	0.38	1.74
chr1.CM0591.60.r2.m	no hit	3.76	0.03	0.85	27.61	0.50	1.80	19.77	0.57	2.87
LjSGA_142964.1	nodulin-like protein	0.73	0.07	10.03	9.15	0.51	5.55	15.28	1.14	7.44
chr4.CM0165.230.r2.d	calmodulin-like protein	4.40	0.19	4.40	14.11	0.66	4.69	14.07	0.43	3.03
chr4.CM0075.30.r2.m	uncharacterized protein	5.52	0.29	5.27	9.90	0.29	2.93	14.04	0.83	5.95
chr3.CM0160.370.r2.m	uncharacterized protein	5.10	0.06	1.19	13.33	0.25	1.91	13.48	0.54	4.04
chr3.CM0160.350.r2.m	proline-rich protein	5.27	0.16	3.12	13.02	0.14	1.09	13.35	0.58	4.36



Cluster3 (374)

ID number	Annotation	2Wpi Average normalized	2Wpi SD normalized	2Wpi %CV	4Wpi Average normalized	4Wpi SD normalized	4Wpi %CV	8Wpi Average normalized	8Wpi SD normalized	8Wpi %CV
chr1.CM0104.2620.r2.m	arabinogalactan peptide 14	157.19	6.16	3.92	77.18	0.20	0.26	73.07	3.94	5.39
chr1.CM0125.390.r2.m	probable peptide nitrate transporter at2g40460-like	70.29	2.57	3.66	46.27	3.04	6.58	28.98	1.30	4.49
chr4.CM0337.580.r2.m	EKN protein	57.04	5.60	9.81	42.54	3.05	7.16	24.94	1.50	6.01
chr4.CM0227.40.r2.d	AP2 erf domain-containing transcription factor	41.62	2.69	6.46	25.98	0.20	0.76	7.87	0.24	3.00
chr1.CM0544.890.r2.m	cu zn superoxide dismutase	36.45	2.04	5.60	21.99	3.06	13.93	5.77	1.08	18.70
chr3.CM0282.1000.r2.m	early nodulin-like protein 2-like	32.96	2.06	6.26	5.06	0.33	6.44	7.62	0.45	5.87
chr4.CM0042.2230.r2.m	calmodulin 24-like protein	26.36	0.46	1.73	6.84	0.34	4.98	11.61	0.16	1.39
chr5.CM1077.360.r2.a	glutamine expressed	25.35	1.12	4.40	8.07	0.31	3.82	8.53	0.20	2.34
chr1.CM0104.2710.r2.a	uncharacterized protein loc100798848 isoform 1	23.50	1.02	4.33	7.39	0.16	2.19	7.91	0.16	1.96
chr2.CM0021.560.r2.m	uncharacterized protein	21.61	0.02	0.08	11.69	0.54	4.61	8.98	0.16	1.76
chr4.CM0046.1620.r2.m	aquaporin NIP1-2	21.09	1.97	9.34	13.69	1.75	12.78	8.84	0.98	11.13
chr1.CM0017.1450.r2.d	farnesylated protein	20.63	1.86	8.99	5.80	0.55	9.49	8.62	0.86	10.02
chr1.CM0398.350.r2.d	dehydration-induced protein ERD15	20.51	0.94	4.58	6.42	0.08	1.23	9.97	0.44	4.42
chr4.CM0006.210.r2.d	no hit	18.99	1.16	6.09	9.66	0.01	0.11	8.25	0.18	2.22
chr3.CM0590.380.r2.d	uncharacterized protein	18.42	1.48	8.01	8.50	0.46	5.37	7.54	0.75	9.89
chr2.CM0608.1430.r2.m	uncharacterized protein	17.86	0.44	2.47	3.49	0.31	8.87	6.70	0.54	8.04
chr3.CM1570.70.r2.a	IAA-amino acid hydrolase ILR1-like protein	17.51	0.49	2.79	2.84	0.96	33.83	3.48	1.29	37.05
LjSGA_023779.1	coproporphyrinogen III oxidase	17.47	1.47	8.42	7.98	0.26	3.25	6.15	0.57	9.27
chr2.CM0903.320.r2.a	uncharacterized protein loc100815940	16.71	0.16	0.96	5.63	0.14	2.42	7.28	0.02	0.31
chr1.LjT04N09.160.r2.d	NAC domain protein	16.50	0.12	0.73	5.31	0.09	1.66	7.91	0.10	1.21



Cluster4 (42)

ID number	Annotation	2Wpi Average normalized	2Wpi SD normalized	2Wpi %CV	4Wpi Average normalized	4Wpi SD normalized	4Wpi %CV	8Wpi Average normalized	8Wpi SD normalized	8Wpi %CV
chr4.CM0337.590.r2.m	vacuolar iron transporter homolog 4-like	72.10	6.53	9.06	115.67	11.23	9.70	51.63	2.09	4.05
chr6.CM1514.140.r2.m	dihydroneopterin aldolase	28.40	2.48	8.72	24.97	3.69	14.78	13.89	3.40	24.49
LjT36K06.70.r2.d	sugar transporter sweet1-like	15.06	4.14	27.51	26.85	7.31	27.23	6.78	1.72	25.32
chr4.CM0414.440.r2.d	metal transporter	13.43	2.25	16.79	22.61	5.03	22.24	8.84	1.94	22.01
chr5.LjT43D06.110.r2.d	vegetative lectin	4.79	0.23	4.80	8.58	0.00	0.03	1.80	0.10	5.27
chr2.CM0021.1330.r2.m	expansin-like B1-like	4.26	0.34	7.96	5.54	0.50	9.01	1.90	0.13	7.06
chr1.CM1868.110.r2.a	ubiquitin system component CUE protein	1.67	0.01	0.87	1.97	0.06	3.25	0.55	0.03	4.65
LjSGA_060891.2	inositol phosphate kinase	1.66	0.12	7.18	2.77	0.35	12.61	0.91	0.07	7.67
chr4.CM0307.380.r2.d	mitochondrial substrate carrier family protein	1.35	0.02	1.26	1.47	0.03	2.26	0.67	0.01	2.02
chr1.CM0012.190.r2.m	probable membrane-associated kinase regulator 4-li	1.15	0.02	1.74	1.11	0.04	3.66	0.49	0.01	1.03
chr2.CM0081.530.r2.d	quinone oxidoreductase-like protein	0.92	0.05	5.22	0.93	0.04	4.73	0.31	0.02	5.09
LjSGA_016572.1	ethylene-responsive transcription factor ERF118	0.82	0.04	5.34	0.84	0.05	5.97	0.40	0.00	0.03
chr1.CM0109.110.r2.d	uncharacterized protein	0.80	0.05	6.54	1.01	0.08	7.53	0.36	0.04	11.35
LjSGA_047220.1	zinc finger protein constans-like 9	0.77	0.04	4.66	0.67	0.03	4.92	0.24	0.01	3.38
LjSGA_039721.1	glucose 1-dehydrogenase-like	0.75	0.02	3.10	1.04	0.04	3.79	0.31	0.02	6.31
chr2.CM0373.110.r2.d	phospholipase a2	0.65	0.03	4.54	0.57	0.03	5.22	0.33	0.00	0.67
chr5.CM0657.290.r2.m	cytosolic Fe-S cluster assembly factor nbp35	0.63	0.06	8.79	0.82	0.12	14.38	0.22	0.03	11.66
LjSGA_084433.1	expansin B3	0.63	0.05	7.61	0.50	0.00	0.01	0.16	0.00	1.82
LjSGA_087846.1	peptide chain release factor 2	0.61	0.01	1.31	0.69	0.02	3.38	0.24	0.01	2.78
chr6.CM0013.1230.r2.m	uncharacterized protein	0.57	0.00	0.16	0.71	0.03	4.81	0.17	0.01	4.36

Figure 2. Expression profiles of genes differentially expressed during nodule senescence. The graphs show the expression patterns of significant genes for each cluster. The total number of genes in each cluster is indicated in parentheses. The data are expressed as average normalization and standard deviation (SD). The coefficient of variation (CV) is the percentage of the mean represented by the SD. The top twenty genes in 1 and 2 clusters and 3 and 4 clusters according to the expression pattern of 8 and 2 wpi are shown, respectively. The complete list of differentially expressed genes in each cluster is available in the Supplemental Tables 1–4.

r2.a), which catalyzes acetyl-CoA to *O*-acetylserine, was classified in cluster 2. Genes for metallothionein (LjSGA_019294.2) and heat shock protein (chr3.CM0127.770.r2.d) were also in cluster 2. These genes were induced under oxidative stress or defense response (Büttner and Singh 1997; Cvjetko et al. 2014; Hondo et al. 2007; Mehta et al. 1996; Mir et al. 2004). A gene for iron-storage protein, ferritin (chr3.CM0116.300.r2.m), was classified in cluster 2 (Supplemental Table 2, Figure 3). During nodule senescence, membranes in nodule tissue degrade and iron is released to cytoplasm, inhibiting nitrogen fixation (Arosio et al. 2009; Ravet et al. 2009). Increased ferritin observed within the nodules might reduce iron content in cytoplasm and restrict induced senescence, resulting in prolonged nitrogen fixation. These genes classified in cluster 2 might be

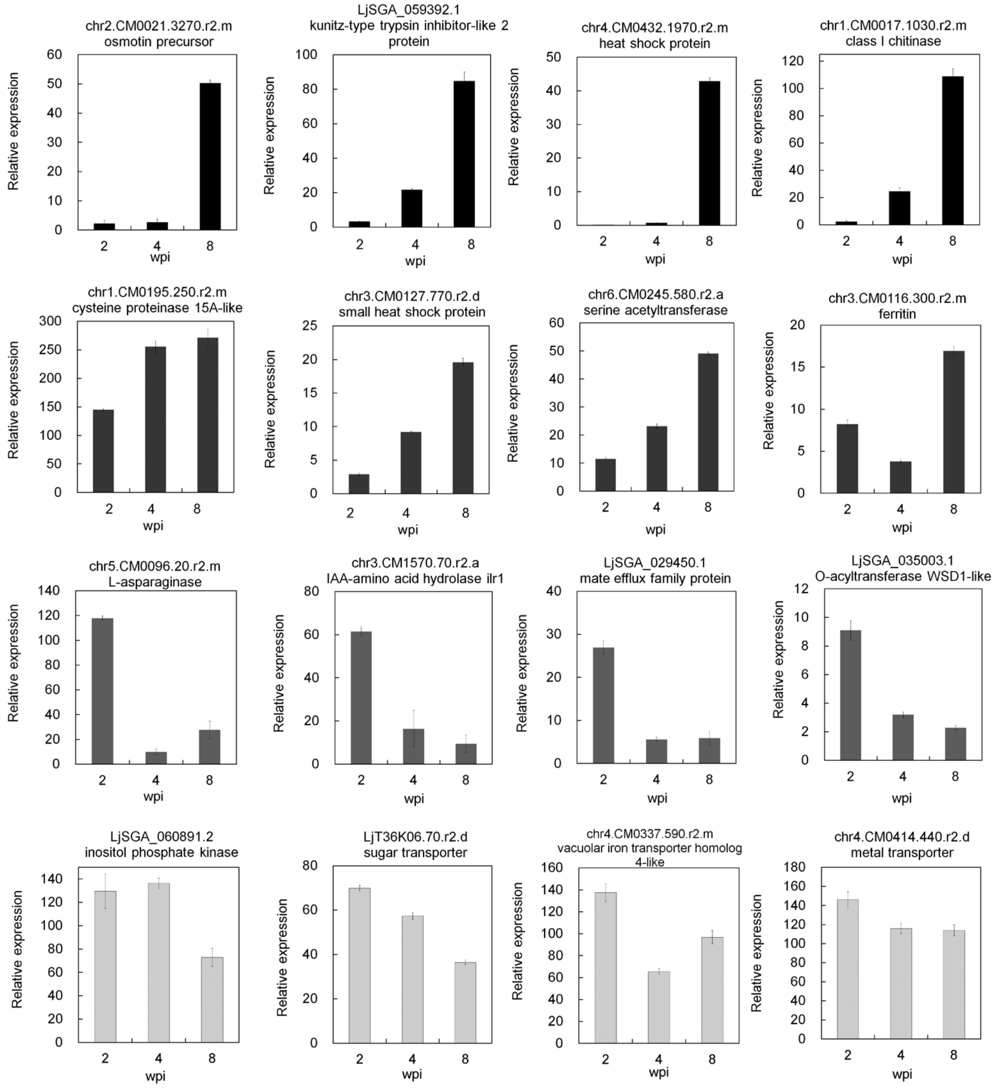


Figure 3. Comparison of relative expression levels in the microarray analysis with qRT-PCR. Representatives of genes in cluster 1 (■), cluster 2 (■), cluster 3 (■) and cluster 4 (■) during nodule development. The expression profile was normalized to ubiquitin. All of the data are shown as±SD wpi: weeks post inoculation.

important to maintain nitrogen fixation in the nodules.

Four hundred sixteen down-regulated genes during nodule senescence were also classified into two clusters, cluster 3 and cluster 4. Their expressions of 374 genes in cluster 3 were highest at 2 wpi and were down-regulated from 4 wpi (Figure 2, Supplemental Table 3). Forty two genes of cluster 4 were up-regulated until 4 wpi and were down-regulated at 8 wpi (Figure 2, Supplemental Table 4). Genes of clusters 3 and 4 were expressed in the stages of nitrogen fixation in fully developed nodule. Functional classification according to classified KOGs database indicated many defense mechanisms genes (2.77%) were identified in these down-regulated genes of clusters 3 and 4 (Figure 1). Although 2.56% of the genes had similarity to ones of function unknown or no similarity to deposited sequences. A full interpretation of the genes have to wait until completion of *L. japonicus* genome annotation. These clusters contained a number of genes for antioxidant-related proteins such as L-ascorbate oxidase (LjSGA_025815.1), peroxidase (chr1.CM0207.130.r2.m, LjSGA_036806.1), glutathione S-transferase (LjSGA_057970.1, LjSGA_010022.2) and leghemoglobin (chr5.CM0909.860.r2.a) (Figure 2, Supplemental Tables 3 and 4). Becana et al. (2010) showed that antioxidants are important for nodule function. Drought or other types of abiotic stress lead to decreases of antioxidant activities that are associated with nodule senescence (Gogorcena et al. 1997; Pérez Guerra et al. 2010; Porcel et al. 2003; Swaraj et al. 1994). Our data support that decreased activities of antioxidants induced nodule senescence.

To confirm the fidelity of microarray analysis in this study, selected genes were subjected to quantitative reverse transcription PCR (qRT-PCR) according to the manufacturer's protocol (Thermal Cycler Dice Real Time System II; Takara). For qRT-PCR analysis, thirtytwo genes were selected. These specific primers used for qRT-PCR are shown in Supplemental Table 5. The result demonstrated that the expression profiles obtained using the two methods were consistent (Figure 3, Supplemental Figure 1).

To conclude, senescence-associated genes might correspond to trigger degradation of the organs, and conversely preserve and protect cells from environmental stimulus, which leads to aging classified in metabolism, and cellular process. Different expression clusters might reflect the developmental stage of nodule senescence. Especially, genes in cluster 1 appeared specifically in nodule senescence, indicating that these genes can be good markers for the senescence. For many legume crops, nodule senescence coincides with pod filling (Lawn and Brun 1974). Therefore, extending the period of active nitrogen fixation by delaying nodule senescence might have a beneficial effect on crop yield. This microarray data should be helpful in future study of senescence-related genes.

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Supplemental Tables and Figure

Supplemental Table 1. Expression profile of 217 genes in cluster 1 during nodule senescence

Supplemental Table 2. Expression profile of 424 genes in cluster 2 during nodule senescence

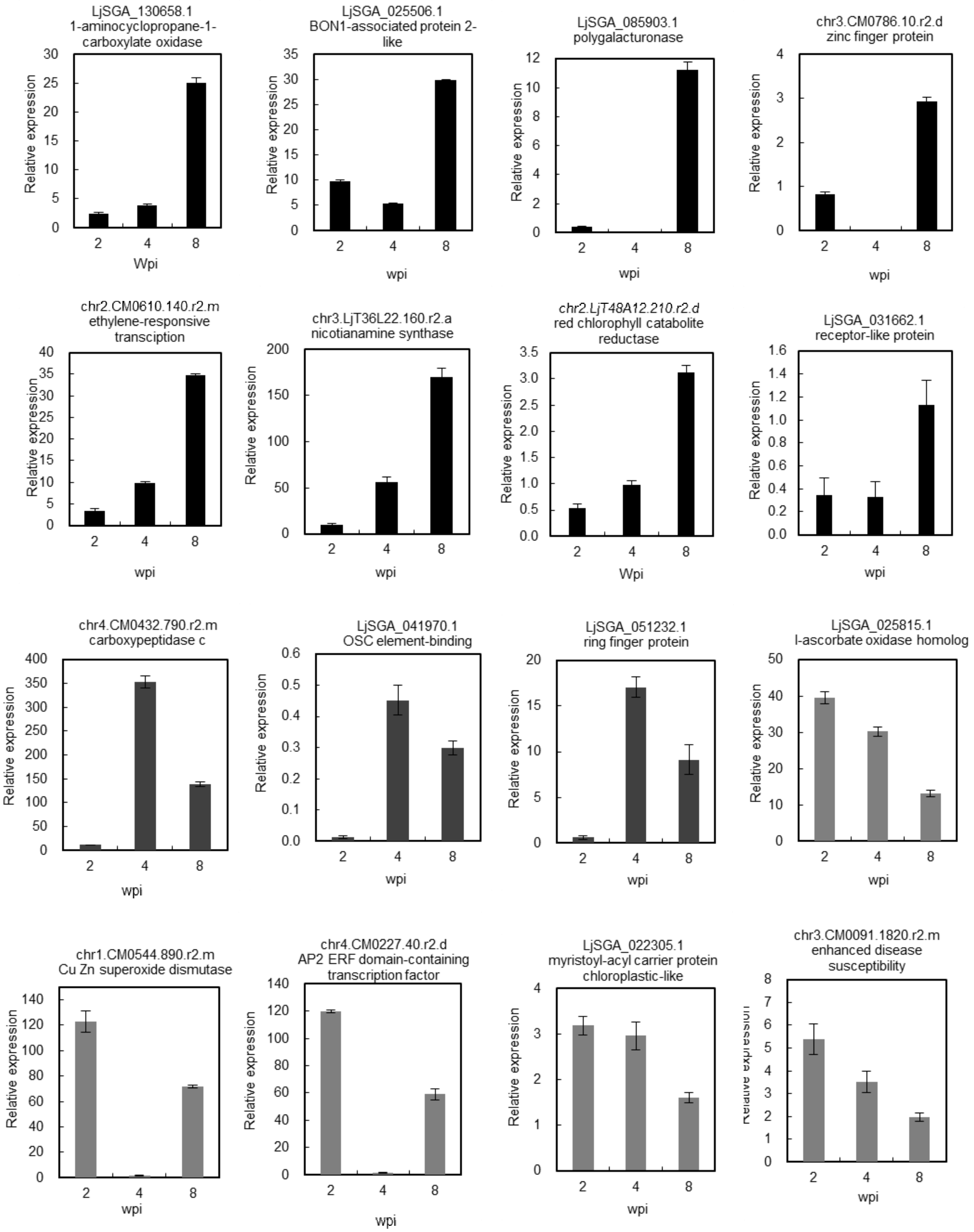
Supplemental Table 3. Expression profile of 374 genes in cluster 3 during nodule senescence

Supplemental Table 4. Expression profile of 42 genes in cluster 4 during nodule senescence

Supplemental Table 5. Primers list used in this study

Supplemental Figure 1 Comparison of relative expression levels in the microarray analysis with qRT-PCR. The other expression profiles classified in cluster 1 (■), cluster 2 (■), and cluster 3 (■). The expression profile was normalized to ubiquitin. All of the data are shown as ± SD. Wpi: weeks post inoculation

Supplemental Figure1, Chungopast et al.,



Supplemental Table 1. Expression profile of 217 genes in cluster 1 during nodule senescence

ID number	Annotation	2 wpi			4 wpi			8 wpi		
		Average Normalized	SD Normalized	CV (%)	Average Normalized	SD Normalized	CV (%)	Average Normalized	SD Normalized	CV (%)
chr2.CM0191.580.r2.m	Nlj21 [Lotus japonicus]	52.299	5.419	10.361	77.671	16.035	20.645	148.909	14.810	9.945
chr1.CM0012.2130.r2.m	tonoplast intrinsic protein	46.639	1.881	4.033	28.841	0.737	2.555	93.886	2.643	2.815
chr5.CM0456.170.r2.d	acidic chitinase	27.983	2.529	9.036	27.087	4.310	15.911	76.861	7.261	9.447
LjSGA_096088.1	pathogenesis-related protein PR10	24.915	2.362	9.481	32.129	1.733	5.395	90.146	6.289	6.977
LjSGA_043683.1	U-box domain-containing protein 20-like	9.800	0.331	3.379	11.513	0.250	2.173	23.093	0.180	0.780
chr5.CM0071.800.r2.m	CBL-interacting protein kinase 4	8.498	0.794	9.341	8.418	0.069	0.823	17.988	1.247	6.932
LjSGA_025506.1	bon1-associated protein 2-like	7.175	0.809	11.270	5.941	0.371	6.252	18.246	1.430	7.835
chr2.CM0608.1150.r2.m	uncharacterized protein	6.864	0.402	5.852	4.383	0.428	9.775	15.333	0.933	6.082
LjSGA_057224.1	trypsin inhibitor	6.006	0.189	3.141	5.669	0.503	8.869	25.848	1.452	5.616
chr1.CM0433.130.r2.d	BURP domain-containing protein	5.209	0.365	7.003	2.038	0.381	18.691	13.034	0.505	3.875
chr1.LjT14M06.150.r2.d	uncharacterized protein	5.083	0.158	3.109	4.639	0.109	2.350	13.659	0.409	2.998
chr3.LjT36L22.160.r2.a	nicotianamine synthase	3.821	0.372	9.730	4.404	0.654	14.844	60.671	5.328	8.781
chr3.CM0213.540.r2.m	ATP-binding cassette	3.409	0.040	1.164	3.858	0.238	6.162	6.835	0.310	4.532
chr4.CM0432.2980.r2.d	S-adenosyl-L-methionine: 2,7,4-trihydroxyisoflavanone 4 -O-methyltransferase	3.185	0.096	3.005	2.933	0.006	0.219	8.826	0.117	1.325
chr1.CM0320.110.r2.d	probable wrky transcription factor 70-like	2.574	0.058	2.271	1.958	0.010	0.506	6.756	0.170	2.510
chr2.CM0610.140.r2.m	ethylene-responsive transciptional coactivator-like protein	2.353	0.872	37.034	11.414	4.060	35.573	26.402	9.515	36.038
chr4.CM0026.1220.r2.a	cytochrome P450	2.292	0.037	1.610	2.665	0.186	6.998	15.808	1.005	6.355
chr5.CM0180.30.r2.d	aspartic proteinase nepenthesin-1-like	2.194	0.090	4.085	2.518	0.025	0.998	5.162	0.183	3.547
LjSGA_059392.1	kunitz-type trypsin inhibitor-like 2 protein	2.182	0.026	1.212	9.571	0.851	8.890	42.649	1.610	3.774
chr2.CM0249.1390.r2.m	isoflavone reductase	2.147	0.160	7.441	3.865	0.458	11.844	14.021	0.286	2.040
LjSGA_042762.1	bon1-associated protein 2-like	1.967	0.052	2.644	2.262	0.108	4.791	5.799	0.024	0.408
LjSGA_030260.1	bon1-associated protein 2-like	1.918	0.150	7.797	1.967	0.223	11.330	4.538	0.426	9.391
chr2.CM0272.460.r2.d	lysine histidine transporter	1.886	0.084	4.475	1.786	0.015	0.839	4.025	0.342	8.501
chr2.CM0249.1380.r2.m	isoflavone reductase	1.817	0.112	6.162	3.374	0.260	7.719	12.617	0.485	3.841
chr5.CM1323.310.r2.d	benzyl alcohol o-benzoyltransferase-like	1.752	0.081	4.637	0.888	0.065	7.353	5.537	0.037	0.665
LjSGA_134572.1	pathogenesis-related protein 1	1.653	0.036	2.197	0.285	0.001	0.452	9.670	0.059	0.611
chr2.CM0826.310.r2.m	brassinosteroid insensitive 1-associated receptor kinase 1	1.583	0.055	3.445	0.963	0.194	20.188	3.223	0.303	9.406
chr6.LjT47B05.40.r2.a	serine threonine-protein kinase-like protein ccr3-like	1.482	0.009	0.613	1.474	0.004	0.265	3.004	0.033	1.100
LjSGA_039552.2	heavy metal transport detoxification domain-containing protein	1.403	0.033	2.318	1.564	0.066	4.194	4.082	0.246	6.032
chr1.CM0375.240.r2.d	cytochrome p450	1.376	0.125	9.105	1.954	0.462	23.658	3.916	0.252	6.425
chr5.CM0335.70.r2.d	dehydrin	1.236	0.037	2.969	1.144	0.132	11.506	3.012	0.187	6.211
chr2.CM0021.3270.r2.m	osmotin precursor	1.231	0.002	0.133	1.287	0.025	1.906	8.503	0.437	5.135
chr1.CM0088.510.r2.d	brassinosteroid insensitive 1-associated receptor kinase 1 precursor	1.186	0.006	0.468	0.997	0.047	4.705	2.520	0.165	6.564
chr2.CM0904.50.r2.d	tripeptidyl-peptidase 2-like	1.165	0.016	1.395	1.386	0.013	0.913	2.465	0.034	1.391
chr3.CM0213.210.r2.a	uncharacterized protein loc100801941	1.164	0.067	5.719	1.210	0.037	3.051	4.924	0.065	1.327
chr3.CM0279.1000.r2.m	metalloendoproteinase 1-like	1.134	0.011	1.005	2.268	0.032	1.418	4.535	0.004	0.085
chr4.CM0087.1770.r2.m	F-box family protein	1.129	0.073	6.503	1.273	0.089	6.975	3.357	0.269	8.028
chr6.CM0055.360.r2.d	ISP4-like protein	1.094	0.028	2.573	0.421	0.081	19.191	2.544	0.228	8.977
chr6.CM0584.140.r2.d	uncharacterized protein	1.049	0.108	10.291	1.277	0.089	6.979	2.885	0.153	5.314
chr1.CM0109.390.r2.m	cytochrome p450	1.048	0.194	18.497	1.436	0.191	13.305	3.288	0.296	9.016
chr4.CM0042.1210.r2.m	uncharacterized protein	0.881	0.089	10.133	0.552	0.050	8.984	1.997	0.134	6.693
LjSGA_012246.1	G-type lectin S-receptor-like serine threonine-protein kinase RLK1-like	0.872	0.168	19.268	0.577	0.105	18.131	3.376	0.315	9.341
LjSGA_135673.1	low quality protein: probably inactive leucine-rich repeat receptor-like protein kinase at5g48380-lik	0.860	0.013	1.531	0.739	0.074	10.039	1.897	0.107	5.643
chr5.CM1392.180.r2.m	probable lrr receptor-like serine threonine-protein kinase at2g16250-like	0.799	0.020	2.565	0.828	0.025	2.991	1.803	0.116	6.452
LjSGA_085903.1	polygalacturonase	0.746	0.035	4.701	0.050	0.007	14.495	3.035	0.064	2.121
chr1.CM0017.1030.r2.m	class I chitinase	0.728	0.057	7.770	1.665	0.108	6.463	26.538	2.285	8.609
LjSGA_040710.1	uncharacterized protein	0.644	0.078	12.103	0.376	0.052	13.782	1.456	0.131	9.016
LjSGA_040698.1	universal stress protein family protein	0.634	0.013	1.981	0.743	0.069	9.294	3.861	0.115	2.967
chr6.LjT41B20.110.r2.d	wall-associated receptor kinase-like 20	0.624	0.012	1.902	0.250	0.010	3.958	1.987	0.015	0.758
chr2.CM0608.560.r2.m	ribonuclease t2	0.610	0.062	10.209	0.197	0.018	9.351	1.498	0.116	7.722
chr1.CM0050.450.r2.d	protein ZCF37	0.560	0.035	6.249	0.311	0.012	3.935	1.197	0.090	7.521
chr5.CM0186.280.r2.d	ethylene receptor	0.516	0.061	11.767	0.700	0.049	7.067	1.143	0.111	9.727
chr2.CM0021.1440.r2.a	phospholipase a1- chloroplastic-like	0.500	0.008	1.514	0.499	0.010	2.047	1.802	0.014	0.760
LjSGA_018057.1	non-specific lipid-transfer protein	0.469	0.005	1.153	0.290	0.021	7.265	2.640	0.058	2.200
chr5.CM1125.340.r2.m	adenylate isopentenyltransferase	0.444	0.026	5.755	1.202	0.127	10.583	4.055	0.186	4.581
chr6.CM0314.280.r2.m	bacterial-induced peroxidase	0.444	0.036	8.011	0.146	0.016	11.067	1.426	0.116	8.164
LjSGA_010097.2	uncharacterized protein	0.442	0.009	2.125	0.547	0.010	1.876	0.925	0.008	0.819
LjSGA_036927.1	desacetoxyvindoline 4-hydroxylase	0.406	0.045	11.095	0.470	0.027	5.802	0.903	0.048	5.259
LjSGA_046847.1	uncharacterized protein	0.404	0.026	6.425	0.477	0.033	6.944	0.988	0.078	7.912
chr2.LjT43I20.160.r2.d	Peroxisomal fatty acid beta-oxidation multifunctional protein	0.390	0.006	1.645	0.542	0.032	5.946	1.090	0.032	2.949
chr3.CM0460.20.r2.d	NAC domain-containing	0.378	0.007	1.726	0.510	0.080	15.685	1.005	0.019	1.841
LjSGA_144365.1	phosphate transporter	0.358	0.012	3.278	0.229	0.006	2.547	0.801	0.009	1.155
chr6.CM0573.60.r2.d	AP2 erf domain-containing transcription factor	0.358	0.024	6.749	0.203	0.020	9.912	0.908	0.037	4.081
chr3.CM0208.430.r2.d	late elongated hypocotyl and circadian clock associated-1-like protein 1	0.347	0.031	8.941	0.117	0.002	2.077	0.718	0.039	5.372
chr5.CM0239.410.r2.d	universal stress protein a-like	0.346	0.033	9.448	0.283	0.011	4.053	2.205	0.135	6.115
LjSGA_050544.1	wrky transcription factor 11	0.336	0.077	22.748	0.614	0.101	16.505	1.130	0.109	9.616
chr5.CM0071.470.r2.d	basic 7S globulin 2 precursor small	0.323	0.007	2.233	0.171	0.015	8.973	0.715	0.003	0.488
chr3.CM0091.590.r2.m	uncharacterized protein	0.320	0.042	13.047	0.304	0.019	6.087	0.685	0.066	9.640
chr4.CM0126.600.r2.m	senescence-inducible chloroplast stay-green protein	0.317	0.005	1.680	0.511	0.013	2.632	1.201	0.021	1.715
chr4.CM0006.500.r2.m	saur family protein	0.307	0.023	7.462	0.421	0.053	12.692	0.772	0.041	5.315
chr2.CM0803.430.r2.m	uncharacterized protein	0.303	0.000	0.127	0.506	0.005	1.044	0.966	0.018	1.898
chr3.CM0142.550.r2.d	protein LURP-one-related 12-like	0.301	0.021	7.050	0.192	0.022	11.324	0.627	0.047	7.449
chr4.CM0046.1480.r2.m	glutathione s-transferase gst	0.296	0.006	2.152	0.289	0.022	7.553	0.623	0.033	5.340
chr2.CM0803.290.r2.m	urea active transporter-like protein	0.284	0.005	1.751	0.189	0.023	12.230	0.597	0.040	6.722
chr4.CM0182.190.r2.m	dentin sialophospho protein	0.279	0.014	4.900	0.312	0.010	3.067	0.625	0.033	5.356
chr3.CM0786.10.r2.d	zinc finger protein	0.277	0.031	11.137	0.055	0.003	5.382	0.906	0.122	13.425
chr6.CM1625.100.r2.m	hypoxia induced protein conserved region containing expressed	0.273	0.013	4.731	0.166	0.022	13.274	0.789	0.029	3.684
LjSGA_007368.1	myb-like transcription factor 1	0.265	0.010	3.627	0.512	0.042	8.216	1.014	0.094	9.280
chr4.LjT16L01.220.r2.d	uncharacterized protein	0.258	0.030	11.609	0.121	0.012	10.223	0.906	0.038	4.183
chr3.CM0649.10.r2.d	uncharacterized protein loc100787205	0.257	0.008	3.275	0.174	0.010	5.722	1.097	0.019	1.688
chr4.CM0004.1470.r2.m	ring finger protein	0.244	0.001	0.250	0.229	0.017	7.276	0.776	0.019	2.448
LjSGA_017029.2	adenine nucleotide alpha hydrolases-like protein	0.244	0.016	6.546	0.249	0.014	5.604	1.389	0.023	1.644
LjSGA_008568.2	PLAC8 family protein	0.240	0.028	11.855	0.174	0.014	8.231	0.577	0.035	6.021
chr1.CM0105.1690.r2.m	uncharacterized protein	0.239	0.000	0.055	0.306	0.006	1.959	0.535	0.005	0.900
LjSGA_019896.1	malonyl-COA :isoflavone 7-O-glucoside-6 -O-malonyltransferase	0.231	0.000	0.076	0.212	0.012	5.581	0.733	0.069	9.391
chr6.CM0114.170.r2.m	AP2 erf domain-containing transcription factor	0.228	0.003	1.210	0.399	0.035	8.661	0.702	0.013	1.849
LjSGA_130658.1	1-aminocyclopropane-1-carboxylate oxidase	0.225	0.002	0.948	0.516	0.002	0.302	2.687	0.002	0.085
chr1.CM0600.80.r2.m	uncharacterized protein	0.219	0.002	0.910	0.136	0.004	2.650	0.885	0.013	1.487
chr5.CM1574.330.r2.a	exostosin family protein	0.214	0.072	33.822	0.055	0.027	48.979	0.448	0.028	6.344
chr3.CM0091.1170.r2.d	isoflavone reductase-like protein	0.208	0.005	2.429	0.295	0.037	12.408	0.776	0.065	8.314
chr2.CM0028.560.r2.d	WD repeat-containing protein	0.206	0.021	10.255	0.345	0.023	6.550	0.739	0.055	7.440
LjSGA_009761.2	subtilisin inhibitor	0.198	0.001	0.411	0.368	0.019	5.076	0.928	0.056	5.994
chr2.CM0018.520.r2.d	AP2 erf domain-containing transcription factor	0.192	0.001	0.430	0.347	0.005	1.562	0.705	0.009	1.264
chr1.CM0760.300.r2.m	potassium channel	0.187	0.007	3.730	0.358	0.038	10.624	0.712	0.071	9.906
LjSGA_094101.1	beta-1,3-glucanase	0.185	0.004	2.332	0.107	0.010	9.727	0.670	0.026	3.915
chr5.CM0211.260.r2.d	E3 ubiquitin-protein ligase ATL6-like	0.185	0.014	7.696	0.337	0.017	5.166	0.990	0.005	0.465
chr6.CM0679.560.r2.d	lipid transfer protein	0.182	0.012	6.856	0.341	0.021	6.151	7.581	0.698	9.201
chr5.CM0186.200.r2.d	enzyme of the cupin superfamily	0.175	0.001	0.593	0.463	0.023	4.946	0.822	0.072	8.712
LjSGA_062409.1	uncharacterized protein loc100811015	0.172	0.000	0.188	0.153	0.006	3.614	0.419	0.002	0.451
chr1.CM0178.320.r2.m	protein kinase	0.165	0.019	11.767	0.183	0.009	5.113	0.381	0.025	6.693
LjSGA_101716.1.1	AP-1 complex subunit mu1 like	0.159	0.022	13.706	0.162	0.017	10.761	0.338	0.026	7.645
LjSGA_043690.1	plant cell wall protein 88	0.159	0.016	9.896	0.176	0.012	6.761	0.744	0.071	9.604
LjSGA_038109.1	vacuolar-sorting receptor 7-like	0.153	0.002	1.492	0.112	0.009	8.075	0.364	0.005	1.428
LjSGA_020632.1	clathrin interactor epsin 2	0.148	0.018	11.837	0.190	0.004	2.287	0.338	0.011	3.356
LjT13J03.140.r2.d	uncharacterized protein	0.147	0.007	4.578	0.367	0.014	3.816	0.778	0.059	7.530
LjSGA_091313.0.1	gibberellin 20 oxidase	0.146	0.002	1.192	0.207	0.001	0.722	0.324	0.021	6.583
chr3.CM0649.250.r2.d	zinc finger, protein binding protein	0.146	0.010	6.821	0.214	0.016	7.494	0.356	0.021	5.948
chr1.CM0195.320.r2.m	s-type anion channel SLAH1-like	0.140	0.015	10.716	0.145	0.001	0.906	0.820	0.021	2.518
chr1.LjT41J07.90.r2.d	Ser Thr protein kinase	0.137	0.010	7.238	0.157	0.002	1.462	0.351	0.016	4.682
chr5.LjT24B10.90.r2.m	uncharacterized protein	0.134	0.004	2.731	0.176	0.013	7.186	0.338	0.014	4.268
LjSGA_025993.1	galactoside 2-alpha-L-fucosyltransferase	0.132	0.016	12.111	0.030	0.005	16.236	0.369	0.007	1.785
LjSGA_076799.1	glucosyltransferase	0.125	0.008	6.627	0.507	0.063	12.514	0.920	0.038	4.146
chr5.CM1323.260.r2.d	benzyl alcohol o-benzoyltransferase-like	0.125	0.005	3.939	0.086	0.011	13.008	0.263	0.001	0.436
chr4.CM0680.260.r2.m	uncharacterized protein	0.115	0.000	0.320	0.090	0.002	2.599	0.276	0.020	7.140
chr1.CM0064.870.r2.m	calcium-binding protein CML38	0.115	0.000	0.318	0.354	0.004	1.233	0.848	0.007	0.820
LjSGA_042036.1	ABC transporter G family member 39-like	0.110	0.008	7.370	0.106	0.015	13.787	0.407	0.005	1.184
chr1.CM0315.190.r2.m	quinohaemoprotein ethanol dehydrogenase type-1	0.107	0.005	4.656	0.082	0.009	11.215	0.479	0.038	7.836
chr2.LjT48A12.210.r2.d	red chlorophyll catabolite reductase	0.106	0.008	7.525	0.190	0.003	1.433	0.377	0.010	2.709
chr5.LjT43N20.90.r2.m	uncharacterized protein	0.105	0.011	10.224	0.098	0.001	0.952	0.489	0.035	7.146
LjSGA_030430.1	beta-glucosidase 40-like	0.105	0.006	5.451	0.074	0.005	6.422	0.391	0.023	5.848
chr4.CM0337.760.r2.m	NAC domain ipr003441	0.101	0.011	11.162	0.025	0.000	1.504	0.535	0.023	4.288
LjT10O10.50.r2.d	alpha-expansin 4	0.100	0.001	0.838	0.085	0.005	6.203	0.331	0.020	5.977
chr1.CM0122.2400.r2.a	uncharacterized protein	0.097	0.001	0.944	0.250	0.005	1.975	0.214	0.004	2.025
LjSGA_104176.1	glycosyltransferase gt19j14	0.097	0.010	10.135	0.159	0.013	7.967	0.314	0.011	3.617
LjSGA_013173.2	glucose-6-phosphate dehydrogenase 5	0.095	0.010	11.025	0.134	0.004	2.759	0.261	0.019	7.475
chr4.CM0432.1860.r2.m	TIR-NBS-LRR disease resistance-like protein	0.094	0.016	17.226	0.089	0.013	15.124	0.262	0.008	3.162
chr5.LjT43N20.70.r2.m	uncharacterized protein	0.094	0.011	11.487	0.093	0.002	1.684	0.649	0.034	5.167
chr1.CM0009.330.r2.m	receptor protein kinase clavata1	0.092	0.007	7.194	0.044	0.001	2.561	0.228	0.009	3.769
LjSGA_066904.1	uncharacterized protein	0.087	0.000	0.185	0.191	0.005	2.379	0.217	0.003	1.241
LjSGA_034602.1	disease resistance response protein	0.086	0.010	11.127	0.042	0.002	4.391	0.552	0.033	5.901
chr6.CM2021.110.r2.m	uncharacterized protein	0.085	0.000	0.359	0.124	0.011	8.906	0.577	0.049	8.425
LjSGA_100451.1	Zinc finger homeodomain protein at4g24660-like	0.080	0.007	8.254	0.227	0.004	1.783	0.224	0.016	7.318
chr2.CM0803.310.r2.m	alternative oxidase	0.080	0.010	12.255	0.128	0.001	1.057	0.230	0.013	5.845
LjSGA_061228.1	glutathione s-transferase	0.077	0.041	53.615	0.056	0.031	55.140	1.017	0.038	3.744
chr1.CM0375.470.r2.d	phospholipase A1-Igamma2	0.076	0.007	9.080	0.131	0.008	6.138	0.353	0.020	5.721
chr2.CM0065.90.r2.d	receptor-like protein kinase hsl1-like	0.075	0.013	17.173	0.082	0.002	2.896	0.178	0.009	5.132
chr6.CM0830.360.r2.a	ankyrin repeat-containing protein	0.075	0.001	1.140	0.084	0.003	4.100	0.391	0.034	8.747
chr3.CM0292.340.r2.m	beta-amyrin synthase	0.073	0.006	8.722	0.111	0.002	1.358	0.258	0.018	7.171
chr3.CM0261.600.r2.a	receptor protein kinase clavata1	0.073	0.008	11.339	0.088	0.001	0.999	0.182	0.014	7.815
LjSGA_027923.2	Ca2+ antiporter cation exchanger	0.072	0.008	11.330	0.043	0.016	37.778	0.246	0.009	3.547
LjSGA_018632.2	cationic peroxidase 1-like	0.072	0.004	6.027	0.058	0.031	54.246	0.334	0.021	6.298
chr1.CM0104.2380.r2.a	probable receptor-like protein kinase at1g67000-like	0.069	0.002	3.207	0.079	0.000	0.030	0.217	0.015	7.039
LjSGA_018845.1	nadph:quinone oxidoreductase	0.069	0.008	12.296	0.104	0.005	4.965	0.190	0.001	0.552
LjSGA_031662.1	receptor-like protein 12-like	0.068	0.004	5.611	0.054	0.006	10.633	0.210	0.015	6.958
chr4.CM0617.360.r2.d	uncharacterized protein	0.066	0.005	7.204	0.061	0.006	9.814	0.401	0.036	8.927
LjSGA_026352.1	sodium calcium exchanger family protein	0.064	0.003	5.268	0.048	0.000	0.375	0.144	0.006	4.493
LjSGA_033937.1	disease resistance response protein	0.063	0.004	6.308	0.086	0.006	6.700	0.441	0.036	8.119
LjSGA_023898.1	senescence-associated nodulin 1a	0.063	0.002	2.503	0.093	0.000	0.362	0.246	0.018	7.244
chr1.CM0316.520.r2.a	quinone-oxidoreductase-like protein	0.063	0.004	6.666	0.084	0.002	2.180	0.140	0.004	3.179
chr3.CM0792.320.r2.d	cytochrome p450 monooxygenase cyp72a61	0.062	0.007	11.847	0.068	0.005	7.657	0.167	0.016	9.291
LjSGA_084705.1	anthocyanidin 3-o-glucosyltransferase	0.061	0.005	8.329	0.124	0.016	12.755	0.236	0.001	0.461
chr1.CM0039.290.r2.d	uncharacterized protein	0.060	0.006	9.479	0.134	0.004	2.670	0.256	0.011	4.197
chr1.CM0316.500.r2.a	uncharacterized protein	0.059	0.012	20.740	0.103	0.018	17.314	0.247	0.019	7.524
LjSGA_011701.2	SAUR family protein	0.059	0.004	6.235	0.081	0.005	6.384	0.151	0.005	3.230
LjSGA_052231.1	receptor protein kinase-like protein	0.058	0.005	9.553	0.053	0.028	53.084	0.147	0.005	3.173
LjSGA_126580.1	Cytochrome P450, 716b2-like	0.057	0.005	7.965	0.037	0.005	13.324	0.122	0.009	7.065
chr6.CM0118.650.r2.m	heat-shock protein	0.057	0.001	1.960	0.080	0.009	10.815	0.191	0.014	7.418
chr5.CM0311.190.r2.d	protein IDA-like 1	0.054	0.001	1.577	0.045	0.003	7.148	0.348	0.008	2.233
chr1.CM0295.1210.r2.a	ATP-binding cassette	0.053	0.003	5.894	0.120	0.004	3.196	0.236	0.006	2.605
LjSGA_019312.1	probable inactive receptor kinase at4g23740-like	0.053	0.004	7.469	0.096	0.002	2.487	0.283	0.010	3.389
chr4.CM0004.2380.r2.d	CCCH-type zinc finger protein	0.053	0.002	4.335	0.918	0.045	4.915	0.221	0.001	0.650
chr1.LjT35C19.20.r2.a	heat stress transcription factor b-3	0.051	0.006	10.906	0.055	0.005	8.448	0.206	0.006	3.088
LjSGA_016571.1	hydroquinone glucosyltransferase-like	0.049	0.024	50.073	0.069	0.017	24.008	0.199	0.007	3.620
chr5.CM0200.1860.r2.d	ATP binding protein	0.047	0.001	1.398	0.092	0.000	0.489	0.473	0.014	3.046
LjSGA_031126.1	phenylcoumaran benzylic ether reductase -like protein	0.047	0.002	3.832	0.043	0.007	17.096	0.134	0.011	8.056
chr2.CM0124.510.r2.m	serine-threonine kinase	0.046	0.002	4.879	0.067	0.003	4.897	0.128	0.006	4.922
chr6.LjT06I08.70.r2.m	uncharacterized protein	0.045	0.001	2.807	0.075	0.003	3.505	0.182	0.005	3.011
chr6.CM0013.730.r2.d	AP2 erf domain-containing transcription factor	0.042	0.002	4.309	0.024	0.007	28.241	0.131	0.007	5.144
chr2.CM0021.1710.r2.m	uncharacterized protein	0.042	0.002	4.789	0.405	0.017	4.294	0.225	0.014	6.074
chr1.CM0064.1050.r2.m	peroxidase 55	0.041	0.007	16.191	0.073	0.001	0.815	0.591	0.024	4.141
chr1.CM0393.880.r2.d	uncharacterized protein	0.040	0.023	57.703	0.082	0.016	19.775	0.164	0.013	8.116
LjSGA_064062.1	s-locus-specific glycoprotein	0.039	0.004	9.609	0.041	0.002	5.143	0.080	0.006	7.209
chr4.CM0026.590.r2.m	uncharacterized protein	0.039	0.002	6.103	0.133	0.001	0.508	0.316	0.001	0.256
LjSGA_028551.1	stachyose synthase	0.037	0.006	16.909	0.029	0.001	5.081	0.201	0.009	4.700
chr4.CM0182.400.r2.m	2-nitropropane dioxygenase	0.037	0.002	6.491	0.046	0.004	8.833	0.221	0.012	5.393
LjSGA_017360.1	cysteine-rich receptor-like protein kinase	0.037	0.002	6.075	0.052	0.011	21.985	0.095	0.001	0.532
LjSGA_014003.1	wrky transcription factor	0.037	0.011	28.744	0.040	0.001	2.350	0.236	0.002	1.022
chr4.CM0026.10.r2.d	s-type anion channel SLAH1-like	0.036	0.002	5.686	0.392	0.067	16.981	0.219	0.012	5.344
chr5.CM0456.270.r2.d	acidic endochitinase-like	0.036	0.006	15.357	0.137	0.029	21.478	0.589	0.036	6.166
LjT03D12.130.r2.d	no hit	0.036	0.008	20.963	0.064	0.005	7.215	0.116	0.005	4.693
LjSGA_021092.0.1	uncharacterized protein	0.035	0.001	3.912	0.066	0.003	4.928	0.132	0.006	4.352
chr1.LjT35C22.30.r2.m	uncharacterized protein	0.035	0.001	2.131	0.660	0.036	5.509	0.222	0.020	9.017
chr4.CM0831.260.r2.d	expansin-like b1-like	0.034	0.004	12.039	0.055	0.001	1.683	0.169	0.016	9.682
LjSGA_030867.1	reticuline oxidase-like	0.034	0.007	19.147	0.059	0.013	22.732	0.430	0.022	5.041
chr4.CM0026.600.r2.m	uncharacterized protein	0.033	0.002	5.911	0.143	0.005	3.349	0.337	0.015	4.334
LjSGA_078537.1	disease resistance response protein	0.033	0.005	16.569	0.028	0.004	15.265	0.325	0.002	0.614
chr4.CM0003.50.r2.a	kinase-like protein	0.031	0.002	7.559	0.040	0.004	9.807	0.212	0.005	2.249
LjSGA_122490.1	brefeldin a-inhibited guanine nucleotide-exchange protein 1-like	0.031	0.003	10.793	0.042	0.000	0.973	0.066	0.004	6.735
LjSGA_022785.1	homeobox protein knotted 1 like	0.031	0.007	23.466	0.020	0.002	11.783	0.067	0.003	5.142
chr5.CM0148.665.r2.a	CLE10 protein	0.031	0.002	7.374	0.040	0.004	9.862	0.292	0.008	2.729
chr1.CM0315.280.r2.d	quinohaemoprotein ethanol dehydrogenase type-1	0.028	0.002	7.353	0.030	0.018	60.415	0.085	0.003	3.454
LjSGA_018721.1	probable receptor-like protein kinase at5g56460-like	0.028	0.002	6.509	0.032	0.005	17.126	0.064	0.006	9.322

LjT13F18.100.r2.d	no hit	0.027	0.006	23.633	0.043	0.002	4.020	0.095	0.006	6.815
LjSGA_018600.1	high affinity inorganic phosphate transporter	0.027	0.005	20.270	0.021	0.006	29.853	0.075	0.000	0.572
chr3.CM0792.360.r2.d	tropinone reductase homolog at1g07440-like	0.026	0.000	1.150	0.146	0.014	9.611	0.265	0.006	2.115
LjSGA_086310.1	wall-associated receptor kinase 2-like	0.026	0.005	19.885	0.053	0.004	8.075	0.285	0.024	8.517
chr2.CM0008.40.r2.d	carbonic anhydrase	0.026	0.002	6.969	0.033	0.008	24.286	0.084	0.007	8.235
LjSGA_088447.2	uncharacterized protein	0.026	0.002	9.214	0.050	0.010	19.702	0.162	0.014	8.431
chr3.CM0106.400.r2.d	electron transfer flavoprotein-ubiquinone oxidoreductase	0.025	0.004	14.406	0.032	0.005	15.437	0.064	0.004	5.952
LjSGA_064042.1	protein SRG1-like	0.025	0.001	2.593	0.039	0.001	1.374	0.075	0.006	8.523
LjSGA_031726.2	TIR-NBS-LRR resistance protein	0.025	0.005	20.798	0.032	0.001	4.078	0.184	0.002	1.105
LjSGA_072637.1	glutamyl-tRNA amidotransferase subunit A	0.025	0.002	6.114	0.035	0.005	13.720	0.067	0.002	3.567
LjSGA_061348.1	uncharacterized protein	0.024	0.002	10.475	0.029	0.002	7.543	0.053	0.001	1.979
LjSGA_037080.2	uncharacterized protein	0.023	0.004	15.518	0.027	0.005	17.170	0.055	0.004	7.638
chr4.CM0432.1970.r2.m	heat shock protein	0.023	0.003	11.984	0.971	0.049	5.016	13.033	0.291	2.233
chr2.CM0124.1350.r2.d	protein SRG1-like	0.023	0.002	10.042	0.032	0.004	12.131	0.224	0.011	4.801
chr4.LjT06B21.90.r2.d	RCC1 and BTB domain-containing protein	0.023	0.001	2.370	0.038	0.008	22.152	0.070	0.006	8.161
LjSGA_031326.1	MATE efflux family protein 8-like	0.022	0.000	2.215	0.026	0.008	32.130	0.048	0.002	3.746
LjSGA_029281.1	Cytochrome P450	0.022	0.009	42.413	0.037	0.011	30.693	0.066	0.006	8.896
LjSGA_088259.3	beta-glucan-binding protein	0.022	0.003	14.975	0.046	0.004	8.886	0.086	0.007	7.944
LjSGA_034269.2	ATP binding protein	0.021	0.000	0.474	0.034	0.003	9.370	0.413	0.017	4.045
chr5.CM0200.390.r2.d	protein kinase family protein	0.021	0.007	34.043	0.030	0.003	8.246	0.056	0.003	4.642
chr6.CM0336.460.r2.d	uncharacterized protein	0.018	0.000	0.976	0.051	0.003	6.800	0.109	0.003	3.016
LjSGA_084215.1	sarcosine oxidase	0.017	0.006	36.697	0.036	0.005	14.205	0.120	0.012	9.919
LjSGA_014954.1	expansin precursor	0.017	0.005	32.861	0.032	0.002	6.621	0.101	0.004	3.973
chr2.CM0081.1450.r2.a	ABC transporter b family member	0.015	0.004	27.167	0.040	0.008	19.668	0.121	0.006	4.845
chr5.CM1547.30.r2.m	disease resistance response protein 206-like	0.013	0.000	1.450	0.018	0.003	18.342	0.038	0.002	5.414

Supplemental Table 2. Expression profile of 424 genes in cluster 2 during nodule senescence

ID number	Annotation	2 wpi			4 wpi			8 wpi		
		Average Normalized	SD Normalized	CV (%)	Average Normalized	SD Normalized	CV (%)	Average Normalized	SD Normalized	CV (%)
chr1.CM0195.250.r2.m	cysteine proteinase 15A-like	32.063	1.321	4.119	97.327	2.516	2.585	66.842	2.977	4.454
chr1.CM0295.970.r2.m	peptide transporter PTR3-a	30.016	3.191	10.630	110.695	8.459	7.642	65.695	5.053	7.692
chr2.CM0065.600.r2.d	uncharacterized protein	21.034	0.030	0.142	66.629	0.772	1.158	54.483	1.051	1.929
chr3.CM0135.890.r2.a	cyclophilin	24.452	1.173	4.796	41.991	0.192	0.456	52.823	1.251	2.368
LjSGA_015484.1	cysteine protease	17.528	0.630	3.593	34.974	0.853	2.438	47.979	1.244	2.593
chr4.CM0126.510.r2.m	subtilisin-like protease SDD1-like	20.264	0.904	4.460	36.201	3.614	9.984	47.111	2.197	4.664
LjSGA_062791.1	no hit	15.811	1.524	9.636	30.233	1.528	5.053	43.706	2.985	6.829
chr1.CM2079.120.r2.a	UNC93-like protein	11.243	0.661	5.877	30.391	1.732	5.700	25.932	1.658	6.392
chr1.CM0017.470.r2.a	transaldolase	11.315	1.215	10.739	19.464	2.518	12.934	25.809	2.436	9.437
LjT42E21.90.r2.m	wound-induced protein	11.065	0.606	5.477	26.925	1.850	6.872	25.750	1.170	4.544
chr4.CM0432.790.r2.m	carboxypeptidase C	2.882	0.038	1.330	29.320	1.487	5.071	23.293	0.418	1.796
LjSGA_051679.1	cysteine synthase	9.101	0.159	1.742	16.159	0.491	3.036	23.160	0.119	0.513
chr4.LjT13G24.170.r2.a	cytochrome p450 like TBP	9.947	0.118	1.183	25.658	0.951	3.705	23.018	0.516	2.241
LjSGA_019294.2	type 2 metallothionein	5.134	0.103	2.005	15.755	0.061	0.384	21.900	0.380	1.737
chr1.CM0591.60.r2.m	no hit	3.764	0.032	0.849	27.609	0.497	1.799	19.768	0.567	2.866
LjSGA_142964.1	nodulin-like protein	0.731	0.073	10.031	9.155	0.508	5.554	15.282	1.137	7.437
chr4.CM0165.230.r2.d	calmodulin-like protein	4.398	0.193	4.396	14.110	0.662	4.693	14.072	0.426	3.027
chr4.CM0075.30.r2.m	uncharacterized protein	5.517	0.291	5.271	9.903	0.290	2.928	14.037	0.835	5.948
chr3.CM0160.370.r2.m	uncharacterized protein	5.099	0.061	1.189	13.330	0.255	1.910	13.479	0.545	4.040
chr3.CM0160.350.r2.m	14 kDa proline-rich protein	5.269	0.164	3.118	13.018	0.142	1.091	13.351	0.582	4.356
LjSGA_019308.1	uncharacterized protein	5.938	0.108	1.818	16.181	0.396	2.445	13.325	0.364	2.730
chr3.CM0160.360.r2.m	14 kDa proline-rich protein	5.274	0.091	1.716	12.902	0.585	4.535	13.297	0.772	5.806
chr2.CM0250.230.r2.d	no hit	4.536	0.277	6.098	9.562	0.685	7.161	12.966	0.236	1.822
chr5.CM0696.540.r2.a	copper chaperone	2.413	0.103	4.262	27.586	1.856	6.728	11.984	0.702	5.860
chr3.CM0127.770.r2.d	small heat shock protein	1.670	0.125	7.484	4.736	0.678	14.310	10.519	0.441	4.190
chr5.CM0200.1660.r2.d	uncharacterized protein	1.253	0.008	0.666	7.139	0.338	4.737	9.824	0.583	5.934
chr4.CM0244.350.r2.d	Zn Cd P-type ATPase	4.193	0.140	3.333	15.852	1.090	6.877	9.083	0.408	4.491
chr1.CM0178.490.r2.m	glycine-rich RNA-binding protein	2.733	2.044	74.770	13.322	1.564	11.741	8.918	0.753	8.445
chr3.CM0416.890.r2.m	uncharacterized protein	4.207	0.394	9.372	13.466	1.490	11.067	8.564	0.834	9.743
chr4.CM0528.400.r2.d	R2R3-myb transcription	4.032	0.063	1.566	13.060	0.031	0.237	8.381	0.323	3.851
chr5.CM0909.220.r2.m	intracellular chloride channel	3.269	0.020	0.614	11.910	1.256	10.545	8.300	0.400	4.820
chr6.CM0245.580.r2.a	serine acetyltransferase mitochondrial	1.185	0.007	0.623	12.167	0.354	2.908	8.095	0.319	3.942
LjSGA_026650.1	auxin-induced protein 5ng4-like	1.105	0.083	7.502	3.693	0.482	13.059	8.000	0.580	7.255
LjSGA_021104.1	with no lysine kinase	3.356	0.087	2.595	10.732	0.258	2.408	7.296	0.102	1.393
LjSGA_104322.1	acyl-coenzyme a oxidase peroxisomal-like	2.319	0.098	4.225	8.586	0.453	5.281	7.123	0.451	6.336
chr1.CM0023.30.r2.d	putative copper ion-binding laccase	3.026	0.501	16.568	5.508	1.016	18.449	6.501	0.573	8.812
chr3.CM1303.220.r2.m	glycerol-3-phosphate acyltransferase	2.431	0.084	3.449	10.642	0.315	2.958	6.474	0.312	4.817
chr3.CM0116.300.r2.m	ferritin	3.371	0.970	28.781	2.197	0.664	30.204	6.058	1.755	28.973
LjSGA_023908.1	homeobox-leucine zipper protein HAT22-like	1.901	0.077	4.034	3.364	0.135	3.999	5.662	0.071	1.259
chr1.CM2079.250.r2.m	zinc finger protein zat11-like	1.323	0.110	8.313	3.614	0.182	5.030	5.251	0.500	9.523
chr3.CM0226.90.r2.m	sulfate transporter	2.076	0.026	1.239	3.218	0.124	3.854	4.901	0.016	0.334
chr4.CM0432.950.r2.m	RNA polymerase-associated protein RTF1 homolog	2.195	0.320	14.567	6.094	1.196	19.624	4.700	0.419	8.907
chr5.LjT34O04.60.r2.d	E3 ubiquitin-protein ligase ATL23-like	1.891	0.034	1.795	10.326	0.001	0.009	4.457	0.232	5.198
LjSGA_044058.1	uncharacterized protein	0.527	0.029	5.491	4.431	0.309	6.975	4.004	0.337	8.411
chr3.LjT07B06.60.r2.m	uncharacterized protein	1.595	0.049	3.066	3.309	0.149	4.496	3.906	0.063	1.624
chr3.CM0155.30.r2.d	uncharacterized protein	0.493	0.050	10.133	2.489	0.234	9.400	3.815	0.274	7.180
chr3.CM0226.310.r2.d	F-box kelch-repeat protein	1.458	0.031	2.124	5.015	0.052	1.041	3.781	0.245	6.481
LjT15A10.70.r2.a	regulator of osome expressed	1.504	0.004	0.273	2.888	0.168	5.801	3.740	0.100	2.663
LjSGA_030826.1	chaperone protein dnaj	1.728	0.120	6.941	3.949	0.268	6.783	3.634	0.034	0.942
LjSGA_055604.1	uncharacterized protein	1.721	0.046	2.677	3.643	0.130	3.577	3.576	0.171	4.771
chr1.CM0017.280.r2.m	probable carboxylesterase 17-like	0.752	0.028	3.755	5.371	0.498	9.267	3.487	0.263	7.543
chr5.CM0077.520.r2.d	no hit	1.740	0.106	6.102	4.146	0.385	9.277	3.485	0.286	8.217
LjSGA_070708.1	alpha-trehalose-phosphate synthase	1.480	0.047	3.166	2.133	0.081	3.812	3.422	0.223	6.526
LjSGA_141755.1	phospholipase D	1.605	0.128	7.969	7.713	0.675	8.757	3.350	0.218	6.497
LjSGA_010144.1	white-brown-complex abc transporter family	0.708	0.044	6.240	2.155	0.207	9.604	3.283	0.305	9.286
LjSGA_056007.1	response to low sulfur 2	1.601	0.050	3.111	2.401	0.036	1.508	3.226	0.153	4.745
chr4.CM0087.1030.r2.d	heat shock protein 101	1.323	0.118	8.959	2.368	0.191	8.065	3.149	0.211	6.693
LjSGA_014372.1	bon1-associated protein 2-like	1.001	0.024	2.371	2.389	0.110	4.623	3.077	0.073	2.372
chr1.CM0269.620.r2.d	10 kda chaperonin-like	1.433	0.022	1.541	3.732	0.206	5.514	3.051	0.142	4.662
chr1.CM0010.190.r2.m	uncharacterized protein	0.265	0.013	4.827	4.073	0.466	11.430	3.028	0.233	7.690
chr6.CM0437.510.r2.m	saur family protein	1.316	0.104	7.903	2.732	0.101	3.683	2.964	0.230	7.756
LjSGA_085944.1	2-hydroxyphytanoyl- lyase-like protein	1.232	0.002	0.173	1.991	0.035	1.750	2.825	0.036	1.259
LjSGA_044971.1	callose synthase	1.087	0.073	6.704	2.601	0.156	5.989	2.821	0.016	0.575
LjSGA_041970.1	OCS element-binding	0.097	0.001	1.229	1.320	0.016	1.218	2.773	0.034	1.235
chr5.CM0200.20.r2.m	uncharacterized protein	0.914	0.024	2.653	3.071	0.225	7.339	2.771	0.274	9.890
chr5.CM0052.410.r2.a	no hit	0.732	0.081	11.134	2.502	0.016	0.620	2.717	0.180	6.608
LjSGA_040947.1	zinc finger ccch domain-containing protein	1.227	0.085	6.905	2.009	0.083	4.132	2.619	0.175	6.696
chr5.CM0909.550.r2.m	uncharacterized protein	0.786	0.031	3.939	6.026	0.141	2.348	2.543	0.016	0.638
LjSGA_085949.1	DNA-binding protein escarola-like	1.068	0.079	7.354	2.013	0.151	7.485	2.407	0.186	7.711
chr6.CM0314.680.r2.m	vacuolar iron transporter-like protein	0.743	0.041	5.545	3.149	0.194	6.153	2.386	0.084	3.537
chr1.CM0105.1600.r2.m	hypoersensitive response protein	0.696	0.016	2.248	2.383	0.197	8.252	2.312	0.100	4.327
LjSGA_022317.1	auxin-induced protein 5ng4-like	1.123	0.134	11.958	2.556	0.340	13.308	2.306	0.146	6.323
LjSGA_112884.1	aminophospholipid atpase	1.094	0.016	1.506	2.230	0.018	0.827	2.250	0.024	1.067
LjSGA_097658.1	protein SRG1-like	0.401	0.013	3.276	1.369	0.066	4.845	2.249	0.030	1.321
LjSGA_118123.1	uncharacterized protein	0.585	0.039	6.599	1.751	0.112	6.406	2.245	0.004	0.177
chr5.CM0040.200.r2.d	kinase-like protein	0.637	0.014	2.171	0.911	0.043	4.761	2.226	0.031	1.389
chr1.CM0064.640.r2.a	brain protein 44-like protein	0.938	0.091	9.671	1.180	0.060	5.089	2.217	0.167	7.539
LjSGA_017457.1	u-box domain-containing protein 8-like	0.874	0.033	3.742	2.292	0.080	3.477	2.198	0.138	6.275
chr5.CM0456.180.r2.d	acidic endochitinase-like	0.748	0.015	1.944	0.942	0.048	5.123	2.178	0.053	2.442
chr1.CM0578.70.r2.d	serine-threonine protein kinase	0.171	0.006	3.777	0.449	0.024	5.345	2.174	0.042	1.922
LjSGA_061146.1	uncharacterized protein	0.221	0.008	3.499	0.622	0.015	2.412	2.158	0.069	3.195
chr1.CM0063.340.r2.d	cationic amino acid transporter	0.519	0.018	3.551	2.133	0.076	3.557	2.127	0.086	4.046
chr5.CM0456.190.r2.d	acidic endochitinase	0.713	0.003	0.417	0.969	0.003	0.267	2.125	0.081	3.806
chr2.CM0021.50.r2.d	bZip transcription factor family protein	0.766	0.012	1.621	1.317	0.011	0.853	2.098	0.004	0.210
chr4.CM0007.660.r2.d	urease accessory protein	0.858	0.040	4.688	2.737	0.150	5.493	2.056	0.027	1.296
chr2.CM0099.250.r2.m	uncharacterized protein loc100800669	0.722	0.029	3.984	1.860	0.013	0.673	2.049	0.151	7.376
chr6.CM0037.910.r2.m	cytochrome p450	0.123	0.012	9.716	0.435	0.032	7.354	2.024	0.121	5.976
chr4.CM0179.50.r2.a	BTB/POZ domain with WD40 yvtn repeat-containing protein	0.719	0.004	0.613	3.307	0.098	2.970	2.020	0.039	1.914
chr5.CM0200.3120.r2.m	uncharacterized protein	0.163	0.024	14.534	0.361	0.037	10.246	1.959	0.030	1.545
LjSGA_121222.1	squamosa promoter binding-like protein	0.968	0.026	2.641	2.227	0.037	1.670	1.952	0.082	4.211
LjSGA_045783.1	lipase class 3 family protein	0.852	0.028	3.266	1.004	0.082	8.212	1.936	0.050	2.559
chr1.CM0032.170.r2.d	wrky transcription factor	0.082	0.000	0.479	0.303	0.006	1.951	1.922	0.165	8.567
chr5.CM0200.3570.r2.d	cyclase family protein	0.943	0.103	10.904	2.556	0.041	1.614	1.898	0.030	1.560
LjSGA_020504.1	uncharacterized protein	0.289	0.014	4.900	1.363	0.014	1.062	1.878	0.081	4.305
LjSGA_059387.1	sulfurtransferase 18	0.087	0.005	5.684	1.654	0.075	4.561	1.857	0.109	5.856
chr5.CM0158.160.r2.m	autophagy-related protein 8h	0.409	0.003	0.833	1.545	0.115	7.458	1.849	0.125	6.767
chr3.CM0059.200.r2.m	auxin-responsive family protein	0.611	0.028	4.590	1.184	0.009	0.773	1.845	0.034	1.850
LjSGA_023918.1	GRAS family transcription factor	0.368	0.026	7.031	1.270	0.036	2.798	1.811	0.017	0.923
LjSGA_020805.2	phloem specific protein	0.230	0.003	1.348	2.835	0.115	4.059	1.798	0.134	7.441
chr2.LjT46G02.230.r2.d	nematode-resistance protein	0.685	0.021	3.133	0.932	0.030	3.242	1.783	0.079	4.457
LjSGA_047781.1	uncharacterized protein	0.586	0.032	5.436	1.789	0.071	3.968	1.774	0.127	7.154
LjSGA_019117.2	DNA-directed RNA polymerase 3	0.868	0.005	0.548	2.008	0.172	8.560	1.748	0.027	1.552
chr1.CM0012.640.r2.m	CCAAT-binding transcription factor subunit	0.817	0.074	9.062	2.807	0.249	8.882	1.660	0.086	5.160
chr5.CM1667.270.r2.a	leucine-rich repeat family protein	0.652	0.058	8.864	0.791	0.108	13.645	1.657	0.137	8.255
LjSGA_086698.1	saur family protein	0.617	0.082	13.339	1.542	0.155	10.081	1.639	0.059	3.628
chr1.LjT38J19.120.r2.d	Vamp-like protein	0.662	0.043	6.544	1.476	0.079	5.342	1.632	0.080	4.897
LjSGA_024313.1	oxidoreductase -like	0.581	0.037	6.339	2.071	0.140	6.770	1.597	0.135	8.452
LjSGA_020634.1.1	peroxidase	0.321	0.009	2.863	1.497	0.087	5.845	1.564	0.079	5.070
LjSGA_011457.1	temperature-induced lipocalin	0.281	0.032	11.315	1.345	0.097	7.233	1.557	0.115	7.401
chr4.CM0432.2020.r2.d	1-aminocyclopropane-1-carboxylate oxidase homolog 1-like	0.721	0.038	5.258	2.011	0.293	14.579	1.529	0.108	7.043
LjSGA_014261.1	uncharacterized protein	0.616	0.041	6.724	0.997	0.127	12.762	1.524	0.106	6.928
chr5.CM0180.660.r2.m	chalcone isomerase	0.151	0.025	16.586	0.371	0.074	19.934	1.503	0.104	6.916
LjSGA_127288.1	nuclear transcription factor Y subunit B5-like	0.403	0.050	12.339	0.624	0.027	4.264	1.465	0.119	8.157
LjSGA_053543.1	glycine-rich protein	0.187	0.012	6.166	1.356	0.153	11.284	1.423	0.050	3.538
LjSGA_081256.1	calcium-dependent protein kinase	0.639	0.007	1.100	1.019	0.006	0.541	1.418	0.040	2.836
chr5.CM0200.2670.r2.d	LOB domain-containing protein 38-like	0.481	0.003	0.630	4.987	0.031	0.618	1.397	0.026	1.867
chr4.CM0026.570.r2.m	uncharacterized protein	0.388	0.005	1.192	0.939	0.022	2.368	1.390	0.093	6.718
chr2.CM0373.470.r2.m	cytidine deaminase	0.459	0.035	7.535	1.698	0.090	5.306	1.387	0.059	4.237
chr1.CM0122.180.r2.m	nicotianamine synthase	0.115	0.011	9.251	0.511	0.050	9.870	1.364	0.094	6.901
chr2.CM0021.1470.r2.a	g-type lectin s-receptor-like serine threonine-protein kinase rlk1-like	0.270	0.023	8.522	0.421	0.012	2.739	1.364	0.046	3.364
LjSGA_083412.1	uncharacterized protein	0.572	0.039	6.845	1.415	0.088	6.246	1.355	0.100	7.406
LjSGA_126557.1	ATPase splayed	0.502	0.028	5.583	1.043	0.069	6.594	1.237	0.020	1.641
chr5.CM0186.410.r2.d	RNA-binding protein 42-like	0.307	0.036	11.810	0.840	0.048	5.674	1.236	0.038	3.057
LjSGA_051232.1	ring finger protein	0.114	0.004	3.725	2.435	0.135	5.550	1.233	0.041	3.361
LjSGA_097845.2	open stomata 1	0.480	0.002	0.516	1.664	0.028	1.670	1.214	0.030	2.436
chr5.CM0344.90.r2.d	sucrose transporter 1	0.541	0.022	4.008	1.034	0.024	2.331	1.210	0.025	2.033
LjSGA_033620.1	cellulose synthase-like protein h1	0.110	0.020	17.719	0.611	0.110	17.955	1.190	0.084	7.089
chr3.CM0246.100.r2.d	uncharacterized protein	0.417	0.001	0.323	1.322	0.097	7.315	1.144	0.003	0.246
chr1.LjT35C22.70.r2.m	calcium-binding protein cml42	0.414	0.027	6.597	2.282	0.026	1.140	1.136	0.041	3.589
chr1.CM0295.980.r2.m	peptide transporter ptr3-a	0.385	0.069	18.021	1.831	0.196	10.720	1.136	0.105	9.197
LjSGA_109425.1.1	uncharacterized protein	0.237	0.032	13.318	1.581	0.239	15.098	1.135	0.094	8.311
LjSGA_148517.1	saur family protein	0.540	0.009	1.641	1.040	0.003	0.296	1.132	0.019	1.642
LjSGA_140008.1	zinc finger AN1 and C2H2 domain-containing stress-associated protein 16-like	0.539	0.051	9.494	1.676	0.315	18.773	1.121	0.048	4.249
LjSGA_145059.1	heat shock protein binding	0.294	0.037	12.624	1.223	0.137	11.173	1.114	0.075	6.763
LjSGA_143579.1	acetyl-coenzyme A carboxyl transferase	0.367	0.005	1.484	0.861	0.062	7.157	1.087	0.023	2.115
LjSGA_065179.1	senescence-associated protein	0.300	0.042	14.160	1.276	0.156	12.229	1.046	0.092	8.837
chr5.CM0852.200.r2.d	uncharacterized protein	0.386	0.007	1.919	0.674	0.024	3.503	1.039	0.068	6.534
LjSGA_031704.1	RJ2 protein	0.204	0.045	22.124	0.843	0.160	18.966	1.031	0.050	4.863
chr6.CM1613.310.r2.m	math domain-containing protein	0.493	0.029	5.803	0.968	0.054	5.572	1.030	0.064	6.180
LjSGA_123715.1	esterase PIR7B	0.160	0.016	9.729	0.801	0.002	0.306	1.025	0.083	8.107
chr4.CM1983.100.r2.a	uncharacterized protein	0.208	0.013	6.430	0.770	0.004	0.557	1.016	0.045	4.436
chr1.LjT44L17.130.r2.d	heat shock protein	0.077	0.001	1.137	1.231	0.013	1.090	1.009	0.076	7.546
chr4.CM0337.430.r2.m	auxin-induced protein 5NG4	0.182	0.006	3.474	0.582	0.014	2.468	0.992	0.073	7.359
LjSGA_126326.1.1	phospholipase D	0.381	0.015	3.834	2.260	0.227	10.036	0.939	0.034	3.591
chr1.CM0600.70.r2.m	uncharacterized protein	0.385	0.004	1.083	0.763	0.057	7.480	0.917	0.005	0.504
LjSGA_041312.1	heat shock protein	0.301	0.010	3.188	1.465	0.074	5.024	0.894	0.023	2.602
chr2.CM0608.910.r2.d	mucin-like protein	0.433	0.017	3.942	1.167	0.006	0.478	0.874	0.014	1.653
chr6.CM0553.320.r2.d	core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	0.405	0.023	5.636	0.984	0.039	3.965	0.859	0.060	6.989
chr2.LjT42A12.70.r2.m	protein translation factor SUI1	0.195	0.001	0.552	0.782	0.023	2.991	0.849	0.015	1.736
chr1.CM0029.1570.r2.a	uncharacterized protein	0.386	0.001	0.332	0.734	0.037	5.005	0.830	0.034	4.121
LjSGA_018271.1.1	cell division protease	0.402	0.001	0.245	0.594	0.013	2.127	0.823	0.019	2.324
chr2.LjT03F24.90.r2.d	AP2/ERF domain-containing transcription factor	0.276	0.024	8.796	0.799	0.031	3.828	0.810	0.033	4.093
chr2.CM0124.730.r2.m	protein NSP-interacting kinase 1-like	0.285	0.049	16.997	0.680	0.078	11.480	0.805	0.065	8.117
LjSGA_048998.1	WD repeat-containing protein 5-like	0.339	0.002	0.696	1.892	0.039	2.044	0.802	0.026	3.226
LjSGA_012012.1	oleosin 16kDa-like	0.195	0.003	1.347	0.625	0.015	2.393	0.791	0.004	0.452
LjSGA_027803.2	OSBP(oxysterol binding protein)-related protein 1c	0.211	0.020	9.366	0.722	0.027	3.791	0.790	0.011	1.372
LjSGA_036411.1	Fimbriata-associated protein	0.319	0.001	0.206	3.074	0.126	4.113	0.786	0.009	1.129
LjSGA_028172.2	uncharacterized protein loc100791221	0.370	0.019	5.203	1.040	0.024	2.300	0.785	0.009	1.085
LjSGA_034935.1	ATP-dependent Clp protease adaptor protein	0.327	0.022	6.669	1.491	0.058	3.917	0.777	0.010	1.329
LjSGA_020559.2	protein phosphatase-2C	0.332	0.019	5.713	1.395	0.046	3.287	0.758	0.026	3.487
LjSGA_009276.2	uncharacterized protein loc100786776	0.340	0.000	0.024	0.698	0.011	1.505	0.757	0.011	1.399
chr3.LjT35E03.150.r2.d	cytochrome P450	0.136	0.007	5.489	0.605	0.007	1.082	0.751	0.017	2.315
chr2.CM0002.450.r2.m	RING-H2 finger protein ATL66-like	0.183	0.003	1.880	0.485	0.019	3.861	0.720	0.007	1.020
chr4.CM0570.190.r2.a	probable calcium-binding protein CML17-like	0.124	0.007	5.501	0.661	0.022	3.287	0.709	0.033	4.673
LjSGA_106315.1	p-aminobenzoate synthase	0.327	0.001	0.162	2.442	0.032	1.296	0.707	0.001	0.078
LjSGA_011044.2	uncharacterized protein	0.218	0.016	7.152	0.501	0.068	13.671	0.696	0.058	8.319

chr5.LjT29P04.10.r2.d	uncharacterized protein	0.227	0.010	4.555	0.628	0.014	2.288	0.684	0.028	4.131
chr2.CM0021.2440.r2.m	uncharacterized protein	0.153	0.008	4.910	0.537	0.015	2.754	0.682	0.039	5.653
chr4.LjT16L01.70.r2.d	auxin-induced protein 5ng4-like	0.018	0.002	9.322	0.503	0.072	14.287	0.659	0.066	9.948
chr2.CM0177.120.r2.d	cinnamyl alcohol dehydrogenase	0.245	0.012	4.767	0.445	0.039	8.667	0.658	0.054	8.247
LjSGA_032403.1	protein transport protein sec31	0.291	0.008	2.741	0.431	0.011	2.663	0.613	0.040	6.564
chr1.LjT04O21.80.r2.d	phox domain-containing protein	0.294	0.035	11.989	0.576	0.099	17.142	0.611	0.056	9.138
chr1.CM0012.2260.r2.d	thaumatin-like protein	0.045	0.004	8.479	0.598	0.014	2.426	0.600	0.029	4.796
chr6.CM0573.140.r2.m	topless-related protein 3-like	0.276	0.013	4.651	0.508	0.032	6.292	0.585	0.043	7.293
chr4.CM0131.170.r2.d	uncharacterized protein	0.108	0.000	0.126	0.650	0.025	3.912	0.584	0.020	3.475
LjSGA_051596.1	senescence-associated protein	0.140	0.002	1.736	0.390	0.013	3.392	0.575	0.024	4.127
chr2.CM0099.240.r2.m	uncharacterized protein loc100800669	0.286	0.022	7.528	0.465	0.024	5.234	0.574	0.025	4.426
chr2.CM0124.480.r2.m	pho1-like protein	0.061	0.005	8.632	0.626	0.042	6.740	0.570	0.003	0.591
LjSGA_015944.1	protein wax2-like	0.248	0.027	10.774	1.153	0.047	4.085	0.558	0.015	2.745
LjSGA_015617.1	uncharacterized protein	0.193	0.001	0.767	0.495	0.005	1.107	0.554	0.004	0.772
LjSGA_006701.1	transcription factor UNE10-like	0.255	0.002	0.923	0.501	0.006	1.235	0.553	0.015	2.775
chr4.CM0831.250.r2.d	probable purine permease 11-like	0.253	0.013	5.186	1.119	0.039	3.512	0.532	0.026	4.955
chr1.CM0012.2230.r2.d	thaumatin-like protein	0.046	0.005	10.993	0.629	0.082	13.005	0.524	0.035	6.709
chr1.LjT31L11.70.r2.d	phosphoribosylaminoimidazole-succinocarboxamide synthase	0.212	0.005	2.303	0.677	0.036	5.317	0.519	0.004	0.759
LjT31N04.80.r2.m	F-box protein ORE9-like	0.164	0.014	8.777	0.687	0.032	4.687	0.504	0.038	7.520
chr1.CM0145.370.r2.d	phosphoribosylaminoimidazole-succinocarboxamide synthase	0.203	0.025	12.404	0.593	0.119	20.090	0.485	0.006	1.158
chr3.CM1570.240.r2.m	kinase family protein	0.179	0.015	8.377	0.400	0.060	15.018	0.479	0.016	3.258
chr5.CM1729.40.r2.a	transcription factor TCP15	0.160	0.013	7.888	0.654	0.019	2.928	0.456	0.016	3.444
LjSGA_050225.1	uncharacterized protein	0.143	0.004	2.556	0.621	0.055	8.860	0.452	0.005	1.215
chr6.CM0314.540.r2.d	phosphatidylserine decarboxylase	0.212	0.006	2.648	0.373	0.031	8.380	0.445	0.020	4.479
LjSGA_034647.1	agenet domain containing protein expressed	0.172	0.012	6.715	0.289	0.024	8.270	0.442	0.019	4.353
LjSGA_014379.1	alpha beta-hydrolase domain-containing protein	0.177	0.015	8.501	0.411	0.023	5.637	0.439	0.021	4.687
LjSGA_085110.1	ubiquitin-protein ligase 1	0.201	0.020	9.809	0.339	0.033	9.689	0.438	0.030	6.944
chr5.CM0052.670.r2.d	transcription factor	0.144	0.022	15.384	0.459	0.018	3.909	0.427	0.020	4.703
chr2.LjT16L14.80.r2.m	receptor-like protein kinase hsl1-like	0.091	0.014	14.873	0.746	0.033	4.362	0.424	0.028	6.512
LjSGA_081253.1	zinc finger ccch domain-containing protein 30-like	0.140	0.002	1.458	0.330	0.006	1.730	0.418	0.003	0.825
chr4.CM0006.630.r2.a	lysine-ketoglutarate reductase saccharopine dehydrogenase bifunctional enzyme	0.096	0.010	10.805	0.288	0.015	5.234	0.414	0.030	7.142
LjSGA_020916.1	cytosolic alpha-amylase	0.035	0.002	6.912	0.186	0.009	4.664	0.412	0.020	4.960
chr1.CM1664.10.r2.a	La protein 1	0.174	0.011	6.268	0.574	0.027	4.750	0.409	0.021	5.037
LjSGA_018929.1	auxin-induced protein 5ng4-like	0.038	0.003	7.101	0.205	0.007	3.625	0.404	0.016	3.924
chr1.CM0637.160.r2.d	ABC transporter B family member 20-like	0.198	0.006	3.160	0.727	0.031	4.205	0.399	0.028	7.061
chr1.CM0284.300.r2.m	SPX domain-containing membrane protein at4g22990-like isoform 1	0.014	0.003	19.116	0.404	0.059	14.643	0.395	0.039	9.845
LjSGA_075588.1	RNA polymerase II second largest subunit	0.133	0.002	1.405	0.470	0.023	4.888	0.391	0.010	2.684
chr5.CM0341.340.r2.a	uncharacterized protein	0.158	0.009	5.598	0.440	0.001	0.314	0.391	0.030	7.782
LjSGA_017232.1	ethylene-responsive transcription factor 1b-like	0.059	0.010	16.379	0.239	0.000	0.016	0.387	0.030	7.797
LjSGA_025450.1	uncharacterized protein	0.120	0.007	6.174	0.332	0.010	3.060	0.385	0.035	9.115
LjSGA_054056.1	nucleolar protein 10-like	0.157	0.003	1.804	0.667	0.002	0.353	0.384	0.004	1.162
chr2.CM0021.3450.r2.m	uncharacterized protein	0.174	0.005	2.710	0.545	0.038	6.960	0.384	0.013	3.416
LjSGA_121516.1	soul heme-binding family protein	0.091	0.001	1.005	0.398	0.008	1.911	0.383	0.009	2.372
LjSGA_104119.1.1	uncharacterized protein	0.171	0.006	3.395	0.251	0.018	7.367	0.381	0.021	5.436
chr3.CM0111.50.r2.d	no hit	0.152	0.015	9.711	0.458	0.023	4.984	0.381	0.003	0.801
LjSGA_023264.1	B-block binding subunit of TFIIIC	0.096	0.000	0.064	0.328	0.018	5.563	0.377	0.005	1.211
LjSGA_040996.2	aminophospholipid ATPase	0.175	0.013	7.550	0.333	0.014	4.166	0.377	0.012	3.130
LjSGA_033644.2	thaumatin-like protein	0.061	0.008	12.258	0.459	0.032	7.072	0.374	0.017	4.506
chr2.CM0168.300.r2.d	galactomannan galactosyltransferase	0.152	0.014	9.279	0.312	0.005	1.694	0.371	0.025	6.840
chr5.CM0180.970.r2.d	kinase family protein	0.162	0.004	2.727	0.334	0.003	0.899	0.369	0.012	3.363
LjSGA_129120.1	remorin family protein	0.111	0.008	7.089	0.492	0.016	3.203	0.359	0.017	4.847
chr5.CM0200.3040.r2.m	zinc finger protein 4	0.072	0.008	10.642	1.056	0.051	4.788	0.357	0.019	5.312
LjSGA_052668.1	s-adenosyl-L-methionine-dependent methyltransferase-like protein	0.169	0.016	9.405	0.253	0.009	3.572	0.355	0.004	1.241
LjSGA_075073.1	gibberellin-regulated protein	0.113	0.011	9.818	0.385	0.002	0.421	0.350	0.024	6.991
chr1.CM0295.990.r2.m	peptide transporter PTR3A	0.026	0.006	24.323	0.545	0.031	5.640	0.348	0.005	1.352
chr4.CM0061.250.r2.m	uncharacterized protein	0.171	0.001	0.377	0.346	0.013	3.836	0.347	0.014	4.150
LjSGA_062034.1	LON protease homolog peroxisomal-like	0.142	0.013	9.313	0.274	0.027	9.883	0.345	0.020	5.769
LjSGA_091062.1	pre-mRNA splicing factor	0.168	0.005	3.206	0.331	0.002	0.479	0.343	0.008	2.453
chr5.CM0052.500.r2.d	one helix protein 2 protein	0.166	0.007	4.206	0.587	0.015	2.514	0.341	0.026	7.596
chr5.CM0456.340.r2.d	DNA-directed RNA polymerase III subunit RPC5	0.114	0.002	2.083	0.395	0.011	2.821	0.341	0.032	9.524
LjSGA_024632.1	ATP binding protein	0.115	0.003	2.483	0.241	0.021	8.598	0.338	0.003	0.781
LjSGA_010785.1	cysteine-rich repeat secretory protein	0.123	0.000	0.196	0.657	0.008	1.281	0.337	0.006	1.758
LjSGA_029395.1.1	WD40 repeat compass complex protein	0.165	0.004	2.726	0.708	0.010	1.360	0.334	0.020	5.877
LjSGA_075081.1	acetyl-CoA carboxylase	0.136	0.003	2.247	0.329	0.003	0.842	0.332	0.000	0.038
LjSGA_052934.2	RAS-related protein Rab-18	0.025	0.004	16.168	0.662	0.063	9.578	0.331	0.032	9.659
chr1.CM0105.2280.r2.m	ankyrin repeat-containing protein at5g02620-like	0.147	0.003	1.794	0.328	0.008	2.512	0.325	0.010	3.122
chr1.CM0591.620.r2.d	uncharacterized protein loc100810757	0.106	0.012	10.853	0.289	0.002	0.582	0.315	0.030	9.494
chr1.LjT05B18.150.r2.d	AHA1 domain-containing protein	0.141	0.022	15.562	0.334	0.007	2.013	0.315	0.009	2.794
LjSGA_013005.1	suppressor-like protein	0.082	0.001	1.461	0.293	0.007	2.370	0.313	0.018	5.827
chr5.CM0852.80.r2.m	BRI1 kinase inhibitor 1-like	0.095	0.041	42.710	0.199	0.003	1.276	0.311	0.002	0.632
LjSGA_097410.1	uncharacterized protein	0.139	0.006	4.207	1.232	0.006	0.459	0.305	0.017	5.649
LjSGA_047696.1	protein sensitive to proton rhizotoxicity 1-like	0.118	0.005	4.613	0.299	0.010	3.289	0.297	0.010	3.477
chr1.CM0410.140.r2.m	UDP-glycosyltransferase 83a1-like	0.117	0.007	6.319	0.290	0.007	2.262	0.297	0.027	9.014
LjSGA_128679.1	ATP-binding cassette transporter	0.098	0.001	0.701	0.265	0.020	7.417	0.297	0.024	8.240
LjSGA_026760.1	uncharacterized protein	0.084	0.002	1.991	0.751	0.018	2.391	0.297	0.003	1.039
LjSGA_068216.1	auxin response factor-like protein	0.137	0.002	1.809	0.316	0.011	3.329	0.296	0.011	3.641
LjSGA_013484.2	nucleotide-diphospho-sugar transferase	0.061	0.005	8.406	0.363	0.009	2.608	0.294	0.009	3.110
chr1.CM0295.1020.r2.m	uncharacterized protein	0.094	0.012	12.803	0.171	0.013	7.607	0.292	0.025	8.564
LjSGA_081570.1	myosin-like protein	0.133	0.010	7.682	0.278	0.018	6.358	0.289	0.001	0.377
chr4.CM0126.630.r2.m	MADS-box protein agl14	0.018	0.001	7.465	0.151	0.002	1.227	0.288	0.003	0.946
chr5.CM0200.1370.r2.d	PSI reaction center subunit II	0.141	0.013	9.541	1.076	0.064	5.961	0.284	0.020	6.933
LjSGA_010384.1	uncharacterized protein	0.125	0.013	10.276	0.353	0.034	9.599	0.283	0.022	7.655
chr2.CM0272.980.r2.d	histidine kinase osmosensor protein	0.012	0.000	1.392	0.222	0.006	2.840	0.278	0.009	3.144
LjSGA_057043.1	uncharacterized protein	0.132	0.002	1.361	0.202	0.015	7.604	0.273	0.012	4.570
chr6.CM0139.1170.r2.d	s-adenosylmethionine decarboxylase	0.020	0.001	5.194	0.138	0.018	13.192	0.273	0.002	0.820
chr3.CM0091.1990.r2.m	probable E3 ubiquitin-protein ligase ARI7-like	0.080	0.007	8.654	0.249	0.000	0.001	0.272	0.019	6.895
chr5.CM0062.210.r2.d	acyl carrier protein	0.107	0.002	1.967	0.396	0.007	1.891	0.269	0.010	3.742
LjSGA_061086.1.1	bZip transcription factor-like protein	0.065	0.006	9.550	0.171	0.007	4.068	0.268	0.009	3.166
chr5.CM0180.140.r2.m	trx fold-containing protein	0.084	0.001	0.793	0.490	0.041	8.360	0.267	0.024	9.002
chr4.CM1987.150.r2.a	uncharacterized protein	0.097	0.023	24.146	0.217	0.041	18.702	0.265	0.017	6.270
LjSGA_011803.1	uncharacterized protein at5g65660-like	0.045	0.006	13.476	0.512	0.042	8.263	0.260	0.014	5.357
LjSGA_033977.1	nuclear export mediator factor nemf-like	0.100	0.014	14.023	0.237	0.003	1.182	0.255	0.017	6.725
LjSGA_067865.1	WD40 repeat protein	0.102	0.000	0.315	0.247	0.011	4.538	0.254	0.001	0.539
LjSGA_016567.2	uncharacterized protein	0.124	0.001	0.844	0.350	0.028	8.125	0.254	0.007	2.818
LjSGA_014426.1	zinc ion binding protein	0.102	0.004	3.680	0.322	0.003	1.083	0.250	0.006	2.225
chr1.CM0133.780.r2.m	wrky transcription factor 50	0.052	0.003	4.798	0.167	0.019	11.427	0.247	0.013	5.470
chr2.CM0346.220.r2.d	uncharacterized protein	0.107	0.002	1.903	0.258	0.023	8.894	0.241	0.006	2.316
LjSGA_027448.2	lecithine-cholesterol acyltransferase-like 4-like	0.089	0.010	10.867	0.168	0.013	7.697	0.237	0.005	2.222
LjSGA_051658.1	peroxisomal targeting signal 1 receptor	0.088	0.015	17.661	0.214	0.005	2.547	0.234	0.011	4.689
LjSGA_019770.1	wall-associated receptor kinase-like 14-like	0.084	0.003	3.078	0.358	0.039	10.828	0.233	0.014	6.122
LjSGA_031176.1	zeaxanthin epoxidase	0.108	0.005	4.332	0.206	0.009	4.409	0.231	0.009	3.723
LjSGA_099985.1	calcium-dependent protein kinase	0.098	0.002	2.337	0.153	0.009	5.993	0.229	0.011	4.724
chr5.CM0328.240.r2.d	uncharacterized protein	0.107	0.006	5.443	0.219	0.001	0.270	0.227	0.013	5.584
LjSGA_031097.1	ADP-ribosylation factor GTPase-activating protein AGD14	0.072	0.011	15.707	0.236	0.014	5.892	0.203	0.008	4.115
chr5.CM0096.720.r2.d	protein zcf37	0.082	0.007	8.466	0.132	0.009	6.728	0.201	0.006	3.164
chr1.CM0001.80.r2.a	protein lateral organ boundaries-like	0.024	0.003	13.692	0.294	0.014	4.719	0.201	0.020	9.734
LjSGA_041246.1	proline-rich protein	0.085	0.011	13.468	0.159	0.007	4.201	0.198	0.011	5.725
chr1.CM0012.1610.r2.d	heme oxygenase 1 protein 2	0.039	0.002	5.128	0.189	0.013	7.039	0.197	0.007	3.690
LjSGA_010472.2	histone transcription regulator hira	0.084	0.015	18.414	0.170	0.009	5.035	0.196	0.017	8.834
LjSGA_039118.1	tRNA-dihydrouridine synthase 2-like protein	0.088	0.001	0.829	0.275	0.006	2.035	0.191	0.002	0.978
chr1.CM0433.220.r2.d	uncharacterized protein	0.038	0.006	14.805	0.117	0.013	11.160	0.191	0.013	6.645
chr1.CM0001.180.r2.a	erythrocyte membrane-associated giant protein antigen 332	0.066	0.006	9.119	0.136	0.015	11.203	0.190	0.011	5.883
LjSGA_092688.1	pentatricopeptide repeat-containing protein mitochondrial-like	0.087	0.004	5.133	0.192	0.008	3.938	0.189	0.016	8.646
chr2.CM0021.680.r2.m	glycine decarboxylase multi-enzyme h subunit	0.012	0.002	20.000	0.436	0.047	10.762	0.187	0.006	3.158
LjSGA_036309.1	octicosapeptide phox domain-containing protein kinase	0.062	0.001	2.259	0.138	0.043	31.366	0.182	0.009	4.746
chr4.CM0004.750.r2.d	zinc finger protein	0.079	0.001	1.772	0.122	0.008	6.399	0.178	0.004	2.166
LjSGA_055091.1	cytoe P450 monooxygenase cyp72a65	0.058	0.003	4.467	0.112	0.000	0.017	0.178	0.005	2.748
chr4.CM0165.200.r2.d	s-adenosyl-L-homocysteine hydrolase	0.033	0.002	6.118	0.130	0.001	1.027	0.169	0.001	0.818
LjSGA_049510.2	uncharacterized protein	0.041	0.008	19.879	0.104	0.004	4.139	0.168	0.013	7.604
chr2.CM0177.510.r2.m	hydroxyproline-rich glycoprotein	0.039	0.001	2.895	0.334	0.030	8.984	0.167	0.009	5.623
LjSGA_063109.1	zinc finger protein	0.066	0.015	22.991	0.125	0.026	20.917	0.167	0.008	4.613
LjSGA_038141.1	uncharacterized protein	0.066	0.012	18.831	0.113	0.014	12.747	0.167	0.005	2.951
LjSGA_019513.1	uncharacterized protein	0.068	0.001	1.131	0.155	0.027	17.378	0.166	0.001	0.323
LjSGA_029197.1	mannose-binding lectin-like protein	0.077	0.000	0.341	0.127	0.002	1.761	0.164	0.006	3.657
LjSGA_101291.1	ATPase splayed	0.080	0.002	2.539	0.154	0.006	3.950	0.163	0.009	5.613
LjSGA_035257.1	auxin response factor 2	0.078	0.009	11.300	0.197	0.002	0.908	0.163	0.007	4.345
LjSGA_132775.1	type II inositol- -trisphosphate 5-phosphatase FRA3-like	0.077	0.004	5.384	0.175	0.018	10.467	0.161	0.004	2.449
LjSGA_037651.1.1	multidrug pheromone MDR ABC transporter family	0.067	0.005	6.870	0.140	0.005	3.446	0.156	0.006	3.806
chr5.CM0062.250.r2.d	ubiquitin-protein ligase	0.073	0.007	9.490	0.143	0.010	6.963	0.155	0.014	8.804
LjSGA_029905.1	G patch domain-containing protein	0.066	0.002	2.346	0.134	0.007	5.242	0.149	0.014	9.665
chr3.LjT35E03.220.r2.d	cytochrome P450	0.029	0.006	21.704	0.118	0.004	3.425	0.148	0.011	7.368
chr1.CM0393.250.r2.d	Phospholipase A1	0.048	0.004	7.981	0.161	0.017	10.683	0.145	0.007	4.567
chr4.CM0087.1640.r2.d	galactose oxidase kelch repeat domain-containing protein	0.068	0.012	18.354	0.147	0.010	6.729	0.142	0.010	6.678
chr5.CM1439.120.r2.d	transportin 1	0.069	0.003	4.447	0.179	0.011	6.066	0.141	0.000	0.257
chr4.CM0006.520.r2.m	alpha beta-hydrolases-like protein	0.055	0.002	3.784	0.140	0.010	6.874	0.141	0.009	6.257
chr3.CM0396.710.r2.m	zinc finger protein ZAT5-like	0.035	0.003	8.640	0.096	0.003	3.131	0.140	0.003	2.201
LjSGA_040371.1	transcription elongation factor SPT6	0.053	0.000	0.594	0.142	0.013	8.987	0.137	0.008	5.679
LjSGA_092088.2	agenet domain-containing protein bromo-adjacent homology domain-containing protein	0.060	0.010	16.377	0.115	0.010	8.831	0.133	0.007	5.285
LjSGA_022326.1	F-box family protein	0.057	0.003	4.471	0.146	0.007	4.626	0.131	0.000	0.120
LjSGA_011634.1	constans interacting protein 5-like protein	0.046	0.005	10.973	0.187	0.008	4.424	0.130	0.005	3.797
LjSGA_050602.1	uncharacterized protein	0.064	0.007	11.433	0.117	0.009	7.344	0.129	0.005	3.681
LjSGA_065566.2	serine threonine-protein phosphatase BSL2-like	0.052	0.002	4.352	0.161	0.001	0.847	0.128	0.000	0.142
CM0905.30.r2.d	serine esterase family protein	0.055	0.001	2.364	0.109	0.007	6.421	0.124	0.004	3.628
chr1.CM0318.20.r2.d	uncharacterized protein	0.039	0.005	12.733	0.139	0.008	6.026	0.122	0.000	0.326
chr1.CM0122.2700.r2.d	universal stress protein A-like protein	0.025	0.001	5.550	0.063	0.000	0.318	0.120	0.001	0.820
chr1.LjT04O21.120.r2.d	adenine phosphoribosyltransferase	0.041	0.004	9.493	0.104	0.009	8.657	0.120	0.001	1.248
LjSGA_013865.1	nucleolar protein 10-like	0.046	0.005	10.986	0.180	0.005	2.929	0.119	0.001	0.709
LjSGA_040464.1	transcription elongation factor spt6	0.055	0.009	15.550	0.100	0.010	10.408	0.118	0.008	6.693
chr3.CM0080.430.r2.d	uncharacterized protein	0.052	0.005	8.704	0.084	0.006	7.709	0.117	0.001	0.753
LjSGA_084236.1	polyadenylate-binding protein 2A	0.058	0.002	4.277	0.125	0.009	7.096	0.117	0.009	7.552
LjSGA_103895.1	golgi-body localisation and RNA pol II promoter FMP27 domain-containing protein	0.043	0.001	2.639	0.105	0.022	20.928	0.116	0.005	4.429
LjSGA_029835.1	uncharacterized protein	0.056	0.007	13.244	0.483	0.054	11.073	0.115	0.003	2.558
LjSGA_045519.1	bZip transcription factor-like protein	0.026	0.003	11.187	0.060	0.009	15.206	0.111	0.001	0.867
LjSGA_004924.2	CRS2-associated factor 1	0.045	0.005	10.695	0.115	0.014	12.436	0.109	0.001	1.035
LjSGA_041144.2	calcium ion binding	0.038	0.002	6.452	0.134	0.008	6.324	0.107	0.001	1.147
chr3.CM0049.320.r2.d	TIR-NBS-IRR resistance protein	0.035	0.008	23.217	0.073	0.006	8.242	0.106	0.003	3.108
chr3.CM0047.470.r2.d	sucrose-phosphate synthase	0.049	0.005	10.631	0.224	0.026	11.573	0.105	0.009	8.711
LjSGA_051865.1	protein kinase chloroplastic-like	0.030	0.003	8.698	0.060	0.005	8.621	0.105	0.010	9.870
LjSGA_019299.1	proline-rich receptor-like protein kinase PERK13-like	0.045	0.002	4.344	0.286	0.022	7.705	0.104	0.001	0.488
chr4.CM0042.720.r2.m	NBS-IRR resistance-like protein 4G	0.043	0.009	21.876	0.096	0.016	16.251	0.101	0.000	0.159
LjSGA_025454.2	nuclear receptor corepressor	0.049	0.005	9.920	0.115	0.010	9.015	0.101	0.001	1.215
LjSGA_052669.1	protein embryo defective 2423	0.041	0.003	8.250	0.102	0.013	12.465	0.100	0.005	5.201
LjSGA_016449.2	vacuolar protein sorting-associated	0.040	0.001	3.171	0.085	0.007	8.559	0.099	0.006	5.879
chr3.CM0246.510.r2.d	E3 sumo-protein ligase SIZ1	0.036	0.013	34.834	0.075	0.009	12.047	0.097	0.004	4.590
LjSGA_027943.1	armadillo beta-catenin-like repeat-containing protein	0.043	0.003	7.764	0.140	0.000	0.163	0.097	0.002	1.905
chr6.CM0169.110.r2.d	neutral ceramidase	0.033	0.002	6.576	0.056	0.006	10.499	0.095	0.001	1.365
LjSGA_081703.2	helicase, DNA binding protein	0.040	0.000	0.733	0.091	0.005	5.381	0.095	0.005	5.366
LjSGA_077714.1	uncharacterized protein	0.043	0.004	8.623	0.070	0.007	9.293	0.093	0.008	8.278
chr1.CM0295.870.r2.d	tetratricopeptide repeat protein 7A-like	0.045	0.004	8.121	0.091	0.001	0.641	0.092	0.007	7.926
CM1102.50.r2.m	uncharacterized protein	0.042	0.001	3.415	0.098	0.005	5.548	0.092	0.007	7.435
LjSGA_013253.1	uncharacterized protein	0.044	0.002	5.213	0.069	0.002	2.805	0.092	0.004	4.381
chr4.CM0042.560.r2.d	stomatal cytokinesis defective SCD1 protein	0.039	0.007	19.143	0.087	0.003	3.211	0.092	0.008	8.736
LjSGA_013848.1	NBS-IRR resistance protein	0.035	0.001	2.717	0.115	0.006	4.954	0.091	0.002	1.844
LjB14E16.10.r2.a	lysophosphatidylcholine acyltransferase lyso-paf acetyltransferase	0.042	0.006	14.918	0.096	0.000	0.293	0.091	0.001	1.401
chr2.CM0237.280.r2.m	protein binding protein	0.042	0.001	3.334	0.084	0.005	5.892	0.089	0.008	9.190
LjSGA_028017.2	VPS51 VPS67 family (components of vesicular transport) protein	0.043	0.002	5.382	0.091	0.005	5.139	0.089	0.000	0.554
LjSGA_043693.1	glutamate receptor	0.029	0.001	2.635	0.077	0.001	1.586	0.089	0.002	2.254
LjSGA_056241.1	ring u-box domain-containing protein	0.041	0.011	27.998	0.093	0.011	12.271	0.087	0.001	0.686
LjSGA_028192.1	G patch domain-containing protein 1	0.034	0.002	5.429	0.070	0.017	24.705	0.084	0.007	8.522
chr6.CM0013.330.r2.d	zinc finger protein	0.016	0.000	1.438	0.069	0.001	1.077	0.084	0.002	2.836
LjSGA_018151.1	homeobox protein knotted-1-like 6	0.033	0.002	5.659	0.059	0.005	8.101	0.084	0.000	0.078
LjSGA_040160.1	RAC-GTP binding protein	0.038	0.002	6.289	0.062	0.001	2.356	0.083	0.004	4.693
chr3.LjT37F23.40.r2.d	zinc transporter ZTP29-like	0.027	0.002	8.358	0.131	0.018	13.779	0.082	0.003	3.229
LjSGA_072549.1.1	DNA-directed RNA polymerase I subunit RPA2-like	0.027	0.002	6.212	0.128	0.000	0.237	0.081	0.002	2.419
LjT11B21.40.r2.d	uncharacterized protein	0.028	0.011	39.298	0.080	0.003	3.943	0.081	0.003	3.538
LjSGA_034573.1	agenet domain containing protein expressed	0.036	0.004	11.567	0.057	0.007	11.695	0.079	0.003	4.324
LjSGA_081862.1	uncharacterized protein	0.036	0.004	10.259	0.116	0.006	5.380	0.079	0.005	6.361
LjSGA_015272.1	uncharacterized protein loc100810572	0.031	0.002	5.767	0.060	0.002	4.009	0.079	0.008	9.941
LjT24M05.70.r2.m	uncharacterized protein	0.036	0.004	11.159	0.094	0.014	15.083	0.077	0.003	3.519
LjSGA_037430.1	regulatory-associated protein of TOR 1-like	0.038	0.007	18.159	0.070	0.002	3.225	0.077	0.007	8.806
chr1.CM0794.130.r2.d	senescence-associated protein DIN1	0.017	0.004	23.472	0.050	0.000	0.367	0.077	0.007	8.564
chr3.CM0127.740.r2.m	glucan endo-1,3-beta-glucosidase	0.031	0.000	1.443	0.051	0.001	2.899	0.076	0.007	9.202
LjSGA_053986.1	urease	0.034	0.002	5.024	0.061	0.005	7.970	0.075	0.001	1.145
chr1.CM0284.390.r2.a	(+)-neomenthol dehydrogenase	0.029	0.011	36.378	0.052	0.001	1.097	0.075	0.007	9.479
LjT33L02.10.r2.a	uncharacterized protein	0.032	0.009	26.902	0.051	0.000	0.659	0.075	0.001	1.111
LjSGA_017092.1	TMV resistance protein N	0.019	0.002	9.496	0.055	0.005	9.086	0.075	0.003	3.643
chr6.CM0830.70.r2.d	helicase-like protein	0.037	0.006	17.401	0.091	0.008	8.672	0.074	0.007	9.378

chr1.CM0113.220.r2.m	pentatricopeptide repeat-containing	0.027	0.004	14.723	0.066	0.001	1.130	0.073	0.003	4.455
LjSGA_050580.1	wrky transcription factor 17	0.015	0.001	6.603	0.042	0.001	2.855	0.073	0.001	1.589
chr2.CM1882.120.r2.m	membrane-anchored ubiquitin-fold protein 2	0.036	0.003	7.147	0.064	0.007	11.348	0.072	0.001	1.990
chr4.CM0244.90.r2.m	uncharacterized protein	0.025	0.010	38.856	0.079	0.006	7.494	0.072	0.007	9.432
chr2.CM0168.310.r2.d	galactomannan galactosyltransferase	0.023	0.004	15.880	0.047	0.001	1.739	0.069	0.004	5.486
LjSGA_110475.1	uncharacterized protein	0.032	0.003	9.537	0.048	0.005	10.957	0.069	0.002	3.231
chr4.CM0046.990.r2.m	uncharacterized protein	0.018	0.003	18.226	0.061	0.008	13.280	0.068	0.000	0.512
LjSGA_036017.1	uncharacterized protein	0.030	0.002	7.042	0.062	0.001	1.850	0.067	0.000	0.523
LjSGA_145237.1	uncharacterized protein	0.015	0.004	27.395	0.089	0.001	1.309	0.067	0.006	9.285
chr1.CM0029.340.r2.d	armadillo beta-catenin-like repeat-containing protein	0.032	0.003	8.588	0.071	0.007	10.305	0.067	0.002	2.581
LjSGA_017441.2	galacturonosyltransferase	0.029	0.001	4.733	0.059	0.000	0.124	0.066	0.006	8.811
LjSGA_033849.1	transducin family protein	0.032	0.001	3.097	0.109	0.001	0.756	0.066	0.006	9.885
LjSGA_050156.1	phosphatidylinositol-4-phosphate 5-kinase	0.031	0.006	20.289	0.073	0.003	4.358	0.065	0.003	3.941
LjSGA_011511.1	ankyrin repeat-containing	0.024	0.000	1.387	0.072	0.015	21.339	0.065	0.001	2.163
LjSGA_026864.1	cytosolic purine 5 -nucleotidase-like	0.014	0.000	2.528	0.035	0.011	31.858	0.064	0.002	3.217
CM0457.270.r2.d	inorganic phosphate transporter 2-1	0.030	0.001	3.105	0.042	0.003	6.836	0.064	0.000	0.439
LjSGA_039654.1	phagocyte signaling-impaired	0.021	0.002	11.659	0.052	0.003	4.986	0.063	0.003	5.061
LjSGA_119330.1	RNA-dependent RNA polymerase	0.022	0.001	5.574	0.037	0.002	4.145	0.060	0.003	5.401
LjSGA_129393.1	myosin-like protein	0.024	0.002	8.302	0.061	0.014	23.090	0.060	0.002	3.863
LjSGA_063966.1	WD-40 repeat protein	0.029	0.002	8.241	0.056	0.004	6.421	0.058	0.003	5.990
LjSGA_013644.1	basic helix-loop-helix protein bHLH6	0.024	0.002	8.725	0.053	0.008	15.143	0.058	0.002	3.533
LjSGA_145058.1	probable protein phosphatase 2C 52-like	0.028	0.007	24.795	0.049	0.002	4.726	0.057	0.005	8.954
LjSGA_037221.1	xylosyltransferase 1-like	0.022	0.002	7.531	0.050	0.001	2.096	0.056	0.002	4.035
LjSGA_020117.3	leucine-rich repeat receptor-like protein kinase	0.023	0.001	5.168	0.047	0.010	20.620	0.056	0.003	4.875
chr5.CM0186.70.r2.m	uncharacterized protein	0.027	0.000	0.827	0.065	0.007	11.220	0.056	0.004	6.501
LjSGA_051568.1	kinesin-like protein	0.018	0.004	22.327	0.038	0.002	5.391	0.054	0.005	9.843
LjSGA_041338.1	CC-NBS-IRR resistance protein	0.026	0.001	4.931	0.052	0.008	15.952	0.054	0.001	0.978
LjSGA_058760.1	dnaJ homolog subfamily C member 13-like	0.021	0.003	13.738	0.037	0.012	32.115	0.052	0.004	6.731
LjSGA_147348.1	uncharacterized protein	0.026	0.003	12.446	0.043	0.005	12.614	0.052	0.005	9.083
LjSGA_028255.1	uncharacterized protein	0.020	0.005	23.488	0.104	0.001	1.338	0.052	0.004	8.463
LjSGA_148154.1	protein kinase domain-containing protein	0.016	0.000	2.437	0.044	0.002	5.185	0.051	0.000	0.830
LjSGA_038793.1	AAA ATPase containing von willebrand factor type a domain-containing protein	0.022	0.001	2.456	0.076	0.005	7.071	0.050	0.002	3.085
chr4.LjB17I07.20.r2.a	aminotransferase class I and II family protein	0.017	0.002	12.475	0.131	0.020	15.202	0.050	0.004	7.814
chr5.CM0813.340.r2.d	TPR domain protein	0.024	0.003	13.760	0.093	0.011	11.672	0.049	0.000	0.325
chr5.CM0089.110.r2.m	no hit	0.023	0.000	1.543	0.046	0.002	5.077	0.049	0.004	7.227
chr2.CM0028.780.r2.d	NBS-IRR resistance protein	0.014	0.001	6.806	0.050	0.002	3.130	0.047	0.001	2.126
LjSGA_045031.1	kinesin-like protein kif15	0.014	0.002	12.549	0.044	0.009	21.144	0.047	0.004	9.437
LjSGA_127687.1	B-block binding subunit of TFIIIC	0.023	0.002	9.757	0.047	0.007	14.128	0.047	0.002	3.951
LjSGA_075598.1	uncharacterized protein	0.023	0.005	20.546	0.045	0.005	11.326	0.047	0.005	9.671
chr5.CM0696.240.r2.m	pentatricopeptide repeat-containing protein	0.019	0.001	3.069	0.130	0.006	4.990	0.046	0.004	9.603
chr3.LjT01D08.70.r2.d	serine threonine protein kinase	0.021	0.000	0.170	0.032	0.013	38.874	0.046	0.003	7.416
LjSGA_044807.1	AMP deaminase	0.020	0.002	8.624	0.074	0.002	2.869	0.045	0.000	0.325
LjSGA_014139.1	squamosa promoter-binding-like protein 7	0.021	0.001	7.282	0.054	0.015	27.141	0.045	0.001	1.414
chr1.CM0316.790.r2.d	pentatricopeptide repeat-containing protein	0.022	0.002	8.745	0.046	0.005	10.587	0.045	0.003	6.947
LjSGA_069382.1	ABC transporter D family member	0.022	0.001	2.326	0.042	0.007	17.359	0.044	0.002	4.896
LjSGA_015452.1	trihelix transcription factor GT-2-like	0.014	0.001	10.338	0.057	0.003	4.572	0.043	0.002	4.884
chr1.LjT12B11.60.r2.d	NBS-IRR resistance protein	0.019	0.002	10.739	0.059	0.005	9.195	0.043	0.003	6.967
LjSGA_012074.2	PAP-specific phosphatase HAL2-like	0.019	0.002	9.330	0.030	0.001	3.442	0.042	0.004	9.910
LjSGA_108877.1	sensitive to freezing 6 protein	0.016	0.001	5.372	0.037	0.002	5.301	0.042	0.002	3.685
chr3.CM0129.70.r2.d	DNA mismatch repair protein mlh1	0.019	0.003	14.778	0.075	0.000	0.380	0.042	0.000	0.062
chr1.CM0442.20.r2.a	phospholipase D	0.017	0.002	14.331	0.026	0.001	5.317	0.041	0.001	2.137
chr3.CM0590.140.r2.m	uncharacterized protein loc100786119	0.018	0.003	16.407	0.041	0.006	14.523	0.040	0.001	2.052
chr1.CM0088.130.r2.d	presequence protease 2	0.017	0.002	8.827	0.043	0.003	6.940	0.039	0.003	8.721
LjSGA_051351.1	protein kinase family protein	0.018	0.002	10.621	0.032	0.005	14.856	0.039	0.001	2.574
LjSGA_131588.1	phosphoribosylformylglycinamidine synthase	0.019	0.004	19.754	0.050	0.002	4.889	0.038	0.003	7.369
LjSGA_130957.1	probable lrr receptor-like serine threonine-protein kinase RKF3-like	0.018	0.001	5.943	0.026	0.004	16.430	0.038	0.000	1.061
LjSGA_022114.1	two-component response regulator ARR11-like	0.015	0.003	18.615	0.046	0.006	14.052	0.037	0.002	4.167
chr1.CM0178.120.r2.d	ribosome biogenesis protein	0.017	0.003	16.764	0.040	0.005	13.314	0.035	0.002	6.353
chr6.CM0830.550.r2.d	at4g20130-like protein	0.015	0.001	8.450	0.048	0.005	9.866	0.034	0.001	4.349
chr1.CM0113.560.r2.d	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily a member 3-like	0.015	0.001	3.662	0.041	0.002	3.935	0.032	0.002	6.894
LjSGA_048592.1	pantothenate kinase 2-like	0.013	0.001	3.931	0.024	0.002	8.914	0.030	0.002	6.066

Supplemental Table 3. Expression profile of 374 genes in cluster 3 during nodule senescence

ID number	Annotation	2 wpi			4 wpi			8 wpi		
		Average Normalized	SD Normalized	CV (%)	Average Normalized	SD Normalized	CV (%)	Average Normalized	SD Normalized	CV (%)
chr1.CM0104.2620.r2.m	arabinogalactan peptide 14	157.189	6.158	3.918	77.180	0.197	0.255	73.073	3.936	5.386
chr1.CM0125.390.r2.m	probable peptide nitrate transporter at2g40460-like	70.287	2.572	3.660	46.267	3.043	6.576	28.978	1.301	4.490
chr4.CM0337.580.r2.m	EKN protein	57.041	5.595	9.809	42.538	3.046	7.161	24.935	1.497	6.005
chr4.CM0227.40.r2.d	AP2 erf domain-containing transcription factor	41.622	2.690	6.464	25.976	0.198	0.763	7.872	0.236	3.003
chr1.CM0544.890.r2.m	cu zn superoxide dismutase	36.447	2.041	5.599	21.988	3.062	13.927	5.765	1.078	18.704
chr3.CM0282.1000.r2.m	early nodulin-like protein 2-like	32.960	2.064	6.261	5.056	0.326	6.440	7.619	0.448	5.874
chr4.CM0042.2230.r2.m	calmodulin 24-like protein	26.356	0.456	1.729	6.840	0.340	4.976	11.611	0.161	1.386
chr5.CM1077.360.r2.a	glutamine expressed	25.349	1.116	4.404	8.071	0.308	3.819	8.525	0.199	2.336
chr1.CM0104.2710.r2.a	uncharacterized protein loc100798848 isoform 1	23.502	1.019	4.334	7.393	0.162	2.187	7.912	0.155	1.963
chr2.CM0021.560.r2.m	uncharacterized protein	21.612	0.018	0.082	11.687	0.538	4.607	8.980	0.158	1.760
chr4.CM0046.1620.r2.m	aquaporin NIP1-2	21.090	1.969	9.338	13.689	1.750	12.785	8.840	0.984	11.128
chr1.CM0017.1450.r2.d	farnesylated protein	20.628	1.855	8.995	5.804	0.551	9.491	8.621	0.864	10.021
chr1.CM0398.350.r2.d	dehydration-induced protein ERD15	20.508	0.939	4.577	6.425	0.079	1.225	9.966	0.440	4.415
chr4.CM0006.210.r2.d	no hit	18.992	1.156	6.087	9.661	0.011	0.110	8.247	0.183	2.218
chr3.CM0590.380.r2.d	uncharacterized protein	18.423	1.475	8.007	8.501	0.456	5.367	7.536	0.745	9.891
chr2.CM0608.1430.r2.m	uncharacterized protein	17.858	0.442	2.474	3.486	0.309	8.866	6.702	0.539	8.038
chr3.CM1570.70.r2.a	IAA-amino acid hydrolase ILR1-like protein	17.512	0.488	2.789	2.843	0.962	33.829	3.476	1.288	37.049
LjSGA_023779.1	coproporphyrinogen III oxidase	17.467	1.470	8.418	7.982	0.259	3.247	6.146	0.569	9.265
chr2.CM0903.320.r2.a	uncharacterized protein loc100815940	16.708	0.160	0.957	5.633	0.136	2.416	7.284	0.022	0.305
chr1.LjT04N09.160.r2.d	NAC domain protein	16.498	0.120	0.726	5.306	0.088	1.658	7.911	0.095	1.206
chr5.CM0048.40.r2.d	hydrophobic protein LTI6a	15.436	0.435	2.820	7.003	0.107	1.521	5.651	0.156	2.753
chr4.CM0003.1090.r2.m	bifunctional inhibitor lipid-transfer protein seed storage 2S albumin-like protein	13.013	0.524	4.030	1.598	0.057	3.589	4.707	0.043	0.918
chr2.CM0249.1560.r2.d	dnaJ homolog subfamily C member 2-like	12.603	0.499	3.958	2.041	0.106	5.196	3.026	0.114	3.755
LjSGA_069348.1	haloacid dehalogenase-like hydrolase domain-containing protein	12.407	0.358	2.883	7.744	0.017	0.221	5.644	0.357	6.334
chr1.CM0133.160.r2.m	no hit	12.347	0.250	2.025	3.645	0.002	0.054	4.263	0.180	4.234
LjSGA_041467.1.1	bifunctional dihydroflavonol 4-reductase flavanone 4-reductase-like	12.004	0.762	6.348	3.399	0.077	2.260	5.832	0.025	0.433
chr2.CM0056.620.r2.d	beta-glucosidase	11.942	1.010	8.459	2.715	0.321	11.839	5.098	0.556	10.908
chr4.CM0100.70.r2.m	uncharacterized protein	11.831	0.275	2.321	5.754	0.359	6.232	4.681	0.043	0.929
chr1.CM0104.3050.r2.a	serine threonine-protein kinase	11.780	0.202	1.716	7.337	0.143	1.953	5.800	0.245	4.218
LjSGA_046195.1	desiccation protectant protein LEA14-like protein	11.778	0.933	7.920	1.877	0.000	0.022	3.240	0.068	2.114
chr1.LjT10G23.110.r2.m	oligopeptide transporter OPT family	11.495	0.642	5.582	1.176	0.163	13.827	3.353	0.481	14.345
LjSGA_019228.1	anthranilate N-hydroxycinnamoyl benzoyltransferase	11.147	0.312	2.802	5.775	0.097	1.684	3.786	0.204	5.379
chr4.CM0026.1170.r2.a	uncharacterized protein	10.873	0.901	8.285	8.944	0.417	4.667	5.347	0.469	8.774
LjSGA_007556.3	metallothionein-like protein	10.840	0.432	3.985	0.662	0.045	6.791	3.470	0.179	5.169
LjSGA_022879.1	bifunctional inhibitor lipid-transfer protein seed storage 2S albumin-like protein	10.812	0.886	8.191	2.735	0.184	6.718	5.152	0.368	7.135
chr3.CM0396.100.r2.m	uncharacterized protein at4g22758-like	10.784	0.703	6.518	2.709	0.037	1.374	3.748	0.272	7.265
chr6.CM1034.80.r2.d	polygalacturonase at1g48100-like	10.367	0.128	1.238	1.640	0.104	6.327	3.925	0.169	4.314
LjSGA_024327.1	histone H2A	9.660	0.648	6.711	2.169	0.084	3.879	3.365	0.385	11.440
chr5.CM0096.20.r2.m	L-asparaginase	9.422	0.321	3.402	1.133	0.028	2.439	1.317	0.148	11.225
LjSGA_040860.1	uncharacterized protein	9.195	0.754	8.201	4.107	0.409	9.960	4.016	0.344	8.556
chr3.CM0460.120.r2.d	L-ascorbate oxidase homolog	9.167	0.298	3.254	1.196	0.005	0.451	3.405	0.035	1.016
LjSGA_127000.1	catalytic hydrolase	9.157	0.283	3.088	0.650	0.018	2.779	0.955	0.052	5.448
chr3.CM0160.190.r2.m	uncharacterized protein	7.961	0.169	2.127	3.874	0.144	3.705	3.664	0.149	4.055
LjSGA_052139.1	uncharacterized protein at5g01610-like	7.916	0.087	1.105	2.500	0.128	5.110	2.812	0.241	8.579
LjSGA_022729.1	protein exordium like 2	7.637	0.042	0.556	6.755	0.490	7.256	2.769	0.009	0.311
LjSGA_023624.0.1	Calcium-binding EF-hand	7.595	0.241	3.174	0.878	0.001	0.134	1.455	0.052	3.566
chr1.CM2121.240.r2.m	probable protein phosphatase 2C 8-like	7.215	0.174	2.405	5.238	0.056	1.078	3.491	0.140	4.016
chr3.CM0616.180.r2.d	histone H4	6.808	0.063	0.931	2.377	0.019	0.815	3.160	0.080	2.528
LjSGA_025815.1	L-ascorbate oxidase homolog	6.705	0.641	9.565	1.030	0.131	12.720	1.124	0.206	18.309
chr2.CM0373.1220.r2.d	actin 4	6.602	0.242	3.673	1.077	0.328	30.481	2.324	0.219	9.404
chr2.LjT46G02.250.r2.d	60S acidic ribosomal protein P0	6.434	0.216	3.359	2.191	0.095	4.320	2.530	0.011	0.421
chr3.CM0127.90.r2.m	uncharacterized protein	6.333	0.209	3.307	2.306	0.143	6.211	1.878	0.060	3.183
LjSGA_051582.1	monocopper oxidase-like protein SKU5	6.292	0.227	3.601	1.462	0.036	2.456	3.010	0.100	3.310
LjSGA_018703.2	scarecrow-like protein 5-like	6.246	0.290	4.650	1.733	0.040	2.289	2.265	0.348	15.382
chr6.CM0679.230.r2.d	DNA repair protein RAD50	6.242	0.400	6.403	5.210	0.063	1.206	2.801	0.242	8.636
chr1.CM0104.3070.r2.a	no hit	6.192	0.537	8.679	6.378	0.254	3.977	1.568	0.065	4.146
chr1.CM0145.260.r2.d	protein transport protein SFT1	6.085	0.460	7.568	2.026	0.127	6.265	2.908	0.231	7.928
chr3.CM0091.110.r2.d	hydroxyacylglutathione hydrolase	5.752	0.440	7.644	3.519	0.059	1.679	2.392	0.091	3.806
chr3.CM0416.270.r2.a	subtilisin-like protease-like	5.724	0.026	0.446	1.374	0.051	3.739	2.325	0.037	1.580
LjT33G24.10.r2.d	AP2/ERF domain-containing transcription factor	5.005	0.462	9.224	1.220	0.080	6.564	2.079	0.190	9.149
chr4.CM0387.120.r2.m	1-deoxy-D-xylulose 5-phosphate synthase	4.841	0.089	1.843	3.154	0.333	10.560	1.895	0.022	1.176
chr4.LjT40J14.160.r2.m	hydroxymethylbilane synthase	4.717	0.028	0.584	2.568	0.010	0.374	1.996	0.062	3.095
chr1.CM0207.220.r2.m	NAC transcription factor-like 9	4.711	0.430	9.126	1.287	0.117	9.079	2.113	0.211	9.989
chr3.CM0426.80.r2.a	60S acidic ribosomal protein	4.664	0.363	7.788	3.843	0.268	6.966	2.326	0.198	8.532
chr3.CM0135.180.r2.d	enoyl-ACP reductase	4.552	0.404	8.883	1.464	0.046	3.146	2.116	0.011	0.510
chr1.CM0113.240.r2.m	saur family protein	4.512	0.351	7.777	0.886	0.125	14.074	1.076	0.080	7.454
LjSGA_016165.1	L-gulonolactone oxidase-like	4.468	0.052	1.174	0.327	0.002	0.486	0.413	0.007	1.715
chr3.CM0142.520.r2.d	tetratricopeptide repeat domain-containing protein	4.413	0.256	5.804	0.317	0.047	14.911	2.005	0.099	4.928
chr6.CM0139.530.r2.m	basic 7S globulin-like	4.404	0.011	0.251	0.623	0.077	12.323	1.951	0.168	8.600
chr4.CM1864.550.r2.m	nucleoside diphosphate kinase	4.259	0.137	3.210	2.040	0.072	3.524	1.036	0.048	4.636
chr3.CM0136.250.r2.a	structural constituent of cell	3.823	0.296	7.749	1.367	0.090	6.573	1.406	0.158	11.275
chr5.LjT14L10.20.r2.m	nitrate and chloride transporter	3.816	0.169	4.428	2.349	0.027	1.160	1.205	0.080	6.633
chr5.CM0200.280.r2.d	alpha-L-fucosidase 1-like	3.750	0.007	0.183	0.599	0.038	6.366	1.410	0.082	5.827
LjSGA_129702.1	probable xyloglucan endotransglucosylase hydrolase protein 28-like	3.702	0.346	9.351	1.491	0.040	2.699	1.819	0.145	7.947
chr4.CM2115.30.r2.a	glycine decarboxylase complex H-protein	3.689	0.108	2.928	1.881	0.093	4.954	1.714	0.091	5.321
LjSGA_070244.1	basic blue copper protein	3.683	0.224	6.091	1.263	0.017	1.381	1.799	0.079	4.383
LjSGA_044797.1	60S ribosomal protein L10	3.676	0.277	7.544	1.106	0.126	11.364	1.041	0.140	13.493
chr3.CM0396.310.r2.d	argonaute protein group	3.665	0.206	5.616	2.461	0.285	11.591	1.359	0.002	0.178
LjSGA_073816.1	uncharacterized protein	3.634	0.093	2.570	2.471	0.088	3.578	1.801	0.074	4.106
chr4.CM0617.450.r2.d	senescence dehydration-associated protein	3.548	0.299	8.431	0.629	0.082	12.953	0.962	0.101	10.506
chr1.CM0029.730.r2.d	dihydroneopterin aldolase	3.538	0.345	9.744	1.123	0.063	5.588	0.793	0.062	7.766
LjSGA_063118.0.1	microsomal omega-3 fatty acid desaturase	3.499	0.062	1.786	0.331	0.011	3.250	0.650	0.016	2.472
chr5.CM0239.480.r2.m	dnaJ heat shock N-terminal domain-containing protein	3.423	0.003	0.089	0.737	0.003	0.362	1.383	0.011	0.762
chr1.CM0010.150.r2.m	Iron-sulfur assembly protein IscA-like protein	3.422	0.001	0.043	2.526	0.018	0.722	1.545	0.079	5.115
chr5.CM0909.820.r2.a	histone H2	3.400	0.022	0.655	0.923	0.035	3.780	1.494	0.031	2.070
LjSGA_060223.1	multicopper oxidase	3.362	0.053	1.577	0.778	0.028	3.540	1.545	0.069	4.467
chr3.CM0127.70.r2.m	uncharacterized protein	3.252	0.310	9.541	1.323	0.088	6.674	1.144	0.102	8.886
chr3.LjT48P15.80.r2.m	type-a response regulator	3.248	0.295	9.075	1.298	0.089	6.838	1.107	0.069	6.217
LjT09J04.40.r2.d	uncharacterized protein	3.124	0.260	8.334	0.688	0.064	9.233	0.974	0.067	6.876
LjSGA_130412.1	uncharacterized protein	3.010	0.103	3.433	1.621	0.036	2.215	1.255	0.038	3.050
LjSGA_076798.1.1	inactive rhomboid protein 1-like	2.971	0.213	7.163	0.786	0.036	4.542	0.664	0.051	7.674
chr1.CM0207.130.r2.m	peroxidase 5-like	2.924	0.163	5.590	0.609	0.062	10.127	1.355	0.139	10.246
chr4.CM0161.180.r2.d	high affinity nitrate transporter	2.745	0.055	1.989	0.540	0.003	0.561	1.099	0.008	0.701
LjSGA_057970.1	glutathione s-transferase GST	2.723	0.016	0.572	1.000	0.029	2.932	1.164	0.076	6.553
chr1.CM0284.440.r2.a	phosphomannomutase	2.649	0.008	0.289	1.140	0.038	3.334	1.214	0.034	2.784
LjSGA_021446.1	uncharacterized protein	2.591	0.031	1.201	0.644	0.036	5.578	1.148	0.001	0.126
chr5.CM0492.290.r2.m	uncharacterized protein	2.559	0.024	0.954	0.415	0.020	4.706	0.557	0.003	0.542
chr6.CM0037.430.r2.m	carboxypeptidase D	2.530	0.180	7.104	0.186	0.030	16.049	0.899	0.037	4.129
LjSGA_026569.1.1	uncharacterized protein	2.521	0.121	4.805	1.452	0.072	4.965	1.245	0.008	0.659
chr5.CM0456.530.r2.m	metal ion binding	2.336	0.200	8.556	0.293	0.004	1.481	0.730	0.087	11.847
chr2.CM0018.180.r2.m	hexokinase	2.317	0.131	5.640	0.736	0.049	6.601	0.804	0.019	2.394
LjT37O09.130.r2.d	auxin-induced in root cultures protein 12	2.234	0.105	4.703	0.666	0.017	2.546	0.760	0.060	7.841
chr2.CM0058.340.r2.d	no hit	2.200	0.030	1.382	1.563	0.121	7.717	0.621	0.042	6.774
LjSGA_018803.2	early-responsive to dehydration 4	2.197	0.135	6.165	1.156	0.038	3.255	0.984	0.074	7.525
chr2.CM0903.380.r2.m	dihydrolipoamide s-acetyltransferase	2.181	0.177	8.130	0.761	0.045	5.941	0.951	0.100	10.510
LjSGA_062319.1	zinc finger protein	2.170	0.091	4.197	0.144	0.000	0.019	0.447	0.016	3.674
chr4.CM0087.140.r2.d	GDSL esterase lipase at1g74460-like	2.155	0.065	3.009	0.454	0.002	0.434	0.522	0.000	0.022
chr6.LjT01P07.200.r2.d	5'-adenylylsulfate reductase 3, chloroplastic-like	2.152	0.171	7.965	0.713	0.009	1.274	0.994	0.045	4.560
LjSGA_033127.1	leucine-rich repeat receptor-like protein kinase	2.143	0.191	8.898	0.662	0.068	10.315	0.798	0.064	8.028
LjT41D17.110.r2.a	auxin-induced protein 10A5-like	2.112	0.001	0.040	0.951	0.053	5.537	0.589	0.047	7.964
chr5.CM0048.210.r2.m	rhicadhesin receptor	2.080	0.002	0.081	0.558	0.020	3.573	0.734	0.041	5.627
chr1.CM0398.230.r2.d	gibberellin 20	2.073	0.059	2.844	0.088	0.000	0.142	0.479	0.020	4.187
chr5.CM0909.860.r2.a	leghemoglobin	2.056	0.117	5.678	1.643	0.115	7.002	0.963	0.168	17.401
LjSGA_010895.1	cytochrome P450	2.050	0.140	6.852	0.564	0.041	7.323	0.687	0.022	3.231
LjSGA_036806.1	peroxidase	2.043	0.035	1.698	0.175	0.001	0.602	0.997	0.042	4.220
chr3.CM0279.790.r2.a	NAC domain ipr003441	2.032	0.027	1.322	0.309	0.001	0.469	0.401	0.009	2.130
chr1.CM1664.60.r2.a	uncharacterized protein	1.995	0.137	6.876	0.405	0.030	7.519	0.931	0.099	10.610
chr1.CM0104.1160.r2.a	zinc knuckle (CCHC-type) family protein	1.881	0.092	4.884	1.132	0.043	3.797	0.928	0.003	0.345
chr2.CM0102.530.r2.m	uncharacterized protein	1.865	0.120	6.435	0.420	0.011	2.570	0.698	0.010	1.372
LjSGA_074183.1	hexose transporter	1.823	0.044	2.387	0.208	0.020	9.578	0.507	0.016	3.180
chr2.CM0272.810.r2.m	protein mitochondrial-like	1.811	0.010	0.576	1.419	0.037	2.615	0.848	0.004	0.516
chr1.CM0166.1190.r2.m	ADP-glucose pyrophosphorylase-like protein	1.788	0.177	9.880	0.251	0.031	12.311	0.574	0.042	7.346
chr2.CM0021.2380.r2.m	lipid binding protein	1.785	0.024	1.366	1.333	0.010	0.734	0.337	0.002	0.587
chr1.CM0088.570.r2.d	ribosomal RNA large subunit methyltransferase n	1.757	0.113	6.428	0.887	0.048	5.434	0.721	0.030	4.110
LjSGA_026718.1	protein trichome birefringence-like 38	1.737	0.125	7.210	0.115	0.000	0.291	0.574	0.040	6.936
chr3.CM0127.370.r2.m	mitochondrial import inner membrane translocase subunit TIM22	1.713	0.087	5.085	0.661	0.043	6.453	0.351	0.021	5.837
chr2.CM0056.580.r2.d	beta--glucosidase 11-like	1.712	0.154	9.009	0.264	0.051	19.270	0.612	0.100	16.266
LjSGA_017346.1	GTP-binding protein SAS1	1.710	0.113	6.609	0.634	0.046	7.252	0.602	0.080	13.245
chr2.CM0021.1550.r2.a	homeobox-leucine zipper protein	1.679	0.037	2.205	0.731	0.009	1.259	0.625	0.079	12.693

LjSGA_043692.1.1	expansin B1	1.640	0.126	7.695	1.382	0.072	5.193	0.452	0.038	8.351
LjSGA_096057.1	pyruvate kinase	1.626	0.103	6.346	0.589	0.050	8.523	0.672	0.045	6.663
chr6.CM0573.150.r2.m	probable polygalacturonase-like	1.600	0.087	5.420	0.111	0.000	0.364	0.493	0.053	10.690
LjSGA_099348.1	hexose transporter	1.595	0.099	6.226	0.586	0.052	8.839	0.731	0.062	8.463
LjSGA_018693.2	strubbelig-receptor family 6	1.590	0.084	5.309	0.563	0.021	3.775	0.707	0.045	6.422
chr1.CM0012.330.r2.m	arginine serine-rich splicing	1.583	0.000	0.001	0.916	0.004	0.457	0.584	0.025	4.223
LjSGA_036303.1	NAC domain protein NAC4	1.559	0.066	4.223	0.156	0.018	11.443	0.506	0.037	7.409
LjSGA_014096.1	uncharacterized protein	1.550	0.146	9.414	0.412	0.030	7.272	0.558	0.061	10.867
chr3.CM0091.130.r2.d	glyoxalase II	1.544	0.130	8.430	0.851	0.055	6.426	0.687	0.057	8.361
chr2.LjT16G06.40.r2.d	3-ketoacyl- reductase	1.486	0.054	3.666	0.815	0.042	5.190	0.176	0.000	0.131
LjSGA_075593.1	haloacid dehalogenase-like hydrolase domain-containing protein	1.462	0.049	3.341	0.668	0.070	10.434	0.614	0.022	3.649
LjSGA_114821.1	ER glycerol-phosphate acyltransferase	1.458	0.092	6.305	0.365	0.007	1.855	0.548	0.037	6.793
LjSGA_041552.1	TRANSPARENT TESTA 12 protein	1.432	0.079	5.501	0.533	0.039	7.229	0.702	0.018	2.493
chr3.CM0091.1820.r2.m	enhanced disease susceptibility	1.432	0.113	7.859	0.183	0.047	25.630	0.280	0.035	12.640
chr4.CM0042.1810.r2.m	RING finger protein	1.426	0.100	7.026	0.257	0.010	3.959	0.628	0.086	13.616
LjSGA_047206.1	rhamnogalacturonate lyase	1.413	0.111	7.819	0.185	0.027	14.658	0.392	0.007	1.679
LjSGA_015358.2	type-A response regulator	1.407	0.113	8.037	0.696	0.056	8.071	0.612	0.057	9.244
LjSGA_100223.1	uncharacterized protein	1.403	0.080	5.737	0.337	0.007	1.968	0.637	0.004	0.609
LjSGA_029450.1	mate efflux family protein dtx1-like	1.400	0.664	47.428	0.148	0.064	43.056	0.072	0.022	30.260
chr2.CM0021.3240.r2.m	uncharacterized protein loc100306532	1.338	0.079	5.936	0.452	0.003	0.742	0.483	0.001	0.120
chr6.CM0037.1460.r2.m	protein MEI2-like 2-like	1.321	0.067	5.069	1.149	0.115	10.037	0.632	0.062	9.750
chr5.CM0052.160.r2.d	dihydroflavonol reductase	1.307	0.013	0.974	0.247	0.022	9.087	0.570	0.010	1.735
chr6.CM1034.220.r2.d	UDP-arabinose 4-epimerase	1.285	0.107	8.352	0.781	0.073	9.300	0.634	0.059	9.368
chr6.CM0013.770.r2.d	auxin response factor	1.271	0.018	1.447	0.917	0.004	0.480	0.576	0.007	1.217
chr2.CM0249.1490.r2.m	aldose 1-epimerase family protein	1.268	0.007	0.561	0.284	0.009	3.196	0.543	0.017	3.107
LjSGA_035003.1	o-acyltransferase wsd1-like	1.255	0.490	39.069	0.642	0.249	38.730	0.191	0.075	39.404
chr5.CM0909.320.r2.m	blue copper protein	1.235	0.059	4.761	0.242	0.011	4.444	0.365	0.010	2.714
LjSGA_062924.1	serine carboxypeptidase-like protein	1.222	0.082	6.689	0.167	0.010	6.103	0.107	0.008	7.443
chr1.CM0105.1860.r2.m	RNA-binding region-containing	1.207	0.074	6.124	0.121	0.000	0.332	0.272	0.027	10.055
chr4.CM0244.70.r2.m	uncharacterized protein	1.199	0.090	7.530	0.239	0.021	8.951	0.390	0.022	5.728
LjSGA_025191.2	B-cell receptor-associated 31-like protein	1.192	0.078	6.536	0.291	0.030	10.221	0.477	0.054	11.363
chr2.CM0021.2030.r2.m	aspartic proteinase nepenthesin-2	1.187	0.049	4.149	0.884	0.071	8.066	0.457	0.037	8.121
chr1.CM0322.80.r2.d	uncharacterized protein	1.184	0.068	5.756	0.851	0.091	10.663	0.333	0.027	8.220
LjSGA_121922.1	uncharacterized protein	1.165	0.008	0.729	0.531	0.002	0.291	0.372	0.005	1.478
chr6.CM0013.470.r2.m	saur33 - auxin-responsive saur family member	1.161	0.007	0.609	0.440	0.022	5.056	0.220	0.031	14.025
chr5.CM0328.920.r2.d	protein phosphatase 2C 15	1.124	0.085	7.545	0.373	0.011	2.995	0.486	0.018	3.768
chr3.CM0241.610.r2.m	UDP-glycosyltransferase 85A3-like	1.098	0.105	9.588	0.466	0.143	30.716	0.315	0.064	20.314
LjSGA_010711.1	wrky transcription factor	1.096	0.002	0.161	0.213	0.008	3.594	0.232	0.008	3.362
chr6.CM0055.850.r2.d	2-oxoglutarate malate translocator	1.081	0.107	9.934	0.392	0.036	9.078	0.515	0.030	5.874
LjSGA_014827.2.1	glucan -beta-glucosidase	1.064	0.088	8.267	0.177	0.010	5.922	0.189	0.009	4.631
LjSGA_042146.1	probable protein phosphatase 2C 10-like	1.056	0.047	4.488	0.708	0.049	6.983	0.411	0.029	6.981
chr6.CM0139.1100.r2.d	auxin-induced protein 5NG4-like	1.055	0.073	6.957	0.421	0.134	31.870	0.363	0.076	21.031
chr5.CM0052.250.r2.d	uncharacterized protein	1.046	0.007	0.649	0.290	0.025	8.761	0.383	0.011	2.952
chr4.CM0414.20.r2.d	uncharacterized protein	1.021	0.030	2.911	0.312	0.016	5.275	0.353	0.005	1.406
chr2.CM0018.470.r2.d	no hit	1.013	0.036	3.579	0.433	0.016	3.674	0.449	0.018	4.044
chr4.CM0044.310.r2.d	pentatricopeptide repeat-containing protein	0.999	0.060	5.992	0.414	0.055	13.298	0.375	0.017	4.430
chr2.CM0308.180.r2.a	plectin-related protein	0.989	0.070	7.126	0.463	0.023	4.891	0.477	0.037	7.662
chr5.CM0200.1570.r2.m	AMP-binding protein	0.989	0.045	4.549	0.298	0.021	7.030	0.469	0.025	5.225
chr5.CM0096.670.r2.d	no hit	0.986	0.052	5.318	0.645	0.004	0.665	0.391	0.007	1.789
chr3.CM1468.210.r2.d	dihydrodipicolinate reductase 2	0.966	0.063	6.558	0.432	0.014	3.132	0.441	0.002	0.522
chr6.CM0139.1190.r2.d	methionine sulfoxide reductase type	0.958	0.095	9.926	0.720	0.106	14.780	0.465	0.081	17.432
chr1.CM0001.400.r2.d	ribosomal RNA-processing protein 8-like	0.946	0.040	4.187	0.703	0.032	4.525	0.432	0.019	4.309
chr3.CM2163.290.r2.m	disease resistance response	0.942	0.024	2.560	0.722	0.167	23.167	0.242	0.008	3.445
chr4.CM0119.160.r2.m	uncharacterized protein	0.921	0.050	5.399	0.141	0.019	13.669	0.259	0.017	6.743
chr2.CM0081.810.r2.a	serine-threonine protein kinase	0.919	0.011	1.160	0.121	0.001	1.241	0.237	0.013	5.617
LjSGA_022002.1	diphenol oxidase laccase	0.912	0.090	9.839	0.141	0.004	3.009	0.301	0.029	9.678
chr6.CM0118.210.r2.d	auxin response factor 6-like	0.911	0.033	3.640	0.317	0.020	6.457	0.402	0.004	0.942
chr5.CM0089.420.r2.d	no hit	0.904	0.001	0.076	0.582	0.023	3.923	0.448	0.014	3.071
chr1.CM0121.70.r2.m	ornithine decarboxylase	0.899	0.026	2.863	0.223	0.019	8.698	0.441	0.016	3.643
chr1.CM0295.1200.r2.a	tyrosine decarboxylase	0.882	0.072	8.204	0.438	0.052	11.829	0.404	0.048	11.895
LjSGA_062280.1	protein rhomboid-like 1	0.871	0.002	0.277	0.195	0.003	1.432	0.168	0.003	1.855
LjSGA_054725.1	uncharacterized protein	0.866	0.024	2.821	0.258	0.007	2.680	0.430	0.041	9.563
chr5.CM1574.510.r2.m	auxin-induced protein AUX28-like	0.865	0.022	2.491	0.411	0.003	0.658	0.283	0.019	6.874
LjSGA_041976.1.1	anthranilate N-hydroxycinnamoyl benzoyltransferase	0.839	0.010	1.200	0.384	0.013	3.370	0.255	0.009	3.441
chr4.CM0528.40.r2.d	haloacid dehalogenase-like hydrolase domain-containing protein	0.836	0.044	5.211	0.396	0.084	21.242	0.385	0.066	17.164
LjSGA_024944.1	uncharacterized protein	0.824	0.071	8.596	0.195	0.009	4.420	0.304	0.056	18.472
chr2.CM0608.870.r2.d	transcription factor bHLH135-like	0.817	0.078	9.596	0.094	0.003	3.307	0.290	0.013	4.332
LjSGA_123578.1	early nodulin-like protein 1-like	0.813	0.009	1.128	0.174	0.001	0.584	0.233	0.013	5.398
chr2.CM0249.720.r2.m	actin interacting protein	0.808	0.072	8.899	0.399	0.044	10.965	0.392	0.039	10.052
chr6.CM0821.190.r2.d	uncharacterized protein	0.806	0.032	3.940	0.196	0.001	0.508	0.359	0.019	5.270
chr2.CM1882.100.r2.m	uncharacterized protein	0.790	0.037	4.650	0.560	0.038	6.740	0.364	0.041	11.179
LjSGA_023991.1	leucoanthocyanidin	0.789	0.069	8.759	0.106	0.011	10.516	0.094	0.006	6.313
chr2.CM0230.60.r2.m	jumonji domain protein	0.766	0.053	6.978	0.173	0.002	0.873	0.298	0.035	11.763
LjSGA_012491.1	uncharacterized protein	0.749	0.007	0.948	0.487	0.002	0.438	0.373	0.006	1.616
LjSGA_011556.1	leucine rich repeat receptor	0.734	0.019	2.560	0.242	0.025	10.361	0.230	0.034	14.753
chr4.CM0006.420.r2.m	peroxiredoxin Q	0.731	0.067	9.112	0.117	0.018	15.316	0.158	0.011	6.959
chr3.CM0164.90.r2.d	momilactone A synthase-like	0.721	0.066	9.211	0.136	0.027	20.075	0.344	0.041	11.898
chr2.LjT31P23.30.r2.a	uncharacterized protein	0.720	0.016	2.207	0.410	0.008	1.847	0.337	0.012	3.611
LjSGA_071495.1.1	Tubby-like F-box protein	0.708	0.056	7.983	0.261	0.027	10.431	0.186	0.015	8.123
LjSGA_085276.1.1	delta -sterol-C5 -desaturase-like	0.705	0.023	3.274	0.078	0.001	1.115	0.195	0.021	10.910
LjSGA_059948.1	glycerol-3-phosphate acyltransferase	0.701	0.015	2.127	0.451	0.032	7.008	0.341	0.003	0.806
LjSGA_016012.1	4-coumarate: ligase	0.666	0.037	5.621	0.213	0.006	2.970	0.282	0.009	3.055
chr4.CM0087.820.r2.m	flavin-containing monooxygenase-like protein	0.652	0.056	8.588	0.044	0.018	41.335	0.038	0.001	3.247
chr3.CM0160.240.r2.m	uncharacterized protein	0.647	0.011	1.719	0.152	0.011	6.942	0.189	0.008	4.302
LjSGA_092050.1	major pollen allergen bet V 1-l	0.643	0.056	8.627	0.135	0.001	0.907	0.092	0.004	3.820
LjSGA_086307.1	glyceraldehyde-3-phosphate dehydrogenase	0.633	0.038	6.042	0.368	0.044	11.949	0.223	0.079	35.290
LjSGA_006032.2	prolyl-tRNA synthetase	0.624	0.059	9.424	0.414	0.025	6.035	0.302	0.041	13.438
LjSGA_039497.1	uncharacterized protein at5g01610-like	0.620	0.012	1.982	0.160	0.001	0.802	0.199	0.012	5.803
chr2.CM0065.460.r2.d	probable pectinesterase 53-like	0.611	0.059	9.738	0.122	0.002	1.597	0.197	0.013	6.529
chr3.CM0468.380.r2.d	diacylglycerol kinase 5	0.609	0.028	4.593	0.188	0.027	14.173	0.299	0.025	8.503
chr1.CM1868.270.r2.m	uncharacterized protein	0.607	0.045	7.454	0.254	0.032	12.672	0.264	0.035	13.238
LjSGA_033111.2	uncharacterized protein	0.602	0.041	6.891	0.355	0.013	3.689	0.196	0.019	9.497
chr6.CM0055.520.r2.m	GMP synthase	0.584	0.036	6.186	0.110	0.007	6.491	0.213	0.012	5.815
chr3.CM0091.960.r2.d	uncharacterized protein	0.584	0.020	3.347	0.308	0.004	1.407	0.267	0.007	2.552
LjSGA_022426.1	uncharacterized protein ycf45-like	0.582	0.014	2.334	0.462	0.058	12.637	0.210	0.025	11.710
chr2.CM0803.930.r2.a	conidiospore surface protein	0.580	0.012	1.998	0.089	0.009	10.273	0.185	0.019	10.518
LjSGA_041493.1	mitochondrial carrier protein	0.560	0.004	0.772	0.318	0.018	5.576	0.264	0.029	10.825
LjSGA_118121.1	ABC transporter A family member	0.558	0.017	3.106	0.094	0.004	3.836	0.119	0.003	2.684
LjSGA_022305.1	myristoyl-acyl carrier protein chloroplastic-like	0.557	0.003	0.458	0.099	0.015	14.648	0.102	0.005	4.584
chr1.CM0393.1070.r2.d	cyclin-dependent protein	0.542	0.053	9.699	0.040	0.002	6.222	0.109	0.002	2.280
chr3.CM0396.290.r2.d	uncharacterized protein	0.541	0.023	4.257	0.253	0.008	3.254	0.235	0.014	5.952
LjSGA_030627.1	AP2 domain-containing transcription factor	0.538	0.043	8.062	0.124	0.033	26.826	0.237	0.035	14.656
chr5.CM0072.500.r2.d	replicon protein A2	0.536	0.039	7.231	0.319	0.010	3.027	0.158	0.009	5.672
chr5.LjT42F22.120.r2.m	ATP-dependent DNA helicase 2 subunit KU70-like	0.535	0.035	6.570	0.231	0.023	9.865	0.186	0.037	19.871
chr5.CM0200.3060.r2.m	uncharacterized protein	0.534	0.013	2.420	0.107	0.006	5.191	0.209	0.002	0.958
LjSGA_067661.1	late embryogenesis abundant group 6	0.525	0.021	4.085	0.283	0.002	0.599	0.136	0.016	11.887
chr1.LjT41J07.180.r2.d	cyclin-dependent kinase g-2-like	0.520	0.011	2.072	0.119	0.007	5.600	0.213	0.008	3.627
LjSGA_033086.1	phytol kinase	0.519	0.021	4.142	0.116	0.005	4.528	0.058	0.010	18.134
chr3.CM1468.150.r2.d	uncharacterized protein chloroplastic-like	0.516	0.026	4.982	0.342	0.006	1.716	0.185	0.008	4.404
chr2.CM1835.130.r2.m	gibberellin-regulated protein	0.498	0.036	7.187	0.087	0.011	13.091	0.091	0.003	3.422
chr3.CM0292.620.r2.d	pectinesterase	0.484	0.003	0.651	0.023	0.009	38.952	0.074	0.001	1.382
LjSGA_072640.1	L-ascorbate oxidase homolog	0.478	0.046	9.534	0.084	0.009	10.301	0.169	0.013	7.848
LjSGA_038408.1	uncharacterized protein	0.475	0.026	5.483	0.080	0.001	1.355	0.112	0.010	8.982
LjSGA_018189.1	SWI/SNF -related matrix-associated actin-dependent regulator of atin subfamily A-like protein 1-like	0.467	0.025	5.329	0.240	0.007	2.772	0.180	0.021	11.571
LjSGA_137625.2	probable LRR receptor-like serine threonine-protein kinase at4g20940-like	0.467	0.022	4.769	0.100	0.004	3.783	0.175	0.000	0.068
chr2.CM1285.240.r2.d	uncharacterized protein	0.466	0.039	8.310	0.313	0.003	1.029	0.224	0.016	6.985
chr6.CM0245.500.r2.a	zinc finger protein constans-like 5-like	0.448	0.027	6.016	0.242	0.026	10.850	0.205	0.011	5.179
chr6.CM0367.380.r2.d	Blue (type 1) copper domain	0.447	0.013	2.936	0.086	0.005	6.131	0.175	0.004	2.499
chr2.CM0346.70.r2.m	replication factor a protein	0.440	0.009	2.061	0.116	0.002	2.129	0.136	0.011	7.967
LjSGA_005709.1	protein SRG1-like	0.432	0.031	7.174	0.204	0.006	3.073	0.159	0.019	12.233
LjSGA_010291.1	uncharacterized protein	0.426	0.008	1.808	0.133	0.002	1.377	0.156	0.002	0.968
LjSGA_011717.2	auxin transporter protein 1	0.421	0.034	8.176	0.121	0.000	0.190	0.128	0.006	4.854
LjSGA_022582.1	gamma-tubulin complex	0.420	0.036	8.528	0.280	0.034	12.247	0.205	0.016	7.808
chr2.CM0153.40.r2.d	sigma factor sigB regulation protein rsbQ-like	0.419	0.024	5.673	0.187	0.010	5.472	0.196	0.006	2.941
chr4.CM0075.190.r2.m	CAAX amino terminal motif-containing protease	0.401	0.036	8.964	0.173	0.024	13.848	0.169	0.023	13.773
chr2.CM0308.430.r2.m	uncharacterized protein	0.395	0.003	0.853	0.177	0.018	10.079	0.067	0.005	6.970
LjSGA_021876.1	ATP binding protein	0.375	0.029	7.723	0.172	0.005	3.037	0.150	0.009	5.875
chr3.CM0226.320.r2.d	sulfate transporter	0.374	0.030	7.967	0.036	0.003	8.110	0.062	0.021	33.880
LjSGA_083364.1	ATP binding	0.373	0.018	4.722	0.131	0.022	17.045	0.179	0.013	7.168
chr6.LjT46F23.70.r2.d	nucleotide sugar transporter family protein	0.372	0.027	7.337	0.121	0.008	6.528	0.162	0.004	2.318
chr2.CM0210.540.r2.d	uncharacterized protein	0.372	0.011	2.912	0.081	0.017	20.622	0.163	0.002	0.955
LjSGA_037422.1	alpha beta-hydrolases family protein	0.370	0.016	4.235	0.244	0.013	5.397	0.183	0.002	0.859
chr4.CM0536.100.r2.d	Nucleic acid binding protein, DUF579	0.358	0.020	5.586	0.206	0.009	4.565	0.123	0.002	1.608
LjSGA_058334.1	cyclin-dependent protein	0.357	0.032	8.931	0.044	0.003	5.738	0.067	0.005	7.891
LjSGA_068650.1	myb transcription factor	0.356	0.023	6.460	0.139	0.019	13.629	0.160	0.029	17.998
LjSGA_063898.1	inactive rhomboid protein 1-like	0.354	0.006	1.600	0.039	0.005	13.701	0.079	0.001	1.082
chr2.CM0065.670.r2.d	arginyl-tRNA synthetase	0.350	0.015	4.368	0.155	0.003	2.214	0.166	0.011	6.538
chr3.CM0155.70.r2.d	early nodulin-like protein 1-like	0.350	0.029	8.427	0.207	0.014	6.670	0.158	0.013	8.103
chr5.CM1323.30.r2.m	pollen-specific protein SF21-like	0.348	0.006	1.751	0.056	0.003	5.218	0.050	0.002	4.797
chr5.CM0239.170.r2.d	uncharacterized protein	0.346	0.003	0.887	0.257	0.036	14.080	0.164	0.021	12.919
chr4.CM0004.1320.r2.m	serine protease APRX	0.342	0.001	0.353	0.135	0.014	10.593	0.097	0.010	9.860
LjB04I14.50.r2.d	long chain acyl-CoA synthetase 2-like	0.340	0.005	1.405	0.103	0.002	1.601	0.127	0.000	0.176
chr1.CM0181.340.r2.m	amino acid permease	0.330	0.006	1.894	0.162	0.010	6.396	0.102	0.005	4.774
LjSGA_071437.1.1	serpin-like protein	0.323	0.014	4.284	0.120	0.018	15.063	0.158	0.005	3.314
chr3.CM0135.450.r2.d	uncharacterized protein	0.323	0.021	6.459	0.090	0.002	1.938	0.109	0.008	7.088
LjSGA_135074.1	aspartic proteinase nepenthesin-2	0.312	0.023	7.502	0.071	0.003	3.941	0.123	0.012	9.521
LjSGA_067521.2.1	calmodulin-like isoform 4	0.309	0.001	0.423	0.218	0.026	11.982	0.118	0.004	3.557
LjSGA_015029.1	GDSL esterase lipase at5g62930-like	0.307	0.020	6.630	0.185	0.026	14.022	0.142	0.027	18.936
chr1.CM0088.360.r2.d	no hit	0.303	0.017	5.469	0.153	0.001	0.717	0.095	0.001	0.812
chr3.CM0176.230.r2.d	zinc ion binding protein	0.302	0.008	2.620	0.094	0.005	5.583	0.113	0.005	4.180
chr4.CM0042.1120.r2.m	DUF26 domain-containing protein 1	0.296	0.029	9.655	0.202	0.009	4.266	0.137	0.004	2.663
LjT13I15.50.r2.d	uncharacterized oxidoreductase at4g09670-like	0.289	0.022	7.490	0.044	0.009	21.002	0.072	0.002	2.623
chr1.CM0064.830.r2.m	uncharacterized protein	0.284	0.012	4.304	0.081	0.029	35.278	0.100	0.014	14.079
LjSGA_007122.1	D-arabinono-1,4-lactone oxidase family protein	0.275	0.022	7.953	0.025	0.003	11.282	0.046	0.001	2.567
LjSGA_037479.1	cellulose synthase-like C1-glycosyltransferase family 2 protein	0.275	0.017	6.358	0.135	0.008	6.251	0.121	0.004	3.353
chr1.CM0017.1380.r2.m	uncharacterized protein	0.273	0.013	4.683	0.094	0.020	21.691	0.127	0.016	12.833
chr5.CM0096.240.r2.m	CLE11 protein	0.263	0.008	2.922	0.130	0.002	1.698	0.086	0.014	16.052
LjSGA_050424.1	uncharacterized protein	0.261	0.011	4.199	0.112	0.003	2.593	0.101	0.002	1.729
LjSGA_062134.1	nodulation protein H-like	0.259	0.025	9.662	0.070	0.010	14.241	0.091	0.016	17.363
chr3.CM0135.170.r2.d	enoyl-[acyl-carrier-protein] reductase	0.249	0.015	5.990	0.054	0.001	2.096	0.093	0.001	0.667
chr4.CM0333.780.r2.m	DNA-directed RNA polymerase II	0.245	0.000	0.094	0.133	0.001	0.566	0.119	0.010	8.513
LjSGA_090710.1	serine carboxypeptidase-like protein	0.243	0.001	0.216	0.024	0.004	17.791	0.025	0.003	12.837
LjSGA_052424.1	oxidoreductase transition metal ion binding protein	0.242	0.013	5.542	0.195	0.013	6.432	0.117	0.003	2.201
chr4.CM0004.640.r2.a	ATP binding	0.241	0.020	8.329	0.121	0.031	25.310	0.105	0.039	37.101
chr4.CM0007.1310.r2.d	uncharacterized protein	0.239	0.011	4.444	0.178	0.007	4.104	0.117	0.034	29.434
chr4.CM0026.470.r2.m	arogenate dehydratase prephenate dehydratase	0.239	0.014	5.877	0.072	0.007	9.269	0.098	0.018	18.066
LjT41D17.240.r2.a	auxin-induced protein 15a-like	0.234	0.020	8.744	0.050	0.002	4.334	0.072	0.003	3.687
chr5.CM0328.910.r2.d	receptor serine threonine	0.233	0.011	4.549	0.083	0.033	39.760	0.108	0.037	34.085
chr6.LjT35D18.10.r2.m	subtilase family protein	0.231	0.013	5.742	0.050	0.001	2.761	0.092	0.001	1.570
chr4.CM0851.440.r2.d	uncharacterized protein	0.224	0.006	2.827	0.072	0.013	17.940	0.035	0.003	7.326
chr3.CM1488.40.r2.d	somatic embryogenesis receptor kinase	0.218	0.016	7.430	0.030	0.013	44.092	0.077	0.026	33.017
chr3.CM1543.200.r2.m	uncharacterized protein	0.217	0.012	5.545	0.116	0.005	4.423	0.086	0.005	6.001
chr3.CM1468.250.r2.d	dihydrodipicolinate reductase 2	0.216	0.011	4.981	0.092	0.005	5.571	0.101	0.009	9.252
chr3.CM1488.30.r2.d	ATP binding	0.216	0.001	0.308	0.034	0.001	1.915	0.081	0.003	3.909
chr3.CM0160.1040.r2.m	bZip transcription factor family protein	0.209	0.004	2.031	0.055	0.008	13.996	0.060	0.006	10.265
chr2.CM0056.590.r2.d	beta-glucosidase 11-like	0.208	0.001	0.697	0.047	0.003	5.552	0.091	0.004	4.031
LjSGA_025567.1	protease inhibitor seed storage lipid transfer protein family protein	0.205	0.020	9.814	0.105	0.011	10.782	0.100	0.010	9.725
chr5.CM0909.510.r2.m	uncharacterized protein	0.205	0.018	8.885	0.033	0.005	15.136	0.031	0.003	9.567
LjSGA_032039.1	2-phytyl-1,4-naphtoquinone chloroplastic-like	0.203	0.001	0.511	0.121	0.010	8.534	0.071	0.005	6.388
chr1.LjT39M20.120.r2.m	D3-type cyclin	0.199	0.009	4.395	0.072	0.005	7.055	0.057	0.008	13.841
chr6.CM0118.1410.r2.a	uncharacterized protein	0.199	0.002	0.905	0.030	0.005	17.829	0.086	0.013	14.874
chr5.CM0040.610.r2.d	BTB/POZ domain-containing protein npy1-like	0.197	0.018	8.908	0.095	0.005	5.682	0.075	0.003	4.652
chr3.CM0213.470.r2.m	tRNA (guanine-N-7)-methyltransferase-like	0.196	0.015	7.747	0.138	0.011	8.145	0.086	0.003	2.991
chr2.CM0249.1200.r2.d	auxilin-related protein 2-like	0.196	0.002	1.217	0.101	0.004	4.066	0.096	0.000	0.343
chr3.LjB13E21.80.r2.m	malate dehydrogenase	0.194	0.003	1.510	0.132	0.006	4.214	0.077	0.004	5.533
LjSGA_014975.1.1	uncharacterized protein	0.193	0.003	1.713	0.094	0.005	5.311	0.094	0.012	12.637
chr3.CM0164.70.r2.d	uncharacterized protein	0.189	0.000	0.167	0.030	0.009	28.946	0.050	0.003	6.341
LjSGA_008486.1	uncharacterized protein	0.185	0.015	8.221	0.080	0.004	5.598	0.083	0.016	19.512
LjSGA_116558.0.1	3-oxo-5-alpha-steroid 4-dehydrogenase	0.184	0.014	7.788	0.115	0.004	3.584	0.086	0.011	13.351
chr2.CM0177.300.r2.m	MADS box	0.183	0.017	9.165	0.080	0.013	16.593	0.073	0.019	25.863
chr1.CM0029.20.r2.a	uncharacterized protein	0.182	0.015	8.424	0.095	0.010	10.478	0.076	0.006	8.118
LjSGA_027817.1	magnesium transporter NIPA2-like	0.176	0.005	2.569	0.085	0.012	14.687	0.059	0.005	8.518
LjSGA_138105.1	nucleobase ascorbate transporter	0.172	0.008	4.468	0.069	0.007	10.716	0.077	0.000	0.369
chr4.CM0184.110.r2.d	uncharacterized protein	0.172	0.008	4.543	0.042	0.002	5.274	0.045	0.004	8.554
chr3.CM0226.260.r2.m	auxin-induced protein	0.170	0.016	9.141	0.115	0.002	1.620	0.070	0.004	5.238
LjT19F24.60.r2.d	serine threonine-protein kinase PBS1-like	0.169	0.011	6.591	0.046	0.002	4.585	0.068	0.011	16.598

LjSGA_030160.1	flavin-containing monooxygenase FMO GS-OX5	0.169	0.006	3.268	0.084	0.007	8.458	0.074	0.001	1.766
LjSGA_060722.1	o-glycosyl hydrolases family 17 protein	0.167	0.008	4.865	0.040	0.002	6.165	0.074	0.010	13.271
LjSGA_046425.1.1	SUN protein,Ribosomal RNA small subunit methyltransferase B	0.165	0.000	0.121	0.124	0.003	2.271	0.080	0.005	5.687
LjSGA_050157.1	Nucleic acid binding protein	0.161	0.011	6.950	0.093	0.002	2.221	0.064	0.000	0.339
chr6.CM0041.120.r2.a	histone H3	0.161	0.004	2.681	0.033	0.001	3.855	0.051	0.003	6.181
LjSGA_125993.1	auxin transporter-like protein 2-like	0.157	0.007	4.599	0.056	0.016	29.469	0.065	0.004	5.946
LjSGA_145334.1	GDSL esterase lipase CPRD49	0.157	0.006	3.867	0.024	0.004	14.692	0.049	0.002	4.744
chr2.CM0435.840.r2.m	RNA polymerase II C-terminal domain phosphatase-like 4-like	0.156	0.005	3.030	0.106	0.024	22.968	0.073	0.006	8.382
chr1.CM0012.880.r2.m	fasciclin-like arabinogalactan protein 11-like	0.153	0.012	8.054	0.068	0.010	15.308	0.026	0.001	2.820
chr3.LjT13N17.80.r2.m	uncharacterized protein	0.152	0.002	1.247	0.036	0.004	12.135	0.069	0.004	6.464
LjSGA_005613.1	WEE1-like protein kinase	0.151	0.001	0.827	0.041	0.001	2.431	0.075	0.008	10.119
chr4.CM0044.520.r2.m	uncharacterized protein	0.149	0.009	5.724	0.059	0.011	18.304	0.043	0.004	9.886
chr4.CM0165.120.r2.d	STS14 protein	0.147	0.008	5.622	0.043	0.004	9.708	0.067	0.005	6.928
LjSGA_098290.1	transcription factor bHLH122	0.139	0.010	7.015	0.081	0.000	0.138	0.068	0.004	5.795
LjSGA_065093.1	male sterility 5 family protein	0.139	0.004	2.825	0.036	0.004	12.043	0.054	0.005	8.742
LjSGA_004719.1	bifunctional nuclease BFN1	0.138	0.009	6.301	0.025	0.009	35.813	0.050	0.005	9.589
LjT44L11.20.r2.d	glucan 1,3-beta-glucosidase	0.135	0.006	4.501	0.019	0.002	12.574	0.030	0.001	4.422
chr5.CM1125.1050.r2.a	patatin group A-3-like	0.126	0.011	8.533	0.027	0.005	20.079	0.042	0.006	14.089
chr1.CM0544.420.r2.d	GDSL esterase lipase	0.126	0.008	6.464	0.078	0.021	26.663	0.048	0.013	25.891
chr5.CM0431.90.r2.d	alph/ beta hydrolase fold family protein	0.120	0.006	5.305	0.034	0.001	1.816	0.054	0.008	14.769
chr1.LjT01F21.10.r2.m	F-actin-capping protein subunit alpha	0.111	0.003	2.577	0.051	0.006	11.416	0.045	0.007	16.512
chr5.CM0200.2030.r2.d	MADS-box transcription factor	0.108	0.010	9.426	0.028	0.003	12.466	0.030	0.004	12.503
LjSGA_010022.2	probable glutathione s-transferase-like	0.107	0.004	3.317	0.059	0.012	19.542	0.031	0.019	60.861
LjSGA_056374.1	casparian strip protein 3	0.106	0.000	0.335	0.058	0.003	4.734	0.022	0.001	4.170
chr4.LjT33M20.250.r2.d	beta-ketoacyl-coa synthase family protein	0.105	0.008	7.171	0.030	0.004	14.218	0.048	0.001	2.386
LjSGA_044744.1	GDSL esterase lipase	0.104	0.004	4.278	0.035	0.003	7.748	0.041	0.007	15.990
chr1.CM0378.220.r2.a	probable leucine-rich repeat receptor-like protein kinase at1g68400-like	0.104	0.004	3.922	0.047	0.009	18.134	0.020	0.000	2.361
chr4.CM0004.1310.r2.m	esterase-like protein	0.103	0.005	4.548	0.037	0.006	14.899	0.029	0.006	20.896
LjT37O09.290.r2.d	GRF1-interacting factor 3	0.102	0.007	6.775	0.021	0.001	3.684	0.028	0.001	3.997
LjSGA_069132.1	zinc-finger domain of monoamine-oxidase a repressor r1 protein	0.101	0.007	7.209	0.038	0.023	60.428	0.038	0.023	58.642
LjT33G24.80.r2.d	xylan 1 4-beta-xylosidase	0.100	0.006	5.597	0.025	0.005	19.846	0.040	0.001	3.598
chr2.CM0608.1440.r2.m	protein kinase domain-containing protein	0.094	0.006	6.588	0.025	0.006	22.838	0.047	0.001	2.472
LjSGA_013238.2	probable ubiquitin-conjugating enzyme E2 25-like	0.093	0.003	3.125	0.046	0.000	0.064	0.036	0.006	17.246
LjSGA_052141.1	uncharacterized protein	0.085	0.008	9.904	0.035	0.005	13.739	0.040	0.003	8.623
chr4.CM0046.1310.r2.d	uncharacterized protein	0.085	0.004	4.318	0.057	0.005	9.376	0.031	0.008	24.280
LjSGA_014939.0.1	uncharacterized protein	0.084	0.006	7.387	0.032	0.010	32.159	0.037	0.002	5.547
chr5.CM0089.490.r2.d	phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase p	0.074	0.003	3.983	0.018	0.002	12.305	0.033	0.000	0.420
LjSGA_026555.1	mitogen-activated protein kinase kinase kinase 1-like	0.073	0.006	8.274	0.023	0.004	15.808	0.020	0.001	5.923
LjSGA_028605.1	uncharacterized protein	0.072	0.001	1.022	0.017	0.002	8.890	0.028	0.001	2.058
chr1.CM0029.310.r2.d	N-acetyltransferase ESCO2-like	0.070	0.002	2.957	0.024	0.002	8.987	0.032	0.002	5.419
LjSGA_098316.1.1	uncharacterized protein	0.070	0.007	9.331	0.024	0.002	10.258	0.032	0.010	32.949
chr2.CM0338.230.r2.d	DUF246 domain-containing protein at1g04910-like	0.067	0.006	9.104	0.028	0.006	20.789	0.028	0.001	3.884
chr1.CM0760.60.r2.d	serine threonine protein phosphatase 2A 57 kda regulatory subunit B iota isoform-like	0.064	0.002	3.425	0.026	0.006	24.521	0.031	0.010	33.599
LjSGA_019785.1	phospholipid glycerol acyltransferase family protein	0.064	0.002	3.277	0.030	0.002	5.722	0.030	0.004	13.731
LjSGA_039494.1	uncharacterized protein	0.064	0.001	2.339	0.027	0.003	10.186	0.029	0.007	23.167
chr2.CM0177.160.r2.m	cinnamyl alcohol dehydrogenase-like protein	0.060	0.001	1.969	0.039	0.002	6.125	0.027	0.003	9.306
chr4.CM0042.2460.r2.m	uncharacterized protein at3g17950-like	0.052	0.004	7.872	0.022	0.000	0.334	0.025	0.002	6.893
chr5.CM0428.400.r2.m	arginine biosynthesis bifunctional protein	0.051	0.004	7.466	0.022	0.004	20.269	0.022	0.001	4.269
LjSGA_028933.2	protein trichome birefringence-like 33	0.042	0.002	3.557	0.022	0.003	14.586	0.019	0.003	17.851

Supplemental Table 4. Expression profile of 42 genes in cluster 4 during nodule senescence

ID number	Annotation	2 wpi			4 wpi			8 wpi		
		Average Normalized	SD Normalized	CV (%)	Average Normalized	SD Normalized	CV (%)	Average Normalized	SD Normalized	CV (%)
chr4.CM0337.590.r2.m	vacuolar iron transporter homolog 4-like	72.096	6.530	9.057	115.674	11.226	9.705	51.627	2.090	4.049
chr6.CM1514.140.r2.m	dihydroneopterin aldolase	28.401	2.476	8.718	24.968	3.690	14.778	13.890	3.401	24.485
LjT36K06.70.r2.d	sugar transporter sweet1-like	15.061	4.144	27.513	26.852	7.312	27.231	6.782	1.717	25.323
chr4.CM0414.440.r2.d	metal transporter	13.428	2.254	16.787	22.607	5.027	22.237	8.836	1.945	22.007
chr5.LjT43D06.110.r2.d	vegetative lectin	4.789	0.230	4.802	8.585	0.003	0.035	1.804	0.095	5.267
chr2.CM0021.1330.r2.m	expansin-like B1-like	4.263	0.339	7.955	5.541	0.499	9.012	1.898	0.134	7.059
chr1.CM1868.110.r2.a	ubiquitin system component CUE protein	1.671	0.015	0.871	1.973	0.064	3.247	0.546	0.025	4.646
LjSGA_060891.2	inositol phosphate kinase	1.656	0.119	7.183	2.766	0.349	12.614	0.905	0.069	7.672
chr4.CM0307.380.r2.d	mitochondrial substrate carrier family protein	1.347	0.017	1.257	1.473	0.033	2.259	0.673	0.014	2.020
chr1.CM0012.190.r2.m	probable membrane-associated kinase regulator 4-like	1.149	0.020	1.744	1.111	0.041	3.659	0.493	0.005	1.031
chr2.CM0081.530.r2.d	quinone oxidoreductase-like protein	0.925	0.048	5.217	0.929	0.044	4.729	0.309	0.016	5.090
LjSGA_016572.1	ethylene-responsive transcription factor ERF118	0.815	0.044	5.336	0.842	0.050	5.969	0.404	0.000	0.026
chr1.CM0109.110.r2.d	uncharacterized protein	0.804	0.053	6.543	1.006	0.076	7.531	0.361	0.041	11.353
LjSGA_047220.1	zinc finger protein constans-like 9	0.767	0.036	4.663	0.668	0.033	4.924	0.240	0.008	3.378
LjSGA_039721.1	glucose 1-dehydrogenase-like	0.751	0.023	3.104	1.040	0.039	3.788	0.314	0.020	6.309
chr2.CM0373.110.r2.d	phospholipase a2	0.653	0.030	4.536	0.566	0.030	5.222	0.325	0.002	0.673
chr5.CM0657.290.r2.m	cytosolic Fe-S cluster assembly factor nbp35	0.632	0.055	8.787	0.822	0.118	14.380	0.221	0.026	11.662
LjSGA_084433.1	expansin B3	0.625	0.048	7.615	0.503	0.000	0.006	0.164	0.003	1.817
LjSGA_087846.1	peptide chain release factor 2	0.609	0.008	1.307	0.693	0.023	3.375	0.236	0.007	2.779
chr6.CM0013.1230.r2.m	uncharacterized protein	0.574	0.001	0.159	0.714	0.034	4.810	0.169	0.007	4.362
chr1.CM0393.670.r2.d	glyoxysomal fatty acid beta-oxidation multifunctional protein multifunctional protein	0.519	0.006	1.133	1.020	0.012	1.183	0.250	0.015	6.006
chr2.LjT44B19.150.r2.d	plasma membrane H+-ATPase	0.490	0.000	0.081	1.609	0.032	2.020	0.196	0.000	0.080
chr2.CM0788.290.r2.m	probable LRR receptor-like serine threonine-protein kinase at1g14390-like	0.406	0.028	6.945	0.364	0.006	1.692	0.202	0.004	1.762
chr6.CM0055.980.r2.d	2-dehydro-3-deoxyphosphoheptonate aldolase 3-deoxy-d-arabino-heptulosonate 7-phosphate synthetase	0.380	0.022	5.761	0.311	0.018	5.864	0.190	0.026	13.509
chr3.CM0152.130.r2.m	S-locus lectin protein kinase family protein	0.354	0.028	7.992	0.266	0.031	11.472	0.082	0.027	32.621
chr2.CM0608.1100.r2.m	AP2 domain-containing transcription factor	0.344	0.014	3.965	0.568	0.012	2.070	0.132	0.003	2.315
chr1.CM0113.250.r2.m	uncharacterized protein	0.274	0.007	2.390	0.334	0.000	0.122	0.131	0.005	3.887
chr2.CM0081.1090.r2.m	uncharacterized protein	0.259	0.025	9.681	0.239	0.002	0.642	0.119	0.012	10.457
chr5.CM0359.140.r2.m	phytosulfokine peptide precursor	0.252	0.014	5.739	0.869	0.051	5.900	0.053	0.025	46.564
chr5.CM1077.70.r2.m	pectate lyase	0.252	0.001	0.333	0.178	0.001	0.619	0.060	0.003	5.312
chr4.CM0126.1120.r2.m	DNA topoisomerase 6 subunit B	0.209	0.009	4.249	0.216	0.025	11.749	0.091	0.014	15.494
chr5.CM0494.290.r2.m	CDT1-like protein chloroplastic-like	0.195	0.004	2.277	0.178	0.007	3.870	0.081	0.003	4.145
chr2.CM0058.320.r2.d	no hit	0.161	0.008	5.236	0.138	0.015	11.027	0.074	0.005	6.994
chr4.CM0307.540.r2.d	50s ribosomal protein l23-like	0.155	0.012	7.584	0.128	0.007	5.659	0.072	0.002	2.445
chr5.CM0200.3730.r2.m	metal ion binding	0.125	0.009	6.839	0.157	0.005	3.123	0.058	0.005	8.518
LjSGA_037651.1	uncharacterized protein	0.121	0.003	2.525	0.171	0.002	1.259	0.028	0.002	8.657
chr3.CM0996.170.r2.a	peroxisomal membrane	0.116	0.003	2.917	0.092	0.004	4.670	0.045	0.005	10.157
chr4.CM0194.200.r2.m	oxygen-evolving enhancer protein chloroplastic-like	0.084	0.002	2.227	0.156	0.003	1.752	0.039	0.005	12.036
LjSGA_068069.1	Cytochrome P450 71a26-like	0.076	0.006	8.420	0.164	0.013	8.105	0.026	0.002	7.444
chr5.CM0200.3750.r2.m	metal ion binding	0.069	0.001	1.726	0.066	0.008	12.083	0.030	0.007	24.111
LjSGA_023096.1	protein trichome birefringence-like 41	0.064	0.001	1.358	0.386	0.015	3.828	0.026	0.000	1.011
chr5.CM0052.120.r2.d	probable LRR receptor-like serine threonine-protein kinase at1g34110-like	0.052	0.005	8.769	0.054	0.004	6.658	0.023	0.007	30.525

Supplemental Table 5. Primers list used in this study.

ID	Anotation	Forward primer (5'→3')	Reverse primer (5'→3')
chr1.CM0017.1030.r2.m	class I chitinase	TGTGACTTGCTTGGAGTTGG	TGTCGAGAAGGAGCTGTGAA
chr1.CM0195.250.r2.m	cysteine proteinase 15a-like	TGGAGTTTCATGCCCATACA	CACCAGAAGAACCCCATGAT
chr1.CM0544.890.r2.m	Cu/Zn superoxide dismutase	GGCCATGAGCTTAGCAAGAC	CACAAGCTACTCTGCCACCA
chr2.CM0021.3270.r2.m	osmotin precursor	GGACAGGTGCCATGATTCTT	GAAAGTGCTGGTGGGATCAT
chr2.CM0610.140.r2.m	ethylene-responsive transciptional coactivator-like protein	CGCGTTTGGAGAAGAAGATG	CACCGCCTTACCATTCTCAT
chr2.LjT48A12.210.r2.d	red chlorophyll catabolite reductase	TTGGTTCAAGCTTTCCAAGG	ACTCCTTGATGGCTTCCAGT
chr3.CM0091.1820.r2.m	enhanced disease susceptibility	CTCTCACCCAATGGCATTTT	TGCAGCTCATACTGGCCTAA
chr3.CM0116.300.r2.m	Ferritin	AAAGAGGGCATGCAGAGAAA	CCTTCCACCACGAATGTTCT
chr3.CM0127.770.r2.d	small heat shock protein	GACTTGCCGGACAAGCTTTA	TGACCTTGAGCACACCATTC
chr3.CM0786.10.r2.d	zinc finger protein	CAAGGCTTGAGGGAGAAGAA	CCTCCAAGTGCTTGACCAAT
chr3.CM1570.70.r2.a	IAA-amino acid hydrolase ilr1-like protein	GCTGCACTTCATGCATCATT	TAGCGATGGGTCTCTCTTGC
chr3.LjT36L22.160.r2.a	nicotianamine synthase	TGAAGGAGGGAGGTGTTTTG	AAAGCTCTAGCCCCTTTTGC
chr4.CM0227.40.r2.d	AP2 erf domain-containing transcription factor	GGGAATGGAATTGGAAGGAG	CCCCAATCCTATCCCAAAAT
chr4.CM0337.590.r2.m	vacuolar iron transporter homolog 4-like	GCTTTGGTGGCTTTTGGTAG	CTCGTCATGGGAGTCTTTCC
chr4.CM0414.440.r2.d	metal transporter	CATGTAGAAAAGGGGACTTTGG	TTCTGGTAGTGGGATACTTGCT
chr4.CM0432.1970.r2.m	heat shock protein	CAGTGGGAAATTCCAGAGGA	AGTGAGAACCCCATTCTCCA
chr4.CM0432.790.r2.m	carboxypeptidase C	CATGGAGGCCTTGGTATCAT	ATGACCAGCTCCTCGAAATG
chr5.CM0096.20.r2.m	L-asparaginase	AAGCATCGTTTGGATGAAGG	ATGCCGTTGCAGTTAAAACC
chr6.CM0245.580.r2.a	serine acetyltransferase mitochondrial	TGGTGCTAAGATTGGTGCTG	TAACAACCTTGCTGGGTTCC
LjSGA_022305.1	myristoyl-acyl carrier protein chloroplastic-like	TCAGAAGACCTGACCTGCAA	GGCTCGGACAACATCTGATT
LjSGA_025506.1	BON1-associated protein 2-like	TGGTGGGTTCTTGTGGATTT	CACAGAAGGGGAACACCAGT
LjSGA_025815.1	L-ascorbate oxidase homolog	ATGTGGAATTTGAGGTCTGC	GCTTTGCTGTGCATTCCATA
LjSGA_029450.1	mate efflux family protein dtx1-like	GTGGCTGGGGATCGTATGT	GGCCTTCTTTTCCTCTTGCT
LjSGA_031662.1	receptor-like protein 12-like	TGGTATTGGCAACTTGTGGA	CCCTTGTCCTCTGTGGGTTA
LjSGA_035003.1	O-acyltransferase WSD1-like	TGACTTTGTTTGGCACTCCA	CCAAATCCAAGAGCATACCC
LjSGA_041970.1	OCS element-binding	AGAGCTTCGCCAAATGCTAA	CATCTTCAAGAGGGGCAAAG
LjSGA_051232.1	RING finger protein	TGGTCACACCAAACCTTCTG	CTCGAGTGGTGCTATGGTCA
LjSGA_059392.1	Kunitz-type trypsin inhibitor-like 2 protein	ATGGAAGGCGTCTCATTCTG	ACACGAGCAAACACAACTCG
LjSGA_060891.2	inositol phosphate kinase	TGCTGCAGGAGTTTGTGAAC	GCAAGGACTTCCTCTTCACG
LjSGA_085903.1	polygalacturonase	GGCAGCATATGGGGAGATAA	GGTTGCCTCTCTCCAAACAA
LjSGA_130658.1	1-aminocyclopropane-1-carboxylate oxidase	AGAGTGTGGAGCATCGTGTG	GGAGCAGGGTAGATGACAGC
LjT36K06.70.r2.d	bidirectional sugar transporter sweet1-like	GCCACAACAAAGGAGGAATC	GCTTGAGCTCCATTTGCATT
chr3.CM0996.1420.r2.m	Ubiquitin	ATGCAGATCTTCGTCAAGACCTTG	ACCTCCCCTCAGACGAAG