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Molecular mechanisms underlying the transition to ripening in tomato fruit

Mécanismes moléculaires sous-jacents à la transition vers la maturation des fruits chez la tomate

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Oral Communication

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Poster

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Abstract

Ripening is the last step in the developmental program of fleshy fruits, during which the fruits become edible and acquire their unique sensory qualities. In climacteric fruits such as tomato, ripening is characterized by a burst of autocatalytic ethylene production and an increase in respiration. Because of this burst, ethylene has been considered the key hormone in climacteric fruit ripening. Although our knowledge of the mechanisms that regulate fruit ripening has improved considerably over the past decades, the molecular mechanisms underlying the transition to ripening remain poorly understood. Previous studies of tomato fruit ripening have focused on deciphering the dynamic changes in the pericarp tissues between Mature Green (MG) and Breaker (Br) stages, neglecting what occurs in the locular tissues. The first part of this thesis addresses the transcriptomic changes between the Early Mature Green (EMG) and Late Mature Green (LMG) stages, in gel and pericarp separately. The data shows that the shift from the inability to initiate ripening to the capacity to undergo full ripening requires a massive transcriptomic reprogramming that takes place first in the locular tissues and then extends to the pericarp. Genome-wide transcriptomic profiling revealed that 48 out of 54 transcription factor families are engaged in the global reprogramming of gene expression, thus highlighting the extent of the transcriptomic changes underlying fruit ripening. We observed extensive reformed hormone homeostasis during ripening onset, underlining the multi-hormonal control of ripening initiation. In addition, our data unveil the antagonistic roles of ethylene and auxin during the onset of ripening and show that auxin treatment represses climacteric ethylene production through the downregulation of genes involved in System-2 of ethylene biosynthesis. The second part of the thesis addresses the role of the Ethylene Response Factors (ERF) in ripening initiation. ERFs mediate the last step in the ethylene signaling pathway and members of the *ERF.E* clade in the tomato display a remarkable ripening-associated expression pattern. ERF.E members are characterized by a conserved N-terminal domain, described as the substrate for degradation by the N-end rule pathway in normal oxygen conditions. Using physiological approaches, we demonstrated that the locular gel tissue undergoes drastic depletion of oxygen (hypoxia) as the ripening progresses. In contrast, other tissues, such as the pericarp and columella maintain their normoxia status and fail to experience hypoxia. Whereas all previous studies considered the MG stage as homogeneous, we show that the physiology of the gel tissues differs significantly between the EMG (normoxia), and the LMG stage (hypoxia). Altogether, the data suggest that tomato fruits experience dramatic physiological and transcriptomic changes during the MG stage that lead the fruit to gain competency to ripen, a fate-determining point of the whole process of ripening. To further investigate the putative role of SlERF.E members during the transition to ripening, we addressed their regulation under

hypoxia at the protein level. The data show that hypoxia induces a decrease in membrane localization of SlERF.E proteins while promoting their accumulation in the nucleus. Moreover, normoxia promotes the degradation of SlERF.E proteins, while hypoxia leads to their stabilization, revealing the role of oxygen concentration in the post-translational regulation of SlERF.E. We generated knocked-out and over-expressing tomato lines for *SlERF.E2* and *SlERF.E4* to gain insight on their functional significance. Over-expressing lines display delayed ripening, reduced ethylene production, and retarded depletion of oxygen, supporting the hypothesis that these genes encode for negative regulators of climacteric ripening. Overall, the outcome of the study sheds new light on the complex mechanisms and molecular factors regulating the initiation of the ripening process.

Résumé

La maturation est la dernière étape du programme de développement des fruits charnus. Pendant cette étape, les fruits deviennent comestibles et acquièrent leurs qualités organoleptiques. Chez les fruits climactériques tels que la tomate, la maturation se caractérise par une production autocatalytique d'éthylène et une augmentation de la respiration. Pendant longtemps l'éthylène a été considéré comme l'hormone clé de la maturation des fruits climatériques. Même si le nombre d'études portant sur les mécanismes régulant la maturation s'est multiplié pendant les dernières décennies, les mécanismes moléculaires expliquant la transition vers la maturation restent mal compris. De plus, alors que la plupart des études se sont concentrées sur le péricarpe entre les stades Mature Green (MG) et Breaker (Br), les études portant sur le tissu loculaire restent rares. La première partie de cette thèse porte sur l'étude des changements transcriptionnel qui surviennent au cours du stade qui précède l'entrée en maturation appelé Mature Green (MG). Nous avons analysé l'évolution du profil transcriptomique global entre les stades MG précoce (Early MG ; EMG) et MG tardif (Late MG ; LMG), dans le gel et le péricarpe, séparément. L'étude montre que la transition du stade EMG au stade LMG s'accompagne d'une reprogrammation transcriptomique massive qui a lieu d'abord dans les tissus loculaires et qui s'étend ensuite au péricarpe. Ce changement est particulièrement remarquable pour 48 familles de facteurs de transcription, sur les 54 présentes dans la tomate, soulignant ainsi l'ampleur des changements transcriptomiques qui s'opèrent dans le gel au cours des évènements précoces. La combinaison des données transcriptomiques et métabolomiques suggèrent un changement de l'homéostasie hormonale entre les stades EMG et LMG, mettant en évidence le contrôle multi-hormonal de l'initiation de la maturation. De plus, l'étude met en évidence les rôles antagonistes de l'éthylène et de l'auxine lors de l'initiation de la maturation et montre que le traitement du fruit par l'auxine exogène induit la répression de la production autocatalytique d'éthylène à travers la régulation négative des gènes de biosynthèse impliqués dans le Système 2 de biosynthèse autocatalytique d'éthylène. La deuxième partie de la thèse porte sur le rôle des facteurs de transcription appartenant à la famille des Ethylene Response Factors (ERF) dans l'initiation de la maturation. Les ERF sont les derniers acteurs de la voie de signalisation de l'éthylène et les membres la sous-classe E présentent une expression associée à la maturation. Les protéines de la clade ERF.E sont caractérisées par la présence d'un domaine N-terminal conservé, décrit comme le substrat de la dégradation par la voie de la "N-end rule" en conditions normales d'oxygène. Des mesures d'oxygène au cours de la maturation dans différents tissus du fruit ont montré que contrairement au péricarpe qui se maintient en état de normoxia (concentration normale d'oxygène), le gel loculaire subit une baisse de la concentration d'oxygène pour se retrouver en condition d'hypoxie suggérant que la

physiologie du gel diffère significativement entre le stade EMG (normoxie), et le stade LMG (hypoxie). L'ensemble de ces données suggère qu'au cours du stade MG, les fruits subissent des changements physiologiques et transcriptomiques importants qui pourraient être à l'origine de l'acquisition de la compétence à mûrir. Afin de déterminer le rôle des SlERF.E au cours de cette étape, leur régulation post-traductionnelle a été étudiée en réponse à l'hypoxie. Les études d'expression transitoire ont démontré qu'en condition d'hypoxie les ERF.E s'accumulent préférentiellement dans le noyau. De plus, la dégradation des protéines SlERF.E est favorisée en condition normoxique, tandis que l'hypoxie conduit à leur stabilisation, confirmant le rôle de l'oxygène dans la régulation des protéines SlERF.E. Enfin, pour mieux comprendre le rôle des ERF.E dans la maturation, des tomates transgéniques surexprimant *SlERF.E2* ou *SlERF.E4* ainsi que des lignées *knock-out* pour ces gènes ont été générées. Les lignées de surexpresssion montrent une maturation retardée, une production réduite d'éthylène et un retard de la déplétion en oxygène, suggérant que ces ERF codent pour des régulateurs négatifs de la maturation.

Abbreviations

AADC1A	Aromatic amino acid decarboxylase
AAOs	abscisic aldehyde oxidases family
AAT1	alcohol acetyltransferase
ABA	Abscisic acid
ABFs	ABA-responsive element binding factors
ACC	1-aminocyclopropane-1-carboxylate
ACO	ACC oxidase
ACS	ACC synthase
ADH	alcohol dehydrogenase
AP2	Apetala2
ARFs	Auxin Response Factors
ATEs	Arginyl tRNA-Treansferases
Aux/IAA	Auxin/INDOLE-3-ACETIC ACID
BCAA	branched-chain amino acids derivatives
BCAT1	Branched-chain amino acid aminotransferases
BES1	BRI1-EMS-SUPPRESSOR1
BL	brassinolide
BRs	brassinosteroids
CCD1	carotenoid cleavage dioxygenases
CHX	carotene hydroxylase
CK	Cytokinines
Cnr	colorless non-ripening
CRTISO	carotene isomerase
CTR1	Constitutive Triple Response 1
DAO	Dioxygenase for Auxin Oxidation
DEGs	Differentially Expressed Genes
DPA	days post-anthesis
DRE/CRT	dehydration-responsive element/C-repeat
EAR	ERF Amphiphilic Repression domain
EBF	Ethylene Insensitive3-binding F-box
EIN2	Ethylene Insensitive 2
EIN3/EIL	Ethylene Insensitive 3/ Ethylene Insensitive 3-Like
ERFs	Ethylene Response Factors
ETR	ethylene receptors
EXP	expansin
FUL	Fruitfull
GA	Gibberellins
GGPP	geranylgeranyl pyrophosphate
GH3	Gretchen Hagen 3
HDAs	histone deacetylases
HRE	Hypoxia Response Element
IAA	Indole-3-Acetic Acid
IAM	indole-3-acetamide
ICS	isochorismate synthase
IPyA	indole-3-pyruvic acid
JA	jasmonic acid
JAZ 3	Jasmonate Zim Domain Protein 3
KO	Knock out
LCY	lycopene cyclase
LDH	lactate dehydrogenase
LOX	lipoxygenase
MAPs	Methionine Aminopeptidases
MC	Macrocalyx
MeJA	methyl jasmonate
MEP	methylerythritol-4-phosphate
MeSA	Methyl salicylate
MoCo	molybdenum cofactor
NCED	9-cis-epoxycarotenoid dioxygenase
nor	non-ripening
NR	Nitrate reductase
PAL	phenylalanine ammonia-lyase
PAL3	L-phenylalanine ammonia lyase
PCOs	Plant Cysteine Oxidases
PDC	pyruvate decarboxylase
PDS	phytoene desaturase
PE	pectinesterase
PG	polygalacturonase
PGB or HB	nonsymbiotic hemoglobins
PL	pectate lyase
PME	pectin methylesterase
PP2Cs	protein phosphatases 2C
PSY	phytoene synthase
rin	ripening inhibitor
SA	Salicylic acid
SAUR	Small Auxin Upregulated
SDR	short-chain dehydrogenase/reductase
SnRK2	SNF1- related protein kinase 2

TAA	Tryptophan Aminotransferase of Arabidopsis
TAGL1	TOMATO AGAMOUS-LIKE1
TF	Transcription Factor
TPS	TOPLESS
UGT	uridine diphosphate glucosyltransferase
VOCs	volatile chemicals
WT	Wild Type
XTH	1,4-β-glucanase, xyloglucan transglycosylase/hydrolase
ZDS	ζ-carotene desaturase
ZISO	ζ-carotene isomerase
β-GAL	β-galactosidase

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Chapter I

Bibliographic review
&
Objectives of the study

Bibliographic review

1.1 Angiosperms and fruit classification

Only angiosperms produce true fruits, and their Latin name, angio-hidden, sperm-seed, relates to the structures that encase and safeguard seeds. Angiosperms, or flowering plants, make up the majority of the world's tropical, subtropical, and temperate zones vegetation and are made up of over 295,383 species split into four primary clades (APG IV, 2016). Angiosperms first appeared around 200 million years ago, during the early Cretaceous period (Zhang et al., 2019). A true fruit is a mature ovary; however, in some taxa, other flower and inflorescence parts also form a part of the fruit. Angiosperms have a large variety of fruit types. On the basis of their shape and development, fruits are classed as follows: simple (fruit from a single ovary), accessory (fruit from an inferior ovary), aggregate (fruit from numerous separate ovaries), and multiple (fruit from several independent flowers) (Malik et al., 2014). In addition to this classification the plethora of fruit types recognized in angiosperms can be simplified using combinations of the following characteristics: dehiscent (opening to release seeds) or indehiscent (not opening to release seeds), dry or fleshy exterior, and free (apocarpous) or fused (syncarpous) carpels (see Table 1 for examples) (Knapp and Litt, 2013).

To improve seed dispersal, fleshy fruits have evolved to be appealing to frugivores, and they have become an essential part of the human diet. Berries with seeds enclosed in a dense fleshy pulp, such as tomato, grapes, and bananas, drupes with a stony endocarp that protects a single seed, such as peach and nectarine, and aggregate drupelets, such as raspberry, are among the most well-known classes (Karlova et al., 2014). In general, fleshy fruits are indehiscent: animals chew and digest the fruit, thereby opening it. If the fruit is not consumed, the seeds are released upon decomposition. As the fruits ripen, they become more appealing to animals. Changes in parenchymal tissues cause fruit juiciness and attractiveness. Softening, starch and chlorophyll hydrolysis, and sugar accumulation are examples of such changes. Furthermore, anthocyanins and carotenoids accumulate in the epidermis, making the fruit more visible to animals (Rodríguez et al., 2013).

Climacteric and non-climacteric fruits are two main classes of fleshy fruits. In climacteric fruits, ripening is characterized by a peak in respiration and autocatalytic ethylene production, which is necessary for normal fruit ripening in tomato and other climacteric fruits such as apple, melon, and banana. Conversely, non-climacteric fruits do not show a dramatic change in respiration, and ethylene production remains at basal levels (Alexander and Grierson, 2002). The ecological characteristics and environment of a plant play an important role in determining the fate of the fruit, supporting the reproductive mechanism, seed dispersal, and ultimately species propagation.

Table 1. Some often found fruit-type names and examples (adapted from Knapp and Litt, 2013).

		Definition	Some examples
Dry indehiscent fruits	Achene	One-seeded, seed attached to fruit wall at one point only.	Sunflower or lettuce
	Grain	One-seeded, seed coat fused to seed.	Wheat or rice
	Nut	One-seeded, pericarp hard	Hazelnuts or acorns
	Samara	One-seeded, winged	Maples or dipterocarps
Dry dehiscent fruits	Capsule	Syncarpous gynoecium of two or more carpels, opening in a variety of ways.	Tobacco, poppies or violet
	Follicle	Apocarpous gynoecium of one carpel, splits along one suture.	Columbine or magnolia
	Legume	Apocarpous gynoecium of one carpel, splits along two sutures.	Peas and beans
	Silique or silicle	Syncarpous gynoecium of two or more carpels, splits along two sutures, has a persistent partition.	*Arabidopsis* or canola
Fleshy indehiscent fruits	Berry	Syncarpous gynoecium of one-several fused carpels, one-many seeds imbedded in fleshy mass.	Grape, tomato, pepper or orange
	Drupe/pyrene	Seed(s) enclosed in a stony endocarp.	Peach or almond

1.2 Tomato as a model plant

Tomato (*Solanum lycopersicum*) is a highly valuable model organism for studying fleshy fruit development, ripening, and metabolic pathways. It is also a reference species for research on the Solanaceae family. Tomatoes are a significant source of various metabolites, including vitamin C, potassium, and folic acid (Fraser and Bramley, 2004; Klee and Giovannoni, 2011), and one of the most important vegetable crops worldwide, with over 100 million tons of fresh fruit produced globally (FAO, 2021).

A wealth of molecular tools have been developed for tomato. . Its compact, diploid, and sequenced genome spans approximately 900 megabases (Tomato Genome Consortium et al., 2012), enabling the generation of resources for high-throughput reverse genetics and transcriptomics. The availability of well-characterized spontaneous or induced mutants, wild species introgression, recombinant inbred lines, abundant RNAseq data (Fernandez-Pozo et al., 2017; Zouine, 2017), and various biological resources and tools (e.g. EST database, TILLING resources, genetic and physical maps) provide an extensive toolkit for fruit development research. Additionally, thanks to its short generation time (3-4 generations per year), routine transformation technology, and the existence of a dwarf variety (MicroTom) (Scott et al., 1989) with a sequenced genome, high-density culture is

possible. Therefore, tomato has been widely selected as a core model system for fruit research.

1.3 Tomato fruit development

1.3.1 Tomato fruit structure

Solanaceae plants have a diverse range of fruit structures, including dry fruits such as capsules (e.g., tobacco and petunia) and pyxides, as well as fleshy fruits like berries or drupes (Knapp and Litt, 2013). Berries are a large, monophyletic clade in the family, suggesting that fruit evolution has a phylogenetic component (Knapp, 2002). The genus *Solanum*, for example, produces soft berries with intricate fruit anatomy that includes multiple types of tissue and cells that interact with one another. During fruit development, these tissues and cells undergo significant morphological changes as their functions diversify and become more specialized.

Tomato berries (Figure 1A) consist of two or more carpels separated by a septa. The septa divides the ovary and fruit into two or more locules, resulting in bilocular or multilocular berry. Multilocular fruits have three or more cavities separated by septa (e.g., beefsteak tomato). The septa join at the columella, or core, which connects the fruit to the plant via the pedicel. The seeds are attached to the placenta by the funiculus and are located and protected by the locular gel that fills the locules. After fertilization, the ovary wall transforms into the pericarp, which comprises three distinct tissues known as the exocarp, mesocarp, and endocarp (Figure 1B). The exocarp is the outer layer of the tomato fruit that protects the flesh and seeds. It is composed of several cell layers, including the cuticle layer, which thickens as the fruit ages, and the skin, which consists of an epidermal cell layer and three to four layers of collenchymatous tissue (Grierson and Kader, 1986; Ho and Hewitt, 1986; Pesaresi et al., 2014; Van de Poel et al., 2014).

1.3.2 Tomato fruit development

The development of a fruit begins with the opening of a flower. At the time of anthesis, the anther lobes go through a process called dehiscence, which allows the pollen to be released. The pollen then quickly germinates after landing on the stigma. Pollen tubes begin to develop close to the base of the style roughly six hours after pollination, and they eventually make their way to the ovules approximately two hours later. It takes ten to twelve hours after pollination for the pollen tubes to release their contents, which led to fertilization of the ovules (Stage 0). During development other three major stages can be distinguished: a phase of cell proliferation (Stage I), a phase of cell expansion (Stage II),

and finally a ripening and senescence phase (Stage III) (Pirrello, 2009). Immediately after fertilization, Stage I is characterized by rapid cell division that leads to a progressive increase in pericarp cell number. In tomato cv. MicroTom cell division begins at two days post-anthesis (2 DPA) when the ovary is 1 mm in diameter and has 10 cell layers (Figure 1B). Cell divisions are both periclinal and anticlinal, and by 4 DPA the fruit is 1.5 mm in diameter with 30 cell layers. At 7-8 DPA, cell division continues, but cell expansion becomes apparent, and the number of cell layers increases to 35 at the fruit apex and 20 at the equator. During Stage II, the fruit undergoes a steady increase in size, mostly through cell expansion, it is important to point out that Stage I and Stage II overlap since 7-8 DPA and for about 5 days. By 10-13 DPA, cell division has ceased and cell expansion progresses at a dramatic rate until approximately 30 DPA when the fruit reaches a diameter of 1.5–2 cm (Figure 1B and Figure 1C). At the end of the cell expansion phase, the fruit reaches its final size and is ready to ripe (Seymour et al., 2013; Pesaresi et al., 2014). This trait timing, like many others, varies among different cultivars, it is under strong genetic control and is influenced by environmental conditions, such as the availability of water and nutrients.

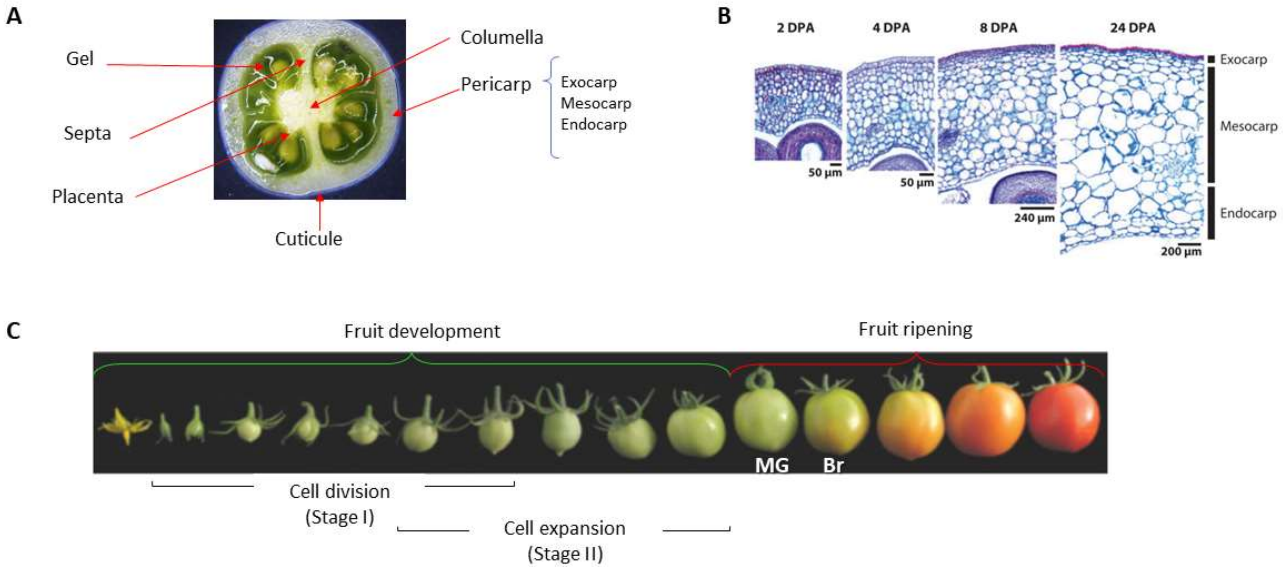

Figure 1. Tissues and fruit structure of *Solanum lycopersicum cv.* Micro Tom. (A) Transverse section of tomato fruit shows the different tissues of the fruit. **(B)** Transverse section of tomato fruit at different days postanthesis (DPA), showing pericarp layers and illustrating cell division and cell expansion phases (from Seymour et al., 2013). **(C)** Development and ripening stages of tomato fruit. MG, mature green; Br, breaker.

1.4 Tomato fruit ripening

Ripening is a complex and coordinated process that marks the final stage of fruit development (Stage III) and plays a vital role in aiding seed dispersal. Ripening coincides with seed maturation, occurring around the same time (Klee and Giovannoni, 2011). This process involves numerous biochemical changes that require the expression of hundreds to thousands of genes. Ripening leads to the softening of the fruit, and an increase in the accumulation of sugars, acids, and volatile compounds that make it more appealing and palatable to animals. Additionally, the fruit undergoes a distinct color change that acts as a signal to animals, indicating that the fruit is mature. The following bibliographic review will focus on the key traits that characterize tomato ripening.

1.4.1 Color formation

One of the most notable characteristics of ripe fruit is the biosynthesis of a wide range of secondary metabolites. In the case of tomatoes, red pigment accumulation is emblematic of the ripening process. There are two primary processes involved in color change in tomato fruit: first, chlorophyll loss from chloroplasts accompanied by the disassembly and recycling of specific thylakoid membranes and photosynthetic proteins; and second, the buildup of colored carotenoids such as β-carotene and lycopene in lipid globules or other membrane-bound structures in the developing chromoplasts, which can occur either from the conversion of chloroplasts or from other types of plastids (Kahlau and Bock, 2008; Egea et al., 2010; Barsan et al., 2012). Carotenoid pigments, such as lycopene, greatly contribute to the sensory and nutritional qualities of both fresh ripe and processed tomato fruits. Fruits rich in carotenoids provide a rich source of dietary pro-vitamin A (Fraser and Bramley, 2004; Klee and Giovannoni, 2011).

In-depth molecular research has been done on the synthesis of carotenoids during ripening, and involves the selective expression of genes encoding specific enzymes in their respective metabolic pathways. In summary, the carotenoid biosynthetic pathway is as follows (Figure 2): The precursor of carotenoid biosynthesis, geranylgeranyl pyrophosphate (GGPP), is synthesized via the methylerythritol-4-phosphate (MEP) pathway. Two GGPP molecules combine to form phytoene, which is catalyzed by phytoene synthase (PSY). Phytoene is transformed to lycopene by a sequence of desaturation and isomerization processes catalyzed by phytoene desaturase (PDS), ζ-carotene isomerase (ZISO), ζ-carotene desaturase (ZDS) and carotene isomerase (CRTISO). Lycopene can be cyclised by lycopene cyclase (LCY) to form α-carotene, which can then be catalyzed by carotene hydroxylase (CHX) to produce lutein. Alternatively, lycopene can be cyclized by LCY or chromoplast-specific lycopene β-cyclase (LYCB) to form β-carotene, which is

converted into β-cryptoxanthin and then into zeaxanthin by β-carotene hydroxylase (CHYB) (Luan et al., 2020). Downstream reactions lead to the production of absiscic acid and are explained in Section 1.5.3.

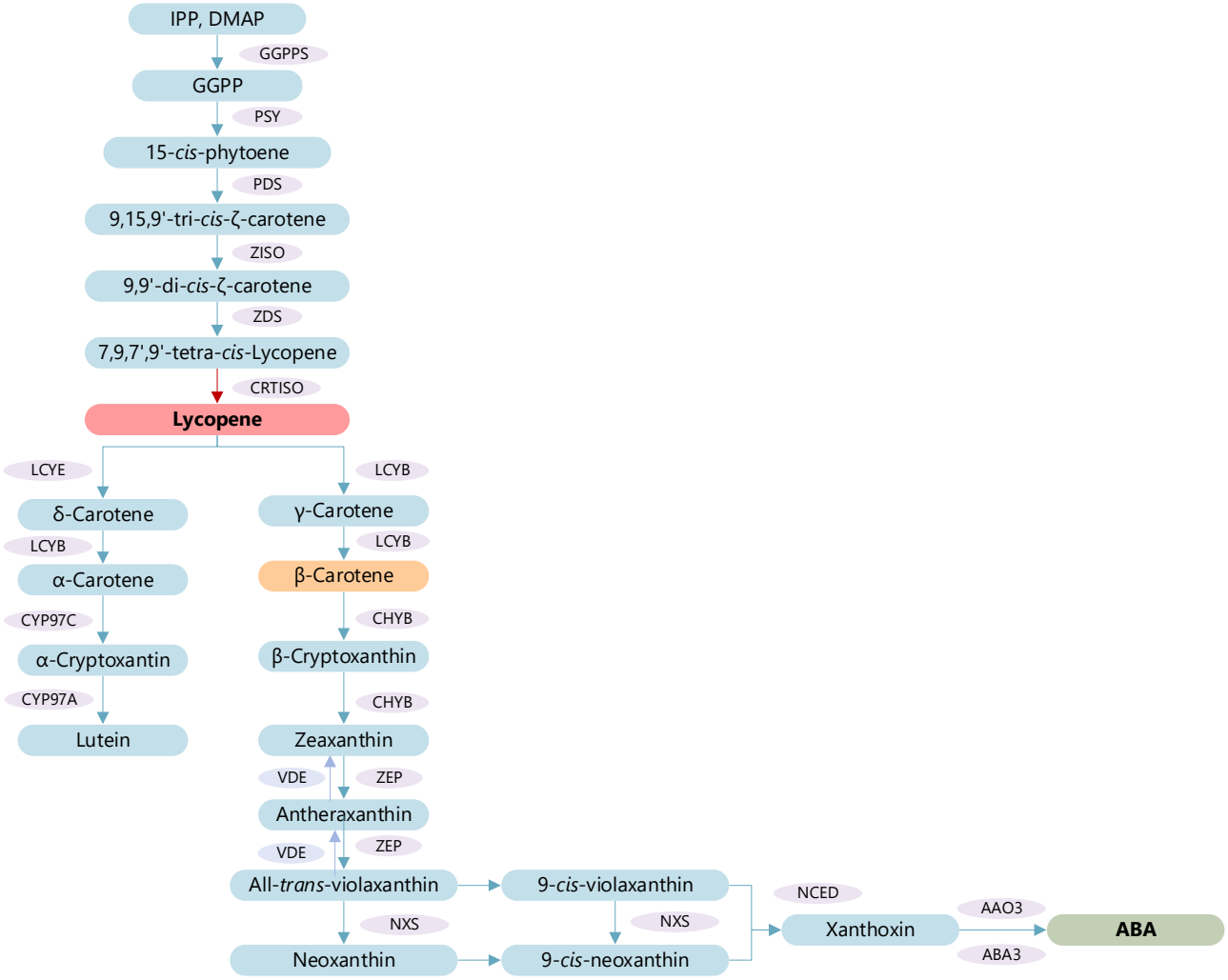

Figure 2. The carotenoid biosynthesis pathway. IPP, isopentenyl pyrophosphate; DMAPP, dimethylallyl diphosphate; GGPS, geranylgeranyl diphosphate synthase; PSY, phytoene synthase; PDS, phytoene desaturase; ZISO, ζ-carotene isomerase; ZDS, ζ-carotene desaturase; CRTISO, lycopene isomerase; LCYE, lycopene e-cyclase; LCYB, chromoplast-specific lycopene β-cyclase; CHYB, β-carotene hydroxylase; ZEP, zeaxanthin epoxidase; VDE, violaxanthin de-epoxidase; NXS, neoxanthin synthase; NCED, 9-cis-epoxycarotenoid dioxygenase; SDR, short-chain dehydrogenase/reductase; AAO, aldehyde oxidase; ABA, abscisic acid (redrawn and modified from Galpaz et al., 2006).

In tomato, several mutants have been identified and the pathways and enzymatic steps for carotenoid production are now well-established. Indeed, most of the phenotypes observed as a result of these mutations produce yellow or orange fruits and not fully developed red color. Table 2 provides a summary of the mutants, genes, and phenotypes observed. Interestingly, unlike *Arabidopsis*, which has a single *PSY* gene, tomato has three, with neofunctionalization of additional genes occurring during evolution (Gupta et al., 2022). Among these genes, PSY1 mediates fruit-specific carotenoid biosynthesis in chromoplasts (Fray and Grierson, 1993) , and it is known to be rate-limiting for lycopene production. PSY2 and PSY3 are likewise tissue-specific, with PSY2 driving leaf-specific carotenoids production (Fraser et al., 1999) and recently shown to play a role in abscisic acid biosynthesis in fruit (Gupta et al., 2022). On the other hand, *PSY3* expression is limited to roots under stress conditions (Fraser et al., 1999; Fantini et al., 2013).

Table 2. Mutations in the functional genes related to carotenoid biosynthetic pathway in tomato (adapted from Luan et al., 2020).

Variety/Mutant	Phenotype and changes in carotenoid composition	Gene	Mutation site	Enzyme activity and mutation details	References
fcd1 (*fruit carotenoid deficient 1*)	Pale orange fruit; little carotenoid accumulation	*IDI1*	Gene	Loss of or decreased enzyme activity; due to either a nonsense mutation (*fcd1-2*, *fcd1*^{at}), a deletion (*fcd1-1*) or a missense mutation (*fcd1-3*)	(Pankratov et al., 2016)
og (*old-gold*), *og*^{c} (*old- gold crimson*)	Deep red fruit; lacking β-carotene and increased lycopene accumulation	*CYCB*	Gene	Loss of enzyme activity; caused by a single base insertion	(Ronen et al., 2000)
r (*yellow flesh*), *r*^{y}	Yellow fruit; lacking carotenoids (yellow pigments are flavonoids)	*PSY1*	Gene	Loss of enzyme activity; due to a deletion (*r*^{y}) or mutation(s) with detail not revealed (*r*)	(Fray and Grierson, 1993)
tangerine^{mic}	Orange fruit; accumulation of prolycopene instead of lycopene	*CRTISO*	Gene	Loss of enzyme activity; due to a deletion	(Isaacson et al., 2002)
wf1 (*white flower 1*)	White flower; lacking carotenoids	*CrtR-b2* (flower-specific CHYB)	Gene	Loss of enzyme activity; due to a deletion (*wf1-1*, *wf1-3*) or a single base substitution (*wf1-2*)	(Galpaz et al., 2006)
B (*Beta*)	Orange fruit; increased accumulation of b-Carotene and decreased accumulation of lycopene	*CYCB*	Promoter	Enhanced expression; due to six insertions and a deletion in the promoter	(Ronen et al., 2000)
nxd1 (*neoxanthin-deficient 1*)	Pale yellow flower; lacking neoxanthin	*Nxd1* (*NSY*)	Promoter	Decreased expression; due to a deletion (nxd1-1) or a single base substitution (nxd1-2)	(Neuman et al., 2014)
tangerine^{3183}	Orange fruit; accumulation of prolycopene instead of lycopene CRTISO	*CRTISO*	Promoter	No expression; due to a deletion in the promoter	(Isaacson et al., 2002)

1.4.2 Fruit softening

Texture change and softening are two of the most noticeable characteristics of fruit ripening, and it has long been assumed that this phenomenon is caused, at least in part, by cell wall disassembly and reorganization. The cell wall consists of cellulose fibrils encased in a matrix of hemicelluloses, pectin, and structural proteins such as hydroxyproline-rich extensin and arabinogalactan proteins (Figure 3) (Carpita and Gibeaut, 1993). Enzymes responsible for the turnover of cell wall components to accommodate cell expansion and the textural changes associated with fruit ripening are likely present in the cell wall. Studies on many fruits have revealed that at least ten different types of cell wall-modifying enzymes are expressed during ripening (Tucker et al., 2017)). These enzymes collectively contribute to the change in texture, leading to alterations in the structure and hydration of cell wall polymers, resulting in softening (Li et al., 2021).

Among the main cell wall modifying enzymes we found, pectin-modifying enzymes include pectinesterase (PE), pectate lyase (PL), polygalacturonase (PG) and β-galactosidase (β-GAL), whereas hemicellulose/cellulose-modifying enzymes include 1,4-β-glucanase, xyloglucan transglycosylase/hydrolase (XTH) and expansin (EXP). Although there is no single enzyme that contributes significantly to softening, it is clear that several of these enzymes have specific actions affecting cell wall structure (Tucker et al., 2017; Wang et al., 2018), with some of the major contributions shown in Figure 3. Indeed, the pectin-rich middle lamella of the cell wall is modified and partially hydrolyzed during the ripening process, and the structural change of this pectin gel is responsible for the loss of cohesion between cells and, at least partly, for the softening of the ripe fruit. PG catalyses the hydrolytic cleavage of α-(1-4)-galacturonan linkages and is responsible for the change in pectin structure, although minor increase in firmness has been detected in knockdown PG tomatoes (Langley et al., 1994). Expansin has a significant effect on cell walls during ripening, despite the fact that it is not an enzyme in the strict sense of the term because it does not catalyze a chemical reaction. Instead, it is thought to interact at the cellulose fibril-coating hemicellulose polymer junction to disrupt hydrogen bonds (Brummell et al., 1999; Tucker et al., 2017). Recently, a study that simultaneously knocked-down PG and EXP1 showed a remarkable phenotype with firmer fruits, with more total soluble solids, denser cell walls and thicker cuticles (Jiang et al., 2019). Recent RNAi knockdown and CRISPR/Cas9 knockout experiments revealed that removing PL resulted in firmer tomatoes, though softening was not eliminated (Uluisik et al., 2016). Overall, this confirms the high level of complexity in the softening process during ripening. Moreover different tissues, such as locular gel tissue, show different pattern of cell wall modification, for example it was demonstrated that the nature of pectins in this tissue and their changes during ripening differ greatly from those from pericarp (Huber and Lee, 1986). It is

important to point that recently it was demonstrated that locular gel formation play a key role in the further softening process and therefore in the fruit quality (Huang et al., 2021). Because some of these enzymes are encoded by more than one gene in the tomato genome, a tissue-specific analysis should be further performed.

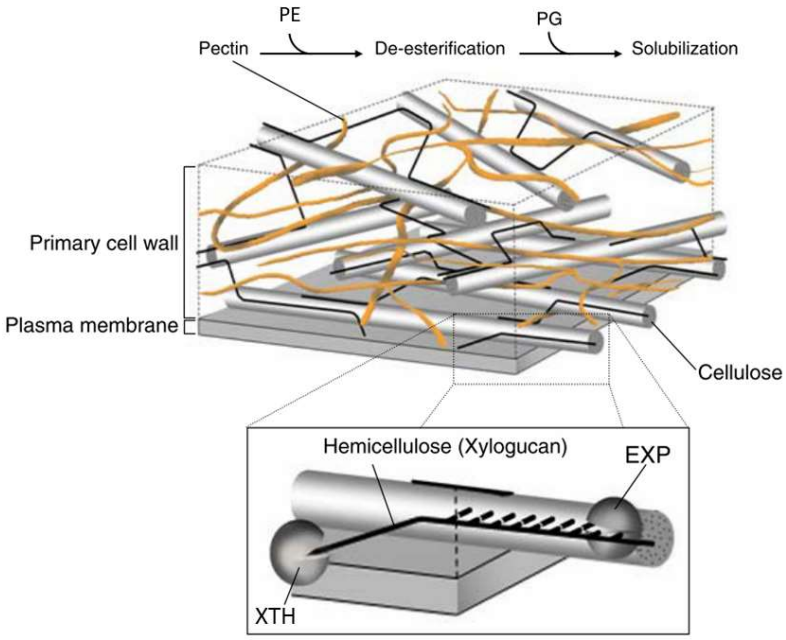

Figure 3. General structure of primary cell and representation of some cell wall modification sites. In the primary cell wall, proteins like expansin and extensin are embedded in a complex network of carbohydrates, primarily cellulose, hemicellulose, and pectin. The cellulose-hemicellulose network, which is enmeshed in the pectin matrix, is made up of cellulose microfibrils connected by hemicellulosic tethers. Xyloglucan is the most prevalent hemicellulose found in primary cell walls. Fruit softening and texture changes during ripening are linked to an enzyme-driven breakdown of the cell wall. For subsequent pectin de-polymerization and solubilization by PG, PE must first perform pectin de-methylation and de-esterification. Another cell wall protein called expansin is in charge of breaking the hydrogen bonds between the polysaccharide matrix and the cellulose microfibrils. In growing tomato fruit, XTH enzyme activity is very high, falls towards the beginning of ripening, and then slightly increases at the end of ripening (from Pirrello, 2009).

1.4.3 Volatile production

Tomato flavor is the sum and interaction of different components, including sweetness, which is primarily dictated by sugars; acidity, which is defined by the presence of organic acids; texture, driven by firmness and juiciness; and a huge number of volatile compounds (Mathieu et al., 2009). According to Petró-Turza (2009), ripe tomato fruit contains over

400 volatile chemicals (VOCs), which are derived from primary metabolites such as fatty acids and amino acids or secondary metabolites such as phenylpropanoids and carotenoids. However, only a subset of these volatiles have been identified as being responsible for the distinctive aroma of tomatoes, with only 13 being linked to specific human sensorial characteristics and acceptance. (Tieman et al., 2017). Nonetheless, the presence of sugar or organic acids alters the perception of aromatic panel descriptors in samples containing the same concentration of volatile compounds (Tandon et al., 2003; Baldwin et al., 2008), demonstrating the complexity of the aroma trait. As result of efforts made to develop the prediction of this trait, top 21 VOCs have been identified (Table 3) (Tandon et al., 2003; Abegaz et al., 2004; Tieman et al., 2012; Piombino et al., 2013). According to their biosynthetic origins, the compounds can be classified into five groups: (1) fatty acids derivatives; (2) branched-chain amino acids derivatives (BCAA); (3) carotenoid catabolism derivatives; (4) phenolic; and (5) phenylpropanoid (Martina et al., 2021).

Table 3. Summary of the primary 21 main components of tomato aroma (adapted from Martina et al., 2021)

Class	Compound	Odor Descriptors
Carotenoid	6-Methyl-5-hepten-2-one	Citrus, green, musty, lemongrass, apple
Carotenoid	Geranial	Sharp, lemon, sweet
Carotenoid	β-Damascenone	Apple, rose, honey, tobacco, sweet
Carotenoid	Geranylacetone	Fresh, green, fruity, waxy, rose, woody, magnolia, tropical
Carotenoid	β-Ionone	Floral, woody, sweet, fruity, berry, tropical, beeswax
BCAA	3-Methylbutanal	Ethereal, aldehydic, chocolate, peach, fatty
BCAA	2-Methylbutanal	Musty, cocoa, coffee, nutty
BCAA	3-Methylbutanol	Fusel, oil, alcoholic, whiskey, fruity, banana
BCAA	2-Isobuthylthiazole	Green, wasabi, privet, tomato, leaf, earthy, vegetable,
Fatty acids	1-Penten-3-one	Pungent, peppery, mustard, garlic, onion
Fatty acids	(Z)-3-Hexenal	Green, fatty, grassy, weedy, fruity, apple
Fatty acids	Hexenal	Sweet, almond, fruity, green, leafy, apple, plum, vegetable
Fatty acids	(E)-2-Hexenal	Sharp, fresh, leafy, green, clean, fruity, spicy, herbal
Fatty acids	(E)-2-Heptenal	Pungent, green, vegetable, fresh, fatty
Fatty acids	(E,E)-2.4-Decadienal	Oily, cucumber, melon, citrus, pumpkin, nut, meat
Phenolic	Phenylacetaldehyde	Green, sweet, floral, hyacinth, clover, honey, cocoa
Phenolic	2-Phenylethanol	Sweet, floral, fresh, bready, rose, honey
Phenolic	1-Nitro-2-phenylethane	Flower, spice
Phenylpropanoid	Guaiacol	Phenolic, smoke, spice, vanilla, woody
Phenylpropanoid	Methyl salicylate	Wintergreen, mint
Phenylpropanoid	Eugenol	Sweet, spicy, clove, woody

The first enzymes identified to be linked with aroma and flavor production in tomato ripening were lipoxygenase (LOX) and alcohol dehydrogenase (ADH) (Speirs et al., 1998; Chen et al., 2004). The tomato genome contains 21 putative LOX genes that are thought to be involved in a variety of metabolic processes, including the synthesis of jasmonic acid (JA), making it difficult to identify the volatile associated one. However, targeting several LOX genes demonstrated that the plastid-located TomLOX C (LOXC) is essential for the

generation of lipid-derived C6 and later C5 volatiles (Shen et al., 2014; Gao et al., 2019). During ripening *ADH2* transcript levels increase and its activity is required for conversion of aldehydes to alcohols (Speirs et al., 1998). Several genes are now known to be associated in the production of flavor volatiles (Figure 4). Acetate esters are synthetized by alcohol acetyltransferase (AAT1) using an alcohol as precursor and its lower activity leads to lower amount of this compounds (Yahyaoui et al., 2002; Goulet et al., 2015). Branched-chain amino acid aminotransferases (BCAT1) is important for the production of BCAAs (Maloney et al., 2010; Zhang et al., 2016). The initial phase in the creation of phenylalanine-derived fragrances in tomato fruits is facilitated by Aromatic Amino Acid Decarboxylase (AADC1A) (Tieman et al., 2006). L-phenylalanine ammonia lyase (PAL3) converts L-phenylalanine to trans-cinnamic acid, which is then used to synthesize benzenoids (C6-C1) (Aragüez and Valpuesta Fernández, 2013). Cleavage of carotenoids by carotenoid cleavage dioxygenases (CCD1) which are particularly expressed during fruit ripening (Wei et al., 2015) leads to the production of carotenoid derivative VOCs (Simkin et al., 2004).

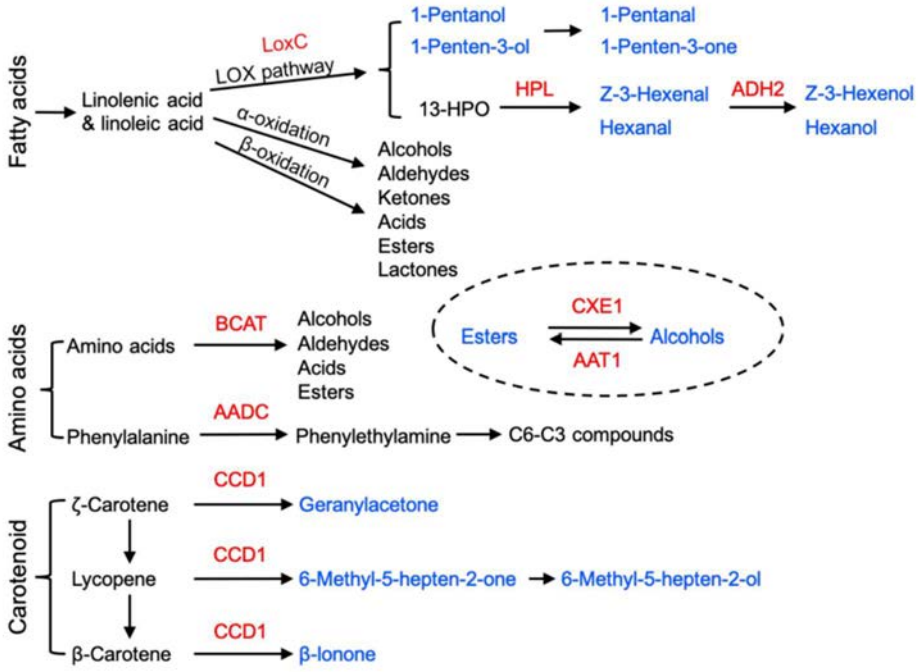

Figure 4. Simplified volatile compound biosynthesis pathways in fruits. Volatiles derived from different pathways fatty acids, amino acids or carotenoids. Additionally, the enzymes alcohol acetyltransferase (AAT1) and carboxymethylesterase (CXE1) can reversibly convert volatile alcohols to esters. Volatiles are indicated in blue and enzymes in red. LoxC, lipoxygenase C; HPL, fatty acid hydroperoxide lyase; ADH2, alcohol dehydrogenase 2; BCAT, branched-chain amino acid aminotransferases; AADC, aromatic amino acid decarboxylase; CCD1, carotenoid cleavage deoxygenase 1 (From Li et al., 2021).

1.5 Hormonal control of ripening

In fleshy fruits, the change from growth to ripening is marked by distinct shifts in the phytohormone profiles. These shifts are necessary to halt fruit expansion and to promote fruit ripening (Forlani et al., 2019; Chirinos et al., 2023).

1.5.1 Ethylene

Ethylene plays a role in a wide variety of developmental processes and physiological responses in plants, including flowering, fruit ripening, organ senescence, abscission, root nodulation, seed germination, programmed cell death, cell expansion, and responses to abiotic stresses, such as flooding, and pathogen attacks (Abeles et al., 1992). Burg and Burg (1965) were the first to describe the role of ethylene in fruit ripening, and since then, direct evidence has accumulated to show that ethylene mediates tomato fruit ripening at the physiological, biochemical, and molecular levels. Indeed, as mentioned in Section 1.1.2, climacteric fruits show a peak in autocatalytic ethylene production and rely on it to fully ripe. Changing ethylene at the biosynthesis, perception, signal transduction, or transcriptional level has been shown to affect fruit ripening (Hamilton et al., 1990; Oeller et al., 1991; Lanahan et al., 1994; Lee et al., 2012; Liu et al., 2014).

The ethylene biosynthetic pathway (Figure 5A) involves two specific steps catalyzed by ACC synthase (ACS) and ACC oxidase (ACO), both encoded by multigene families. In tomato, two ethylene biosynthesis systems have been identified: System-1, which is autoinhibitory and active in vegetative tissues and during fruit development, and System-2, which is autocatalytic and active once the fruit has reached full size. (Lelièvre et al., 1997; Giovannoni et al., 2017). In tomato, 14 ACS genes (ACS1A/B-13) and 7 ACO genes (ACO1-7) have been identified (Liu et al., 2015). System-1 ethylene production mainly relies on ACS1A, ACS6, and ACO1, while System-2 is dependent on ACO1, ACO4, ACS2, and ACS4 (Oeller et al., 1991; Nakatsuka et al., 1998; Barry et al., 2000; Liu et al., 2015). The transition from System-1 to System-2 ethylene biosynthesis marks the beginning of the climacteric phase and acquisition of ripening competency (McMurchie et al., 1972). Direct evidence that ethylene is critical for the induction of ripening in climacteric fruit come from studies in tomato, where antisense-mediated suppression of the ethylene biosynthetic genes, ACS and ACO, showed a significant delay or blocked ripening. Exposure to exogenous ethylene can initiate the ripening of these transgenic fruits (Hamilton et al., 1990; Oeller et al., 1991). However, it is still unknown how ethylene production switches from auto-inhibitory to auto-catalytic during the ripening process.

The current accepted model of ethylene signaling is based on a linear transduction pathway in which in the absence of ethylene, ethylene receptors (ETR) interact with the protein kinase Constitutive Triple Response 1 (CTR1) that phosphorylates Ethylene

Insensitive 2 (EIN2) and as a result shut down the ethylene transduction pathway (Figure 5B). On the other hand, in the presence of ethylene, both ETR and CTR1 are inactivated, and the C-terminus of EIN2 undergoes dephosphorylation and proteolytic cleavage at the same time. C-terminus of EIN2 activates the transcriptional cascade that involves primary transcription factors, EIN3/EIL (Ethylene Insensitive 3/ Ethylene Insensitive 3-Like), and then secondary transcription factors as Ethylene Response Factors (ERFs) (Figure 5C). The tomato genome encodes 7 ETR (Chen et al., 2018), 4 SlCTRs, 1 SlEIN2, 6 SlEILs, 4 SlEBFs, and 81 SlERFs (Pirrello et al., 2012; Liu et al., 2016; Deng et al., 2022), indicating a high degree of adaptability during the ethylene signaling process in tomato. Several genes of the ethylene transduction pathway have been functionally characterized. *Nr* (mutated in SlETR3) shows severe ripening defect (Lanahan et al., 1994). *SlEIN2* null or knock-down mutants showed a severe inhibited fruit size and blocked ripening (Gao et al., 2016; Huang et al., 2022). The suppression of four *SlEIL* genes simultaneously or the overexpression of a single *SlEBF3* gene resulted in transgenic tomatoes with impaired ripening (Tieman et al., 2001; Deng et al., 2018; Huang et al., 2022). ERF transcription factors regulate many genes that influence various fruit phenotypic traits such as color, firmness, aroma, taste, and postharvest shelf life. Their role in ripening is described in the Section 1.6.3 of this Chapter.

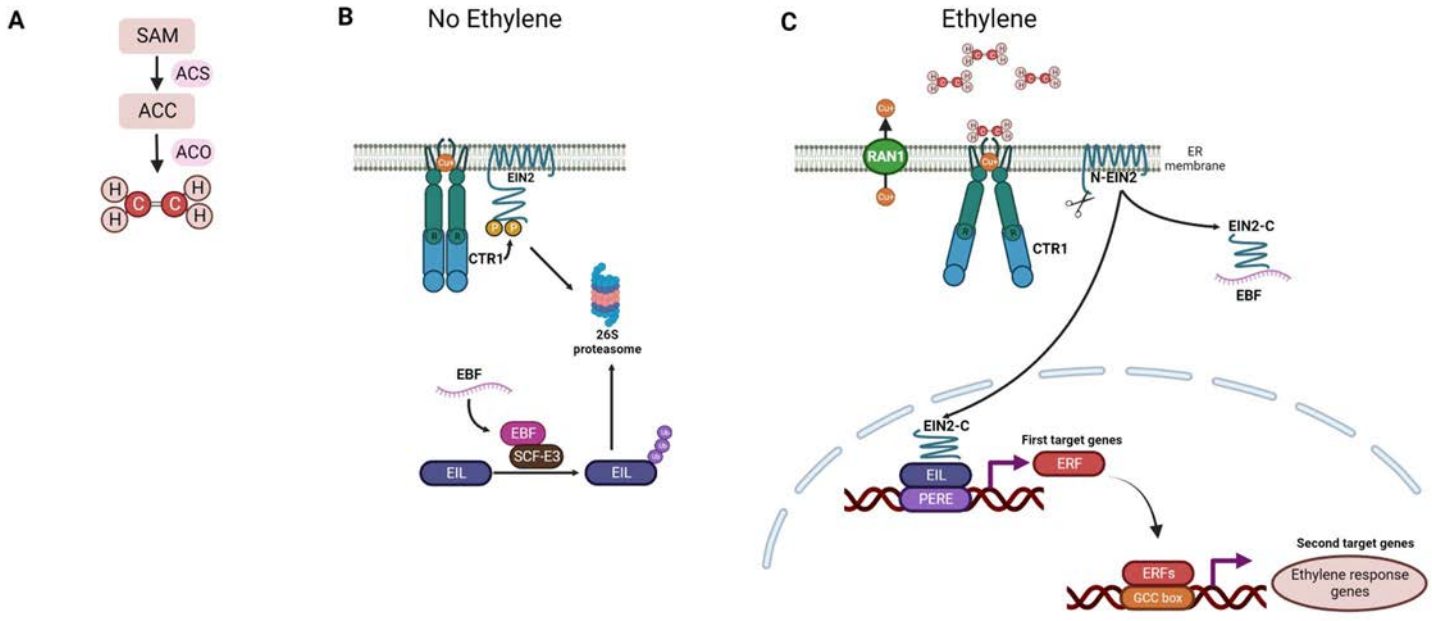

Figure 5. Ethylene biosynthesis and signalling pathways. (A) Ethylene biosynthesis, S-adenosylmethionine is converted to 1-aminocyclopropane-1- carboxylate (ACC) by ACC synthase (ACS). ACC is subsequently converted to ethylene by ACC oxidase (ACO). **(B)** In the absence of

ethylene, the receptors activate Constitutive Triple-Response1 (CTR1), which suppresses the ethylene response via phosphorylation of Ethylene Insensitive2 (EIN2). This results in EIN2 degradation by the proteasome. Because EIN2 levels are low, an SCF-E3 containing the Ethylene Insensitive3-binding F-box (EBF) proteins ubiquitinates EIN3 and EILs (here represented only as EIL), leading to their degradation by the proteasome and preventing them from affecting transcription in the nucleus. **(C)** In the presence of ethylene, the receptor proteins (ETR), located in the endoplasmic reticulum (ER), bind ethylene via a copper cofactor delivered by RAN1. Ethylene binding to the receptors induces their inactivation, and by consequence, switches off CTR1 phosphorylation activity. EIN2 in its active state stabilizes EIL transcription factors, which then induce the expression of target genes by binding to primary ethylene response elements (PEREs). This includes genes that encode ERF transcription factors. ERFs, in turn, modulate the transcription of ethylene-regulated genes through binding to GCC-box type cis-elements present in their target promoters (redrawn and modified from Liu et al., 2015 and Binder, 2020).

1.5.2 Auxin

The role of auxins in fruit development is well known (Kumar et al., 2014); however, data on the role of auxin in the control of fruit ripening initiation is limited. Several studies have pointed an antagonistic role towards ripening (Lieberman et al., 1977; Shinozaki et al., 2018), which is supported by reverse genetics experiments (Jones et al., 2002; Hao et al., 2015; Su et al., 2015; Breitel et al., 2016; Shin et al., 2019). Indeed, the beginning of ripening is linked with a decline in auxin levels and signaling. This results in increased ethylene sensitivity, which further activates the production of System-2 ethylene, causing the onset of climacteric ripening (Shin et al., 2019; Li et al., 2021, Chirinos et al., 2023). Auxin synthesis occur in the chloroplasts via tryptophan, followed by conversion to IAA either through indole-3-acetamide (IAM) or indole-3-pyruvic acid (IPyA) (Mano and Nemoto, 2012). *TRYPTOPHAN AMINOTRANSFERASE OF ARABIDOPSIS* (TAA) and a multigene family of *YUCCA* genes, which encode flavin-containing monooxygenases, also play important roles in tryptophan-independent auxin biosynthesis in the cytosol (Wang et al., 2015; Cao et al., 2019). The IPyA pathway appears to be dominant in tomato fruit auxin production (Matsuo et al., 2018). In addition, to the decrease in auxin concentration at ripening initiation it has been demonstrated silencing of a *Gretchen Hagen 3* (*GH3*) *IAA– amido synthetases* (*SlGH3-2*) involved in auxin catabolism, inhibited both ethylene biosynthesis and lycopene accumulation (Sravankumar et al., 2018), supporting the idea of the negative role of auxin in ripening initiation.

Auxin Response Factors (ARFs) transcription factors, Auxin/INDOLE-3-ACETIC ACID (Aux/IAA) transcriptional repressors, and TOPLESS (TPS) co-repressors are the

main players in the auxin signaling pathway. The tomato genome is composed of 22 ARF genes (Zouine et al., 2014). Most of these genes have an N-terminal DNA-binding domain, a central transcriptional regulatory region that can serve as either an activator or repressor domain, and a carboxy-terminal dimerization domain. These domains facilitate the formation of ARF/ARF homodimers or ARF/Aux/IAA heterodimers. Several reverse genetic experiments have addressed the role of ARFs during ripening. The over-expression of *SlARF2A* in tomatoes caused uneven ripening, where certain areas of the fruit ripened faster than others, resulting in a patchy appearance (Hao et al., 2015; Breitel et al., 2016). Downregulation of tomato SlARF4 also changed ripening-related traits such firmness, sugar, and chlorophyll content, resulting in dark green fruit and blotchy ripening (Jones et al., 2002; Sagar et al., 2013). Interestingly, similar phenotypes were found when *SlARF6A* or *SlARF10* are downregulated (Yuan et al., 2018; Yuan et al., 2019), which is involved in regulating chlorophyll during tomato fruit development. *SlARF2A* expression is ethylene and auxin-regulated and show a ripening associated profile (Hao et al., 2015; Breitel et al., 2016). The tomato genome harbours two ARF2 paralogs, SlARF2A and SlARF2B, are nuclear localized and repress auxin-responsive genes (Hao et al., 2015). The presence of auxin and ethylene *cis*-regulatory elements in the promoter regions of several ARFs suggests a cross-talk between these two hormones at this level. (Muday et al., 2012; Hao et al., 2014). Small auxin-upregulated RNAs (SAURs), in addition to ARFs, are thought to be involved in a variety of auxin-related actions (Ren and Gray, 2015). *SlSAUR69* has been shown to be involved in changing auxin signaling or transport and altering its expression delays ripening initiation (Su et al., 2015; Shin et al., 2019).

1.5.3 Abscisic acid

Abscisic acid (ABA) is an important hormone in the regulation of photosynthesis, transpiration and many physiological processes like root growth, senescence, and fruit ripening (Pilati et al., 2017). It is generally agreed upon that ABA is the primary regulatory phytohormone present in non-climacteric fruits during the ripening process; however recent evidence point also a significant role in tomato ripening. Indeed, exogenous ABA enhances the amplitude of the ethylene peak, accelerating ripening, whereas the application of fluridone, which is an inhibitor of carotenoid biosynthesis, or nordihydroguaiaretic acid, which is an inhibitor of ABA biosynthesis, produces the opposite result (Zhang et al., 2009).

The first committed step in the ABA biosynthetic pathway (Figure 6) is the oxidative cleavage of 9′-cis-neoxanthin and/or 9-cis-violaxanthin, which produces xanthoxin, a neutral growth inhibitor with physiological properties similar to ABA. This is a rate-

limiting regulatory step and is catalyzed by 9-cis-epoxycarotenoid dioxygenase (NCED). Then, the Short Chain Dehydrogenase/Reductase (SDR) catalyzes the transformation of xanthoxin into abscisic aldehyde. The final step is catalyzed by abscisic aldehyde oxidases family (AAOs), which all require a molybdenum cofactor (MoCo). ABA catabolism is accomplished through hydroxylation by ABA 8′-hydroxylases or conjugation by uridine diphosphate glucosyltransferase (UGT) (Li et al., 2017). In tomato, the inhibition of SlNCED1 leads to a reduction in endogenous ABA levels and an increase in ethylene production (Ji et al., 2014).Conversely, suppressing three CYP707A2 isoforms that encode ABA 8'-hydroxylases, or SlUGT75C1 which generates esterified ABA-glucose, produces over-ripe fruits with elevated ABA concentrations (Ji et al., 2014; Sun et al., 2017).

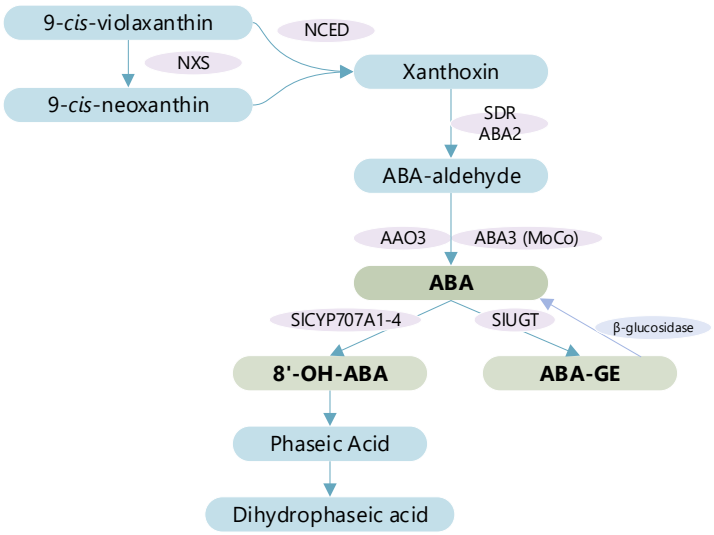

Figure 6. The abscisic acid (ABA) biosynthetic pathway. Carotenoid precursor synthesis in the early steps of ABA biosynthesis can be seen in Figure 2. ABA, abscisic acid; ABA-GE, ABA-glucosyl ester; AAO, aldehyde oxidase; SlCYP707A1-4, ABA 8'-hydroxylase; NCED, 9-cis-epoxycarotenoid dioxygenase; NXS, neoxanthin synthase; SDR, short-chain dehydrogenase/reductase; SlUGT, uridine diphosphate glucosyltransferase (Adapted and redrawn from Chernys and Zeevaart, 2000; Chen et al., 2016).

The ABA signaling pathway (Figure 7) has three core components: PYR/PYL/RCAR ABA receptors (PYLs), protein phosphatases 2C (PP2Cs) and SNF1- related protein kinase 2 (SnRK2) (Fujii et al., 2009; Ma et al., 2009; Melcher et al., 2009). In the absence of ABA, PP2Cs repress ABA signal transduction by inhibiting the activity of SnRK2 kinase. In the presence of ABA, ABA-bound receptors block PP2C activity while permitting SNRK2 and the subsequent phosphorylation of ABA-responsive element binding factors (ABFs) to

activate ABA-responsive genes (Furihata et al., 2006; Fujii et al., 2009). In tomato, early ripening was observed in RNAi lines of SlPP2C1, SlPP2C3, or SlPP2C5, which function as negative regulators of ABA signaling, while lines that overexpressed these genes experienced a ripening delay (Zhang et al., 2018; Liang et al., 2021; Wang et al., 2021). Based on these results, it appears that ABA biosynthesis genes affect ripening in a manner distinct from that of ABA signaling genes.

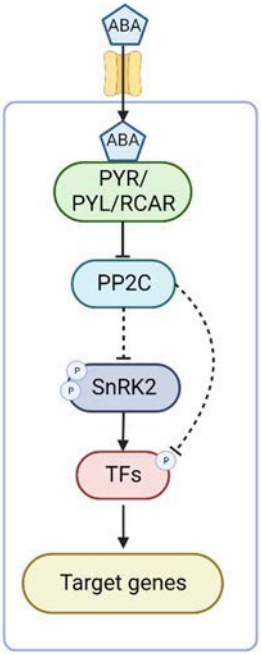

Figure 7. Simplified Abscisic Acid signaling pathway. Schematic representation of the core ABA signaling components. Pyrabactin Resistance 1/PYR1-Like, PYR/PYLs; group-A type 2 C of protein phosphatases, PP2Cs; subclass III Snf1-related protein kinases2, SnRK2s; TFs, transcription factors (Adapted from Xiong et al., 2021).

1.5.4 Brassinosteroids

The brassinosteroids (BRs) are steroid hormones that have significant effects on plant growth, development, and response to environmental cues. Furthermore, they greatly impact various facets of fruit ripening in multiple fruits, including tomatoes (Zhu et al., 2015; Nolan et al., 2020). Some data have pointed the role of BRs in tomato fruit ripening. Tomato fruit ripening was hastened by the application of brassinolide (BL), which increased the accumulation of transcripts encoding the ethylene biosynthesis genes *ACS2*, *ACS4*, *ACO1*, *ACO4* (Zhu et al., 2015) and the key carotenoid biosynthesis gene *PSY1* (Liu et al., 2014a). Additionally, Li et al. (2016) reported that BRs are actively synthesized and accumulated during tomato fruit ripening, suggesting a potential role for BRs in this

process. Recently, the functional role in ripening of some BRs-related genes have been characterized. Overexpressing *SlCYP90B3*, which encodes a cytochrome P450 monooxygenase that catalyzes the rate-limiting step of BR synthesis, enhanced softening and increased soluble sugar and flavor volatile contents in an ethylene-dependent manner (Hu et al., 2020). Notably, it has recently been demonstrated that a key basic helix-loop-helix TF in the BR signaling pathway, called BRI1-EMS-SUPPRESSOR1 (BES1), can mediate ethylene-independent fruit softening by repressing PMEU1, a pectin methylesterase (PME) (Liu et al., 2021).

1.5.5 Jasmonates

Jasmonates (JAs) are a class of important plant hormones derived from linolenic acid, with volatile ester methyl jasmonate (MeJA) and other derivatives of jasmonic acid being included in this group (Pérez-Llorca et al., 2019). Despite the importance of JAs in plant development, knowledge on their function during fruit ripening is limited, with most studies focusing on the effects of MeJA exogenous treatments. Treatment with MeJA has been shown to induce earlier ripening and the upregulation of ethylene System-2 biosynthesis genes (Saniewski et al., 1987; Tao et al., 2021). Notably, transient increases in JA and MeJA concentration in tomatoes have been observed during the onset of fruit ripening, suggesting a potential role in the regulation of this process (Fan et al., 1998). Further investigations are needed to determine the precise mechanisms underlying the regulation of ripening by JAs.

1.5.6 Salicylic Acid

Salicylic acid (SA) is synthesized in plants from chorismite in the plastids via the isochorismate synthase (ICS) and/or phenylalanine ammonia-lyase (PAL) pathways (Pérez-Llorca et al., 2019; Li et al., 2021), while methyl salicylate (MeSA) is produced when SA is methylated by a particular type of O-methyltransferase (Tieman et al., 2010). There is very little data regarding the role of SA during fruit ripening, a report showed that high concentration MeSA (0.5 mM), inhibited ethylene production, respiration, and color development, which was associated with suppression of *ACS2* and *ACS4* transcript accumulation and delayed *ACO1* accumulation (Ding and Wang, 2003). More research research is needed to elucidate the mechanisms by which SA regulates fruit ripening.

1.6 Transcriptional regulation of ripening

Tomato ripening is controlled by a number of transcription factors (TFs), as well as the plant hormone ethylene and its downstream effector genes (Wang et al., 2019). A significant step forward in understanding the transcriptional control of fruit ripening was the identification of the mutations affecting the ripening-defective natural mutants *ripening inhibitor* (*rin*), *non-ripening* (*nor*) and *colorless non-ripening* (*Cnr*), positional cloning showed that *rin* encoded a MADS TF, MADS-RIN, *nor* encoded a NAC TF, NAC-NOR, and *cnr* encoded a SQUAMOSA promoter-binding protein-like TF, SPL-CNR (Vrebalov et al., 2002; Manning et al., 2006; Giovannoni, 2007).

1.6.1 MADS

The transcriptional factors encoded by the highly conserved MADS-box gene family, control a variety of plant developmental processes. MADS-RIN (or RIN) is a MADS-box transcription factor related to the *SEPALLATA* clade (E-class) of *MADS-box* genes, it was identified and characterized by the cloning of the *rin* tomato ripening mutation (Vrebalov et al., 2002). The deletion characterised in *rin* mutant produce the fusion of two adjacent MADS genes (*RIN* and *MACROCALYX* (MC)) located on tomato chromosome 5, generating a chimeric gene *RIN-MC*. *rin* mutant fruit lack an autocatalytic ethylene burst, do not accumulate lycopene or produce flavor volatiles or soften, and fruit do not ripen when ethylene is supplied externally (Vrebalov et al., 2002). However, significant differences between the phenotypes of *RIN* knockout or knockdown, which could only undergo partial ripening, and the phenotype of the severely ripening-inhibited *rin* mutant (Ito et al., 2017; Li et al., 2019; Li et al., 2020). The chimeric *RIN-MC* transcripts accumulate significantly in *rin* mutant and it is thought to be translated in a dominant negative TF with a strong repressor function (Li et al., 2019). RIN is still considered a key regulator of ripening and it is absolutely required for full progression of ripening (Ito et al., 2017; Li et al., 2019; Li et al., 2020). ChIP-chip or ChIP-Seq assays have demonstrated that RIN has hundreds of target genes (Fujisawa et al., 2013; Zhong et al., 2013), including the ethylene biosynthesis genes ACS2 and ACS4, the ethylene receptor NR/ETR3, many genes involved in color, flavor, texture, and aroma, like LoxC and ADH2, cell wall-softening genes PG, TBG4, EXP1, CEL2, and transcription factor genes, NAC-NOR, SBP-CNR, AP2a, FUL1/2 (Fujisawa et al., 2011; Fujisawa et al., 2013; Zhong et al., 2013), revealing the big extend of RIN in the control of ripening. Several other MADS-box transcription factors essential for expression of multiple ripening genes, including TOMATO AGAMOUS-LIKE1 (TAGL1) and FRUITFULL (FUL1 and FUL2), form

DNA binding complexes with MADS-RIN (Itkin et al., 2009; Bemer et al., 2012; Fujisawa et al., 2014). Inhibition of FUL1/2 interferes with ripening (Fujisawa et al., 2014).

1.6.2 NAC

The NAC TF family is highly diverse and unique to plants; the tomato genome contains 101 putative NAC and is thus they are involved in a wide variety of biological processes (Liu et al., 2022). The name NAC is originally derived from three proteins no apical meristem (NAM), ATAF1-2 and CUC2 (cup-shaped cotyledon). The tomato *nor* mutation produces a severe ripening-impaired phenotype. The mutation was due to a 2 bp deletion in the third exon of NAC-NOR (Giovannoni, 2004), generating a truncated protein of 186 amino acids, which retains the NAC domain. NAC-NOR complete knock-out produced a less severe phenotype and, thus suggesting that the mutation carried by *nor* generate a dominant negative TF (Wang et al., 2019; Gao et al., 2020). In recent years many other NAC TFs have been associated to play a role in ripening. *NOR-like1, NAC4,* and *NAC9* positively regulate ethylene biosynthesis and lycopene production (Gao et al., 2018; Kou et al., 2018). Particularly, NOR-like1 targets genes involved in ethylene biosynthesis (*ACS2*, *ACS4*), colour formation (*GGPPS2*, *SGR1*) and cell wall metabolism (*PG2a*, *PL*, *CEL2* and *EXP1*) (Gao et al., 2018). Although there are conflicting reports as to whether NAC1 delays or accelerates ripening, it is clear that NAC1 is involved in tomato ripening and that manipulating its expression affects *ACS2*, *ACS4*, *ACO1*, and ethylene biosynthesis (Ma et al., 2014).

1.6.3 ERF

The last actors in ethylene transduction pathway are the Ethylene Response Factors (ERFs). ERFs are one of the most numerous plant transcription factor families, and they are responsible for ethylene effects at the genetic level. In this regard, these transcription factors may be able to mediate the wide range of ethylene responses seen in various aspects of climacteric fruit ripening (Pirrello et al., 2012; Liu et al., 2016). ERFs are members of the AP2/ERF multi-gene family, which is defined by the presence of the AP2/ERF domain. ERF proteins bind to the GCC box or dehydration-responsive element/C-repeat (DRE/CRT) *cis*-acting elements in the promoter regions of ethylene-responsive genes (Pirrello et al., 2012). The tomato genome contains 81 ERFs, which can be further subdivided into nine subclades (A-J) based on structural features (Pirrello et al., 2012; Deng et al., 2022). A study of the expression pattern of these ERF genes has showed that 27 are upregulated while 28 are downregulated upon ripening (Liu et al., 2016). Particularly, *SlERF.E1*, *SlERF.E2*, and *SlERF.E4*, from the subclade E, were the most upregulated during ripening and dramatically downregulated in the ripening mutants Nr,

rin, and nor (Liu et al., 2016). Up to date the role of several ERFs on ripening has been already described, *SlERF.H1* (formerly known as LeERF1) overexpression accelerates fruit ripening and softening through a constitutive ethylene response (Li et al., 2007). Similarly, *SlERF.E4* (formerly known as *ERF6*) is involved in tomato fruit ripening by connecting ethylene and carotenoid synthesis pathways (Lee et al., 2012), while *SlERF.B3* regulates climacteric ethylene production and carotenoid accumulation to control fruit ripening (Liu et al., 2013). Downregulation of *SlERF.A3* (formerly known as *SlPti4*) showed early ripening, reduced ethylene production and less lycopene content; however, it also showed higher levels in ABA but reduced sensitivity to ABA (Sun et al., 2018), suggesting that SlERF.A3 could be in the crosstalk between ABA and ethylene. Members of the ERF F subclade have the Ethylene-responsive element-binding factor-associated Amphiphilic Repression (EAR) motif for transcriptional repression (Kagale and Rozwadowski, 2011), and recently the role of SlERF.F12 in tomato ripening has been deciphered. SlERF.F12 inhibits tomato fruit ripening by engaging the co-repressor TOPLESS protein 2 (TPL2) and the histone deacetylases (HDAs) HDA1/HDA3 to repress the transcription of ripening-related genes (Deng et al., 2022). Understanding the role of ERFs in ripening and determining their target genes will be crucial for elucidating their unique contribution to this process (Liu et al., 2015).

1.7 Hypoxia in plant development and ripening

Molecular oxygen plays an important role in many plant biochemical reactions. Light energy is converted into chemical energy in the form of ATP by photosystems in the thylakoid membranes of chloroplasts, resulting in oxygen production (Van Dongen and Licausi, 2015). However, it also contributes to the synthesis of extremely reactive molecules and competes with carbon dioxide as a substrate for the enzyme Rubisco, making careful homeostasis of oxygen concentrations essential (Weits et al., 2021). In plants, steep oxygen gradients within tissues are not unusual but rather a typical occurrence. Unlike animals, plants lack of an active oxygen transport system, therefore the supply of oxygen to tissues depends on passive transport methods like diffusion and convection (Ho et al., 2011). When the rate of diffusion from the atmosphere exceeds the rate of consumption by cellular respiration, oxygen concentrations in plant tissues typically fall. Specific environmental conditions, such as flooding, ice encasement, or artificially altered atmospheres, have a significant impact on plant cell oxygen availability (Weits et al., 2021). Endogenously generated oxygen gradients, on the other hand, are very common in plants, where the anatomy and physiology of the specific tissue determines oxygen release, retention, or diffusion (Van Dongen and Licausi, 2015). In pears and apples, oxygen gradients can be seen macroscopically, with the lowest oxygen concentrations found in the

fruit core (Joseph et al., 2021). Other examples of oxygen gradients in plant tissues include avocados, carrots and potatoes (Van Dongen et al., 2003). Oxygen concentrations of less than 5 kPa have been measured in developing seed centers such as pea, maize, sunflower, and bean (Borisjuk and Rolletschek, 2009). The active metabolism and resistance to gas diffusions in growing potato tubers result in the formation of a significant oxygen gradient from the surface to the core, where the oxygen concentration falls below 5% (Geigenberger et al., 2000) (Figure 8).

When the oxygen concentration falls to the point where oxygen becomes limiting as a substrate for cytochrome c oxidase, ATP production via oxidative phosphorylation is no longer capable of meeting cellular ATP demands (Van Dongen and Licausi, 2015). This can be compensated by increasing ATP production through substrate-level phosphorylation by activating glycolytic activity (Gibbs and Greenway, 2003). Nevertheless, the ATP yield per glucose unit that can be derived through glycolysis alone is much lower than that of oxidative phosphorylation. This phenomenon necessitates the efficient recycling of NAD^+ from NADH; otherwise, glycolysis will be constrained by NAD^+ availability. As a result, the ethanol fermentation pathway is activated by inducing the expression of the enzymes pyruvate decarboxylase (PDC) and alcohol dehydrogenase (ADH), while the lactate fermentation pathway is also activated by inducing the expression of lactate dehydrogenase (LDH), and both pathways use pyruvate and NADH as substrates (Van Dongen and Licausi, 2015). Nitric oxide (NO) cycle can be used to recycle NAD+ from NADH as an alternative. Under low-oxygen conditions (hypoxia), the nitric oxide (NO) cycle can be used to recycle NAD+ from NADH. Nitrate reductase (NR) increases nitrite reduction under hypoxic conditions, which results in NO production. Class-1 nonsymbiotic hemoglobins (PGB or HB), which are specifically expressed when the oxygen concentration is low, oxidize NO to nitrate again. This cycle balances the cytosol's antioxidant status and requires NADH as a cosubstrate (Dordas et al., 2003; Igamberdiev and Hill, 2004; Van Dongen and Licausi, 2015). Transcripts encoding enzymes in metabolic reprogramming, such as those involved in fermentative adaptation, ethylene biosyntesis (genes ACS and ACO), and JASMONATE ZIM DOMAIN PROTEIN 3 (JAZ 3), accumulate in plants in response to low oxygen. In *Arabidopsis*, 49 genes have been described as hypoxia «core response» genes and are involved in low oxygen response of diverse cell types and tissues (Mustroph et al., 2009). Among them, some are coding for TFs, signaling proteins, anaerobic metabolism enzymes, and uncharacterized proteins.

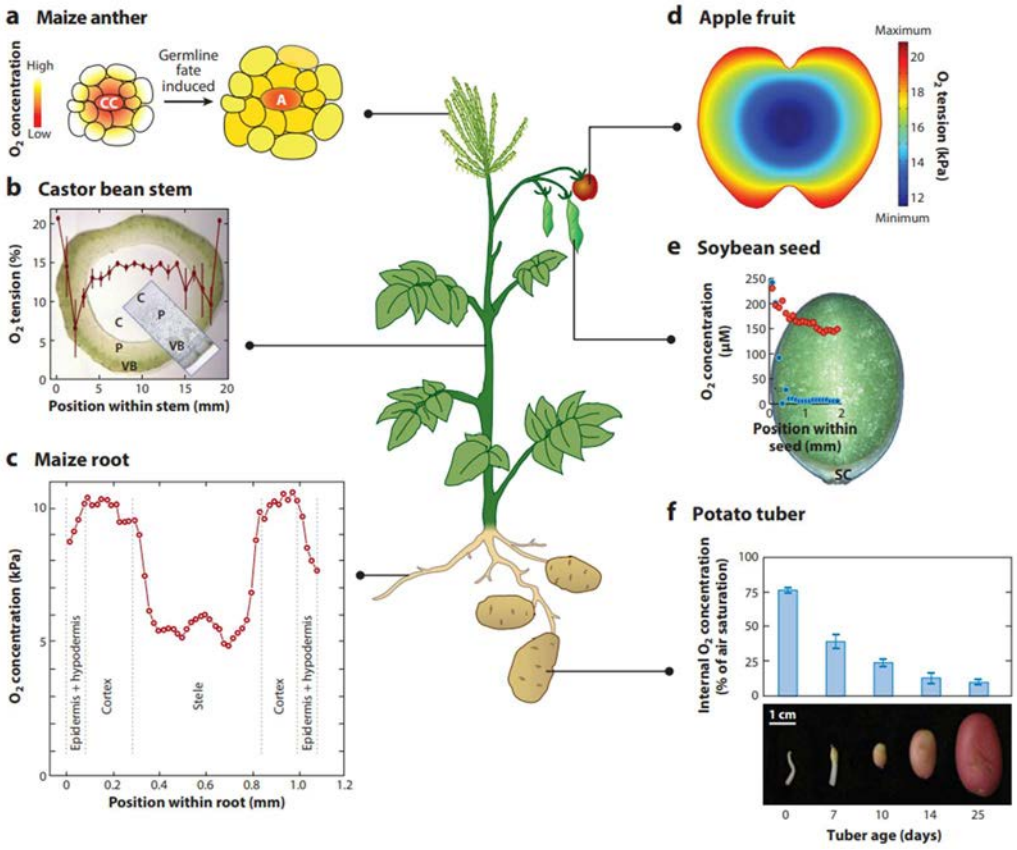

Figure 8. Differences in oxygen content between plant tissues and over time. (A) Oxygen concentration in maize anthers. CC, central cells; A, archespores **(B)** Oxygen profile through a castor bean (*Ricinus communis*) stem. C, hollow center; P, parenchyma cells; VB vascular bundle. **(C)** Radial oxygen profile across the primary root of maize. **(D)** Model of the oxygen partial pressure distribution along the vertical axis of an apple fruit. The color bar indicates oxygen partial pressure (in kPa). **(E)** Oxygen distribution map of soybean seeds measured under light (red circles) or dark (blue circles) conditions. SC, seed coat. **(F)** Internal oxygen levels in the cores of tubers at different developmental stages. (From Van Dongen and Licausi, 2015).

1.7.1 ERFs and oxygen sensing and signalling

Plant oxygen sensing research has advanced enormously in recent decades, as a result now we have a very detailed understanding of how plants sense oxygen and react to low-oxygen conditions. Notably, the transcription factors Ethylene Response Factor (ERF)-VII have been shown to play an important role in the oxygen-sensing process. Interestingly, *Arabidopsis* group VII ERFs that are characterized by a MCGGAII/L N-terminal motif (Nakano et al., 2006) are orthologues of the tomato ERF subclade E genes (Liu et al., 2016). In *Arabidopsis*, in normal oxygen conditions ERFs-VII are targeted by the N-end rule pathway of protein degradation. In brief, after removal of the first methionine by a

Methionine Aminopeptidases (MAPs) and oxidation of the penultimate position cysteine by Plant Cysteine Oxidases (PCOs) using O_2 as co-factor. The oxidized N-terminal cysteine (C*) is then arginylated by the Arginyl tRNA-Treansferases (ATEs). Finally, the protein is targeted by the E3 ubiquitin-protein ligase (PRT6) to be finally degraded by proteasome (Figure 9A). Degradation of ERFs-VII is suppressed in hypoxia due to a lack of oxygen-dependent cysteine oxidation. ERFs-VII can then accumulate and drive the expression of downstream genes in response to hypoxia (Figure 9B) (Gibbs et al., 2011; Licausi et al., 2011; Gibbs et al., 2014). When oxygen availability returns to aerobic levels, ERFs-VII are destabilized again, restoring oxygen homeostasis (Hartman et al., 2019) (Figure 9). Four of five ERF-VIIs (RAP2.12, RAP2.2, HRE1 and HRE2) have been reported to be associated with the regulation of hypoxia-response genes in *Arabidopsis* (Bailey-Serres et al., 2012). As previously mentioned, ERFs functional analysis in different fruits has identified this large plant family as important player in several different aspects of ripening. However, genes that have the same molecular function as RAP2.12 have not yet been identify in fruits.

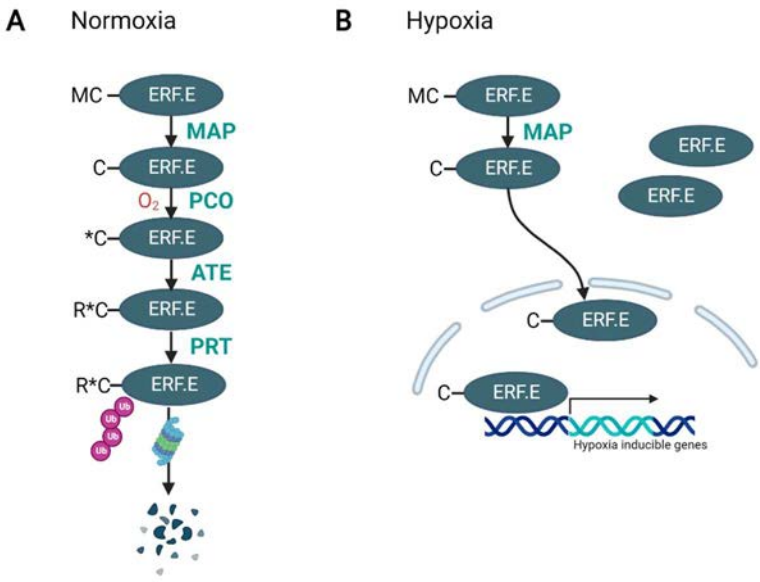

Figure 9. Oxygen sensing and signaling mechanisms. Graphical representation of the N-end rule branch that leads to oxygen-dependent protein degradation via the 26S proteasome. ERF subclade E (or ERF-VII) bear a conserved N-terminal sequence that **(A)** under normoxia, targets them to constitutive proteasomal degradation, through a branch of the N-end rule pathway that relies on the production of oxidized cysteine (*C) as an intermediate. **(B)** On the other hand, oxygen limiting conditions lead to stabilization of the Met-Cys N terminal sequence, thereby allowing ERF to migrate into the nucleus and activate transcription of low oxygen-responsive genes (Adapted and re-drawn from Banti et al., 2013).

Objectives of the study

Fruits are an important source of mineral salts, antioxidants, and essential vitamins, making them essential for a healthy human diet. Every year, approximately 14% of the world's food, valued at $400 billion, is lost between harvest and the retail market (FAO, 2019). Because of their high-water content, fruits are especially vulnerable to post-harvest losses. Reduction in these losses and yield improvement are major challenges in the context of rapid growth of human population and an improved understanding of the ripening process of perishable fruits is a critical component in meeting this challenge. Fruit ripening is a complexly orchestrated developmental process that occurs only in plants and results in significant physiological and metabolic changes, ultimately leading to fruit decay and seed dispersal. This process is distinguished by the emergence of quality characteristics such as color, aroma, or softening. The development of these characteristics makes the fruit appealing to animals that will aid in seed dispersal. Fruits are classified as climacteric or non-climacteric based on their ripening profiles, which include whether or not they experience an increase in respiration and autocatalytic ethylene production (Klee and Giovannoni, 2011). Therefore, ethylene is essential for the initiation of ripening in climacteric fruits, ethylene biosynthesis is governed by two systems (McMurchie et al., 1972). System 1 is in charge of producing the basal ethylene levels found in all tissues. System 1 is known to be ethylene autoinhibitory and is reported to function during fruit growth, whereas System 2 is autocatalytic and operates during climacteric ripening. The switch from System-1 to System-2 ethylene biosynthesis signals the start of the climacteric phase and the acquisition of ripening competency (McMurchie et al., 1972). However, it is still unknown how ethylene production switches from auto-inhibitory to auto-catalytic during the ripening process. Whereas the onset and progression of tomato ripening is typically associated with changes in the external color of the pericarp tissue, few studies have pointed to the role of inner tissues where key ripening transcription factors are induced first in the locular gel prior to the pericarp (Giovannoni et al., 2017; Shinozaki et al., 2018). Based on this knowledge, firstly this thesis aimed to decipher the early transcriptomic changes associated with ripening initiation in two different fruit tissues, gel and pericarp, as well as the interaction of auxin and ethylene during this process (Chapter II).

As mentioned before, ripening of climacteric fruits is characterized by a significant increase in respiration, as evidenced by the high CO_2 production, as well as the autocatalytic ethylene production. Whereas the link between these two events remains unexplained, it is widely recognized that ethylene plays a key role in the initiation of climacteric fruit ripening (Liu et al. 2015), and that this hormone recruits the ripening-related genes via Ethylene Response Factors (ERFs) which belong to a large multigene

family of transcription factors (Pirrello et al., 2012). However, the mechanism by which ERFs control specific aspects of fruit ripening remains yet to be deciphered. Transcriptomic analysis recently revealed that ERFs subclade E (ERF.E1, E2, E4) have an expression pattern that is associated with ripening. Furthermore, the gene expression of these ERFs is low in the known maturation mutants (*rin*, *nr* and *nor*), suggesting their potential requirement for fruit ripening (Liu et al. 2016). On the other hand, it was shown that *Arabidopsis* ERFs-VII, orthologues of tomato ERF subclade E, work as oxygen sensors exhibiting degradation in normoxia (normal oxygen conditions) via the N-end rule pathway. On the other hand, under hypoxic conditions (low O_2 levels) these ERFs are stabilized and can then function as transcription factors (Licausi et al., 2011). Taking together, this raise the hypothesis that these ERFs might be the "missing link" between the concomitant increase in respiration and the ethylene peak characteristic of the climacteric ripening. Building on this new hypothesis, the second part (Chapter III) of this thesis aimed (i) to determine if switches in oxygen concentration occurs during ripening, (ii) to uncover the putative role of ERFs subclade E triggering fruit ripening initiation by integrating oxygen sensing and the N-end rule pathway.

Chapter II

Transition to ripening in tomato requires hormone-controlled genetic reprogramming initiated in gel tissue

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Research Article

Transition to ripening in tomato requires hormone-controlled genetic reprogramming initiated in gel tissue

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J.P. and M.B. planned and designed the research. X.C., S.Y., M.A.R., and E.P. performed experiments. S.F. performed metabolomics experiments and data analysis. X.C., S.Y., A.D., and E.M. contributed to computational analysis. X.C., S.Y., G.H., M.L., F.R., J.P., and M.B. analyzed data. X.C., J.P., and M.B. wrote the manuscript.
The author responsible for distribution of materials integral to the findings presented in this article in accordance with the policy described in the Instructions for Authors (https://academic.oup.com/plphys/pages/general-instructions) is: Julien Pirrello (julien.pirrello@toulouse-inp.fr).

Abstract

Ripening is the last stage of the developmental program in fleshy fruits. During this phase, fruits become edible and acquire their unique sensory qualities and post-harvest potential. Although our knowledge of the mechanisms that regulate fruit ripening has improved considerably over the past decades, the processes that trigger the transition to ripening remain poorly deciphered. While transcriptomic profiling of tomato (*Solanum lycopersicum* L.) fruit ripening to date has mainly focused on the changes occurring in pericarp tissues between the Mature Green and Breaker stages, our study addresses the changes between the Early Mature Green and Late Mature Green stages in the gel and pericarp separately. The data showed that the shift from an inability to initiate ripening to the capacity to undergo full ripening requires extensive transcriptomic reprogramming that takes place first in the locular tissues before extending to the pericarp. Genome-wide transcriptomic profiling revealed the wide diversity of transcription factor (TF) families engaged in the global reprogramming of gene expression and identified those specifically regulated at the Mature Green stage in the gel but not in the pericarp, thereby providing potential targets toward deciphering the initial factors and events that trigger the transition to ripening. The study also uncovered an extensive reformed homeostasis for most plant hormones, highlighting the multihormonal control of ripening initiation. Our data unveil the antagonistic roles of ethylene and auxin during the onset of ripening and show that auxin treatment delays fruit ripening via impairing the expression of genes required for System-2 autocatalytic ethylene production that is essential for climacteric ripening. This study unveils the detailed features of the transcriptomic reprogramming associated with the transition to ripening of tomato fruit and shows that the first changes occur in the

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locular gel before extending to pericarp and that a reformed auxin homeostasis is essential for the ripening to proceed.

Introduction

Fruit ripening is the last phase of fleshy fruit development that ultimately leads to fruit decay and seed dispersal. During this process, most fruit quality traits occur as a result of the activation of major physiological and metabolic pathways, leading to changes in color, aroma, and texture. These traits are essential in making the fruit attractive to consumers and frugivores that promote seed dispersal. It is commonly accepted that ripening starts at the breaker stage when the fruit color shifts from green to light yellow. Based on their ripening profiles, fruits are classified as climacteric or nonclimacteric depending on whether or not they undergo a rise in respiration and in autocatalytic ethylene production (Klee and Giovannoni, 2011). A typical characteristic of climacteric fruit is their capacity to initiate ripening when detached from the plant, once they gain the competence to ripen, a stage commonly named Mature Green (MG). Ethylene has been considered the primary hormone orchestrating climacteric fruit ripening. Consequently, a plethora of studies have been devoted to the role of this hormone in the ripening process (Lelièvre et al., 1997; Liu et al., 2015). Also, it is worth mentioning that, so far, most studies have focused on deciphering the dynamic changes taking place in the pericarp tissues while neglecting what occurs in inner tissues.

The ethylene biosynthetic pathway involves two specific steps catalyzed by 1-aminocyclopropane-1-carboxylate (ACC) synthase (ACS) and ACC oxidase (ACO), both encoded by multigene families. In climacteric fruit like tomato (*Solanum lycopersicum* L.), at the pre-ripening immature green stages, ethylene biosynthesis is controlled by the so-called System-1 characterized by auto-inhibitory ethylene production, whereas System-2 prevails at MG stages and is characterized by autocatalytic ethylene production (Lelièvre et al., 1997; Giovannoni et al., 2017). System-1 ethylene production mainly relies on ACS1A, ACS6, and ACO1, while System-2 is dependent on ACO1, ACO4, ACS2, and ACS4 (Oeller et al., 1991; Nakatsuka et al., 1998; Barry et al., 2000; Liu et al., 2015). The transition from System-1 to System-2 ethylene biosynthesis marks the beginning of the climacteric phase and acquisition of ripening competency (McMurchie et al., 1972). How ethylene production shifts from auto-inhibitory to auto-catalytic during the transition to ripening is still unclear.

It is remarkable that potential roles of other hormones during the transition to ripening of climacteric fruit remains poorly understood. Several studies have reported that exogenous applications of auxin (indole-3-acetic acid, IAA), gibberellic acid (GA), or cytokinin (CK) delay ripening (Dostal and Leopold, 1967; Davey and Van Staden, 1978; Su et al., 2015). On the other hand, exogenous applications of abscisic acid (ABA), brassinosteroid (BR), or jasmonate (JA) have been reported to promote ripening and enhance climacteric ethylene production (Zhang et al., 2009; Zhu et al., 2015; Tao et al., 2021). Although these studies support the hypothesis that these hormones may have important roles in fruit ripening, there is little understanding of their possible interactions with ethylene. It was recently shown that auxin, ABA, and JA influence the expression of genes involved in the ripening control network, including those involved in ethylene biosynthesis (Li et al., 2021). In addition, a growing body of evidence supports the importance of crosstalk between different hormones in controlling tomato fruit ripening. It was demonstrated that *ETHYLENE RESPONSE FACTOR B3* (*SlERF.B3*), encoding a TF from the Ethylene Response Factor (ERF) family, is responsive to both ethylene and auxin and integrates these two signaling pathways via regulation of the auxin signaling component *SlIAA27* (Liu et al., 2018). Moreover, the expression of the auxin conjugating gene *GRETCHEN HAGEN 3* (*GH3*) is upregulated by ABA and ethylene during grape (*Vitis vinifera*) and tomato ripening, suggesting the existence of complex multihormonal crosstalk associated with the process of fleshy fruit ripening (Böttcher et al., 2011; SravanKumar et al., 2018). ABA has been reported to induce ripening by promoting ethylene biosynthesis in banana (*Musa sapientum* L.), tomato, and peach (*Prunus persica laevis* L. Batsch) (Zhang et al., 2009; Soto et al., 2013; Jiang et al., 2014) in line with enhanced transcript levels of *ACS2*, *ACS4*, and *ACO1* genes upon exogenous ABA application (Chernys and Zeevaart, 2000; Zhang et al., 2009).

Overall, our knowledge of the molecular mechanisms and factors underlying the shift from ripening incompetency to ripening competency associated with the transition to ripening is sparse. We recently proposed a model in which RIPENING INHIBITOR (SlRIN) and SMALL AUXIN UPREGULATED 69 (SlSAUR69) define a regulation loop that acts as a modulator of the balance between auxin and ethylene via repressing auxin transport and tissue distribution, resulting in enhanced ethylene sensitivity (Shin et al., 2019). However, a more comprehensive understanding of the molecular events controlling the developmental transition leading to the initiation of the ripening process is still missing.

The development of high-throughput sequencing technologies has paved the way for transcriptomic profiling aimed at deciphering the dynamic changes in gene expression on a genome-wide scale. This effort has greatly benefited from the characterization of ripening-impaired mutants, including *ripening inhibitor* (*rin*) and *non-ripening* (*nor*) (Kumar et al., 2018). Both mutants produce dominant-negative TFs capable of repressing many key ripening-related genes (Ito et al.,

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2017; Wang et al., 2019; Li et al., 2020). Knockout or knockdown lines have demonstrated that *RIN* and *NOR* are required for the full progression of ripening (Ito et al., 2017; Wang et al., 2019; Li et al., 2020). Several other MADS-box TFs essential for the expression of multiple ripening genes, including *TOMATO AGAMOUS-LIKE1 (TAGL1)* and *FRUITFULL (FUL1* and *FUL2*), form DNA-binding complexes with MADS-RIN (Itkin et al., 2009; Bemer et al., 2012; Fujisawa et al., 2014). Among the NAC TFs, *NOR-like1*, *NAC4*, and *NAC9* positively regulate ethylene biosynthesis and lycopene production (Gao et al., 2018; Kou et al., 2018). Re-evaluation of the regulatory hierarchy of key ripening regulators has been made with the recent insights provided by clustered regularly interspaced short palindromic repeats/Cas9 (CRISPR/Cas9) technology (Wang et al., 2019; Li et al., 2021), but data exploring their role in hormone biosynthesis and signaling genes during the ripening process are scarce.

In tomato, the ripening process has been addressed by focusing mainly on the pericarp tissue, likely due to the fact that the onset and progression of ripening are typically associated with visible changes in the external color of the pericarp. However, although fruit texture and softening are associated with the ripening phase, it was recently demonstrated that this major fruit quality trait is dependent on differentiation of the locular tissue and determined at early pre-ripening stages (Huang et al., 2021). This finding represents a paradigm shift in thinking and clearly points out the important role of tissues besides pericarp in controlling the ripening process. Previous studies have indicated that initial ripening steps, including pigment accumulation and locular differentiation, take place within the fruit inner tissues (Shinozaki et al., 2018). Furthermore, the rise in the expression of many important ripening-associated genes like *RIN*, *NOR*, *PECTIN-LYASE1 (PL1)*, *PHYTOENE SYNTHASE1* (*PSY1*), and *CAROTENOID ISOMERASE* (*CRTISO*) begins in the locular tissue and then radiates out to the placenta and other tissues. Altogether, these data call for more attention to the investigation of physiological and transcriptomic regulation in the gel and pericarp tissues separately. In the present study, we present genome-wide transcriptomic profiling of the transition to ripening in tomato pericarp and gel, spanning four ripening stages. Notably, while most studies exploring the transition to ripening considered the transcriptomic changes in the whole fruit, a distinctive feature of our study is to sample separately the gel and pericarp in order to reveal potential differences and shifted dynamics of the transcriptomic reprogramming associated with the transition to ripening in the two tissues. Moreover, whereas the MG stage is commonly considered as a homogeneous stage, and in an attempt to capture the very early events heralding the transition to ripening, our study distinguishes Early Mature Green (EMG) and Late Mature Green (LMG) as two different development stages. The data reveal that the transcriptomic reprogramming associated with initiation of ripening occurs first in the gel tissue before extending to the pericarp. The transcriptomic analysis also comprehensively identified TF families contributing to the transcriptomic reprogramming underlying the ripening initiation and provided several potential candidate TFs putatively involved in the transition to ripening. In addition, the study documents changes in multiple hormone signaling pathways, indicating that fruit ripening is under complex multihormonal control. Finally, the study uncovered a key role for auxin and its interplay with ethylene during the onset of ripening.

Results

Transcriptomic changes associated with the transition to ripening are initiated in the locular gel tissue

To unravel the transcriptomic reprogramming associated with the transition to ripening, we performed whole-genome transcriptomic profiling by RNA sequencing (RNA-Seq) of tomato fruit at four developmental stages, including EMG, LMG, Breaker (Br), and 4-day post-breaker (Br + 4). Moreover, to investigate whether ripening initiation is synchronized in all parts of the fruit organ, we sampled the pericarp and locular gel tissues separately. On average, 44 million clean reads were generated per sample and mapped to the SlyMIC v.1.0 assembly and annotation of the *S. lycopersicum cv.* MicroTom reference genome (BioProject: PRJNA553986). The total number of differentially expressed genes (DEGs) during the transition to ripening was 18,134 genes in gel tissue and 16,863 in the pericarp (Figure 1A). Principal component analysis (PCA) revealed major differences between the transcriptomes generated, with 57% of the variance (PC1) associated with the ripening stages and 24% of the variance (PC2) with the tissue type. The gel transcriptome gives rise to clusters distinct from those of the pericarp at both ripening (Br and Br + 4) and pre-ripening (EMG and LMG) stages. Notably, the two pericarp transcriptomes corresponding to the pre-ripening stages cluster together, while these EMG and LMG stages cluster separately in the gel, with the LMG gel transcriptome starting to shift toward that of the ripening stages. This clustering suggests that the transition to ripening starts earlier in the gel than in pericarp tissue, as shown by the higher extent of transcriptomic changes revealed during the transition from EMG to LMG in the gel tissue (Figure 1B). Consistent with this idea, the number of DEGs between EMG and LMG is more than twice higher in the gel (829) than in the pericarp (318; Figure 1A). However, throughout the progression toward ripening, the number of DEGs between LMG and Br becomes similar in the gel (11,867) and pericarp (9,515), and this trend continues when considering the DEGs between Br and Br + 4 (5,210 in pericarp and 5,601 in the gel). As a complementary nontargeted approach, we examined co-expressed gene sets reflecting tissue or stage specificity, using weighted gene co-expression network analysis (WGCNA). A total of 21 modules were identified based on the similar expression patterns (Supplemental Figure S1, A and B) highlighting the existence of tissue or stage-specific modules. In particular, M7 and M8

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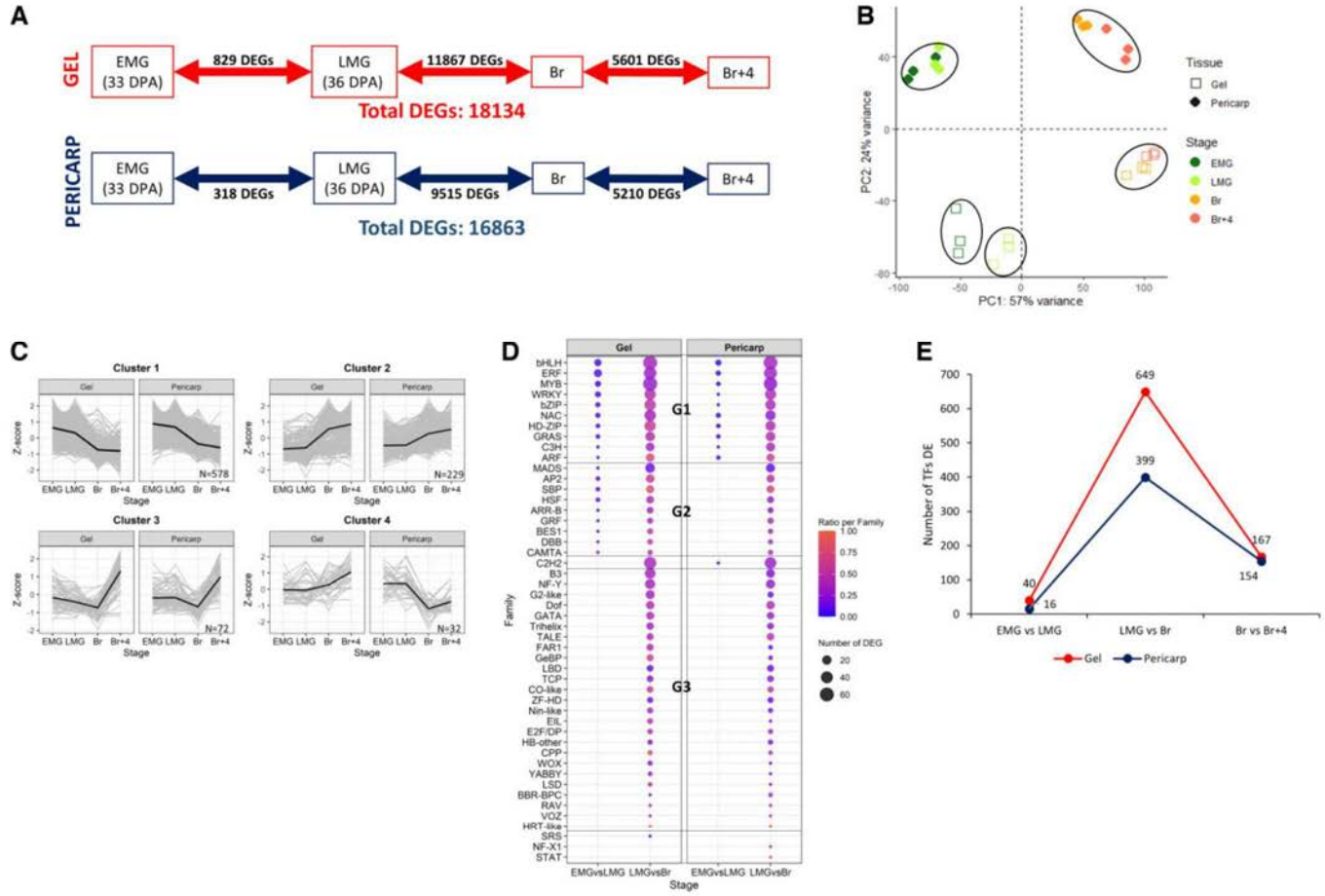

Figure 1 Global transcriptomic changes during the transition to ripening in tomato fruit. A, Transcriptional dynamics throughout ripening showing the number of DEGs at early stages of the transition to ripening. B, PCA of transcriptomic profiles of EMG, LMG, Br, and Br + 4 in gel and pericarp tissues. Every symbol represents one replicate. C, Clustering analysis of DEGs corresponding to TFs at four ripening stages in gel and pericarp according to their expression pattern. The bold black line represents the mean z-score for each cluster. D, Dot-plot showing the number of TF family members that are DEGs when comparing pre-ripening and early-ripening stages. The dot color indicates the ratio between the number of DEGs per family/total number of family members in the tomato genome. E, The number of TFs displaying differential expression during ripening in gel and pericarp. Adjusted $P < 0.05$.

modules gather genes whose expression is highly correlated with the gel tissue while the expression of genes in M18, M19, and M3 modules is strongly correlated with pericarp. On the other hand, the expression of genes in modules M1, M4, and M13 is highly correlated with the developmental stages.

Because any transcriptomic reprogramming requires the intervention of TFs, we sought to capture all DEGs annotated as putative TFs. Among a total of 1,994 TF genes in the tomato genome, 911 exhibit differential expression (DE) during the transition to ripening in the pericarp and gel tissues. The clustering of DEG TFs based on their expression pattern during ripening revealed four main clusters (Figure 1C). Cluster 1 includes 578 genes that show downregulation at the transition from LMG to Br in both gel and pericarp. Cluster 2 contains 229 TF genes that are upregulated during the initiation of ripening, including several known ripening regulators (*RIN*, *NOR*, *FUL2*, *CNR*, *TAGL1*, *NAC4*, *AP2A*, and *SlARF2A*). In particular, *RIN*, *NOR*, and *AP2a* show substantial increases in their transcript levels between EMG and LMG in locular gel tissues and only moderate upregulation in the pericarp (Supplemental Figure S2). In contrast, the upregulation of *FUL1* in the pericarp precedes that in the gel. Cluster 3 includes 72 genes that are upregulated once ripening has been initiated. Finally, Cluster 4 includes 32 genes showing opposite trends, upregulated in the gel, while downregulated in the pericarp. Taken together, the data support the idea that transcriptomic reprogramming associated with ripening initiation follows shifted dynamics in the gel and pericarp.

The high number and enormous diversity of TF families involved in the transition to ripening in tomato fruit reflect the extent of transcriptomic reprogramming underlying this process (Figure 1C; Supplemental Table S1). Indeed, out of 54 TF families identified in the tomato genome, 48 showed at least one differentially expressed member during ripening initiation (Figure 1D). Three main groups of TF families were defined based on their expression profiles. Group 1 (G1)

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contains 10 TF families whose members show DE between the four ripening stages in both gel and pericarp. Of these, basic helix–loop–helix (bHLH), ERF, NAC, and MYB TF families are the most representative of G1 and contain more members potentially engaged in these transitions. The second group (G2) contains TF families whose members display DE only in locular gel between the pre-ripening stages EMG and LMG, with APETALA2 (AP2), SQUAMOSA promoter Binding Protein-like (SBP), HEAT SHOCK FACTOR (HSF), and MADS-Box being the most represented families in this group. The third group (G3) includes TF families specifically differentially expressed between LMG and Br. Given that Group 2 members are differentially expressed specifically in the gel at the pre-ripening stages and become DEGs in the pericarp only later at the transition from LMG to Br, they are good candidates for active regulators orchestrating the initiation of ripening. In line with the idea that transcriptomic reprogramming is more intensive in the gel than in the pericarp at ripening initiation, 40 genes encoding putative TFs are differentially expressed between the EMG and LMG stages in the gel but only 16 in the pericarp (Figure 1E). At the transition from LMG to Br, 649 TF genes are DEGs in the gel and 399 in the pericarp. Finally, the number of TF genes that exhibit a statistically significant change in their expression level between Br and Br + 4 becomes similar in the gel (167) and the pericarp (154). The dynamics and changes that occur in TF genes reflect the extent of the global transcriptomic reprogramming and support the idea that the pericarp undergoes similar changes to those occurring in the gel but with a time lag. Notably, the comprehensive analysis of TF genes during the transition to ripening defines potential candidates putatively involved in the regulation of the transcriptional network associated with the initiation of the ripening process in tomato fruit (Supplemental Table S1).

The transcriptomic reprogramming underlying the transition to ripening is associated with multiple hormone-associated processes

To further define the biological processes associated with fruit ripening, we performed a GO term enrichment analysis of all DEGs in gel and pericarp separately. The analysis indicated that, among the top 20 most enriched GO terms, the GO:0009755 corresponding to hormone-mediated signaling pathway was highly enriched in both tissues (Supplemental Figure S3A). To gain better insight into the hormonal control of the transition to ripening in tomato fruit, we identified all DEGs related to hormone signaling, metabolism, and transport. Remarkably, genes associated with almost all plant hormones are affected at the transition to ripening, including auxin, ethylene, ABA, JA, BR, SA, CK, and GA, ordered based on the number of DEGs (Supplemental Figure S3B). Strikingly, while ethylene is known to be the primary hormone regulating climacteric fruit ripening, transcriptomic profiling revealed that auxin-related processes exhibit the highest number of DEGs (Supplemental Figure S3B). The data indicate that several genes related to the biosynthesis and signaling of CK, GA, and auxin are downregulated (Supplemental Figure S4, A–C). On the other hand, JA, ABA, and BR biosynthesis and signaling genes are upregulated, while the expression of genes involved in the catabolism of these hormones is decreased (Supplemental Figure S4, D–F). Hormone profiling showed that the levels of the CK active form dihydrozeatin decrease during the onset of ripening (Supplemental Figure S5A). This finding is consistent with the downregulation of CK-biosynthesis genes and the previously reported negative role of CKs during ripening (Davey and Van Staden, 1978). On the other hand, ABA and the glucose-conjugated form ABA–glucose ester levels increased at the initiation of ripening, in line with the transcriptomic profile of their related genes (Supplemental Figures 4, E and 5, B). Surprisingly, JA levels decrease at the Br stage, likely due to the transformation of JA into JA-Ile active form by *GRETCHEN HAGEN 3* (*GH3*) *JASMONATE RESISTANT* (*JAR*) genes (Supplemental Figures 4, D and 5, C). Overall, the data clearly indicate that the transition to ripening involves alterations in processes associated with multiple hormones.

Based on the number of the corresponding DEGs between EMG and LMG, auxin, ethylene, BR, and JA appear to be the most involved in the events initiating the ripening program (Figure 2A). Later, at the transition from LMG to Br stage, the highest number of DEGs occurs with auxin and ethylene processes, suggesting that the interplay between these two hormones may have a prominent role at the onset of ripening (Figure 2A). Clustering analysis of auxin-related DEGs at early stages of ripening identified two groups, one includes 81 genes that show downregulation as the main trend during ripening initiation and the second includes 31 genes exhibiting upregulation during later ripening stages (Figure 2B). Interestingly, Cluster 1 contains 23 genes involved in auxin biosynthesis, including one *TRYPTOPHAN AMINOTRANSFERASE* (*TAA*), and two *FLAVIN-CONTAINING MONOOXYGENASES* (*YUC*) genes (Figure 2C). On the other hand, Cluster 2 contains several *SMALL AUXIN UP-REGULATED* (*SAUR*) genes including *Sl-SAUR69* that is greatly upregulated at Br stage and shown to negatively regulate auxin transport (Shin et al., 2019; (Figure 2, B and D); two *GRETCHEN HAGEN 3* (*GH3*) IAA–amido synthetases, including *SlGH3-2*, an ortholog of grape *GH3.1* that preferentially conjugates aspartate to IAA (Böttcher et al., 2011; SravanKumar et al., 2018); and one *DIOXYGENASE FOR AUXIN OXIDATION* (*DAO*) encoding a DAO enzyme that irreversibly oxidizes IAA or IAA-Asp (Hayashi et al., 2021; Figure 2C). Together, these results are consistent with a pattern in which the expression of genes associated with auxin synthesis decrease, whereas those associated with auxin catabolism increase during the transition from LMG to Br. Consistent with the outcome of this interpretation of transcriptomic profiling, levels of active forms of free auxin decrease, while conjugated inactive forms accumulate in the fruit tissue at the onset of ripening (Figure 2E). Altogether,

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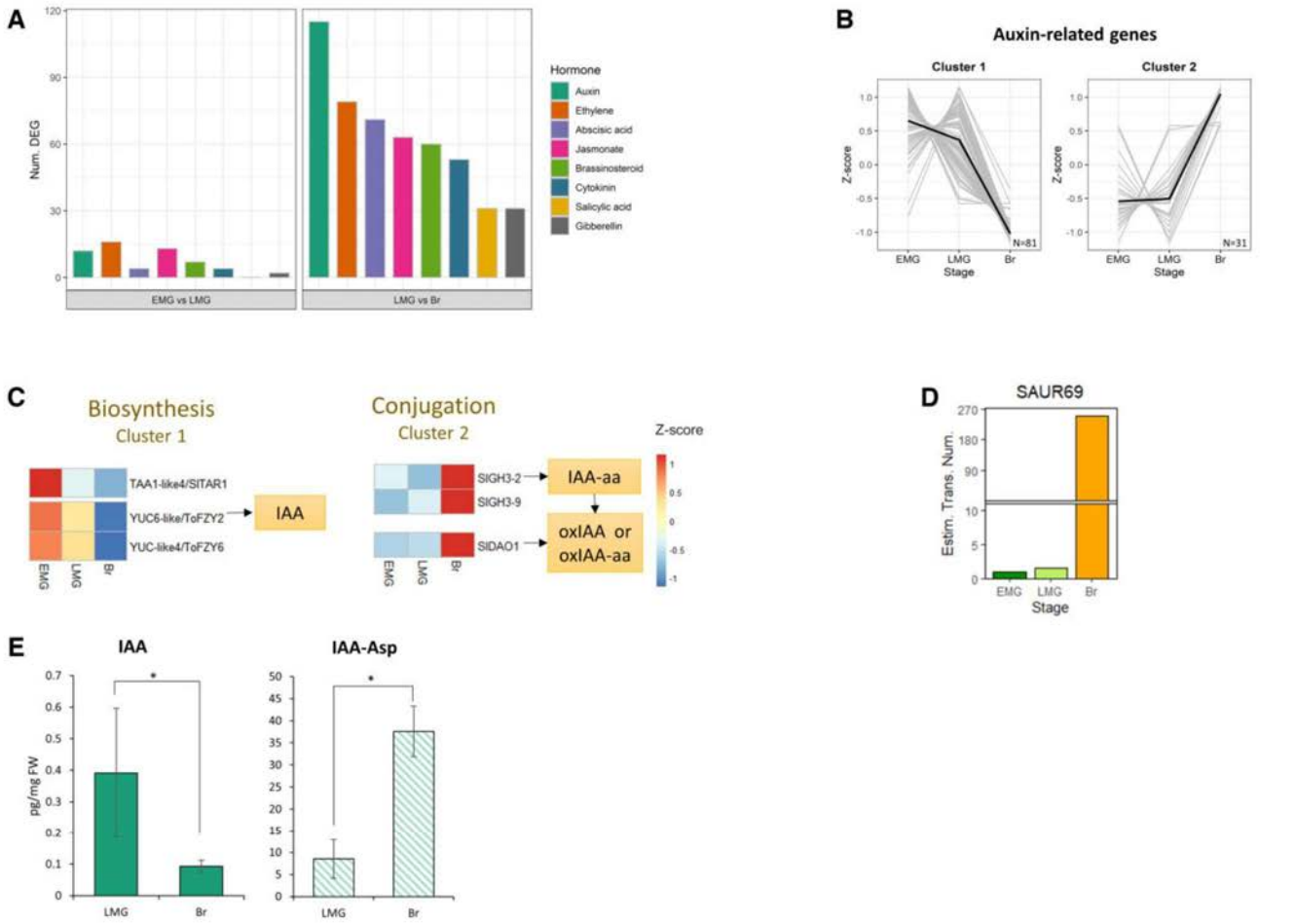

Figure 2 Hormone-associated DEGs during the transition to ripening. A, Number of DEGs related to each hormone at two transition stages EMG versus LMG and LMG versus Br (adjusted $P < 0.05$). B, Cluster analysis of auxin-related DEGs at pre-ripening stages. C, Heatmap the expression level of genes involved in auxin biosynthesis (IPA pathway) and conjugation. D, Estimated transcript number of *SlSAUR69* at pre-ripening stages. E, Endogenous levels of free IAA and its conjugated form IAA–Asp at the initiation of ripening. Results shown are mean ± SE, based on three independent biological replicates. Statistical significance was determined using Student's *t* test: $^*P < 0.05$.

the data suggest that a fundamental shift in auxin metabolism occurs at the onset of ripening, likely through cross-talk with ethylene, as reported previously (Hao et al., 2015; Liu et al., 2018; Shin et al., 2019).

Auxin treatment delays the transition to ripening

Considering the high number of DEGs related to auxin during the transition to ripening, we set out to further explore the role of this hormone in ripening initiation by performing two successive treatments with exogenous auxin (IAA, 100 μM) at 33 DPA (EMG) and 34 DPA (Figure 3A). Because transcriptomic profiling showed that similar changes in the overall gene expression occur in the gel and the pericarp, albeit with some delay in the latter tissue, we decided to address the impact of auxin treatment on the whole fruit. In contrast to the mock-treated fruit that undergo typical ripening as indicated by the color change, the auxin-treated fruit exhibited delayed and incomplete change in color until 12 days after treatment (Figure 3B). This is consistent with the previous reports indicating that auxin acts as a negative regulator of fruit ripening (Su et al., 2015; Li et al., 2016, 2017; Tobaruela et al., 2021). To further decipher the changes induced by auxin treatment during the initiation of ripening, we performed genome-wide transcriptomic profiling on fruit samples collected at three time points. The first transcriptome was from fruit sampled 6 h after the first injection and addressed potential wound effect of the treatment as well as early auxin responses. The second and third transcriptomes correspond to fruit sampled 24 h and 72 h after the second injection, respectively (Figure 3A).

PCA indicated that 6-h and 24-h transcriptome data cluster together, suggesting that these two time points are representative of short-term responses to exogenous auxin treatment and probably responses to mechanical wounding due to the injections (Figure 3C). In contrast, transcriptomes corresponding to 6-h and 24-h samples are separated from the 72-h samples which likely represent long-term responses to auxin. Consistent with this hypothesis, the total numbers of DEGs between auxin-treated and mock samples were 14,038 DEGs and 13,140 after 6 h and 24 h, respectively, and

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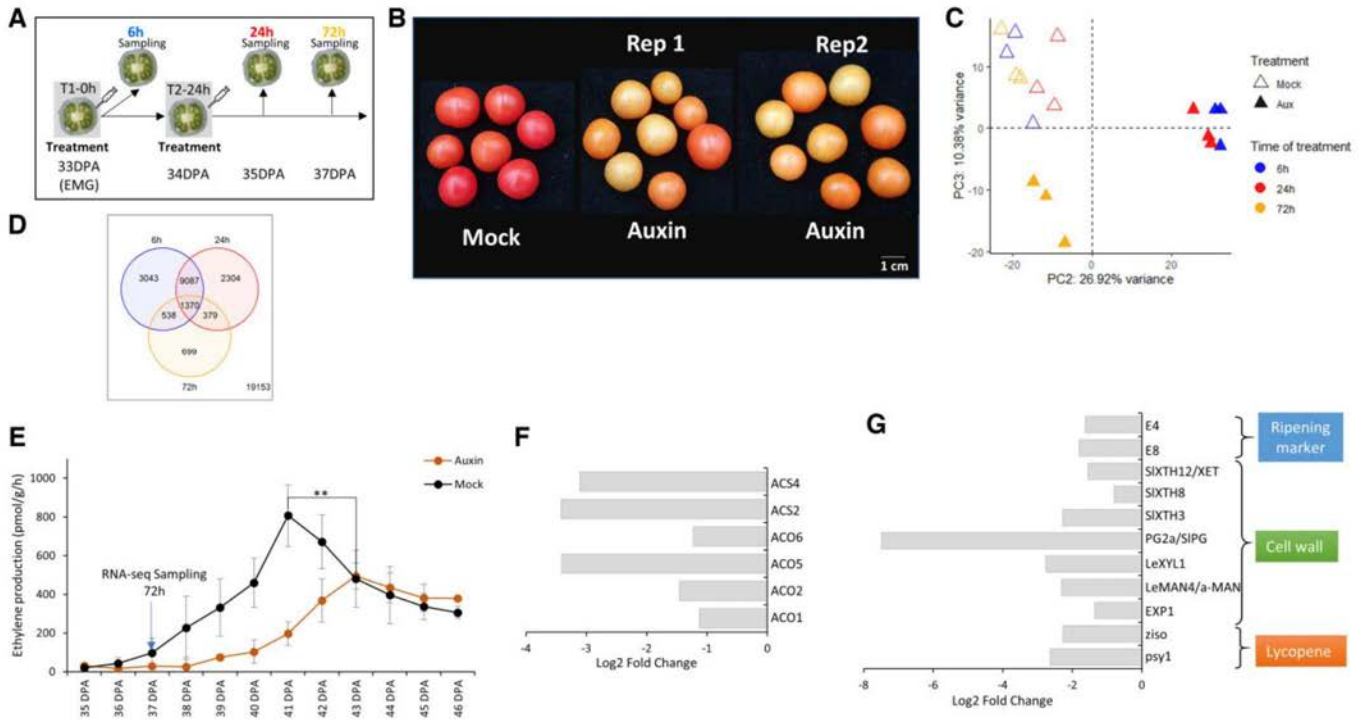

Figure 3 Impact of exogenous auxin treatment on tomato fruit ripening. A, Experimental design of the study. Tomato fruits were injected at 33 DPA (T1) with mock or auxin and the treatment was repeated after 24 h (T2). Samples were collected at three time points: 6 h after T1, 24 h after T2, and 48 h after T2. B, Ripening phenotype at 45 DPA (12 days after T1) of mock and auxin-treated fruits. The pictures are representative of at least 10 independent replicates showing the same trend. Among these independent replicates, three were used for the transcriptomic profiling by RNA-Seq. Images were digitally extracted for comparison. C, PCA of transcriptomic profiles of mock or auxin-treated fruits at 6 h after T1, 24 h, and 72 h after T2. Each symbol represents one replicate. D, Venn diagrams of the number of DEGs (auxin vs. mock) at 6 h after T1, 24 h, and 72 h after T2. E, Ethylene production in tomato fruits treated with mock (black line) or auxin (orange line) (mean ± SD, $n = 10$, based on three independent biological replicates). F, G, Bar plot representing log2(fold change) values of DEGs at 72 h after treatment, auxin vs. mock (adjusted $P < 0.05$) for ethylene biosynthesis genes (F) and ripening-associated genes (G). T1, first treatment; T2, second treatment. Asterisks indicate significant differences determined by Student's *t* test at $^{**}P < 0.01$.

thereafter dropped to 2,986 at 72 h. Most of the DEGs, either up- or downregulated, are shared between the 6-h and 24-h samples (Figure 3D), revealing that auxin treatment induces massive transcriptomic changes early after the injection. Thereafter, the transcriptomic landscape stabilized at 72 h after treatment. We therefore postulated that the 72-h transcriptome data, rather than the 6 h or 24 h ones, reflect a sustainable auxin effect on ripening. This result prompted us to focus our study on the 72-h samples to uncover the genes and networks altered by auxin during the onset of ripening.

To assess the potential effect of auxin treatment on ripening, we first monitored ethylene production in mock- and auxin-treated fruits. The rise in ethylene production is delayed in auxin-treated fruits, which also produced less ethylene than mock-treated fruit (Figure 3E), supporting the hypothesis that auxin negatively controls ethylene production during climacteric fruit ripening. Consistent with this interpretation, transcript levels of the ethylene biosynthesis genes *ACS2*, *ACS4*, *ACO1*, *ACO2*, *ACO5*, and *ACO6*, known to be involved in System-2 ethylene production, were all downregulated 72 h after auxin treatment (Figure 3F).

In order to address whether the reduced ethylene production in IAA-treated tomatoes is due to their inability to induce autocatalytic System-2, we treated the fruit with propylene, an ethylene analog known to mimic the hormone effects. Propylene treatment restored normal ripening and ethylene production in auxin-treated fruits. Notably, both mock- and auxin-treated fruit challenged with 100 ppm propylene leads to almost a complete recovery of ethylene production, indicating that auxin treatment does not hamper the activation of System-2 but rather impairs ethylene biosynthesis (Supplemental Figure 6, A and B). In line with the reduced ethylene production, the expression of *E4* and *E8*, well-known ethylene-responsive and ripening-regulated genes, was also downregulated. Moreover, many important, well-characterized ripening-associated pathways were altered by auxin. For instance, the carotenoid biosynthesis genes *PSY1* and *ZISO* are downregulated in auxin-treated fruits, consistent with the faint red pigmentation in these fruits (Figure 3G). Likewise, the expression of cell wall-related genes, including *EXPANSIN 1* (*EXP1*), *α-MAN*, *LeXYL1*, *POLYGALACTURONASE 2a* (*PG2a*), *SlXTH3*, *SlXTH8*, and *XET*, is reduced in auxin-treated fruit (Figure 3G). Together, these data indicate that auxin treatment alters multiple ripening-

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associated pathways through impairing ethylene biosynthesis.

Auxin alters the expression of TF genes encoding key regulators of fruit ripening

To further decipher how auxin alters the transcriptomic reprogramming underlying the transition to ripening, we analyzed the impact of auxin treatment on the expression of TF genes. A total of 174 TF genes belonging to 35 different TF families are differentially expressed in auxin-treated fruit. Among these, 14 families exhibited members undergoing either up- or downregulation, 10 families exhibited only downregulation, and 11 families exhibited only upregulation (Figure 4A). Consistent with auxin being a negative regulator of ripening, TF genes encoding key regulators of tomato fruit ripening, including *RIN*, *NOR*, *AP2a*, *NAC1*, and *FUL1*, were all downregulated in auxin-treated samples (Figure 4B).

Because the ERF family had the highest number of downregulated genes upon auxin treatment, and considering the important role ascribed to ERFs in mediating ethylene responses, we analyzed their expression patterns during ripening initiation. Notably, among the 77 *ERF* genes present in the tomato genome, 42 (68%) showed a statistically significant change in their transcript levels during the transition to ripening, and based on the expression profiles, two ERF clusters were identified; one cluster includes 13 genes upregulated at the onset of ripening, and the second cluster includes 39 genes that are downregulated (Figure 4C). Interestingly, six out of the nine *ERF* genes that are upregulated during ripening initiation in untreated fruit are downregulated by auxin treatment, including *SlERF.E1* and *SlERF.E4*, both known to be highly induced at the onset of ripening (Figure 4C). On the other hand, among the 33 *ERF* genes that are downregulated during ripening initiation, 12 are differentially regulated by auxin, among which five show upregulation (Figure 4C). The data reveal the strong impact of auxin on the expression of several *ERF* genes, which may reflect altered ethylene responses following auxin application. The data are consistent with previous reports showing that, in addition to their response to ethylene, *ERF* genes can also be regulated by auxin (Pirrello et al., 2012).

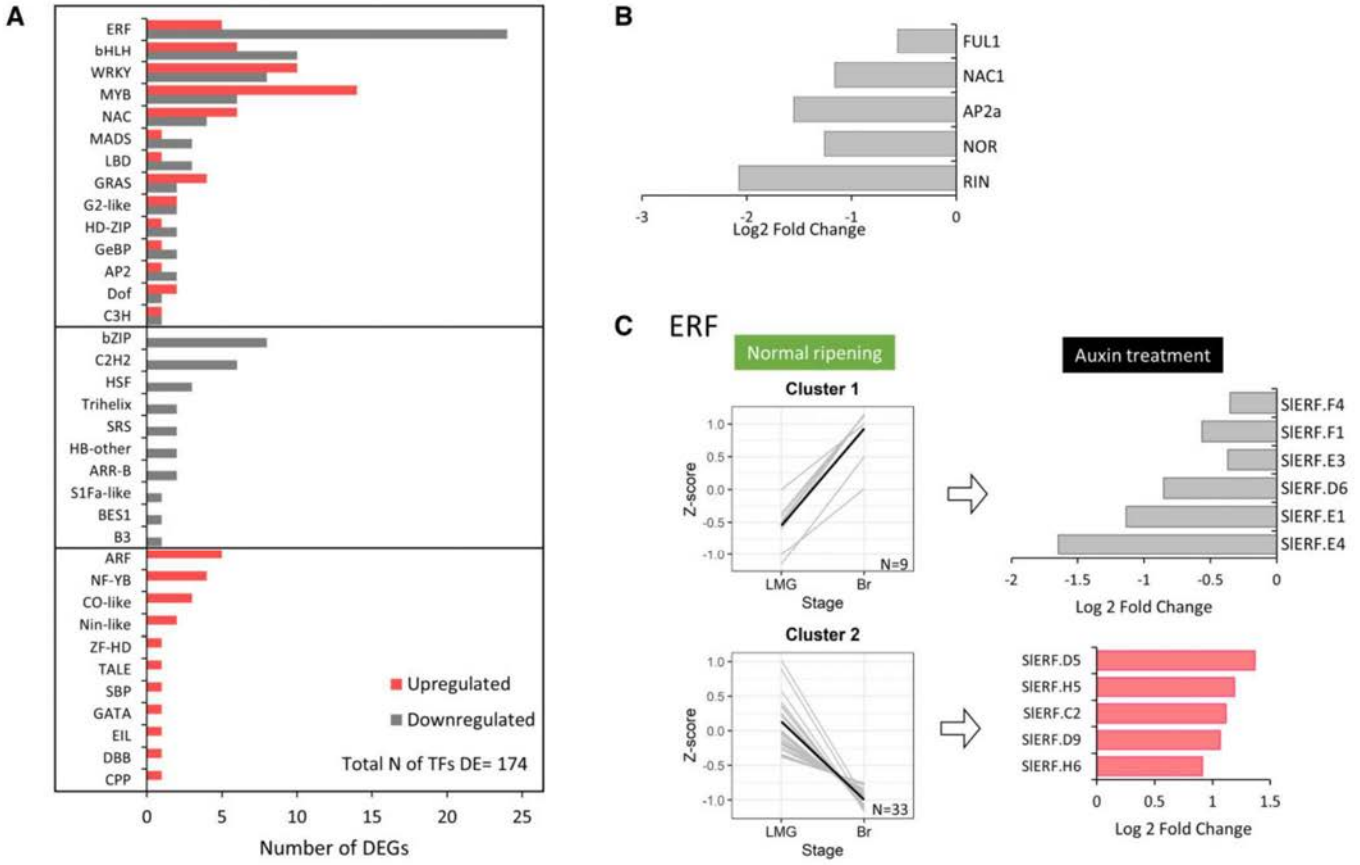

Figure 4 Impact of auxin treatment on the expression of transcription factor genes that are DEGs. A, Number of TF genes being DEGs 72 h after auxin treatment in each family. Downregulated genes are shown in grey (log2(fold change) < 0, adjusted $P < 0.05$), and upregulated genes in red (log2(fold change) > 0, adjusted $P < 0.05$). B, Expression of key ripening regulator TFs after 72 h of auxin treatment. C, Clustering of *ERF* genes being DEGs at the onset of ripening in normal ripening fruit (left). Bar plot representing log2(fold change) values of the expression level of ERF after auxin treatment (right).

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Auxin treatment alters hormonal signaling during ripening

The transcriptomic profiling indicated that the transition to ripening is associated with modulation of several hormones (Figure 2A). Strikingly, among the 673 hormone-related DEGs during ripening (Supplemental Figure S3B; Supplemental Table S2), 113 exhibited DE following auxin treatment (Supplemental Table S2). Under normal ripening, genes related to ethylene are distributed in two clusters. Cluster 1 contains 29 genes that are upregulated at the onset of ripening, 17 of which are downregulated in response to auxin treatment (Figure 5A). Interestingly, these genes whose expression is modulated by auxin are involved in all steps of ethylene signaling, including biosynthesis (*ACS2*, *ACS4*, *ACO1*, *ACO2*), signal transduction (*ETR3*, *ETR6*, *EBF2*, *EBF3*), and transcriptional activation (*SlERFE.E1*, *SlERF.E4*). Cluster 2 includes 48 genes that are downregulated at the transition to ripening, including five ERFs (*SlERF.C2*, *SlERF.D5*, *SlERF.D9*, *SlERF.H5*, and *SlERF.H6*). The copper transporter *RAN1* genes exhibit upregulation upon auxin treatment (Figures 4, C and 5,A). These data indicate that auxin treatment greatly disturbs the expression of many ethylene-associated genes, including those involved in System-2 ethylene production, likely causing the observed delayed ripening. This observation is consistent with the requirement for a decline in auxin signaling essential for initiation of climacteric ripening (Shin et al., 2019).

Abscisic acid has been reported to influence fruit ripening in different ways, depending on the mode and timing of application (Diretto et al., 2020). Cluster analysis shows that 20 ABA-related genes are upregulated (Cluster 1) during normal ripening and four of these genes are downregulated by auxin treatment, including *SlCYP707A3*, an ABA 8′-hydroxylases involved in ABA oxidative catabolism, as well as the putative ABA response genes *HVA22K-like* and *HVA22K-like1* (Figure 5B). Cluster 2 includes 41 genes downregulated during ripening, and among these, auxin treatment remarkably upregulates *MOCOS-like2* and *AAO4-like5* 2 genes

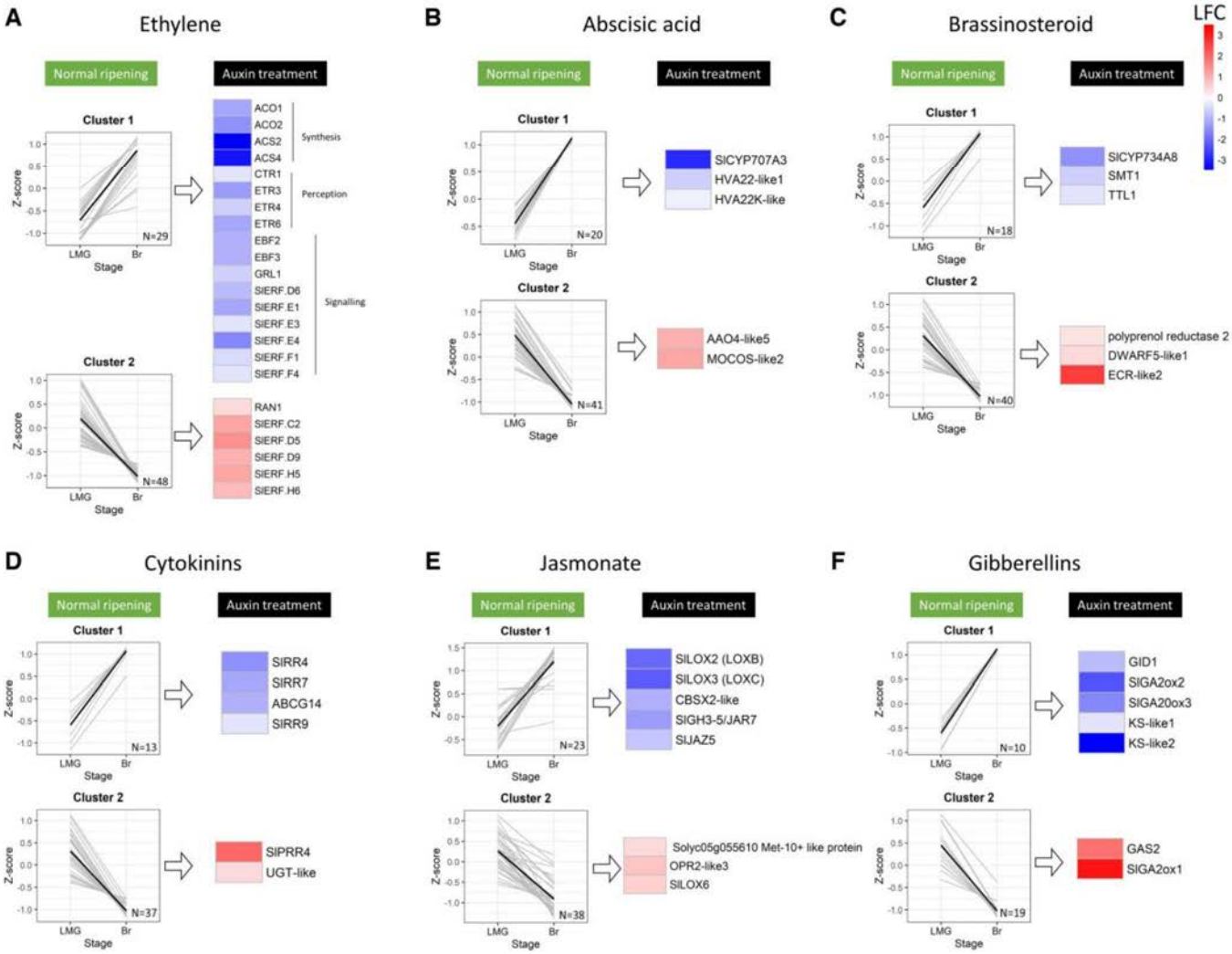

Figure 5 Impact of auxin treatment on the expression of hormone-related genes. Clustering of hormone-related genes in normal ripening (left) or auxin-treated (right). Right shows genes displaying opposite trend upon auxin treatment (72 h). A, Ethylene, (B) abscisic acid, (C) brassinosteroid, (D) cytokinins, (E) jasmonate, and (F) gibberellins. Square color per gene represents log2(fold change). *N*, number of genes. Adjusted $P < 0.05$.

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involved in ABA biosynthesis (Figure 5B). These data indicate that the expression of ABA-related genes is disturbed by exogenous auxin treatment.

Several studies have reported on a positive role for BR in fruit ripening (Hu et al., 2020). Analysis of BR-related genes undergoing differential regulation at the transition to ripening showed that 18 genes are upregulated (Cluster 1), while 40 are downregulated (Cluster 2; Figure 5C). Auxin treatment resulted in downregulation of three genes in Cluster 1, including *SlCYP734A8*, a gene encoding an enzyme putatively involved in BR catabolism. Upon auxin treatment, three genes involved in BR biosynthesis belonging to Cluster 2 were upregulated (Figure 5C). These results support the hypothesis that auxin promotes BR biosynthesis.

Studies on the role of CK in ripening are scarce, although it has been reported that CK levels decrease during ripening (Davey and Van Staden, 1978). Cluster analysis of genes related to CK showed that 13 genes are upregulated (Cluster 1) and 37 are downregulated (Cluster 2) at the onset of ripening. Within Cluster 1, three genes were downregulated after auxin treatment, including *SlRR4* and *SlRR7*, two Type-ARABIDOPSIS RESPONSE REGULATORS (ARRs) known to be negative regulators of cytokinin signaling, as well as *ABCG14*, a putative transporter of CK. In Cluster 2, two genes were upregulated after auxin treatment, including the ARABIDOPSIS PSEUDO-RESPONSE REGULATORS *SlPRR4* gene, described as effectors of cytokinin signal (Figure 5D), suggesting that auxin may enhance cytokinin signaling during the transition to ripening.

Cluster analysis of genes related to JA revealed 23 upregulated (Cluster 1) and 38 downregulated (Cluster 2) genes during ripening. Among Cluster 1 genes, five were downregulated by auxin treatment, including the main lipoxygenases contributing to JA biosynthesis, as well as C5 and C6 flavor volatiles, *SlLOX2* and *SlLOX3* (Figure 5E). Interestingly, *SlLOX2*, also known as *TomLoxC*, is the main contributor to tomato aroma (Shen et al., 2014). This observation is consistent with the previously described negative role of auxin in desirable volatile production (Tobaruela et al., 2021). Importantly, *SlJAR7*, a GH3 involved in the transformation of JA to its active form JA-Ile, is also downregulated, suggesting a negative role of auxin in JA biosynthesis. Surprisingly within Cluster 2, three genes annotated as putatively involved in JA biosynthesis are upregulated after auxin treatment (Figure 5E).

Exogenous application of GA was reported to delay tomato ripening (Dostal and Leopold, 1967). We, therefore, examined the behavior of genes related to GAs during normal fruit ripening, showing that 10 genes are upregulated (Cluster 1), while 19 are downregulated (Cluster 2; Figure 5F). Within Cluster 1, five genes are downregulated upon auxin treatment, including those related to GA biosynthesis *ent*-kaurene synthase *KS-like1* and *KS-like2*, a gibberellin 20-oxidase (*GA20ox3*), and a gibberellin catabolism gene, gibberellin 2-oxidase 2 (*SlGA2ox2*). Within the Cluster 2 downregulated genes, two corresponding to 2-oxoglutarate-dependent dioxygenase (*GAS2*), encoding enzymes mediating the last step in biosynthesis of the bioactive form of GA, DHGA12, undergo upregulation after auxin treatment (Figure 5F).

Altogether, our data suggest that auxin is capable of altering the expression of genes involved in the biosynthesis, catabolism, or signaling of multiple hormones during the transition to the ripening of tomato fruit.

Discussion

Fruit ripening is initiated in the gel

Fruit ripening is a complex process regulated by internal signals such as hormones and external cues like light and temperature. The developmental transition associated with ripening relies on major transcriptomic reprogramming, leading to a large number of biochemical and physiological changes, including changes in color and texture. Our knowledge of the mechanisms regulating fruit ripening has substantially progressed over the last several decades, and recent reports indicated that key ripening transcription factors are induced first in the locular gel prior to the pericarp (Giovannoni et al., 2017; Shinozaki et al., 2018). Most studies addressing fruit ripening have focused on the characterization of events occurring in the pericarp while neglecting the changes in locule and placenta tissues, although few studies indicated that the first changes that herald the onset of ripening occur in the locular gel at the time this inner tissue undergoes liquefaction with an early increase in ACC synthase activity in the gel tissue (Brecht, 1987; Van de Poel et al., 2014). In the case of climacteric fruit, the onset of ripening is a key step marked by the acquisition of ripening competency. The high number and vast diversity of TF families engaged in the transition to ripening revealed by our study reflects the complexity of this developmental process. Our analysis of the TF genes throughout fruit ripening suggests spatiotemporal specialization of distinct family members, thereby defining putative biologically relevant regulatory genes. Transcriptomic profiling of the transition to ripening in tomato fruit performed in our study confirms that the key ripening regulators *RIN* and *NOR* are first induced in the gel tissue between EMG and LMG stages, indicating that fruit ripening is initiated in the locule compartment (Supplemental Figure S2). DE analysis identified over 900 TF genes belonging to 48 different families putatively involved in the transition to ripening, reflecting the complexity of this developmental process. Among these genes, 13 members of the *bHLH* gene family and 12 members of the *GRAS* family undergo significant changes in their transcript levels during the early stages of ripening (Figure 1D; Supplemental Table S1). This observation is in line with the reported downregulation of SlbHLH95 that affects accumulation of total carotenoids, lycopene, as well as ethylene sensitivity (Zhang et al., 2020). Likewise, silencing of *SlGRAS38* results in lower lycopene content and reduced ethylene

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production in tomato fruit, while the overexpression of *SlGRAS4* leads to premature ripening (Liu et al., 2021). Moreover, among the group of TFs that show DE in locular gel tissue earlier than in pericarp, *SlAP2a* has been demonstrated to be a negative regulator of ripening initiation and ethylene production and a positive regulator of chlorophyll degradation and carotenoid biosynthesis (Chung et al., 2010; Karlova et al., 2011; Wang et al., 2019). Overall, the data provide targets for future studies aiming to further decipher the regulatory network underlying the ripening process in tomato fruit.

Transition to ripening is a multihormone-controlled process with a prominent role for the interaction between auxin and ethylene

Given the central role of ethylene in climacteric fruit ripening, a large number of studies have focused on the mode of action of this hormone, whereas comparatively, the roles of other hormones in this transition are less well understood (Grierson, 2014; Liu et al., 2015). Therefore, a major challenge is to gain a comprehensive understanding of the molecular circuits underlying fruit ripening and to uncover the network of interactions between various hormones. Our data support the requirement for a reprogramming of multiple plant hormones at the onset of ripening. Indeed, we observed significant alterations in the expression of genes associated with all of the hormones that we examined, including auxin, ethylene, ABA, BR, CK, SA, JA, and GA. Moreover, the transition to ripening in tomato fruit involves an active interplay between auxin and ethylene. This result is consistent with our previous work showing that ripening initiation is associated with decreased auxin signaling that results in increased ethylene sensitivity, in turn leading to stimulation of System-2 ethylene production triggering climacteric ripening (Shin et al., 2019; Li et al., 2021).

Interestingly, ethylene treatment of IAA-treated fruits restores full ripening (Supplemental Figure S6A), and System-2 ethylene production can be induced by propylene in IAA-treated fruits (Supplemental Figure S6B). The response to propylene is a classic test for the initiation of autocatalytic ethylene synthesis during climacteric ripening (McMurchie et al., 1972). The restored autocatalytic ethylene biosynthesis in IAA-treated fruits suggests that the induction of System-2 ethylene production is tightly regulated by an ethylene/IAA balance in the fruit tissues. These results support the hypothesis that the decrease of auxin content is required for climacteric process to proceed at the onset of ripening. It is known that free auxin levels are highly dependent on conjugation to sugars and amino acids and that this process is integral to auxin homeostasis. While a comprehensive and accurate quantification of auxin and its conjugates at the onset of ripening is still lacking, our data reveal a depletion of free auxin at the onset of ripening and a concomitant increase in conjugated IAA–Asp. The study also revealed upregulation of several *GH3* genes, supporting the hypothesis that modulation of auxin homeostasis is a key step during the transition to ripening. Moreover, our transcriptomic profiling revealed that *SlSAUR69* is highly expressed at the Br stage, supporting the idea that auxin transport and tissue distribution may also contribute to the control of auxin homeostasis. Indeed, SlSAUR69 has been described as a negative regulator of polar auxin transport, generating auxin minima that result in enhanced ethylene sensitivity (Shin et al., 2019).

High auxin levels seem to impair all ripening-associated processes. Indeed, fruits treated with IAA display delayed ripening resulting in fruit that fail to reach full red color (Figure 3B), consistent with the downregulation of carotenoid biosynthesis genes (Figure 3G). The impaired ripening is also associated with downregulation of genes encoding cell wall modifying enzymes. Auxin and ethylene cross-talk has been reported to operate in many physiological processes including fruit ripening. It was shown that 7 days after auxin treatment, the transcript levels of genes involved in System-1 ethylene production are enhanced, whereas a high methylation status of genes involved in System-2 ethylene biosynthesis is maintained, resulting in the repression of their expression (Li et al., 2016). Our study shows that auxin treatment also results in downregulation of the key ripening gene *RIN*, known to control the expression of several ripening-associated genes encoding ethylene biosynthesis enzymes such as *ACS2* and *ACS4*, the ethylene receptor *ETR3*, cell-wall softening enzymes *PG2a* and *EXP*, carotenoid synthesis enzymes *PSY* and *ZDS* as well as TFs like *NAC-NOR*, *CNR*, *AP2a*, and *FUL1/2* (Fujisawa et al., 2011). This pattern of regulation raises the hypothesis that auxin may act through RIN to control the expression of ripening-related genes, in agreement with the recently elaborated model, in which ethylene initiates ripening at the MG stage, which in turn induces *SlSAUR69*, involved in auxin depletion and enhanced ethylene sensitivity (Shin et al., 2019; Li et al., 2020). Our data support this model by showing that high auxin levels block System-2 genes, and that auxin conjugation is a major component involved in the regulation of auxin homeostasis during normal fruit ripening (Figure 6). Nevertheless, the ability of ethylene to trigger ethylene synthesis suggests that the shift from System-1 to System-2 ethylene production is not dependent on auxin only. Although based on our present data, it is not possible to make a solid assumption in this respect, a plausible hypothesis would be that high concentrations of ethylene are required to reverse the inhibitory effect of auxin, which implies that the inhibition of System-2 by auxin can only be alleviated when ethylene concentrations reach a certain threshold level. More experiments are needed to validate this hypothesis.

Overall, the study unravels in a renewed way the transcriptomic reprogramming associated with the transition to ripening of tomato fruit and highlights the

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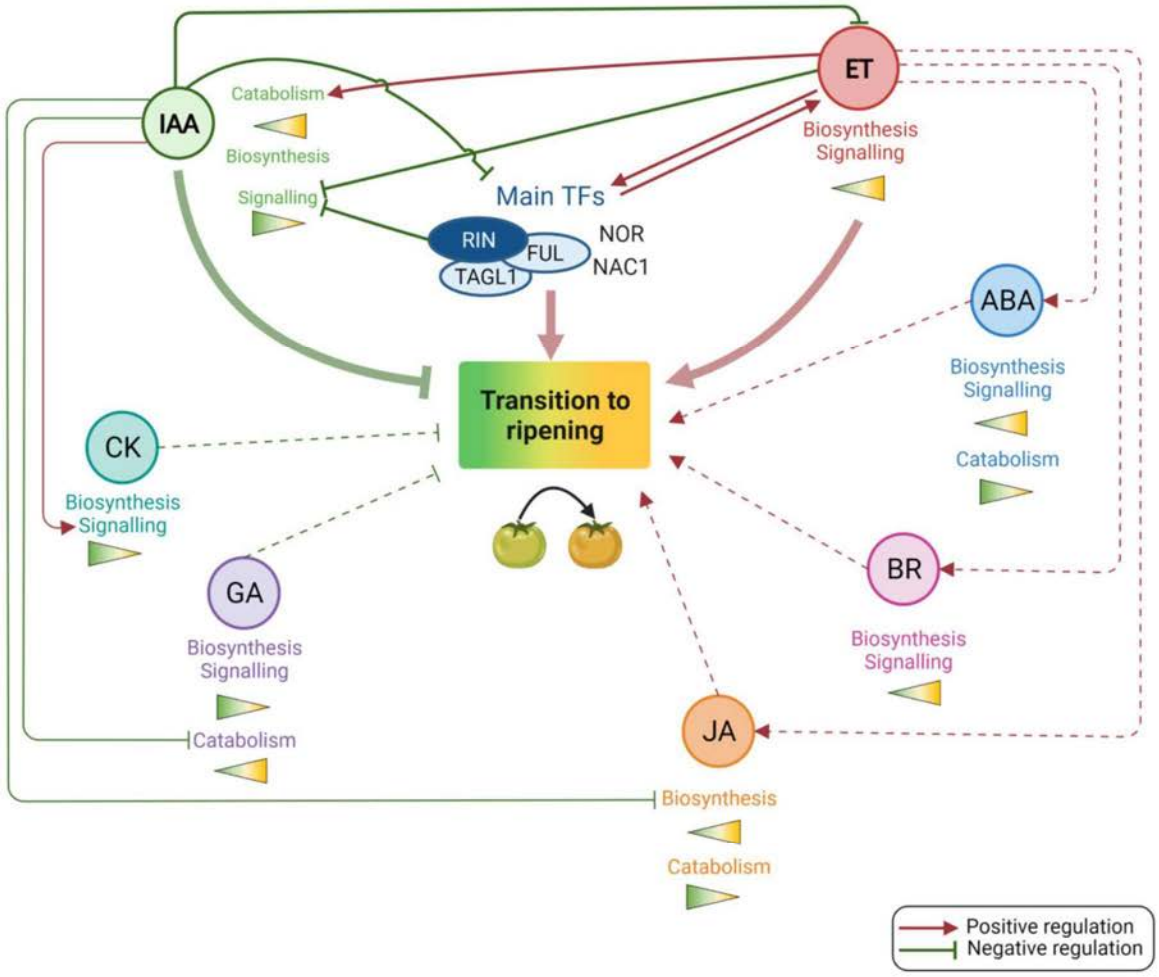

Figure 6 Multihormonal control of the transcriptomic changes associated with the onset of tomato fruit ripening. Ethylene biosynthesis and signaling increases at LMG which promotes ripening initiation in conjunction with key TFs (*RIN*, *FUL1*, *TAGL1*, *NOR*, and *NAC1*). Concomitantly, IAA concentration decreases after LMG stage via downregulation of auxin biosynthesis genes (*TAA1-like4*, *YUC-like4*, and *YUC6-like*) and IAA inactivation via upregulation of auxin conjugation/oxidation genes (*SlGH3.2*, *SlGH3.9*, and *SlDAO1*). These changes in free IAA and conjugated IAA forms are promoted by ethylene. At the ripening onset, genes encoding negative regulators of auxin signaling (*ARF2*, *ARF17*, *AUX/IAA3*, and *SlSAUR69*) are upregulated, leading to the inhibition of auxin signaling and response (Hao et al., 2015; Shin et al., 2019), while positive auxin signaling genes (*TIR1* and *ARF6A*) are downregulated. RIN has been reported to reduce auxin signaling through inducing *SlSAUR69* expression, which alters tissue distribution of auxin by blocking its transport (Shin et al., 2019). High levels of auxin hamper the onset of ripening, through downregulating key ripening regulators (*RIN*, *FUL1*, *TAGL1*, *NOR*, and *NAC1*), System-2 ethylene biosynthesis and signaling genes (*ACS2*, *ACS4*, *ACO1*, *ETR3*, *CTR1*, *AP2a*, and *ERF.E1*). Auxin also represses JA biosynthesis through inactivating their biosynthetic genes (*LOXB*, *LOXC*, and *SlJAR7*). On the other hand, auxin promotes GA signaling by blocking GA catabolism genes (*SlGA2ox2*). Also, auxin seems to promote CK by activating positive regulators of CK signaling genes (*SlPRR4*) and repressing negative regulators (*SlRR7* and *SlRR4*). Notably, consistent with their roles in promoting different aspects of ripening, BR biosynthesis and signaling genes (*SlCPD*, *SlCYP85A1*, *SlBR1*, *SlBES1*, and *SlBZR1*) and ABA biosynthesis and signaling genes (*SlSDR*, *SlMoCo*, *SlPYL1/2*, *SlSnRK2.1*, *SlSnRK2.3*, *SlSnRK2.7*, and *SlABI5-like*) are upregulated (Zhang et al., 2009; Zhu et al., 2015). Dotted arrows indicate possible regulation.

contribution of inner tissues to this process. Moreover, while so far, most transcriptomic profiling of fruit ripening has mainly focused on the changes occurring in pericarp tissues between MG and Br stages, our study addresses the changes between EMG and LMG stages, in gel and pericarp separately. The data reveal that the transition to ripening is initiated at first in locular gel before extending to pericarp. This is consistent with our recent findings that locular tissues play an essential role in controlling fruit texture and firmness (Huang et al., 2021). Our genome-wide transcriptomic analysis reveals that a wide diversity of transcription factor families are engaged in the global reprogramming of gene expression, thereby highlighting the extent of the transcriptomic changes underlying the transition to ripening. In particular, the study identified transcription factors that are specifically regulated during the MG stage in the gel but not in pericarp, thereby providing potential targets toward deciphering the initial factors and events that trigger the transition to ripening. The potential roles of these transcription factors

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in the ripening program remain to be elucidated. In this regard, the outcome of our study provides an essential resource for future studies aiming to further decipher the regulation mechanisms of fruit ripening. Our data also bring evidence for a multihormonal control of the transition to ripening and show that altered auxin homeostasis disturbs the overall hormonal balance. The study reveals the antagonistic cross-talk between auxin and ethylene operating at this developmental shift. Building on the achievement of the present work, we propose a model enriched with the data that depicts the multihormonal control of the transcriptomic reprogramming leading to the transition from System-1 to System-2 of ethylene production at the onset of climacteric ripening (Figure 6).

Materials and methods

Plant material and sampling

Tomato (*Solanum lycopersicum L.* cv Micro-Tom) plants were grown under standard culture chamber conditions (14 h: 10 h, 25°C: 20°C, light: dark cycle, respectively, 80% relative humidity, 250 mol m^{-2} s^{-1} intense light). The flowers were tagged at the anthesis stage and fruits were sampled at different stages. For hormonal profiling and transcriptomic analysis in normal ripening conditions 10 fruits from 6 different plants per replicate were collected at EMG (33-day post anthesis [DPA]), LMG (36 DPA), Breaker (Br), and Br + 4 days. We sampled tomato at different DPAs around the MG stage, which allowed defining two categories differing by their ability to reach full ripening with a few days lag. In this way, we were able to define fruits corresponding to 33 DPA as EMG because 90% of them reach the full ripening stage 2–4 days later than LMG (36 DPA) of which 99% were able to fully ripe. Then gel (without seeds) and pericarp were separated and samples were frozen in liquid nitrogen, immediately after separation and stored at −80°C. Three independent biological replicates were performed for each experiment.

Hormonal profiling

Frozen fruit samples were ground with Tissue Lyser II (Qiagen, France) by applying two cycles of 45 s at 300 Hz. A total of 300 mg of ground tissue was extracted with 700 µL of pre-cooled (−20°C) extraction methyl tert-butyl ether/methanol (75/5, v/v) solvent. After mixing by vortexing, samples were sonicated for 3 min in an ultrasonic bath. A volume of 700 µL of pre-cooled water/methanol (75/25, v/v) solution was added and the samples were again thoroughly vortexed for 30 s and sonicated for 3 min. The samples were centrifuged at 14,000 rpm for 3 min at 5°C. Around 500 µL of the hydrophilic phase was transferred to a fresh 1.5-mL microcentrifuge tube and dried down using a SpeedVac concentrator at 35°C. The dried pellets were resuspended in acetonitrile/water (20/80, v/v) solution with a final concentration of 10 $mg{\cdot}mL^{-1}$. Analysis was performed by ultrahigh-performance liquid chromatography-multiple reaction monitoring (U-HPLC-MRM). U-HPLC system (Dionex Ultimate 3000, Thermo Scientific) was equipped with a Hypersil Gold AQ (100 × 2.1 mm, 1.9 µm Thermo Scientific) heated at 45°C. Five microliter of samples were injected. Separation was performed at a constant flow rate of 0.3 $mL{\cdot}min^{-1}$, in a gradient of solvents A (water + 0.05% v/v formic acid) and B (acetonitrile + 0.05% v/v formic acid): 1 min 5% v/v B; 8 min 5% to 96% v/v B; 1 min 96% v/v B, and re-equilibration to the initial conditions in 4 min. Mass spectrometer analysis was performed with a Qtrap 5500 mass spectrometer (AB Sciex) with electrospray ionization and MRM mode, as described by Pons et al. (2020). Phytohormones quantification was performed using Sciex OS software, concentration of standards is listed in Supplemental Table S3.

Auxin treatment

The IAA solutions were prepared at 100 µM in Milli-Q water at pH 5.6 and injected into fruits harvested at 33DPA (Su et al., 2015; Tobaruela et al., 2021). Fruits from the mock groups were injected with Milli-Q water alone. Injections have been performed using 40 µL of auxin or mock solution in the two opposite parts of fruits. Two successive treatments with exogenous auxin 24 h apart have been performed, the first at 33 DPA (EMG) and the second at 34 DPA. Tissues have been sampled for analysis 0 h, 6 h after the first treatment, and 24 h or 72 h after the second treatment (Figure 3A). Each condition includes 10 fruits collected from six different plants. Three independent biological repeats were performed for each experiment.

Ethylene and propylene treatment

Auxin and mock-treated tomato fruits 72 h after the second treatment (37 DPA), before any color change, were placed in an air-tight 22 L acrylic cabinet (Nalgene) with 10-ppm ethylene or 1,000-ppm propylene. The treatment was conducted continually; the gas environments (air, ethylene, and, propylene) were replenished every 24 h for 3 days, with at least three biological replicates for each treatment.

Ethylene production measurement

Five fruits treated with auxin, mock, auxin plus propylene, and mock plus propylene-treated fruits were placed in 120-mL jars 24 h after the second treatment (35 DPA). Jars were sealed and incubated at room temperature for 1 h, and 1 mL of headspace gas was injected into an Agilent 7820A gas chromatograph equipped with a flame ionization detector (Agilent, Santa Clara, CA, USA). Samples were compared with a reagent-grade ethylene standard of 4 ppm concentration and normalized for fruit weight. Three independent biological replicates were performed for each experiment.

RNA extraction

Fruit samples stored at −80°C were homogenized to powder with the ball grinder Tissue Lyser II (Qiagen, France) by applying two cycles of 45 s at 300 Hz. Total RNA from gel and

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pericarp of ten individual fruits at each developmental stage was extracted, using 200 mg of fruit powder, with ReliaPrep RNA Tissue Miniprep System kit (Promega, France, Ref. Z6112) according to the manufacturer's instructions. The total RNA sample was then treated with DNA-free DNA Removal Kit (Invitrogen, France) to remove DNA. The quantity and quality of RNA were assessed by measuring the optical density (OD) at 260 nm and 280 nm by a spectrophotometer (NanoDrop 330, Thermo Fisher Scientific) and 2% (w/v) gel electrophoresis.

RNA-Seq analyses

For each condition, three biological replicates were prepared. RNA quality was checked on an Agilent 2100 Bioanalyzer System, using the RNA 6000 Nano kit protocol (Agilent Technologies, Germany). RNA samples with RNA Integrity Number values of >7.5 were sent to Novogene Bioinformatics Technology Co., Ltd (Beijing, China) for cDNA library construction and sequencing on Illumina NovaSeq 6000 platform (Illumina, San Diego, CA, USA). Raw sequence corresponding to paired-end reads (2×150 bp) were treated as described by Althiab-Almasaud et al. (2021) and aligned to SLYMIC v.1.0 assembly and annotation of the *S. lycopersicum cv.* MicroTom reference genome (BioProject: PRJNA553986). The quality of alignments is listed in Supplemental Table S4.

DE and downstream analyses

DE analysis was performed with R software version 4.1.1 (https://www.r-project.org/) using the DESeq2 package version 1.30.1 with the default relative log expression (RLE) normalization method, encompassing biases caused by library size and relative size of transcriptomes (Maza et al., 2013; Love et al., 2014). The false discovery rate (FDR) was controlled by the Benjamini–Hochberg method. Genes were declared as DEGs with an adjusted $P_{(padj)} < 0.05$ using a multifactor design, then a likelihood ratio test was performed to determine if the increased likelihood of the data use in the full model is more than expected, which included the paired sample stage or treatment. The RLE normalization by DESeq2 considers that all the transcripts have the same length and does not normalize counts by transcript length. Thus, we extracted such normalized data and normalize it by transcript lengths to be able to compare transcript expressions in downstream analyses, as profile clustering. For this purpose, we divided DESeq2 normalized expressions by transcript sizes and multiplied them by the length of a raw read, as in the TomExpress platform (https://tomexpress.gbfwebtools.fr/). These normalized expressions can then be understood as (relative) estimations of transcript numbers. Lastly, the mean value of the biological replicates was calculated giving as a result the estimated transcript number for the given condition. PCA was performed with the plotPCA function of DESeq2. All graphs were plotted with ggplot2 version 3.3.3 R package. Hierarchical clustering and heatmap for the DEGs were generated with the pheatmap version 1.0.12 R package with Pearson correlation as the distance metric and a complete linkage method.

Identification of hormone-related genes in the tomato genome

Mercator4 V3.0 tool was used to automatically annotate the SLYMIC 1.0 gene/protein model 1.1 and MapMan4 to functionally categorize the genes (Schwacke et al., 2019), annotations were manually curated. In addition, annotations from Hu et al. (2021) were recovered and the database were expanded following the same pipeline (Supplemental Table S2).

Weighted gene co-expression network analysis

Co-expression network modules were identified using normalized expression values and the WGCNA package (v1.71) in R. Genes with a low level of expression below 10 and low coefficient of variation ($CV < 0.5$) among all samples were discarded and the remaining 9,563 genes were used for the analysis. The co-expression modules were obtained using the automatic network construction function with a soft threshold (power) of 8, TOMType was "signed", networkType was "signed hybrid", minModuleSize was 30, and mergeCutHeight was 0.15. The list of genes belonging to each module is available in Supplemental Table S5.

Gene ontology analysis

Gene ontology (GO) analysis of DEGs from gel and pericarp separately was performed by PANTHER GO-slim (Mi et al., 2019). Top 20 significantly enriched GO categories were selected with FDR < 0.05.

Accession numbers

Sequence data from this article can be found in the GenBank/EMBL data libraries under accession numbers listed in Supplemental Table S6. Correspondences between SLYMIC v.1.0 (Sly nomenclature) and ITAG 2.4 (Solyc) annotation (https://solgenomics.net/organism/Solanum_lycopersicum/) are available in Supplemental Table S6. All RNA sequences are available from the Sequence Read Archive at the National Center for Biotechnology Information, under accession PRJNA808237.

Supplemental data

The following materials are available in the online version of this article.

Supplemental Figure S1. Co-expression modules generated by WGCNA.

Supplemental Figure S2. Transcriptomic kinetics of main ripening TFs.

Supplemental Figure S3. GO enrichment.

Supplemental Figure S4. Transcriptomic profile of key genes associated with hormones at the onset of ripening.

Supplemental Figure S5. Endogenous levels of different hormones at ripening initiation.

Supplemental Figure S6. Effect of exogenous auxin, ethylene, and propylene treatment on fruit ripening.

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Supplemental Table S1. Solanum lycopersicum putative TF genes differentially expressed in this study.

Supplemental Table S2. Hormone-related DEGs in this study.

Supplemental Table S3. Concentration of standards used for the hormone profiling.

Supplemental Table S4. Report of the counts of reads that map to a single location and summarized at the gene level.

Supplemental Table S5. Module assignment for the 9,563 genes selected for WGCNA.

Supplemental Table S6. Accession number correspondence between Solyc, Sly, and Gene Bank.

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Conflict of interest statement. The authors declare no conflict of interest.

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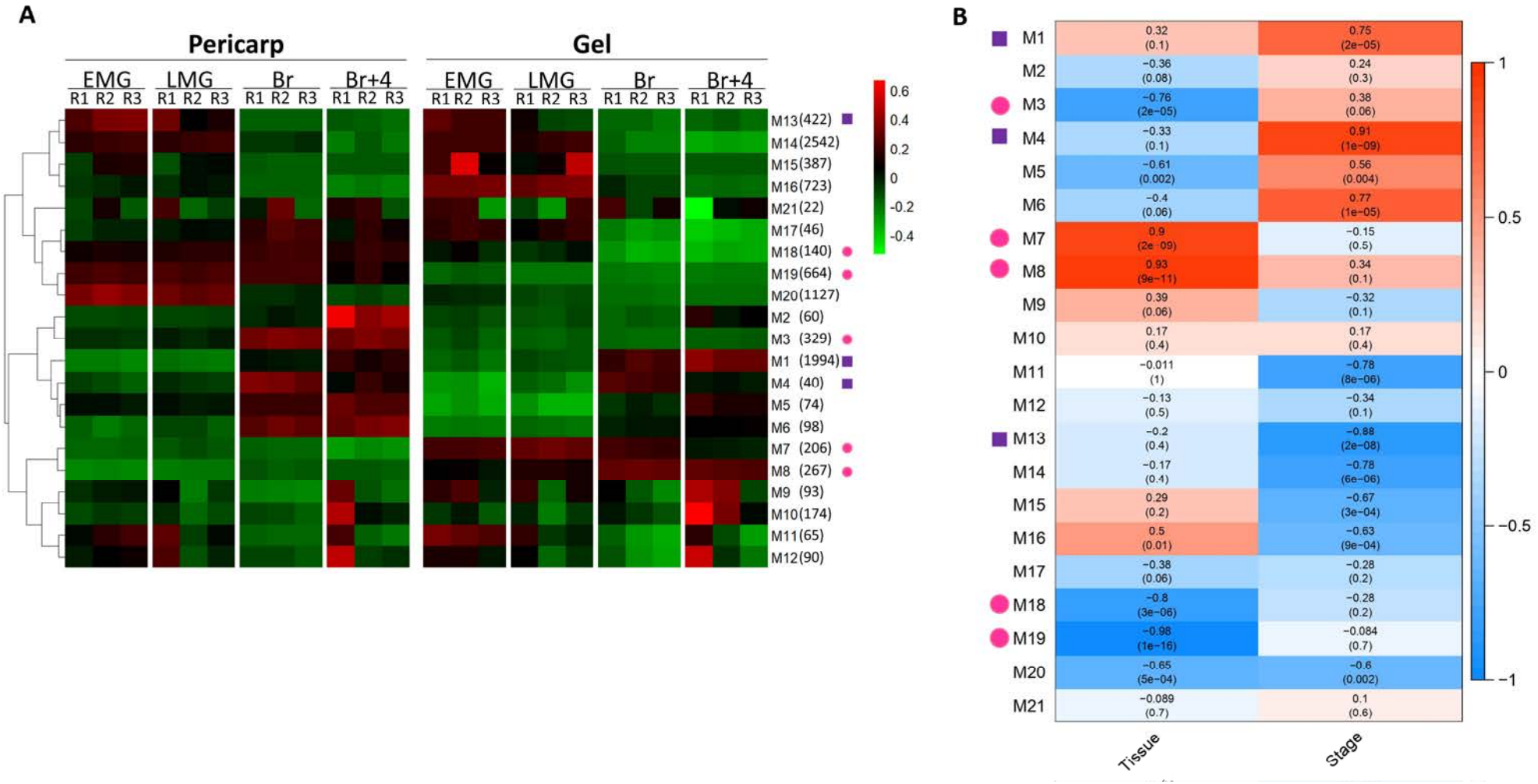
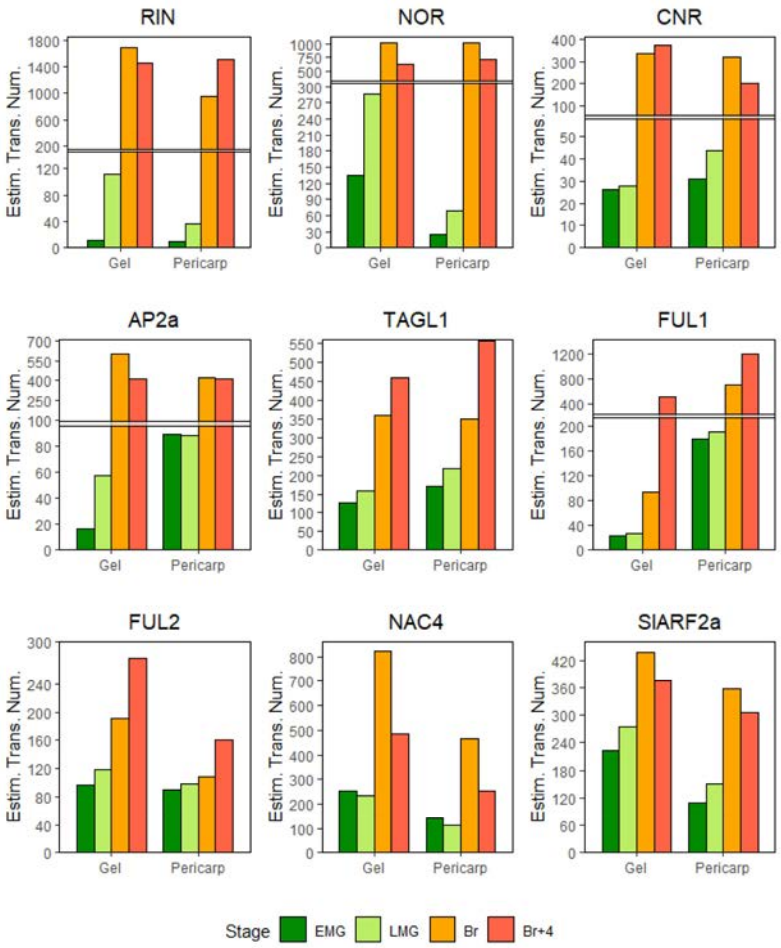
Supplementary tables can be found at the end of this manuscript.

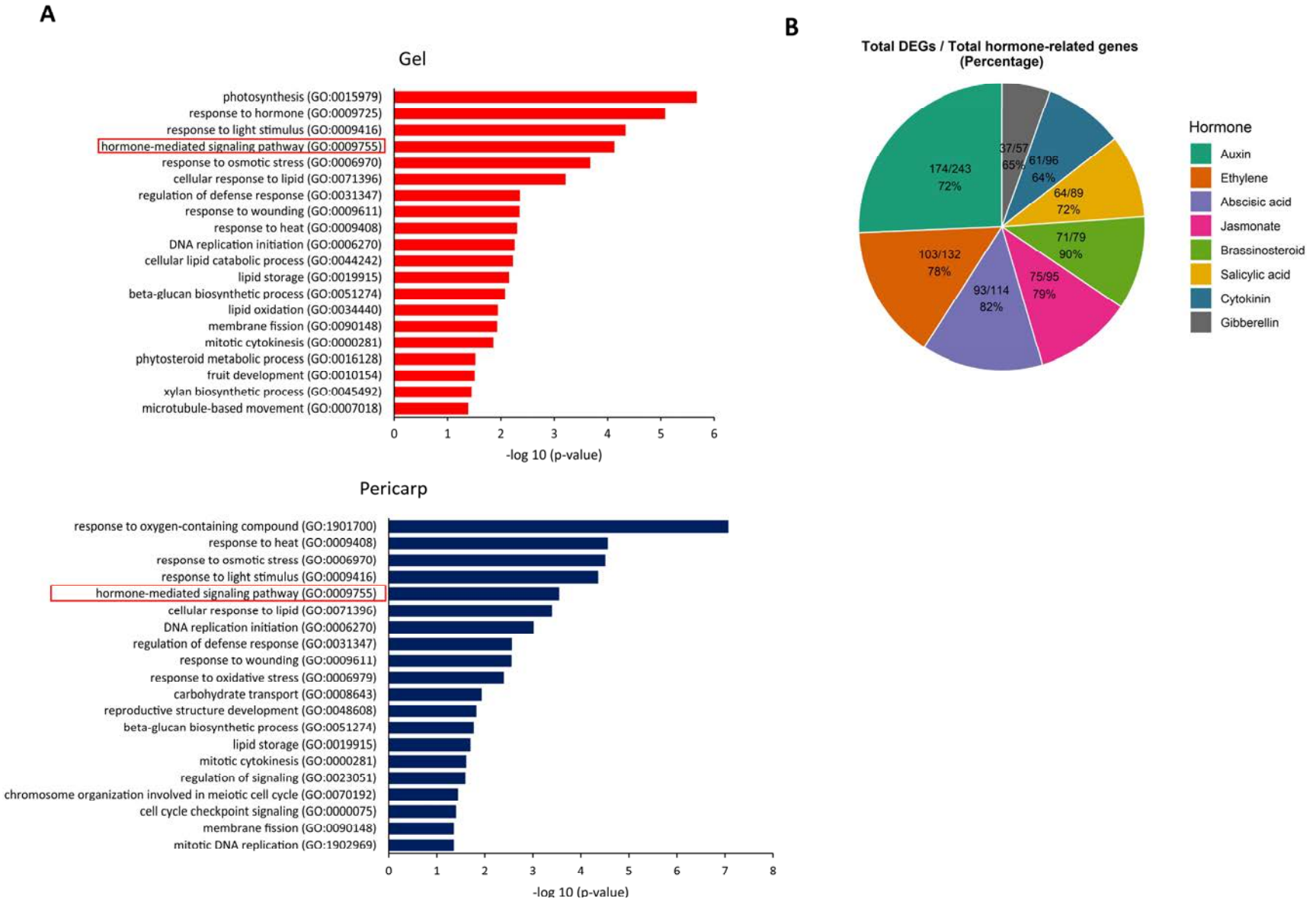
Supplementary Figures



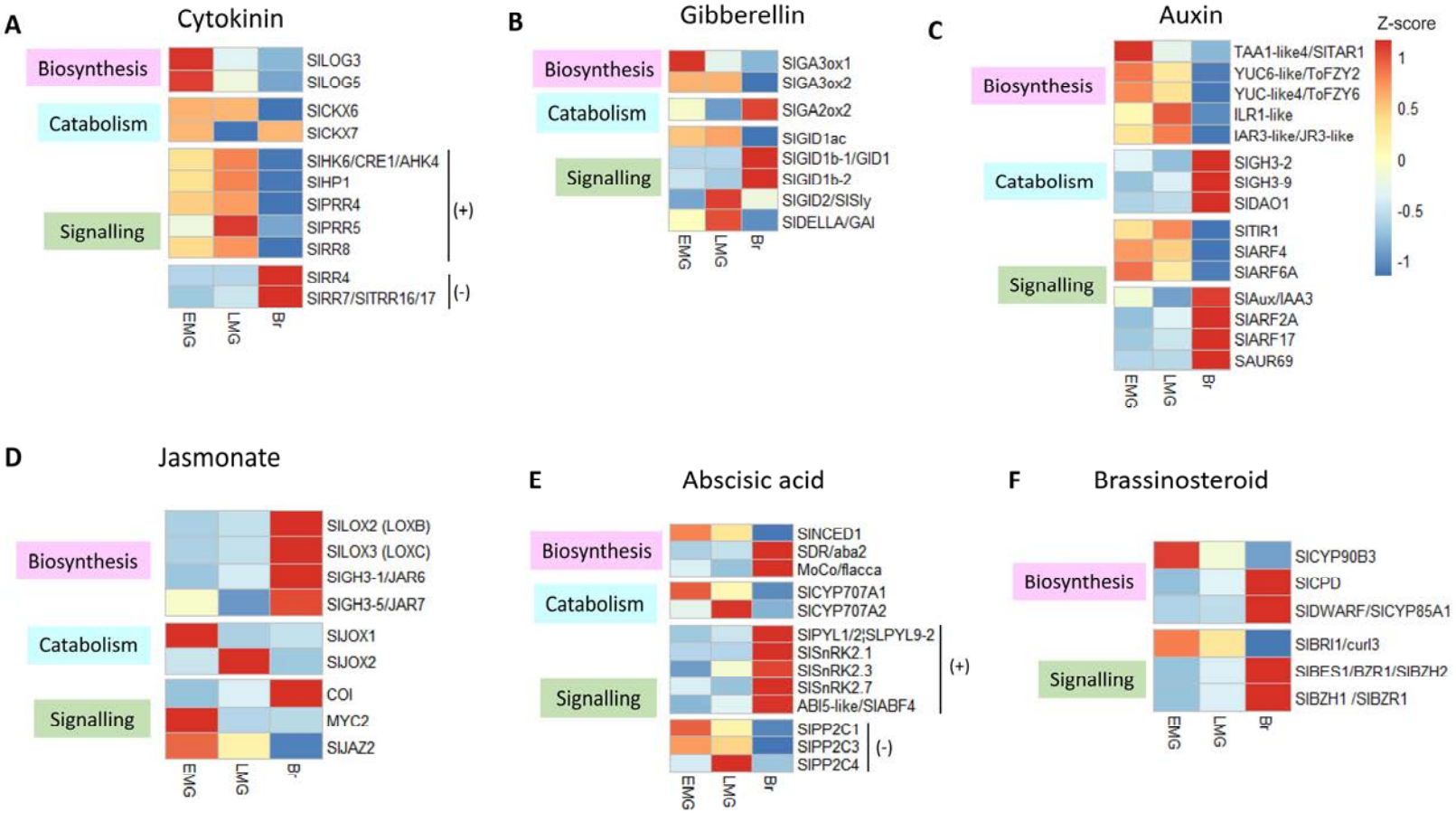
Supplementary Figure 1. Co-expression modules generated by Weighted Gene Co-expression Network Analysis (WGCNA). (A) Heatmap representation of average transcriptomic behavior of co-expressed genes clustered in different modules revealed by a non-targeted approach showing gene sets that reflect tissue or stage specificity. **(B)** Table representing the correlation between the modules (rows) and the tissue or stage factors (columns). Numbers in the table correspond to the correlation *r* and the *p*-value in parentheses. The rows are colored based on the correlation of the module with the factor: red for positive and blue for negative correlation. Main modules related to tissue (pink circle) or stage (purple square). M, module; EMG, early mature green; LMG, late mature green; Br, breaker; Br+4, breaker +4 days.



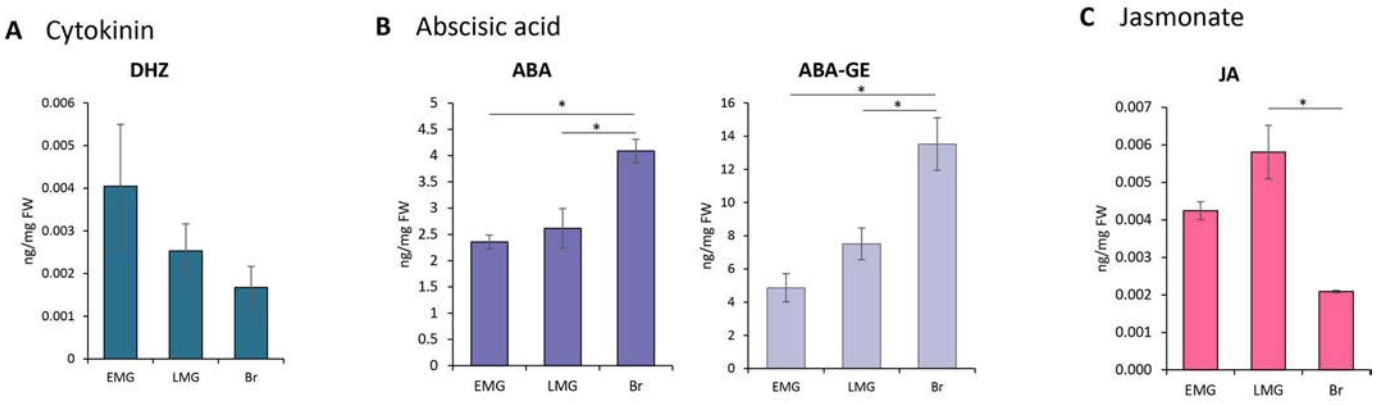
Supplementary Figure 2. Transcriptomic kinetics of main ripening TFs. Expression in terms of Estimated Transcript Number (see Material and Methods) of key ripening regulating transcription factors in two different tissues at four ripening stages. TFs, transcription factors; EMG, early mature green; LMG, late mature green; Br, breaker; Br+4, breaker +4 days.



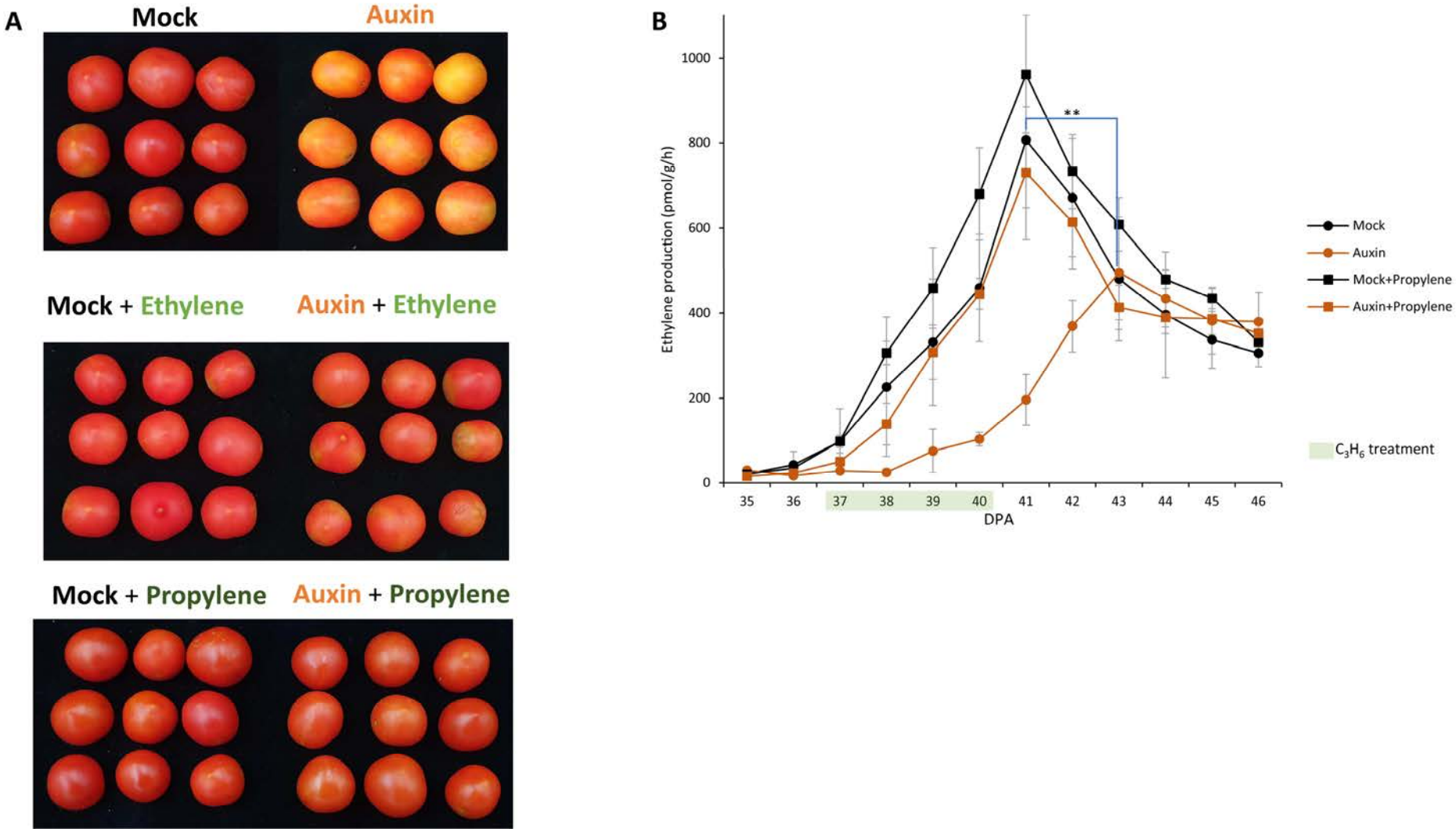
Supplementary Figure 3. Gene ontology enrichment. (A) Top 20 enriched GO - slim biological process terms in gel (red) and pericarp (blue),- log 10 (FDR-adjusted p-value < 0.05) **(B)** Distribution of the total number of DEGs associated with hormones during ripening (Number of DEGs/Total number of genes annotated per hormone, percentage of DEGs). The slice area is proportional to the number of DEGs.



Supplementary Figure 4. Transcriptomic profile of key genes associated with hormones at the onset of ripening. Heatmap representing the expression of hormone-associated DEGs involved in biosynthesis, catabolism, and signaling of **(A)** cytokinins, **(B)** gibberellins, **(C)** auxin, **(D)** jasmonates, **(E)** abscisic acid, and **(F)** brassinosteroids. (+) indicates positive regulators and (-) indicates negative regulators.



Supplementary Figure 5. Endogenous levels of different hormones at ripening initiation. (A) Cytokinin, (B) Abscisic acid, (C) Jasmonate (mean ± SE, n=3). EMG, early mature green; LMG, late mature green; Br, breaker; DHZ, Dihydrozeatin; ABA, Abscisic acid; ABA-GE, ABA-glucose ester; JA, Jasmonic acid. Asterisks indicate significant differences determined by Student's t-test at * $p < 0.05$.



Supplementary Figure 6. Effect of exogenous auxin, ethylene, and propylene treatment on fruit ripening phenotype (A) and ethylene production (B). Fruits treated with mock (black line), auxin (orange line), mock + propylene (dotted black line) or auxin + propylene (dotted orange line) (mean ± SD, n=10). Asterisks indicate significant differences determined by Student's t-test at ** $p < 0.01$.

Chapter III

Oxygen regulated *SlERF.E2* and *SlERF.E4* are negative regulators of ripening initiation

(In preparation)

Oxygen-regulated *SlERF.E2* and *SlERF.E4* are negative regulators of tomato fruit ripening initiation

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Abstract

Ripening of fleshy fruit corresponds to the massive physiological and metabolomic changes underlying the nutritional and sensory traits that make the fruit appealing to consumers. In climacteric fruits, such as tomato (*Solanum lycopersicum*), ripening is characterized by a burst of ethylene production and an increase in respiration, although the link between these two processes remains obscure. The plant hormone ethylene is essential for the initiation and coordination of climacteric ripening and its action is known to be mediated by a linear transduction pathway leading to the activation of Ethylene Response Factors (ERF). Members of the tomato ERF.E clade (SlERF.Es), display a remarkable ripening-associated expression pattern and are characterized by a methionine-cysteine N-terminal domain that targets these proteins for degradation through the N-end rule pathway. Here we demonstrated that, as the ripening progresses, the locular gel tissue undergoes drastic depletion of oxygen (hypoxia). In contrast, other tissues, such as pericarp and columella stay under normal oxygen conditions (normoxia). In this work, we assessed the regulation of ERF.E by oxygen at both transcriptional and protein level. Compared to normoxia, hypoxia induces ERF.E gene expression, significantly decreases their membrane localization, while promoting their accumulation in the nucleus. In addition, normoxia promotes ERF.E protein degradation, while hypoxia leads to their stabilization, revealing the role of oxygen concentration in the post-translational regulation of the ERF.E clade. To further address the role of ERF.E members in ripening, transgenic tomatoes over-expressing or knocking-out *SlERF.E2* or *SlERF.E4* have been generated. Over-expressing lines display delayed ripening, reduced ethylene production, and retarded depletion of oxygen in the gel tissue, supporting the hypothesis that these genes encode for negative

regulators of climacteric ripening. Overall, this study brings new insight into the factors and meachanisms that regulate the initiation of the ripening process.

Introduction

Fruit development is a critical part of the reproductive process in higher plants, serving to protect, develop, and disseminate seeds. Climacteric fruit, such as tomato, banana, apple, and pears, exhibit a sharp increase in fruit respiration and autocatalytic ethylene production during ripening (Biale, 1964; Oeller et al., 1991).While many data point to the importance of ethylene in ripening, the link between increased respiration and ethylene production needs to be clarified in order to fully comprehend the role of climacteric process in ripening. Tomato (*Solanum lycopersicum*) is a widely produced and consumed horticultural crop and is also an essential model organism for studying climacteric ripening (Klee and Giovannoni, 2011). Unlike other bulky fruits such as apple and pear, the tomato fruit is technically a berry that emerges from an ovary, (Knapp and Litt, 2013), and its fleshy tissue comprises septa (between locules), placenta (links to seeds), locular gel tissue (surrounding and protecting the seeds), columella (in the center), and pericarp (Brecht, 1987; Xiao et al., 2021). Despite the fact that interior tissues are as crucial for fruit development, ripening and quality, the majority of tomato research has concentrated on the outer pericarp (Brecht, 1987; Van de Poel et al., 2014; Huang et al., 2021; Chirinos et al., 2023).

Plants require oxygen as a substrate for many biochemical reactions, including energy metabolism (respiration). Oxygen gradients can develop within plants, where the tissue's anatomy and physiology determine oxygen release, retention, or diffusion (Van Dongen and Licausi, 2015). Oxygen levels below 5% (~55 μM) have been observed in mature apple fruit, seeds, and roots with little or no photosynthesis (Van Dongen et al., 2003; Borisjuk and Rolletschek, 2009). Ethylene Response Factor (ERF) group VII (ERFs-VII) transcription factors play a significant role in oxygen sensing, with a common N-terminal consensus motif (MCGGAII/L) distinguishing ERFs-VII proteins (Nakano et al., 2006; Liu et al., 2016). In *Arabidopsis*, ERFs-VII are degraded by the N-end rule pathway of protein degradation under normal oxygen conditions. In brief, after removal of the first methionine by a Methionine Aminopeptidase (MAP) and oxidation of the penultimate position cysteine by Plant Cysteine Oxidases (PCOs) using oxygen as co-factor, the protein is targeted by the E3 ubiquitin-protein ligase (PRT6) to be finally degraded by the proteasome. Degradation of ERFs-VII is suppressed in hypoxia due to a lack of oxygen-dependent cysteine oxidation, enabling ERFs-VII to accumulate and drive downstream gene expression in response to hypoxia (Gibbs et al., 2011; Licausi et al., 2011; Gibbs et al., 2014). Oxygen homeostasis is restored when oxygen availability returns to aerobic

levels (Hartman et al., 2019). Whereas the key elements of oxygen sensing in *Arabidopsis* have been at least partially elucidated, it is still unclear if other plant species exhibit a comparable process.

In tomato, the ripening process is largely controlled by the plant hormone ethylene, but the mechanisms by which it mediates the transcription of downstream target genes, known as ripening-associated genes, are not well understood. Ethylene biosynthesis is carried out by two enzymes, 1-aminocyclopropane-1-carboxylic acid (ACC) synthase (ACS) and 1-aminocyclopropane-1-carboxylic acid oxidase (ACO), which transform S-adenosyl-L-Met (SAM) into ACC and convert ACC into ethylene, respectively (Yang and Hoffman, 1984). Two different systems of ethylene production operate during fruit development and ripening. Two different systems of ethylene production operate during fruit development and ripening, with System-1 dominating at immature stages and System-2 taking over during ripening (Liu et al., 2015). According to the currently accepted model, ethylene signaling relies on a linear transduction pathway where the hormone is perceived by a specific receptor family (ETR, ethylene receptor proteins), which initiates a signaling cascade leading to the activation of transcriptional regulators belonging to the Ethylene Response Factor (ERF) family of transcription factors (Benavente et al., 2006; Tian and Lu, 2006). This in turn regulates genes underlying ripening-related traits, such as color, firmness, aroma, taste, and postharvest shelf life (Barry et al., 2000). However, the mechanisms by which ERFs mediate the regulation of ripening-associated genes remain largely obscure. Moreover, the supposed link between the rise in respiration and into catalytic ethylene production is widely shared hypothesis among scientists although it is not supported by any experimental data.

ERFs are encoded by a large multigene family and specifically bind to the GCC box in the promoter regions of ethylene-responsive genes (Pirrello et al., 2012; Gasch et al., 2016). In the tomato genome, 81 ERFs have been identified and distributed in nine subclasses (ERF.A to ERF.J) (Pirrello et al., 2012), with 27 upregulated and 28 downregulated upon ripening. (Liu et al., 2016). This ripening-related expression pattern highlights their putative role in fruit ripening. Consistent with this hypothesis, the role of some ERFs has been described, tomato *LeERF1* (*SlERF.H1*) overexpression resulted in a constitutive ethylene response and accelerated fruit ripening and softening (Li et al., 2007). Similarly, SlERF.E4 plays an important role in fruit ripening by integrating ethylene and carotenoid synthesis pathways in tomato (Lee et al., 2012). Of particular interest, from the ERFs upregulated during ripening, three of them *SlERF.E1*, *SlERF.E2,* and *SlERF.E4*, show the highest upregulation. In addition, these sub-class E ERFs are downregulated in the ripening mutants *Nr*, *rin,* and *nor* (Liu et al., 2016). Tomato ERF.E genes are orthologues of *Arabidopsis* ERFs-VII and are characterized by a highly conserved MCGGAII/L N-

terminal motif (Liu et al., 2016) making them good candidates as oxygen sensors and ripening regulators.

In the present study, we revealed that the onset of tomato fruit ripening is associated with a dramatic drop in O_2 concentrations in locular gel and an earlier transcriptional reprogramming taking place in this tissue. The present study investigates the role of hypoxia in controlling ERF.E expression, protein stabilization, and subcellular localization, as well as the putative role of SlERF.E2 and SlERF.E4 in the initiation of ripening.

Results

Locular tissue undergoes oxygen depletion

While climacteric ripening has long been associated with a sharp increase in respiration, data assessing oxygen levels during fruit ripening is still missing. In the present study, we assessed the evolution of oxygen concentration throughout all stages of tomato fruit development using a non-destructive probe. At the 34th day post-anthesis (DPA), we observed a dramatic depletion of oxygen concentration specific to the locular gel tissue, eventually leading to hypoxia in this compartment (oxygen concentration below 50 µM; Figure 1A, B, C and D), while other tissues such as columella and pericarp stayed in normoxia (oxygen concentration above 200µM; Figure 1A and B). Interestingly, oxygen depletion occurs 3 to 5 days before the peak of ethylene production (Figure 1B).

To further support our observations, we used a sensor foil for 2D imaging of oxygen distribution at different ripening stages: immature green (IMG, 25 days post-anthesis (DPA), mature green (MG, 36 DPA), breaker (Br), 3 days post-breaker (Br+3) and 7 days post-breaker (Br+7). The imaging revealed oxygen depletion in the locular gel exists from mature green stage onwards (Figure 1D), thus confirming our previous observation.

To test if these events are cultivar-specific, we measured oxygen evolution throughout ripening in Alisa Craig and M82 cultivars, and we confirmed that oxygen depletion in locular tissue takes place in both of these varieties (Supplementary Figure 1A and 1B). To a far lesser extent, pericarp tissues of both of these two varieties showed reduction in oxygen. In addition, we observed that the natural ripening mutant *rin* and his knock-out version show a delay in oxygen depletion that follows the delay of ripening (Supplementary Figure 1C and D). This observation suggests that a new developmental stage can be defined by hypoxia induction in gel, during which underlying molecular changes render the fruit tissue competent to ripen, which is a fate-determining point of the whole process of ripening.

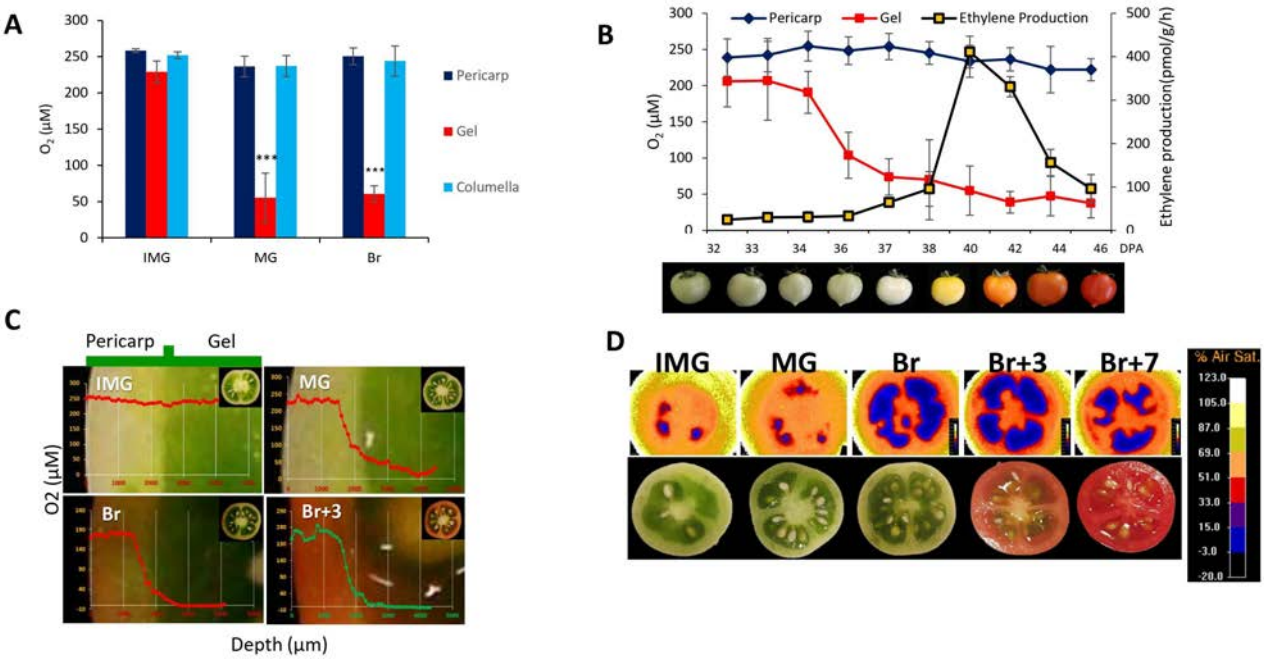

Figure 1. Oxygen concentrations in different fruit tissues during ripening. (A) Barplot representing the oxygen concentration (µM) in pericarp (dark blue), locular gel (red), columella (light blue) at different ripening stages. **(B)** Oxygen concentration (primary axis) in pericarp (blue), locular gel (red), and ethylene production (black) from MG (32 DPA) to red stage (46 DPA) in WT. **(C)** Oxygen concentration (vertical axis) vs depth (µm, horizontal axis) at IMG, MG, Br and Br+3 stage. **(D)** Pictures taken with a chemiluminescent oxygen-sensing foil representing oxygen distribution in different tissues at different ripening stages. DPA, days post anthesis; IMG, immature green; MG, mature green; Br, breaker; Br+3, breaker +3 days; Br+7, breaker +7 days; % Air Sat, percentage of air saturation.

Transcriptomic changes associated with oxygen depletion at pre-ripening stages

This work builds on the finding that the locular gel tissue undergoes dramatic depletion of oxygen at the initiation of fruit ripening, making this pre-ripening event an essential marker of fruit readiness to trigger the transcriptomic reprogramming that leads to ripening. In our previous study, we demonstrated that the MG stage is not as homogeneous as previously thought, and that early ripening signals are first induced in the locular gel tissue (Chirinos et al., 2023). In addition, our data suggest that the physiology of the gel differs significantly between the Early Mature Green (EMG, normal oxygen concentration) and the Late Mature Green (LMG, hypoxic condition).

To identify if early transcriptomic changes are in place at the beginning of oxygen depletion in the locular tissue, we performed a genome-wide transcriptomic profiling by RNA sequencing (RNA-Seq) of locular tissue and pericarp at the following three crucial stages: EMG corresponding to 33 DPA just before oxygen depletion begins, oxygen

concentration of 250 µM; 35 DPA when oxygen concentrations drop to 100-150 µM; 36 DPA corresponding to full hypoxic conditions of the locular gel, Breaker (Br); and 4 days post-breaker (Br+4), when external changes in color are noticeable. We analyzed the transcriptome changes in terms of Differentially Expressed Genes (DEGs) and found that in pre-ripening stages, comparing 33 DPA vs. 35 DPA, the number of DEGs is more than double in the gel (142) than in the pericarp (5), and this trend continues when comparing 35 DPA vs. 36 DPA where we observed 1910 DEGs in the gel compared to 1036 in the pericarp (Figure 2A). These numbers then stabilized during full onset of ripening (Br and Br+4). These observations are in accord with our earlier findings that in the transition to ripening, earlier transcriptomic changes occur first in the gel and then in the pericarp (Chirinos et al., 2023).

Through principal component analysis (PCA), we found significant differences between the transcriptomes, with 57% of the variation (PC1) associated with ripening stages and 24% (PC2) with tissue type (Figure 2B). At pre-ripening stages (33 DPA, 35 DPA and 36 DPA) and ripening stages (Br and Br+4), the gel transcriptomes were in different clusters compared to the pericarp. In the pre-ripening stages of the gel tissue, transcriptomes clustered separately, while those of the pericarp formed a common cluster (Figure 2B). These results suggest that the observed transcriptomic changes may be related to the depletion of oxygen in the gel tissue.

To gain insight into the transcriptional changes associated with the onset of oxygen depletion and early ripening signals, we performed a co-expressing gene sets showing tissue or stage specificity, using weighted gene co-expression network analysis (WGCNA) non-targeted approach. In total, 23 modules were identified, with three modules (M9, M11, and M12) significantly correlated with gel tissue, and two modules specific to pericarp (M1 and M2) (Figure 2C and Supplementary Figure 3A). Notably, M11 and M12 contained key ripening-associated genes that showed higher expression or earlier induction in locular gel tissue compared to pericarp. These genes included key transcription factors *RIN*, *NOR*, *NOR-like1*, genes associated to carotenoid biosynthesis *PHYTOENE SYNTHASE* (*PSY1*), *PHYTOENE DESATURASE* (*PDS*) and *ζ-CAROTENE ISOMERASE* (*ZISO*) and cell wall modification genes *PECTATE LYASE* (*SlPL*), *EXPANSIN 1* (*EXP1*), *CELLULASE 8* (CEL8), *ALPHA MANNOSIDASE* (a-MAN), *β-GALACTOSIDASE 4* (*TBG4*) and a *XYLOGLUCAN ENDOTRANSGLUCOSYLASE-HYDROLASE* (*SlXTH5*) (Supplementary Figure 2C). These results suggest that physiological and transcriptomic changes associated with oxygen depletion may be related to the initiation of ripening. Moreover, genes in M11 and M12 could be promising candidates for investigating the relationship between oxygen depletion and early ripening signals. Supplementary Table 1 lists the genes that make up each module.

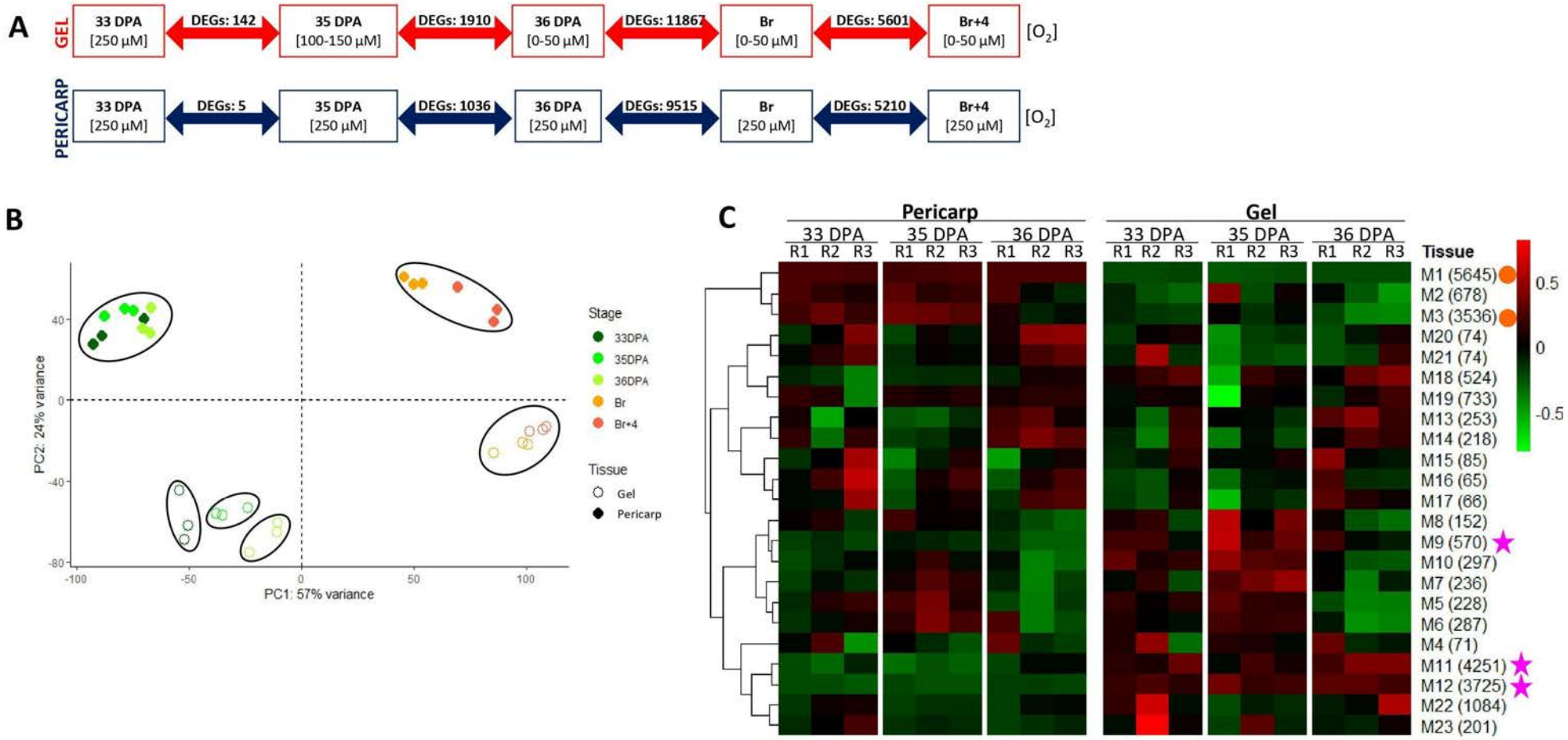

Figure 2. Global transcriptomic changes during ripening and oxygen depletion. (A) Transcriptional dynamics throughout ripening showing the number of DEGs at 33DPA, 35DPA, 36DPA, Br and Br+4 in gel and pericarp tissues. **(B)** Principal component analysis (PCA) of transcriptomic profiles at early stages Each symbol represents a replicate. **(C)** Weighed Gene Co-expression Network Analysis (WGCNA), heatmap representation of average transcriptomic behavior at early stages of co-expressed genes clustered in different modules. The number of genes in each module is indicated by the values in parentheses. Main modules related to pericarp (orange circle) and gel (pink star). DPA, days post anthesis; Br, breaker; Br+4, breaker +4 days; DEGs, differentially expressed genes; [O_2], oxygen concentration; M, module.

Hypoxia response core genes are regulated in gel tissue

The existence of oxygen gradients in plant tissues has been reported since last century (Magness, 1920). In *Arabidopsis*, 49 genes were described as hypoxia core response. These genes encode transcription factors, signaling components, enzymes of anaerobic metabolism, and other uncharacterized proteins (Mustroph et al., 2009). To investigate whether the tomato orthologues of these genes play a role in ripening and are induced during oxygen depletion in gel tissue, we identified all the orthologue genes belonging to M11 or M12 from the WGCNA results, resulting in a total of 70 orthologue genes that showed induction in gel during pre-ripening stages (Supplementary Figure 4A). In particular, two genes of unknown function, *TIL* and *HUP54*, showed induction in gel during oxygen depletion in locular tissue and even higher induction in both gel and pericarp at ripening initiation (Br stage; Supplementary Figure 4B and C), suggesting a link between hypoxia response and ripening initiation.

Ethylene Response Factors belonging to the ERF.E clade (ERF.Es) are essential for activating the response to hypoxia at the transcriptional level (Gibbs et al., 2011; Licausi et al., 2011). Among the five ERF.E genes present in the tomato genome, *SlERF.E1*, *SlERF.E2*, and *SlERF.E4* exhibit a remarkable expression pattern associated with ripening (Liu et al., 2016). To further understand the tissue-specific expression of these genes in fruit, we conducted additional analyses. Our results confirm that after the Br stage, all three *ERF.E* genes are induced at the transcriptional level in both pericarp and locular gel tissue (Supplementary Figure 5A, B and C). We also observed that while the expression of *SlERF.E2* and *SlERF.E4* is concomitant in both gel and pericarp tissues (Supplementary Figure 5B and C), the expression of *SlERF.E1* is initially induced in gel tissue and subsequently shows higher expression in this tissue (Supplementary Figure 5A).

A common response to hypoxia has been identified in higher plants, including the induction of nitric oxide (NO) metabolism and fermentation (Mustroph et al. 2009). It has been also demonstrated that NO negatively affects ERF.E stability (Gibbs et al., 2014) and that it delays ripening (Zuccarelli et al., 2021). The expression of *NITRATE REDUCTASE* (*NR*), the enzyme responsible for NO production, showed upregulation in gel but moderate downregulation in pericarp. Interestingly, non-symbiotic phytoglobins *HB1* and *HB2* showed downregulation at the initiation of ripening, particularly in pericarp tissue (Figure 3B), suggesting that locular gel tissue could be exposed to a higher concentration of NO than pericarp. To identify if fermentation adaptation processes are regulated during ripening, we looked at the expression of related genes. *ALCOHOL DEHYDROGENASE 2* (*ADH2*), known to be involved in several aspects of flavor development during ripening, is early and highly induced in gel compared to pericarp (Figure 3B), indicating that, to some extent, adaptation to hypoxic conditions is in place in gel tissue during ripening.

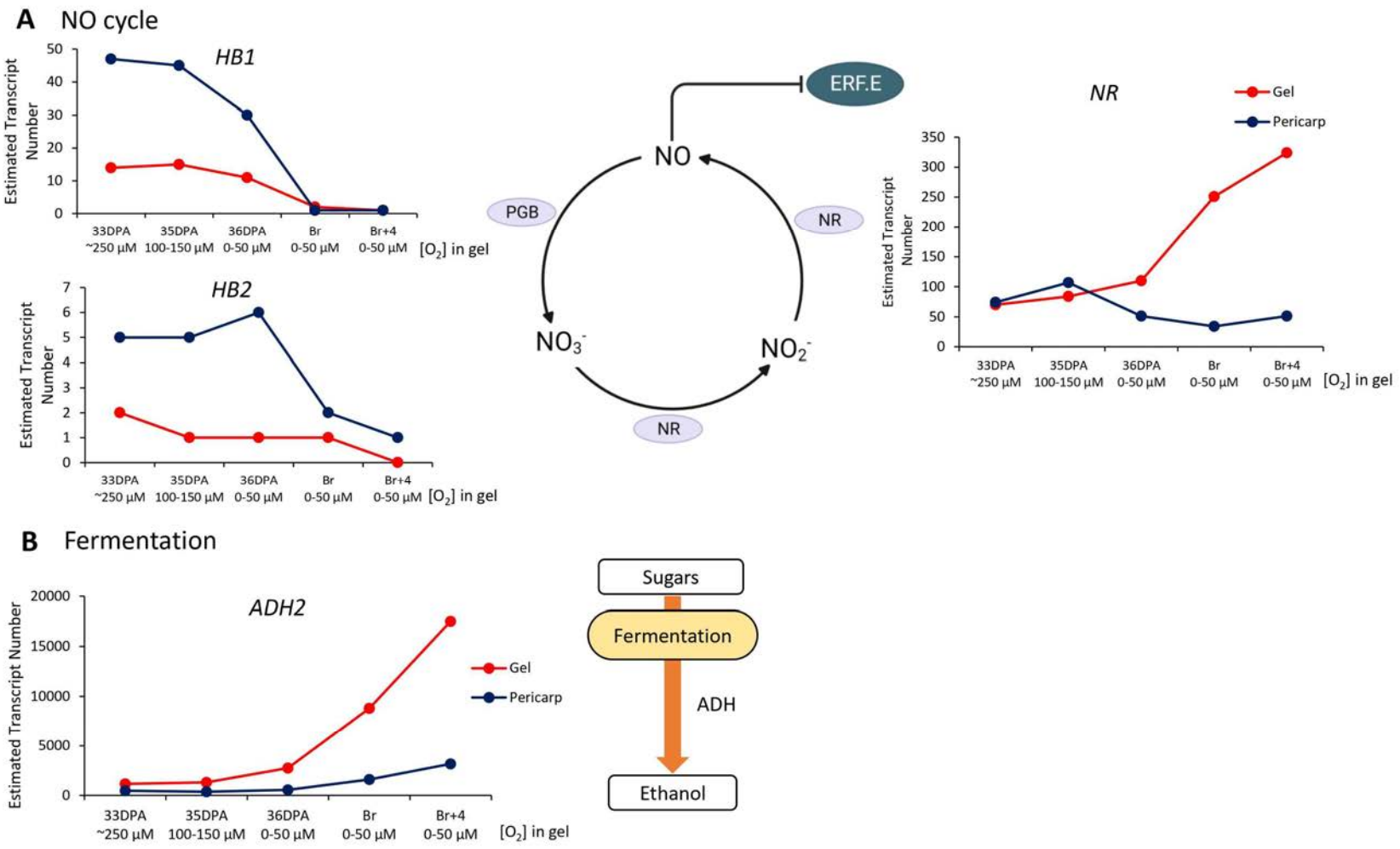

Figure 3. Energy metabolism and fermentation related genes during ripening. Transcriptional expression in terms of Estimated Transcript Number of genes related to **(A)** NO production and primary nitrogen metabolism and **(B)** Fermentation. [O_2], oxygen concentration in locular gel tissue; DPA, days post anthesis; ADH, alcohol dehydrogenase; NO, nitric oxide; HB, phytoglobin; NR, nitrate reductase.

Oxygen-mediated regulation of SlERF.E at the transcriptional and post-translational levels

In *Arabidopsis*, ERF.E stability is dependent on the O_2 concentration, giving them a central role in sensing changes in O_2 concentrations during plant development (Gibbs et al., 2011; Licausi et al., 2011). In particular, under hypoxic conditions, ERF.Es are relocated from the membrane to the nucleus where they activate hypoxia-related genes. Conversely, under normoxic conditions, a pool of ERF.Es is attached to the membrane by binding to Acyl-CoA-binding protein (ACBP) proteins, while free ERF.E proteins are degraded through the N-end rule pathway (Gibbs et al., 2011; Licausi et al., 2011). In this study, we aimed to understand whether the expression of SlERF.E1, SlERF.E2 and SlERF.E4 is regulated by oxygen. First, we exposed plantlets to hypoxic conditions (10-50 µM O_2) and we collected samples at different time points. *SlERF.E1* mRNA levels were dramatically increased after 1 h of treatment and remained high during the time of treatment. *SlERF.E2* showed slow but steady increase in expression, while SlERF.E4 showed a quick but transient induction after exposure (Figure 4A). Taken together, the results showed that tomato *ERF.E*s expression is regulated by hypoxia, although they have different induction patterns.

Then, to explore the effect of oxygen concentrations on the subcellular localization of tomato SlERF.E1, SlERF.E2, and SlERF.E4 proteins, we fused *ERF.E*s with a VENUS C-terminal tag and transiently expressed the proteins in *Nicotiana benthamiana* under normoxia (250 µM O_2) or hypoxic conditions (10-50 µM O_2) (Figure 4B and C). In normoxia, tomato ERF.Es are located in both the nuclei and the plasma membrane. In hypoxic conditions, the localization of SlERF.Es in the membrane decreases, whereas their translocalization into the nucleus is significantly enhanced, revealing the regulation of tomato SlERF.Es' subcellular targeting by oxygen (Figure 4B and 4C). To further assess the requirement of the N-terminal motif in the re-localization process, stabilized versions of these ERFs with a deletion of the first 13 amino acids, lacking the methionine-cysteine N-terminal domain, were generated. Interestingly, the localization pattern of the stabilized ERF.E (d13ERF.E) no longer depends on oxygen, since these proteins display a similar subcellular localization, regardless of the oxygen concentration, and is similar to the localization pattern of the native ERF.E in hypoxia conditions (Figure 4B and 4C).

To further investigate whether the N-end rule pathway is able to control SlERF.E activity and stability in tomato, mesophyll protoplasts were transiently transformed with a plasmid bearing the *35S:ERF.E:FLuc* construct, in which the N-terminal extremity of *Firefly Luciferase* (*FLuc*) is fused to *SlERF.E1*, *SlERF.E2* or *SlERF.E4* or d13 versions (*d13ERF.Es*) (Figure 4D). We compared the stability of this chimeric construct with that

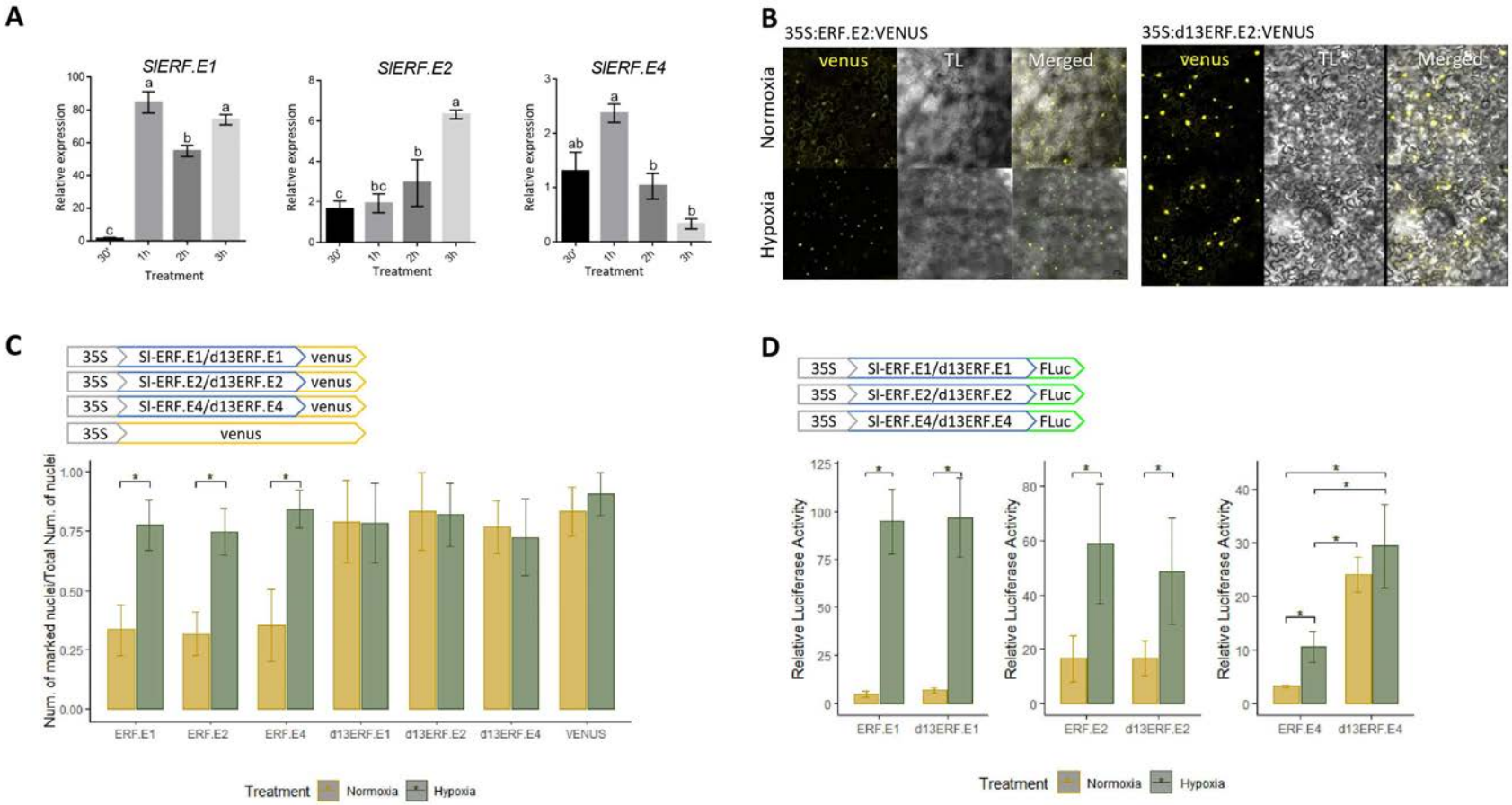

Figure 4. SlERF.E expression, subcellular localization and stability under normoxia and hypoxic conditions. (A) Barplots representing relative expression of *SlERF.E* in plantlets at different time points under hypoxia (10-50µM O_2), expression is relative to normoxic condition. Letters indicate statistically significant difference ($P < 0.05$, one-way analysis of variance (ANOVA)). **(B)** Subcellular localization of transiently expressed SlERF.E2 and Sld13ERF.E2 fused to venus in *N. benthamiana* under normoxia (250µM O_2) and hypoxia (10-50µM O_2) conditions. **(C)** ERF.Es fused to venus in C-terminal construction. Barplots representing the Ratio of marked nuclei / total number of nuclei in normoxia and hypoxia after 4h of incubation. Tobacco leaves have been transiently transformed by the native version of each ERF fused to VENUS, or by the stabilized version of each ERF, lacking the MCGGA/I domain making them insensitive to the N-end rule. **(D)** ERF.Es fused to Firefly Luciferase (Fluc) in C-terminal construction. Bar plots representing the relative luciferase activity of ERF.Es and stabilized versions (d13) under normoxia and hypoxia. The bar plots show Mean ± SE, $*P < 0.05$. Normoxia = 250µM O_2 and hypoxia =10-50µM O_2.

of a stabilized version. *Photinus pyralis* firefly luciferase (Fluc) activity was normalized against that of *Renilla renifor*mis (RLuc), expressed by a 35S:RLuc module. The results demonstrated that in normoxic conditions, only d13ERF.E4-FLuc protein, but not d13ERF.E1-FLuc or d13ERF.E2-FLuc, has a significantly higher signal than the native protein forms (Figure 4D). Moreover, all d13ERF.E and ERF.E proteins are significantly accumulated under hypoxia condition (Figure 4D). These results suggest that all three SlERF.E proteins are stabilized under hypoxia condition and that SlERF.E4 stability is dependent on the N-terminal MCGGAI/L motif.

We have also identified the tomato orthologues of *Arabidopsis* N-end rule members. The tomato genome contains three PCO genes, one ATE gene, and two PRT6 genes, which here are annotated as PCO, PCO1, PCO2, ATE, PRT6a, and PRT6b (Supplementary Figure 6A). To date, we have generated knock-out lines for PCO, ATE and PRT6b. However, when selecting ATE knock-out lines, we encountered a flowerless epinastic phenotype (Supplementary Figure 6B) that we were unable to propagate, thus we used artificial micro RNA (amiATE) lines for this study. Therefore, we addressed the role of the N-end rule enzymes PCO, ATE and PRT6b in the stability of ERF.Es through mesophyll protoplast of this knockout or knock-down lines and DLR (Dual Luciferase Reporter) assay. We see that in *pco*-KO protoplasts SlERF.E2 is stabilized but not SlERF.E1 and SlERF.E4, suggesting that may be a substrate specificity for these PCOs (Supplementary Figure 6C). Interestingly, downregulation of ATE is capable to stabilize SlERF.E2 and SlERF.E4 but not SlERF.E1, suggesting that SlERF.E1 may be regulated by oxygen but not by the N-end rule pathway (Supplementary Figure 6D). In *prt6b*-KO protoplasts there is no difference compared to the WT, demonstrating that the stability of the ERF.Es is not under the control of this enzyme and may be *PRT6a* who is able to regulate the ERF.Es. Taken altogether, we demonstrated that O_2 is capable to regulate the expression, subcellular localization and stability of the SlERF.Es.

SlERF.E2 and *SlERF.E4* are negative regulators of ripening initiation

To address the functional significance of *SlERF.E2* and *SlERF.E4* members during tomato fruit ripening, we overexpressed either their native form or a stabilized version (d13ERF.E) lacking the first 13 amino acids, driven by the constitutive 35S promoter. We also generated knockout or knock-down lines by CRISPR/Cas9 or RNA interference technology. *SlERF.E2-OE* lines display delayed ripening, associated with a reduced ethylene production and delayed oxygen depletion (Figure 5), while *SlERF.E2* knock-down and knock-out lines didn't show a ripening related phenotype (Supplementary Figure 7A and B). In line with these results, lines over-expressing both native or stabilized *SlERF.E4* (d13ERF.E4) also display delayed ripening that is more pronounced in the d13

stabilized lines (Figure 6), associated with delayed oxygen depletion and reduced ethylene production. Meanwhile, *erf.e4*-KO line lacks a ripening associated phenotype (Supplementary Figure 7C). Lacking of these phenotypes in knock-out or knock-down lines compared to overexpressing lines is probably due to their functional redundancy. We also aimed to understand the sensibility of *SlERF.E2-OE* to ethylene and we found that in a triple response assay, contrary to WT, after 1ppm of ethylene treatment, the over-expressing lines showed a moderated hook formation, suggesting that these lines have less sensibility to this hormone (Supplementary Figure 8). These data support the hypothesis that SlERF.E2 and SlERF.E4 are negative regulators of fruit ripening. The stronger phenotypes of the lines expressing the deleted version escaping oxygen regulation suggest a complex interaction between Sl-ERF.E4 and hypoxia that leads to delayed climacteric ripening.

Discussion

Locular gel tissue experience early physiological and transcriptional changes previous to the ripening initiation

Many organs in plants are subjected to low oxygen conditions as part of their normal development and growth. This occurs most frequently in metabolically active bulky tissues such as seeds, seedlings, and tubers (Cukrov et al., 2016). One of the reasons that oxygen concentrations in plant tissues typically fall is because the rate of diffusion from the atmosphere exceeds the rate of consumption by cellular respiration (Weits et al., 2021). In this study, we report that tomato's locular gel undergoes a decline in oxygen concentration previous to ripening initiation, resulting in chronic hypoxia (Figure 1). We hypothesize that this depletion in oxygen could be associated to the climacteric peak in respiration, but more data is needed to confirm this hypothesis since information on respiration rate in locular gel tissue is still lacking. Another hypothesis could be that there is a lack of air spaces for gas exchange between the super expanded gel cells imposing a limit to oxygen diffusion within this tissue, probably due to the fact that cell wall seems to be earlier modified in gel cells based on the expression of related genes (Supplementary Figure 3D) likely producing gel liquefaction. However, pericarp does not experience chronic hypoxia although the cells of the mesocarp undergo also cell expansion, this has been explained as an increase of tissue porosity (Xiao et al., 2021).

We have demonstrated that locular gel tissue is capable of perceive this depletion in oxygen since several hypoxia response genes are induced in this tissue and not in pericarp (Figure 3 and Supplementary Figure 4A). Interestingly, this decrease in oxygen occurs

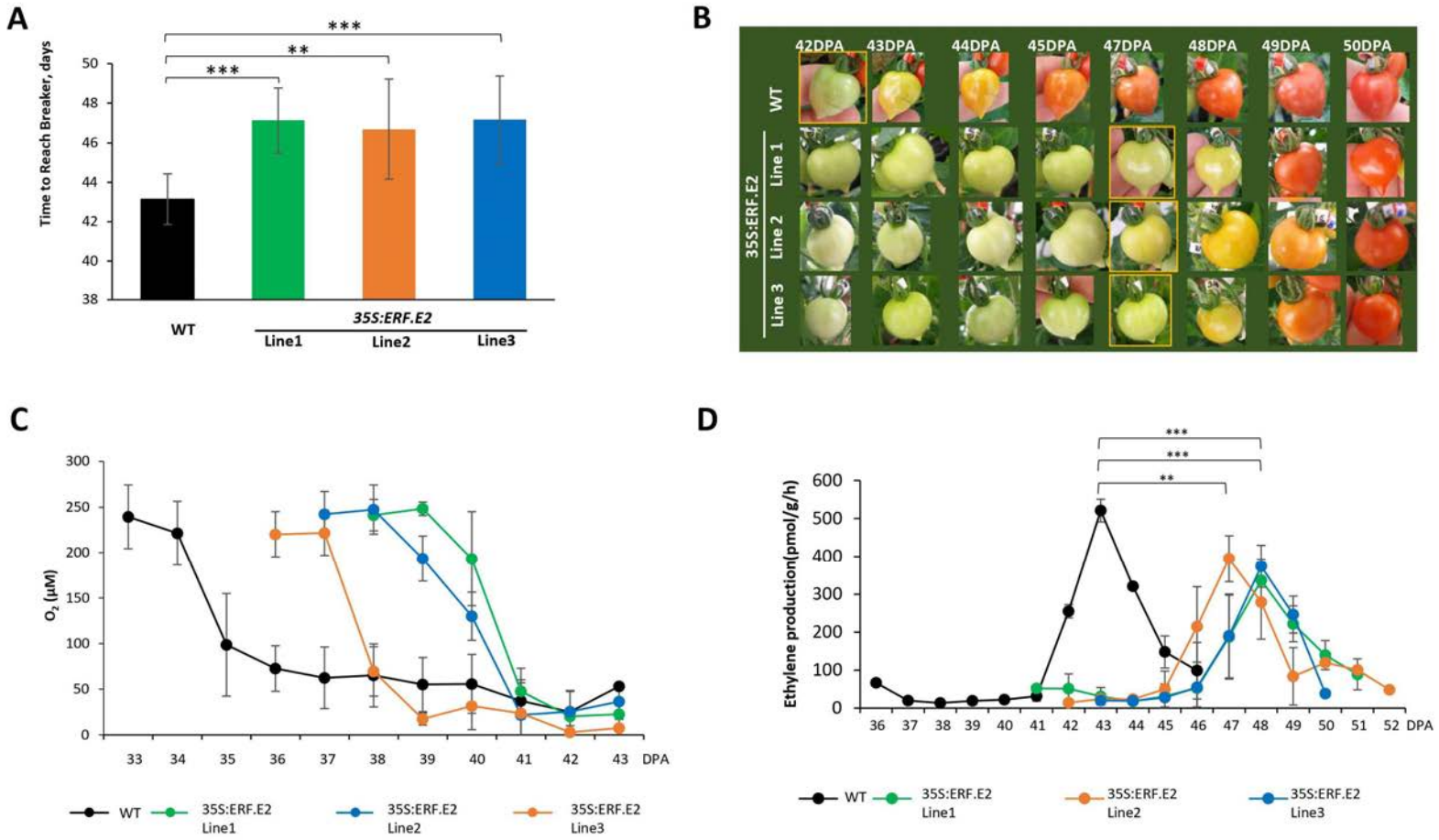

Figure 5. Ripening related phenotype of Sl-ERF.E2 over-expressing lines. (A) Time to reach breaker for WT and ERF.E2-OE lines (in days post anthesis). **(B)** ERF.E2-OE lines show a delay in ripening. **(C)** Oxygen concentration in locular gel and **(D)** ethylene production in WT and ERF.E2-OE lines at during ripening. Data represent mean values from at least 20 fruits. The bar plots show mean ± SD, *P < 0.05, **P <0.01, ***P < 0.001; Student's t-test. DPA, days post anthesis.

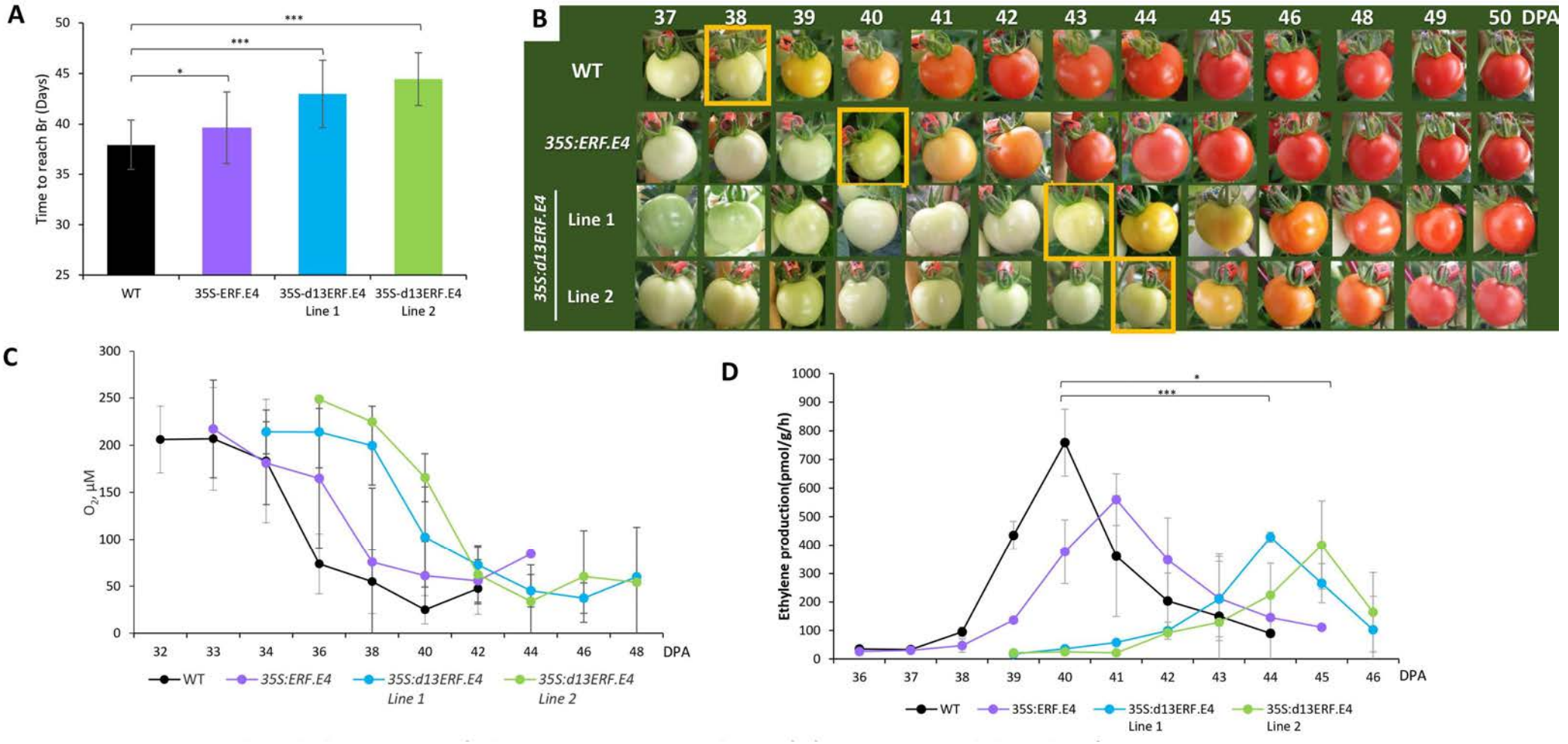

Figure 6. Ripening related phenotype of Sl-ERF.E4 transgenic lines. (A) Time to reach breaker for WT, ERF.E4 over-expressing native and stabilized lines (in days after pollination). **(B)** Ripening related WT, ERF.E4 over-expressing native and stabilized lines phenotypes. **(C)** Oxygen concentration in locular gel **(D)**Ethylene production in WT and ERF.E4 transgenic lines during ripening. Data represent mean values from at least 20 fruits. The bar plots show mean ± SD, *P < 0.05, **P <0.01, ***P < 0.001; Student's t-test.

prior to the climacteric peak of ethylene (Figure 1B), it is not cultivar dependent (Supplementary Figure 1A and B) and is delayed in tomato ripening mutant *rin* and *rin*-KO (Supplementary Figure 1C), whereas other tissues such as the pericarp and columella remained in normal oxygen conditions. Immature fruits (those at the IMG stage) are defined as such because their seeds have not yet fully developed. MG fruits are full size and their seeds are mature (viable), but the fruits themselves have not yet begun climacteric respiration or increased endogenous ethylene production. MG stage occurs in a window of approximately 5–10 days (depending on the cultivar) prior to the onset of tomato ripening, remarkably this window between both stages coincides with the time of decline in oxygen in locular gel. We hypothesized that this low oxygen conditions could be the phenomenon that mark the beginning of MG stage, thus we separated it in EMG (33DPA in cultivar MicroTom), just before the oxygen depletion where most fruit are capable of fully ripe and LMG where locular gel tissue is in hypoxia and most of the ripening machinery is being put in place (Supplementary Figure 3B, C and D; Chirinos et al. 2023). Placing oxygen depletion as a player in the paradigm of ripening initiation.

SlERF.E are the link between oxygen depletion and ripening initiation

ERF.Es play a critical role in the transcriptional activation of the hypoxia response. The presence of the N-terminal MCGGAII/L motif, which was recently shown to be responsible for their post-translational degradation under aerobic conditions in *Arabidopsis*, is a distinguishing feature of these genes. (Gibbs et al., 2011; Licausi et al., 2011). The observed expression profile of *SlERF.E1*, *SlERF.E2* and *SlERF.E4* under hypoxic conditions (Figure 4A) is in line with the already well documented patterns of *ERF.Es* orthologous expression as a response to low oxygen stress in *Arabidopsis* (Gibbs et al., 2011; Licausi et al., 2011) and apple (Cukrov et al., 2016). In contrast to *Arabidopsis*, where AtRAP2.12, the orthologue of SlERF.E2, shows only membrane localization in normoxic conditions and then relocalizes into the nucleus in hypoxia via association with membrane proteins from the ACBP (Acyl-CoA binding protein) family (Licausi et al., 2011). SlERF.Es are found in both the membrane and the nucleus (Figure 4B), with hypoxia resulting in a significant increase in the number of nuclei expressing SlERF.Es compared to normoxia. Confirming that tomato ERF.Es localization is also influenced by oxygen levels. However, no evidence of interaction between tomato ERF.Es and ACBP proteins has been reported yet.

Furthermore, through DLR assay carried out in mesophyll protoplasts of tomato, we demonstrated that oxygen levels are capable of regulating SlERF.E1, SlERF.E2 and SlERF.E4 protein levels, placing these ERF.Es in the core response to hypoxia. More data

is necessary to demonstrate the capacity of SlERF.Es regulating the promoters of hypoxia response genes. Interestingly, deletion of the first 13 aminoacid corresponding to the N-terminal motif of SlERF.Es stabilized only SlERF.E4, making this motif essential for the stability of this ERF. Moreover, we aimed, to analyse if SlERF.Es proteins are post-translationally modified by the N-end rule pathway, remarkably the absence of one of PCO, SlPCO, stabilized SlERF.E2 and but not SlERF.E1 or SlERF.E4. In *Arabidopsis*, individual over expression of *AtPCO1* or *AtPCO2* is able to destabilized AtRAP2.12 while only a double knockout (*pco1pco2*) is capable of its stabilization (Weits et al., 2014). Because we identified three PCO in the tomato genome, it is possible that the other ERF.Es are substrates of the other PCO and that SlPCO is sufficient to regulate SlERF.E2. Another possibility is that there is substrate specificity per PCO. More information about PCO1 and PCO2 in the regulation of SlERF.Es is required. We also showed that downregulating SlATE can stabilize SlERF.E2 and SlERF.E4, but not SlERF.E1 raising the question of whether SlERF.E1 is a substrate for the N-end rule. In rice, *OsSUB1A-1*, a major determinant of submergence tolerance, is not a substrate for the N-end rule pathway despite containing the N-terminal motif (Gibbs et al., 2011), same that *SlERF.E1*, suggesting that may SlERF.E1 is also uncoupled from N-end rule pathway regulation.

Tomato *ERF.E1, ERF.E2* and *ERF.E4* genes show a ripening-associated pattern in pericarp (Liu et al., 2016) and locular gel (Supplementary Figure 5). In addition, they are induced by hypoxia. We demonstrated that over-expression of *SlERF.E2* and *SlERF.E4* leads with a delay in ripening (Figure 5A, 5B, 6A and 6B), delay in O_2 decline in locular gel (Figure 5C and 6C) and reduced ethylene production (Figure 5D and 6D). These results suggest that *SlERF.E2* and *SlERF.E4* exert a negative feedback control over ethylene production during ripening. Similar results were reported for *SlERF.E4* (named *SlERF6* in Lee et al., 2012), where ethylene production is enhanced in RNAi lines. Interestingly, *SlERF.E1*, *SlERF.E2* and *SlERF.E4* are induced by ethylene in maturing fruit (Pirrello et al., 2012), implying that its own expression is connected into the fruit ethylene homeostasis modulating ethylene synthesis during ripening. Of particular note, it was identified that *ERF.Es* possess conserved RIN-binding sites in their promoter regions, this added to the capacity of RIN to induce the transcriptional activity of *SlERF.E1, SlERF.E2* and *SlERF.E4* promoters in transactivation assays (Liu et al., 2016) support the possibility that RIN directly regulates promoter regions of *ERF.Es*. Therefore, regulation of expression of *ERF.Es* could be orchestrated by RIN controlled by the rise of ethylene during ripening. It should be noted that ethylene biosynthesis modulation could be linked to a mechanism that prevents ethylene receptors from becoming saturated and maintains their ability to respond to it (O'Malley et al., 2005).

Considering the putative role of SlERF.E2 and SlERF.E4 as negative regulators of ripening and ethylene biosynthesis, it is important to clarify if these TFs are involved in activating or repressing System-2 genes. It was demonstrated that ethylene production is tissue specific and that locular accumulate a high content of intermediates (ACC, MACC and SAM) (Brecht, 1987; Van de Poel et al., 2014), what is consequent with our hypothesis that in locular gel SlERF.E proteins are stabilized by the low O_2 concentration and that acts as negative regulator of ethylene production. Interestingly, in rice, SUBMERGENCE 1A, an ERF.Es, participates in a feedback restriction mechanism for ethylene biosynthesis during submergence (hypoxic conditions) (Perata and Voesenek, 2007), this in correlation to our results for over-expressing lines *SlERF.E2* and *SlERF.E4.* According to this, we hypothesized that during ripening ERF.E proteins are degraded in pericarp and columella level, nevertheless at locular gel level proteins are not degraded and act as negative regulators. Dark-grown *35S:SlERF.E2* seedlings displayed a reduced ethylene response with reduce apical hook formation in the presence of 1 ppm ethylene compared to the WT. These phenotypes may arise by a decreased sensitivity to ethylene. Seedlings treated with 1-MCP, a potent inhibitor of ethylene receptors completely reverse the phenotype. It was previously reported that over-expressing lines of *ERF.E1* exhibited exaggerated apical hook formation in the absence of exogenous ethylene treatment (Pirrello et al., 2006), which is the opposite of what is observed in over-expressing lines *ERF.E2.* This information could suggest that ethylene perception is regulated in a different way in both ERFs. More information is needed about the role of *SlERF.E1* in ripening.

The study revealed that the onset of tomato fruit ripening is associated with a dramatic drop in O_2 concentrations in locular gel. In parallel, hypoxia condition induces a shift in subcellular localization of SlERF.Es from the plasma membrane to the nucleus and their stability is oxygen dependent. Moreover, the delayed ripening of *SlERF.E2* and *SlERF.E4* over-expressing fruits supports the idea that the ERF.E proteins act as negative regulators of ripening initiation. Based on these observations, we suggest that the hypoxia in the locular tissue has an important role in the early stages of ripening, by acting upon SlERF.Es, which we show to be oxygen-sensitive and to have an important role in the upstream regulation of ripening.

Material and Methods

Plant material and sampling

Tomato plants used in this study *Solanum lycopersicum L.* cv Micro-Tom were sown directly in soil and grown under standard culture chamber conditions (14 h : 10 h, 25°C : 20°C, light : dark cycle, respectively, 80% relative humidity, 250 mol m^{-2} s^{-1}

intense light). The flowers were marked at the anthesis stage and fruits were sampled at different stages. For the transcriptomic analysis 10 fruits from different plants per replicate were collected at 33 Days Post-anthesis (DPA); 35 DPA, corresponding to gel at 100-150 μM oxygen concentration; 36 DPA, corresponding to gel at 0-50 μM oxygen concentration; Breaker (Br); and Br+4 days. Then gel and pericarp were separated and samples were frozen in liquid nitrogen, immediately after separation and stored at −80 °C. Three independent biological repeats were performed for each experiment.

Vector construction and transgenic lines

To generate over-expression lines the full-length of *SlERF.E2* and *SlERF.E4* genes, were amplified from Micro-Tom cDNA and assembled into the pDGB3alpha2 vector with a 2x35S promoter and Tnos terminator, then together with a kanamycin-resistance module (pDGB3alpha1-35S-NPTII-tNos) into the pDGB3omega1 expression vector via Golden Braid 3.0 system. To generate knock-out lines CRISPR-P (http://cbi.hzau.edu.cn/crispr/) was used to design all the sgRNAs that target either *SlERF.E2, SlERF.E4, SlRIN, SlPCO, SlPRT6b* or *SlATE*. Plasmids were assembled by the Golden Braid 3.0 system together with hCas9 module and with a kanamycin-resistance module described in Vazquez-Vilar et al., 2016. Sequences of the sgRNAs and the induced genomic mutations are given in Supplementary Figure 9. The final binary constructions were directly transformed into *A. tumefaciens* strain C58. Stable transformation of tomato was done as previously described (McCormick et al., 1986). Artificial microRNA (*amiATE*) tomato lines were kindly provided by F. Licausi lab.

The 35S:ERF.E-VENUS constructs were obtained by assembling *SlERF.E1, E2* and *E4* full length coding sequence or a version without the first 13 aminoacids (d13ERF.E) with a C- terminal VENUS tag into the pDGB3alpha2 vector and then directly transformed into *A. tumefaciens* strain C58 for transient expression in *N. benthamiana* plants. FRen-35S:ERF.E-FLuc were obtained by assembling full coding sequence of *SlERF.E1*, *E2* and *E4* or d13 versions with a *Firefly Luciferase* (FLuc) tag into the pDGB3alpha2 vector, then together with a module containing *Firefly Renilla* (pDGB3alpha1-35S-FRenilla-Tnos) into the pDGB3omega1 vector to then be used for protoplast transformation.

Transient expression assays and confocal microscopy

Suspensions of A. tumefaciens strain C58 were infiltrated into leaves of *N. benthamiana* as previously described (Martin et al., 2009). Following a 48-h incubation infiltrated plants were placed in an air-tight 22 L acrylic cabinet (Nalgene) under constant flow of either N_2 or air for 4 hours, thus emulating hypoxic (5% oxygen concentration) or normoxic conditions. Then water-mounted sections of leaf tissue were

examined by confocal microscopy. Leaves were observed using 10X dry or 25X objectives with a spectral confocal laser scanning system (SP8; Leica, Mannheim, Germany). An argon laser emitting at 514 nm was used to collect VENUS in the range 515–600 nm. Nuclear staining was performed by using DAPI (molecular probes) according to the manufacturer's instructions. For quantification of nuclear translocation of SlERF.Es after treatment, 2 mm^2 portions of three leaves from 5 plants per condition were analysed with ImageJ software version 1.8.0. The experiments were repeated three times.

Luciferase transactivation and protein stability in protoplast

Transactivation and protein stability assays were carried out using the *Renilla reniformis* (Rluc) and *Photinus pyralis* (Fluc) luciferase enzymes. To compare the stability of native *SlERF.E*s with the modified version *Sld13ERF.E*s, tomato mesophyll protoplasts were transiently transformed with plasmids bearing the construct FRen-35S:ERF.E-FLuc. For protoplast isolation, leaves were taken from 6 weeks-old plants and cut into thin strips. Leaf strips were placed in 20 mL of enzyme solution [2% cellulose R10, 1% macerozyme R10, 0.6 M mannitol, 20 mM KCl, 25 mM MES solution (pH 5.7), 10 mM $CaCl_2$ and 1% BSA] and incubated overnight in dark at 25°C. After the incubation, the enzyme solution was eluted with 20 ml of Wash Solution [WS, (0.6 M mannitol, 5 mM MES pH 5.7, 20 mM KCl, 10mM $CaCl_2$)] and filtered with a 40 µm nylon filter into a 50 ml conical tube. Protoplasts were pelleted by centrifugation, 100 rpm for 2 min, and resuspended in 10 mL of cold WS. Protoplasts were kept to precipitate for 30 min in ice. The WS was removed and protoplasts were resuspended in fresh WS. 2.5 µg of plasmid was added to 100 µL protoplast suspension in a 2 mL centrifuge tube. 110µL of a 40% PEG solution (0.2 M mannitol, 0.1 M $CaCl_2$) was added to each tube and the protoplasts were incubated for 20 min at room temperature in the dark. The transformation was stopped by adding 440 µl of WS solution and tubes were centrifuged at 100 rcf for 2 min. Protoplast were resuspended in 1 mL WS and incubated overnight in 6 multiwell plates in the dark at 25°C. Later, protoplasts were pelletted by centrifugation (700 rcf, 2 min) and flash frozen in liquid nitrogen. Samples were subsequently processed with the Dual-Luciferase Reporter Assay System (Promega, Madison, USA), and luciferase activity was quantified using VICTOR® Nivo™ Multimode Microplate Reader (PerkinElmer Inc., USA). Relative luciferase intensity values (Fluc/Rluc) were reported as means ±SE of four independent transfections. The assays were repeated at least three times independently.

Ethylene and oxygen measurements

To measure ethylene production, 20 fruits harvested at 33 DPA were placed in 120-mL jars, sealed, and incubated at room temperature for 1 hour before, 1 mL of headspace gas

being injected into an Agilent 7820A gas chromatograph equipped with a flame ionization detector (Agilent, Santa Clara, CA, USA). The samples were compared to a 4 ppm reagent-grade ethylene standard and normalized for fruit weight. The same fruits were then analyzed to determine oxygen profiles. Measurements were performed with an oxygen microsensor with a tip diameter of 100 µm (OX-100, Unisense) able to descend in the equatorial part of the fruit to a depth of 5500 µm evaluating oxygen concentration every 100 µm spanning different fruit tissues. The sensor was calibrated against completely aerated water and an anoxia solution of sodium ascorbate and NaOH 0.1 M. Oxygen imaging was done using a DU01 detector and SF-RPSu4 oxygen sensor foil (PreSens Precision Sensing GmbH, Germany). Fruits were cut along the plane perpendicular to columella (equatorial plane) and the chemiluminescent oxygen-sensing foil was deposit on the exposed tissue.

RNA extraction and qRT-PCR

Frozen fruit samples were homogenized to powder with the ball grinder Tissue Lyser II (Qiagen, France) by applying two cycles of 30 s at 300 Hz. From 200 mg of gel or pericarp total RNA was extracted with ReliaPrep™ RNA Tissue Miniprep System kit (Promega, France, Ref. Z6112) according to the manufacturer's instructions. Then DNA was removed from the total RNA sample with DNA-free™ DNA Removal Kit (Invitrogen, France). The quantity and quality of RNA were assessed by measuring the optical density (OD) at 260 nm and 280 nm by a spectrophotometer (NanoDrop 330, Thermo Fisher Scientific) and 2% (w/v) gel electrophoresis. The comparative threshold cycle method (DDCt) was used for quantitative PCR (QuantStudio 6 PCR system; Applied Biosystems, Carlsbad, CA, USA). *SlActin* (Sly11g0286941/Solyc11g005330) was used as an internal reference. The primers used are listed in Supplementary Table 2.

RNA-seq analyses

Five µg of total RNAs were used for high-throughput sequencing. Three biological replicates were prepared for each condition. RNA quality was checked on an Agilent 2100 Bioanalyzer System, using the RNA 6000 Nano kit protocol (Agilent Technologies, Germany). RNA samples with RNA Integrity Numbers greater than 7.5 were sent to Novogene Bioinformatics Technology Co., Ltd (Beijing, China) for cDNA library construction and sequencing on Illumina NovaSeq 6000 platform (Illumina, San Diego, CA). Raw sequence corresponding to paired-end reads (2x150bp) were treated as described by Althiab-Almasaud et al., 2021 and aligned to SLYMIC v.1.0 assembly and annotation of the *S. lycopersicum cv*. MicroTom reference genome (BioProject: PRJNA553986). The quality of alignments is listed in Supplementary Table 3.

Differential expression and downstream analyses

Differential expression (DE) analysis was performed as previously described by Chirinos et al. 2023. PCA analysis was performed with the plotPCA function of DESeq2. All graphs were plotted with ggplot2 version 3.3.3 R package. Hierarchical clustering and heatmap for the DEGs were generated with the pheatmap version 1.0.12 R package with Pearson correlation as the distance metric and a complete linkage method.

Weighted gene co-expression network analysis

Co-expression network modules were identified using normalized expression values and the WGCNA package (v1.71) in R. Genes with a low level of expression below 50 reads in all samples were discarded, leaving 23 062 genes for analysis. The co-expression modules were created with the automatic network construction function and a soft threshold (power) of 4, TOMType was “signed”, networkType was "signed hybrid", minModuleSize was 30, and mergeCutHeight was 0.15. List of genes belonging to each module are available in Supplementary Table 1.

Data availability

All RNA sequences are available from the Sequence Read Archive (SRA) at the National Center for Biotechnology Information, under accession PRJNA808237.

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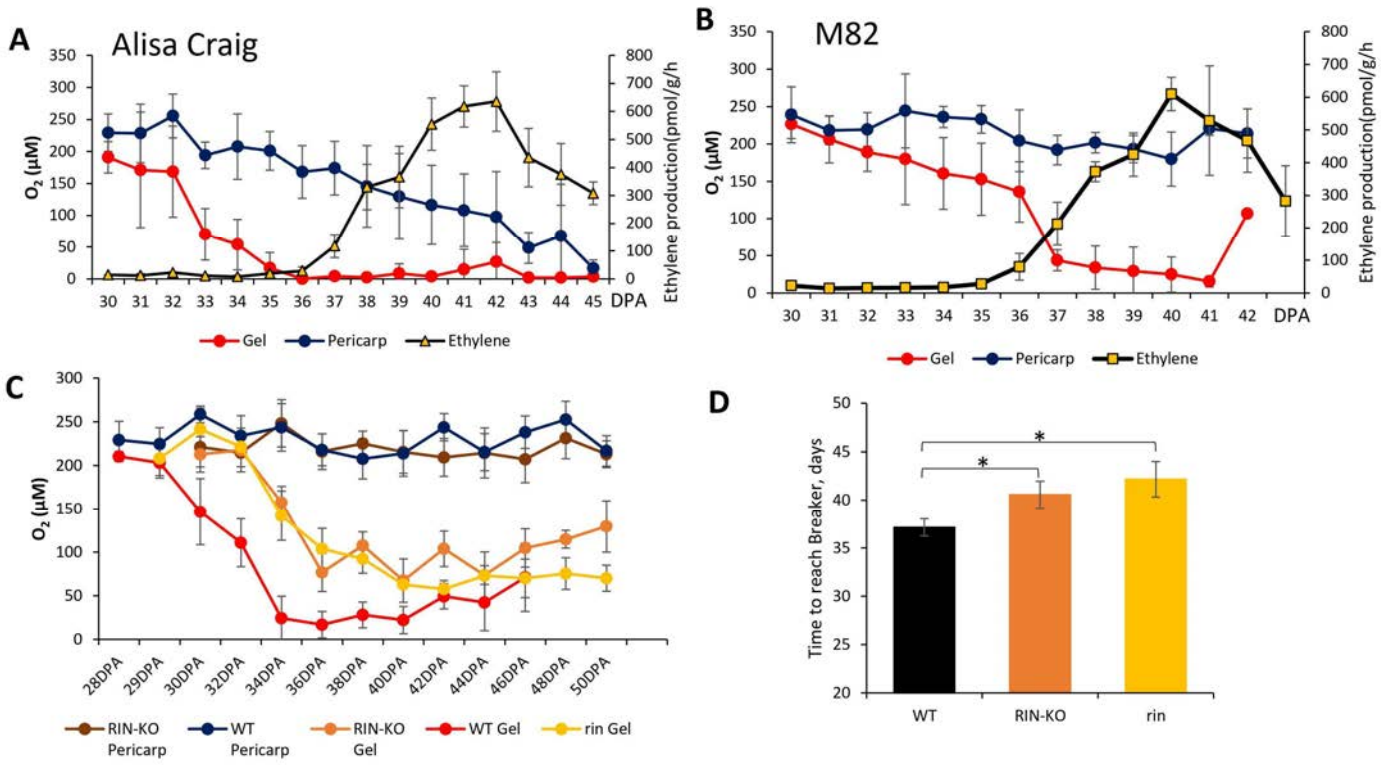
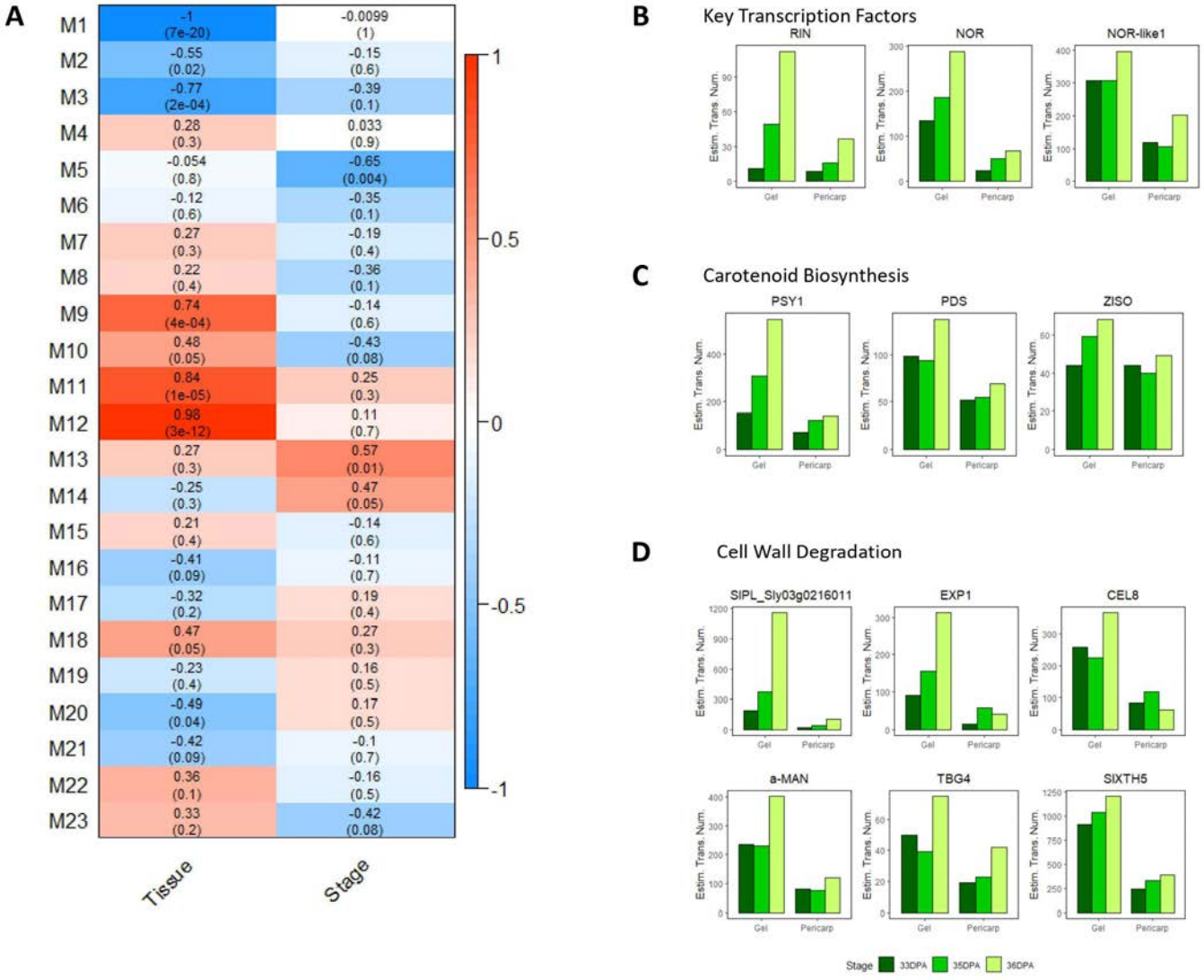
Supplementary tables can be found at the end of this manuscript.

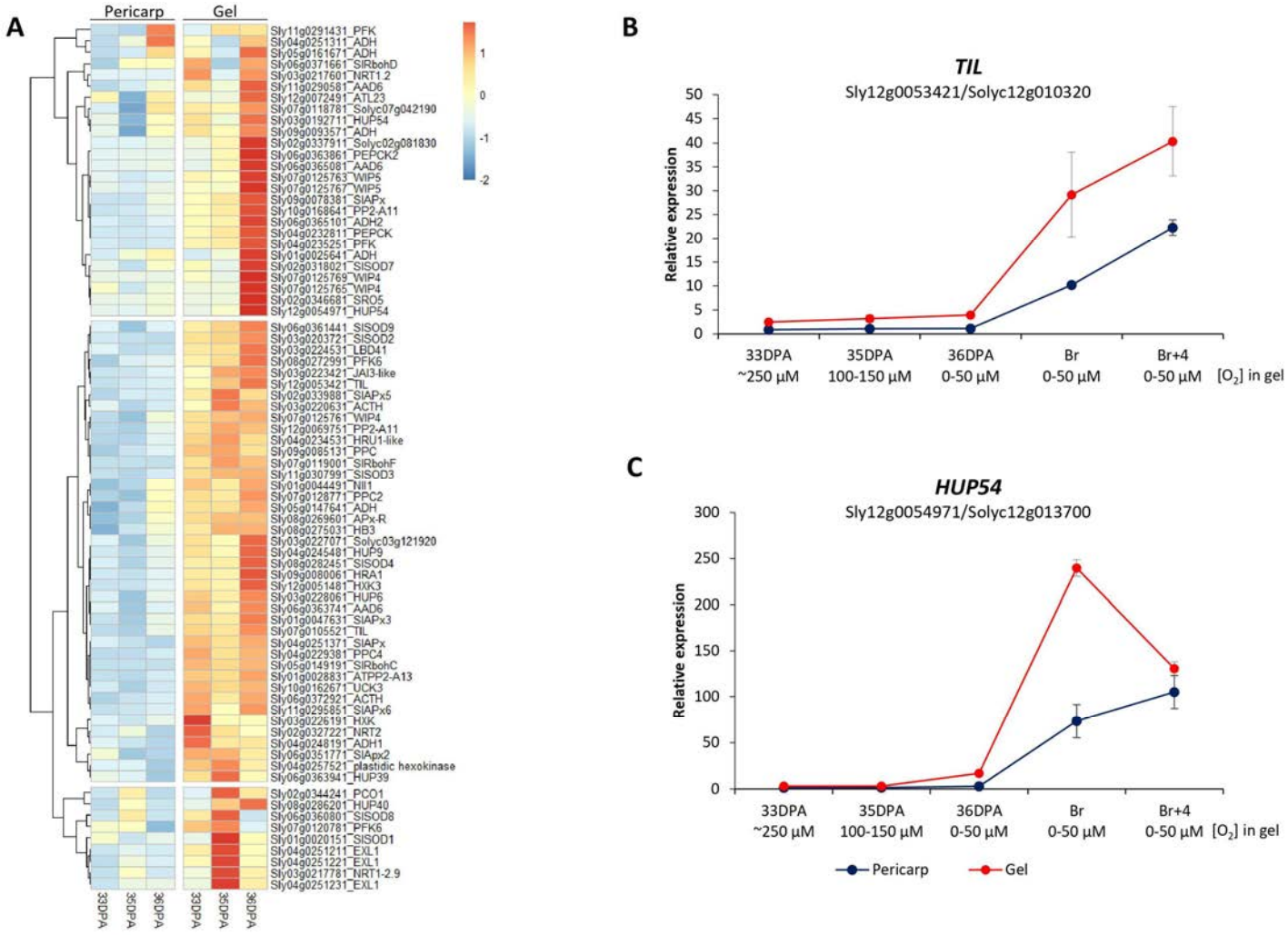
Supplementary Figures



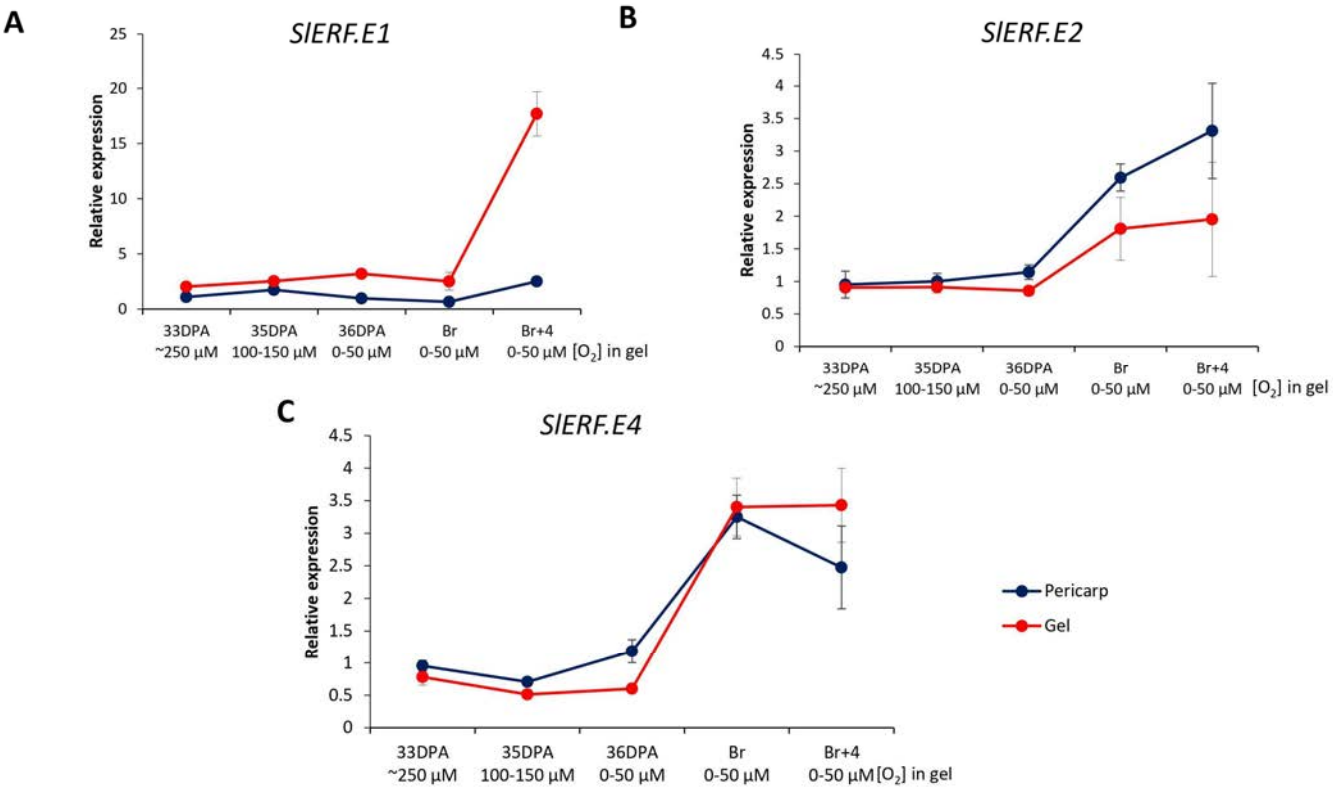
Supplementary Figure 1. Oxygen concentration in different tomato cultivars and *rin* mutants. Oxygen concentration (primary axis) in pericarp (blue), locular gel (red), and ethylene production (black) from MG (30 DPA) to red stage (45 DPA) in **(A)** Alisa Craig and **(B)** M82. **(C)** Oxygen evolution during ripening in WT-Pericarp (blue), RIN-KO-Pericarp (brown), WT-Gel (red), RIN-KO (Gel) and *rin*-Gel (yellow). **(D)** Time to reach breaker for WT and RIN-KO and *rin* (in days after pollination). Data represents mean values from at least 5 fruits. The bar plot show Mean ± SD, asterisks indicate significant differences determined by Student's t-test at * $p < 0.05$.



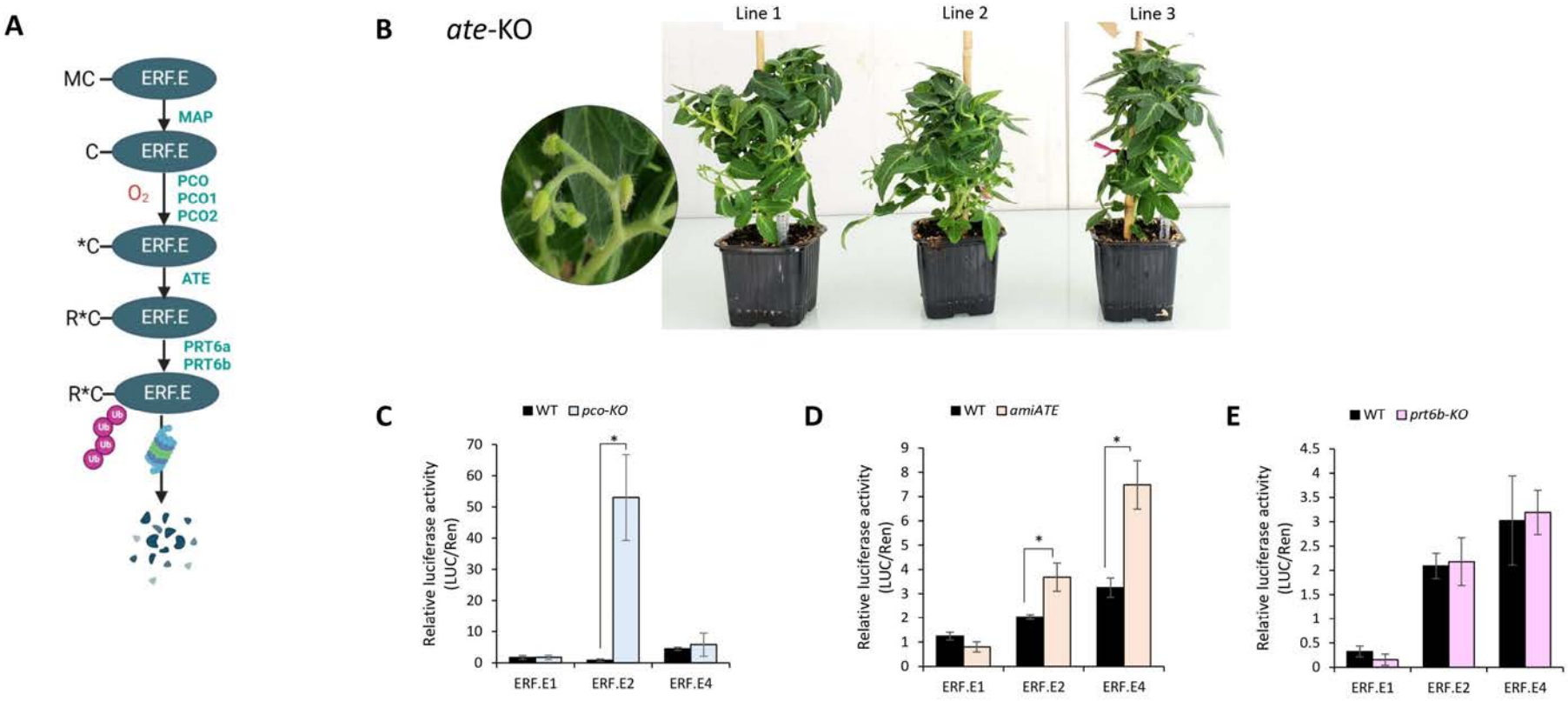
Supplementary Figure 3. Gene Co-expression Network Analysis (WGCNA) module correlation and key ripening gene expression. (A) Table representing the correlation between the modules (rows) and the factord (Tissue or Stage, columns). Numbers correspond to the correlation *r* (top) and the *p*-value in parentheses. The rows are colored based on the correlation of the module with the factor: red for positive and blue for negative correlation. **(B)** Expression in terms of Estimated Transcript Number of ripening-related genes in gel (left) and pericarp (right). M, module; DPA, days post anthesis.



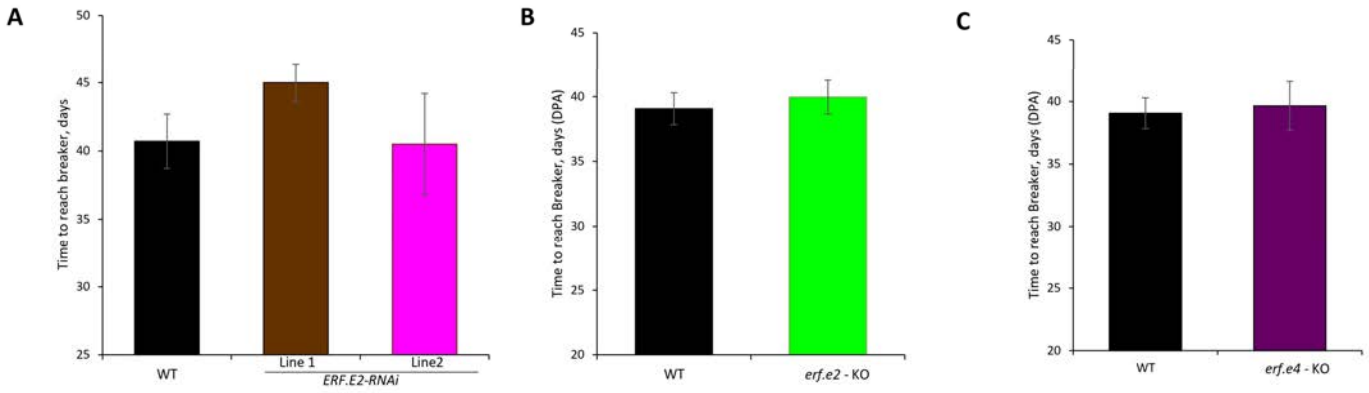
Supplementary Figure 4. Transcriptomic analysis of hypoxia core response genes during ripening. **(A)** Heatmap representing the expression pattern of orthologue hypoxia core response genes **(B and C)** Expression of hypoxic marker genes. Each graph shows qPCR relative expression in gel and pericarp tissues at different ripening stages. [O_2], oxygen concentration in locular gel tissue; DPA, days post anthesis; TIL, temperature-induced lipocalin; HUP, hypoxia-response unknown protein.



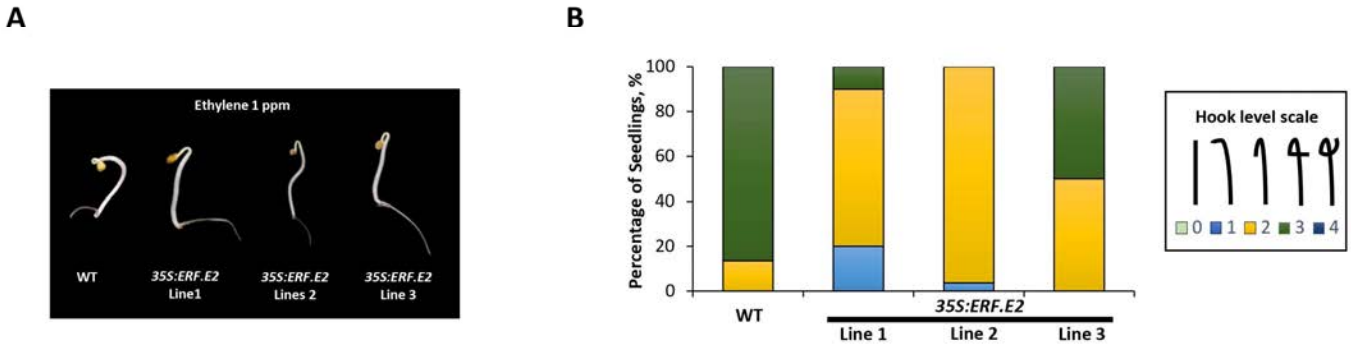
Supplementary Figure 5. Expression of SlERF.Es during ripening. (A) *SlERF.E1*, (B) *SlERF.E2* and (C) *SlERF.E4*. Each graph shows qPCR relative expression in gel and pericarp tissues at different ripening stages. [O_2], oxygen concentration in locular gel tissue; DPA, days post anthesis.



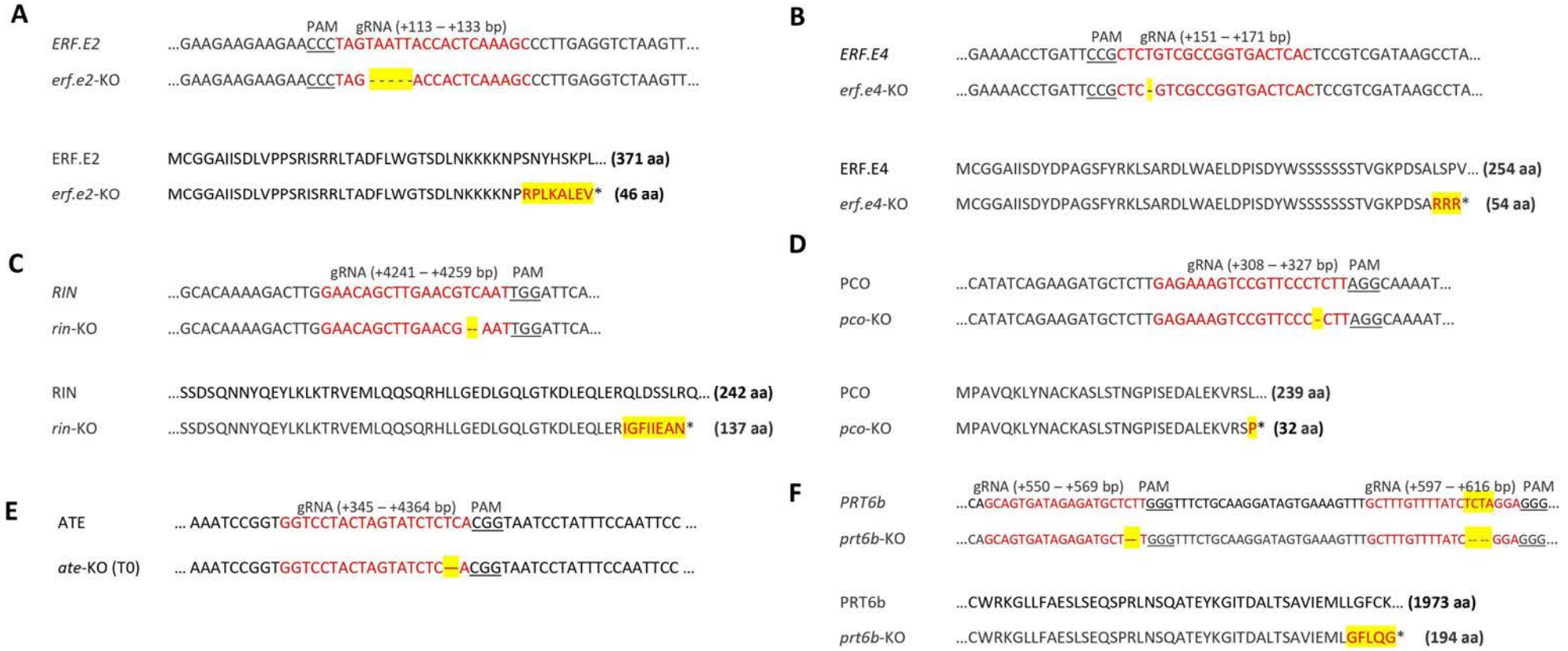
Supplementary Figure 6. (A) Proposed scheme representation of the N-end rule pathway that leads to oxygen-dependent ERF.E protein degradation. Enzymes annotated are the orthologues of *A. thaliana* in *S. lycopersicum*. *C, oxidized cysteine; PCO, Plant Cysteine Oxidase; MAP, Methionine Amino-Peptidase; ATE Arginyl Transferase; PRT6, PROTEOLYSIS E3 ligase. **(B)** *ate*-KO flowerless phenotype. **(C to E)** Oxygen-dependent modulation of luciferase after fusion with SlERF.E N-terminal in WT and (C) *pco-KO*, (D) *amiATE* and (E) *prt6b-KO* mutants. The bar plots show mean ± SD, *P < 0.05; Student's t-test.



Supplementary Figure 7. Time to reach breaker in days after pollination in (A) ERF.E2 downregulating lines, (B) ERF.E2 knock-out lines and (C) ERF.E4 knock-out lines.



Supplementary Figure 8. Ethylene triple response phenotype of WT and *SlERF.E2* over-expressing lines. When treated with 1 ppm ethylene WT seedlings responded with marked hook formation while the mutants had a minor but differential response. **(A)** Picture representative of the phenotype of at least 20 seedlings per line. **(B)** Bar plot representing the percentage of seedlings per line showing different hook level scale.



Supplementary Figure 9. Gene editing targeting of (A) *SlERF.E2,* (B) *SlERF.E4*, (C) *SlRIN*, (D) *SlPCO*, (E) *SlATE*, and (F) *SlPRT6b* genes. Upper panel of each figure show the genomic sequence in the first line and the deletion induced by Cas9 in the second line. Down panel show the aminoacid sequences in the first line and in the second the deletion and size of the protein induced by the mutation.

CHAPTER IV

General Conclusions and Perspectives

In order for fruit to ripen, a number of separate but interdependent processes need to be precisely synchronized. These processes result in color change brought on by pigment accumulation and chlorophyll degradation, flavor improvement due to the production of sugars, acids, and volatile compounds, and fruit softening brought on by cell wall remodeling. The ripening of fruit is comprised of all of these specialized activities that are spatiotemporally regulated and extraordinarily structured by a complex interplay of plant hormones, transcriptional regulators, and epigenomic modifications that ultimately define fruit quality. In particular, ripening of climacteric fruits, such as tomato, is associated with significantly increased respiration in conjunction with or just prior to a burst of the plant hormone ethylene. Because of this burst, which occurrs as a result of autocatalytic ethylene biosynthesis, ethylene has been regarded as the primary orchestrator of the ripening process, with early ripening regulation studies focusing on the role of this hormone (Lelièvre et al., 1997; Liu et al., 2015). However, information on the role of other phytohormes in ripening is limited. To investigate the ripening process in tomato, researchers have concentrated their efforts mostly on the pericarp tissue. This is likely due to the fact that the progression of ripening is often accompanied with discernible changes in the coloration of the pericarp's exterior. Nevertheless, it was recently shown that, despite the common belief that fruit texture and softening are related with the ripening phase, a major component of this fruit quality attribute is based on differentiation of the locular tissue that is determined at early pre-ripening stages (Huang et al., 2021). This is in line with previous studies indicating that initial ripening steps, including pigment accumulation and locular differentiation take place within the fruit inner tissues (Shinozaki et al., 2018). In light of this information, our research first concentrated on the early transcriptomic changes associated with ripening initiation in two different fruit tissues, gel and pericarp, as well as the interaction of auxin and ethylene during this process (Chapter II).

Taken as a whole, the findings of Chapter II study, shed new light on the reprogramming of tomato fruit's transcriptome that occurs during the ripening process, and highlight the role of inner tissues in these transformations. In addition, while so far most transcriptomic profiling of fruit ripening has primarily concentrated on the changes that take place in pericarp tissues between the Mature Green (MG) and Breaker (Br) stages, our study addresses separately the changes occuring in gel and pericarp tissues at the early phases of the transition to ripening. To this end, we defined in unprecedented way two as new stages, the Early Mature Green (EMG) and Late Mature Green (LMG) to better capture the early events of ripening initiation. The comparative study of the transcriptome dynamics reveals that the early events of the ripening process start in the locular gel before extending to the pericarp. Interestingly, the genome-wide transcriptomic analysis shows that a wide range of transcription factor families are engaged in the global reprogramming

of gene expression, thereby highlighting the diversity and complexity of signaling pathways associated with the ripening process. In particular, the study identified a set of transcription factors that are uniquely regulated during the MG stage in the gel but not in the pericarp. In this regard, the findings provide new leads towards the investigation of the initial factors and events underlying the transition from immature to ripe fruit. Nevertheless, there is still a long way before uncovering the potential roles that these transcription factors play in the ripening process. In-depth investigation of these potential candidates needs to be conducted now, beginning with the examination of their expression patterns using tools such as TomExpress. Also, the *in silico* characterisation of their functional domains and the presence of predicted regulatory elements in their promoters should provide clues into their potential functional significance. Finally, for the selected best candidates, reverse genetics approaches, via over-expression or knock-out strategies, can be implemented to address their putative role in triggering and regulating the ripening process. The outcome of the study also provides evidence for a multi-hormonal control of the transitioning to ripening and reveals that a reformed auxin homeostasis is essential for the ripening to proceed. In particular, the data show the antagonistic role of auxin and ethylene regulating shift from System-1 to System-2 ethylene production. In this respect, our study open new research avenues to fully understand the extent of auxin contribution to ripening initiation, and to further define the pathways and gene networks through which auxin is impacting this developmental transition.

It is widely accepted that ethylene is essential for the initiation and coordination of climacteric fruit ripening (Liu et al., 2015) and that EthyleneRresponse Factors (ERFs), which form a large multigene family of transcription factors, are the final actors in the ethylene signaling pathway and the mediators of ethylene responses. However, the mechanisms by which ERFs regulate ripening genes are largely unknown. We previously revealed that sub-class E tomato ERFs (ERF.E1, E2, E4) display a ripening-associated expression pattern (Liu et al., 2016). Notably, the *SlERF.Es* are distinguished by a conserved N-terminal domain (MCGGAII/L) predicted to target the encoded proteins to proteolytic degradation in normal oxygen conditions via the "N-end rule" pathway while hypoxic conditions (low oxygen levels) promote their stabilization and relocalization to the nuclear compartment, as demonstrated in *Arabidopsis* (Gibbs et al., 2011; Licausi et al., 2011). These observations prompted us to assess the oxygen levels in fruit tissues and to address the impact of hypoxia/normoxia on *SlERF.Es* during tomato fruit ripening (Chapter III).

Our findings (Chapter III), reveal that in tomato fruit, locular gel, but not pericarp tissues, undergo a dramatic decrease in oxygen levels prior to ripening initiation. However, further investigation is still needed to determine whether this oxygen depletion plays a role

in the transition to ripening and how it affects ERF.E transcription factors. We have demonstrated that hypoxia and ripening induce the expression of *SlERF.Es* and that low oxygen conditions cause a change in the subcellular localization of SlERF.Es, leading to their relocalization from the plasma membrane to the nucleus. Additionally, we established that SlERF.Es stability is regulated by oxygen concentration. However, data related to SlERF.Es protein levels in tomato fruit during ripening are still lacking. One possible approach to clarify this issue would be to detect the ERF.E proteins by western blot in subcellular fractions at different ripening stages. Another option would be to expresss a recombinant ERF.E proteins tagged with GFP and to use fluorescent microscopy approach, although in our experience, this approach is challenging, because fruit tissues are highly auto-fluorescent preventing low abundant transcription factors like SlERF.Es from being detected.

Our preliminary data showing the stabilization of SlERF.E2 and SlERF.E4 in mesophyll protoplasts, where some members of the N-end rule pathway have been silenced, support the notion that these two ERF members are substrates of this protein degradation pathway. Yet, direct evidence for the functional role of the N-end rule genes in fruit ripening is still missing. Notably, over-expression of SlERF.E2 or SlERF.E4 results in delayed ripening along with reduced climacteric ethylene production, suggesting that these genes are negative regulators of ripening initiation. Strickingly, knock-out or knock-down lines of each of these two transcription factors did not show a ripening-associated phenotypes, likely due to a functional redundancy among the two ERFs. However, the simultaneous knock-out of both *SlERF.E2* and *SlERF.E4* genes may overcome the putative redundancy. Therefore, this approach has to be performed in the future. In addition, combined RNA-Seq and Chromatin Immunoprecipitation Sequencing (ChIP-Seq) or DNA Affinity Purification and sequencing (DAP-Seq) approaches may allow defining the putative direct target genes of these transcription factors. On the other hand, SlERF.E1 is an interesting candidate to investigate in order to better understand the changes in locular gel tissue associated with ripening. It is noteworthy that among all *SlERF.Es*, this genes exhibits higher expression in gel compared to pericarp, in addition of being to be regulated by *SlERF.E4* (Liu et al., 2016). Theses features point to its potential role in controlling the initial events of ripening occurring in the locular tissues.

Overall, the outcome of the studies conducted within the framework of the thesis project provide novel insight into the intricate systems and molecular variables that govern the initiation of the ripening process.

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Supplementary Tables Chapter II

Supplementary Table 1. *Solanum lycopersicum* putative Transcription Factor (TF) genes differentially expressed in this study.

Normal ripening (in blue): estimated trancript number, cluster number, gene expression at different ripening stages in Gel and Pericarp (Per) , and statistical results in normal ripening conditions, adjusted p-value < 0.05, multifactor design test using DESeq2 package.

Auxin treatment (in green): Log 2(fold change) and adjusted p-value after 72h of auxin treatment.

EMG, early mature green; LMG, late mature green; Br, breaker; Br+4, breaker +4 days; padj ,adjusted p-value

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly11g0312491	Solyc11g072600	AP2		C1	28	7	1	1	84	28	1	1	2.2E-10		
Sly03g0222571	Solyc03g117720	AP2		C2	1	1	6	6	8	15	24	12	1.0E-09		
Sly11g0291711	Solyc11g010710	AP2		C2	7	4	12	5	17	12	82	43	8.6E-06	-1.56	1.5E-02
Sly01g0032351	Solyc01g096860	AP2		C1	14	7	1	0	4	3	1	0	4.0E-05		
Sly08g0284641	Solyc08g081650	AP2		C1	4	4	1	1	3	3	2	1	4.2E-04		
Sly02g0348681	Solyc02g092050	AP2		C3	1	1	0	0	1	1	0	1	5.2E-04		
Sly05g0155911	Solyc05g051380	AP2		C1	5	2	1	1	2	1	0	1	7.1E-04		
Sly03g0199301	Solyc03g044300	AP2	*AP2a*	C2	17	57	600	413	89	88	417	409	7.4E-04	-1.55	4.5E-03
Sly02g0325121	Solyc02g064960	AP2		C1	1	1	1	0	1	1	1	1	6.8E-03	1.56	3.0E-03
Sly02g0349841	Solyc02g093150	AP2		C1	48	33	18	7	69	38	17	8	1.2E-02		
Sly09g0078371	Solyc09g007260	AP2		C1	4	4	1	1	5	3	1	1	1.5E-02		
Sly02g0319171	Solyc02g030210	AP2		C3	34	39	29	42	30	38	33	45	1.7E-02		
Sly03g0227551	Solyc03g123430	AP2		C1	1	1	0	0	5	5	2	1	1.9E-02		
Sly07g0112371	Solyc07g018290	AP2		C1	4	1	1	1	2	1	1	1	2.0E-02		
Sly10g0188331	Solyc10g084340	AP2		C1	6	9	3	1	2	3	1	1	3.0E-02		
Sly06g0378171	Solyc06g075510	AP2		C1	1	1	1	1	2	2	2	1	3.2E-02		
Sly04g0242301	Solyc04g049800	AP2		C1	16	16	6	4	4	4	4	4	3.9E-02		
Sly06g0371541	Solyc06g068570	AP2		C1	7	5	1	1	17	16	1	1	4.1E-02		
Sly01g0004061	Solyc01g008890	AP2	*SlERF.H16/CRF3*	C2	19	20	24	31	18	22	21	24	5.0E-02		
Sly01g0038341	Solyc01g103050	ARF	*SlARF1*	C1	119	73	22	20	106	66	24	30	6.7E-17		
Sly03g0223161	Solyc03g118290	ARF	*SlARF2A*	C2	222	274	436	375	110	150	357	306	1.2E-13		
Sly07g0111231	Solyc07g016180	ARF	*SlARF7A*	C1	18	17	1	2	37	47	14	16	1.9E-12		
Sly09g0078981	Solyc09g007810	ARF	*SlARF16A*	C1	6	8	3	4	11	12	12	11	7.4E-10		
Sly02g0321431	Solyc02g037530	ARF	*SlARF8B*	C1	35	34	10	12	14	16	7	8	1.3E-09	0.68	1.6E-04
Sly08g0285761	Solyc08g082630	ARF	*SlARF9A*	C1	22	14	1	1	7	4	1	1	7.8E-09	2.40	1.6E-02
Sly03g0196581	Solyc03g031970	ARF		C1	104	97	76	81	94	98	54	49	2.7E-07		
Sly11g0309901	Solyc11g069190	ARF	*SlARF4*	C1	211	173	10	2	78	83	28	20	3.6E-05		
Sly05g0161121	Solyc05g056040	ARF	*SlARF24*	C1	69	39	11	10	67	42	15	7	3.5E-04		
Sly05g0153701	Solyc05g047460	ARF	*SlARF7B*	C3	20	19	14	14	25	32	21	36	1.1E-03		
Sly08g0263311	Solyc08g008380	ARF	*SlARF9B*	C1	15	11	5	3	19	16	9	9	2.3E-03		
Sly07g0118851	Solyc07g042260	ARF	*SlARF19*	C1	7	7	3	3	6	9	5	4	4.6E-03	0.44	1.0E-02
Sly12g0065841	Solyc12g042070	ARF	*SlARF2B*	C4	108	101	106	112	96	104	77	102	1.2E-02		
Sly06g0378021	Solyc06g075150	ARF	*SlARF10B*	C2	11	12	12	12	6	7	15	10	2.0E-02		
Sly01g0031511	Solyc01g096070	ARF	*SlARF18*	C1	18	14	1	1	9	6	2	1	2.6E-02		
Sly12g0050081	Solyc00g196060	ARF	*SlARF6A*	C1	18	13	7	8	22	20	11	8	2.7E-02	0.31	6.1E-03
Sly11g0310211	Solyc11g069500	ARF	*SlARF10A*	C2	25	25	17	22	20	35	44	32	4.3E-02		
Sly02g0333461	Solyc02g077560	ARF	*SlARF3*	C1	79	82	84	66	75	79	72	61	4.5E-02		
Sly03g0196571	Solyc03g031970	ARF	*SlARF8A*		42	36	27	27	33	36	22	18		0.39	1.4E-03
Sly12g0053431	Solyc12g010330	ARR-B	*SlRR22*	C2	22	24	46	50	19	22	27	30	2.2E-10		
Sly05g0142931	Solyc05g014260	ARR-B	*SlRR21*	C1	20	18	4	1	22	25	10	2	1.3E-07		
Sly05g0159351	Solyc05g054390	ARR-B	*SlRR9*	C1	40	33	32	61	74	56	20	20	2.1E-05	-0.29	3.1E-02
Sly08g0279671	Solyc08g077230	ARR-B	*SlPRR8*	C2	33	65	405	189	8	11	79	34	1.9E-04	-0.66	3.8E-02
Sly06g0366561	Solyc06g061030	ARR-B	*SlPRR7*	C1	3	4	2	1	11	15	6	2	2.1E-04		
Sly04g0230641	Solyc04g008050	ARR-B	*SlRR8*	C1	22	21	12	5	22	26	17	16	1.1E-03		
Sly07g0105451	Solyc07g005140	ARR-B	*SlRR23*	C2	2	1	1	1	9	9	11	10	7.1E-03		
Sly11g0312251	Solyc11g072330	ARR-B	*SlRR14*	C2	18	21	26	27	12	13	13	18	1.2E-02		
Sly01g0017831	Solyc01g065540	ARR-B	*SlRR10*	C1	17	17	14	12	18	17	15	10	4.5E-02		
Sly08g0269141	Solyc08g029090	B3		C1	20	21	9	1	12	17	13	4	1.2E-08		
Sly08g0260721	Solyc08g006220	B3		C2	9	8	20	23	12	15	17	18	1.0E-06		
Sly10g0181281	Solyc10g075030	B3		C1	31	35	16	5	31	34	29	18	2.9E-06		
Sly08g0260731	Solyc08g006230	B3		C2	6	6	15	23	10	11	11	12	2.2E-05		
Sly02g0325561	Solyc02g065350	B3		C1	10	8	2	1	15	13	4	2	6.3E-05		
Sly01g0043941	Solyc01g108120	B3		C2	12	12	20	20	19	18	23	24	6.7E-05		
Sly02g0346731	Solyc02g090170	B3		C1	5	3	1	1	1	1	1	1	8.3E-05		
Sly08g0260741	Solyc08g006230	B3		C2	7	7	22	35	12	10	12	12	1.4E-04		
Sly02g0351321	Solyc02g094460	B3	*FUS3*	C1	7	3	1	1	2	1	1	1	1.4E-04		
Sly01g0041831	Solyc01g106230	B3		C1	2	2	1	1	1	1	1	1	4.1E-04		
Sly06g0381631	Solyc06g083600	B3	*ABI3-like1/ABI3*	C1	3	2	1	1	2	1	0	0	6.3E-04		
Sly10g0186921	Solyc10g083210	B3		C1	4	3	3	2	31	16	6	3	6.5E-04		
Sly02g0335021	Solyc02g079020	B3		C1	20	25	9	5	22	25	16	15	2.6E-03		
Sly06g0376711	Solyc06g073980	B3		C2	1	1	1	0	3	3	4	3	5.7E-03		
Sly08g0260971	Solyc08g006260	B3		C1	5	4	2	1	5	6	5	2	7.0E-03		
Sly03g0215711	Solyc03g111410	B3		C2	12	12	25	27	10	10	15	20	7.9E-03		
Sly03g0215821	Solyc03g111500	B3		C1	4	3	3	2	5	6	6	4	8.6E-03		
Sly06g0380431	Solyc06g082520	B3		C1	19	14	13	6	54	32	19	20	8.7E-03		
Sly07g0125581	Solyc07g054630	B3		C2	9	11	17	16	7	8	12	11	9.0E-03		
Sly02g0347301	Solyc02g090710	B3		C1	40	38	29	35	35	34	32	32	1.2E-02		
Sly08g0286571	Solyc08g083400	B3		C2	1	0	1	1	1	1	1	1	1.4E-02		
Sly01g0032271	Solyc01g096790	B3		C1	2	2	1	2	13	17	6	4	1.6E-02		
Sly01g0043951	Solyc01g108130	B3		C2	14	11	17	21	19	15	15	18	1.7E-02		
Sly11g0302371	Solyc11g045450	B3		C1	2	2	0	0	1	1	0	0	1.7E-02		
Sly01g0043961	Solyc01g108140	B3		C1	5	4	2	1	5	5	3	2	2.1E-02		
Sly01g0044801	Solyc01g108930	B3		C1	28	28	2	1	6	12	2	1	2.2E-02		
Sly06g0353571	Solyc06g007530	B3		C1	7	7	5	4	11	11	8	5	3.2E-02		
Sly01g0044811	Solyc01g108940	B3		C1	7	5	1	1	2	2	1	1	3.4E-02		
Sly08g0275591	Solyc08g068540	B3		C1	8	10	6	7	7	8	8	6	3.6E-02		
Sly12g0051211	Solyc12g007300	B3		C2	4	5	36	42	6	5	14	26	3.9E-02	-0.80	4.3E-02
Sly02g0337871	Solyc02g081780	B3		C1	2	2	0	0	1	1	0	0	4.4E-02		
Sly01g0023671	Solyc01g081400	B3		C4	12	12	16	18	11	14	9	10	4.9E-02		
Sly03g0193441	Solyc03g007140	B3		C1	17	19	13	9	13	16	11	9	5.0E-02		
Sly04g0231121	Solyc04g008380	BBR-BPC		C2	71	70	111	105	77	68	81	75	3.0E-06		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly08g0278571	Solyc08g076230	BBR-BPC		C4	9	10	12	14	9	11	7	9	6.1E-04		
Sly01g0046401	Solyc01g110470	BBR-BPC		C4	15	19	18	20	15	18	12	12	1.3E-03		
Sly06g0374901	Solyc06g072370	BBR-BPC		C1	7	6	7	6	6	6	5	4	4.5E-02		
Sly08g0260221	Solyc08g005780	BES1	*BAM8-like*	C2	10	30	392	936	9	10	61	474	6.6E-16	-1.96	3.2E-05
Sly02g0323991	Solyc02g063010	BES1	*BES1-like*	C1	109	100	43	68	108	97	63	68	3.5E-04		
Sly07g0128531	Solyc07g062260	BES1	*BEH4-like3*	C1	6	5	2	3	11	9	6	7	3.4E-03		
Sly04g0255911	Solyc04g079980	BES1	*SlBES1/BZR1/SlBZH*	C4	24	25	34	35	28	28	24	21	1.1E-02		
Sly02g0331791	Solyc02g071990	BES1	*SLB3*	C1	29	20	15	21	56	44	26	33	1.4E-02		
Sly03g0192101	Solyc03g005990	BES1	*BEH4-like2*	C2	6	4	6	12	11	10	9	13	3.1E-02		
Sly12g0072051	Solyc12g089040	BES1	*SlBZH1 /SlBZR1*	C2	44	47	73	120	46	48	46	71	4.6E-02		
Sly07g0112061	Solyc07g018010	bHLH		C1	85	5	1	1	321	185	1	1	1.3E-34		
Sly01g0027911	Solyc01g090790	bHLH		C1	1	1	1	0	13	19	2	1	2.4E-28		
Sly10g0183521	Solyc10g079070	bHLH		C1	23	20	4	6	27	52	7	7	4.3E-19		
Sly02g0336041	Solyc02g079970	bHLH		C1	285	301	92	113	152	149	118	102	5.7E-15		
Sly10g0166671	Solyc10g009290	bHLH		C1	2	1	0	0	49	13	1	1	1.8E-09		
Sly08g0263571	Solyc08g008600	bHLH		C1	1	0	0	0	7	8	0	0	4.7E-09	-2.10	1.6E-04
Sly06g0368761	Solyc06g065040	bHLH		C2	3	3	25	66	2	3	7	25	2.3E-07		
Sly05g0138721	Solyc05g009880	bHLH		C1	1	1	0	0	2	3	1	0	3.3E-07		
Sly05g0143291	Solyc05g014590	bHLH	*SlybHLH076*	C1	10	2	3	1	206	77	1	1	5.1E-07	2.79	3.7E-04
Sly08g0286341	Solyc08g083170	bHLH		C1	1	1	0	0	13	7	0	0	7.9E-07		
Sly01g0031841	Solyc01g096370	bHLH		C1	2	1	1	0	3	2	0	1	4.2E-06		
Sly09g0094421	Solyc09g065100	bHLH	*SlAN1/SlbHLH150*	C1	14	11	1	1	3	2	1	1	7.8E-06	2.23	3.6E-03
Sly06g0362111	Solyc06g050840	bHLH		C1	44	59	6	1	15	18	3	1	1.5E-05		
Sly12g0074931	Solyc12g098620	bHLH		C2	1	2	35	72	1	1	3	20	1.5E-05		
Sly10g0165441	Solyc10g008250	bHLH		C1	34	14	1	1	35	30	1	0	2.2E-05		
Sly06g0381141	Solyc06g083170	bHLH		C1	2	1	0	1	4	3	1	1	3.6E-05		
Sly05g0135151	Solyc05g006650	bHLH		C1	6	4	3	2	24	31	25	7	4.0E-05		
Sly09g0093251	Solyc09g063010	bHLH		C3	12	11	17	35	10	7	9	33	4.6E-05	0.94	2.3E-02
Sly02g0332731	Solyc02g076920	bHLH		C1	2	2	1	1	1	1	1	1	1.3E-04		
Sly06g0359141	Solyc06g035490	bHLH		C1	6	1	0	0	20	4	1	1	1.6E-04		
Sly09g0095281	Solyc09g065820	bHLH		C1	29	28	14	22	46	46	30	29	3.1E-04	0.43	7.2E-03
Sly04g0254611	Solyc04g078790	bHLH		C2	0	0	1	2	1	1	3	8	3.5E-04		
Sly08g0279241	Solyc08g076820	bHLH		C1	2	1	1	0	1	2	0	0	4.0E-04		
Sly10g0163461	Solyc10g006510	bHLH		C2	16	14	25	36	19	17	21	28	4.5E-04		
Sly01g0045591	Solyc01g109700	bHLH		C1	19	6	2	5	23	10	3	5	4.6E-04		
Sly06g0362511	Solyc06g051260	bHLH		C1	7	6	1	0	12	14	3	1	4.6E-04		
Sly12g0065701	Solyc12g042010	bHLH		C1	2	3	5	7	40	36	12	4	5.2E-04		
Sly02g0344371	Solyc02g087860	bHLH		C1	1	1	0	0	1	1	1	1	7.0E-04		
Sly03g0191411	Solyc03g005350	bHLH		C2	21	25	38	40	21	25	30	31	7.5E-04		
Sly07g0117271	Solyc07g039570	bHLH		C1	4	1	0	0	4	1	1	0	1.1E-03		
Sly03g0224361	Solyc03g119390	bHLH		C1	2	1	0	0	6	3	1	1	1.5E-03		
Sly03g0193191	Solyc03g006910	bHLH		C1	1	1	0	0	7	4	1	1	1.6E-03	-2.90	1.2E-03
Sly07g0120171	Solyc07g043580	bHLH	*SlbHLH052/PIF4*	C1	15	12	2	2	23	29	5	2	1.6E-03		
Sly12g0076521	Solyc12g100140	bHLH		C1	19	16	2	2	19	26	5	3	1.6E-03		
Sly02g0341271	Solyc02g084880	bHLH		C1	1	1	1	1	2	2	1	1	1.7E-03		
Sly09g0104751	Solyc09g098110	bHLH		C1	8	6	5	4	23	13	5	4	1.8E-03		
Sly11g0305281	Solyc11g056650	bHLH		C3	7	7	2	4	5	4	5	11	1.9E-03		
Sly01g0031491	Solyc01g096050	bHLH	*bHLH113*	C1	34	27	42	35	178	62	91	70	1.9E-03	-0.36	1.6E-03
Sly03g0225621	Solyc03g120530	bHLH		C1	15	13	3	1	9	13	6	3	2.0E-03		
Sly02g0349961	Solyc02g093280	bHLH		C1	2	1	1	1	7	5	2	1	2.8E-03		
Sly08g0284061	Solyc08g081140	bHLH	*SlJAF13/SlbHLH90*	C1	20	21	2	1	13	17	10	7	3.4E-03	0.79	1.5E-02
Sly04g0229441	Solyc04g006990	bHLH		C2	1	1	1	1	1	1	2	2	3.5E-03	-1.67	3.1E-02
Sly07g0123551	Solyc07g052670	bHLH		C1	11	7	1	1	6	5	3	2	4.2E-03		
Sly06g0372431	Solyc06g069370	bHLH	*SlBIM1b*	C2	12	11	19	18	8	7	14	15	4.3E-03		
Sly08g0259271	Solyc08g005050	bHLH	*MYC1*	C1	51	17	5	21	81	38	19	45	5.3E-03		
Sly08g0279361	Solyc08g076930	bHLH	*MYC2*	C1	88	51	43	100	138	75	85	158	5.8E-03		
Sly08g0277291	Solyc08g075090	bHLH		C1	120	113	109	81	169	165	100	74	6.1E-03		
Sly10g0183501	Solyc10g079050	bHLH	*SlbHLH95*	C2	2	1	92	211	3	4	12	50	6.4E-03		
Sly07g0130221	Solyc07g063830	bHLH		C1	1	1	0	0	1	2	1	1	6.6E-03		
Sly01g0034251	Solyc01g098720	bHLH		C1	1	0	0	0	3	2	1	0	7.9E-03		
Sly01g0043711	Solyc01g107950	bHLH		C1	3	3	0	0	1	1	0	0	8.9E-03		
Sly06g0371851	Solyc06g068870	bHLH		C1	135	168	125	107	62	77	112	82	9.0E-03	-0.44	2.6E-06
Sly04g0234281	Solyc04g014360	bHLH		C1	1	0	0	0	2	1	0	0	9.1E-03		
Sly01g0037081	Solyc01g102300	bHLH	*PIF3/SlbHLH006*	C1	53	61	37	51	28	48	42	43	9.4E-03		
Sly03g0218721	Solyc03g114230	bHLH		C1	1	0	0	0	4	5	0	0	1.0E-02		
Sly01g0042091	Solyc01g106460	bHLH		C1	4	1	0	0	2	1	1	0	1.0E-02		
Sly05g0154911	Solyc05g050560	bHLH		C1	13	9	7	7	43	16	9	10	1.1E-02		
Sly02g0348311	Solyc02g091690	bHLH		C1	186	114	2	2	24	34	10	4	1.2E-02		
Sly04g0254501	Solyc04g078690	bHLH		C1	8	5	3	2	10	8	5	2	1.3E-02		
Sly03g0223181	Solyc03g118310	bHLH		C1	4	4	0	1	2	2	1	1	1.3E-02		
Sly04g0253251	Solyc04g077480	bHLH		C1	9	9	6	4	7	8	5	3	1.4E-02		
Sly01g0047271	Solyc01g111130	bHLH		C2	17	21	27	25	16	21	20	23	1.7E-02		
Sly01g0015171	Solyc01g057300	bHLH		C3	1	1	1	2	1	1	1	1	1.7E-02		
Sly09g0104501	Solyc09g097870	bHLH	*SlbHLH62*	C1	62	97	96	51	35	39	33	23	2.0E-02	-0.65	2.5E-02
Sly01g0005521	Solyc01g010130	bHLH		C1	5	4	1	1	4	5	3	2	2.0E-02		
Sly04g0228561	Solyc04g005280	bHLH		C2	25	31	36	52	23	26	26	33	2.0E-02		
Sly04g0228401	Solyc04g005130	bHLH		C1	4	3	1	2	5	5	5	2	2.0E-02		
Sly03g0217921	Solyc03g113560	bHLH		C2	1	1	1	1	1	1	2	1	2.1E-02		
Sly03g0219311	Solyc03g114720	bHLH	*SlBIM1a*	C1	30	25	15	21	34	32	19	19	2.1E-02		
Sly02g0324481	Solyc02g063430	bHLH		C1	40	18	2	1	22	7	1	1	2.3E-02		
Sly07g0130461	Solyc07g064040	bHLH		C2	133	123	175	218	210	183	150	166	2.3E-02		
Sly07g0124201	Solyc07g053290	bHLH		C1	18	25	7	5	15	20	17	9	2.4E-02		
Sly03g0213541	Solyc03g097820	bHLH	*SlbHLH22*	C1	8	4	1	1	3	2	1	1	2.5E-02		
Sly06g0367101	Solyc06g062460	bHLH		C1	3	1	1	0	1	1	1	1	2.8E-02		
Sly09g0094211	Solyc09g064920	bHLH		C2	17	16	20	31	19	16	12	20	3.1E-02		
Sly05g0139831	Solyc05g010610	bHLH		C1	9	8	5	5	7	8	6	5	3.3E-02		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly03g0211621	Solyc03g095980	bHLH		C1	2	3	1	1	2	7	2	1	3.6E-02	1.22	7.3E-05
Sly09g0100131	Solyc09g083360	bHLH		C1	24	4	1	0	60	23	1	0	3.6E-02		
Sly02g0326741	Solyc02g067380	bHLH	*SlPRE2*	C1	1	1	0	0	2	2	0	0	4.1E-02		
Sly06g0375091	Solyc06g072520	bHLH		C4	1	4	3	4	1	3	1	1	4.2E-02	-1.17	5.6E-03
Sly06g0354071	Solyc06g008030	bHLH		C1	9	7	10	6	25	39	22	18	4.6E-02		
Sly01g0024731	Solyc01g086870	bHLH		C1	129	92	7	9	114	108	52	25	4.9E-02		
Sly03g0199461	Solyc03g044460	bHLH			0	0	1	1	0	0	0	1		-3.01	1.7E-03
Sly04g0252581	Solyc00g050430	bHLH			1	1	0	1	1	1	1	0		-2.72	4.8E-04
Sly06g0368311	Solyc06g064590	bHLH			1	1	1	1	1	1	1	2		-2.63	1.4E-02
Sly09g0081001	Solyc09g009760	bZIP		C2	1	2	302	180	1	1	11	10	1.7E-12		
Sly02g0348761	Solyc02g092090	bZIP		C1	40	87	38	7	28	30	22	15	2.4E-08		
Sly01g0043901	Solyc01g108080	bZIP	*ABI5-like/SlABF4*	C2	35	42	78	76	40	45	46	54	3.7E-08		
Sly08g0269921	Solyc08g061130	bZIP	*SlHY5*	C2	7	11	97	75	5	9	60	63	9.9E-08		
Sly10g0185991	Solyc10g081350	bZIP	*SlAREB3*	C1	24	30	14	13	12	11	11	11	1.8E-07		
Sly08g0260591	Solyc08g006110	bZIP		C1	99	87	12	4	171	143	28	11	2.0E-07		
Sly01g0040231	Solyc01g104650	bZIP		C2	69	88	394	177	55	63	215	162	2.9E-07	-0.63	1.5E-02
Sly10g0182301	Solyc10g076920	bZIP		C1	16	15	9	4	13	14	16	15	3.7E-07		
Sly03g0197481	Solyc03g033730	bZIP		C1	4	3	1	1	3	3	1	1	3.0E-06		
Sly11g0309011	Solyc11g068370	bZIP		C1	2	2	0	1	1	1	1	1	5.2E-06		
Sly12g0053981	Solyc12g010800	bZIP		C2	13	23	69	38	2	4	10	4	7.0E-06		
Sly10g0178681	Solyc10g054010	bZIP		C1	10	4	2	2	32	12	3	2	5.3E-05		
Sly04g0250181	Solyc04g072460	bZIP		C1	113	134	30	15	30	38	14	8	1.5E-04		
Sly08g0276961	Solyc08g074860	bZIP		C1	2	3	1	1	1	1	1	0	1.7E-04		
Sly04g0254681	Solyc04g078840	bZIP	*ABF3-like4/SlABF2/*	C1	34	33	16	23	37	38	17	18	2.9E-04		
Sly10g0184951	Solyc10g080410	bZIP		C1	7	6	1	1	3	2	1	1	3.1E-04		
Sly08g0259531	Solyc08g005290	bZIP		C2	24	22	34	32	35	32	30	28	3.8E-04		
Sly11g0306561	Solyc11g064950	bZIP		C1	49	40	35	52	59	47	43	50	4.3E-04		
Sly04g0257301	Solyc04g081190	bZIP		C2	69	114	191	67	29	36	110	53	6.5E-04		
Sly01g0045791	Solyc01g109880	bZIP		C2	1020	1249	904	382	379	396	832	732	7.1E-04	-0.38	2.4E-02
Sly05g0154471	Solyc05g050220	bZIP		C2	4	8	39	44	4	4	12	12	1.1E-03	-0.60	1.4E-02
Sly01g0036181	Solyc01g100460	bZIP		C2	7	8	40	60	9	9	28	36	1.4E-03		
Sly06g0355711	Solyc06g009640	bZIP		C3	30	21	28	76	51	32	26	49	2.0E-03	-0.52	4.1E-03
Sly01g0004811	Solyc01g009510	bZIP		C1	8	6	0	0	3	2	0	0	4.2E-03		
Sly12g0070361	Solyc12g056860	bZIP		C1	8	8	3	1	24	25	16	8	4.3E-03		
Sly01g0003901	Solyc01g008730	bZIP		C2	25	29	45	48	32	29	38	42	4.9E-03		
Sly04g0248721	Solyc04g071160	bZIP		C2	42	48	63	71	44	44	48	56	6.3E-03		
Sly01g0030771	Solyc01g095460	bZIP		C3	38	32	16	46	49	43	19	50	6.7E-03		
Sly05g0138471	Solyc05g009660	bZIP		C1	4	1	0	1	5	5	1	1	9.6E-03		
Sly01g0032871	Solyc01g097330	bZIP		C1	18	16	12	9	25	19	17	11	9.7E-03		
Sly04g0256821	Solyc04g080740	bZIP		C2	122	130	207	138	136	105	201	137	1.0E-02	-0.84	1.3E-04
Sly01g0047701	Solyc01g111580	bZIP		C2	21	21	30	28	21	19	19	22	1.4E-02		
Sly02g0342021	Solyc02g085610	bZIP		C1	24	25	23	12	28	28	20	19	1.8E-02		
Sly02g0323911	Solyc02g062950	bZIP		C4	71	87	68	78	70	75	59	57	1.9E-02		
Sly04g0233771	Solyc04g011670	bZIP		C1	30	26	3	2	20	21	8	4	2.3E-02		
Sly10g0185361	Solyc10g080770	bZIP		C2	72	53	74	84	83	62	70	81	2.8E-02	-0.29	4.9E-02
Sly08g0278441	Solyc08g076100	bZIP		C1	42	41	49	43	76	57	44	46	2.9E-02		
Sly11g0303111	Solyc11g044560	bZIP	*ABF3-like2*	C1	156	147	33	45	156	148	85	78	3.0E-02		
Sly01g0021541	Solyc01g079480	bZIP		C3	95	78	73	166	88	74	58	97	3.0E-02	-0.45	8.7E-04
Sly10g0183101	Solyc10g078670	bZIP		C3	2	2	1	6	1	1	1	2	3.1E-02		
Sly06g0365881	Solyc06g060490	bZIP		C1	51	44	26	21	63	47	32	29	3.2E-02		
Sly06g0361401	Solyc06g049040	bZIP		C1	3	2	0	1	3	3	1	1	3.5E-02		
Sly06g0360991	Solyc06g048630	bZIP		C1	36	32	17	19	25	23	22	17	3.7E-02		
Sly06g0377091	Solyc06g074320	bZIP		C2	1	0	0	1	1	1	1	1	4.0E-02		
Sly04g0259071	Solyc04g082890	bZIP			224	192	178	223	206	170	138	175		-0.13	4.6E-02
Sly08g0272041	Solyc08g063040	C2H2		C2	17	17	79	107	4	5	38	53	1.5E-16	-1.05	5.1E-04
Sly09g0078691	Solyc09g007550	C2H2		C1	14	11	3	5	22	12	2	1	4.4E-14		
Sly10g0189651	Solyc10g085560	C2H2	*SlHDT2*	C1	88	90	76	61	117	107	62	55	2.6E-11		
Sly04g0256061	Solyc04g080130	C2H2		C1	6	2	1	1	13	11	1	1	7.7E-11	-0.58	1.7E-02
Sly06g0371321	Solyc06g068390	C2H2		C1	2	1	0	0	21	8	1	1	1.0E-08		
Sly04g0246441	Solyc04g056320	C2H2		C1	28	18	7	6	35	33	13	9	1.3E-08		
Sly06g0369161	Solyc06g065440	C2H2		C1	41	44	6	1	32	46	12	3	1.7E-07		
Sly06g0379691	Solyc06g076820	C2H2		C1	20	13	2	1	28	24	6	5	1.8E-07		
Sly03g0226811	Solyc03g121660	C2H2		C2	56	53	135	161	39	32	65	58	1.1E-06	-0.45	1.8E-02
Sly02g0341991	Solyc02g085580	C2H2		C1	12	8	4	2	14	11	4	3	8.1E-06		
Sly03g0194781	Solyc03g025440	C2H2		C1	27	28	20	25	31	34	24	23	1.8E-05		
Sly01g0000141	Solyc01g005130	C2H2		C3	32	28	14	36	24	22	15	25	2.4E-05		
Sly11g0293181	Solyc11g011890	C2H2		C1	1	1	0	1	2	3	1	1	3.3E-05		
Sly09g0095071	Solyc09g065670	C2H2		C1	60	54	4	3	11	14	7	3	3.3E-05		
Sly06g0367321	Solyc06g062670	C2H2		C1	68	107	64	12	95	89	31	5	5.2E-05		
Sly01g0036991	Solyc01g101250	C2H2		C4	88	81	93	101	85	91	67	67	5.9E-05		
Sly09g0079681	Solyc09g008440	C2H2		C3	1	3	3	4	1	1	1	5	1.3E-04		
Sly01g0027961	Solyc01g090840	C2H2		C1	2	2	0	1	3	3	1	1	1.6E-04		
Sly01g0034921	Solyc01g099340	C2H2		C1	60	57	14	6	52	50	43	34	2.4E-04		
Sly10g0188141	Solyc10g084180	C2H2		C1	37	29	17	8	34	32	10	6	6.1E-04		
Sly03g0208831	Solyc03g083310	C2H2		C2	23	24	36	51	30	28	31	45	6.4E-04		
Sly01g0042911	Solyc01g107170	C2H2		C2	19	31	162	342	24	27	114	243	6.5E-04		
Sly09g0080321	Solyc09g009120	C2H2		C4	23	21	27	25	25	21	21	22	6.8E-04		
Sly06g0378521	Solyc06g075780	C2H2		C3	32	42	10	172	22	48	3	61	1.6E-03	-1.10	4.0E-03
Sly03g0219861	Solyc03g115120	C2H2		C1	5	7	2	1	3	3	1	1	1.6E-03		
Sly06g0366191	Solyc06g060740	C2H2		C1	4	4	1	1	3	2	6	2	2.6E-03		
Sly03g0213761	Solyc03g098070	C2H2		C1	4	4	2	3	3	2	1	1	3.0E-03		
Sly05g0134771	Solyc05g006310	C2H2		C1	1	0	0	0	2	3	0	1	3.4E-03	-3.77	3.5E-05
Sly06g0377621	Solyc06g074800	C2H2		C1	3	2	1	1	2	2	2	2	3.4E-03		
Sly02g0323901	Solyc02g062940	C2H2		C1	24	21	7	7	24	23	14	13	3.5E-03		
Sly03g0215901	Solyc03g111590	C2H2	*SlREF6-1*	C2	22	24	63	96	20	23	50	86	6.7E-03		
Sly07g0132821	Solyc07g066160	C2H2		C2	1	1	7	11	1	1	2	6	8.1E-03		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly04g0253801	Solyc04g077980	C2H2		C3	43	18	5	180	35	41	8	113	8.1E-03		
Sly01g0000071	Solyc01g005060	C2H2		C1	1	1	1	1	7	6	4	3	1.2E-02		
Sly10g0182481	Solyc10g077110	C2H2		C1	51	39	48	42	61	52	40	38	1.6E-02		
Sly11g0308021	Solyc11g066420	C2H2		C1	1	1	0	1	1	2	1	1	1.7E-02		
Sly11g0313041	Solyc11g073060	C2H2		C4	1	2	1	2	1	2	0	1	1.9E-02	-3.38	6.8E-03
Sly11g0308001	Solyc11g066400	C2H2		C1	2	2	1	1	2	2	1	1	1.9E-02		
Sly06g0378111	Solyc06g075250	C2H2		C2	48	53	70	90	34	37	31	37	2.4E-02		
Sly12g0071371	Solyc12g088390	C2H2		C1	2	1	0	0	5	4	1	2	2.5E-02		
Sly11g0305961	Solyc11g062060	C2H2		C2	13	15	8	14	5	5	9	10	3.0E-02		
Sly05g0137921	Solyc05g009170	C2H2		C1	1	1	1	1	10	4	2	1	3.2E-02		
Sly02g0350951	Solyc02g094170	C2H2		C2	32	32	57	66	34	34	40	52	3.3E-02		
Sly03g0220191	Solyc03g115450	C2H2		C1	3	3	1	0	1	1	1	1	4.0E-02		
Sly04g0235621	Solyc04g015570	C2H2		C1	10	11	7	7	8	10	8	6	4.4E-02		
Sly04g0251011	Solyc04g074250	C2H2		C1	4	4	3	2	4	4	4	4	4.5E-02		
Sly01g0000201	Solyc01g005190	C2H2		C2	2	1	3	3	1	2	2	2	4.9E-02		
Sly11g0290821	Solyc11g008900	C3H		C2	25	25	60	64	34	37	44	53	1.6E-17		
Sly10g0174031	Solyc10g047040	C3H		C2	5	5	6	26	5	6	3	12	4.1E-07		
Sly06g0379881	Solyc06g082010	C3H		C1	43	12	2	3	178	139	31	50	7.8E-07		
Sly05g0138131	Solyc05g009350	C3H		C1	22	24	16	18	21	26	13	16	1.6E-06		
Sly11g0310051	Solyc11g069340	C3H		C1	39	41	44	48	54	53	36	41	1.7E-05		
Sly01g0024301	Solyc01g073940	C3H		C2	15	17	21	33	12	12	16	24	4.8E-05		
Sly02g0338241	Solyc02g082110	C3H		C1	15	15	10	6	14	17	11	7	6.0E-05		
Sly12g0051631	Solyc12g008660	C3H		C1	221	209	11	4	28	29	2	8	1.8E-04		
Sly12g0056791	Solyc12g017410	C3H		C2	35	35	47	54	34	37	40	44	2.0E-04		
Sly12g0049341	Solyc12g005770	C3H		C2	16	16	23	28	17	16	18	23	1.8E-03		
Sly07g0124691	Solyc07g053750	C3H		C1	12	9	2	1	6	3	1	1	2.0E-03		
Sly10g0183191	Solyc10g078750	C3H		C1	28	31	27	32	41	35	24	30	2.7E-03		
Sly01g0019951	Solyc01g067550	C3H		C2	39	43	61	50	42	44	56	51	2.8E-03		
Sly01g0025111	Solyc01g087170	C3H		C2	116	123	201	141	197	200	222	163	3.6E-03		
Sly02g0340851	Solyc02g084520	C3H		C2	26	28	45	39	24	22	30	31	4.9E-03	-0.24	5.8E-03
Sly06g0375311	Solyc06g072720	C3H		C4	25	24	25	28	27	21	24	21	5.5E-03		
Sly10g0184791	Solyc10g080260	C3H		C2	24	27	35	42	27	26	38	34	5.5E-03		
Sly09g0097231	Solyc09g074640	C3H		C4	36	36	36	37	41	35	20	27	1.2E-02	0.33	4.6E-02
Sly12g0052461	Solyc12g009390	C3H		C2	6	5	20	24	17	11	16	18	1.7E-02		
Sly01g0036741	Solyc01g100990	C3H		C2	15	15	22	28	13	12	18	26	1.8E-02		
Sly11g0310871	Solyc11g070070	C3H		C4	7	5	6	6	7	8	4	4	2.4E-02		
Sly03g0204101	Solyc03g063200	C3H		C2	36	38	50	67	40	38	45	50	3.4E-02		
Sly10g0171101	Solyc10g038000	C3H		C2	31	35	38	46	24	29	27	30	3.9E-02		
Sly12g0051861	Solyc12g008870	C3H		C2	45	46	45	46	29	32	41	45	4.9E-02		
Sly05g0144401	Solyc05g015650	CAMTA		C1	41	37	25	28	34	33	30	29	4.9E-03		
Sly01g0040831	Solyc01g105230	CAMTA		C2	42	34	40	63	60	46	49	67	9.0E-03		
Sly01g0015151	Solyc01g057270	CAMTA		C2	1	1	1	1	1	1	2	1	1.9E-02		
Sly12g0075661	Solyc12g099340	CAMTA		C1	86	96	71	37	82	88	89	59	2.5E-02		
Sly04g0246391	Solyc04g056270	CAMTA		C1	151	86	52	70	129	97	66	77	4.4E-02		
Sly12g0073731	Solyc12g096500	CO-like		C1	117	143	5	8	166	168	20	17	2.0E-14	1.06	4.7E-04
Sly04g0229701	Solyc04g007210	CO-like		C1	70	85	18	4	28	34	21	4	3.5E-08		
Sly08g0261261	Solyc08g006530	CO-like		C1	55	50	9	1	45	38	10	2	1.1E-07	0.46	9.8E-03
Sly03g0224551	Solyc03g119540	CO-like		C1	9	10	1	0	13	19	2	1	1.1E-05		
Sly05g0138081	Solyc05g009310	CO-like		C1	13	19	1	1	15	25	3	1	4.3E-04		
Sly05g0147271	Solyc05g020020	CO-like		C1	35	36	26	21	35	37	28	19	4.8E-04		
Sly07g0120801	Solyc07g045180	CO-like		C1	37	36	45	24	34	36	53	20	6.0E-04		
Sly09g0097161	Solyc09g074560	CO-like		C3	37	36	31	54	58	57	34	48	1.5E-03		
Sly07g0107221	Solyc07g006630	CO-like		C3	1	1	2	4	2	2	1	7	2.1E-03	1.99	3.1E-03
Sly02g0346081	Solyc02g089540	CO-like		C3	1	1	1	2	1	1	1	1	3.3E-02		
Sly07g0112941	Solyc07g020710	CPP		C1	13	13	13	14	21	18	13	13	4.6E-04		
Sly12g0051081	Solyc12g007180	CPP		C2	20	24	97	173	15	13	34	55	1.3E-03		
Sly09g0099121	Solyc09g082500	CPP		C1	5	5	2	1	5	4	4	3	4.2E-03	1.05	2.2E-03
Sly08g0274041	Solyc08g067150	CPP		C2	15	13	38	22	27	23	20	20	2.0E-02		
Sly07g0128431	Solyc07g062160	DBB		C3	63	73	61	111	55	61	58	105	2.0E-03		
Sly12g0072281	Solyc12g089240	DBB		C2	9	72	245	334	40	73	195	379	3.2E-03		
Sly06g0375781	Solyc06g073180	DBB		C1	43	46	29	32	20	29	15	39	6.0E-03	1.07	2.5E-05
Sly01g0046321	Solyc01g110370	DBB		C1	42	42	17	24	56	50	22	18	6.6E-03		
Sly04g0257121	Solyc04g081020	DBB		C1	14	13	2	1	15	18	4	2	1.5E-02		
Sly00g0383901	Solyc06g075370	Dof		C1	58	42	4	1	79	51	4	3	4.6E-28		
Sly03g0220711	Solyc03g115940	Dof		C1	6	9	1	3	27	24	4	6	3.2E-10		
Sly06g0372971	Solyc06g069760	Dof		C3	13	16	6	23	13	18	4	21	2.3E-09	0.72	4.3E-02
Sly02g0334611	Solyc02g078620	Dof		C1	6	3	0	0	2	3	1	0	8.2E-06		
Sly11g0312381	Solyc11g072500	Dof		C1	4	3	1	1	8	5	1	1	7.7E-05		
Sly02g0344581	Solyc02g088070	Dof		C4	5	4	7	9	8	6	2	3	4.0E-04		
Sly05g0136561	Solyc05g007880	Dof		C1	11	11	1	4	3	4	1	5	4.2E-04		
Sly08g0286071	Solyc08g082910	Dof		C1	4	4	3	4	7	6	3	2	1.4E-03		
Sly11g0291971	Solyc11g010940	Dof		C1	3	4	1	0	2	1	0	0	3.6E-03		
Sly03g0226521	Solyc03g121400	Dof		C3	2	2	5	30	4	4	8	24	4.9E-03		
Sly02g0333861	Solyc02g077950	Dof		C1	1	1	1	1	6	4	4	2	8.5E-03	0.94	1.8E-03
Sly06g0378811	Solyc06g076030	Dof		C1	1	1	1	1	3	2	2	2	1.1E-02		
Sly02g0346871	Solyc02g090310	Dof	*SlDOF10*	C4	41	33	75	64	68	73	23	33	1.2E-02		
Sly06g0373771	Solyc06g071480	Dof		C1	1	1	0	0	1	1	0	0	1.5E-02		
Sly10g0166781	Solyc10g009360	Dof		C1	0	0	0	1	2	2	1	1	2.9E-02		
Sly06g0367161	Solyc06g062520	Dof		C2	5	7	13	19	10	7	4	8	3.5E-02	-0.97	2.7E-03
Sly11g0307691	Solyc11g066050	Dof		C1	1	1	1	0	4	3	1	1	3.8E-02		
Sly10g0182831	Solyc10g078430	E2F/DP	*DPB*	C2	13	11	17	26	19	17	29	46	4.9E-06		
Sly09g0082011	Solyc09g010670	E2F/DP	*DPA*	C1	4	4	1	1	9	7	5	3	1.3E-05		
Sly06g0376741	Solyc06g074010	E2F/DP	*E2FA-like3*	C1	10	11	10	9	14	14	9	9	4.1E-05		
Sly01g0002741	Solyc01g007760	E2F/DP	*E2FA-like1*	C2	28	27	70	60	33	29	25	36	1.4E-03		
Sly03g0218151	Solyc03g113760	E2F/DP	*E2FD/DEL2-like1*	C1	2	1	1	1	1	1	1	1	2.8E-03		
Sly11g0309501	Solyc11g068800	E2F/DP	*E2FA-like2*	C1	17	14	14	9	19	13	10	9	4.4E-03		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly06g0376431	Solyc06g073720	EIL	*EIL1*	C3	161	130	83	258	139	115	78	89	9.2E-09		
Sly06g0376451	Solyc06g073730	EIL	*EIL4*	C4	101	87	131	160	130	108	91	79	2.6E-03	0.21	2.2E-02
Sly01g0001731	Solyc01g006650	EIL	*EIL6*	C2	1	1	2	1	1	1	1	1	9.5E-03		
Sly01g0004361	Solyc01g009170	EIL	*EIL2*	C2	21	19	32	36	53	60	91	62	1.7E-02		
Sly01g0032291	Solyc01g096810	EIL	*EIL3*	C4	156	138	147	220	130	138	104	128	1.9E-02		
Sly01g0008161	Solyc01g014480	EIL	*EIL5*	C2	21	20	28	23	31	25	26	23	3.4E-02		
Sly03g0225921	Solyc03g120840	ERF	*SlERF.H6*	C1	34	49	1	1	6	9	6	5	8.1E-40	0.91	6.7E-03
Sly06g0380511	Solyc06g082590	ERF	*SlERF.G2/CRF1*	C1	29	4	1	2	96	51	2	3	2.2E-21		
Sly05g0156751	Solyc05g052030	ERF	*SlERF.B3*	C1	30	31	3	7	61	60	10	7	1.1E-08		
Sly12g0052571	Solyc12g009490	ERF		C1	0	1	0	0	8	14	0	0	1.5E-08		
Sly06g0362971	Solyc06g051840	ERF	*SlERF.G4/CRF6*	C1	4	1	1	0	13	7	1	1	1.2E-07		
Sly07g0118831	Solyc07g042230	ERF	*SlERF.H9*	C1	17	1	2	1	12	14	1	0	1.0E-06	-1.13	3.9E-02
Sly09g0100781	Solyc09g089910	ERF		C1	7	1	0	0	16	5	0	0	2.2E-05	-5.85	7.0E-05
Sly06g0363491	Solyc06g053240	ERF		C1	6	4	1	1	5	4	1	1	2.5E-05		
Sly06g0370381	Solyc06g066540	ERF	*SlERF.H7*	C4	2	2	7	11	8	8	2	2	3.2E-05		
Sly07g0124681	Solyc07g053740	ERF	*SlERF.F4*	C3	84	41	16	294	178	104	36	162	4.8E-05	-0.35	2.1E-02
Sly05g0156771	Solyc05g052050	ERF	*SlERF.A3/SlPti4*	C1	67	47	32	47	141	86	33	49	1.0E-04		
Sly04g0244341	Solyc04g051360	ERF	*SlERF.D1*	C1	23	7	1	2	27	9	1	1	1.1E-04	-4.64	2.4E-04
Sly09g0095851	Solyc09g066360	ERF	*SlERF.C3*	C1	13	3	2	4	73	19	4	3	2.4E-04	-1.88	6.4E-08
Sly12g0051281	Solyc12g008350	ERF		C1	6	2	1	1	19	16	6	7	4.4E-04	-1.33	6.0E-03
Sly04g0254451	Solyc04g078640	ERF		C2	97	202	245	383	67	78	153	172	5.0E-04		
Sly09g0098001	Solyc09g075420	ERF	*SlERF.E1*	C4	84	89	115	375	54	44	27	38	5.6E-04	-1.13	3.0E-04
Sly01g0027441	Solyc01g090310	ERF	*SlERF.B7*	C1	37	7	0	1	10	4	0	0	8.7E-04		
Sly11g0294281	Solyc11g012980	ERF		C3	2	4	3	20	1	1	1	12	1.1E-03	-2.59	1.8E-10
Sly10g0166471	Solyc10g009110	ERF	*SlERF.F5*	C1	102	49	11	151	513	181	11	121	1.7E-03	-0.82	1.3E-05
Sly01g0027771	Solyc01g090560	ERF	*SlERF.H4*	C1	2	2	0	1	4	2	1	1	1.8E-03		
Sly09g0100801	Solyc09g089930	ERF	*SlERF.C4*	C1	19	5	1	1	80	35	3	1	1.9E-03	-2.09	3.0E-03
Sly04g0238001	Solyc04g012050	ERF	*SlERF.D5*	C4	16	3	2	10	14	6	1	1	2.0E-03	1.37	1.6E-02
Sly06g0371811	Solyc06g068830	ERF	*SlERF.D9*	C4	1	1	1	1	2	2	0	0	2.8E-03	1.07	1.6E-04
Sly03g0210181	Solyc03g093530	ERF		C1	21	21	2	3	15	22	10	5	3.1E-03		
Sly08g0285301	Solyc08g082210	ERF		C2	8	13	5	20	46	79	91	122	3.2E-03		
Sly08g0280591	Solyc08g078180	ERF	*SlERF.A1*	C1	1	1	1	1	6	3	1	1	3.2E-03	-1.25	1.6E-02
Sly06g0367761	Solyc06g063070	ERF	*SlERF.E2*	C2	496	567	1189	1186	828	856	1531	1459	3.5E-03		
Sly03g0195721	Solyc03g026280	ERF		C3	1	7	9	219	1	2	2	148	3.5E-03	-3.11	2.2E-03
Sly02g0333761	Solyc02g077840	ERF	*ERF.F12*	C1	10	2	1	0	24	19	2	1	4.8E-03		
Sly04g0229661	Solyc04g007180	ERF	*SlCRF11*	C1	15	10	5	3	31	21	8	4	5.0E-03		
Sly03g0224591	Solyc03g119580	ERF	*SlCRF9*	C1	4	2	1	2	6	6	4	4	5.2E-03		
Sly11g0303901	Solyc11g042560	ERF		C1	1	1	0	1	1	1	1	0	5.2E-03		
Sly03g0193761	Solyc03g007460	ERF	*SlERF.G3/CRF4*	C1	7	4	1	2	3	5	3	4	6.4E-03		
Sly10g0177631	Solyc10g050970	ERF	*SlERF.D4*	C1	12	7	1	4	4	2	1	2	8.4E-03		
Sly05g0155231	Solyc05g050830	ERF	*SlERF.H5*	C1	1	0	0	1	8	16	3	2	9.5E-03	1.19	2.7E-03
Sly06g0359301	Solyc06g035700	ERF		C3	1	1	1	3	1	1	1	1	1.0E-02		
Sly03g0192491	Solyc03g006320	ERF	*SlERF.F7*	C1	5	5	1	1	6	4	1	1	1.1E-02		
Sly04g0234481	Solyc04g014530	ERF	*SlERF.C2*	C1	1	0	0	0	4	5	1	0	1.1E-02	1.12	4.6E-03
Sly03g0210191	Solyc03g093540	ERF	*SlERF.B4*	C1	19	7	1	4	14	12	5	7	1.2E-02		
Sly04g0246001	Solyc04g054910	ERF	*SlERF.H10*	C1	190	110	30	61	224	228	135	141	1.3E-02		
Sly10g0183051	Solyc10g078610	ERF		C2	0	0	1	2	1	1	3	2	1.4E-02		
Sly03g0210201	Solyc03g093550	ERF	*SlERF.B5*	C1	27	10	2	17	11	14	8	15	1.4E-02		
Sly01g0018261	Solyc01g065980	ERF	*SlERF.E4*	C2	200	183	1076	1142	393	366	748	566	1.5E-02	-1.64	1.1E-08
Sly05g0155691	Solyc05g051200	ERF	*SlERF.C1*	C1	1	0	1	1	22	11	2	11	1.5E-02	-2.46	4.0E-05
Sly06g0364971	Solyc06g054630	ERF		C1	2	1	0	0	1	2	0	0	1.6E-02		
Sly07g0125131	Solyc07g054220	ERF		C1	4	5	2	2	16	17	2	4	1.6E-02		
Sly03g0210271	Solyc03g093610	ERF	*SlERF.A2*	C1	8	2	1	1	18	6	2	2	1.8E-02		
Sly12g0064101	Solyc12g038450	ERF		C1	28	31	2	7	1	2	1	2	1.8E-02		
Sly08g0262041	Solyc08g007230	ERF	*SlERF.A5*	C1	9	3	1	3	15	6	1	2	1.8E-02	-1.56	2.9E-02
Sly03g0223061	Solyc03g118190	ERF	*SlERF.D7*	C2	1	1	5	3	4	5	6	2	2.0E-02		
Sly02g0333231	Solyc02g077370	ERF	*SlERF.C6*	C1	116	34	1	2	79	38	1	4	2.1E-02		
Sly08g0262651	Solyc08g007830	ERF		C1	11	4	1	2	13	2	1	1	2.2E-02		
Sly10g0162951	Solyc10g006130	ERF	*SlERF.F1*	C3	51	35	24	200	50	43	31	153	2.2E-02	-0.56	4.6E-03
Sly09g0091401	Solyc09g059510	ERF		C1	23	18	23	15	39	26	19	12	2.3E-02		
Sly03g0195711	Solyc03g026270	ERF		C3	1	2	1	23	1	1	1	14	2.4E-02		
Sly03g0195731	Solyc03g124110	ERF		C2	1	4	3	133	1	1	2	45	2.4E-02	-5.67	1.5E-04
Sly12g0052281	Solyc12g009240	ERF		C3	5	6	1	58	5	11	3	39	2.5E-02	-2.53	1.3E-03
Sly08g0282941	Solyc08g080290	ERF		C3	2	1	1	3	1	1	1	1	2.5E-02		
Sly03g0227631	Solyc03g123500	ERF	*SlERF.E3*	C2	111	74	114	123	123	85	114	113	2.7E-02	-0.37	4.4E-05
Sly04g0256991	Solyc04g080910	ERF		C1	3	4	1	0	2	1	1	0	2.7E-02		
Sly12g0049611	Solyc12g005960	ERF	*SlERF.F6*	C2	16	17	19	21	8	8	11	13	2.7E-02		
Sly01g0027491	Solyc01g090340	ERF	*SlERF.B9*	C1	1	1	0	0	1	1	0	0	2.8E-02		
Sly01g0044061	Solyc01g108240	ERF	*SlERF.D3*	C3	5	7	1	14	6	2	1	7	2.8E-02		
Sly09g0095841	Solyc09g066350	ERF	*SlERF.B12*	C1	3	0	1	0	1	1	0	0	2.9E-02		
Sly08g0280601	Solyc08g078190	ERF	*SlERF.B13*	C3	9	6	3	38	4	8	6	36	3.3E-02		
Sly06g0371301	Solyc06g068360	ERF	*SlERF.H2*	C1	1	1	1	0	1	1	0	0	3.4E-02		
Sly05g0157141	Solyc05g052410	ERF	*SlERF.H14*	C2	6	10	22	47	4	6	16	36	3.9E-02		
Sly05g0156761	Solyc05g052040	ERF	*SlERF.B1*	C3	49	22	5	50	28	46	29	172	3.9E-02		
Sly01g0030811	Solyc01g095500	ERF	*SlERF.G1/CRF5*	C1	2	1	0	0	2	2	1	1	4.2E-02		
Sly08g0262641	Solyc08g007820	ERF		C3	18	12	6	23	16	8	5	15	4.5E-02	-1.26	4.5E-02
Sly04g0249421	Solyc04g071770	ERF	*SlERF.D6*	C4	31	31	86	69	103	46	20	12	4.5E-02	-0.85	1.1E-02
Sly12g0068621	Solyc12g049560	ERF	*SlERF.E5*	C2	24	27	44	70	33	33	44	59	4.5E-02		
Sly06g0361841	Solyc06g050520	ERF	*SlERF.H15*	C3	2	2	1	7	1	2	4	7	4.6E-02		
Sly04g0250671	Solyc04g072900	ERF	*SlERF.H12/DREB3*	C1	50	26	30	91	234	147	147	152	4.7E-02		
Sly05g0138251	Solyc05g009450	ERF	*SlERF.J3/CRF10*	C1	21	13	15	18	39	20	13	14	5.0E-02		
Sly02g0333221	Solyc02g077360	ERF	*SlERF.C5*		0	0	0	0	0	0	0	1		-2.78	1.5E-03
Sly06g0369551	Solyc06g065820	ERF	*SlERF.H1*		5	5	4	5	1	1	1	3		-0.95	1.9E-02
Sly08g0280581	Solyc08g078170	ERF	*SlERF.A4*		1	0	0	0	1	2	1	1		-2.12	1.8E-03
Sly09g0098211	Solyc09g075640	FAR1		C1	11	11	5	6	9	11	8	9	1.1E-08		
Sly09g0090721	Solyc09g057870	FAR1		C1	17	21	13	12	15	15	14	11	6.2E-05		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly06g0371151	Solyc06g068210	FAR1		C1	17	19	11	11	11	15	10	9	1.1E-03		
Sly01g0048471	Solyc01g112320	FAR1		C2	19	22	32	36	19	21	24	32	1.8E-03		
Sly07g0119921	Solyc07g043260	FAR1		C1	21	20	15	16	18	20	14	12	4.0E-03		
Sly06g0375801	Solyc06g073200	FAR1		C1	16	15	10	11	16	13	11	13	4.8E-03		
Sly07g0121161	Solyc07g045520	FAR1		C1	6	6	4	2	7	8	8	4	6.0E-03		
Sly02g0328081	Solyc02g068550	FAR1		C1	9	9	6	6	8	10	9	7	9.5E-03		
Sly06g0375811	Solyc06g073210	FAR1		C1	7	8	5	3	9	7	5	2	1.0E-02		
Sly01g0032341	Solyc01g096850	FAR1		C2	15	15	22	24	11	13	18	19	2.8E-02		
Sly08g0259491	Solyc08g005260	G2-like		C1	6	8	1	1	3	3	2	1	5.7E-10		
Sly05g0138531	Solyc05g009720	G2-like		C1	7	9	1	1	10	16	10	12	8.8E-09		
Sly01g0044121	Solyc01g108300	G2-like		C1	91	101	32	13	59	64	51	40	1.4E-08		
Sly10g0185611	Solyc10g080960	G2-like		C3	1	1	1	3	1	2	1	2	9.1E-06		
Sly06g0369981	Solyc06g066180	G2-like		C1	2	3	1	1	4	3	4	3	3.3E-05		
Sly11g0293051	Solyc11g011770	G2-like		C2	2	1	1	1	5	9	16	18	2.6E-04		
Sly05g0161011	Solyc05g055940	G2-like		C1	61	71	39	20	37	48	44	28	1.6E-03	0.50	2.0E-03
Sly02g0332491	Solyc02g076670	G2-like	*ARR18-like*	C1	0	0	0	0	2	2	1	1	2.0E-03		
Sly09g0096281	Solyc09g072830	G2-like		C2	36	36	54	50	45	41	49	47	2.1E-03		
Sly12g0074651	Solyc12g098370	G2-like		C1	23	22	8	7	14	14	8	4	2.3E-03		
Sly07g0124581	Solyc07g053630	G2-like		C1	1	1	1	0	1	2	1	0	4.0E-03		
Sly10g0165311	Solyc10g008160	G2-like	*SlGLK2*	C1	1	0	1	1	12	24	12	5	1.2E-02	0.88	4.5E-02
Sly05g0155481	Solyc05g051060	G2-like		C1	9	6	4	3	39	35	21	11	1.5E-02		
Sly06g0354261	Solyc06g008200	G2-like		C2	24	27	34	36	41	39	35	41	1.8E-02		
Sly09g0103231	Solyc09g091880	G2-like		C1	3	2	0	0	1	1	0	0	2.0E-02		
Sly11g0299001	Solyc11g022470	G2-like		C2	38	37	42	48	44	37	38	44	2.0E-02		
Sly02g0346951	Solyc02g090400	G2-like	*ARR13*	C1	1	1	1	1	3	3	1	1	2.1E-02		
Sly11g0308871	Solyc11g067280	G2-like		C2	39	37	69	90	80	67	61	63	2.5E-02		
Sly08g0278301	Solyc08g076010	G2-like		C2	6	6	14	43	4	4	5	18	2.7E-02	-1.26	6.6E-04
Sly10g0182711	Solyc10g078310	G2-like		C1	22	22	14	19	26	26	21	22	2.9E-02		
Sly04g0235341	Solyc04g015290	G2-like		C2	27	25	33	30	34	30	31	30	3.0E-02		
Sly02g0336841	Solyc02g080710	G2-like		C1	1	1	0	0	1	1	1	0	4.2E-02		
Sly10g0185001	Solyc10g080460	G2-like			0	1	0	0	0	0	0	0		-2.74	1.8E-02
Sly08g0261981	Solyc08g007190	GATA		C1	19	14	20	24	55	45	21	27	1.2E-06		
Sly11g0310221	Solyc11g069510	GATA		C4	24	28	18	21	20	22	15	15	3.8E-05		
Sly12g0075691	Solyc12g099370	GATA		C1	29	26	6	9	34	28	12	10	4.1E-05	0.45	1.3E-02
Sly01g0041651	Solyc01g106040	GATA		C1	9	8	2	1	6	5	3	1	4.2E-05		
Sly06g0366411	Solyc06g060940	GATA		C2	8	10	17	20	10	11	21	21	8.0E-05		
Sly05g0159361	Solyc05g054400	GATA		C1	30	25	15	17	38	33	20	17	2.3E-04		
Sly03g0197401	Solyc03g033660	GATA		C1	2	1	1	3	6	5	1	1	8.1E-04		
Sly05g0158381	Solyc05g053500	GATA		C2	12	6	5	26	14	17	20	27	8.3E-04		
Sly01g0041641	Solyc01g106030	GATA		C2	40	44	63	90	39	41	46	63	1.1E-03		
Sly01g0027861	Solyc01g090760	GATA		C1	2	2	1	0	2	3	1	0	1.1E-03		
Sly02g0340921	Solyc02g084590	GATA		C1	7	5	1	1	5	8	3	2	3.1E-03		
Sly05g0161221	Solyc05g056120	GATA		C1	27	25	6	8	13	13	18	13	3.2E-03		
Sly01g0035881	Solyc01g100220	GATA		C1	3	3	1	1	3	2	1	1	3.3E-03		
Sly04g0235421	Solyc04g015360	GATA		C3	14	14	14	169	9	12	9	103	3.4E-03		
Sly09g0102351	Solyc09g091250	GATA		C1	58	60	36	31	72	68	38	29	8.8E-03		
Sly03g0225981	Solyc03g120890	GATA		C1	9	10	1	1	5	6	3	2	2.0E-02		
Sly09g0098191	Solyc09g075610	GATA		C1	4	4	2	3	4	4	3	3	2.3E-02		
Sly04g0252271	Solyc04g076530	GATA		C2	48	54	55	79	31	36	41	55	4.5E-02		
Sly01g0033401	Solyc01g097890	GeBP		C1	27	26	16	16	25	23	22	21	5.3E-04		
Sly07g0123641	Solyc07g052760	GeBP		C1	22	20	16	13	21	20	15	11	5.1E-03		
Sly02g0315521	Solyc02g005290	GeBP		C1	23	24	18	15	24	27	26	28	6.0E-03		
Sly05g0155851	Solyc05g051330	GeBP		C1	9	12	8	8	10	12	12	7	1.2E-02		
Sly02g0315531	Solyc02g005290	GeBP		C1	23	28	18	11	25	28	28	27	2.5E-02	0.32	3.0E-02
Sly02g0340011	Solyc02g083750	GeBP		C2	44	45	34	38	43	42	48	50	2.5E-02		
Sly07g0123731	Solyc07g052830	GeBP		C2	13	13	32	22	16	17	21	18	2.8E-02	-0.29	4.7E-02
Sly07g0123761	Solyc07g052900	GeBP			19	23	22	25	20	17	21	21		-0.32	1.1E-02
Sly04g0234821	Solyc04g014830	GRAS		C1	27	25	1	1	27	33	1	1	7.2E-35	1.33	9.5E-03
Sly02g0341731	Solyc02g085340	GRAS		C1	26	21	2	1	19	16	2	3	7.1E-26		
Sly01g0028051	Solyc01g090950	GRAS		C1	13	15	7	7	20	25	7	6	5.1E-16	0.46	1.0E-02
Sly01g0004081	Solyc01g008910	GRAS		C2	6	6	30	38	3	4	9	12	6.4E-11		
Sly07g0123821	Solyc07g052960	GRAS		C2	11	53	643	335	3	23	368	343	8.8E-07	-2.65	5.3E-04
Sly07g0130351	Solyc07g063940	GRAS		C1	60	19	4	9	192	95	13	14	1.6E-06		
Sly11g0293821	Solyc11g012510	GRAS		C1	85	52	4	4	51	35	13	11	8.8E-06		
Sly09g0082281	Solyc09g010920	GRAS		C2	5	4	11	9	12	7	6	7	1.5E-05		
Sly06g0359791	Solyc06g036170	GRAS		C2	66	98	275	477	73	89	201	400	2.3E-05		
Sly09g0086131	Solyc09g018460	GRAS		C2	2	2	11	4	4	4	12	7	3.7E-05		
Sly03g0194471	Solyc03g025170	GRAS		C2	30	27	36	78	40	52	76	92	5.4E-05		
Sly08g0264091	Solyc08g014030	GRAS		C1	1	1	0	0	3	3	1	0	1.1E-04		
Sly07g0119961	Solyc07g043330	GRAS		C2	6	5	6	6	4	7	13	11	1.3E-04		
Sly02g0342011	Solyc02g085600	GRAS		C2	3	4	14	15	48	52	149	116	1.4E-04		
Sly08g0283051	Solyc08g080400	GRAS		C2	1	1	2	2	1	1	3	3	3.6E-04	0.93	3.7E-02
Sly07g0121601	Solyc07g047950	GRAS		C1	9	9	8	13	16	32	10	12	6.3E-04		
Sly11g0294431	Solyc11g013150	GRAS		C1	2	2	1	2	7	12	6	4	9.1E-04		
Sly05g0157871	Solyc05g053090	GRAS		C2	8	8	14	20	21	20	23	27	1.6E-03		
Sly11g0292301	Solyc11g011260	GRAS	*SlDELLA/GAI*	C1	86	99	64	60	47	51	52	41	3.4E-03		
Sly09g0101801	Solyc09g090830	GRAS		C1	2	2	3	1	2	1	1	1	4.3E-03		
Sly01g0035861	Solyc01g100200	GRAS		C2	28	9	27	36	18	12	24	33	9.9E-03		
Sly03g0227521	Solyc03g123400	GRAS		C1	1	1	0	0	2	1	1	1	1.2E-02		
Sly12g0048881	Solyc12g005340	GRAS		C3	53	27	15	118	40	44	22	112	1.2E-02	-0.51	1.2E-03
Sly04g0248011	Solyc04g064550	GRAS		C3	44	37	22	41	37	42	29	40	1.6E-02		
Sly08g0281241	Solyc08g078800	GRAS		C1	22	19	9	7	18	17	10	7	2.1E-02		
Sly05g0159091	Solyc05g054170	GRAS		C1	79	52	10	12	47	29	15	23	2.3E-02		
Sly12g0076281	Solyc12g099900	GRAS		C1	25	25	27	7	40	36	21	13	2.7E-02		
Sly07g0131811	Solyc07g065270	GRAS		C2	38	51	64	70	33	40	62	91	3.2E-02		
Sly02g0349031	Solyc02g092370	GRAS		C1	1	1	0	0	1	1	1	1	3.5E-02		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly06g0359261	Solyc06g035620	GRAS		C3	19	12	9	29	13	16	7	25	3.6E-02		
Sly06g0379091	Solyc06g076280	GRAS		C1	33	13	7	13	19	14	10	19	4.5E-02		
Sly10g0190531	Solyc10g086380	GRAS	*GAI-like2*	C1	1	1	1	1	8	7	2	1	4.9E-02		
Sly04g0233751	Solyc04g011630	GRAS			19	20	24	25	23	29	28	30		0.22	6.9E-03
Sly04g0253291	Solyc04g077510	GRF		C1	5	3	1	1	5	5	1	1	3.6E-13		
Sly12g0073271	Solyc12g096070	GRF		C2	11	12	22	26	8	7	23	22	2.8E-12		
Sly08g0259711	Solyc08g005430	GRF		C1	9	8	3	1	7	8	3	2	1.8E-06		
Sly02g0348701	Solyc02g092070	GRF		C1	4	2	1	1	2	1	1	1	1.6E-03		
Sly08g0286401	Solyc08g083230	GRF		C1	1	1	1	0	1	1	1	1	8.0E-03		
Sly08g0278221	Solyc08g075950	GRF		C1	5	4	3	1	3	3	2	1	1.2E-02		
Sly07g0118371	Solyc07g041640	GRF		C1	1	1	1	0	3	5	2	1	2.8E-02		
Sly01g0028661	Solyc01g091540	GRF		C1	2	2	1	0	1	1	0	0	4.7E-02		
Sly09g0095521	Solyc09g066060	HB-other		C2	1	1	15	15	1	1	3	3	9.0E-07		
Sly12g0076121	Solyc12g099760	HB-other		C2	27	27	85	81	33	30	49	52	9.7E-07	-0.41	4.5E-02
Sly07g0124551	Solyc07g053610	HB-other		C1	42	46	25	23	27	36	28	31	3.7E-03		
Sly11g0306771	Solyc11g065110	HB-other		C2	17	17	23	17	23	21	26	22	2.4E-02	-0.25	1.8E-02
Sly12g0053511	Solyc12g010410	HB-other	*SlKNATII4*	C4	17	13	15	31	17	24	12	6	3.8E-02		
Sly08g0269931	Solyc08g061140	HB-other		C2	29	39	47	64	29	35	47	58	5.0E-02		
Sly01g0043201	Solyc01g107410	HB-PHD		C1	26	24	17	13	26	25	29	14	9.0E-05		
Sly07g0109661	Solyc07g008730	HB-PHD		C2	6	7	9	6	6	7	9	8	4.6E-03		
Sly05g0156041	Solyc05g051460	HD-ZIP		C1	9	5	2	2	47	11	1	1	8.0E-23		
Sly10g0162071	Solyc10g005330	HD-ZIP		C1	8	5	1	1	14	14	12	12	2.7E-21		
Sly02g0342041	Solyc02g085630	HD-ZIP		C1	25	10	2	2	88	27	1	1	5.6E-11		
Sly03g0225701	Solyc03g120620	HD-ZIP		C1	14	11	2	2	13	14	8	4	1.8E-10	0.82	1.9E-02
Sly03g0217621	Solyc03g113270	HD-ZIP		C2	287	347	981	1005	482	427	558	809	6.7E-10		
Sly08g0273351	Solyc08g066500	HD-ZIP		C1	2	1	1	0	5	3	1	1	3.1E-08		
Sly02g0336341	Solyc02g080260	HD-ZIP		C1	3	3	1	1	2	3	1	2	3.9E-08		
Sly10g0185081	Solyc10g080540	HD-ZIP		C1	1	1	0	0	7	5	1	0	7.3E-08		
Sly05g0135541	Solyc05g006980	HD-ZIP		C1	79	60	11	7	59	57	14	22	4.0E-07		
Sly03g0195501	Solyc03g026070	HD-ZIP		C1	2	1	1	1	4	5	4	4	2.4E-06		
Sly03g0208011	Solyc03g082550	HD-ZIP		C1	1	0	1	2	3	3	2	1	3.3E-04		
Sly04g0251421	Solyc04g074700	HD-ZIP		C1	16	15	3	3	33	13	1	2	3.4E-04		
Sly01g0027661	Solyc01g090460	HD-ZIP		C1	31	34	5	5	5	9	14	5	6.7E-04		
Sly03g0226001	Solyc03g120910	HD-ZIP		C1	38	40	21	12	27	35	10	5	1.0E-03		
Sly06g0361541	Solyc06g050160	HD-ZIP		C2	0	1	1	2	1	0	1	1	1.3E-03	-4.17	3.8E-05
Sly08g0262071	Solyc08g007270	HD-ZIP		C1	2	1	0	0	3	1	1	0	2.2E-03		
Sly11g0291261	Solyc11g010270	HD-ZIP		C1	106	76	16	16	216	255	112	56	2.2E-03		
Sly02g0333501	Solyc02g077590	HD-ZIP		C1	19	8	1	0	35	19	1	0	3.2E-03		
Sly03g0213921	Solyc03g098200	HD-ZIP		C2	1	1	1	0	2	1	5	4	3.6E-03		
Sly02g0323921	Solyc02g062960	HD-ZIP		C1	56	45	1	1	2	1	0	0	3.7E-03		
Sly01g0028751	Solyc01g091630	HD-ZIP		C2	14	9	8	16	72	60	70	68	3.8E-03		
Sly02g0318991	Solyc02g024070	HD-ZIP		C1	3	2	1	1	3	3	2	1	4.1E-03		
Sly02g0324601	Solyc02g063520	HD-ZIP		C1	18	13	3	5	26	30	10	5	4.2E-03	-0.60	1.8E-02
Sly08g0286291	Solyc08g083130	HD-ZIP		C2	32	41	27	72	85	79	127	159	4.6E-03		
Sly02g0343511	Solyc02g086930	HD-ZIP	*LeHb1*	C1	91	58	29	68	132	103	91	83	5.6E-03		
Sly02g0344351	Solyc02g087840	HD-ZIP		C1	47	45	3	2	13	26	2	1	9.6E-03		
Sly02g0329491	Solyc02g069830	HD-ZIP		C1	9	8	8	7	15	13	9	7	1.1E-02		
Sly02g0348561	Solyc02g091930	HD-ZIP		C1	23	21	2	2	43	33	14	9	1.3E-02		
Sly02g0343501	Solyc02g086930	HD-ZIP	*LeHb1*	C1	88	60	20	37	122	119	96	79	1.4E-02		
Sly01g0031771	Solyc01g096320	HD-ZIP		C1	49	56	33	20	58	47	50	21	1.4E-02		
Sly04g0229151	Solyc04g005800	HD-ZIP		C1	1	1	1	0	1	2	1	1	1.6E-02		
Sly05g0135841	Solyc05g007180	HD-ZIP		C1	65	30	2	1	19	19	1	1	1.9E-02		
Sly12g0049471	Solyc12g005830	HD-ZIP		C1	3	2	0	0	1	1	0	0	2.8E-02		
Sly11g0310181	Solyc11g069470	HD-ZIP		C1	18	17	13	14	21	23	13	17	3.1E-02		
Sly11g0293231	Solyc11g011940	HD-ZIP		C1	1	1	1	0	1	1	1	1	3.2E-02		
Sly01g0024271	Solyc01g073910	HD-ZIP		C1	7	4	1	1	9	4	2	1	3.5E-02		
Sly06g0366291	Solyc06g060830	HD-ZIP		C4	10	10	16	32	3	5	4	5	3.6E-02		
Sly08g0280721	Solyc08g078300	HD-ZIP		C1	32	15	1	0	18	8	2	1	3.9E-02		
Sly04g0252971	Solyc04g077220	HD-ZIP		C1	70	100	53	50	36	31	18	31	4.2E-02		
Sly07g0114041	Solyc07g021550	HRT-like		C1	32	36	16	15	29	33	20	16	2.0E-03		
Sly03g0212701	Solyc03g097120	HSF		C2	52	53	110	141	50	48	116	124	1.1E-19		
Sly12g0050931	Solyc12g007070	HSF		C2	18	20	42	55	37	37	163	108	8.7E-13		
Sly03g0192111	Solyc03g006000	HSF		C3	17	16	23	65	31	28	31	85	3.9E-12		
Sly03g0195451	Solyc03g026020	HSF		C3	62	74	73	165	64	72	104	129	2.1E-05		
Sly09g0095061	Solyc09g065660	HSF		C2	0	0	0	2	1	1	9	40	8.0E-05	-3.23	2.0E-02
Sly02g0335201	Solyc02g079180	HSF		C1	10	1	1	1	8	3	1	1	1.1E-04		
Sly12g0074811	Solyc12g098520	HSF		C1	128	150	96	100	81	95	58	70	1.4E-04		
Sly09g0080301	Solyc09g009100	HSF		C3	50	45	29	48	49	57	28	56	4.1E-04		
Sly04g0236021	Solyc04g016000	HSF		C1	6	2	6	1	4	5	1	1	4.4E-03	-0.82	2.5E-03
Sly08g0278981	Solyc08g076590	HSF		C1	2	1	1	1	2	2	2	2	4.8E-03		
Sly02g0347411	Solyc02g090820	HSF		C3	58	30	86	213	125	77	94	190	1.4E-02		
Sly06g0364251	Solyc06g053960	HSF		C2	168	313	959	726	180	357	841	944	1.5E-02		
Sly06g0375341	Solyc06g072750	HSF		C2	7	8	23	35	9	9	10	14	2.7E-02		
Sly02g0334311	Solyc02g078340	HSF		C2	2	3	8	11	1	1	1	2	3.0E-02		
Sly07g0126671	Solyc07g055710	HSF		C1	3	1	1	1	11	11	2	1	4.9E-02		
Sly10g0183871	Solyc10g079380	HSF			0	0	0	0	0	0	0	0		-2.73	1.6E-07
Sly05g0138091	Solyc05g009320	LBD		C1	31	27	1	0	10	5	1	1	3.4E-08		
Sly01g0028531	Solyc01g091420	LBD		C1	16	14	2	3	4	3	2	2	1.9E-06		
Sly02g0327231	Solyc02g067800	LBD		C1	2	1	1	1	30	20	3	1	1.1E-03	0.62	3.1E-02
Sly11g0312351	Solyc11g072470	LBD		C2	174	292	782	562	84	104	229	228	7.1E-03		
Sly01g0042941	Solyc01g107190	LBD		C2	3	3	8	15	12	10	17	19	1.3E-02		
Sly00g0383941	Solyc06g075330	LBD		C1	2	1	0	1	3	1	1	0	1.6E-02		
Sly11g0302261	Solyc11g045530	LBD		C1	1	1	0	0	2	2	1	0	2.0E-02		
Sly02g0346961	Solyc02g090410	LBD		C4	1	1	1	1	1	1	0	1	2.3E-02		
Sly02g0349231	Solyc02g092550	LBD		C1	1	2	1	1	12	7	4	6	3.7E-02		
Sly03g0211571	Solyc03g095940	LBD		C1	1	1	1	2	4	8	4	3	4.7E-02		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly04g0253811	Solyc04g077990	LBD		C1	5	7	3	1	17	14	7	4	4.9E-02	-0.77	1.7E-02
Sly02g0342331	Solyc02g085910	LBD			12	14	20	47	30	11	20	16		-1.84	3.5E-08
Sly03g0224531	Solyc03g119530	LBD			110	131	132	182	85	80	87	112		-0.45	4.6E-02
Sly08g0279511	Solyc08g077060	LSD		C1	133	125	2	2	186	231	9	4	4.4E-09		
Sly02g0334211	Solyc02g078270	LSD		C2	21	24	34	32	19	20	23	27	8.6E-04		
Sly05g0140361	Solyc05g012020	MIKC_MADS	*RIN*	C2	11	112	1684	1452	9	37	955	1506	3.3E-11	-2.08	6.8E-03
Sly11g0300401	Solyc11g028020	MIKC_MADS		C1	94	92	17	29	8	9	2	3	1.2E-08		
Sly12g0070751	Solyc12g087830	MIKC_MADS		C2	47	66	110	122	61	70	126	118	1.6E-06		
Sly06g0372521	Solyc06g069430	MIKC_MADS	*FUL1*	C2	23	28	95	510	180	191	687	1184	1.6E-06	-0.56	1.9E-05
Sly03g0219451	Solyc03g114840	MIKC_MADS	*MADS1*	C1	21	14	3	2	111	106	51	19	5.6E-05		
Sly02g0331511	Solyc02g071730	MIKC_MADS	*TAG1*	C1	15	18	33	35	105	156	142	72	1.7E-04		
Sly10g0184561	Solyc10g080030	MIKC_MADS		C1	16	14	4	2	5	2	1	1	7.0E-04		
Sly07g0126901	Solyc07g055920	MIKC_MADS	*TAGL1*	C2	126	157	359	460	172	217	350	558	1.7E-03		
Sly12g0064201	Solyc12g038510	MIKC_MADS		C1	0	1	1	0	4	4	4	1	2.3E-03		
Sly01g0026061	Solyc01g087990	MIKC_MADS		C2	17	17	16	9	9	11	13	15	3.0E-03		
Sly01g0026051	Solyc01g087990	MIKC_MADS		C2	84	100	89	61	48	58	66	75	3.6E-03		
Sly05g0144461	Solyc05g015750	MIKC_MADS		C1	269	246	200	160	340	328	288	201	3.8E-03		
Sly03g0219441	Solyc03g114830	MIKC_MADS	*FUL2*	C2	96	118	191	276	90	98	109	160	8.3E-03		
Sly03g0193111	Solyc03g006830	MIKC_MADS		C1	8	13	6	7	5	5	4	3	1.2E-02		
Sly02g0340991	Solyc02g084630	MIKC_MADS		C1	26	26	6	5	92	90	32	20	1.6E-02		
Sly11g0291561	Solyc11g010570	MIKC_MADS		C1	3	3	1	1	2	2	2	1	1.6E-02		
Sly02g0345791	Solyc02g089200	MIKC_MADS		C1	498	460	499	534	685	643	517	378	2.1E-02		
Sly04g0254111	Solyc04g078300	MIKC_MADS		C1	3	3	1	1	1	1	1	1	2.8E-02		
Sly04g0228601	Solyc04g005320	MIKC_MADS		C1	1	0	0	0	1	2	1	1	2.9E-02		
Sly03g0214991	Solyc03g019710	MIKC_MADS		C2	1	1	3	11	12	33	104	108	3.8E-02		
Sly01g0037011	Solyc01g102260	M-type_MADS		C1	4	4	1	1	2	2	1	1	7.1E-05		
Sly01g0042301	Solyc01g106700	M-type_MADS		C2	2	3	64	31	2	3	10	19	1.7E-04	-1.23	1.3E-02
Sly03g0220671	Solyc03g115910	M-type_MADS		C4	1	1	1	1	1	1	0	1	3.6E-03	1.66	2.4E-02
Sly07g0123581	Solyc07g052700	M-type_MADS		C2	26	23	46	147	54	60	135	222	4.9E-03		
Sly01g0019091	Solyc01g066730	M-type_MADS		C1	5	6	2	2	2	3	3	2	1.0E-02		
Sly01g0033581	Solyc01g098060	M-type_MADS		C2	1	1	1	2	0	1	1	1	2.1E-02		
Sly04g0248361	Solyc04g064860	M-type_MADS		C1	2	2	1	1	3	3	2	2	3.0E-02		
Sly01g0041761	Solyc01g106170	M-type_MADS		C3	19	19	19	22	19	16	17	29	3.5E-02		
Sly06g0373581	Solyc06g071300	M-type_MADS		C2	2	2	13	11	2	3	6	11	4.3E-02		
Sly03g0216721	Solyc03g112390	MYB		C1	17	19	1	1	18	9	1	1	1.5E-12		
Sly01g0037151	Solyc01g102340	MYB		C1	6	5	1	1	16	12	1	2	1.3E-09	1.57	1.3E-02
Sly01g0021711	Solyc01g079620	MYB		C2	1	1	1	0	12	17	128	66	2.2E-09		
Sly09g0100991	Solyc09g090130	MYB		C1	38	10	1	1	4	4	1	1	3.4E-08		
Sly03g0195261	Solyc03g025870	MYB		C1	3	3	0	0	5	4	1	1	6.1E-07		
Sly07g0124131	Solyc07g053240	MYB		C1	1	1	0	1	8	6	0	0	6.3E-07		
Sly08g0275261	Solyc08g068320	MYB		C1	3	2	1	1	5	3	1	1	6.6E-07	1.11	1.8E-02
Sly12g0068401	Solyc12g049300	MYB		C2	1	1	1	0	1	1	4	3	3.2E-06		
Sly11g0288481	Solyc11g006720	MYB	*SlMYBR11*	C2	52	68	77	108	55	46	29	55	5.1E-06		
Sly06g0368831	Solyc06g065100	MYB		C1	13	12	5	4	51	40	39	28	8.7E-06		
Sly09g0101751	Solyc09g090790	MYB		C2	1	2	20	4	1	1	3	2	8.7E-06	-1.86	3.3E-03
Sly03g0210541	Solyc03g093890	MYB		C1	13	5	1	1	15	16	1	1	1.3E-05	1.85	6.2E-04
Sly02g0326691	Solyc02g067340	MYB		C1	6	4	1	1	6	11	3	1	1.7E-05		
Sly05g0158101	Solyc05g053330	MYB		C2	1	1	1	1	1	1	2	2	4.9E-05		
Sly11g0311971	Solyc11g072060	MYB		C1	3	2	0	0	1	1	1	1	6.6E-05		
Sly06g0381951	Solyc06g083900	MYB		C1	1	1	0	0	6	2	0	0	1.4E-04		
Sly03g0224331	Solyc03g119370	MYB		C1	11	6	1	1	8	6	1	0	2.1E-04		
Sly08g0281701	Solyc08g079270	MYB		C1	3	2	0	0	1	1	1	0	2.6E-04		
Sly05g0160101	Solyc05g055030	MYB		C1	9	1	0	0	4	2	0	1	4.1E-04	-0.99	2.0E-02
Sly12g0075451	Solyc12g099130	MYB		C1	2	1	2	2	75	60	12	2	5.2E-04		
Sly06g0373071	Solyc06g069850	MYB	*MYB30*	C1	6	3	1	1	33	42	11	5	8.2E-04		
Sly00g0383711	Solyc05g048830	MYB		C1	1	1	1	1	9	8	3	1	9.1E-04		
Sly02g0335331	Solyc02g079280	MYB		C1	2	1	1	1	16	6	1	1	1.1E-03		
Sly02g0349581	Solyc02g092930	MYB		C3	35	18	9	116	53	34	10	83	1.2E-03		
Sly10g0172661	Solyc10g044680	MYB		C1	1	1	1	1	2	5	2	1	1.8E-03		
Sly10g0185961	Solyc10g081320	MYB		C1	7	3	1	1	71	18	3	1	2.0E-03		
Sly12g0075441	Solyc12g099120	MYB		C1	2	2	1	1	17	14	5	1	2.6E-03	1.53	1.6E-02
Sly03g0223991	Solyc03g119050	MYB		C1	14	11	10	7	16	14	9	7	4.7E-03		
Sly06g0363851	Solyc06g053610	MYB		C1	6	5	1	1	5	2	1	1	5.1E-03		
Sly10g0180101	Solyc10g055410	MYB		C1	38	29	1	1	42	47	15	5	5.4E-03	0.80	3.0E-02
Sly06g0379641	Solyc06g076770	MYB		C1	38	36	7	21	24	25	13	17	5.7E-03		
Sly11g0311211	Solyc11g071300	MYB		C1	1	1	1	0	1	1	1	0	5.9E-03	1.50	4.6E-03
Sly11g0311411	Solyc11g071500	MYB		C2	11	11	18	23	8	8	11	12	5.9E-03		
Sly05g0160301	Solyc05g055240	MYB		C2	38	44	55	76	37	34	48	71	6.4E-03		
Sly05g0135811	Solyc05g007160	MYB		C1	13	9	5	2	39	42	5	3	6.6E-03		
Sly01g0047621	Solyc01g111500	MYB		C1	4	2	1	1	2	3	5	2	7.3E-03		
Sly03g0220861	Solyc03g116100	MYB		C2	3	2	1	1	10	14	23	17	7.4E-03		
Sly06g0374031	Solyc06g071690	MYB		C1	7	3	0	0	5	4	1	1	7.6E-03		
Sly01g0015921	Solyc01g057910	MYB		C1	2	3	2	1	5	4	4	2	8.2E-03		
Sly03g0191641	Solyc03g005570	MYB		C1	3	1	0	1	1	1	1	1	9.3E-03		
Sly07g0124121	Solyc07g053230	MYB		C1	29	7	1	3	69	34	1	3	1.4E-02		
Sly09g0083791	Solyc09g014250	MYB		C1	7	7	5	3	5	5	8	5	1.5E-02		
Sly01g0004261	Solyc01g009070	MYB		C1	36	36	28	26	28	36	25	18	2.1E-02		
Sly05g0137981	Solyc05g009230	MYB		C1	2	1	0	0	4	3	1	1	2.1E-02		
Sly12g0049191	Solyc12g005640	MYB		C1	1	0	0	0	7	2	0	0	2.1E-02		
Sly04g0255281	Solyc04g079360	MYB		C1	6	3	1	4	16	3	2	2	2.3E-02		
Sly01g0000721	Solyc01g005660	MYB		C1	9	10	7	9	3	2	1	1	2.4E-02		
Sly05g0157611	Solyc05g052850	MYB		C1	7	5	4	3	13	7	6	4	2.4E-02		
Sly02g0344721	Solyc02g088190	MYB		C2	1	1	1	3	15	18	37	38	2.6E-02		
Sly01g0029581	Solyc01g094360	MYB		C1	3	2	1	0	9	16	7	2	2.6E-02		
Sly06g0376351	Solyc06g073640	MYB		C1	7	7	3	3	2	2	1	1	2.9E-02		
Sly09g0083301	Solyc09g011780	MYB		C3	4	4	5	7	6	5	5	8	4.0E-02		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly03g0211971	Solyc03g096350	MYB		C1	1	1	1	0	3	2	2	1	4.3E-02		
Sly04g0254251	Solyc04g078420	MYB		C1	38	32	27	99	173	87	39	91	4.8E-02		
Sly08g0283261	Solyc08g080580	MYB		C1	5	4	2	2	5	5	3	2	4.9E-02	0.86	5.9E-06
Sly03g0224771	Solyc03g119740	MYB			22	26	25	35	22	31	31	34		0.34	3.2E-02
Sly12g0051641	Solyc12g008670	MYB			1	0	0	0	1	0	0	0		1.48	4.7E-02
Sly12g0075461	Solyc12g099140	MYB			4	4	6	5	16	9	5	3		-0.86	8.7E-03
Sly03g0218001	Solyc03g113620	MYB_related		C1	262	322	11	12	247	304	9	10	2.7E-69		
Sly11g0303341	Solyc11g044320	MYB_related		C2	24	28	60	70	21	24	49	58	2.4E-12		
Sly01g0030311	Solyc01g095030	MYB_related		C3	16	13	16	37	13	10	9	28	1.3E-11		
Sly01g0019961	Solyc01g067560	MYB_related		C1	30	29	19	18	28	30	15	12	1.6E-08		
Sly10g0188361	Solyc10g084370	MYB_related		C3	2	2	3	15	3	2	1	16	1.6E-07	2.07	1.4E-03
Sly05g0157361	Solyc05g052610	MYB_related		C1	44	58	24	26	31	42	38	29	2.0E-07		
Sly04g0228371	Solyc04g005100	MYB_related		C2	98	104	15	40	110	167	207	256	3.1E-07		
Sly08g0280761	Solyc08g078340	MYB_related		C1	62	39	5	6	21	20	9	8	6.8E-07		
Sly03g0227141	Solyc03g121990	MYB_related		C2	35	36	52	80	37	38	38	58	3.9E-06	-0.27	2.9E-02
Sly02g0337731	Solyc02g081640	MYB_related		C2	38	43	69	70	36	42	44	54	7.6E-06		
Sly06g0379081	Solyc06g076270	MYB_related		C2	24	23	42	43	26	28	33	43	9.5E-06		
Sly09g0079161	Solyc09g007990	MYB_related		C2	26	28	63	58	18	24	37	41	9.9E-06		
Sly10g0161821	Solyc10g005080	MYB_related		C3	3	3	2	14	2	2	2	19	1.2E-05	2.64	2.5E-10
Sly03g0226991	Solyc03g121840	MYB_related		C2	48	61	126	137	40	48	67	106	2.8E-05	-0.45	1.9E-02
Sly01g0042541	Solyc01g106940	MYB_related		C2	21	24	27	45	18	20	22	33	6.8E-05		
Sly04g0233761	Solyc04g011650	MYB_related		C2	19	21	37	28	26	34	58	53	8.3E-05		
Sly10g0161811	Solyc10g005080	MYB_related		C3	2	2	1	6	2	2	1	13	3.0E-04	2.84	8.9E-10
Sly02g0334791	Solyc02g078810	MYB_related		C2	2	2	2	5	7	5	5	8	3.7E-04		
Sly06g0373501	Solyc06g071230	MYB_related		C1	203	218	55	101	132	178	93	156	6.8E-04		
Sly01g0030981	Solyc01g095640	MYB_related		C1	3	2	0	0	1	1	1	0	1.2E-03		
Sly12g0067461	Solyc12g044610	MYB_related		C1	6	8	2	1	8	10	5	2	1.5E-03		
Sly02g0324731	Solyc02g064630	MYB_related		C2	47	51	64	72	45	42	48	56	1.8E-03		
Sly10g0184811	Solyc10g080300	MYB_related		C3	38	23	24	38	27	24	22	31	3.0E-03		
Sly06g0359971	Solyc06g036300	MYB_related		C2	41	52	75	63	35	36	44	47	3.5E-03		
Sly09g0079311	Solyc09g008100	MYB_related		C2	16	17	21	18	19	21	16	19	6.7E-03		
Sly01g0032181	Solyc01g096700	MYB_related		C1	224	236	262	226	340	368	299	233	1.5E-02	-0.42	1.9E-03
Sly03g0213981	Solyc03g098260	MYB_related		C1	3	2	0	0	1	1	0	0	2.3E-02		
Sly12g0051791	Solyc12g008800	MYB_related		C1	1	1	1	1	3	7	4	3	2.8E-02		
Sly02g0321291	Solyc02g036370	MYB_related		C1	33	29	14	21	25	27	18	10	3.0E-02		
Sly11g0310631	Solyc11g069850	MYB_related		C3	4	3	3	3	2	3	3	7	3.1E-02		
Sly12g0072201	Solyc12g089170	MYB_related		C1	3	7	0	0	2	2	0	0	4.7E-02		
Sly03g0214041	Solyc03g098320	MYB_related			8	8	13	21	5	7	5	10		1.22	5.2E-03
Sly10g0185571	Solyc10g080920	MYB_related			1	1	1	1	5	4	4	5		1.38	1.2E-02
Sly10g0163851	Solyc10g006880	NAC	*NOR*	C2	134	287	1025	632	24	68	1019	704	2.9E-38	-1.26	3.4E-03
Sly04g0232281	Solyc04g009440	NAC	*SlNAC1*	C1	172	45	13	27	163	71	5	9	9.4E-14	-1.16	1.1E-03
Sly11g0289891	Solyc11g008000	NAC		C2	66	57	110	111	116	88	91	107	2.8E-12		
Sly02g0350111	Solyc02g093420	NAC		C1	4	2	1	1	12	5	1	1	7.4E-10	0.95	8.3E-03
Sly11g0287571	Solyc11g005920	NAC		C1	101	97	111	100	161	137	90	102	2.6E-09		
Sly01g0005261	Solyc01g009860	NAC		C1	218	161	47	24	155	93	31	25	8.7E-09		
Sly05g0160551	Solyc05g055470	NAC		C2	47	35	70	74	73	54	69	78	1.3E-08		
Sly11g0295781	Solyc11g017470	NAC	*SlNAC4*	C2	255	233	824	486	143	114	466	255	1.6E-07		
Sly10g0161751	Solyc10g005010	NAC		C1	51	60	1	0	14	8	1	0	1.7E-07		
Sly04g0249911	Solyc04g072220	NAC		C1	41	37	29	33	56	55	38	39	4.9E-07		
Sly05g0138661	Solyc05g009840	NAC		C1	45	31	21	25	47	36	17	22	5.4E-07		
Sly07g0129751	Solyc07g063410	NAC		C1	42	30	24	22	180	85	29	19	2.7E-05		
Sly01g0029711	Solyc01g094490	NAC		C2	6	5	18	29	5	5	7	18	4.2E-04		
Sly04g0254481	Solyc04g078670	NAC		C3	12	9	7	10	12	10	5	11	8.5E-04		
Sly08g0279561	Solyc08g077110	NAC		C1	8	7	1	1	12	4	3	2	1.1E-03		
Sly07g0132981	Solyc07g066330	NAC		C1	3	1	1	1	3	2	1	1	1.2E-03		
Sly08g0275321	Solyc08g068380	NAC		C1	3	2	1	1	3	3	3	2	1.3E-03		
Sly03g0213911	Solyc03g098190	NAC		C1	3	3	1	0	1	2	0	0	2.5E-03		
Sly04g0228921	Solyc04g005610	NAC	*SNAC9*	C1	6	2	1	1	7	8	3	2	3.1E-03		
Sly02g0333521	Solyc02g077610	NAC		C3	4	4	2	10	2	2	1	3	3.4E-03		
Sly06g0366631	Solyc06g061080	NAC		C3	2	1	2	10	4	11	3	3	4.5E-03		
Sly03g0206471	Solyc03g078120	NAC		C1	90	60	44	56	89	58	32	39	4.9E-03		
Sly05g0160561	Solyc05g055480	NAC		C1	45	42	25	27	30	27	12	19	5.1E-03		
Sly03g0220591	Solyc03g115850	NAC		C1	2	2	1	1	2	1	1	1	5.2E-03		
Sly07g0124531	Solyc07g053590	NAC		C1	9	8	0	0	2	2	1	1	5.5E-03		
Sly06g0372901	Solyc06g069710	NAC		C1	12	7	1	1	4	2	1	1	6.2E-03		
Sly02g0322621	Solyc02g061870	NAC		C1	1	1	1	1	1	1	1	0	6.2E-03		
Sly12g0054881	Solyc12g013620	NAC		C2	108	125	269	298	168	107	121	150	6.3E-03		
Sly02g0322501	Solyc02g061780	NAC		C2	4	11	25	4	4	3	4	1	9.1E-03		
Sly06g0376931	Solyc06g074170	NAC	*NAC60*	C2	1	1	1	1	1	2	2	4	9.2E-03		
Sly01g0040491	Solyc01g104900	NAC		C1	209	250	2	1	58	81	10	3	9.6E-03		
Sly04g0235981	Solyc04g015960	NAC		C3	1	1	2	3	2	2	2	3	1.1E-02		
Sly04g0255861	Solyc04g079940	NAC		C1	79	65	32	26	148	108	47	24	1.1E-02	0.68	5.8E-03
Sly06g0375631	Solyc06g073050	NAC		C3	48	39	52	132	67	43	46	106	1.2E-02		
Sly11g0289901	Solyc11g008010	NAC		C1	115	81	72	76	224	202	125	94	1.3E-02		
Sly02g0344711	Solyc02g088180	NAC		C1	3	1	1	0	3	3	1	1	1.6E-02		
Sly11g0309441	Solyc11g068750	NAC		C1	7	6	4	3	7	8	6	4	1.9E-02		
Sly10g0180521	Solyc10g055760	NAC		C1	11	8	2	5	47	50	44	39	1.9E-02	0.71	5.4E-03
Sly12g0070291	Solyc12g056790	NAC		C1	122	86	74	75	96	92	61	53	2.3E-02		
Sly03g0203611	Solyc03g062750	NAC		C1	2	2	1	1	1	2	1	1	3.4E-02		
Sly03g0207501	Solyc03g080090	NAC		C3	176	179	172	361	222	211	137	248	3.5E-02		
Sly05g0150071	Solyc05g026180	NAC		C1	1	1	1	0	1	1	1	1	3.5E-02		
Sly06g0365651	Solyc06g060230	NAC		C3	113	88	41	106	58	33	36	82	3.6E-02		
Sly08g0263631	Solyc08g008660	NAC		C1	3	3	0	0	1	1	0	0	4.0E-02		
Sly05g0136441	Solyc05g007770	NAC	*SlNAP1/SlNAC2*	C4	44	46	139	123	104	64	67	30	4.1E-02		
Sly07g0129761	Solyc07g063420	NAC	*NOR-like1*	C1	307	396	180	138	120	201	202	188	4.6E-02		
Sly11g0309271	Solyc11g068620	NAC		C2	1	0	0	1	2	2	6	6	4.6E-02		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly01g0012201	Solyc01g021730	NAC			1	2	3	43	1	1	1	8		-1.48	3.7E-02
Sly02g0329651	Solyc02g069960	NAC			0	0	0	0	1	1	0	1		1.02	4.4E-02
Sly05g0147371	Solyc05g021090	NAC			2	1	0	0	1	1	0	0		2.40	6.8E-03
Sly06g0358971	Solyc06g034340	NAC			0	0	0	0	1	1	1	1		-3.89	4.8E-03
Sly07g0120651	Solyc07g045030	NAC			1	0	0	0	1	1	1	0		1.88	6.3E-06
Sly03g0223301	Solyc03g118420	NF-X1		C4	57	43	45	53	60	47	32	43	3.7E-02		
Sly11g0307311	Solyc11g065700	NF-YA		C2	41	46	63	125	39	38	35	72	2.1E-04		
Sly12g0052061	Solyc12g009050	NF-YA		C2	4	1	4	20	2	1	3	10	4.6E-04		
Sly01g0002041	Solyc01g006930	NF-YA		C1	1	1	1	1	20	23	19	8	5.3E-04		
Sly01g0025181	Solyc01g087240	NF-YA		C1	48	41	13	10	53	44	27	28	5.4E-04		
Sly03g0227091	Solyc03g121940	NF-YA		C2	9	7	17	13	7	6	11	10	1.3E-03		
Sly08g0271221	Solyc08g062210	NF-YA		C2	20	19	24	25	30	36	43	27	7.4E-03		
Sly10g0183611	Solyc10g079150	NF-YA		C2	4	2	7	2	1	1	2	1	2.1E-02		
Sly02g0329521	Solyc02g069860	NF-YA		C2	31	39	45	44	21	24	26	37	2.2E-02		
Sly01g0003661	Solyc01g008490	NF-YA		C2	19	21	35	43	16	17	24	30	2.9E-02		
Sly05g0133761	Solyc05g005380	NF-YB		C1	17	22	0	0	8	5	0	0	3.5E-05		
Sly05g0133731	Solyc05g005350	NF-YB		C1	17	18	1	0	7	5	1	0	1.5E-04		
Sly05g0133741	Solyc05g005360	NF-YB		C1	10	11	0	0	4	3	0	0	2.2E-04		
Sly05g0133751	Solyc05g005370	NF-YB		C1	5	6	1	0	3	2	0	0	2.2E-04		
Sly07g0132091	Solyc07g065500	NF-YB		C1	113	139	9	9	82	80	17	16	4.4E-04	0.79	2.1E-04
Sly05g0133851	Solyc05g005440	NF-YB		C1	14	13	1	1	6	3	0	0	4.8E-04	4.71	1.2E-02
Sly10g0166871	Solyc10g009440	NF-YB		C1	8	6	0	0	3	2	0	1	9.6E-04		
Sly11g0309131	Solyc11g068480	NF-YB		C3	16	21	24	25	21	23	17	29	1.2E-03		
Sly07g0132191	Solyc07g065570	NF-YB		C1	6	8	0	0	2	1	0	0	1.6E-03		
Sly03g0218921	Solyc03g114400	NF-YB		C2	18	18	25	37	17	16	17	21	3.5E-03		
Sly09g0078401	Solyc09g007290	NF-YB		C2	100	117	174	261	95	108	122	158	4.9E-03		
Sly06g0372331	Solyc06g069310	NF-YB		C3	67	56	54	78	62	63	53	65	5.8E-03		
Sly05g0133791	Solyc05g005390	NF-YB		C1	7	5	0	0	3	2	0	0	9.8E-03		
Sly05g0144321	Solyc05g015550	NF-YB		C1	7	7	2	1	3	3	1	1	1.6E-02	1.22	5.3E-03
Sly04g0232381	Solyc04g009520	NF-YB		C3	3	3	2	2	4	3	2	3	3.0E-02	0.77	2.2E-02
Sly01g0032191	Solyc01g096710	NF-YC		C2	91	85	132	147	97	89	118	125	3.1E-05		
Sly05g0143921	Solyc05g015330	NF-YC		C1	4	4	1	0	3	3	1	1	7.3E-05		
Sly01g0021971	Solyc01g079870	NF-YC		C3	171	181	156	253	224	231	210	220	1.6E-03		
Sly03g0215191	Solyc03g110860	NF-YC		C1	43	52	33	21	29	31	26	19	1.5E-02		
Sly11g0312061	Solyc11g072150	NF-YC		C2	11	11	14	19	12	12	13	15	1.7E-02		
Sly06g0374411	Solyc06g072040	NF-YC		C1	60	59	27	24	80	88	64	75	2.1E-02		
Sly02g0347631	Solyc02g091030	NF-YC		C1	51	48	43	23	48	37	24	21	3.3E-02		
Sly04g0258651	Solyc04g082480	Nin-like		C1	9	7	2	2	7	7	4	3	9.8E-06	0.79	8.2E-03
Sly08g0285891	Solyc08g082750	Nin-like		C1	4	3	2	3	38	19	5	4	8.7E-05	0.86	5.4E-09
Sly11g0302471	Solyc11g045350	Nin-like		C1	37	37	27	28	32	31	33	30	9.4E-04		
Sly08g0263351	Solyc08g008410	Nin-like		C1	37	24	3	3	25	15	7	3	5.5E-03		
Sly01g0048331	Solyc01g112190	Nin-like		C1	1	1	0	1	1	2	1	1	4.5E-02		
Sly08g0263941	Solyc08g013900	Nin-like		C1	16	13	7	4	9	8	7	4	4.9E-02		
Sly05g0138601	Solyc05g009790	RAV		C1	9	4	1	1	36	24	4	2	1.3E-06		
Sly04g0229461	Solyc04g007000	RAV		C1	5	2	2	1	42	41	14	3	2.9E-03		
Sly09g0078631	Solyc09g007500	S1Fa-like			75	78	74	78	70	81	75	61		-0.27	2.4E-04
Sly10g0169501	Solyc10g018780	SBP		C1	2	1	0	0	27	19	1	1	2.1E-18		
Sly10g0183131	Solyc10g078700	SBP		C1	5	5	1	1	6	10	1	1	6.5E-18		
Sly03g0219461	Solyc03g114850	SBP		C1	4	3	1	1	14	15	3	2	1.0E-10		
Sly02g0333841	Solyc02g077920	SBP	*CNR*	C2	26	28	333	374	31	44	319	200	1.2E-10		
Sly01g0027811	Solyc01g090730	SBP		C1	1	1	1	0	5	4	0	0	1.3E-07		
Sly01g0022851	Solyc01g080670	SBP		C1	84	83	44	41	78	91	56	52	3.7E-06		
Sly07g0129231	Solyc07g062980	SBP		C2	1	4	22	11	5	7	3	7	2.5E-05		
Sly05g0158021	Solyc05g053240	SBP		C1	32	29	21	20	41	45	30	30	3.7E-05	0.20	3.5E-02
Sly12g0064221	Solyc12g038520	SBP		C1	5	4	1	1	10	10	4	3	1.0E-03		
Sly05g0140391	Solyc05g012040	SBP		C2	13	13	17	17	19	15	18	19	6.0E-03		
Sly04g0247911	Solyc04g064470	SBP		C2	14	14	23	13	13	17	35	15	1.0E-02		
Sly05g0144261	Solyc05g015510	SBP		C2	39	43	59	57	34	40	57	67	1.6E-02		
Sly05g0144551	Solyc05g015840	SBP		C1	1	1	0	1	6	4	2	2	2.1E-02		
Sly10g0166441	Solyc10g009080	SBP		C1	1	1	0	1	6	5	4	4	2.7E-02		
Sly02g0341041	Solyc02g084680	SRS		C3	1	1	1	2	2	2	1	2	1.0E-03		
Sly11g0306471	Solyc11g064800	SRS		C2	2	2	1	2	1	1	2	2	5.0E-02	-0.76	4.1E-02
Sly08g0279911	Solyc08g077450	SRS			22	24	21	25	18	20	21	26		-0.31	3.2E-02
Sly07g0128301	Solyc07g062050	STAT		C3	16	15	15	22	12	12	17	25	6.8E-04		
Sly07g0107711	Solyc07g007120	TALE	*SlKNATII3*	C1	385	487	234	220	371	513	242	231	7.3E-05		
Sly08g0272331	Solyc08g065420	TALE		C1	1	1	0	0	2	2	1	1	1.5E-04		
Sly08g0284381	Solyc08g081400	TALE		C2	4	4	2	3	13	18	20	12	5.5E-04	0.62	2.0E-04
Sly01g0045891	Solyc01g109980	TALE		C1	27	32	29	22	46	57	35	27	8.4E-04		
Sly11g0310691	Solyc11g069890	TALE		C1	3	2	1	0	11	12	2	1	2.4E-03		
Sly10g0190821	Solyc10g086640	TALE		C1	1	1	1	0	2	2	1	1	4.1E-03		
Sly09g0082851	Solyc09g011380	TALE		C1	2	2	3	4	11	17	11	9	4.7E-03		
Sly02g0346501	Solyc02g089940	TALE		C1	8	7	1	1	11	8	3	3	5.5E-03		
Sly08g0267621	Solyc08g041820	TALE	*SlKNATII5*	C1	43	33	22	30	47	43	32	38	7.4E-03		
Sly04g0255751	Solyc04g079830	TALE		C1	1	1	1	1	4	4	2	1	9.8E-03		
Sly11g0309611	Solyc11g068950	TALE		C1	305	301	305	222	470	517	211	123	1.3E-02		
Sly06g0376861	Solyc06g074120	TALE		C2	31	34	41	64	117	152	225	201	2.1E-02		
Sly01g0036231	Solyc01g100510	TALE		C1	3	3	4	4	14	15	10	9	3.5E-02		
Sly01g0002271	Solyc01g007070	TALE		C1	311	342	179	286	276	309	240	295	4.1E-02		
Sly06g0368871	Solyc06g065190	TCP		C1	17	16	0	0	12	10	4	3	7.5E-07		
Sly08g0266211	Solyc08g048370	TCP		C1	17	14	9	4	19	13	10	4	1.7E-05		
Sly04g0231991	Solyc04g009180	TCP		C1	7	5	1	1	8	7	4	2	2.5E-04		
Sly08g0282801	Solyc08g080150	TCP		C1	3	3	1	1	5	6	2	2	5.5E-04		
Sly02g0345601	Solyc02g089020	TCP		C1	1	1	1	0	5	3	1	1	1.0E-03		
Sly02g0327681	Solyc02g068200	TCP		C3	45	41	43	75	32	36	51	67	3.0E-03		
Sly01g0039091	Solyc01g103780	TCP		C1	134	176	208	140	74	104	99	77	3.3E-03		
Sly02g0333081	Solyc05g012840	TCP		C1	1	1	0	0	1	1	1	1	5.4E-03		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly03g0221091	Solyc03g116320	TCP		C1	11	14	2	4	12	13	6	5	7.1E-03		
Sly01g0003221	Solyc01g008230	TCP		C4	66	70	65	91	53	58	42	53	3.0E-02		
Sly09g0079201	Solyc09g008030	TCP		C1	15	17	6	4	9	9	6	5	4.6E-02		
Sly08g0260341	Solyc08g005900	Trihelix		C2	21	18	38	48	28	27	25	33	1.2E-09		
Sly07g0126061	Solyc07g055100	Trihelix		C1	1	1	1	1	2	3	1	1	4.4E-08		
Sly06g0381421	Solyc06g083430	Trihelix		C2	13	13	21	21	14	12	21	21	9.5E-06		
Sly04g0248971	Solyc04g071360	Trihelix		C2	27	25	14	26	17	27	32	33	1.5E-04		
Sly05g0146371	Solyc05g018350	Trihelix		C2	14	15	28	28	18	16	24	28	4.4E-04		
Sly06g0362371	Solyc06g051120	Trihelix		C2	24	28	23	35	20	23	21	25	2.8E-03		
Sly03g0215571	Solyc03g111260	Trihelix		C2	37	46	45	24	19	27	52	49	3.5E-03		
Sly11g0286991	Solyc11g005380	Trihelix		C2	38	51	31	99	42	73	73	115	4.1E-03		
Sly08g0276231	Solyc08g069160	Trihelix		C2	12	11	15	15	13	13	16	16	9.4E-03		
Sly12g0069881	Solyc12g056510	Trihelix		C1	32	36	12	6	19	26	22	14	1.1E-02		
Sly02g0329051	Solyc02g069390	Trihelix		C2	1	1	2	1	1	1	1	2	1.2E-02		
Sly04g0240811	Solyc04g045430	Trihelix		C2	51	61	85	94	41	47	53	68	1.3E-02		
Sly01g0031951	Solyc01g096470	Trihelix		C1	25	27	4	3	16	20	11	8	2.0E-02		
Sly12g0054121	Solyc12g010890	Trihelix		C1	32	29	18	25	26	24	18	19	3.5E-02		
Sly01g0026931	Solyc01g088820	Trihelix		C1	13	11	7	5	11	8	6	7	4.4E-02		
Sly01g0040341	Solyc01g104760	Trihelix		C1	5	3	1	1	4	2	1	1	4.7E-02		
Sly02g0332611	Solyc02g076810	Trihelix			22	25	33	44	25	27	29	34		-0.39	4.1E-04
Sly09g0077411	Solyc09g005560	Trihelix			8	9	6	9	4	6	3	6		-0.59	1.6E-02
Sly10g0166251	Solyc10g008880	VOZ		C1	13	13	7	13	30	30	18	20	2.9E-02		
Sly05g0135691	Solyc05g007100	Whirly		C3	16	17	18	25	19	20	19	27	3.7E-02		
Sly02g0333261	Solyc02g077390	WOX		C1	4	3	0	0	1	1	0	0	2.9E-05		
Sly02g0333251	Solyc02g077390	WOX		C1	7	3	0	0	1	1	0	0	1.1E-04		
Sly02g0338821	Solyc02g082670	WOX		C1	183	160	160	107	182	158	174	100	1.7E-02		
Sly03g0223711	Solyc03g118770	WOX		C1	1	1	0	0	3	1	1	1	3.2E-02		
Sly06g0375491	Solyc06g072890	WOX		C1	1	1	0	0	1	1	1	0	3.6E-02		
Sly09g0084551	Solyc09g014990	WRKY		C1	43	8	1	1	17	28	1	1	2.1E-12		
Sly08g0274281	Solyc08g067360	WRKY		C1	4	1	1	1	37	16	0	0	6.5E-07	3.92	6.8E-04
Sly08g0285191	Solyc08g082110	WRKY		C1	2	1	1	1	5	19	2	1	1.5E-06		
Sly04g0249771	Solyc04g072070	WRKY		C1	16	3	1	1	8	3	0	0	4.1E-06	2.90	4.1E-03
Sly04g0254381	Solyc04g078550	WRKY		C3	27	14	5	41	41	65	38	89	4.1E-06		
Sly05g0154581	Solyc05g050340	WRKY		C1	4	2	7	4	36	19	8	4	4.2E-06	0.70	2.9E-02
Sly08g0284601	Solyc08g081610	WRKY		C1	1	1	1	1	2	3	0	1	4.5E-06		
Sly08g0263171	Solyc08g008280	WRKY		C1	15	6	3	4	26	86	10	4	7.3E-06		
Sly06g0354681	Solyc06g008610	WRKY		C1	85	79	27	34	57	56	30	41	1.1E-05		
Sly03g0205441	Solyc03g104810	WRKY		C2	73	74	69	66	50	63	93	88	3.4E-05		
Sly02g0330821	Solyc02g071130	WRKY		C1	21	3	1	1	75	38	4	2	6.2E-05		
Sly12g0073591	Solyc12g096350	WRKY		C1	7	6	1	2	12	12	6	7	7.8E-05		
Sly10g0188371	Solyc10g084380	WRKY		C1	6	5	1	1	2	1	0	0	9.7E-05	2.87	4.7E-03
Sly03g0221711	Solyc03g116890	WRKY		C1	62	11	2	6	185	56	4	8	1.2E-04	-1.59	6.8E-04
Sly02g0320841	Solyc02g032950	WRKY		C4	2	1	2	3	3	2	1	1	1.9E-04		
Sly07g0132881	Solyc07g066220	WRKY		C1	113	97	59	70	80	82	73	83	2.2E-04		
Sly07g0121611	Solyc07g047960	WRKY		C1	14	14	9	17	25	29	16	17	3.0E-04		
Sly04g0244661	Solyc04g051690	WRKY		C1	1	1	0	1	16	7	1	1	3.7E-04	3.81	1.3E-04
Sly07g0126241	Solyc07g055280	WRKY		C1	6	5	5	4	18	10	4	2	3.8E-04		
Sly01g0021321	Solyc01g079260	WRKY		C2	22	33	93	101	29	35	48	65	4.1E-04	-0.59	1.2E-02
Sly02g0318571	Solyc02g021680	WRKY		C2	1	1	4	5	3	4	11	9	4.3E-04		
Sly01g0021421	Solyc01g079360	WRKY		C1	35	44	16	10	26	16	10	7	7.3E-04		
Sly12g0066351	Solyc12g042590	WRKY		C1	1	0	0	0	3	2	0	1	8.5E-04		
Sly03g0193691	Solyc03g007380	WRKY		C1	1	1	0	0	2	11	1	1	1.6E-03		
Sly06g0373231	Solyc06g070990	WRKY		C1	1	1	0	0	1	1	1	1	1.6E-03		
Sly10g0167301	Solyc10g011910	WRKY		C4	2	3	1	3	2	2	1	2	2.3E-03	-1.57	1.1E-03
Sly02g0349701	Solyc02g093050	WRKY		C1	19	3	1	1	70	54	23	14	2.7E-03		
Sly01g0027081	Solyc01g089960	WRKY		C2	1	1	2	3	1	1	1	1	2.7E-03		
Sly03g0211411	Solyc03g095770	WRKY		C1	2	1	1	2	44	31	5	8	4.6E-03	2.53	8.1E-04
Sly02g0336991	Solyc02g080890	WRKY		C3	16	5	2	10	3	9	7	20	5.4E-03	-0.70	4.0E-02
Sly01g0016601	Solyc01g058540	WRKY		C1	3	2	0	0	2	3	1	1	7.3E-03		
Sly01g0030381	Solyc01g095100	WRKY		C1	1	1	1	1	5	3	2	1	1.0E-02		
Sly05g0140971	Solyc05g012500	WRKY		C2	20	18	29	60	47	49	55	83	1.4E-02		
Sly12g0055961	Solyc12g014610	WRKY		C1	8	7	2	2	14	18	10	6	1.4E-02		
Sly10g0188381	Solyc10g084380	WRKY		C1	4	3	1	1	1	1	0	0	1.5E-02		
Sly07g0122691	Solyc07g051840	WRKY		C3	8	8	7	25	4	5	16	31	1.6E-02		
Sly05g0141261	Solyc05g012770	WRKY		C2	2	2	7	12	21	13	15	23	1.7E-02		
Sly09g0085441	Solyc09g015770	WRKY	*SlWRKY81*	C1	148	84	57	434	526	311	52	185	1.9E-02	2.63	8.1E-05
Sly05g0144561	Solyc05g015850	WRKY		C1	6	1	2	1	9	7	1	1	2.0E-02	-2.09	2.3E-05
Sly10g0167001	Solyc10g009550	WRKY		C3	9	4	1	7	7	10	1	9	2.0E-02		
Sly01g0030961	Solyc01g095630	WRKY		C1	11	6	1	6	32	45	8	15	3.4E-02		
Sly06g0370181	Solyc06g066370	WRKY		C3	147	85	58	155	120	120	48	146	3.7E-02		
Sly05g0158161	Solyc05g053380	WRKY		C1	4	1	1	1	4	2	1	1	3.8E-02		
Sly10g0165081	Solyc10g007970	WRKY		C1	9	7	1	1	1	1	1	0	4.1E-02		
Sly08g0271441	Solyc08g062490	WRKY		C1	2	2	1	1	4	2	1	1	4.6E-02		
Sly05g0154571	Solyc05g050330	WRKY		C2	7	10	41	23	10	8	11	14	4.9E-02	-0.57	7.0E-03
Sly08g0274271	Solyc08g067340	WRKY	*SlWRKY46*	C1	10	4	1	9	101	56	2	14	4.9E-02	3.95	8.8E-09
Sly02g0351091	Solyc02g094270	WRKY			0	0	0	0	0	0	0	0		-5.68	6.3E-09
Sly03g0217451	Solyc03g113120	WRKY			0	0	0	0	0	0	0	0		-2.04	3.3E-02
Sly05g0135701	Solyc05g007110	WRKY			0	0	0	0	1	1	0	0		1.83	4.3E-03
Sly12g0054451	Solyc12g011200	WRKY			1	0	0	0	1	1	1	0		1.11	2.7E-02
Sly06g0376651	Solyc06g073920	YABBY		C2	5	2	7	6	311	400	679	297	4.6E-03		
Sly11g0311731	Solyc11g071810	YABBY		C2	1	1	1	1	47	72	222	116	2.6E-02		
Sly08g0281531	Solyc08g079100	YABBY		C1	1	1	0	0	11	8	6	3	4.5E-02		
Sly05g0136241	Solyc05g007580	ZF-HD		C1	2	2	1	1	6	4	1	1	1.4E-05	1.65	3.3E-02
Sly02g0326671	Solyc02g067320	ZF-HD		C1	5	4	1	0	5	6	1	1	1.6E-05		
Sly02g0326661	Solyc02g067310	ZF-HD		C1	3	2	0	0	2	1	1	0	2.5E-04		
Sly09g0100351	Solyc09g089550	ZF-HD		C2	16	18	29	32	13	15	18	21	2.1E-02		

					Estimated Transcript Number - Normal ripening								padj_ ripening	72h auxin treatment	
Sly	Solyc	Family	Symbol	Cluster	EMG_Gel	LMG_Gel	Br_Gel	Br+4_Gel	EMG_Per	LMG_Per	Br_Per	Br+4_Per		Log2 FoldChange	padj
Sly02g0344481	Solyc02g087970	ZF-HD		C1	92	112	70	86	134	124	65	59	2.3E-02		
Sly04g0251741	Solyc04g074990	ZF-HD		C1	1	1	0	0	4	2	1	0	4.6E-02		

Supplementary Table 2. Hormone related differentially expressed genes in this study.

Normal ripening (in blue): estimated trancript number, gene expression at different ripening stages, and statistical results in normal ripening conditions, adjusted p-value < 0.05, multifactor design test using DESeq2 package.

Auxin treatment (in green): Log2 (fold change) and adjusted p-value after 72h of auxin treatment.

EMG, early mature green; LMG, late mature green; Br, breaker; Br+4, breaker +4 days; padj ,adjusted p-value

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly01g0026261	Solyc01g088180	Abscisic acid	Abscisic acid biosynthesis	aldehyde oxidase	AAO1-like1	3	3	3	2				1.41E-02		
Sly01g0004421	Solyc01g009230	Abscisic acid	Abscisic acid biosynthesis	aldehyde oxidase	AAO4-like2/SIT	6	6	3	1		8.64E-13	7.08E-08	7.08E-08		
Sly11g0311531	Solyc11g071600	Abscisic acid	Abscisic acid biosynthesis	aldehyde oxidase	AAO4-like3	1	1	1	1				4.23E-03		
Sly11g0311551	Solyc11g071620	Abscisic acid	Abscisic acid biosynthesis	aldehyde oxidase	AAO4-like5/SlAO1	5	7	5	2			7.24E-03	3.16E-03	1.06	3.16E-03
Sly02g0347471	Solyc02g090890	Abscisic acid	Abscisic acid biosynthesis	Zeaxanthin epoxidase	ABA1-like	53	80	28	41		4.57E-19	4.89E-02	4.89E-02		
Sly02g0342471	Solyc02g086050	Abscisic acid	Abscisic acid biosynthesis	synthase	aba4	15	17	32	31		3.58E-07		1.75E-08		
Sly08g0277721	Solyc08g075490	Abscisic acid	Abscisic acid biosynthesis	carotenoid cleavage dioxygenase	CCD4B	14	23	1	1		4.91E-22	9.97E-03	9.97E-03		
Sly08g0273621	Solyc08g066720	Abscisic acid	Abscisic acid biosynthesis	carotenoid cleavage dioxygenase	CCD9	12	12	1	1		6.92E-06	1.61E-02	1.75E-06		
Sly07g0133161	Solyc07g066480	Abscisic acid	Abscisic acid biosynthesis	Molybdenum cofactor sulfurase	MoCo/flacca	18	17	25	32		1.41E-06		1.18E-02		
Sly02g0346751	Solyc02g090190	Abscisic acid	Abscisic acid biosynthesis	Molybdenum cofactor sulfurase	MOCOS-like1	22	24	30	35		2.79E-02		1.30E-03		
Sly08g0282831	Solyc08g080180	Abscisic acid	Abscisic acid biosynthesis	Molybdenum cofactor sulfurase	MOCOS-like2	2	2	1	1		4.52E-04		1.74E-02	1.12	1.74E-02
Sly08g0265671	Solyc08g016720	Abscisic acid	Abscisic acid biosynthesis	nine-cis-epoxycarotenoid dioxygenase	NCED5/SlNCED2	32	28	4	6		1.01E-05		6.28E-03		
Sly04g0249631	Solyc04g071940	Abscisic acid	Abscisic acid biosynthesis	alcohol dehydrogenase	SDR/aba2	28	29	55	41		9.53E-07	1.06E-02	9.16E-03		
Sly01g0025191	Solyc01g087250	Abscisic acid	Abscisic acid biosynthesis	carotenoid cleavage dioxygenase	SlCCD1A	22	23	28	29		2.02E-03		9.53E-04		
Sly01g0025201	Solyc01g087260	Abscisic acid	Abscisic acid biosynthesis	carotenoid cleavage dioxygenase	SlCCD1B	144	176	245	391		7.30E-04	9.99E-08	9.99E-08		
Sly04g0254741	Solyc04g078900	Abscisic acid	Abscisic acid biosynthesis	ABA 8'-hydroxylase	SlCYP707A1	7	5	3	2		1.76E-09		4.13E-02		
Sly08g0259951	Solyc08g005610	Abscisic acid	Abscisic acid biosynthesis	ABA 8'-hydroxylase	SlCYP707A2	20	31	16	43				5.64E-09	-2.72	5.64E-09
Sly08g0277511	Solyc08g075320	Abscisic acid	Abscisic acid biosynthesis	ABA 8'-hydroxylase	SlCYP707A3	1	2	4	58	2.88E-02		1.50E-05	2.13E-05	-2.82	2.13E-05
Sly01g0044031	Solyc01g108210	Abscisic acid	Abscisic acid biosynthesis	ABA 8'-hydroxylase	SlCYP707A4	7	5	3	9			6.86E-03	2.44E-04		
Sly07g0127591	Solyc07g056570	Abscisic acid	Abscisic acid biosynthesis	nine-cis-epoxycarotenoid dioxygenase	SlNCED1	270	264	243	139		3.27E-06		2.60E-12		
Sly09g0104041	Solyc09g092500	Abscisic acid	Abscisic acid biosynthesis	UDP	SlUGT75C1	83	140	544	821		1.85E-04		1.41E-06		
Sly11g0307571	Solyc11g065920	Abscisic acid	Abscisic acid biosynthesis	xanthine dehydrogenase	XDH1	99	121	174	188		3.14E-06		1.15E-06		
Sly07g0114031	Solyc07g021540	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like1	71	76	95	190			2.47E-04	2.47E-04		
Sly04g0231751	Solyc04g008970	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like10	21	24	2	2		4.67E-03		6.94E-05		
Sly11g0292721	Solyc11g011580	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like11	6	7	5	4		5.94E-06		1.49E-04		
Sly03g0214411	Solyc03g098660	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like12	18	9	1	5		8.16E-05	6.15E-03	6.15E-03		
Sly04g0231711	Solyc04g008930	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like13	3	4	2	3		2.58E-05		4.02E-02		
Sly04g0231721	Solyc04g008940	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like14	3	4	3	3		1.15E-05		3.33E-05		
Sly08g0280931	Solyc08g078510	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like5	149	82	85	342			2.90E-04	2.90E-04		
Sly04g0231741	Solyc04g008960	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like6	5	6	1	2		2.27E-07		1.31E-07		
Sly11g0292731	Solyc11g011590	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like7	7	8	4	3		1.48E-05		1.04E-04		
Sly04g0231731	Solyc04g008950	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like8	5	8	5	5		4.00E-08		4.59E-05		
Sly11g0292751	Solyc11g011600	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GEM-like9	4	4	2	2		2.35E-03		2.35E-03		
Sly04g0234121	Solyc04g014250	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GLABRA2-like1	55	54	81	89		9.95E-06		4.30E-07		
Sly11g0291421	Solyc11g010440	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	GLABRA2-like2	65	66	38	35		1.41E-02		1.10E-04		
Sly10g0174761	Solyc10g047670	Abscisic acid	Abscisic acid response	Abscisic acid-responsive family protein	HVA22A-like1	34	32	21	16		4.31E-08	2.86E-05	8.59E-10		
Sly03g0221121	Solyc03g116350	Abscisic acid	Abscisic acid response	Abscisic acid-responsive family protein	HVA22A-like2	46	56	59	76			1.74E-03	8.14E-07		
Sly04g0252331	Solyc04g076610	Abscisic acid	Abscisic acid response	Abscisic acid-responsive family protein	HVA22C-like	44	16	12	11				8.07E-05		
Sly06g0375261	Solyc06g072680	Abscisic acid	Abscisic acid response	Abscisic acid-responsive family protein	HVA22E	7	6	16	23		2.76E-03		2.37E-05		
Sly03g0213041	Solyc03g097420	Abscisic acid	Abscisic acid response	Abscisic acid-responsive family protein	HVA22E-like2	2	1	0	0		1.56E-03		1.43E-03		
Sly03g0215261	Solyc03g110920	Abscisic acid	Abscisic acid response	Abscisic acid-responsive family protein	HVA22K-like	20	22	30	36		2.39E-02		3.76E-02	-0.23	3.76E-02
Sly12g0072351	Solyc12g089290	Abscisic acid	Abscisic acid response	Abscisic acid-responsive family protein	HVA22-like1	17	19	19	8			7.11E-04	1.46E-03	-0.63	1.46E-03
Sly04g0257461	Solyc04g081340	Abscisic acid	Abscisic acid response	Abscisic acid-responsive family protein	HVA22-like2	28	32	37	39		1.92E-02		1.00E-02		
Sly01g0002761	Solyc01g007780	Abscisic acid	Abscisic acid response	Abscisic acid-responsive family protein	HVA22-like3	12	7	4	6		3.94E-06	4.50E-02	9.78E-03		
Sly09g0097471	Solyc09g074910	Abscisic acid	Abscisic acid response	GRAM domain-containing protein	TSPO-like	8	7	5	4			3.61E-02	1.02E-02		
Sly11g0303111	Solyc11g044560	Abscisic acid	Abscisic acid signal transduction	abscisic acid responsive elements-binding	ABF3-like2/SlAREB2	154	146	58	61		2.95E-02		7.89E-03		
Sly04g0254681	Solyc04g078840	Abscisic acid	Abscisic acid signal transduction	abscisic acid responsive elements-binding	ABF3-like4/SlABF2/	35	35	16	20		2.89E-04		3.47E-04		
Sly06g0381621	Solyc06g083590	Abscisic acid	Abscisic acid signal transduction	AP2/B3-like transcriptional factor family	ABI3	1	1	1	0				3.22E-02		
Sly06g0381631	Solyc06g083600	Abscisic acid	Abscisic acid signal transduction	AP2/B3-like transcriptional factor family	ABI3-like1/ABI3	3	2	1	1		6.26E-04		5.49E-04		
Sly01g0043901	Solyc01g108080	Abscisic acid	Abscisic acid signal transduction	abscisic acid responsive elements-binding	ABI5-like/SlABF4	37	43	61	64		3.68E-08		3.70E-06		
Sly02g0351321	Solyc02g094460	Abscisic acid	Abscisic acid signal transduction	AP2/B3-like transcriptional factor family	FUS3	5	2	1	1		1.39E-04		7.46E-04		
Sly01g0020711	Solyc01g068200	Abscisic acid	Abscisic acid signal transduction	glycosyltransferase	KOBITO1	27	26	22	23		6.55E-03		6.55E-03		
Sly10g0183671	Solyc10g079210	Abscisic acid	Abscisic acid signal transduction	AP2/B4-like transcriptional factor family	sdl1-like1	1	1	1	1		2.59E-03		6.49E-04		
Sly06g0357081	Solyc06g024310	Abscisic acid	Abscisic acid signal transduction	AP2/B4-like transcriptional factor family	sdl1-like2	35	23	1	1		1.24E-04		1.50E-03		
Sly10g0185991	Solyc10g081350	Abscisic acid	Abscisic acid signal transduction	abscisic acid responsive elements-binding	SlAREB3	18	20	12	12		1.79E-07		3.39E-08		
Sly04g0249241	Solyc04g071610	Abscisic acid	Abscisic acid signal transduction	Abscicic acid stress ripening	SlASR1	12400	17053	33845	55659		7.68E-04	2.67E-08	2.67E-08		
Sly04g0249191	Solyc04g071580	Abscisic acid	Abscisic acid signal transduction	Abscicic acid stress ripening	SlASR2	88	74	22	12		6.07E-08		2.61E-14		
Sly04g0249201	Solyc04g071590	Abscisic acid	Abscisic acid signal transduction	Abscicic acid stress ripening	SlASR3	6	7	1	1		1.48E-06	1.76E-02	1.51E-02	-2.22	1.51E-02
Sly04g0249251	NA	Abscisic acid	Abscisic acid signal transduction	Abscicic acid stress ripening	SlASR4	845	1148	340	69		1.66E-02	1.28E-02	4.66E-02	0.61	4.66E-02
Sly04g0249221	Solyc04g071600	Abscisic acid	Abscisic acid signal transduction	Abscicic acid stress ripening	SlASR5	3	2	1	1	1.84E-02	7.26E-04		7.26E-04		
Sly07g0129221	Solyc07g062970	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C	125	168	546	710	7.34E-03	4.00E-10	1.02E-02	1.02E-02		
Sly03g0212231	Solyc03g096670	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C1	122	95	56	57		1.64E-02		1.06E-02		
Sly03g0193221	Solyc03g006930	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C11	3	2	1	1		6.78E-04		4.24E-03		
Sly03g0193231	Solyc03g006940	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C12	2	2	0	0		9.58E-03		8.54E-03		

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly03g0193251	Solyc03g006960	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C14	6	9	91	64		8.93E-27	9.29E-03	2.09E-17		
Sly05g0157761	Solyc05g052980	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C2	142	150	129	253			4.92E-02	4.92E-02		
Sly06g0379221	Solyc06g076400	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C3	38	34	12	7		3.49E-03	2.87E-02	4.42E-05		
Sly07g0117781	Solyc07g040990	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C4	86	110	81	51		1.85E-07	4.18E-05	8.08E-03		
Sly03g0227031	Solyc03g121880	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C5	218	173	142	139				3.27E-02		
Sly12g0073221	Solyc12g096020	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C6	30	30	25	31				4.20E-02		
Sly08g0271611	Solyc08g062640	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C7	25	23	23	17			9.77E-03	9.77E-03		
Sly03g0193541	Solyc03g007230	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C8	124	241	334	193	1.76E-04		4.25E-02	5.94E-06	-0.95	5.94E-06
Sly06g0363081	Solyc06g051940	Abscisic acid	Abscisic acid signal transduction	type 2C protein phosphatases	SlPP2C9	35	27	5	5		1.01E-07		2.12E-07		
Sly12g0069201	Solyc12g055990	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL1/2¦SLPYL9-2	35	37	56	56		2.79E-03		2.79E-03		
Sly03g0193611	Solyc03g007310	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL10/SlPYL8-2	29	28	19	28		3.26E-03		3.01E-02		
Sly01g0031031	Solyc01g095700	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL3/SlPYL8-1	84	57	9	7		1.19E-10	6.06E-03	6.06E-03		
Sly03g0211421	Solyc03g095780	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL4/SlPYL6-1	1	1	1	1		4.51E-02		4.53E-02		
Sly08g0279401	Solyc08g076960	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL5/PYR1	3	3	6	6		1.66E-02		1.66E-02		
Sly06g0361821	Solyc06g050500	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL6/SlPYL4-1	15	19	7	16		1.31E-02	1.02E-14	1.31E-02		
Sly05g0157151	Solyc05g052420	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL6-2	1	1	1	0				3.68E-02		
Sly10g0189401	Solyc10g085310	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL7/PYL4-2	6	3	2	1		6.25E-03		3.95E-06		
Sly06g0366761	Solyc06g061180	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL8/PYR1	19	15	4	4		4.98E-11	1.13E-02	6.68E-13		
Sly09g0085001	Solyc09g015380	Abscisic acid	Abscisic acid signal transduction	ABA receptor-like	SlPYL9/SlPYL6-3	1	1	2	1		2.62E-02	2.12E-02	2.12E-02		
Sly01g0039351	Solyc01g103940	Abscisic acid	Abscisic acid signal transduction	SNF1-regulated protein kinase 2	SlSnRK2.2	120	117	76	75		2.30E-05		6.20E-04		
Sly01g0044101	Solyc01g108280	Abscisic acid	Abscisic acid signal transduction	SNF1-regulated protein kinase 2	SlSnRK2.3	53	59	68	51		2.67E-03	3.26E-02	3.26E-02		
Sly02g0346941	Solyc02g090390	Abscisic acid	Abscisic acid signal transduction	SNF1-regulated protein kinase 2	SlSnRK2.4	137	154	100	105		8.48E-03		1.50E-02		
Sly11g0291121	Solyc11g010130	Abscisic acid	Abscisic acid signal transduction	SNF1-regulated protein kinase 2	SlSnRK2.5	1	1	0	0				4.67E-02		
Sly04g0251281	Solyc04g074500	Abscisic acid	Abscisic acid signal transduction	SNF1-regulated protein kinase 2	SlSnRK2.7	19	17	29	25		7.58E-19		4.66E-11		
Sly04g0238111	Solyc04g012160	Abscisic acid	Abscisic acid signal transduction	SNF1-regulated protein kinase 2	SlSnRK2.8	79	77	245	195		6.68E-07		6.04E-03		
Sly07g0107471	Solyc07g006880	Abscisic acid	Abscisic acid signal transduction	TF	SlZFP2	92	153	207	142				3.49E-02		
Sly10g0164961	Solyc10g007840	Auxin	Auxin biosynthesis	AMI1	AMI1-like1	18	20	20	20		2.05E-02		3.87E-02		
Sly01g0041951	Solyc01g106340	Auxin	Auxin biosynthesis	AMI1	AMI1-like2	3	4	3	1		4.02E-02	7.16E-03	5.25E-03		
Sly10g0174331	Solyc10g047300	Auxin	Auxin biosynthesis	AMI1	AMI1-like3	30	22	19	27	2.04E-02	6.44E-04	1.30E-02	1.30E-02		
Sly10g0190291	Solyc10g086170	Auxin	Auxin biosynthesis	AMI1	AMI1-like4	14	22	38	12		6.91E-03	4.33E-04	4.33E-04		
Sly03g0222871	Solyc03g118030	Auxin	Auxin biosynthesis	AMI1	AMI1-like5	35	36	33	37			1.89E-02	1.89E-02		
Sly01g0041941	Solyc01g106330	Auxin	Auxin biosynthesis	AMI1	AMI1-like6	19	21	14	13	1.42E-03	3.44E-02		8.86E-03		
Sly03g0223641	Solyc03g118690	Auxin	Auxin biosynthesis	AMI1	AMI1-like7	42	40	55	41		2.24E-11	1.64E-07	1.64E-07		
Sly01g0041991	Solyc01g106360	Auxin	Auxin biosynthesis	AMI1	AMI1-like8	61	63	80	80		2.77E-03		1.17E-02		
Sly01g0041971	Solyc01g106350	Auxin	Auxin biosynthesis	AMI1	AMI1-like9	6	4	1	1		2.03E-04		2.30E-03		
Sly03g0226401	Solyc03g121270	Auxin	Auxin biosynthesis	IAA-amino acid hydrolase ILR1	IAR3-like/JR3-like	127	146	75	73		1.10E-05		3.34E-06		
Sly12g0051671	Solyc12g008690	Auxin	Auxin biosynthesis	IAA-amino acid hydrolase	ILL2-like	23	28	37	37		2.27E-04		3.30E-05		
Sly01g0000531	Solyc01g005490	Auxin	Auxin biosynthesis	IAA-amino acid hydrolase	ILR1-like	30	32	44	37		4.72E-03		4.72E-03		
Sly05g0134721	Solyc05g006220	Auxin	Auxin biosynthesis	IAA-amino acid hydrolase	ILR1-like	130	70	1	1		7.51E-26		4.70E-02	1.11	4.70E-02
Sly06g0364751	Solyc06g054410	Auxin	Auxin biosynthesis	IAA-amino acid hydrolase	ILR1-like	19	21	16	15		3.50E-03	3.81E-02	3.81E-02		
Sly06g0375641	Solyc06g073060	Auxin	Auxin biosynthesis	IAA-amino acid hydrolase	ILR1-like	70	64	89	73		2.54E-03	6.69E-05	3.58E-02		
Sly10g0184151	Solyc10g079640	Auxin	Auxin biosynthesis	IAA-amino acid hydrolase	ILR1-like	40	28	2	2		4.30E-31	1.75E-02	1.34E-24		
Sly11g0309411	Solyc11g068730	Auxin	Auxin biosynthesis	NIT	NIT-like	38	44	86	199		5.11E-04	9.73E-03	9.73E-03		
Sly02g0323021	Solyc02g062190	Auxin	Auxin biosynthesis	TAA/IPA Pathway	TAA1-like1/SlTAR5	1	1	1	1				4.55E-03		
Sly05g0150661	Solyc05g031600	Auxin	Auxin biosynthesis	TAA/IPA Pathway	TAA1-like3/SlTAR3	1	1	1	1				2.35E-03		
Sly03g0216781	Solyc03g112460	Auxin	Auxin biosynthesis	TAA/IPA Pathway	TAA1-like4/SlTAR1	4	2	1	1		5.65E-03		2.56E-02		
Sly06g0373971	Solyc06g071640	Auxin	Auxin biosynthesis	TAA/IPA Pathway	TAA1-like5/SlTAR2	1	0	0	0				4.90E-02		
Sly10g0163341	Solyc10g006400	Auxin	Auxin biosynthesis	TSB	TSB-like2	37	38	55	80		1.06E-03	9.86E-06	4.90E-02	-0.27	4.90E-02
Sly07g0130701	Solyc07g064280	Auxin	Auxin biosynthesis	TSB	TSB-like3	27	30	24	12		3.10E-02	2.09E-05	2.09E-05		
Sly12g0073401	Solyc12g096190	Auxin	Auxin biosynthesis	TSB	TSB-like4	168	199	140	102		2.15E-07		8.35E-10		
Sly10g0162061	Solyc10g005320	Auxin	Auxin biosynthesis	TSB	TSB-like6	192	93	1	1	1.62E-04	1.40E-30		2.26E-21		
Sly09g0103221	Solyc09g091870	Auxin	Auxin biosynthesis	YUC/IPA Pathway	YUC10-like3/ToFZY8	1	1	1	0				1.76E-03		
Sly09g0093411	Solyc09g064160	Auxin	Auxin biosynthesis	YUC/IPA Pathway	YUC5-like/ToFZY7	1	1	1	1				4.21E-02		
Sly08g0275111	Solyc08g068160	Auxin	Auxin biosynthesis	YUC/IPA Pathway	YUC6-like/ToFZY2	5	4	1	1		5.47E-04		5.27E-04		
Sly06g0381761	Solyc06g083700	Auxin	Auxin biosynthesis	YUC/IPA Pathway	YUC-like1/ToFYZ5	1	1	0	0				1.80E-02		
Sly06g0354101	Solyc06g008050	Auxin	Auxin biosynthesis	YUC/IPA Pathway	YUC-like2/ToFYZ4	3	10	67	110		3.32E-04		8.00E-07		
Sly09g0102131	Solyc09g091090	Auxin	Auxin biosynthesis	YUC/IPA Pathway	YUC-like3/ToFZY3	1	1	1	1				4.22E-03		
Sly09g0097021	Solyc09g074430	Auxin	Auxin biosynthesis	YUC/IPA Pathway	YUC-like4/ToFZY6	10	8	1	1		5.41E-09		1.45E-04	2.29	1.45E-04
Sly03g0196581	Solyc03g031970	Auxin	Auxin signal transduction	ARF	ARF	98	97	64	65		2.65E-07		7.94E-10		
Sly06g0382471	Solyc06g084390	Auxin	Auxin signal transduction	ABP1	SlABP1	27	34	111	254		2.17E-08	4.63E-03	4.63E-03		
Sly01g0038341	Solyc01g103050	Auxin	Auxin signal transduction	ARF	SlARF1	111	69	23	25	6.30E-03	6.66E-17		1.40E-10		
Sly11g0310211	Solyc11g069500	Auxin	Auxin signal transduction	ARF	SlARF10A	22	30	31	27	1.37E-03	5.54E-03	4.33E-02	4.33E-02		
Sly06g0378021	Solyc06g075150	Auxin	Auxin signal transduction	ARF	SlARF10B	9	9	13	11		2.61E-07	2.05E-02	2.05E-02		
Sly09g0078981	Solyc09g007810	Auxin	Auxin signal transduction	ARF	SlARF16A	8	9	7	7		7.40E-10		1.78E-05		
Sly11g0294791	Solyc11g013470	Auxin	Auxin signal transduction	ARF	SlARF17	6	9	33	38		1.53E-07		2.48E-09		
Sly01g0031511	Solyc01g096070	Auxin	Auxin signal transduction	ARF	SlARF18	13	9	2	1		2.63E-02		5.86E-05		
Sly07g0118851	Solyc07g042260	Auxin	Auxin signal transduction	ARF	SlARF19	6	8	4	3		4.58E-03		1.04E-02	0.44	1.04E-02
Sly05g0161121	Solyc05g056040	Auxin	Auxin signal transduction	ARF	SlARF24	67	40	13	8		1.52E-06	3.47E-04	3.47E-04		
Sly03g0223161	Solyc03g118290	Auxin	Auxin signal transduction	ARF	SlARF2A	164	210	393	336		1.18E-13		7.50E-10		

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly12g0065841	Solyc12g042070	Auxin	Auxin signal transduction	ARF	SlARF2B	101	102	91	105		2.57E-03	1.25E-02	1.25E-02		
Sly02g0333461	Solyc02g077560	Auxin	Auxin signal transduction	ARF	SlARF3	76	80	77	63			4.48E-02	4.48E-02		
Sly11g0309901	Solyc11g069190	Auxin	Auxin signal transduction	ARF	SlARF4	143	127	19	11		3.63E-05	9.37E-09	1.29E-08		
Sly04g0257351	Solyc04g081240	Auxin	Auxin signal transduction	ARF	SlARF5	33	56	42	26				4.71E-03		
Sly12g0050081	Solyc00g196060	Auxin	Auxin signal transduction	ARF	SlARF6A	20	16	9	8		2.65E-02		6.12E-03	0.31	6.12E-03
Sly07g0120211	Solyc07g043620	Auxin	Auxin signal transduction	ARF	SlARF6B	28	30	24	24				4.67E-02		
Sly07g0111231	Solyc07g016180	Auxin	Auxin signal transduction	ARF	SlARF7A	27	32	8	9		1.91E-12		5.97E-10		
Sly05g0153701	Solyc05g047460	Auxin	Auxin signal transduction	ARF	SlARF7B	22	25	17	25		6.10E-03	1.06E-03	1.06E-03		
Sly03g0196571	Solyc03g031970	Auxin	Auxin signal transduction	ARF	SlARF8A	37	35	24	22				1.44E-03	0.39	1.44E-03
Sly02g0321431	Solyc02g037530	Auxin	Auxin signal transduction	ARF	SlARF8B	24	25	9	10		1.34E-09		1.64E-04	0.68	1.64E-04
Sly08g0285761	Solyc08g082630	Auxin	Auxin signal transduction	ARF	SlARF9A	15	9	1	1		7.78E-09		1.59E-02	2.40	1.59E-02
Sly08g0263311	Solyc08g008380	Auxin	Auxin signal transduction	ARF	SlARF9B	17	13	7	6		2.27E-03		6.40E-04		
Sly09g0100051	Solyc09g083280	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA1	28	3	1	1	8.57E-10	2.97E-06		5.97E-06		
Sly12g0074201	Solyc12g096980	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA11	1	1	0	0				4.93E-02	-3.92	4.93E-02
Sly09g0093741	Solyc09g064530	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA12	36	37	6	13		2.93E-24	2.46E-03	2.46E-03		
Sly09g0101901	Solyc09g090910	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA13	20	24	1	1		2.47E-05		2.92E-06		
Sly03g0225481	Solyc03g120390	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA15	674	530	210	154		1.57E-08		6.14E-12		
Sly01g0032831	Solyc01g097290	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA16	15	12	1	1		2.22E-22		1.62E-21		
Sly06g0354661	Solyc06g008590	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA17	87	95	1	1		6.01E-16		1.86E-14		
Sly03g0225461	Solyc03g120380	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA19	13	6	1	0		6.74E-11		6.24E-11		
Sly06g0382131	Solyc06g084070	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA2	3	2	1	0		1.52E-03		1.71E-03	-3.48	1.71E-03
Sly06g0354651	Solyc06g008580	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA22	1	1	0	0				4.80E-02		
Sly03g0226181	Solyc03g121060	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA26	9	6	2	2		1.49E-03		2.71E-05		
Sly03g0225581	Solyc03g120500	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA27	102	127	15	6		6.30E-17	1.79E-03	5.58E-03	0.81	5.58E-03
Sly08g0268651	Solyc08g021820	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA29	138	59	7	2	2.48E-04	2.30E-11	3.41E-06	2.24E-02	-1.63	2.24E-02
Sly09g0095311	Solyc09g065850	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA3	80	48	131	488		1.77E-02	4.20E-02	8.93E-12	-1.55	8.93E-12
Sly07g0108881	Solyc07g008020	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA35	18	10	1	1		3.08E-10		1.80E-02	-2.53	1.80E-02
Sly06g0369751	Solyc06g066020	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA36	12	7	1	0		3.05E-06		2.81E-06		
Sly06g0364111	Solyc06g053840	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA4	300	396	47	43		4.27E-07		6.43E-06		
Sly06g0364101	Solyc06g053830	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA7	2	2	1	1		1.98E-04		8.68E-05		
Sly12g0051141	Solyc12g007230	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA8	20	13	6	3		6.49E-03	2.30E-02	2.30E-02		
Sly04g0252591	Solyc04g076850	Auxin	Auxin signal transduction	AUX/IAA	SlAux/IAA9	1392	1405	795	609		8.22E-11	5.08E-04	3.81E-04	-1.23	3.81E-04
Sly09g0097121	Solyc09g074520	Auxin	Auxin signal transduction	TIR	SlTIR1	59	69	24	32		2.61E-06		2.30E-02	0.51	2.30E-02
Sly02g0335221	Solyc02g079190	Auxin	Auxin signal transduction	TIR	SlTIR1-like1	24	31	26	15			1.17E-02	1.17E-02		
Sly04g0251731	Solyc04g074980	Auxin	Auxin signal transduction	TIR	SlTIR1-like2	24	18	18	19				3.40E-02		
Sly03g0222191	Solyc03g117360	Auxin	Auxin signal transduction	TPL	SlTPL1	70	47	13	8		8.77E-10	2.09E-02	3.21E-18		
Sly08g0278331	Solyc08g076030	Auxin	Auxin signal transduction	TPL	SlTPL2	41	32	23	18		1.81E-03	5.26E-03	1.80E-03		
Sly01g0035671	Solyc01g100050	Auxin	Auxin signal transduction	TPL	SlTPL3	143	168	199	201				1.62E-04		
Sly03g0221551	Solyc03g116750	Auxin	Auxin signal transduction	TPL	SlTPL4	100	83	102	123		5.83E-04		4.15E-06		
Sly07g0108901	Solyc07g008040	Auxin	Auxin signal transduction	TPL	SlTPL5	31	32	33	37			3.03E-02	3.03E-02		
Sly08g0269151	Solyc08g029050	Auxin	Auxin signal transduction	TPL	SlTPL6	14	13	9	3		4.28E-02	1.75E-05	1.75E-05		
Sly12g0050091	Solyc12g006350	Auxin	Auxin signal transduction	ARF		14	11	9	7				2.82E-02	0.30	2.82E-02
Sly02g0347831	Solyc02g091240	Auxin	Auxin transport	PILS	SlPILS2	52	62	54	61		1.17E-03	2.18E-02	3.21E-03		
Sly03g0196601	Solyc03g031990	Auxin	Auxin transport	PILS	SlPILS3	2	2	1	1		4.46E-03	3.78E-03	3.78E-03		
Sly04g0259011	Solyc04g082830	Auxin	Auxin transport	PILS	SlPILS4	31	40	88	65		2.84E-09		3.29E-04		
Sly02g0338601	Solyc02g082450	Auxin	Auxin transport	PILS	SlPILS5	36	35	5	2		2.03E-04	3.21E-02	3.21E-02		
Sly10g0181041	Solyc10g074790	Auxin	Auxin transport	PILS	SlPILS6	348	504	202	311	3.80E-02	5.20E-04	2.38E-02	5.20E-04		
Sly03g0196721	Solyc03g032080	Auxin	Auxin transport	PILS	SlPILS7	1	1	1	1			9.77E-03	9.77E-03		
Sly12g0072961	Solyc12g095750	Auxin	Auxin transport	PILS	SlPILS8	1	1	1	2			4.59E-02	7.41E-04		
Sly03g0223681	Solyc03g118740	Auxin	Auxin transport-efflux	PIN	SlPIN1	2	1	1	1		5.39E-03		2.28E-03		
Sly07g0107491	Solyc07g006900	Auxin	Auxin transport-efflux	PIN	SlPIN2	0	1	0	1				1.80E-02		
Sly04g0230221	Solyc04g007690	Auxin	Auxin transport-efflux	PIN	SlPIN3	7	3	1	1		1.70E-10		2.63E-10		
Sly05g0136731	Solyc05g008060	Auxin	Auxin transport-efflux	PIN	SlPIN4	48	24	6	7		1.87E-02		2.91E-04		
Sly01g0020901	Solyc01g068410	Auxin	Auxin transport-efflux	PIN	SlPIN5	4	2	8	16		2.77E-02		3.29E-03		
Sly06g0365091	Solyc06g059730	Auxin	Auxin transport-efflux	PIN	SlPIN6	1	1	0	1				6.73E-03		
Sly10g0185521	Solyc10g080880	Auxin	Auxin transport-efflux	PIN	SlPIN7	2	2	10	14		1.15E-05	3.09E-04	1.95E-07		
Sly02g0344161	Solyc02g087660	Auxin	Auxin transport-efflux	PIN	SlPIN8	1	1	2	2				3.63E-03		
Sly10g0182771	Solyc10g078370	Auxin	Auxin transport-efflux	PIN	SlPIN9	2	2	1	1		3.63E-03		1.29E-04		
Sly09g0083871	Solyc09g014370	Auxin	Auxin transport-influx	LAX	SlLAX1	7	7	7	6				1.33E-02		
Sly01g0047461	Solyc01g111310	Auxin	Auxin transport-influx	LAX	SlLAX2	2	2	1	1		2.35E-03		8.94E-04		
Sly11g0294601	Solyc11g013310	Auxin	Auxin transport-influx	LAX	SlLAX3	40	45	50	12			6.12E-04	6.12E-04		
Sly10g0182171	Solyc10g076790	Auxin	Auxin transport-influx	LAX	SlLAX4	1	1	1	1				4.20E-02		
Sly10g0179911	Solyc10g055260	Auxin	Auxin transport-influx	LAX	SlLAX5	1	1	0	0				4.92E-02		
Sly02g0327791	Solyc02g068310	Auxin	Catabolism	Dioxygenase for auxin oxidation	SlDAO1	11	18	253	421		3.03E-31	1.38E-06	5.88E-05	-1.75	5.88E-05
Sly02g0327801	Solyc02g068320	Auxin	Catabolism	Dioxygenase for auxin oxidation	SlDAO2	59	40	14	17	2.04E-05	8.82E-07	3.24E-02	3.24E-02		
Sly02g0327811	Solyc02g068330	Auxin	Catabolism	Dioxygenase for auxin oxidation	SlDAO3	2	2	0	0		7.40E-04		6.42E-04		
Sly00g0384101	Solyc10g010650	Auxin	Conjugation	Conjugation	GH3-22	1	1	0	0				3.85E-02		
Sly07g0125501	Solyc07g054580	Auxin	Conjugation	Conjugation	GH3-8	1	1	1	1				3.61E-02		
Sly10g0165801	Solyc10g008520	Auxin	Conjugation	Conjugation	SlGH3-10	8	5	1	1		9.40E-11		1.81E-10		

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly12g0048851	Solyc12g005310	Auxin	Conjugation	Conjugation	SlGH3-15	1	1	1	1		4.46E-02		1.20E-02		
Sly07g0123901	Solyc07g053030	Auxin	Conjugation	Conjugation	SlGH3-17	6	4	1	2		6.45E-09	4.84E-05	2.12E-02	1.22	2.12E-02
Sly01g0043161	Solyc01g107390	Auxin	Conjugation	II IAA-amido synthetase	SlGH3-2	126	64	59	166	2.36E-02		4.92E-02	2.70E-06	-1.96	2.70E-06
Sly02g0324951	Solyc02g064830	Auxin	Conjugation	II IAA-amido synthetase	SlGH3-3	32	9	1	1		1.07E-05	3.44E-02	1.20E-05	-1.99	1.20E-05
Sly02g0349491	Solyc02g092820	Auxin	Conjugation	II IAA-amido synthetase	SlGH3-4	25	14	1	1		1.52E-03		1.35E-08	-2.59	1.35E-08
Sly10g0163571	Solyc10g006610	Auxin	Conjugation	Conjugation	SlGH3-7	2	2	2	6			7.42E-10	7.42E-10		
Sly07g0130251	Solyc07g063850	Auxin	Conjugation	II IAA-amido synthetase	SlGH3-9	2	2	7	8		8.61E-05		6.02E-03	-1.52	6.02E-03
Sly00g0384091	Solyc00g212260	Auxin	Conjugation	Conjugation	Solyc00g167300	1	1	0	0		1.38E-02		1.97E-02		
Sly00g0384071	Solyc00g254910	Auxin	Conjugation	Conjugation	Solyc00g212260	1	1	0	0				3.93E-02		
Sly01g0000241	Solyc01g005230	Auxin	Conjugation	Conjugation	Solyc00g322630	1	1	1	1				2.82E-02		
Sly01g0043191	Solyc01g107400	Auxin	Conjugation	II IAA-amido synthetase	Solyc01g107400/Sl	50	21	175	38		4.38E-08	7.39E-03	7.39E-03		
Sly01g0047071	Solyc01g111010	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR or Auaporin	2	1	2	5				4.04E-03		
Sly01g0028131	Solyc01g091030	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR1	6	4	1	1		2.22E-06		2.07E-03		
Sly01g0046691	Solyc01g110710	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR10	1	1	1	2				1.87E-02		
Sly01g0046651	Solyc01g110680	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR12	3	2	3	3				4.39E-02		
Sly01g0046821	Solyc01g110800	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR19	1	1	0	1				3.67E-02		
Sly01g0031811	Solyc01g096340	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR2	28	29	102	112		1.03E-03		4.20E-03	-0.84	4.20E-03
Sly01g0046971	Solyc01g110920	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR26	12	10	3	1		5.32E-03	1.27E-03	1.27E-03		
Sly01g0046501	Solyc01g110560	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR3	16	19	7	2		5.25E-04	1.50E-03	1.50E-03		
Sly02g0323091	Solyc02g062230	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR32	3	2	1	2		1.85E-02	1.43E-02	1.43E-02		
Sly02g0340331	Solyc02g084010	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR33	8	9	2	1		2.98E-04	2.25E-02	2.25E-02		
Sly03g0207951	Solyc03g082510	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR35	2	1	1	1		4.27E-03		4.86E-04	1.04	4.86E-04
Sly03g0207961	Solyc03g082520	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR36	5	6	1	3		2.95E-03		8.03E-08	-4.15	8.03E-08
Sly03g0207971	Solyc03g082530	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR37	14	20	3	42		1.22E-02	3.02E-03	2.30E-03	-2.77	2.30E-03
Sly03g0227681	Solyc03g123550	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR39	4	4	3	9		3.07E-03	4.67E-03	1.60E-07		
Sly01g0046511	Solyc01g110570	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR4	3	2	0	0		1.46E-02		1.36E-02		
Sly04g0257361	Solyc04g081250	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR51	6	27	46	10			2.12E-02	2.12E-02		
Sly04g0257381	Solyc04g081270	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR52	5	9	14	5		1.64E-02		3.86E-02		
Sly05g0153531	Solyc05g046320	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR55	3	2	1	1		2.92E-03		9.65E-03		
Sly05g0161531	Solyc05g056430	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR56	1	1	1	1				2.21E-02		
Sly01g0046518	Solyc01g110590	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR6	1	1	1	0				3.21E-02		
Sly06g0375231	Solyc06g072650	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR61	9	16	71	54	1.28E-02	5.20E-05		1.09E-05	-1.55	1.09E-05
Sly07g0110691	Solyc07g014620	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR63	20	25	10	5		8.77E-08		1.84E-02	0.66	1.84E-02
Sly07g0133231	Solyc07g066560	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR65	2	2	1	1		2.84E-03		1.37E-02		
Sly08g0281581	Solyc08g079140	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR67	2	2	1	1		3.39E-02	9.27E-03	1.94E-02		
Sly09g0079141	Solyc09g007970	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR68	1	1	0	1				3.14E-02		
Sly09g0079381	Solyc09g008170	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR69	1	1	248	55		9.87E-17	1.23E-02	9.40E-04	-3.83	9.40E-04
Sly09g0081221	Solyc09g009980	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR70	1	1	1	1				5.64E-03		
Sly10g0169031	Solyc10g018340	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR71	1	1	1	1				1.53E-03		
Sly10g0178291	Solyc10g052580	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR76	1	1	1	0				3.93E-02		
Sly01g0046541	Solyc01g110620	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR8	1	0	1	1				3.49E-02		
Sly10g0179341	Solyc10g054770	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR81	1	2	0	0				3.83E-02		
Sly01g0046551	Solyc01g110630	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	SAUR9	1	1	1	1		4.17E-02		4.17E-02		
Sly01g0046631	Solyc01g110660	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110660	4	3	7	13		4.44E-02		9.69E-04		
Sly01g0046641	Solyc01g110670	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110670	3	3	3	4				3.42E-02		
Sly01g0046701	Solyc01g110720	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110720	1	1	3	5		2.01E-02		4.38E-02		
Sly01g0046711	Solyc01g110730	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110730	1	1	2	2				3.78E-02		
Sly01g0046881	Solyc01g110860	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110860	2	2	3	3				4.47E-02		
Sly01g0046891	Solyc01g110870	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110870	1	1	2	2				4.63E-02		
Sly01g0046901	Solyc01g110880	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110880	1	1	2	4				5.03E-03		
Sly01g0046911	Solyc01g110890	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110890	1	0	1	1				4.34E-02		
Sly01g0046921	Solyc01g110900	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110900	1	1	2	1				4.53E-02		
Sly01g0046981	Solyc01g110930	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110930	3	2	2	1				4.42E-03		
Sly01g0047021	Solyc01g111180	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g110970	1	1	1	0		1.55E-02		1.43E-02		
Sly01g0047061	Solyc01g111000	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc01g111000	2	1	2	4		1.48E-02	4.64E-02	1.09E-02		
Sly03g0197311	Solyc03g033590	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc03g033590	1	1	1	0				4.94E-02		
Sly06g0363501	Solyc06g053260	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc06g053260	2	1	2	1		2.08E-03		5.43E-03	-2.73	5.43E-03
Sly06g0363521	Solyc06g053290	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc06g053290	18	36	83	26	8.67E-03	1.33E-02	1.05E-02	1.05E-02		
Sly07g0119051	Solyc07g042490	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc07g042490	87	64	91	49			4.53E-02	5.64E-10	-0.96	5.64E-10
Sly08g0281591	Solyc08g079150	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc08g079150	1	1	1	1		4.33E-02		4.33E-02		
Sly10g0187851	Solyc10g084020	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc10g084020	1	1	0	1				4.55E-02		
Sly12g0052361	Solyc12g009290	Auxin	Small auxin up-regulated RNA	Small auxin up-regulated RNA	Solyc12g009290	1	1	0	0				4.34E-02		
Sly03g0227461	Solyc03g122350	Brassinosteroid	Brassinosteroid biosynthesis	Cytochrome P450	CYP71A1	326	149	208	363			8.78E-04	8.78E-04		
Sly03g0227471	Solyc03g122360	Brassinosteroid	Brassinosteroid biosynthesis	Cytochrome P450	CYP71A1-like	1	1	44	23		1.77E-18	3.24E-02	6.61E-14		
Sly02g0341111	Solyc02g084740	Brassinosteroid	Brassinosteroid biosynthesis	3-epi-6-deoxocathasterone 23-monooxyg	CYP90C1	11	10	3	13		1.19E-04	6.82E-05	6.82E-05		
Sly09g0080271	Solyc09g009040	Brassinosteroid	Brassinosteroid biosynthesis	sterol reductase	delta14-sterol redu	27	28	13	6		9.67E-07	1.71E-05	1.71E-05		
Sly09g0083621	Solyc09g013070	Brassinosteroid	Brassinosteroid biosynthesis	3-oxo-5-alpha-steroid 6-dehydrogenase	DET2-like	37	43	48	63		1.86E-04	3.21E-02	3.21E-02		
Sly02g0329151	Solyc02g069490	Brassinosteroid	Brassinosteroid biosynthesis	sterol reductase	DWARF1-like	12	3	1	1		5.87E-06		8.19E-03		
Sly01g0004571	Solyc01g009310	Brassinosteroid	Brassinosteroid biosynthesis	Δ7-sterol reductase DWF5	DWARF5-like1	179	164	76	65		9.25E-12		1.88E-04	0.37	1.88E-04

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly06g0376831	Solyc06g074090	Brassinosteroid	Brassinosteroid biosynthesis	Δ7-sterol reductase DWF5	DWARF5-like2	23	22	14	6		1.69E-06	5.40E-11	5.40E-11		
Sly02g0319151	Solyc02g030170	Brassinosteroid	Brassinosteroid biosynthesis	sterol reductase	DWF1	343	443	249	222		2.38E-03		1.93E-02		
Sly11g0287941	Solyc11g006270	Brassinosteroid	Brassinosteroid biosynthesis	3-oxo-5-alpha-steroid 4-dehydrogenase	enoyl-CoA reductas	42	82	373	94	1.29E-03	7.62E-09	2.49E-07	2.49E-07		
Sly11g0287981	Solyc11g006300	Brassinosteroid	Brassinosteroid biosynthesis	3-oxo-5-alpha-steroid 4-dehydrogenase	enoyl-CoA reductas	1	2	2	19		3.28E-04	3.23E-06	3.49E-02	2.56	3.49E-02
Sly06g0380931	Solyc06g082980	Brassinosteroid	Brassinosteroid biosynthesis	sterol reductase	HYD1-like	111	115	82	51		1.15E-03	2.14E-03	2.14E-03		
Sly01g0046391	Solyc01g110460	Brassinosteroid	Brassinosteroid biosynthesis	3-oxo-5-alpha-steroid 4-dehydrogenase	polyprenol reductas	9	9	8	6		1.87E-04	4.81E-06	5.84E-03	0.34	5.84E-03
Sly06g0362891	Solyc06g051750	Brassinosteroid	Brassinosteroid biosynthesis	steroid 3-dehydrogenase (CPD)	SlCPD	34	55	134	91	2.07E-02	9.26E-03		9.26E-03		
Sly07g0127131	Solyc07g056160	Brassinosteroid	Brassinosteroid biosynthesis	steroid 22-alpha-hydroxylase (DWF4)	SlCYP724B2	1	1	1	1		1.96E-06		4.26E-06		
Sly12g0050621	Solyc12g006860	Brassinosteroid	Brassinosteroid biosynthesis	brassinosteroid hydroxylase	SlCYP734A8	3	2	8	8		7.32E-07		4.67E-03	-1.46	4.67E-03
Sly02g0341751	Solyc02g085360	Brassinosteroid	Brassinosteroid biosynthesis	steroid 22-alpha-hydroxylase (DWF4)	SlCYP90B3	23	14	7	8		1.51E-07	2.35E-02	2.35E-02		
Sly10g0190651	Solyc10g086500	Brassinosteroid	Brassinosteroid biosynthesis	3-oxo-5-alpha-steroid 5-dehydrogenase	SlDET2	27	13	3	3	1.32E-04	3.96E-05		5.40E-07		
Sly02g0345751	Solyc02g089160	Brassinosteroid	Brassinosteroid biosynthesis	6-deoxocastasterone 6-oxidase	SlDWARF/SlCYP85A	15	16	31	59		4.66E-04	2.78E-02	2.31E-06		
Sly10g0184691	Solyc10g080150	Brassinosteroid	Brassinosteroid biosynthesis	sterol methyltransferase	SMT1-like	6	5	3	2		2.95E-04		3.14E-07		
Sly10g0180401	Solyc10g055680	Brassinosteroid	Brassinosteroid biosynthesis	sterol methyltransferase	SMT2-like1	7	3	2	2	2.90E-04	5.06E-06		2.22E-02		
Sly01g0047951	Solyc01g111830	Brassinosteroid	Brassinosteroid biosynthesis	sterol methyltransferase	SMT2-like3	40	46	16	10		3.76E-13		3.13E-04		
Sly04g0253211	Solyc04g077440	Brassinosteroid	Brassinosteroid biosynthesis	Squalene monooxygenase	SQE1-like	80	101	35	35		3.11E-17		6.18E-15		
Sly00g0393281	Solyc00g085070	Brassinosteroid	Brassinosteroid biosynthesis	Squalene monooxygenase	SQE3-like	6	5	6	9				6.80E-04		
Sly11g0287971	Solyc11g006290	Brassinosteroid	Brassinosteroid biosynthesis	3-oxo-5-alpha-steroid 4-dehydrogenase	SRD5A-like	3	5	7	5		2.25E-08		2.72E-02	0.83	2.72E-02
Sly02g0342611	Solyc02g086180	Brassinosteroid	Brassinosteroid biosynthesis	sterol reductase	STE1-like2	10	11	1	1		9.71E-07		3.37E-08		
Sly02g0324251	Solyc02g063240	Brassinosteroid	Brassinosteroid biosynthesis	sterol reductase	STE1-like3	75	66	55	39		1.45E-03	4.49E-06	1.32E-04		
Sly05g0140211	Solyc05g011890	Brassinosteroid	Brassinosteroid biosynthesis	steroid sulphotransferase	steroid sulphotrans	7	8	26	108		6.60E-07	2.44E-08	2.44E-08		
Sly03g0219311	Solyc03g114720	Brassinosteroid	Brassinosteroid response	Cell size transcription factor	SlBIM1a	31	28	17	20		2.12E-02		1.41E-02		
Sly01g0008171	Solyc01g014490	Brassinosteroid	Brassinosteroid response	topoisomerase 6 subunit B	TOP6B-like2	21	23	25	26				4.39E-02		
Sly04g0250321	Solyc04g072570	Brassinosteroid	Brassinosteroid signal transduction & response	co-receptor protein kinase (BAK)	BAK1C	14	11	4	2		2.98E-03	6.53E-03	6.53E-03		
Sly03g0192101	Solyc03g005990	Brassinosteroid	Brassinosteroid signal transduction & response	BRASSINAZOLE-RESISTANT	BEH4-like2	9	7	7	12			3.06E-02	3.06E-02		
Sly07g0128531	Solyc07g062260	Brassinosteroid	Brassinosteroid signal transduction & response	BRASSINAZOLE-RESISTANT	BEH4-like3	8	7	4	5		3.36E-03		3.36E-03		
Sly02g0323991	Solyc02g063010	Brassinosteroid	Brassinosteroid signal transduction & response	BRASSINAZOLE-RESISTANT	BES1-like	107	98	53	67		3.46E-04	3.92E-04	2.24E-03		
Sly01g0028741	Solyc01g091620	Brassinosteroid	Brassinosteroid signal transduction & response	GSK3-type protein kinase (BIN2)	BIN2	70	72	52	46		2.86E-02		3.60E-05		
Sly01g0036751	Solyc01g101000	Brassinosteroid	Brassinosteroid signal transduction & response	GSK3-type protein kinase (BIN2)	BIN2	299	311	393	509		1.99E-03	3.34E-02	3.34E-02		
Sly01g0038731	Solyc01g103430	Brassinosteroid	Brassinosteroid signal transduction & response	GSK3-type protein kinase (BIN2)	BIN2	147	171	39	34		9.37E-19		3.01E-24		
Sly02g0343191	Solyc02g086670	Brassinosteroid	Brassinosteroid signal transduction & response	GSK3-type protein kinase (BIN2)	BIN2	83	87	109	159			3.11E-02	3.11E-02		
Sly05g0155471	Solyc05g051050	Brassinosteroid	Brassinosteroid signal transduction & response	GSK3-type protein kinase (BIN2)	BIN2	44	52	31	25		2.34E-02		2.06E-04		
Sly12g0060831	Solyc12g062870	Brassinosteroid	Brassinosteroid signal transduction & response	GSK3-type protein kinase (BIN2)	BIN2	206	216	273	293		1.78E-02		1.75E-03		
Sly02g0343931	Solyc02g087460	Brassinosteroid	Brassinosteroid signal transduction & response	Leucine-rich Repeat Receptor Kinase	BIR3	33	30	19	24		7.49E-06	6.18E-04	8.08E-04		
Sly05g0135071	Solyc05g006570	Brassinosteroid	Brassinosteroid signal transduction & response	Leucine-rich Repeat Receptor Kinase	BIR3	2	2	1	1		1.82E-03		3.12E-05		
Sly04g0255001	Solyc04g079110	Brassinosteroid	Brassinosteroid signal transduction & response	receptor kinase inhibitor (BKI)	BKI1	6	7	4	1		2.18E-05	6.80E-05	6.80E-05		
Sly01g0023081	Solyc01g080880	Brassinosteroid	Brassinosteroid signal transduction & response	signalling protein kinase (BSK)	BSK	64	59	51	87		6.21E-03	2.68E-08	2.68E-08		
Sly06g0379481	Solyc06g076600	Brassinosteroid	Brassinosteroid signal transduction & response	signalling protein kinase (BSK)	BSK	2	2	1	1		1.90E-05		3.73E-05		
Sly10g0189071	Solyc10g085000	Brassinosteroid	Brassinosteroid signal transduction & response	signalling protein kinase (BSK)	BSK	45	34	8	14		1.17E-09	2.33E-02	2.33E-02		
Sly04g0258441	Solyc04g082260	Brassinosteroid	Brassinosteroid signal transduction & response	signalling protein kinase (BSK)	BSK1	95	89	103	100		2.21E-02		2.21E-02		
Sly11g0306521	Solyc11g064890	Brassinosteroid	Brassinosteroid signal transduction & response	signalling protein kinase (BSK)	BSK3	103	90	82	86		9.97E-03		6.24E-03		
Sly12g0076211	Solyc12g099830	Brassinosteroid	Brassinosteroid signal transduction & response	signalling protein kinase (BSK)	BSK3-like	14	14	2	1		6.85E-15	2.04E-04	2.04E-04		
Sly01g0004501	Solyc01g009280	Brassinosteroid	Brassinosteroid signal transduction & response	protein phosphatase (BSU)	BSU	28	30	36	36		6.13E-03		5.55E-05		
Sly06g0376691	Solyc06g073960	Brassinosteroid	Brassinosteroid signal transduction & response	protein phosphatase (BSU)	BSU	39	37	41	47				3.31E-03	0.18	3.31E-03
Sly11g0311841	Solyc11g071920	Brassinosteroid	Brassinosteroid signal transduction & response	protein phosphatase (BSU)	BSU	39	35	38	43				6.15E-03		
Sly09g0096881	Solyc09g074320	Brassinosteroid	Brassinosteroid signal transduction & response	protein phosphatase (BSU)	BSU1	73	71	72	77				9.21E-03		
Sly01g0019781	Solyc01g067400	Brassinosteroid	Brassinosteroid signal transduction & response	NA	CDG1	33	30	32	36				1.38E-02		
Sly06g0373071	Solyc06g069850	Brassinosteroid	Brassinosteroid signal transduction & response	TF	MYB30	20	23	6	3		8.18E-04		7.47E-09		
Sly03g0195371	Solyc03g025950	Brassinosteroid	Brassinosteroid signal transduction & response	receptor kinase regulator protein (MSBP)	receptor kinase reg	269	267	337	414		2.61E-03		9.52E-08		
Sly10g0174161	Solyc10g047140	Brassinosteroid	Brassinosteroid signal transduction & response	co-receptor protein kinase (BAK)	SERK3A/BAK1A	64	36	22	22	1.50E-02	1.76E-07		1.97E-03		
Sly01g0040591	Solyc01g104970	Brassinosteroid	Brassinosteroid signal transduction & response	co-receptor protein kinase (BAK)	SERK3B/BAK1B	42	18	6	5	1.77E-06	2.62E-05		2.27E-07		
Sly02g0331791	Solyc02g071990	Brassinosteroid	Brassinosteroid signal transduction & response	BRASSINAZOLE-RESISTANT	SLB3	42	32	20	26		1.40E-02		1.40E-02		
Sly04g0255911	Solyc04g079980	Brassinosteroid	Brassinosteroid signal transduction & response	BRASSINAZOLE-RESISTANT	SlBES1/BZR1/SlBZH	26	26	29	28		1.06E-02		1.72E-02		
Sly02g0332101	Solyc02g072300	Brassinosteroid	Brassinosteroid signal transduction & response	GSK3-type protein kinase (BIN2)	SlBIN2.1	189	151	99	101		9.38E-03		4.56E-03		
Sly07g0126161	Solyc07g055200	Brassinosteroid	Brassinosteroid signal transduction & response	GSK3-type protein kinase (BIN2)	SlBIN2.2/SlSK	81	90	55	46		9.35E-03	4.22E-03	4.22E-03		
Sly03g0192241	Solyc03g006070	Brassinosteroid	Brassinosteroid signal transduction & response	GSK3-type protein kinase (BIN2)	SlBIN2.3	71	66	75	91		2.11E-02		1.56E-04		
Sly04g0244531	Solyc04g051510	Brassinosteroid	Brassinosteroid signal transduction & response	receptor protein kinase (BRI)	SlBRI1/curl3	45	34	5	5		1.74E-04		3.37E-06		
Sly04g0231181	Solyc04g008430	Brassinosteroid	Brassinosteroid signal transduction & response	receptor protein kinase (BRI)	SlBRL1	1	1	1	1				2.02E-02		
Sly07g0132891	Solyc07g066230	Brassinosteroid	Brassinosteroid signal transduction & response	receptor protein kinase (BRI)	SlBRL2	16	10	6	6	5.13E-03	2.58E-10		1.39E-03		
Sly12g0072051	Solyc12g089040	Brassinosteroid	Brassinosteroid signal transduction & response	BRASSINAZOLE-RESISTANT	SlBZH1 /SlBZR1	44	47	59	94		2.44E-02	4.55E-02	4.55E-02		
Sly07g0128821	Solyc07g062580	Brassinosteroid	Brassinosteroid signal transduction & response	TETRATRICOPEPTIDE THIOREDOXIN-LIKE	TTL1-like	19	16	17	14				7.36E-03	-0.37	7.36E-03
Sly05g0135091	Solyc05g006590	Brassinosteroid	Abscisic acid signal transduction	protein phosphatase 2A catalytic subunit	PP2AC1	53	41	59	70		3.66E-04		4.54E-03		
Sly01g0025561	Solyc01g087560	Brassinosteroid	Brassinosteroid biosynthesis	sterol methyltransferase	SMT1	77	92	171	173		9.06E-11		4.11E-05	-0.67	4.11E-05
Sly04g0229371	Solyc04g006960	Cytokinin	Cytokinin biosynthesis	cytokinin transporter (ABCG14)	ABCG14	2	2	2	2		4.35E-02		3.61E-03	-1.10	3.61E-03
Sly08g0259881	Solyc08g005580	Cytokinin	Cytokinin biosynthesis	cytokinin transporter (ABCG14)	ABCG14	1	1	2	1		5.13E-04		5.13E-04		
Sly08g0277661	Solyc08g075430	Cytokinin	Cytokinin biosynthesis	cytokinin transporter (ABCG14)	ABCG14	4	5	11	10		3.33E-08		1.40E-06		
Sly12g0055501	Solyc12g014190	Cytokinin	Cytokinin biosynthesis	adenylate isopentenyltransferase	IPT9	16	17	18	23			5.40E-03	5.40E-03		
Sly08g0270921	Solyc08g061930	Cytokinin	Cytokinin biosynthesis	cytokinin oxidase/dehydrogenase-like	SlCKX1	1	1	1	1		1.72E-05		3.68E-05		
Sly01g0026241	Solyc01g088160	Cytokinin	Cytokinin biosynthesis	cytokinin oxidase/dehydrogenase-like	SlCKX2	2	2	1	1		1.15E-05		2.27E-07		

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly04g0256901	Solyc04g080820	Cytokinin	Cytokinin biosynthesis	cytokinin oxidase/dehydrogenase-like	SlCKX4	34	12	1	1		2.31E-05		1.18E-09		
Sly12g0051891	Solyc12g008900	Cytokinin	Cytokinin biosynthesis	cytokinin oxidase/dehydrogenase-like	SlCKX6	150	150	1	1		5.92E-34	4.69E-04	1.44E-22		
Sly10g0184401	Solyc10g079870	Cytokinin	Cytokinin biosynthesis	cytokinin oxidase/dehydrogenase-like	SlCKX7	10	4	10	4	2.82E-02	1.03E-03	1.06E-02	1.10E-02		
Sly02g0342321	Solyc02g094860	Cytokinin	Cytokinin biosynthesis	CK-hydroxylase-like2	SlCYP735A1	15	15	0	0		5.65E-09		5.58E-09		
Sly02g0342311	Solyc02g085880	Cytokinin	Cytokinin biosynthesis	CK-hydroxylase-like1	SlCYP735A2	3	2	1	0		6.83E-05		4.11E-03		
Sly05g0138201	Solyc05g009410	Cytokinin	Cytokinin biosynthesis	adenylate isopentenyltransferase	SlIPT1	7	3	2	3	4.86E-02	5.33E-03	1.03E-02	4.34E-02		
Sly04g0229731	Solyc04g007240	Cytokinin	Cytokinin biosynthesis	adenylate isopentenyltransferase	SlIPT2	2	1	1	1				2.05E-02		
Sly01g0022261	Solyc01g080150	Cytokinin	Cytokinin biosynthesis	adenylate isopentenyltransferase	SlIPT3/IPT5	3	2	3	1		1.72E-03	2.80E-02	2.80E-02		
Sly11g0308581	Solyc11g066960	Cytokinin	Cytokinin biosynthesis	adenylate isopentenyltransferase	SlIPT5	8	10	8	9		1.71E-02		1.71E-02		
Sly11g0310291	Solyc11g069570	Cytokinin	Cytokinin biosynthesis	cytokinin riboside 5'-monophosphate ph	SlLOG1	6	5	1	1		6.17E-05		2.41E-04		
Sly09g0079001	Solyc09g007830	Cytokinin	Cytokinin biosynthesis	cytokinin riboside 5'-monophosphate ph	SlLOG2/LOG1	1	1	0	0		8.06E-03		1.10E-02		
Sly04g0257401	Solyc04g081290	Cytokinin	Cytokinin biosynthesis	cytokinin riboside 5'-monophosphate ph	SlLOG3	18	8	4	5		4.27E-03		2.01E-05		
Sly08g0271811	Solyc08g062820	Cytokinin	Cytokinin biosynthesis	cytokinin riboside 5'-monophosphate ph	SlLOG5	59	45	37	57		2.07E-02	5.25E-09	2.07E-02		
Sly10g0186721	Solyc10g082020	Cytokinin	Cytokinin biosynthesis	cytokinin riboside 5'-monophosphate ph	SlLOG7	1	1	1	1				3.34E-02		
Sly12g0066361	Solyc12g042600	Cytokinin	Cytokinin biosynthesis	UDP-glucose iridoid glucosyltransferase-li	UGT73C1-like	11	2	1	0	1.16E-02	1.06E-07		1.50E-09		
Sly10g0189971	Solyc10g085870	Cytokinin	Cytokinin biosynthesis	UDP-glucose iridoid glucosyltransferase-li	UGT73C3-like	1	1	1	1				2.75E-02		
Sly10g0189961	Solyc10g085860	Cytokinin	Cytokinin biosynthesis	UDP-glucose iridoid glucosyltransferase-li	UGT73D1	2	1	1	1		1.01E-02		1.21E-03		
Sly04g0231041	Solyc04g008310	Cytokinin	Cytokinin biosynthesis	UDP-dependent glycosyl transferase	UGT-like	49	38	23	16		1.23E-07	6.60E-03	1.63E-05	0.45	1.63E-05
Sly06g0379381	Solyc06g076550	Cytokinin	Cytokinin biosynthesis	UDP-glucose iridoid glucosyltransferase-li	UGT-like1	3	2	1	1		8.11E-03		2.01E-02		
Sly10g0189331	Solyc10g085280	Cytokinin	Cytokinin biosynthesis	UDP-glucose iridoid glucosyltransferase-li	UGT-like2	6	7	10	4		1.62E-05	2.01E-06	2.01E-06		
Sly04g0251151	Solyc04g074360	Cytokinin	Cytokinin biosynthesis	UDP-glucose iridoid glucosyltransferase-li	UGT-like5	3	1	1	1		9.35E-03		8.69E-03		
Sly04g0251181	Solyc04g074390	Cytokinin	Cytokinin biosynthesis	UDP-glucose iridoid glucosyltransferase-li	UGT-like6	1	1	1	1		1.20E-02		1.12E-02		
Sly02g0346951	Solyc02g090400	Cytokinin	Cytokinin signal transduction	two-component response regulator	ARR13	2	2	1	1		2.13E-02		9.74E-03		
Sly02g0332491	Solyc02g076670	Cytokinin	Cytokinin signal transduction	two-component response regulator	ARR18-like	1	1	1	1		2.00E-03		1.37E-03		
Sly11g0312801	Solyc11g072850	Cytokinin	Cytokinin signal transduction	two-component response regulator	ARR5-like1	4	3	1	1		1.75E-07		2.77E-07		
Sly04g0229661	Solyc04g007180	Cytokinin	Cytokinin signal transduction	Cytokinin Response Factor	SlCRF11	23	15	7	3		1.11E-04	4.96E-03	4.96E-03		
Sly03g0224591	Solyc03g119580	Cytokinin	Cytokinin signal transduction	Cytokinin Response Factor	SlCRF9	5	4	3	3		5.17E-03		5.17E-03		
Sly07g0121391	Solyc07g047770	Cytokinin	Cytokinin signal transduction	histidine kinase	SlHK4/AHK2	34	40	21	27		8.01E-03		8.01E-03		
Sly04g0230751	Solyc04g008110	Cytokinin	Cytokinin signal transduction	histidine kinase	SlHK6/CRE1/AHK4	57	66	32	27		3.36E-02		2.68E-03		
Sly01g0033921	Solyc01g098400	Cytokinin	Cytokinin signal transduction	Histidine phosphotransfer	SlHP1	22	27	8	7		3.69E-07		3.15E-09		
Sly01g0022701	Solyc01g080540	Cytokinin	Cytokinin signal transduction	Histidine phosphotransfer	SlHP2	55	43	13	10		4.79E-05	2.21E-06	7.79E-05		
Sly06g0382491	Solyc06g084410	Cytokinin	Cytokinin signal transduction	Histidine phosphotransfer	SlHP3	43	37	60	89		4.46E-12	3.31E-03	3.15E-03		
Sly03g0221511	Solyc03g116720	Cytokinin	Cytokinin signal transduction	pseudo signal transducer (AHP)	SlPHP2 (AHP6)	1	1	1	1				1.04E-02		
Sly06g0372871	Solyc06g069690	Cytokinin	Cytokinin signal transduction	two-component response regulator	SlPRR2	49	49	69	91		5.78E-11	8.52E-03	8.52E-03		
Sly03g0207651	Solyc03g081240	Cytokinin	Cytokinin signal transduction	two-component response regulator	SlPRR3	15	26	13	24				4.80E-02		
Sly10g0161771	Solyc10g005030	Cytokinin	Cytokinin signal transduction	two-component response regulator	SlPRR4	7	7	3	6		9.60E-06	1.80E-06	3.91E-06	1.99	3.91E-06
Sly04g0242161	Solyc04g049670	Cytokinin	Cytokinin signal transduction	two-component response regulator	SlPRR5	231	296	198	223		1.47E-02		2.27E-02		
Sly10g0190111	Solyc10g086000	Cytokinin	Cytokinin signal transduction	two-component response regulator	SlPRR6	31	34	26	22				1.41E-02		
Sly06g0366561	Solyc06g061030	Cytokinin	Cytokinin signal transduction	two-component response regulator	SlPRR7	7	9	4	1		2.58E-03	2.08E-04	2.08E-04		
Sly08g0279671	Solyc08g077230	Cytokinin	Cytokinin signal transduction	two-component response regulator type	SlPRR8	20	38	239	110	1.75E-02	1.45E-22	1.93E-04	3.83E-02	-0.66	3.83E-02
Sly05g0134911	Solyc05g006420	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR1/SlTRR3/4	99	99	11	11		1.66E-41		1.21E-39		
Sly01g0017831	Solyc01g065540	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR10	17	17	15	11			4.51E-02	4.51E-02		
Sly11g0312251	Solyc11g072330	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR14	15	17	19	22		3.17E-02	1.21E-02	1.21E-02		
Sly03g0218111	Solyc03g113720	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR2/SlTRR7/15	4	3	1	2		9.22E-03	7.00E-03	7.00E-03		
Sly05g0142931	Solyc05g014260	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR21	21	21	7	2		2.51E-04	1.29E-07	1.29E-07		
Sly12g0053431	Solyc12g010330	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR22	20	23	36	39		2.16E-10		7.12E-03		
Sly07g0105451	Solyc07g005140	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR23	5	5	6	5		7.07E-03		1.05E-03		
Sly02g0330921	Solyc02g071220	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR3/SlTRR8/9b	16	13	5	10		1.32E-03		1.32E-03		
Sly10g0184211	Solyc10g079700	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR4	2	2	10	9		3.85E-02		1.50E-02	-1.46	1.50E-02
Sly10g0184111	Solyc10g079600	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR5/SlTRR8/9a	35	33	10	22		8.52E-04	5.30E-04	5.30E-04		
Sly06g0361271	Solyc06g048930	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR7/SlTRR16/17	2	3	14	24		2.06E-05		1.52E-02	-1.24	1.52E-02
Sly04g0230641	Solyc04g008050	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR8	22	24	15	11		1.13E-03	1.97E-10	4.49E-05		
Sly05g0159351	Solyc05g054390	Cytokinin	Cytokinin signal transduction	two-component response regulator type-	SlRR9	56	44	25	40		2.08E-05	1.61E-02	3.12E-02	-0.29	3.12E-02
Sly10g0189301	Solyc10g085230	Cytokinin/ABA	Cytokinin biosynthesis	UDP-glucose iridoid glucosyltransferase-li	SlUGT76E1	17	50	1606	1593		8.96E-21		6.78E-03	-2.50	6.78E-03
Sly03g0225111	Solyc03g120060	Cytokinin/Brass	Cytokinin biosynthesis	cytochrome P450	SlCYP734A7	6	3	1	1		3.77E-05		5.44E-04		
Sly07g0122291	Solyc07g049530	Ethylene	Ethylene biosynthesis	ACC oxidase	ACO1	2405	1480	2147	1393	7.55E-03			1.80E-02	-1.13	1.80E-02
Sly12g0049591	Solyc12g005940	Ethylene	Ethylene biosynthesis	ACC oxidase	ACO2	4	2	2	13		1.79E-02	8.59E-05	2.41E-03	-1.46	2.41E-03
Sly07g0122311	Solyc07g049550	Ethylene	Ethylene biosynthesis	ACC oxidase	ACO3	57	43	14	3		2.41E-03	6.51E-04	6.51E-04		
Sly02g0337251	Solyc02g081190	Ethylene	Ethylene biosynthesis	ACC oxidase	ACO4	68	33	10	8		6.83E-03		2.77E-04		
Sly07g0115061	Solyc07g026650	Ethylene	Ethylene biosynthesis	ACC oxidase	ACO5	27	15	2	1		1.33E-04		6.12E-07	-3.41	6.12E-07
Sly02g0321271	Solyc02g036350	Ethylene	Ethylene biosynthesis	ACC oxidase	ACO6	1570	1402	1053	145			3.19E-04	3.20E-05	-1.23	3.20E-05
Sly12g0051731	Solyc12g008740	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS10	0	0	0	1				2.36E-04	2.22	2.36E-04
Sly03g0193371	Solyc03g007070	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS11	21	24	24	28				4.35E-03		
Sly08g0282371	Solyc08g079750	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS12	18	23	13	31		7.50E-04	1.44E-03	1.44E-03		
Sly12g0069441	Solyc12g056180	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS13	3	2	0	0		2.45E-06		2.19E-06		
Sly08g0284531	Solyc00g095860	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS1A	60	54	356	208	1.08E-07	2.17E-07		1.78E-04		
Sly08g0284521	Solyc00g095760	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS1B	1	1	1	1		1.14E-03		2.43E-04		
Sly01g0030361	Solyc01g095080	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS2	11	20	374	562		1.64E-03		1.58E-07	-3.42	1.58E-07
Sly02g0348621	Solyc02g091990	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS3	1	1	1	1		2.66E-02		1.19E-02	-1.40	1.19E-02

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly05g0154241	Solyc05g050010	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS4	3	4	162	216		3.31E-22		1.55E-03	-3.11	1.55E-03
Sly04g0253181	Solyc04g077410	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS5	1	1	0	0				3.85E-02	-3.23	3.85E-02
Sly08g0262991	Solyc08g008110	Ethylene	Ethylene biosynthesis	ACC synthase (ACS)	ACS6	137	67	6	9		9.98E-11		4.55E-07		
Sly01g0036821	Solyc01g101060	Ethylene	Ethylene biosynthesis	S-adenosyl-L-methionine synthetase	SAMS	2672	3006	1176	895		6.00E-21	2.55E-02	2.55E-02		
Sly09g0079511	Solyc09g008280	Ethylene	Ethylene biosynthesis	S-adenosyl-L-methionine synthetase Z241	SAMS	609	361	217	212				1.69E-03		
Sly10g0187791	Solyc10g083970	Ethylene	Ethylene biosynthesis	S-adenosylmethionine synthase	SAMS	333	146	74	53	1.16E-02	7.94E-04	3.61E-02	3.61E-02		
Sly12g0075331	Solyc12g099000	Ethylene	Ethylene biosynthesis	S-adenosylmethionine synthase	SAMS	306	203	234	142			1.76E-02	1.76E-02		
Sly10g0187381	Solyc10g083610	Ethylene	Ethylene signal transduction	CTR	CTR1	93	54	72	58		9.34E-04		4.14E-02	-0.31	4.14E-02
Sly01g0033491	Solyc01g097980	Ethylene	Ethylene signal transduction	CTR	CTR2	35	32	29	37			1.65E-02	1.65E-02		
Sly09g0080291	Solyc09g009090	Ethylene	Ethylene signal transduction	CTR	CTR3	32	26	27	29				9.59E-03	0.17	9.59E-03
Sly08g0269681	Solyc08g060810	Ethylene	Ethylene signal transduction	EBF	EBF1	200	131	211	204		9.17E-03		2.79E-03		
Sly12g0052631	Solyc12g009560	Ethylene	Ethylene signal transduction	EBF	EBF2	190	86	194	112		8.44E-04		1.23E-08	-1.11	1.23E-08
Sly07g0109101	Solyc07g008250	Ethylene	Ethylene signal transduction	EBF	EBF3	120	51	62	20		2.60E-02	8.58E-04	4.53E-10	-1.08	4.53E-10
Sly06g0376431	Solyc06g073720	Ethylene	Ethylene signal transduction	EIN-like	EIL1	148	122	80	171		2.37E-02	9.20E-09	1.25E-02		
Sly01g0004361	Solyc01g009170	Ethylene	Ethylene signal transduction	EIN-like	EIL2	36	39	61	48		1.73E-02		1.13E-02		
Sly01g0032291	Solyc01g096810	Ethylene	Ethylene signal transduction	EIN-like	EIL3	142	137	124	172		1.91E-02	7.97E-04	1.91E-02		
Sly06g0376451	Solyc06g073730	Ethylene	Ethylene signal transduction	EIN-like	EIL4	114	97	110	118		2.64E-03		2.18E-02	0.21	2.18E-02
Sly01g0008161	Solyc01g014480	Ethylene	Ethylene signal transduction	EIN-like	EIL5	26	22	27	23		3.42E-02		3.42E-02		
Sly01g0001731	Solyc01g006650	Ethylene	Ethylene signal transduction	EIN-like	EIL6	1	1	2	1		1.59E-03	9.50E-03	9.50E-03		
Sly09g0079041	Solyc09g007870	Ethylene	Ethylene signal transduction	EIN2	EIN2	62	69	52	48		3.53E-05		1.39E-02		
Sly02g0333761	Solyc02g077840	Ethylene	Ethylene signal transduction	ERF	ERF.F12	16	10	1	1	1.86E-05	5.05E-12	4.81E-03	4.81E-03		
Sly12g0054571	Solyc12g011330	Ethylene	Ethylene signal transduction	ETR and partner	ETR1	39	38	29	29		3.88E-02		3.88E-02		
Sly07g0127601	Solyc07g056580	Ethylene	Ethylene signal transduction	ETR and partner	ETR2	10	14	26	34	4.02E-02	2.79E-09	9.83E-04	1.61E-13		
Sly09g0098021	Solyc09g075440	Ethylene	Ethylene signal transduction	ETR and partner	ETR3	140	117	727	773		2.71E-07		7.97E-05	-1.29	7.97E-05
Sly06g0363951	Solyc06g053710	Ethylene	Ethylene signal transduction	ETR and partner	ETR4	234	118	266	135	1.60E-02	1.16E-03	1.94E-04	4.39E-03	-0.69	4.39E-03
Sly09g0100471	Solyc09g089610	Ethylene	Ethylene signal transduction	ETR and partner	ETR6	32	19	37	15		3.94E-04	6.36E-03	7.10E-05	-1.22	7.10E-05
Sly05g0160141	Solyc05g055070	Ethylene	Ethylene signal transduction	ETR and partner	ETR7	29	25	35	28		5.44E-05		4.34E-02		
Sly01g0039811	Solyc01g104330	Ethylene	Ethylene signal transduction	ETR and partner	GR	4	4	2	2		4.35E-03		1.37E-02		
Sly08g0272241	Solyc08g065320	Ethylene	Ethylene signal transduction	ETR and partner	GRL1	84	56	62	47				7.58E-04	-0.66	7.58E-04
Sly02g0323351	Solyc02g062420	Ethylene	Ethylene signal transduction	ETR and partner	GRL2	7	7	14	23		4.40E-03	1.66E-03	1.66E-03		
Sly02g0328021	Solyc02g068490	Ethylene	Ethylene signal transduction	ETR and partner	RAN1	36	35	19	16		8.32E-04		1.49E-02	0.39	1.49E-02
Sly08g0280591	Solyc08g078180	Ethylene	Ethylene signal transduction	ERF	SlERF.A1	3	2	1	1		3.25E-03		1.56E-02	-1.25	1.56E-02
Sly03g0210271	Solyc03g093610	Ethylene	Ethylene signal transduction	ERF	SlERF.A2	13	4	1	1	4.28E-02	1.75E-02		1.04E-03		
Sly05g0156771	Solyc05g052050	Ethylene	Ethylene signal transduction	ERF	SlERF.A3/SlPti4	103	66	32	48		1.00E-04		2.51E-02		
Sly08g0280581	Solyc08g078170	Ethylene	Ethylene signal transduction	ERF	SlERF.A4	1	1	1	1				1.78E-03	-2.12	1.78E-03
Sly08g0262041	Solyc08g007230	Ethylene	Ethylene signal transduction	ERF	SlERF.A5	12	4	1	3		1.80E-02		2.88E-02	-1.56	2.88E-02
Sly05g0156761	Solyc05g052040	Ethylene	Ethylene signal transduction	ERF	SlERF.B1	38	34	17	109		4.29E-02	3.93E-02	3.93E-02		
Sly09g0095841	Solyc09g066350	Ethylene	Ethylene signal transduction	ERF	SlERF.B12	2	1	1	0	2.93E-02			1.70E-03		
Sly08g0280601	Solyc08g078190	Ethylene	Ethylene signal transduction	ERF	SlERF.B13	6	7	4	36			3.32E-02	3.32E-02		
Sly05g0156751	Solyc05g052030	Ethylene	Ethylene signal transduction	ERF	SlERF.B3	45	45	6	7		1.14E-08	2.81E-02	1.27E-12		
Sly03g0210191	Solyc03g093540	Ethylene	Ethylene signal transduction	ERF	SlERF.B4	16	10	3	5		1.23E-02		1.16E-02		
Sly03g0210201	Solyc03g093550	Ethylene	Ethylene signal transduction	ERF	SlERF.B5	19	12	5	16		3.38E-02	1.43E-02	1.43E-02		
Sly01g0027441	Solyc01g090310	Ethylene	Ethylene signal transduction	ERF	SlERF.B7	23	5	0	1		8.69E-04		7.30E-04		
Sly01g0027491	Solyc01g090340	Ethylene	Ethylene signal transduction	ERF	SlERF.B9	1	1	0	0		2.80E-02		2.54E-02		
Sly05g0155691	Solyc05g051200	Ethylene	Ethylene signal transduction	ERF	SlERF.C1	11	6	1	6	1.03E-02	7.58E-03	1.52E-02	3.96E-05	-2.46	3.96E-05
Sly04g0234481	Solyc04g014530	Ethylene	Ethylene signal transduction	ERF	SlERF.C2	2	3	1	0		1.04E-09	1.12E-02	4.55E-03	1.12	4.55E-03
Sly09g0095851	Solyc09g066360	Ethylene	Ethylene signal transduction	ERF	SlERF.C3	42	11	3	4	2.35E-02	2.38E-04	2.48E-02	6.38E-08	-1.88	6.38E-08
Sly09g0100801	Solyc09g089930	Ethylene	Ethylene signal transduction	ERF	SlERF.C4	49	20	2	1	2.25E-02	1.26E-09	1.86E-03	3.01E-03	-2.09	3.01E-03
Sly02g0333221	Solyc02g077360	Ethylene	Ethylene signal transduction	ERF	SlERF.C5	0	0	0	1				1.46E-03	-2.78	1.46E-03
Sly02g0333231	Solyc02g077370	Ethylene	Ethylene signal transduction	ERF	SlERF.C6	97	36	1	3		9.70E-11	2.10E-02	2.10E-02		
Sly04g0244341	Solyc04g051360	Ethylene	Ethylene signal transduction	ERF	SlERF.D1	25	8	1	2		1.15E-04	2.60E-02	2.41E-04	-4.64	2.41E-04
Sly12g0070011	Solyc12g056590	Ethylene	Ethylene signal transduction	ERF	SlERF.D2	36	17	15	16				1.78E-03		
Sly01g0044061	Solyc01g108240	Ethylene	Ethylene signal transduction	ERF	SlERF.D3	5	4	1	10		5.08E-03	2.84E-02	2.84E-02		
Sly10g0177631	Solyc10g050970	Ethylene	Ethylene signal transduction	ERF	SlERF.D4	8	5	1	3		3.56E-04	8.43E-03	5.81E-03		
Sly04g0238001	Solyc04g012050	Ethylene	Ethylene signal transduction	ERF	SlERF.D5	15	4	1	5		1.98E-03		1.62E-02	1.37	1.62E-02
Sly04g0249421	Solyc04g071770	Ethylene	Ethylene signal transduction	ERF	SlERF.D6	66	38	52	40		4.49E-02		1.06E-02	-0.85	1.06E-02
Sly03g0223061	Solyc03g118190	Ethylene	Ethylene signal transduction	ERF	SlERF.D7	3	3	5	2		7.15E-08	1.98E-02	1.98E-02		
Sly06g0371811	Solyc06g068830	Ethylene	Ethylene signal transduction	ERF	SlERF.D9	2	1	1	1		2.77E-03		1.60E-04	1.07	1.60E-04
Sly09g0098001	Solyc09g075420	Ethylene	Ethylene signal transduction	ERF	SlERF.E1	69	66	70	204			5.55E-04	2.97E-04	-1.13	2.97E-04
Sly06g0367761	Solyc06g063070	Ethylene	Ethylene signal transduction	ERF	SlERF.E2	655	704	1346	1305		3.45E-03		5.50E-03		
Sly03g0227631	Solyc03g123500	Ethylene	Ethylene signal transduction	ERF	SlERF.E3	116	78	113	116		2.66E-02		4.39E-05	-0.37	4.39E-05
Sly01g0018261	Solyc01g065980	Ethylene	Ethylene signal transduction	ERF	SlERF.E4	294	272	902	843		1.48E-02		1.12E-08	-1.64	1.12E-08
Sly12g0068621	Solyc12g049560	Ethylene	Ethylene signal transduction	ERF	SlERF.E5	28	30	44	63		4.80E-02	4.53E-02	4.53E-02		
Sly10g0162951	Solyc10g006130	Ethylene	Ethylene signal transduction	ERF	SlERF.F1	50	39	27	174			2.24E-02	4.64E-03	-0.56	4.64E-03
Sly07g0131421	Solyc07g064890	Ethylene	Ethylene signal transduction	ERF	SlERF.F2	96	113	118	120				1.87E-02		
Sly07g0124681	Solyc07g053740	Ethylene	Ethylene signal transduction	ERF	SlERF.F4	130	72	25	225			4.84E-05	2.11E-02	-0.35	2.11E-02
Sly10g0166471	Solyc10g009110	Ethylene	Ethylene signal transduction	ERF	SlERF.F5	304	114	11	134		6.01E-05	1.69E-03	1.29E-05	-0.82	1.29E-05
Sly12g0049611	Solyc12g005960	Ethylene	Ethylene signal transduction	ERF	SlERF.F6	12	12	15	17		2.74E-02		3.70E-04		
Sly03g0192491	Solyc03g006320	Ethylene	Ethylene signal transduction	ERF	SlERF.F7	5	5	1	1		2.02E-03	1.11E-02	1.11E-02		

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly05g0142121	Solyc05g013540	Ethylene	Ethylene signal transduction	ERF	SlERF.F9	1	1	1	1				4.02E-02		
Sly01g0030811	Solyc01g095500	Ethylene	Ethylene signal transduction	ERF	SlERF.G1/CRF5	2	1	1	1		4.23E-02		1.72E-03		
Sly06g0380511	Solyc06g082590	Ethylene	Ethylene signal transduction	ERF	SlERF.G2/CRF1	62	27	2	2	5.22E-07	2.18E-21	4.80E-03	4.78E-20		
Sly03g0193761	Solyc03g007460	Ethylene	Ethylene signal transduction	ERF	SlERF.G3/CRF4	5	5	2	3		6.40E-03		6.40E-03		
Sly06g0362971	Solyc06g051840	Ethylene	Ethylene signal transduction	ERF	SlERF.G4/CRF6	8	4	1	1	5.00E-03	1.21E-07		3.58E-09		
Sly06g0369551	Solyc06g065820	Ethylene	Ethylene signal transduction	ERF	SlERF.H1	3	3	2	4				1.87E-02	-0.95	1.87E-02
Sly04g0246001	Solyc04g054910	Ethylene	Ethylene signal transduction	ERF	SlERF.H10	205	167	81	100		1.32E-02	1.06E-03	1.87E-02		
Sly05g0157141	Solyc05g052410	Ethylene	Ethylene signal transduction	ERF	SlERF.H14	5	8	19	41		1.15E-02	3.90E-02	3.90E-02		
Sly06g0361841	Solyc06g050520	Ethylene	Ethylene signal transduction	ERF	SlERF.H15	1	2	3	7		4.79E-03	4.63E-02	4.63E-02		
Sly01g0004061	Solyc01g008890	Ethylene	Ethylene signal transduction	ERF	SlERF.H16/CRF3	19	21	22	27			4.98E-02	1.93E-02		
Sly06g0371301	Solyc06g068360	Ethylene	Ethylene signal transduction	ERF	SlERF.H2	1	1	1	0		3.35E-02		3.09E-02		
Sly01g0027771	Solyc01g090560	Ethylene	Ethylene signal transduction	ERF	SlERF.H4	3	2	1	1		1.83E-03		2.33E-02		
Sly05g0155231	Solyc05g050830	Ethylene	Ethylene signal transduction	ERF	SlERF.H5	4	8	2	1		9.51E-03		2.73E-03	1.19	2.73E-03
Sly03g0225921	Solyc03g120840	Ethylene	Ethylene signal transduction	ERF	SlERF.H6	20	29	4	3		8.12E-40		6.74E-03	0.91	6.74E-03
Sly06g0370381	Solyc06g066540	Ethylene	Ethylene signal transduction	ERF	SlERF.H7	5	5	4	6		3.24E-05		1.33E-04		
Sly07g0118831	Solyc07g042230	Ethylene	Ethylene signal transduction	ERF	SlERF.H9	15	8	1	1	2.51E-03	1.00E-06		3.92E-02	-1.13	3.92E-02
Sly05g0138251	Solyc05g009450	Ethylene	Ethylene signal transduction	ERF	SlERF.J3/CRF10	29	16	13	16	4.95E-02			9.59E-06		
Sly07g0106691	Solyc07g006180	Ethylene	Ethylene signal transduction	ETR and partner	TPR1	36	37	82	149		1.95E-02	7.32E-03	7.67E-06		
Sly09g0099081	Solyc09g082460	Ethylene upstre	Ethylene biosynthesis	homocysteine S-methyltransferase	HMT3	23	129	1408	434	2.36E-02	2.01E-06	1.04E-02	4.37E-03	-1.41	4.37E-03
Sly04g0250671	Solyc04g072900	Ethylene/ABA	Ethylene signal transduction	ERF	SlERF.H12/DREB3	140	86	88	120			4.72E-02	4.72E-02		
Sly03g0210961	Solyc03g095310	Gibberellin	Gibberellin biosynthesis	gibberellin modification enzyme	CYP714A1-like	47	23	5	3		4.06E-08	5.52E-03	1.35E-02		
Sly01g0026871	Solyc01g088760	Gibberellin	Gibberellin biosynthesis	gibberellin modification enzyme (ELA)	CYP714A2-like	44	60	107	97	7.66E-03	1.41E-04		3.52E-04		
Sly06g0379901	Solyc06g082030	Gibberellin	Gibberellin biosynthesis	GA2ox8 GA 2-oxidase	GA2ox10	1	1	2	1		4.47E-02		4.47E-02		
Sly09g0079811	Solyc09g008560	Gibberellin	Gibberellin biosynthesis	gibberellin-A12 hydration enzyme (GAS2)	GAS2-1	54	28	2	1		4.28E-14	1.85E-02	1.89E-21		
Sly11g0289761	Solyc11g007890	Gibberellin	Gibberellin biosynthesis	gibberellin-A12 hydration enzyme (GAS2)	GAS2-2	2	1	0	0				1.56E-02	1.85	1.56E-02
Sly01g0023101	Solyc01g080900	Gibberellin	Gibberellin biosynthesis	KAO1 ent-kaurenoic acid oxidase	KAO2-like	8	9	7	23		6.80E-18	3.64E-06	3.64E-06		
Sly12g0050201	Solyc12g006460	Gibberellin	Gibberellin biosynthesis	KAO1 ent-kaurenoic acid oxidase	KAO2-like2	7	12	8	3		2.45E-10	4.17E-02	4.17E-02		
Sly08g0260171	Solyc08g005720	Gibberellin	Gibberellin biosynthesis	KS (GA2) ent-kaurene synthase	KS-like1	1	0	2	31		9.24E-07	3.63E-27	2.54E-02	-3.52	2.54E-02
Sly05g0138301	Solyc05g009500	Gibberellin	Gibberellin biosynthesis	multi-functional transporter (NPF3)	NPF3	3	2	1	1		2.51E-02		8.13E-05		
Sly06g0382311	Solyc06g084240	Gibberellin	Gibberellin biosynthesis	CPS-GA1-ent-copalyl diphosphate syntha	SlCPS	1	1	1	1		3.15E-03		3.15E-03		
Sly03g0193161	Solyc03g006880	Gibberellin	Gibberellin biosynthesis	GA20ox1 (GA5) GA 20-oxidase	SlGA20ox1	28	31	1	1		2.42E-07		1.67E-07		
Sly11g0312231	Solyc11g072310	Gibberellin	Gibberellin biosynthesis	GA20ox1 (GA5) GA 20-oxidase	SlGA20ox3	32	78	260	222		9.36E-10		2.46E-05	-1.66	2.46E-05
Sly01g0029171	Solyc01g093980	Gibberellin	Gibberellin biosynthesis	GA20ox1 (GA5) GA 20-oxidase	SlGA20ox4	1	1	1	1			1.25E-02	1.25E-02		
Sly05g0158111	Solyc05g053340	Gibberellin	Gibberellin biosynthesis	GA2ox1 GA 2-oxidase	SlGA2ox1	1	1	1	0		2.75E-03		8.35E-03	3.14	8.35E-03
Sly04g0231421	Solyc04g008670	Gibberellin	Gibberellin biosynthesis	GA2ox8 GA 2-oxidase	SlGA2ox11	1	1	1	1		1.32E-02		1.32E-02		
Sly10g0162111	Solyc10g005360	Gibberellin	Gibberellin biosynthesis	GA2ox8 GA 2-oxidase	SlGA2ox12	11	9	18	5			1.46E-02	1.46E-02		
Sly07g0127701	Solyc07g056670	Gibberellin	Gibberellin biosynthesis	GA2ox1 GA 2-oxidase	SlGA2ox2	135	57	242	186		1.57E-02		3.25E-03	-2.32	3.25E-03
Sly01g0021261	Solyc01g079200	Gibberellin	Gibberellin biosynthesis	GA2ox6 GA 2-oxidase	SlGA2ox3	2	2	1	1		5.21E-05		4.57E-05		
Sly07g0127941	Solyc07g061720	Gibberellin	Gibberellin biosynthesis	GA2ox1 GA 2-oxidase	SlGA2ox4	28	19	1	0		3.29E-09		2.37E-10		
Sly07g0127951	Solyc07g061730	Gibberellin	Gibberellin biosynthesis	GA2ox1 GA 2-oxidase	SlGA2ox5	118	73	5	6		1.74E-11		1.92E-08		
Sly02g0330131	Solyc02g070430	Gibberellin	Gibberellin biosynthesis	GA2ox1 GA 2-oxidase	SlGA2ox7	2	1	1	1		9.35E-05		1.75E-04		
Sly08g0265651	Solyc08g016660	Gibberellin	Gibberellin biosynthesis	GA2ox1 GA 2-oxidase	SlGA2ox8	1	1	1	1		3.06E-02		3.06E-02		
Sly10g0164661	Solyc10g007570	Gibberellin	Gibberellin biosynthesis	GA2ox2 GA 2-oxidase	SlGA2ox9	21	25	19	21		1.45E-04		2.91E-02		
Sly06g0370701	Solyc06g066820	Gibberellin	Gibberellin biosynthesis	GA3ox1 (GA4) GA 3-oxidase	SlGA3ox1	5	2	1	1		1.96E-02		1.96E-02		
Sly04g0255491	Solyc04g083160	Gibberellin	Gibberellin biosynthesis	KO (GA3) ent-kaurene oxidase	SlKO	23	17	1	1		3.15E-09		8.64E-11		
Sly07g0133361	Solyc07g066670	Gibberellin	Gibberellin biosynthesis	KS (GA2) ent-kaurene synthase	SlKS/gib3	37	40	76	142		1.42E-06	1.40E-16	3.41E-02	-0.34	3.41E-02
Sly01g0037081	Solyc01g102300	Gibberellin	Gibberellin response	TF	PIF3/SlbHLH006	40	54	39	46	9.41E-03	9.07E-04		5.62E-05		
Sly07g0120171	Solyc07g043580	Gibberellin	Gibberellin response	TF	SlbHLH052/PIF4	19	21	4	2		2.40E-15	1.61E-03	1.61E-03		
Sly10g0190531	Solyc10g086380	Gibberellin	Gibberellin signal transduction	RGA DELLA, GA signaling repressor	GAI-like2	5	4	1	1		5.78E-04	4.94E-02	4.94E-02		
Sly11g0292301	Solyc11g011260	Gibberellin	Gibberellin signal transduction	RGA DELLA, GA signaling repressor	SlDELLA/GAI	66	74	58	50		3.40E-03		4.59E-04		
Sly01g0033911	Solyc01g098390	Gibberellin	Gibberellin signal transduction	GID1a GA receptor	SlGID1ac	9	10	4	3		3.39E-04		1.04E-06		
Sly09g0096821	Solyc09g074270	Gibberellin	Gibberellin signal transduction	GID1a GA receptor	SlGID1b-1/GID1	9	9	26	59		4.49E-04	2.60E-02	2.24E-03	-0.98	2.24E-03
Sly06g0354991	Solyc06g008870	Gibberellin	Gibberellin signal transduction	GID1a GA receptor	SlGID1b-2	18	17	47	80		1.00E-09		2.34E-04		
Sly04g0254221	NA	Gibberellin	Gibberellin signal transduction	F-box protein	SlGID2/SlSly	69	84	74	108			6.93E-04	6.93E-04		
Sly07g0121311	Solyc07g047680	Gibberellin	Gibberellin signal transduction	signal transducer (SLY)	SLY1-like2	3	3	5	3			1.66E-02	1.66E-02		
Sly09g0094351	Solyc09g065020	Gibberellin	Gibberellin signal transduction	signal transducer (SLY)	SLY1-like3	6	7	15	14		1.58E-03		1.30E-04		
Sly09g0081451	Solyc09g010180	Gibberellin	Gibberellin signal transduction	SPY OGT, GA signaling repressor	SPY	72	77	84	98			9.71E-03	8.83E-03		
Sly08g0280811	Solyc08g078390	Jasmonate	Jasmonate biosynthesis	OPC-8:CoA oxidase	ACOX1A	225	180	91	71		2.62E-05		2.83E-09		
Sly04g0245981	Solyc04g054890	Jasmonate	Jasmonate biosynthesis	OPC-8:CoA oxidase	ACOX2	35	42	97	93		3.51E-13		1.72E-18		
Sly10g0165241	Solyc10g008110	Jasmonate	Jasmonate biosynthesis	OPC-8:CoA oxidase	ACOX3	79	75	40	33		2.23E-13		9.76E-22		
Sly10g0181971	Solyc10g076600	Jasmonate	Jasmonate biosynthesis	OPC-8:CoA oxidase	ACOX4	41	52	167	185		5.36E-32		4.59E-39		
Sly10g0189251	Solyc10g085200	Jasmonate	Jasmonate biosynthesis	OPC-8:CoA oxidase	ACOX4-2	42	49	49	38		7.17E-05		8.63E-03	0.34	8.63E-03
Sly12g0072671	Solyc12g094520	Jasmonate	Jasmonate biosynthesis	OPC-8:CoA synthetase	ACS (acyl)/opcl1	152	72	36	62	8.11E-04	2.34E-03	4.85E-04	2.34E-03		
Sly01g0029751	Solyc01g094530	Jasmonate	Jasmonate biosynthesis	acyl-CoA thioesterase	acyl-CoA thioestera	17	18	16	21			4.11E-07	4.11E-07		
Sly01g0029771	Solyc01g094550	Jasmonate	Jasmonate biosynthesis	acyl-CoA thioesterase	acyl-CoA thioestera	72	51	29	36		2.33E-06		4.44E-05		
Sly02g0342181	Solyc02g085730	Jasmonate	Jasmonate biosynthesis	allene oxide cyclase	AOC	634	487	41	27	4.44E-10	4.06E-25		2.29E-34		
Sly04g0255661	Solyc04g079730	Jasmonate	Jasmonate biosynthesis	allene oxide synthase	AOS	111	41	2	3	5.96E-05	8.76E-18		5.49E-15		
Sly11g0310581	Solyc11g069800	Jasmonate	Jasmonate biosynthesis	allene oxide synthase	AOS2	50	28	14	9		9.93E-07		2.89E-09		
Sly10g0165071	Solyc10g007960	Jasmonate	Jasmonate biosynthesis	allene oxide synthase	AOS3	2	1	0	0				1.70E-03		

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly01g0044981	Solyc01g109160	Jasmonate	Jasmonate biosynthesis	allene oxide synthase	AOS3-like	1	1	1	2		7.63E-05	3.67E-02	3.67E-02		
Sly01g0044961	Solyc01g109140	Jasmonate	Jasmonate biosynthesis	allene oxide synthase	AOS-like4	1	1	0	0		2.41E-02		8.96E-04	-3.18	8.96E-04
Sly02g0325111	Solyc02g064950	Jasmonate	Jasmonate biosynthesis	CBS domain-containing protein	CBSX1-like1	37	37	69	178		8.61E-07	9.11E-08	9.11E-08		
Sly02g0349831	Solyc02g093140	Jasmonate	Jasmonate biosynthesis	CBS domain-containing protein	CBSX1-like2	30	35	62	85		4.71E-06	1.73E-02	1.73E-02		
Sly06g0377201	Solyc06g074420	Jasmonate	Jasmonate biosynthesis	jasmonoyl-amino acid carboxylase	CYP94C1	8	2	1	1		1.13E-04		6.47E-04		
Sly09g0080951	NA	Jasmonate	Jasmonate biosynthesis	jasmonoyl-amino acid carboxylase	CYP94C1-like1	17	14	1	1		2.01E-12	2.67E-02	3.34E-10		
Sly09g0080961	NA	Jasmonate	Jasmonate biosynthesis	jasmonoyl-amino acid carboxylase	CYP94C1-like2	9	6	0	0		3.58E-10		3.44E-10		
Sly07g0122471	Solyc07g049690	Jasmonate	Jasmonate biosynthesis	fatty acid hydroperoxide lyase	HPO lyase	58	64	94	106		3.48E-03		3.27E-02		
Sly01g0003021	Solyc01g008010	Jasmonate	Jasmonate biosynthesis	oxophytodienoate export protein (JASSY)	JASSY	15	11	16	20		3.46E-02		6.82E-03		
Sly09g0093091	Solyc09g061840	Jasmonate	Jasmonate biosynthesis	3-ketoacyl-CoA thi- olase (KAT)	KAT	484	322	12	7		6.28E-17		2.05E-02	0.67	2.05E-02
Sly09g0102761	Solyc09g091470	Jasmonate	Jasmonate biosynthesis	3-ketoacyl-CoA thi- olase (KAT)	KAT	284	323	1035	1402		5.73E-32	9.73E-03	2.23E-02	-0.45	2.23E-02
Sly01g0034721	Solyc01g099150	Jasmonate	Jasmonate biosynthesis	lipoxygenase	LOX1-like2	1	1	3	4		4.89E-08		9.93E-09		
Sly09g0089321	Solyc09g055890	Jasmonate	Jasmonate biosynthesis	lipoxygenase	LOX1-like6	8	7	6	4			5.18E-03	1.62E-02		
Sly01g0019021	Solyc01g066620	Jasmonate	Jasmonate biosynthesis	Fatty acid beta-oxidation multifunctional	MFP	3	3	2	2			8.42E-03	6.64E-03		
Sly06g0355301	Solyc06g009160	Jasmonate	Jasmonate biosynthesis	Fatty acid beta-oxidation multifunctional	MFP	14	19	17	37			1.30E-09	1.30E-09		
Sly07g0112881	Solyc07g019670	Jasmonate	Jasmonate biosynthesis	Fatty acid beta-oxidation multifunctional	MFP	212	142	123	163	3.45E-02	1.65E-02		3.32E-02		
Sly08g0275361	Solyc08g068390	Jasmonate	Jasmonate biosynthesis	Fatty acid beta-oxidation multifunctional	MFP	55	26	8	4	4.07E-04	4.68E-04		2.15E-08		
Sly12g0051071	Solyc12g007170	Jasmonate	Jasmonate biosynthesis	Fatty acid beta-oxidation multifunctional	MFP	165	134	83	83		4.76E-04		1.14E-04		
Sly12g0075781	Solyc12g099440	Jasmonate	Jasmonate biosynthesis	Fatty acid beta-oxidation multifunctional	MFP	243	299	430	473		2.50E-06		3.05E-07		
Sly11g0301811	Solyc11g032130	Jasmonate	Jasmonate biosynthesis	12-oxophytodienoate reductase	OPR1-like2	40	31	34	56			8.59E-06	1.23E-03		
Sly10g0190341	Solyc10g086220	Jasmonate	Jasmonate biosynthesis	12-oxophytodienoate reductase	OPR2-like3	19	22	5	1	1.11E-03	1.21E-15	6.98E-14	4.54E-02	0.70	4.54E-02
Sly01g0038691	Solyc01g103390	Jasmonate	Jasmonate biosynthesis	12-oxophytodienoate reductase	OPR2-like6	4	4	2	2		7.46E-03		2.71E-04		
Sly07g0108701	Solyc07g007870	Jasmonate	Jasmonate biosynthesis	12-oxophytodienoate reductase	OPR3-like	397	219	13	8	6.28E-04	3.44E-30	2.08E-02	2.08E-02		
Sly01g0030901	Solyc01g095580	Jasmonate	Jasmonate biosynthesis	JAR1	SlGH3-1/JAR6	40	51	114	167		1.24E-03	3.93E-03	8.37E-09		
Sly10g0167071	Solyc10g009610	Jasmonate	Jasmonate biosynthesis	JAR1	SlGH3-12/JAR3	1	1	1	1		5.58E-03		5.58E-03		
Sly00g0384051	Solyc10g009620	Jasmonate	Jasmonate biosynthesis	JAR1	SlGH3-21/JAR2	1	1	0	0		3.20E-03		4.63E-02		
Sly05g0154531	Solyc05g050280	Jasmonate	Jasmonate biosynthesis	JAR1	SlGH3-5/JAR7	53	35	76	84		8.10E-07		1.38E-07	-1.36	1.38E-07
Sly03g0211701	Solyc03g096050	Jasmonate	Jasmonate biosynthesis	NA	SlJOX1	13	6	7	10		4.84E-03		2.79E-03		
Sly10g0182041	Solyc10g076660	Jasmonate	Jasmonate biosynthesis	NA	SlJOX2	18	26	16	5		1.57E-02	6.12E-06	3.80E-02	-1.15	3.80E-02
Sly10g0189241	Solyc10g085190	Jasmonate	Jasmonate biosynthesis	NA	SlJOX3	2	1	0	0		4.21E-02		3.84E-02		
Sly08g0264051	Solyc08g014000	Jasmonate	Jasmonate biosynthesis	lipoxygenase	SlLOX1 (LOXA)	836	1203	2242	1673	1.27E-02	9.54E-07	2.46E-03	2.46E-03		
Sly12g0054291	Solyc12g011040	Jasmonate	Jasmonate biosynthesis	13-LOX	SlLOX10	31	17	1	1		4.14E-08		8.14E-08		
Sly05g0143441	Solyc05g014790	Jasmonate	Jasmonate biosynthesis	lipoxygenase	SlLOX11	28	28	38	38		9.85E-03		7.18E-04		
Sly01g0001611	Solyc01g006560	Jasmonate	Jasmonate biosynthesis	13-LOX	SlLOX12 (LOXF)	2	2	1	1		3.90E-05		1.84E-05		
Sly01g0034791	Solyc01g099210	Jasmonate	Jasmonate biosynthesis	lipoxygenase	SlLOX13	1	1	2	1			6.30E-03	1.82E-02	1.85	1.82E-02
Sly09g0098471	Solyc09g075870	Jasmonate	Jasmonate biosynthesis	lipoxygenase	SlLOX14	1	1	0	0				4.20E-03	4.52	4.20E-03
Sly01g0034771	Solyc01g099190	Jasmonate	Jasmonate biosynthesis	13-LOX	SlLOX2 (LOXB)	550	1222	11167	10150	3.45E-02	2.06E-14		4.20E-04	-2.06	4.20E-04
Sly01g0001591	Solyc01g006540	Jasmonate	Jasmonate biosynthesis	13-LOX	SlLOX3 (LOXC)	15	120	1902	3108	3.61E-08	1.66E-41	1.69E-02	3.23E-02	-2.11	3.23E-02
Sly03g0227451	Solyc03g122340	Jasmonate	Jasmonate biosynthesis	13-LOX	SlLOX4 (LOXD)	94	60	6	19		3.04E-05	6.51E-04	2.09E-02	-0.69	2.09E-02
Sly01g0034741	Solyc01g099160	Jasmonate	Jasmonate biosynthesis	lipoxygenase	SlLOX5 (LOXE)	6	8	40	66		2.39E-04		3.49E-08		
Sly09g0098461	Solyc09g075860	Jasmonate	Jasmonate biosynthesis	lipoxygenase	SlLOX6	23	16	5	3		1.10E-07		7.02E-03	0.56	7.02E-03
Sly01g0034781	Solyc01g099200	Jasmonate	Jasmonate biosynthesis	lipoxygenase	SlLOX7	6	4	3	7		3.23E-05	1.26E-05	4.99E-02		
Sly08g0269231	Solyc08g029000	Jasmonate	Jasmonate biosynthesis	lipoxygenase	SlLOX8	1	1	0	0				2.13E-04	-2.98	2.13E-04
Sly01g0034761	Solyc01g099180	Jasmonate	Jasmonate biosynthesis	lipoxygenase	SlLOX9	1	1	2	2		1.57E-03		9.86E-03		
Sly01g0043621	Solyc01g107860	Jasmonate	Jasmonate response	Cystathionine β-Synthase Domain–Conta	CBSX2-like	60	76	343	191		1.36E-13	2.54E-02	3.53E-02	-1.03	3.53E-02
Sly05g0157371	Solyc05g052620	Jasmonate	Jasmonate signal transduction	receptor complex component	COI	26	30	53	46		3.37E-26		1.40E-17		
Sly05g0160681	Solyc05g055610	Jasmonate	Jasmonate signal transduction	Met-10+ like family protein	Met-10+ like protei	22	23	18	15		1.10E-02		4.24E-02	0.36	4.24E-02
Sly08g0259271	Solyc08g005050	Jasmonate	Jasmonate signal transduction	transcription factor MYC1	MYC1	65	27	12	33		9.64E-03	5.28E-03	2.05E-04		
Sly08g0279361	Solyc08g076930	Jasmonate	Jasmonate signal transduction	jasmonic acid 3	MYC2	112	62	63	127			5.77E-03	6.83E-03		
Sly05g0146331	Solyc05g018320	Jasmonate	Jasmonate signal transduction	arabinogalactan	NINJA	60	57	40	39		1.51E-02		7.77E-04		
Sly05g0148761	Solyc05g024410	Jasmonate	Jasmonate signal transduction	Galactose oxidase	nitrile-specifier prot	122	149	154	147		6.18E-03		2.98E-02		
Sly07g0118761	Solyc07g042170	Jasmonate	Jasmonate signal transduction	jasmonate ZIM-domain protein	SlJAZ1	220	108	12	22		2.83E-12		1.56E-10		
Sly08g0265841	Solyc08g036620	Jasmonate	Jasmonate signal transduction	jasmonate ZIM-domain protein/no COI at	SlJAZ10	11	3	1	1		4.05E-03		5.87E-03		
Sly08g0265811	Solyc08g036660	Jasmonate	Jasmonate signal transduction	jasmonate ZIM-domain protein/no COI at	SlJAZ11	16	6	0	1		1.04E-07		3.01E-06		
Sly01g0038911	Solyc01g103600	Jasmonate	Jasmonate signal transduction	Jasmonate ZIM-domain protein 4	SlJAZ13	6	6	7	8				2.93E-02		
Sly12g0052261	Solyc12g009220	Jasmonate	Jasmonate signal transduction	jasmonate ZIM-domain protein	SlJAZ2	170	106	1	3		5.07E-10		2.72E-03	-1.27	2.72E-03
Sly03g0227341	Solyc03g122190	Jasmonate	Jasmonate signal transduction	jasmonate ZIM-domain protein	SlJAZ3	204	61	9	10	1.03E-04	1.17E-17		4.59E-16		
Sly12g0068501	Solyc12g049400	Jasmonate	Jasmonate signal transduction	jasmonate ZIM-domain protein	SlJAZ4	92	41	1	2	4.43E-06	2.03E-26	6.71E-04	8.35E-24		
Sly03g0223421	Solyc03g118540	Jasmonate	Jasmonate signal transduction	Jasmonate ZIM-domain protein 7b	SlJAZ5	29	71	103	50	1.24E-02		3.51E-03	3.54E-03	-0.77	3.54E-03
Sly01g0000471	Solyc01g005440	Jasmonate	Jasmonate signal transduction	Jasmonate ZIM-domain protein 3	SlJAZ6	346	292	60	58		6.48E-29		4.24E-38		
Sly11g0292061	Solyc11g011030	Jasmonate	Jasmonate signal transduction	Pto-responsive gene 1	SlJAZ7	58	40	1	1		2.95E-33		1.41E-27		
Sly08g0265821	Solyc08g036640	Jasmonate	Jasmonate signal transduction	jasmonate ZIM-domain protein/no COI at	SlJAZ9	24	11	1	1		2.00E-04		4.73E-04		
Sly10g0178751	Solyc10g054100	Salicylic acid	Salicylic acid signal transduction	salicylic acid transporter (EDS5)	EDS5	3	3	2	1		5.60E-05		1.23E-02		
Sly07g0117491	Solyc07g040690	Salicylic acid	Salicylic acid signal transduction	receptor protein (NPR1)	NPR1	36	25	26	27				7.71E-05		
Sly02g0328951	Solyc02g069310	Salicylic acid	Salicylic acid signal transduction	receptor protein (NPR3|4)	NPR3|4	40	25	17	42			3.59E-02	3.59E-02		
Sly07g0120611	Solyc07g044980	Salicylic acid	Salicylic acid signal transduction	receptor protein (NPR3|4)	NPR3|4	106	61	23	18		3.25E-04		3.69E-07		
Sly03g0216521	Solyc03g112190	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	BIR6-like	4	5	5	6				1.72E-02		
Sly01g0046201	Solyc01g110280	Salicylic acid	Salicylic acid synthesis	salicylic acid transporter (EDS5)	EDS5	8	7	8	12			2.73E-02	2.73E-02		
Sly01g0038451	Solyc01g103160	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	emb1796-like1	38	32	28	25				1.49E-02		

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly03g0208801	Solyc03g083280	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	emb1796-like2	41	37	68	97		7.12E-06	1.71E-04	1.71E-04		
Sly02g0318171	Solyc02g021280	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	EMB2794	6	6	4	2		4.45E-05		5.10E-04		
Sly12g0055841	Solyc12g014500	Salicylic acid	Salicylic acid synthesis	IAA carboxylmethyltransferase	IAMT1-like	1	1	1	0				4.72E-03		
Sly06g0373271	Solyc06g071030	Salicylic acid	Salicylic acid synthesis	isochorismate synthase	isochorismate synth	2	2	2	2		2.82E-02	3.55E-02	3.55E-02		
Sly09g0081751	Solyc09g010450	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	MEE40	5	6	7	7		1.62E-02		7.60E-04		
Sly07g0114741	Solyc07g025230	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	NFD5-like1	14	13	16	13				4.55E-02		
Sly07g0114721	Solyc07g025200	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	NFD5-like2	18	16	17	14			5.20E-05	3.72E-02		
Sly03g0218141	Solyc03g113750	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	OTP43-like	9	7	7	7				1.07E-02		
Sly03g0219641	Solyc03g114920	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PNM1	22	22	23	26				4.08E-02		
Sly08g0280701	Solyc08g078280	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like1	3	3	3	2		5.56E-03		2.51E-05		
Sly04g0252121	Solyc04g076370	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like10	4	5	4	3		2.02E-03		3.01E-03		
Sly12g0055301	Solyc12g014000	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like12	4	6	6	6				4.42E-02		
Sly11g0286721	Solyc11g005140	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like13	25	20	20	18				3.67E-02		
Sly02g0339121	Solyc02g082970	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like14	9	8	10	11		9.30E-03		2.50E-04		
Sly03g0209771	Solyc03g093150	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like15	8	7	7	5			3.65E-04	6.53E-04		
Sly02g0351141	Solyc02g094310	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like16	4	5	4	3				6.84E-04		
Sly11g0288441	Solyc11g006680	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like18	20	24	20	18		2.91E-03		1.88E-03		
Sly10g0164601	Solyc10g007520	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like19	7	8	9	6			4.72E-02	4.72E-02		
Sly04g0232031	Solyc04g009220	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like2	4	5	4	3				1.14E-02		
Sly12g0055641	Solyc12g014330	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like21	4	5	4	3				2.10E-02		
Sly09g0099851	Solyc09g083110	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like22	6	6	7	9				4.49E-03		
Sly05g0140681	Solyc05g012250	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like23	8	8	8	6				2.86E-03		
Sly01g0032651	Solyc01g097130	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like24	10	11	10	10				3.64E-02		
Sly03g0211581	Solyc03g095950	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like26	8	9	10	12		9.25E-03	8.22E-04	8.22E-04		
Sly08g0269101	Solyc08g029150	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like30	6	5	7	8		1.64E-02		1.92E-04		
Sly02g0336261	Solyc02g080170	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like31	3	3	4	3		4.21E-02	4.17E-02	4.17E-02		
Sly03g0195951	Solyc03g031460	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like32	14	15	13	12		8.38E-03		9.58E-03		
Sly06g0353901	Solyc06g007850	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like33	10	10	6	4		9.00E-03		2.27E-03		
Sly08g0276061	Solyc08g069010	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like34	7	8	4	1		2.41E-05	1.61E-08	1.61E-08		
Sly02g0335881	Solyc02g079830	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like36	10	10	15	17		1.12E-04		3.06E-03		
Sly04g0248851	Solyc04g071280	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like37	9	11	9	12				2.15E-02	0.32	2.15E-02
Sly01g0030391	Solyc01g095110	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like38	6	7	6	5				4.33E-03		
Sly03g0216881	Solyc03g112560	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like39	13	15	15	16				2.72E-02		
Sly01g0047611	Solyc01g111470	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like4	9	11	9	8		3.07E-02		3.20E-02		
Sly01g0022611	Solyc01g080450	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like40	13	14	19	16		1.17E-02		1.17E-02		
Sly12g0073341	Solyc12g096140	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like42	61	47	44	42		2.93E-03		1.87E-02		
Sly03g0193701	Solyc03g007390	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like43	7	7	11	10		2.61E-02		9.20E-03		
Sly11g0287591	Solyc11g005940	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like44	13	11	11	11				8.18E-03		
Sly02g0344681	Solyc02g088150	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like45	2	2	2	2				3.99E-02		
Sly12g0061501	Solyc12g035170	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like47	10	12	12	13				1.51E-02		
Sly02g0342661	Solyc02g086230	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like48	4	4	3	4				3.11E-02		
Sly01g0044881	Solyc01g109060	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like49	5	6	4	4				3.85E-03		
Sly10g0162021	Solyc10g005280	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like5	22	17	17	14				1.89E-02		
Sly11g0313221	Solyc11g073230	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like50	4	4	6	4		1.27E-03	2.16E-03	2.16E-03		
Sly06g0353801	Solyc06g007740	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like52	4	5	3	3		3.56E-03	2.02E-03	2.02E-03		
Sly02g0326541	Solyc02g067200	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like53	8	8	12	10		6.37E-06		3.00E-03		
Sly06g0381171	Solyc06g083200	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like6	16	15	15	13			4.54E-02	4.54E-02		
Sly04g0255041	Solyc04g079150	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like7	3	3	3	3				4.68E-02		
Sly01g0036901	Solyc01g101150	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like8	3	3	2	1		1.55E-04	9.21E-03	9.21E-03		
Sly01g0022451	Solyc01g080310	Salicylic acid	Salicylic acid synthesis	pentatricopeptide repeat-containing prot	PPR-like9	8	9	8	8				5.47E-03		
Sly06g0353871	Solyc06g007820	Salicylic acid	Salicylic acid synthesis	rna processing factor	RPF2-like	3	4	2	1		1.66E-02	3.14E-02	3.14E-02		
Sly02g0347731	Solyc02g091140	Salicylic acid	Salicylic acid synthesis	S-adenosyl-L-methionine-dependent met	SAM-METT-like10	14	12	16	34		6.63E-03	4.15E-03	4.15E-03		
Sly09g0102821	Solyc09g091530	Salicylic acid	Salicylic acid synthesis	S-adenosyl-L-methionine-dependent met	SAM-METT-like11	1	1	1	1		2.42E-02		2.42E-02		
Sly02g0341331	Solyc02g084950	Salicylic acid	Salicylic acid synthesis	S-adenosyl-L-methionine-dependent met	SAM-METT-like4	3	5	9	8				3.93E-02		
Sly04g0246371	Solyc00g033460	Salicylic acid	Salicylic acid synthesis	S-adenosyl-L-methionine-dependent met	SAM-METT-like8	6	3	0	0		3.96E-06		3.49E-06		
Sly09g0102841	Solyc09g091550	Salicylic acid	Salicylic acid synthesis	S-adenosyl-L-methionine-dependent met	SlSAMT1	15	9	0	0		1.51E-10		1.29E-10		
Sly08g0271231	Solyc08g062220	Salicylic acid	Salicylic acid synthesis	UDP-dependent glycosyl transferase	UDP-dependent gly	14	6	7	5		8.41E-03	3.13E-02	3.13E-02		
Sly10g0179051	Solyc10g054440	Polyamines	Plolyamines biosynthesis	Arginine decarboxylase	ADC1	511	248	27	31		3.25E-05		3.25E-05		
Sly12g0064591	Solyc12g038970	Polyamines	Plolyamines biosynthesis	agmatine iminohydrolase/deiminase	AIH	37	38	56	75		3.45E-02	1.64E-02	1.64E-02	-0.42	7.82E-05
Sly01g0028241	Solyc01g091160	Polyamines	Plolyamines biosynthesis	Arginase	ARG1	79	91	72	59		1.45E-03	7.17E-03	7.17E-03		
Sly01g0028251	Solyc01g091170	Polyamines	Plolyamines biosynthesis	Arginase	ARG2	134	158	1	1		1.37E-48	6.41E-04	6.41E-04		
Sly11g0309191	Solyc11g068540	Polyamines	Plolyamines biosynthesis	N-carbamoyl putrescine amidase	CPA	84	91	108	93		7.23E-03	4.67E-02	4.67E-02		
Sly04g0258151	Solyc04g082030	Polyamines	Plolyamines biosynthesis	ornithine decarboxylase	ODC1	55	16	6	3	9.27E-08	8.24E-03	1.80E-02	1.80E-02		
Sly03g0214011	Solyc03g098300	Polyamines	Plolyamines biosynthesis	ornithine decarboxylase	ODC2	1	1	1	0	3.64E-02			3.64E-02		
Sly05g0139441	Solyc05g010420	Polyamines	Plolyamines biosynthesis	S-adenosylmethionine decarboxylase	SlSAMDc1	1614	1349	5525	4467		1.53E-16		1.53E-16	-0.66	1.11E-05
Sly02g0346161	Solyc02g089610	Polyamines	Plolyamines biosynthesis	S-adenosylmethionine decarboxylase	SlSAMDc2	166	71	36	348			3.24E-06	3.24E-06		
Sly01g0005451	Solyc01g010040	Polyamines	Plolyamines biosynthesis	S-adenosylmethionine decarboxylase	SlSAMDc3	108	108	75	66		4.92E-02		4.92E-02		
Sly05g0134161	Solyc05g005710	Polyamines	Plolyamines biosynthesis	spermidine synthase	SlSPDS1	202	212	193	266		7.97E-03	3.68E-04	7.97E-03	-0.21	2.95E-02
Sly04g0238801	Solyc04g026030	Polyamines	Plolyamines biosynthesis	Spermidine synthase	SlSPDS2	28	30	44	34		3.77E-03		3.77E-03		

						Estimated Transcript Number - Normal ripening								72h auxin treatment	
Sly	Solyc	Tag	Functional_category	Family	Symbol	EMG	LMG	Br	Br+4	padj_EMGvsLMG	padj_LMGvsBr	padj_BrvsBr+4	padj_general_ripening	Log2FoldChange	padj
Sly08g0270991	Solyc08g061970	Polyamines	Plolyamines biosynthesis	spermine synthase	SlSPMS	6	7	1	0		1.80E-06		1.80E-06		
Sly08g0281931	Solyc08g079430	Polyamines	Plolyamines catabolism	copper-dependent amine oxidases	SlCuAO4	66	78	64	42		1.99E-36		1.99E-36		
Sly05g0142021	Solyc05g013440	Polyamines	Plolyamines catabolism	copper-dependent amine oxidases	SlCuAO4- like	55	60	80	79		1.41E-07		1.41E-07	-0.41	1.27E-02
Sly01g0025591	Solyc01g087590	Polyamines	Plolyamines catabolism	Polyamine oxidase	SlPAO2	27	20	1	4		7.17E-06	1.48E-03	1.48E-03		
Sly02g0337471	Solyc02g081390	Polyamines	Plolyamines catabolism	Polyamine oxidase	SlPAO4- like	208	156	503	625		1.09E-09	5.06E-03	1.09E-09		

Supplementary Table 3.Concentration of standards used for the hormone profiling.

Standard Concentration nM	Name
0	Cal00
0.1761	Cal01
0.3521	Cal02
0.7043	Cal03
1.409	Cal04
2.817	Cal05
5.634	Cal06
11.27	Cal07
22.54	Cal08
45.07	Cal09
90.14	Cal10
180.3	Cal11
360.6	Cal12
721.2	Cal13
1442	Cal14
2885	Cal15

Supplementary Table 4. Report of the counts of reads that map to a single location and summarized at the gene level. Total read count is associated with a gene (meta-feature) which correspond to the sum of reads associated with each of the exons (feature) that belong to that gene.

[a]Assigned: Number of reads or fragments that were assigned to features (exon)

[b]Unassigned multiMapping : Number of alignment records that were not assigned because corresponding reads mapped to multiple locations (genome coordinates)

[c]Unassigned noFeatures: Number of reads or fragments not assigned to any features of the gene model

[d]Unassigned Ambiguous: Number of reads or fragments not assigned because they overlap multiple features (exons) or meta-features (genes)

Normal ripening

ID	Tissue	Stage	Assigned[a]	Unassigned MultiMapping[b]	Unassigned NoFeatures[c]	Unassigned Ambiguous[d]	Total	Total Unassigned	% Assigned	% Unassigned
N_1A	Pericarp	33 DPA	21,782,908	1,198,762	791,005	50,393	23,823,068	2,040,160	91.44	8.56
N_1B	Gel	33 DPA	20,529,790	2,668,654	816,973	47,622	24,063,039	3,533,249	85.32	14.68
N_3A	Pericarp	36 DPA	20,810,432	1,269,812	739,645	48,877	22,868,766	2,058,334	91.00	9.00
N_3B	Gel	36 DPA	22,355,294	2,310,885	780,733	58,468	25,505,380	3,150,086	87.65	12.35
N_4A	Pericarp	Br	20,773,386	1,178,085	754,678	56,776	22,762,925	1,989,539	91.26	8.74
N_4B	Gel	Br	21,028,911	1,015,798	1,016,163	49,982	23,110,854	2,081,943	90.99	9.01
N_5A	Pericarp	Br+4	22,344,032	1,000,847	825,992	71,100	24,241,971	1,897,939	92.17	7.83
N_5B	Gel	Br+4	21,281,120	864,052	859,014	83,085	23,087,271	1,806,151	92.18	7.82
N_6A	Pericarp	33 DPA	20,091,482	1,608,748	874,600	46,797	22,621,627	2,530,145	88.82	11.18
N_6B	Gel	33 DPA	19,973,619	3,881,480	897,416	47,638	24,800,153	4,826,534	80.54	19.46
N_8A	Pericarp	36 DPA	21,410,534	1,350,931	781,682	52,390	23,595,537	2,185,003	90.74	9.26
N_8B	Gel	36 DPA	22,292,094	2,252,261	921,629	54,748	25,520,732	3,228,638	87.35	12.65
N_9A	Pericarp	Br	21,242,150	1,091,226	705,684	55,405	23,094,465	1,852,315	91.98	8.02
N_9B	Gel	Br	21,425,782	970,386	911,686	53,232	23,361,086	1,935,304	91.72	8.28
N_10A	Pericarp	Br+4	20,441,387	1,046,583	718,615	57,585	22,264,170	1,822,783	91.81	8.19
N_10B	Gel	Br+4	18,784,228	907,564	935,145	47,177	20,674,114	1,889,886	90.86	9.14
N_11A	Pericarp	33 DPA	21,177,421	1,603,806	631,550	55,120	23,467,897	2,290,476	90.24	9.76
N_11B	Gel	33 DPA	21,063,423	2,167,929	886,882	48,565	24,166,799	3,103,376	87.16	12.84
N_13A	Pericarp	36 DPA	21,842,764	1,442,004	888,677	56,629	24,230,074	2,387,310	90.15	9.85
N_13B	Gel	36 DPA	19,743,751	4,231,959	910,855	47,830	24,934,395	5,190,644	79.18	20.82
N_14A	Pericarp	Br	21,146,235	1,146,793	727,233	56,791	23,077,052	1,930,817	91.63	8.37
N_14B	Gel	Br	23,679,489	994,711	1,104,603	55,725	25,834,528	2,155,039	91.66	8.34
N_15A	Pericarp	Br+4	21,453,802	795,460	705,156	55,566	23,009,984	1,556,182	93.24	6.76
N_15B	Gel	Br+4	19,254,101	852,204	947,039	47,895	21,101,239	1,847,138	91.25	8.75

Auxin treatment

ID	Tissue	Stage	Assigned[a]	Unassigned MultiMapping[b]	Unassigned NoFeatures[c]	Unassigned Ambiguous[d]	Total	Total Unassigned	% Assigned	% Unassigned
N_61A	Pericarp	Auxin_T6h	20,368,042	1,314,412	544,046	46,819	22,273,319	1,905,277	91.45	8.55
N_61B	Gel	Auxin_T6h	22,549,181	1,736,808	664,922	51,445	25,002,356	2,453,175	90.19	9.81
N_82A	Pericarp	Auxin_T24h	20,480,673	1,413,480	583,485	52,743	22,530,381	2,049,708	90.90	9.10
N_82B	Gel	Auxin_T24h	19,283,342	1,883,398	571,126	44,520	21,782,386	2,499,044	88.53	11.47
N_83A	Pericarp	Auxin_T72h	22,092,061	1,402,683	888,563	57,198	24,440,505	2,348,444	90.39	9.61
N_83B	Gel	Auxin_T72h	18,123,866	2,227,201	825,944	45,695	21,222,706	3,098,840	85.40	14.60
N_81A	Pericarp	Auxin_T6h	18,983,360	2,360,526	750,227	48,365	22,142,478	3,159,118	85.73	14.27
N_81B	Gel	Auxin_T6h	18,592,739	1,864,767	537,765	53,875	21,049,146	2,456,407	88.33	11.67
N_62A	Pericarp	Auxin_T24h	19,811,062	1,735,598	565,770	53,400	22,165,830	2,354,768	89.38	10.62
N_62B	Gel	Auxin_T24h	23,024,423	2,028,216	889,915	58,681	26,001,235	2,976,812	88.55	11.45
N_63A	Pericarp	Auxin_T72h	21,086,599	1,801,317	830,739	54,190	23,772,845	2,686,246	88.70	11.30
N_63B	Gel	Auxin_T72h	20,029,183	1,503,266	743,244	50,213	22,325,906	2,296,723	89.71	10.29
N_64A	Pericarp	Auxin_T6h	19,521,061	1,288,498	503,616	47,207	21,360,382	1,839,321	91.39	8.61
N_64B	Gel	Auxin_T6h	18,931,854	2,072,185	483,117	54,553	21,541,709	2,609,855	87.88	12.12
N_85A	Pericarp	Auxin_T24h	20,345,943	1,253,219	549,534	52,134	22,200,830	1,854,887	91.64	8.36
N_85B	Gel	Auxin_T24h	20,059,517	2,034,112	583,927	54,454	22,732,010	2,672,493	88.24	11.76
N_86A	Pericarp	Auxin_T72h	19,856,631	1,645,787	778,937	60,167	22,341,522	2,484,891	88.88	11.12
N_86B	Gel	Auxin_T72h	19,480,309	1,919,069	799,455	61,588	22,260,421	2,780,112	87.51	12.49
N_84A	Pericarp	Auxin_T6h	17,618,023	2,141,315	673,724	46,086	20,479,148	2,861,125	86.03	13.97
N_84B	Gel	Auxin_T6h	19,011,778	1,539,515	625,214	49,506	21,226,013	2,214,235	89.57	10.43
N_65A	Pericarp	Auxin_T24h	18,248,941	1,515,070	749,614	49,824	20,563,449	2,314,508	88.74	11.26
N_65B	Gel	Auxin_T24h	19,588,995	1,863,637	763,757	59,998	22,276,387	2,687,392	87.94	12.06
N_66A	Pericarp	Auxin_T72h	20,723,806	1,715,163	783,076	50,279	23,272,324	2,548,518	89.05	10.95
N_66B	Gel	Auxin_T72h	17,583,733	1,708,587	667,022	50,301	20,009,643	2,425,910	87.88	12.12
N_67A	Pericarp	Mock_T6h	20,704,280	1,356,310	571,352	48,932	22,680,874	1,976,594	91.29	8.71
N_70B	Gel	Mock_T6h	19,021,693	2,394,375	588,687	41,334	22,046,089	3,024,396	86.28	13.72
N_88A	Pericarp	Mock_T24h	19,725,219	1,511,196	524,519	48,080	21,809,014	2,083,795	90.45	9.55
N_88B	Gel	Mock_T24h	19,675,677	2,166,729	524,888	49,057	22,416,351	2,740,674	87.77	12.23
N_89A	Pericarp	Mock_T72h	17,816,360	1,666,795	767,043	44,953	20,295,151	2,478,791	87.79	12.21
N_89B	Gel	Mock_T72h	19,201,039	2,282,254	749,823	59,444	22,292,560	3,091,521	86.13	13.87
N_90A	Pericarp	Mock_T6h	19,834,812	2,668,101	760,706	63,379	23,326,998	3,492,186	85.03	14.97
N_90B	Gel	Mock_T6h	18,986,331	2,018,567	684,287	58,021	21,747,206	2,760,875	87.30	12.70
N_71A	Pericarp	Mock_T24h	18,797,161	906,273	730,841	55,098	20,489,373	1,692,212	91.74	8.26
N_68B	Gel	Mock_T24h	19,229,857	1,531,607	822,227	56,141	21,639,832	2,409,975	88.86	11.14
N_69A	Pericarp	Mock_T72h	24,143,175	2,485,404	913,363	66,571	27,608,513	3,465,338	87.45	12.55
N_69B	Gel	Mock_T72h	21,351,093	2,446,516	732,309	51,088	24,581,006	3,229,913	86.86	13.14

Supplementary Data 5. Module assignmentfor the 9563 genes selected for WGCNA.

Gene	Module	Gene	Module	Gene	Module	Gene	Module	Gene	Module
Sly00g0384181	M1	Sly12g0067451	M1	Sly05g0142851	M14	Sly02g0344351	M16	Sly05g0138631	M20
Sly00g0384561	M1	Sly12g0067621	M1	Sly05g0142931	M14	Sly02g0344671	M16	Sly05g0139421	M20
Sly00g0384611	M1	Sly12g0067881	M1	Sly05g0143191	M14	Sly02g0344691	M16	Sly05g0140641	M20
Sly00g0385041	M1	Sly12g0067961	M1	Sly05g0143221	M14	Sly02g0345051	M16	Sly05g0140731	M20
Sly00g0385371	M1	Sly12g0068371	M1	Sly05g0143371	M14	Sly02g0345481	M16	Sly05g0140841	M20
Sly00g0392031	M1	Sly12g0068611	M1	Sly05g0143411	M14	Sly02g0345661	M16	Sly05g0141071	M20
Sly00g0393251	M1	Sly12g0068691	M1	Sly05g0143921	M14	Sly02g0346011	M16	Sly05g0142471	M20
Sly00g0394031	M1	Sly12g0068701	M1	Sly05g0144211	M14	Sly02g0346061	M16	Sly05g0142891	M20
Sly00g0394041	M1	Sly12g0068771	M1	Sly05g0144661	M14	Sly02g0346191	M16	Sly05g0143291	M20
Sly00g0394201	M1	Sly12g0068781	M1	Sly05g0145041	M14	Sly02g0346261	M16	Sly05g0143751	M20
Sly01g0000151	M1	Sly12g0068951	M1	Sly05g0145051	M14	Sly02g0346581	M16	Sly05g0144551	M20
Sly01g0000181	M1	Sly12g0069141	M1	Sly05g0145911	M14	Sly02g0347051	M16	Sly05g0144851	M20
Sly01g0000191	M1	Sly12g0069581	M1	Sly05g0146211	M14	Sly02g0347211	M16	Sly05g0145901	M20
Sly01g0000201	M1	Sly12g0069741	M1	Sly05g0146481	M14	Sly02g0347661	M16	Sly05g0146601	M20
Sly01g0001071	M1	Sly12g0069891	M1	Sly05g0146831	M14	Sly02g0348231	M16	Sly05g0148531	M20
Sly01g0001591	M1	Sly12g0069901	M1	Sly05g0146841	M14	Sly02g0348461	M16	Sly05g0150491	M20
Sly01g0002631	M1	Sly12g0070021	M1	Sly05g0146851	M14	Sly02g0348761	M16	Sly05g0150631	M20
Sly01g0002891	M1	Sly12g0070061	M1	Sly05g0146901	M14	Sly02g0349351	M16	Sly05g0151301	M20
Sly01g0002911	M1	Sly12g0070071	M1	Sly05g0147121	M14	Sly02g0349361	M16	Sly05g0151311	M20
Sly01g0003081	M1	Sly12g0070081	M1	Sly05g0147411	M14	Sly02g0349491	M16	Sly05g0152331	M20
Sly01g0003161	M1	Sly12g0070281	M1	Sly05g0147681	M14	Sly02g0351161	M16	Sly05g0153271	M20
Sly01g0003251	M1	Sly12g0070351	M1	Sly05g0147691	M14	Sly03g0191201	M16	Sly05g0153861	M20
Sly01g0003681	M1	Sly12g0070671	M1	Sly05g0147701	M14	Sly03g0191861	M16	Sly05g0154401	M20
Sly01g0003851	M1	Sly12g0071161	M1	Sly05g0147861	M14	Sly03g0191871	M16	Sly05g0154581	M20
Sly01g0004081	M1	Sly12g0071171	M1	Sly05g0148481	M14	Sly03g0192051	M16	Sly05g0154641	M20
Sly01g0004191	M1	Sly12g0071351	M1	Sly05g0148741	M14	Sly03g0192261	M16	Sly05g0154911	M20
Sly01g0005551	M1	Sly12g0071391	M1	Sly05g0148791	M14	Sly03g0192411	M16	Sly05g0155321	M20
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Sly01g0006011	M1	Sly12g0072141	M1	Sly05g0150091	M14	Sly03g0194271	M16	Sly05g0156391	M20
Sly01g0006151	M1	Sly12g0072251	M1	Sly05g0150281	M14	Sly03g0194771	M16	Sly05g0156631	M20
Sly01g0006171	M1	Sly12g0072261	M1	Sly05g0150741	M14	Sly03g0194911	M16	Sly05g0156771	M20
Sly01g0006931	M1	Sly12g0072281	M1	Sly05g0150961	M14	Sly03g0196071	M16	Sly05g0157021	M20
Sly01g0007451	M1	Sly12g0072411	M1	Sly05g0151291	M14	Sly03g0196341	M16	Sly05g0157031	M20
Sly01g0007901	M1	Sly12g0072531	M1	Sly05g0151361	M14	Sly03g0196931	M16	Sly05g0157401	M20
Sly01g0008271	M1	Sly12g0073261	M1	Sly05g0151371	M14	Sly03g0197211	M16	Sly05g0157411	M20
Sly01g0008281	M1	Sly12g0073431	M1	Sly05g0151631	M14	Sly03g0197871	M16	Sly05g0157421	M20
Sly01g0008291	M1	Sly12g0073711	M1	Sly05g0152381	M14	Sly03g0198721	M16	Sly05g0158501	M20
Sly01g0009071	M1	Sly12g0073891	M1	Sly05g0152391	M14	Sly03g0199141	M16	Sly05g0158511	M20
Sly01g0009271	M1	Sly12g0074261	M1	Sly05g0152541	M14	Sly03g0199731	M16	Sly05g0159351	M20
Sly01g0009281	M1	Sly12g0074931	M1	Sly05g0152741	M14	Sly03g0200101	M16	Sly05g0159371	M20
Sly01g0011531	M1	Sly12g0074941	M1	Sly05g0152771	M14	Sly03g0200841	M16	Sly05g0159931	M20
Sly01g0011541	M1	Sly12g0075021	M1	Sly05g0153801	M14	Sly03g0200911	M16	Sly05g0160461	M20
Sly01g0013061	M1	Sly12g0075501	M1	Sly05g0153871	M14	Sly03g0202781	M16	Sly05g0160711	M20
Sly01g0013271	M1	Sly12g0076191	M1	Sly05g0154221	M14	Sly03g0202881	M16	Sly05g0160951	M20
Sly01g0014461	M1	Sly00g0382751	M10	Sly05g0154391	M14	Sly03g0203281	M16	Sly05g0161241	M20
Sly01g0014861	M1	Sly00g0384621	M10	Sly05g0154621	M14	Sly03g0203561	M16	Sly05g0161481	M20
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Sly01g0015681	M1	Sly01g0009141	M10	Sly05g0155381	M14	Sly03g0206061	M16	Sly06g0353081	M20
Sly01g0015691	M1	Sly01g0012201	M10	Sly05g0155411	M14	Sly03g0207751	M16	Sly06g0353481	M20
Sly01g0015841	M1	Sly01g0014761	M10	Sly05g0156301	M14	Sly03g0208141	M16	Sly06g0353491	M20
Sly01g0016201	M1	Sly01g0017821	M10	Sly05g0156451	M14	Sly03g0208991	M16	Sly06g0354161	M20
Sly01g0016251	M1	Sly01g0020341	M10	Sly05g0156551	M14	Sly03g0209131	M16	Sly06g0354331	M20
Sly01g0016691	M1	Sly01g0021051	M10	Sly05g0156611	M14	Sly03g0209511	M16	Sly06g0354341	M20
Sly01g0017191	M1	Sly01g0024861	M10	Sly05g0156691	M14	Sly03g0209581	M16	Sly06g0354831	M20
Sly01g0018261	M1	Sly01g0026041	M10	Sly05g0156751	M14	Sly03g0209801	M16	Sly06g0355281	M20
Sly01g0019451	M1	Sly01g0030171	M10	Sly05g0156821	M14	Sly03g0210251	M16	Sly06g0355331	M20
Sly01g0019461	M1	Sly01g0033571	M10	Sly05g0157341	M14	Sly03g0210631	M16	Sly06g0355431	M20
Sly01g0019581	M1	Sly01g0034331	M10	Sly05g0157571	M14	Sly03g0211281	M16	Sly06g0355821	M20
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Gene	Module	Gene	Module	Gene	Module	Gene	Module	Gene	Module
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Sly01g0019611	M1	Sly01g0039701	M10	Sly05g0157771	M14	Sly03g0212451	M16	Sly06g0359111	M20
Sly01g0019621	M1	Sly01g0040321	M10	Sly05g0157801	M14	Sly03g0213121	M16	Sly06g0359221	M20
Sly01g0019921	M1	Sly01g0041901	M10	Sly05g0157881	M14	Sly03g0213201	M16	Sly06g0359421	M20
Sly01g0019931	M1	Sly01g0043061	M10	Sly05g0158081	M14	Sly03g0213761	M16	Sly06g0360051	M20
Sly01g0020151	M1	Sly01g0044041	M10	Sly05g0158091	M14	Sly03g0214331	M16	Sly06g0361061	M20
Sly01g0020261	M1	Sly01g0044071	M10	Sly05g0158151	M14	Sly03g0214871	M16	Sly06g0361141	M20
Sly01g0020331	M1	Sly01g0044081	M10	Sly05g0158761	M14	Sly03g0215761	M16	Sly06g0361681	M20
Sly01g0020351	M1	Sly01g0044941	M10	Sly05g0158781	M14	Sly03g0215991	M16	Sly06g0361701	M20
Sly01g0020361	M1	Sly01g0045461	M10	Sly05g0158841	M14	Sly03g0216001	M16	Sly06g0362191	M20
Sly01g0020441	M1	Sly01g0046371	M10	Sly05g0159001	M14	Sly03g0216261	M16	Sly06g0362441	M20
Sly01g0020471	M1	Sly01g0047581	M10	Sly05g0159031	M14	Sly03g0216901	M16	Sly06g0362811	M20
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Sly01g0020901	M1	Sly02g0324381	M10	Sly05g0159121	M14	Sly03g0217431	M16	Sly06g0364261	M20
Sly01g0020981	M1	Sly02g0325661	M10	Sly05g0159151	M14	Sly03g0217791	M16	Sly06g0364271	M20
Sly01g0020991	M1	Sly02g0326111	M10	Sly05g0159261	M14	Sly03g0218071	M16	Sly06g0364301	M20
Sly01g0021001	M1	Sly02g0333521	M10	Sly05g0159321	M14	Sly03g0218451	M16	Sly06g0364451	M20
Sly01g0021281	M1	Sly02g0338761	M10	Sly05g0159381	M14	Sly03g0218851	M16	Sly06g0364671	M20
Sly01g0021321	M1	Sly02g0338801	M10	Sly05g0159601	M14	Sly03g0219631	M16	Sly06g0364801	M20
Sly01g0021661	M1	Sly02g0339351	M10	Sly05g0159611	M14	Sly03g0219651	M16	Sly06g0364981	M20
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Sly01g0021891	M1	Sly02g0342331	M10	Sly05g0159951	M14	Sly03g0220571	M16	Sly06g0365271	M20
Sly01g0021941	M1	Sly02g0343781	M10	Sly05g0160601	M14	Sly03g0220661	M16	Sly06g0365531	M20
Sly01g0021961	M1	Sly02g0343961	M10	Sly05g0160621	M14	Sly03g0221021	M16	Sly06g0366041	M20
Sly01g0022321	M1	Sly02g0345301	M10	Sly05g0160641	M14	Sly03g0221171	M16	Sly06g0366211	M20
Sly01g0022441	M1	Sly02g0346201	M10	Sly05g0160831	M14	Sly03g0221881	M16	Sly06g0366521	M20
Sly01g0022581	M1	Sly02g0346551	M10	Sly05g0160871	M14	Sly03g0221891	M16	Sly06g0366561	M20
Sly01g0022621	M1	Sly02g0346911	M10	Sly05g0160911	M14	Sly03g0222121	M16	Sly06g0366801	M20
Sly01g0022871	M1	Sly02g0347761	M10	Sly05g0160941	M14	Sly03g0222141	M16	Sly06g0367751	M20
Sly01g0023091	M1	Sly02g0348121	M10	Sly05g0160981	M14	Sly03g0222421	M16	Sly06g0367871	M20
Sly01g0023211	M1	Sly03g0194211	M10	Sly05g0161121	M14	Sly03g0224911	M16	Sly06g0368131	M20
Sly01g0023261	M1	Sly03g0195711	M10	Sly05g0161161	M14	Sly03g0225231	M16	Sly06g0368241	M20
Sly01g0023291	M1	Sly03g0195721	M10	Sly05g0161221	M14	Sly03g0225421	M16	Sly06g0368441	M20
Sly01g0023451	M1	Sly03g0195731	M10	Sly06g0351631	M14	Sly03g0225491	M16	Sly06g0369741	M20
Sly01g0023551	M1	Sly03g0195931	M10	Sly06g0351901	M14	Sly03g0225641	M16	Sly06g0370141	M20
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Sly11g0310571	M1	Sly04g0258831	M14	Sly01g0042411	M16	Sly04g0230501	M20		
Sly11g0310641	M1	Sly04g0258931	M14	Sly01g0042821	M16	Sly04g0230661	M20		
Sly11g0310981	M1	Sly04g0259091	M14	Sly01g0043321	M16	Sly04g0231111	M20		
Sly11g0310991	M1	Sly04g0259141	M14	Sly01g0043591	M16	Sly04g0232511	M20		
Sly11g0311001	M1	Sly04g0259181	M14	Sly01g0043821	M16	Sly04g0232691	M20		
Sly11g0311401	M1	Sly05g0133371	M14	Sly01g0044171	M16	Sly04g0232731	M20		
Sly11g0311421	M1	Sly05g0133431	M14	Sly01g0044781	M16	Sly04g0232761	M20		
Sly11g0311571	M1	Sly05g0133441	M14	Sly01g0044801	M16	Sly04g0232961	M20		
Sly11g0311751	M1	Sly05g0133531	M14	Sly01g0045361	M16	Sly04g0233091	M20		
Sly11g0311921	M1	Sly05g0133541	M14	Sly01g0046271	M16	Sly04g0234291	M20		
Sly11g0312231	M1	Sly05g0133551	M14	Sly01g0046511	M16	Sly04g0234481	M20		
Sly11g0312241	M1	Sly05g0133571	M14	Sly01g0047221	M16	Sly04g0234711	M20		
Sly11g0312351	M1	Sly05g0133721	M14	Sly01g0047491	M16	Sly04g0234811	M20		
Sly11g0312841	M1	Sly05g0133971	M14	Sly01g0047571	M16	Sly04g0234901	M20		
Sly11g0313691	M1	Sly05g0133981	M14	Sly01g0047761	M16	Sly04g0234911	M20		
Sly11g0313881	M1	Sly05g0134121	M14	Sly01g0048131	M16	Sly04g0235001	M20		
Sly12g0048591	M1	Sly05g0134191	M14	Sly01g0048201	M16	Sly04g0235021	M20		
Sly12g0049031	M1	Sly05g0134211	M14	Sly01g0048221	M16	Sly04g0235211	M20		
Sly12g0049301	M1	Sly05g0134331	M14	Sly01g0048271	M16	Sly04g0235501	M20		
Sly12g0049591	M1	Sly05g0134411	M14	Sly02g0314751	M16	Sly04g0235721	M20		
Sly12g0049641	M1	Sly05g0134421	M14	Sly02g0315101	M16	Sly04g0237411	M20		
Sly12g0049741	M1	Sly05g0134431	M14	Sly02g0317641	M16	Sly04g0237421	M20		
Sly12g0049961	M1	Sly05g0134441	M14	Sly02g0318321	M16	Sly04g0237531	M20		
Sly12g0050111	M1	Sly05g0134451	M14	Sly02g0318851	M16	Sly04g0237541	M20		
Sly12g0050431	M1	Sly05g0134471	M14	Sly02g0318951	M16	Sly04g0239761	M20		
Sly12g0050641	M1	Sly05g0134551	M14	Sly02g0319471	M16	Sly04g0241331	M20		
Sly12g0050721	M1	Sly05g0134611	M14	Sly02g0319631	M16	Sly04g0243681	M20		
Sly12g0050731	M1	Sly05g0134651	M14	Sly02g0319721	M16	Sly04g0244391	M20		
Sly12g0050741	M1	Sly05g0134911	M14	Sly02g0320331	M16	Sly04g0244661	M20		
Sly12g0050751	M1	Sly05g0134931	M14	Sly02g0321431	M16	Sly04g0245181	M20		
Sly12g0050761	M1	Sly05g0135051	M14	Sly02g0322991	M16	Sly04g0245371	M20		
Sly12g0050871	M1	Sly05g0135131	M14	Sly02g0323921	M16	Sly04g0245631	M20		
Sly12g0050941	M1	Sly05g0135281	M14	Sly02g0323941	M16	Sly04g0246051	M20		
Sly12g0050971	M1	Sly05g0135541	M14	Sly02g0324031	M16	Sly04g0246361	M20		
Sly12g0051081	M1	Sly05g0135641	M14	Sly02g0324171	M16	Sly04g0246371	M20		
Sly12g0051091	M1	Sly05g0135711	M14	Sly02g0324271	M16	Sly04g0247161	M20		

Gene	Module	Gene	Module	Gene	Module	Gene	Module	Gene	Module
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Sly12g0051221	M1	Sly05g0135801	M14	Sly02g0324431	M16	Sly04g0247641	M20		
Sly12g0051371	M1	Sly05g0136121	M14	Sly02g0324811	M16	Sly04g0247701	M20		
Sly12g0051581	M1	Sly05g0136131	M14	Sly02g0324951	M16	Sly04g0248071	M20		
Sly12g0052061	M1	Sly05g0136151	M14	Sly02g0325131	M16	Sly04g0248341	M20		
Sly12g0052301	M1	Sly05g0136361	M14	Sly02g0325651	M16	Sly04g0248371	M20		
Sly12g0052471	M1	Sly05g0136451	M14	Sly02g0325801	M16	Sly04g0249001	M20		
Sly12g0052481	M1	Sly05g0136461	M14	Sly02g0325811	M16	Sly04g0249421	M20		
Sly12g0052631	M1	Sly05g0136731	M14	Sly02g0325871	M16	Sly04g0249571	M20		
Sly12g0053231	M1	Sly05g0136761	M14	Sly02g0326561	M16	Sly04g0249581	M20		
Sly12g0053281	M1	Sly05g0136811	M14	Sly02g0327321	M16	Sly04g0249601	M20		
Sly12g0053301	M1	Sly05g0137201	M14	Sly02g0327761	M16	Sly04g0249691	M20		
Sly12g0053421	M1	Sly05g0137281	M14	Sly02g0328431	M16	Sly04g0249711	M20		
Sly12g0053541	M1	Sly05g0137361	M14	Sly02g0328441	M16	Sly04g0250321	M20		
Sly12g0053561	M1	Sly05g0137561	M14	Sly02g0329101	M16	Sly04g0251501	M20		
Sly12g0053791	M1	Sly05g0137651	M14	Sly02g0329111	M16	Sly04g0251751	M20		
Sly12g0054191	M1	Sly05g0137831	M14	Sly02g0330701	M16	Sly04g0252301	M20		
Sly12g0054371	M1	Sly05g0137961	M14	Sly02g0330711	M16	Sly04g0252331	M20		
Sly12g0054551	M1	Sly05g0138011	M14	Sly02g0330713	M16	Sly04g0252341	M20		
Sly12g0054691	M1	Sly05g0138021	M14	Sly02g0330716	M16	Sly04g0252781	M20		
Sly12g0054721	M1	Sly05g0138071	M14	Sly02g0330719	M16	Sly04g0252981	M20		
Sly12g0054751	M1	Sly05g0138081	M14	Sly02g0330721	M16	Sly04g0253041	M20		
Sly12g0054771	M1	Sly05g0138111	M14	Sly02g0330731	M16	Sly04g0253161	M20		
Sly12g0054811	M1	Sly05g0138271	M14	Sly02g0330751	M16	Sly04g0253511	M20		
Sly12g0054881	M1	Sly05g0138371	M14	Sly02g0331541	M16	Sly04g0254091	M20		
Sly12g0054961	M1	Sly05g0138461	M14	Sly02g0333001	M16	Sly04g0254101	M20		
Sly12g0054971	M1	Sly05g0138481	M14	Sly02g0333011	M16	Sly04g0254251	M20		
Sly12g0055091	M1	Sly05g0138491	M14	Sly02g0333091	M16	Sly04g0254741	M20		
Sly12g0055121	M1	Sly05g0138531	M14	Sly02g0333251	M16	Sly04g0254941	M20		
Sly12g0056161	M1	Sly05g0138571	M14	Sly02g0333691	M16	Sly04g0255101	M20		
Sly12g0056171	M1	Sly05g0138691	M14	Sly02g0333891	M16	Sly04g0255111	M20		
Sly12g0056241	M1	Sly05g0138811	M14	Sly02g0333961	M16	Sly04g0255281	M20		
Sly12g0056541	M1	Sly05g0139601	M14	Sly02g0333971	M16	Sly04g0255341	M20		
Sly12g0056621	M1	Sly05g0139621	M14	Sly02g0334581	M16	Sly04g0255391	M20		
Sly12g0056641	M1	Sly05g0139631	M14	Sly02g0334651	M16	Sly04g0255471	M20		
Sly12g0056871	M1	Sly05g0139641	M14	Sly02g0334691	M16	Sly04g0255751	M20		
Sly12g0056921	M1	Sly05g0139651	M14	Sly02g0336021	M16	Sly04g0256501	M20		
Sly12g0057281	M1	Sly05g0139701	M14	Sly02g0336041	M16	Sly04g0257491	M20		
Sly12g0057431	M1	Sly05g0139811	M14	Sly02g0336251	M16	Sly04g0258671	M20		
Sly12g0057441	M1	Sly05g0139901	M14	Sly02g0336561	M16	Sly05g0133871	M20		
Sly12g0057481	M1	Sly05g0139911	M14	Sly02g0336581	M16	Sly05g0133961	M20		
Sly12g0057501	M1	Sly05g0140101	M14	Sly02g0337121	M16	Sly05g0134261	M20		
Sly12g0058041	M1	Sly05g0140411	M14	Sly02g0337981	M16	Sly05g0134531	M20		
Sly12g0058611	M1	Sly05g0140461	M14	Sly02g0338331	M16	Sly05g0135251	M20		
Sly12g0059131	M1	Sly05g0140831	M14	Sly02g0338411	M16	Sly05g0135401	M20		
Sly12g0059391	M1	Sly05g0140981	M14	Sly02g0338441	M16	Sly05g0135811	M20		
Sly12g0059451	M1	Sly05g0141101	M14	Sly02g0339051	M16	Sly05g0136141	M20		
Sly12g0059751	M1	Sly05g0141181	M14	Sly02g0339091	M16	Sly05g0136161	M20		
Sly12g0060011	M1	Sly05g0141271	M14	Sly02g0339151	M16	Sly05g0136181	M20		
Sly12g0060131	M1	Sly05g0141281	M14	Sly02g0339161	M16	Sly05g0136511	M20		
Sly12g0060821	M1	Sly05g0141311	M14	Sly02g0339291	M16	Sly05g0136631	M20		
Sly12g0062601	M1	Sly05g0141381	M14	Sly02g0339681	M16	Sly05g0136741	M20		
Sly12g0062631	M1	Sly05g0141391	M14	Sly02g0340431	M16	Sly05g0136921	M20		
Sly12g0063691	M1	Sly05g0141661	M14	Sly02g0341111	M16	Sly05g0137081	M20		
Sly12g0064071	M1	Sly05g0141791	M14	Sly02g0341211	M16	Sly05g0137811	M20		
Sly12g0064731	M1	Sly05g0141821	M14	Sly02g0341321	M16	Sly05g0137921	M20		
Sly12g0064811	M1	Sly05g0141881	M14	Sly02g0341371	M16	Sly05g0137981	M20		
Sly12g0065371	M1	Sly05g0141951	M14	Sly02g0341901	M16	Sly05g0138121	M20		
Sly12g0065381	M1	Sly05g0142031	M14	Sly02g0342211	M16	Sly05g0138181	M20		
Sly12g0066281	M1	Sly05g0142051	M14	Sly02g0342321	M16	Sly05g0138281	M20		
Sly12g0066541	M1	Sly05g0142251	M14	Sly02g0342751	M16	Sly05g0138291	M20		
Sly12g0066681	M1	Sly05g0142401	M14	Sly02g0343281	M16	Sly05g0138301	M20		
Sly12g0066721	M1	Sly05g0142641	M14	Sly02g0343411	M16	Sly05g0138421	M20		
Sly12g0067341	M1	Sly05g0142791	M14	Sly02g0343581	M16	Sly05g0138441	M20		
Sly12g0067401	M1	Sly05g0142821	M14	Sly02g0344341	M16	Sly05g0138601	M20		

Supplementary Table 6. Gene correspondance Solyc and Sly locus.

Solyc	Sly	Solyc	Sly	Solyc	Sly	Solyc	Sly	Solyc	Sly	Solyc	Sly
Solyc00g005080	Sly00g0386171	Solyc11g064880	Sly11g0306511	Solyc02g077950	Sly02g0333861	Solyc04g072730	Sly04g0250501	Solyc07g039610	Sly07g0117341	Solyc10g007690	Sly10g0164791
Solyc00g006540	Sly00g0382811	Solyc11g065040	Sly11g0306671	Solyc02g077960	Sly02g0333871	Solyc04g015520	Sly04g0235571	Solyc07g039620	Sly07g0117351	Solyc10g007700	Sly10g0164801
Solyc00g006540	Sly00g0382821	Solyc11g065140	Sly11g0306801	Solyc02g077970	Sly02g0333881	Solyc04g072740	Sly04g0250511	Solyc07g005520	Sly07g0105861	Solyc10g007710	Sly10g0164811
Solyc00g006540	Sly00g0382831	Solyc11g065150	Sly11g0306801	Solyc02g077980	Sly02g0333891	Solyc04g072760	Sly04g0250521	Solyc07g039650	Sly07g0117371	Solyc10g005240	Sly10g0161981
Solyc00g006900	Sly11g0302001	Solyc11g065160	Sly11g0306801	Solyc02g077990	Sly02g0333901	Solyc04g072770	Sly04g0250531	Solyc07g040680	Sly07g0117481	Solyc10g038130	Sly10g0171251
Solyc00g007110	Sly02g0321921	Solyc11g065200	Sly11g0306831	Solyc02g078000	Sly02g0333911	Solyc04g072780	Sly04g0250551	Solyc07g040690	Sly07g0117491	Solyc10g007720	Sly10g0164841
Solyc00g007120	Sly02g0321921	Solyc11g065270	Sly11g0306901	Solyc02g078010	Sly02g0333921	Solyc04g072790	Sly04g0250561	Solyc07g040700	Sly07g0117501	Solyc10g007730	Sly10g0164851
Solyc00g007140	Sly10g0177581	Solyc11g065310	Sly11g0306941	Solyc02g078020	Sly02g0333931	Solyc04g072800	Sly04g0250571	Solyc07g040710	Sly07g0117511	Solyc10g038140	Sly10g0171261
Solyc00g013130	Sly00g0385091	Solyc11g065420	Sly11g0307061	Solyc02g078040	Sly02g0333961	Solyc04g072810	Sly04g0250591	Solyc07g040720	Sly07g0117531	Solyc10g007740	Sly10g0164861
Solyc00g013130	Sly00g0385101	Solyc11g065520	Sly11g0307141	Solyc02g078050	Sly02g0333971	Solyc04g072850	Sly04g0250621	Solyc07g040740	Sly07g0117551	Solyc10g007750	Sly10g0164871
Solyc00g013170	Sly11g0313691	Solyc11g065550	Sly11g0307181	Solyc02g078060	Sly02g0333981	Solyc04g072860	Sly04g0250631	Solyc07g040750	Sly07g0117571	Solyc10g007760	Sly10g0164881
Solyc00g014390	Sly00g0393351	Solyc11g065610	Sly11g0307221	Solyc02g078070	Sly02g0333991	Solyc04g072870	Sly04g0250641	Solyc07g040790	Sly07g0117591	Solyc10g038150	Sly10g0171281
Solyc00g014790	Sly11g0313531	Solyc11g065670	Sly11g0307281	Solyc02g078090	Sly02g0334011	Solyc04g072880	Sly04g0250651	Solyc07g005530	Sly07g0105871	Solyc10g007770	Sly10g0164891
Solyc00g014800	Sly11g0313521	Solyc11g065780	Sly11g0307401	Solyc02g078100	Sly02g0334021	Solyc04g072890	Sly04g0250661	Solyc07g005030	Sly07g0105331	Solyc10g007800	Sly10g0164921
Solyc00g014830	Sly01g0037901	Solyc11g065790	Sly11g0307401	Solyc02g078130	Sly02g0334051	Solyc04g072910	Sly04g0250681	Solyc07g040850	Sly07g0117611	Solyc10g038170	Sly10g0171301
Solyc00g014830	Sly01g0037921	Solyc11g065900	Sly11g0307551	Solyc02g078140	Sly02g0334061	Solyc04g072920	Sly04g0250691	Solyc07g040890	Sly07g0117671	Solyc10g007820	Sly10g0164941
Solyc00g014830	Sly01g0037961	Solyc11g065980	Sly11g0307621	Solyc02g078150	Sly02g0334071	Solyc04g072940	Sly04g0250711	Solyc07g040900	Sly07g0117681	Solyc10g007830	Sly10g0164951
Solyc00g014850	Sly01g0037971	Solyc11g066000	Sly11g0307641	Solyc02g078160	Sly02g0334081	Solyc04g073940	Sly04g0250721	Solyc07g014580	Sly07g0110651	Solyc10g038190	Sly10g0171331
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Solyc00g017540	Sly00g0383991	Solyc11g066080	Sly11g0307721	Solyc02g078180	Sly02g0334121	Solyc04g015530	Sly04g0235581	Solyc07g040960	Sly07g0117731	Solyc10g007850	Sly10g0164971
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Solyc00g019730	Sly00g0386991	Solyc11g066430	Sly11g0308031	Solyc02g078200	Sly02g0334141	Solyc04g073970	Sly04g0250751	Solyc07g014590	Sly07g0110661	Solyc10g039190	Sly10g0171341
Solyc00g020840	Sly03g0194351	Solyc11g066450	Sly11g0308051	Solyc02g078210	Sly02g0334151	Solyc04g073980	Sly04g0250761	Solyc07g040980	Sly07g0117771	Solyc10g007860	Sly10g0164981
Solyc00g021630	Sly11g0313811	Solyc11g066460	Sly11g0308061	Solyc02g078220	Sly02g0334161	Solyc04g073990	Sly04g0250771	Solyc07g040990	Sly07g0117781	Solyc10g039210	Sly10g0171371
Solyc00g022100	Sly00g0387661	Solyc11g066470	Sly11g0308071	Solyc02g078230	Sly02g0334171	Solyc04g074000	Sly04g0250781	Solyc07g041000	Sly07g0117791	Solyc10g007870	Sly10g0164991
Solyc00g022110	Sly11g0314041	Solyc11g066540	Sly11g0308141	Solyc02g078240	Sly02g0334181	Solyc04g074010	Sly04g0250791	Solyc07g041010	Sly07g0117801	Solyc10g039220	Sly10g0171411
Solyc00g023590	Sly11g0313361	Solyc11g066630	Sly11g0308221	Solyc02g078250	Sly02g0334191	Solyc04g074020	Sly04g0250801	Solyc07g041020	Sly07g0117811	Solyc10g007880	Sly10g0165001
Solyc00g023590	Sly11g0313371	Solyc11g066750	Sly11g0308361	Solyc02g078260	Sly02g0334201	Solyc04g074030	Sly04g0250811	Solyc07g005540	Sly07g0105881	Solyc10g039260	Sly10g0171441
Solyc00g025290	Sly00g0387421	Solyc11g066760	Sly11g0308361	Solyc02g078270	Sly02g0334211	Solyc04g074040	Sly04g0250821	Solyc07g014600	Sly07g0110671	Solyc10g007890	Sly10g0165011
Solyc00g027770	Sly11g0310981	Solyc11g066770	Sly11g0308361	Solyc02g078280	Sly02g0334221	Solyc04g074050	Sly04g0250831	Solyc07g014610	Sly07g0110681	Solyc10g039270	Sly10g0171451
Solyc00g030520	Sly12g0050031	Solyc11g066860	Sly11g0308471	Solyc02g078290	Sly02g0334261	Solyc04g005880	Sly04g0229231	Solyc07g041070	Sly07g0117821	Solyc10g039280	Sly10g0171461
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Solyc11g063530	Sly00g0392461	Solyc02g077850	Sly02g0333771	Solyc04g072660	Sly04g0250421	Solyc07g039540	Sly07g0117241	Solyc10g038080	Sly10g0171201		
Solyc11g063540	Sly11g0314071	Solyc02g077860	Sly02g0333781	Solyc04g072670	Sly04g0250431	Solyc07g039550	Sly07g0117251	Solyc10g038090	Sly10g0171221		
Solyc11g063620	Sly11g0313621	Solyc02g077880	Sly02g0333801	Solyc04g072680	Sly04g0250441	Solyc07g009540	Sly07g0110591	Solyc10g038100	Sly10g0171231		
Solyc11g063630	Sly11g0313621	Solyc02g077890	Sly02g0333811	Solyc04g072690	Sly04g0250451	Solyc07g039570	Sly07g0117271	Solyc10g007650	Sly10g0164751		
Solyc11g063700	Sly00g0392321	Solyc02g077900	Sly02g0333821	Solyc04g072700	Sly04g0250461	Solyc07g039580	Sly07g0117281	Solyc10g007660	Sly10g0164761		
Solyc11g063730	Sly11g0306381	Solyc02g077910	Sly02g0333831	Solyc04g072710	Sly04g0250471	Solyc07g039590	Sly07g0117301	Solyc10g007670	Sly10g0164771		
Solyc11g064860	Sly11g0306511	Solyc02g077920	Sly02g0333841	Solyc04g072720	Sly04g0250481	Solyc07g005510	Sly07g0105851	Solyc10g007680	Sly10g0164781		

Supplementary Tables Chapter III

Supplementary Table 1. Module assignmentfor the 23067 genes selected for WGCNA.

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly00g0382751	M8	NA	10	11	8	5	11	13	14	7	9	22
Sly00g0382761	M12	NA	26	27	27	26	29	31	30	31	36	38
Sly00g0383491	M2	NA	5	6	5	4	3	5	6	4	7	5
Sly00g0383511	M1	NA	1	2	1	1	1	1	1	1	1	1
Sly00g0383691	M12	NA	49	46	51	53	54	76	75	95	116	132
Sly00g0383701	M9	NA	0	1	0	0	0	1	2	1	0	0
Sly00g0383711	M1	NA	9	9	8	3	1	1	1	1	1	1
Sly00g0383731	M1	NA	14	16	15	21	25	11	13	13	23	24
Sly00g0383851	M12	NA	1	2	1	1	1	2	2	2	1	1
Sly00g0383861	M12	NA	1	1	1	1	0	2	1	1	1	0
Sly00g0383871	M3	NA	20	24	13	13	9	16	21	13	8	7
Sly00g0383881	M12	NA	79	78	79	57	48	94	101	111	104	117
Sly00g0383901	M3	NA	78	90	50	4	3	56	66	41	4	1
Sly00g0383911	M1	NA	136	139	156	62	51	27	29	21	20	71
Sly00g0383921	M1	NA	26	26	29	14	14	8	9	8	11	24
Sly00g0383931	M19	NA	50	52	60	61	88	51	49	53	49	71
Sly00g0383941	M3	NA	2	3	1	1	0	2	3	1	0	1
Sly00g0383951	M3	NA	3	3	2	1	2	1	1	1	1	1
Sly00g0383961	M1	NA	12	10	9	4	3	4	5	5	5	5
Sly00g0384051	M22	GH3-21	1	0	1	0	0	2	1	1	0	0
Sly00g0384091	M22	Solyc00g167300	1	1	1	0	0	1	1	1	0	0
Sly00g0384141	M2	NA	28	33	25	25	21	20	29	18	26	22
Sly00g0384151	M2	NA	39	44	33	34	34	26	34	23	37	29
Sly00g0384181	M1	NA	18	18	17	60	107	11	12	14	50	91
Sly00g0384191	M1	NA	123	105	62	16	9	10	7	5	2	4
Sly00g0384201	M1	NA	54	49	28	6	4	4	4	3	2	2
Sly00g0384211	M13	NA	13	11	14	26	40	14	12	17	17	16
Sly00g0384221	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly00g0384231	M3	NA	15	14	13	12	14	12	13	10	13	13
Sly00g0384251	M12	NA	26	23	29	33	41	58	61	89	65	106
Sly00g0384261	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly00g0384271	M22	NA	1	1	1	1	1	3	1	3	1	1
Sly00g0384291	M11	NA	174	161	181	187	175	185	184	199	170	176
Sly00g0384381	M22	NA	3	4	3	1	2	9	1	3	0	0
Sly00g0384431	M22	NA	1	1	1	1	1	1	1	1	0	1
Sly00g0384441	M16	NA	3	2	2	2	1	2	2	2	1	1
Sly00g0384461	M3	NA	11	11	10	11	10	7	7	7	8	7
Sly00g0384511	M22	NA	1	1	1	0	0	2	1	2	1	0
Sly00g0384521	M1	NA	40	44	39	39	38	35	29	30	23	22
Sly00g0384531	M6	NA	11	41	26	3	45	21	38	8	3	69
Sly00g0384541	M12	NA	114	102	117	143	267	150	143	151	236	343
Sly00g0384551	M3	NA	97	106	72	42	22	62	80	39	57	28
Sly00g0384561	M12	NA	3	3	3	7	7	4	4	5	10	8
Sly00g0384571	M3	E2FD/DEL2-like2	11	11	9	8	10	10	11	8	8	9
Sly00g0384581	M3	NA	138	136	110	102	91	116	129	106	101	131
Sly00g0384591	M14	NA	25	21	27	16	18	25	21	24	8	10
Sly00g0384601	M1	NA	5	4	4	2	3	3	2	2	1	1
Sly00g0384611	M6	NA	5	6	3	4	5	5	6	4	5	7
Sly00g0384621	M6	NA	32	39	27	31	50	33	44	26	28	64
Sly00g0384691	M22	NA	2	1	1	0	0	8	1	6	0	0
Sly00g0384751	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0384781	M1	NA	6	6	7	5	5	5	4	6	2	3
Sly00g0384821	M22	NA	1	2	2	2	2	2	1	2	1	2
Sly00g0385001	M1	NA	4	5	4	5	5	3	2	3	1	2
Sly00g0385031	M1	NA	1	2	2	3	2	1	1	1	1	2
Sly00g0385041	M1	NA	1	2	2	2	3	1	1	1	1	2
Sly00g0385081	M18	NA	2	3	3	4	4	4	4	4	2	2
Sly00g0385241	M1	NA	4	4	3	2	2	4	2	3	2	6
Sly00g0385371	M12	NA	24	21	22	43	71	23	24	24	62	88
Sly00g0385401	M3	NA	2	2	2	1	1	1	1	1	1	1
Sly00g0385411	M1	NA	11	9	7	1	2	4	4	4	2	2
Sly00g0385431	M12	NA	19	19	18	14	17	20	21	19	13	19
Sly00g0385441	M11	NA	44	36	58	43	24	104	72	133	36	12
Sly00g0385451	M19	NA	58	61	64	57	47	66	58	66	55	45
Sly00g0385471	M9	NA	1	1	1	2	1	1	1	1	2	1
Sly00g0385481	M5	NA	11	11	7	7	9	11	12	8	11	7
Sly00g0385801	M19	NA	7	8	8	11	13	8	7	10	2	4
Sly00g0385811	M19	NA	8	9	9	12	12	9	8	11	3	4
Sly00g0385851	M19	NA	8	8	8	9	5	6	7	9	3	4
Sly00g0385871	M19	NA	9	11	11	11	8	8	8	10	3	4
Sly00g0385901	M18	NA	2	3	2	3	5	3	3	4	2	3
Sly00g0385921	M19	NA	2	2	2	3	5	2	2	2	1	2
Sly00g0385931	M22	NA	1	2	1	2	5	2	1	2	1	2
Sly00g0385951	M22	NA	2	2	2	3	6	3	2	2	1	2
Sly00g0385961	M22	NA	1	1	2	2	3	1	1	1	1	1
Sly00g0385971	M12	NA	3	3	3	5	5	3	3	3	1	2
Sly00g0385981	M22	NA	5	6	5	7	8	6	5	5	2	3
Sly00g0385991	M19	NA	7	8	7	7	9	7	5	7	2	3
Sly00g0386001	M19	NA	9	9	11	11	10	11	7	11	2	4
Sly00g0386011	M19	NA	3	3	3	3	4	4	3	4	1	1
Sly00g0386031	M11	NA	6	5	6	6	17	7	7	8	3	11
Sly00g0386051	M12	NA	6	5	6	6	11	9	8	8	5	7
Sly00g0386061	M11	NA	4	4	5	6	9	6	6	6	3	5
Sly00g0386081	M22	NA	4	4	4	9	12	6	5	5	2	4
Sly00g0386121	M6	NA	3	4	3	3	4	4	3	3	2	5
Sly00g0386581	M1	NA	3	2	2	3	2	1	2	3	1	1
Sly00g0386721	M6	NA	13	34	9	1	1	11	19	2	0	0
Sly00g0386731	M6	NA	1	3	1	0	1	2	3	1	0	0
Sly00g0386741	M6	NA	7	24	7	1	1	10	14	1	1	1
Sly00g0386761	M22	NA	1	1	1	1	1	1	1	1	0	1
Sly00g0386811	M5	NA	39	52	28	16	21	42	49	25	21	31
Sly00g0387011	M1	NA	3	3	3	3	4	2	3	3	2	3
Sly00g0387031	M1	NA	2	3	3	2	2	2	1	3	1	1
Sly00g0387121	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0387151	M19	NA	1	2	1	1	1	1	1	1	1	1
Sly00g0387161	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0387361	M1	NA	2	2	3	2	2	2	2	2	1	2
Sly00g0387371	M1	NA	2	3	4	3	3	2	2	2	1	2
Sly00g0387421	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0387431	M22	NA	2	2	2	3	3	2	1	1	1	2
Sly00g0387451	M3	NA	1	2	1	1	1	1	1	1	1	2
Sly00g0387491	M16	NA	1	1	1	1	2	1	1	1	1	1
Sly00g0387501	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0387511	M1	NA	3	3	2	3	3	1	2	2	1	2
Sly00g0387571	M19	NA	1	2	2	2	1	1	1	2	1	1
Sly00g0387931	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0387971	M18	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0388051	M22	NA	2	3	2	3	4	2	1	2	1	3
Sly00g0388101	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0390261	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0390391	M22	NA	1	1	1	2	3	1	1	1	1	1
Sly00g0391151	M1	NA	1	1	1	1	2	1	1	1	1	1
Sly00g0391241	M12	NA	17	26	11	5	16	32	45	24	21	39
Sly00g0391461	M19	NA	3	4	3	3	4	4	3	3	1	3
Sly00g0391481	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0391521	M18	NA	1	3	1	4	4	2	2	3	1	1
Sly00g0391591	M12	NA	1	1	1	1	3	2	2	1	0	1
Sly00g0391601	M1	NA	2	2	1	2	4	1	1	1	1	1
Sly00g0391621	M1	NA	4	4	4	4	6	3	3	4	2	3
Sly00g0392031	M22	NA	1	2	1	1	1	2	1	2	2	2
Sly00g0392041	M12	NA	12	12	10	10	9	11	13	13	11	13
Sly00g0392061	M12	NA	5	6	6	4	5	6	6	6	6	5
Sly00g0392091	M1	NA	1	1	1	1	1	1	1	1	1	2
Sly00g0392111	M2	NA	1	1	2	1	2	1	2	1	1	2
Sly00g0392121	M12	NA	2	3	3	3	3	3	3	3	4	4
Sly00g0392261	M1	NA	90	87	81	80	88	61	67	60	78	82
Sly00g0392271	M12	NA	2	1	1	2	1	1	2	2	1	1
Sly00g0392371	M22	NA	5	6	6	1	1	52	1	35	0	0
Sly00g0392411	M5	NA	1	1	1	0	0	1	1	0	0	0
Sly00g0392611	M11	NA	4	5	5	5	5	5	6	7	3	4
Sly00g0392631	M11	NA	2	1	1	3	4	2	2	2	1	2

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0353811	M11	NA	72	68	79	136	70	160	156	177	152	58
Sly06g0353821	M1	NA	3	2	3	2	1	2	2	1	1	1
Sly06g0353831	M11	NA	14	14	17	13	13	15	15	17	21	19
Sly06g0353851	M11	NA	52	51	54	57	89	74	67	87	91	143
Sly06g0353861	M12	NA	3	2	3	2	1	4	3	4	2	1
Sly06g0353871	M12	RPF2-like	3	3	2	2	1	3	4	5	2	1
Sly06g0353881	M12	NA	7	6	7	6	5	10	11	10	7	5
Sly06g0353891	M11	NA	7	7	8	6	4	12	9	13	8	5
Sly06g0353901	M18	PPR-like33	7	7	9	7	4	12	9	11	6	4
Sly06g0353921	M3	NA	55	51	40	34	37	40	37	30	39	41
Sly06g0353931	M12	NA	1	1	1	1	1	3	3	3	1	1
Sly06g0353961	M12	NA	6	5	4	1	1	7	8	9	5	1
Sly06g0353971	M22	NA	2	0	1	0	0	8	0	6	0	0
Sly06g0353981	M10	NA	149	167	103	217	243	149	204	134	593	626
Sly06g0353991	M12	NA	2	2	1	2	3	4	3	2	4	3
Sly06g0354011	M12	NA	1	1	1	2	1	3	2	1	47	4
Sly06g0354021	M11	NA	97	85	120	68	76	158	144	174	53	43
Sly06g0354031	M11	NA	10	9	10	14	23	11	10	12	18	32
Sly06g0354051	M1	NA	30	27	32	35	40	27	27	24	35	87
Sly06g0354061	M2	NA	42	43	41	42	38	32	36	32	44	42
Sly06g0354071	M1	NA	25	21	38	22	18	9	10	7	9	5
Sly06g0354081	M11	NA	25	29	33	44	39	40	38	42	28	27
Sly06g0354101	M1	YUC-like2	5	13	15	99	178	1	3	4	33	37
Sly06g0354151	M1	NA	35	33	34	22	20	19	15	17	13	9
Sly06g0354161	M1	NA	7	7	3	1	0	1	1	0	0	0
Sly06g0354171	M1	NA	40	38	42	46	58	34	29	36	41	52
Sly06g0354181	M1	NA	61	50	52	43	31	47	44	44	31	24
Sly06g0354191	M1	NA	34	32	31	38	182	31	28	29	31	176
Sly06g0354211	M3	NA	13	12	12	12	14	12	11	13	21	21
Sly06g0354221	M11	NA	11	11	12	24	28	14	14	15	26	25
Sly06g0354231	M3	NA	351	321	316	366	300	249	308	277	395	333
Sly06g0354241	M11	NA	3	2	4	3	5	6	5	7	4	4
Sly06g0354251	M1	NA	4	4	4	4	3	4	3	4	4	3
Sly06g0354261	M1	NA	40	38	38	34	40	24	24	26	33	35
Sly06g0354271	M3	NA	6	7	5	3	2	6	6	5	1	1
Sly06g0354281	M11	NA	44	40	49	52	54	47	44	58	78	103
Sly06g0354291	M1	NA	16	17	18	38	49	15	14	15	38	39
Sly06g0354311	M12	NA	10	10	11	21	42	12	16	13	32	56
Sly06g0354321	M16	NA	411	373	340	302	215	289	280	302	319	206
Sly06g0354331	M3	NA	30	32	11	2	1	5	8	2	1	1
Sly06g0354341	M3	NA	24	33	12	0	1	3	7	1	0	1
Sly06g0354351	M3	NA	74	69	42	28	37	50	68	35	43	52
Sly06g0354361	M1	NA	38	53	40	166	114	4	2	2	2	7
Sly06g0354371	M1	NA	25	26	22	25	23	17	16	16	16	16
Sly06g0354381	M1	NA	40	34	41	41	40	31	30	30	33	26
Sly06g0354391	M1	NA	13	14	11	22	18	7	7	7	14	7
Sly06g0354401	M1	NA	38	41	40	65	93	30	28	35	60	89
Sly06g0354411	M13	NA	28	28	29	53	74	27	26	31	63	76
Sly06g0354421	M1	NA	3	4	4	9	9	1	1	1	1	1
Sly06g0354431	M12	NA	8	9	5	5	2	8	9	9	3	1
Sly06g0354461	M1	NA	3	3	2	1	1	2	2	1	1	0
Sly06g0354491	M1	NA	7	7	6	3	1	1	1	1	1	0
Sly06g0354531	M1	SlJMJ16	16	16	16	17	25	13	11	13	16	23
Sly06g0354541	M12	NA	2	3	2	2	1	5	6	5	2	1
Sly06g0354551	M11	CDT1A-like	3	2	4	3	5	3	4	3	1	1
Sly06g0354561	M15	NA	38	36	33	33	34	34	35	37	39	44
Sly06g0354571	M18	NA	2	2	2	2	2	2	2	2	2	2
Sly06g0354661	M11	SlAux/IAA17	14	8	21	1	1	157	94	165	1	1
Sly06g0354671	M3	BMI-like3	17	21	17	17	19	18	18	15	15	11
Sly06g0354681	M12	NA	56	51	55	29	39	83	92	77	26	33
Sly06g0354701	M3	NA	35	25	15	1	1	20	20	15	2	2
Sly06g0354771	M1	NA	33	31	27	23	21	22	23	21	21	21
Sly06g0354781	M9	NA	3	3	2	2	1	5	5	4	2	1
Sly06g0354801	M1	NA	37	41	39	44	42	31	31	31	60	55
Sly06g0354811	M12	NA	35	39	35	49	48	47	44	44	51	48
Sly06g0354821	M14	NA	30	21	29	27	31	24	23	29	32	32
Sly06g0354831	M1	NA	5	4	4	1	1	0	1	0	0	0
Sly06g0354851	M1	NA	22	22	20	9	11	1	1	1	1	1
Sly06g0354861	M1	NA	1	1	1	1	0	1	0	1	0	0
Sly06g0354881	M1	NA	1	1	1	0	0	1	1	0	0	0
Sly06g0354891	M1	NA	2	2	1	2	1	1	1	1	1	0
Sly06g0354901	M23	NA	2	2	2	6	5	2	2	2	4	4
Sly06g0354911	M22	NA	1	2	2	5	4	2	1	2	3	2
Sly06g0354921	M1	NA	16	13	16	3	2	6	4	7	2	1
Sly06g0354961	M11	NA	1	1	1	1	1	2	1	1	1	1
Sly06g0354971	M11	NA	24	23	24	25	24	28	24	31	27	27
Sly06g0354981	M2	NA	31	34	29	30	36	26	32	25	43	55
Sly06g0354991	M3	GID1B-like	27	28	25	41	75	9	11	8	50	81
Sly06g0355001	M11	NA	48	47	58	77	103	77	68	88	92	135
Sly06g0355011	M1	NA	1	2	2	2	2	1	1	1	1	1
Sly06g0355051	M1	NA	6	6	6	8	7	5	5	6	8	4
Sly06g0355071	M1	NA	50	43	49	67	60	8	10	9	203	189
Sly06g0355081	M1	NA	4	5	4	3	2	1	0	1	0	1
Sly06g0355091	M2	NA	37	43	37	29	22	27	35	27	38	28
Sly06g0355111	M18	NA	16	18	20	38	42	22	18	23	31	47
Sly06g0355121	M18	NA	11	12	11	11	13	13	10	13	14	12
Sly06g0355131	M11	NA	1	0	1	1	0	1	1	2	0	0
Sly06g0355141	M11	NA	1	1	1	1	0	2	1	2	0	0
Sly06g0355181	M2	NA	810	767	550	563	670	484	555	330	354	544
Sly06g0355191	M12	NA	1	1	1	0	1	1	2	1	0	0
Sly06g0355211	M12	NA	118	173	226	1339	2502	637	719	850	2431	4242
Sly06g0355221	M1	NA	213	200	184	169	178	187	173	191	210	189
Sly06g0355231	M18	NA	9	10	12	11	11	12	10	12	14	10
Sly06g0355251	M5	NA	46	57	25	3	7	36	46	11	1	3
Sly06g0355261	M11	NA	11	7	10	7	12	17	14	15	13	17
Sly06g0355271	M1	NA	24	27	33	29	16	21	19	17	14	14
Sly06g0355281	M3	NA	628	863	458	362	288	425	626	214	231	411
Sly06g0355291	M3	NA	2	3	1	2	1	1	1	1	1	1
Sly06g0355301	M1	NA	22	21	29	23	49	7	6	8	11	23
Sly06g0355311	M1	NA	43	42	41	23	15	18	15	18	22	14
Sly06g0355331	M1	NA	23	15	43	1	1	2	1	2	0	0
Sly06g0355351	M17	NA	755	683	760	626	519	655	634	740	623	480
Sly06g0355361	M11	ISA3	35	35	38	60	58	45	43	44	44	37
Sly06g0355401	M11	NA	2	2	2	2	2	2	2	2	2	2
Sly06g0355411	M11	NA	21	20	27	31	35	30	32	42	46	54
Sly06g0355421	M18	NA	14	15	19	25	25	21	20	30	30	25
Sly06g0355431	M3	NA	70	94	41	14	13	25	30	9	5	13
Sly06g0355451	M3	NA	24	17	7	1	1	24	18	2	1	1
Sly06g0355461	M1	NA	10	12	9	4	5	6	5	3	2	3
Sly06g0355471	M1	NA	45	45	46	38	38	37	36	29	23	29
Sly06g0355481	M11	NA	38	32	48	61	50	60	56	75	65	62
Sly06g0355491	M3	NA	169	175	113	178	139	59	107	59	222	180
Sly06g0355501	M3	NA	13	15	9	9	9	5	6	5	7	11
Sly06g0355511	M11	NA	64	48	78	196	358	62	57	63	67	95
Sly06g0355531	M1	NA	21	18	16	9	6	12	13	15	14	4
Sly06g0355541	M3	NA	18	15	13	8	11	13	13	9	11	8
Sly06g0355551	M1	NA	18	15	15	11	8	11	12	11	11	9
Sly06g0355591	M5	NA	11	13	11	11	6	12	12	10	5	3
Sly06g0355601	M1	NA	4	3	4	3	3	2	2	3	3	2
Sly06g0355621	M11	NA	41	42	40	47	85	56	52	57	50	70
Sly06g0355631	M1	NA	52	57	54	58	44	49	49	46	38	32
Sly06g0355661	M22	NA	2	1	1	1	1	4	1	4	0	0
Sly06g0355691	M3	NA	4	4	3	3	3	3	3	2	3	2
Sly06g0355701	M11	NA	357	307	414	627	510	568	510	725	655	665
Sly06g0355711	M3	NA	50	45	31	25	47	30	44	21	27	73
Sly06g0355721	M11	NA	37	36	35	37	36	37	36	38	36	46
Sly06g0355731	M2	NA	46	46	39	40	28	32	44	27	39	30
Sly06g0355741	M11	NA	1	1	1	1	1	2	2	1	1	0
Sly06g0355751	M22	NA	4	3	3	1	1	4	3	3	1	1
Sly06g0355761	M11	NA	10	10	11	11	11	13	12	15	11	9
Sly06g0355801	M1	NA	82	83	87	96	100	52	54	55	90	97

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly00g0392641	M12	NA	2	2	2	4	6	3	3	3	1	4
Sly00g0392691	M1	NA	2	4	3	4	5	3	3	2	1	2
Sly00g0392711	M22	NA	3	4	3	4	8	3	3	4	1	3
Sly00g0392731	M18	NA	3	4	4	4	7	4	4	5	2	3
Sly00g0393121	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly00g0393141	M1	NA	7	7	7	6	11	7	5	5	6	11
Sly00g0393251	M12	NA	2	2	1	2	2	2	2	2	3	5
Sly00g0393281	M3	SQE3-like	6	7	5	6	8	5	7	5	7	9
Sly00g0394011	M2	NA	16	15	14	15	14	14	16	15	18	21
Sly00g0394021	M12	NA	27	25	28	51	34	24	31	38	64	31
Sly00g0394031	M12	NA	1	1	2	3	3	1	1	2	3	2
Sly00g0394041	M12	NA	1	1	2	2	2	2	2	2	2	2
Sly00g0394051	M2	NA	16	14	14	24	20	11	17	17	36	18
Sly00g0394101	M22	NA	1	1	1	0	0	2	1	2	1	0
Sly00g0394201	M11	NA	6	4	3	5	8	5	4	6	8	13
Sly00g0394601	M12	NA	1	1	1	2	1	1	3	6	6	2
Sly00g0394611	M12	NA	6	6	12	11	6	110	98	207	117	69
Sly00g0394621	M12	NA	540	411	720	76	14	11728	9709	11722	565	44
Sly00g0394741	M12	NA	1	1	1	1	1	1	1	1	1	2
Sly01g0000011	M12	NA	35	28	38	3	6	137	134	153	1	2
Sly01g0000021	M1	NA	7	5	13	6	2	5	3	4	1	0
Sly01g0000031	M18	NA	34	35	43	37	22	62	50	64	6	3
Sly01g0000041	M11	NA	23	24	35	73	49	79	65	108	79	50
Sly01g0000071	M1	NA	7	9	6	4	3	1	1	1	1	1
Sly01g0000091	M1	NA	6	6	11	7	8	1	1	1	1	1
Sly01g0000111	M11	NA	14	14	20	18	19	26	23	26	26	24
Sly01g0000121	M3	NA	9	9	8	10	10	6	9	7	10	12
Sly01g0000131	M3	NA	6	7	4	4	6	4	3	3	5	4
Sly01g0000141	M11	NA	23	22	21	15	24	31	30	28	13	35
Sly01g0000151	M13	NA	10	14	20	36	144	18	17	34	82	364
Sly01g0000171	M3	NA	2	5	7	1	1	1	2	1	1	4
Sly01g0000181	M1	NA	1	2	2	3	4	2	1	1	3	4
Sly01g0000191	M11	NA	4	6	6	8	12	8	7	9	11	22
Sly01g0000201	M1	NA	1	2	2	2	2	1	2	1	3	3
Sly01g0000221	M13	NA	65	67	94	123	123	87	76	118	91	150
Sly01g0000231	M6	NA	19	26	18	10	21	21	25	15	4	20
Sly01g0000241	M3	Solyc00g322630	1	1	1	1	1	1	1	1	0	0
Sly01g0000261	M1	NA	81	80	87	60	59	62	68	60	60	49
Sly01g0000271	M1	NA	50	44	48	53	68	40	36	36	32	45
Sly01g0000281	M1	NA	16	16	12	9	6	6	7	5	3	2
Sly01g0000291	M1	NA	7	8	9	40	16	3	4	2	3	2
Sly01g0000301	M1	NA	5	5	9	115	33	1	1	1	1	0
Sly01g0000311	M1	NA	2	2	3	146	221	1	1	1	5	38
Sly01g0000321	M11	NA	111	81	143	159	136	135	104	179	111	131
Sly01g0000331	M12	NA	1	1	1	1	1	2	1	2	1	1
Sly01g0000351	M1	NA	39	37	46	35	28	31	28	32	13	13
Sly01g0000361	M11	NA	39	31	41	42	56	89	67	124	37	43
Sly01g0000401	M12	NA	29	34	30	51	51	28	37	40	71	75
Sly01g0000411	M11	SISDG43	9	9	11	15	16	12	12	13	9	9
Sly01g0000421	M3	NA	1	3	2	1	4	1	1	1	2	6
Sly01g0000431	M22	NA	2	2	2	11	11	6	2	2	1	1
Sly01g0000441	M1	NA	41	50	29	1	1	22	13	18	1	1
Sly01g0000451	M1	NA	10	12	8	1	1	3	3	1	0	1
Sly01g0000461	M12	NA	11	11	10	10	12	19	23	21	24	21
Sly01g0000471	M1	NA	420	343	314	58	45	265	250	260	60	68
Sly01g0000481	M11	NA	7	7	7	5	2	10	11	13	4	2
Sly01g0000491	M3	NA	2	1	1	1	1	1	1	1	0	0
Sly01g0000501	M1	NA	63	71	29	2	1	2	1	1	1	0
Sly01g0000511	M3	NA	12	11	7	3	4	5	7	5	3	4
Sly01g0000521	M3	NA	15	16	12	6	7	8	9	8	3	3
Sly01g0000531	M12	NA	29	28	29	40	35	31	34	33	45	39
Sly01g0000541	M3	NA	2	3	0	0	0	1	1	1	0	0
Sly01g0000561	M11	NA	18	16	21	32	46	22	19	28	27	46
Sly01g0000571	M12	NA	6	5	7	6	4	8	9	8	6	4
Sly01g0000581	M18	NA	11	12	12	17	21	14	12	15	10	9
Sly01g0000601	M1	NA	21	16	30	15	11	11	9	12	6	4
Sly01g0000611	M1	SlICDH1	183	162	171	404	135	21	9	18	27	18
Sly01g0000621	M1	NA	30	23	30	28	32	20	15	21	19	15
Sly01g0000631	M3	NA	56	54	53	76	65	43	47	47	78	76
Sly01g0000641	M21	NA	44	24	43	3	3	32	14	26	9	9
Sly01g0000651	M12	NA	68	66	79	98	130	72	81	82	131	199
Sly01g0000671	M11	NA	206	189	200	215	202	197	221	224	217	241
Sly01g0000701	M1	NA	33	29	32	48	49	18	19	20	37	29
Sly01g0000721	M12	NA	3	2	2	1	1	9	5	10	7	8
Sly01g0000731	M3	NA	17	15	13	8	9	10	11	9	11	11
Sly01g0000751	M8	NA	65	63	57	42	41	66	64	59	26	38
Sly01g0000761	M1	NA	12	12	12	10	11	13	11	12	10	9
Sly01g0000771	M1	NA	2	1	1	0	1	1	1	0	1	0
Sly01g0000781	M1	NA	2	2	1	1	1	1	1	0	0	0
Sly01g0000791	M1	NA	1	2	1	1	1	1	1	1	0	0
Sly01g0000801	M1	NA	15	10	7	5	6	2	2	1	1	2
Sly01g0000811	M12	NA	10	11	10	10	8	12	13	13	10	9
Sly01g0000821	M3	NA	1	3	2	1	2	1	2	1	0	1
Sly01g0000831	M3	NA	116	116	115	84	65	103	104	112	90	70
Sly01g0000841	M3	NA	344	336	262	219	221	253	255	213	189	189
Sly01g0000851	M11	NA	10	8	13	9	4	15	16	15	3	1
Sly01g0000861	M11	NA	24	23	27	36	37	30	31	43	41	44
Sly01g0000871	M11	NA	2	1	1	1	1	2	2	2	1	1
Sly01g0000881	M11	NA	1	1	1	1	1	1	1	1	0	1
Sly01g0000891	M1	NA	5	6	3	1	1	1	1	0	0	0
Sly01g0000911	M3	NA	5	7	4	4	4	3	4	3	2	2
Sly01g0000921	M3	NA	12	12	8	6	8	8	7	7	10	11
Sly01g0000931	M3	NA	33	37	26	22	27	21	21	20	27	31
Sly01g0000951	M3	NA	2	2	2	1	1	1	1	1	1	1
Sly01g0000961	M1	NA	9	13	8	3	2	2	2	2	1	1
Sly01g0000971	M11	NA	23	22	27	43	53	27	28	31	57	72
Sly01g0001001	M1	NA	58	57	62	78	68	42	52	48	54	65
Sly01g0001011	M1	NA	36	34	35	49	61	31	29	31	50	47
Sly01g0001021	M1	NA	14	13	12	9	8	8	9	7	7	7
Sly01g0001031	M9	NA	13	12	13	10	4	26	36	16	6	2
Sly01g0001041	M1	NA	9	7	17	3	1	1	1	1	1	0
Sly01g0001051	M4	NA	22	22	22	25	32	26	24	22	24	25
Sly01g0001061	M1	NA	17	18	18	18	17	14	15	14	20	17
Sly01g0001071	M11	NA	39	33	71	76	130	104	78	154	57	99
Sly01g0001081	M18	NA	18	19	19	24	26	22	19	22	24	21
Sly01g0001131	M3	NA	15	14	10	7	4	11	11	7	10	8
Sly01g0001141	M11	SlCMT3-like3	2	2	2	1	1	5	4	4	1	1
Sly01g0001151	M3	NA	111	121	105	110	117	77	86	63	76	104
Sly01g0001161	M3	NA	156	173	122	109	125	129	143	111	95	116
Sly01g0001171	M11	NA	52	49	74	66	66	77	65	102	60	49
Sly01g0001181	M11	NA	46	32	50	42	39	56	48	69	46	42
Sly01g0001191	M13	CDT1A	11	8	13	9	10	13	12	14	9	10
Sly01g0001211	M1	NA	24	21	24	16	14	6	5	7	13	24
Sly01g0001221	M1	NA	518	493	513	418	279	322	365	330	337	264
Sly01g0001231	M3	NA	70	73	47	28	28	36	46	28	39	44
Sly01g0001241	M3	NA	17	18	17	14	9	16	16	14	13	7
Sly01g0001251	M3	NA	60	63	50	55	52	30	34	29	45	43
Sly01g0001261	M2	NA	21	19	18	24	22	17	22	17	24	21
Sly01g0001271	M1	NA	4	5	4	2	2	3	3	3	2	1
Sly01g0001281	M11	SISDG15	6	6	6	4	4	9	8	10	7	3
Sly01g0001291	M2	NA	45	53	48	97	98	40	49	48	112	95
Sly01g0001311	M11	NA	13	9	11	10	11	13	12	15	11	12
Sly01g0001321	M1	NA	13	11	12	7	4	8	9	8	6	3
Sly01g0001341	M11	NA	101	95	106	160	71	148	140	152	115	64
Sly01g0001351	M12	NA	1	1	2	3	1	5	7	4	24	17
Sly01g0001381	M3	NA	10	10	4	1	1	1	2	1	0	0
Sly01g0001391	M3	NA	14	20	8	3	1	3	7	2	1	1
Sly01g0001401	M11	NA	2	1	2	2	3	3	2	4	1	2
Sly01g0001411	M3	NA	12	13	12	14	16	12	12	12	13	15
Sly01g0001421	M19	NA	56	61	61	57	53	55	54	53	35	35
Sly01g0001431	M11	NA	30	27	40	23	17	51	35	48	10	7
Sly01g0001441	M3	NA	2	1	1	1	0	0	1	0	0	0
Sly01g0001461	M1	NA	42	37	18	1	2	5	5	2	1	1
Sly01g0001481	M12	NA	384	363	386	72	232	470	440	361	131	350

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0355821	M1	NA	29	28	39	3	1	1	1	1	1	0
Sly06g0355831	M1	NA	2	2	1	1	1	1	1	1	0	0
Sly06g0355841	M11	NA	17	19	23	24	21	24	25	26	18	25
Sly06g0355851	M11	NA	3	3	3	3	2	3	3	3	3	3
Sly06g0355861	M12	NA	3	3	4	2	3	4	4	4	2	3
Sly06g0355871	M18	NA	11	14	13	12	13	14	12	15	13	18
Sly06g0355881	M12	NA	9	8	10	8	13	11	12	13	19	26
Sly06g0355981	M9	NA	4	8	7	4	3	5	17	6	3	8
Sly06g0355991	M7	NA	9	18	12	5	5	8	35	13	5	15
Sly06g0356011	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly06g0356041	M22	NA	2	1	2	1	1	3	1	2	1	1
Sly06g0356061	M1	NA	944	868	907	678	494	673	727	643	613	448
Sly06g0356071	M11	NA	19	20	21	19	22	24	23	25	26	32
Sly06g0356081	M19	NA	27	29	30	33	44	28	25	31	41	53
Sly06g0356111	M1	NA	31	44	17	9	4	2	1	1	0	1
Sly06g0356171	M12	NA	17	18	19	24	19	18	18	19	28	22
Sly06g0356181	M12	NA	1	1	1	1	1	1	1	1	4	5
Sly06g0356201	M12	NA	4	3	3	3	4	4	4	4	4	5
Sly06g0356211	M11	NA	1	1	1	1	0	1	1	1	0	0
Sly06g0356221	M10	NA	1	1	1	0	0	1	1	1	0	0
Sly06g0356411	M12	NA	3	5	5	5	5	6	7	7	5	2
Sly06g0356441	M18	MOM1-like	14	16	17	20	20	19	16	19	17	20
Sly06g0356451	M12	NA	1	1	1	1	1	1	2	1	1	1
Sly06g0356471	M12	NA	16	16	19	19	20	18	18	20	31	36
Sly06g0356511	M1	NA	3	3	4	13	12	2	3	4	18	20
Sly06g0356541	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0356551	M3	NA	597	562	519	332	247	423	477	393	382	304
Sly06g0356631	M3	NA	12	8	4	5	6	7	7	7	17	39
Sly06g0356651	M12	NA	23	25	34	98	278	44	39	51	68	144
Sly06g0356671	M12	NA	31	32	42	129	376	53	54	61	106	284
Sly06g0356681	M11	NA	4	4	6	6	5	7	6	9	7	6
Sly06g0356691	M12	NA	2	3	2	3	3	2	3	3	3	4
Sly06g0356701	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0356711	M22	NA	1	1	1	0	0	7	1	4	0	0
Sly06g0356741	M9	NA	14	15	13	4	2	21	20	16	3	1
Sly06g0356751	M1	NA	2	2	2	4	2	1	1	0	1	0
Sly06g0356761	M7	NA	7	14	5	2	3	11	18	8	2	10
Sly06g0356811	M9	NA	5	5	5	6	15	6	6	5	16	33
Sly06g0356821	M11	NA	7	7	7	10	13	8	6	9	14	28
Sly06g0356871	M11	NA	18	20	26	24	32	29	21	26	27	34
Sly06g0356881	M11	NA	30	31	42	40	64	45	34	47	45	77
Sly06g0356891	M12	NA	29	30	38	31	55	45	38	40	44	74
Sly06g0356901	M12	NA	29	27	37	32	53	35	34	37	39	86
Sly06g0356911	M12	NA	28	28	34	68	55	32	41	38	58	51
Sly06g0356921	M12	NA	24	22	24	16	8	25	24	25	21	20
Sly06g0356931	M7	NA	8	13	5	5	17	9	28	10	12	75
Sly06g0356951	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0357081	M12	sdl1-like2	3	3	6	0	1	66	67	40	1	2
Sly06g0357351	M18	NA	34	31	29	31	31	32	27	34	33	28
Sly06g0357371	M3	NA	39	38	35	45	47	30	34	37	46	54
Sly06g0357391	M1	NA	4	4	6	5	6	2	2	2	1	1
Sly06g0357421	M9	NA	11	9	6	4	2	16	20	10	4	2
Sly06g0357461	M7	NA	5	6	6	3	4	4	9	4	3	10
Sly06g0357521	M3	NA	22	20	19	11	13	14	15	12	13	14
Sly06g0357531	M1	NA	75	70	74	49	46	49	48	47	49	42
Sly06g0357541	M22	NA	2	1	2	1	1	3	1	5	1	1
Sly06g0357581	M3	NA	6	6	4	2	2	3	4	3	2	2
Sly06g0357591	M1	NA	8	8	5	2	2	4	3	3	2	1
Sly06g0357641	M19	NA	26	27	28	34	34	29	25	30	23	23
Sly06g0357691	M12	NA	5	5	4	5	4	6	7	6	5	3
Sly06g0357701	M2	NA	26	27	30	31	33	26	28	27	26	27
Sly06g0357731	M11	NA	1	1	1	0	0	1	1	2	1	1
Sly06g0357751	M1	NA	11	7	8	4	2	7	7	5	1	1
Sly06g0357761	M1	NA	22	22	16	15	18	11	13	12	19	20
Sly06g0357951	M14	NA	88	83	110	284	231	81	83	98	149	105
Sly06g0357981	M11	NA	28	26	35	36	9	77	66	99	37	8
Sly06g0358001	M1	NA	6	9	7	37	103	2	3	3	9	78
Sly06g0358011	M3	NA	47	41	41	51	54	33	40	38	45	48
Sly06g0358021	M12	NA	7	7	9	12	21	10	10	10	17	34
Sly06g0358031	M11	NA	6	6	7	8	11	9	7	10	9	10
Sly06g0358041	M9	NA	3	3	3	3	3	3	3	3	3	2
Sly06g0358061	M12	NA	44	45	49	50	33	70	72	78	76	54
Sly06g0358091	M19	NA	30	33	31	56	96	31	27	32	70	92
Sly06g0358181	M12	NA	13	13	12	8	5	12	16	13	9	10
Sly06g0358211	M11	NA	53	46	54	67	81	59	45	72	81	85
Sly06g0358221	M11	NA	22	23	27	35	34	23	23	32	36	25
Sly06g0358231	M11	NA	48	46	60	67	80	53	58	70	77	85
Sly06g0358241	M23	NA	2	2	2	1	1	3	2	2	1	1
Sly06g0358261	M9	NA	6	7	3	3	3	10	14	4	4	8
Sly06g0358281	M1	NA	20	18	18	12	9	15	16	16	13	16
Sly06g0358291	M12	NA	19	17	13	13	16	18	22	17	12	18
Sly06g0358351	M22	NA	1	0	1	0	0	2	1	3	0	0
Sly06g0358411	M1	NA	46	88	118	43	5	23	16	29	6	1
Sly06g0358421	M3	NA	2	1	1	1	0	1	1	1	1	1
Sly06g0358551	M2	NA	3	4	2	3	5	3	4	3	6	6
Sly06g0358561	M3	NA	3	3	3	2	3	2	3	2	4	6
Sly06g0358571	M3	NA	9	8	7	7	6	7	8	7	8	8
Sly06g0358621	M12	NA	52	48	51	71	103	63	65	80	105	156
Sly06g0358641	M22	NA	124	35	49	5	1	266	94	175	22	2
Sly06g0358671	M3	NA	11	12	9	6	4	8	9	7	6	4
Sly06g0358681	M1	NA	42	44	40	47	39	41	39	41	46	40
Sly06g0358691	M1	NA	1	2	1	2	2	1	1	1	1	1
Sly06g0358701	M1	NA	15	16	12	57	38	4	4	5	11	9
Sly06g0358711	M11	NA	50	49	54	60	44	76	71	82	40	23
Sly06g0358731	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0358741	M11	NA	6	4	7	13	7	13	11	12	8	5
Sly06g0358771	M2	NA	82	81	82	95	122	65	78	76	99	163
Sly06g0358821	M23	NA	1	1	1	0	0	2	1	1	0	0
Sly06g0358851	M1	NA	32	33	35	47	53	26	27	31	64	75
Sly06g0358861	M12	NA	13	14	13	12	12	14	15	16	13	9
Sly06g0358911	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly06g0358931	M3	NA	5	5	3	4	5	2	4	3	1	2
Sly06g0358941	M2	NA	4	4	4	6	6	4	5	4	6	5
Sly06g0358951	M11	NA	20	18	20	38	36	24	20	28	23	27
Sly06g0358961	M11	NA	72	75	74	76	82	82	76	82	80	85
Sly06g0358971	M1	NA	1	1	1	1	1	0	1	0	0	0
Sly06g0359011	M3	NA	96	206	10	1	1	38	44	5	1	1
Sly06g0359031	M11	NA	1	1	2	0	0	2	1	2	1	0
Sly06g0359061	M12	NA	1	1	1	0	0	1	1	1	1	0
Sly06g0359091	M1	NA	1	1	1	2	5	1	1	1	4	8
Sly06g0359101	M3	NA	8	7	6	4	2	4	5	3	3	2
Sly06g0359111	M1	NA	78	75	54	34	20	28	32	21	16	11
Sly06g0359121	M11	NA	4	3	4	2	1	44	41	63	15	2
Sly06g0359131	M1	NA	517	505	547	412	293	394	345	411	429	367
Sly06g0359141	M3	NA	20	18	4	1	1	6	3	1	0	0
Sly06g0359171	M11	NA	1	1	2	1	1	1	1	2	1	1
Sly06g0359181	M1	NA	2	2	2	0	1	2	2	2	0	1
Sly06g0359191	M23	GA20OX2	0	1	1	0	0	1	1	1	0	0
Sly06g0359221	M1	NA	61	25	120	20	6	2	1	1	1	0
Sly06g0359231	M11	NA	6	8	7	6	4	10	10	11	7	4
Sly06g0359241	M12	NA	5	4	3	3	2	7	7	6	5	3
Sly06g0359251	M12	NA	8	6	12	3	1	30	24	29	6	2
Sly06g0359261	M10	NA	12	20	16	7	24	18	28	12	9	28
Sly06g0359271	M6	NA	12	23	23	9	24	19	30	13	8	13
Sly06g0359291	M1	NA	26	23	32	37	61	20	24	28	39	77
Sly06g0359301	M7	NA	1	2	1	1	1	1	13	1	1	3
Sly06g0359311	M1	NA	1	1	1	1	0	1	0	1	0	0
Sly06g0359321	M1	NA	207	170	112	9	4	50	51	39	5	5
Sly06g0359341	M3	NA	1	1	1	0	0	0	0	0	0	0
Sly06g0359361	M1	NA	1	0	2	0	0	1	1	1	0	0
Sly06g0359391	M12	NA	3	3	4	3	6	6	6	6	5	3
Sly06g0359421	M

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0001501	M11	NA	32	27	33	48	79	66	63	70	89	108
Sly01g0001531	M3	NA	19	19	16	21	24	17	16	19	29	26
Sly01g0001541	M14	NA	23	26	27	27	26	22	25	27	24	28
Sly01g0001551	M11	NA	12	13	15	12	13	17	15	20	17	15
Sly01g0001561	M11	NA	102	105	116	119	83	147	127	170	114	139
Sly01g0001571	M1	NA	7	6	5	3	1	3	2	3	1	1
Sly01g0001591	M12	SlLOX3 (LOXC)	4	14	31	2005	4877	25	78	204	1716	1220
Sly01g0001601	M1	NA	3	4	3	2	1	1	1	2	1	1
Sly01g0001611	M1	SlLOX12	3	2	3	1	1	1	1	1	1	1
Sly01g0001681	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly01g0001691	M23	NA	11	4	4	1	0	41	14	5	1	1
Sly01g0001711	M12	NA	18	20	21	32	22	24	25	24	12	4
Sly01g0001731	M3	EIL6	1	2	1	1	1	1	1	1	2	1
Sly01g0001741	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0001751	M13	NA	12	13	15	25	23	13	12	14	12	9
Sly01g0001761	M11	SlJMJ24	29	25	38	78	48	48	35	54	69	44
Sly01g0001771	M21	NA	2	2	2	6	3	2	1	1	0	1
Sly01g0001781	M12	NA	34	33	36	25	32	34	36	34	31	34
Sly01g0001791	M1	NA	17	18	19	19	21	15	12	15	19	29
Sly01g0001801	M1	NA	3	2	4	2	2	1	1	1	1	1
Sly01g0001841	M11	NA	8	7	10	8	5	10	8	10	8	4
Sly01g0001881	M22	NA	1	0	1	0	0	1	1	2	0	0
Sly01g0001891	M11	NA	1	1	1	1	0	2	1	2	1	0
Sly01g0001901	M11	NA	3	2	4	1	1	6	5	9	1	1
Sly01g0001911	M19	NA	100	98	98	74	74	95	82	94	68	73
Sly01g0001921	M3	NA	21	23	24	28	16	18	22	21	38	15
Sly01g0001931	M8	NA	88	73	71	23	40	87	141	54	29	78
Sly01g0001941	M1	NA	34	35	38	26	23	26	27	27	26	28
Sly01g0001961	M1	NA	2	3	2	2	2	2	2	2	2	2
Sly01g0001971	M12	NA	16	16	18	31	35	15	19	18	28	32
Sly01g0001981	M1	NA	27	28	31	39	28	17	15	14	7	4
Sly01g0001991	M11	SlSDG20	20	22	23	28	28	25	22	26	44	38
Sly01g0002001	M1	NA	41	44	22	3	2	9	4	4	5	5
Sly01g0002011	M11	NA	395	313	393	403	341	469	407	428	241	226
Sly01g0002031	M1	NA	2	3	3	3	3	3	2	2	2	2
Sly01g0002041	M1	NA	20	21	22	18	8	1	1	1	1	1
Sly01g0002051	M11	NA	25	25	32	49	45	44	40	47	22	14
Sly01g0002061	M5	Syntaxin121-like	69	154	64	5	4	86	92	18	3	10
Sly01g0002071	M12	NA	34	36	39	36	33	43	42	43	31	37
Sly01g0002141	M18	NA	31	31	38	42	36	46	38	53	33	31
Sly01g0002151	M11	NA	51	46	51	89	93	53	51	50	66	74
Sly01g0002161	M3	NA	42	37	26	27	32	29	28	29	30	44
Sly01g0002191	M7	NA	1	3	1	0	0	2	3	1	1	1
Sly01g0002211	M7	NA	1	3	1	1	1	2	6	1	1	1
Sly01g0002221	M7	NA	8	24	6	1	2	10	24	8	1	2
Sly01g0002241	M11	NA	8	10	10	12	12	11	11	12	9	9
Sly01g0002261	M12	NA	15	17	17	21	18	19	21	20	22	21
Sly01g0002271	M12	NA	271	242	301	233	286	304	310	333	173	275
Sly01g0002311	M1	NA	15	12	15	9	11	14	10	11	8	7
Sly01g0002321	M3	NA	289	333	209	118	181	204	379	175	161	289
Sly01g0002331	M3	NA	38	40	36	35	35	26	29	26	42	37
Sly01g0002341	M1	NA	10	9	14	16	8	4	4	5	6	2
Sly01g0002351	M1	NA	10	12	11	11	9	7	7	8	13	12
Sly01g0002361	M3	NA	73	78	71	65	53	66	69	52	44	40
Sly01g0002371	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly01g0002381	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0002391	M11	NA	21	20	21	16	19	21	20	24	22	24
Sly01g0002611	M12	NA	20	15	12	11	16	24	23	16	31	24
Sly01g0002621	M12	NA	3	3	3	11	14	17	13	18	63	82
Sly01g0002651	M9	NA	481	658	529	245	192	649	777	694	671	533
Sly01g0002661	M3	NA	22	22	19	17	18	15	16	15	20	20
Sly01g0002681	M3	NA	57	64	52	40	37	31	41	29	49	46
Sly01g0002691	M22	NA	1	1	1	1	1	1	1	1	0	1
Sly01g0002711	M11	NA	4	3	4	6	7	5	4	5	6	5
Sly01g0002721	M11	PrxII	61	52	62	86	113	74	76	80	83	112
Sly01g0002731	M11	NA	10	8	13	11	11	15	15	22	15	12
Sly01g0002741	M3	E2FA-like1	33	34	28	24	35	28	29	27	68	58
Sly01g0002761	M3	HVA22-like3	17	22	9	6	10	8	6	4	1	2
Sly01g0002771	M12	NA	9	10	11	15	18	14	15	15	16	14
Sly01g0002801	M11	NA	4	4	4	6	6	4	4	6	8	10
Sly01g0002811	M1	NA	1	1	1	2	1	2	1	1	1	1
Sly01g0002821	M11	NA	19	18	19	25	36	23	21	27	37	45
Sly01g0002831	M19	NA	11	12	12	14	16	12	10	12	16	20
Sly01g0002841	M1	NA	227	195	207	209	158	127	129	149	173	199
Sly01g0002851	M12	NA	5	5	5	1	1	11	10	4	1	1
Sly01g0002861	M11	NA	6	6	8	8	12	8	7	10	9	10
Sly01g0002871	M1	NA	7	5	6	2	4	5	2	4	1	4
Sly01g0002891	M3	NA	27	24	21	29	46	20	18	15	40	67
Sly01g0002901	M3	NA	143	144	110	80	59	77	91	65	53	39
Sly01g0002911	M11	NA	34	33	43	80	72	60	60	71	87	178
Sly01g0002921	M11	NA	24	22	28	15	27	35	33	33	14	23
Sly01g0002931	M22	NA	8	2	4	1	1	18	5	10	1	1
Sly01g0002961	M1	NA	12	11	8	2	1	5	5	2	1	1
Sly01g0002971	M3	NA	2	2	1	1	0	1	1	1	1	1
Sly01g0002991	M6	NA	2	2	1	0	1	1	1	1	1	1
Sly01g0003001	M3	NA	29	32	21	10	10	13	12	5	3	7
Sly01g0003011	M12	NA	457	422	442	386	345	413	465	467	531	625
Sly01g0003021	M3	oxophytodienoate exp	17	17	12	20	22	13	14	9	12	17
Sly01g0003031	M11	NA	19	12	23	2	2	34	23	39	1	1
Sly01g0003071	M1	NA	44	45	43	37	42	38	37	39	34	35
Sly01g0003081	M11	NA	67	66	79	159	293	72	70	92	207	337
Sly01g0003091	M1	NA	843	747	820	445	216	470	493	513	280	204
Sly01g0003101	M1	NA	214	193	178	143	128	118	140	116	145	136
Sly01g0003111	M14	NA	35	30	39	44	40	33	34	34	32	33
Sly01g0003121	M12	NA	132	120	123	181	205	136	151	129	169	205
Sly01g0003131	M1	SlHAC1	39	44	37	35	36	31	29	28	27	26
Sly01g0003141	M1	NA	44	51	45	20	17	5	2	4	1	1
Sly01g0003151	M1	NA	19	23	21	29	25	16	13	17	14	14
Sly01g0003161	M1	NA	12	10	11	36	40	8	8	8	33	32
Sly01g0003171	M1	NA	39	36	35	36	37	30	28	28	33	40
Sly01g0003181	M1	NA	16	17	18	11	7	11	8	6	1	1
Sly01g0003191	M1	NA	14	12	13	19	22	12	12	14	20	22
Sly01g0003201	M8	NA	6	11	4	3	1	7	19	4	2	1
Sly01g0003211	M7	NA	4	7	3	2	1	6	9	3	1	1
Sly01g0003221	M11	NA	52	45	56	41	51	64	60	68	62	87
Sly01g0003251	M11	NA	21	16	23	23	40	40	34	40	39	79
Sly01g0003261	M12	NA	16	13	22	27	35	20	21	22	30	43
Sly01g0003271	M12	NA	55	50	51	48	47	57	60	51	60	76
Sly01g0003281	M3	NA	81	76	70	63	58	47	55	48	52	38
Sly01g0003291	M11	NA	14	15	14	12	13	17	18	20	16	11
Sly01g0003301	M1	NA	3	3	3	2	1	2	2	2	1	1
Sly01g0003311	M1	NA	130	136	147	136	129	117	122	111	126	130
Sly01g0003321	M18	NA	18	19	20	27	35	23	20	24	40	58
Sly01g0003401	M1	NA	85	73	87	230	252	74	77	74	129	187
Sly01g0003411	M3	NA	32	33	26	38	39	24	27	21	27	26
Sly01g0003431	M3	NA	93	90	93	116	131	73	83	83	148	164
Sly01g0003441	M1	NA	158	151	160	163	214	138	137	154	189	272
Sly01g0003451	M1	NA	5	5	5	4	4	3	5	4	4	2
Sly01g0003461	M3	NA	3	3	2	3	2	1	2	2	2	2
Sly01g0003481	M1	NA	24	30	18	6	1	1	1	0	1	1
Sly01g0003501	M1	NA	15	15	10	15	11	1	1	1	6	6
Sly01g0003511	M1	NA	15	28	11	4	1	1	1	1	1	1
Sly01g0003521	M1	NA	2	2	1	1	1	1	1	0	0	0
Sly01g0003571	M1	NA	9	9	13	17	3	1	1	1	1	1
Sly01g0003591	M19	NA	18	20	21	28	34	19	14	16	24	31
Sly01g0003621	M1	NA	37	38	41	33	32	23	27	25	33	27
Sly01g0003631	M1	NA	20	20	19	17	16	12	16	12	18	13
Sly01g0003641	M19	EMB3111-like	12	13	17	17	17	15	12	15	16	14
Sly01g0003651	M11	NA	15	14	16	19	18	15	14	16	22	26
Sly01g0003661	M12	NA	16	15	16	23	29	18	18	20	34	41
Sly01g0003671	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0003681	M12	NA	1	2	1	29	19	5	5	4	10	18
Sly01g0003691	M21	NA	6	5	7	4	3	5	5	5	2	1
Sly01g0003701	M22	NA	5	5	4	2	1	5	3	4	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0359481	M11	NA	145	118	147	202	245	159	158	192	188	247
Sly06g0359541	M11	NA	92	84	105	100	82	151	142	182	155	173
Sly06g0359551	M1	NA	3	4	4	6	3	3	3	4	3	1
Sly06g0359561	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly06g0359581	M3	NA	84	156	102	38	30	117	110	44	30	43
Sly06g0359591	M11	NA	294	280	357	247	238	563	504	645	273	274
Sly06g0359621	M1	NA	8	7	10	9	8	7	5	6	6	7
Sly06g0359701	M11	NA	279	253	277	227	206	275	269	319	260	242
Sly06g0359711	M19	NA	7	7	5	4	3	6	5	6	3	1
Sly06g0359721	M1	NA	11	10	10	6	5	10	8	8	3	1
Sly06g0359731	M1	NA	22	22	21	16	17	18	19	18	16	14
Sly06g0359741	M1	NA	14	15	14	12	11	12	12	12	8	8
Sly06g0359751	M11	NA	6	5	6	5	2	6	6	8	4	1
Sly06g0359761	M6	NA	163	216	106	63	58	138	270	127	75	49
Sly06g0359771	M3	NA	29	30	26	16	14	26	31	21	18	17
Sly06g0359781	M3	NA	29	40	26	230	187	18	21	25	51	97
Sly06g0359791	M13	NA	72	74	87	195	388	64	65	96	265	459
Sly06g0359801	M1	NA	2	2	2	1	1	1	1	1	1	0
Sly06g0359811	M3	NA	2	3	2	3	3	2	2	2	8	6
Sly06g0359881	M12	NA	3	3	3	4	10	22	28	32	40	43
Sly06g0359921	M12	NA	2	1	3	6	38	15	17	23	81	111
Sly06g0359931	M12	NA	1	1	2	4	26	12	14	17	67	89
Sly06g0359941	M12	crtrb1	37	31	36	36	69	135	127	145	168	151
Sly06g0359961	M4	HSP90	51	17	63	34	166	62	28	32	86	252
Sly06g0359971	M11	NA	35	28	35	43	45	40	41	51	72	61
Sly06g0359981	M10	NA	97	80	35	4	1	143	195	59	3	2
Sly06g0359991	M10	NA	30	37	27	25	40	44	54	38	30	47
Sly06g0360001	M13	NA	11	12	17	54	62	16	14	21	48	42
Sly06g0360011	M11	NA	59	51	55	87	101	85	83	93	121	129
Sly06g0360041	M3	NA	3	3	2	1	1	1	1	1	1	1
Sly06g0360051	M3	NA	6	6	3	1	1	1	2	1	1	1
Sly06g0360061	M12	NA	61	49	60	39	24	155	151	146	69	35
Sly06g0360071	M9	NA	1	1	1	1	1	12	13	2	1	1
Sly06g0360081	M1	NA	1	2	1	1	1	1	1	1	1	0
Sly06g0360091	M5	NA	20	20	19	17	24	19	20	18	27	45
Sly06g0360101	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly06g0360151	M11	NA	1	1	2	3	3	5	4	6	7	9
Sly06g0360171	M3	NA	2	2	1	0	0	1	1	0	0	0
Sly06g0360191	M11	NA	36	35	46	72	73	52	49	63	63	60
Sly06g0360201	M11	NA	178	150	150	294	337	218	212	259	311	398
Sly06g0360211	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly06g0360221	M12	NA	7	7	6	3	1	8	9	7	2	2
Sly06g0360241	M3	NA	6	2	1	5	2	2	4	1	3	1
Sly06g0360251	M1	NA	37	38	34	35	38	28	27	28	33	33
Sly06g0360261	M19	NA	20	18	18	20	21	14	12	15	13	11
Sly06g0360301	M12	NA	25	25	35	85	49	67	76	97	132	65
Sly06g0360361	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0360391	M11	NA	43	42	45	44	48	55	46	59	56	62
Sly06g0360401	M12	NA	10	11	11	12	15	15	15	15	15	14
Sly06g0360411	M5	NA	36	36	34	18	12	37	37	33	16	12
Sly06g0360421	M12	NA	2	2	2	2	2	2	3	3	2	2
Sly06g0360551	M1	NA	2	2	2	4	3	0	0	0	0	0
Sly06g0360561	M1	ARP5	26	27	24	29	32	21	20	21	25	26
Sly06g0360581	M22	Cell cycle switch 52B	1	1	1	0	0	1	1	1	0	0
Sly06g0360641	M22	NA	2	2	2	2	1	3	2	2	2	2
Sly06g0360651	M3	NA	25	23	21	15	18	17	19	17	28	31
Sly06g0360661	M12	NA	17	19	19	21	25	26	25	28	27	33
Sly06g0360741	M12	NA	12	15	14	13	14	15	16	14	13	13
Sly06g0360791	M1	SlSOD5	214	179	187	304	797	146	124	141	151	485
Sly06g0360801	M12	SlSOD8	1	1	1	1	1	1	2	1	2	2
Sly06g0360811	M1	NA	4	2	4	2	2	3	3	3	3	3
Sly06g0360821	M22	NA	138	77	82	1	1	867	229	664	1	2
Sly06g0360831	M3	NA	12	13	11	8	7	12	11	10	7	5
Sly06g0360841	M11	NA	10	7	13	3	2	18	12	16	4	1
Sly06g0360851	M11	NA	19	20	21	20	25	22	21	23	21	23
Sly06g0360861	M12	NA	59	55	59	52	55	67	67	72	59	73
Sly06g0360871	M1	NA	35	34	36	42	41	30	29	32	53	48
Sly06g0360891	M13	NA	37	37	42	99	158	40	39	50	124	161
Sly06g0360921	M11	NA	8	5	8	1	2	14	8	11	3	8
Sly06g0360951	M22	NA	14	14	13	11	6	16	13	13	6	1
Sly06g0360971	M3	NA	48	48	46	55	59	36	39	32	50	54
Sly06g0360981	M1	NA	2	2	3	2	2	1	1	1	1	1
Sly06g0360991	M9	NA	24	26	23	22	16	35	35	31	16	18
Sly06g0361001	M12	NA	8	6	9	9	25	9	8	10	13	51
Sly06g0361021	M1	NA	2	2	2	1	1	1	1	0	0	1
Sly06g0361041	M11	NA	26	28	30	51	56	31	30	36	48	46
Sly06g0361051	M1	NA	1	1	1	1	1	1	1	0	0	0
Sly06g0361061	M1	NA	13	8	20	1	0	1	0	0	0	0
Sly06g0361131	M3	NA	41	54	36	28	24	21	28	20	26	29
Sly06g0361141	M1	NA	481	386	402	20	14	118	103	71	11	13
Sly06g0361151	M11	NA	7	8	6	4	1	14	13	12	34	3
Sly06g0361181	M8	NA	3	3	3	2	6	3	4	2	5	12
Sly06g0361221	M11	NA	17	17	19	17	15	20	20	20	19	19
Sly06g0361231	M1	NA	4	4	4	3	3	2	2	2	2	2
Sly06g0361251	M12	NA	10	15	11	20	20	18	20	19	27	22
Sly06g0361261	M12	NA	4	7	8	30	27	10	16	20	50	70
Sly06g0361271	M12	SlRR7	1	2	2	3	6	2	3	4	24	41
Sly06g0361281	M3	NA	51	53	44	38	30	35	40	32	35	31
Sly06g0361291	M22	NA	4	4	3	1	1	5	3	4	1	1
Sly06g0361301	M19	NA	5	7	6	5	4	6	5	6	5	4
Sly06g0361311	M1	NA	22	23	21	9	8	16	16	17	10	9
Sly06g0361321	M19	NA	14	14	15	9	5	14	11	15	5	6
Sly06g0361371	M7	NA	21	31	17	36	64	36	27	19	10	78
Sly06g0361391	M12	NA	10	9	12	4	2	17	18	12	1	1
Sly06g0361401	M1	NA	3	3	3	1	1	3	3	2	0	1
Sly06g0361411	M1	expansin 2	2	1	2	1	1	1	1	1	2	1
Sly06g0361421	M3	NA	37	42	30	33	38	25	28	24	36	53
Sly06g0361431	M3	NA	50	54	43	36	24	38	53	24	26	20
Sly06g0361441	M11	SlSOD9	106	90	105	174	255	132	142	159	221	317
Sly06g0361451	M12	NA	13	9	11	17	20	16	14	17	14	25
Sly06g0361461	M12	NA	8	9	9	10	15	11	10	12	11	15
Sly06g0361471	M11	NA	5	3	5	6	7	6	5	6	6	6
Sly06g0361481	M22	GA2OOX2-like2	1	1	1	1	1	1	1	1	1	1
Sly06g0361491	M1	NA	494	497	563	590	563	411	421	446	798	669
Sly06g0361501	M19	NA	17	18	32	33	20	19	14	21	5	4
Sly06g0361511	M3	NA	2	3	1	1	1	1	1	1	0	1
Sly06g0361551	M11	NA	38	54	89	49	16	191	175	303	134	34
Sly06g0361581	M2	NA	16	17	16	13	14	16	18	16	14	14
Sly06g0361591	M3	NA	51	48	22	22	21	29	28	27	25	30
Sly06g0361601	M9	LSF2	76	77	81	82	117	89	105	93	103	162
Sly06g0361621	M1	NA	7	6	5	6	3	3	2	5	1	1
Sly06g0361661	M8	NA	25	25	20	25	24	24	34	20	84	101
Sly06g0361671	M11	NA	56	65	80	78	111	80	67	98	89	141
Sly06g0361681	M1	NA	26	14	22	12	12	7	5	7	5	3
Sly06g0361691	M1	NA	2	1	2	1	1	1	1	1	0	1
Sly06g0361701	M1	NA	8	7	9	5	4	3	2	3	2	2
Sly06g0361711	M1	NA	15	15	13	4	2	8	8	9	3	1
Sly06g0361721	M12	NA	5	7	6	5	5	9	11	7	9	12
Sly06g0361731	M12	NA	23	17	17	3	1	62	60	57	1	0
Sly06g0361761	M1	NA	2	4	1	1	1	0	1	0	3	1
Sly06g0361821	M1	SlPYL6	16	19	22	12	17	13	10	15	2	13
Sly06g0361831	M18	CLSY1-like	34	35	45	39	23	48	38	45	24	11
Sly06g0361841	M11	SlERF.H15	1	1	2	4	7	2	1	2	1	7
Sly06g0361851	M22	NA	2	1	1	1	0	16	1	6	0	0
Sly06g0361861	M1	NA	3	3	2	1	1	1	1	1	1	1
Sly06g0361871	M19	NA	100	93	93	96	92	89	83	97	113	117
Sly06g0361891	M8	NA	39	36	31	25	12	38	50	31	28	17
Sly06g0361901	M3	NA	83	73	73	162	157	49	63	51	119	134
Sly06g0361911	M11	NA	1	1	1	1	1	2	1	2	1	1
Sly06g0361921	M11	NA	1	1	1	0	1	2

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0003711	M1	NA	1	1	5	75	27	1	0	1	1	1
Sly01g0003721	M1	NA	59	49	47	18	7	19	6	15	2	1
Sly01g0003731	M3	NA	63	89	46	23	30	32	33	14	9	14
Sly01g0003761	M11	NA	15	14	20	21	21	23	23	34	29	25
Sly01g0003811	M1	NA	1	1	1	0	0	1	1	0	0	0
Sly01g0003831	M1	NA	14	12	11	9	10	10	10	11	7	11
Sly01g0003841	M3	NA	1	1	1	1	1	1	1	0	0	0
Sly01g0003851	M3	NA	1	2	1	4	9	1	1	1	11	14
Sly01g0003861	M1	NA	11	19	5	0	0	1	1	1	0	0
Sly01g0003871	M1	NA	18	18	36	276	125	13	13	17	58	42
Sly01g0003881	M1	LeMAN4/a-MAN	1	8	15	5254	4272	1	1	1	24	63
Sly01g0003901	M3	NA	31	33	28	37	41	24	24	28	44	46
Sly01g0003921	M11	NA	11	9	10	9	7	11	10	14	8	7
Sly01g0003931	M18	NA	27	25	28	23	24	29	27	27	19	17
Sly01g0003941	M12	NA	42	47	53	86	118	64	68	91	153	154
Sly01g0003951	M1	NA	65	67	109	20	9	44	35	50	5	2
Sly01g0003961	M1	TIR-NBS11	5	6	5	4	2	1	1	1	1	1
Sly01g0003971	M14	NA	21	19	23	15	14	21	19	23	20	23
Sly01g0003981	M2	NA	95	105	81	97	83	68	79	55	79	72
Sly01g0003991	M1	NA	5	6	4	3	2	1	1	1	1	0
Sly01g0004001	M1	NA	67	74	69	81	85	58	58	58	76	78
Sly01g0004011	M9	NA	131	160	131	135	184	247	428	213	288	460
Sly01g0004061	M19	SIERF.H16	18	19	22	20	23	19	16	20	23	30
Sly01g0004071	M11	NA	6	6	6	7	7	6	6	6	5	4
Sly01g0004081	M12	NA	3	3	3	9	12	5	5	5	29	37
Sly01g0004091	M11	NA	7	6	8	6	8	17	15	20	9	13
Sly01g0004101	M11	NA	5	5	7	11	10	9	7	9	6	5
Sly01g0004111	M22	NA	4	1	3	1	0	7	2	8	1	0
Sly01g0004121	M2	NA	223	205	195	249	218	188	210	205	220	205
Sly01g0004131	M11	AGO4A	182	150	199	135	110	271	200	273	94	91
Sly01g0004141	M11	NA	212	201	208	175	176	236	204	252	226	244
Sly01g0004151	M18	NA	10	10	10	8	9	11	10	11	10	13
Sly01g0004161	M11	NA	25	22	27	26	33	25	25	29	35	40
Sly01g0004171	M3	NA	21	21	20	25	26	19	20	19	27	28
Sly01g0004181	M11	NA	59	56	58	41	41	60	56	67	39	45
Sly01g0004191	M19	NA	45	47	43	122	167	44	44	46	105	136
Sly01g0004201	M1	NA	99	96	98	126	151	68	66	76	88	84
Sly01g0004211	M3	NA	30	31	26	37	43	23	25	21	35	39
Sly01g0004231	M22	SlCycB1;4	1	1	1	1	1	1	1	1	0	0
Sly01g0004241	M11	NA	24	27	33	39	53	38	34	43	36	54
Sly01g0004251	M2	NA	35	36	32	34	43	30	32	31	35	31
Sly01g0004261	M11	NA	28	27	35	24	18	35	31	35	27	25
Sly01g0004271	M12	NA	2	2	3	4	3	6	7	5	2	1
Sly01g0004281	M11	NA	3	2	3	4	2	5	5	6	2	1
Sly01g0004291	M19	NA	68	65	69	64	68	61	54	63	56	70
Sly01g0004301	M2	NA	235	219	158	145	101	111	152	83	143	85
Sly01g0004311	M11	SlHDA7	14	12	15	19	24	15	14	17	23	40
Sly01g0004331	M8	NA	25	26	22	21	14	25	31	23	15	13
Sly01g0004341	M7	NA	7	26	11	4	13	12	24	15	3	16
Sly01g0004361	M1	EIL2	52	51	59	88	60	20	12	18	31	35
Sly01g0004371	M1	NA	31	32	31	46	47	20	20	20	25	27
Sly01g0004391	M1	NA	1	1	1	1	1	1	0	1	0	0
Sly01g0004421	M1	AAO4-like2	8	9	8	5	2	5	4	4	1	1
Sly01g0004451	M1	NA	6	8	7	2	0	6	6	6	1	0
Sly01g0004461	M1	NA	1	1	2	1	1	2	1	1	2	2
Sly01g0004501	M11	BSU	24	26	27	35	38	31	27	32	35	33
Sly01g0004511	M12	NA	23	22	24	24	25	23	23	23	24	24
Sly01g0004521	M9	NA	26	26	27	16	7	37	41	19	14	5
Sly01g0004551	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly01g0004571	M1	DWARF5-like1	231	181	203	97	76	122	132	119	52	52
Sly01g0004601	M22	NA	1	0	1	1	1	6	1	3	0	0
Sly01g0004611	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly01g0004651	M1	NA	13	14	15	17	34	13	14	14	16	18
Sly01g0004661	M3	NA	27	30	31	34	28	22	28	25	40	39
Sly01g0004691	M1	NA	412	373	421	337	262	300	346	303	282	268
Sly01g0004711	M1	NA	520	517	527	521	270	178	148	112	89	55
Sly01g0004741	M1	NA	151	147	157	146	119	130	141	158	145	154
Sly01g0004751	M3	NA	64	57	55	44	37	37	46	37	43	32
Sly01g0004761	M23	NA	2	1	1	1	0	6	2	1	1	1
Sly01g0004791	M12	NA	9	9	10	8	7	10	13	11	12	12
Sly01g0004811	M22	NA	3	1	2	0	0	8	1	6	0	0
Sly01g0004821	M1	NA	328	296	289	244	190	252	234	244	247	165
Sly01g0004851	M3	NA	2	1	1	0	0	1	1	1	1	0
Sly01g0004891	M1	NA	46	41	37	26	16	30	28	26	13	9
Sly01g0004911	M12	NA	28	26	30	34	45	32	35	31	50	60
Sly01g0004921	M1	NA	26	25	29	39	53	23	23	25	37	63
Sly01g0004961	M22	NA	2	1	1	1	0	3	2	1	2	1
Sly01g0004981	M11	NA	2	2	3	1	1	3	2	3	1	1
Sly01g0005001	M1	NA	1	1	1	1	0	0	1	0	0	0
Sly01g0005021	M3	NA	2	2	1	1	0	1	1	1	0	0
Sly01g0005031	M1	NA	2	1	3	1	1	1	1	0	0	0
Sly01g0005041	M1	NA	1	1	1	1	1	1	1	0	0	0
Sly01g0005091	M15	NA	199	163	167	176	220	162	167	181	246	342
Sly01g0005101	M1	GEM-like4	3	4	2	3	3	1	1	1	1	0
Sly01g0005111	M3	NA	2	2	1	1	1	1	1	1	0	0
Sly01g0005121	M1	NA	4	2	2	6	5	2	1	1	1	2
Sly01g0005131	M7	NA	68	81	59	54	119	62	83	61	88	269
Sly01g0005211	M10	NA	34	43	29	23	29	39	42	31	27	35
Sly01g0005221	M1	NA	4	6	8	4	1	1	1	1	0	0
Sly01g0005251	M1	NA	36	33	35	42	45	24	24	23	36	39
Sly01g0005261	M12	NA	152	126	90	30	24	212	190	157	46	23
Sly01g0005271	M1	NA	27	34	44	3	10	3	3	3	1	1
Sly01g0005341	M3	NA	1	2	1	0	0	1	1	0	0	0
Sly01g0005381	M11	NA	10	9	13	25	27	16	17	20	23	19
Sly01g0005401	M11	NA	89	80	89	156	199	128	124	125	196	213
Sly01g0005411	M1	NA	11	8	10	20	26	9	8	9	10	13
Sly01g0005421	M2	NA	8	12	10	7	3	3	6	2	1	1
Sly01g0005431	M1	NA	4	4	4	5	3	3	3	3	5	3
Sly01g0005441	M11	NA	52	62	61	39	37	102	102	113	68	39
Sly01g0005451	M11	NA	80	82	68	52	56	133	126	144	95	73
Sly01g0005461	M10	NA	29	67	22	8	47	70	162	41	7	152
Sly01g0005471	M3	NA	2	3	2	3	2	1	1	1	1	1
Sly01g0005481	M22	NA	1	1	1	1	1	2	1	2	1	1
Sly01g0005521	M1	NA	4	4	4	3	2	4	4	4	1	1
Sly01g0005551	M12	NA	6	6	5	11	16	26	17	16	9	18
Sly01g0005571	M3	NA	209	139	95	7	4	44	54	18	1	1
Sly01g0005581	M1	NA	35	25	26	8	12	11	13	9	12	29
Sly01g0005591	M1	NA	311	227	291	61	53	119	137	105	80	168
Sly01g0005601	M3	NA	40	38	26	16	7	24	32	13	7	4
Sly01g0005611	M3	NA	21	19	12	5	5	10	12	5	2	6
Sly01g0005621	M1	NA	97	69	45	19	22	22	20	15	3	23
Sly01g0005641	M2	NA	45	50	51	71	43	37	58	53	257	283
Sly01g0005661	M16	NA	115	91	93	56	64	87	78	83	52	68
Sly01g0005681	M1	NA	26	25	27	18	12	24	23	25	28	36
Sly01g0005701	M12	NA	16	11	18	16	3	17	20	14	6	1
Sly01g0005721	M1	NA	3	3	4	7	7	2	2	2	1	1
Sly01g0005731	M1	NA	4	4	4	4	2	2	1	2	1	1
Sly01g0005751	M22	NA	19	25	11	7	6	29	15	23	5	3
Sly01g0005791	M12	NA	6	6	5	8	7	8	8	8	12	9
Sly01g0005801	M10	NA	39	73	42	12	25	77	109	43	13	18
Sly01g0005811	M11	NA	74	71	92	66	63	89	79	109	77	81
Sly01g0005821	M11	NA	9	11	10	11	10	13	11	15	13	10
Sly01g0005831	M13	NA	61	42	109	99	81	79	62	88	36	17
Sly01g0005841	M12	NA	3	5	6	50	46	35	46	43	66	58
Sly01g0005921	M1	NA	3	3	3	3	3	3	2	2	2	2
Sly01g0005931	M20	NA	6	5	8	3	1	5	4	5	1	1
Sly01g0005951	M3	NA	219	198	165	118	101	130	143	117	137	106
Sly01g0005971	M11	NA	31	29	33	27	26	38	32	41	33	35
Sly01g0005981	M1	NA	421	384	381	271	203	343	328	402	320	288
Sly01g0005991	M11	NA	29	31	36	28	28	37	35	34	27	31
Sly01g0006011	M11	NA	17	15	17	36	81	32	29	33	73	192
Sly01g0006021	M12	NA	36	33	43	53	53	55	48	53	32	39
Sly01g0006031	M3	NA	27	42	20	16	36	13	23	11	10	51
Sly01g0006051	M9	NA	1	1	1	1	1	1	2	1	2	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0362011	M3	NA	27	27	22	31	33	25	24	23	33	38
Sly06g0362021	M1	NA	163	116	145	198	201	108	95	67	22	26
Sly06g0362031	M12	NA	129	130	140	173	220	151	163	169	238	310
Sly06g0362051	M11	NA	7	7	8	8	8	10	10	11	6	3
Sly06g0362061	M12	NA	8	13	15	4	4	13	22	14	3	1
Sly06g0362071	M6	NA	45	76	34	2	2	67	93	27	2	1
Sly06g0362091	M11	NA	12	15	16	9	5	16	15	14	3	2
Sly06g0362111	M11	NA	15	12	17	3	1	43	43	57	6	1
Sly06g0362141	M11	NA	13	13	14	10	9	15	14	15	12	11
Sly06g0362151	M1	NA	9	9	10	2	1	5	5	5	1	1
Sly06g0362161	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly06g0362191	M3	NA	68	74	38	17	22	20	26	16	12	11
Sly06g0362211	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0362221	M1	NA	216	172	233	130	191	160	181	182	215	261
Sly06g0362231	M1	NA	26	26	26	34	35	18	19	21	47	37
Sly06g0362251	M3	NA	10	10	6	9	13	3	4	1	1	1
Sly06g0362261	M11	NA	33	33	49	116	137	56	49	63	46	34
Sly06g0362271	M5	NA	25	41	28	17	24	30	39	20	13	21
Sly06g0362281	M3	NA	2	1	1	1	1	1	1	1	1	1
Sly06g0362321	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0362341	M18	NA	14	15	18	27	42	17	14	19	23	30
Sly06g0362371	M11	NA	20	19	22	21	24	24	22	27	22	33
Sly06g0362381	M1	NA	3	3	4	1	1	3	3	3	1	1
Sly06g0362421	M11	NA	16	15	14	18	20	15	16	20	15	15
Sly06g0362441	M1	NA	5	6	5	3	2	3	3	2	1	1
Sly06g0362451	M11	NA	29	26	31	71	112	46	45	54	102	124
Sly06g0362461	M1	NA	21	22	17	20	14	17	14	14	11	9
Sly06g0362481	M1	NA	17	14	11	7	8	8	8	7	2	3
Sly06g0362491	M3	NA	4	6	3	2	3	2	4	1	1	3
Sly06g0362501	M1	NA	7	6	13	15	5	4	4	5	1	2
Sly06g0362511	M1	NA	12	9	13	3	1	6	3	6	1	0
Sly06g0362521	M1	NA	129	100	99	62	93	76	77	88	92	185
Sly06g0362531	M12	NA	3	2	2	0	1	3	4	3	1	1
Sly06g0362541	M3	NA	83	96	77	84	59	77	87	54	45	51
Sly06g0362551	M23	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0362561	M1	NA	3	4	4	5	7	2	3	2	7	4
Sly06g0362571	M1	NA	5	5	6	9	8	4	3	5	10	17
Sly06g0362601	M23	NA	1	1	1	1	1	3	2	2	1	1
Sly06g0362611	M11	NA	46	34	49	28	30	52	47	56	29	51
Sly06g0362621	M12	NA	24	27	26	30	30	30	31	30	37	35
Sly06g0362631	M3	NA	337	388	237	100	85	225	213	190	82	52
Sly06g0362641	M12	NA	17	18	18	52	26	30	34	35	18	9
Sly06g0362661	M12	NA	48	45	44	48	57	52	57	55	63	73
Sly06g0362671	M3	NA	76	68	60	38	32	60	64	49	42	39
Sly06g0362681	M3	NA	60	66	55	37	27	54	50	45	34	24
Sly06g0362691	M11	NA	36	37	44	26	19	50	42	58	24	18
Sly06g0362701	M11	NA	39	37	42	22	22	51	50	54	29	19
Sly06g0362711	M11	NA	37	32	38	23	22	36	41	45	26	20
Sly06g0362721	M11	NA	9	6	10	1	1	12	9	12	1	0
Sly06g0362731	M21	NA	12	12	13	12	10	10	7	11	4	3
Sly06g0362741	M12	NA	39	36	42	66	42	46	56	53	88	66
Sly06g0362751	M12	NA	8	10	8	8	12	12	13	12	12	13
Sly06g0362771	M12	NA	1	1	1	3	7	3	3	4	44	47
Sly06g0362781	M12	NA	15	16	16	16	16	19	20	19	17	17
Sly06g0362801	M3	NA	81	89	53	29	32	50	89	35	23	23
Sly06g0362811	M3	NA	6	7	4	5	2	3	3	2	1	1
Sly06g0362821	M12	NA	51	52	54	70	66	69	73	80	57	45
Sly06g0362831	M12	NA	38	34	31	19	9	38	46	45	27	13
Sly06g0362841	M11	NA	1	2	1	2	1	2	1	2	1	1
Sly06g0362851	M1	NA	27	24	28	57	27	21	20	18	17	12
Sly06g0362861	M11	NA	21	21	27	30	30	31	30	34	29	37
Sly06g0362871	M3	NA	12	12	9	8	9	10	11	10	12	12
Sly06g0362881	M12	NA	17	24	20	20	15	18	23	23	18	17
Sly06g0362891	M1	SlCPD	52	64	79	137	88	15	25	29	126	90
Sly06g0362901	M11	NA	23	24	26	24	24	26	27	31	22	23
Sly06g0362921	M3	NA	64	71	43	25	29	46	41	33	22	24
Sly06g0362931	M12	EXP1	16	57	41	666	443	89	152	303	2424	1097
Sly06g0362941	M11	IDN2	116	104	136	145	166	161	129	184	251	275
Sly06g0362951	M12	NA	31	37	27	28	35	42	48	42	53	70
Sly06g0362961	M22	NA	1	1	1	1	1	3	1	3	0	0
Sly06g0362971	M3	SlERF.G4	13	19	7	1	1	4	3	1	1	0
Sly06g0362981	M3	NA	1	1	1	1	0	1	1	1	0	0
Sly06g0362991	M1	NA	14	13	18	16	48	1	1	1	1	7
Sly06g0363011	M1	NA	56	35	60	78	96	3	1	2	3	13
Sly06g0363021	M1	NA	65	43	73	103	134	4	2	2	5	18
Sly06g0363031	M1	NA	59	33	70	98	118	3	2	2	5	24
Sly06g0363041	M1	NA	9	9	10	8	14	8	7	8	6	11
Sly06g0363061	M3	NA	59	72	54	45	51	53	66	33	30	45
Sly06g0363071	M12	NA	18	16	17	6	29	21	22	21	12	41
Sly06g0363081	M1	SlPP2C9	55	24	38	8	9	14	10	14	1	1
Sly06g0363091	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0363111	M3	NA	6	3	2	1	1	3	2	2	1	1
Sly06g0363121	M3	NA	8	12	4	2	2	6	6	2	1	1
Sly06g0363131	M11	NA	25	24	29	27	27	31	27	37	32	41
Sly06g0363151	M23	DMS3	1	1	1	1	1	2	1	1	1	1
Sly06g0363171	M1	NA	3	2	3	1	1	2	1	1	1	0
Sly06g0363201	M1	NA	61	57	62	58	55	48	49	52	57	52
Sly06g0363221	M11	NA	10	7	13	21	15	19	17	24	17	6
Sly06g0363241	M3	NA	25	25	23	13	6	27	24	19	7	2
Sly06g0363251	M6	NA	11	16	11	7	11	10	13	7	10	15
Sly06g0363261	M1	NA	23	22	19	21	22	14	13	13	12	18
Sly06g0363271	M22	NA	2	1	1	1	0	3	1	3	0	0
Sly06g0363311	M22	NA	1	1	1	0	0	3	1	2	0	0
Sly06g0363321	M22	NA	1	0	1	0	0	3	0	2	0	1
Sly06g0363351	M22	NA	1	1	1	0	0	3	0	1	0	0
Sly06g0363361	M22	NA	1	1	1	0	0	2	1	2	0	0
Sly06g0363401	M11	NA	9	5	16	4	18	24	22	27	7	7
Sly06g0363411	M6	NA	14	22	12	3	2	15	20	5	2	1
Sly06g0363421	M6	NA	60	65	55	50	54	55	69	50	48	55
Sly06g0363441	M2	NA	393	421	385	449	329	260	364	253	382	312
Sly06g0363451	M12	NA	25	24	31	27	17	27	34	41	27	17
Sly06g0363461	M1	NA	57	52	54	61	78	40	39	37	42	77
Sly06g0363471	M13	NA	31	24	42	27	37	29	22	42	21	23
Sly06g0363481	M12	NA	58	45	62	48	40	66	79	80	72	52
Sly06g0363491	M22	NA	4	3	4	1	1	6	2	4	1	1
Sly06g0363501	M3	Solyc06g053260	3	3	2	0	1	1	1	1	3	2
Sly06g0363511	M1	NA	9	10	9	5	2	6	5	5	1	1
Sly06g0363521	M1	Solyc06g053290	24	43	28	49	16	11	23	42	113	35
Sly06g0363541	M12	NA	30	28	34	51	51	33	34	33	50	49
Sly06g0363551	M2	NA	79	95	72	92	177	66	94	77	140	239
Sly06g0363561	M3	NA	21	22	18	17	17	21	19	17	19	14
Sly06g0363571	M3	NA	52	53	44	36	29	41	44	36	42	34
Sly06g0363581	M12	NA	20	17	22	36	32	32	37	65	190	110
Sly06g0363591	M12	NA	19	16	16	16	15	22	22	23	19	18
Sly06g0363601	M3	NA	5	6	5	8	9	5	6	5	12	9
Sly06g0363611	M12	NA	8	8	8	16	16	9	11	9	13	15
Sly06g0363621	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0363631	M12	NA	1	1	1	1	1	2	1	1	1	0
Sly06g0363641	M2	NA	22	23	18	20	18	17	20	16	24	19
Sly06g0363661	M1	NA	50	48	51	38	70	33	27	29	28	48
Sly06g0363681	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0363691	M9	NA	61	58	58	72	70	56	70	57	72	65
Sly06g0363711	M11	NA	98	93	122	118	229	120	100	131	195	268
Sly06g0363721	M2	NA	48	51	44	40	33	35	43	34	49	42
Sly06g0363731	M1	NA	34	36	37	39	38	27	29	28	41	55
Sly06g0363741	M11	AAD6	90	81	90	104	157	115	102	123	110	154
Sly06g0363751	M3	NA	42	44	38	43	44	32	38	33	58	53
Sly06g0363761	M3	NA	6	5	5	3	3	4	5	4	6	5
Sly06g0363801	M1	NA	25	25	25	24	21	22	22	20	18	15
Sly06g0363811	M8	NA	7	6	3	1	1	8	10	3	1	1
Sly06g0363821	M2	NA

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0006061	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0006071	M11	NA	32	29	33	36	30	35	40	46	55	41
Sly01g0006081	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly01g0006091	M1	NA	3	2	2	0	0	2	1	1	1	0
Sly01g0006141	M11	NA	333	288	327	441	595	355	351	385	530	733
Sly01g0006171	M1	NA	90	93	88	170	272	56	67	66	125	275
Sly01g0006181	M11	NA	42	43	58	31	8	73	73	96	38	20
Sly01g0006191	M12	NA	34	35	34	39	41	51	51	53	65	61
Sly01g0006221	M12	NA	63	59	59	60	57	56	65	63	62	66
Sly01g0006231	M3	NA	2	1	1	1	1	1	2	1	1	2
Sly01g0006291	M16	NA	14	14	13	14	19	12	14	13	20	23
Sly01g0006311	M1	NA	37	34	30	33	29	25	23	24	22	21
Sly01g0006321	M11	NA	19	18	22	37	43	22	25	26	38	40
Sly01g0006371	M1	NA	29	23	26	24	30	20	21	25	28	32
Sly01g0006381	M11	NA	74	77	95	211	216	88	77	109	167	145
Sly01g0006391	M3	NA	13	17	14	8	10	10	13	9	7	8
Sly01g0006471	M3	NA	3	4	3	3	1	3	3	3	2	1
Sly01g0006481	M9	NA	45	46	42	59	54	48	54	52	122	59
Sly01g0006491	M11	NA	18	19	19	20	31	21	20	24	27	36
Sly01g0006511	M13	NA	5	4	9	5	5	6	4	8	2	2
Sly01g0006531	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0006551	M12	NA	13	14	12	14	13	20	19	16	14	16
Sly01g0006561	M1	NA	207	196	173	177	148	110	133	121	177	192
Sly01g0006581	M3	NA	334	360	342	322	229	192	264	216	301	239
Sly01g0006601	M1	NA	20	18	23	35	24	14	14	17	9	10
Sly01g0006611	M2	NA	96	103	85	87	80	79	108	61	63	68
Sly01g0006691	M1	NA	24	18	20	19	19	14	17	16	22	29
Sly01g0006701	M1	NA	44	43	42	48	58	37	35	36	23	32
Sly01g0006711	M1	NA	3	2	2	2	1	1	1	1	0	0
Sly01g0006751	M11	NA	4	2	3	2	3	5	3	4	3	4
Sly01g0006761	M11	NA	1	2	3	1	2	3	2	3	2	2
Sly01g0006771	M11	NA	3	3	3	4	4	3	3	4	4	3
Sly01g0006781	M19	NA	2	2	1	2	2	2	2	2	1	1
Sly01g0006871	M3	NA	98	95	76	87	90	78	90	65	94	105
Sly01g0006881	M11	NA	79	61	120	62	60	116	95	136	35	32
Sly01g0006911	M1	NA	7	12	15	7	1	1	2	2	1	1
Sly01g0006931	M22	NA	5	7	3	4	1	6	4	4	9	9
Sly01g0007021	M3	NA	33	35	35	43	35	22	27	18	6	6
Sly01g0007041	M12	NA	1	2	1	1	1	3	2	3	1	1
Sly01g0007061	M12	NA	12	13	14	6	2	25	24	22	5	3
Sly01g0007221	M1	NA	5	4	6	3	5	5	4	5	6	8
Sly01g0007441	M3	NA	25	31	20	13	11	11	14	7	3	9
Sly01g0007451	M12	NA	49	36	64	122	119	127	103	129	127	261
Sly01g0007501	M12	NA	7	7	9	5	2	21	20	16	2	1
Sly01g0007511	M12	NA	4	4	6	4	1	13	13	13	2	1
Sly01g0007521	M11	NA	3	5	5	3	1	12	10	11	1	1
Sly01g0007761	M12	NA	1	1	1	0	0	8	4	7	0	0
Sly01g0007771	M11	NA	2	1	2	1	1	4	4	4	1	1
Sly01g0007781	M1	NA	2	1	1	0	1	1	0	0	0	0
Sly01g0007841	M12	NA	403	381	433	529	543	506	488	684	888	923
Sly01g0007861	M12	NA	8	8	7	5	2	8	9	8	2	1
Sly01g0007891	M1	NA	22	24	18	14	13	4	3	3	2	2
Sly01g0007901	M12	NA	32	33	42	94	100	52	62	68	217	266
Sly01g0007921	M11	NA	34	31	39	37	35	57	54	62	50	44
Sly01g0008041	M12	NA	1	1	1	1	1	3	3	3	2	2
Sly01g0008051	M12	NA	1	1	2	1	1	4	4	4	2	3
Sly01g0008151	M1	NA	2	1	2	2	2	1	1	1	1	1
Sly01g0008161	M3	EIL5	30	31	25	25	22	21	22	19	27	23
Sly01g0008171	M1	TOP6B-like2	22	23	23	27	27	20	18	22	23	23
Sly01g0008201	M1	NA	21	19	31	42	40	1	1	1	2	12
Sly01g0008281	M1	NA	7	12	10	45	37	4	3	7	49	28
Sly01g0008291	M1	NA	14	15	16	33	56	5	7	5	31	66
Sly01g0008301	M3	NA	20	23	18	13	19	10	13	9	17	28
Sly01g0008371	M12	NA	8	8	9	9	12	8	8	9	13	20
Sly01g0008481	M1	NA	2	1	3	8	3	1	1	1	1	1
Sly01g0008541	M1	NA	18	14	11	9	3	1	2	0	0	0
Sly01g0008651	M12	NA	1	1	1	1	0	3	5	4	1	0
Sly01g0008671	M3	NA	4	8	3	2	2	3	4	2	1	2
Sly01g0008681	M9	NA	40	40	38	40	46	41	45	40	40	49
Sly01g0008841	M22	NA	1	0	1	0	1	3	1	2	0	1
Sly01g0008861	M3	NA	47	46	34	41	43	35	30	32	37	38
Sly01g0008941	M18	NA	1	1	1	1	1	2	1	2	2	2
Sly01g0009061	M1	NA	24	26	22	25	29	18	20	20	27	37
Sly01g0009071	M8	NA	8	8	5	10	21	6	10	7	21	42
Sly01g0009091	M3	NA	12	15	9	9	9	10	10	8	12	16
Sly01g0009121	M3	NA	12	10	6	7	6	7	5	5	7	6
Sly01g0009141	M7	NA	40	47	28	31	47	34	67	30	34	102
Sly01g0009251	M3	NA	1	2	1	0	0	1	1	0	0	0
Sly01g0009271	M12	NA	1	2	1	4	3	3	3	3	4	10
Sly01g0009281	M12	NA	15	14	16	28	36	15	18	19	49	51
Sly01g0009291	M1	NA	1	1	1	1	2	1	1	1	1	1
Sly01g0009351	M3	NA	114	112	97	61	47	54	68	42	49	45
Sly01g0009441	M1	NA	35	40	33	19	17	21	19	20	15	15
Sly01g0009451	M3	NA	23	23	15	12	12	10	14	8	12	12
Sly01g0009661	M12	NA	4	4	5	5	3	6	5	5	3	1
Sly01g0009771	M11	NA	7	6	8	6	7	8	7	9	10	15
Sly01g0010011	M12	NA	1	1	3	9	6	9	18	28	95	57
Sly01g0010391	M18	NA	3	4	2	4	5	3	3	4	2	2
Sly01g0010791	M11	NA	1	1	2	1	2	2	2	2	1	2
Sly01g0010941	M9	NA	2	2	2	2	2	2	2	2	1	1
Sly01g0011041	M12	NA	15	14	16	21	24	21	21	20	29	33
Sly01g0011061	M12	NA	3	4	4	3	1	6	6	6	4	2
Sly01g0011071	M11	NA	2	3	2	2	2	4	2	3	3	2
Sly01g0011271	M3	NA	11	11	9	7	7	8	8	9	8	6
Sly01g0011281	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0011431	M12	NA	0	1	1	2	1	4	4	4	8	1
Sly01g0011451	M22	NA	1	1	0	0	0	2	1	1	1	0
Sly01g0011461	M22	NA	1	1	1	1	1	3	1	2	1	1
Sly01g0011501	M11	NA	5	5	9	7	6	9	8	10	8	11
Sly01g0011511	M11	NA	5	10	8	7	11	12	9	13	9	14
Sly01g0011521	M11	NA	2	1	2	2	2	2	2	2	2	4
Sly01g0011531	M11	NA	3	2	2	4	4	5	5	5	6	8
Sly01g0011541	M11	NA	17	16	17	27	41	24	22	28	47	65
Sly01g0011571	M12	NA	6	6	6	8	6	7	7	8	10	12
Sly01g0011591	M22	NA	3	3	3	3	3	3	3	3	3	3
Sly01g0011601	M11	NA	4	5	5	5	6	4	4	5	6	7
Sly01g0011651	M1	NA	1	1	1	1	1	0	0	0	0	0
Sly01g0011771	M11	NA	23	22	25	17	12	26	21	23	11	10
Sly01g0011861	M22	NA	4	4	4	5	2	5	3	4	3	2
Sly01g0011871	M3	NA	4	6	6	4	4	5	5	4	4	4
Sly01g0011881	M2	NA	7	8	8	7	6	8	9	6	9	7
Sly01g0011901	M1	NA	4	4	5	4	3	3	3	3	3	2
Sly01g0011961	M10	NA	3	3	1	0	0	11	4	1	0	0
Sly01g0012021	M22	NA	1	0	1	0	0	2	0	2	0	0
Sly01g0012031	M1	NA	22	23	22	18	21	17	17	19	26	26
Sly01g0012041	M11	NA	112	109	129	142	141	149	144	155	127	85
Sly01g0012101	M11	NA	4	3	6	3	3	8	5	8	4	7
Sly01g0012121	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0012201	M12	NA	1	1	1	1	8	1	1	2	3	41
Sly01g0012261	M12	NA	7	6	6	7	8	7	8	8	9	10
Sly01g0012271	M2	NA	67	67	65	131	131	59	80	65	99	100
Sly01g0012991	M12	NA	2	2	2	2	3	3	2	2	4	4
Sly01g0013001	M3	NA	4	5	4	4	5	4	4	3	4	6
Sly01g0013021	M12	NA	63	60	56	77	64	66	69	67	70	77
Sly01g0013061	M3	NA	4	4	5	4	6	4	4	3	9	13
Sly01g0013071	M22	NA	1	1	1	1	1	1	1	1	0	1
Sly01g0013081	M12	NA	2	2	1	2	1	2	2	2	2	2
Sly01g0013101	M1	NA	21	22	19	15	16	13	13	14	14	15
Sly01g0013181	M3	NA	33	34	30	29	34	28	30	29	35	41
Sly01g0013211	M2	NA	190	192	172	158	168	160	179	150	164	195
Sly01g0013221	M11	NA	28	29	33	44	62	34	32	42	50	76
Sly01g0013231	M1	NA	403	400	381	277	316	325	313	306	331	424
Sly01g0013251	M2	NA	48	47	40	30	19	35	42	28	25	22
Sly01g0013271	M11	NA	492	442	504	782	1568	604	529	544	734	1290

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0363861	M12	phosphoenolpyruvate	5	6	7	509	1043	10	28	86	2560	3257
Sly06g0363871	M7	NA	75	93	62	77	117	73	89	74	102	161
Sly06g0363881	M7	NA	1	3	1	1	1	1	4	1	1	2
Sly06g0363891	M6	NA	2	4	1	1	1	2	2	1	0	1
Sly06g0363911	M3	NA	56	57	54	50	26	53	54	50	62	28
Sly06g0363921	M11	NA	123	127	113	110	105	184	167	236	195	214
Sly06g0363941	M12	HUP39	10	10	8	5	5	14	17	12	7	7
Sly06g0363951	M3	ETR4	323	352	137	310	186	141	165	96	210	79
Sly06g0363971	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly06g0363981	M11	NA	29	29	34	81	102	46	45	63	153	144
Sly06g0363991	M11	NA	31	31	43	29	25	42	34	50	26	25
Sly06g0364011	M22	KNOLLE	1	1	1	1	1	1	1	1	1	1
Sly06g0364021	M11	NA	7	8	8	6	5	9	9	10	11	7
Sly06g0364031	M12	NA	7	7	7	3	1	17	16	20	7	2
Sly06g0364061	M11	NA	215	204	200	286	262	197	188	231	371	453
Sly06g0364071	M3	NA	69	72	63	51	55	50	57	44	70	72
Sly06g0364081	M11	NA	10	11	13	6	4	39	37	54	17	15
Sly06g0364091	M1	NA	84	82	76	61	53	66	76	76	73	58
Sly06g0364101	M1	SlAux/IAA7	3	2	4	1	1	1	1	1	1	0
Sly06g0364111	M11	SlAux/IAA4	155	129	208	41	50	436	338	569	51	34
Sly06g0364121	M1	NA	4	4	4	4	3	2	2	2	2	2
Sly06g0364141	M12	NA	21	21	23	28	30	41	44	43	66	43
Sly06g0364191	M12	NA	72	56	86	68	43	115	114	145	85	35
Sly06g0364201	M11	NA	9	9	11	12	15	13	12	18	27	23
Sly06g0364211	M12	NA	1	1	2	1	3	1	2	5	2	7
Sly06g0364241	M13	NA	130	117	221	584	720	127	154	229	741	634
Sly06g0364251	M13	NA	176	173	348	817	915	164	206	305	924	699
Sly06g0364261	M1	NA	4	6	4	2	1	2	1	1	0	0
Sly06g0364271	M1	chl2	30	25	30	8	15	5	5	6	1	1
Sly06g0364301	M1	NA	6	5	7	4	3	3	2	2	2	1
Sly06g0364321	M11	NA	27	25	34	47	30	43	37	57	47	13
Sly06g0364361	M22	NA	10	7	9	6	4	18	6	12	4	3
Sly06g0364371	M11	NA	25	23	24	32	40	34	34	41	44	53
Sly06g0364381	M11	NA	5	5	4	2	1	6	5	8	4	2
Sly06g0364401	M12	NA	2	2	1	1	1	2	2	2	1	1
Sly06g0364411	M11	NA	1	1	1	1	1	1	1	1	0	0
Sly06g0364421	M18	NA	5	5	5	4	4	7	4	6	2	2
Sly06g0364431	M22	NA	3	4	4	3	3	4	4	4	2	1
Sly06g0364441	M1	NA	4	5	5	3	3	4	4	4	2	2
Sly06g0364451	M3	NA	5	4	3	1	2	2	2	1	1	1
Sly06g0364551	M3	NA	18	17	11	9	31	11	14	12	48	90
Sly06g0364571	M12	NA	1	1	2	2	2	2	2	2	1	1
Sly06g0364581	M14	NA	39	32	50	72	47	30	26	35	20	12
Sly06g0364591	M11	NA	205	127	215	218	55	506	418	660	425	84
Sly06g0364601	M11	NA	2	2	3	1	1	30	13	25	1	1
Sly06g0364621	M12	NA	2	3	2	3	1	4	5	3	1	1
Sly06g0364651	M13	NA	5	4	6	8	7	6	6	7	9	8
Sly06g0364661	M11	NA	2	2	3	6	4	4	2	3	4	3
Sly06g0364671	M1	NA	12	7	12	1	1	3	3	3	1	1
Sly06g0364681	M12	NA	15	15	16	22	19	18	17	19	18	16
Sly06g0364691	M11	NA	6	5	5	6	8	8	8	10	11	15
Sly06g0364711	M23	NA	1	0	1	0	0	2	1	1	0	0
Sly06g0364721	M2	NA	13	12	13	18	21	13	13	13	17	20
Sly06g0364731	M11	NA	1	1	1	1	1	1	1	1	0	1
Sly06g0364741	M19	NA	13	13	13	13	15	13	11	15	11	13
Sly06g0364751	M12	NA	12	10	13	9	7	26	24	28	23	23
Sly06g0364761	M11	NA	77	68	100	89	133	106	98	134	119	185
Sly06g0364771	M12	NA	11	11	10	10	11	14	12	13	12	14
Sly06g0364781	M12	NA	17	17	18	21	20	21	21	23	28	32
Sly06g0364791	M12	NA	1	2	2	1	1	1	2	2	1	1
Sly06g0364801	M3	NA	5	6	5	2	3	3	3	2	2	3
Sly06g0364811	M3	NA	4	4	3	2	2	3	3	2	1	1
Sly06g0364821	M2	SlP4H2	57	61	57	52	68	44	57	45	42	46
Sly06g0364841	M15	NA	386	304	348	673	783	382	379	429	664	974
Sly06g0364871	M1	NA	27	27	29	35	30	24	20	23	25	25
Sly06g0364881	M1	NA	33	28	35	33	36	25	23	28	28	37
Sly06g0364891	M11	NA	10	8	14	4	1	17	13	21	3	1
Sly06g0364901	M11	NA	42	34	40	38	47	41	40	46	44	51
Sly06g0364911	M19	CHR11-like2	19	23	21	17	15	16	11	15	9	6
Sly06g0364921	M1	NA	29	32	30	24	24	22	21	22	13	11
Sly06g0364941	M5	NA	14	15	10	10	9	14	13	12	10	10
Sly06g0364951	M15	NA	32	28	23	19	18	28	31	30	32	27
Sly06g0364961	M12	NA	6	6	6	10	10	15	18	27	37	26
Sly06g0364971	M6	NA	1	4	2	0	0	2	2	1	0	0
Sly06g0364981	M1	NA	7	7	5	1	1	2	2	1	1	1
Sly06g0365011	M10	NA	34	37	33	37	34	35	39	33	33	35
Sly06g0365031	M11	NA	1	0	1	0	0	1	1	1	1	1
Sly06g0365081	M12	AAD6	1	6	16	192	1348	5	75	234	2007	5800
Sly06g0365091	M3	SlPIN6	2	2	1	0	1	1	1	0	0	0
Sly06g0365101	M11	ADH2	460	360	535	1557	3070	1123	1264	2665	8480	16819
Sly06g0365111	M1	NA	40	43	46	51	55	41	40	38	46	46
Sly06g0365121	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0365131	M12	NA	35	39	38	42	42	47	47	47	40	41
Sly06g0365141	M11	NA	10	8	8	9	9	10	10	12	11	8
Sly06g0365171	M11	NA	56	42	70	12	10	195	123	211	9	6
Sly06g0365181	M11	NA	3	3	4	1	1	10	8	11	2	1
Sly06g0365241	M1	NA	12	19	30	8	1	2	1	2	0	0
Sly06g0365251	M1	NA	3	2	4	1	1	1	1	0	0	0
Sly06g0365261	M1	NA	6	6	6	5	2	2	2	1	2	1
Sly06g0365271	M1	NA	110	41	46	4	7	11	11	7	1	1
Sly06g0365281	M9	NA	2	2	1	1	1	9	27	6	5	1
Sly06g0365291	M1	NA	2	2	2	1	0	0	1	1	1	1
Sly06g0365311	M3	NA	7	8	7	6	12	6	7	6	8	33
Sly06g0365321	M22	NA	1	1	1	0	0	1	0	1	0	0
Sly06g0365361	M18	SlSDG34	10	10	13	13	14	17	14	18	14	11
Sly06g0365381	M19	NA	12	14	12	15	13	13	12	13	10	9
Sly06g0365411	M1	NA	2	2	2	1	1	2	1	1	1	1
Sly06g0365471	M3	NA	4	4	3	4	4	2	3	2	3	3
Sly06g0365481	M16	NA	14	12	12	12	23	13	12	12	15	20
Sly06g0365501	M15	NA	104	93	79	110	77	95	104	91	90	66
Sly06g0365511	M3	NA	122	153	85	58	101	87	134	61	101	191
Sly06g0365521	M8	NA	13	14	10	12	10	14	17	10	11	11
Sly06g0365531	M6	NA	52	127	37	49	31	36	131	8	2	22
Sly06g0365541	M11	NA	47	47	60	47	47	78	63	88	50	53
Sly06g0365551	M11	NA	87	62	100	38	30	232	211	207	23	17
Sly06g0365561	M11	NA	8	7	7	2	2	9	7	8	2	2
Sly06g0365571	M1	NA	31	31	32	21	25	27	24	25	22	22
Sly06g0365581	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0365591	M12	NA	5	7	5	12	8	7	8	7	23	13
Sly06g0365651	M12	NA	57	80	32	35	79	110	99	86	39	101
Sly06g0365671	M21	NA	50	45	52	24	33	52	35	52	25	43
Sly06g0365681	M3	SlAPx7	63	60	59	133	168	58	63	56	125	144
Sly06g0365691	M1	NA	2	1	2	3	4	2	1	1	5	6
Sly06g0365701	M23	NA	2	1	2	2	4	2	1	1	4	10
Sly06g0365711	M1	NA	137	122	143	177	126	134	121	125	60	51
Sly06g0365721	M12	NA	6	5	6	14	26	11	12	13	19	30
Sly06g0365751	M11	NA	32	36	27	12	9	45	41	37	1	1
Sly06g0365761	M18	NA	8	8	8	7	9	10	9	10	8	7
Sly06g0365771	M23	NA	1	1	1	1	1	2	1	1	1	1
Sly06g0365781	M9	NA	50	61	58	96	62	62	94	62	82	84
Sly06g0365791	M3	NA	23	28	14	10	13	20	18	12	10	12
Sly06g0365801	M18	SlSDG31	14	14	16	18	19	14	13	16	19	18
Sly06g0365811	M17	NA	525	435	522	347	295	464	412	508	407	312
Sly06g0365821	M22	NA	1	1	1	1	4	1	1	1	0	1
Sly06g0365831	M12	NA	48	48	50	53	60	48	52	51	63	72
Sly06g0365851	M12	NA	15	14	16	15	18	19	21	18	18	20
Sly06g0365881	M3	NA	62	58	46	32	28	50	51	43	25	20
Sly06g0365901	M12	NA	3	3	3	2	1	8	10	8	2	1
Sly06g0365911	M7	NA	1	2	1	1	1	2	2	1	1	0
Sly06g0365931	M12	NA	4	4	5	4	3	6	7	6	5	5
Sly06g0365941	M2	NA	20	18

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0013281	M1	NA	3	2	3	2	1	2	2	2	2	1
Sly01g0013291	M12	NA	6	6	11	22	14	6	8	10	17	10
Sly01g0013301	M1	NA	4	4	6	15	12	2	3	4	10	5
Sly01g0013311	M1	NA	57	94	115	103	68	28	24	40	7	7
Sly01g0013321	M1	NA	117	163	179	201	119	39	34	50	13	10
Sly01g0013331	M3	NA	14	16	14	19	20	13	13	12	15	16
Sly01g0013371	M1	NA	27	26	24	23	26	16	15	17	18	22
Sly01g0013381	M1	NA	182	186	180	124	105	140	142	130	123	109
Sly01g0013391	M22	NA	1	1	1	1	1	2	1	1	0	1
Sly01g0013401	M11	NA	7	7	8	7	3	10	9	11	9	12
Sly01g0013411	M11	NA	9	10	10	10	4	15	14	13	14	13
Sly01g0013421	M18	NA	5	7	8	7	3	8	9	10	10	8
Sly01g0013441	M3	NA	41	44	43	50	60	31	37	31	44	52
Sly01g0013461	M12	NA	1	1	1	0	0	2	1	1	0	0
Sly01g0013481	M1	NA	11	5	7	3	3	3	4	3	4	6
Sly01g0013491	M1	NA	84	69	95	32	22	67	66	58	28	25
Sly01g0013531	M3	NA	98	98	90	119	134	84	87	86	108	124
Sly01g0013651	M12	NA	10	9	10	10	9	13	11	12	16	17
Sly01g0013691	M1	NA	3	2	4	2	1	2	1	2	1	1
Sly01g0013701	M3	NA	2	2	1	2	2	1	1	1	1	1
Sly01g0013761	M1	NA	10	9	21	20	15	3	3	4	2	1
Sly01g0013771	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly01g0013791	M12	NA	296	285	317	383	316	432	448	467	461	394
Sly01g0013801	M11	NA	4	3	4	3	4	4	3	4	4	4
Sly01g0013811	M2	NA	8	10	10	7	2	6	10	3	3	1
Sly01g0013821	M3	NA	3	3	3	3	1	2	4	2	2	1
Sly01g0013831	M12	NA	1	1	1	2	1	3	3	2	3	2
Sly01g0013841	M12	NA	1	2	1	1	1	1	1	2	2	1
Sly01g0013861	M11	NA	60	55	61	76	73	77	73	80	49	48
Sly01g0013891	M9	NA	17	17	13	13	9	16	17	16	17	9
Sly01g0013901	M10	NA	15	16	16	18	21	17	21	16	20	27
Sly01g0013911	M3	NA	19	19	15	17	12	18	18	16	17	15
Sly01g0014021	M11	NA	1	1	1	1	1	2	2	2	1	0
Sly01g0014091	M1	NA	7	7	9	7	7	6	5	7	6	9
Sly01g0014101	M19	NA	4	5	4	5	4	5	4	4	6	8
Sly01g0014121	M1	NA	12	11	11	15	13	10	10	11	11	11
Sly01g0014131	M1	NA	15	15	16	8	7	5	5	5	2	2
Sly01g0014141	M1	NA	18	17	18	9	7	6	5	6	2	1
Sly01g0014151	M12	NA	2	2	1	0	1	5	6	7	1	1
Sly01g0014341	M12	NA	1	1	1	1	1	1	1	1	1	2
Sly01g0014351	M7	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0014361	M12	NA	2	3	2	3	3	3	4	4	4	4
Sly01g0014371	M11	NA	3	5	4	6	5	4	5	5	7	6
Sly01g0014391	M12	NA	14	16	13	19	31	16	16	16	20	29
Sly01g0014411	M11	NA	26	26	28	36	39	29	27	29	32	38
Sly01g0014421	M5	NA	1	1	1	0	0	1	1	1	0	0
Sly01g0014441	M12	NA	11	11	13	14	17	13	12	13	16	16
Sly01g0014461	M11	ENOLASE	9	5	12	9	14	10	6	12	14	30
Sly01g0014501	M11	NA	19	17	19	20	20	23	20	26	23	25
Sly01g0014541	M3	NA	66	65	51	41	42	42	51	32	40	34
Sly01g0014561	M19	NA	14	18	14	7	5	13	11	13	6	4
Sly01g0014571	M3	NA	15	16	11	7	4	14	11	11	6	5
Sly01g0014581	M3	NA	20	22	15	9	6	17	15	16	8	8
Sly01g0014591	M3	NA	9	9	6	3	2	5	6	4	2	3
Sly01g0014601	M11	NA	11	10	12	21	16	21	17	25	19	18
Sly01g0014611	M1	NA	3	2	3	2	1	2	1	1	1	1
Sly01g0014621	M1	NA	2	3	2	2	1	1	1	1	1	1
Sly01g0014631	M1	NA	12	11	14	10	6	10	9	10	6	3
Sly01g0014651	M11	NA	53	24	26	12	8	57	44	46	2	4
Sly01g0014671	M12	NA	3	5	5	7	5	5	6	5	6	6
Sly01g0014761	M7	NA	5	6	3	3	3	4	8	3	3	8
Sly01g0014771	M3	NA	2	1	2	1	1	2	2	1	2	1
Sly01g0014841	M3	NA	19	21	17	18	21	15	17	16	25	31
Sly01g0014851	M12	NA	2	3	2	1	1	3	3	3	2	1
Sly01g0014861	M12	NA	244	255	428	1017	1041	1190	1226	1906	2797	2604
Sly01g0014881	M11	NA	19	19	21	24	35	23	22	25	25	42
Sly01g0014911	M3	NA	1	2	1	0	0	1	1	1	0	0
Sly01g0014921	M11	NA	30	29	33	31	34	36	30	40	35	35
Sly01g0015031	M3	NA	3	2	2	1	1	1	1	1	1	2
Sly01g0015041	M1	NA	2	3	2	1	1	1	1	2	2	1
Sly01g0015051	M12	NA	6	4	6	5	5	9	8	8	5	5
Sly01g0015071	M11	NA	9	9	9	13	15	12	12	14	14	11
Sly01g0015081	M1	NA	61	54	51	37	30	49	48	50	42	36
Sly01g0015151	M22	NA	1	1	1	2	1	1	1	1	1	1
Sly01g0015171	M1	NA	1	1	1	1	1	1	0	1	1	2
Sly01g0015181	M11	NA	2	2	2	2	2	3	3	4	3	3
Sly01g0015201	M3	NA	28	25	21	17	17	24	27	21	22	25
Sly01g0015281	M13	NA	4	3	4	5	5	3	3	4	5	4
Sly01g0015291	M11	NA	5	3	5	6	10	4	5	5	9	23
Sly01g0015301	M1	NA	4	5	5	6	9	4	3	5	8	12
Sly01g0015311	M3	NA	103	93	65	36	47	61	59	49	28	23
Sly01g0015341	M11	NA	11	13	14	10	11	14	14	15	16	16
Sly01g0015361	M11	NA	8	8	8	9	6	9	8	9	14	9
Sly01g0015381	M3	NA	30	35	30	13	12	29	28	26	7	6
Sly01g0015411	M2	NA	14	15	9	5	1	7	10	7	2	1
Sly01g0015441	M11	NA	17	19	20	24	22	22	19	23	21	21
Sly01g0015491	M1	NA	3	2	3	1	0	1	0	0	1	0
Sly01g0015531	M12	NA	3	5	4	5	3	5	9	7	6	5
Sly01g0015541	M3	NA	2	2	1	2	1	2	1	1	1	1
Sly01g0015551	M22	NA	2	0	1	0	0	12	1	7	0	0
Sly01g0015601	M3	NA	8	9	8	9	7	7	7	7	7	8
Sly01g0015621	M1	NA	1	1	1	1	1	1	1	1	1	5
Sly01g0015681	M12	NA	10	9	8	9	10	13	16	17	22	67
Sly01g0015691	M12	NA	6	4	4	4	7	10	13	8	20	48
Sly01g0015751	M1	NA	46	47	39	45	43	35	32	33	27	26
Sly01g0015761	M7	NA	16	44	13	9	11	22	54	13	16	27
Sly01g0015771	M7	NA	38	103	33	18	28	48	123	33	34	83
Sly01g0015791	M12	NA	1	2	1	1	1	2	2	2	3	1
Sly01g0015801	M11	NA	23	22	23	23	35	25	25	25	35	35
Sly01g0015831	M1	NA	10	13	11	7	5	6	10	7	6	4
Sly01g0015841	M11	NA	39	39	49	128	180	70	65	95	151	203
Sly01g0015851	M1	NA	25	26	23	21	23	22	21	23	20	17
Sly01g0015881	M19	NA	22	24	23	21	20	18	16	20	15	12
Sly01g0015901	M12	NA	13	13	12	11	6	21	21	20	4	4
Sly01g0015911	M1	NA	37	40	39	46	57	34	33	33	30	43
Sly01g0015921	M1	NA	5	3	4	4	2	2	2	3	2	1
Sly01g0016021	M5	NA	24	28	17	13	14	27	30	14	10	12
Sly01g0016121	M18	NA	39	41	45	33	31	53	47	52	42	38
Sly01g0016131	M11	NA	18	21	17	17	14	21	23	21	22	22
Sly01g0016141	M11	NA	16	14	16	12	12	18	17	18	17	19
Sly01g0016171	M18	NA	5	5	9	6	4	13	9	16	8	3
Sly01g0016181	M11	NA	8	7	12	11	7	19	16	22	14	6
Sly01g0016201	M11	NA	35	31	36	68	160	33	37	43	102	171
Sly01g0016211	M12	NA	6	6	6	8	10	7	7	7	8	10
Sly01g0016231	M11	NA	21	20	22	20	18	25	20	25	28	24
Sly01g0016281	M12	NA	152	141	145	175	174	206	210	259	375	402
Sly01g0016291	M20	NA	17	13	17	12	13	16	16	14	14	14
Sly01g0016301	M1	NA	39	34	39	39	34	36	36	35	45	44
Sly01g0016311	M7	NA	1	2	1	1	1	3	14	1	1	1
Sly01g0016351	M20	NA	38	26	43	3	2	33	29	28	4	5
Sly01g0016411	M12	NA	1	1	1	1	2	2	2	2	2	3
Sly01g0016451	M11	NA	50	43	47	26	17	51	41	44	11	10
Sly01g0016501	M19	NA	22	23	21	29	30	22	22	21	29	30
Sly01g0016541	M12	NA	14	12	16	12	13	16	16	15	19	27
Sly01g0016581	M22	NA	3	2	1	2	2	2	2	2	1	1
Sly01g0016591	M3	NA	4	4	4	3	2	4	3	3	2	2
Sly01g0016601	M21	NA	2	1	2	1	1	3	1	1	0	0
Sly01g0016671	M12	NA	2	1	1	2	2	5	5	6	5	3
Sly01g0016681	M11	NA	3	3	2	2	4	6	4	5	4	4
Sly01g0016691	M12	NA	29	25	34	31	51	48	56	55	59	97
Sly01g0016811	M6	NA	8	14	12	1	1	16	19	2	1	1
Sly01g0016821	M3	NA	1	2	1	1	0	1	1	1	0	0
Sly01g0016831	M12	NA	69	64	75	74	65	88	83	85	63	63
Sly01g0016941	M11	NA	68	66	69	114	111	73	74	92	113	104

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0366041	M1	NIT2	54	91	15	1	1	2	3	1	0	1
Sly06g0366091	M19	SIPRMT4	8	9	8	6	6	9	8	8	5	5
Sly06g0366101	M18	NA	14	15	15	10	11	15	16	14	10	13
Sly06g0366111	M3	NA	5	5	5	15	14	3	3	4	16	27
Sly06g0366121	M6	NA	13	28	12	19	57	13	24	10	10	34
Sly06g0366131	M6	NA	16	31	14	3	15	11	20	5	1	12
Sly06g0366141	M12	NA	3	4	2	1	1	5	5	3	10	6
Sly06g0366161	M6	NA	59	120	32	6	9	41	55	21	10	9
Sly06g0366171	M14	NA	98	88	101	96	100	85	84	98	106	133
Sly06g0366181	M3	NA	14	16	13	14	18	13	12	13	14	16
Sly06g0366191	M22	NA	3	2	2	6	2	4	2	4	1	1
Sly06g0366201	M1	NA	14	16	14	19	15	13	12	13	19	15
Sly06g0366211	M1	NA	12	10	5	1	1	1	1	1	1	1
Sly06g0366221	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly06g0366231	M11	NA	22	23	23	20	23	24	22	23	23	27
Sly06g0366251	M12	NA	99	89	90	122	226	87	98	104	166	244
Sly06g0366261	M11	NA	3	4	5	13	19	5	4	6	18	22
Sly06g0366271	M1	NA	41	40	41	41	42	34	35	35	42	53
Sly06g0366281	M21	NA	2	1	2	1	1	2	1	1	1	0
Sly06g0366291	M11	NA	3	3	5	3	5	10	9	10	15	31
Sly06g0366301	M22	NA	64	13	27	255	218	143	37	119	384	244
Sly06g0366311	M12	NA	43	41	42	37	37	41	47	43	44	40
Sly06g0366321	M11	NA	2	2	2	1	0	3	2	2	1	0
Sly06g0366331	M3	NA	3	6	1	0	1	2	1	1	1	1
Sly06g0366341	M1	ZEP1	2	2	2	1	1	2	1	2	1	1
Sly06g0366361	M1	NA	9	9	9	8	11	9	9	9	9	9
Sly06g0366381	M12	NA	2	2	2	7	6	5	5	6	12	8
Sly06g0366391	M3	NA	11	9	8	10	10	6	7	6	9	7
Sly06g0366411	M3	NA	10	11	11	20	21	8	10	10	17	20
Sly06g0366421	M12	NA	4	2	2	2	3	4	5	6	4	2
Sly06g0366431	M11	SISDG7	14	15	14	15	16	15	14	16	13	13
Sly06g0366491	M11	NA	16	16	16	21	25	17	18	22	26	30
Sly06g0366501	M11	NA	240	220	251	193	171	306	304	334	380	374
Sly06g0366521	M1	Solyc06g061010	15	25	17	2	1	1	1	1	0	0
Sly06g0366531	M1	NA	100	93	202	439	173	31	49	40	82	89
Sly06g0366541	M11	NA	5	3	8	2	1	21	19	21	1	1
Sly06g0366551	M11	NA	1	1	3	1	1	7	6	7	1	1
Sly06g0366561	M1	SIPRR7	11	11	15	6	2	3	3	4	2	1
Sly06g0366571	M19	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0366581	M3	NA	11	12	12	23	20	8	10	10	26	20
Sly06g0366601	M11	NA	24	22	31	33	56	31	29	38	40	68
Sly06g0366621	M11	NA	52	56	66	62	34	86	81	96	45	59
Sly06g0366631	M1	NA	4	7	11	3	3	2	1	1	2	9
Sly06g0366641	M11	NA	5	5	7	3	1	20	19	27	2	1
Sly06g0366681	M11	NA	3	2	3	1	1	7	4	6	3	1
Sly06g0366691	M12	NA	33	32	35	27	42	35	39	40	55	68
Sly06g0366701	M11	NA	9	8	8	10	11	11	11	12	17	20
Sly06g0366711	M1	glutathione peroxidas	22	21	20	17	14	15	17	15	19	14
Sly06g0366721	M2	NA	62	63	50	48	41	45	59	39	44	54
Sly06g0366751	M1	NA	44	56	51	266	603	38	29	82	1465	1609
Sly06g0366761	M1	SIPYL8	26	31	20	6	6	12	9	10	2	3
Sly06g0366781	M6	NA	13	19	16	10	17	12	20	10	8	21
Sly06g0366801	M1	NA	155	78	100	4	5	4	3	2	1	1
Sly06g0366821	M1	NA	1	1	2	0	0	1	0	1	0	0
Sly06g0366851	M3	NA	3	6	2	1	1	1	1	0	0	0
Sly06g0366861	M11	NA	115	121	103	57	70	195	151	207	52	68
Sly06g0366871	M1	NA	3	3	2	1	1	1	1	1	1	1
Sly06g0366901	M1	NA	63	116	96	26	3	3	1	1	1	1
Sly06g0366921	M1	NA	10	12	11	11	8	11	9	11	8	7
Sly06g0366941	M12	NA	7	8	6	9	9	9	9	9	10	12
Sly06g0366961	M11	NA	4	2	4	3	2	4	3	4	2	1
Sly06g0366971	M11	NA	3	3	3	2	2	4	3	3	2	2
Sly06g0366991	M1	NA	19	19	15	12	15	13	12	13	15	18
Sly06g0367011	M12	NA	38	40	42	42	47	40	38	41	44	50
Sly06g0367031	M1	NA	2	2	1	0	0	0	1	0	0	0
Sly06g0367051	M1	NA	5	5	5	5	4	2	2	2	1	1
Sly06g0367061	M3	NA	10	14	6	1	1	3	8	4	0	1
Sly06g0367071	M11	NA	11	13	22	30	18	19	18	33	38	31
Sly06g0367081	M1	NA	16	18	14	11	11	13	13	13	9	8
Sly06g0367101	M12	NA	1	1	1	1	1	3	2	1	1	0
Sly06g0367111	M12	NA	12	17	13	23	19	16	18	16	23	18
Sly06g0367121	M12	NA	17	18	17	31	27	21	24	20	31	27
Sly06g0367131	M12	NA	1	1	1	2	2	2	2	2	1	2
Sly06g0367141	M12	NA	155	148	134	87	80	227	242	258	146	176
Sly06g0367151	M11	NA	169	149	183	172	247	180	173	216	293	393
Sly06g0367161	M1	NA	9	6	7	4	8	5	4	7	13	18
Sly06g0367171	M3	NA	49	53	41	32	28	42	51	38	22	24
Sly06g0367181	M22	NA	2	3	2	1	1	5	2	5	1	5
Sly06g0367241	M1	NA	2	2	2	1	1	2	1	1	1	1
Sly06g0367251	M12	NA	87	82	98	197	292	128	128	169	289	317
Sly06g0367261	M1	NA	20	22	25	80	31	18	15	12	16	19
Sly06g0367271	M18	NA	3	4	4	4	3	4	4	4	4	3
Sly06g0367281	M12	NA	4	4	4	4	5	6	5	5	7	5
Sly06g0367291	M11	NA	2	2	1	2	1	2	2	2	2	2
Sly06g0367301	M3	NA	65	63	45	33	39	38	41	33	53	60
Sly06g0367311	M1	NA	70	67	50	35	39	44	39	36	48	48
Sly06g0367321	M13	NA	93	75	87	30	5	66	78	104	62	12
Sly06g0367331	M12	NA	2	2	2	2	1	3	5	2	1	1
Sly06g0367341	M12	NA	11	12	11	27	69	11	16	17	36	84
Sly06g0367351	M12	NA	16	15	15	11	13	21	20	22	19	23
Sly06g0367401	M11	NA	10	7	9	10	13	9	9	10	12	11
Sly06g0367411	M1	NA	16	13	17	15	24	11	11	15	20	23
Sly06g0367421	M1	NA	54	57	39	16	11	24	24	22	10	9
Sly06g0367431	M12	NA	70	69	70	109	145	69	72	74	173	169
Sly06g0367451	M1	NA	1	2	1	5	3	1	1	1	18	21
Sly06g0367461	M3	NA	51	50	44	46	44	47	48	43	49	53
Sly06g0367481	M11	NA	5	5	6	5	5	7	7	8	7	5
Sly06g0367491	M11	NA	25	25	24	22	9	28	24	24	6	2
Sly06g0367501	M3	NA	26	27	24	25	27	22	25	25	34	37
Sly06g0367511	M12	NA	42	45	42	42	56	51	50	49	67	102
Sly06g0367521	M11	NA	21	25	23	23	21	28	24	25	22	35
Sly06g0367531	M18	NA	26	28	29	30	36	32	25	34	39	51
Sly06g0367551	M22	NA	1	1	1	1	1	2	1	1	1	1
Sly06g0367561	M19	NA	14	18	18	14	11	17	12	16	9	7
Sly06g0367571	M19	NA	13	14	14	10	8	14	11	14	10	7
Sly06g0367581	M5	NA	33	33	24	19	14	29	31	27	18	12
Sly06g0367591	M5	NA	4	4	3	2	2	4	4	3	3	2
Sly06g0367601	M6	NA	10	31	9	1	1	8	10	2	1	1
Sly06g0367621	M3	NA	124	124	105	122	123	99	107	102	136	151
Sly06g0367631	M3	NA	128	120	116	110	68	117	124	88	28	10
Sly06g0367641	M5	NA	10	13	5	2	1	11	10	6	1	1
Sly06g0367661	M12	NA	8	7	8	6	5	11	10	9	10	8
Sly06g0367671	M6	NA	13	17	12	8	8	14	16	9	10	11
Sly06g0367681	M11	NA	160	148	171	148	231	190	178	209	221	431
Sly06g0367691	M11	NA	28	28	28	40	37	30	29	34	76	53
Sly06g0367701	M3	NA	20	18	18	14	14	15	14	13	13	15
Sly06g0367711	M9	NA	35	35	36	37	38	36	37	37	37	37
Sly06g0367721	M22	NA	4	3	4	10	7	6	4	6	4	3
Sly06g0367731	M11	NA	2	2	2	3	2	4	4	5	4	3
Sly06g0367751	M3	NA	29	50	31	10	9	8	11	5	8	27
Sly06g0367761	M1	SIERF.E2	812	768	835	1488	1413	483	599	551	1146	1139
Sly06g0367781	M2	ALAAT1	54	62	54	90	59	40	42	30	61	33
Sly06g0367791	M12	NA	13	15	14	20	22	23	21	21	25	25
Sly06g0367801	M3	NA	2	3	1	1	2	2	2	1	1	1
Sly06g0367811	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly06g0367821	M1	NA	4	5	4	4	3	2	2	1	2	1
Sly06g0367831	M3	NA	146	150	143	177	187	136	140	139	172	193
Sly06g0367841	M1	NA	2	2	2	2	2	1	1	1	1	1
Sly06g0367851	M18	NA	3	4	3	2	2	5	3	5	3	1
Sly06g0367861	M12	NA	7	9	7	5	3	8	7	8	6	3
Sly06g0367871	M3	NA	16	30	11	2	1	5	5	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0016971	M11	NA	26	25	31	17	4	39	33	35	10	3
Sly01g0017001	M18	NA	13	12	18	16	14	22	19	21	9	9
Sly01g0017011	M3	NA	67	76	56	90	48	31	36	19	11	10
Sly01g0017091	M11	NA	5	5	5	3	4	5	5	5	3	3
Sly01g0017101	M11	NA	102	91	93	58	55	107	110	124	92	91
Sly01g0017121	M11	NA	1	1	1	1	1	1	1	2	1	1
Sly01g0017151	M1	NA	2	2	1	1	0	0	0	0	0	0
Sly01g0017161	M3	NA	1	2	1	0	0	0	0	0	0	0
Sly01g0017171	M1	NA	44	40	45	1	1	1	1	0	1	0
Sly01g0017181	M17	NA	87	80	95	98	104	77	67	91	125	145
Sly01g0017191	M1	NA	1	1	2	2	2	1	1	1	2	3
Sly01g0017201	M19	NA	11	12	12	14	17	12	10	12	15	15
Sly01g0017221	M11	NA	6	6	6	3	2	8	8	7	4	1
Sly01g0017231	M3	NA	26	30	29	33	36	27	28	27	37	38
Sly01g0017241	M19	NA	10	10	14	14	13	10	13	10	10	9
Sly01g0017261	M8	NA	40	46	39	63	42	50	59	38	42	35
Sly01g0017271	M3	NA	126	118	95	62	66	88	81	71	48	51
Sly01g0017281	M1	NA	2	2	2	1	1	0	0	0	0	0
Sly01g0017291	M1	NA	46	46	38	14	18	24	25	18	7	6
Sly01g0017321	M1	NA	8	7	8	9	7	7	6	8	3	2
Sly01g0017331	M5	NA	4	6	4	7	4	5	4	4	2	1
Sly01g0017341	M19	NA	3	4	5	5	1	3	3	4	1	1
Sly01g0017371	M1	NA	51	53	41	22	31	19	14	18	21	40
Sly01g0017391	M11	NA	7	7	8	7	7	9	9	8	6	6
Sly01g0017421	M8	NA	34	35	25	33	34	32	40	28	42	44
Sly01g0017631	M12	NA	18	16	20	18	15	23	21	28	37	45
Sly01g0017641	M11	NA	34	28	38	25	25	41	36	44	45	65
Sly01g0017691	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0017731	M12	NA	1	1	1	1	1	1	1	1	3	1
Sly01g0017741	M1	NA	286	275	264	265	278	250	244	260	290	317
Sly01g0017761	M5	NA	1	1	1	1	0	2	1	1	0	0
Sly01g0017791	M11	NA	29	25	27	27	29	32	30	34	36	38
Sly01g0017801	M1	NA	6	5	4	1	1	1	1	1	1	1
Sly01g0017811	M3	NA	6	7	2	1	1	2	2	1	1	1
Sly01g0017821	M12	NA	23	44	20	48	305	42	139	58	126	513
Sly01g0017831	M2	SlRR10	17	16	17	15	10	16	17	17	14	12
Sly01g0017841	M5	NA	21	26	18	19	18	23	25	18	16	18
Sly01g0017851	M2	NA	16	16	13	15	15	12	14	12	19	13
Sly01g0017861	M11	NA	1	1	1	1	1	2	1	2	1	1
Sly01g0017891	M1	NA	50	50	45	28	24	31	32	28	26	22
Sly01g0018031	M9	NA	4	4	3	1	1	4	5	4	1	1
Sly01g0018041	M1	NA	9	8	7	4	4	1	2	2	2	3
Sly01g0018061	M12	NA	8	8	7	5	4	9	8	7	5	2
Sly01g0018071	M1	NA	34	37	40	67	78	31	32	32	67	83
Sly01g0018081	M1	NA	6	6	6	5	9	4	4	4	4	3
Sly01g0018091	M9	NA	4	6	4	3	3	13	20	11	4	4
Sly01g0018171	M12	NA	17	16	16	16	23	19	19	18	23	28
Sly01g0018241	M3	NA	2	2	2	1	1	1	2	1	1	1
Sly01g0018261	M1	SIERF.E4	385	397	358	726	549	196	224	178	1037	1096
Sly01g0018271	M8	NA	15	15	11	10	12	14	19	12	11	24
Sly01g0018291	M12	NA	4	5	5	5	4	5	6	5	8	9
Sly01g0018301	M22	NA	1	1	1	0	0	1	1	1	1	1
Sly01g0018341	M3	NA	92	90	73	93	87	73	81	68	96	108
Sly01g0018351	M3	NA	19	21	20	22	28	17	18	18	27	35
Sly01g0018531	M1	NA	3	3	1	0	1	1	0	0	0	0
Sly01g0018551	M1	NA	5	3	2	1	2	1	1	1	1	1
Sly01g0018571	M1	NA	12	10	12	10	6	1	1	1	1	0
Sly01g0018591	M12	NA	1	1	1	1	0	2	2	2	3	1
Sly01g0018641	M18	NA	14	14	13	13	12	17	11	17	4	14
Sly01g0018651	M19	NA	89	91	81	81	72	87	77	93	94	91
Sly01g0018671	M1	NA	13	14	12	9	8	11	11	13	10	10
Sly01g0018681	M3	NA	5	7	6	5	5	6	6	5	6	8
Sly01g0018781	M10	NA	33	77	47	34	172	92	154	46	8	127
Sly01g0018791	M11	NA	8	6	12	4	2	56	49	73	6	2
Sly01g0018801	M12	NA	2	2	2	1	1	18	21	22	4	2
Sly01g0018821	M22	NA	2	1	2	2	1	11	3	14	28	2
Sly01g0018871	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0018881	M11	NA	34	34	34	48	53	33	34	35	49	54
Sly01g0018891	M23	NA	1	1	1	1	0	1	1	1	0	1
Sly01g0018911	M9	NA	1	1	1	1	1	1	1	1	1	0
Sly01g0018921	M1	NA	84	80	51	36	44	28	30	27	47	50
Sly01g0018941	M23	NA	5	2	1	1	0	9	6	2	0	0
Sly01g0018951	M23	NA	3	2	1	0	0	9	7	2	0	0
Sly01g0018961	M23	NA	3	1	1	0	0	7	5	1	0	0
Sly01g0018981	M19	NA	2	2	3	2	3	2	2	3	2	2
Sly01g0018991	M13	NA	89	60	153	129	143	144	141	193	51	45
Sly01g0019001	M11	NA	47	39	49	34	46	58	46	67	44	46
Sly01g0019011	M11	NA	2	2	2	1	1	3	3	3	1	1
Sly01g0019021	M1	NA	3	5	4	3	2	2	2	2	1	1
Sly01g0019031	M20	NA	6	4	14	4	1	6	3	6	1	0
Sly01g0019051	M1	NA	52	52	49	47	45	45	45	46	54	51
Sly01g0019061	M1	NA	7	8	6	9	5	2	2	2	1	1
Sly01g0019071	M1	NA	9	10	8	14	7	3	3	2	1	1
Sly01g0019081	M3	NA	309	308	272	411	431	204	270	309	610	585
Sly01g0019091	M11	NA	2	2	3	3	2	5	5	5	2	2
Sly01g0019101	M1	NA	18	14	30	4	4	7	4	6	3	2
Sly01g0019121	M3	NA	2	1	1	1	0	1	0	0	0	0
Sly01g0019131	M3	NA	19	19	21	12	11	20	20	17	9	7
Sly01g0019191	M11	NA	3	3	3	4	2	5	4	4	4	3
Sly01g0019201	M1	NA	22	25	23	22	23	18	18	19	18	18
Sly01g0019211	M1	NA	468	436	392	363	307	294	320	278	377	307
Sly01g0019231	M1	NA	4	2	4	1	0	1	1	1	0	0
Sly01g0019241	M11	NA	7	6	9	8	8	9	10	10	6	6
Sly01g0019251	M1	NA	6	5	6	12	8	3	1	1	1	1
Sly01g0019261	M3	NA	13	13	10	6	4	9	10	7	4	3
Sly01g0019271	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly01g0019301	M3	NA	33	42	27	21	17	28	34	23	23	19
Sly01g0019321	M9	NA	5	4	5	2	3	5	7	4	3	2
Sly01g0019351	M1	NA	9	10	7	19	10	2	2	2	1	1
Sly01g0019361	M2	NA	36	34	33	30	31	35	35	33	41	58
Sly01g0019371	M10	NA	54	65	49	26	23	66	72	53	14	22
Sly01g0019391	M12	NA	12	11	14	18	23	26	25	38	31	43
Sly01g0019401	M3	NA	21	36	16	10	8	5	8	2	1	1
Sly01g0019411	M9	NA	1	1	1	0	1	1	1	1	0	1
Sly01g0019421	M5	NA	6	6	5	5	5	5	6	5	3	3
Sly01g0019441	M1	NA	30	27	28	19	22	22	21	20	14	19
Sly01g0019451	M1	NA	11	10	11	25	98	9	9	12	112	128
Sly01g0019461	M11	NA	8	9	7	10	26	10	10	10	19	48
Sly01g0019471	M11	NA	107	108	126	124	157	121	111	137	121	139
Sly01g0019481	M3	NA	6	7	2	1	0	3	2	1	1	0
Sly01g0019501	M3	NA	1	4	2	3	2	1	1	1	0	0
Sly01g0019531	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly01g0019541	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0019561	M11	NA	4	3	3	3	2	5	4	5	3	3
Sly01g0019581	M19	NA	1	1	1	1	1	1	1	1	3	6
Sly01g0019591	M18	NA	1	1	1	1	3	1	1	1	3	4
Sly01g0019601	M18	NA	2	2	2	2	3	3	2	2	5	8
Sly01g0019611	M19	NA	4	4	5	5	4	4	4	4	10	16
Sly01g0019621	M12	NA	4	5	6	6	7	6	6	6	20	32
Sly01g0019631	M18	NA	6	7	7	7	7	7	7	9	10	6
Sly01g0019641	M11	NA	7	7	6	6	7	8	6	8	10	9
Sly01g0019651	M11	NA	20	17	21	17	18	22	21	26	18	19
Sly01g0019661	M11	NA	11	10	15	12	7	16	15	18	10	4
Sly01g0019671	M12	NA	52	65	58	41	11	104	153	226	430	104
Sly01g0019701	M1	NA	15	33	21	19	5	8	3	9	10	7
Sly01g0019731	M12	NA	3	2	3	1	1	27	18	25	2	1
Sly01g0019741	M12	NA	0	1	0	0	0	4	3	3	0	0
Sly01g0019751	M3	NA	3	4	1	1	0	3	3	1	1	0
Sly01g0019761	M11	NA	26	28	38	37	44	46	45	64	70	74
Sly01g0019771	M19	CHR11-like1	102	106	111	95	110	95	78	97	78	82
Sly01g0019781	M8	CDG1	33	31	30	32	36	32	33	30	29	34
Sly01g0019801	M22	NA	1	0	1	0	0	2	1	1	0	0
Sly01g0019831	M1	NA	6	6	7	16	7	1	1	1	1	1
Sly01g0019841	M12	NA	3	3	2	2	1	5	5	3	3	3

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0367911	M12	NA	72	60	68	75	58	64	72	72	65	53
Sly06g0367921	M11	NA	37	32	37	26	12	61	60	70	22	10
Sly06g0367931	M3	NA	285	232	222	76	28	201	255	154	54	17
Sly06g0367941	M3	NA	29	31	29	24	27	29	30	29	29	31
Sly06g0367951	M3	NA	2	2	2	1	1	2	2	2	1	1
Sly06g0367961	M12	NA	9	9	10	6	7	10	10	10	9	11
Sly06g0367971	M2	NA	4	3	3	3	4	3	3	3	3	2
Sly06g0367981	M1	NA	35	35	30	35	45	27	27	28	38	43
Sly06g0367991	M11	NA	17	13	21	12	12	20	16	22	9	10
Sly06g0368001	M11	NA	225	189	196	290	257	255	251	263	290	294
Sly06g0368011	M12	NA	100	108	91	112	155	167	175	163	145	220
Sly06g0368021	M12	NA	1	1	2	1	1	13	13	15	11	7
Sly06g0368031	M12	NA	4	3	2	1	1	5	5	5	1	1
Sly06g0368041	M11	NA	4	4	4	3	4	5	4	5	5	6
Sly06g0368051	M11	NA	122	53	182	116	121	359	321	493	156	47
Sly06g0368091	M12	NA	21	22	21	35	36	25	24	24	18	19
Sly06g0368101	M14	NA	15	15	16	16	19	16	13	15	16	23
Sly06g0368121	M12	NA	5	5	7	7	3	6	7	7	4	2
Sly06g0368131	M1	NA	48	30	44	17	17	22	22	24	18	19
Sly06g0368141	M1	NA	17	16	18	18	21	14	14	15	17	15
Sly06g0368151	M11	NA	39	31	46	33	37	69	59	87	113	124
Sly06g0368161	M1	NA	408	387	371	241	170	261	269	252	238	169
Sly06g0368181	M11	NA	7	6	8	8	7	8	7	7	9	10
Sly06g0368191	M12	NA	11	10	15	66	82	9	14	15	276	287
Sly06g0368201	M9	NA	1	1	1	1	2	2	2	1	5	11
Sly06g0368211	M12	NA	3	3	4	4	8	11	7	10	9	13
Sly06g0368221	M12	NA	1	0	1	0	0	1	1	1	1	1
Sly06g0368241	M1	NA	4	5	4	3	1	2	3	2	1	1
Sly06g0368271	M20	NA	6	5	7	2	2	5	3	4	1	1
Sly06g0368281	M1	NA	3	3	5	5	5	3	3	3	2	2
Sly06g0368291	M11	NA	15	15	19	35	59	19	18	22	35	50
Sly06g0368321	M5	NA	3	3	3	3	3	3	3	3	3	2
Sly06g0368331	M10	NA	1	1	1	1	0	2	2	1	0	1
Sly06g0368351	M16	NA	426	368	352	253	203	315	297	300	292	212
Sly06g0368361	M22	NA	12	9	9	11	10	15	8	10	8	8
Sly06g0368371	M22	NA	7	2	3	1	0	17	3	10	1	1
Sly06g0368381	M22	NA	7	2	3	0	0	16	4	8	1	1
Sly06g0368401	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0368421	M1	NA	1	1	1	1	0	1	0	1	0	0
Sly06g0368441	M1	NA	6	6	5	1	1	1	1	1	0	0
Sly06g0368471	M1	NA	1	1	1	1	1	0	1	1	1	0
Sly06g0368491	M11	NA	1	1	1	0	0	1	1	1	0	1
Sly06g0368511	M1	NA	2	2	1	1	2	0	0	0	0	1
Sly06g0368521	M11	NA	26	25	30	44	37	41	35	42	44	43
Sly06g0368531	M23	NA	2	1	1	1	1	6	2	1	1	0
Sly06g0368541	M11	NA	34	33	37	37	47	34	34	37	39	46
Sly06g0368551	M12	NA	32	29	37	23	34	466	456	489	377	564
Sly06g0368561	M11	NA	1	1	1	1	1	3	3	3	1	1
Sly06g0368581	M1	NA	6	8	6	3	3	5	3	4	2	2
Sly06g0368591	M1	NA	19	22	18	8	9	12	11	10	9	8
Sly06g0368601	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0368611	M3	NA	74	72	68	83	100	60	70	61	93	127
Sly06g0368621	M9	NA	1	1	1	4	14	1	1	1	13	42
Sly06g0368631	M18	NA	38	40	44	54	66	57	48	64	54	61
Sly06g0368661	M12	NA	30	51	52	102	51	115	109	168	112	55
Sly06g0368731	M22	NA	3	2	2	1	0	6	2	5	1	1
Sly06g0368741	M11	NA	174	156	184	214	196	183	163	221	398	291
Sly06g0368751	M3	NA	25	28	13	5	15	5	8	3	2	4
Sly06g0368761	M11	NA	2	2	3	7	24	3	2	3	24	63
Sly06g0368771	M12	NA	3	3	4	1	1	39	34	35	2	1
Sly06g0368831	M1	NA	50	42	39	38	28	13	10	12	5	4
Sly06g0368851	M19	NA	30	31	30	41	42	30	30	28	28	27
Sly06g0368861	M3	NA	211	211	200	241	178	144	182	144	163	159
Sly06g0368871	M11	NA	12	13	10	4	2	17	15	15	0	0
Sly06g0368881	M3	NA	11	9	8	8	9	7	8	7	8	7
Sly06g0368891	M11	NA	24	25	30	25	14	35	30	36	11	4
Sly06g0368911	M12	NA	72	65	66	108	117	74	87	80	159	158
Sly06g0368921	M2	NA	14	14	16	15	14	11	15	15	14	10
Sly06g0368931	M1	NA	21	21	21	20	21	19	18	21	19	17
Sly06g0368941	M10	NA	10	10	9	11	11	11	11	10	10	8
Sly06g0368951	M1	NA	55	60	83	49	13	6	5	6	6	4
Sly06g0368961	M11	NA	49	35	49	84	146	65	61	74	108	150
Sly06g0369001	M2	NA	20	17	15	21	22	17	17	16	31	30
Sly06g0369041	M3	NA	5	4	4	4	2	2	3	2	5	3
Sly06g0369051	M3	NA	72	69	61	47	40	46	50	44	35	27
Sly06g0369061	M11	NA	29	28	49	100	150	55	46	76	115	148
Sly06g0369071	M22	NA	3	2	2	1	1	3	2	2	1	1
Sly06g0369081	M18	NA	9	9	9	13	20	10	10	10	9	14
Sly06g0369091	M11	NA	153	135	163	176	237	155	141	164	150	147
Sly06g0369111	M11	NA	51	44	62	89	92	86	81	104	116	124
Sly06g0369121	M3	NA	29	34	22	29	25	18	21	12	12	15
Sly06g0369161	M11	NA	31	26	45	12	3	40	35	42	6	1
Sly06g0369181	M3	NA	43	50	39	43	34	43	44	40	32	35
Sly06g0369191	M3	NA	118	107	106	97	96	92	100	97	116	127
Sly06g0369201	M11	NA	67	72	80	111	146	68	66	88	132	174
Sly06g0369211	M11	NA	1	1	1	2	1	3	2	3	1	1
Sly06g0369221	M12	NA	19	22	19	35	52	26	30	27	43	58
Sly06g0369231	M11	NA	7	7	8	7	9	8	8	8	8	8
Sly06g0369241	M1	NA	85	82	90	76	68	81	85	80	63	61
Sly06g0369251	M12	NA	2	1	1	1	1	10	4	7	1	0
Sly06g0369261	M1	NA	24	25	25	24	28	14	14	13	22	23
Sly06g0369271	M1	NA	1	6	3	2	1	3	1	1	1	0
Sly06g0369281	M3	NA	37	50	31	11	6	33	38	12	9	8
Sly06g0369291	M8	NA	120	141	109	194	105	120	188	121	256	156
Sly06g0369301	M3	NA	36	37	37	53	65	34	36	35	64	79
Sly06g0369341	M1	NA	217	199	214	184	184	140	152	146	177	177
Sly06g0369361	M3	NA	30	30	23	26	27	21	25	20	39	34
Sly06g0369371	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0369391	M1	NA	71	74	76	85	86	55	50	58	61	58
Sly06g0369401	M11	NA	16	16	23	49	41	43	44	57	100	63
Sly06g0369411	M1	NA	1	1	2	1	1	1	1	1	1	0
Sly06g0369421	M1	NA	9	6	16	3	1	4	2	3	2	1
Sly06g0369431	M21	SlCycA2;2	2	2	3	1	1	2	2	2	1	0
Sly06g0369441	M8	NA	16	16	13	13	4	19	20	11	6	1
Sly06g0369451	M19	NA	42	41	40	39	42	40	37	41	49	48
Sly06g0369461	M1	NA	97	102	101	108	112	71	67	72	85	81
Sly06g0369471	M3	NA	21	23	14	23	23	16	16	11	19	17
Sly06g0369481	M19	PKL	28	31	35	47	36	30	31	33	32	26
Sly06g0369491	M9	NA	18	19	17	21	21	21	23	18	25	29
Sly06g0369501	M6	NA	13	14	9	13	16	13	15	12	18	20
Sly06g0369541	M3	NA	9	10	9	7	7	8	8	8	7	6
Sly06g0369551	M12	SlERF.H1	1	2	1	1	3	4	8	5	4	4
Sly06g0369561	M12	NA	19	20	23	57	76	21	25	28	42	46
Sly06g0369581	M3	NA	35	37	35	36	37	34	35	32	29	35
Sly06g0369601	M3	NA	4	3	2	0	1	1	1	1	0	0
Sly06g0369631	M12	NA	25	22	25	46	45	31	33	25	19	52
Sly06g0369641	M12	NA	8	7	8	6	6	29	22	30	5	5
Sly06g0369651	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0369661	M12	NA	16	16	19	22	26	21	20	21	27	34
Sly06g0369671	M2	NA	76	79	68	29	9	71	71	76	25	11
Sly06g0369681	M17	NA	5	5	6	4	3	4	4	6	4	4
Sly06g0369691	M11	NA	1	1	1	0	0	6	6	6	1	1
Sly06g0369701	M12	NA	77	82	81	93	69	94	99	101	89	73
Sly06g0369711	M11	NA	5	3	4	2	1	11	9	12	1	1
Sly06g0369721	M12	NA	4	4	4	3	2	7	7	7	5	2
Sly06g0369731	M11	NA	54	51	65	74	43	90	82	103	71	45
Sly06g0369741	M1	NA	15	18	7	6	2	3	3	2	2	1
Sly06g0369751	M22	SlAux/IAA36	10	11	3	0	0	13	6	10	1	0
Sly06g0369761	M3	NA	38	38	36	21	8	38	40	32	10	5
Sly06g0369771	M3	NA	109	97	91	56	22	96	106	77	29	15
Sly06g0369811	M3	NA	27	23	18	18	25	22	24	20	29	28
Sly06g0369831	M1	NA	164

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0019851	M12	NA	2	2	2	2	1	4	7	2	2	1
Sly01g0019861	M1	NA	10	7	7	0	1	1	1	1	0	0
Sly01g0019871	M18	NA	11	11	13	9	5	16	13	16	5	4
Sly01g0019881	M18	NA	17	18	19	16	15	18	17	19	20	15
Sly01g0019901	M12	NA	39	39	42	47	47	46	43	46	46	51
Sly01g0019911	M22	NA	2	1	2	0	0	2	1	2	0	0
Sly01g0019931	M12	NA	18	19	19	55	60	39	39	41	125	166
Sly01g0019951	M11	NA	42	39	43	54	49	38	39	42	59	49
Sly01g0019961	M18	NA	28	28	29	14	12	30	28	28	18	18
Sly01g0019971	M12	NA	14	15	17	22	20	22	19	23	30	35
Sly01g0019981	M11	NA	19	17	21	24	28	26	24	26	41	56
Sly01g0019991	M3	NA	13	14	11	14	15	12	11	12	15	15
Sly01g0020001	M3	NA	42	42	35	35	31	38	39	34	29	28
Sly01g0020011	M19	NA	24	27	24	29	29	25	21	24	27	25
Sly01g0020021	M11	NA	22	21	19	23	28	23	20	22	33	42
Sly01g0020031	M22	NA	4	4	4	1	1	7	4	4	1	1
Sly01g0020041	M11	NA	16	15	15	17	11	22	22	25	8	6
Sly01g0020051	M11	NA	19	19	22	19	9	29	27	31	11	5
Sly01g0020061	M22	NA	19	21	15	12	9	23	17	18	8	4
Sly01g0020081	M1	BAM9-like	423	332	450	437	775	292	297	364	599	1008
Sly01g0020091	M11	NA	125	107	148	158	185	142	160	211	263	226
Sly01g0020101	M12	NA	5	6	6	5	5	7	7	7	9	6
Sly01g0020111	M9	NA	16	17	16	31	30	20	27	17	28	25
Sly01g0020121	M3	NA	17	16	13	15	12	12	13	12	16	13
Sly01g0020131	M3	NA	12	8	8	9	7	8	8	8	9	8
Sly01g0020141	M1	NA	573	483	550	1078	790	307	374	324	657	912
Sly01g0020151	M9	SISOD1	867	812	835	1360	1479	836	1030	876	2059	2542
Sly01g0020161	M18	NA	8	9	8	16	10	11	9	8	16	8
Sly01g0020171	M5	NA	48	45	39	85	53	48	47	40	74	45
Sly01g0020211	M22	NA	1	1	1	1	0	2	1	2	1	0
Sly01g0020231	M19	NA	4	4	4	1	1	4	3	4	1	1
Sly01g0020241	M9	NA	56	54	40	26	21	98	93	65	18	18
Sly01g0020251	M1	NA	16	16	15	19	22	14	14	17	32	33
Sly01g0020261	M3	NA	19	18	20	32	47	14	18	14	25	46
Sly01g0020321	M11	NA	1	0	0	0	0	2	1	1	0	0
Sly01g0020331	M14	DXS1	86	65	140	220	534	80	64	94	303	190
Sly01g0020341	M3	NA	3	3	2	2	5	2	2	2	3	10
Sly01g0020351	M11	NA	36	32	35	88	80	35	35	38	105	97
Sly01g0020361	M12	NA	31	34	41	268	109	33	43	62	207	116
Sly01g0020381	M5	NA	77	79	58	51	82	70	83	56	44	80
Sly01g0020391	M1	NA	6	4	5	5	3	2	2	2	2	2
Sly01g0020441	M10	NA	38	52	39	75	115	45	59	48	108	174
Sly01g0020461	M3	NA	10	10	8	9	10	8	8	8	8	3
Sly01g0020471	M12	NA	15	14	20	48	72	26	30	30	48	45
Sly01g0020491	M1	NA	346	291	264	212	142	195	206	177	207	150
Sly01g0020501	M1	NA	16	14	15	11	7	12	11	12	7	5
Sly01g0020511	M11	NA	54	44	43	60	113	75	68	85	139	267
Sly01g0020531	M19	NA	12	12	12	9	8	12	9	12	7	5
Sly01g0020551	M12	NA	6	5	5	13	17	17	18	18	92	131
Sly01g0020571	M12	NA	1	1	1	1	1	1	1	1	2	1
Sly01g0020591	M12	NA	1	1	2	2	2	2	2	2	1	2
Sly01g0020601	M1	NA	6	6	6	6	7	4	4	5	8	9
Sly01g0020621	M3	NA	169	184	143	154	149	162	161	139	131	134
Sly01g0020641	M1	NA	22	22	18	4	3	4	4	3	1	2
Sly01g0020651	M11	NA	2	2	2	2	3	2	2	3	2	2
Sly01g0020661	M1	NA	14	14	16	12	13	12	12	14	13	11
Sly01g0020671	M11	NA	20	18	20	23	26	23	22	28	32	39
Sly01g0020681	M3	NA	13	12	11	9	6	12	11	11	7	5
Sly01g0020691	M3	NA	9	12	8	9	8	10	9	9	7	6
Sly01g0020701	M11	NA	10	10	11	17	19	12	12	14	17	19
Sly01g0020711	M1	KOBITO1	34	28	32	30	32	21	19	18	13	14
Sly01g0020721	M19	NA	37	37	40	49	59	36	30	38	41	55
Sly01g0020731	M3	NA	41	44	36	38	31	22	26	21	41	26
Sly01g0020741	M22	NA	1	1	1	3	3	3	1	2	1	1
Sly01g0020751	M11	NA	9	8	9	10	27	9	9	10	5	17
Sly01g0020761	M18	NA	42	31	49	37	33	71	57	81	75	35
Sly01g0020771	M18	NA	6	8	7	7	4	8	7	7	4	3
Sly01g0020781	M11	NA	10	12	15	23	29	22	17	26	20	24
Sly01g0020831	M1	NA	48	49	40	31	31	27	24	21	19	22
Sly01g0020841	M1	NA	4	3	4	2	2	3	2	3	2	2
Sly01g0020851	M1	NA	1	1	1	1	2	1	1	1	1	1
Sly01g0020861	M19	SISDG11	6	7	7	8	9	6	6	7	5	6
Sly01g0020871	M3	NA	2	3	2	2	1	2	2	1	1	1
Sly01g0020881	M1	NA	44	45	40	36	36	31	30	29	32	32
Sly01g0020891	M11	NA	86	82	97	103	93	97	102	112	118	107
Sly01g0020901	M22	SIPIN5	1	1	1	1	2	7	2	4	14	30
Sly01g0020921	M22	NA	4	1	3	3	5	28	4	15	44	57
Sly01g0020941	M12	NA	35	37	37	41	44	43	44	43	61	69
Sly01g0020951	M1	NA	154	138	165	32	11	48	35	51	5	2
Sly01g0020961	M11	NA	6	8	8	8	10	11	9	13	6	7
Sly01g0020971	M18	NA	36	37	45	40	34	49	40	52	37	38
Sly01g0020981	M10	NA	5	7	3	4	4	6	7	4	9	9
Sly01g0020991	M22	NA	3	3	3	11	23	3	2	3	16	19
Sly01g0021021	M1	NA	217	192	197	161	134	171	175	175	157	163
Sly01g0021031	M12	NA	3	2	2	2	3	2	2	3	3	3
Sly01g0021051	M11	NA	17	11	18	7	25	14	15	16	10	24
Sly01g0021061	M3	NA	38	40	33	34	40	18	21	18	38	40
Sly01g0021071	M1	NA	17	28	20	9	8	11	9	11	5	5
Sly01g0021081	M1	NA	50	57	40	29	23	28	26	27	19	22
Sly01g0021091	M11	NA	14	13	13	21	31	17	16	19	27	31
Sly01g0021101	M1	NA	3	5	3	1	1	1	2	2	1	1
Sly01g0021111	M3	NA	20	21	12	11	7	10	13	7	8	4
Sly01g0021121	M12	NA	10	9	10	10	10	15	14	16	10	10
Sly01g0021131	M3	NA	4	4	2	1	1	2	3	2	1	1
Sly01g0021141	M11	NA	36	35	42	68	88	70	56	80	75	87
Sly01g0021151	M1	NA	1	1	1	0	1	1	1	1	0	1
Sly01g0021161	M11	NA	21	12	11	1	1	34	27	29	1	1
Sly01g0021201	M3	NA	2	2	1	0	0	1	1	1	0	0
Sly01g0021211	M9	NA	4	3	2	1	1	7	8	4	1	1
Sly01g0021221	M11	NA	1	1	1	0	0	1	1	1	1	0
Sly01g0021231	M12	NA	9	7	6	1	2	26	21	25	6	5
Sly01g0021261	M3	GA2ox3	2	8	3	0	0	2	2	1	1	1
Sly01g0021271	M12	NA	23	23	23	24	25	24	24	26	28	26
Sly01g0021281	M12	NA	19	20	20	36	67	27	26	30	57	81
Sly01g0021291	M19	NA	56	59	60	66	64	60	51	62	67	55
Sly01g0021301	M1	NA	21	17	22	92	46	9	5	8	2	2
Sly01g0021311	M12	NA	206	205	213	167	160	268	253	288	243	225
Sly01g0021321	M2	NA	28	51	34	46	63	21	40	32	90	97
Sly01g0021351	M3	NA	2	2	2	2	2	2	2	1	3	3
Sly01g0021361	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly01g0021371	M11	NA	16	14	16	19	17	18	15	18	9	9
Sly01g0021381	M1	NA	16	16	15	9	6	12	13	13	10	5
Sly01g0021391	M1	NA	34	34	33	31	35	32	30	33	34	32
Sly01g0021401	M1	NA	33	32	36	32	23	32	29	29	15	14
Sly01g0021411	M18	NA	65	60	68	49	50	73	57	77	60	51
Sly01g0021421	M11	NA	26	22	16	10	7	34	30	43	15	10
Sly01g0021431	M12	NA	1	1	1	1	0	1	1	1	1	1
Sly01g0021441	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0021451	M11	EZ1	47	47	59	53	54	72	58	82	44	52
Sly01g0021461	M11	NA	13	14	16	10	10	20	18	22	3	3
Sly01g0021471	M1	NA	7	5	9	1	1	3	2	2	0	1
Sly01g0021481	M3	NA	278	255	242	279	255	202	258	230	274	269
Sly01g0021491	M3	NA	6	6	5	6	6	5	6	5	6	5
Sly01g0021501	M19	NA	6	5	5	3	4	4	4	5	4	3
Sly01g0021511	M11	NA	77	79	90	113	129	88	78	90	70	79
Sly01g0021531	M11	NA	22	11	29	71	19	67	52	120	26	2
Sly01g0021541	M10	NA	86	83	73	56	94	93	149	76	70	159
Sly01g0021551	M8	NA	16	19	16	13	13	17	19	16	14	15
Sly01g0021561	M1	NA	14	12	15	4	5	10	12	10	2	2
Sly01g0021571	M19	NA	34	38	36	38	34	39	33	40	31	27
Sly01g0021581	M11	NA	4	4	4	3	3	5	5	4	2	2
Sly01g0021591	M12	NA	27	24	29	8	11	44	51	45	9	26
Sly01g0021601	M3	NA	297	309	271	303	284	249	312	263	344	349
Sly01g0021611	M3	NA	2	1	1	1	1	1	1	1	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0369871	M2	NA	75	77	66	81	78	66	74	68	98	110
Sly06g0369881	M3	NA	6	7	2	1	0	5	6	3	1	1
Sly06g0369961	M22	NA	2	1	1	5	2	5	1	3	0	0
Sly06g0369971	M22	NA	2	2	2	10	5	8	2	6	1	0
Sly06g0369981	M1	NA	4	3	3	4	3	2	1	3	1	1
Sly06g0369991	M2	NA	45	45	41	62	63	40	44	42	62	71
Sly06g0370011	M3	NA	29	32	24	17	15	22	29	18	15	14
Sly06g0370021	M10	NA	2	5	1	0	0	10	6	1	0	1
Sly06g0370031	M1	NA	5	4	2	1	0	0	0	0	0	0
Sly06g0370091	M3	NA	9	10	8	12	6	8	8	10	17	14
Sly06g0370101	M1	NA	37	34	32	27	23	31	30	32	32	35
Sly06g0370111	M3	NA	23	22	16	13	7	20	17	14	6	2
Sly06g0370121	M1	NA	138	138	119	138	153	119	109	112	124	141
Sly06g0370131	M1	NA	39	39	45	78	130	30	26	32	78	96
Sly06g0370141	M1	NA	6	7	6	6	4	2	3	2	2	1
Sly06g0370171	M6	NA	7	18	14	1	0	15	11	6	1	0
Sly06g0370181	M6	NA	117	209	117	47	142	143	213	83	56	149
Sly06g0370191	M3	NA	18	21	13	13	13	10	11	9	11	12
Sly06g0370211	M12	NA	7	8	8	11	13	8	8	9	17	20
Sly06g0370221	M11	NA	0	1	1	1	1	1	1	4	5	2
Sly06g0370231	M11	NA	8	8	14	18	23	70	65	133	52	31
Sly06g0370241	M1	NA	27	23	38	14	20	11	4	18	7	13
Sly06g0370251	M3	HXK2	23	25	18	13	12	15	14	12	9	7
Sly06g0370261	M12	NA	86	89	82	69	122	108	124	122	171	292
Sly06g0370271	M12	NA	74	92	85	70	121	113	102	116	144	210
Sly06g0370281	M18	NA	26	32	32	23	39	37	32	42	43	59
Sly06g0370321	M1	NA	2	2	2	0	1	1	1	1	0	0
Sly06g0370351	M12	NA	1	1	1	0	1	1	1	1	1	0
Sly06g0370371	M10	NA	1	1	2	1	1	2	2	1	1	1
Sly06g0370381	M3	SlERF.H7	8	13	8	2	2	2	6	2	6	10
Sly06g0370391	M11	NA	26	26	33	58	56	36	35	62	163	84
Sly06g0370441	M11	NA	44	41	44	46	57	43	43	49	55	78
Sly06g0370451	M1	NA	3	3	3	1	1	1	1	1	1	1
Sly06g0370461	M1	NA	10	20	9	2	1	4	3	3	1	0
Sly06g0370471	M7	NA	32	42	27	52	67	42	53	30	44	80
Sly06g0370481	M3	NA	49	55	49	52	48	51	49	47	50	52
Sly06g0370491	M11	NA	81	84	86	89	116	135	126	142	131	256
Sly06g0370501	M5	NA	13	17	5	1	1	7	11	3	1	2
Sly06g0370511	M11	NA	9	6	8	6	1	31	30	47	7	1
Sly06g0370521	M3	NA	2	3	1	1	1	1	1	1	1	1
Sly06g0370531	M16	NA	227	183	187	166	145	161	150	163	153	119
Sly06g0370541	M5	NA	2	2	2	1	1	2	2	2	1	1
Sly06g0370551	M12	NA	7	8	10	10	4	20	21	24	17	14
Sly06g0370611	M3	NA	40	47	35	36	24	39	46	29	20	18
Sly06g0370621	M3	NA	22	21	19	15	13	18	22	16	18	24
Sly06g0370641	M11	NA	30	26	32	34	35	38	36	44	46	44
Sly06g0370651	M12	NA	1	3	3	8	17	2	4	11	16	31
Sly06g0370661	M12	NA	15	16	17	17	19	19	16	19	19	19
Sly06g0370671	M19	NA	46	48	53	43	21	47	45	51	46	22
Sly06g0370681	M7	NA	40	74	18	7	8	52	169	46	8	64
Sly06g0370691	M3	NA	24	25	23	22	23	23	23	23	18	19
Sly06g0370701	M3	GA3ox1	8	20	3	1	1	1	1	1	1	1
Sly06g0370721	M11	NA	1	1	1	0	0	1	1	1	0	1
Sly06g0370761	M7	NA	2	2	1	2	2	2	3	2	3	5
Sly06g0370821	M12	NA	91	80	85	104	108	118	128	137	145	167
Sly06g0370831	M3	NA	10	10	8	4	4	5	5	3	4	2
Sly06g0370861	M2	NA	55	53	47	48	51	48	53	47	51	57
Sly06g0370881	M2	NA	110	105	89	82	55	72	93	66	63	47
Sly06g0370891	M1	NA	59	46	33	13	12	14	12	12	24	36
Sly06g0370901	M2	NA	60	61	55	79	89	50	62	56	96	106
Sly06g0370911	M11	NA	55	47	54	39	48	56	58	64	49	72
Sly06g0370921	M1	NA	9	8	8	27	12	8	5	6	3	4
Sly06g0370931	M12	NA	22	23	24	20	22	23	25	24	22	22
Sly06g0370941	M18	NA	13	12	14	10	12	15	12	13	12	10
Sly06g0370961	M11	NA	37	39	39	74	89	48	47	52	77	102
Sly06g0370971	M2	NA	9	6	6	9	9	5	7	5	9	11
Sly06g0370981	M11	NA	47	45	47	48	52	51	57	64	82	92
Sly06g0371001	M3	NA	45	45	40	18	14	25	31	19	13	16
Sly06g0371011	M11	NA	21	26	26	31	27	32	30	32	26	21
Sly06g0371041	M9	NA	41	43	31	25	24	50	63	44	41	48
Sly06g0371051	M8	NA	127	180	99	104	116	161	238	111	82	121
Sly06g0371081	M11	NA	27	28	38	39	31	35	36	42	30	28
Sly06g0371091	M11	NA	1	1	1	0	0	5	3	3	0	0
Sly06g0371101	M14	MBD11	77	60	100	73	98	73	64	92	91	173
Sly06g0371111	M12	NA	2	2	2	2	2	1	3	2	2	4
Sly06g0371121	M11	NA	8	5	10	10	14	17	14	20	17	11
Sly06g0371141	M1	NA	4	4	6	7	11	4	5	4	6	13
Sly06g0371151	M11	NA	11	9	14	10	8	17	14	19	10	11
Sly06g0371161	M11	NA	25	23	32	45	51	37	37	48	89	92
Sly06g0371171	M18	NA	30	25	33	17	19	57	45	61	16	29
Sly06g0371181	M12	NA	2	2	3	4	5	5	5	4	4	2
Sly06g0371211	M12	NA	1	2	3	14	15	7	6	11	30	36
Sly06g0371221	M11	NA	15	14	17	23	32	17	14	19	24	44
Sly06g0371231	M11	NA	3	3	5	4	2	5	4	7	3	2
Sly06g0371241	M12	NA	2	2	1	1	2	2	2	2	1	1
Sly06g0371251	M12	NA	1	1	1	1	0	1	1	1	1	0
Sly06g0371261	M3	NA	276	276	219	138	121	172	188	142	113	114
Sly06g0371271	M2	NA	5	5	4	5	8	3	4	2	6	11
Sly06g0371291	M23	NA	1	1	1	1	0	2	1	1	1	0
Sly06g0371301	M3	SlERF.H2	1	3	1	0	0	1	1	1	1	0
Sly06g0371311	M1	NA	40	41	37	21	23	22	25	21	22	25
Sly06g0371321	M1	NA	21	15	7	1	1	2	2	1	0	0
Sly06g0371331	M1	NA	62	56	54	34	22	36	36	34	31	22
Sly06g0371341	M3	NA	47	42	35	41	43	43	40	35	42	48
Sly06g0371361	M1	NA	6	7	7	7	8	3	2	3	4	3
Sly06g0371371	M1	NA	9	10	9	13	15	1	1	2	4	8
Sly06g0371381	M4	NA	14	17	15	144	60	23	21	26	490	287
Sly06g0371391	M11	NA	44	43	57	80	70	99	75	102	55	77
Sly06g0371401	M5	NA	56	119	49	60	48	54	105	21	9	32
Sly06g0371411	M1	NA	9	7	9	11	5	6	5	5	3	2
Sly06g0371421	M11	NA	27	23	36	64	34	30	28	36	24	20
Sly06g0371431	M11	NA	13	14	20	22	34	19	17	23	42	35
Sly06g0371441	M11	NA	22	20	33	26	43	29	23	40	47	35
Sly06g0371451	M13	NA	185	154	306	466	651	209	174	364	513	620
Sly06g0371461	M1	NA	7	6	6	2	1	1	1	1	1	1
Sly06g0371471	M12	NA	2	2	2	8	9	2	2	3	16	9
Sly06g0371481	M1	NA	103	111	108	15	9	6	4	4	1	1
Sly06g0371501	M13	NA	6	6	7	24	22	5	6	8	20	31
Sly06g0371511	M19	NA	7	7	9	30	28	6	7	10	22	25
Sly06g0371521	M23	NA	1	1	1	0	1	1	1	1	0	0
Sly06g0371531	M3	NA	12	12	8	8	9	8	8	7	8	8
Sly06g0371541	M1	NA	16	20	16	1	1	7	5	5	1	1
Sly06g0371561	M12	NA	11	12	13	16	8	13	17	16	21	11
Sly06g0371571	M1	NA	30	37	37	76	47	14	13	19	39	26
Sly06g0371581	M1	NA	19	21	23	50	27	9	7	15	25	17
Sly06g0371591	M1	NA	6	6	6	7	8	5	5	5	7	6
Sly06g0371601	M11	NA	18	8	16	2	1	17	10	17	1	1
Sly06g0371611	M12	NA	6	7	7	3	3	7	8	6	4	4
Sly06g0371631	M12	NA	10	16	6	1	1	31	28	11	1	0
Sly06g0371651	M14	NA	45	37	66	79	41	50	43	59	38	32
Sly06g0371661	M11	SlRbohD	2	3	3	1	1	4	2	4	1	0
Sly06g0371671	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0371681	M3	NA	5	7	4	2	1	5	6	4	2	1
Sly06g0371691	M3	NA	18	16	15	13	11	12	14	11	19	14
Sly06g0371701	M3	NA	39	35	23	16	17	16	17	13	17	15
Sly06g0371721	M3	NA	33	35	30	36	47	26	28	29	52	61
Sly06g0371731	M12	NA	31	28	33	12	5	78	74	69	12	5
Sly06g0371741	M11	NA	64	58	71	63	87	77	75	81	79	91
Sly06g0371751	M12	NA	5	4	5	3	1	10	8	7	1	1
Sly06g0371761	M3	NA	35	32	28	29	27	31	36	27	26	26
Sly06g0371771	M1	NA	14	13	19	23	7	7	6	6	3	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0021641	M20	NA	6	5	7	1	1	6	5	5	1	1
Sly01g0021661	M12	NA	74	60	82	187	406	107	108	123	165	311
Sly01g0021671	M9	NA	23	35	24	47	110	29	45	30	28	94
Sly01g0021681	M3	NA	56	74	49	57	31	48	73	30	33	28
Sly01g0021711	M1	NA	12	9	17	125	64	1	1	1	1	0
Sly01g0021721	M1	NA	10	9	11	9	13	8	9	9	10	13
Sly01g0021731	M11	NA	8	7	10	7	7	10	9	12	10	7
Sly01g0021741	M1	NA	21	19	28	34	51	10	6	9	4	8
Sly01g0021751	M7	NA	3	14	7	2	22	8	50	12	8	55
Sly01g0021761	M9	NA	1	1	1	1	1	1	2	1	1	2
Sly01g0021771	M1	NA	26	25	28	20	15	20	18	20	12	13
Sly01g0021781	M19	CHR12-like	17	18	18	16	18	14	13	15	12	14
Sly01g0021791	M1	NA	60	63	72	40	37	58	54	58	51	51
Sly01g0021801	M18	NA	44	45	50	64	87	60	53	65	52	58
Sly01g0021831	M10	NA	1	1	1	0	1	2	2	1	1	0
Sly01g0021841	M1	NA	4	3	3	3	3	3	2	2	2	1
Sly01g0021851	M1	NA	22	21	22	33	37	17	20	21	40	39
Sly01g0021861	M11	NA	5	5	6	16	10	11	9	14	17	9
Sly01g0021871	M9	NA	64	69	63	84	55	71	89	70	78	61
Sly01g0021881	M11	SlAGPase-L3	6	6	4	3	2	7	7	6	2	1
Sly01g0021891	M12	NA	5	5	5	9	26	18	16	22	16	22
Sly01g0021901	M10	NA	62	79	41	20	37	73	76	58	14	13
Sly01g0021911	M11	PrxII	64	61	73	89	111	89	90	99	86	109
Sly01g0021931	M1	NA	66	61	70	95	116	61	55	67	93	107
Sly01g0021941	M12	NA	1	1	1	3	7	3	2	3	4	2
Sly01g0021951	M12	NA	8	6	7	9	16	8	8	8	12	14
Sly01g0021961	M11	NA	17	17	18	45	80	23	19	23	29	58
Sly01g0021971	M1	NA	220	196	226	204	213	167	155	176	150	243
Sly01g0021981	M11	NA	703	539	914	323	497	785	811	902	258	566
Sly01g0022041	M3	NA	2	5	2	1	0	3	3	2	1	1
Sly01g0022051	M6	NA	6	16	9	2	1	9	12	8	2	1
Sly01g0022061	M3	NA	3	7	4	1	1	1	2	1	1	1
Sly01g0022071	M7	NA	9	18	6	3	28	18	45	7	4	36
Sly01g0022121	M22	NA	7	2	5	0	0	16	4	21	1	0
Sly01g0022131	M1	NA	224	217	219	197	205	50	35	24	2	2
Sly01g0022141	M11	NA	113	85	168	41	23	216	178	305	34	9
Sly01g0022151	M11	NA	1	1	1	1	1	3	4	7	10	3
Sly01g0022161	M12	NA	11	12	13	17	18	15	17	18	23	26
Sly01g0022181	M1	NA	40	37	42	10	3	24	13	16	1	1
Sly01g0022191	M14	NA	15	14	16	12	13	14	12	15	10	13
Sly01g0022201	M18	NA	55	45	65	43	35	58	53	62	36	37
Sly01g0022211	M11	NA	2	1	1	0	0	3	2	3	1	0
Sly01g0022221	M14	NA	24	24	31	32	39	25	24	26	31	31
Sly01g0022241	M12	NA	9	7	12	5	5	12	13	10	5	6
Sly01g0022251	M2	NA	28	31	24	31	42	22	22	19	35	44
Sly01g0022261	M1	IPT5/SlIPT3	4	3	4	5	2	1	1	1	1	1
Sly01g0022271	M12	NA	15	16	17	11	10	33	33	30	21	10
Sly01g0022281	M18	NA	27	32	32	22	42	34	24	38	23	33
Sly01g0022291	M12	NA	12	10	9	15	15	12	12	13	14	13
Sly01g0022301	M1	NA	8	9	9	13	11	7	7	8	13	10
Sly01g0022311	M22	NA	52	43	38	8	7	45	33	45	4	4
Sly01g0022321	M13	NA	8	9	10	42	59	7	7	11	29	36
Sly01g0022331	M1	NA	21	20	29	139	219	2	2	2	6	13
Sly01g0022351	M1	NA	65	67	67	66	61	51	51	46	37	43
Sly01g0022381	M3	NA	109	108	96	106	88	83	93	81	87	71
Sly01g0022391	M12	NA	1	1	1	5	2	4	2	3	1	1
Sly01g0022401	M3	NA	41	44	39	46	46	38	41	37	49	53
Sly01g0022411	M1	NA	24	23	24	66	12	10	8	8	1	1
Sly01g0022431	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0022441	M11	NA	12	13	14	26	26	12	14	14	41	37
Sly01g0022451	M19	PPR-like9	7	7	10	8	6	8	7	8	8	11
Sly01g0022461	M12	NA	6	6	8	7	6	8	7	8	9	10
Sly01g0022471	M12	NA	1	2	2	1	2	4	4	6	3	5
Sly01g0022481	M9	NA	277	262	296	348	414	330	414	336	339	468
Sly01g0022491	M1	NA	19	18	18	18	21	9	8	11	19	22
Sly01g0022501	M12	NA	10	11	12	16	17	15	16	15	19	17
Sly01g0022511	M11	NA	17	18	22	23	24	25	23	30	30	28
Sly01g0022521	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0022571	M11	NA	14	13	16	19	22	24	23	28	43	51
Sly01g0022581	M12	NA	14	13	11	285	401	15	18	23	573	418
Sly01g0022591	M12	NA	49	53	51	65	82	64	62	67	57	64
Sly01g0022611	M12	PPR-like40	11	12	13	17	14	14	14	15	21	18
Sly01g0022621	M11	NA	134	127	248	510	981	337	269	392	379	761
Sly01g0022631	M14	NA	35	30	33	27	27	32	27	32	26	26
Sly01g0022651	M12	NA	3	3	1	5	5	11	8	7	1	1
Sly01g0022661	M3	NA	284	390	239	132	255	201	250	109	44	141
Sly01g0022671	M11	NA	22	22	24	30	31	30	34	36	39	44
Sly01g0022691	M12	NA	28	26	30	27	18	30	33	33	22	16
Sly01g0022701	M12	SlHP2	32	32	30	14	15	77	58	54	12	4
Sly01g0022731	M3	NA	4	5	11	1	0	8	4	1	0	0
Sly01g0022741	M1	NA	1	1	1	1	1	0	0	1	0	0
Sly01g0022751	M11	NA	19	17	22	51	62	31	31	39	44	60
Sly01g0022761	M11	NA	5	3	4	1	1	8	7	7	1	1
Sly01g0022781	M11	NA	22	21	24	24	27	28	26	32	29	26
Sly01g0022801	M3	NA	104	141	70	56	40	45	68	29	36	39
Sly01g0022811	M2	NA	294	377	223	159	131	123	213	89	124	134
Sly01g0022831	M12	NA	17	16	14	13	14	20	18	17	20	27
Sly01g0022841	M11	NA	20	18	18	16	16	24	19	24	21	23
Sly01g0022851	M14	NA	77	72	89	55	51	82	62	80	42	40
Sly01g0022861	M21	NA	3	2	3	2	1	2	1	2	0	1
Sly01g0022871	M1	NA	34	35	40	74	116	28	25	33	65	118
Sly01g0022881	M11	NA	9	9	10	10	5	11	10	10	7	3
Sly01g0022901	M3	NA	8	8	6	3	4	4	4	3	4	4
Sly01g0022921	M22	NA	1	1	1	0	0	1	0	1	0	0
Sly01g0022931	M3	NA	19	20	16	17	15	18	19	14	12	8
Sly01g0022941	M1	NA	3	3	2	1	1	1	1	1	1	1
Sly01g0022951	M18	NA	7	7	8	11	8	8	7	8	10	7
Sly01g0023011	M11	NA	15	16	17	22	25	27	23	28	15	18
Sly01g0023031	M1	NA	12	10	12	13	24	8	6	9	9	17
Sly01g0023041	M18	NA	29	31	36	46	55	52	41	57	47	63
Sly01g0023051	M12	NA	62	66	69	75	66	78	76	73	64	67
Sly01g0023061	M12	NA	82	80	73	97	109	86	91	89	115	137
Sly01g0023071	M12	NA	35	38	40	86	48	110	114	97	176	151
Sly01g0023081	M3	signalling protein kina	65	70	63	49	81	61	62	52	51	89
Sly01g0023091	M9	NA	75	74	62	68	383	91	123	94	381	1027
Sly01g0023101	M21	KAO1-like	8	6	9	13	44	8	4	9	1	2
Sly01g0023111	M12	NA	137	101	196	82	79	520	543	660	136	111
Sly01g0023131	M11	NA	70	65	71	118	163	88	91	100	124	172
Sly01g0023141	M13	NA	36	32	40	38	46	38	37	48	46	61
Sly01g0023211	M12	NA	2	2	2	3	4	3	3	3	6	6
Sly01g0023221	M11	NA	454	440	510	371	319	460	439	539	444	398
Sly01g0023231	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0023241	M12	NA	34	37	37	55	57	53	59	54	49	51
Sly01g0023251	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly01g0023261	M22	NA	17	19	16	19	36	21	18	18	34	61
Sly01g0023291	M12	SlXTH5	235	328	382	942	1143	891	1008	1172	1917	2083
Sly01g0023301	M2	NA	54	57	53	86	111	51	62	52	103	112
Sly01g0023341	M11	NA	2	2	3	3	2	2	2	3	3	2
Sly01g0023351	M11	NA	22	17	19	21	17	19	21	25	26	19
Sly01g0023391	M11	NA	70	61	64	63	63	74	72	81	108	103
Sly01g0023401	M11	NA	2	1	3	1	0	5	5	5	4	7
Sly01g0023411	M12	NA	15	14	14	2	2	47	34	35	17	18
Sly01g0023421	M11	NA	9	10	11	2	1	34	24	28	11	10
Sly01g0023451	M1	NA	3	4	4	2	3	2	2	3	4	4
Sly01g0023461	M12	NA	23	22	24	36	38	38	38	49	64	57
Sly01g0023481	M11	NA	4	5	5	5	5	5	6	5	5	6
Sly01g0023491	M19	NA	5	6	5	5	5	5	5	5	5	4
Sly01g0023501	M4	NA	111	71	125	139	1621	86	61	47	36	200
Sly01g0023521	M1	NA	10	7	10	16	115	2	1	2	2	26
Sly01g0023531	M11	NA	3	3	3	4	3	4	3	4	3	2
Sly01g0023541	M12	NA	9	8	8	12	16	9	8	9	14	18
Sly01g0023551	M2	NA	19	21	18	28	77	14	17	14	84	120
Sly01g0023561	M3	NA	107	130	128	93	72	127	135	69	24	26
Sly01g0023571	M18	NA	6	7	9	7	6	13	10	13	12	11

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0371811	M3	SlERF.D9	2	3	2	0	0	1	1	1	1	1
Sly06g0371821	M12	NA	22	23	20	27	30	31	30	33	39	50
Sly06g0371831	M1	NA	21	24	22	23	28	20	21	21	25	29
Sly06g0371841	M18	NA	40	37	44	34	22	45	38	47	19	12
Sly06g0371851	M11	NA	60	56	75	109	79	131	117	164	121	103
Sly06g0371861	M1	NA	18	23	28	48	19	13	13	13	3	1
Sly06g0371871	M1	NA	3	5	4	5	2	1	1	1	1	1
Sly06g0371881	M1	NA	11	14	22	155	174	8	10	22	307	407
Sly06g0371891	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly06g0371901	M19	NA	44	44	46	47	49	43	39	44	46	46
Sly06g0371931	M12	NA	1	1	1	0	0	1	1	1	1	1
Sly06g0371941	M11	NA	12	7	12	3	1	21	15	18	3	1
Sly06g0371951	M3	NA	54	86	24	8	3	8	11	3	1	1
Sly06g0371961	M1	NA	6	8	7	16	12	5	5	4	5	2
Sly06g0371971	M11	NA	10	10	10	8	7	14	13	12	5	8
Sly06g0371981	M12	NA	4	4	3	8	9	6	6	8	7	2
Sly06g0371991	M1	NA	2	1	1	1	1	1	1	1	0	1
Sly06g0372001	M1	NA	428	405	382	296	248	309	334	313	301	291
Sly06g0372011	M1	NA	209	215	214	190	179	176	176	174	199	199
Sly06g0372021	M11	NA	20	19	28	45	54	29	26	36	19	20
Sly06g0372031	M10	NA	2	2	1	2	2	5	6	2	2	1
Sly06g0372071	M1	NA	2	1	2	1	1	1	0	0	1	1
Sly06g0372081	M4	NA	4	4	4	6	5	5	5	5	5	3
Sly06g0372091	M1	NA	594	552	527	353	262	348	397	328	362	277
Sly06g0372141	M23	NA	2	1	1	0	1	3	2	1	1	1
Sly06g0372151	M12	NA	703	613	820	685	404	1622	1297	1887	1032	531
Sly06g0372161	M6	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0372181	M1	NA	2	1	3	1	1	1	1	1	0	1
Sly06g0372191	M11	NA	126	112	130	187	209	196	181	219	169	211
Sly06g0372201	M12	NA	55	54	57	83	118	55	61	60	88	137
Sly06g0372211	M3	NA	79	89	59	19	17	62	64	39	15	9
Sly06g0372221	M12	NA	53	63	56	92	104	68	72	73	167	137
Sly06g0372241	M23	NA	5	4	3	3	5	55	8	24	6	6
Sly06g0372251	M1	NA	5	5	5	3	4	3	3	2	1	2
Sly06g0372281	M22	NA	7	2	4	0	0	18	3	13	1	0
Sly06g0372291	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly06g0372301	M11	NA	11	13	16	54	53	15	14	20	29	20
Sly06g0372331	M3	NA	61	70	61	52	63	65	67	54	52	75
Sly06g0372351	M1	NA	3	4	4	5	3	1	2	1	1	5
Sly06g0372371	M8	NA	31	27	26	30	29	28	35	25	26	27
Sly06g0372401	M12	NA	4	4	5	6	10	6	7	6	6	11
Sly06g0372411	M23	NA	9	10	6	0	1	89	20	49	1	0
Sly06g0372421	M11	NA	9	9	9	8	9	10	9	10	9	8
Sly06g0372431	M12	NA	8	9	7	14	15	12	11	10	19	18
Sly06g0372441	M1	NA	6	5	4	3	2	3	3	3	2	1
Sly06g0372451	M14	NA	90	62	95	23	20	53	47	69	3	5
Sly06g0372461	M1	NA	17	17	16	13	12	18	14	16	12	11
Sly06g0372471	M22	NA	1	1	1	0	0	3	1	3	0	0
Sly06g0372481	M22	NA	1	1	1	1	1	3	1	3	0	0
Sly06g0372491	M11	NA	15	13	19	20	23	19	20	31	60	30
Sly06g0372501	M5	NA	20	22	14	47	48	22	21	15	10	38
Sly06g0372511	M3	NA	4	4	2	15	15	1	1	1	2	7
Sly06g0372521	M1	FUL1	176	205	186	668	1147	23	33	27	91	491
Sly06g0372531	M1	NA	65	67	54	82	87	36	36	34	35	42
Sly06g0372541	M13	NA	10	11	15	24	20	13	13	17	16	18
Sly06g0372571	M9	NA	105	115	85	36	37	168	239	142	45	46
Sly06g0372581	M19	NA	21	24	28	34	46	19	15	19	20	25
Sly06g0372651	M11	NA	51	45	52	66	93	46	49	55	88	101
Sly06g0372661	M19	NA	19	19	19	18	18	16	16	16	15	17
Sly06g0372671	M11	NA	13	15	14	13	13	15	14	17	13	15
Sly06g0372681	M16	NA	400	370	356	390	458	338	334	381	566	600
Sly06g0372691	M8	NA	26	24	21	29	19	25	27	21	20	16
Sly06g0372711	M1	NA	2	4	2	1	1	1	1	1	0	0
Sly06g0372731	M3	NA	39	42	35	35	31	36	37	39	35	30
Sly06g0372741	M10	NA	8	8	6	4	4	8	10	6	3	3
Sly06g0372751	M3	NA	89	125	62	76	131	40	57	32	20	59
Sly06g0372761	M1	NA	5	6	6	3	2	5	4	4	1	1
Sly06g0372811	M12	NA	5	5	7	4	3	13	12	14	4	2
Sly06g0372821	M1	NA	2	2	2	1	1	1	1	1	1	0
Sly06g0372831	M5	NA	3	7	2	1	0	4	4	1	0	1
Sly06g0372841	M11	NA	1	1	1	1	1	1	2	2	4	4
Sly06g0372851	M12	NA	2	2	2	3	4	3	3	5	13	13
Sly06g0372871	M1	SlPRR2	57	61	55	47	67	40	37	40	88	110
Sly06g0372881	M1	NA	3	3	3	3	2	2	2	2	3	2
Sly06g0372891	M3	NA	3	2	2	3	2	2	2	3	2	2
Sly06g0372901	M22	NA	4	2	2	1	1	12	3	7	1	1
Sly06g0372921	M12	ACTH	5	6	7	5	2	24	17	24	7	4
Sly06g0372931	M3	NA	20	19	15	5	8	10	12	11	8	8
Sly06g0372951	M11	NA	1	1	1	1	1	2	2	3	0	0
Sly06g0372961	M10	NA	5	13	9	0	1	14	31	5	1	1
Sly06g0372971	M11	NA	13	8	18	4	20	13	10	16	6	22
Sly06g0372981	M17	NA	61	55	57	48	53	54	44	56	47	57
Sly06g0372991	M3	NA	27	29	23	27	43	22	20	16	16	31
Sly06g0373001	M21	NA	3	2	4	1	1	5	0	2	0	0
Sly06g0373041	M9	NA	9	7	10	13	31	18	21	17	45	103
Sly06g0373051	M12	NA	4	4	5	3	7	5	5	5	9	23
Sly06g0373061	M9	NA	3	3	3	2	6	4	4	3	5	11
Sly06g0373071	M1	MYB30	33	38	41	11	5	6	2	3	1	1
Sly06g0373081	M1	NA	395	349	320	223	131	272	270	242	209	117
Sly06g0373111	M2	NRP2-like1	74	77	75	45	45	52	62	50	56	50
Sly06g0373191	M22	NA	2	1	1	1	1	6	1	3	1	1
Sly06g0373201	M22	NA	2	1	1	1	1	6	1	3	1	1
Sly06g0373211	M12	NA	430	337	324	361	306	538	518	634	636	670
Sly06g0373221	M12	NA	867	790	854	864	612	1187	1260	1428	1268	1110
Sly06g0373231	M1	NA	1	2	1	1	1	1	1	1	0	0
Sly06g0373241	M11	NA	79	73	95	127	131	115	105	120	91	82
Sly06g0373251	M3	NA	46	48	44	41	43	41	44	44	65	76
Sly06g0373261	M11	SlPL	1	1	1	1	1	1	1	1	1	1
Sly06g0373271	M11	isochorismate synthas	1	1	2	2	2	2	2	2	1	2
Sly06g0373281	M19	NA	46	48	45	44	40	46	44	45	45	39
Sly06g0373291	M3	NA	210	198	106	34	46	112	139	76	30	51
Sly06g0373311	M10	NA	54	61	37	7	3	137	152	80	14	6
Sly06g0373321	M12	NA	6	7	9	9	14	12	19	15	12	10
Sly06g0373331	M9	NA	2	2	3	3	4	4	5	3	4	3
Sly06g0373341	M12	NA	2	2	2	3	3	3	5	2	3	3
Sly06g0373351	M12	NA	2	1	2	2	2	3	3	2	2	1
Sly06g0373361	M18	NA	166	162	172	195	122	180	154	168	77	45
Sly06g0373371	M18	NA	7	8	7	10	11	9	7	8	11	11
Sly06g0373381	M19	NA	43	46	46	45	41	38	35	36	29	31
Sly06g0373401	M11	NA	60	62	66	68	64	75	73	83	94	113
Sly06g0373411	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly06g0373421	M1	NA	33	42	29	13	16	15	15	10	5	7
Sly06g0373431	M11	NA	71	66	74	82	125	76	74	89	116	155
Sly06g0373441	M12	NA	22	21	26	32	21	31	36	34	41	27
Sly06g0373471	M3	NA	69	72	52	80	60	59	56	40	40	46
Sly06g0373481	M8	NA	80	87	76	132	126	79	90	80	162	150
Sly06g0373491	M11	NA	2	1	2	1	0	16	8	20	0	0
Sly06g0373501	M11	NA	130	104	174	90	151	197	170	212	53	97
Sly06g0373511	M12	NA	10	11	9	1	1	193	105	170	1	1
Sly06g0373521	M3	NA	19	19	17	16	16	16	15	14	16	16
Sly06g0373531	M16	NA	23	20	21	21	20	16	18	19	23	25
Sly06g0373541	M11	NA	25	20	23	30	40	24	18	26	32	39
Sly06g0373551	M3	NA	59	68	26	4	2	23	31	6	1	2
Sly06g0373561	M1	NA	30	28	29	30	15	3	2	2	1	1
Sly06g0373581	M3	NA	2	2	3	6	10	2	2	2	13	11
Sly06g0373591	M3	NA	14	14	14	11	5	14	13	11	7	3
Sly06g0373601	M23	NA	1	1	1	0	1	1	1	1	1	1
Sly06g0373611	M11	NA	12	10	10	1	4	21	18	17	1	1
Sly06g0373621	M1	NA	9	10	8	5	4	7	8	9	8	6
Sly06g0373631	M19	NA	33	34	36	48	46	35	32	37	32	30
Sly06g0373641	M12	NA	9

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0023581	M1	NA	8	10	9	7	8	9	9	9	7	6
Sly01g0023591	M3	NAMT1	1	1	1	1	1	1	1	1	1	1
Sly01g0023601	M22	NA	1	0	1	0	1	1	0	1	0	0
Sly01g0023631	M22	NA	1	1	1	0	0	4	1	2	1	0
Sly01g0023641	M12	NA	9	7	10	11	12	11	12	12	16	11
Sly01g0023651	M9	NA	17	17	16	33	40	20	25	16	28	33
Sly01g0023671	M13	NA	10	9	13	9	10	12	9	12	15	18
Sly01g0023681	M1	NA	6	6	6	7	6	6	5	4	3	3
Sly01g0023691	M19	NA	23	25	26	32	40	26	21	28	29	33
Sly01g0023701	M1	NA	13	12	14	10	12	12	9	11	6	10
Sly01g0023711	M7	NA	77	75	64	77	95	71	76	72	112	130
Sly01g0023721	M11	NA	9	9	9	9	13	11	11	12	15	15
Sly01g0023731	M9	NA	15	16	16	24	21	17	18	16	25	19
Sly01g0023741	M11	NA	7	6	9	6	5	13	11	13	8	5
Sly01g0023751	M11	NA	10	11	16	37	41	18	17	25	35	23
Sly01g0023761	M3	LHP1-like1	100	98	84	77	80	89	87	83	46	65
Sly01g0023771	M11	NA	13	11	13	16	17	14	12	17	17	18
Sly01g0023781	M3	NA	56	61	55	54	51	53	55	50	61	53
Sly01g0023801	M3	NA	65	70	55	27	15	38	42	22	23	9
Sly01g0023811	M3	NA	2	3	2	2	2	1	2	2	2	2
Sly01g0023821	M1	NA	20	26	23	7	3	21	18	20	2	1
Sly01g0023881	M1	NA	20	18	16	37	41	11	11	12	44	45
Sly01g0023891	M3	NA	3	2	1	2	1	2	1	1	1	1
Sly01g0023911	M22	NA	1	1	1	1	0	2	1	2	1	0
Sly01g0023921	M3	GAD3	23	22	9	1	2	8	18	6	2	3
Sly01g0023931	M1	NA	154	159	159	175	160	134	131	123	111	139
Sly01g0023941	M1	NA	5	8	8	18	26	2	1	2	1	3
Sly01g0023971	M12	NA	9	5	6	1	1	23	15	17	1	1
Sly01g0023991	M1	NA	2	2	2	5	5	1	1	1	2	1
Sly01g0024001	M1	NA	1	2	2	5	5	1	1	1	1	1
Sly01g0024051	M15	NA	2	2	1	1	2	2	2	2	3	4
Sly01g0024071	M5	NA	25	25	17	10	7	22	21	20	9	11
Sly01g0024081	M10	NA	1	4	2	0	1	5	5	2	1	0
Sly01g0024091	M12	NA	1	1	1	2	2	2	1	2	4	2
Sly01g0024101	M1	NA	24	18	18	14	20	13	13	13	7	5
Sly01g0024111	M3	NA	102	93	82	47	57	69	78	55	36	39
Sly01g0024121	M18	NA	75	77	82	52	52	85	69	71	27	31
Sly01g0024131	M11	NA	15	13	18	20	24	21	16	26	23	30
Sly01g0024181	M1	NA	4	11	5	1	0	1	0	0	0	0
Sly01g0024191	M1	NA	2	5	2	1	0	1	0	1	0	0
Sly01g0024201	M1	NA	1	7	2	1	0	0	1	0	0	0
Sly01g0024221	M1	NA	2	11	2	1	0	1	0	0	0	0
Sly01g0024231	M19	NA	38	42	39	39	48	39	35	44	59	60
Sly01g0024241	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0024251	M3	NA	3	11	3	1	1	1	2	1	1	1
Sly01g0024261	M3	NA	50	55	37	35	36	34	34	32	29	30
Sly01g0024271	M3	NA	9	11	4	2	1	7	6	4	1	1
Sly01g0024281	M3	NA	27	28	22	14	18	16	18	13	13	17
Sly01g0024291	M11	NA	10	11	12	15	19	14	13	16	24	23
Sly01g0024301	M12	NA	12	11	12	15	24	14	17	16	21	32
Sly01g0024311	M3	NA	34	43	27	36	31	29	30	23	30	33
Sly01g0024321	M11	NA	44	47	48	56	57	55	50	53	58	54
Sly01g0024351	M18	NA	7	7	10	9	3	15	10	15	3	2
Sly01g0024361	M11	NA	3	4	6	4	2	7	7	9	2	1
Sly01g0024371	M12	NA	9	11	14	11	5	20	21	20	5	2
Sly01g0024381	M11	NA	34	26	30	1	1	63	63	50	1	1
Sly01g0024391	M5	NA	47	50	39	38	34	51	49	41	31	30
Sly01g0024401	M1	NA	14	14	11	11	13	8	8	7	10	10
Sly01g0024411	M11	NA	50	43	52	4	1	128	94	93	2	1
Sly01g0024461	M12	NA	7	9	5	2	2	15	18	8	3	2
Sly01g0024471	M10	NA	22	29	13	15	10	25	37	15	47	10
Sly01g0024481	M3	NA	9	10	4	1	1	7	9	3	3	1
Sly01g0024491	M6	NA	14	17	7	1	1	18	30	5	1	1
Sly01g0024501	M10	NA	14	15	8	2	4	35	30	9	2	3
Sly01g0024511	M10	NA	18	27	19	3	10	49	65	13	2	2
Sly01g0024521	M11	NA	2	2	2	1	1	3	3	2	1	1
Sly01g0024541	M1	NA	42	47	43	21	22	34	32	30	18	18
Sly01g0024561	M6	NA	7	14	6	1	3	12	14	2	1	4
Sly01g0024571	M1	NA	74	77	70	65	88	51	50	45	63	72
Sly01g0024581	M1	NA	78	85	87	75	56	66	61	66	50	43
Sly01g0024611	M11	NA	10	9	9	7	5	11	10	15	9	8
Sly01g0024651	M14	NA	9	8	12	11	13	9	8	10	3	1
Sly01g0024671	M11	NA	23	17	17	1	1	35	31	30	1	1
Sly01g0024701	M3	NA	32	32	25	27	27	18	20	16	16	20
Sly01g0024711	M11	NA	51	50	73	56	33	52	58	80	36	33
Sly01g0024721	M13	NA	56	51	66	41	36	55	51	57	36	32
Sly01g0024731	M5	NA	112	176	106	50	24	126	178	90	7	8
Sly01g0024761	M11	NA	218	232	216	189	198	232	229	235	253	268
Sly01g0024771	M11	NA	6	6	6	9	16	9	8	12	10	12
Sly01g0024781	M20	NA	7	4	15	0	0	6	3	5	0	0
Sly01g0024791	M20	NA	14	10	33	1	0	9	7	10	0	0
Sly01g0024801	M11	NA	2	2	2	1	1	3	2	2	1	1
Sly01g0024811	M11	NA	3	2	2	3	3	3	2	3	6	4
Sly01g0024821	M1	NA	31	30	35	43	42	24	23	25	35	28
Sly01g0024841	M1	NA	10	13	16	17	16	12	10	10	14	15
Sly01g0024851	M1	NA	26	24	25	34	32	18	18	19	30	30
Sly01g0024861	M3	NA	188	232	145	109	242	135	212	108	121	386
Sly01g0024871	M11	NA	3	3	5	7	9	6	5	7	9	13
Sly01g0024881	M11	NA	2	2	2	3	2	2	2	2	5	3
Sly01g0024891	M11	NA	421	414	491	545	547	492	537	657	1181	1329
Sly01g0024901	M18	NA	33	31	31	32	32	33	30	34	38	29
Sly01g0024911	M12	NA	1	1	1	1	3	1	1	1	2	5
Sly01g0024921	M18	NA	45	44	46	39	37	49	43	47	35	29
Sly01g0024931	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0024941	M8	NA	22	25	19	26	32	21	25	22	36	50
Sly01g0024961	M9	NA	113	151	108	89	42	395	470	309	56	58
Sly01g0024971	M9	NA	19	28	24	15	7	67	99	55	10	12
Sly01g0024981	M11	NA	54	52	62	64	71	66	60	77	79	82
Sly01g0024991	M11	NA	19	15	23	20	19	42	37	54	32	18
Sly01g0025011	M11	NA	2	1	2	1	1	5	3	5	1	1
Sly01g0025021	M1	NA	14	17	11	4	2	7	7	7	1	1
Sly01g0025031	M12	NA	14	14	19	14	14	24	25	32	19	23
Sly01g0025061	M11	NA	240	223	231	290	259	290	291	315	211	224
Sly01g0025101	M22	NA	1	1	1	1	1	2	1	2	0	0
Sly01g0025111	M1	NA	193	199	195	216	158	113	131	119	193	136
Sly01g0025121	M1	NA	5	5	16	7	3	2	1	2	5	4
Sly01g0025131	M1	NA	9	8	8	10	13	6	5	7	13	14
Sly01g0025141	M14	NA	5	3	6	7	9	4	4	4	7	7
Sly01g0025151	M11	NA	3	3	4	6	3	5	5	5	4	2
Sly01g0025161	M23	NA	192	160	176	73	57	193	199	148	37	51
Sly01g0025171	M2	NA	23	24	21	19	23	22	23	22	22	26
Sly01g0025181	M19	NA	52	44	43	27	27	47	40	40	13	10
Sly01g0025191	M12	CCD1A	17	16	18	15	15	27	25	28	40	40
Sly01g0025201	M11	SlCCD1B	119	106	131	163	313	166	165	214	316	450
Sly01g0025241	M11	NA	26	26	30	37	42	43	39	49	49	58
Sly01g0025251	M2	NA	26	29	28	37	36	25	30	27	50	49
Sly01g0025261	M14	NA	18	17	20	17	20	20	16	20	21	25
Sly01g0025301	M19	NA	18	15	17	16	13	21	9	21	16	11
Sly01g0025311	M12	NA	16	16	17	14	22	17	16	17	34	57
Sly01g0025321	M1	NA	14	14	14	13	16	13	13	15	24	30
Sly01g0025331	M12	NA	7	7	9	7	7	9	11	11	15	18
Sly01g0025341	M12	NA	2	2	2	2	3	3	2	2	3	5
Sly01g0025351	M11	NA	15	13	17	23	27	21	18	28	38	45
Sly01g0025361	M11	NA	12	11	13	17	19	18	15	20	28	26
Sly01g0025371	M11	NA	12	11	17	21	24	17	18	24	30	30
Sly01g0025381	M11	NA	19	20	23	29	38	31	31	39	45	46
Sly01g0025391	M18	NA	35	37	40	51	52	47	41	52	77	78
Sly01g0025401	M18	NA	13	17	19	18	19	19	14	20	21	17
Sly01g0025411	M19	NA	15	19	22	25	22	25	18	27	27	26
Sly01g0025421	M11	NA	15	16	14	14	10	19	15	22	27	16
Sly01g0025431	M19	NA	4	5	5	6	3	6	4	6	7	3
Sly01g0025441	M18	NA	27	25	27	29	34	35	29	39	32	32
Sly01g0025451	M1	NA	6	7	7	5	2	3	2	3	2	1
Sly01g0025471	M1	NA	36	35	38	71	82	35	30	34	44	71

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0373691	M11	NA	54	54	68	69	107	64	56	72	71	99
Sly06g0373701	M11	NA	22	19	20	23	36	24	21	24	27	47
Sly06g0373711	M2	NA	17	16	15	17	17	14	16	13	19	17
Sly06g0373721	M3	NA	16	17	15	16	20	13	15	13	19	20
Sly06g0373741	M2	NA	33	34	28	23	12	20	27	17	16	6
Sly06g0373751	M11	NA	149	155	165	225	274	186	199	210	293	319
Sly06g0373761	M4	NA	2	2	2	2	2	2	1	2	12	18
Sly06g0373771	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly06g0373781	M1	NA	32	29	35	54	65	22	20	27	33	41
Sly06g0373801	M14	NA	18	21	33	38	18	17	15	21	4	2
Sly06g0373811	M1	NA	11	11	11	16	12	6	8	9	7	5
Sly06g0373841	M3	NA	171	153	112	109	102	101	110	94	128	128
Sly06g0373851	M3	NA	3	4	2	1	1	2	4	1	1	1
Sly06g0373861	M1	NA	33	31	22	8	4	15	14	11	2	1
Sly06g0373871	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0373891	M22	DMS11-like2	1	1	1	2	5	3	1	2	1	2
Sly06g0373911	M12	NA	1	2	1	1	1	2	1	1	1	0
Sly06g0373921	M1	NA	6	6	6	3	2	6	6	5	2	2
Sly06g0373941	M1	NA	4	3	3	3	4	2	2	1	2	4
Sly06g0373951	M1	NA	2	2	2	1	2	1	1	1	1	1
Sly06g0373961	M12	NA	8	8	9	7	9	9	10	10	9	11
Sly06g0374011	M11	NA	8	8	11	13	20	10	9	12	11	21
Sly06g0374021	M1	SlHDA3	65	58	64	53	66	45	47	49	54	60
Sly06g0374031	M1	NA	5	4	4	1	1	7	1	3	0	0
Sly06g0374061	M16	NA	676	571	573	479	344	558	526	612	519	509
Sly06g0374071	M1	NA	2	1	2	3	1	1	1	0	1	0
Sly06g0374091	M3	NA	14	12	11	42	36	11	12	10	49	66
Sly06g0374111	M12	NA	83	85	86	120	147	86	84	92	170	182
Sly06g0374121	M9	NA	23	33	22	44	96	84	132	52	62	134
Sly06g0374131	M11	NA	46	39	56	100	171	70	56	84	100	182
Sly06g0374141	M3	NA	20	22	18	23	22	18	20	20	35	25
Sly06g0374151	M3	NA	56	77	29	5	10	16	23	5	1	3
Sly06g0374171	M13	NA	186	87	331	132	222	218	158	329	141	81
Sly06g0374181	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly06g0374201	M1	NA	17	18	19	18	19	16	16	16	18	23
Sly06g0374211	M11	NA	27	25	33	36	41	36	26	35	32	32
Sly06g0374221	M1	NA	187	174	184	134	127	122	140	120	115	119
Sly06g0374231	M3	NA	292	273	288	179	165	217	244	202	190	166
Sly06g0374241	M12	NA	41	38	41	27	24	71	80	85	27	19
Sly06g0374251	M11	NA	16	17	16	16	15	19	19	22	16	13
Sly06g0374261	M16	NA	76	64	64	82	50	62	67	62	58	43
Sly06g0374271	M13	NA	238	205	255	568	711	224	240	251	402	488
Sly06g0374311	M12	NA	5	5	5	4	2	6	6	6	3	1
Sly06g0374321	M11	NA	19	18	24	41	42	35	32	41	61	43
Sly06g0374341	M3	NA	8	8	7	7	9	8	7	8	11	9
Sly06g0374351	M3	NA	67	77	50	31	35	39	52	84	25	63
Sly06g0374361	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0374371	M12	NA	4	4	6	17	17	9	7	9	12	13
Sly06g0374381	M12	NA	4	3	4	14	17	6	6	5	10	16
Sly06g0374391	M3	NA	567	635	429	559	459	439	666	394	631	539
Sly06g0374401	M6	NA	5	7	5	6	5	6	9	5	10	5
Sly06g0374411	M1	NA	79	58	86	63	72	58	38	58	26	23
Sly06g0374431	M11	NA	53	50	61	49	43	61	51	65	47	51
Sly06g0374451	M12	NA	8	8	6	7	5	8	9	9	5	3
Sly06g0374471	M22	NA	2	2	2	3	2	3	2	2	2	2
Sly06g0374501	M11	NA	26	28	26	23	40	39	37	37	22	34
Sly06g0374511	M3	NA	319	307	276	240	186	187	220	163	213	162
Sly06g0374521	M22	NA	39	8	14	1	1	82	19	50	4	1
Sly06g0374531	M1	NA	23	21	20	18	23	16	17	19	28	24
Sly06g0374541	M11	NA	34	32	35	38	40	38	37	42	45	42
Sly06g0374551	M3	NA	12	12	11	10	9	11	11	9	11	11
Sly06g0374561	M9	NA	8	8	7	19	8	10	10	7	3	1
Sly06g0374571	M3	NA	29	28	25	31	26	25	26	25	31	28
Sly06g0374671	M3	NA	2	2	1	0	0	1	1	0	0	0
Sly06g0374681	M1	NA	3	2	2	0	0	1	1	0	0	0
Sly06g0374691	M11	NA	1	1	1	0	0	2	1	1	0	0
Sly06g0374701	M3	NA	47	49	39	24	23	34	35	29	33	30
Sly06g0374731	M11	NA	3	1	1	0	1	3	2	5	0	0
Sly06g0374771	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly06g0374801	M12	NA	7	8	8	11	11	9	8	9	10	10
Sly06g0374811	M1	NA	30	28	24	16	16	17	18	16	17	13
Sly06g0374831	M1	NA	107	95	100	97	77	72	56	65	40	35
Sly06g0374841	M1	NA	1	1	1	2	1	1	1	1	1	0
Sly06g0374861	M10	NA	3	3	3	8	22	5	6	2	14	41
Sly06g0374871	M12	NA	5	4	4	3	4	8	7	7	6	6
Sly06g0374901	M12	NA	6	6	6	5	3	7	7	6	7	6
Sly06g0374911	M11	NA	41	38	45	41	26	49	37	56	39	19
Sly06g0374961	M4	NA	10	6	11	21	120	8	6	8	29	135
Sly06g0374971	M1	NA	53	43	46	54	51	38	43	39	40	39
Sly06g0375031	M3	NA	53	92	29	2	1	13	21	3	1	1
Sly06g0375041	M11	NA	26	25	32	29	27	59	58	73	32	26
Sly06g0375061	M3	NA	472	436	401	293	241	310	347	293	330	265
Sly06g0375071	M12	NA	6	6	7	11	12	8	7	7	12	14
Sly06g0375081	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0375091	M2	NA	1	2	3	1	1	1	2	4	3	4
Sly06g0375101	M12	NA	3	2	1	27	6	4	3	3	1	0
Sly06g0375121	M3	NA	8	7	2	1	1	4	2	1	1	0
Sly06g0375141	M1	NA	48	44	53	63	38	40	40	41	33	27
Sly06g0375151	M11	NA	53	49	51	64	52	58	56	63	72	69
Sly06g0375171	M2	NA	51	47	41	42	34	32	38	28	42	35
Sly06g0375181	M3	NA	46	50	31	14	12	32	33	20	17	12
Sly06g0375201	M1	NA	2	1	1	1	0	1	1	1	1	0
Sly06g0375231	M12	SAUR61	2	2	6	12	10	17	22	25	126	96
Sly06g0375241	M11	NA	14	15	14	2	1	20	19	15	1	1
Sly06g0375251	M12	NA	12	13	5	1	1	27	37	13	4	3
Sly06g0375261	M3	HVA22E	10	21	7	27	42	4	10	4	4	3
Sly06g0375271	M3	NA	9	8	8	4	3	8	9	8	4	5
Sly06g0375291	M21	NA	25	15	26	6	2	19	7	12	1	1
Sly06g0375301	M11	NA	6	4	7	9	7	10	9	14	7	3
Sly06g0375311	M5	NA	26	25	20	23	21	24	27	23	24	27
Sly06g0375321	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly06g0375331	M2	NA	25	22	17	9	8	12	12	6	9	10
Sly06g0375341	M2	NA	9	11	9	9	14	7	9	8	22	34
Sly06g0375351	M12	NA	1	1	1	12	19	2	2	3	215	234
Sly06g0375361	M3	NA	9	9	10	19	27	6	9	9	102	126
Sly06g0375381	M11	NA	5	5	5	6	6	6	6	8	10	8
Sly06g0375391	M2	NA	24	25	23	22	25	23	26	21	27	29
Sly06g0375401	M12	NA	16	17	19	28	36	15	18	19	43	35
Sly06g0375421	M18	NA	13	13	12	12	12	13	12	13	12	11
Sly06g0375431	M12	NA	91	80	112	161	53	289	317	488	204	84
Sly06g0375441	M12	NA	1150	1004	1702	2742	2088	3299	3894	5623	4953	2352
Sly06g0375471	M10	NA	1	1	1	1	2	1	1	1	1	1
Sly06g0375481	M9	NA	1	1	1	1	1	2	3	1	1	1
Sly06g0375491	M1	NA	1	1	1	1	0	1	1	1	0	0
Sly06g0375521	M11	NA	12	11	13	13	12	13	11	13	16	14
Sly06g0375541	M1	NA	1	2	1	1	2	1	1	1	1	2
Sly06g0375551	M1	NA	6	6	7	4	8	5	4	6	6	9
Sly06g0375561	M3	NA	46	44	33	39	42	24	28	29	64	57
Sly06g0375571	M12	NA	1	1	1	0	0	1	1	1	2	2
Sly06g0375601	M12	NA	23	24	24	20	17	29	33	29	23	23
Sly06g0375611	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0375631	M3	NA	65	86	42	45	103	47	73	38	50	126
Sly06g0375641	M1	NA	95	76	69	82	99	43	49	56	93	45
Sly06g0375661	M3	NA	30	28	3	1	1	6	22	6	5	17
Sly06g0375671	M11	NA	45	37	53	74	69	76	58	100	45	64
Sly06g0375691	M12	NA	43	38	26	18	6	57	48	39	11	5
Sly06g0375701	M3	NA	30	30	26	20	15	21	25	19	18	15
Sly06g0375711	M1	NA	5	6	4	5	4	3	2	4	2	2
Sly06g0375721	M1	NA	17	16	16	18	11	15	16	15	7	4
Sly06g0375731	M22	NA	1	1	1	2	3	2	1	1	1	1
Sly06g0375741	M12	NA	37	37	40	42	53	41	44	43	61	70
Sly06g0375751	M1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0025491	M1	NA	46	48	40	37	41	38	36	35	25	25
Sly01g0025501	M22	NA	1	1	1	1	0	1	1	1	0	1
Sly01g0025521	M11	NA	32	31	39	49	71	59	62	72	65	100
Sly01g0025531	M3	NA	41	39	28	25	22	22	23	19	17	15
Sly01g0025541	M1	NA	40	45	45	8	3	32	29	31	2	1
Sly01g0025551	M1	NA	48	48	47	49	45	43	40	46	48	59
Sly01g0025561	M12	SMT1	57	60	64	133	125	96	122	116	201	213
Sly01g0025571	M3	NA	15	32	18	9	6	7	9	4	4	2
Sly01g0025581	M10	NA	3	16	8	2	23	19	29	9	1	22
Sly01g0025591	M12	NA	19	37	6	1	3	34	42	35	1	6
Sly01g0025601	M12	NA	22	20	24	19	17	22	23	21	11	10
Sly01g0025611	M11	NA	20	19	19	24	19	24	21	23	17	13
Sly01g0025621	M9	NA	395	406	321	509	939	435	634	468	894	1087
Sly01g0025631	M10	NA	1	3	3	1	1	2	4	2	1	1
Sly01g0025641	M11	ADH	61	62	63	117	103	60	61	67	109	106
Sly01g0025651	M12	NA	30	27	30	34	39	34	38	39	41	47
Sly01g0025661	M15	NA	3	3	2	2	3	2	3	3	5	6
Sly01g0025671	M1	NA	39	40	39	25	29	32	33	31	29	36
Sly01g0025681	M13	NA	34	21	41	82	133	34	33	53	96	106
Sly01g0025741	M11	NA	27	28	38	55	67	35	30	44	64	66
Sly01g0025751	M11	NA	89	77	114	127	131	163	132	210	148	153
Sly01g0025761	M1	NA	1	1	1	1	0	1	0	1	0	1
Sly01g0025771	M1	NA	1	1	1	1	0	1	0	1	0	0
Sly01g0025791	M1	NA	1	1	1	1	0	1	0	0	0	0
Sly01g0025821	M1	NA	2	1	2	1	0	1	1	1	0	0
Sly01g0025831	M1	NA	12	10	16	4	1	5	3	5	1	0
Sly01g0025841	M1	NA	55	44	54	2	1	8	4	4	1	0
Sly01g0025851	M3	NA	40	43	21	1	1	8	9	2	1	1
Sly01g0025861	M2	NA	80	92	76	12	2	53	56	25	2	1
Sly01g0025891	M1	NA	4	4	5	2	1	3	3	3	1	1
Sly01g0025901	M1	NA	5	5	7	2	1	5	5	5	1	1
Sly01g0025911	M1	NA	126	132	71	6	3	14	13	9	2	1
Sly01g0025921	M3	NA	4	5	3	4	5	3	5	3	7	7
Sly01g0025931	M3	NA	10	12	9	5	2	5	6	4	2	1
Sly01g0025941	M3	NA	37	37	32	22	16	22	26	20	29	18
Sly01g0025951	M1	NA	32	30	36	70	102	24	19	26	25	27
Sly01g0025961	M17	NA	162	153	168	163	160	138	128	160	167	156
Sly01g0025971	M1	NA	22	20	26	23	24	14	12	15	15	23
Sly01g0025981	M22	NA	1	1	0	1	1	1	1	1	0	0
Sly01g0025991	M12	NA	0	1	1	4	2	1	2	2	30	5
Sly01g0026001	M12	NA	3	7	12	247	92	43	93	164	558	204
Sly01g0026021	M12	NA	1	1	1	2	1	9	11	10	15	7
Sly01g0026041	M12	NA	6	6	8	8	28	11	15	27	24	78
Sly01g0026051	M12	NA	47	47	56	64	73	82	84	97	86	58
Sly01g0026061	M12	NA	9	9	11	12	14	17	16	17	15	9
Sly01g0026071	M3	NA	45	40	36	25	24	40	38	38	28	29
Sly01g0026081	M23	NA	1	1	1	1	1	2	1	1	1	1
Sly01g0026111	M3	NA	134	142	132	154	127	125	128	108	101	87
Sly01g0026121	M12	NA	4	6	6	12	22	8	12	10	23	34
Sly01g0026131	M15	NA	159	140	126	171	183	138	143	134	161	168
Sly01g0026141	M1	NA	3	3	3	5	9	3	3	3	7	10
Sly01g0026151	M12	NA	4	4	4	5	6	6	5	6	5	5
Sly01g0026161	M1	NA	110	112	115	83	75	96	104	94	86	81
Sly01g0026171	M1	SIPPH	25	24	26	101	362	18	18	18	154	352
Sly01g0026181	M19	NA	41	43	60	49	26	43	39	44	48	61
Sly01g0026211	M13	NA	3	3	3	3	4	2	3	4	4	4
Sly01g0026221	M1	NA	22	23	26	30	37	19	19	20	34	41
Sly01g0026231	M3	NA	21	24	15	10	7	18	21	13	8	7
Sly01g0026241	M1	SlCKX2	3	3	2	1	1	1	1	1	1	0
Sly01g0026251	M1	AO4-like	23	25	23	25	24	16	16	16	16	16
Sly01g0026261	M12	AAO1-like1	2	2	2	1	1	4	5	4	4	4
Sly01g0026311	M11	NA	11	12	15	24	22	13	11	16	25	27
Sly01g0026321	M11	NA	14	13	14	28	28	15	15	17	34	38
Sly01g0026331	M1	NA	22	20	27	8	10	11	12	10	5	5
Sly01g0026391	M3	NA	12	12	9	13	19	11	12	9	9	16
Sly01g0026401	M1	NA	4	4	3	2	2	2	2	1	1	1
Sly01g0026411	M1	NA	4	4	2	1	2	1	2	1	1	0
Sly01g0026421	M1	NA	3	3	3	1	2	2	2	1	1	0
Sly01g0026431	M12	NA	18	16	21	32	38	19	27	24	35	43
Sly01g0026451	M1	NA	233	237	208	190	151	180	180	168	175	170
Sly01g0026461	M11	NA	1	2	2	1	1	2	3	2	1	1
Sly01g0026471	M1	NA	7	7	7	10	3	5	5	4	8	3
Sly01g0026481	M1	NA	17	18	22	1027	461	1	1	2	795	406
Sly01g0026491	M2	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0026501	M3	NA	5	4	4	3	2	4	4	4	3	1
Sly01g0026511	M9	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0026531	M12	NA	4	6	5	5	5	6	10	7	4	4
Sly01g0026541	M12	NA	13	15	19	26	23	31	34	40	23	36
Sly01g0026551	M11	NA	9	8	7	7	6	10	8	9	3	6
Sly01g0026561	M11	NA	21	20	26	25	21	36	35	42	22	18
Sly01g0026571	M2	NA	127	131	86	48	22	63	100	61	33	20
Sly01g0026581	M3	NA	3	4	3	4	4	2	3	2	5	3
Sly01g0026601	M3	NA	17	17	11	5	3	12	16	10	5	3
Sly01g0026611	M3	NA	104	112	85	92	89	86	101	73	82	92
Sly01g0026621	M1	NA	9	11	8	2	1	2	1	1	1	1
Sly01g0026641	M5	NA	43	44	29	26	21	36	51	25	17	17
Sly01g0026651	M7	NA	158	198	130	135	174	170	310	159	148	353
Sly01g0026661	M12	NA	56	52	47	63	65	55	58	55	58	57
Sly01g0026681	M12	NA	15	18	19	175	176	31	67	89	875	595
Sly01g0026691	M11	NA	12	11	15	9	4	21	18	25	13	5
Sly01g0026701	M12	NA	102	92	91	160	251	150	155	134	208	309
Sly01g0026711	M12	NA	1	1	1	1	1	6	6	6	2	1
Sly01g0026721	M22	NA	1	1	1	1	1	2	1	1	1	1
Sly01g0026741	M11	NA	23	21	23	22	27	25	22	28	34	37
Sly01g0026751	M12	NA	26	25	26	18	10	49	43	40	8	4
Sly01g0026761	M11	NA	320	235	322	191	141	453	514	496	172	78
Sly01g0026771	M18	NA	4	4	5	4	4	7	5	6	4	3
Sly01g0026781	M12	NA	5	5	5	4	4	6	5	6	4	4
Sly01g0026791	M3	NA	21	32	26	45	73	20	24	20	34	40
Sly01g0026801	M1	NA	131	147	117	117	103	94	85	81	67	62
Sly01g0026811	M3	NA	26	27	22	19	18	22	28	20	26	30
Sly01g0026821	M18	NA	21	22	24	28	30	26	23	27	31	39
Sly01g0026831	M11	NA	49	48	52	53	55	52	50	64	74	86
Sly01g0026841	M3	NA	35	35	26	18	23	26	28	24	29	24
Sly01g0026851	M2	NA	7	7	7	7	5	7	7	6	5	5
Sly01g0026871	M11	gibberellin modificatio	31	37	47	72	69	55	58	71	138	121
Sly01g0026881	M1	NA	63	59	64	66	64	44	45	43	71	68
Sly01g0026911	M19	NA	50	52	45	53	50	47	37	42	38	38
Sly01g0026921	M3	NA	2	2	1	1	1	2	2	1	1	1
Sly01g0026931	M12	NA	11	9	8	5	7	12	10	11	6	5
Sly01g0026961	M12	SlCycU4;1	1	1	1	1	1	1	2	1	2	1
Sly01g0026971	M3	NA	29	28	23	27	16	25	25	17	43	32
Sly01g0026981	M14	NA	32	32	37	59	65	27	29	35	67	60
Sly01g0026991	M1	NA	13	18	20	5	1	5	5	4	1	1
Sly01g0027001	M1	NA	4	7	5	1	1	1	1	1	3	3
Sly01g0027011	M12	NA	13	13	14	18	23	15	15	15	21	27
Sly01g0027021	M12	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0027071	M11	NA	4	3	4	6	7	6	6	8	10	10
Sly01g0027081	M1	NA	1	1	1	1	1	1	1	1	2	3
Sly01g0027091	M16	NA	769	714	704	439	378	612	629	659	546	501
Sly01g0027101	M11	NA	30	25	39	30	38	60	48	64	38	34
Sly01g0027111	M12	NA	1	2	1	1	1	3	2	4	4	3
Sly01g0027161	M8	NA	5	6	5	3	4	6	6	5	4	5
Sly01g0027251	M3	NA	1	2	2	1	1	1	1	1	1	1
Sly01g0027271	M3	NA	2	2	1	1	1	2	1	2	1	1
Sly01g0027281	M12	NA	7	8	10	21	30	14	13	13	32	38
Sly01g0027291	M9	NA	72	69	74	80	84	78	101	80	87	100
Sly01g0027301	M11	NA	2	1	2	3	1	4	2	3	1	0
Sly01g0027311	M11	NA	201	177	197	240	280	197	174	232	199	230
Sly01g0027321	M12	NA	38	42	37	44	75	51	46	49	72	91
Sly01g0027331	M1	NA	13	14	12	7	3	8	7	6	4	5
Sly01g0027341	M3	PLA1 phospholipase A	1	1	1	1	1	1	1	1	1	1
Sly01g0027351	M14	NA	38	35	42	34	43	35	32	38	50	64
Sly01g0027361	M3	NA	39	41	40	34	30	38	37	37	28	22

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0375781	M11	NA	20	12	28	14	38	42	39	45	28	30
Sly06g0375791	M20	NA	481	358	442	171	111	362	309	353	136	125
Sly06g0375801	M11	NA	16	13	13	11	12	15	13	15	10	11
Sly06g0375811	M3	NA	8	8	7	5	2	7	7	8	5	3
Sly06g0375831	M11	NA	25	20	25	14	18	24	23	27	19	25
Sly06g0375841	M12	NA	24	22	26	29	18	34	34	33	34	24
Sly06g0375851	M12	NA	5	7	6	8	29	11	12	10	4	36
Sly06g0375861	M12	NA	1	1	1	1	2	2	2	1	0	1
Sly06g0375871	M11	NA	9	11	10	5	2	15	14	16	3	2
Sly06g0375881	M9	NA	59	63	60	67	59	69	89	73	78	73
Sly06g0375901	M11	NA	93	86	101	138	250	104	99	117	140	233
Sly06g0375921	M11	NA	6	3	9	4	2	16	15	24	4	2
Sly06g0375931	M1	NA	900	755	713	624	425	574	584	656	683	497
Sly06g0375941	M3	NA	481	430	388	347	361	317	353	293	388	364
Sly06g0375961	M1	NA	497	469	387	330	600	269	255	195	189	457
Sly06g0375971	M1	NA	147	143	154	122	109	103	99	102	104	115
Sly06g0375981	M3	NA	43	42	41	40	44	40	36	37	39	47
Sly06g0375991	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0376001	M12	NA	136	133	136	176	180	121	146	142	174	156
Sly06g0376011	M1	NA	427	403	414	316	240	279	318	276	321	288
Sly06g0376021	M3	NA	11	12	9	9	12	13	12	6	2	2
Sly06g0376031	M3	NA	38	38	35	37	49	30	32	29	37	42
Sly06g0376041	M12	NA	13	15	14	16	15	13	13	16	21	17
Sly06g0376051	M11	NA	11	10	11	13	10	11	11	11	10	6
Sly06g0376061	M12	NA	30	24	24	21	23	31	34	37	37	29
Sly06g0376071	M1	NA	959	828	805	651	374	648	649	723	814	415
Sly06g0376091	M12	NA	188	156	169	208	81	400	393	468	325	110
Sly06g0376101	M12	glutathione peroxidas	134	130	161	400	552	326	421	520	2257	1984
Sly06g0376111	M11	NA	25	23	29	50	74	38	35	42	42	53
Sly06g0376121	M12	NA	1	1	1	1	1	2	3	3	1	1
Sly06g0376131	M3	NA	11	10	10	13	16	10	9	9	12	14
Sly06g0376141	M3	NA	30	31	31	32	36	26	30	26	35	34
Sly06g0376151	M1	ORC2-like1	23	22	22	9	8	14	15	13	7	7
Sly06g0376161	M11	NA	15	13	15	27	34	15	14	15	31	47
Sly06g0376181	M11	AGO4B	88	77	115	80	66	139	100	131	56	62
Sly06g0376191	M19	NA	37	39	42	30	30	35	31	37	30	25
Sly06g0376291	M1	NA	79	75	74	61	56	73	64	70	55	59
Sly06g0376321	M1	SlCycB1;3	2	3	2	2	2	3	2	2	1	1
Sly06g0376331	M11	NA	41	35	38	35	24	37	38	43	44	31
Sly06g0376341	M19	CDKC;1-1	52	51	53	61	72	47	46	54	63	71
Sly06g0376351	M12	NA	2	2	2	1	1	7	6	7	3	3
Sly06g0376361	M12	NA	13	12	10	11	12	15	15	14	16	15
Sly06g0376371	M12	NA	4	3	3	3	1	8	8	8	2	1
Sly06g0376381	M11	NA	24	26	29	35	31	33	31	38	33	30
Sly06g0376391	M12	NA	8	7	7	5	4	9	9	9	4	3
Sly06g0376401	M11	NA	105	99	106	122	147	106	96	124	137	181
Sly06g0376431	M12	EIL1	136	142	113	76	86	157	152	126	80	248
Sly06g0376451	M3	EIL4	127	129	106	89	76	98	107	85	126	154
Sly06g0376461	M11	NA	56	54	67	91	82	171	149	194	239	244
Sly06g0376481	M12	NA	10	12	11	6	1	89	92	119	36	7
Sly06g0376491	M11	NA	68	60	68	72	87	70	68	76	72	84
Sly06g0376501	M11	NA	29	33	39	39	43	36	32	39	32	28
Sly06g0376511	M19	NA	27	29	33	34	32	35	25	33	24	19
Sly06g0376531	M1	NA	222	191	202	149	108	149	148	147	153	120
Sly06g0376541	M1	NA	250	226	189	172	140	137	135	134	160	132
Sly06g0376551	M12	NA	26	25	25	28	31	28	26	29	40	45
Sly06g0376561	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0376571	M10	CML38	13	30	14	1	2	57	138	35	4	3
Sly06g0376581	M10	NA	69	84	60	64	67	84	104	67	80	74
Sly06g0376591	M7	NA	9	15	6	6	23	12	21	6	4	20
Sly06g0376601	M3	NA	71	73	49	36	55	47	53	43	59	88
Sly06g0376611	M1	NA	118	100	103	133	167	90	89	84	146	177
Sly06g0376621	M1	NA	74	70	56	47	54	31	34	32	52	80
Sly06g0376631	M12	NA	111	97	122	247	240	192	189	223	234	248
Sly06g0376641	M1	NA	19	13	20	9	4	12	10	11	4	3
Sly06g0376651	M1	NA	305	286	390	660	288	5	1	2	7	6
Sly06g0376661	M12	NA	6	6	7	9	12	8	7	8	6	11
Sly06g0376671	M1	NA	12	10	10	6	3	7	6	9	1	3
Sly06g0376681	M11	NA	54	50	62	71	89	55	50	73	107	131
Sly06g0376691	M12	BSU	37	41	34	38	46	41	40	39	42	45
Sly06g0376701	M1	NA	92	96	101	138	80	41	42	42	31	23
Sly06g0376711	M1	NA	3	3	3	4	3	1	1	1	1	0
Sly06g0376721	M1	NA	77	72	47	29	14	6	7	4	3	1
Sly06g0376731	M12	NA	2	3	2	1	1	3	3	3	1	0
Sly06g0376741	M1	E2FA-like3	13	11	14	8	9	10	10	11	10	9
Sly06g0376761	M6	NA	26	68	31	8	111	36	67	34	5	153
Sly06g0376781	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0376791	M1	NA	11	8	9	7	8	8	6	8	5	8
Sly06g0376811	M1	NA	10	7	9	1	1	7	5	6	2	1
Sly06g0376821	M11	SlHDA6	24	20	28	29	28	26	24	30	43	41
Sly06g0376831	M11	DWARF5-like2	21	17	21	15	5	24	28	23	11	6
Sly06g0376851	M12	NA	2	3	3	2	2	10	12	8	4	2
Sly06g0376861	M1	NA	114	122	149	219	195	31	32	33	39	61
Sly06g0376871	M2	NA	14	15	14	14	15	14	14	12	17	18
Sly06g0376881	M6	NA	6	18	11	0	0	7	10	1	1	0
Sly06g0376931	M1	NAC60	1	1	2	2	4	1	1	1	1	1
Sly06g0376951	M11	NA	11	8	15	12	4	18	14	18	5	1
Sly06g0376961	M11	NA	77	37	90	48	11	275	221	332	95	6
Sly06g0376971	M12	NA	100	94	113	69	55	113	122	133	113	94
Sly06g0376981	M3	NA	54	55	52	47	51	53	52	49	60	58
Sly06g0377001	M9	cyc	2	5	3	4	2	11	15	7	13	3
Sly06g0377011	M12	NA	61	57	68	79	90	67	74	83	103	134
Sly06g0377021	M1	NA	591	292	846	3	2	15	8	9	8	5
Sly06g0377031	M3	NA	16	15	8	6	5	11	11	9	13	8
Sly06g0377061	M12	NA	118	102	123	243	302	154	185	259	706	824
Sly06g0377071	M3	NA	429	401	363	267	207	266	312	241	283	248
Sly06g0377081	M11	NA	16	15	18	16	10	19	18	20	13	10
Sly06g0377101	M12	NA	28	26	27	37	36	35	40	41	47	45
Sly06g0377141	M1	NA	4	3	4	3	2	3	2	2	1	1
Sly06g0377151	M1	NA	26	28	26	21	27	13	14	14	18	25
Sly06g0377161	M1	NA	20	54	53	15	1	2	1	1	2	1
Sly06g0377171	M1	NA	37	37	37	18	18	32	28	29	19	18
Sly06g0377191	M12	NA	2	2	2	2	2	2	2	3	4	6
Sly06g0377201	M3	jasmonoyl-amino acid	15	30	4	0	1	1	1	0	1	0
Sly06g0377211	M3	NA	572	524	512	367	282	375	449	374	385	310
Sly06g0377221	M18	NA	8	9	12	14	9	11	10	13	11	10
Sly06g0377231	M11	NA	12	13	12	16	17	13	15	15	16	20
Sly06g0377241	M3	NA	21	18	14	9	9	12	14	12	17	13
Sly06g0377251	M12	NA	11	12	12	10	14	13	12	12	14	13
Sly06g0377261	M15	NA	205	160	172	230	292	188	205	201	221	276
Sly06g0377271	M11	NA	468	420	422	575	546	484	514	546	457	513
Sly06g0377281	M1	NA	1	1	1	0	0	1	1	0	0	0
Sly06g0377291	M11	NA	7	7	9	7	7	18	15	22	9	5
Sly06g0377311	M6	NA	66	120	41	13	8	129	170	28	5	3
Sly06g0377321	M1	NA	1	2	1	1	1	1	1	1	0	0
Sly06g0377341	M3	NA	4	6	4	1	1	2	3	2	1	1
Sly06g0377391	M3	NA	10	13	10	9	15	8	10	8	6	25
Sly06g0377421	M3	NA	10	10	6	4	3	8	8	7	4	3
Sly06g0377431	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0377441	M3	NA	37	40	33	26	23	27	27	24	22	20
Sly06g0377461	M7	NA	32	63	21	7	10	33	69	22	5	30
Sly06g0377471	M22	NA	3	2	3	2	1	8	5	8	2	1
Sly06g0377481	M1	NA	20	20	20	13	12	17	16	17	20	19
Sly06g0377491	M1	NA	54	52	49	38	40	48	43	49	44	45
Sly06g0377501	M1	NA	9	5	6	105	220	2	3	2	151	339
Sly06g0377511	M11	NA	617	606	736	684	647	683	700	819	1073	1278
Sly06g0377521	M3	NA	5	3	2	1	1	2	2	2	1	1
Sly06g0377531	M11	NA	32	35	43	35	39	43	41	42	27	51
Sly06g0377541	M1	NA	36	41	62	80	71	5	4	5	49	114
Sly06g0377551	M1	NA	10	10	19	29	24	2	2	3	39	51
S

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0027371	M9	NA	11	6	5	1	1	10	9	6	1	1
Sly01g0027381	M19	NA	8	8	9	5	4	8	7	8	4	3
Sly01g0027391	M1	NA	10	10	9	7	7	9	8	9	7	6
Sly01g0027401	M1	NA	74	69	65	19	9	51	53	45	14	12
Sly01g0027411	M12	NA	45	47	48	57	63	54	57	58	78	76
Sly01g0027421	M2	NA	63	64	59	75	84	56	60	52	96	100
Sly01g0027431	M23	SIERF.B6	1	1	1	0	0	2	1	1	1	0
Sly01g0027441	M10	SIERF.B7	9	18	4	0	0	36	34	6	0	1
Sly01g0027451	M23	SIERF.B8	1	1	1	0	0	1	1	1	0	0
Sly01g0027491	M18	SIERF.B9	1	1	1	0	0	1	1	1	0	0
Sly01g0027511	M11	NA	61	37	30	4	2	81	155	121	47	4
Sly01g0027521	M11	NA	156	96	71	8	2	248	421	323	88	7
Sly01g0027541	M2	NA	11	13	12	13	12	10	12	9	9	11
Sly01g0027551	M19	NA	4	5	4	3	2	4	3	4	3	2
Sly01g0027561	M1	NA	5	6	5	3	3	5	4	4	4	3
Sly01g0027571	M12	NA	11	12	11	18	14	18	21	20	28	27
Sly01g0027581	M19	NA	19	20	20	20	18	20	18	20	12	9
Sly01g0027631	M3	NA	40	39	23	9	6	21	23	15	7	5
Sly01g0027641	M22	NA	2	1	2	1	1	4	2	3	1	1
Sly01g0027651	M1	NA	17	16	18	19	23	16	16	16	29	34
Sly01g0027661	M12	NA	5	5	9	13	5	30	22	33	5	5
Sly01g0027671	M1	NA	59	68	68	76	79	55	58	62	104	92
Sly01g0027681	M11	NA	36	34	34	30	28	43	39	44	38	44
Sly01g0027691	M11	NA	3	3	3	4	5	4	3	4	6	6
Sly01g0027701	M11	NA	33	30	31	48	54	34	31	38	62	56
Sly01g0027711	M1	NA	5	5	4	3	3	3	3	4	3	2
Sly01g0027721	M22	NA	3	0	2	0	0	17	1	10	0	0
Sly01g0027741	M3	NA	2	1	1	1	1	1	1	1	1	1
Sly01g0027761	M11	NA	100	100	123	238	291	142	128	187	349	353
Sly01g0027771	M3	SIERF.H4	4	3	2	1	1	2	1	2	0	1
Sly01g0027781	M12	NA	14	14	14	29	22	14	17	20	34	16
Sly01g0027791	M22	NA	1	1	1	1	1	1	1	2	1	0
Sly01g0027801	M11	NA	34	32	34	28	31	32	34	35	40	36
Sly01g0027811	M1	NA	4	2	4	0	0	1	1	1	1	0
Sly01g0027821	M11	NA	24	21	19	15	18	34	29	57	67	102
Sly01g0027831	M18	NA	86	95	108	122	137	98	89	104	108	112
Sly01g0027841	M1	NA	83	99	107	120	131	90	86	97	111	121
Sly01g0027851	M2	NA	110	111	112	135	172	108	118	109	140	210
Sly01g0027861	M22	NA	2	1	3	1	0	2	1	2	1	0
Sly01g0027871	M11	NA	19	16	20	27	35	26	24	28	26	31
Sly01g0027881	M12	NA	14	14	15	18	26	21	18	20	19	21
Sly01g0027891	M19	NA	44	47	48	45	53	44	38	42	38	47
Sly01g0027911	M1	NA	13	9	18	2	1	1	1	1	1	0
Sly01g0027921	M12	SlCycU2;1	1	0	1	0	0	1	1	1	0	0
Sly01g0027931	M22	NA	1	1	2	1	1	4	1	1	1	1
Sly01g0027961	M1	NA	3	4	3	1	1	2	1	2	0	1
Sly01g0027971	M12	NA	15	15	16	19	22	17	18	16	22	24
Sly01g0027981	M19	NA	18	21	21	24	28	25	19	25	27	31
Sly01g0027991	M11	NA	17	14	17	12	14	25	23	27	23	26
Sly01g0028011	M2	NA	37	34	31	42	67	28	33	30	58	93
Sly01g0028021	M3	NA	68	58	50	30	17	32	33	23	5	5
Sly01g0028031	M2	NA	5	6	6	4	7	5	6	6	6	9
Sly01g0028041	M11	NA	21	22	21	25	36	26	28	27	35	44
Sly01g0028051	M1	NA	20	17	25	7	6	13	13	14	7	7
Sly01g0028091	M2	NA	22	22	18	16	20	20	22	17	16	21
Sly01g0028101	M11	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0028111	M22	NA	1	1	1	0	1	1	1	1	1	1
Sly01g0028121	M8	NA	33	34	31	34	34	32	41	31	28	24
Sly01g0028131	M10	SAUR1	4	4	3	1	1	9	12	5	1	1
Sly01g0028141	M1	NA	5	5	5	6	5	1	1	1	1	1
Sly01g0028151	M12	NA	1	1	1	0	1	6	2	3	1	1
Sly01g0028161	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly01g0028171	M1	NA	86	82	89	71	71	73	71	78	80	85
Sly01g0028181	M12	NA	15	16	15	18	14	17	17	17	13	10
Sly01g0028191	M12	NA	0	1	0	0	1	5	1	1	1	1
Sly01g0028211	M1	NA	62	63	58	64	70	47	48	48	68	80
Sly01g0028221	M4	NA	6	6	6	15	40	6	6	5	14	34
Sly01g0028231	M18	NA	3	3	3	2	1	4	3	4	1	1
Sly01g0028241	M13	NA	74	73	83	79	72	81	78	96	63	43
Sly01g0028251	M1	NA	242	259	299	2	1	24	24	13	1	0
Sly01g0028261	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly01g0028271	M3	NA	105	103	75	142	107	75	75	47	73	56
Sly01g0028281	M10	NA	5	5	4	4	2	6	8	4	3	2
Sly01g0028291	M1	NA	25	25	25	24	31	20	20	23	28	35
Sly01g0028301	M3	NA	142	143	141	93	73	101	117	105	116	85
Sly01g0028311	M22	NA	1	1	1	0	1	2	1	1	0	0
Sly01g0028321	M13	NA	3	3	3	3	3	3	2	3	3	3
Sly01g0028341	M12	NA	20	15	14	11	25	43	37	20	13	55
Sly01g0028351	M4	NA	23	24	28	131	429	31	28	35	154	645
Sly01g0028361	M9	NA	45	45	43	51	44	42	48	46	50	48
Sly01g0028401	M3	NA	1	1	1	1	2	1	1	1	1	1
Sly01g0028411	M3	NA	48	47	42	46	42	42	48	37	42	35
Sly01g0028431	M11	NA	2	1	2	0	0	6	5	2	0	0
Sly01g0028441	M1	NA	5	4	3	6	2	2	2	2	1	1
Sly01g0028451	M1	NA	23	21	21	8	10	13	13	12	6	6
Sly01g0028461	M3	NA	35	42	29	18	25	18	19	15	12	12
Sly01g0028471	M3	NA	30	37	17	1	1	9	8	3	1	1
Sly01g0028481	M1	NA	37	46	47	13	8	19	15	12	1	1
Sly01g0028491	M1	NA	5	4	5	3	2	3	3	3	2	1
Sly01g0028501	M1	NA	12	12	11	12	14	11	10	12	12	13
Sly01g0028531	M12	NA	4	4	3	2	2	16	11	13	2	3
Sly01g0028541	M12	NA	2	1	1	2	1	2	3	3	5	7
Sly01g0028551	M12	NA	2	2	2	2	2	3	3	4	8	6
Sly01g0028561	M11	NA	4	4	5	13	15	8	7	9	15	15
Sly01g0028571	M9	NA	31	32	29	29	28	35	35	29	22	24
Sly01g0028581	M3	NA	3	2	1	1	0	1	1	1	0	0
Sly01g0028591	M3	NA	1	2	1	1	1	1	2	1	1	1
Sly01g0028601	M19	NA	8	10	9	8	9	10	8	8	6	5
Sly01g0028621	M18	NA	9	9	11	10	13	12	9	11	12	13
Sly01g0028631	M3	NA	43	44	34	24	24	31	31	28	28	28
Sly01g0028641	M11	NA	74	60	73	25	16	73	65	90	85	33
Sly01g0028651	M12	NA	31	29	35	6	2	61	71	44	2	2
Sly01g0028661	M22	NA	1	1	1	0	0	2	1	2	1	0
Sly01g0028681	M11	NA	24	23	23	23	30	31	27	33	37	42
Sly01g0028701	M12	NA	28	29	23	34	35	32	29	29	38	40
Sly01g0028711	M10	NA	6	25	24	4	53	34	72	22	6	149
Sly01g0028721	M3	NA	47	43	34	24	34	40	47	30	20	35
Sly01g0028731	M18	NA	4	4	4	5	4	4	4	4	5	4
Sly01g0028741	M3	BIN2	72	90	78	60	49	67	67	63	41	41
Sly01g0028751	M1	NA	70	92	58	68	66	14	11	9	8	15
Sly01g0028761	M2	NA	30	31	26	28	28	25	30	20	16	20
Sly01g0028771	M2	NA	115	107	87	99	100	81	94	68	103	102
Sly01g0028781	M3	NA	22	23	20	19	20	18	18	17	22	18
Sly01g0028811	M11	NA	56	90	110	565	416	155	171	307	465	368
Sly01g0028831	M12	ATPP2-A13	8	7	10	4	3	34	31	38	12	10
Sly01g0028841	M12	NA	14	14	18	22	20	42	41	55	61	79
Sly01g0028851	M11	NA	21	21	21	23	26	28	28	28	27	30
Sly01g0028861	M12	NA	23	23	23	24	23	31	32	35	51	48
Sly01g0028871	M1	NA	111	117	118	156	245	43	44	55	58	70
Sly01g0028881	M1	NA	8	7	8	6	7	6	7	5	3	8
Sly01g0028891	M11	NA	53	50	49	50	51	49	49	53	48	42
Sly01g0028911	M12	NA	5	5	4	1	1	6	7	5	1	1
Sly01g0028921	M11	NA	15	15	19	14	14	21	19	22	7	6
Sly01g0028931	M11	NA	8	10	10	14	7	13	12	15	8	6
Sly01g0028941	M11	NA	7	5	7	14	10	11	9	11	6	5
Sly01g0028961	M11	NA	14	14	14	11	14	15	14	15	16	18
Sly01g0028981	M22	NA	4	3	3	2	4	8	2	5	1	2
Sly01g0028991	M22	NA	1	2	1	1	1	3	2	2	1	1
Sly01g0029001	M18	NA	15	16	18	17	24	17	14	18	17	24
Sly01g0029011	M23	NA	1	1	1	1	0	2	1	1	1	1
Sly01g0029021	M3	NA	41	45	38	55	58	34	35	28	36	56
Sly01g0029041	M13	NA	67	58	69	62	68	62	58	70	81	92
Sly01g0029051	M11	NA	20	19	19	19	28	23	21	23	21	34
Sly01g0029061	M7	NA	21	31	12	9	6	43	65	17	4	18

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0377601	M11	NA	111	90	106	185	238	141	128	162	119	191
Sly06g0377611	M11	NA	42	30	36	8	7	84	74	82	11	8
Sly06g0377621	M22	NA	2	2	2	2	2	3	1	2	1	1
Sly06g0377631	M11	NA	9	8	9	9	8	11	10	11	9	8
Sly06g0377641	M12	NA	167	129	210	16	25	212	213	257	24	32
Sly06g0377651	M10	NA	2	3	1	1	0	3	4	1	1	1
Sly06g0377661	M10	NA	2	3	1	1	0	3	4	1	1	1
Sly06g0377681	M3	NA	22	26	17	12	15	16	19	12	10	11
Sly06g0377691	M3	NA	90	112	64	40	52	62	69	42	34	49
Sly06g0377701	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0377741	M11	NA	5	5	7	4	2	10	9	12	4	1
Sly06g0377751	M12	NA	3	4	4	3	3	5	5	5	4	2
Sly06g0377791	M3	NA	68	66	43	33	43	43	42	32	39	36
Sly06g0377811	M12	NA	13	15	10	11	12	17	17	15	11	11
Sly06g0377821	M11	NA	9	9	13	6	5	23	16	21	3	3
Sly06g0377831	M11	NA	284	268	316	276	237	329	298	367	288	252
Sly06g0377851	M1	NRT2	2	4	2	1	1	1	1	0	0	0
Sly06g0377871	M1	NA	10	8	7	2	1	1	2	2	4	2
Sly06g0377881	M3	NA	5	4	4	5	4	4	4	4	5	4
Sly06g0377891	M18	NA	61	52	57	30	10	62	57	50	2	1
Sly06g0377911	M1	NA	11	12	9	7	4	7	7	7	4	4
Sly06g0377951	M12	NA	4	2	2	1	0	12	8	9	1	0
Sly06g0377961	M11	NA	38	38	41	37	33	47	45	45	32	38
Sly06g0377981	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0377991	M22	NA	43	41	43	42	50	63	42	61	49	50
Sly06g0378001	M3	NA	1	2	1	1	1	2	1	1	1	1
Sly06g0378011	M23	NA	1	1	1	0	0	1	1	1	0	0
Sly06g0378021	M12	SlARF10B	6	6	7	15	10	11	11	11	11	11
Sly06g0378031	M1	NA	34	36	38	21	23	21	17	19	17	21
Sly06g0378041	M1	NA	19	14	17	12	13	9	9	12	24	25
Sly06g0378051	M1	NA	315	269	284	84	38	144	166	132	58	33
Sly06g0378071	M3	NA	43	50	44	19	13	34	39	25	12	18
Sly06g0378101	M22	NA	1	1	1	0	0	2	0	1	0	0
Sly06g0378111	M12	NA	34	34	36	30	36	47	57	52	68	87
Sly06g0378131	M9	NA	1	1	0	0	1	1	1	0	0	1
Sly06g0378171	M1	NA	2	2	2	2	1	1	1	1	1	1
Sly06g0378191	M12	NA	3	2	2	1	1	3	5	4	3	1
Sly06g0378201	M1	NA	29	22	16	5	13	5	6	4	6	8
Sly06g0378211	M9	NA	52	50	52	56	70	62	67	61	97	98
Sly06g0378221	M1	NA	17	14	23	33	80	8	8	10	11	10
Sly06g0378261	M11	NA	7	7	9	3	1	17	14	14	1	2
Sly06g0378271	M12	NA	1	1	3	22	5	3	10	28	317	53
Sly06g0378301	M12	NA	59	63	68	88	91	82	81	93	92	96
Sly06g0378311	M1	NA	1	2	1	0	1	1	1	1	0	0
Sly06g0378321	M3	NA	44	100	23	6	6	5	6	2	1	1
Sly06g0378331	M1	NA	55	41	44	31	36	38	37	41	38	37
Sly06g0378361	M3	NA	4	3	3	1	1	1	1	0	0	0
Sly06g0378371	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly06g0378381	M12	NA	1	2	2	2	1	6	7	8	8	10
Sly06g0378391	M12	NA	1	1	1	1	1	2	1	2	2	2
Sly06g0378401	M6	NA	73	156	62	6	13	107	145	27	2	11
Sly06g0378511	M2	NA	2	3	3	1	7	1	3	3	3	23
Sly06g0378521	M7	NA	22	56	47	3	59	31	92	41	9	165
Sly06g0378531	M1	NA	32	35	41	38	50	29	31	35	17	34
Sly06g0378551	M11	NA	66	58	52	43	54	70	64	51	20	54
Sly06g0378561	M11	NA	117	95	111	219	248	155	153	189	217	206
Sly06g0378581	M15	NA	97	80	76	109	90	114	90	114	91	85
Sly06g0378591	M12	NA	23	17	19	7	6	25	27	19	9	7
Sly06g0378701	M11	NA	33	23	26	10	10	40	32	37	12	13
Sly06g0378731	M11	NA	134	113	168	93	114	211	197	202	82	76
Sly06g0378761	M11	NA	13	13	12	12	15	15	15	16	12	11
Sly06g0378771	M12	NA	2	2	2	1	1	5	5	3	2	0
Sly06g0378791	M12	NA	8	8	10	14	20	13	13	14	19	28
Sly06g0378801	M3	HSP70	272	219	194	25	105	243	283	99	74	279
Sly06g0378811	M1	NA	2	3	2	2	2	1	1	1	1	1
Sly06g0378831	M5	NA	158	226	69	22	50	163	210	66	7	15
Sly06g0378841	M7	NA	70	145	50	33	103	96	164	65	28	87
Sly06g0378861	M1	NA	2	5	3	1	0	3	1	2	0	0
Sly06g0378871	M6	NA	8	34	9	2	3	6	14	3	1	5
Sly06g0378881	M3	NA	5	9	2	1	1	1	1	1	1	0
Sly06g0378891	M1	NA	31	34	29	26	18	11	7	8	3	3
Sly06g0378901	M11	NA	12	11	20	15	11	26	22	17	3	4
Sly06g0378911	M11	NA	11	11	17	13	11	22	20	15	3	4
Sly06g0378921	M1	NA	15	21	20	5	2	2	1	1	1	1
Sly06g0378931	M1	MT2B	596	592	926	2239	1420	137	167	438	1242	947
Sly06g0378941	M1	NA	62	62	56	59	66	47	43	42	63	55
Sly06g0378951	M1	NA	9	17	8	42	58	2	2	1	1	1
Sly06g0378971	M22	NA	2	1	2	0	1	6	1	7	1	0
Sly06g0379021	M22	NA	1	1	1	1	2	2	1	2	3	3
Sly06g0379031	M5	NA	6	8	3	1	1	9	6	4	1	1
Sly06g0379041	M11	NA	10	10	15	9	9	14	12	14	7	9
Sly06g0379051	M18	NA	5	5	7	4	3	8	5	8	3	3
Sly06g0379061	M1	NA	22	23	20	15	23	21	20	20	20	25
Sly06g0379071	M3	NA	27	31	20	17	20	9	10	7	19	18
Sly06g0379081	M3	NA	26	25	27	32	42	23	25	22	41	41
Sly06g0379091	M6	NA	19	33	13	10	19	32	33	13	7	13
Sly06g0379101	M3	NA	7	10	8	16	18	4	4	3	2	2
Sly06g0379111	M3	NA	63	81	36	5	9	58	55	10	1	4
Sly06g0379121	M12	NA	1	1	1	2	3	1	2	1	2	4
Sly06g0379131	M12	NA	24	37	22	162	356	60	107	36	170	249
Sly06g0379151	M19	NA	65	70	73	76	73	62	58	63	56	58
Sly06g0379161	M11	NA	34	36	38	55	31	62	58	76	62	46
Sly06g0379171	M18	NA	80	73	79	100	159	82	70	79	121	151
Sly06g0379201	M11	NA	53	47	53	44	44	52	51	59	49	49
Sly06g0379211	M11	NA	94	92	115	90	74	112	96	119	94	79
Sly06g0379221	M12	SlPP2C3	34	30	32	13	9	41	39	35	11	5
Sly06g0379231	M11	NA	48	42	58	98	147	56	58	78	147	186
Sly06g0379241	M12	NA	3	7	1	1	0	6	8	5	1	1
Sly06g0379251	M1	NA	57	52	60	44	38	34	32	42	38	40
Sly06g0379261	M3	NA	14	14	14	7	8	12	12	10	6	6
Sly06g0379271	M3	NA	48	50	32	18	14	15	16	12	15	13
Sly06g0379281	M11	NA	34	33	36	39	45	43	33	47	54	60
Sly06g0379301	M1	NA	3	3	4	1	2	2	2	2	1	1
Sly06g0379311	M11	NA	27	25	30	44	41	54	50	69	53	48
Sly06g0379331	M12	NA	20	25	28	21	11	43	50	60	19	16
Sly06g0379341	M9	NA	36	36	45	170	539	46	71	52	99	412
Sly06g0379351	M12	NA	343	297	223	1339	5925	434	441	426	672	3165
Sly06g0379361	M12	NA	205	190	243	1081	2360	308	364	299	458	1670
Sly06g0379381	M10	UGT-like1	1	1	1	1	1	5	7	2	1	0
Sly06g0379411	M12	NA	33	31	36	621	2632	57	70	64	144	1575
Sly06g0379441	M12	NA	48	41	44	297	1596	97	86	91	155	1787
Sly06g0379461	M3	NA	18	18	14	13	17	17	17	12	8	12
Sly06g0379481	M12	signalling protein kina	1	1	1	1	1	2	2	2	1	1
Sly06g0379491	M11	NA	8	7	10	7	5	9	8	12	7	4
Sly06g0379501	M10	NA	27	29	25	23	26	27	29	27	28	28
Sly06g0379511	M1	NA	4	4	6	3	3	1	1	1	1	1
Sly06g0379521	M9	NA	85	76	77	42	13	90	97	76	30	21
Sly06g0379531	M3	NA	36	42	34	33	32	37	37	32	33	34
Sly06g0379541	M3	PCNA1	22	21	18	7	6	16	18	12	3	4
Sly06g0379551	M4	NA	106	84	90	203	334	144	133	128	438	641
Sly06g0379561	M22	NA	5	5	5	3	2	6	5	6	4	4
Sly06g0379571	M12	NA	31	27	24	105	122	24	30	32	159	176
Sly06g0379581	M12	NA	4	4	4	20	22	8	6	7	25	17
Sly06g0379591	M1	NA	1	1	1	2	5	1	1	1	1	6
Sly06g0379621	M1	NA	184	201	126	111	59	41	45	36	25	34
Sly06g0379641	M11	NA	24	19	24	13	16	37	33	35	7	20
Sly06g0379651	M1	NA	78	99	105	98	17	37	45	46	36	11
Sly06g0379661	M1	NA	10	19	10	4	1	1	0	1	0	0
Sly06g0379671	M11	NA	18	20	18	22	19	24	20	25	15	23
Sly06g0379691	M1	NA	28	33	23	6	5	19	16	13	2	1
Sly06g0379711	M22	NA	1	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0029071	M1	NA	1	1	1	1	1	1	1	0	0	0
Sly01g0029081	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0029091	M3	NA	10	10	10	11	13	10	10	9	8	7
Sly01g0029101	M11	NA	60	54	70	30	30	61	51	64	22	20
Sly01g0029151	M3	NA	3	2	1	1	1	1	1	1	0	1
Sly01g0029161	M9	NA	20	24	19	27	23	26	36	24	32	25
Sly01g0029171	M1	GA20OX4	1	1	1	2	1	1	0	0	0	0
Sly01g0029181	M12	NA	4	4	3	4	1	7	7	7	2	1
Sly01g0029191	M14	NA	37	32	42	37	45	36	30	38	31	37
Sly01g0029201	M1	NA	71	66	75	25	5	7	8	7	2	2
Sly01g0029211	M11	NA	5	4	7	6	2	25	20	31	9	2
Sly01g0029221	M11	NA	42	42	50	71	83	73	68	82	55	67
Sly01g0029231	M10	NA	133	138	90	49	57	161	238	136	62	72
Sly01g0029241	M12	NA	17	21	19	21	20	28	24	26	15	13
Sly01g0029261	M1	NA	30	32	43	94	104	21	22	24	25	30
Sly01g0029301	M11	NA	1	1	1	0	0	1	1	1	1	1
Sly01g0029321	M1	NA	5	4	7	3	1	3	3	3	1	1
Sly01g0029331	M19	NA	24	23	23	36	45	23	22	25	39	50
Sly01g0029361	M12	NA	11	11	12	19	33	16	17	19	28	65
Sly01g0029371	M12	NA	4	4	5	5	4	5	7	5	6	5
Sly01g0029381	M11	NA	8	8	10	9	11	11	11	13	9	12
Sly01g0029391	M1	NA	95	92	89	78	81	68	63	66	27	27
Sly01g0029401	M1	NA	46	34	33	4	2	9	8	8	1	1
Sly01g0029411	M11	NA	26	24	25	57	82	27	29	26	62	91
Sly01g0029421	M12	NA	1	2	1	1	1	1	2	2	1	1
Sly01g0029431	M1	NA	44	48	115	26	4	4	2	5	1	1
Sly01g0029441	M1	NA	70	57	152	32	6	10	9	9	1	0
Sly01g0029451	M1	NA	74	61	90	33	12	34	32	17	2	1
Sly01g0029461	M1	NA	96	95	70	5	1	5	4	1	1	0
Sly01g0029471	M1	NA	20	29	68	23	3	1	1	1	1	0
Sly01g0029481	M1	NA	38	38	34	26	33	26	25	25	26	31
Sly01g0029491	M1	NA	12	12	15	14	21	9	9	11	12	18
Sly01g0029501	M19	NA	26	27	34	40	53	21	17	26	25	30
Sly01g0029541	M12	NA	2	2	2	2	2	2	2	3	8	6
Sly01g0029551	M11	NA	15	16	17	21	17	24	24	29	63	33
Sly01g0029561	M11	NA	19	18	37	26	22	78	61	103	51	47
Sly01g0029571	M3	NA	57	59	47	32	28	39	41	32	28	23
Sly01g0029581	M1	NA	9	5	16	7	2	3	2	2	1	0
Sly01g0029591	M9	NA	71	76	61	56	73	128	211	101	29	79
Sly01g0029631	M6	NA	89	161	85	50	135	125	169	64	42	123
Sly01g0029641	M1	NA	45	44	45	39	38	37	34	35	40	39
Sly01g0029651	M9	NA	1	1	1	0	1	1	3	1	1	0
Sly01g0029661	M12	NA	1	1	1	1	1	2	1	1	1	0
Sly01g0029671	M12	NA	1	1	1	1	1	1	1	1	1	0
Sly01g0029681	M1	NA	18	24	25	8	3	17	13	19	1	1
Sly01g0029691	M1	NA	28	26	22	22	18	17	15	17	22	22
Sly01g0029701	M11	NA	99	91	106	104	113	118	103	124	147	158
Sly01g0029711	M11	NA	5	4	5	7	17	5	4	5	17	28
Sly01g0029721	M1	NA	7	5	6	6	3	5	5	6	2	1
Sly01g0029741	M12	NA	8	7	6	8	8	9	8	9	10	10
Sly01g0029751	M1	acyl-CoA thioesterase	20	19	21	19	19	15	12	14	13	21
Sly01g0029761	M3	NA	63	61	49	31	25	40	42	35	38	31
Sly01g0029771	M3	acyl-CoA thioesterase	96	103	68	31	34	47	55	32	27	37
Sly01g0029781	M1	NA	71	73	73	56	49	56	60	62	77	76
Sly01g0029791	M12	NA	15	20	21	19	18	38	38	35	14	17
Sly01g0029801	M12	BAM3-like1	21	23	21	24	22	26	22	23	20	20
Sly01g0029811	M11	NA	1	2	2	2	3	3	3	3	4	6
Sly01g0029821	M12	NA	4	4	5	6	6	6	6	6	8	6
Sly01g0029831	M18	NA	2	3	2	2	2	2	2	3	4	3
Sly01g0029851	M1	NA	16	17	15	17	19	12	11	11	10	12
Sly01g0029861	M2	NA	38	38	32	29	36	30	34	27	40	54
Sly01g0029871	M1	NA	38	39	48	39	36	40	36	38	34	30
Sly01g0029881	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0029891	M1	NA	35	39	38	31	27	26	22	28	35	30
Sly01g0029901	M12	NA	9	7	6	7	8	9	9	8	10	9
Sly01g0029911	M3	NA	49	44	29	22	27	41	46	28	23	25
Sly01g0029921	M22	NA	17	9	14	40	65	23	5	16	6	72
Sly01g0029931	M1	NA	53	48	90	8	1	15	5	11	1	1
Sly01g0029951	M11	NA	20	16	21	32	36	36	28	37	37	29
Sly01g0029961	M1	NA	4	3	5	2	2	3	1	2	1	0
Sly01g0029971	M1	ORC5	9	8	8	2	2	5	4	4	2	1
Sly01g0029981	M11	NA	92	90	98	102	92	96	95	112	100	89
Sly01g0029991	M3	NA	12	13	12	19	15	10	11	9	13	12
Sly01g0030001	M12	NA	186	171	202	252	120	252	296	273	1308	503
Sly01g0030021	M19	BRM	42	48	44	44	49	49	44	45	27	30
Sly01g0030031	M1	NA	91	96	114	65	68	95	89	98	80	109
Sly01g0030041	M12	NA	4	4	4	5	6	6	6	7	10	9
Sly01g0030051	M14	NA	7	7	9	8	6	6	5	6	2	2
Sly01g0030061	M19	NA	7	7	11	10	8	7	6	8	2	1
Sly01g0030081	M1	NA	19	19	17	11	17	11	12	11	16	23
Sly01g0030101	M18	NA	2	3	3	4	5	3	3	3	4	3
Sly01g0030111	M3	NA	29	28	17	12	12	11	14	9	9	8
Sly01g0030121	M11	NA	2	2	2	4	5	4	4	5	6	5
Sly01g0030131	M12	NA	28	30	30	33	32	40	38	36	30	33
Sly01g0030141	M22	FRO02	6	4	4	1	1	15	3	11	1	1
Sly01g0030151	M12	FRO03	3	4	7	4	1	28	47	93	37	2
Sly01g0030161	M13	NA	1	1	1	2	1	1	1	3	2	0
Sly01g0030171	M7	NA	117	151	96	81	177	115	154	93	94	238
Sly01g0030181	M2	NA	87	87	87	123	135	77	95	79	108	113
Sly01g0030191	M22	NA	13	13	18	11	6	18	13	13	3	3
Sly01g0030201	M10	NA	341	405	321	317	476	377	447	342	426	710
Sly01g0030211	M3	NA	22	27	17	12	14	13	15	9	9	13
Sly01g0030221	M3	NA	1	2	1	1	1	1	1	1	1	0
Sly01g0030231	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly01g0030271	M12	NA	7	6	8	15	46	11	11	12	13	32
Sly01g0030281	M1	NA	7	8	10	24	21	7	6	8	26	23
Sly01g0030291	M19	NA	31	31	37	48	36	32	30	35	47	34
Sly01g0030301	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly01g0030311	M12	NA	13	8	10	8	27	16	14	13	15	36
Sly01g0030321	M11	NA	66	62	76	51	43	71	67	79	50	43
Sly01g0030331	M1	NA	632	562	591	556	458	493	523	610	612	723
Sly01g0030341	M12	NA	18	18	16	16	16	19	21	22	33	24
Sly01g0030351	M1	NA	71	60	57	23	14	28	26	36	37	23
Sly01g0030361	M1	ACS2	18	11	28	424	559	3	3	12	307	541
Sly01g0030371	M1	NA	4	5	3	9	4	2	2	2	3	3
Sly01g0030381	M1	NA	5	7	3	2	1	1	1	1	1	1
Sly01g0030391	M1	PPR-like38	7	7	6	7	6	6	6	7	6	4
Sly01g0030401	M11	NA	26	27	32	30	34	31	26	30	25	26
Sly01g0030411	M12	NA	1	2	2	1	2	3	2	2	1	1
Sly01g0030441	M6	NA	348	571	159	6	53	247	814	140	29	213
Sly01g0030451	M3	NA	721	891	415	303	583	509	952	352	466	918
Sly01g0030461	M11	NA	2	2	2	3	3	3	2	3	3	3
Sly01g0030471	M1	NA	90	102	87	110	77	5	3	3	2	2
Sly01g0030481	M12	NA	8	8	13	24	14	10	10	12	6	6
Sly01g0030501	M9	NA	171	159	176	226	260	175	199	182	229	329
Sly01g0030511	M3	NA	25	28	26	27	27	26	24	23	23	22
Sly01g0030521	M1	NA	33	26	27	11	9	17	18	15	12	10
Sly01g0030541	M18	NA	11	11	11	7	8	12	11	13	11	8
Sly01g0030561	M22	NA	3	4	2	1	2	4	2	3	1	1
Sly01g0030581	M13	NA	32	22	36	36	81	34	31	54	53	104
Sly01g0030591	M1	NA	17	19	25	19	15	13	9	11	7	6
Sly01g0030601	M2	NA	9	9	9	11	8	8	10	8	7	7
Sly01g0030621	M1	NA	16	16	18	8	4	2	1	1	1	1
Sly01g0030631	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0030641	M1	NA	2004	3049	3865	17436	19176	1059	1207	2568	7194	8526
Sly01g0030671	M23	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0030681	M1	NA	12	8	10	12	14	8	7	12	29	30
Sly01g0030701	M1	NA	9	9	6	4	2	4	4	3	1	1
Sly01g0030711	M3	NA	150	126	109	57	45	82	85	79	48	44
Sly01g0030721	M11	NA	1302	1193	1244	1402	1476	1304	1221	1547	1437	1466
Sly01g0030731	M3	NA	39	34	34	34	47	30	31	32	45	56
Sly01g0030741	M11	NA	72	54	79	49	34	175	151	218	70	27
Sly01g0030761	M11	NA	4	2	5	1	1	59	38	62	1	1
Sly01g0030771	M3	NA	48	47	42	18	49	37	44	31	15	44

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0379761	M11	NA	38	36	37	38	53	44	39	46	59	82
Sly06g0379771	M11	NA	70	58	63	65	83	69	65	78	87	105
Sly06g0379781	M12	NA	4	4	5	8	11	5	5	6	7	9
Sly06g0379821	M15	NA	62	61	63	89	103	62	63	63	102	146
Sly06g0379831	M3	NA	17	18	14	21	22	14	14	12	20	17
Sly06g0379841	M11	NA	17	15	17	19	24	19	18	22	30	40
Sly06g0379851	M13	NA	195	180	210	276	258	179	191	199	242	256
Sly06g0379871	M1	NA	98	84	73	103	151	47	54	57	221	294
Sly06g0379881	M3	NA	175	231	136	31	48	42	48	12	2	2
Sly06g0379901	M11	GA2ox10	1	1	1	1	1	1	1	1	3	2
Sly06g0379911	M11	NA	2	2	2	3	2	3	3	4	2	3
Sly06g0379921	M18	NA	8	7	10	9	6	10	7	11	6	6
Sly06g0379931	M1	NA	8	9	7	3	1	2	3	1	1	1
Sly06g0379941	M3	NA	10	15	11	10	19	9	10	5	3	15
Sly06g0379951	M1	NA	176	174	157	115	89	99	103	94	66	50
Sly06g0379961	M19	NA	47	47	49	45	46	42	37	42	29	32
Sly06g0379981	M12	NA	98	88	91	90	101	94	109	102	126	136
Sly06g0380001	M1	NA	300	284	329	224	153	192	219	211	134	123
Sly06g0380011	M18	PFK	17	21	21	32	31	22	17	25	26	28
Sly06g0380041	M12	NA	28	27	28	38	40	29	30	34	47	48
Sly06g0380061	M3	NA	4	3	4	4	3	2	3	2	5	3
Sly06g0380071	M9	NA	11	10	9	10	8	12	16	12	9	10
Sly06g0380081	M12	NA	13	9	14	24	12	24	24	35	55	12
Sly06g0380091	M11	NA	10	11	12	24	25	14	13	15	25	27
Sly06g0380101	M11	NA	26	26	30	68	57	29	31	39	40	37
Sly06g0380121	M3	NA	109	103	85	91	106	73	74	74	89	113
Sly06g0380131	M11	NA	1	2	2	2	1	3	2	3	2	1
Sly06g0380141	M1	NA	1	1	1	1	1	0	1	0	0	0
Sly06g0380161	M3	NA	59	59	48	43	46	47	50	41	52	60
Sly06g0380171	M11	NA	14	14	21	32	65	26	24	31	49	63
Sly06g0380191	M3	NA	35	39	27	28	22	28	30	21	24	19
Sly06g0380201	M11	NA	2	3	2	1	0	5	5	6	1	0
Sly06g0380221	M1	NA	3	3	3	2	1	2	2	1	1	1
Sly06g0380251	M11	NA	2	1	1	1	1	2	2	2	1	1
Sly06g0380261	M3	NA	30	26	25	16	21	20	24	17	28	29
Sly06g0380271	M2	NA	34	30	26	17	19	24	28	19	28	25
Sly06g0380281	M19	NA	87	77	86	80	105	80	73	84	92	122
Sly06g0380291	M3	NA	10	8	6	5	5	6	7	6	7	7
Sly06g0380301	M11	RDM4-like	55	49	66	51	89	72	62	74	68	108
Sly06g0380321	M1	NA	1	1	3	5	22	1	1	2	19	37
Sly06g0380341	M9	NA	1	1	1	0	0	2	2	1	1	1
Sly06g0380351	M6	NA	12	28	22	2	8	15	34	14	3	10
Sly06g0380371	M11	NA	2	1	4	1	0	5	3	4	0	0
Sly06g0380381	M1	NA	37	46	41	44	24	19	21	25	35	14
Sly06g0380391	M1	NA	6	5	6	2	3	5	3	3	1	2
Sly06g0380401	M5	NA	38	41	30	36	29	37	42	34	42	42
Sly06g0380411	M3	NA	20	18	20	15	7	18	21	17	11	3
Sly06g0380421	M19	NA	18	17	17	18	21	17	14	17	18	24
Sly06g0380431	M3	NA	53	53	32	18	20	18	18	13	12	6
Sly06g0380451	M3	NA	78	101	74	441	267	104	106	31	22	11
Sly06g0380491	M1	NA	94	102	26	10	2	2	1	1	0	0
Sly06g0380501	M3	NA	189	170	165	157	182	162	165	164	174	186
Sly06g0380511	M3	SlERF.G2	95	99	50	2	3	28	36	4	1	2
Sly06g0380521	M12	NA	98	90	111	171	169	97	109	115	179	219
Sly06g0380531	M11	NA	9	8	12	29	24	28	22	25	32	33
Sly06g0380541	M1	NA	509	504	536	325	239	428	436	471	294	228
Sly06g0380551	M12	NA	113	112	115	173	196	129	143	143	205	223
Sly06g0380561	M19	NA	3	2	3	4	3	2	1	3	7	6
Sly06g0380571	M4	NA	3	3	5	5	5	5	3	3	10	14
Sly06g0380581	M3	NA	553	513	487	384	317	382	427	325	367	339
Sly06g0380591	M12	NA	116	112	112	175	189	114	115	132	232	276
Sly06g0380601	M1	NA	293	265	263	201	157	212	227	227	199	187
Sly06g0380611	M15	NA	85	64	65	102	111	82	73	87	93	115
Sly06g0380621	M1	NA	2	2	1	1	1	2	1	1	1	1
Sly06g0380631	M3	NA	2	2	2	1	1	2	2	1	1	1
Sly06g0380641	M3	NA	50	56	54	79	87	43	49	46	113	111
Sly06g0380681	M11	NA	31	29	34	58	59	57	55	70	65	88
Sly06g0380691	M12	NA	5	5	5	8	10	10	9	10	12	11
Sly06g0380701	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0380711	M7	NA	18	20	16	13	30	14	24	14	10	40
Sly06g0380721	M1	NA	61	60	59	49	45	56	55	56	60	54
Sly06g0380731	M1	NA	18	17	16	5	6	13	9	10	2	2
Sly06g0380751	M11	NA	216	202	206	188	209	206	208	254	288	348
Sly06g0380761	M19	NA	82	89	82	82	76	86	78	78	78	76
Sly06g0380791	M22	NA	1	1	1	0	0	3	1	3	0	0
Sly06g0380801	M1	NA	361	338	379	245	214	313	312	323	248	201
Sly06g0380811	M3	NA	2	3	2	2	3	3	2	2	3	2
Sly06g0380821	M1	NA	2	3	3	2	3	1	2	2	3	2
Sly06g0380831	M2	NA	27	27	27	36	41	24	28	26	40	61
Sly06g0380841	M1	NA	21	22	21	22	23	19	19	20	32	37
Sly06g0380851	M1	NA	14	13	15	1	1	9	7	4	1	1
Sly06g0380861	M3	NA	161	185	96	26	33	121	139	50	22	39
Sly06g0380871	M1	NA	117	112	120	90	99	89	85	84	86	108
Sly06g0380881	M11	NA	115	90	135	54	8	250	229	299	45	3
Sly06g0380891	M11	NA	110	76	125	88	31	246	219	317	127	30
Sly06g0380921	M11	NA	6	6	7	6	3	19	19	22	7	7
Sly06g0380931	M11	HYD1-like	88	77	96	84	49	132	114	130	77	51
Sly06g0380941	M11	NA	16	13	20	16	23	26	20	29	29	32
Sly06g0380951	M10	NA	1	1	1	1	1	3	2	1	1	1
Sly06g0380961	M11	NA	99	90	102	175	228	146	147	189	290	393
Sly06g0380971	M22	NA	1	1	1	1	0	3	1	2	0	0
Sly06g0380981	M11	NA	4	3	4	1	1	10	8	10	1	0
Sly06g0380991	M22	NA	2	1	2	0	0	15	3	12	1	1
Sly06g0381021	M3	NA	24	26	18	23	25	21	21	18	34	34
Sly06g0381031	M3	NA	9	11	8	8	8	9	10	7	11	11
Sly06g0381041	M20	NA	23	20	29	6	1	19	12	17	1	1
Sly06g0381051	M1	NA	3	2	2	1	1	1	1	1	1	1
Sly06g0381061	M1	NA	11	11	12	11	12	10	10	10	14	18
Sly06g0381071	M12	NA	1	1	1	1	1	1	1	1	1	0
Sly06g0381081	M3	NA	40	39	32	49	58	24	29	25	48	51
Sly06g0381101	M3	NA	19	36	7	2	2	25	13	12	3	6
Sly06g0381111	M1	NA	10	14	4	2	1	6	2	4	0	0
Sly06g0381121	M5	NA	40	51	35	24	35	43	45	35	30	41
Sly06g0381141	M1	NA	4	4	3	1	1	2	1	1	0	1
Sly06g0381151	M1	NA	272	241	230	208	169	152	161	143	175	160
Sly06g0381161	M4	NA	242	219	245	326	506	222	217	201	330	533
Sly06g0381171	M12	PPR-like6	15	15	14	12	12	17	15	15	17	13
Sly06g0381181	M11	NA	41	45	52	46	64	46	42	57	63	81
Sly06g0381191	M12	NA	22	24	30	44	37	38	38	42	47	37
Sly06g0381201	M3	NA	18	18	14	6	2	14	15	9	2	1
Sly06g0381221	M11	NA	10	7	10	13	11	8	9	11	16	18
Sly06g0381231	M13	SlCycC1;1	63	70	89	95	141	86	84	115	116	152
Sly06g0381241	M3	NA	18	22	20	57	34	15	19	9	24	15
Sly06g0381251	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0381261	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0381271	M1	NA	349	331	346	238	153	261	246	286	214	181
Sly06g0381281	M12	NA	201	260	156	86	72	333	473	253	45	91
Sly06g0381301	M3	NA	2	3	2	3	2	2	2	1	1	1
Sly06g0381311	M1	NA	78	69	72	80	64	56	61	60	71	58
Sly06g0381321	M13	NA	27	24	26	30	44	25	23	25	83	94
Sly06g0381331	M12	NA	155	146	164	137	193	153	162	164	182	248
Sly06g0381341	M3	NA	2	3	2	1	1	2	2	1	1	1
Sly06g0381351	M9	NA	21	21	20	31	50	24	24	23	36	52
Sly06g0381361	M3	NA	247	350	159	102	146	166	178	66	30	82
Sly06g0381381	M12	NA	6	7	8	25	30	14	15	14	25	18
Sly06g0381401	M4	NA	36	26	29	37	52	56	48	41	158	187
Sly06g0381411	M19	NA	25	27	26	27	21	26	23	25	19	17
Sly06g0381421	M3	NA	14	16	11	20	20	13	13	12	20	20
Sly06g0381441	M22	NA	28	29	27	21	8	36	33	29	5	2
Sly06g0381471	M9	NA	56	60	56	108	120	83	83	74	115	147
Sly06g0381481	M1	NA	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0030781	M12	NA	8	9	9	22	20	56	75	50	311	201
Sly01g0030791	M1	NA	46	47	52	35	38	43	41	45	46	43
Sly01g0030801	M3	NA	45	46	39	63	56	41	50	39	91	82
Sly01g0030811	M3	SIERF.G1	2	2	2	1	1	2	2	1	0	0
Sly01g0030821	M3	NA	8	7	5	5	14	5	4	3	6	12
Sly01g0030831	M12	NA	1	1	2	7	2	12	15	44	78	12
Sly01g0030841	M1	NA	161	77	241	219	23	22	19	31	110	26
Sly01g0030851	M12	NA	16	19	20	44	51	27	31	29	53	58
Sly01g0030861	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0030871	M3	NA	2	1	1	3	1	1	1	1	1	1
Sly01g0030881	M3	NA	47	39	31	22	30	37	37	22	20	20
Sly01g0030901	M11	SIGH3-1	37	37	51	79	107	43	43	49	143	219
Sly01g0030921	M12	NA	15	16	13	12	10	44	43	47	18	10
Sly01g0030931	M12	NA	3	3	2	2	2	3	3	3	2	2
Sly01g0030941	M1	NA	13	12	11	2	1	8	8	9	1	1
Sly01g0030951	M3	NA	377	389	191	5	1	188	154	50	3	1
Sly01g0030961	M6	NA	32	99	44	7	15	11	30	5	1	6
Sly01g0030971	M3	NA	3	5	1	0	1	1	0	0	0	0
Sly01g0030981	M22	NA	1	1	1	1	0	3	2	2	0	0
Sly01g0030991	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0031001	M11	NA	27	24	32	32	45	54	49	57	39	35
Sly01g0031011	M19	NA	21	19	21	29	45	18	17	22	32	37
Sly01g0031021	M12	NA	2	2	2	2	1	6	6	7	4	1
Sly01g0031031	M1	SIPYL3	158	155	108	17	7	8	4	4	1	6
Sly01g0031041	M19	NA	13	14	15	15	17	13	11	14	14	16
Sly01g0031051	M22	NA	7	4	8	2	5	12	2	5	1	1
Sly01g0031061	M19	NA	21	22	21	24	23	24	20	23	23	20
Sly01g0031071	M11	NA	34	33	36	36	46	37	35	41	39	36
Sly01g0031081	M22	NA	2	2	2	8	3	3	1	2	1	1
Sly01g0031091	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly01g0031101	M3	NA	3	5	1	1	1	2	1	1	1	0
Sly01g0031111	M22	NA	1	1	1	0	0	2	0	1	0	0
Sly01g0031121	M11	NA	86	72	85	76	86	127	102	150	126	149
Sly01g0031131	M11	NA	10	10	10	13	12	13	11	12	11	11
Sly01g0031141	M12	NA	0	1	1	3	1	1	2	1	1	1
Sly01g0031161	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0031261	M1	NA	1	2	1	1	1	1	1	1	0	0
Sly01g0031301	M19	SISDG25	16	16	19	15	16	18	15	17	15	18
Sly01g0031321	M11	NA	11	14	16	144	216	18	18	27	243	238
Sly01g0031341	M1	NA	3	4	8	299	369	1	1	1	4	6
Sly01g0031351	M1	NA	289	338	521	1761	1861	43	37	48	243	318
Sly01g0031391	M1	NA	2	2	2	52	11	0	1	0	1	0
Sly01g0031401	M3	NA	70	80	45	30	28	49	77	34	38	52
Sly01g0031411	M12	NA	3	3	3	6	8	6	6	7	5	5
Sly01g0031421	M12	NA	31	41	26	27	47	44	48	36	25	47
Sly01g0031431	M12	NA	18	19	16	26	25	19	24	20	34	37
Sly01g0031441	M18	NA	18	20	19	36	41	19	19	22	38	30
Sly01g0031451	M1	NA	20	19	18	14	11	11	14	12	8	6
Sly01g0031461	M1	NA	16	16	15	12	11	14	12	13	9	8
Sly01g0031471	M12	NA	143	143	131	172	110	136	181	183	197	57
Sly01g0031491	M3	NA	175	193	61	89	68	33	40	27	41	33
Sly01g0031501	M3	NA	48	52	37	30	26	32	32	25	23	20
Sly01g0031511	M22	SIARF18	9	5	6	2	1	17	4	13	1	1
Sly01g0031521	M11	NA	14	13	22	16	20	26	26	58	33	16
Sly01g0031531	M11	NA	128	110	109	177	217	140	143	153	176	240
Sly01g0031541	M13	NA	118	95	158	271	325	150	141	239	444	504
Sly01g0031551	M19	NA	11	12	12	18	21	14	12	14	14	17
Sly01g0031571	M11	NA	65	55	68	57	54	69	64	87	61	69
Sly01g0031581	M12	NA	1	1	1	1	0	1	1	1	1	1
Sly01g0031591	M9	NA	13	11	9	23	23	21	22	23	53	51
Sly01g0031601	M1	NA	14	15	14	17	19	12	11	12	11	13
Sly01g0031621	M12	NA	1	1	1	2	2	1	1	1	2	1
Sly01g0031631	M12	NA	35	36	31	35	48	62	58	56	57	69
Sly01g0031641	M9	NA	4	4	3	2	2	11	12	5	1	2
Sly01g0031651	M7	NA	9	13	6	2	2	13	23	8	5	8
Sly01g0031661	M11	NA	7	7	8	7	10	10	9	11	10	10
Sly01g0031671	M12	NA	22	19	23	64	48	87	84	144	74	20
Sly01g0031681	M12	NA	17	17	17	50	60	24	34	38	126	89
Sly01g0031691	M11	NA	44	38	51	53	76	95	93	118	76	77
Sly01g0031701	M1	NA	4	4	6	2	2	2	1	2	1	1
Sly01g0031711	M1	NA	2	1	2	1	0	1	1	1	1	1
Sly01g0031721	M12	NA	158	154	155	276	354	163	174	176	212	265
Sly01g0031731	M1	NA	2	2	2	1	1	2	1	1	1	1
Sly01g0031741	M1	NA	354	326	324	233	205	230	225	216	265	275
Sly01g0031751	M12	NA	4	4	4	2	2	8	9	9	8	5
Sly01g0031771	M12	NA	57	38	46	48	20	48	45	54	32	19
Sly01g0031781	M1	NA	2	2	2	3	1	1	2	2	3	4
Sly01g0031801	M2	NA	6	5	7	6	5	5	8	4	7	19
Sly01g0031811	M12	SAUR2	30	24	25	60	93	26	31	33	139	125
Sly01g0031821	M12	NA	28	30	29	55	55	42	39	42	55	70
Sly01g0031831	M12	NA	2	2	3	1	1	7	7	6	1	1
Sly01g0031841	M3	NA	3	2	2	0	1	2	2	1	1	0
Sly01g0031851	M12	NA	1	1	1	2	2	1	1	1	1	1
Sly01g0031861	M18	NPRE1-like	14	15	20	19	21	31	21	30	13	17
Sly01g0031881	M1	NA	10	7	9	10	26	5	5	8	11	16
Sly01g0031891	M11	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0031901	M3	NA	44	35	32	3	2	15	14	3	1	1
Sly01g0031911	M5	NA	95	84	67	38	37	91	83	69	26	22
Sly01g0031921	M18	NA	3	4	4	3	3	4	3	5	2	2
Sly01g0031931	M12	NA	8	6	6	1	1	9	10	6	1	1
Sly01g0031941	M1	NA	23	27	22	14	22	13	13	11	8	12
Sly01g0031951	M11	NA	16	13	19	11	8	24	22	27	4	3
Sly01g0031961	M11	NA	22	20	27	26	32	34	31	42	28	30
Sly01g0031971	M19	NA	35	38	36	50	50	41	35	43	38	43
Sly01g0031981	M5	NA	51	59	40	34	38	55	50	46	44	58
Sly01g0031991	M10	NA	8	21	10	1	1	22	33	9	1	1
Sly01g0032001	M1	NA	85	76	73	65	74	58	58	57	57	73
Sly01g0032011	M11	NA	41	39	41	59	53	46	51	54	72	64
Sly01g0032021	M3	NA	31	38	30	28	30	29	29	29	27	37
Sly01g0032031	M3	SIPRMT1	26	30	23	12	11	13	16	11	13	11
Sly01g0032041	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0032051	M1	NA	140	121	163	151	191	123	121	142	150	218
Sly01g0032061	M1	NA	312	271	303	192	148	200	211	200	177	128
Sly01g0032071	M1	NA	331	295	325	233	178	221	249	217	246	180
Sly01g0032081	M19	NA	47	48	48	48	49	48	46	50	50	48
Sly01g0032091	M3	NA	48	43	40	43	47	40	42	44	51	50
Sly01g0032101	M11	NA	16	9	17	11	29	15	17	17	34	44
Sly01g0032111	M11	NA	20	11	18	11	30	22	21	20	42	63
Sly01g0032121	M11	NA	5	2	4	2	9	4	4	4	11	19
Sly01g0032141	M11	NA	26	25	32	88	285	44	44	44	158	274
Sly01g0032151	M10	NA	27	28	10	16	8	55	46	16	2	2
Sly01g0032161	M11	NA	1	1	1	1	0	2	2	2	1	1
Sly01g0032181	M1	NA	334	321	359	290	226	219	196	230	252	217
Sly01g0032191	M2	NA	95	99	87	115	121	89	100	82	127	141
Sly01g0032201	M10	NA	4	4	1	1	1	15	16	1	7	2
Sly01g0032211	M3	NA	16	25	14	3	2	13	17	3	2	2
Sly01g0032231	M12	AGO4D	1	1	1	1	1	1	1	1	1	1
Sly01g0032241	M1	NA	61	60	54	36	31	49	46	45	46	40
Sly01g0032251	M18	NA	35	34	41	24	16	38	34	40	24	14
Sly01g0032261	M3	NA	63	59	59	37	30	59	57	56	39	32
Sly01g0032271	M1	NA	13	7	16	6	3	2	1	2	1	2
Sly01g0032281	M3	NA	46	46	42	25	21	26	31	19	29	27
Sly01g0032291	M11	EIL3	128	135	134	101	124	152	158	134	142	212
Sly01g0032301	M1	NA	2	3	2	5	1	1	0	0	0	0
Sly01g0032311	M18	NA	44	48	46	75	72	48	46	49	56	53
Sly01g0032321	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0032341	M11	NA	11	11	13	18	18	14	12	15	22	23
Sly01g0032351	M22	NA	4	1	3	1	0	13	2	7	1	0
Sly01g0032361	M11	NA	50	47	54	79	103	73	64	80	87	87
Sly01g0032371	M1	NA	5	4	3	1	1	1	1	1	0	0
Sly01g0032381	M1	NA	12	13	12	12	10	9	9	9	12	10
Sly01g0032391	M18	NA	18	18	23	21	27	25	21	25	22	22
Sly01g0032401	M11	NA	23	19	21	19	17	20	16	25	22	19
Sly01g0032411	M1	NA	33	34	32	19	23	25	27	25	24	32

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0381551	M19	NA	27	26	30	17	15	26	23	28	16	16
Sly06g0381561	M22	NA	89	85	92	105	99	80	88	90	125	171
Sly06g0381571	M17	NA	43	38	43	38	49	35	36	44	54	63
Sly06g0381581	M3	NA	6	7	7	7	3	5	6	4	5	3
Sly06g0381601	M11	NA	15	12	15	12	14	14	15	15	14	18
Sly06g0381611	M13	SIPL	89	68	132	22	6	102	122	128	27	6
Sly06g0381621	M23	ABI3	1	1	1	1	0	1	1	1	1	0
Sly06g0381631	M22	ABI3-like1/ABI3	2	1	1	0	0	3	1	2	1	1
Sly06g0381661	M1	NA	287	258	266	261	310	221	223	225	298	334
Sly06g0381671	M8	NA	62	63	57	69	69	59	68	57	75	85
Sly06g0381681	M1	NA	31	31	26	16	17	22	21	20	14	18
Sly06g0381691	M1	NA	3	2	6	0	0	0	0	1	0	0
Sly06g0381701	M1	NA	12	11	15	3	7	11	11	10	2	3
Sly06g0381711	M3	NA	3	4	3	2	1	2	1	1	2	2
Sly06g0381721	M3	NA	7	7	6	4	6	5	7	4	5	10
Sly06g0381731	M11	NA	76	59	94	48	31	113	103	137	46	62
Sly06g0381741	M11	NA	21	18	21	44	61	28	25	30	42	61
Sly06g0381771	M12	NA	1	1	1	1	1	4	2	3	1	1
Sly06g0381791	M3	NA	96	101	90	88	75	89	97	78	79	69
Sly06g0381801	M1	NA	5	6	4	4	5	2	2	2	3	3
Sly06g0381811	M12	NA	7	8	9	17	19	10	12	10	3	4
Sly06g0381821	M22	SISDG14	16	17	20	15	14	20	15	17	12	8
Sly06g0381831	M11	NA	5	6	6	10	20	10	9	11	18	30
Sly06g0381841	M1	NA	476	444	408	329	350	339	334	327	393	449
Sly06g0381851	M3	NA	235	233	189	182	142	168	178	127	164	138
Sly06g0381861	M3	NA	11	8	7	14	8	7	6	5	4	2
Sly06g0381871	M11	NA	117	112	126	146	128	131	145	155	155	139
Sly06g0381881	M1	NA	150	132	118	100	80	77	76	73	86	71
Sly06g0381891	M12	NA	66	65	63	99	151	83	87	82	114	121
Sly06g0381901	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0381911	M1	NA	22	23	18	7	4	3	3	2	1	2
Sly06g0381921	M19	NA	46	47	51	42	43	40	35	43	32	35
Sly06g0381931	M23	NA	2	1	1	1	1	5	2	2	1	1
Sly06g0381941	M11	NA	16	18	21	27	32	31	27	36	48	50
Sly06g0381951	M3	NA	6	7	2	0	0	1	1	1	0	0
Sly06g0381971	M11	NA	7	7	8	8	9	7	8	9	9	9
Sly06g0382041	M3	NA	75	94	51	32	36	58	65	34	35	41
Sly06g0382051	M3	NA	21	22	16	15	14	18	19	15	14	14
Sly06g0382061	M13	NA	113	111	131	95	91	140	127	153	151	130
Sly06g0382071	M11	NA	371	348	533	812	949	699	659	837	736	805
Sly06g0382081	M11	NA	5	5	6	10	4	7	5	6	2	1
Sly06g0382101	M3	BMI-like2	5	5	4	5	5	4	5	5	3	3
Sly06g0382111	M11	NA	35	22	39	8	1	75	66	90	7	2
Sly06g0382121	M12	NA	12	11	12	10	14	12	13	16	23	34
Sly06g0382131	M22	SIAux/IAA2	3	2	2	0	0	3	1	2	1	0
Sly06g0382141	M11	NA	1	1	1	1	1	2	2	2	1	1
Sly06g0382151	M11	NA	8	6	6	1	1	13	11	10	1	1
Sly06g0382161	M12	NA	1	1	1	3	2	1	1	2	3	4
Sly06g0382181	M12	NA	9	9	11	15	12	11	10	14	34	31
Sly06g0382191	M12	NA	2	3	2	1	1	4	4	2	1	1
Sly06g0382201	M3	NA	1	1	1	1	1	1	1	1	0	1
Sly06g0382211	M1	NA	10	5	13	1	1	1	1	1	1	1
Sly06g0382221	M3	NA	9	9	8	9	11	8	8	8	12	12
Sly06g0382231	M1	NA	88	84	80	81	101	65	66	69	80	110
Sly06g0382241	M3	NA	76	92	79	17	8	26	65	29	9	15
Sly06g0382261	M1	NA	5	6	2	1	0	2	1	1	0	0
Sly06g0382271	M12	NA	48	49	43	39	46	53	60	50	57	85
Sly06g0382281	M3	NA	122	125	114	104	86	101	106	87	81	75
Sly06g0382291	M3	NA	11	14	9	13	18	10	13	10	17	27
Sly06g0382301	M1	NA	311	265	265	225	160	206	206	198	181	134
Sly06g0382311	M22	CPS	1	1	1	1	1	2	1	1	0	1
Sly06g0382331	M1	NA	18	19	21	15	3	15	12	12	6	1
Sly06g0382341	M12	NA	10	9	9	13	12	12	13	12	12	6
Sly06g0382351	M11	NA	41	40	45	80	99	42	43	50	66	91
Sly06g0382371	M12	NA	27	38	31	35	32	34	40	38	43	34
Sly06g0382381	M12	NA	17	20	15	24	19	26	26	29	37	21
Sly06g0382391	M16	NA	54	49	48	32	25	44	40	45	35	20
Sly06g0382401	M11	NA	14	11	17	17	17	20	14	22	11	7
Sly06g0382411	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly06g0382431	M1	NA	37	31	32	30	23	26	28	28	39	35
Sly06g0382441	M11	NA	75	77	75	124	191	98	92	105	215	280
Sly06g0382451	M2	NA	3	2	2	5	6	2	3	2	13	10
Sly06g0382461	M12	NA	1	1	1	1	0	1	1	1	1	0
Sly06g0382471	M12	SIABP1	25	25	31	110	228	29	33	35	106	268
Sly06g0382481	M11	NA	19	19	23	18	21	21	23	23	23	26
Sly06g0382491	M1	SIHP3	59	59	50	56	77	26	28	23	61	97
Sly06g0382501	M22	NA	2	1	1	1	1	2	1	1	1	0
Sly06g0382511	M3	NA	19	22	16	5	9	15	17	15	7	17
Sly06g0382521	M2	NA	59	57	50	68	72	44	48	43	68	73
Sly06g0382541	M1	NA	9	9	13	6	3	7	6	6	1	1
Sly06g0382551	M11	NA	7	7	9	7	4	13	12	14	7	4
Sly06g0382561	M11	NA	2	2	2	2	1	3	2	3	2	1
Sly06g0382581	M3	NA	46	45	33	33	33	30	35	29	37	35
Sly06g0382591	M1	NA	42	43	44	61	80	31	34	36	67	91
Sly06g0382601	M11	NA	100	96	103	90	110	106	99	111	123	126
Sly06g0382611	M19	NA	60	65	66	80	67	69	61	63	52	44
Sly06g0382621	M12	NA	48	39	48	356	661	64	68	85	334	742
Sly06g0382631	M20	NA	27	25	32	23	27	23	19	25	24	27
Sly06g0382641	M3	NA	3	4	2	3	2	1	2	1	1	1
Sly06g0382651	M1	NA	6	6	6	9	11	3	3	4	4	5
Sly06g0382661	M1	NA	4	5	5	5	4	2	2	2	4	2
Sly06g0382671	M11	NA	50	53	54	66	82	55	58	61	83	91
Sly06g0382681	M1	NA	4	3	4	5	3	2	2	2	2	1
Sly06g0382691	M1	NA	9	9	9	10	6	8	8	7	4	2
Sly06g0382701	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0382711	M1	NA	12	9	10	10	6	9	7	8	4	2
Sly07g0105301	M19	NA	31	33	32	47	57	28	25	31	50	55
Sly07g0105311	M11	NA	5	3	5	2	2	19	10	16	2	1
Sly07g0105321	M13	NA	24	22	25	15	24	21	23	22	12	11
Sly07g0105331	M1	NA	25	23	23	13	16	18	16	15	12	11
Sly07g0105361	M16	NA	376	334	313	253	177	273	265	297	217	151
Sly07g0105371	M11	NA	36	32	36	32	34	39	35	46	41	37
Sly07g0105401	M3	NA	1	2	1	0	0	1	1	1	0	0
Sly07g0105411	M1	NA	1	1	1	1	1	1	0	0	0	1
Sly07g0105421	M5	NA	1	1	1	0	1	1	1	1	0	0
Sly07g0105431	M11	NA	20	19	21	12	11	24	21	23	14	16
Sly07g0105441	M3	NA	14	13	15	9	5	8	7	4	2	1
Sly07g0105451	M1	SIRR23	9	9	9	11	9	2	1	1	1	1
Sly07g0105481	M1	NA	1	1	2	2	3	1	1	1	1	1
Sly07g0105491	M1	NA	64	61	62	25	14	20	24	14	2	1
Sly07g0105501	M22	NA	2	1	2	1	0	8	2	7	1	1
Sly07g0105511	M2	NA	78	81	69	57	62	45	56	42	78	97
Sly07g0105521	M11	TIL	76	69	97	79	53	150	138	172	108	100
Sly07g0105531	M22	NA	3	3	3	2	1	4	3	3	2	1
Sly07g0105541	M1	NA	12	12	12	6	3	11	9	8	5	3
Sly07g0105551	M1	NA	11	10	11	7	6	11	8	8	6	5
Sly07g0105561	M11	NA	16	13	13	9	13	16	14	18	22	24
Sly07g0105571	M11	NA	7	7	7	4	5	8	7	8	7	9
Sly07g0105581	M18	NA	8	8	10	6	5	13	9	13	11	11
Sly07g0105591	M11	NA	11	10	12	8	7	15	10	15	14	12
Sly07g0105601	M11	NA	52	48	75	19	8	79	61	100	18	8
Sly07g0105611	M11	NA	9	9	11	9	9	11	9	11	15	16
Sly07g0105621	M11	NA	8	6	8	7	6	10	8	11	11	8
Sly07g0105631	M18	NA	26	24	27	24	27	30	22	30	21	20
Sly07g0105641	M3	NA	103	136	66	31	51	66	116	46	52	132
Sly07g0105651	M11	NA	71	65	62	77	103	77	71	97	116	157
Sly07g0105671	M3	NA	2	2	2	2	3	2	2	2	2	3
Sly07g0105681	M2	NA	15	17	15	26	32	12	14	12	22	24
Sly07g0105701	M5	NA	18	26	5	1	0	20	15	2	1	0
Sly07g0105721	M14	NA	20	13	19	22	14	14	12	13	5	3
Sly07g0105731	M1	NA	10	11	7

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0032421	M3	NA	13	20	12	16	16	14	12	7	8	7
Sly01g0032431	M11	NA	3	2	5	1	2	4	3	3	1	1
Sly01g0032441	M3	NA	13	15	14	13	16	11	13	11	15	15
Sly01g0032451	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly01g0032461	M11	NA	19	20	16	20	25	16	18	20	24	18
Sly01g0032471	M3	NA	11	12	10	13	15	12	10	10	16	13
Sly01g0032491	M12	NA	35	32	34	39	48	33	33	38	50	50
Sly01g0032501	M11	NA	5	4	7	3	1	7	5	5	1	1
Sly01g0032511	M11	NA	84	79	83	72	72	83	82	91	97	109
Sly01g0032521	M9	NA	20	18	16	33	41	20	27	21	36	47
Sly01g0032531	M1	NA	19	17	18	15	19	17	15	18	13	15
Sly01g0032541	M5	NA	25	35	22	7	3	36	33	18	4	1
Sly01g0032561	M3	NA	20	22	7	0	0	4	4	1	0	0
Sly01g0032571	M3	NA	4	4	2	0	1	2	2	2	1	0
Sly01g0032601	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly01g0032611	M11	NA	1	1	1	0	0	2	2	1	0	0
Sly01g0032621	M11	NA	1	1	1	0	0	1	1	1	1	0
Sly01g0032641	M3	NA	133	132	86	38	34	68	65	58	59	54
Sly01g0032651	M11	PPR-like24	9	9	9	10	11	12	11	11	10	9
Sly01g0032661	M1	NA	46	45	50	45	31	41	43	43	49	46
Sly01g0032671	M11	NA	42	35	60	58	71	60	63	84	77	100
Sly01g0032681	M11	NA	18	19	23	32	33	48	37	53	29	25
Sly01g0032691	M10	NA	15	14	13	12	18	15	19	13	14	21
Sly01g0032711	M3	NA	100	94	72	111	155	61	64	53	89	139
Sly01g0032721	M12	NA	6	6	3	6	5	7	7	8	16	12
Sly01g0032731	M9	NA	9	10	5	7	6	10	13	10	36	35
Sly01g0032741	M22	NA	2	1	1	1	1	2	1	2	1	1
Sly01g0032761	M12	NA	3	2	4	3	4	5	5	6	5	7
Sly01g0032771	M12	NA	18	11	12	15	16	30	27	22	22	24
Sly01g0032781	M1	NA	245	149	191	298	615	59	50	10	6	3
Sly01g0032791	M2	NA	27	25	25	29	29	26	28	24	29	27
Sly01g0032801	M23	NA	8	7	6	7	6	8	7	7	8	10
Sly01g0032811	M1	NA	95	57	66	1	1	2	1	1	1	0
Sly01g0032821	M1	NA	1	1	1	1	1	0	0	0	0	0
Sly01g0032831	M22	SlAux/IAA16	14	7	13	1	1	16	11	12	1	0
Sly01g0032841	M11	NA	37	34	35	42	48	41	40	47	67	79
Sly01g0032851	M3	NA	86	78	70	86	119	74	78	69	98	153
Sly01g0032861	M19	NA	13	14	15	15	18	15	13	15	11	14
Sly01g0032871	M3	NA	25	26	19	17	11	18	17	16	12	8
Sly01g0032881	M11	NA	30	24	28	25	19	63	62	69	69	59
Sly01g0032891	M3	NA	119	141	97	48	49	75	89	49	46	50
Sly01g0032901	M1	NA	45	44	41	43	42	33	31	35	54	45
Sly01g0032921	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly01g0032931	M3	NA	4	4	4	2	3	3	3	3	1	1
Sly01g0032941	M12	NA	1	1	1	1	1	1	1	1	1	3
Sly01g0032951	M12	NA	1	1	1	2	2	1	1	1	14	9
Sly01g0032961	M1	NA	52	53	50	50	52	41	42	43	55	59
Sly01g0032971	M1	NA	160	154	163	216	269	100	119	108	191	248
Sly01g0032981	M11	NA	57	52	57	122	197	80	80	93	145	221
Sly01g0032991	M1	NA	44	22	61	29	15	2	3	1	1	2
Sly01g0033001	M12	NA	1	1	1	1	1	1	1	1	1	0
Sly01g0033011	M12	NA	56	62	52	99	76	107	110	85	54	37
Sly01g0033021	M1	NA	143	111	99	12	5	16	14	13	2	1
Sly01g0033031	M1	NA	1133	817	453	25	21	45	46	22	15	20
Sly01g0033051	M7	NA	1	1	1	0	1	1	1	1	1	0
Sly01g0033061	M12	NA	16	17	19	51	83	23	23	25	77	113
Sly01g0033101	M1	NA	25	29	25	18	17	19	17	16	9	7
Sly01g0033111	M12	NA	14	12	11	17	22	13	14	15	25	33
Sly01g0033141	M22	NA	1	1	1	1	1	3	1	2	1	1
Sly01g0033151	M1	NA	39	43	36	21	20	23	23	20	18	15
Sly01g0033191	M1	NA	3	2	2	2	2	1	1	1	1	1
Sly01g0033211	M1	NA	4	4	3	6	7	3	3	3	5	4
Sly01g0033221	M19	NA	13	13	13	10	9	13	12	13	9	9
Sly01g0033231	M3	NA	62	61	56	66	62	51	53	48	54	55
Sly01g0033261	M1	NA	539	549	537	418	292	389	423	360	402	290
Sly01g0033271	M11	NA	23	20	35	2	1	53	37	42	2	1
Sly01g0033291	M3	NA	24	23	24	21	20	23	23	20	23	23
Sly01g0033301	M11	NA	26	26	29	37	52	25	27	32	42	52
Sly01g0033311	M11	zds	43	41	45	119	301	46	45	53	153	313
Sly01g0033321	M11	NA	7	7	9	5	4	8	7	10	4	2
Sly01g0033331	M12	NA	3	4	4	3	3	11	11	13	5	2
Sly01g0033341	M12	NA	14	19	17	24	22	17	20	17	8	9
Sly01g0033371	M11	NA	29	28	35	14	11	54	47	60	16	7
Sly01g0033381	M1	NA	436	380	392	207	101	294	289	298	188	119
Sly01g0033391	M12	NA	107	118	111	396	279	111	139	159	1479	506
Sly01g0033401	M18	NA	24	21	23	22	21	26	20	25	16	15
Sly01g0033421	M11	NA	25	20	30	35	39	43	37	56	49	84
Sly01g0033431	M12	NA	2	2	2	1	1	10	6	11	10	11
Sly01g0033441	M12	NA	0	1	1	0	0	1	1	1	1	1
Sly01g0033461	M11	NA	2	1	1	1	1	3	2	2	0	0
Sly01g0033481	M3	NA	15	11	12	4	2	14	13	9	3	2
Sly01g0033491	M3	CTR2	35	39	32	32	38	35	32	31	24	34
Sly01g0033501	M12	NA	2	2	1	1	1	3	3	2	1	1
Sly01g0033511	M3	NA	124	110	95	54	42	70	86	64	80	66
Sly01g0033521	M1	NA	2	1	1	1	0	1	1	1	1	0
Sly01g0033531	M1	NA	21	15	13	3	2	8	6	10	1	1
Sly01g0033541	M1	NA	47	42	44	38	47	36	33	35	35	53
Sly01g0033551	M11	NA	57	51	56	41	27	70	67	67	35	38
Sly01g0033571	M7	NA	1	2	1	1	2	1	5	1	1	9
Sly01g0033581	M12	NA	0	1	1	1	1	1	3	1	1	2
Sly01g0033611	M1	NA	10	11	14	12	14	10	10	9	4	2
Sly01g0033621	M19	NA	65	72	71	94	107	62	54	63	51	61
Sly01g0033631	M3	NA	88	82	58	46	40	39	46	27	81	75
Sly01g0033641	M14	NA	7	6	11	102	329	6	7	12	391	657
Sly01g0033651	M1	NA	18	17	17	20	20	2	2	2	11	3
Sly01g0033661	M1	NA	5	6	4	18	27	3	3	4	9	8
Sly01g0033671	M5	NA	45	49	42	44	41	53	48	38	42	29
Sly01g0033681	M11	NA	21	22	21	17	20	25	23	21	20	17
Sly01g0033691	M19	NA	52	55	60	57	58	52	46	53	60	58
Sly01g0033701	M11	NA	54	55	93	188	158	128	131	139	203	106
Sly01g0033711	M11	NA	24	21	26	32	44	27	27	30	47	52
Sly01g0033721	M12	NA	23	19	20	35	37	33	28	36	49	55
Sly01g0033741	M1	NA	34	38	35	33	31	25	27	25	32	29
Sly01g0033751	M12	NA	1	1	1	0	0	1	1	1	1	1
Sly01g0033761	M9	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0033771	M3	NA	29	31	27	25	25	27	25	25	22	20
Sly01g0033781	M11	NA	1	1	2	2	2	2	2	2	2	4
Sly01g0033791	M22	NA	1	1	1	1	2	1	1	1	1	4
Sly01g0033801	M3	NA	4	6	4	9	7	3	3	3	4	8
Sly01g0033851	M3	NA	9	9	10	14	10	5	7	5	12	6
Sly01g0033871	M1	NA	17	16	19	16	10	16	14	17	11	7
Sly01g0033881	M1	SlCycL1;1	34	32	30	19	21	26	25	23	22	20
Sly01g0033891	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0033901	M1	NA	34	33	35	37	36	31	30	32	21	14
Sly01g0033911	M1	GID1C	16	14	17	7	5	3	2	2	1	1
Sly01g0033921	M11	SlHP1	20	15	25	3	2	23	19	28	14	12
Sly01g0033931	M1	NA	3	3	3	3	3	1	1	1	1	1
Sly01g0033951	M1	NA	37	37	40	45	51	22	24	24	41	50
Sly01g0033961	M10	NA	1	1	1	0	0	1	1	1	1	1
Sly01g0033971	M18	NA	10	10	12	10	13	13	12	14	14	14
Sly01g0033981	M11	NA	14	13	15	17	21	14	13	16	19	26
Sly01g0033991	M11	NA	3	3	3	4	4	3	3	4	3	3
Sly01g0034001	M1	NA	15	18	19	52	39	2	2	1	4	5
Sly01g0034011	M20	NA	61	64	88	58	49	65	51	56	25	25
Sly01g0034021	M20	NA	116	94	124	93	99	99	90	90	51	53
Sly01g0034031	M9	NA	3	3	2	2	2	5	5	3	5	7
Sly01g0034041	M5	NA	28	36	19	12	21	28	38	20	24	57
Sly01g0034051	M8	NA	26	31	19	10	17	24	33	24	32	62
Sly01g0034061	M3	NA	14	15	13	17	21	10	14	12	18	23
Sly01g0034071	M3	NA	41	41	37	69	91	36	40	37	59	87
Sly01g0034081	M1	NA	17	16	18	21	8	9	5	7	3	5
Sly01g0034091	M1	NA	4	4	4	49	63	1	2	3	89	142
Sly01g0034101	M6	NA	9	15	8	8	9	10	12	6	6	9
Sly01g0034111	M3	NA	299	352	177	81	62	129	120	35	4	12

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0105811	M3	NA	27	24	19	14	10	19	18	19	14	10
Sly07g0105821	M1	NA	38	37	32	27	27	25	24	26	28	29
Sly07g0105831	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly07g0105841	M12	NA	51	66	70	66	52	72	100	87	137	86
Sly07g0105851	M3	NA	57	74	82	32	49	46	71	56	57	87
Sly07g0105861	M22	NA	10	10	7	6	4	11	7	9	3	4
Sly07g0105871	M11	NA	425	430	496	499	392	512	472	595	591	450
Sly07g0105881	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly07g0105891	M9	NA	51	52	48	87	177	54	56	51	110	193
Sly07g0105901	M1	NA	514	484	504	454	609	429	455	471	429	505
Sly07g0105921	M11	NA	18	16	25	30	48	30	22	45	34	48
Sly07g0105931	M2	NA	18	18	16	23	33	17	19	16	27	33
Sly07g0105941	M1	NA	40	39	37	41	44	34	28	27	11	24
Sly07g0105951	M8	NA	246	260	234	260	194	235	310	212	212	195
Sly07g0105961	M10	NA	19	27	19	39	58	25	34	23	50	75
Sly07g0105971	M9	NA	13	17	14	24	37	17	24	16	29	39
Sly07g0106021	M3	NA	28	29	24	19	21	20	20	18	22	33
Sly07g0106031	M11	NA	13	14	17	20	21	20	18	24	22	27
Sly07g0106041	M22	NA	2	0	2	0	0	6	0	7	0	0
Sly07g0106071	M11	NA	49	46	60	39	30	80	74	95	31	30
Sly07g0106091	M22	NA	1	0	1	0	0	3	0	1	0	0
Sly07g0106151	M2	NA	64	68	72	116	84	54	68	61	129	107
Sly07g0106161	M1	NA	36	39	37	25	28	29	24	29	30	30
Sly07g0106171	M1	NA	78	73	84	64	71	50	59	54	68	68
Sly07g0106181	M15	NA	98	88	85	71	40	100	100	106	163	116
Sly07g0106191	M11	NA	114	102	115	123	97	128	132	143	115	85
Sly07g0106201	M3	NA	4	4	4	4	4	4	3	3	3	3
Sly07g0106211	M1	NA	2	3	4	2	4	2	3	4	2	4
Sly07g0106221	M12	NA	107	117	170	687	1259	216	334	391	1801	1654
Sly07g0106231	M11	NA	4	4	5	2	1	8	8	11	4	1
Sly07g0106241	M1	NA	28	30	24	30	17	2	3	2	1	1
Sly07g0106281	M2	NA	55	53	48	36	32	40	51	41	54	38
Sly07g0106291	M2	NA	417	367	326	274	220	323	367	330	394	251
Sly07g0106301	M1	NA	295	299	294	244	172	265	256	266	268	137
Sly07g0106311	M12	NA	1	1	1	1	1	1	3	1	3	1
Sly07g0106321	M11	NA	22	20	25	45	52	34	31	45	45	49
Sly07g0106331	M22	NA	5	3	4	2	2	13	2	10	2	2
Sly07g0106341	M19	NA	3	3	3	3	2	3	3	3	2	2
Sly07g0106351	M1	NA	13	12	12	23	14	7	7	7	19	15
Sly07g0106371	M11	NA	7	6	8	9	10	10	8	11	11	9
Sly07g0106381	M18	NA	42	43	46	39	44	48	41	50	46	52
Sly07g0106391	M1	NA	16	15	18	17	15	9	8	10	13	14
Sly07g0106401	M1	NA	2	2	3	6	2	1	1	1	0	0
Sly07g0106411	M1	NA	1	1	1	1	1	1	0	1	1	1
Sly07g0106431	M18	NA	19	21	27	22	31	29	23	32	26	35
Sly07g0106441	M12	NA	129	124	132	160	138	170	188	177	177	168
Sly07g0106471	M11	NA	10	9	11	9	7	11	9	12	6	5
Sly07g0106481	M1	NA	20	11	22	4	1	3	3	3	1	1
Sly07g0106491	M1	NA	13	15	13	13	15	13	12	11	12	13
Sly07g0106511	M3	NA	165	159	129	90	89	94	103	93	124	118
Sly07g0106521	M11	NA	19	20	20	38	38	31	29	37	32	39
Sly07g0106531	M12	NA	24	22	20	17	17	26	28	28	28	31
Sly07g0106541	M9	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0106551	M18	NA	10	12	12	17	22	14	11	14	16	33
Sly07g0106561	M11	NA	2	2	2	2	0	2	2	2	0	0
Sly07g0106571	M11	SlSDG16	4	4	5	2	2	9	6	8	6	17
Sly07g0106581	M3	NA	32	32	24	38	35	23	27	21	31	40
Sly07g0106591	M22	NA	2	1	2	1	2	2	2	2	2	2
Sly07g0106611	M12	NA	1	1	1	2	2	2	2	3	7	6
Sly07g0106621	M1	NA	4	4	4	9	7	2	1	1	1	1
Sly07g0106631	M1	NA	18	18	19	23	24	11	11	13	16	24
Sly07g0106641	M2	NA	75	68	59	83	93	46	53	43	98	71
Sly07g0106651	M3	NA	67	68	51	14	10	47	63	41	8	4
Sly07g0106661	M5	NA	69	67	59	72	56	67	68	60	60	43
Sly07g0106671	M3	NA	59	56	48	61	61	47	45	40	86	78
Sly07g0106691	M3	TPR1	39	43	42	76	119	32	37	31	84	171
Sly07g0106701	M3	NA	23	26	22	22	23	15	17	14	19	15
Sly07g0106711	M11	NA	33	23	26	38	57	32	29	37	51	63
Sly07g0106741	M3	NA	317	371	240	272	254	148	213	109	62	164
Sly07g0106761	M1	NA	20	21	18	17	18	13	13	15	16	15
Sly07g0106771	M11	NA	26	21	25	19	24	55	46	58	21	24
Sly07g0106781	M12	NA	68	63	57	107	103	74	78	82	156	146
Sly07g0106791	M12	NA	259	466	356	1219	1726	642	991	725	2255	2390
Sly07g0106811	M1	NA	17	17	29	38	11	1	1	1	1	0
Sly07g0106831	M18	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0106841	M3	NA	4	4	4	3	2	3	4	3	3	1
Sly07g0106851	M12	NA	13	13	17	72	128	25	29	39	116	121
Sly07g0106861	M1	NA	19	21	19	13	8	9	9	9	6	3
Sly07g0106871	M1	NA	2	1	2	1	1	1	1	1	1	1
Sly07g0106881	M1	NA	46	30	44	29	50	4	3	2	6	8
Sly07g0106891	M1	NA	80	2	107	0	0	7	9	6	0	0
Sly07g0106911	M22	NA	3	0	2	0	0	19	1	16	0	0
Sly07g0106931	M11	NA	41	35	37	40	31	40	42	45	47	41
Sly07g0106941	M1	NA	1	1	1	1	1	1	0	0	0	1
Sly07g0107031	M22	NA	1	0	1	0	0	1	0	1	0	0
Sly07g0107051	M3	NA	19	29	6	1	1	7	11	1	0	1
Sly07g0107071	M11	NA	23	28	23	35	38	36	37	42	35	34
Sly07g0107081	M14	NA	38	59	57	90	91	40	39	66	80	84
Sly07g0107091	M3	NA	75	83	68	50	54	64	66	56	41	45
Sly07g0107101	M11	NA	24	30	32	93	94	39	34	54	61	60
Sly07g0107111	M1	NA	50	57	48	49	53	33	29	35	36	43
Sly07g0107121	M1	NA	47	57	47	67	56	48	42	48	32	37
Sly07g0107131	M1	NA	1	1	1	1	1	0	0	0	0	0
Sly07g0107141	M11	NA	6	3	9	1	1	22	7	22	1	0
Sly07g0107151	M1	NA	100	75	112	83	116	56	27	45	2	3
Sly07g0107161	M11	NA	21	18	21	21	26	32	29	37	34	37
Sly07g0107171	M1	NA	5	7	6	4	2	1	1	1	1	1
Sly07g0107181	M12	NA	63	53	138	356	169	301	349	570	1195	644
Sly07g0107191	M2	NA	2	2	2	1	1	2	2	1	1	1
Sly07g0107221	M1	NA	2	1	2	1	6	1	1	1	2	4
Sly07g0107231	M1	NA	123	108	126	104	80	100	112	112	86	73
Sly07g0107241	M11	NA	218	214	280	282	284	323	284	398	237	214
Sly07g0107251	M1	NA	5	3	8	1	1	2	2	2	1	1
Sly07g0107261	M1	NA	26	27	26	24	35	15	13	14	16	28
Sly07g0107301	M12	NA	8	7	9	4	2	39	35	29	7	1
Sly07g0107331	M19	NA	27	25	30	21	20	22	20	23	18	15
Sly07g0107351	M1	NA	50	71	35	11	12	2	2	1	2	4
Sly07g0107361	M11	NA	22	21	25	40	32	31	28	38	79	91
Sly07g0107371	M3	NA	92	86	79	84	85	70	69	56	51	52
Sly07g0107391	M11	NA	9	8	11	6	4	21	17	21	3	3
Sly07g0107401	M19	SlHAF1	19	22	22	24	30	20	19	21	20	21
Sly07g0107411	M1	NA	122	111	110	98	93	85	84	90	93	83
Sly07g0107451	M12	NA	1	2	1	1	1	1	2	1	1	1
Sly07g0107461	M1	NA	2	2	3	4	4	0	0	0	1	0
Sly07g0107471	M11	NA	55	52	80	86	61	127	147	220	318	216
Sly07g0107481	M6	NA	80	120	61	4	16	67	93	19	2	17
Sly07g0107501	M11	NA	41	56	72	116	82	98	104	155	155	124
Sly07g0107511	M12	NA	11	11	11	11	7	15	17	15	10	6
Sly07g0107521	M6	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0107541	M12	NA	33	31	32	38	48	31	35	41	53	68
Sly07g0107551	M12	NA	38	37	38	27	20	42	45	46	34	38
Sly07g0107561	M14	NA	26	24	31	36	26	20	16	25	17	16
Sly07g0107571	M18	NA	3	4	2	2	3	4	2	3	5	3
Sly07g0107581	M1	NA	3	4	3	3	4	3	2	3	4	4
Sly07g0107591	M3	NA	6	4	3	4	7	3	3	5	9	9
Sly07g0107621	M1	NA	2	2	2	2	2	2	2	2	2	2
Sly07g0107631	M3	NA	87	81	61	82	59	48	57	33	44	34
Sly07g0107641	M11	NA	51	51	63	83	118	72	63	88	123	132
Sly07g0107651	M3	NA	12	14	13	5	2	9	9	3	1	1
Sly07g0107661	M1	NA	35	36	34	39	54	10	9	9	25	61
Sly07g0107691	M11	NA	15	14	21	34	57	23	21	31	37	66
Sly07g0107701	M11

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0034121	M12	NA	8	10	12	12	4	39	45	36	44	14
Sly01g0034131	M5	NA	31	27	26	21	22	31	29	24	25	26
Sly01g0034141	M11	NA	12	15	14	15	11	17	14	14	12	10
Sly01g0034161	M12	NA	20	23	21	23	30	23	25	23	35	38
Sly01g0034171	M11	NA	35	28	45	26	19	98	86	119	40	40
Sly01g0034181	M11	NA	40	33	47	44	62	93	75	83	23	37
Sly01g0034201	M10	NA	1	1	1	1	1	3	4	2	1	1
Sly01g0034221	M3	NA	12	21	6	2	3	5	9	5	2	3
Sly01g0034231	M12	NA	19	20	22	65	94	50	44	63	156	211
Sly01g0034241	M3	NA	19	18	11	3	2	6	8	3	2	1
Sly01g0034251	M1	NA	3	3	2	1	0	1	1	0	0	0
Sly01g0034261	M3	NA	81	99	74	210	277	39	42	24	89	180
Sly01g0034271	M1	NA	1	2	2	34	30	1	1	1	1	2
Sly01g0034281	M3	NA	19	23	17	14	25	18	21	15	17	38
Sly01g0034291	M3	NA	391	413	231	22	13	242	279	156	16	14
Sly01g0034301	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0034311	M1	NA	94	92	101	102	94	67	80	73	95	93
Sly01g0034321	M12	NA	2	2	2	1	1	8	6	7	3	1
Sly01g0034331	M7	NA	23	38	21	29	60	26	43	19	28	70
Sly01g0034341	M3	NA	15	18	12	10	8	7	11	7	8	8
Sly01g0034351	M1	NA	1	1	2	1	1	1	1	0	1	0
Sly01g0034361	M12	NA	17	21	21	24	35	26	24	25	33	39
Sly01g0034371	M10	NA	10	10	9	13	17	10	12	10	17	22
Sly01g0034381	M3	NA	84	100	51	56	41	48	45	21	7	8
Sly01g0034391	M7	NA	5	6	3	1	1	5	10	6	8	1
Sly01g0034401	M12	NA	4	4	3	1	1	5	5	5	3	1
Sly01g0034411	M8	NA	46	52	43	62	54	49	53	44	52	47
Sly01g0034421	M1	NA	116	115	108	96	97	62	65	59	89	100
Sly01g0034431	M10	NA	46	51	39	50	43	60	78	48	54	51
Sly01g0034441	M3	NA	253	296	131	56	119	94	122	38	45	137
Sly01g0034451	M18	NA	162	165	169	165	204	190	170	201	206	237
Sly01g0034461	M15	NA	47	42	36	38	57	43	46	43	58	78
Sly01g0034471	M1	SlCycU3;2	5	3	4	4	5	1	1	1	1	1
Sly01g0034481	M23	NA	1	1	1	1	0	1	1	1	0	0
Sly01g0034491	M12	NA	8	9	7	13	11	14	12	15	27	21
Sly01g0034521	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0034531	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0034541	M11	NA	29	29	36	47	63	49	40	59	57	70
Sly01g0034551	M3	NA	4	4	4	5	4	4	4	4	4	4
Sly01g0034561	M12	NA	2	1	2	7	6	2	3	3	11	9
Sly01g0034581	M22	NA	1	1	1	1	1	1	1	1	1	3
Sly01g0034591	M12	NA	1	1	3	401	245	1	3	5	598	524
Sly01g0034611	M1	NA	1	1	1	9	2	0	0	0	4	2
Sly01g0034641	M11	NA	2	1	2	1	3	2	2	2	3	3
Sly01g0034651	M11	NA	43	42	69	123	116	108	83	125	78	108
Sly01g0034661	M11	NA	84	106	123	411	392	98	107	117	240	283
Sly01g0034671	M11	NA	24	26	36	42	55	42	40	53	46	57
Sly01g0034681	M12	NA	15	13	15	16	11	19	22	19	16	8
Sly01g0034691	M11	NA	31	29	31	41	64	32	32	36	64	100
Sly01g0034701	M12	NA	2	2	3	12	8	2	2	3	21	7
Sly01g0034731	M11	NA	1	1	1	20	53	1	2	4	112	111
Sly01g0034741	M1	SlLOX5 (LOXE)	11	23	15	63	118	1	1	1	16	12
Sly01g0034761	M11	SlLOX9	1	1	1	1	1	1	1	1	2	2
Sly01g0034771	M12	SlLOX2 (LOXB)	392	494	829	6268	6155	695	981	1569	15542	13647
Sly01g0034781	M22	SlLOX7	3	2	3	5	5	9	3	6	1	7
Sly01g0034791	M1	SlLOX13	1	4	2	4	1	1	1	1	0	0
Sly01g0034801	M3	NA	17	20	17	16	19	17	15	15	15	14
Sly01g0034811	M1	NA	17	15	15	10	12	14	12	13	12	13
Sly01g0034821	M11	NA	15	14	14	14	15	15	14	14	13	14
Sly01g0034841	M11	NA	33	32	47	46	46	51	46	51	43	44
Sly01g0034851	M5	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0034861	M12	NA	29	28	27	38	32	30	33	29	60	43
Sly01g0034871	M3	NA	28	15	13	3	3	17	18	12	2	1
Sly01g0034881	M11	DMS11-like1	23	26	28	33	39	29	26	30	47	58
Sly01g0034891	M1	SlCycH1;1	9	10	10	11	7	6	7	6	4	1
Sly01g0034911	M3	NA	3	3	1	1	1	1	1	1	1	1
Sly01g0034921	M11	NA	51	63	49	41	33	59	59	55	13	6
Sly01g0034931	M2	NA	79	84	66	61	47	60	70	49	43	40
Sly01g0034941	M19	NA	24	23	21	25	26	22	20	21	20	21
Sly01g0034951	M7	NA	94	196	88	38	307	184	412	104	47	621
Sly01g0034961	M9	NA	22	22	21	33	35	34	47	35	76	104
Sly01g0034971	M2	NA	2	2	2	2	2	2	4	1	2	2
Sly01g0034981	M11	NA	103	99	122	133	147	165	154	176	145	192
Sly01g0034991	M11	NA	97	69	70	21	24	167	144	145	19	31
Sly01g0035001	M3	NA	6	9	7	7	12	6	7	7	12	24
Sly01g0035011	M9	NA	7	11	8	8	14	9	10	10	21	38
Sly01g0035021	M7	NA	5	6	5	5	10	4	7	6	11	22
Sly01g0035031	M2	NA	5	7	5	5	11	4	7	5	11	23
Sly01g0035041	M9	NA	7	8	6	2	2	13	14	10	3	5
Sly01g0035051	M9	NA	4	4	4	2	2	7	8	5	2	4
Sly01g0035061	M7	NA	4	6	3	1	5	4	8	7	4	15
Sly01g0035071	M7	NA	3	3	2	1	3	2	3	2	2	6
Sly01g0035091	M9	NA	4	6	5	3	9	7	13	8	8	27
Sly01g0035111	M12	NA	35	57	48	46	91	71	115	61	77	128
Sly01g0035121	M18	NA	3	4	5	6	8	7	6	8	9	9
Sly01g0035181	M9	NA	6	7	6	17	41	8	15	8	153	195
Sly01g0035191	M12	NA	147	133	184	322	429	244	313	318	1012	1180
Sly01g0035201	M12	NA	44	37	79	221	362	166	173	284	1629	1900
Sly01g0035211	M3	SlRbohA	2	3	1	4	3	1	1	3	42	30
Sly01g0035221	M1	XTH1	38	28	48	3	1	5	3	4	1	1
Sly01g0035231	M3	NA	18	17	14	34	40	16	16	15	80	79
Sly01g0035241	M20	NA	1	1	1	1	1	1	1	1	1	0
Sly01g0035251	M22	NA	2	2	2	21	45	5	2	3	6	32
Sly01g0035261	M3	NA	623	582	522	381	304	398	454	358	418	301
Sly01g0035271	M3	NA	622	753	414	294	436	409	664	399	545	881
Sly01g0035281	M11	NA	136	133	160	415	810	176	183	224	482	798
Sly01g0035291	M3	NA	98	102	74	76	69	59	63	56	52	54
Sly01g0035301	M3	NA	72	91	47	52	55	41	53	44	45	45
Sly01g0035311	M3	NA	69	70	57	62	69	50	52	50	63	77
Sly01g0035321	M12	NA	28	31	34	64	68	40	41	40	73	69
Sly01g0035341	M2	NA	34	38	31	33	39	25	29	27	53	59
Sly01g0035351	M11	NA	107	97	111	95	117	105	101	121	133	174
Sly01g0035361	M11	NA	56	53	86	70	52	182	129	197	76	64
Sly01g0035371	M1	NA	203	189	209	171	190	155	152	167	174	222
Sly01g0035381	M13	NA	7050	6622	7387	8037	6396	5777	6465	8185	10629	8290
Sly01g0035391	M15	NA	47	45	42	43	40	43	55	51	53	69
Sly01g0035401	M10	NA	121	119	108	124	123	137	151	115	93	119
Sly01g0035411	M1	NA	246	248	250	429	455	191	201	245	661	696
Sly01g0035421	M1	NA	2	2	2	1	1	1	2	1	1	1
Sly01g0035431	M1	NA	477	402	398	295	204	327	341	337	328	230
Sly01g0035451	M1	NA	718	425	684	240	203	305	196	293	47	101
Sly01g0035461	M1	NA	40	34	40	35	39	30	27	32	35	34
Sly01g0035471	M12	NA	25	26	25	35	28	26	30	31	41	31
Sly01g0035491	M1	NA	10	9	9	2	1	0	0	0	0	0
Sly01g0035501	M2	NA	64	68	60	82	95	54	77	57	109	104
Sly01g0035511	M16	NA	763	689	721	584	489	572	565	620	533	502
Sly01g0035521	M3	NA	2	3	2	1	1	3	2	1	0	0
Sly01g0035531	M12	NA	14	16	15	47	37	72	123	107	131	130
Sly01g0035541	M12	NA	113	111	122	146	192	123	117	142	293	395
Sly01g0035551	M11	NA	2	2	2	3	3	3	3	5	3	3
Sly01g0035571	M12	NA	1	2	1	2	4	2	2	1	2	2
Sly01g0035581	M12	NA	10	11	10	13	13	21	18	19	28	27
Sly01g0035591	M14	NA	24	15	41	13	8	20	15	24	3	2
Sly01g0035611	M12	NA	4	4	7	14	24	11	13	18	61	60
Sly01g0035621	M13	NA	65	64	84	62	36	49	73	75	39	15
Sly01g0035631	M6	NA	20	42	26	3	4	28	42	15	2	10
Sly01g0035641	M12	NA	2	2	2	1	1	3	3	4	2	1
Sly01g0035651	M1	NA	26	19	24	2	2	17	16	13	1	1
Sly01g0035661	M3	NA	77	75	39	6	6	49	42	29	2	3
Sly01g0035671	M11	SlTPL3	123	127	167	197	194	159	139	163	192	198
Sly01g0035681	M17	NA	75	71	67	74	86	68	67	74	83	100
Sly01g0035691	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0035701	M1	NA	23	25	27	22	21	22	21	24	23	26
Sly01g0035741	M12	NA	18	17	14	15	18	29	36	31	33	35

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0107731	M9	NA	62	83	88	48	170	100	197	79	30	196
Sly07g0107741	M1	NA	14	15	14	23	32	9	10	13	31	20
Sly07g0107751	M13	NA	51	29	68	13	7	63	62	104	7	7
Sly07g0107761	M12	NA	19	18	30	11	13	33	43	32	21	23
Sly07g0107771	M10	NA	94	152	76	22	67	142	220	63	15	62
Sly07g0107781	M13	NA	30	22	52	42	46	39	31	69	53	57
Sly07g0107801	M11	NA	3	2	3	2	5	3	3	3	2	1
Sly07g0107811	M19	NA	56	59	61	56	60	56	50	53	50	62
Sly07g0107821	M1	NA	17	19	15	6	9	5	6	3	2	8
Sly07g0107831	M19	NA	52	48	49	47	49	51	43	49	44	47
Sly07g0107851	M20	NA	149	53	241	2	2	75	45	61	1	1
Sly07g0107861	M11	NA	1	1	2	0	0	4	3	4	0	0
Sly07g0107871	M12	NA	4	8	5	0	1	41	51	22	0	0
Sly07g0107881	M11	NA	6	8	7	3	1	18	15	19	1	1
Sly07g0107901	M11	NA	14	13	15	23	33	18	16	20	27	25
Sly07g0107911	M11	NA	20	18	23	21	25	22	21	22	19	24
Sly07g0107941	M1	NA	4	4	7	8	8	3	2	3	7	8
Sly07g0107981	M1	NA	52	46	64	31	31	38	33	33	24	14
Sly07g0107991	M1	NA	24	19	33	12	8	15	14	15	3	2
Sly07g0108001	M1	NA	11	8	21	18	7	8	2	9	3	1
Sly07g0108011	M22	NA	20	17	23	22	28	21	17	21	27	38
Sly07g0108021	M1	NA	32	29	28	20	27	21	18	20	27	30
Sly07g0108031	M1	NA	49	52	54	62	53	33	36	32	39	39
Sly07g0108041	M19	NA	46	53	40	53	75	47	47	44	48	68
Sly07g0108051	M11	NA	282	223	410	124	71	1192	1079	1738	962	853
Sly07g0108061	M12	NA	73	77	65	37	35	83	86	97	55	45
Sly07g0108071	M9	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0108081	M3	NA	5	6	7	7	4	4	4	5	7	3
Sly07g0108151	M11	NA	0	1	1	1	1	3	2	3	1	1
Sly07g0108161	M11	NA	1	1	1	1	1	2	1	2	1	1
Sly07g0108181	M1	NA	24	22	21	23	27	20	19	20	25	34
Sly07g0108191	M1	NA	22	19	20	21	22	20	18	19	22	26
Sly07g0108231	M22	NA	13	9	14	4	3	32	10	25	2	1
Sly07g0108241	M1	NA	7	7	9	8	13	6	6	5	5	7
Sly07g0108261	M10	NA	6	11	4	4	9	10	16	5	4	11
Sly07g0108271	M10	NA	17	33	17	12	30	48	62	16	11	25
Sly07g0108281	M1	NA	269	254	255	304	268	96	70	83	27	107
Sly07g0108291	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0108301	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0108311	M12	NA	40	41	43	43	52	45	49	48	64	77
Sly07g0108321	M12	NA	3	3	5	9	9	8	6	7	8	11
Sly07g0108331	M9	NA	5	5	5	9	10	8	9	8	12	14
Sly07g0108341	M3	NA	26	27	25	28	28	23	24	26	34	29
Sly07g0108351	M9	NA	16	20	16	27	101	19	26	19	71	132
Sly07g0108361	M12	NA	10	9	11	4	2	30	24	22	1	1
Sly07g0108371	M12	NA	30	31	30	33	34	31	33	33	33	28
Sly07g0108391	M20	NA	6	5	7	8	6	5	4	5	3	2
Sly07g0108401	M12	NA	7	6	8	12	15	9	8	9	16	19
Sly07g0108411	M12	NA	5	4	2	1	1	10	10	8	4	1
Sly07g0108501	M1	NA	4	3	3	1	0	1	0	0	0	0
Sly07g0108511	M1	NA	2	6	9	12	20	6	0	4	1	1
Sly07g0108521	M22	NA	1	0	1	0	0	3	0	3	0	0
Sly07g0108531	M11	NA	678	535	887	142	38	1057	1070	1126	40	8
Sly07g0108541	M1	NA	504	790	936	1063	605	129	147	184	121	84
Sly07g0108621	M3	NA	70	76	60	58	87	54	60	56	61	80
Sly07g0108631	M18	NA	160	156	205	233	252	173	182	194	191	201
Sly07g0108641	M1	NA	93	122	162	58	7	4	2	2	1	1
Sly07g0108651	M19	NA	16	17	19	19	17	17	16	18	18	19
Sly07g0108661	M5	NA	61	79	44	41	44	69	73	42	45	52
Sly07g0108671	M12	NA	55	57	68	96	119	79	87	98	171	176
Sly07g0108681	M1	NA	16	18	19	15	15	12	10	11	13	16
Sly07g0108701	M3	OPR3-like	642	656	384	22	11	146	155	48	3	4
Sly07g0108721	M3	NA	27	28	25	28	29	26	26	27	31	27
Sly07g0108741	M11	NA	1	1	1	1	1	1	2	1	1	1
Sly07g0108751	M11	TBG	91	75	190	352	208	164	171	287	283	190
Sly07g0108761	M11	NA	5	5	6	6	7	6	5	5	4	6
Sly07g0108781	M1	NA	5	4	9	2	1	3	2	2	1	0
Sly07g0108791	M6	NA	10	13	12	12	25	9	15	7	7	32
Sly07g0108801	M3	NA	44	40	33	44	51	29	28	27	46	43
Sly07g0108811	M12	NA	10	12	11	13	12	13	14	15	12	11
Sly07g0108821	M1	NA	1	1	1	1	1	1	0	0	0	0
Sly07g0108851	M22	NA	1	1	1	1	1	2	1	2	1	1
Sly07g0108861	M3	NA	42	45	34	36	44	39	38	33	42	53
Sly07g0108871	M12	NA	1	1	1	1	1	1	1	1	1	2
Sly07g0108881	M1	SlAux/IAA35	31	25	17	1	1	4	1	2	1	0
Sly07g0108891	M12	NA	6	6	7	3	1	14	12	9	1	1
Sly07g0108901	M12	SlTPL5	25	26	29	28	38	36	32	34	36	35
Sly07g0108911	M22	NA	15	13	14	12	16	14	13	13	14	15
Sly07g0108921	M1	NA	46	47	31	20	29	22	22	16	15	22
Sly07g0108941	M12	NA	18	19	17	14	13	21	20	17	10	11
Sly07g0108951	M11	NA	7	6	8	3	3	14	11	15	3	2
Sly07g0108961	M10	NA	189	283	144	43	11	274	329	147	75	34
Sly07g0108971	M6	NA	1	2	2	1	1	2	2	1	1	1
Sly07g0108991	M3	NA	7	12	7	3	1	3	3	1	1	1
Sly07g0109001	M1	NA	30	27	27	11	12	13	12	10	6	8
Sly07g0109011	M18	NA	27	30	29	29	27	37	30	35	22	21
Sly07g0109021	M11	NA	13	12	15	39	43	18	13	21	25	28
Sly07g0109031	M1	NA	123	78	167	115	61	3	1	1	1	1
Sly07g0109041	M18	NA	28	27	29	25	34	29	27	31	30	43
Sly07g0109051	M1	NA	3	2	2	1	1	0	1	0	0	0
Sly07g0109061	M23	NA	2	1	1	0	0	2	2	1	1	0
Sly07g0109091	M1	HB1	46	44	29	1	1	14	14	11	2	1
Sly07g0109101	M3	EBF3	171	176	74	58	24	68	72	26	63	15
Sly07g0109111	M12	NA	19	20	21	32	29	25	28	30	36	35
Sly07g0109121	M3	NA	24	23	21	27	24	19	22	20	24	21
Sly07g0109131	M1	NA	3	4	5	2	2	4	2	2	1	1
Sly07g0109141	M11	NA	2	1	1	1	1	3	4	4	2	1
Sly07g0109161	M11	NA	16	17	20	38	55	24	26	33	46	45
Sly07g0109171	M5	NA	152	160	79	46	42	123	143	58	26	49
Sly07g0109181	M1	NA	60	64	59	40	32	36	40	35	43	35
Sly07g0109191	M1	NA	167	181	154	140	128	107	119	99	144	134
Sly07g0109201	M3	NA	66	64	59	68	60	55	57	59	73	89
Sly07g0109211	M1	NA	1	1	2	1	1	1	1	1	11	5
Sly07g0109221	M3	NA	373	341	334	266	235	251	288	235	291	233
Sly07g0109261	M12	NA	1	1	1	1	1	3	3	2	3	1
Sly07g0109271	M23	NA	1	1	1	0	0	1	1	1	1	1
Sly07g0109281	M23	NA	1	1	1	1	1	1	1	1	2	2
Sly07g0109301	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly07g0109311	M1	NA	3	1	1	0	1	1	1	1	0	0
Sly07g0109321	M9	NA	111	128	72	89	106	118	197	145	344	231
Sly07g0109361	M1	NA	1	1	1	4	3	1	1	1	1	2
Sly07g0109371	M19	NA	20	23	23	25	20	21	20	21	20	17
Sly07g0109381	M12	SlSDG37	15	17	18	24	35	17	17	19	34	44
Sly07g0109391	M11	NA	7	8	8	9	5	11	11	13	8	5
Sly07g0109411	M1	NA	11	12	13	13	14	10	9	11	13	15
Sly07g0109421	M3	NA	58	57	47	50	32	44	43	41	42	24
Sly07g0109451	M12	NA	4	4	4	7	4	7	4	5	12	3
Sly07g0109461	M1	NA	11	10	13	20	23	10	10	12	18	14
Sly07g0109471	M11	NA	7	6	9	10	9	12	12	16	16	23
Sly07g0109481	M22	NA	1	1	1	3	2	2	0	1	0	1
Sly07g0109491	M1	NA	9	10	8	6	8	1	1	1	1	1
Sly07g0109501	M1	NA	1	2	1	1	1	1	1	1	1	2
Sly07g0109521	M3	NA	12	18	8	1	1	3	3	1	1	1
Sly07g0109531	M1	NA	7	11	7	1	0	1	1	1	0	1
Sly07g0109541	M1	NA	101	104	97	93	72	78	73	81	111	86
Sly07g0109551	M3	NA	34	49	12	6	7	16	29	6	2	3
Sly07g0109561	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0109581	M1	NA	6	7	7	8	6	4	5	4	6	9
Sly07g0109591	M3	NA	25	27	21	28	29	18	22	17	21	23
Sly07g0109601	M5	NA	5	6	4	1	1	6	5	3	1	0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0035751	M12	NA	43	45	40	40	40	70	80	74	59	53
Sly01g0035771	M22	NA	1	1	1	0	1	2	1	2	0	0
Sly01g0035781	M3	NA	25	28	24	35	41	24	24	27	53	54
Sly01g0035791	M11	NA	47	42	48	35	35	55	53	56	37	40
Sly01g0035811	M3	NA	44	47	38	44	45	36	39	33	47	51
Sly01g0035831	M11	NA	7	7	8	11	15	8	8	7	6	6
Sly01g0035841	M11	NA	12	12	14	16	17	15	16	17	14	16
Sly01g0035861	M10	NA	17	26	11	23	32	27	35	9	26	35
Sly01g0035871	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0035881	M12	NA	3	2	2	1	1	3	3	3	1	1
Sly01g0035901	M2	NA	31	24	25	53	98	28	27	24	66	136
Sly01g0035911	M6	NA	6	11	8	11	52	8	10	5	15	81
Sly01g0035921	M12	NA	5	6	4	8	18	6	7	6	10	17
Sly01g0035931	M11	NA	18	16	19	26	42	21	20	20	30	42
Sly01g0035941	M11	NA	2	2	2	3	4	8	5	7	7	13
Sly01g0035951	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0035961	M1	NA	6	6	5	2	2	5	4	4	2	1
Sly01g0035971	M5	NA	18	20	14	14	9	19	21	12	8	6
Sly01g0035981	M1	NA	16	16	19	31	24	16	14	14	13	16
Sly01g0035991	M9	NA	172	189	192	625	473	257	315	260	716	620
Sly01g0036021	M12	NA	27	28	27	35	39	28	28	31	48	46
Sly01g0036051	M11	NA	3	3	4	3	5	3	3	5	5	5
Sly01g0036071	M11	NA	493	422	467	495	495	444	428	554	633	664
Sly01g0036081	M11	NA	101	97	104	233	220	103	111	112	179	196
Sly01g0036091	M2	NA	322	323	271	384	368	204	254	371	622	841
Sly01g0036101	M9	NA	584	657	738	1155	580	782	841	736	1058	583
Sly01g0036111	M9	NA	1	1	1	1	1	2	1	1	2	1
Sly01g0036121	M12	NA	9	11	10	8	10	10	11	11	9	8
Sly01g0036131	M3	NA	24	25	21	31	39	18	20	21	45	39
Sly01g0036141	M12	NA	15	16	15	23	27	15	17	16	29	27
Sly01g0036151	M3	NA	45	44	33	19	18	23	26	18	24	18
Sly01g0036161	M22	NA	1	1	1	0	0	2	1	2	0	0
Sly01g0036171	M19	NA	4	4	4	5	4	4	4	5	5	4
Sly01g0036181	M3	NA	9	13	9	28	35	7	9	8	39	58
Sly01g0036201	M2	NA	35	36	32	38	51	30	35	31	39	57
Sly01g0036211	M1	NA	2	2	2	11	6	1	1	1	1	1
Sly01g0036221	M11	NA	54	51	57	73	103	58	53	66	134	168
Sly01g0036231	M1	NA	14	13	14	9	8	3	3	3	4	4
Sly01g0036241	M13	NA	174	156	188	441	692	197	189	245	429	735
Sly01g0036251	M11	NA	4	4	5	2	1	16	9	12	1	1
Sly01g0036261	M18	NA	11	9	13	9	9	15	11	16	8	8
Sly01g0036271	M3	NA	4	4	3	2	2	3	3	3	3	2
Sly01g0036281	M1	NA	269	259	276	156	135	203	205	207	169	164
Sly01g0036291	M1	NA	20	18	21	15	12	16	17	16	16	18
Sly01g0036301	M3	NA	107	100	68	39	31	78	98	59	68	60
Sly01g0036311	M12	NA	2	2	3	1	1	14	11	9	1	0
Sly01g0036321	M11	NA	20	19	20	22	28	31	30	36	38	32
Sly01g0036331	M22	NA	3	1	2	1	0	10	2	3	1	0
Sly01g0036341	M18	NA	8	8	10	21	32	14	9	14	49	70
Sly01g0036351	M11	Catalase	10	11	11	23	37	15	12	17	60	75
Sly01g0036361	M11	NA	5	12	16	20	41	12	13	11	58	96
Sly01g0036371	M12	Catalase	17	20	24	35	68	19	19	23	112	173
Sly01g0036381	M11	NA	19	22	24	32	50	38	32	42	50	47
Sly01g0036411	M12	NA	68	68	37	22	14	151	140	132	33	17
Sly01g0036441	M12	NA	29	31	25	29	36	47	55	55	58	65
Sly01g0036451	M3	NA	47	43	38	36	36	32	35	34	40	48
Sly01g0036461	M1	NA	504	336	400	65	44	48	38	39	12	17
Sly01g0036471	M11	NA	77	69	77	75	79	98	89	97	105	113
Sly01g0036481	M11	NA	12	13	15	14	14	14	13	17	16	18
Sly01g0036491	M3	NA	11	12	10	11	11	8	8	7	11	13
Sly01g0036501	M1	NA	2	2	3	6	2	1	1	1	3	2
Sly01g0036511	M1	NA	27	60	74	695	182	3	2	2	14	14
Sly01g0036521	M1	NA	13	11	11	8	4	10	12	12	6	4
Sly01g0036531	M1	NA	2	2	2	2	2	1	1	1	2	1
Sly01g0036541	M1	NA	3	3	3	4	3	3	3	3	3	2
Sly01g0036551	M3	NA	34	32	24	21	28	21	23	25	30	37
Sly01g0036561	M12	NA	22	24	22	26	29	27	29	25	31	33
Sly01g0036571	M12	NA	1	1	1	1	1	2	2	2	3	1
Sly01g0036581	M3	NA	37	38	29	32	32	33	36	35	51	41
Sly01g0036601	M3	NA	28	30	23	33	21	25	26	21	25	14
Sly01g0036611	M3	NA	627	590	572	558	468	506	584	526	604	643
Sly01g0036621	M12	NA	655	593	675	657	451	885	992	1095	937	820
Sly01g0036631	M12	NA	9	7	11	11	3	109	133	166	152	34
Sly01g0036641	M1	NA	1	2	1	0	0	1	1	0	0	0
Sly01g0036651	M22	NA	3	2	4	2	1	4	2	3	1	1
Sly01g0036661	M1	NA	1	1	2	1	1	1	1	1	0	1
Sly01g0036681	M1	NA	11	7	15	2	2	2	1	2	1	1
Sly01g0036691	M1	NA	16	11	17	4	2	10	9	9	1	1
Sly01g0036701	M1	NA	4	5	4	1	1	2	2	2	1	1
Sly01g0036711	M11	NA	12	14	16	22	37	16	15	16	30	32
Sly01g0036721	M11	NA	381	299	332	272	323	480	393	466	349	435
Sly01g0036741	M12	NA	13	11	12	18	25	15	15	15	21	27
Sly01g0036751	M1	BIN2	311	311	332	398	497	279	295	281	370	498
Sly01g0036761	M1	NA	41	42	40	44	66	38	34	41	67	81
Sly01g0036771	M1	SPT16-like	60	63	54	57	58	46	39	43	46	47
Sly01g0036781	M1	NA	5	4	5	4	3	5	4	3	1	1
Sly01g0036791	M23	NA	115	108	109	156	112	120	118	99	62	66
Sly01g0036821	M1	SAMS	2695	2308	3331	844	568	2586	2133	2581	1455	1178
Sly01g0036831	M11	NA	15	15	17	15	15	19	15	17	21	18
Sly01g0036841	M12	NA	13	16	13	18	28	16	22	17	26	47
Sly01g0036851	M11	NA	12	13	18	16	16	24	24	23	13	8
Sly01g0036861	M3	NA	3	3	2	1	1	2	2	2	1	1
Sly01g0036871	M1	NA	10	10	11	3	4	3	3	4	1	1
Sly01g0036881	M7	NA	3	5	2	4	10	4	8	2	3	13
Sly01g0036891	M3	NA	77	93	61	72	79	69	73	52	68	78
Sly01g0036901	M1	PPR-like8	4	4	4	2	1	3	3	3	2	2
Sly01g0036911	M1	NA	20	19	17	17	19	14	14	14	17	24
Sly01g0036941	M5	NA	1	1	1	0	0	1	1	0	0	0
Sly01g0036951	M5	NA	1	2	1	0	0	2	1	0	0	0
Sly01g0036971	M11	NA	29	27	28	27	29	27	26	30	25	25
Sly01g0036981	M11	NA	311	299	429	272	258	373	348	462	353	304
Sly01g0036991	M1	NA	83	80	88	65	65	85	75	79	90	97
Sly01g0037001	M6	NA	4	5	3	1	1	7	7	3	0	1
Sly01g0037011	M11	NA	2	3	2	1	1	3	3	3	1	1
Sly01g0037021	M1	NA	15	14	14	7	2	6	8	6	3	2
Sly01g0037031	M11	NA	10	7	9	6	25	12	11	15	41	87
Sly01g0037041	M1	NA	9	11	10	3	4	5	5	4	7	11
Sly01g0037051	M11	NA	84	71	89	144	235	139	127	180	444	673
Sly01g0037061	M9	NA	430	513	333	175	382	484	932	531	882	1300
Sly01g0037081	M11	NA	27	24	46	41	41	52	42	59	36	49
Sly01g0037091	M11	NA	20	18	31	9	13	89	71	99	10	26
Sly01g0037111	M11	NA	1	1	1	1	1	2	2	3	2	1
Sly01g0037141	M12	NA	64	58	66	48	12	117	125	153	98	63
Sly01g0037151	M1	NA	15	13	12	1	2	6	3	5	1	1
Sly01g0037161	M12	NA	12	16	17	12	7	37	56	56	22	15
Sly01g0037181	M11	NA	28	28	31	19	21	35	27	34	18	16
Sly01g0037201	M6	NA	15	17	12	5	6	18	22	11	6	4
Sly01g0037211	M1	NA	14	13	13	9	8	10	7	8	2	2
Sly01g0037221	M2	NA	98	99	89	80	62	78	91	99	73	63
Sly01g0037251	M12	NA	2	2	2	2	1	3	2	2	1	1
Sly01g0037281	M12	NA	5	4	4	9	10	8	8	11	17	14
Sly01g0037291	M12	NA	5	4	4	7	12	6	5	7	12	18
Sly01g0037301	M9	NA	24	24	26	25	29	27	30	24	25	31
Sly01g0037311	M12	NA	39	52	35	32	52	48	54	49	50	101
Sly01g0037321	M3	NA	36	36	29	29	26	25	27	20	25	21
Sly01g0037331	M3	NA	43	48	43	44	37	46	46	40	32	35
Sly01g0037341	M1	NA	4	4	4	2	3	4	3	4	2	1
Sly01g0037351	M12	NA	36	34	29	16	19	43	39	39	15	13
Sly01g0037361	M12	NA	25	26	25	15	14	34	31	30	12	7
Sly01g0037371	M18	NA	21	23	25	23	25	28	27	29	22	22
Sly01g0037381	M19	NA	75	74	67	51	48	67	65	65	49	48
Sly01g0037391	M3	cel3	75	79	51	65	103	57	56	49	58	152
Sly01g0037401	M3	NA	50	50	39	41	40	36	36	33	41	41
Sly01g0037411	M12	FRO04	5	4	6	11	27	14	13	12	46	56

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0109671	M11	NA	14	14	13	8	4	20	21	28	5	1
Sly07g0109701	M11	NA	62	54	64	62	70	58	60	72	90	88
Sly07g0109711	M19	NA	29	31	32	17	14	23	19	24	17	17
Sly07g0109721	M11	NA	83	69	74	91	130	85	80	99	108	169
Sly07g0109731	M12	NA	44	51	46	74	81	47	49	54	77	87
Sly07g0109741	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0109761	M3	NA	57	55	49	45	31	38	47	41	55	34
Sly07g0109771	M6	NA	4	9	3	1	3	9	10	2	1	6
Sly07g0109781	M10	NA	5	7	4	1	1	8	11	4	1	1
Sly07g0109791	M1	NA	125	101	85	53	82	61	59	46	48	67
Sly07g0109801	M1	NA	10	9	10	11	12	9	9	8	8	9
Sly07g0109811	M3	NA	54	51	43	28	26	29	34	27	30	31
Sly07g0109831	M19	NA	84	90	104	105	116	99	81	100	66	67
Sly07g0109841	M12	NA	7	7	7	7	6	6	7	7	4	4
Sly07g0109851	M18	NA	74	71	112	87	63	99	72	93	15	24
Sly07g0109861	M12	NA	20	23	25	23	22	27	24	24	26	36
Sly07g0109871	M12	NA	2	3	3	3	1	2	3	4	3	2
Sly07g0109881	M1	NA	18	27	36	8	1	4	3	7	8	4
Sly07g0109891	M3	NA	69	73	63	43	34	48	51	40	24	26
Sly07g0109901	M1	NA	133	140	138	141	156	95	99	95	123	131
Sly07g0109921	M1	NA	19	20	27	46	41	20	16	23	41	40
Sly07g0109971	M12	NA	3	3	4	7	7	16	13	49	93	33
Sly07g0110031	M1	NA	6	6	8	8	8	4	2	5	1	1
Sly07g0110061	M1	NA	189	173	192	198	241	171	167	188	252	290
Sly07g0110091	M11	NA	9	10	11	12	11	12	11	13	15	11
Sly07g0110101	M3	NA	71	66	67	68	62	49	61	55	61	60
Sly07g0110131	M12	NA	5	4	5	10	10	8	9	9	12	7
Sly07g0110141	M1	NA	3	3	2	1	1	2	1	1	1	1
Sly07g0110181	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0110201	M3	NA	3	3	3	3	2	3	3	3	3	1
Sly07g0110211	M12	NA	1	1	1	1	1	3	1	1	1	1
Sly07g0110291	M3	NA	34	35	30	34	30	25	28	22	30	23
Sly07g0110301	M3	NA	450	416	366	309	182	251	291	223	246	173
Sly07g0110321	M1	NA	38	43	43	40	54	27	24	26	30	42
Sly07g0110361	M1	SIXTH2	30	39	119	171	47	3	1	1	1	1
Sly07g0110371	M1	NA	2	2	1	1	1	1	1	1	1	1
Sly07g0110441	M12	NA	2	2	2	2	1	3	3	3	1	1
Sly07g0110451	M1	NA	3	4	3	2	1	2	1	2	1	1
Sly07g0110461	M1	NA	6	6	10	42	99	1	1	2	14	58
Sly07g0110471	M1	NA	4	4	8	24	72	0	0	2	13	30
Sly07g0110481	M11	NA	22	18	27	17	23	31	32	44	21	14
Sly07g0110491	M3	NA	4	4	3	3	2	4	3	3	3	4
Sly07g0110501	M1	NA	54	49	50	42	159	4	6	8	49	59
Sly07g0110511	M1	NA	86	81	91	70	75	73	73	78	57	59
Sly07g0110531	M1	NA	6	2	4	7	1	5	1	1	1	1
Sly07g0110571	M3	NA	48	64	54	83	26	61	88	18	136	170
Sly07g0110581	M1	NA	10	1	1	1	1	1	1	1	9	2
Sly07g0110661	M11	ISA1	9	9	13	8	2	18	13	16	2	1
Sly07g0110671	M11	NA	2	2	2	1	1	3	2	6	1	1
Sly07g0110681	M3	NA	15	15	14	21	22	13	15	13	19	17
Sly07g0110691	M11	SAUR63	18	12	23	17	9	21	20	26	3	2
Sly07g0110701	M22	NA	7	6	8	5	2	12	6	10	1	1
Sly07g0110711	M11	NA	70	67	74	75	69	86	74	96	90	86
Sly07g0110731	M1	NA	100	74	59	22	17	6	6	6	3	2
Sly07g0110761	M1	NA	118	114	116	109	86	88	100	86	78	73
Sly07g0110771	M18	NA	2	1	3	3	2	5	3	5	1	1
Sly07g0110781	M11	NA	14	12	15	17	23	22	22	23	29	40
Sly07g0110811	M11	NA	20	17	21	15	12	24	22	26	18	19
Sly07g0110871	M11	NA	9	9	11	8	4	18	15	19	6	3
Sly07g0110931	M12	NA	1	1	1	1	3	7	5	7	2	1
Sly07g0110981	M3	NA	52	45	48	69	59	43	49	45	78	78
Sly07g0110991	M11	NA	7	7	8	10	8	9	9	10	7	4
Sly07g0111041	M3	NA	1	1	1	0	0	1	0	0	0	0
Sly07g0111171	M3	NA	21	24	22	13	16	12	16	13	13	7
Sly07g0111211	M15	NA	356	325	337	247	192	330	339	347	352	279
Sly07g0111221	M11	NA	14	14	18	10	4	57	52	68	22	6
Sly07g0111231	M1	SIARF7A	36	35	46	14	16	18	13	17	1	2
Sly07g0111251	M15	NA	130	116	107	127	138	120	116	129	159	164
Sly07g0111281	M12	NA	25	24	35	29	39	28	27	27	22	23
Sly07g0111301	M12	NA	13	12	14	15	10	11	15	13	20	8
Sly07g0111311	M22	NA	11	10	12	17	11	13	10	11	14	6
Sly07g0111321	M3	NA	21	22	19	23	22	18	20	18	22	25
Sly07g0111331	M12	NA	2	2	2	8	5	3	3	5	31	23
Sly07g0111391	M12	NA	59	61	58	67	69	66	69	69	104	106
Sly07g0111401	M11	NA	22	20	22	22	20	25	23	27	25	26
Sly07g0111411	M2	NA	3	2	4	4	5	3	3	3	5	6
Sly07g0111421	M5	NA	40	42	35	38	39	46	42	34	34	32
Sly07g0111471	M11	NA	56	62	67	73	92	70	59	75	85	130
Sly07g0111491	M11	NA	43	40	46	126	143	42	39	48	122	146
Sly07g0111501	M18	NA	77	84	119	198	146	160	128	159	121	96
Sly07g0111541	M3	NA	15	14	12	17	14	15	12	10	16	23
Sly07g0111551	M3	NA	5	6	4	3	4	6	6	3	5	7
Sly07g0111561	M22	NA	8	8	7	8	8	8	7	8	8	9
Sly07g0111571	M12	NA	12	14	13	14	13	16	12	13	10	14
Sly07g0111581	M1	NA	5	5	4	1	1	3	3	2	1	1
Sly07g0111611	M3	NA	14	14	10	2	1	6	8	4	1	1
Sly07g0111621	M1	NA	2	2	2	1	2	1	1	1	3	4
Sly07g0111631	M1	NA	126	94	59	28	7	5	4	2	1	1
Sly07g0111641	M11	NA	100	99	157	341	440	136	119	189	419	642
Sly07g0111671	M19	NA	13	14	16	20	25	14	11	14	18	20
Sly07g0111681	M19	NA	6	7	9	11	12	7	5	7	7	14
Sly07g0111691	M19	NA	5	7	9	9	11	7	7	6	6	11
Sly07g0111701	M1	NA	6	6	6	8	12	6	5	5	7	7
Sly07g0111711	M19	NA	7	10	11	12	19	9	8	8	10	16
Sly07g0111721	M19	NA	6	7	9	8	13	7	6	7	9	10
Sly07g0111731	M1	NA	7	9	9	10	17	9	7	8	12	18
Sly07g0111741	M1	NA	10	9	9	11	16	8	8	7	14	23
Sly07g0111751	M12	NA	6	6	8	8	9	6	6	7	10	13
Sly07g0111761	M11	NA	10	11	14	16	22	12	9	13	16	28
Sly07g0111771	M2	NA	59	64	53	42	36	47	47	34	54	47
Sly07g0111781	M3	NA	39	41	32	29	23	33	31	23	34	31
Sly07g0111811	M1	NA	1	1	1	0	0	1	0	1	0	0
Sly07g0111821	M9	NA	73	71	66	73	89	74	71	70	73	79
Sly07g0111831	M18	NA	6	7	8	9	8	8	8	8	8	4
Sly07g0111841	M11	NA	22	20	25	72	82	27	24	30	69	101
Sly07g0111851	M1	NA	108	127	85	94	54	30	19	21	4	7
Sly07g0111861	M12	NA	33	29	29	39	108	32	31	37	44	159
Sly07g0111881	M3	NA	3	3	3	2	2	3	2	2	4	3
Sly07g0111891	M3	NA	5	4	3	3	2	3	4	3	3	4
Sly07g0111911	M8	NA	18	20	18	18	17	19	20	17	12	14
Sly07g0111941	M12	NA	66	58	65	72	61	81	85	87	73	54
Sly07g0111991	M1	NA	34	38	26	19	17	23	23	22	20	16
Sly07g0112001	M22	NA	5	1	5	5	3	6	2	3	1	1
Sly07g0112011	M11	NA	106	97	108	81	81	101	97	120	105	90
Sly07g0112021	M22	NA	1	0	1	0	0	3	0	4	0	0
Sly07g0112031	M3	NA	4	4	3	4	3	2	2	3	4	2
Sly07g0112051	M1	NA	11	9	11	8	12	10	8	8	8	7
Sly07g0112061	M3	NA	315	358	181	1	1	82	62	5	1	1
Sly07g0112081	M3	NA	4	7	6	1	1	2	2	1	1	0
Sly07g0112091	M3	NA	7	7	3	2	1	3	2	1	1	2
Sly07g0112111	M1	NA	8	8	8	5	6	7	5	5	3	4
Sly07g0112121	M1	NA	4	3	2	1	1	1	1	1	0	1
Sly07g0112131	M22	NA	4	0	3	0	0	34	0	26	0	0
Sly07g0112141	M22	NA	2	0	1	0	0	10	0	11	0	0
Sly07g0112161	M12	NA	17	17	17	16	15	20	20	19	16	15
Sly07g0112211	M11	NA	9	8	15	1	1	14	10	14	1	3
Sly07g0112251	M3	NA	2	1	1	1	1	1	1	1	0	0
Sly07g0112261	M3	NA	2	1	1	1	1	1	1	1	0	0
Sly07g0112271	M1	NA	9	13	13	5	4	2	2	1	1	1
Sly07g0112281	M3	NA	3	6	1	0	0	0	1	0	0	0
Sly07g0112291	M8	NA	13	10	11	14	14	12	15	10	12	13
Sly07g0112301	M8

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0037421	M9	NA	1	1	1	1	2	2	2	1	2	5
Sly01g0037451	M1	NA	4	4	4	2	3	4	3	3	4	3
Sly01g0037461	M3	NA	3	3	3	2	4	3	2	2	4	3
Sly01g0037471	M11	NA	530	518	566	902	1731	573	611	648	1176	1672
Sly01g0037481	M12	NA	4	4	6	4	6	10	8	11	9	15
Sly01g0037491	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0037501	M19	NA	2	4	3	3	2	3	3	3	3	2
Sly01g0037511	M12	NA	2	2	2	1	3	3	2	2	3	2
Sly01g0037521	M3	NA	25	49	26	18	13	14	14	7	5	6
Sly01g0037821	M19	NA	1	2	3	3	4	2	2	2	1	1
Sly01g0037851	M19	NA	2	4	2	2	6	4	2	3	1	4
Sly01g0037991	M1	NA	4	3	4	1	1	1	1	1	1	0
Sly01g0038001	M1	NA	3	2	3	1	1	1	1	1	0	0
Sly01g0038011	M12	NA	14	11	9	7	11	14	17	12	17	19
Sly01g0038031	M14	NA	53	54	64	88	140	50	54	60	97	122
Sly01g0038041	M16	NA	75	75	59	69	67	73	64	64	83	75
Sly01g0038051	M18	NA	26	28	24	26	30	27	24	27	35	34
Sly01g0038061	M1	NA	3	3	3	3	4	3	2	3	3	3
Sly01g0038071	M2	NA	38	42	37	40	38	28	31	26	35	32
Sly01g0038081	M1	NA	9	9	9	4	1	9	8	6	1	1
Sly01g0038091	M11	NA	22	20	19	23	28	23	21	22	15	13
Sly01g0038101	M15	NA	109	95	90	116	110	109	111	116	112	134
Sly01g0038111	M7	NA	10	25	13	13	60	16	30	11	16	76
Sly01g0038131	M11	NA	12	11	15	12	4	27	24	33	6	1
Sly01g0038141	M3	NA	4	6	2	1	1	1	1	1	1	1
Sly01g0038161	M1	NA	8	11	7	7	5	3	2	3	2	1
Sly01g0038171	M3	NA	8	9	5	4	3	3	4	3	2	2
Sly01g0038211	M3	NA	22	22	17	37	20	11	9	5	2	1
Sly01g0038221	M1	NA	1	2	2	4	5	1	1	1	1	1
Sly01g0038231	M11	NA	15	14	27	846	1323	18	9	31	153	428
Sly01g0038241	M19	NA	33	31	33	28	26	32	28	32	29	28
Sly01g0038261	M11	NA	20	20	22	21	27	25	23	26	25	29
Sly01g0038271	M1	NA	1	2	2	3	7	1	1	1	3	9
Sly01g0038281	M4	NA	2	1	2	5	8	2	2	2	3	5
Sly01g0038291	M1	NA	3	4	4	6	12	3	3	3	7	16
Sly01g0038301	M18	NA	52	55	61	67	56	60	56	58	51	41
Sly01g0038311	M3	NA	86	85	80	71	70	83	81	78	98	84
Sly01g0038321	M10	NA	5	11	5	3	1	9	11	6	2	1
Sly01g0038331	M11	NA	12	11	13	11	11	20	15	17	8	7
Sly01g0038341	M5	SlARF1	104	96	64	23	29	116	104	71	22	20
Sly01g0038371	M1	NA	55	56	64	46	52	53	48	57	49	58
Sly01g0038381	M19	NA	23	22	22	22	22	24	21	25	19	21
Sly01g0038391	M3	NA	17	16	17	18	22	17	16	16	20	22
Sly01g0038401	M19	NA	17	18	17	23	44	19	14	18	34	54
Sly01g0038411	M1	NA	20	20	20	26	51	18	16	20	40	87
Sly01g0038421	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly01g0038431	M12	NA	47	47	71	228	159	161	181	236	428	299
Sly01g0038441	M3	NA	17	15	16	20	20	14	16	13	20	23
Sly01g0038451	M3	emb1796-like1	42	39	34	27	24	33	32	30	28	25
Sly01g0038461	M1	NA	15	18	20	28	42	14	18	17	46	62
Sly01g0038471	M3	NA	16	16	14	11	15	13	12	11	13	15
Sly01g0038481	M3	NA	46	43	40	49	55	41	45	42	53	56
Sly01g0038491	M12	NA	83	73	69	55	68	102	110	97	70	103
Sly01g0038501	M3	NA	345	338	261	338	310	282	356	282	356	357
Sly01g0038511	M11	NA	18	18	21	14	11	30	22	26	6	4
Sly01g0038521	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0038531	M18	NA	47	46	64	36	11	86	60	83	21	7
Sly01g0038541	M11	NA	63	58	78	46	15	106	80	107	31	13
Sly01g0038551	M11	NA	65	57	72	44	14	108	86	100	34	13
Sly01g0038561	M18	NA	3	4	4	4	2	4	4	6	2	1
Sly01g0038571	M18	NA	3	5	4	3	2	5	5	5	3	1
Sly01g0038581	M11	NA	4	6	6	5	3	7	7	8	5	1
Sly01g0038591	M18	NA	7	6	7	5	4	7	6	8	4	2
Sly01g0038621	M19	NA	13	14	15	16	17	14	14	17	24	26
Sly01g0038651	M12	NA	13	11	14	21	23	21	20	22	40	30
Sly01g0038661	M22	NA	1	0	1	0	0	3	0	1	0	0
Sly01g0038671	M1	NA	113	111	115	100	115	12	12	11	13	41
Sly01g0038681	M3	NA	41	40	34	35	34	34	39	34	37	43
Sly01g0038691	M6	OPR2-like6	3	7	4	2	1	4	5	4	2	2
Sly01g0038701	M2	NA	77	75	75	62	60	70	84	69	49	50
Sly01g0038711	M12	NA	187	179	208	281	305	283	291	367	474	524
Sly01g0038721	M1	NA	93	89	79	78	82	68	68	66	113	98
Sly01g0038731	M11	BIN2	116	114	165	46	39	174	147	170	29	27
Sly01g0038741	M1	NA	22	21	19	33	61	17	15	17	32	45
Sly01g0038751	M11	NA	346	304	352	470	661	400	351	407	524	596
Sly01g0038761	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly01g0038771	M11	NA	9	8	7	8	5	14	14	21	13	7
Sly01g0038781	M3	NA	6	7	3	1	1	3	5	2	1	1
Sly01g0038791	M9	NA	169	172	172	161	152	190	230	195	200	209
Sly01g0038801	M3	NA	34	31	21	10	10	17	14	12	4	7
Sly01g0038821	M1	NA	60	70	53	34	23	25	24	22	17	16
Sly01g0038831	M1	NA	4	2	3	1	1	1	1	1	1	0
Sly01g0038841	M11	NA	664	687	832	1033	974	1135	1008	1375	1551	1801
Sly01g0038861	M1	NA	12	11	11	10	9	9	10	10	8	7
Sly01g0038871	M1	NA	26	28	25	14	15	18	16	16	13	11
Sly01g0038891	M12	NA	5	6	4	5	5	8	10	8	6	7
Sly01g0038901	M1	NA	84	54	34	11	24	4	7	3	1	8
Sly01g0038911	M12	NA	5	6	5	6	8	7	7	6	8	9
Sly01g0038921	M19	NA	5	5	4	6	5	6	5	5	6	5
Sly01g0038931	M12	NA	4	5	4	5	6	6	5	4	5	4
Sly01g0038941	M11	NA	9	10	10	11	11	12	12	12	11	8
Sly01g0038961	M3	NA	7	9	5	4	4	7	6	5	4	5
Sly01g0038971	M3	NA	141	129	58	5	2	76	60	11	2	2
Sly01g0038981	M3	NA	2	3	2	3	1	2	3	1	1	1
Sly01g0038991	M1	NA	34	32	34	38	37	24	23	30	36	35
Sly01g0039001	M3	NA	167	173	177	214	214	159	168	151	158	163
Sly01g0039011	M18	NA	18	20	20	21	23	24	22	25	28	28
Sly01g0039031	M3	NA	40	42	44	71	140	35	39	40	97	170
Sly01g0039041	M1	NA	140	145	129	81	84	92	101	84	98	93
Sly01g0039051	M1	NA	100	108	111	71	59	74	70	72	67	53
Sly01g0039061	M11	NA	56	47	55	50	43	65	64	67	42	23
Sly01g0039071	M3	NA	18	18	15	16	15	18	21	14	11	12
Sly01g0039081	M11	NA	14	14	12	8	8	15	16	23	20	19
Sly01g0039091	M11	NA	72	67	102	96	75	131	137	171	201	135
Sly01g0039101	M1	NA	2	3	2	1	1	1	1	1	1	1
Sly01g0039111	M1	NA	438	384	410	248	149	329	364	360	206	145
Sly01g0039141	M22	NA	2	1	2	2	1	2	1	2	0	0
Sly01g0039211	M12	NA	25	21	30	29	27	51	56	53	20	24
Sly01g0039221	M12	NA	1	1	1	1	2	2	3	2	3	2
Sly01g0039241	M3	NA	17	21	17	15	14	15	19	13	14	22
Sly01g0039261	M12	NA	2	1	1	3	1	5	5	2	3	1
Sly01g0039271	M12	NA	1	1	1	2	1	2	2	2	4	2
Sly01g0039291	M13	NA	8	9	11	15	14	8	8	10	14	11
Sly01g0039301	M1	NA	51	51	43	46	49	39	38	39	56	49
Sly01g0039331	M12	NA	13	13	26	117	384	34	28	31	7	70
Sly01g0039341	M1	NA	70	65	66	42	32	38	38	34	18	15
Sly01g0039351	M12	SlSnRK2.2	117	118	115	74	81	122	123	116	74	65
Sly01g0039361	M11	NA	20	18	20	19	21	26	24	28	20	20
Sly01g0039371	M11	NA	6	6	7	2	3	9	6	8	2	2
Sly01g0039381	M11	NA	53	59	55	62	98	55	59	60	56	90
Sly01g0039391	M12	NA	36	35	42	50	49	60	63	79	84	78
Sly01g0039401	M19	NA	87	75	95	215	306	79	68	86	183	275
Sly01g0039411	M3	NA	39	40	29	54	51	33	33	28	63	54
Sly01g0039421	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly01g0039431	M1	NA	15	15	13	28	19	5	5	4	5	9
Sly01g0039441	M12	NA	50	51	54	53	25	75	87	74	10	7
Sly01g0039451	M1	NA	65	67	53	36	26	38	39	30	19	16
Sly01g0039461	M5	NA	21	30	16	15	11	20	24	10	4	4
Sly01g0039471	M11	NA	24	23	23	45	61	30	28	33	48	48
Sly01g0039481	M2	NA	55	63	56	40	31	46	54	43	45	32
Sly01g0039491	M9	NA	66	66	62	66	89	78	94	78	95	111
Sly01g0039511	M1	NA	2	2	2	2	2	2	1	2	2	1
Sly01g0039581	M12	NA	41	41	76	257	235	26	51	105	239	222
Sly01g0039591	M18	NA	40	41	39	69	70	41	42	46	73	63

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0112361	M8	VIN3	18	17	15	20	20	17	18	17	18	18
Sly07g0112371	M23	NA	2	1	1	1	1	4	1	1	1	1
Sly07g0112381	M3	RPA2A-like	6	6	6	3	4	5	6	4	2	2
Sly07g0112411	M19	NA	19	22	24	14	8	21	18	20	10	6
Sly07g0112421	M1	NA	31	31	33	19	13	29	27	28	17	11
Sly07g0112441	M18	NA	73	75	92	151	136	135	109	149	131	97
Sly07g0112481	M11	NA	4	3	3	1	1	3	4	3	1	1
Sly07g0112491	M11	NA	4	6	4	7	10	8	8	9	11	15
Sly07g0112501	M11	NA	4	5	4	6	7	6	5	7	5	7
Sly07g0112511	M11	NA	9	8	8	9	7	11	8	12	7	13
Sly07g0112521	M11	NA	2	3	2	3	2	4	3	3	1	3
Sly07g0112561	M1	NA	6	8	3	1	1	1	0	0	0	0
Sly07g0112571	M22	NA	3	3	3	2	1	4	3	3	1	0
Sly07g0112591	M12	NA	2	1	2	1	1	3	2	2	1	1
Sly07g0112601	M11	SlAGPase-L2	55	56	58	72	91	54	57	62	79	101
Sly07g0112621	M10	NA	206	334	128	89	159	414	449	122	85	140
Sly07g0112671	M12	NA	27	25	23	20	13	28	26	26	16	14
Sly07g0112841	M11	NA	10	9	10	5	1	18	12	18	2	1
Sly07g0112871	M11	NA	2	2	3	4	3	9	8	12	6	2
Sly07g0112881	M3	NA	271	299	197	189	265	148	203	83	52	55
Sly07g0112941	M1	NA	21	20	18	13	12	12	13	13	13	14
Sly07g0112951	M23	NA	1	1	1	0	0	1	1	1	1	1
Sly07g0112961	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly07g0112971	M3	NA	164	163	134	79	35	100	126	80	59	23
Sly07g0112991	M11	NA	6	6	5	8	5	6	6	8	12	8
Sly07g0113001	M11	NA	19	16	22	20	22	23	20	24	20	13
Sly07g0113011	M23	NA	2	1	1	1	1	3	1	2	0	1
Sly07g0113031	M1	NA	3	3	3	3	6	2	2	2	6	11
Sly07g0113041	M11	PrxII	505	446	478	652	723	496	495	536	496	559
Sly07g0113051	M3	NA	13	24	6	1	1	3	3	1	1	0
Sly07g0113061	M3	NA	7	13	4	1	0	2	1	1	0	0
Sly07g0113091	M22	NA	1	1	0	0	0	3	1	1	0	0
Sly07g0113251	M1	NA	25	24	28	19	12	4	3	4	6	5
Sly07g0113481	M11	NA	6	6	5	5	6	8	7	7	5	3
Sly07g0113521	M12	NA	1	1	1	0	0	3	3	1	0	0
Sly07g0113531	M12	NA	1	1	1	0	0	2	4	3	1	1
Sly07g0113731	M1	NA	4	3	5	1	0	0	1	0	0	0
Sly07g0113741	M12	NA	19	19	26	59	94	37	38	56	88	123
Sly07g0113931	M12	NA	1	0	1	2	4	2	2	2	7	9
Sly07g0114021	M11	NA	1	1	2	1	1	4	1	3	1	1
Sly07g0114031	M12	GEM-like1	67	63	63	78	139	75	84	86	108	231
Sly07g0114041	M11	NA	28	28	32	20	16	31	31	35	16	14
Sly07g0114071	M7	NA	15	24	13	13	18	16	26	18	28	54
Sly07g0114101	M1	NA	16	15	12	8	6	9	9	10	6	6
Sly07g0114111	M14	NA	8	7	8	12	13	7	7	9	12	7
Sly07g0114121	M11	NA	1	1	1	2	1	1	1	1	1	1
Sly07g0114151	M2	NA	23	23	20	21	20	19	22	23	28	26
Sly07g0114191	M12	NA	14	14	13	11	13	16	19	16	19	20
Sly07g0114201	M12	NA	2	2	1	3	1	3	3	3	4	2
Sly07g0114211	M12	NA	1	1	1	3	5	3	8	5	39	109
Sly07g0114221	M12	NA	3	4	4	4	5	4	8	5	19	36
Sly07g0114241	M9	NA	43	59	34	23	34	92	172	78	45	78
Sly07g0114271	M19	NA	41	42	41	41	42	47	38	48	61	77
Sly07g0114291	M11	NA	32	33	35	34	28	39	38	38	24	25
Sly07g0114321	M3	NA	24	24	25	16	14	23	23	22	18	9
Sly07g0114341	M1	NA	23	25	24	24	23	24	23	23	21	22
Sly07g0114371	M11	NA	23	20	21	18	4	54	48	51	10	2
Sly07g0114381	M19	NA	50	67	62	100	115	44	59	72	149	169
Sly07g0114391	M3	NA	26	27	23	25	18	22	25	20	24	20
Sly07g0114401	M1	NA	24	19	19	15	13	14	16	15	14	8
Sly07g0114411	M1	NA	23	25	18	10	9	5	5	3	4	4
Sly07g0114451	M11	NA	78	80	110	262	267	99	119	149	327	286
Sly07g0114461	M11	NA	2	2	2	1	1	2	2	2	1	1
Sly07g0114511	M11	NA	4	4	4	1	1	7	6	5	1	1
Sly07g0114561	M11	NA	11	9	12	13	7	16	17	15	14	5
Sly07g0114641	M11	NA	0	1	1	3	2	1	1	3	7	3
Sly07g0114701	M11	NA	16	16	16	19	11	18	17	19	20	10
Sly07g0114721	M1	NFD5-like2	20	21	18	17	17	15	15	14	16	10
Sly07g0114741	M3	NFD5-like1	16	16	14	17	15	12	14	12	14	11
Sly07g0114751	M18	NA	8	7	8	7	6	8	7	8	5	4
Sly07g0114771	M3	NA	9	5	5	2	1	4	6	3	1	1
Sly07g0114821	M3	NA	22	21	21	10	4	18	20	16	5	2
Sly07g0114831	M11	NA	8	8	7	1	1	11	10	9	1	1
Sly07g0114841	M12	NA	20	24	23	24	22	20	26	23	23	21
Sly07g0114851	M11	NA	44	43	53	76	107	63	54	75	101	140
Sly07g0114941	M11	NA	5	5	8	6	4	7	6	6	4	2
Sly07g0114961	M12	NA	13	12	15	11	11	14	19	14	8	11
Sly07g0114971	M11	NA	14	12	15	19	16	16	14	16	11	8
Sly07g0115021	M11	NA	42	46	54	47	58	58	49	62	88	94
Sly07g0115031	M12	NA	5	5	4	5	4	6	5	6	8	10
Sly07g0115041	M11	NA	5	4	6	4	3	6	6	6	5	2
Sly07g0115061	M1	ACO5	52	65	20	4	1	2	2	9	1	1
Sly07g0115081	M3	NA	9	13	8	3	2	9	10	7	2	2
Sly07g0115101	M12	NA	19	20	18	26	29	25	21	23	26	38
Sly07g0115111	M1	NA	1	2	1	1	0	1	1	1	1	0
Sly07g0115131	M1	NA	9	9	9	9	10	7	6	8	10	6
Sly07g0115141	M1	NA	15	16	14	14	13	10	10	12	13	12
Sly07g0115151	M3	NA	16	16	14	15	14	10	13	12	16	19
Sly07g0115161	M1	NA	5	5	6	4	2	5	4	4	4	3
Sly07g0115171	M1	NA	5	6	5	4	2	4	4	4	3	3
Sly07g0115181	M12	NA	5	5	5	4	3	6	6	5	4	3
Sly07g0115191	M12	NA	4	4	5	4	2	5	6	4	4	2
Sly07g0115201	M1	NA	3	2	3	4	4	2	2	2	2	3
Sly07g0115211	M11	NA	274	260	296	289	227	307	333	367	359	314
Sly07g0115251	M11	NA	1	1	1	1	0	1	1	1	0	0
Sly07g0115271	M19	NA	44	46	48	56	59	47	41	47	47	50
Sly07g0115371	M1	NA	12	12	15	9	12	11	10	10	10	11
Sly07g0115381	M12	NA	1	1	1	15	5	1	2	2	9	3
Sly07g0115411	M12	NA	122	119	141	223	232	211	214	251	324	327
Sly07g0115421	M19	NA	2	3	2	2	1	3	2	2	2	1
Sly07g0115431	M12	NA	3	3	2	2	2	3	3	3	3	2
Sly07g0115461	M1	NA	34	33	35	24	22	28	25	28	19	18
Sly07g0115471	M19	NA	21	22	22	18	14	20	15	19	12	10
Sly07g0115551	M11	NA	5	5	5	6	6	6	5	7	9	10
Sly07g0115581	M1	NA	1	1	1	1	0	1	1	1	0	0
Sly07g0115591	M13	NA	58	52	57	52	69	50	53	60	67	85
Sly07g0115611	M9	NA	44	49	39	48	48	49	56	42	31	50
Sly07g0115621	M18	NA	12	13	13	12	8	16	13	16	10	9
Sly07g0115661	M12	NA	15	13	13	11	17	14	19	14	16	15
Sly07g0115691	M19	NA	26	27	30	25	22	28	23	25	26	29
Sly07g0115701	M2	NA	41	37	39	34	36	39	40	37	48	70
Sly07g0115711	M19	NA	25	29	25	22	20	23	24	22	18	21
Sly07g0115721	M19	NA	7	8	7	11	8	10	7	9	8	9
Sly07g0115731	M18	NA	10	13	12	13	12	13	12	12	14	18
Sly07g0115741	M3	NA	42	48	43	42	43	36	41	41	56	72
Sly07g0115751	M10	NA	37	64	38	43	109	58	71	37	42	82
Sly07g0115761	M1	SlPRMT5	26	25	21	15	14	18	17	16	21	18
Sly07g0115771	M9	NA	18	25	24	45	31	23	29	22	30	18
Sly07g0115781	M3	NA	40	41	40	33	22	37	39	37	30	21
Sly07g0115791	M11	NA	5	3	4	3	3	7	5	9	3	4
Sly07g0115891	M12	NA	10	11	13	11	27	14	18	15	11	34
Sly07g0115901	M12	NA	6	6	9	12	21	8	8	12	15	39
Sly07g0115911	M11	NA	2	2	4	9	11	5	3	5	6	11
Sly07g0115921	M12	NA	11	9	15	22	44	15	14	20	28	79
Sly07g0116031	M2	NA	11	11	9	8	6	7	9	6	8	9
Sly07g0116071	M3	SlCycT1;2	69	72	43	23	26	35	41	24	33	37
Sly07g0116091	M11	NA	5	5	5	5	4	7	6	8	22	12
Sly07g0116251	M8	NA	1	2	1	1	1	1	3	1	0	1
Sly07g0116271	M12	NA	1	2	2	1	1	8	7	10	2	1
Sly07g0116281	M12	NA	5	5	5	6	3	6	6	5	2	1
Sly07g0116301	M12	NA	114	114	122	148	123

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0039601	M12	NA	2	1	2	7	2	4	3	2	1	1
Sly01g0039621	M11	NA	122	117	125	138	166	146	127	153	225	283
Sly01g0039631	M11	NA	434	396	452	436	380	484	455	576	557	527
Sly01g0039651	M12	NA	30	25	27	17	13	33	40	33	23	19
Sly01g0039681	M11	NA	55	56	58	82	76	59	63	69	86	81
Sly01g0039691	M1	NA	1	1	1	1	0	1	1	1	1	1
Sly01g0039701	M2	NA	18	20	18	20	33	15	18	14	16	33
Sly01g0039711	M11	NA	32	31	37	62	70	38	39	43	56	71
Sly01g0039731	M11	NA	54	47	62	98	145	69	62	88	136	183
Sly01g0039741	M12	NA	8	8	7	12	10	10	10	10	9	9
Sly01g0039751	M3	NA	2	2	1	1	1	3	3	1	1	1
Sly01g0039761	M3	NA	63	62	46	22	32	29	30	18	21	26
Sly01g0039781	M11	NA	40	37	36	44	72	46	40	50	65	79
Sly01g0039791	M11	NA	26	25	40	40	69	52	38	68	79	82
Sly01g0039811	M22	GR	3	2	2	2	1	6	3	6	3	3
Sly01g0039821	M12	NA	36	35	35	48	58	41	45	43	60	54
Sly01g0039871	M3	NA	492	467	410	400	324	296	340	270	364	282
Sly01g0039881	M22	NA	5	0	3	0	0	30	1	22	0	0
Sly01g0039901	M11	NA	5	3	4	0	0	9	3	8	0	0
Sly01g0039921	M18	NA	13	14	16	21	27	17	15	18	17	30
Sly01g0039931	M19	NA	2	2	2	2	2	2	2	2	2	3
Sly01g0039941	M7	NA	2	5	3	3	3	2	4	3	3	7
Sly01g0039951	M22	NA	3	3	3	3	5	3	3	4	5	9
Sly01g0039961	M7	NA	6	11	8	6	7	8	13	9	11	19
Sly01g0039971	M3	NA	44	61	39	16	22	33	40	26	28	43
Sly01g0039981	M3	NA	20	25	12	3	7	12	19	9	9	20
Sly01g0039991	M12	NA	11	11	13	14	15	21	21	24	35	44
Sly01g0040001	M11	NA	8	10	10	11	12	15	13	18	20	21
Sly01g0040011	M1	NA	34	35	37	34	37	25	26	26	32	33
Sly01g0040021	M17	NA	863	826	905	720	542	799	730	971	877	909
Sly01g0040031	M3	NA	48	51	37	33	42	35	36	30	28	34
Sly01g0040041	M18	NA	2	2	2	1	1	4	3	3	1	1
Sly01g0040051	M11	NA	3	3	3	1	1	7	5	6	2	2
Sly01g0040061	M11	NA	84	81	103	307	303	96	103	147	582	559
Sly01g0040071	M3	MSI1-like	61	60	54	43	48	44	43	38	50	52
Sly01g0040081	M10	NA	1	1	1	0	0	2	2	1	1	1
Sly01g0040091	M5	NA	48	55	42	43	46	49	48	46	47	44
Sly01g0040101	M12	NA	29	28	27	36	43	33	35	37	70	53
Sly01g0040121	M1	NA	141	136	138	97	123	120	102	118	134	182
Sly01g0040131	M1	NA	9	8	6	3	3	5	5	5	2	2
Sly01g0040141	M1	NA	15	14	21	10	9	5	4	6	4	13
Sly01g0040151	M1	NA	834	736	794	534	477	703	685	701	635	603
Sly01g0040161	M1	NA	51	62	51	58	50	52	50	55	67	61
Sly01g0040171	M2	NA	33	32	29	37	42	30	30	31	46	55
Sly01g0040201	M13	NA	8	5	10	25	57	6	5	9	48	93
Sly01g0040211	M3	NA	13	12	10	7	7	11	11	10	8	5
Sly01g0040221	M1	NA	27	27	29	26	24	23	23	23	31	21
Sly01g0040231	M4	NA	54	50	61	209	157	67	63	86	380	170
Sly01g0040241	M12	NA	46	42	44	111	130	43	49	49	176	190
Sly01g0040251	M5	NA	94	104	76	78	99	84	111	62	104	116
Sly01g0040261	M2	NA	280	295	251	226	306	145	194	137	206	218
Sly01g0040271	M3	NA	98	106	66	7	3	58	44	18	1	1
Sly01g0040281	M3	NA	177	176	165	180	256	124	140	159	335	310
Sly01g0040291	M11	NA	207	198	304	90	37	221	211	260	104	132
Sly01g0040301	M1	NA	1350	1507	1758	1941	1168	1063	851	941	628	760
Sly01g0040311	M10	NA	55	47	49	26	35	56	62	44	51	56
Sly01g0040321	M8	NA	40	35	39	18	90	67	73	28	57	132
Sly01g0040331	M6	NA	1	1	1	1	1	2	1	1	1	1
Sly01g0040341	M22	HRA1	4	4	2	1	1	5	3	3	1	1
Sly01g0040351	M3	NA	519	533	385	124	113	359	400	264	169	209
Sly01g0040361	M3	NA	14	12	12	1	1	6	6	9	1	1
Sly01g0040371	M1	NA	21	18	19	17	19	16	17	19	16	16
Sly01g0040421	M11	NA	105	96	90	86	73	109	102	122	115	112
Sly01g0040431	M12	NA	24	23	41	6	2	186	198	233	76	14
Sly01g0040441	M22	NA	12	4	9	0	0	59	8	52	1	0
Sly01g0040471	M3	NA	51	52	37	26	32	38	37	32	18	17
Sly01g0040481	M12	NA	8	8	9	7	8	12	14	16	10	8
Sly01g0040491	M11	NA	57	64	80	10	3	204	197	244	2	1
Sly01g0040501	M14	NA	162	152	266	245	146	145	150	194	134	97
Sly01g0040511	M3	NA	166	167	132	64	75	101	123	91	73	77
Sly01g0040541	M12	NA	3	3	2	3	2	5	5	6	8	5
Sly01g0040551	M12	NA	3	3	5	4	3	10	9	8	12	7
Sly01g0040561	M12	NA	1	1	1	1	0	1	1	1	1	0
Sly01g0040571	M11	NA	38	33	56	39	14	148	154	172	470	140
Sly01g0040591	M3	SERK3B	67	75	32	11	9	17	17	5	1	1
Sly01g0040601	M11	NA	41	38	43	40	40	47	43	51	62	56
Sly01g0040611	M14	NA	5	5	6	3	5	4	5	5	13	11
Sly01g0040631	M12	NA	25	27	24	23	15	79	158	78	79	55
Sly01g0040641	M11	NA	4	4	5	6	5	9	8	11	5	2
Sly01g0040651	M12	NA	73	36	78	58	17	257	210	309	169	12
Sly01g0040661	M1	NA	6	5	5	7	6	5	5	5	8	6
Sly01g0040671	M11	NA	47	26	53	44	7	193	176	231	108	5
Sly01g0040681	M3	NA	34	32	27	68	82	25	26	22	35	42
Sly01g0040691	M1	NA	17	21	11	2	4	1	1	1	0	1
Sly01g0040711	M11	NA	18	17	23	13	14	26	24	33	19	23
Sly01g0040731	M3	NA	148	152	134	110	93	98	105	90	85	81
Sly01g0040751	M14	NA	46	29	55	25	168	41	33	46	45	229
Sly01g0040771	M1	NA	39	38	35	27	24	28	27	31	31	29
Sly01g0040781	M4	NA	52	47	46	73	111	52	49	50	97	162
Sly01g0040791	M3	NA	20	21	18	20	19	17	17	15	12	13
Sly01g0040801	M11	NA	33	31	31	37	38	39	37	40	32	31
Sly01g0040811	M1	NA	18	22	13	5	2	1	1	1	1	1
Sly01g0040821	M1	NA	4	5	5	6	11	2	2	2	1	2
Sly01g0040831	M3	NA	59	70	45	48	65	41	44	33	38	61
Sly01g0040841	M1	NA	72	72	68	91	88	62	58	58	61	59
Sly01g0040871	M12	NA	9	9	10	13	15	10	10	10	14	10
Sly01g0040881	M3	NA	67	83	51	51	67	46	57	34	61	80
Sly01g0040891	M3	NA	29	28	25	16	14	25	24	22	13	21
Sly01g0040901	M3	NA	4	6	3	1	1	3	3	3	2	1
Sly01g0040911	M1	NA	1	1	1	1	1	1	0	0	0	1
Sly01g0040921	M1	NA	3	4	2	3	4	1	1	1	1	3
Sly01g0040931	M1	NA	14	13	12	10	13	11	10	11	10	11
Sly01g0040941	M1	NA	372	350	403	757	1138	310	312	382	799	1038
Sly01g0040961	M12	NA	1	1	1	2	2	1	2	2	19	19
Sly01g0040971	M1	NA	30	36	23	2	2	5	6	4	2	2
Sly01g0040981	M12	NA	48	51	39	57	63	61	62	58	87	56
Sly01g0040991	M1	NA	25	41	14	1	1	2	1	1	1	1
Sly01g0041001	M3	NA	5	4	2	1	1	2	1	1	0	0
Sly01g0041011	M1	EXL1	939	966	574	11	12	65	65	18	2	12
Sly01g0041021	M11	NA	88	92	102	132	277	99	90	105	87	116
Sly01g0041031	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly01g0041041	M1	NA	1	2	2	1	1	2	1	2	1	1
Sly01g0041051	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0041061	M1	NA	3	5	6	1	2	1	1	1	0	0
Sly01g0041071	M11	NA	17	19	21	37	31	25	26	28	28	23
Sly01g0041081	M12	NA	6	7	7	6	5	8	9	9	7	6
Sly01g0041091	M22	NA	23	22	20	17	15	35	24	32	23	23
Sly01g0041101	M22	NA	5	2	3	0	0	11	5	15	1	0
Sly01g0041111	M18	NA	11	14	14	12	10	18	15	17	17	12
Sly01g0041121	M12	NA	12	13	14	13	12	17	15	17	23	18
Sly01g0041131	M19	NA	5	5	6	3	4	5	5	5	2	2
Sly01g0041141	M1	NA	7	7	10	25	12	5	4	5	4	3
Sly01g0041151	M12	NA	27	26	25	32	21	31	34	33	57	32
Sly01g0041171	M6	NA	79	148	62	82	118	122	155	72	96	144
Sly01g0041181	M12	NA	25	22	21	26	24	24	23	24	38	34
Sly01g0041211	M3	NA	3	3	1	3	4	2	2	2	1	1
Sly01g0041221	M3	NA	4	6	1	1	1	1	2	1	0	0
Sly01g0041231	M1	NA	13	15	6	9	8	2	1	1	1	1
Sly01g0041241	M3	NA	12	14	6	1	1	3	5	1	1	1
Sly01g0041251	M1	NA	252	217	146	1	0	11	10	6	1	1
Sly01g0041261	M11	NA	232	211	337	715	924	321	257	435	295	770
Sly01g0041281	M11	NA	27	26	32	44	51	35	32	39	43	43
Sly01g0041291	M7	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0041301	M1	NA	17	18	20	12	12	16	13	16	12	12

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0116461	M11	NA	7	6	8	7	5	9	8	10	8	4
Sly07g0116501	M12	NA	1	1	1	1	3	1	1	4	20	15
Sly07g0116521	M12	NA	1	1	1	2	2	1	2	3	27	22
Sly07g0116531	M11	NA	2	1	2	1	1	2	2	4	5	1
Sly07g0116541	M1	NA	13	13	15	13	22	9	12	12	26	30
Sly07g0116551	M2	NA	8	8	7	9	9	4	7	5	5	6
Sly07g0116561	M12	NA	32	34	33	39	34	35	38	35	24	24
Sly07g0116611	M11	NA	11	10	12	12	27	14	13	14	13	25
Sly07g0116621	M11	NA	1	1	1	2	2	2	1	2	1	2
Sly07g0116681	M9	NA	2	3	3	3	2	3	4	3	3	2
Sly07g0116691	M11	NA	11	13	16	10	3	21	18	23	6	2
Sly07g0116731	M1	NA	106	100	97	72	97	80	83	84	104	120
Sly07g0116741	M1	NA	30	30	33	38	39	29	30	30	42	38
Sly07g0116821	M12	NA	1	1	1	1	1	1	1	2	2	3
Sly07g0116901	M1	NA	3	3	3	1	1	1	1	0	0	1
Sly07g0116921	M11	NA	29	34	44	53	42	59	52	67	58	42
Sly07g0116931	M11	NA	2	2	3	2	3	4	4	5	3	2
Sly07g0116941	M12	NA	120	114	136	209	179	241	208	259	275	222
Sly07g0116951	M12	MSI4-like	104	96	122	166	147	184	182	200	227	213
Sly07g0116961	M19	NA	27	26	33	32	20	24	19	25	7	8
Sly07g0116981	M4	NA	2	1	2	3	6	2	2	2	4	14
Sly07g0116991	M12	NA	3	3	2	3	2	3	3	3	3	3
Sly07g0117021	M1	NA	8	8	10	7	2	5	6	6	1	1
Sly07g0117061	M3	NA	1	1	1	2	12	1	1	1	21	30
Sly07g0117071	M19	NA	5	6	7	9	10	5	4	6	8	10
Sly07g0117081	M1	NA	4	3	3	4	5	2	2	2	6	7
Sly07g0117091	M12	NA	1	1	1	2	3	2	2	2	3	4
Sly07g0117101	M12	NA	1	1	1	2	3	1	2	2	3	4
Sly07g0117111	M11	NA	1	2	2	1	3	1	2	2	2	7
Sly07g0117121	M18	NA	2	2	2	2	2	2	2	2	3	3
Sly07g0117131	M12	NA	5	5	7	6	9	5	7	8	14	14
Sly07g0117141	M12	NA	3	4	5	6	8	4	5	6	9	15
Sly07g0117151	M3	NA	58	54	56	55	54	52	56	51	61	57
Sly07g0117191	M11	NA	5	6	6	9	10	7	7	8	10	9
Sly07g0117201	M12	NA	14	12	13	8	3	17	16	17	7	3
Sly07g0117251	M19	NA	16	16	16	16	12	14	13	14	13	12
Sly07g0117261	M3	NA	8	8	6	5	4	5	6	5	2	3
Sly07g0117271	M5	NA	4	8	1	1	0	4	4	1	0	0
Sly07g0117321	M1	NA	2	1	2	2	1	1	1	1	2	1
Sly07g0117331	M1	NA	26	51	75	24	6	14	21	32	17	12
Sly07g0117421	M1	NA	4	5	5	4	4	5	4	5	4	5
Sly07g0117441	M18	NA	2	2	2	2	0	2	3	2	3	1
Sly07g0117451	M1	NA	1	2	2	0	1	1	1	1	2	0
Sly07g0117461	M11	NA	2	1	1	1	1	2	1	2	1	1
Sly07g0117481	M11	NA	23	17	27	22	32	35	28	47	35	46
Sly07g0117491	M3	receptor protein (NPR	40	45	28	26	27	30	36	21	25	25
Sly07g0117511	M6	NA	14	44	15	0	0	33	36	7	1	1
Sly07g0117531	M3	NA	81	106	62	58	77	53	77	55	65	82
Sly07g0117541	M1	NA	109	86	89	44	35	77	64	65	41	42
Sly07g0117551	M3	NA	6	7	5	2	1	5	4	4	1	1
Sly07g0117561	M11	NA	14	15	16	17	17	31	23	32	20	33
Sly07g0117571	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly07g0117581	M8	NA	4	4	3	1	1	5	4	3	1	1
Sly07g0117591	M11	NA	10	10	10	11	12	12	12	13	15	13
Sly07g0117671	M3	NA	4	8	1	1	1	3	3	1	0	0
Sly07g0117691	M1	NA	40	38	38	41	47	28	29	27	36	40
Sly07g0117711	M11	NA	33	35	43	46	60	46	44	53	51	66
Sly07g0117721	M11	NA	17	18	19	28	58	22	21	24	25	56
Sly07g0117731	M6	NA	38	107	74	17	486	62	154	41	18	551
Sly07g0117751	M3	NA	2	3	3	2	3	3	2	2	4	4
Sly07g0117771	M19	NA	31	31	30	35	39	29	27	28	36	39
Sly07g0117781	M11	SlPP2C4	60	64	79	99	70	108	103	138	61	30
Sly07g0117791	M1	NA	2	2	2	1	1	1	1	1	1	0
Sly07g0117801	M9	NA	81	71	64	54	58	115	150	80	43	75
Sly07g0117811	M3	NA	34	34	30	23	19	28	29	30	29	18
Sly07g0117821	M3	NA	7	4	4	1	0	6	6	3	1	1
Sly07g0117831	M1	NA	28	24	26	15	9	10	11	10	6	3
Sly07g0117881	M19	NA	23	28	30	28	23	22	17	23	17	14
Sly07g0117891	M19	NA	71	84	80	85	78	68	55	62	53	52
Sly07g0117901	M3	NA	136	149	135	140	150	116	124	107	122	134
Sly07g0117911	M2	NA	70	86	66	77	90	54	74	52	96	128
Sly07g0117931	M1	NA	2	3	2	1	1	1	1	1	1	1
Sly07g0117941	M13	NA	48	44	74	124	107	69	63	98	199	198
Sly07g0117951	M2	NA	57	55	51	45	43	47	55	40	33	36
Sly07g0117961	M12	NA	13	15	17	18	29	35	34	34	22	23
Sly07g0117971	M9	NA	3	3	3	2	2	3	5	4	2	2
Sly07g0117991	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0118011	M12	NA	9	8	9	4	2	18	19	22	8	3
Sly07g0118041	M11	NA	3	2	3	2	1	5	4	4	1	1
Sly07g0118051	M11	NA	2	2	2	1	1	2	2	3	1	1
Sly07g0118061	M11	NA	3	3	4	2	1	6	4	4	1	1
Sly07g0118071	M3	NA	1	1	1	0	0	1	1	1	0	0
Sly07g0118081	M11	NA	1	1	1	0	1	1	1	1	1	1
Sly07g0118091	M1	NA	158	145	134	95	70	112	121	114	99	70
Sly07g0118101	M1	NA	457	399	444	287	195	340	347	350	270	181
Sly07g0118111	M12	NA	5	4	6	6	11	7	9	9	9	28
Sly07g0118121	M1	NA	102	108	109	82	30	88	101	95	63	26
Sly07g0118131	M11	NA	8	9	9	9	9	9	9	10	12	10
Sly07g0118141	M13	NA	25	18	44	21	21	40	34	48	12	13
Sly07g0118201	M1	NA	1	1	2	1	0	1	1	1	1	0
Sly07g0118261	M11	NA	19	14	25	28	37	23	21	27	30	33
Sly07g0118271	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly07g0118281	M7	NA	1	4	1	1	3	2	3	1	1	2
Sly07g0118291	M11	NA	25	27	29	30	33	39	32	39	28	30
Sly07g0118301	M7	NA	13	22	11	12	41	17	29	12	16	93
Sly07g0118311	M9	NA	2	5	1	1	2	4	10	3	2	5
Sly07g0118321	M7	NA	2	5	2	1	1	3	9	2	1	1
Sly07g0118331	M7	NA	24	42	23	23	76	38	55	26	57	198
Sly07g0118371	M1	NA	3	3	4	2	1	1	1	1	1	0
Sly07g0118391	M3	NA	55	54	49	31	30	47	44	41	35	34
Sly07g0118401	M1	NA	2	1	2	1	0	0	0	1	0	0
Sly07g0118411	M12	NA	8	7	8	8	7	16	18	14	7	5
Sly07g0118421	M9	NA	1	3	1	1	1	2	6	3	2	2
Sly07g0118431	M7	NA	54	90	48	30	34	63	85	54	29	51
Sly07g0118441	M9	NA	5	6	5	2	2	5	7	5	2	1
Sly07g0118471	M12	NA	6	5	7	10	15	8	6	8	10	19
Sly07g0118491	M11	NA	32	30	35	28	29	47	39	59	42	39
Sly07g0118501	M12	NA	12	12	13	13	11	14	14	14	16	15
Sly07g0118531	M1	NA	54	56	58	53	48	44	42	42	43	41
Sly07g0118561	M11	NA	630	619	910	1053	911	966	900	1364	1152	589
Sly07g0118581	M3	NA	37	37	32	26	26	26	29	26	31	29
Sly07g0118621	M12	NA	26	29	30	11	9	57	46	59	19	19
Sly07g0118641	M12	NA	4	4	4	3	1	6	6	4	2	1
Sly07g0118651	M1	NA	14	11	17	8	9	6	4	5	3	2
Sly07g0118661	M1	NA	4	4	4	5	8	4	3	4	5	6
Sly07g0118671	M3	NA	12	16	12	16	14	12	15	10	13	9
Sly07g0118681	M12	NA	9	10	8	8	6	11	11	9	5	3
Sly07g0118691	M12	NA	9	10	12	25	28	24	25	28	35	26
Sly07g0118701	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly07g0118711	M12	NA	1	1	1	1	0	2	3	2	0	0
Sly07g0118721	M3	NA	15	27	7	19	21	10	16	6	13	13
Sly07g0118741	M11	NA	16	13	15	14	14	24	23	26	15	11
Sly07g0118751	M12	NA	12	11	12	6	4	48	42	42	5	4
Sly07g0118761	M3	JAZ1-like2	288	265	115	9	12	148	191	99	13	30
Sly07g0118771	M11	NA	102	94	109	110	190	121	122	129	187	271
Sly07g0118781	M11	Solyc07g042190	203	152	272	412	302	265	247	316	458	231
Sly07g0118801	M2	NA	5	6	5	3	4	5	5	5	5	5
Sly07g0118821	M12	NA	1	1	1	0	0	1	1	1	1	0
Sly07g0118831	M6	SlERF.H9	12	31	14	1	0	17	22	1	2	1
Sly07g0118841	M12	NA	161	140	151	462	1240	180	191	185	650	1336
Sly07g0118851	M18	SlARF19	6	6	9	5	4	7	7	7	3	3

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0041311	M19	NA	13	15	17	8	8	14	8	14	9	6
Sly01g0041321	M15	NA	116	83	88	93	92	107	96	107	73	80
Sly01g0041331	M1	NA	200	136	208	49	22	39	37	39	27	19
Sly01g0041341	M1	NA	284	262	541	255	15	27	6	13	1	0
Sly01g0041371	M3	NA	1	2	1	1	1	1	0	1	0	0
Sly01g0041381	M3	NA	1	2	1	1	0	0	0	0	0	0
Sly01g0041391	M19	NA	29	27	29	28	30	27	23	27	23	30
Sly01g0041411	M1	NA	2	1	2	1	1	1	0	0	0	0
Sly01g0041431	M11	NA	28	33	27	27	36	33	31	33	41	48
Sly01g0041481	M1	NA	2	2	2	0	0	1	1	0	0	0
Sly01g0041491	M3	NA	1	1	1	1	1	0	0	0	0	0
Sly01g0041501	M1	NA	54	41	30	0	0	2	4	1	1	0
Sly01g0041531	M3	NA	1	1	1	1	1	1	1	0	1	1
Sly01g0041551	M3	NA	2	1	1	1	2	1	1	1	4	8
Sly01g0041571	M1	NA	1	1	1	1	2	1	0	1	1	1
Sly01g0041581	M1	NA	240	228	237	272	491	164	188	204	393	572
Sly01g0041591	M11	NA	18	15	22	27	33	33	31	37	30	28
Sly01g0041601	M11	NA	36	36	43	48	70	47	40	61	53	71
Sly01g0041611	M13	NA	150	140	189	255	184	137	144	176	141	139
Sly01g0041621	M12	NA	23	23	26	24	30	31	31	37	28	27
Sly01g0041631	M3	NA	19	20	16	15	14	17	16	17	10	8
Sly01g0041641	M11	NA	39	37	40	45	61	39	38	43	60	86
Sly01g0041651	M22	NA	6	4	5	3	1	9	6	8	2	1
Sly01g0041661	M3	NA	76	84	68	72	81	62	66	55	91	97
Sly01g0041671	M12	NA	6	6	7	8	9	9	9	9	8	6
Sly01g0041681	M11	NA	78	64	84	68	70	291	219	534	247	225
Sly01g0041691	M11	NA	30	29	34	69	78	54	48	57	73	65
Sly01g0041701	M11	NA	15	16	22	68	106	41	39	61	139	141
Sly01g0041711	M11	NA	8	7	8	10	9	9	8	11	9	7
Sly01g0041721	M1	NA	15	17	17	13	15	14	15	14	20	17
Sly01g0041741	M1	NA	2	1	2	1	1	1	1	1	2	1
Sly01g0041761	M11	NA	18	20	16	17	28	18	13	19	18	21
Sly01g0041771	M19	NA	16	17	14	18	26	16	11	16	21	20
Sly01g0041781	M19	NA	6	6	6	7	8	6	5	6	8	10
Sly01g0041801	M3	NA	132	141	126	147	181	95	98	79	128	147
Sly01g0041811	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0041821	M1	NA	3	3	3	2	1	3	3	3	2	1
Sly01g0041831	M11	NA	1	1	1	1	1	2	2	2	1	1
Sly01g0041841	M19	NA	9	11	10	6	5	8	8	8	4	4
Sly01g0041851	M12	NA	1	1	1	1	1	3	2	2	1	1
Sly01g0041861	M3	NA	77	84	67	65	52	51	62	46	73	59
Sly01g0041891	M3	NA	142	133	102	113	164	94	101	70	69	134
Sly01g0041901	M7	NA	17	21	11	10	45	21	36	15	13	83
Sly01g0041921	M1	NA	5	5	4	13	57	1	1	1	1	62
Sly01g0041931	M11	NA	156	142	140	229	179	225	185	199	86	124
Sly01g0041941	M1	AMI1-like6	36	37	39	26	25	2	1	1	0	1
Sly01g0041951	M1	AMI1-like2	5	5	6	5	2	1	2	1	1	0
Sly01g0041961	M1	NA	3	3	3	3	2	1	1	1	1	1
Sly01g0041971	M1	AMI1-like9	6	5	5	1	2	5	4	4	1	1
Sly01g0041981	M3	NA	9	7	5	2	2	6	4	4	1	1
Sly01g0041991	M1	AMI1-like8	69	68	74	99	94	52	44	50	56	62
Sly01g0042001	M12	NA	11	11	11	15	16	15	15	16	15	18
Sly01g0042011	M1	NA	7	5	6	6	7	4	5	5	5	9
Sly01g0042021	M6	NA	9	15	13	8	27	10	12	8	12	23
Sly01g0042031	M11	NA	2	2	2	2	2	4	3	4	1	1
Sly01g0042041	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0042051	M9	NA	9	9	8	12	13	10	11	9	9	10
Sly01g0042061	M11	NA	67	64	71	58	29	100	95	107	43	23
Sly01g0042071	M12	NA	21	20	21	21	24	24	25	22	22	27
Sly01g0042081	M11	NA	53	44	59	55	54	75	69	82	86	76
Sly01g0042091	M10	NA	2	2	1	1	0	4	2	1	0	0
Sly01g0042111	M12	NA	33	35	48	92	144	48	50	65	186	113
Sly01g0042121	M11	NA	37	33	35	26	17	64	54	64	22	20
Sly01g0042131	M5	NA	70	90	34	25	47	68	78	26	7	25
Sly01g0042141	M10	NA	2	1	1	0	0	2	3	1	1	0
Sly01g0042191	M11	NA	19	16	16	13	15	16	16	19	14	17
Sly01g0042201	M11	NA	26	23	30	34	37	28	26	30	10	7
Sly01g0042211	M9	NA	38	36	40	31	17	56	72	53	14	8
Sly01g0042221	M12	NA	8	8	9	9	8	12	13	13	7	7
Sly01g0042251	M1	NA	22	23	18	3	2	1	1	1	1	1
Sly01g0042281	M11	NA	47	46	63	55	49	53	52	57	45	43
Sly01g0042291	M11	NA	26	18	30	35	89	29	36	31	93	120
Sly01g0042301	M12	NA	2	2	3	10	18	2	2	3	61	30
Sly01g0042341	M18	NA	31	35	33	54	68	32	32	36	72	71
Sly01g0042361	M19	NA	14	17	21	21	20	20	15	21	11	11
Sly01g0042371	M18	NA	27	29	35	38	45	37	30	37	26	30
Sly01g0042381	M1	NA	37	35	33	26	23	20	20	16	19	20
Sly01g0042391	M11	NA	4	3	6	7	15	7	6	7	8	29
Sly01g0042401	M1	NA	10	11	10	11	9	5	3	3	1	1
Sly01g0042411	M12	NA	10	9	9	6	5	17	21	18	9	6
Sly01g0042421	M12	NA	14	14	21	52	199	111	108	118	114	376
Sly01g0042461	M12	NA	26	26	26	31	40	30	34	33	49	56
Sly01g0042471	M3	NA	17	20	11	11	17	11	14	10	23	15
Sly01g0042481	M3	NA	14	12	5	7	13	7	12	6	15	15
Sly01g0042491	M6	NA	17	18	10	21	50	17	18	12	40	32
Sly01g0042501	M11	NA	55	53	57	61	73	59	53	68	71	82
Sly01g0042511	M1	NA	1	1	1	1	0	1	1	0	0	0
Sly01g0042521	M22	NA	2	1	1	1	1	9	2	8	0	0
Sly01g0042541	M11	NA	18	18	19	21	32	20	18	24	26	43
Sly01g0042551	M18	NA	22	25	24	28	37	27	26	28	39	60
Sly01g0042561	M12	NA	19	21	17	19	34	21	24	21	40	65
Sly01g0042601	M11	NA	4	3	3	4	5	3	4	6	7	8
Sly01g0042621	M1	NA	3	4	4	3	4	3	3	4	4	6
Sly01g0042721	M12	NA	1	1	1	0	0	2	1	1	0	0
Sly01g0042751	M11	NA	18	22	19	34	49	19	23	26	58	76
Sly01g0042761	M11	NA	6	6	9	10	8	9	8	12	13	14
Sly01g0042771	M18	NA	58	54	52	53	54	57	49	59	70	63
Sly01g0042781	M2	NA	33	31	32	35	42	31	31	30	37	38
Sly01g0042791	M12	NA	1	1	1	1	0	2	2	2	1	0
Sly01g0042801	M11	NA	6	6	8	7	8	8	7	10	4	4
Sly01g0042811	M11	NA	3	3	4	3	3	3	3	4	2	2
Sly01g0042821	M12	NA	2	3	2	1	16	10	10	10	1	2
Sly01g0042831	M9	NA	7	12	11	1	1	12	18	14	1	2
Sly01g0042841	M3	NA	10	25	15	1	1	5	7	9	1	0
Sly01g0042861	M2	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0042871	M6	NA	109	116	110	137	155	111	116	106	101	134
Sly01g0042891	M8	NA	48	50	42	53	51	50	58	46	57	60
Sly01g0042901	M1	NA	26	24	22	19	20	18	19	17	22	27
Sly01g0042911	M7	NA	24	28	26	111	235	18	37	30	156	328
Sly01g0042921	M1	NA	8	7	11	14	36	3	1	2	1	1
Sly01g0042931	M3	NA	3	5	3	5	5	2	3	2	8	11
Sly01g0042941	M3	NA	12	15	10	17	18	3	5	3	8	14
Sly01g0042951	M21	NA	3	3	4	3	3	3	2	3	3	2
Sly01g0042961	M12	NA	7	6	6	8	9	7	7	7	12	13
Sly01g0042981	M3	NA	12	12	10	6	7	8	8	5	3	4
Sly01g0042991	M3	NA	107	94	61	23	25	92	67	41	7	6
Sly01g0043001	M22	NA	1	1	1	1	1	1	1	1	0	1
Sly01g0043011	M19	NA	4	5	4	2	2	4	4	4	3	3
Sly01g0043061	M10	NA	29	71	28	37	139	66	97	37	49	174
Sly01g0043071	M1	NA	15	22	14	23	41	12	12	11	30	70
Sly01g0043081	M3	NA	21	27	18	27	54	14	17	14	36	119
Sly01g0043091	M11	NA	7	6	8	18	21	8	8	10	18	15
Sly01g0043101	M11	NA	34	29	39	58	48	40	38	49	45	31
Sly01g0043111	M1	NA	5	3	2	7	1	1	1	1	1	1
Sly01g0043121	M22	NA	7	7	5	2	2	8	7	5	1	1
Sly01g0043131	M9	NA	15	16	14	27	56	30	34	26	29	59
Sly01g0043151	M12	NA	110	106	126	219	278	197	188	242	267	327
Sly01g0043161	M10	SlGH3-2	129	113	33	59	154	121	105	93	56	170
Sly01g0043191	M10	Solyc01g107400	42	27	19	311	64	57	136	22	32	10
Sly01g0043201	M19	NA	25	23	24	29	14	25	21	23	17	12
Sly01g0043211	M11	NA	7	6	9	8	10	10	8	11	9	9
Sly01g0043221	M3	NA	66	71	56	74	54	58	68	50	73	56
Sly01g0043241	M12	NA	7	7	6	8	7	16	18	21	19	13
Sly01g0043251	M22	NA	1	1	1	0	1	2	1	1	1	0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0118921	M11	NA	29	29	35	68	78	43	40	47	53	38
Sly07g0118931	M1	NA	7	8	7	7	5	7	7	7	6	5
Sly07g0118941	M12	NA	1	1	1	1	1	1	1	1	1	2
Sly07g0118951	M19	NA	50	48	52	33	29	46	43	42	27	21
Sly07g0118961	M12	NA	28	20	41	3	1	408	328	545	23	3
Sly07g0118971	M12	NA	5	5	5	9	8	34	37	42	65	50
Sly07g0118981	M9	NA	1	1	1	6	4	1	1	1	1	2
Sly07g0118991	M11	Peroxiredoxin Q	19	19	19	46	56	41	45	45	25	25
Sly07g0119001	M12	SlRbohF	7	6	6	11	10	9	10	10	11	9
Sly07g0119031	M1	NA	6	7	5	16	13	2	3	2	3	5
Sly07g0119041	M1	NA	2	2	2	6	1	1	1	2	1	0
Sly07g0119051	M1	Solyc07g042490	136	138	92	139	69	36	32	35	38	27
Sly07g0119081	M18	NA	13	14	16	46	59	15	14	16	42	59
Sly07g0119091	M3	NA	1	2	1	1	0	1	0	0	0	0
Sly07g0119141	M22	SUS4-like	1	1	1	0	0	10	1	6	0	0
Sly07g0119151	M3	NA	32	40	16	5	4	7	9	4	2	5
Sly07g0119161	M7	NA	1	2	1	1	1	1	4	1	1	1
Sly07g0119171	M3	NA	17	21	20	7	6	10	26	7	3	18
Sly07g0119181	M3	SUS4-like	290	295	205	151	133	203	219	109	79	58
Sly07g0119201	M3	NACK2	1	1	1	0	1	1	1	1	0	0
Sly07g0119211	M3	NA	78	78	73	54	40	55	66	49	54	43
Sly07g0119221	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0119231	M10	NA	24	32	23	23	16	33	35	24	10	12
Sly07g0119251	M1	NA	109	110	97	110	94	70	84	83	117	126
Sly07g0119321	M11	NA	176	162	157	127	127	173	166	162	140	157
Sly07g0119331	M12	NA	1	1	1	1	0	4	4	4	1	1
Sly07g0119341	M3	NA	29	29	27	25	23	25	26	24	24	23
Sly07g0119351	M1	NA	40	40	38	45	59	23	27	24	27	42
Sly07g0119381	M2	NA	25	26	22	18	17	17	21	18	19	17
Sly07g0119391	M3	NA	13	16	14	12	9	13	12	11	10	9
Sly07g0119401	M1	NA	13	15	15	11	10	14	10	10	9	8
Sly07g0119411	M3	NA	25	29	22	19	20	20	20	16	17	18
Sly07g0119421	M1	NA	4	4	4	4	3	2	2	2	3	2
Sly07g0119451	M11	NA	3	4	3	6	5	5	4	7	3	1
Sly07g0119461	M12	NA	3	3	2	4	3	4	3	3	3	2
Sly07g0119471	M22	STS5	10	10	11	27	54	11	10	12	48	75
Sly07g0119491	M9	NA	1	2	1	1	1	2	2	1	2	0
Sly07g0119501	M1	NA	12	13	13	11	9	6	4	5	6	3
Sly07g0119521	M3	NA	160	186	123	96	99	132	132	106	98	121
Sly07g0119531	M1	NA	19	20	20	15	15	11	10	10	13	13
Sly07g0119561	M12	NA	30	32	32	37	34	36	36	34	29	28
Sly07g0119601	M4	NA	10	9	11	36	57	12	11	12	38	100
Sly07g0119621	M3	NA	10	10	8	13	13	9	9	10	12	12
Sly07g0119631	M11	NA	18	15	21	22	24	23	21	27	25	25
Sly07g0119641	M11	NA	16	13	14	15	15	18	16	17	20	23
Sly07g0119651	M11	NA	1	1	1	1	0	1	1	1	0	1
Sly07g0119661	M11	NA	18	9	45	1	1	78	50	75	1	0
Sly07g0119711	M11	NA	9	10	10	4	6	14	12	13	2	6
Sly07g0119751	M1	NA	8	8	9	2	2	6	5	4	1	1
Sly07g0119791	M14	NA	11	10	17	26	33	8	6	11	11	20
Sly07g0119801	M1	NA	6	5	9	8	71	3	3	3	23	84
Sly07g0119811	M8	NA	4	3	2	2	1	4	4	2	2	2
Sly07g0119821	M12	NA	28	29	31	21	20	67	68	57	27	29
Sly07g0119831	M12	NA	3	3	3	3	3	6	5	4	4	5
Sly07g0119851	M12	NA	1	1	1	1	1	2	3	2	2	1
Sly07g0119861	M11	NA	1	1	1	1	1	2	2	2	1	1
Sly07g0119891	M1	NA	47	81	25	1	1	10	5	1	0	1
Sly07g0119901	M12	NA	1	1	1	2	2	2	2	1	1	1
Sly07g0119911	M5	NA	14	24	12	5	6	18	23	7	2	2
Sly07g0119921	M18	NA	17	17	19	14	11	21	16	20	14	16
Sly07g0119931	M19	NA	61	67	65	71	75	63	58	64	80	72
Sly07g0119941	M2	NA	356	357	329	315	123	242	311	212	490	205
Sly07g0119951	M3	NA	283	309	248	132	146	228	216	170	112	163
Sly07g0119961	M11	NA	4	5	6	13	10	5	5	5	6	6
Sly07g0119971	M1	NA	140	126	126	90	72	90	91	87	93	89
Sly07g0119981	M11	NA	3	1	4	1	0	14	12	4	0	1
Sly07g0119991	M23	NA	0	0	1	0	0	1	1	1	0	0
Sly07g0120021	M11	NA	58	51	99	27	5	114	82	64	5	1
Sly07g0120061	M23	NA	3	2	3	1	1	6	3	3	1	0
Sly07g0120071	M12	NA	1	1	1	0	0	4	4	2	1	0
Sly07g0120091	M3	NA	11	13	7	4	1	7	9	3	1	1
Sly07g0120101	M1	NA	4	3	5	2	1	1	1	1	0	0
Sly07g0120121	M7	NA	28	39	27	57	92	28	48	27	61	123
Sly07g0120141	M1	NA	22	23	23	8	3	8	7	7	4	1
Sly07g0120151	M2	NA	55	64	53	71	38	39	42	27	24	20
Sly07g0120161	M11	NA	43	37	46	69	56	114	97	117	16	8
Sly07g0120171	M1	NA	22	25	29	5	2	15	14	12	2	2
Sly07g0120181	M3	NA	115	95	88	145	150	65	71	69	185	135
Sly07g0120191	M13	NA	18	18	24	31	45	22	20	25	31	34
Sly07g0120201	M12	NA	38	38	40	36	43	41	43	38	37	40
Sly07g0120211	M19	SlARF6B	26	28	29	25	27	30	28	29	23	19
Sly07g0120221	M12	NA	1	1	1	3	1	1	3	5	27	9
Sly07g0120411	M11	NA	7	7	7	6	6	7	7	8	6	7
Sly07g0120421	M1	NA	142	135	158	142	161	115	113	140	186	192
Sly07g0120431	M9	NA	14	16	16	25	31	18	20	15	28	37
Sly07g0120441	M6	NA	2	2	1	1	2	2	2	2	2	2
Sly07g0120451	M2	NA	61	59	64	60	58	58	61	59	68	69
Sly07g0120461	M22	NA	2	1	1	0	0	1	1	3	0	0
Sly07g0120471	M3	NA	42	36	34	28	20	30	33	25	14	13
Sly07g0120481	M12	NA	373	352	375	503	391	426	428	456	511	503
Sly07g0120491	M19	NA	52	52	49	86	87	53	50	53	74	69
Sly07g0120501	M11	NA	272	192	323	271	406	574	490	684	298	179
Sly07g0120521	M15	NA	11	8	10	12	8	9	9	9	10	7
Sly07g0120531	M12	NA	1	1	1	0	0	2	3	2	1	0
Sly07g0120571	M18	NA	8	8	9	8	7	8	8	9	7	4
Sly07g0120591	M7	NA	2	3	1	1	1	4	4	1	1	1
Sly07g0120601	M11	NA	1	1	1	1	0	3	1	2	1	1
Sly07g0120611	M1	receptor protein (NPR	187	190	106	37	26	24	35	13	8	10
Sly07g0120621	M2	NA	18	18	23	61	81	19	17	19	66	86
Sly07g0120641	M3	NA	3	2	2	1	1	2	2	2	1	1
Sly07g0120661	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0120671	M11	NA	18	18	20	26	45	22	22	27	32	47
Sly07g0120691	M17	NA	21	19	20	19	14	19	18	19	18	11
Sly07g0120701	M1	NA	2	1	2	13	3	1	1	2	7	1
Sly07g0120721	M12	NA	1	2	3	252	100	2	12	19	635	317
Sly07g0120731	M6	NA	4	10	12	6	15	7	13	9	7	21
Sly07g0120761	M11	NA	4	4	4	50	72	7	4	11	67	53
Sly07g0120771	M2	NA	63	62	47	45	38	44	48	38	44	39
Sly07g0120781	M9	PFK6	17	18	11	15	22	22	24	15	33	74
Sly07g0120791	M1	NA	9	9	10	6	7	8	6	7	6	6
Sly07g0120801	M7	NA	33	39	35	52	19	36	42	35	43	23
Sly07g0120811	M1	NA	185	172	140	51	35	49	50	42	43	29
Sly07g0120821	M1	NA	10	8	5	3	3	2	2	2	2	3
Sly07g0120831	M11	NA	60	51	59	47	35	64	58	56	22	19
Sly07g0120841	M22	NA	7	6	6	5	5	7	5	7	4	4
Sly07g0120851	M18	NA	33	33	39	31	28	37	32	37	27	25
Sly07g0120861	M1	NA	95	90	84	86	104	76	73	74	104	123
Sly07g0120871	M15	NA	44	33	34	38	26	38	34	37	22	16
Sly07g0120881	M1	NA	11	12	11	10	7	11	9	10	6	3
Sly07g0120911	M1	NA	56	53	57	66	78	50	54	55	52	64
Sly07g0120921	M11	NA	38	38	44	61	49	58	56	68	80	70
Sly07g0120931	M11	SlSDG52	12	11	15	39	44	20	18	24	35	34
Sly07g0120941	M12	NA	9	9	12	40	44	17	15	19	32	61
Sly07g0120951	M3	NA	22	21	23	32	34	19	22	18	30	37
Sly07g0120971	M11	NA	178	184	233	380	299	172	198	238	401	475
Sly07g0120981	M1	NA	467	485	397	56	28	84	80	34	33	11
Sly07g0120991	M3	NA	6	6	4	1	2	3	3	2	2	2
Sly07g0121001	M1	NA	15	16	14	14	17	11	11	11	15	17
Sly07g0121011	M19	NA	15	13	15	13	15	12	11	14	11	15
Sly07g0121021	M1	NA	5	5	6	7	8	4	4	4	8	15
Sly07g0121031	M17	NA	38	35	36	29

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0043256	M3	NA	41	52	37	31	40	40	38	34	47	65
Sly01g0043261	M1	NA	1	3	2	0	1	1	1	1	1	0
Sly01g0043271	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0043281	M3	NA	118	120	98	115	103	69	73	62	125	110
Sly01g0043291	M1	NA	5	5	4	2	2	2	1	1	1	1
Sly01g0043311	M3	NA	10	11	8	6	6	6	6	5	4	4
Sly01g0043321	M12	NA	26	20	22	4	2	182	122	164	2	1
Sly01g0043331	M2	NA	37	40	33	35	28	30	37	25	30	31
Sly01g0043341	M1	NA	39	34	32	31	35	28	25	26	32	35
Sly01g0043351	M2	NA	31	29	27	19	17	18	25	18	18	16
Sly01g0043361	M3	NA	16	16	12	7	6	9	11	8	5	6
Sly01g0043371	M12	NA	54	51	55	106	140	63	69	68	96	114
Sly01g0043381	M23	NA	1	1	1	0	1	1	1	1	1	1
Sly01g0043391	M11	NA	55	43	47	67	68	76	69	86	86	138
Sly01g0043401	M1	NA	20	21	25	18	26	5	8	3	2	9
Sly01g0043411	M1	NA	7	8	7	6	8	6	4	4	5	4
Sly01g0043421	M1	NA	5	6	6	5	8	5	5	4	4	3
Sly01g0043431	M11	NA	44	42	57	193	157	57	59	84	120	89
Sly01g0043441	M1	NA	66	74	79	142	114	61	74	69	82	76
Sly01g0043491	M1	SlCycD3;1	2	1	4	0	0	1	1	1	0	1
Sly01g0043501	M6	NA	24	33	20	33	95	21	29	22	65	134
Sly01g0043511	M11	NA	75	80	78	105	109	96	93	106	131	166
Sly01g0043541	M3	NA	1	2	1	0	0	1	1	0	0	0
Sly01g0043551	M3	NA	63	97	27	6	3	19	17	11	2	1
Sly01g0043571	M12	NA	27	39	22	23	11	91	106	148	80	24
Sly01g0043581	M1	NA	1	1	1	0	1	1	1	1	0	0
Sly01g0043591	M10	NA	275	284	177	29	59	400	518	229	184	173
Sly01g0043611	M12	NA	27	33	52	213	398	95	184	283	2180	1578
Sly01g0043621	M2	CBSX2-like	76	88	58	80	72	43	71	91	590	299
Sly01g0043631	M17	NA	637	647	650	714	650	638	612	626	675	647
Sly01g0043641	M1	NA	126	130	132	110	120	118	113	113	80	103
Sly01g0043651	M20	NA	15	9	19	1	1	8	4	7	0	0
Sly01g0043661	M1	NA	129	132	113	91	109	79	69	46	28	42
Sly01g0043671	M22	NA	12	10	9	7	7	37	10	29	1	2
Sly01g0043681	M3	NA	11	10	5	6	10	4	4	2	4	6
Sly01g0043691	M3	NA	21	23	19	23	30	21	21	19	26	28
Sly01g0043701	M3	NA	17	19	16	14	13	17	17	15	12	7
Sly01g0043711	M22	NA	1	1	1	0	0	3	1	3	0	0
Sly01g0043751	M10	NA	15	21	14	11	7	30	33	20	3	3
Sly01g0043761	M12	NA	12	11	12	14	6	15	12	12	2	1
Sly01g0043771	M12	NA	1	1	1	1	2	1	1	1	1	1
Sly01g0043781	M11	NA	38	38	33	45	64	41	38	41	67	73
Sly01g0043791	M1	NA	62	42	42	30	38	30	29	31	39	57
Sly01g0043801	M1	NA	121	105	140	151	193	88	88	116	92	118
Sly01g0043821	M12	NA	19	22	16	10	7	29	25	23	15	13
Sly01g0043831	M19	NA	21	21	19	17	15	24	20	19	12	17
Sly01g0043841	M1	NA	4	3	3	4	4	3	2	2	1	3
Sly01g0043851	M1	NA	3	5	4	5	4	3	4	2	2	3
Sly01g0043861	M3	NA	25	33	23	19	22	24	26	19	19	21
Sly01g0043871	M3	NA	39	45	34	28	35	35	40	29	27	46
Sly01g0043881	M7	NA	5	6	5	3	7	8	8	4	2	5
Sly01g0043891	M11	NA	11	12	12	15	14	22	22	23	19	16
Sly01g0043901	M14	ABI5-like/SlABF4	40	31	44	45	52	34	30	40	75	73
Sly01g0043921	M11	NA	19	21	27	35	33	40	37	56	82	79
Sly01g0043931	M12	NA	10	10	9	14	12	10	11	10	17	18
Sly01g0043941	M1	NA	19	20	17	23	24	12	12	11	19	19
Sly01g0043951	M2	NA	19	18	15	15	17	14	15	11	17	21
Sly01g0043961	M1	NA	5	6	5	3	1	4	4	4	1	1
Sly01g0043971	M3	NA	108	112	116	104	125	100	102	101	88	92
Sly01g0043981	M19	NA	22	23	20	21	22	20	19	19	17	19
Sly01g0044001	M1	NA	17	17	15	10	10	13	12	12	9	10
Sly01g0044011	M1	NA	12	10	8	20	11	2	2	2	2	2
Sly01g0044021	M3	NA	11	15	7	6	5	8	10	5	3	2
Sly01g0044031	M7	SlCYP707A4	6	10	4	2	4	7	9	5	3	13
Sly01g0044041	M3	NA	6	13	5	2	5	6	11	4	4	16
Sly01g0044051	M8	NA	26	27	18	17	15	25	32	20	11	14
Sly01g0044061	M7	SlERF.D3	6	9	2	1	7	5	15	7	1	13
Sly01g0044071	M7	NA	54	66	47	46	184	63	110	58	83	299
Sly01g0044081	M9	NA	53	52	54	42	70	56	70	52	58	138
Sly01g0044101	M11	SlSnRK2.3	37	38	45	67	49	69	55	71	67	52
Sly01g0044111	M1	NA	24	24	24	21	20	21	20	23	22	22
Sly01g0044121	M11	NA	58	45	63	50	39	88	80	99	31	12
Sly01g0044161	M1	NA	3	2	3	1	1	1	1	1	0	1
Sly01g0044171	M11	NA	21	18	35	16	15	52	39	50	15	13
Sly01g0044181	M3	NA	6	8	1	0	0	1	1	0	0	0
Sly01g0044191	M3	NA	2	4	1	0	0	0	0	1	0	0
Sly01g0044211	M3	NA	10	8	3	1	0	1	0	1	1	0
Sly01g0044221	M1	NA	85	99	36	215	129	2	1	1	3	4
Sly01g0044231	M19	NA	12	14	13	22	30	14	11	15	21	25
Sly01g0044241	M12	NA	9	9	10	14	25	11	10	11	26	37
Sly01g0044251	M12	NA	6	5	6	8	16	7	7	8	19	32
Sly01g0044261	M1	NA	26	23	27	27	29	24	24	23	23	26
Sly01g0044271	M2	NA	22	20	23	23	20	20	20	20	20	15
Sly01g0044281	M1	NA	35	38	35	28	31	28	28	28	31	38
Sly01g0044291	M3	NA	23	45	18	2	1	14	18	4	1	1
Sly01g0044301	M22	NA	4	1	3	0	1	20	5	21	1	1
Sly01g0044341	M3	NA	7	4	3	1	0	4	4	2	1	1
Sly01g0044351	M1	NA	314	251	223	29	16	201	172	128	15	18
Sly01g0044361	M1	NA	1209	1131	1159	517	465	650	569	543	280	335
Sly01g0044371	M11	NA	11	11	15	14	12	17	15	18	5	6
Sly01g0044381	M12	NA	15	12	20	53	47	47	42	55	7	7
Sly01g0044401	M11	NA	7	6	9	22	33	8	7	11	4	11
Sly01g0044411	M11	NA	6	5	7	10	21	12	10	12	7	15
Sly01g0044421	M12	NA	5	3	4	2	2	8	6	6	1	1
Sly01g0044431	M3	NA	24	24	18	24	20	18	21	18	12	17
Sly01g0044441	M1	NA	8	7	11	107	55	5	4	8	107	45
Sly01g0044451	M3	NA	30	26	33	389	257	14	20	22	494	303
Sly01g0044461	M14	NA	38	40	45	69	118	41	37	44	66	69
Sly01g0044471	M9	NA	1	1	1	1	0	1	1	1	0	0
Sly01g0044481	M12	NA	28	34	30	12	22	37	41	35	16	25
Sly01g0044491	M11	NII1	4	5	7	52	45	9	8	9	4	3
Sly01g0044501	M11	NA	1	1	2	3	6	3	3	3	5	5
Sly01g0044511	M12	NA	6	6	7	11	11	7	8	8	13	12
Sly01g0044521	M12	NA	44	42	43	67	104	46	51	47	66	94
Sly01g0044531	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0044551	M22	NA	2	2	2	3	6	3	3	2	7	11
Sly01g0044561	M7	NA	2	3	2	2	3	2	3	2	5	15
Sly01g0044571	M12	NA	1	2	2	1	1	3	2	3	1	1
Sly01g0044591	M1	NA	1	1	4	1	1	0	1	1	1	2
Sly01g0044601	M1	NA	1	1	1	13	32	0	1	1	68	191
Sly01g0044621	M1	NA	2	2	2	4	3	1	1	1	3	5
Sly01g0044631	M1	NA	3	1	4	1	0	1	1	1	0	0
Sly01g0044641	M1	NA	8	6	10	4	8	2	1	2	1	1
Sly01g0044651	M1	NA	11	9	9	2	3	6	6	4	1	1
Sly01g0044661	M3	NA	6	6	4	1	1	3	3	2	1	0
Sly01g0044671	M1	NA	2	1	1	1	1	1	0	1	0	0
Sly01g0044681	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly01g0044711	M11	NA	14	17	18	18	28	20	17	20	12	19
Sly01g0044721	M23	NA	1	0	0	0	0	1	1	1	0	0
Sly01g0044731	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0044751	M3	NA	4	4	3	39	210	2	2	2	342	469
Sly01g0044761	M11	NA	39	39	47	42	33	58	56	65	44	36
Sly01g0044771	M11	NA	1	1	1	1	2	1	1	1	1	1
Sly01g0044781	M11	NA	465	400	673	478	444	838	692	1352	785	533
Sly01g0044791	M18	NA	21	24	24	23	24	30	25	32	22	22
Sly01g0044801	M11	NA	6	6	11	2	1	27	23	27	2	1
Sly01g0044811	M22	NA	2	2	2	1	1	7	4	5	1	1
Sly01g0044821	M18	NA	8	9	11	10	10	10	7	10	13	12
Sly01g0044831	M12	NA	11	12	11	12	15	11	12	12	26	29
Sly01g0044861	M11	NA	28	23	27	13	2	49	48	57	13	2
Sly01g0044871	M1	NA	3	4	3	1	1	1	1	1	1	1
Sly01g0044881	M11	PPR-like49	5	4	6	4	4	5	5	5	4	3
Sly01g0044891	M3	NA	48	40	32	21	21	24	28	20	33	26
Sly01g0044901	M19	NA	11	13	14	16	16	15	12	15	11	13

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0121071	M1	NA	21	19	21	12	7	7	11	8	2	3
Sly07g0121081	M12	NA	75	66	72	4	2	140	162	117	2	1
Sly07g0121091	M23	NA	1	1	1	0	0	1	1	1	1	0
Sly07g0121101	M12	NA	5	4	6	5	4	49	48	45	35	45
Sly07g0121111	M1	NA	24	22	20	13	13	15	14	13	8	7
Sly07g0121121	M12	NA	9	10	11	11	11	11	11	11	11	11
Sly07g0121141	M10	NA	2	3	2	3	2	3	3	3	2	3
Sly07g0121151	M3	NA	2	3	2	2	2	2	2	1	1	1
Sly07g0121161	M1	NA	7	10	8	7	4	6	6	6	4	2
Sly07g0121171	M1	NA	21	23	17	1	1	2	4	1	0	1
Sly07g0121181	M11	NA	18	17	24	15	6	29	22	32	7	2
Sly07g0121201	M22	NA	3	2	2	1	1	2	2	2	1	1
Sly07g0121211	M19	NA	2	2	2	1	0	2	1	2	1	0
Sly07g0121251	M1	NA	22	23	23	21	19	20	19	17	16	14
Sly07g0121261	M1	NA	5	6	5	7	6	3	4	4	5	4
Sly07g0121281	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly07g0121301	M1	NA	284	273	323	184	199	173	160	198	112	89
Sly07g0121311	M1	signal transducer (SLY	4	4	4	8	2	1	1	1	2	3
Sly07g0121321	M1	NA	10	9	10	11	12	9	7	11	5	7
Sly07g0121331	M1	NA	80	64	68	76	86	59	58	63	83	87
Sly07g0121341	M1	NA	3	4	2	1	3	1	2	1	1	2
Sly07g0121351	M2	NA	60	62	55	57	62	49	57	47	62	78
Sly07g0121361	M3	NA	9	8	7	9	9	7	8	5	8	14
Sly07g0121381	M22	NA	14	13	16	48	56	15	11	15	36	49
Sly07g0121391	M19	SlHK4	34	31	43	25	33	34	27	35	16	20
Sly07g0121401	M1	NA	1	2	3	3	2	1	1	0	0	1
Sly07g0121421	M3	NA	78	86	48	39	57	34	40	28	38	59
Sly07g0121431	M1	NA	99	110	112	96	146	81	83	70	85	145
Sly07g0121441	M3	NA	1044	1053	750	2141	2645	679	883	651	3093	3322
Sly07g0121451	M10	NA	8	8	7	16	16	8	8	7	12	12
Sly07g0121481	M11	NA	4	5	6	4	2	8	7	9	4	2
Sly07g0121491	M11	NA	23	19	21	13	4	21	21	25	10	5
Sly07g0121501	M11	NA	40	19	46	14	15	83	70	91	16	10
Sly07g0121511	M19	NA	13	15	15	14	18	15	12	14	11	12
Sly07g0121531	M1	NA	55	50	51	53	39	48	48	46	40	31
Sly07g0121541	M19	NA	14	14	14	12	14	14	13	15	13	13
Sly07g0121581	M22	NA	4	3	4	1	1	5	2	4	1	0
Sly07g0121601	M1	NA	16	27	31	10	12	9	6	9	8	13
Sly07g0121611	M1	NA	25	24	28	16	17	13	11	14	9	16
Sly07g0121621	M2	NA	42	42	34	38	45	33	39	30	41	48
Sly07g0121631	M3	NA	30	35	28	35	122	29	28	27	30	94
Sly07g0121651	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0121661	M3	NA	12	13	10	4	4	9	8	7	5	6
Sly07g0121691	M3	NA	42	44	35	32	23	38	40	33	29	21
Sly07g0121701	M3	NA	31	34	34	47	57	21	22	11	15	26
Sly07g0121721	M22	NA	1	1	1	1	0	2	1	1	1	0
Sly07g0121731	M7	NA	5	11	1	0	1	5	23	1	1	2
Sly07g0121741	M10	NA	1	2	1	1	1	7	4	1	0	1
Sly07g0121751	M11	NA	17	17	20	31	46	30	26	31	26	23
Sly07g0121761	M12	NA	20	18	22	69	13	100	87	124	44	12
Sly07g0121771	M3	NA	2	2	2	1	1	1	2	1	1	1
Sly07g0121781	M1	NA	3	3	4	1	1	2	1	1	1	1
Sly07g0121791	M3	NA	20	19	17	23	36	16	16	16	29	41
Sly07g0121821	M12	NA	9658	8943	12016	22234	49714	40426	42597	41320	68616	124587
Sly07g0121831	M1	NA	183	136	192	105	47	83	122	102	191	94
Sly07g0121841	M2	NA	20	17	21	16	13	18	20	17	18	11
Sly07g0121881	M5	NA	41	63	30	13	14	43	47	25	13	17
Sly07g0121891	M11	NA	9	14	10	5	3	16	14	15	5	9
Sly07g0121901	M1	NA	6	8	7	6	3	1	1	1	0	1
Sly07g0121911	M1	NA	23	23	26	50	58	14	18	14	48	71
Sly07g0121921	M14	NA	22	17	23	36	42	17	17	19	12	18
Sly07g0121931	M1	NA	32	31	30	50	43	23	23	22	21	24
Sly07g0121941	M11	NA	36	31	36	47	47	41	40	56	59	55
Sly07g0121971	M2	NA	35	34	31	40	50	27	30	26	50	58
Sly07g0121981	M11	NA	6	5	6	8	9	8	7	8	11	16
Sly07g0121991	M1	NA	11	13	12	11	4	13	10	9	4	1
Sly07g0122001	M11	NA	36	35	55	15	3	50	39	53	2	1
Sly07g0122011	M11	NA	7	4	9	0	0	27	19	24	1	0
Sly07g0122021	M11	NA	8	8	10	10	10	12	10	12	6	5
Sly07g0122031	M10	NA	2	2	1	1	1	2	2	1	1	1
Sly07g0122091	M14	NA	3	2	3	3	2	2	3	3	3	2
Sly07g0122101	M2	NA	55	64	64	64	55	53	80	55	42	37
Sly07g0122111	M15	NA	130	102	103	177	188	104	99	120	180	200
Sly07g0122121	M3	NA	12	19	4	1	1	9	16	1	1	1
Sly07g0122141	M9	NA	12	14	12	9	6	15	20	16	17	13
Sly07g0122151	M3	NA	4	3	3	1	3	2	3	2	2	4
Sly07g0122161	M3	NA	16	15	13	14	16	15	14	13	15	20
Sly07g0122191	M1	NA	197	280	454	756	104	8	1	1	1	1
Sly07g0122201	M6	NA	88	94	92	128	79	89	113	79	77	49
Sly07g0122211	M3	NA	1	2	1	1	0	1	1	1	0	1
Sly07g0122221	M1	NA	11	10	10	12	13	7	7	7	17	19
Sly07g0122231	M11	NA	24	22	27	24	29	26	22	28	27	30
Sly07g0122241	M3	SlERF.F3	47	49	37	46	45	38	39	34	41	44
Sly07g0122251	M22	AGO6	8	8	8	7	9	9	7	8	8	10
Sly07g0122291	M3	ACO1	3765	3971	2656	3735	2394	1000	1248	263	477	339
Sly07g0122301	M22	NA	1	1	1	0	0	1	1	2	0	0
Sly07g0122311	M1	ACO3	109	128	82	19	3	5	8	2	10	3
Sly07g0122321	M3	NA	20	18	11	8	10	9	8	7	5	9
Sly07g0122331	M1	NA	2	1	2	2	1	1	2	1	1	1
Sly07g0122341	M12	NA	12	14	11	17	22	12	13	13	19	19
Sly07g0122351	M3	NA	20	21	20	11	7	20	20	19	6	4
Sly07g0122361	M11	NA	6	7	8	11	11	9	9	10	11	10
Sly07g0122381	M9	NA	10	8	6	3	3	12	14	6	1	3
Sly07g0122391	M3	NA	47	47	37	21	16	36	41	24	4	6
Sly07g0122411	M3	NA	13	7	3	1	1	2	2	2	1	1
Sly07g0122421	M3	NA	5	7	3	2	1	2	3	2	3	4
Sly07g0122431	M3	NA	4	3	2	1	2	2	2	2	2	2
Sly07g0122441	M3	NA	8	7	3	0	1	2	2	1	1	1
Sly07g0122451	M3	NA	1	3	2	0	0	1	1	1	1	1
Sly07g0122461	M3	NA	2	2	2	1	1	2	2	2	1	1
Sly07g0122471	M1	HPO lyase	87	78	93	125	119	28	29	33	60	88
Sly07g0122481	M1	NA	3	4	4	5	9	1	1	1	1	1
Sly07g0122491	M12	NA	55	52	55	72	74	66	73	70	74	69
Sly07g0122501	M18	MGO1-like	104	106	114	114	123	125	105	127	138	148
Sly07g0122511	M3	NA	99	119	75	53	54	90	127	63	47	58
Sly07g0122521	M11	NA	5	4	5	4	4	6	6	6	7	5
Sly07g0122531	M12	NA	15	15	14	17	18	18	20	18	16	15
Sly07g0122551	M3	NA	2	3	2	3	3	1	1	0	1	1
Sly07g0122581	M22	NA	1	1	1	1	2	5	1	2	1	1
Sly07g0122661	M22	NA	1	0	1	0	0	1	1	1	0	0
Sly07g0122671	M1	NA	6	9	11	2	1	1	1	1	1	1
Sly07g0122691	M12	NA	4	6	5	16	30	7	9	7	7	24
Sly07g0122701	M13	NA	397	350	451	470	456	448	411	521	402	538
Sly07g0122711	M12	NA	3	2	1	5	9	7	6	4	5	6
Sly07g0122721	M3	NA	3	3	1	11	4	1	1	1	3	2
Sly07g0122731	M12	NA	3	3	3	109	74	4	4	6	57	62
Sly07g0122761	M12	NA	1	1	1	0	0	1	1	1	1	1
Sly07g0122771	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0122791	M9	NA	1	0	0	0	0	1	1	1	1	0
Sly07g0122801	M12	NA	1	2	4	15	96	5	16	11	178	437
Sly07g0122861	M1	NA	1	1	1	1	5	1	1	1	1	1
Sly07g0122871	M1	NA	5	4	4	2	4	2	2	2	2	4
Sly07g0122961	M1	NA	66	67	64	44	43	48	42	47	46	46
Sly07g0123031	M1	NA	37	43	28	1	0	3	1	1	0	0
Sly07g0123041	M1	NA	16	26	17	0	0	1	0	1	0	0
Sly07g0123051	M1	NA	8	8	4	2	0	0	1	0	0	0
Sly07g0123061	M1	NA	17	17	13	1	1	2	2	1	1	1
Sly07g0123071	M22	NA	3	2	2	0	0	5	2	4	1	0
Sly07g0123091	M12	NA	6	4	6	3	3	73	60	149	34	27
Sly07g0123111	M22	NA	5	4	3	3	3	6	3	5	1	1
Sly07g0123121

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0044921	M11	NA	240	163	301	176	181	338	250	485	195	231
Sly01g0044931	M6	NA	20	42	27	18	41	20	31	18	15	32
Sly01g0044941	M12	NA	1	1	1	1	12	2	2	3	1	23
Sly01g0044951	M16	NA	18	13	15	39	56	16	15	16	32	68
Sly01g0044961	M6	AOS-like4	1	2	2	0	0	1	2	0	0	0
Sly01g0044971	M1	AOS-like5	1	1	1	0	0	1	0	1	0	0
Sly01g0044991	M1	NA	160	195	226	549	696	116	114	164	973	1401
Sly01g0045001	M1	NA	103	86	107	109	151	22	18	25	228	324
Sly01g0045021	M12	NA	22	22	23	10	13	29	25	31	6	8
Sly01g0045031	M22	NA	9	8	8	5	4	10	7	10	3	2
Sly01g0045041	M3	NA	43	42	39	35	26	32	35	34	48	40
Sly01g0045051	M1	NA	5	4	4	7	6	2	1	1	1	1
Sly01g0045071	M6	NA	6	22	18	1	1	6	12	4	1	1
Sly01g0045081	M12	NA	19	18	18	21	22	19	19	19	25	26
Sly01g0045111	M19	NA	25	26	25	31	36	24	25	26	26	26
Sly01g0045121	M1	NA	12	10	13	11	12	10	10	11	9	8
Sly01g0045131	M11	NA	284	254	310	456	961	347	302	422	614	1121
Sly01g0045141	M1	NA	3	6	7	21	11	2	1	1	1	1
Sly01g0045151	M6	NA	1	2	1	34	9	1	1	1	1	1
Sly01g0045161	M12	NA	3	2	2	8	8	7	4	3	1	1
Sly01g0045171	M2	NA	42	38	36	8	2	19	29	11	3	2
Sly01g0045181	M11	NA	79	73	78	76	76	91	85	87	67	64
Sly01g0045191	M1	NA	169	176	173	148	120	135	154	165	174	176
Sly01g0045201	M11	NA	3	3	6	3	3	7	6	7	2	1
Sly01g0045211	M1	NA	4	3	4	5	4	3	1	2	1	1
Sly01g0045251	M5	NA	25	26	22	23	23	25	30	20	22	23
Sly01g0045261	M2	NA	286	282	253	226	174	191	227	175	162	143
Sly01g0045271	M3	NA	15	18	10	11	10	8	11	3	3	4
Sly01g0045281	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly01g0045301	M3	NA	15	20	12	10	10	11	13	12	12	15
Sly01g0045311	M1	NA	611	881	309	27	8	20	5	3	1	2
Sly01g0045321	M2	NA	1	1	1	0	0	1	1	1	1	1
Sly01g0045361	M11	NA	2	1	3	1	1	5	3	4	1	0
Sly01g0045371	M22	NA	1	0	1	0	1	1	1	1	1	1
Sly01g0045381	M18	NA	29	28	34	35	47	33	29	35	31	48
Sly01g0045391	M12	NA	342	342	317	430	456	363	390	403	501	646
Sly01g0045411	M2	NA	151	160	131	137	101	125	147	103	94	87
Sly01g0045421	M19	NA	1	2	1	1	1	1	2	1	1	1
Sly01g0045431	M2	NA	87	87	74	66	71	61	69	55	72	95
Sly01g0045441	M3	NA	114	124	81	37	47	63	81	41	17	32
Sly01g0045451	M9	NA	6	6	5	1	1	7	8	5	2	2
Sly01g0045461	M11	NA	20	19	28	12	28	33	24	32	14	81
Sly01g0045471	M11	NA	56	49	81	59	54	86	73	110	65	66
Sly01g0045481	M22	NA	1	1	1	1	1	2	1	2	1	0
Sly01g0045491	M12	NA	114	114	118	173	190	155	167	177	212	201
Sly01g0045501	M11	NA	6	6	9	8	9	12	10	15	7	8
Sly01g0045511	M3	NA	14	14	12	15	15	12	13	12	15	15
Sly01g0045531	M5	NA	6	9	6	9	9	9	8	6	1	3
Sly01g0045541	M14	NA	1369	1015	1597	1745	1683	914	731	1257	1334	1505
Sly01g0045551	M3	NA	10	6	1	2	1	2	3	1	1	0
Sly01g0045571	M1	NA	30	32	28	46	81	22	23	22	42	101
Sly01g0045581	M23	NA	2	1	1	1	1	2	1	1	0	1
Sly01g0045591	M3	NA	22	30	10	3	4	18	17	6	2	5
Sly01g0045601	M3	NA	255	302	130	38	49	107	122	49	40	54
Sly01g0045611	M1	NA	38	51	20	1	2	3	4	1	1	1
Sly01g0045661	M3	NA	20	21	16	17	11	14	17	13	14	11
Sly01g0045671	M2	NA	158	153	147	132	116	134	163	133	116	123
Sly01g0045681	M11	NA	29	31	29	52	53	26	31	32	89	94
Sly01g0045691	M11	SlAGPase-L1	7	5	11	1	1	9	7	9	1	1
Sly01g0045701	M1	NA	4	2	2	1	1	1	1	1	0	0
Sly01g0045711	M1	NA	22	11	22	9	9	5	3	6	1	1
Sly01g0045721	M1	NA	30	15	27	16	11	4	2	3	1	1
Sly01g0045741	M1	NA	48	42	44	61	80	37	38	42	59	52
Sly01g0045751	M11	NA	118	100	122	104	107	138	133	147	91	89
Sly01g0045761	M1	NA	9	6	7	4	1	1	1	1	1	1
Sly01g0045771	M12	NA	121	130	127	136	136	137	141	147	119	119
Sly01g0045781	M9	NA	1	1	1	2	1	3	3	1	1	0
Sly01g0045791	M12	NA	372	344	386	808	709	994	1332	1216	872	367
Sly01g0045801	M9	NA	44	52	36	36	53	62	84	64	53	81
Sly01g0045811	M12	NA	1	1	1	1	1	1	2	2	1	1
Sly01g0045821	M12	NA	41	42	29	32	50	48	48	46	21	27
Sly01g0045831	M12	NA	19	13	11	16	87	50	42	51	71	306
Sly01g0045841	M12	NA	15	14	15	28	38	26	24	26	23	23
Sly01g0045851	M11	NA	198	183	189	204	256	190	201	203	255	330
Sly01g0045871	M1	NA	24	26	21	20	23	16	15	15	18	16
Sly01g0045881	M11	CLSY3	18	16	23	20	22	32	23	37	21	21
Sly01g0045891	M1	NA	45	40	55	34	27	26	24	31	28	21
Sly01g0045901	M19	NA	41	45	44	39	37	36	31	38	40	41
Sly01g0045911	M1	NA	135	158	282	106	19	102	59	106	10	3
Sly01g0045921	M1	NA	4	4	4	3	4	4	3	4	2	3
Sly01g0045931	M13	NA	61	51	68	52	66	65	56	73	60	90
Sly01g0045941	M8	NA	34	34	30	32	31	35	40	31	39	39
Sly01g0045961	M1	NA	6	6	8	5	2	4	4	4	1	1
Sly01g0045991	M9	NA	4	3	3	3	5	6	8	4	4	5
Sly01g0046001	M22	NA	4	4	3	12	11	13	5	9	1	2
Sly01g0046011	M12	NA	185	183	219	282	281	314	325	328	275	293
Sly01g0046021	M1	NA	25	23	29	9	9	20	21	20	3	3
Sly01g0046041	M2	NA	22	22	19	30	25	19	21	19	55	49
Sly01g0046051	M11	NA	2	2	2	1	1	3	3	3	1	1
Sly01g0046081	M3	NA	2	3	2	3	1	1	1	1	0	0
Sly01g0046091	M1	NA	3	3	2	3	1	1	1	1	0	0
Sly01g0046191	M12	NA	12	10	13	30	37	20	23	29	52	83
Sly01g0046201	M3	salicylic acid transport	8	7	7	7	10	7	7	7	9	13
Sly01g0046211	M6	NA	74	78	53	45	44	73	91	51	99	211
Sly01g0046221	M10	NA	73	76	69	63	60	76	79	71	78	88
Sly01g0046231	M6	NA	40	57	47	50	39	47	48	48	46	37
Sly01g0046271	M12	NA	2	1	2	2	1	2	3	3	3	2
Sly01g0046291	M12	NA	8	7	6	8	8	8	8	8	9	8
Sly01g0046301	M20	NA	364	288	316	118	15	313	229	316	30	4
Sly01g0046311	M1	NA	563	440	489	179	26	449	350	467	50	7
Sly01g0046321	M1	NA	55	41	49	22	17	41	38	41	16	23
Sly01g0046331	M3	NA	37	32	31	29	25	34	32	29	15	19
Sly01g0046341	M12	NA	141	131	146	277	331	160	183	184	269	373
Sly01g0046351	M15	NA	24	19	20	19	20	21	20	24	29	29
Sly01g0046361	M2	NA	150	142	141	161	175	132	139	144	163	193
Sly01g0046371	M7	NA	237	283	132	170	399	223	428	117	252	539
Sly01g0046381	M11	NA	66	62	74	94	100	106	103	113	100	110
Sly01g0046391	M12	polyprenol reductase	9	9	9	9	8	9	9	9	6	4
Sly01g0046401	M11	NA	15	14	17	12	12	14	15	18	18	19
Sly01g0046411	M7	NA	68	104	74	69	95	99	121	83	78	101
Sly01g0046431	M1	NA	40	38	37	36	32	25	23	26	24	25
Sly01g0046451	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0046461	M1	NA	64	61	69	99	122	55	54	54	162	202
Sly01g0046471	M1	NA	102	84	89	66	42	73	73	72	24	28
Sly01g0046481	M2	NA	118	119	113	121	101	105	126	99	133	84
Sly01g0046491	M11	NA	7	6	10	14	18	14	12	19	24	35
Sly01g0046501	M12	SAUR3	13	9	11	6	2	20	19	27	7	2
Sly01g0046511	M12	SAUR4	1	1	1	0	0	5	3	4	0	0
Sly01g0046571	M11	NA	1	1	1	0	1	2	2	2	1	1
Sly01g0046581	M12	NA	1	2	1	2	10	5	4	5	17	29
Sly01g0046591	M12	NA	2	2	3	3	7	6	6	5	19	18
Sly01g0046601	M12	NA	1	1	1	3	3	4	2	2	10	6
Sly01g0046611	M12	NA	2	2	2	3	5	4	3	4	13	13
Sly01g0046631	M12	Solyc01g110660	3	2	1	3	5	5	4	5	11	21
Sly01g0046641	M12	Solyc01g110670	2	2	2	2	2	5	4	4	4	6
Sly01g0046651	M12	SAUR12	2	1	1	1	2	4	4	4	4	3
Sly01g0046661	M12	NA	4	4	4	5	9	14	9	11	19	25
Sly01g0046671	M11	NA	4	5	3	5	10	11	7	7	19	17
Sly01g0046681	M12	NA	2	2	2	2	4	7	4	5	7	10
Sly01g0046701	M12	Solyc01g110720	1	1	1	2	2	1	2	2	4	7
Sly01g0046711	M12	Solyc01g110730	1	1	1	1	2	1	1	2	3	3
Sly01g0046721	M12	NA	2	2	1	2	2	2	3	2	4	4
Sly01g0046731	M12	NA	1	1	1	1	1	2	2	1	2	2
Sly01g0046741	M12	NA	4	6	5	9	13	16	10	11	22	24

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0123181	M1	NA	9	10	10	5	6	7	6	6	3	2
Sly07g0123191	M1	NA	228	216	162	125	92	128	119	100	60	53
Sly07g0123221	M3	NA	6	9	1	1	1	2	2	1	1	0
Sly07g0123231	M22	NA	3	2	3	2	1	6	4	7	2	1
Sly07g0123241	M1	NA	37	30	19	6	6	8	7	7	2	1
Sly07g0123251	M1	NA	37	36	21	4	2	3	3	2	1	1
Sly07g0123271	M15	HXK1	50	42	42	98	91	42	40	46	76	74
Sly07g0123281	M12	NA	6	4	5	12	13	10	10	7	12	7
Sly07g0123291	M22	NA	1	1	1	1	1	2	1	1	1	1
Sly07g0123311	M1	NA	111	146	138	3	0	25	18	16	1	1
Sly07g0123341	M13	NA	33	45	48	234	285	39	40	45	122	120
Sly07g0123351	M1	NA	40	54	52	93	34	36	24	27	20	5
Sly07g0123391	M7	NA	3	4	2	1	2	2	5	2	1	5
Sly07g0123411	M11	NA	1	1	1	0	0	2	1	3	0	0
Sly07g0123421	M11	NA	1	0	1	0	0	1	1	2	1	0
Sly07g0123431	M22	NA	5	1	4	1	1	39	3	32	1	1
Sly07g0123441	M1	NA	7	7	6	4	4	3	3	3	4	6
Sly07g0123451	M11	SISDG39	26	30	25	19	26	30	28	27	36	39
Sly07g0123461	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0123471	M11	NA	3	3	3	4	4	3	3	3	3	2
Sly07g0123481	M1	NA	61	60	59	48	48	37	47	39	49	50
Sly07g0123491	M22	SlCycU1;1	9	8	10	4	1	11	8	10	4	1
Sly07g0123501	M1	NA	3	2	2	1	1	1	1	1	1	1
Sly07g0123521	M5	NA	35	43	25	16	10	30	33	20	16	12
Sly07g0123531	M22	NA	1	1	1	0	0	3	1	1	0	0
Sly07g0123551	M12	NA	6	6	5	3	2	10	8	7	1	1
Sly07g0123561	M12	NA	1	1	2	1	1	4	5	4	1	0
Sly07g0123571	M1	BAM-like	12	14	22	36	56	3	4	6	45	68
Sly07g0123581	M1	NA	53	56	58	131	215	25	29	22	44	141
Sly07g0123591	M1	NA	40	46	42	40	41	23	25	23	51	56
Sly07g0123601	M1	NA	2	1	1	2	1	1	1	1	1	1
Sly07g0123611	M1	NA	2	2	2	2	1	1	1	1	1	1
Sly07g0123621	M3	NA	20	22	17	19	18	18	19	18	26	25
Sly07g0123631	M16	NA	3	2	4	2	2	2	4	3	8	5
Sly07g0123641	M23	NA	21	20	19	14	11	21	19	19	15	12
Sly07g0123681	M1	NA	1	1	1	1	0	0	0	0	0	0
Sly07g0123691	M3	NA	10	14	4	1	0	2	2	1	1	0
Sly07g0123701	M3	NA	29	33	9	1	1	3	4	1	1	1
Sly07g0123731	M1	NA	16	17	16	21	17	12	12	13	30	21
Sly07g0123741	M1	NA	7	7	9	8	8	6	5	6	15	13
Sly07g0123751	M1	NA	11	9	13	12	13	8	9	10	31	38
Sly07g0123761	M12	NA	19	20	17	21	20	18	20	22	22	24
Sly07g0123781	M11	NA	27	23	26	39	47	32	30	35	60	73
Sly07g0123791	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0123801	M19	SISDG29	26	31	29	37	41	31	25	28	31	35
Sly07g0123811	M1	NA	1	1	2	1	1	1	1	1	1	0
Sly07g0123821	M12	NA	3	13	22	358	333	11	25	52	620	322
Sly07g0123831	M1	NA	1	1	1	1	2	1	1	1	3	8
Sly07g0123841	M1	SlXTH16	89	62	42	1	1	28	4	20	1	1
Sly07g0123851	M3	NA	7	10	11	11	52	6	11	5	13	135
Sly07g0123871	M1	NA	8	6	4	10	6	1	1	1	1	1
Sly07g0123881	M1	NA	14	12	10	6	3	5	4	4	1	1
Sly07g0123901	M12	SlGH3-17	1	2	1	1	1	12	7	6	1	3
Sly07g0123921	M6	NA	14	17	13	4	19	15	22	8	3	41
Sly07g0123931	M12	NA	23	21	22	19	19	22	22	24	24	28
Sly07g0123951	M3	NA	2	1	1	1	0	1	1	1	0	0
Sly07g0123961	M12	NA	12	11	14	16	14	19	19	20	25	19
Sly07g0123971	M3	NA	2	1	1	1	1	1	1	1	1	1
Sly07g0123981	M3	NA	4	4	2	1	0	2	1	1	0	0
Sly07g0123991	M1	NA	11	14	6	2	1	2	2	1	1	1
Sly07g0124011	M10	NA	10	11	6	3	45	18	18	5	7	62
Sly07g0124021	M2	NA	15	15	15	21	36	14	15	14	32	48
Sly07g0124031	M11	NA	63	56	65	69	80	61	58	64	77	98
Sly07g0124041	M7	NA	64	83	55	45	60	75	87	53	39	60
Sly07g0124051	M3	NA	59	63	43	34	31	33	30	21	18	18
Sly07g0124061	M1	NA	36	35	33	21	27	23	21	21	17	18
Sly07g0124071	M1	NA	2	2	3	2	3	2	1	2	1	0
Sly07g0124081	M1	NA	2	2	2	2	1	1	1	1	1	1
Sly07g0124091	M1	NA	16	17	21	14	17	14	13	15	7	10
Sly07g0124121	M3	NA	68	110	33	1	3	28	41	7	1	3
Sly07g0124131	M3	NA	8	11	5	0	0	1	1	1	0	1
Sly07g0124141	M19	NA	10	12	12	10	9	12	7	11	9	10
Sly07g0124151	M19	NA	8	12	11	8	8	10	7	10	8	12
Sly07g0124161	M1	NA	40	40	46	32	41	38	39	37	41	64
Sly07g0124171	M11	NA	392	361	447	354	287	411	411	485	386	313
Sly07g0124181	M3	NA	2	2	2	5	1	2	2	1	2	1
Sly07g0124191	M11	NA	536	483	575	703	933	833	803	1007	1426	2393
Sly07g0124201	M14	NA	14	15	20	16	9	18	16	24	7	5
Sly07g0124221	M12	NA	28	30	30	37	44	36	36	39	48	52
Sly07g0124231	M11	NA	14	14	17	20	24	28	25	30	27	24
Sly07g0124261	M3	NA	14	15	11	1	0	4	7	2	1	0
Sly07g0124271	M3	NA	27	24	15	1	1	9	12	3	1	1
Sly07g0124291	M11	NA	3	2	3	3	2	11	12	20	12	4
Sly07g0124311	M1	NA	2	2	2	2	2	2	2	2	2	2
Sly07g0124351	M3	NA	1	1	1	1	1	1	1	0	0	0
Sly07g0124361	M22	NA	1	1	1	1	0	1	1	0	0	0
Sly07g0124371	M1	NA	24	20	23	14	11	20	21	18	7	7
Sly07g0124381	M1	NA	43	45	38	38	36	35	31	31	32	31
Sly07g0124411	M1	NA	70	78	74	51	52	47	51	48	51	53
Sly07g0124421	M3	NA	33	26	20	8	2	27	31	17	5	3
Sly07g0124431	M1	NA	19	17	19	20	24	11	12	11	13	19
Sly07g0124441	M12	NA	3	3	2	3	4	3	4	4	7	5
Sly07g0124451	M18	NA	4	4	4	4	6	4	4	4	4	5
Sly07g0124461	M11	NA	164	129	158	109	80	156	143	186	137	109
Sly07g0124471	M21	NA	1	1	1	0	0	1	1	1	0	0
Sly07g0124481	M20	NA	19	14	34	0	0	11	7	13	1	1
Sly07g0124491	M1	NA	122	131	109	163	330	25	39	45	338	713
Sly07g0124501	M12	NA	6	6	6	8	7	6	7	6	8	8
Sly07g0124511	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly07g0124521	M11	NA	32	27	33	32	43	35	31	38	38	47
Sly07g0124531	M22	NA	2	1	2	1	1	9	1	7	0	0
Sly07g0124541	M1	NA	32	34	28	16	4	3	3	1	1	1
Sly07g0124551	M19	NA	26	30	35	27	30	41	29	45	24	22
Sly07g0124561	M4	NA	54	47	50	81	115	51	51	53	108	166
Sly07g0124581	M1	NA	1	1	2	1	0	1	1	1	1	0
Sly07g0124591	M12	NA	6	15	8	65	20	17	31	32	113	12
Sly07g0124601	M1	NA	142	150	144	164	152	112	108	105	128	125
Sly07g0124611	M1	NA	56	57	59	38	42	48	44	46	44	43
Sly07g0124621	M2	NA	26	26	21	18	17	15	21	15	20	22
Sly07g0124631	M1	NA	103	86	85	55	53	61	67	64	75	78
Sly07g0124651	M14	NA	25	23	30	20	13	25	25	24	16	7
Sly07g0124661	M1	NA	25	22	22	2	1	11	12	10	1	2
Sly07g0124671	M1	NA	40	43	35	26	21	22	23	18	12	11
Sly07g0124681	M3	SlERF.F4	175	211	102	35	157	82	112	40	15	281
Sly07g0124691	M22	NA	6	2	3	1	1	12	4	9	2	1
Sly07g0124701	M3	NA	70	108	38	5	5	12	10	3	2	5
Sly07g0124731	M1	NA	1	1	1	0	0	1	1	1	0	1
Sly07g0124741	M12	RING1a	8	8	8	9	10	14	13	14	9	8
Sly07g0124761	M12	NA	1	1	1	1	0	2	2	2	1	1
Sly07g0124771	M16	NA	180	175	176	200	258	166	171	173	189	292
Sly07g0124791	M3	NA	14	16	14	14	16	13	13	11	13	15
Sly07g0124801	M11	NA	24	26	29	24	33	31	29	35	38	48
Sly07g0124811	M12	NA	8	8	8	11	11	9	9	10	10	12
Sly07g0124821	M19	NA	9	8	9	10	10	9	7	10	9	9
Sly07g0124831	M22	NA	1	1	1	1	1	1	1	1	0	1
Sly07g0124841	M1	NA	2	3	1	1	1	1	0	0	0	0
Sly07g0124861	M1	NA	58	93	77	58	88	38	46	36	23	31
Sly07g0124881	M9	NA	15	18	11	6	2	17	22	15	6	2
Sly07g0124891	M4	NA	4	3	4	3	4	4	4	4	3	7
Sly07g0124901	M11	NA	1	1	1	1	1	2	2	2	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0046751	M11	NA	2	2	4	5	5	3	6	5	6	9
Sly01g0046761	M11	NA	3	3	3	4	6	5	4	6	10	8
Sly01g0046771	M11	NA	2	2	2	3	5	4	4	5	7	6
Sly01g0046831	M12	NA	10	9	9	9	11	11	11	11	14	19
Sly01g0046841	M11	NA	12	10	14	12	15	17	15	19	16	17
Sly01g0046871	M1	NA	3	3	6	2	2	3	3	3	3	6
Sly01g0046881	M11	Solyc01g110860	2	2	2	2	4	2	2	2	3	3
Sly01g0046891	M22	Solyc01g110870	1	1	1	1	2	1	2	1	2	2
Sly01g0046941	M12	NA	1	2	1	3	4	3	6	7	3	4
Sly01g0046961	M12	NA	5	6	4	6	7	8	11	9	10	11
Sly01g0046971	M12	SAUR26	10	11	9	4	2	14	16	10	2	1
Sly01g0046981	M5	Solyc01g110930	2	4	2	2	1	3	3	2	1	1
Sly01g0046991	M12	Solyc01g110940	1	1	1	1	1	1	1	1	1	1
Sly01g0047011	M3	NA	5	6	3	1	1	5	3	3	1	1
Sly01g0047021	M2	Solyc01g110970	1	1	1	0	0	1	1	1	1	0
Sly01g0047041	M3	NA	28	30	21	20	21	22	24	18	20	21
Sly01g0047051	M6	NA	3	4	3	3	5	3	3	3	6	10
Sly01g0047061	M9	Solyc01g111000	2	1	1	2	3	2	2	1	3	6
Sly01g0047071	M12	SAUR or Auaporin	1	0	1	1	2	3	3	2	4	7
Sly01g0047081	M7	NA	1	1	2	1	1	1	2	1	3	6
Sly01g0047101	M11	NA	14	14	16	27	30	25	23	28	24	25
Sly01g0047119	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly01g0047141	M11	NA	1	1	1	4	6	1	1	1	2	5
Sly01g0047151	M11	NA	1	1	1	1	1	2	1	2	1	1
Sly01g0047181	M1	NA	4	4	8	55	70	2	4	4	21	55
Sly01g0047201	M1	NA	126	116	126	138	157	89	86	94	135	152
Sly01g0047211	M9	NA	1	1	1	2	5	3	4	3	3	6
Sly01g0047221	M12	NA	127	105	159	32	102	2136	2079	1543	167	173
Sly01g0047231	M8	NA	78	80	68	87	75	74	92	59	81	91
Sly01g0047241	M22	NA	2	1	1	1	0	2	1	1	1	1
Sly01g0047251	M20	NA	36	20	51	7	5	27	19	23	64	79
Sly01g0047261	M11	Triosephosphate isom	144	120	135	188	194	194	196	204	214	216
Sly01g0047271	M11	NA	15	12	20	19	23	17	16	20	26	24
Sly01g0047281	M11	NA	31	27	35	27	30	36	27	40	34	39
Sly01g0047291	M2	NA	192	176	145	222	154	121	150	118	223	177
Sly01g0047301	M11	NA	71	41	143	1	1	107	114	117	1	1
Sly01g0047311	M1	NA	1381	1083	1358	893	626	944	801	947	183	218
Sly01g0047321	M11	NA	6	6	6	6	6	7	7	7	7	8
Sly01g0047331	M12	NA	11	11	11	12	12	16	16	15	17	19
Sly01g0047341	M3	NA	129	117	91	81	81	108	102	99	79	73
Sly01g0047351	M12	NA	4	4	6	3	1	10	7	8	2	1
Sly01g0047361	M11	NA	2	2	3	1	1	4	3	3	1	1
Sly01g0047371	M1	NA	43	31	52	1	0	9	5	7	1	0
Sly01g0047381	M22	NA	1	1	1	0	0	1	1	1	1	1
Sly01g0047391	M19	NA	87	87	90	76	71	91	72	97	57	54
Sly01g0047401	M2	NA	144	150	111	155	137	42	87	59	329	253
Sly01g0047411	M3	NA	126	110	111	44	34	70	87	65	30	61
Sly01g0047421	M1	NA	19	16	22	11	2	6	6	5	1	1
Sly01g0047431	M11	NA	26	17	32	11	9	22	19	27	23	17
Sly01g0047451	M17	NA	267	184	211	153	153	200	163	251	224	244
Sly01g0047461	M1	SILAX2	3	2	2	1	1	2	1	1	1	0
Sly01g0047471	M11	NA	44	35	49	37	33	56	50	59	28	41
Sly01g0047481	M23	NA	1	1	1	1	0	2	1	1	1	0
Sly01g0047491	M11	NA	44	47	42	222	57	262	253	273	274	23
Sly01g0047501	M11	NA	405	355	480	799	467	845	830	964	761	318
Sly01g0047511	M14	NA	50	59	57	68	34	56	50	61	28	18
Sly01g0047521	M11	NA	20	18	20	17	16	25	27	28	15	17
Sly01g0047531	M13	NA	69	59	108	44	16	99	82	120	17	6
Sly01g0047541	M11	NA	58	61	83	44	38	77	62	96	24	19
Sly01g0047551	M12	NA	22	24	24	37	45	30	28	28	38	52
Sly01g0047561	M1	NA	62	61	57	33	25	42	45	40	34	31
Sly01g0047571	M12	NA	2	1	2	2	1	2	2	2	1	1
Sly01g0047581	M7	NA	135	194	78	77	154	118	274	95	87	294
Sly01g0047591	M3	NA	94	87	83	110	146	79	87	78	128	166
Sly01g0047601	M12	NA	8	8	8	9	10	9	9	9	9	10
Sly01g0047611	M18	PPR-like4	7	8	9	10	9	11	9	12	7	7
Sly01g0047621	M5	NA	2	5	3	5	2	4	3	2	1	1
Sly01g0047631	M11	SIAPx3	194	185	208	262	273	245	232	267	135	131
Sly01g0047641	M9	NA	143	181	127	95	107	160	225	160	99	111
Sly01g0047651	M19	NA	79	92	76	76	78	72	67	63	56	62
Sly01g0047671	M11	NA	4	3	3	1	1	4	4	3	1	0
Sly01g0047681	M11	NA	57	48	75	56	51	70	60	76	43	64
Sly01g0047691	M1	NA	61	46	54	7	2	28	24	16	11	5
Sly01g0047701	M11	NA	21	18	18	19	22	21	20	21	29	27
Sly01g0047711	M1	MSI2-like	5	4	5	2	2	4	2	3	2	1
Sly01g0047721	M17	NA	94	73	90	76	53	73	62	87	51	45
Sly01g0047731	M3	NA	4	6	6	1	0	2	3	1	1	1
Sly01g0047741	M1	NA	55	71	45	48	39	13	18	11	20	17
Sly01g0047751	M11	NA	90	76	91	74	65	127	103	120	24	7
Sly01g0047761	M11	NA	7	4	6	3	2	13	9	13	3	1
Sly01g0047771	M1	NA	226	198	221	201	240	159	141	184	214	279
Sly01g0047781	M1	NA	4	5	5	6	2	2	2	3	1	1
Sly01g0047791	M3	NA	19	18	13	13	18	11	12	7	11	17
Sly01g0047801	M19	NA	20	23	21	25	19	21	20	21	23	19
Sly01g0047811	M12	NA	23	24	26	25	25	23	29	26	18	16
Sly01g0047821	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly01g0047831	M2	NA	186	173	176	143	167	139	156	136	152	182
Sly01g0047841	M1	NA	43	48	52	48	53	37	36	42	52	59
Sly01g0047851	M1	NA	77	108	86	74	54	42	46	35	34	38
Sly01g0047861	M11	NA	4	4	6	2	2	7	5	7	1	1
Sly01g0047871	M2	NA	41	39	38	85	153	35	36	43	104	187
Sly01g0047881	M12	NA	336	343	362	436	272	426	466	426	348	289
Sly01g0047891	M2	NA	22	21	23	27	23	22	24	20	22	20
Sly01g0047901	M1	NA	108	115	115	106	93	106	108	106	100	93
Sly01g0047921	M1	NA	4	3	4	2	3	2	2	3	1	2
Sly01g0047931	M12	NA	18	18	17	13	18	19	22	18	15	14
Sly01g0047951	M11	SMT2-like3	31	24	45	28	13	49	43	44	4	7
Sly01g0047961	M1	NA	4	3	3	6	2	3	2	2	1	1
Sly01g0047981	M12	NA	12	10	10	13	18	12	14	11	24	30
Sly01g0047991	M11	NA	20	21	21	25	36	24	21	24	33	36
Sly01g0048001	M18	NA	2	2	3	2	2	3	2	3	2	1
Sly01g0048011	M1	NA	22	19	17	6	2	4	3	4	2	1
Sly01g0048021	M11	NA	40	40	42	29	21	48	41	47	30	22
Sly01g0048041	M11	NA	20	20	25	24	35	26	23	28	30	40
Sly01g0048051	M12	NA	16	13	15	25	30	28	28	26	27	33
Sly01g0048061	M11	NA	8	7	7	3	3	13	11	13	2	1
Sly01g0048071	M18	NA	44	41	39	59	69	42	37	43	66	68
Sly01g0048081	M3	NA	1	1	1	1	1	1	1	1	2	2
Sly01g0048101	M12	NA	19	30	41	98	32	171	255	349	785	255
Sly01g0048111	M3	NA	212	468	184	50	33	78	96	14	2	15
Sly01g0048121	M18	NA	17	20	23	32	48	29	23	30	27	47
Sly01g0048131	M12	expansin	35	68	50	13	29	105	164	145	18	188
Sly01g0048141	M1	NA	6	5	7	3	3	5	5	5	4	5
Sly01g0048151	M1	NA	4	3	6	2	2	5	4	3	3	3
Sly01g0048161	M3	NA	68	75	69	72	72	68	70	65	81	90
Sly01g0048171	M1	NA	8	8	8	10	9	8	8	7	7	8
Sly01g0048181	M3	NA	70	94	45	27	29	47	49	36	20	24
Sly01g0048191	M11	NA	15	14	15	27	34	21	20	22	13	16
Sly01g0048201	M9	NA	2	3	2	2	1	7	10	4	2	2
Sly01g0048211	M9	NA	25	25	17	3	2	70	79	41	2	2
Sly01g0048221	M12	NA	2	2	2	1	2	4	4	3	1	1
Sly01g0048231	M12	NA	243	255	372	768	562	662	671	929	1129	857
Sly01g0048241	M1	NA	35	38	57	138	68	24	33	41	125	127
Sly01g0048251	M1	NA	30	33	44	161	237	15	19	22	219	188
Sly01g0048261	M1	NA	19	23	30	82	59	9	15	16	192	127
Sly01g0048271	M12	NA	7	7	6	3	3	20	20	15	4	3
Sly01g0048281	M3	NA	51	56	43	62	58	48	48	44	54	56
Sly01g0048291	M2	NA	16	18	16	19	18	16	18	15	17	12
Sly01g0048301	M1	NA	37	39	44	44	46	22	25	22	27	31
Sly01g0048311	M19	NA	8	6	5	9	10	7	5	7	7	8
Sly01g0048321	M12	NA	23	27	25	33	39	25	25	28	37	48
Sly01g0048331	M1	NA	1	2	2	1	1	1	1	1	0	1
Sly01g0048341	M1	NA	4	4	4	4	4	3	4	4	3	3
Sly01g0048351	M12	NA	19	17	20	21	15	22	21	22	10	10

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0124951	M1	NA	59	55	58	38	33	45	44	50	42	39
Sly07g0124961	M11	NA	3	3	3	22	14	3	4	5	47	37
Sly07g0124971	M12	NA	65	64	169	1179	1147	161	243	457	2858	2296
Sly07g0124981	M12	NA	10	10	15	85	119	13	20	34	521	619
Sly07g0124991	M11	NA	54	37	73	23	15	108	87	127	27	19
Sly07g0125001	M11	NA	14	14	14	13	14	15	14	15	13	15
Sly07g0125011	M3	NA	7	8	6	5	4	5	6	6	3	1
Sly07g0125021	M1	NA	4	6	6	4	3	3	4	5	2	1
Sly07g0125031	M3	NA	3	3	1	0	0	1	1	1	0	0
Sly07g0125041	M3	NA	3	4	1	1	0	1	1	1	0	0
Sly07g0125051	M3	NA	6	7	4	4	1	5	5	3	3	2
Sly07g0125061	M12	NA	3	2	3	4	11	7	6	8	6	39
Sly07g0125081	M11	NA	45	46	49	61	66	54	55	60	61	68
Sly07g0125091	M22	NA	2	1	1	1	0	4	1	3	1	0
Sly07g0125111	M1	NA	27	25	24	32	35	24	21	24	28	28
Sly07g0125121	M12	NA	29	22	39	71	137	111	102	148	149	130
Sly07g0125131	M1	NA	16	19	16	2	4	4	2	4	1	2
Sly07g0125161	M12	NA	1	1	1	1	1	3	2	2	1	1
Sly07g0125171	M12	NA	7	5	2	1	0	18	12	13	1	1
Sly07g0125181	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly07g0125191	M11	NA	60	56	85	27	21	85	65	101	46	34
Sly07g0125211	M11	NA	24	17	30	58	54	47	46	61	36	30
Sly07g0125221	M1	NA	17	16	19	22	15	3	1	2	1	1
Sly07g0125231	M1	NA	52	11	126	0	0	1	1	1	0	0
Sly07g0125241	M2	NA	5	7	5	6	4	5	7	6	5	3
Sly07g0125251	M1	NA	29	29	34	44	74	25	25	27	32	46
Sly07g0125261	M12	NA	7	8	7	9	10	8	9	10	12	16
Sly07g0125271	M19	NA	4	5	6	6	6	4	3	4	7	9
Sly07g0125281	M19	NA	6	9	8	10	11	7	6	6	13	16
Sly07g0125291	M4	NA	10	12	13	14	16	11	11	12	23	33
Sly07g0125341	M12	NA	3	3	3	1	1	5	4	4	1	1
Sly07g0125351	M9	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0125361	M11	NA	3	4	4	4	3	4	4	6	5	3
Sly07g0125371	M11	NA	2	2	3	3	3	4	4	4	4	3
Sly07g0125381	M13	NA	10	6	14	3	2	8	6	16	7	2
Sly07g0125391	M12	NA	27	26	25	40	52	29	28	28	63	81
Sly07g0125401	M12	NA	38	37	47	287	273	62	64	85	313	362
Sly07g0125411	M1	NA	46	43	36	15	11	23	25	20	17	10
Sly07g0125421	M1	NA	30	28	23	21	5	4	4	3	4	2
Sly07g0125431	M1	NA	11	12	10	7	6	8	8	8	6	5
Sly07g0125441	M12	NA	32	34	35	33	13	60	68	58	30	17
Sly07g0125451	M3	NA	17	19	12	2	2	10	14	8	1	1
Sly07g0125461	M12	NA	39	41	43	63	94	47	45	49	75	107
Sly07g0125481	M11	NA	1	1	1	0	1	2	1	1	1	1
Sly07g0125501	M1	GH3-8	1	1	1	1	1	0	1	0	0	0
Sly07g0125541	M1	NA	9	9	7	5	5	5	5	4	4	4
Sly07g0125551	M12	NA	3	3	4	4	3	4	4	4	4	3
Sly07g0125561	M12	NA	8	10	9	13	9	12	12	11	19	10
Sly07g0125581	M11	NA	7	8	8	12	11	9	8	11	17	16
Sly07g0125631	M12	NA	4	4	4	7	2	6	6	5	7	3
Sly07g0125641	M12	NA	10	10	8	10	8	9	10	10	10	9
Sly07g0125661	M1	NA	2	2	2	1	1	1	2	2	0	0
Sly07g0125691	M12	NA	3	4	3	3	6	4	4	4	11	22
Sly07g0125711	M11	NA	160	139	151	192	183	223	182	249	101	98
Sly07g0125721	M1	NA	5	5	7	2	2	2	1	1	1	1
Sly07g0125741	M1	NA	26	28	30	9	6	12	10	9	3	4
Sly07g0125751	M12	NA	1	1	1	0	1	1	1	7	1	3
Sly07g0125761	M12	WIP4	140	117	185	253	261	251	269	281	465	656
Sly07g0125763	M12	WIP5	27	20	24	33	43	57	47	115	181	604
Sly07g0125765	M12	WIP4	278	217	263	410	1292	261	257	461	2071	3533
Sly07g0125767	M12	WIP5	16	11	17	14	16	26	25	73	109	356
Sly07g0125769	M12	WIP4	0	1	0	0	1	1	1	8	1	5
Sly07g0125771	M12	NA	2	2	1	1	2	2	2	4	3	7
Sly07g0125781	M11	NA	48	43	68	79	104	64	55	77	79	73
Sly07g0125791	M11	NA	57	47	77	97	134	71	72	92	91	93
Sly07g0125801	M3	NA	66	95	43	20	27	41	59	35	36	60
Sly07g0125811	M6	NA	1	4	1	1	0	1	2	1	0	0
Sly07g0125821	M12	NA	16	11	17	9	4	45	36	55	4	1
Sly07g0125831	M11	NA	21	13	35	2	1	248	237	266	8	1
Sly07g0125881	M22	NA	8	1	5	0	0	17	2	18	0	0
Sly07g0125891	M22	NA	2	1	1	0	0	6	1	3	0	0
Sly07g0125901	M22	NA	6	1	4	0	0	17	2	16	0	0
Sly07g0125961	M1	NA	8	16	5	1	1	1	1	1	1	0
Sly07g0125971	M12	NA	17	16	18	17	24	24	22	23	29	48
Sly07g0125981	M1	NA	8	8	9	7	8	7	5	7	5	5
Sly07g0125991	M11	NA	2	2	3	3	3	3	3	5	10	10
Sly07g0126001	M11	NA	39	29	60	48	22	84	64	108	30	7
Sly07g0126011	M1	PPC	96	96	99	140	113	71	78	71	286	198
Sly07g0126021	M1	NA	60	54	61	32	22	7	6	4	2	3
Sly07g0126031	M1	NA	20	15	18	27	59	15	12	12	24	36
Sly07g0126061	M1	NA	2	2	3	1	1	1	1	1	1	1
Sly07g0126081	M11	NA	8	8	11	8	14	13	11	17	10	16
Sly07g0126091	M3	NA	26	25	20	18	14	23	21	20	11	15
Sly07g0126101	M11	NA	7	7	10	11	11	8	10	14	33	60
Sly07g0126111	M17	NA	25	23	25	36	42	22	20	26	41	46
Sly07g0126121	M12	NA	12	10	9	4	2	14	12	9	2	1
Sly07g0126131	M1	NA	4	3	3	3	3	3	2	3	2	2
Sly07g0126141	M19	NA	4	4	5	2	1	5	3	4	1	1
Sly07g0126151	M1	NA	2	3	3	2	3	2	2	2	1	11
Sly07g0126161	M1	BIN2	82	81	97	68	45	77	72	81	39	46
Sly07g0126171	M3	NA	135	137	121	174	163	111	138	118	190	190
Sly07g0126181	M12	NA	4	4	5	5	6	7	7	7	9	9
Sly07g0126191	M1	NA	121	108	115	80	56	84	83	85	86	62
Sly07g0126211	M1	NA	61	55	57	34	21	40	39	40	25	18
Sly07g0126221	M11	NA	8	6	11	14	29	8	7	11	11	11
Sly07g0126231	M3	NA	10	14	4	2	2	6	5	4	2	2
Sly07g0126241	M3	NA	17	19	10	4	2	6	6	5	4	4
Sly07g0126251	M12	NA	28	24	27	26	33	32	33	29	45	46
Sly07g0126261	M6	NA	28	27	25	26	32	29	28	24	27	29
Sly07g0126271	M1	NA	9	8	7	9	7	6	6	6	9	8
Sly07g0126281	M11	NA	99	92	126	260	393	136	117	159	187	257
Sly07g0126291	M1	NA	3	4	2	2	2	1	1	1	2	3
Sly07g0126301	M12	NA	7	8	8	20	48	12	12	13	25	65
Sly07g0126311	M11	NA	6	5	6	17	44	10	7	12	18	37
Sly07g0126431	M22	NA	1	1	1	1	0	1	1	1	1	1
Sly07g0126451	M22	NA	1	1	1	1	0	1	1	1	1	1
Sly07g0126461	M11	NA	12	19	29	23	4	43	36	65	21	2
Sly07g0126481	M1	NA	7	9	8	3	1	1	0	1	0	0
Sly07g0126521	M12	NA	8	8	10	8	8	16	15	20	10	9
Sly07g0126531	M11	NA	27	29	32	20	15	37	35	58	31	26
Sly07g0126551	M12	NA	5	4	8	9	6	16	22	18	26	20
Sly07g0126561	M12	NA	1	1	0	1	1	1	1	1	1	1
Sly07g0126601	M1	NA	1	3	2	1	0	1	1	1	0	0
Sly07g0126611	M1	NA	6	10	11	19	9	2	2	1	1	1
Sly07g0126621	M5	NA	10	10	8	10	9	9	11	9	9	8
Sly07g0126631	M11	NA	18	16	17	33	68	19	17	25	64	139
Sly07g0126641	M6	NA	12	28	10	2	2	5	11	3	1	1
Sly07g0126651	M12	NA	1	1	1	0	0	1	1	10	1	0
Sly07g0126661	M3	NA	33	35	29	28	21	27	28	22	18	14
Sly07g0126671	M1	NA	11	19	11	2	1	3	5	1	1	1
Sly07g0126681	M13	NA	3	2	5	2	1	3	3	6	1	0
Sly07g0126711	M1	NA	4	4	4	1	0	1	0	0	0	0
Sly07g0126741	M1	NA	9	9	8	9	8	8	8	9	10	9
Sly07g0126751	M2	NA	7	8	7	7	9	7	8	7	9	10
Sly07g0126771	M22	NA	1	1	1	0	0	3	1	2	1	0
Sly07g0126791	M3	NA	16	24	7	1	1	3	3	1	1	0
Sly07g0126811	M2	NA	58	59	49	48	50	39	47	38	57	48
Sly07g0126821	M12	NA	7	7	7	10	10	16	16	19	16	19
Sly07g0126831	M1	NA	13	13	11	11	12	10	8	9	9	13
Sly07g0126841	M14	NA	85	84	90	97	104	81	81	88	104	145

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly01g0048361	M1	NA	17	29	18	12	8	6	4	3	1	1
Sly01g0048371	M23	NA	32	8	10	2	1	67	18	28	4	2
Sly01g0048381	M12	NA	99	92	93	100	98	92	109	97	106	111
Sly01g0048391	M12	NA	41	46	42	47	41	47	46	45	49	40
Sly01g0048401	M2	NA	82	87	78	68	50	70	74	69	60	44
Sly01g0048411	M12	NA	20	18	16	2	2	23	32	17	2	5
Sly01g0048421	M3	NA	2	3	1	1	1	2	3	1	1	1
Sly01g0048431	M12	NA	1	1	1	2	2	1	2	2	2	1
Sly01g0048441	M11	NA	65	58	82	83	84	104	87	114	81	66
Sly01g0048451	M11	NA	104	96	114	154	233	137	128	151	162	226
Sly01g0048461	M18	NA	13	13	13	15	16	17	14	17	13	16
Sly01g0048471	M11	NA	18	17	21	24	31	18	19	22	31	35
Sly01g0048491	M12	NA	46	50	46	54	71	56	58	64	111	92
Sly02g0314371	M1	NA	5	9	6	2	1	2	2	2	1	1
Sly02g0314431	M12	NA	2	3	3	4	2	3	3	3	3	1
Sly02g0314441	M18	NA	2	4	5	8	2	5	4	4	3	2
Sly02g0314451	M19	NA	3	5	4	8	2	5	4	3	3	1
Sly02g0314461	M19	NA	4	6	4	6	2	4	3	4	3	1
Sly02g0314471	M19	NA	5	5	5	8	3	5	4	5	4	1
Sly02g0314581	M18	NA	38	39	46	50	57	49	45	51	47	42
Sly02g0314601	M11	NA	42	39	44	47	60	45	46	45	52	66
Sly02g0314631	M19	NA	1	1	1	2	1	1	1	1	1	1
Sly02g0314641	M23	NA	2	2	2	1	1	2	1	1	1	1
Sly02g0314671	M12	NA	4	3	4	2	2	10	7	6	1	3
Sly02g0314681	M11	NA	31	29	32	34	36	33	29	42	46	37
Sly02g0314741	M11	NA	15	15	17	21	21	21	19	20	21	25
Sly02g0314751	M11	NA	26	25	26	8	1	99	82	110	11	2
Sly02g0314811	M11	NA	1	1	1	1	1	1	1	2	1	1
Sly02g0314821	M11	NA	5	6	7	7	5	8	7	7	6	5
Sly02g0314831	M11	NA	9	11	14	13	10	17	14	16	10	12
Sly02g0314841	M12	NA	12	14	15	15	13	20	16	19	15	17
Sly02g0314851	M12	NA	24	24	23	37	45	34	36	38	47	44
Sly02g0314891	M11	NA	5	5	6	6	5	8	6	8	6	7
Sly02g0315001	M3	NA	2	2	2	2	4	1	2	1	1	1
Sly02g0315021	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0315041	M11	NA	4	6	7	5	7	8	7	9	8	8
Sly02g0315051	M18	NA	5	5	6	4	4	7	6	6	4	4
Sly02g0315091	M19	NA	45	49	44	47	43	51	47	50	39	40
Sly02g0315101	M11	NA	3	3	3	3	4	5	4	4	4	3
Sly02g0315111	M12	NA	47	43	42	45	42	49	53	45	48	50
Sly02g0315121	M1	NA	7	8	8	5	4	6	5	6	3	3
Sly02g0315131	M19	NA	24	25	27	23	23	24	20	23	18	16
Sly02g0315201	M1	NA	24	23	28	10	5	21	22	21	11	10
Sly02g0315231	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0315261	M2	NA	73	76	71	91	80	69	72	71	94	81
Sly02g0315311	M12	NA	11	11	11	9	8	14	13	14	13	16
Sly02g0315321	M12	NA	27	27	27	24	20	34	38	32	40	50
Sly02g0315331	M18	NA	4	3	6	2	2	4	4	5	9	5
Sly02g0315341	M11	NA	8	3	5	6	3	8	6	6	12	11
Sly02g0315371	M3	NA	12	15	10	13	11	10	13	11	7	7
Sly02g0315381	M19	NA	1	1	1	2	1	1	1	1	1	1
Sly02g0315391	M8	NA	2	2	2	3	2	2	2	2	1	2
Sly02g0315401	M3	NA	2	3	2	3	2	2	2	2	2	2
Sly02g0315411	M3	NA	2	2	1	2	3	1	3	1	2	2
Sly02g0315421	M1	NA	21	20	23	14	4	17	19	16	5	1
Sly02g0315471	M18	NA	10	11	14	11	13	14	10	11	10	10
Sly02g0315481	M11	NA	64	75	112	454	425	102	103	136	282	271
Sly02g0315491	M11	NA	14	14	19	51	103	22	22	29	49	109
Sly02g0315501	M1	NA	6	4	6	5	4	2	1	2	1	1
Sly02g0315511	M1	NA	2	3	3	4	4	2	2	3	4	3
Sly02g0315521	M1	NA	24	25	26	26	27	23	23	24	17	15
Sly02g0315531	M14	NA	24	24	27	27	26	23	23	27	17	11
Sly02g0315551	M12	NA	3	2	3	2	1	4	3	4	1	1
Sly02g0315571	M12	NA	6	5	6	8	7	7	9	8	9	10
Sly02g0315581	M12	NA	2	2	2	3	3	2	3	2	6	9
Sly02g0315591	M11	NA	8	9	9	13	17	9	9	11	17	26
Sly02g0315601	M18	NA	3	3	5	4	5	4	3	4	7	7
Sly02g0315631	M12	NA	6	4	6	6	8	5	6	6	8	9
Sly02g0315641	M12	NA	13	14	13	20	21	13	15	13	12	22
Sly02g0315651	M19	NA	20	22	19	25	25	22	20	23	20	25
Sly02g0315781	M11	NA	49	48	52	52	56	70	71	85	87	85
Sly02g0315821	M11	NA	36	34	39	50	47	45	45	48	62	60
Sly02g0315831	M12	NA	7	7	9	11	9	9	12	12	15	15
Sly02g0315921	M12	NA	77	72	80	131	244	79	81	91	150	344
Sly02g0315961	M1	NA	10	20	27	29	7	4	3	5	5	4
Sly02g0316151	M1	NA	3	3	3	4	3	2	2	2	3	2
Sly02g0316691	M1	NA	14	22	9	2	1	2	2	1	1	1
Sly02g0316701	M3	NA	2	2	1	1	1	1	2	1	1	1
Sly02g0316751	M3	NA	34	38	30	24	25	33	35	29	36	38
Sly02g0316761	M19	NA	27	27	28	27	28	27	25	26	24	24
Sly02g0316791	M12	NA	37	37	34	62	46	74	68	74	47	44
Sly02g0316811	M19	NA	14	16	14	19	25	12	10	11	14	19
Sly02g0316821	M12	NA	3	3	3	7	4	4	6	6	6	5
Sly02g0316871	M3	NA	43	56	27	17	17	17	18	8	5	3
Sly02g0316881	M3	NA	43	56	22	17	14	15	15	10	5	2
Sly02g0316891	M1	NA	22	28	16	10	8	9	7	5	3	1
Sly02g0316921	M1	NA	11	9	10	5	5	8	9	9	6	8
Sly02g0316941	M1	NA	407	403	405	206	169	245	244	232	171	152
Sly02g0316981	M19	NA	31	34	31	38	38	28	25	28	27	23
Sly02g0316991	M1	NA	9	11	11	12	8	9	9	9	10	6
Sly02g0317031	M1	NA	11	8	9	12	11	5	4	5	8	9
Sly02g0317041	M3	NA	35	38	33	30	32	33	35	31	24	28
Sly02g0317131	M11	NA	4	5	6	2	1	6	5	5	2	1
Sly02g0317161	M14	NA	9	7	11	16	38	8	9	7	12	12
Sly02g0317171	M11	NA	1	1	1	1	2	1	1	1	3	10
Sly02g0317191	M12	NA	1	1	1	2	2	1	1	1	3	3
Sly02g0317211	M12	NA	19	20	22	24	25	27	25	28	24	31
Sly02g0317541	M11	NA	1	1	1	1	1	2	2	2	1	1
Sly02g0317581	M11	NA	92	86	97	115	123	118	116	157	178	155
Sly02g0317591	M11	NA	28	25	26	41	47	31	34	43	74	75
Sly02g0317601	M22	NA	3	2	2	1	1	17	2	12	1	2
Sly02g0317641	M11	NA	6	5	6	1	2	15	16	18	3	3
Sly02g0317681	M1	NA	14	14	15	11	12	12	11	12	8	7
Sly02g0317701	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0317711	M7	NA	16	22	13	10	29	18	24	14	21	59
Sly02g0317721	M1	NA	11	10	12	15	4	9	6	12	11	3
Sly02g0317731	M11	NA	7	11	12	6	7	10	7	10	2	3
Sly02g0317741	M14	NA	77	55	125	247	356	73	54	138	166	130
Sly02g0317751	M12	NA	106	95	103	156	178	123	138	132	202	209
Sly02g0317791	M12	NA	3	2	2	3	3	5	4	5	6	3
Sly02g0317801	M3	NA	16	31	9	9	10	11	16	8	10	12
Sly02g0317821	M18	NA	29	29	35	32	36	41	34	42	27	31
Sly02g0317831	M9	NA	4	5	3	2	3	6	8	4	5	6
Sly02g0317841	M11	NA	39	38	50	24	3	67	55	69	12	1
Sly02g0317871	M23	NA	2	1	1	1	1	2	1	1	2	1
Sly02g0317891	M11	DPE2	39	41	43	67	56	60	60	62	36	26
Sly02g0317941	M11	NA	22	28	29	27	22	33	41	32	22	30
Sly02g0317951	M3	NA	39	41	35	30	31	31	35	33	33	36
Sly02g0317961	M18	NA	11	11	12	12	11	16	15	18	12	10
Sly02g0317971	M11	NA	12	12	13	39	56	14	16	18	23	19
Sly02g0317981	M1	NA	10	10	10	6	5	6	5	4	3	2
Sly02g0318001	M1	NA	40	41	40	36	34	30	29	34	34	33
Sly02g0318021	M11	SISOD7	64	63	65	90	108	66	63	70	86	109
Sly02g0318101	M1	NA	2	1	4	5	4	1	2	2	2	5
Sly02g0318111	M22	NA	22	10	19	33	31	53	23	63	52	45
Sly02g0318121	M9	NA	10	11	11	19	33	11	16	13	22	37
Sly02g0318131	M1	NA	53	47	53	82	94	40	40	45	45	57
Sly02g0318151	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0318161	M11	NA	8	6	8	6	6	9	7	8	5	5
Sly02g0318171	M19	EMB2794	5	6	6	4	3	6	5	6	3	2
Sly02g0318181	M11	NA	22	20	22	10	9	27	23	26	8	11
Sly02g0318201	M12	NA	20	19	19	26	27	19	24	23	35	35
Sly02g0318231	M1	NA	15	16	16	15	12	15	13	14	11	10
Sly02g0318281	M16	NA	310	244	233	181	139	179	206	187	210	153

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0126901	M1	TAGL1	169	172	212	341	541	123	135	153	346	442
Sly07g0126911	M11	NA	34	40	46	89	91	200	164	282	527	424
Sly07g0126921	M12	NA	7	6	6	8	9	9	9	12	9	10
Sly07g0126931	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0126951	M12	NA	14	14	14	22	25	13	15	15	25	23
Sly07g0126961	M9	NA	12	20	20	2	3	49	94	72	4	12
Sly07g0126971	M7	SIXTH10	9	72	25	4	39	54	181	48	11	94
Sly07g0126981	M8	NA	53	49	47	51	48	50	52	48	57	49
Sly07g0126991	M18	NA	36	38	51	67	89	84	62	101	63	54
Sly07g0127001	M1	NA	115	122	101	102	109	92	83	87	92	101
Sly07g0127011	M1	NA	11	8	17	39	16	8	6	8	3	1
Sly07g0127021	M7	NA	77	88	63	72	64	94	145	63	44	64
Sly07g0127031	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0127041	M3	NA	29	30	24	27	31	23	23	20	27	26
Sly07g0127051	M3	NA	2	5	8	1	1	2	2	2	0	1
Sly07g0127081	M1	NA	31	35	32	25	29	22	23	21	19	20
Sly07g0127091	M11	NA	12	12	15	13	16	15	14	16	14	17
Sly07g0127111	M11	SlAGPase-L4	37	32	49	26	9	68	65	76	5	2
Sly07g0127121	M1	NA	105	100	106	58	81	80	94	94	83	104
Sly07g0127131	M12	SlCYP724B2	1	1	1	1	1	2	1	2	0	0
Sly07g0127141	M9	NA	8	8	4	1	1	26	27	14	4	1
Sly07g0127161	M6	NA	6	24	23	4	11	7	19	4	2	14
Sly07g0127171	M3	NA	63	68	30	2	1	16	28	9	1	3
Sly07g0127191	M1	NA	47	31	22	1	1	2	3	1	1	1
Sly07g0127211	M11	NA	34	35	35	37	43	39	35	40	29	35
Sly07g0127221	M11	NA	7	5	7	2	6	8	7	9	3	3
Sly07g0127231	M3	NA	4	4	2	1	1	1	1	1	1	1
Sly07g0127271	M1	NA	18	20	21	14	13	14	13	14	14	14
Sly07g0127281	M1	NA	10	9	11	8	4	9	6	7	1	1
Sly07g0127291	M3	NA	4	8	7	6	3	4	5	2	1	1
Sly07g0127321	M22	NA	1	1	2	2	1	2	1	2	2	1
Sly07g0127331	M3	NA	33	61	50	7	12	19	31	10	2	3
Sly07g0127361	M3	NA	11	7	8	2	1	6	6	3	1	1
Sly07g0127371	M19	NA	44	41	55	24	12	35	28	38	13	9
Sly07g0127381	M22	NA	51	38	39	25	21	48	39	47	22	18
Sly07g0127391	M3	NA	1	1	1	0	0	1	1	0	0	0
Sly07g0127401	M1	NA	88	87	71	81	67	42	46	41	80	83
Sly07g0127411	M3	NA	37	42	25	26	18	17	16	10	13	9
Sly07g0127421	M5	NA	7	15	2	1	1	11	13	2	1	0
Sly07g0127431	M1	NA	3	4	2	10	29	1	1	1	1	2
Sly07g0127441	M13	NA	145	132	179	758	4563	187	150	244	230	2072
Sly07g0127451	M1	NA	5	4	6	101	425	3	2	5	125	375
Sly07g0127461	M1	NA	12	10	8	9	12	5	4	5	2	12
Sly07g0127481	M23	NA	2	2	1	1	1	3	3	2	1	1
Sly07g0127491	M4	NA	6	5	9	1	1	8	8	5	2	1
Sly07g0127501	M1	NA	97	91	105	6	26	23	26	9	2	1
Sly07g0127511	M11	NA	186	150	218	164	121	215	165	237	78	40
Sly07g0127521	M12	NA	51	60	62	111	159	99	101	94	87	101
Sly07g0127531	M10	NA	1	2	4	275	378	11	7	2	3	31
Sly07g0127541	M1	NA	33	32	30	23	25	25	27	27	27	24
Sly07g0127551	M12	NA	5	5	5	3	1	9	8	8	2	1
Sly07g0127561	M18	NA	90	94	90	42	9	105	66	109	17	3
Sly07g0127571	M3	NA	105	119	102	80	77	77	87	74	83	93
Sly07g0127581	M9	NA	10	9	7	9	7	10	15	11	14	13
Sly07g0127591	M3	NCED3-like/SlNCED1	299	350	245	394	226	235	230	274	83	48
Sly07g0127601	M11	ETR2	9	8	13	25	29	11	8	15	25	38
Sly07g0127611	M3	NA	18	18	17	34	42	15	17	16	35	43
Sly07g0127631	M22	NA	1	1	1	1	0	5	0	6	0	0
Sly07g0127641	M22	NA	2	1	1	0	0	7	1	5	0	0
Sly07g0127651	M12	NA	1	1	2	4	3	5	4	13	11	3
Sly07g0127661	M11	NA	21	20	21	21	29	26	25	29	27	29
Sly07g0127671	M1	NA	24	13	6	7	4	3	2	2	0	1
Sly07g0127681	M1	NA	2	1	1	1	1	1	1	1	0	1
Sly07g0127691	M18	NA	26	25	30	27	30	29	23	30	20	19
Sly07g0127701	M3	SlGA2ox2	248	280	95	388	289	19	24	16	85	77
Sly07g0127721	M1	NA	1	2	1	8	22	1	0	1	7	11
Sly07g0127751	M12	NA	6	9	18	67	139	108	176	359	1013	1006
Sly07g0127761	M1	NA	4	3	3	3	4	1	2	2	4	4
Sly07g0127831	M1	NA	2	3	2	3	2	1	0	1	0	0
Sly07g0127941	M1	GA2ox4	35	39	10	1	0	20	11	26	0	0
Sly07g0127951	M1	SlGA2ox5	163	179	52	1	2	72	47	91	9	10
Sly07g0127961	M17	NA	7	6	6	4	2	6	4	6	1	1
Sly07g0128001	M12	NA	26	28	30	25	31	32	31	30	38	34
Sly07g0128011	M12	NA	55	53	69	133	84	175	174	205	122	58
Sly07g0128021	M22	NA	40	5	40	12	16	401	5	202	1	1
Sly07g0128031	M3	NA	10	8	7	6	5	7	6	6	6	5
Sly07g0128111	M1	NA	2	1	1	2	1	1	0	0	0	0
Sly07g0128141	M11	NA	14	15	19	51	65	30	28	37	57	64
Sly07g0128151	M11	NA	1	1	1	1	1	3	2	3	2	2
Sly07g0128161	M1	NA	2	2	1	2	2	1	1	1	1	1
Sly07g0128171	M16	NA	96	74	64	46	36	72	66	81	70	93
Sly07g0128181	M3	NA	63	74	56	27	23	54	61	40	24	31
Sly07g0128191	M11	NA	41	38	40	46	68	45	42	48	61	75
Sly07g0128201	M1	NA	38	32	31	19	6	33	29	30	6	1
Sly07g0128211	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0128221	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly07g0128231	M11	NA	16	19	20	40	140	25	28	29	54	119
Sly07g0128261	M22	NA	1	1	1	0	0	3	1	1	0	0
Sly07g0128271	M11	NA	11	12	14	22	13	17	16	20	12	7
Sly07g0128281	M12	NA	21	24	25	37	24	31	39	36	28	19
Sly07g0128291	M3	NA	35	25	18	2	2	23	17	18	2	1
Sly07g0128301	M12	NA	11	12	12	17	24	16	14	15	14	22
Sly07g0128311	M11	NA	24	24	35	190	571	35	36	57	218	674
Sly07g0128321	M14	NA	31	27	31	27	25	27	27	38	24	19
Sly07g0128331	M3	NA	95	95	54	60	67	76	73	86	90	82
Sly07g0128361	M1	NA	4	2	3	0	0	3	3	2	0	0
Sly07g0128371	M3	NA	43	44	39	41	42	35	37	34	44	39
Sly07g0128381	M12	NA	1	1	1	1	1	2	1	1	1	1
Sly07g0128391	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly07g0128401	M3	NA	80	80	39	49	11	67	86	28	2	8
Sly07g0128411	M1	NA	47	45	39	18	8	25	22	21	8	4
Sly07g0128421	M12	NA	13	12	16	20	36	18	20	21	25	37
Sly07g0128431	M11	NA	54	53	60	56	102	61	76	71	59	107
Sly07g0128441	M21	NA	5	4	7	2	3	5	3	5	1	1
Sly07g0128451	M9	NA	18	19	16	37	64	18	20	18	39	70
Sly07g0128461	M11	NA	112	105	116	121	115	147	142	167	120	133
Sly07g0128491	M11	NA	22	25	35	28	7	30	30	33	5	2
Sly07g0128521	M1	NA	80	73	71	50	67	62	53	59	39	64
Sly07g0128531	M3	BEH4-like3	11	12	8	6	6	6	11	5	2	3
Sly07g0128541	M1	NA	19	18	19	24	29	15	15	14	19	21
Sly07g0128551	M7	NA	2	2	2	1	1	2	3	2	1	1
Sly07g0128561	M1	NA	3	2	4	3	1	1	1	1	0	0
Sly07g0128571	M1	NA	17	17	18	9	8	13	9	11	3	2
Sly07g0128581	M1	NA	28	33	20	4	3	8	6	5	1	2
Sly07g0128591	M22	NA	2	0	1	0	0	4	0	3	0	0
Sly07g0128611	M22	NA	1	1	1	0	0	1	1	1	1	0
Sly07g0128621	M12	NA	20	20	20	17	23	23	22	21	13	18
Sly07g0128631	M1	NA	75	80	84	99	103	52	55	83	241	135
Sly07g0128641	M1	NA	13	10	10	5	4	10	8	8	5	2
Sly07g0128661	M1	ZDP	15	16	16	14	15	15	13	13	8	5
Sly07g0128671	M1	NA	6	6	5	9	7	6	5	5	9	7
Sly07g0128681	M12	NA	8	6	6	9	8	9	11	11	11	11
Sly07g0128691	M12	NA	3	2	2	1	1	9	9	7	1	1
Sly07g0128701	M11	NA	43	28	39	7	4	108	96	110	21	12
Sly07g0128711	M12	NA	12	7	6	1	0	303	187	160	1	1
Sly07g0128721	M1	NA	180	165	97	2	1	41	27	25	1	1
Sly07g0128731	M12	NA	85	68	66	4	9	187	181	146	8	8
Sly07g0128751	M1	NA	2	2	3	3	3	2	1	2	1	1
Sly07g0128761	M11	NA	25	23	33	23	17	38	37	40	17	8
Sly07g0128771	M11	PPC2	524	427	994	434	179	1294	1178	1556	226	142
Sly07g0128781	M1	NA	28	28	27	25	27

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0318301	M8	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0318311	M19	NA	46	50	49	52	41	48	50	48	40	35
Sly02g0318321	M11	NA	5	3	5	3	1	7	7	10	6	1
Sly02g0318331	M3	NA	290	289	221	152	172	192	199	149	116	148
Sly02g0318351	M11	CULLIN4	43	43	46	55	51	48	45	45	42	44
Sly02g0318361	M1	NA	23	22	24	22	24	22	22	21	14	7
Sly02g0318381	M19	NA	16	18	19	19	19	17	13	18	10	4
Sly02g0318431	M12	NA	3	3	2	1	2	8	9	7	5	7
Sly02g0318441	M3	NA	47	46	44	57	55	37	40	39	63	83
Sly02g0318451	M1	NA	78	74	76	64	68	67	65	63	73	90
Sly02g0318471	M12	NA	1	0	1	1	2	2	3	2	8	19
Sly02g0318481	M1	NA	18	20	19	12	11	20	16	15	5	5
Sly02g0318491	M3	NA	29	31	20	11	11	26	24	13	3	4
Sly02g0318501	M12	NA	21	23	21	19	16	30	31	29	21	17
Sly02g0318531	M1	NA	14	13	13	9	4	12	11	12	7	3
Sly02g0318541	M18	SIDDB1	37	40	43	54	78	46	39	44	41	64
Sly02g0318571	M1	NA	3	3	4	11	8	1	1	1	3	5
Sly02g0318581	M11	NA	50	44	54	50	69	56	55	67	90	115
Sly02g0318651	M11	NA	12	10	12	14	13	12	10	12	9	6
Sly02g0318741	M1	NA	20	22	22	18	16	18	16	18	14	10
Sly02g0318751	M1	NA	94	137	54	5	2	10	6	4	1	1
Sly02g0318781	M1	NA	24	28	23	23	22	21	20	20	21	20
Sly02g0318791	M11	NA	20	20	20	22	18	24	24	26	25	25
Sly02g0318801	M11	NA	2	2	2	3	2	2	2	3	2	1
Sly02g0318841	M3	NA	7	6	5	10	13	6	6	5	10	9
Sly02g0318851	M11	NA	22	18	21	11	5	36	30	36	20	7
Sly02g0318861	M11	NA	22	22	25	21	19	25	23	26	30	33
Sly02g0318871	M1	NA	6	4	5	5	6	5	4	4	2	10
Sly02g0318881	M1	NA	2	2	3	1	1	2	2	2	1	0
Sly02g0318891	M1	NA	165	162	171	174	161	137	142	142	180	162
Sly02g0318901	M1	NA	53	47	43	33	37	24	20	21	17	21
Sly02g0318911	M1	NA	2	2	2	4	2	1	1	1	1	1
Sly02g0318921	M18	NA	17	19	19	19	16	21	20	22	17	14
Sly02g0318931	M5	NA	6	9	4	2	1	6	9	4	1	1
Sly02g0318941	M12	NA	5	6	7	6	2	30	57	58	71	20
Sly02g0318951	M11	NA	13	12	15	11	5	24	23	35	27	9
Sly02g0318961	M12	NA	32	33	43	76	74	63	65	72	71	64
Sly02g0318981	M11	NA	10	8	10	18	17	12	11	13	45	48
Sly02g0318991	M1	NA	3	3	3	2	1	3	3	2	1	1
Sly02g0319011	M22	NA	1	1	1	1	0	1	0	1	0	0
Sly02g0319021	M11	NA	11	10	11	13	8	13	12	14	11	7
Sly02g0319041	M1	NA	79	77	83	55	59	74	65	76	68	74
Sly02g0319081	M9	NA	22	25	21	24	24	30	32	29	22	21
Sly02g0319091	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0319151	M11	DWARF1	261	187	382	245	278	416	339	489	242	157
Sly02g0319161	M18	NA	21	19	31	25	29	30	18	33	15	20
Sly02g0319171	M11	NA	29	26	37	33	43	34	27	38	28	40
Sly02g0319191	M1	NA	23	25	28	61	21	17	18	28	38	12
Sly02g0319201	M9	NA	90	98	91	100	88	93	119	104	137	124
Sly02g0319241	M1	NA	1	1	1	1	1	0	0	0	0	0
Sly02g0319321	M12	NA	1	1	1	1	0	1	1	1	1	0
Sly02g0319441	M3	NA	3	4	2	1	1	2	2	2	1	2
Sly02g0319451	M1	NA	3	4	2	1	1	1	1	2	2	1
Sly02g0319461	M1	NA	2	2	2	1	1	2	1	1	1	0
Sly02g0319471	M12	NA	1	1	1	0	0	3	7	7	1	0
Sly02g0319491	M12	NA	1	1	1	1	0	1	1	1	0	0
Sly02g0319511	M18	NA	8	9	12	19	25	15	14	16	19	24
Sly02g0319531	M12	NA	12	14	15	35	49	25	27	30	52	65
Sly02g0319591	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0319611	M5	NA	92	116	52	24	27	82	105	75	32	28
Sly02g0319621	M1	NA	21	21	14	9	8	1	1	1	1	1
Sly02g0319631	M11	NA	2	2	2	1	1	10	9	17	2	2
Sly02g0319641	M3	NA	10	12	11	14	13	11	11	10	15	14
Sly02g0319651	M12	NA	15	22	11	4	11	46	74	20	6	34
Sly02g0319661	M3	NA	4	5	2	1	1	1	1	1	0	0
Sly02g0319671	M1	NA	5	4	2	1	1	1	1	1	0	0
Sly02g0319691	M3	NA	35	36	31	32	40	32	38	30	29	41
Sly02g0319701	M11	NA	43	44	60	87	82	68	66	83	101	99
Sly02g0319711	M19	NA	75	81	76	92	93	87	79	80	71	67
Sly02g0319721	M12	NA	1	1	2	1	1	3	5	3	1	2
Sly02g0319761	M12	NA	98	106	105	175	171	154	147	148	125	113
Sly02g0319771	M12	NA	7	8	10	9	10	108	128	131	151	106
Sly02g0319781	M12	NA	8	6	8	10	9	122	150	135	193	164
Sly02g0319791	M12	NA	11	11	16	34	49	175	198	200	216	197
Sly02g0319801	M12	NA	4	3	5	13	15	19	25	16	47	24
Sly02g0319811	M12	NA	131	136	265	1018	2320	2558	3056	3439	8606	10022
Sly02g0319821	M12	SIPL	6	8	20	125	93	20	20	20	12	10
Sly02g0319831	M12	NA	11	12	14	28	50	28	27	29	35	47
Sly02g0319841	M22	NA	1	1	1	2	3	3	2	3	1	1
Sly02g0319861	M1	NA	21	16	17	17	6	4	5	1	1	1
Sly02g0319911	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0319921	M12	NA	1	1	1	1	1	1	1	1	2	2
Sly02g0319931	M12	NA	6	8	7	9	10	7	7	8	13	16
Sly02g0320011	M22	NA	4	3	5	18	11	9	2	8	8	11
Sly02g0320021	M12	NA	35	37	41	46	56	46	51	52	92	104
Sly02g0320031	M22	NA	1	1	1	0	1	3	1	1	0	0
Sly02g0320111	M19	NA	17	18	20	14	10	15	10	15	8	5
Sly02g0320121	M1	NA	20	20	23	15	13	19	15	18	9	8
Sly02g0320201	M19	NA	23	24	24	19	21	21	20	22	25	25
Sly02g0320211	M3	NA	30	29	28	27	32	27	26	29	37	50
Sly02g0320241	M11	NA	17	17	22	20	17	24	23	25	20	14
Sly02g0320251	M3	NA	17	13	13	6	5	10	12	11	6	6
Sly02g0320301	M11	NA	1	1	2	1	1	1	2	2	2	1
Sly02g0320311	M11	NA	2	3	2	3	2	2	2	3	3	2
Sly02g0320321	M18	NA	2	2	3	2	2	3	2	3	2	1
Sly02g0320331	M11	NA	2	2	3	1	2	4	2	3	2	3
Sly02g0320361	M13	NA	18	18	21	22	22	18	18	20	28	30
Sly02g0320371	M11	NA	1	3	2	5	4	4	3	4	5	11
Sly02g0320381	M19	NA	10	12	14	15	14	13	10	12	15	13
Sly02g0320391	M19	NA	10	13	13	15	13	12	10	13	14	10
Sly02g0320401	M1	NA	9	8	8	6	8	5	7	5	7	4
Sly02g0320411	M19	NA	8	5	7	9	8	8	5	10	9	6
Sly02g0320421	M19	NA	10	13	12	14	12	12	9	12	12	7
Sly02g0320431	M3	NA	32	36	33	60	79	25	30	32	76	107
Sly02g0320601	M1	NA	5	6	4	3	2	1	1	1	1	1
Sly02g0320611	M6	NA	2	3	2	2	2	2	2	2	3	2
Sly02g0320621	M1	NA	5	4	8	1	1	1	1	1	1	1
Sly02g0320701	M1	NA	21	16	25	11	7	17	17	13	6	3
Sly02g0320711	M5	NA	20	21	13	3	2	25	25	6	3	3
Sly02g0320721	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0320751	M22	NA	1	1	1	0	1	5	2	2	1	0
Sly02g0320771	M3	NA	42	40	30	16	26	25	33	20	17	27
Sly02g0320781	M9	NA	9	9	7	51	32	39	34	22	162	57
Sly02g0320791	M11	NA	15	15	16	11	11	22	19	23	17	12
Sly02g0320801	M22	NA	1	1	1	3	3	3	1	2	1	0
Sly02g0320811	M3	NA	40	46	32	25	21	22	24	17	22	21
Sly02g0320821	M9	NA	109	109	107	180	169	157	182	162	231	187
Sly02g0320831	M22	NA	17	11	12	4	4	33	7	27	8	7
Sly02g0320841	M6	NA	3	8	2	1	1	2	3	1	2	3
Sly02g0320851	M11	NA	25	27	27	39	37	36	31	34	29	21
Sly02g0320901	M11	NA	2	2	2	2	1	2	2	2	2	1
Sly02g0320911	M11	NA	1	1	1	1	1	2	2	2	1	1
Sly02g0320931	M11	NA	2	3	4	2	1	4	3	5	1	1
Sly02g0321201	M3	NA	10	11	7	6	3	6	5	6	5	4
Sly02g0321211	M12	NA	13	14	14	17	20	13	14	15	22	28
Sly02g0321221	M11	NA	14	12	16	17	21	14	12	15	24	22
Sly02g0321231	M11	NA	11	11	11	12	15	13	12	12	17	21
Sly02g0321241	M19	NA	5	8	5	9	7	6	6	6	9	10
Sly02g0321251	M11	NA	39	39	40	44	43	47	45	52	52	56
Sly02g0321261	M1	NA	38	37	26	24	8	4	6	3	2	1
Sly02g0321271	M1	ACO6	3073	2912	2752	2038	282	40	15	17	30	2
Sly02g0321281	M3	NA	14	15	10	16	20	11	13	10	15	15
Sly02g0321291	M12	NA	24	20	26	17	10	32	32	29	14	20
Sly02g0321301	M12	NA	44	48	46	39	48	50	52	57	54	73

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0128831	M3	NA	15	18	12	14	15	13	16	11	13	12
Sly07g0128841	M12	NA	25	28	23	21	22	26	27	38	17	35
Sly07g0128851	M11	NA	53	49	51	71	84	72	66	80	68	83
Sly07g0128861	M1	NA	57	61	42	38	37	27	27	28	35	41
Sly07g0128881	M1	NA	37	41	35	20	21	31	29	36	33	28
Sly07g0128891	M12	NA	211	204	211	287	233	244	278	256	242	211
Sly07g0128901	M19	NA	44	48	42	43	39	46	43	44	31	29
Sly07g0128911	M12	NA	12	8	6	108	18	109	101	105	349	46
Sly07g0128921	M12	NA	4	4	4	4	5	5	6	5	4	4
Sly07g0128951	M6	NA	400	580	211	64	207	303	833	161	95	414
Sly07g0128971	M22	NA	3	1	2	1	1	5	2	5	1	1
Sly07g0128981	M1	NA	8	9	10	5	3	7	4	5	2	2
Sly07g0128991	M12	NA	3	4	5	13	23	5	5	7	15	32
Sly07g0129001	M11	NA	2	2	2	2	2	2	2	3	2	1
Sly07g0129011	M1	NA	16	20	15	19	16	11	11	10	12	10
Sly07g0129021	M1	NA	14	14	17	4	4	8	8	8	1	1
Sly07g0129031	M1	NA	2	2	2	1	1	0	0	0	0	0
Sly07g0129051	M12	NA	1	1	1	1	1	3	3	3	1	1
Sly07g0129061	M1	NA	6	6	7	9	12	4	4	5	7	5
Sly07g0129071	M12	NA	1	1	1	1	1	1	1	1	2	2
Sly07g0129081	M12	NA	38	44	44	106	109	53	56	64	160	160
Sly07g0129091	M11	NA	28	27	34	69	92	56	45	74	70	104
Sly07g0129101	M11	NA	41	35	39	51	66	44	41	56	75	81
Sly07g0129111	M12	NA	19	26	21	20	19	35	28	25	22	23
Sly07g0129121	M9	NA	60	55	47	42	50	87	85	60	56	80
Sly07g0129131	M18	NA	16	17	20	20	17	21	18	21	20	21
Sly07g0129141	M11	NA	28	35	31	34	32	39	33	43	35	45
Sly07g0129151	M11	NA	22	21	24	27	26	30	28	31	36	37
Sly07g0129161	M11	NA	18	17	22	23	25	28	25	28	33	45
Sly07g0129171	M12	NA	27	31	29	39	30	30	32	30	35	28
Sly07g0129181	M12	NA	5	5	4	6	6	5	5	5	8	8
Sly07g0129191	M22	NA	27	30	26	32	34	33	29	31	34	32
Sly07g0129201	M3	NA	11	12	8	4	3	9	9	7	4	2
Sly07g0129221	M11	SIPP2C-like	134	126	140	347	533	112	132	189	719	854
Sly07g0129231	M1	NA	5	5	7	3	7	1	4	4	21	10
Sly07g0129241	M23	NA	2	1	1	1	0	3	2	1	1	1
Sly07g0129251	M1	NA	6	8	6	7	10	5	3	4	1	1
Sly07g0129261	M12	NA	43	45	49	71	101	69	68	103	202	298
Sly07g0129271	M11	NA	1	1	1	1	2	1	1	1	2	2
Sly07g0129281	M12	NA	1	1	1	3	3	1	1	1	3	3
Sly07g0129301	M11	NA	73	68	73	95	128	72	74	81	124	147
Sly07g0129311	M11	NA	107	93	121	96	80	127	111	149	133	116
Sly07g0129321	M11	NA	1	1	1	1	2	3	2	3	1	1
Sly07g0129331	M1	NA	10	9	13	15	19	7	8	7	13	19
Sly07g0129341	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly07g0129371	M11	NA	385	379	422	424	366	442	429	485	452	323
Sly07g0129381	M1	NA	28	27	33	117	107	6	9	16	101	38
Sly07g0129391	M18	NA	27	29	24	26	28	28	28	27	44	40
Sly07g0129421	M11	CDKC;1-3	13	14	17	16	14	19	20	19	13	12
Sly07g0129431	M11	NA	12	9	12	15	22	11	14	14	17	22
Sly07g0129441	M12	NA	2	1	1	1	3	2	2	2	3	2
Sly07g0129451	M9	NA	16	17	16	18	14	20	22	21	26	19
Sly07g0129461	M3	NA	40	35	28	38	35	19	23	17	47	47
Sly07g0129471	M2	NA	22	20	13	9	9	11	16	9	12	16
Sly07g0129481	M1	NA	6	6	4	2	2	3	3	2	2	2
Sly07g0129491	M11	NA	59	53	71	77	95	84	79	99	63	111
Sly07g0129501	M3	NA	29	32	24	21	35	21	24	18	16	34
Sly07g0129521	M2	NA	9	11	8	9	8	7	9	7	6	5
Sly07g0129531	M19	NA	14	13	22	9	4	14	8	15	1	1
Sly07g0129541	M9	NA	71	87	45	13	17	282	275	176	13	24
Sly07g0129551	M11	NA	39	31	35	43	46	51	40	58	58	79
Sly07g0129561	M3	NA	12	17	12	17	8	9	13	11	17	10
Sly07g0129571	M1	NA	184	182	212	118	116	161	152	179	120	154
Sly07g0129591	M11	NA	7	6	9	8	8	7	9	8	9	11
Sly07g0129601	M2	NA	22	20	17	18	19	16	18	12	20	20
Sly07g0129611	M13	NA	34	31	45	44	91	43	40	59	55	169
Sly07g0129621	M1	NA	1	1	1	1	14	1	1	1	2	25
Sly07g0129631	M12	NA	20	21	18	26	44	28	28	25	25	44
Sly07g0129641	M12	NA	236	194	237	231	142	401	436	471	366	313
Sly07g0129671	M20	NA	5	5	10	1	1	4	2	4	0	0
Sly07g0129731	M11	NA	23	30	43	90	71	70	67	93	92	76
Sly07g0129741	M3	NA	1	1	1	1	1	1	1	1	0	0
Sly07g0129751	M3	NA	177	224	83	29	19	40	40	29	23	21
Sly07g0129761	M11	NOR-like1	118	105	196	196	182	299	299	385	173	133
Sly07g0129771	M11	NA	267	228	296	298	376	473	372	526	410	417
Sly07g0129781	M11	NA	35	38	43	42	38	54	50	54	32	30
Sly07g0129791	M18	SlHDMA4	7	7	9	9	6	11	9	12	7	6
Sly07g0129801	M12	NA	10	11	12	12	8	16	14	13	9	10
Sly07g0129811	M12	NA	12	10	11	13	10	17	17	19	13	12
Sly07g0129831	M12	NA	84	82	87	33	20	294	257	353	50	21
Sly07g0129841	M1	NA	3	7	6	1	0	1	1	1	0	0
Sly07g0129851	M12	NA	10	17	12	42	32	26	32	37	65	41
Sly07g0129861	M3	SlHDMA5	1	1	1	1	1	1	1	1	1	1
Sly07g0129871	M11	NA	4	5	6	6	7	9	8	12	7	4
Sly07g0129881	M6	NA	424	544	276	223	124	378	628	187	69	56
Sly07g0129891	M11	NA	76	72	103	216	231	135	126	203	261	250
Sly07g0129901	M1	NA	37	29	31	38	39	20	22	22	34	42
Sly07g0129911	M17	NA	147	147	152	101	91	136	144	155	88	119
Sly07g0129921	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly07g0129931	M11	NA	19	17	22	41	76	26	26	30	36	54
Sly07g0129941	M11	NA	27	22	27	24	19	27	23	30	25	24
Sly07g0129951	M1	NA	2	2	3	3	4	2	1	1	1	1
Sly07g0129961	M11	NA	38	22	40	26	6	88	89	133	26	3
Sly07g0129971	M3	NA	50	61	37	30	32	39	56	30	82	94
Sly07g0129981	M3	NA	80	89	58	89	71	65	99	64	202	182
Sly07g0129991	M3	WIP5	58	57	57	189	89	27	43	62	417	349
Sly07g0130011	M1	NA	36	37	38	40	51	29	29	28	39	45
Sly07g0130051	M2	NA	81	77	74	91	103	71	74	71	94	134
Sly07g0130061	M1	NA	4	2	2	0	0	1	0	0	0	0
Sly07g0130071	M3	NA	3	4	2	0	0	2	2	1	0	0
Sly07g0130081	M3	NA	2	2	1	0	1	1	1	1	0	0
Sly07g0130091	M3	NA	1	1	1	0	1	1	1	1	0	0
Sly07g0130101	M3	NA	4	7	2	1	1	1	1	1	0	0
Sly07g0130121	M12	NA	20	15	15	4	2	21	22	15	1	2
Sly07g0130131	M1	NA	4	5	6	28	14	1	1	1	1	1
Sly07g0130151	M1	NA	13	14	7	4	1	1	1	1	1	1
Sly07g0130161	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly07g0130211	M3	NA	8	11	6	2	2	3	3	2	1	1
Sly07g0130221	M1	NA	1	2	2	1	1	1	1	1	0	0
Sly07g0130251	M12	SlGH3-9	1	2	1	1	1	2	2	3	13	14
Sly07g0130261	M3	NA	49	44	35	9	7	40	50	22	12	21
Sly07g0130271	M11	NA	113	99	118	105	106	120	115	156	181	152
Sly07g0130281	M11	NA	304	238	303	274	278	289	305	370	464	457
Sly07g0130291	M11	NA	5	5	4	11	11	7	7	8	56	63
Sly07g0130301	M1	NA	235	206	212	181	148	165	171	183	203	210
Sly07g0130311	M1	NA	142	135	131	233	314	107	118	135	274	434
Sly07g0130341	M1	NA	44	49	51	128	105	3	5	11	107	123
Sly07g0130351	M3	NA	188	288	93	13	14	58	74	18	4	8
Sly07g0130361	M1	NA	5	4	4	4	3	2	1	1	1	1
Sly07g0130371	M11	NA	28	25	35	115	209	43	43	57	85	222
Sly07g0130421	M1	NA	3	3	2	3	2	2	2	2	1	1
Sly07g0130431	M1	NA	9	9	7	11	9	1	1	1	1	1
Sly07g0130451	M22	NA	8	8	9	4	2	14	5	12	2	1
Sly07g0130461	M2	NA	206	227	178	145	161	129	175	120	169	210
Sly07g0130481	M12	NA	46	50	50	93	105	70	73	73	109	119
Sly07g0130501	M12	NA	26	26	27	41	34	30	31	27	38	29
Sly07g0130511	M11	FIE	38	36	43	44	52	54	48	55	59	64
Sly07g0130521	M1	NA	17	18	18	23	29	15	15	16	22	27
Sly07g0130541	M1	NA	3994	3161	3274	3803	4762	2391	2348	2601	4172	4430
Sly07g0130551	M1	NA	4	3	4	9	19	2	1	1	8	9
Sly07g0130561	M11	NA	701	599	643	453	380	749	719

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0321341	M11	NA	44	41	40	49	51	42	44	46	51	43
Sly02g0321351	M12	NA	5	6	7	10	10	9	9	10	10	11
Sly02g0321361	M11	NA	20	18	28	31	46	35	30	43	34	47
Sly02g0321371	M6	NA	66	159	97	2	1	94	84	24	3	1
Sly02g0321401	M1	NA	376	393	292	660	951	17	26	52	360	536
Sly02g0321411	M11	NA	19	21	18	19	17	22	19	20	18	14
Sly02g0321431	M11	SIARF8B	14	13	16	7	7	34	30	33	10	12
Sly02g0321461	M3	NA	2	2	1	0	0	1	1	1	0	0
Sly02g0321481	M3	NA	2	1	1	0	1	0	0	1	1	0
Sly02g0321491	M11	NA	6	6	7	6	8	6	6	7	10	13
Sly02g0321591	M12	NA	4	4	3	1	1	5	5	4	1	1
Sly02g0321601	M12	NA	11	12	13	19	21	11	12	13	46	49
Sly02g0321711	M5	NA	21	33	13	7	7	23	22	11	7	3
Sly02g0321721	M2	NA	62	68	59	55	53	40	48	40	72	69
Sly02g0321731	M11	NA	37	31	32	29	27	32	36	38	35	38
Sly02g0321791	M3	NA	23	22	15	26	41	20	23	11	61	126
Sly02g0321801	M3	NA	338	270	277	185	208	205	245	189	183	223
Sly02g0321811	M11	NA	14	15	18	15	18	17	15	18	18	17
Sly02g0321821	M12	NA	10	8	12	86	89	29	34	48	124	111
Sly02g0321831	M12	NA	1	1	1	1	0	2	2	2	1	1
Sly02g0321841	M3	NA	2	3	2	2	1	1	2	2	2	1
Sly02g0321881	M5	NA	9	9	6	2	2	9	10	4	1	6
Sly02g0321891	M5	NA	9	13	8	3	3	10	17	5	1	3
Sly02g0321911	M11	NA	2	2	3	4	5	4	5	5	3	3
Sly02g0321921	M12	NA	10	11	10	9	8	14	14	11	6	6
Sly02g0321931	M12	NA	39	41	35	19	15	51	48	50	12	9
Sly02g0321941	M12	NA	18	18	17	19	21	31	31	34	28	29
Sly02g0321951	M1	NA	4	3	3	3	2	3	3	2	3	1
Sly02g0321961	M1	NA	120	107	108	100	133	88	86	89	123	185
Sly02g0321971	M3	NA	40	44	25	12	8	18	23	14	8	7
Sly02g0321991	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly02g0322001	M22	NA	1	1	1	0	0	3	1	3	1	0
Sly02g0322021	M3	NA	5	5	5	7	8	5	5	4	9	8
Sly02g0322031	M1	NA	16	16	17	22	23	14	15	14	17	14
Sly02g0322041	M1	NA	6	8	9	4	6	6	5	8	6	5
Sly02g0322191	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0322481	M11	NA	4	3	3	3	3	4	4	4	2	2
Sly02g0322491	M5	NA	9	8	4	3	2	11	8	3	33	16
Sly02g0322501	M12	NA	4	5	3	4	1	4	13	10	25	4
Sly02g0322511	M12	NA	12	10	12	29	66	17	14	16	34	83
Sly02g0322531	M1	NA	11	10	12	13	17	7	8	7	11	11
Sly02g0322561	M11	NA	14	16	18	35	60	18	16	23	37	37
Sly02g0322571	M3	NA	78	77	69	64	77	64	63	61	80	84
Sly02g0322581	M3	NA	96	94	80	71	85	74	72	74	85	86
Sly02g0322591	M12	NA	1	1	1	2	4	2	2	2	12	10
Sly02g0322621	M12	NA	1	1	1	1	0	1	2	1	1	1
Sly02g0322641	M11	NA	1	1	1	1	0	2	2	2	1	1
Sly02g0322661	M3	NA	2	2	1	1	1	1	1	1	0	1
Sly02g0322701	M11	NA	6	4	4	7	6	13	12	12	13	8
Sly02g0322711	M11	NA	9	9	10	13	17	19	18	22	25	24
Sly02g0322721	M7	NA	84	91	82	110	127	84	92	84	164	162
Sly02g0322741	M3	NA	62	63	56	66	61	56	57	50	66	59
Sly02g0322751	M1	NA	1	1	1	1	0	1	1	1	0	0
Sly02g0322761	M12	NA	58	57	47	75	105	66	79	65	87	143
Sly02g0322771	M9	NA	29	35	30	43	52	37	46	33	48	72
Sly02g0322781	M9	NA	56	64	60	88	99	71	82	72	101	125
Sly02g0322791	M3	NA	2	2	3	3	8	2	3	1	1	4
Sly02g0322801	M3	NA	19	21	14	11	8	10	12	7	6	4
Sly02g0322821	M1	NA	29	27	29	26	21	19	18	21	22	13
Sly02g0322911	M3	NA	15	21	10	11	19	12	15	10	11	18
Sly02g0322921	M3	NA	48	49	34	39	43	40	38	33	36	40
Sly02g0322931	M1	NA	12	14	14	15	18	13	12	13	23	26
Sly02g0322941	M19	NA	19	20	20	25	30	20	16	21	33	35
Sly02g0322951	M12	NA	7	8	8	11	34	11	9	10	5	5
Sly02g0322961	M1	NA	30	27	30	16	26	4	4	6	4	8
Sly02g0322981	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0322991	M12	NA	2	6	2	1	1	6	10	5	2	1
Sly02g0323011	M1	NA	10	10	9	8	12	3	3	3	4	6
Sly02g0323021	M12	TAA1-like1	1	1	1	1	2	1	2	1	1	1
Sly02g0323091	M1	SAUR32	5	6	4	1	4	1	1	1	0	1
Sly02g0323121	M1	NA	41	31	35	18	19	27	26	28	19	12
Sly02g0323131	M2	NA	88	91	85	93	82	65	79	59	82	70
Sly02g0323141	M19	NA	32	33	32	32	33	32	28	32	25	27
Sly02g0323151	M12	NA	1	1	1	1	1	2	3	1	1	1
Sly02g0323201	M22	NA	2	1	2	0	0	10	1	8	0	0
Sly02g0323211	M22	NA	9	2	8	0	0	22	2	29	0	0
Sly02g0323241	M11	NA	64	70	53	17	2	125	98	121	9	1
Sly02g0323251	M2	NA	29	30	27	57	90	24	30	31	78	102
Sly02g0323271	M3	NA	66	83	47	31	33	52	59	38	29	38
Sly02g0323311	M3	NA	1	2	2	2	1	1	1	1	1	1
Sly02g0323321	M12	NA	29	35	88	492	793	56	117	195	1523	1028
Sly02g0323351	M12	GRL2	7	7	6	10	15	7	7	8	17	30
Sly02g0323361	M12	NA	12	13	14	22	28	15	16	18	24	33
Sly02g0323391	M3	NA	910	1237	523	428	917	420	824	423	1684	1784
Sly02g0323431	M1	NA	14	13	13	16	15	12	12	13	23	22
Sly02g0323441	M3	NA	30	26	22	28	24	19	18	16	28	26
Sly02g0323451	M1	NA	39	37	39	33	25	31	31	34	30	20
Sly02g0323461	M6	NA	18	30	30	1	1	20	22	10	2	3
Sly02g0323471	M22	NA	2	1	2	1	1	6	2	6	1	1
Sly02g0323491	M1	NA	5	5	5	4	4	5	4	5	2	2
Sly02g0323501	M1	NA	4	3	4	3	2	3	3	3	1	1
Sly02g0323511	M10	NA	1	1	1	1	0	1	1	0	1	1
Sly02g0323521	M12	NA	50	51	45	78	73	55	67	52	62	57
Sly02g0323531	M11	NA	3	4	4	6	11	5	4	4	2	3
Sly02g0323541	M11	NA	52	46	51	53	51	66	65	77	69	68
Sly02g0323551	M1	NA	3	4	4	3	3	4	3	3	4	3
Sly02g0323561	M5	NA	2	3	2	2	2	2	2	2	2	1
Sly02g0323571	M1	NA	81	73	71	81	90	65	66	67	104	121
Sly02g0323611	M3	NA	6	8	5	3	6	6	7	4	2	7
Sly02g0323621	M3	NA	33	32	32	23	21	28	30	27	21	24
Sly02g0323631	M3	NA	2	2	1	1	2	1	1	1	1	3
Sly02g0323641	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0323651	M3	NA	27	30	23	14	12	17	20	14	14	12
Sly02g0323671	M1	NA	6	10	8	18	18	6	6	9	19	10
Sly02g0323681	M11	NA	18	17	17	19	22	17	18	18	24	26
Sly02g0323691	M11	SIDRM2-like	33	30	36	38	41	36	35	39	44	48
Sly02g0323721	M7	NA	2	1	1	1	0	1	2	1	2	1
Sly02g0323741	M18	DDM1-like1	5	5	6	2	4	8	6	8	1	1
Sly02g0323751	M10	NA	1	1	1	1	1	2	1	1	1	1
Sly02g0323761	M3	NA	53	59	45	28	51	30	38	20	17	29
Sly02g0323771	M12	NA	35	38	34	34	29	40	41	36	29	26
Sly02g0323781	M12	NA	2	3	2	3	3	4	4	3	3	6
Sly02g0323811	M12	NA	1	1	1	1	0	1	1	1	0	0
Sly02g0323831	M11	NA	0	1	1	0	0	1	1	1	0	0
Sly02g0323851	M3	NA	1	3	1	0	0	1	1	0	1	0
Sly02g0323861	M3	NA	29	30	22	16	15	18	20	12	16	16
Sly02g0323871	M11	NA	70	77	77	87	97	89	72	85	89	98
Sly02g0323881	M3	NA	57	59	34	49	50	46	65	41	82	129
Sly02g0323891	M7	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0323901	M1	NA	23	22	22	14	13	23	20	20	7	7
Sly02g0323911	M11	NA	69	71	73	57	55	69	71	85	66	75
Sly02g0323921	M11	NA	2	3	1	0	0	55	28	44	1	1
Sly02g0323931	M11	NA	129	116	146	158	229	239	221	267	312	480
Sly02g0323941	M12	NA	1	1	1	0	0	4	4	5	0	0
Sly02g0323951	M12	NA	0	0	1	0	0	2	3	2	0	0
Sly02g0323971	M1	NA	1	1	1	1	0	0	0	0	1	0
Sly02g0323981	M1	NA	3	2	2	1	1	0	0	0	0	0
Sly02g0323991	M12	BES1-like	106	103	95	62	66	106	113	97	42	65
Sly02g0324001	M3	NA	2	2	1	1	0	1	2	1	1	0
Sly02g0324031	M11	NA	2	1	3	1	1	7	5	6	1	1
Sly02g0324041	M7	NA	1	1	1	1	1	1	1	1	1	2
Sly02g0324051	M3	NA	44	46	40	37	37	41	38	33	32	35
Sly02g0324061	M3	NA	18	16	14	6	5	14	14	13	6	5
Sly02g0324071	M12	NA	330	317	331	361	341	333	373	381	515	493

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0130611	M22	NA	1	1	1	1	3	1	1	1	0	1
Sly07g0130621	M22	NA	173	39	89	1	1	512	69	389	1	1
Sly07g0130631	M22	NA	6	2	2	1	0	12	3	4	1	0
Sly07g0130641	M3	NA	5	4	3	3	2	5	3	3	1	1
Sly07g0130651	M1	NA	4	2	3	1	1	1	1	1	1	4
Sly07g0130661	M12	NA	55	56	67	77	93	74	74	75	65	84
Sly07g0130681	M11	NA	2	2	2	3	4	3	2	3	3	7
Sly07g0130691	M3	NA	173	159	133	322	267	142	164	88	194	150
Sly07g0130701	M12	TSB-like3	17	15	18	16	9	36	35	41	31	14
Sly07g0130711	M3	NA	55	72	34	21	25	30	37	15	8	18
Sly07g0130721	M11	NA	29	32	36	37	42	36	35	39	49	54
Sly07g0130731	M1	NA	27	29	24	25	29	15	17	15	21	20
Sly07g0130751	M11	NA	10	7	9	5	2	11	10	11	3	2
Sly07g0130761	M19	NA	16	16	18	18	19	16	14	18	16	13
Sly07g0130771	M1	NA	10	9	10	10	8	10	8	9	11	9
Sly07g0130781	M3	NA	42	41	29	24	22	28	26	20	24	19
Sly07g0130821	M3	NA	3	4	2	1	2	3	4	2	2	2
Sly07g0130831	M3	NA	7	10	5	2	2	7	7	5	4	3
Sly07g0130861	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly07g0130871	M12	NA	1	1	1	1	1	2	2	2	1	0
Sly07g0130881	M12	NA	1	1	1	1	1	3	3	2	1	1
Sly07g0130911	M1	NA	10	10	10	13	26	6	6	6	15	26
Sly07g0130921	M11	NA	22	19	27	50	78	22	20	30	60	89
Sly07g0130931	M11	NA	1	1	1	1	2	1	1	2	2	2
Sly07g0130941	M11	NA	2	3	3	4	5	3	3	4	6	6
Sly07g0130951	M3	NA	38	38	29	31	24	27	30	22	14	20
Sly07g0130961	M11	NA	2	2	2	1	1	3	2	3	1	1
Sly07g0130971	M11	NA	6	6	6	11	11	7	6	8	15	16
Sly07g0130981	M2	NA	97	95	89	105	114	73	93	73	81	99
Sly07g0130991	M11	NA	206	193	212	264	272	311	275	369	368	395
Sly07g0131001	M1	NA	28	26	28	16	17	21	19	23	15	18
Sly07g0131031	M3	NA	14	13	11	9	10	7	9	5	9	11
Sly07g0131041	M1	NA	40	35	41	37	45	30	26	33	36	44
Sly07g0131051	M11	NA	19	19	18	13	12	20	18	19	14	14
Sly07g0131061	M1	NA	21	22	18	12	6	16	14	14	4	2
Sly07g0131071	M13	NA	60	57	58	77	88	54	57	61	89	120
Sly07g0131081	M1	NA	280	257	239	8	1	25	27	8	1	1
Sly07g0131091	M3	NA	80	82	46	21	19	33	36	14	5	8
Sly07g0131101	M3	NA	207	185	96	228	312	115	154	76	235	258
Sly07g0131111	M3	NA	10	11	9	10	10	9	9	8	7	6
Sly07g0131121	M2	NA	20	23	20	19	21	18	22	21	26	27
Sly07g0131131	M3	NA	9	9	9	11	10	9	10	8	11	11
Sly07g0131141	M3	NA	36	54	19	7	4	22	22	8	7	5
Sly07g0131151	M3	NA	16	15	12	6	2	3	5	6	33	8
Sly07g0131161	M3	NA	88	75	76	58	40	74	78	72	75	49
Sly07g0131171	M11	NA	107	93	130	225	341	147	139	223	382	678
Sly07g0131181	M11	NA	43	38	45	105	154	56	56	68	145	180
Sly07g0131191	M3	NA	19	27	11	10	12	7	8	3	6	6
Sly07g0131201	M3	NA	27	29	22	24	25	22	21	19	21	22
Sly07g0131211	M3	NA	5	6	4	4	3	5	5	5	4	4
Sly07g0131221	M3	NA	4	18	3	1	2	5	10	3	1	3
Sly07g0131241	M22	NA	1	0	1	4	13	1	1	1	48	74
Sly07g0131251	M3	NA	20	23	14	13	9	17	19	11	6	3
Sly07g0131261	M11	NA	2	1	1	1	1	3	2	4	1	1
Sly07g0131271	M3	NA	3	1	1	0	0	1	1	1	1	0
Sly07g0131291	M22	NA	45	5	6	1	0	45	8	11	2	1
Sly07g0131301	M2	NA	107	110	99	112	81	75	91	65	66	51
Sly07g0131321	M11	NA	26	25	30	29	50	31	29	35	31	48
Sly07g0131331	M3	NA	6	12	5	1	1	3	8	4	1	4
Sly07g0131341	M11	SBE3	7	8	9	10	11	10	8	11	7	6
Sly07g0131361	M2	NA	24	22	21	21	22	18	22	19	24	28
Sly07g0131371	M2	NA	25	28	21	15	17	18	21	18	22	21
Sly07g0131391	M1	NA	15	18	9	2	1	4	3	3	1	1
Sly07g0131401	M1	NA	109	113	106	109	101	71	72	68	83	99
Sly07g0131411	M1	NA	76	88	103	101	68	59	73	69	61	54
Sly07g0131421	M1	SIERF.F2	109	118	130	142	121	81	97	92	89	114
Sly07g0131431	M12	NA	26	29	30	53	79	56	58	55	167	356
Sly07g0131441	M12	NA	19	20	20	25	17	27	28	25	15	9
Sly07g0131451	M11	NA	19	21	25	24	35	22	21	24	24	29
Sly07g0131471	M2	NA	51	50	39	38	39	29	40	27	54	47
Sly07g0131481	M13	NA	22	21	27	39	48	19	19	25	33	43
Sly07g0131491	M13	NA	21	22	25	62	73	23	22	31	59	61
Sly07g0131501	M11	NA	1	1	1	1	1	2	2	3	1	0
Sly07g0131511	M11	NA	34	35	53	85	67	103	91	121	71	69
Sly07g0131521	M6	NA	67	74	57	61	77	64	87	58	86	115
Sly07g0131561	M1	NA	23	24	21	20	20	20	18	19	17	17
Sly07g0131571	M11	NA	57	57	72	71	52	60	62	72	51	53
Sly07g0131581	M1	NA	58	54	60	56	53	56	53	51	65	67
Sly07g0131591	M12	NA	127	119	131	146	174	172	175	193	297	341
Sly07g0131601	M11	NA	5	5	6	5	4	6	7	7	6	4
Sly07g0131611	M11	NA	8	7	8	10	10	8	7	9	10	6
Sly07g0131621	M10	NA	4	3	2	1	1	4	7	3	1	1
Sly07g0131631	M11	NA	1	1	1	0	0	1	1	2	1	1
Sly07g0131641	M3	NA	48	52	39	51	53	30	40	23	38	64
Sly07g0131651	M12	NA	81	81	74	57	20	92	89	80	22	9
Sly07g0131661	M11	NA	3	1	6	1	0	3	3	2	1	1
Sly07g0131671	M12	NA	55	72	52	94	108	87	134	83	183	210
Sly07g0131681	M1	NA	8	7	8	7	9	8	7	7	8	9
Sly07g0131691	M11	NA	1	1	1	1	1	1	1	1	0	0
Sly07g0131701	M3	NA	44	37	27	19	19	36	36	22	15	14
Sly07g0131711	M12	NA	5	8	3	1	1	23	15	12	6	1
Sly07g0131721	M1	NA	285	265	235	181	152	189	187	179	205	172
Sly07g0131731	M3	NA	18	18	11	12	33	11	14	12	13	13
Sly07g0131751	M14	NA	94	82	91	109	152	77	78	98	124	136
Sly07g0131761	M22	NA	1	1	1	0	0	1	0	1	1	0
Sly07g0131771	M12	NA	159	173	195	254	211	439	471	478	356	350
Sly07g0131791	M3	NA	44	49	22	7	8	20	20	5	5	5
Sly07g0131801	M1	NA	27	27	28	24	19	22	22	22	25	30
Sly07g0131811	M11	NA	32	34	39	60	88	37	32	50	62	67
Sly07g0131831	M15	NA	49	42	45	72	70	44	44	53	75	83
Sly07g0131841	M12	NA	2	4	5	46	39	5	10	13	27	28
Sly07g0131861	M11	NA	18	19	18	39	51	21	20	22	43	46
Sly07g0131871	M10	NA	4	3	2	1	1	5	4	2	1	1
Sly07g0131881	M12	NA	1	1	1	1	2	2	1	2	5	3
Sly07g0131891	M12	NA	26	31	25	100	213	48	64	80	488	401
Sly07g0131921	M1	NA	79	91	72	79	93	54	55	51	78	66
Sly07g0131931	M3	NA	154	137	90	92	121	70	93	59	79	66
Sly07g0131941	M11	NA	7	6	5	8	11	10	11	11	18	11
Sly07g0131951	M11	NA	11	12	14	13	15	16	19	19	23	16
Sly07g0131961	M12	NA	19	15	21	88	229	109	153	171	222	141
Sly07g0131981	M12	NA	1	1	2	20	17	2	1	2	3	1
Sly07g0131991	M1	NA	3	3	3	1	1	2	1	2	1	1
Sly07g0132001	M22	NA	3	3	4	3	1	4	3	3	1	1
Sly07g0132011	M1	NA	2	2	2	2	1	2	1	1	1	1
Sly07g0132021	M1	NA	17	12	10	4	2	5	4	3	1	1
Sly07g0132031	M1	NA	24	22	29	19	18	21	20	25	22	18
Sly07g0132041	M11	NA	166	157	159	222	251	161	171	174	294	339
Sly07g0132051	M1	NA	144	145	138	194	193	133	130	133	161	186
Sly07g0132071	M1	NA	111	121	127	168	150	118	110	114	135	124
Sly07g0132091	M11	NA	81	53	78	17	16	110	84	135	9	8
Sly07g0132101	M11	NA	37	34	33	30	34	38	35	35	35	45
Sly07g0132111	M3	NA	24	21	19	19	22	20	20	20	24	29
Sly07g0132121	M18	NA	6	4	6	6	6	6	5	7	5	5
Sly07g0132131	M9	NA	3	3	3	4	2	5	6	4	3	4
Sly07g0132141	M12	NA	8	11	11	4	1	26	31	30	11	2
Sly07g0132151	M12	SISRT1	6	5	6	4	5	9	10	9	5	5
Sly07g0132181	M22	NA	1	1	1	0	0	2	1	5	0	0
Sly07g0132191	M22	NA	2	1	1	0	0	5	1	8	0	0
Sly07g0132201	M22	NA	1	0	1	1	0	2	0	2	0	0
Sly07g0132211	M12	NA	12	14	14	24	23	14	15	19	35	23
Sly07g0132221	M11	NA	2	2	2	1	1	2	2	2	1	1
Sly07g0132231

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0324081	M2	NA	37	40	34	32	33	30	31	27	31	32
Sly02g0324101	M2	NA	39	35	35	38	31	32	38	35	35	30
Sly02g0324111	M1	NA	69	65	66	55	47	58	60	57	63	57
Sly02g0324141	M14	NA	153	133	153	122	142	133	129	141	120	137
Sly02g0324151	M1	NA	2	1	2	1	1	1	1	1	0	0
Sly02g0324161	M11	NA	78	59	95	4	1	121	105	137	2	1
Sly02g0324171	M9	NA	8	13	8	7	8	19	40	15	15	3
Sly02g0324181	M1	NSY2/ABA4	8	6	6	1	4	6	5	6	2	2
Sly02g0324191	M11	NA	2	2	2	2	1	3	2	3	2	1
Sly02g0324231	M1	NA	13	11	14	7	14	6	6	7	2	4
Sly02g0324251	M8	STE1-like3	78	72	68	45	42	71	92	61	62	34
Sly02g0324261	M3	NA	72	84	53	6	14	22	31	9	6	6
Sly02g0324271	M12	NA	7	6	7	9	8	47	39	37	14	10
Sly02g0324281	M1	NA	2	1	3	1	1	1	1	1	1	0
Sly02g0324291	M1	NA	292	275	282	168	119	248	238	222	128	112
Sly02g0324301	M3	NA	49	48	39	26	28	31	33	31	42	35
Sly02g0324311	M9	NA	9	8	9	9	9	8	10	9	12	12
Sly02g0324321	M11	NA	12	11	14	12	12	15	16	16	17	13
Sly02g0324341	M12	NA	4	3	3	6	6	6	7	7	8	5
Sly02g0324361	M11	NA	7	5	7	3	1	93	74	129	5	2
Sly02g0324381	M12	NA	1	2	1	1	2	4	9	2	2	14
Sly02g0324391	M3	NA	102	140	85	129	343	77	88	52	151	373
Sly02g0324401	M3	NA	2	4	2	0	1	2	2	1	0	1
Sly02g0324431	M11	NA	1	1	1	1	1	4	3	5	1	2
Sly02g0324441	M22	NA	3	3	3	1	1	3	3	3	1	1
Sly02g0324451	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0324461	M1	NA	2	2	1	1	0	1	1	1	0	0
Sly02g0324471	M1	NA	8	5	6	2	8	6	4	4	10	95
Sly02g0324481	M7	NA	22	32	7	1	1	39	88	17	2	1
Sly02g0324501	M1	NA	25	21	22	8	16	1	1	1	1	2
Sly02g0324511	M19	NA	131	105	149	135	244	93	37	114	36	46
Sly02g0324521	M12	NA	9	8	10	13	16	15	16	18	20	33
Sly02g0324541	M3	NA	2	2	1	0	0	1	1	1	0	0
Sly02g0324551	M12	NA	47	44	48	154	568	64	67	68	289	1007
Sly02g0324591	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly02g0324601	M3	NA	25	24	30	10	5	17	20	12	3	5
Sly02g0324641	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0324651	M11	NA	25	23	25	36	45	30	27	35	34	38
Sly02g0324681	M12	NA	17	18	18	21	29	18	19	21	22	29
Sly02g0324701	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0324711	M18	NA	2	2	2	2	2	2	2	2	2	2
Sly02g0324731	M11	NA	45	41	41	46	54	46	45	50	62	69
Sly02g0324741	M11	NA	28	21	37	20	16	39	33	39	29	22
Sly02g0324751	M9	NA	14	13	13	19	30	15	16	14	15	20
Sly02g0324771	M1	NA	144	130	138	129	118	101	113	103	131	119
Sly02g0324781	M7	NA	56	155	58	42	126	86	165	52	32	144
Sly02g0324791	M11	NA	4	4	7	21	25	7	7	13	13	21
Sly02g0324801	M6	NA	115	127	99	111	125	116	131	100	108	119
Sly02g0324811	M12	NA	2	2	2	1	1	3	4	2	1	1
Sly02g0324821	M1	NA	7	6	13	5	1	4	3	3	1	1
Sly02g0324831	M11	NA	460	356	404	470	814	678	597	737	751	950
Sly02g0324841	M11	NA	21	24	27	24	43	45	40	52	35	44
Sly02g0324851	M3	SlP4H1	72	70	68	36	33	61	63	56	36	36
Sly02g0324881	M1	NA	3	3	6	25	57	1	1	1	6	17
Sly02g0324911	M3	NA	23	20	17	7	6	17	17	12	9	9
Sly02g0324921	M11	NA	30	29	41	20	10	84	53	80	8	4
Sly02g0324931	M3	NA	1	2	1	2	3	1	1	1	1	0
Sly02g0324951	M9	SlGH3-3	5	12	4	1	1	57	41	14	1	1
Sly02g0325091	M1	NA	17	11	12	1	2	2	3	2	2	4
Sly02g0325101	M12	NA	1	1	1	0	0	2	1	1	0	0
Sly02g0325111	M11	CBSX1-like1	33	32	31	69	176	41	42	42	66	172
Sly02g0325121	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0325131	M11	NA	2	1	1	0	1	2	3	4	1	1
Sly02g0325141	M3	NA	25	39	6	3	1	5	7	2	1	1
Sly02g0325171	M1	NA	13	14	14	11	8	13	13	11	5	5
Sly02g0325191	M1	NA	8	9	8	11	5	1	1	1	1	1
Sly02g0325201	M1	NA	4	5	3	3	3	1	1	1	1	0
Sly02g0325221	M3	NA	3	4	4	4	4	3	3	2	4	3
Sly02g0325251	M1	NA	13	14	21	3	1	2	2	1	1	1
Sly02g0325281	M11	NA	8	6	7	1	1	10	8	7	1	0
Sly02g0325291	M12	NA	11	11	13	9	9	45	44	57	34	16
Sly02g0325301	M11	NA	17	15	20	22	30	26	24	34	36	46
Sly02g0325331	M11	NA	7	7	9	6	4	8	9	9	8	6
Sly02g0325341	M1	NA	8	7	7	4	3	7	6	7	6	5
Sly02g0325361	M22	NA	1	1	1	1	0	1	1	1	1	0
Sly02g0325371	M3	NA	39	43	21	2	2	27	36	11	8	6
Sly02g0325381	M11	NA	15	16	16	18	21	16	18	20	25	27
Sly02g0325391	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0325401	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0325411	M12	NA	2	2	2	1	3	2	3	3	2	3
Sly02g0325421	M12	NA	1	1	1	1	4	3	3	3	8	13
Sly02g0325431	M1	NA	123	109	87	38	495	3	4	2	475	2199
Sly02g0325491	M1	NA	3	2	3	10	210	1	1	1	22	31
Sly02g0325501	M12	NA	2	2	2	1	1	2	2	2	2	2
Sly02g0325511	M1	NA	116	118	109	90	79	83	79	79	70	67
Sly02g0325521	M4	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0325541	M12	NA	1	1	1	1	1	2	2	2	2	1
Sly02g0325561	M1	NA	15	12	13	4	2	10	9	8	2	1
Sly02g0325571	M14	NA	14	14	15	15	19	14	13	15	18	21
Sly02g0325581	M1	NA	119	110	116	88	87	101	95	103	103	121
Sly02g0325591	M12	NA	57	55	48	84	79	68	79	62	37	32
Sly02g0325601	M3	NA	2	6	2	3	3	1	2	1	1	3
Sly02g0325621	M11	NA	264	170	292	228	185	460	351	534	263	230
Sly02g0325631	M11	NA	4	4	6	4	4	8	6	7	5	3
Sly02g0325641	M11	NA	29	23	42	43	33	96	93	108	87	61
Sly02g0325651	M12	NA	2	2	2	1	1	4	4	4	0	1
Sly02g0325721	M1	NA	83	91	102	42	14	60	59	65	13	4
Sly02g0325731	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0325741	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly02g0325751	M3	NA	16	20	13	11	11	15	14	11	6	7
Sly02g0325761	M1	NA	5	5	5	5	3	4	4	4	4	3
Sly02g0325771	M1	NA	3	4	3	4	4	3	3	3	4	3
Sly02g0325781	M11	NA	7	4	4	1	0	9	6	8	0	1
Sly02g0325791	M12	NA	22	19	20	18	22	25	27	26	29	41
Sly02g0325801	M12	NA	71	61	77	24	13	124	141	140	65	43
Sly02g0325811	M12	NA	94	88	107	35	18	183	190	199	91	49
Sly02g0325831	M6	NA	4	5	3	3	3	3	4	3	2	3
Sly02g0325851	M10	NA	14	15	14	1	1	24	25	14	1	1
Sly02g0325861	M2	NA	54	51	49	39	34	43	53	37	38	32
Sly02g0325871	M12	NA	3	3	3	2	2	8	8	9	4	2
Sly02g0325881	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0325891	M3	NA	17	21	12	4	1	11	13	5	3	2
Sly02g0325901	M12	NA	15	15	16	13	15	17	19	18	20	20
Sly02g0325911	M18	NA	35	33	34	31	29	37	32	41	30	32
Sly02g0325931	M12	NA	17	16	13	22	21	17	16	20	27	33
Sly02g0325941	M1	NA	18	19	19	25	24	17	18	17	22	20
Sly02g0325961	M11	NA	79	63	102	42	28	96	96	100	17	9
Sly02g0325971	M1	NA	13	13	11	16	12	10	11	13	14	15
Sly02g0325981	M14	NA	28	22	31	16	19	25	21	29	17	13
Sly02g0325991	M22	NA	2	1	2	0	1	4	1	5	0	0
Sly02g0326001	M11	NA	30	27	35	28	33	29	34	36	32	35
Sly02g0326061	M9	NA	92	67	72	18	5	87	94	60	5	3
Sly02g0326081	M20	NA	23	16	30	10	9	19	15	20	9	11
Sly02g0326111	M3	NA	6	6	6	10	27	5	5	4	7	53
Sly02g0326121	M1	NA	2	2	2	1	1	2	1	1	1	1
Sly02g0326131	M12	NA	9	7	11	9	21	11	11	14	24	53
Sly02g0326201	M12	NA	21	20	20	29	30	23	30	23	27	32
Sly02g0326211	M11	NA	13	15	16	11	2	22	19	27	3	1
Sly02g0326221	M11	NA	34	29	40	59	148	41	37	47	78	228
Sly02g0326231	M1	NA	131	132	140	117	109	116	112	127	206	213
Sly02g0326261	M19	NA	16	16	16	12	6	16	14	14	3	1
Sly02g0326281	M12	NA	0	1	1	0	1	1	1	1	1	0
Sly02g0326331	M1	NA	3	4	4	2	2	4	2	3	1	1
Sly02g0326341	M3	NA	2	2	2	2	1	3	2	2	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly07g0132261	M1	NA	184	165	168	102	58	147	161	152	89	69
Sly07g0132271	M2	NA	105	108	99	136	120	95	104	94	139	113
Sly07g0132281	M23	NA	3	3	2	2	3	7	3	5	4	3
Sly07g0132291	M11	NA	7	5	10	17	17	18	16	42	43	31
Sly07g0132301	M12	NA	70	68	68	47	45	69	72	77	45	39
Sly07g0132311	M3	NA	17	16	17	18	17	14	16	16	16	19
Sly07g0132321	M1	NA	97	83	99	68	36	42	40	35	9	15
Sly07g0132341	M11	NA	27	28	28	23	20	43	39	41	14	14
Sly07g0132351	M11	NA	2	2	2	2	1	3	4	2	1	1
Sly07g0132371	M2	NA	10	10	8	11	11	8	11	7	12	10
Sly07g0132381	M14	NA	4	4	5	9	10	4	4	5	8	9
Sly07g0132391	M2	NA	59	56	51	44	46	43	50	37	38	44
Sly07g0132401	M1	NA	5	7	6	6	4	5	5	5	5	2
Sly07g0132411	M12	NA	18	18	19	22	27	18	17	20	22	30
Sly07g0132441	M3	NA	64	65	53	33	25	36	41	28	19	23
Sly07g0132451	M11	NA	71	68	77	91	93	83	79	103	235	174
Sly07g0132461	M12	NA	1	1	1	10	21	1	1	2	62	58
Sly07g0132471	M9	NA	49	49	47	68	66	48	65	48	91	81
Sly07g0132491	M11	NA	1795	1659	1980	1270	1357	4117	3519	4745	3720	3312
Sly07g0132501	M2	NA	32	34	29	42	37	28	36	27	51	43
Sly07g0132511	M1	NA	11	13	18	49	53	4	6	3	24	36
Sly07g0132521	M1	NA	5	5	6	6	5	4	4	4	5	3
Sly07g0132531	M1	NA	1	1	1	1	0	1	1	1	0	1
Sly07g0132541	M3	UCK3	83	103	48	25	26	47	82	31	29	30
Sly07g0132551	M20	NA	8	8	8	2	1	8	6	8	1	1
Sly07g0132571	M3	NA	1	1	1	1	1	0	1	0	0	1
Sly07g0132581	M1	NA	33	20	38	4	6	4	4	6	2	1
Sly07g0132591	M1	NA	56	67	80	20	15	10	11	11	30	13
Sly07g0132601	M11	NA	3	2	2	4	3	4	3	4	4	2
Sly07g0132611	M1	NA	68	72	70	54	40	53	51	47	22	15
Sly07g0132621	M10	NA	14	14	11	10	13	20	20	12	26	28
Sly07g0132631	M12	NA	7	9	8	12	20	16	18	23	27	40
Sly07g0132641	M1	NA	89	110	127	280	182	22	26	33	111	36
Sly07g0132651	M11	NA	5	4	3	3	2	11	6	9	3	4
Sly07g0132661	M12	NA	1	1	1	1	1	2	1	1	1	1
Sly07g0132681	M1	NA	16	22	23	64	81	14	11	10	19	30
Sly07g0132691	M1	NA	6	7	9	9	4	1	1	1	2	2
Sly07g0132701	M1	NA	46	50	48	49	58	29	24	26	24	28
Sly07g0132711	M1	NA	4	3	4	9	8	2	1	2	1	1
Sly07g0132721	M1	NA	16	17	17	42	42	11	10	9	19	29
Sly07g0132731	M1	NA	136	121	127	88	101	108	88	98	53	75
Sly07g0132741	M9	NA	40	48	47	54	70	60	72	56	63	63
Sly07g0132751	M12	NA	18	19	19	31	28	25	22	24	24	27
Sly07g0132761	M9	NA	39	49	40	45	53	53	94	51	56	100
Sly07g0132781	M14	NA	41	38	52	71	81	37	37	46	57	64
Sly07g0132811	M11	NA	89	51	82	93	24	254	233	329	230	23
Sly07g0132821	M12	NA	1	1	1	2	6	1	1	1	6	11
Sly07g0132831	M3	NA	47	47	33	24	22	25	25	24	24	23
Sly07g0132841	M3	NA	4	6	2	2	1	1	1	1	1	0
Sly07g0132851	M3	NA	8	9	7	6	4	4	5	3	2	1
Sly07g0132861	M11	NA	22	23	22	22	25	26	23	26	29	29
Sly07g0132871	M3	NA	17	18	17	18	21	17	16	14	15	16
Sly07g0132881	M10	NA	78	101	80	71	80	110	115	94	57	67
Sly07g0132891	M10	BRI1-like	12	15	9	10	8	19	21	10	3	3
Sly07g0132901	M1	NA	23	29	21	16	21	8	10	9	21	26
Sly07g0132921	M3	NA	53	74	38	23	24	37	50	27	15	24
Sly07g0132931	M10	NA	32	32	27	20	14	34	39	28	21	15
Sly07g0132941	M18	NA	15	16	18	20	33	22	19	24	30	38
Sly07g0132951	M1	NA	34	32	46	19	11	17	17	16	10	7
Sly07g0132961	M1	NA	13	16	16	17	15	7	6	8	16	10
Sly07g0132971	M11	NA	203	156	245	176	290	267	208	306	218	259
Sly07g0132981	M3	NA	3	5	2	1	1	3	2	1	1	1
Sly07g0132991	M11	NA	5	5	4	3	2	7	6	6	5	2
Sly07g0133011	M3	NA	3	3	2	1	1	3	3	1	1	1
Sly07g0133041	M11	NA	35	28	26	23	17	30	31	34	24	30
Sly07g0133051	M3	NA	165	163	156	241	268	127	145	132	248	269
Sly07g0133061	M11	NA	4	4	5	5	3	6	6	7	3	1
Sly07g0133071	M11	NA	1	1	1	0	1	1	1	1	1	1
Sly07g0133081	M1	NA	40	41	41	27	25	30	29	30	25	25
Sly07g0133091	M11	NA	30	26	30	25	26	37	29	38	33	31
Sly07g0133101	M12	NA	19	25	20	28	33	20	22	22	31	29
Sly07g0133111	M11	NA	2	1	3	1	1	4	2	4	1	1
Sly07g0133121	M20	NA	29	30	33	34	37	29	23	28	35	32
Sly07g0133131	M11	NA	13	13	14	12	13	16	13	16	15	14
Sly07g0133141	M11	NA	39	42	54	110	106	59	61	76	116	105
Sly07g0133151	M11	NA	71	77	89	272	319	110	111	130	255	290
Sly07g0133161	M3	ABA3/flacca	20	22	18	20	26	15	16	15	29	36
Sly07g0133181	M11	NA	32	29	34	23	22	32	30	35	31	29
Sly07g0133191	M11	NA	13	14	13	8	9	15	14	13	11	8
Sly07g0133201	M11	NA	7	5	8	6	4	10	7	10	4	4
Sly07g0133211	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly07g0133221	M12	NA	2	2	2	2	1	9	6	9	2	1
Sly07g0133231	M12	SAUR65	2	2	1	1	1	3	2	3	1	1
Sly07g0133241	M1	NA	13	14	14	7	9	3	1	3	1	1
Sly07g0133251	M1	NA	136	155	135	119	152	91	97	90	93	103
Sly07g0133281	M11	NA	446	386	498	553	492	562	552	671	532	465
Sly07g0133291	M11	NA	90	82	98	102	122	166	155	174	96	98
Sly07g0133301	M11	NA	12	13	14	15	20	15	16	17	26	33
Sly07g0133311	M11	NA	121	121	137	151	191	143	143	156	162	213
Sly07g0133331	M12	NA	167	160	166	179	247	170	167	174	261	344
Sly07g0133341	M15	NA	9	8	6	9	13	9	8	8	14	20
Sly07g0133351	M14	SlCycB3;1	17	17	19	11	9	18	16	19	11	7
Sly07g0133361	M19	KS-like1	38	42	38	63	147	36	38	39	86	131
Sly08g0259201	M1	NA	5	4	3	4	3	1	1	1	1	1
Sly08g0259211	M11	NA	38	29	45	16	5	69	54	86	18	4
Sly08g0259231	M17	NA	106	100	100	91	105	99	86	107	99	115
Sly08g0259251	M1	NA	16	15	14	11	12	14	13	15	12	12
Sly08g0259271	M5	NA	79	108	37	18	44	50	62	17	5	20
Sly08g0259281	M1	NA	14	12	11	9	9	6	6	5	2	2
Sly08g0259291	M12	NA	81	78	78	56	50	87	102	87	75	79
Sly08g0259301	M9	NA	69	64	61	48	48	73	83	72	69	80
Sly08g0259321	M1	NA	10	13	11	7	9	5	5	3	1	1
Sly08g0259331	M3	NA	6	5	5	3	2	3	4	2	1	1
Sly08g0259351	M1	NA	1	1	1	7	6	1	1	1	2	3
Sly08g0259361	M3	NA	3	3	2	2	1	2	2	2	1	1
Sly08g0259381	M1	NA	14	16	15	20	22	11	12	12	18	27
Sly08g0259391	M1	NA	19	18	23	14	30	11	8	11	7	14
Sly08g0259411	M1	NA	25	24	22	25	30	22	21	23	23	28
Sly08g0259431	M18	NA	27	28	33	29	29	38	31	41	26	27
Sly08g0259441	M2	NA	27	29	25	23	23	21	25	19	25	17
Sly08g0259451	M2	NA	22	20	22	34	28	19	23	20	34	29
Sly08g0259461	M1	NA	4	3	3	2	3	2	2	2	1	1
Sly08g0259471	M11	NA	186	176	187	190	239	186	183	212	238	284
Sly08g0259481	M23	SlJMJ4	1	1	1	1	1	1	1	1	1	1
Sly08g0259491	M22	NA	3	3	2	2	1	6	3	8	1	1
Sly08g0259501	M19	NA	174	178	176	148	190	168	144	173	122	173
Sly08g0259521	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0259531	M3	NA	34	35	31	29	27	23	24	22	33	31
Sly08g0259541	M19	NA	15	14	14	19	21	14	13	16	14	14
Sly08g0259551	M1	NA	8	8	10	13	12	7	4	6	3	3
Sly08g0259561	M1	NA	3	3	3	4	2	2	1	1	1	1
Sly08g0259571	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly08g0259621	M1	NA	9	11	12	26	35	3	2	3	9	17
Sly08g0259671	M1	NA	4	4	4	4	4	2	2	2	3	3
Sly08g0259681	M12	SlCMT3-like2	11	13	11	7	5	15	16	13	4	3
Sly08g0259701	M12	NA	26	28	31	32	30	46	48	54	110	85
Sly08g0259711	M11	NA	7	6	7	3	2	9	8	8	2	1
Sly08g0259721	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly08g0259731	M11	NA	195	170	215	158	144	215	168	275	159	171
Sly08g0259741	M23	NA	2	1	2	1	2	4	2	3	1	4
Sly08g0259751	M11	NA	132	138	121	145	161

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0326361	M11	NA	36	33	39	35	37	39	38	43	42	46
Sly02g0326371	M1	NA	3	4	4	18	25	2	2	2	26	45
Sly02g0326381	M11	NA	13	13	15	13	10	19	21	21	18	14
Sly02g0326391	M1	NA	16	16	15	6	2	14	12	10	1	1
Sly02g0326401	M11	NA	17	16	20	22	35	16	17	21	31	33
Sly02g0326411	M2	NA	151	141	106	115	69	104	126	80	52	48
Sly02g0326421	M11	NA	32	29	43	45	51	61	48	67	58	76
Sly02g0326431	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0326451	M3	NA	8	8	6	4	5	7	5	4	3	4
Sly02g0326471	M12	NA	21	24	29	31	31	48	77	46	74	112
Sly02g0326481	M3	NA	3	3	2	8	4	2	2	1	2	4
Sly02g0326491	M1	NA	17	17	17	30	23	12	12	14	18	21
Sly02g0326501	M1	NA	23	20	17	45	16	2	3	2	3	2
Sly02g0326511	M1	NA	497	479	460	898	394	106	128	94	155	56
Sly02g0326521	M22	NA	1	1	1	0	0	8	0	5	0	0
Sly02g0326541	M12	PPR-like53	8	8	7	11	10	9	8	8	12	10
Sly02g0326551	M1	NA	70	69	65	63	74	54	48	53	66	84
Sly02g0326561	M11	NA	1	1	1	1	1	3	3	4	1	0
Sly02g0326571	M12	NA	3	3	3	2	3	4	4	4	5	8
Sly02g0326591	M1	NA	15	15	16	31	49	11	11	10	36	48
Sly02g0326601	M1	NA	6	7	5	6	6	6	5	5	5	5
Sly02g0326611	M19	NA	4	6	4	4	4	4	3	4	2	2
Sly02g0326621	M19	NA	2	5	3	4	3	4	3	3	2	2
Sly02g0326631	M19	NA	6	7	6	5	5	6	5	6	4	4
Sly02g0326641	M22	NA	9	7	5	4	6	11	6	11	6	5
Sly02g0326651	M18	NA	8	13	8	9	7	14	10	15	8	5
Sly02g0326661	M22	NA	2	1	1	1	0	3	1	2	0	0
Sly02g0326671	M21	NA	5	4	6	1	1	5	2	4	1	0
Sly02g0326691	M1	NA	6	8	11	3	1	6	5	4	1	1
Sly02g0326701	M1	NA	2	2	3	3	1	1	1	1	1	1
Sly02g0326721	M11	NA	4	3	5	6	4	5	5	7	2	1
Sly02g0326731	M11	NRP2-like3	69	72	81	104	120	89	91	109	161	152
Sly02g0326741	M1	NA	2	1	2	0	0	1	1	1	0	0
Sly02g0326751	M3	NA	41	43	39	31	38	31	35	34	46	54
Sly02g0326791	M12	NA	82	74	79	75	50	86	88	104	109	128
Sly02g0326811	M1	PCO2	13	13	9	7	7	3	4	10	3	2
Sly02g0326841	M2	NA	313	295	245	272	224	221	285	192	228	204
Sly02g0326851	M1	NA	24	24	24	16	8	20	20	18	11	7
Sly02g0326861	M11	NA	2	2	3	5	6	5	3	4	10	8
Sly02g0326871	M9	NA	4	5	3	38	22	6	11	9	143	45
Sly02g0326911	M2	NA	189	164	122	87	58	107	148	92	119	59
Sly02g0326931	M6	SIP4H4	33	42	28	9	13	36	47	22	8	11
Sly02g0326941	M11	NA	15	14	16	30	40	19	18	23	32	37
Sly02g0326951	M1	NA	9	8	7	7	7	5	5	5	4	4
Sly02g0326971	M19	NA	33	34	35	37	41	36	30	34	32	39
Sly02g0326981	M12	NA	144	117	125	193	132	129	147	219	322	334
Sly02g0327001	M6	NA	2	7	2	1	1	1	2	1	0	1
Sly02g0327011	M1	NA	20	20	22	32	31	18	18	19	22	23
Sly02g0327061	M1	NA	21	23	16	2	1	3	5	1	1	1
Sly02g0327071	M19	NA	32	35	37	35	41	34	31	36	32	33
Sly02g0327081	M3	NA	5	8	3	1	1	1	2	1	1	0
Sly02g0327091	M11	NA	47	39	71	47	39	93	86	143	25	8
Sly02g0327101	M13	NA	2	1	3	15	73	2	2	3	5	5
Sly02g0327111	M3	NA	5	5	2	1	1	1	2	1	1	1
Sly02g0327121	M11	NA	2	2	2	2	1	3	2	2	1	1
Sly02g0327171	M1	NA	16	17	15	17	21	15	15	14	22	17
Sly02g0327181	M3	NA	3	22	13	11	267	9	6	2	458	4237
Sly02g0327201	M11	NA	1	1	1	0	1	2	1	2	1	1
Sly02g0327211	M12	NA	1	1	1	1	2	2	2	2	2	3
Sly02g0327221	M12	NRT2	2	2	1	4	6	6	4	3	2	2
Sly02g0327231	M1	NA	29	32	19	3	1	2	2	1	1	1
Sly02g0327241	M6	NA	5	8	2	1	1	7	9	3	1	2
Sly02g0327251	M11	NA	29	28	39	37	36	45	40	49	39	38
Sly02g0327261	M1	NA	3	2	2	1	1	1	1	1	1	0
Sly02g0327271	M1	NA	43	40	33	75	101	21	19	15	34	41
Sly02g0327281	M15	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0327291	M3	NA	29	33	28	49	66	23	27	28	102	149
Sly02g0327301	M22	NA	4	1	1	1	2	4	2	2	1	3
Sly02g0327321	M12	NA	19	17	18	17	14	51	47	47	20	14
Sly02g0327331	M8	NA	27	32	21	19	23	26	32	25	32	35
Sly02g0327341	M12	NA	24	23	24	25	24	28	30	29	29	23
Sly02g0327351	M5	NA	30	34	20	18	31	28	33	18	10	23
Sly02g0327361	M11	NA	3	2	2	1	1	6	4	4	1	1
Sly02g0327381	M10	NA	2	2	1	0	0	4	4	1	0	0
Sly02g0327391	M2	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0327401	M12	NA	7	7	6	8	7	9	8	8	10	9
Sly02g0327411	M3	NA	7	8	7	9	8	8	7	8	9	10
Sly02g0327431	M1	NA	31	33	33	28	23	24	26	23	27	21
Sly02g0327441	M12	NA	7	7	7	12	8	10	11	11	9	7
Sly02g0327451	M1	NA	13	11	11	8	9	10	9	10	5	4
Sly02g0327461	M3	NA	46	38	28	39	47	17	21	17	37	42
Sly02g0327481	M12	NA	66	64	75	61	62	73	77	88	99	143
Sly02g0327491	M18	NA	8	8	7	2	1	13	6	18	1	1
Sly02g0327501	M11	NA	18	15	18	22	42	20	18	23	19	26
Sly02g0327511	M1	NA	2	2	2	1	1	2	1	1	1	1
Sly02g0327521	M1	NA	7	6	7	1	1	3	2	2	0	1
Sly02g0327531	M1	NA	24	29	22	4	2	5	5	6	1	1
Sly02g0327541	M11	NA	69	61	66	103	114	87	85	113	93	92
Sly02g0327551	M1	SWP73A-like	126	119	132	154	171	96	99	105	184	163
Sly02g0327561	M12	NA	39	35	41	77	79	54	68	70	130	133
Sly02g0327571	M1	NA	33	24	23	1	1	15	14	8	1	1
Sly02g0327581	M14	NA	81	76	87	80	82	77	81	87	88	91
Sly02g0327591	M1	NA	31	17	18	2	1	2	2	2	1	1
Sly02g0327611	M16	NA	61	48	55	49	39	41	48	48	53	37
Sly02g0327661	M12	NA	19	19	20	37	54	24	27	28	59	69
Sly02g0327671	M1	NA	3	2	3	2	2	2	1	2	3	3
Sly02g0327681	M11	NA	32	30	35	50	65	44	47	40	41	72
Sly02g0327711	M1	NA	66	61	57	49	43	29	30	29	30	41
Sly02g0327721	M1	NA	43	41	40	34	21	22	22	23	23	12
Sly02g0327741	M11	NA	4	4	4	5	5	6	7	7	7	4
Sly02g0327751	M11	NA	13	11	19	19	13	20	18	28	20	9
Sly02g0327761	M12	NA	36	36	56	61	16	72	80	110	114	25
Sly02g0327771	M13	NA	30	29	33	21	23	28	28	32	20	19
Sly02g0327781	M12	NA	31	34	26	14	4	46	47	39	7	3
Sly02g0327791	M12	NA	5	4	6	65	185	17	19	28	428	635
Sly02g0327801	M12	NA	60	35	25	11	17	57	54	53	17	17
Sly02g0327811	M1	NA	3	3	2	0	0	1	1	1	0	0
Sly02g0327821	M22	NA	13	13	14	6	9	25	18	21	4	2
Sly02g0327841	M1	NA	4	3	4	2	1	2	2	1	1	1
Sly02g0327851	M11	NA	28	24	30	26	27	40	35	43	33	32
Sly02g0327861	M3	NA	38	41	30	29	24	26	27	21	14	15
Sly02g0327871	M1	NA	167	147	161	148	173	135	129	156	167	233
Sly02g0327901	M1	NA	17	16	17	18	15	14	16	17	14	12
Sly02g0327911	M22	NA	2	1	1	1	0	5	1	4	1	1
Sly02g0327931	M22	NA	1	1	1	0	0	3	1	2	1	1
Sly02g0327951	M11	NA	177	178	197	164	138	183	176	210	204	215
Sly02g0327961	M3	NA	232	258	186	120	168	163	230	135	114	287
Sly02g0327971	M11	NA	19	19	22	23	27	26	25	27	22	23
Sly02g0327981	M9	NA	115	113	118	172	156	105	137	115	159	174
Sly02g0327991	M10	NA	1	1	1	1	0	1	2	1	1	0
Sly02g0328001	M10	NA	1	2	1	0	0	3	3	1	0	0
Sly02g0328011	M11	NA	30	26	31	44	53	32	28	35	43	57
Sly02g0328021	M19	RAN1	37	36	33	18	19	35	25	35	19	13
Sly02g0328031	M12	NA	41	42	45	58	86	48	56	53	69	101
Sly02g0328061	M12	NA	75	78	84	63	33	115	126	102	40	30
Sly02g0328071	M3	NA	10	18	6	2	2	6	6	3	1	1
Sly02g0328081	M19	NA	8	9	9	8	7	9	8	9	6	6
Sly02g0328101	M19	NA	17	21	18	20	16	22	19	20	14	13
Sly02g0328111	M1	SlHAG4	22	20	17	11	13	12	11	11	11	13
Sly02g0328121	M8	NA	88	128	118	112	89	102	151	105	107	80
Sly02g0328131	M1	NA	3	3	3	1	1	1	1	1	1	0
Sly02g0328141	M1	NA	6	4	4	3	1	1	1	1	0	0
Sly02g0328151	M22	NA	19	15	15	1	1	79	16	44	1	0
Sly02g0328161	M1	NA	2	3	2	2	2	1	2	1	2	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0259791	M1	NA	1	2	2	6	8	1	0	1	0	1
Sly08g0259801	M1	NA	1	2	3	8	11	1	1	0	1	1
Sly08g0259821	M1	NA	25	23	22	27	27	18	23	24	23	23
Sly08g0259831	M12	NA	12	12	15	28	26	15	14	26	53	44
Sly08g0259841	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly08g0259861	M11	NA	79	76	133	32	16	374	267	382	16	6
Sly08g0259871	M3	NA	21	21	18	14	13	19	20	16	11	10
Sly08g0259881	M1	ABCG14	1	1	1	3	1	1	1	1	1	1
Sly08g0259891	M1	NA	10	9	9	8	11	8	8	8	12	12
Sly08g0259911	M22	NA	3	0	2	0	0	18	0	12	0	0
Sly08g0259921	M22	NA	1	0	1	0	0	3	0	4	0	0
Sly08g0259931	M22	NA	2	0	2	0	0	19	1	14	0	0
Sly08g0259941	M22	NA	1	0	1	0	0	11	0	5	0	0
Sly08g0259951	M3	SlCYP707A2	33	66	33	22	43	7	17	27	9	41
Sly08g0259971	M12	NA	8	18	45	245	1318	143	276	645	2297	2657
Sly08g0260001	M1	NA	14	11	7	1	1	2	2	1	1	1
Sly08g0260051	M12	NA	27	26	23	11	12	41	56	43	42	54
Sly08g0260061	M12	NA	22	22	18	9	10	33	47	39	35	41
Sly08g0260091	M11	NA	1	1	1	0	0	3	2	2	0	0
Sly08g0260141	M3	NA	24	21	20	17	7	15	17	12	9	4
Sly08g0260181	M1	NA	1	1	1	5	62	1	1	1	4	13
Sly08g0260211	M12	NA	1	1	1	6	11	1	1	2	90	51
Sly08g0260221	M12	BAM8-like	8	8	10	60	459	10	14	29	378	899
Sly08g0260231	M1	NA	1	2	1	2	6	0	1	0	1	0
Sly08g0260241	M1	NA	543	520	422	52	15	9	5	4	2	2
Sly08g0260281	M22	NA	1	0	1	0	0	2	0	2	0	0
Sly08g0260291	M12	NA	12	12	13	31	59	17	17	21	46	58
Sly08g0260321	M12	NA	1	0	1	1	1	1	1	1	0	0
Sly08g0260331	M12	NA	2	2	3	1	0	9	8	9	1	1
Sly08g0260341	M1	NA	28	27	26	24	32	21	19	18	37	46
Sly08g0260351	M11	NA	158	145	154	127	120	154	160	162	152	130
Sly08g0260361	M12	NA	25	24	25	19	18	28	30	33	22	24
Sly08g0260371	M1	NA	1	1	2	1	0	1	1	1	0	0
Sly08g0260381	M22	NA	2	1	2	1	0	14	1	10	0	1
Sly08g0260401	M11	NA	2	2	2	2	1	4	3	2	0	0
Sly08g0260411	M11	NA	9	4	11	1	1	22	20	37	6	2
Sly08g0260421	M12	SlPRMT6	66	65	68	51	46	81	79	90	71	80
Sly08g0260431	M5	NA	22	26	12	12	16	19	22	14	8	14
Sly08g0260441	M1	NA	25	29	30	45	59	25	27	27	46	62
Sly08g0260451	M12	NA	69	67	78	128	148	103	115	113	172	204
Sly08g0260461	M1	NA	5	5	4	7	9	2	2	2	6	8
Sly08g0260491	M1	NA	14	13	11	15	9	5	5	4	3	1
Sly08g0260521	M1	NA	305	285	290	181	130	215	212	214	191	128
Sly08g0260531	M16	NA	7	6	7	10	7	5	7	8	34	30
Sly08g0260541	M19	NA	77	75	79	67	70	76	71	77	64	87
Sly08g0260551	M11	NA	14	13	15	12	16	21	21	27	17	20
Sly08g0260561	M12	NA	24	20	19	11	8	29	29	23	12	14
Sly08g0260571	M1	NA	25	21	27	31	33	21	17	20	31	31
Sly08g0260591	M3	NA	167	136	140	27	11	97	106	84	12	4
Sly08g0260611	M11	NA	20	16	19	28	36	22	21	24	35	43
Sly08g0260641	M3	NA	160	155	82	45	30	72	63	55	85	41
Sly08g0260651	M12	NA	4	5	4	6	9	5	5	5	10	14
Sly08g0260661	M14	NA	23	12	24	30	242	15	14	17	64	201
Sly08g0260671	M1	NA	10	10	11	10	11	9	9	8	9	6
Sly08g0260681	M1	KIB1	5	5	5	4	3	4	4	4	4	3
Sly08g0260721	M1	NA	12	13	15	17	17	9	7	7	20	22
Sly08g0260731	M1	NA	10	10	11	11	12	6	6	6	14	22
Sly08g0260741	M1	NA	12	8	10	12	12	7	6	7	21	33
Sly08g0260761	M20	NA	31	29	34	25	10	29	26	30	15	10
Sly08g0260971	M21	NA	5	4	5	4	2	5	4	4	2	1
Sly08g0261011	M1	NA	7	5	6	2	1	3	3	2	1	1
Sly08g0261021	M3	NA	145	218	122	64	85	80	96	45	28	63
Sly08g0261031	M9	NA	16	25	22	61	28	33	39	32	149	57
Sly08g0261041	M1	NA	1	1	1	2	1	1	1	1	1	1
Sly08g0261051	M11	NA	2	3	3	3	1	3	3	5	2	1
Sly08g0261111	M2	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0261121	M19	NA	20	24	20	21	24	21	19	19	17	22
Sly08g0261131	M1	NA	77	73	71	58	56	62	63	65	84	101
Sly08g0261181	M11	NA	40	41	51	46	24	61	60	78	60	36
Sly08g0261191	M5	NA	60	42	26	2	2	59	64	18	6	6
Sly08g0261201	M1	NA	23	22	23	20	21	20	21	20	18	20
Sly08g0261221	M11	NA	53	58	78	27	19	86	76	90	17	15
Sly08g0261231	M1	NA	3	3	3	2	3	3	3	3	3	4
Sly08g0261241	M12	NA	23	24	25	59	79	28	29	28	44	58
Sly08g0261251	M11	NA	1	1	1	1	1	1	1	1	0	0
Sly08g0261261	M11	NA	44	31	37	10	2	53	46	49	9	1
Sly08g0261271	M11	NA	6	6	6	6	4	11	11	11	2	1
Sly08g0261301	M11	NA	40	37	44	44	48	39	37	49	44	51
Sly08g0261311	M14	NA	7	6	8	6	7	7	7	7	5	7
Sly08g0261321	M1	NA	30	28	26	14	16	16	14	13	11	13
Sly08g0261331	M12	NA	12	12	14	14	13	14	13	14	14	18
Sly08g0261341	M3	NA	18	23	16	16	22	18	19	16	15	27
Sly08g0261351	M12	NA	2	3	2	2	1	3	3	3	1	1
Sly08g0261361	M3	NA	443	407	214	23	20	96	89	33	23	17
Sly08g0261371	M2	NA	143	137	120	146	130	89	115	83	127	120
Sly08g0261381	M3	NA	18	17	12	15	12	16	17	13	13	11
Sly08g0261391	M11	NA	37	35	37	33	36	37	31	42	40	43
Sly08g0261401	M3	NA	28	29	15	8	10	14	15	8	10	8
Sly08g0261421	M1	NA	75	67	71	57	69	50	54	59	73	105
Sly08g0261441	M13	Glutathione peroxidas	51	45	68	141	372	62	62	81	186	421
Sly08g0261451	M1	NA	7	27	11	1	0	1	0	1	0	0
Sly08g0261461	M3	NA	2	6	2	2	1	1	1	0	0	0
Sly08g0261471	M3	NA	1	3	1	1	1	1	1	0	1	0
Sly08g0261501	M1	NA	14	16	15	9	6	11	11	12	7	9
Sly08g0261511	M3	NA	4	15	3	1	1	1	1	1	1	1
Sly08g0261521	M3	NA	166	190	194	302	239	141	192	146	697	919
Sly08g0261531	M12	NA	58	58	62	219	240	95	111	130	583	611
Sly08g0261541	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly08g0261551	M23	NA	3	1	2	1	0	5	3	2	2	1
Sly08g0261561	M23	NA	1	1	1	0	0	3	2	2	1	1
Sly08g0261581	M9	NA	30	31	28	49	28	44	53	41	31	25
Sly08g0261591	M11	NA	6	6	10	7	3	13	11	15	6	2
Sly08g0261601	M1	NA	46	47	44	41	39	41	37	40	33	30
Sly08g0261631	M18	NA	9	11	16	5	6	15	12	12	2	1
Sly08g0261641	M19	NA	42	43	38	19	9	43	39	34	7	3
Sly08g0261651	M9	NA	2038	1913	1760	993	345	2612	2877	2399	551	331
Sly08g0261661	M1	NA	177	164	149	97	68	110	116	96	101	79
Sly08g0261671	M1	NA	14	14	14	14	16	11	10	13	21	25
Sly08g0261701	M11	NA	187	127	277	105	19	445	396	581	132	9
Sly08g0261711	M1	NA	44	41	38	41	54	22	19	20	17	40
Sly08g0261721	M22	NA	6	5	6	5	5	9	5	9	4	2
Sly08g0261731	M2	NA	72	72	59	64	57	52	61	45	47	52
Sly08g0261741	M1	NA	13	12	12	10	9	8	8	7	10	8
Sly08g0261751	M5	NA	81	85	67	110	151	85	81	71	109	130
Sly08g0261771	M12	NA	6	8	6	2	3	11	10	8	1	1
Sly08g0261781	M11	NA	20	19	20	55	105	23	25	26	64	108
Sly08g0261801	M2	NA	23	27	20	20	21	17	20	19	21	23
Sly08g0261811	M11	NA	11	12	11	4	1	14	14	16	1	0
Sly08g0261831	M2	NRT1.5	1	1	2	1	1	1	2	1	1	1
Sly08g0261841	M3	NA	88	122	48	21	23	32	35	19	25	24
Sly08g0261851	M3	expansin	1	3	1	0	0	1	0	0	1	0
Sly08g0261861	M11	NA	7	6	8	9	8	9	8	9	10	10
Sly08g0261871	M12	NA	7	7	7	9	8	9	9	8	10	11
Sly08g0261881	M19	NA	63	63	74	68	69	71	58	73	57	62
Sly08g0261901	M11	NA	2	1	3	1	1	3	2	4	1	1
Sly08g0261911	M11	BAM3-like2	2	2	3	1	2	13	9	15	1	1
Sly08g0261921	M1	NA	365	316	272	238	201	246	233	230	245	169
Sly08g0261931	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0261941	M3	NA	16	20	14	6	4	14	13	11	6	3
Sly08g0261961	M3	NA	22	24	20	20	22	22	21	18	15	19
Sly08g0261971	M11	NA	17	15	17	26

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0328171	M15	NA	61	58	60	57	52	56	57	61	65	56
Sly02g0328181	M3	NA	28	26	19	19	19	18	20	16	22	24
Sly02g0328191	M1	NA	6	9	8	1	1	1	1	1	1	1
Sly02g0328201	M3	NA	5	12	3	1	1	3	6	1	1	1
Sly02g0328211	M3	NA	6	11	2	1	1	3	5	1	0	1
Sly02g0328221	M6	NA	9	28	22	1	1	7	13	3	1	3
Sly02g0328231	M9	NA	19	18	18	21	23	22	23	21	17	18
Sly02g0328241	M13	NA	23	20	24	32	31	25	24	30	39	45
Sly02g0328251	M11	NA	9	10	13	14	18	14	11	15	24	44
Sly02g0328261	M18	NA	18	19	19	23	26	22	19	19	18	20
Sly02g0328271	M14	NA	25	24	28	25	26	27	23	31	31	32
Sly02g0328281	M9	NA	59	52	50	97	70	66	83	61	67	58
Sly02g0328291	M1	NA	44	43	40	38	39	32	30	27	32	42
Sly02g0328301	M11	NA	1	1	2	1	1	2	1	3	1	1
Sly02g0328311	M15	NA	75	73	65	78	69	70	70	67	73	77
Sly02g0328321	M1	NA	17	22	17	15	16	12	11	10	15	16
Sly02g0328331	M12	NA	39	45	40	38	33	47	50	44	36	30
Sly02g0328341	M3	NA	3	2	2	2	1	3	3	2	1	2
Sly02g0328351	M1	NA	3	2	3	1	2	2	2	3	1	1
Sly02g0328371	M1	NA	3	3	2	1	1	1	1	1	1	0
Sly02g0328381	M3	NA	21	24	18	19	21	19	21	21	26	30
Sly02g0328401	M19	NA	3	4	3	4	4	4	3	4	3	4
Sly02g0328411	M11	NA	2	2	2	2	2	4	3	4	3	4
Sly02g0328421	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0328431	M12	NA	62	73	116	17	2	1209	1294	1988	157	9
Sly02g0328441	M11	NA	4	5	5	4	3	7	7	8	4	3
Sly02g0328451	M1	NA	58	54	54	63	50	30	31	26	32	21
Sly02g0328481	M11	NA	37	35	46	29	19	52	43	61	27	20
Sly02g0328491	M14	NA	142	139	196	247	230	155	134	194	175	255
Sly02g0328501	M11	NA	8	7	9	12	18	12	11	14	7	4
Sly02g0328541	M12	NA	32	30	32	26	24	32	32	31	31	30
Sly02g0328561	M11	NA	28	25	29	57	64	30	28	34	63	67
Sly02g0328571	M1	NA	3	4	5	5	6	2	2	2	3	3
Sly02g0328581	M1	NA	3	4	2	3	4	2	2	2	4	4
Sly02g0328591	M11	NA	2	3	3	4	6	3	3	3	6	5
Sly02g0328611	M3	NA	2	4	1	1	1	1	0	0	0	0
Sly02g0328651	M3	NA	6	6	2	2	2	0	1	0	0	0
Sly02g0328681	M3	NA	5	4	5	2	2	4	4	4	1	1
Sly02g0328691	M11	NA	21	21	29	27	30	37	30	43	22	23
Sly02g0328701	M14	NA	214	186	245	256	180	185	144	172	114	93
Sly02g0328711	M1	NA	318	254	342	380	277	84	84	96	158	197
Sly02g0328721	M1	NA	32	34	41	34	15	4	3	3	1	1
Sly02g0328731	M1	NA	20	22	19	40	93	12	13	12	34	103
Sly02g0328751	M11	NA	15	14	19	17	11	23	21	24	8	3
Sly02g0328761	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0328771	M11	NA	255	225	244	228	252	239	234	262	226	294
Sly02g0328781	M13	NA	66	67	69	48	64	63	66	71	70	85
Sly02g0328791	M1	NA	6	5	5	4	4	2	2	2	1	2
Sly02g0328801	M1	NA	242	234	174	127	178	104	106	76	36	64
Sly02g0328811	M1	NA	148	158	106	36	33	4	2	1	1	1
Sly02g0328831	M23	NA	1	1	1	0	0	1	1	1	0	1
Sly02g0328841	M12	NA	6	5	5	7	9	6	6	6	15	20
Sly02g0328851	M12	NA	6	6	7	8	11	8	7	6	13	14
Sly02g0328871	M1	NA	48	43	39	35	33	28	28	28	30	26
Sly02g0328881	M19	NA	9	10	9	22	30	9	7	12	93	98
Sly02g0328891	M3	NA	21	16	9	1	1	5	6	2	1	0
Sly02g0328901	M5	NA	113	99	62	26	53	105	125	47	21	47
Sly02g0328911	M3	NA	2	3	1	1	0	1	1	1	0	0
Sly02g0328931	M1	NA	18	12	23	4	2	4	4	4	1	1
Sly02g0328951	M7	receptor protein (NPR	40	49	26	19	35	40	60	23	15	48
Sly02g0328961	M12	NA	4	4	4	4	4	4	5	5	8	7
Sly02g0328971	M12	NA	5	6	6	5	5	7	6	6	8	7
Sly02g0328981	M22	NA	1	0	1	0	0	8	1	3	0	0
Sly02g0328991	M3	NA	48	67	42	35	35	49	54	47	44	32
Sly02g0329001	M3	NA	29	34	25	20	20	22	30	24	27	23
Sly02g0329011	M12	NA	10	9	7	5	3	12	12	9	5	2
Sly02g0329031	M3	NA	63	60	46	39	38	41	47	36	26	25
Sly02g0329041	M1	NA	24	21	21	16	19	20	19	21	16	21
Sly02g0329051	M11	NA	1	1	1	1	2	1	1	1	2	1
Sly02g0329061	M1	NA	18	19	18	11	9	14	14	13	11	10
Sly02g0329071	M11	NA	7	6	10	17	26	12	10	17	19	17
Sly02g0329081	M1	NA	11	12	26	98	322	4	1	2	271	482
Sly02g0329101	M11	NA	35	21	40	34	26	104	91	129	46	28
Sly02g0329111	M11	NA	58	42	74	60	52	167	164	209	71	45
Sly02g0329121	M3	NA	21	21	23	48	60	14	17	13	26	35
Sly02g0329151	M12	DWARF1-like	5	2	3	1	1	19	12	4	1	0
Sly02g0329161	M1	NA	2	2	2	1	1	1	2	2	1	1
Sly02g0329171	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly02g0329181	M1	NA	21	20	22	16	13	13	14	12	11	13
Sly02g0329231	M18	NA	6	6	7	16	40	7	5	7	17	21
Sly02g0329241	M3	NA	81	102	62	86	101	57	76	43	89	85
Sly02g0329251	M8	NA	111	98	99	96	88	104	119	99	91	97
Sly02g0329261	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0329271	M2	NA	67	65	62	77	79	53	67	60	88	98
Sly02g0329281	M11	NA	16	16	16	8	2	27	24	24	7	2
Sly02g0329291	M22	NA	1	1	1	1	1	2	1	1	1	0
Sly02g0329301	M12	NA	54	51	55	79	97	62	66	70	120	124
Sly02g0329311	M11	NA	24	26	27	25	31	38	31	36	28	30
Sly02g0329331	M11	NA	18	15	29	11	5	70	58	63	2	1
Sly02g0329341	M22	NA	4	4	5	2	3	7	3	5	1	2
Sly02g0329351	M22	NA	1	1	1	1	1	2	1	1	1	0
Sly02g0329361	M12	NA	2	1	2	2	2	2	2	2	3	3
Sly02g0329371	M10	NA	11	12	10	11	14	13	14	9	10	12
Sly02g0329381	M3	NA	70	74	65	51	59	62	72	57	61	75
Sly02g0329401	M22	SlIMJ8	1	1	1	1	1	1	1	1	1	1
Sly02g0329411	M3	NA	19	21	16	11	8	16	17	12	9	8
Sly02g0329431	M3	NA	31	35	22	12	9	15	18	11	10	9
Sly02g0329441	M11	NA	34	37	38	49	62	48	43	49	63	87
Sly02g0329451	M11	NA	38	36	35	34	36	36	35	40	43	44
Sly02g0329461	M6	NA	423	543	213	318	531	409	677	223	298	627
Sly02g0329471	M12	NA	3	3	4	3	2	8	5	11	11	3
Sly02g0329481	M1	NA	36	35	43	54	66	24	26	32	55	59
Sly02g0329491	M1	NA	15	15	13	9	7	9	8	8	7	7
Sly02g0329501	M3	NA	39	35	35	41	45	32	37	32	49	55
Sly02g0329511	M16	NA	336	278	250	245	200	233	227	217	237	196
Sly02g0329521	M12	NA	20	22	23	25	36	31	35	38	43	42
Sly02g0329541	M1	NA	17	17	19	18	24	16	15	16	26	37
Sly02g0329561	M12	NA	5	9	4	5	7	7	20	6	4	11
Sly02g0329571	M11	NA	3	3	4	11	7	6	5	8	2	1
Sly02g0329601	M1	NA	8	15	19	216	87	1	1	1	1	2
Sly02g0329611	M19	NA	8	9	9	15	18	8	7	9	19	23
Sly02g0329641	M1	NA	115	119	122	86	65	99	102	115	103	87
Sly02g0329661	M12	NA	2	1	2	1	1	3	3	3	1	1
Sly02g0329671	M11	NA	19	18	22	16	17	26	25	31	21	22
Sly02g0329681	M1	NA	4	4	5	4	3	3	3	3	2	1
Sly02g0329701	M11	NA	6	5	8	8	10	10	8	7	8	9
Sly02g0329711	M1	NA	8	7	8	12	16	7	6	8	14	18
Sly02g0329721	M9	NA	33	46	35	344	575	47	80	45	1067	1331
Sly02g0329731	M1	NA	20	19	18	15	9	14	14	12	11	5
Sly02g0329741	M3	NA	22	24	8	1	2	12	13	5	1	3
Sly02g0329751	M12	NA	23	21	24	34	33	27	36	33	46	48
Sly02g0329761	M22	NA	1	1	1	1	0	1	1	1	0	0
Sly02g0329791	M2	NA	1	3	2	1	1	1	2	2	1	1
Sly02g0329801	M1	NA	66	69	68	41	49	48	51	53	60	65
Sly02g0329811	M10	NA	5	5	1	0	1	17	9	1	0	0
Sly02g0329911	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0329921	M11	NA	13	13	15	20	18	25	20	29	20	20
Sly02g0329931	M19	NA	23	21	20	22	30	22	19	21	18	21
Sly02g0329941	M2	NA	31	29	32	39	47	25	32	30	49	56
Sly02g0329951	M11	NA	30	30	36	13	9	47	36	37	9	7
Sly02g0329971	M3	NA	9	14	7	5	6	5	4	3	3	7
Sly02g0329981	M3	NA	17	17	14	17	17	15	15	13	11	11
Sly02g0329991	M1	NA	8	7	7	4	7	5	3	3	3	4
Sly02g0330001	M16	NA	619	515	504	387	293	435	430	476	404	339

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0262011	M1	NA	299	278	216	181	143	136	150	108	156	119
Sly08g0262021	M1	NA	284	272	204	178	139	134	141	109	149	108
Sly08g0262031	M3	NA	2	2	2	3	6	2	2	2	3	4
Sly08g0262041	M3	SlERF.A5	15	14	6	1	2	8	9	3	1	3
Sly08g0262051	M11	NA	222	146	245	55	42	324	279	487	54	84
Sly08g0262061	M3	NA	4	4	3	2	1	2	2	2	2	2
Sly08g0262071	M3	NA	3	2	1	1	0	2	1	1	0	0
Sly08g0262081	M19	NA	16	17	15	15	14	16	14	17	14	12
Sly08g0262091	M12	NA	12	17	11	9	7	19	26	15	14	15
Sly08g0262101	M9	NA	24	28	24	41	36	33	39	31	49	39
Sly08g0262111	M1	NA	3	4	4	2	3	3	2	3	2	1
Sly08g0262121	M3	NA	37	39	30	32	32	31	28	24	26	28
Sly08g0262131	M12	NA	2	2	2	2	4	2	4	2	4	10
Sly08g0262141	M3	NA	49	54	41	48	44	44	44	38	40	39
Sly08g0262151	M12	NA	18	19	19	25	35	19	18	19	35	38
Sly08g0262161	M1	NA	2	1	2	3	7	1	1	1	1	3
Sly08g0262171	M12	NA	13	13	14	24	40	16	14	18	48	71
Sly08g0262181	M11	NA	5	5	7	7	5	6	6	4	10	9
Sly08g0262191	M14	NA	39	37	51	70	86	40	37	52	88	125
Sly08g0262201	M12	NA	16	15	16	20	24	17	17	18	24	26
Sly08g0262211	M3	LeLDH2	13	13	9	4	2	13	13	7	1	1
Sly08g0262241	M11	NA	12	13	12	16	24	12	13	12	28	36
Sly08g0262261	M10	NA	23	35	32	12	10	45	43	50	24	27
Sly08g0262271	M11	NA	11	13	12	11	17	15	13	15	17	20
Sly08g0262281	M11	NA	28	31	35	37	33	34	34	32	39	35
Sly08g0262311	M3	NA	11	10	11	12	12	8	10	9	10	12
Sly08g0262321	M1	NA	21	21	20	21	21	18	18	19	24	22
Sly08g0262331	M1	NA	19	17	22	24	21	11	9	10	11	11
Sly08g0262341	M1	ACR7	3	4	4	4	4	2	2	2	2	3
Sly08g0262351	M1	NA	5	5	4	3	3	3	3	3	3	3
Sly08g0262381	M12	NA	3	3	3	21	6	6	7	9	31	6
Sly08g0262391	M11	NA	35	33	39	31	24	71	59	83	40	22
Sly08g0262421	M22	NA	2	1	2	0	0	10	4	11	0	1
Sly08g0262431	M1	NA	2	2	3	1	1	1	1	1	1	1
Sly08g0262441	M1	NA	3	3	5	2	1	2	2	1	1	1
Sly08g0262471	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly08g0262511	M12	NA	10	11	9	8	8	11	12	13	9	10
Sly08g0262521	M11	NA	10	10	8	6	5	10	9	10	7	7
Sly08g0262531	M1	NA	3	4	3	2	2	2	3	3	2	3
Sly08g0262541	M11	NA	27	29	27	29	36	30	27	29	42	50
Sly08g0262551	M13	NA	31	30	32	27	25	31	29	34	35	34
Sly08g0262561	M11	NA	72	64	78	47	27	120	98	117	50	31
Sly08g0262591	M1	NA	15	17	9	15	28	4	3	5	10	20
Sly08g0262611	M12	NA	13	14	26	28	13	12	23	20	56	46
Sly08g0262621	M1	NA	1	3	2	1	1	1	2	2	1	1
Sly08g0262631	M7	NA	7	10	3	3	7	6	19	5	3	10
Sly08g0262641	M7	NA	15	21	8	5	14	17	56	11	6	22
Sly08g0262651	M7	NA	13	24	2	1	1	11	37	3	1	2
Sly08g0262671	M8	NA	1	1	1	0	0	1	3	0	0	0
Sly08g0262681	M12	NA	2	7	11	318	184	9	31	28	263	125
Sly08g0262691	M2	NA	70	69	63	110	137	62	75	64	112	110
Sly08g0262761	M3	NA	33	38	28	19	24	16	17	15	26	32
Sly08g0262771	M1	NA	9	15	7	1	1	2	1	1	3	1
Sly08g0262781	M3	NA	6	6	4	2	3	4	3	3	4	4
Sly08g0262811	M18	NA	12	12	14	21	25	15	12	16	14	13
Sly08g0262841	M3	NA	55	61	41	15	30	42	40	32	11	14
Sly08g0262851	M11	NA	2	2	3	3	3	2	2	4	22	33
Sly08g0262861	M11	NA	105	94	109	67	77	102	91	111	100	69
Sly08g0262881	M11	NA	6	5	6	7	9	7	6	8	9	11
Sly08g0262891	M11	NA	11	9	12	12	18	13	12	15	16	21
Sly08g0262911	M11	NA	2	2	3	3	3	5	4	3	1	1
Sly08g0262921	M1	NA	31	33	23	27	25	10	10	10	24	21
Sly08g0262931	M1	NA	74	72	60	51	46	48	46	46	49	44
Sly08g0262941	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly08g0262961	M10	NA	10	11	11	9	10	15	20	10	11	11
Sly08g0262971	M1	NA	16	16	23	6	4	10	8	8	1	1
Sly08g0262981	M1	NA	20	23	19	23	27	14	14	14	30	32
Sly08g0262991	M3	ACS6	200	262	103	8	13	71	66	30	3	5
Sly08g0263001	M12	NA	10	6	8	2	1	16	13	24	6	3
Sly08g0263011	M14	NA	22	23	25	23	22	21	19	25	21	19
Sly08g0263021	M14	NA	8	10	13	13	12	9	6	11	11	10
Sly08g0263041	M1	NA	6	13	9	1	1	2	1	1	0	1
Sly08g0263061	M1	NA	28	30	27	21	22	19	19	21	21	23
Sly08g0263071	M3	NA	52	49	46	38	38	43	44	47	33	29
Sly08g0263081	M1	NA	31	27	28	20	26	23	22	26	30	33
Sly08g0263111	M9	NA	218	212	210	171	107	222	287	232	223	186
Sly08g0263121	M11	NA	376	354	398	362	324	400	405	495	599	562
Sly08g0263141	M3	NA	28	29	23	24	21	24	27	22	23	27
Sly08g0263161	M12	NA	6	8	7	7	6	9	9	8	6	5
Sly08g0263171	M3	NA	26	66	83	10	4	14	33	6	3	3
Sly08g0263181	M3	NA	26	77	101	12	5	18	34	7	2	5
Sly08g0263191	M12	NA	90	90	106	129	127	128	139	139	118	120
Sly08g0263201	M1	NA	2	2	2	1	0	0	0	0	0	0
Sly08g0263211	M1	NA	4	3	5	0	1	1	1	1	0	0
Sly08g0263221	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly08g0263231	M3	NA	16	17	13	9	10	12	17	12	10	11
Sly08g0263251	M9	NA	28	30	26	122	165	30	42	37	264	279
Sly08g0263261	M12	NA	6	6	6	17	6	6	7	9	15	2
Sly08g0263271	M19	NA	69	68	72	66	83	70	62	70	104	121
Sly08g0263301	M6	NA	157	327	186	75	388	99	180	65	48	425
Sly08g0263311	M1	SlARF9B	18	19	16	9	9	14	12	11	4	3
Sly08g0263351	M10	NA	24	25	14	7	3	36	37	23	3	2
Sly08g0263361	M12	NA	0	0	1	0	0	2	2	1	0	1
Sly08g0263381	M9	NA	2	2	2	2	1	3	4	3	1	2
Sly08g0263411	M12	NA	41	40	32	36	31	52	42	47	32	37
Sly08g0263421	M12	NA	60	59	56	72	64	81	75	82	77	87
Sly08g0263441	M1	NA	31	34	31	82	99	23	24	26	36	44
Sly08g0263461	M3	NA	75	70	62	55	71	58	61	49	61	65
Sly08g0263471	M3	NA	101	87	66	67	81	60	61	56	79	92
Sly08g0263481	M12	NA	19	19	24	59	64	38	42	48	131	152
Sly08g0263491	M12	NA	17	15	17	20	24	22	21	23	32	32
Sly08g0263511	M12	NA	32	32	28	31	41	56	54	58	42	56
Sly08g0263541	M12	NA	1	1	1	1	1	2	1	2	1	1
Sly08g0263551	M3	NA	162	163	134	131	96	83	110	75	125	87
Sly08g0263571	M1	NA	7	10	8	0	0	1	1	0	0	0
Sly08g0263581	M1	NA	9	12	9	3	1	2	1	2	0	0
Sly08g0263601	M11	NA	37	26	30	11	2	43	34	39	4	1
Sly08g0263631	M11	NA	1	1	1	0	0	3	1	3	0	0
Sly08g0263641	M12	NA	9	8	11	10	6	16	15	15	12	6
Sly08g0263651	M11	NA	22	10	31	5	3	63	47	63	8	2
Sly08g0263691	M3	NA	21	21	16	16	15	17	20	16	18	15
Sly08g0263701	M11	NA	12	11	14	15	8	15	14	18	13	7
Sly08g0263711	M1	NA	99	100	92	39	14	28	28	18	6	5
Sly08g0263721	M1	NA	2	1	1	1	0	0	1	1	0	0
Sly08g0263731	M3	NA	13	13	12	8	5	9	10	9	9	9
Sly08g0263741	M2	NA	2	2	1	2	2	1	2	2	4	4
Sly08g0263751	M3	NA	83	82	70	47	34	68	79	62	45	38
Sly08g0263761	M3	NA	31	26	20	10	8	24	29	21	15	11
Sly08g0263771	M3	NA	1	2	1	1	3	1	1	1	1	1
Sly08g0263781	M12	NA	1	1	1	1	2	3	2	2	1	0
Sly08g0263791	M12	NA	2	2	2	1	1	11	10	14	7	4
Sly08g0263801	M12	NA	1	1	1	1	1	4	4	4	5	2
Sly08g0263841	M12	NA	15	13	14	10	9	18	16	15	13	12
Sly08g0263881	M12	NA	2	1	2	2	2	3	4	2	3	2
Sly08g0263891	M11	NA	4	4	6	5	3	11	9	13	4	2
Sly08g0263911	M1	NA	91	101	93	90	62	83	86	85	67	57
Sly08g0263921	M3	NA	1	1	1	1	1	1	1	0	1	1
Sly08g0263931	M12	NA	15	17	17	23	23	22	24	22	29	24
Sly08g0263941	M12	NA	9	11	8	7	4	15	17	13	7	4
Sly08g0263981	M3	NA	3	2	1	1	1	2	2	2	1	1
Sly08g0263991	M3	NA	10	8	5	6	6	5	4	2	4	3
Sly08g0264011	M3	NA	20

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0330011	M1	NA	254	236	236	202	195	192	195	192	233	267
Sly02g0330021	M1	NA	317	287	267	232	226	221	219	214	261	252
Sly02g0330031	M1	NA	189	165	173	129	120	143	138	147	175	176
Sly02g0330041	M1	NA	201	186	175	160	185	156	153	155	186	227
Sly02g0330051	M1	NA	304	280	256	224	206	187	189	171	223	220
Sly02g0330061	M1	NA	3	3	2	2	2	2	2	2	1	1
Sly02g0330071	M1	NA	2	3	2	1	1	2	1	2	1	1
Sly02g0330081	M13	NA	27	29	35	89	135	36	32	44	97	112
Sly02g0330091	M1	NA	19	18	19	13	13	14	14	15	10	9
Sly02g0330131	M22	GA2ox6	1	1	1	1	1	2	1	2	0	0
Sly02g0330141	M1	NA	21	21	22	34	32	19	17	19	23	44
Sly02g0330161	M12	CULLIN4-like	30	28	29	28	24	36	39	45	39	28
Sly02g0330171	M3	NA	14	21	49	3	0	7	15	8	1	0
Sly02g0330181	M11	NA	45	38	41	46	46	62	59	63	42	55
Sly02g0330191	M12	NA	13	12	14	37	24	18	19	18	69	85
Sly02g0330201	M1	NA	105	110	105	253	56	48	56	29	203	98
Sly02g0330211	M2	NA	81	76	78	101	113	73	79	74	136	146
Sly02g0330221	M1	NA	37	42	36	57	51	19	24	21	47	44
Sly02g0330231	M3	NA	2	3	2	2	2	1	3	1	2	3
Sly02g0330241	M1	NA	15	14	17	5	4	3	2	1	1	1
Sly02g0330251	M11	NA	245	225	266	259	368	339	318	387	491	595
Sly02g0330261	M12	NA	19	17	20	19	23	26	33	35	49	42
Sly02g0330271	M17	NA	511	458	451	297	190	402	403	492	313	204
Sly02g0330281	M9	NA	12	16	25	18	25	22	35	23	39	45
Sly02g0330311	M1	NA	1	1	1	1	1	1	1	0	1	1
Sly02g0330331	M11	NA	111	104	107	95	102	136	136	156	140	155
Sly02g0330341	M3	NA	223	213	189	150	131	143	151	125	167	122
Sly02g0330351	M3	NA	213	193	177	125	112	142	149	134	152	110
Sly02g0330361	M23	NA	1	1	1	1	0	3	1	2	0	1
Sly02g0330371	M11	NA	39	36	35	43	32	38	36	45	42	66
Sly02g0330391	M3	NA	70	92	55	52	55	69	59	63	51	77
Sly02g0330411	M6	NA	3	5	2	5	8	4	4	2	2	4
Sly02g0330421	M12	NA	1	1	1	1	0	1	1	1	1	0
Sly02g0330441	M1	NA	3	4	4	3	3	3	3	3	4	5
Sly02g0330451	M23	NA	1	1	1	1	2	1	1	1	2	4
Sly02g0330491	M1	NA	3	3	3	2	3	2	2	3	1	1
Sly02g0330501	M11	NA	24	18	26	51	75	39	34	45	62	84
Sly02g0330511	M1	NA	23	23	26	5	7	19	18	18	2	2
Sly02g0330521	M1	NA	17	15	17	18	13	11	7	8	3	3
Sly02g0330531	M13	NA	91	67	146	222	43	138	110	227	71	10
Sly02g0330541	M1	NA	9	9	8	6	5	7	7	6	2	2
Sly02g0330551	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0330571	M19	NA	4	5	6	6	4	5	5	4	6	5
Sly02g0330581	M18	NA	4	7	9	12	9	7	7	8	11	8
Sly02g0330591	M1	NA	8	12	13	10	8	8	8	10	11	13
Sly02g0330601	M12	NA	11	13	12	15	13	16	14	15	18	17
Sly02g0330611	M11	NA	8	8	9	9	10	9	9	10	12	14
Sly02g0330621	M12	NA	22	20	22	23	23	24	23	23	24	25
Sly02g0330631	M11	NA	18	16	16	16	14	17	16	19	20	21
Sly02g0330641	M3	NA	90	99	71	84	90	78	91	81	102	134
Sly02g0330651	M7	NA	13	29	9	15	11	25	39	18	25	31
Sly02g0330661	M1	NA	5	7	4	2	1	2	3	2	1	1
Sly02g0330671	M5	NA	4	6	4	3	4	5	5	5	6	6
Sly02g0330681	M11	NA	8	5	11	5	3	33	32	44	15	5
Sly02g0330701	M11	NA	2	1	2	1	0	15	14	21	1	1
Sly02g0330711	M11	NA	2	1	2	1	0	8	9	10	1	0
Sly02g0330713	M12	NA	1	2	2	1	0	9	11	13	1	0
Sly02g0330716	M12	NA	3	3	2	1	1	16	18	29	1	0
Sly02g0330719	M11	NA	14	8	23	5	1	100	91	142	6	1
Sly02g0330721	M11	NA	144	77	180	27	6	936	791	1295	66	4
Sly02g0330731	M11	STS3	30	28	37	45	42	101	93	131	34	25
Sly02g0330741	M12	NA	19	27	33	32	6	398	599	559	144	18
Sly02g0330751	M12	NA	2	1	1	1	1	5	5	3	1	1
Sly02g0330771	M1	NA	18	24	54	455	315	6	13	34	492	282
Sly02g0330781	M13	NA	11	16	26	147	160	10	13	27	161	253
Sly02g0330791	M1	NA	11	14	22	71	66	6	7	10	63	79
Sly02g0330801	M11	NA	10	9	14	48	76	16	21	23	86	88
Sly02g0330811	M8	NA	57	56	43	42	33	64	88	46	28	30
Sly02g0330821	M3	NA	74	102	37	4	2	21	14	3	1	1
Sly02g0330841	M1	NA	7	8	9	7	7	3	3	2	1	2
Sly02g0330851	M11	NA	120	110	121	158	162	112	121	133	212	229
Sly02g0330861	M1	NA	28	26	29	22	17	23	26	21	10	8
Sly02g0330871	M12	NA	81	83	91	94	75	88	110	101	96	112
Sly02g0330881	M3	NA	67	75	64	55	52	59	61	45	50	51
Sly02g0330891	M1	NA	12	12	14	22	35	9	8	10	19	23
Sly02g0330911	M11	NA	22	20	25	12	8	30	28	33	8	5
Sly02g0330921	M6	SIRR3	16	39	20	5	9	16	23	5	5	11
Sly02g0330931	M3	NA	5	6	5	4	6	6	6	5	5	6
Sly02g0330941	M1	NA	38	38	37	29	33	29	31	31	41	46
Sly02g0330951	M11	NA	8	7	11	4	3	12	9	12	1	1
Sly02g0330961	M19	NA	25	26	28	30	40	27	24	28	38	39
Sly02g0330971	M13	NA	16	15	21	53	107	23	18	32	62	112
Sly02g0330981	M3	NA	21	21	13	6	6	11	14	7	7	5
Sly02g0331001	M3	NA	90	93	62	26	23	40	51	28	32	26
Sly02g0331021	M11	NA	1	2	2	2	1	2	1	2	2	1
Sly02g0331031	M3	NA	1	1	1	2	1	1	1	1	1	1
Sly02g0331041	M1	NA	30	30	39	51	61	25	28	25	38	49
Sly02g0331051	M2	NA	30	30	30	42	45	25	27	25	55	55
Sly02g0331071	M1	NA	2	2	1	1	3	1	1	1	1	1
Sly02g0331081	M3	NA	40	41	33	26	40	24	28	27	35	44
Sly02g0331101	M11	NA	34	35	45	50	21	54	51	64	5	3
Sly02g0331131	M3	NA	2	1	1	1	1	2	2	1	1	1
Sly02g0331141	M12	NA	1	1	1	0	1	1	1	1	1	1
Sly02g0331151	M1	NA	11	17	20	10	3	3	1	4	3	2
Sly02g0331161	M1	NA	8	12	15	6	2	2	1	2	2	1
Sly02g0331171	M1	NA	2	3	3	2	1	1	1	1	1	1
Sly02g0331181	M1	NA	28	29	31	39	40	26	28	27	26	27
Sly02g0331201	M3	NA	18	28	6	0	0	14	12	3	1	1
Sly02g0331221	M1	NA	16	13	11	9	7	2	3	1	2	2
Sly02g0331231	M1	NA	3	2	2	3	1	1	1	1	1	1
Sly02g0331241	M17	NA	65	61	68	42	56	55	49	61	54	58
Sly02g0331251	M3	NA	1	1	1	1	0	1	1	1	1	0
Sly02g0331261	M11	NA	1	1	2	1	1	2	2	2	1	0
Sly02g0331351	M1	NA	2	4	2	1	1	1	1	0	0	0
Sly02g0331361	M3	NA	26	32	25	25	36	23	23	25	31	45
Sly02g0331371	M12	NA	2	2	3	4	5	15	15	16	9	11
Sly02g0331381	M22	NA	2	2	2	1	2	3	1	3	1	1
Sly02g0331391	M1	NA	22	22	19	18	19	19	16	17	17	12
Sly02g0331401	M1	NA	56	45	42	1	1	2	1	1	0	1
Sly02g0331411	M1	NA	260	346	228	49	10	21	8	16	1	1
Sly02g0331421	M3	NA	9	9	7	5	6	5	5	4	6	6
Sly02g0331431	M18	NA	3	3	4	4	4	4	3	4	3	4
Sly02g0331441	M11	NA	3	3	4	4	4	4	5	5	5	5
Sly02g0331451	M1	NA	11	10	9	7	8	8	8	8	14	13
Sly02g0331461	M3	NA	5	6	5	4	5	4	5	3	8	10
Sly02g0331481	M1	NA	14	11	14	0	1	4	2	2	1	0
Sly02g0331501	M1	NA	2	2	2	1	1	1	1	1	1	0
Sly02g0331511	M1	TAG1	103	109	152	138	70	14	12	18	32	34
Sly02g0331521	M1	NA	38	53	28	8	7	14	14	11	10	10
Sly02g0331531	M3	NA	7	9	8	13	19	6	7	7	16	38
Sly02g0331541	M11	NA	4	3	2	1	1	8	8	6	3	1
Sly02g0331551	M12	NA	11	12	13	42	40	23	24	38	96	79
Sly02g0331561	M6	NA	24	56	24	15	18	38	49	17	7	14
Sly02g0331571	M1	NA	11	19	22	38	40	9	13	19	28	33
Sly02g0331581	M1	NA	9	8	10	2	1	2	2	2	1	1
Sly02g0331591	M5	NA	109	157	37	6	2	58	77	24	6	3
Sly02g0331601	M19	NA	4	4	4	4	4	3	3	3	2	2
Sly02g0331631	M11	NA	42	45	61	61	37	135	119	162	102	58
Sly02g0331641	M1	NA	8	8	8	3	4	3	2	2	1	1
Sly02g0331651	M1	NA	5	6	6	2	2	2	2	1	1	1
Sly02g0331661	M1	NA	16	15	23	5	3	6	5	6	2	1
Sly02g0331671	M1	NA	39	37	44	66	89	32	30	34	43	44
Sly02g0331681	M12	NA	9	9	9	12	13	11	11	11	13	18
Sly02g0331691	M19	Solyc02g071910	1	2	1	1	2	1	1	2	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0264051	M1	SILOX1 (LOXA)	1628	1772	2367	4338	2981	31	5	6	62	304
Sly08g0264061	M1	NA	4	2	3	2	1	2	1	1	0	0
Sly08g0264071	M3	NA	5	9	4	9	15	2	2	2	2	2
Sly08g0264081	M12	NA	33	28	34	22	15	36	38	36	32	26
Sly08g0264091	M1	NA	3	2	3	1	0	1	0	1	0	0
Sly08g0264101	M11	NA	12	11	14	14	16	17	16	21	20	19
Sly08g0264111	M12	NA	1	1	1	1	1	1	1	1	2	2
Sly08g0264121	M11	NA	37	35	38	38	35	38	38	42	38	30
Sly08g0264141	M1	NA	31	29	39	15	10	24	18	23	6	4
Sly08g0264161	M1	NA	10	12	12	12	8	10	10	11	10	6
Sly08g0264181	M3	NA	195	254	175	85	107	85	96	86	50	115
Sly08g0264191	M11	NA	51	44	85	603	488	58	56	128	1127	2117
Sly08g0264201	M1	NA	41	43	30	7	5	9	8	5	2	2
Sly08g0264211	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0264251	M22	NA	2	1	1	1	1	5	2	4	1	1
Sly08g0264271	M3	NA	18	17	10	11	12	8	10	6	12	14
Sly08g0264281	M3	NA	11	14	11	11	10	9	10	8	16	14
Sly08g0264311	M23	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0264321	M11	NA	133	134	169	132	92	179	145	185	144	181
Sly08g0264371	M1	NA	13	13	15	9	5	8	6	8	2	1
Sly08g0264411	M2	NA	45	44	41	33	41	40	48	39	40	60
Sly08g0264421	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0264431	M12	NA	16	15	13	4	6	14	16	15	7	7
Sly08g0264441	M1	NA	26	29	27	23	17	16	15	15	22	11
Sly08g0264451	M12	NA	63	64	72	62	87	206	203	228	134	194
Sly08g0264461	M18	NA	43	43	47	43	36	47	42	47	26	23
Sly08g0264481	M11	NA	11	10	11	12	14	14	12	15	14	14
Sly08g0264521	M2	NA	96	92	77	68	56	65	78	65	103	78
Sly08g0264541	M3	NA	4	4	4	5	5	3	4	4	4	5
Sly08g0264551	M4	NA	4	4	5	5	6	4	4	4	5	8
Sly08g0264561	M12	NA	4	4	4	4	4	5	5	6	6	6
Sly08g0264571	M10	NA	39	72	29	2	1	98	110	27	2	2
Sly08g0264581	M11	NA	1	1	1	1	1	2	2	3	1	1
Sly08g0264601	M3	NA	10	11	8	5	4	7	7	6	1	1
Sly08g0264611	M22	NA	1	1	1	0	0	3	1	1	0	0
Sly08g0264621	M12	NA	16	17	17	28	41	17	18	19	34	37
Sly08g0264631	M12	NA	14	16	16	21	19	18	20	19	28	25
Sly08g0264671	M1	NA	9	9	9	8	5	5	6	7	6	6
Sly08g0264681	M1	NA	46	44	37	37	48	25	24	27	33	43
Sly08g0264691	M11	NA	13	12	14	10	7	16	15	15	7	6
Sly08g0264721	M17	NA	269	244	253	312	293	241	230	262	253	224
Sly08g0264791	M2	NA	3	10	6	2	3	3	7	4	1	3
Sly08g0264801	M3	NA	2	9	5	3	4	2	5	4	2	4
Sly08g0264811	M1	NA	1	8	6	2	3	2	4	4	1	2
Sly08g0264821	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0264861	M1	NA	1	2	1	1	1	1	1	1	0	1
Sly08g0264871	M11	NA	2	2	2	1	1	3	2	2	1	1
Sly08g0264881	M19	NA	36	32	40	32	32	32	28	33	17	20
Sly08g0264891	M11	NA	1	1	1	1	1	3	3	5	7	4
Sly08g0264911	M1	NA	6	6	6	4	3	4	4	4	4	5
Sly08g0264921	M9	NA	5	5	5	3	5	5	6	5	8	19
Sly08g0265051	M2	NA	138	148	140	142	110	100	125	103	105	88
Sly08g0265061	M12	NA	113	111	98	80	126	130	138	102	71	115
Sly08g0265091	M1	NA	9	8	7	2	1	4	2	2	1	0
Sly08g0265101	M11	NA	20	16	20	34	34	31	27	35	24	29
Sly08g0265121	M3	NA	62	65	64	112	152	50	56	54	111	146
Sly08g0265131	M12	NA	46	48	47	52	43	52	50	48	33	42
Sly08g0265151	M19	NA	23	23	25	22	18	26	22	24	13	14
Sly08g0265161	M11	NA	22	21	29	27	86	35	30	41	31	38
Sly08g0265181	M3	NA	31	36	29	27	27	26	28	26	26	26
Sly08g0265201	M6	NA	5	28	11	1	2	5	14	3	1	1
Sly08g0265211	M6	NA	1	4	3	1	0	2	3	1	0	0
Sly08g0265231	M3	NA	69	74	56	130	122	56	74	52	104	92
Sly08g0265251	M1	NA	309	287	287	218	171	205	239	198	234	164
Sly08g0265261	M12	NA	27	26	28	34	40	30	35	37	59	60
Sly08g0265281	M3	NA	12	22	4	1	1	2	2	1	1	1
Sly08g0265291	M3	NA	7	14	3	1	1	1	2	1	1	1
Sly08g0265331	M3	NA	1	1	1	1	1	1	2	1	2	3
Sly08g0265351	M3	NA	87	96	37	2	1	17	18	10	1	1
Sly08g0265411	M23	NA	1	1	1	1	1	1	1	1	1	2
Sly08g0265421	M11	NA	12	8	16	58	62	24	19	23	150	219
Sly08g0265431	M11	NA	32	27	29	20	16	37	34	43	25	28
Sly08g0265451	M2	NA	50	49	43	49	53	40	49	36	53	73
Sly08g0265461	M11	NA	2	2	2	2	4	3	2	3	4	9
Sly08g0265471	M12	NA	6	8	6	7	14	9	12	8	12	45
Sly08g0265481	M12	NA	5	8	3	7	18	17	59	12	22	73
Sly08g0265501	M1	NA	2	3	3	14	5	1	1	0	1	1
Sly08g0265511	M12	NA	74	75	75	110	106	86	85	92	126	134
Sly08g0265521	M12	NA	13	11	14	21	43	17	15	20	55	145
Sly08g0265531	M18	NA	6	6	7	12	19	8	6	8	21	48
Sly08g0265551	M12	NA	3	4	3	1	1	4	5	5	8	4
Sly08g0265561	M7	NA	1	2	1	1	0	1	1	1	1	1
Sly08g0265571	M12	NA	6	6	6	4	2	8	9	8	7	5
Sly08g0265581	M1	NA	23	28	25	16	5	13	16	14	11	8
Sly08g0265591	M12	NA	2	2	3	3	3	4	4	3	3	4
Sly08g0265601	M3	NA	5	3	1	1	4	3	4	1	1	2
Sly08g0265611	M5	NA	8	12	6	6	14	8	10	4	8	21
Sly08g0265621	M13	NA	1	1	1	1	1	1	1	1	1	0
Sly08g0265631	M11	NA	4	4	4	4	4	5	4	6	4	4
Sly08g0265651	M22	GA2ox11	1	1	1	0	1	1	1	1	1	1
Sly08g0265661	M2	NA	69	61	79	201	401	65	68	62	158	508
Sly08g0265671	M11	NCED5/SINCED2	23	22	25	5	10	40	26	30	2	3
Sly08g0265731	M8	NA	42	39	40	63	84	40	46	39	60	72
Sly08g0265751	M12	NA	1	2	1	1	2	6	9	12	5	3
Sly08g0265761	M12	NA	1	1	1	1	1	5	6	8	5	2
Sly08g0265771	M12	NA	1	1	1	1	0	6	7	11	7	4
Sly08g0265781	M12	NA	4	5	6	3	2	63	76	102	53	14
Sly08g0265811	M3	NA	27	41	9	0	1	4	10	2	0	0
Sly08g0265821	M3	NA	33	57	9	1	1	14	32	12	1	2
Sly08g0265831	M3	NA	7	7	8	12	10	5	6	6	26	14
Sly08g0265841	M3	NA	11	14	3	1	1	10	22	2	0	1
Sly08g0265851	M3	NA	27	45	5	0	0	7	8	1	0	0
Sly08g0265861	M3	NA	3	3	2	2	1	3	3	3	2	1
Sly08g0265881	M3	NA	5	6	4	4	4	3	3	2	3	2
Sly08g0265911	M2	NA	25	25	22	25	21	18	20	18	19	19
Sly08g0265971	M3	NA	2	3	3	2	2	1	2	1	3	2
Sly08g0265981	M12	NA	1	2	1	2	1	2	2	2	5	3
Sly08g0265991	M12	NA	2	3	2	2	1	3	3	3	5	3
Sly08g0266031	M1	NA	21	22	25	10	6	5	6	3	5	6
Sly08g0266051	M12	NA	5	5	6	5	4	5	7	6	7	7
Sly08g0266081	M11	NA	21	19	23	31	28	32	30	35	28	20
Sly08g0266091	M2	NA	8	8	7	10	8	7	8	7	11	13
Sly08g0266121	M2	NA	29	30	26	31	36	27	28	29	39	40
Sly08g0266131	M18	NA	25	26	28	46	62	30	26	39	63	61
Sly08g0266141	M11	NA	47	50	54	97	141	57	51	66	142	182
Sly08g0266151	M11	NA	19	16	18	21	22	21	21	21	23	24
Sly08g0266161	M11	NA	65	59	52	65	59	68	64	73	72	64
Sly08g0266171	M9	NA	1	1	1	1	1	2	4	2	1	1
Sly08g0266201	M14	NA	53	51	57	41	21	44	42	49	36	21
Sly08g0266211	M3	NA	19	18	12	10	4	16	18	14	9	4
Sly08g0266291	M12	NA	11	14	20	10	10	32	37	39	49	57
Sly08g0266301	M12	NA	3	4	7	3	6	7	14	9	14	23
Sly08g0266321	M11	NA	33	33	35	65	81	38	43	45	111	96
Sly08g0266331	M12	NA	22	21	21	23	17	26	25	27	26	16
Sly08g0266371	M12	NA	4	5	5	7	6	5	6	5	9	11
Sly08g0266381	M1	NA	2	2	2	3	4	1	2	2	4	4
Sly08g0266741	M13	NA	27	23	34	46	92	31	27	42	42	53
Sly08g0266751	M11	NA	5	4	3	3	2	6	5	6	3	1
Sly08g0266781	M11	NA	16	15	21	19	13	26	22	29	20	14
Sly08g0266811	M2	NA	18	14	17	14	14	16	16	16	14	15
Sly08g0266861	M11	NA	17	18	21	17	12	24	22	29	20	16
Sly08g

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0331711	M1	Solyc02g071920	64	70	50	22	7	23	10	17	4	2
Sly02g0331731	M12	NA	12	9	10	6	7	14	14	13	10	12
Sly02g0331771	M1	NA	182	259	127	15	5	11	10	4	1	0
Sly02g0331781	M12	NA	35	39	35	46	51	37	39	42	53	62
Sly02g0331791	M3	SLB3	55	72	43	25	32	28	38	19	14	20
Sly02g0331801	M6	NA	15	15	14	14	20	14	19	12	15	18
Sly02g0331811	M1	NA	3	3	4	4	3	3	2	4	3	3
Sly02g0331821	M22	NA	1	1	1	1	0	2	1	1	1	0
Sly02g0331831	M22	NA	1	1	1	0	1	4	1	3	1	0
Sly02g0331841	M22	NA	1	1	1	0	0	4	1	4	0	1
Sly02g0331861	M1	NA	1	2	1	1	0	1	0	1	0	0
Sly02g0331871	M3	NA	16	23	21	13	55	15	19	16	9	58
Sly02g0331881	M22	NA	5	5	5	8	9	6	5	4	2	2
Sly02g0331891	M3	NA	4	4	3	2	2	4	4	3	2	2
Sly02g0331901	M1	NA	6	6	6	6	6	2	2	1	1	1
Sly02g0331911	M12	NA	13	12	13	16	17	16	16	14	17	14
Sly02g0331921	M2	NA	475	493	393	348	287	362	417	329	246	238
Sly02g0331931	M22	NA	2	1	1	1	1	2	2	2	1	1
Sly02g0331941	M12	NA	48	56	36	13	22	57	67	49	15	27
Sly02g0331951	M6	NA	3	9	8	6	14	6	7	2	1	5
Sly02g0331961	M11	NA	15	14	20	37	104	22	19	24	32	69
Sly02g0331971	M1	NA	5	3	8	9	10	4	3	4	16	32
Sly02g0331981	M3	NA	21	20	15	9	4	13	14	8	2	1
Sly02g0331991	M1	NA	1	2	2	3	3	1	1	1	3	3
Sly02g0332011	M10	NA	2	2	1	1	1	3	4	2	1	2
Sly02g0332021	M7	NA	1	1	1	0	0	1	2	1	1	1
Sly02g0332031	M11	NA	17	19	16	20	28	26	23	29	36	34
Sly02g0332041	M22	NA	2	1	2	1	1	14	1	10	1	1
Sly02g0332061	M11	NA	4	4	5	19	58	5	6	7	60	68
Sly02g0332071	M3	NA	12	15	10	15	15	10	12	11	14	14
Sly02g0332091	M22	NA	1	1	1	0	0	3	0	3	0	0
Sly02g0332101	M3	BIN2	199	230	165	105	103	175	181	132	88	94
Sly02g0332111	M1	NA	2	2	3	1	5	1	1	1	1	2
Sly02g0332121	M1	NA	1	1	1	1	2	1	1	1	1	1
Sly02g0332231	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0332241	M11	NA	3	4	5	4	4	5	5	5	5	6
Sly02g0332271	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0332281	M1	NA	3	3	4	2	1	1	1	1	1	0
Sly02g0332291	M1	NA	5	4	6	2	1	2	1	2	1	0
Sly02g0332301	M1	NA	3	4	3	2	3	1	2	2	1	2
Sly02g0332311	M3	NA	6	7	7	10	10	5	6	6	10	13
Sly02g0332321	M1	NA	20	29	19	12	9	1	1	1	2	3
Sly02g0332331	M1	NA	1	1	1	1	1	1	0	0	1	1
Sly02g0332341	M22	NA	1	1	1	0	1	3	1	3	0	0
Sly02g0332351	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0332361	M3	NA	26	25	25	23	25	24	24	26	30	28
Sly02g0332371	M1	NA	5	7	7	15	14	4	3	4	4	6
Sly02g0332381	M1	NA	28	24	21	18	22	13	8	12	6	6
Sly02g0332431	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0332481	M4	NA	6	6	6	3	5	7	5	5	2	1
Sly02g0332491	M1	ARR18-like	2	3	2	1	1	0	1	0	0	0
Sly02g0332501	M12	NA	13	24	16	91	43	86	91	153	273	81
Sly02g0332511	M11	NA	25	19	42	14	5	93	61	117	7	3
Sly02g0332521	M3	NA	4	5	2	3	4	4	3	3	5	3
Sly02g0332531	M12	NA	229	300	352	986	1342	646	659	720	706	804
Sly02g0332541	M1	NA	44	41	45	29	36	27	23	27	18	26
Sly02g0332551	M1	NA	5	5	8	5	3	3	2	3	3	2
Sly02g0332561	M3	NA	16	18	14	18	31	14	17	13	18	34
Sly02g0332581	M3	NA	10	11	8	12	13	10	10	7	6	9
Sly02g0332591	M1	NA	33	31	35	30	34	29	30	33	35	35
Sly02g0332601	M1	NA	46	36	49	12	29	2	1	1	2	5
Sly02g0332611	M1	NA	25	26	26	28	33	22	22	24	31	43
Sly02g0332621	M1	NA	113	100	124	151	186	72	78	75	139	233
Sly02g0332641	M18	NA	13	13	16	15	11	17	14	15	12	10
Sly02g0332681	M11	NA	25	25	30	74	135	28	29	36	137	175
Sly02g0332711	M3	NA	10	13	11	8	10	10	9	8	9	17
Sly02g0332731	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly02g0332741	M1	NA	3	4	3	1	1	2	1	1	1	2
Sly02g0332751	M3	NA	2	3	2	2	2	2	2	2	3	2
Sly02g0332761	M18	NA	4	5	5	7	7	6	5	6	6	6
Sly02g0332771	M11	NA	7	8	7	10	10	7	8	8	9	9
Sly02g0332781	M11	NA	1	1	1	1	2	1	2	1	1	1
Sly02g0332791	M3	NA	1	3	1	0	1	2	1	0	0	0
Sly02g0332851	M3	NA	187	171	62	98	90	15	39	53	1130	817
Sly02g0332861	M1	NA	10	10	3	1	1	1	1	1	0	0
Sly02g0332871	M6	NA	2	6	2	1	1	2	4	2	0	1
Sly02g0332881	M1	NA	3	4	4	7	3	1	1	1	2	2
Sly02g0332891	M1	NA	402	408	526	495	280	9	6	6	12	42
Sly02g0332901	M1	NA	4	4	3	2	2	2	2	1	1	1
Sly02g0332911	M3	NA	48	64	38	29	49	25	33	15	65	128
Sly02g0332921	M3	NA	56	117	34	3	7	10	13	1	1	3
Sly02g0332931	M1	NA	3	2	2	2	2	1	0	1	1	1
Sly02g0332961	M11	NA	12	9	13	10	8	10	10	12	4	4
Sly02g0332991	M11	NA	1	1	2	1	1	2	2	2	1	0
Sly02g0333001	M11	NA	2	2	1	1	1	4	3	4	1	1
Sly02g0333011	M11	NA	1	1	2	2	1	5	3	3	1	0
Sly02g0333021	M12	NA	2	3	3	1	1	4	5	5	1	1
Sly02g0333041	M22	NA	3	3	3	2	4	3	3	4	6	10
Sly02g0333051	M1	NA	3	3	3	2	2	2	2	2	2	3
Sly02g0333071	M13	PDC2	94	95	77	244	286	66	83	140	116	131
Sly02g0333081	M12	NA	1	1	1	1	1	1	1	1	0	0
Sly02g0333091	M12	NA	2	1	2	1	0	13	10	14	1	1
Sly02g0333111	M1	NA	7	6	5	8	5	1	1	1	1	0
Sly02g0333121	M11	NA	23	22	32	40	23	29	24	31	14	11
Sly02g0333131	M6	NA	1	2	1	1	1	1	1	1	1	1
Sly02g0333151	M22	NA	9	7	8	6	6	11	6	10	3	4
Sly02g0333161	M1	NA	11	10	14	10	7	9	8	9	5	4
Sly02g0333171	M3	NA	34	36	31	21	23	30	32	26	28	36
Sly02g0333191	M1	NA	59	41	59	1	1	1	1	1	0	1
Sly02g0333201	M22	NA	1	0	1	0	0	1	0	2	0	0
Sly02g0333231	M6	SIERF.C6	78	123	37	1	4	113	144	33	1	2
Sly02g0333251	M12	NA	1	1	1	0	0	7	3	3	0	0
Sly02g0333261	M12	NA	1	1	1	0	0	4	4	3	0	0
Sly02g0333271	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0333281	M1	NA	301	299	297	228	200	221	224	224	216	209
Sly02g0333291	M3	NA	2	2	1	0	0	1	0	0	0	0
Sly02g0333301	M1	NA	21	18	15	1	1	1	1	1	1	0
Sly02g0333321	M11	NA	35	31	35	29	37	43	38	48	45	39
Sly02g0333331	M11	NA	63	57	69	59	68	68	59	81	74	81
Sly02g0333341	M11	NA	13	11	14	15	13	14	14	15	13	15
Sly02g0333351	M5	NA	59	88	30	12	23	48	79	23	9	23
Sly02g0333361	M12	NA	94	79	70	79	56	100	97	78	19	7
Sly02g0333461	M18	SIARF3	73	76	77	70	59	77	74	80	81	64
Sly02g0333471	M1	NA	3	2	3	1	1	1	1	1	1	1
Sly02g0333481	M1	NA	10	7	14	3	1	1	1	0	1	1
Sly02g0333491	M1	NA	3	3	2	1	0	1	1	1	1	0
Sly02g0333501	M3	NA	34	28	19	1	0	19	19	8	1	0
Sly02g0333511	M1	NA	10	11	12	8	10	10	10	9	8	7
Sly02g0333521	M22	NA	2	2	2	1	3	4	2	4	2	10
Sly02g0333531	M2	NA	10	10	9	7	7	8	9	8	13	13
Sly02g0333541	M12	NA	19	20	34	46	24	74	65	77	16	15
Sly02g0333551	M22	NA	5	4	3	3	3	4	3	4	3	3
Sly02g0333561	M19	NA	4	4	3	3	2	3	3	4	3	2
Sly02g0333571	M19	NA	42	50	41	50	59	37	36	35	39	47
Sly02g0333581	M4	NA	17	15	22	89	171	26	23	26	79	204
Sly02g0333591	M11	NA	25	26	26	40	34	34	32	39	35	34
Sly02g0333601	M12	NA	11	10	13	15	8	12	14	15	39	17
Sly02g0333611	M12	NA	11	19	16	55	41	33	46	69	215	96
Sly02g0333621	M12	NA	109	203	281	2007	1685	444	849	1212	6787	2817
Sly02g0333631	M1	NA	20	13	32	49	26	13	7	12	4	2
Sly02g0333651	M1	NA	43	42	47	41	35	34	41	35	50	46
Sly02g0333661	M3	NA	51	57	55	57	52	46	50	48	45	43
Sly02g0333671	M11	NA	204	181	229	148	121	205	186	218	175	202
Sly02g0333681	M11	NA	49	36	50	41	39	56	41	53	52	72

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0267111	M1	NA	13	13	12	18	13	7	7	6	7	6
Sly08g0267181	M22	NA	1	1	1	1	0	3	1	1	1	0
Sly08g0267191	M1	NA	30	26	39	48	12	4	5	3	1	1
Sly08g0267241	M22	NA	1	1	1	1	0	1	1	2	1	0
Sly08g0267261	M2	NA	4	5	4	5	2	2	4	3	4	2
Sly08g0267271	M13	NA	37	39	43	68	58	36	38	43	49	45
Sly08g0267281	M1	NA	62	66	61	51	39	48	47	44	41	30
Sly08g0267291	M1	NA	2	2	2	3	3	1	1	1	2	2
Sly08g0267301	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly08g0267321	M12	NA	8	7	8	11	14	12	13	13	14	17
Sly08g0267331	M3	NA	18	20	18	18	19	17	18	18	17	14
Sly08g0267341	M2	NA	22	22	26	23	25	21	24	20	25	23
Sly08g0267361	M12	NA	1	1	1	1	1	2	2	1	0	1
Sly08g0267371	M2	NA	15	15	16	13	23	13	14	14	29	62
Sly08g0267381	M19	NA	15	15	17	16	17	16	14	17	18	22
Sly08g0267391	M21	NA	4	2	3	2	2	4	2	2	2	2
Sly08g0267401	M1	NA	4	5	4	2	2	2	2	2	5	2
Sly08g0267411	M11	NA	57	55	66	112	149	108	87	127	93	120
Sly08g0267421	M1	NA	6	7	6	2	2	4	3	3	1	1
Sly08g0267451	M1	NA	2	3	2	2	1	2	2	1	1	1
Sly08g0267461	M12	NA	1	1	1	1	1	3	2	2	1	1
Sly08g0267481	M3	NA	2	1	1	1	1	1	1	1	1	1
Sly08g0267491	M2	NA	98	97	95	100	76	69	92	72	75	64
Sly08g0267521	M12	NA	8	9	10	11	9	8	14	14	25	29
Sly08g0267531	M12	NA	13	13	18	19	18	14	14	26	36	41
Sly08g0267541	M11	NA	22	20	26	22	10	32	32	39	15	12
Sly08g0267561	M15	NA	177	173	161	88	72	175	166	180	98	97
Sly08g0267581	M11	NA	201	192	226	468	546	297	301	341	534	696
Sly08g0267591	M6	NA	25	33	28	24	105	25	37	23	25	186
Sly08g0267621	M3	NA	46	60	42	31	36	42	44	32	22	29
Sly08g0267671	M12	NA	43	42	42	61	93	49	46	45	51	104
Sly08g0267681	M3	NA	32	29	27	17	6	28	31	20	7	2
Sly08g0267731	M1	NA	22	19	25	11	4	15	14	14	2	1
Sly08g0267741	M1	NA	1	1	1	1	0	1	1	1	1	0
Sly08g0267821	M12	NA	1	1	0	1	0	1	2	1	0	0
Sly08g0267831	M3	NA	3	4	3	3	3	2	3	3	2	2
Sly08g0267841	M1	NA	3	3	3	3	2	3	3	3	3	2
Sly08g0267851	M12	NA	32	28	35	23	19	35	37	35	57	56
Sly08g0267871	M19	NA	10	12	12	11	11	12	10	13	12	8
Sly08g0267881	M11	NA	14	14	12	13	14	15	12	14	17	14
Sly08g0267891	M12	NA	5	5	5	4	3	6	6	5	8	7
Sly08g0267901	M9	NA	14	17	14	12	10	17	22	15	28	30
Sly08g0267911	M9	NA	33	33	32	28	28	32	35	32	63	78
Sly08g0267951	M6	NA	2	4	2	0	1	4	5	2	4	1
Sly08g0267961	M12	NA	14	13	15	17	18	19	17	20	19	11
Sly08g0267981	M18	NA	7	7	8	6	4	9	8	10	7	8
Sly08g0268011	M3	SIGPS	34	37	34	45	45	26	29	28	48	45
Sly08g0268021	M3	NA	19	20	17	22	28	18	18	18	27	32
Sly08g0268051	M12	NA	1	1	1	0	0	1	1	1	1	0
Sly08g0268061	M12	NA	23	34	31	32	37	96	169	123	40	44
Sly08g0268071	M3	NA	2	3	1	1	0	2	2	1	0	0
Sly08g0268081	M3	NA	2	4	2	0	0	3	3	1	0	0
Sly08g0268091	M3	NA	4	4	2	0	1	3	4	1	0	0
Sly08g0268161	M15	NA	29	20	12	17	14	20	19	19	16	20
Sly08g0268171	M11	NA	7	7	7	6	5	5	7	9	7	6
Sly08g0268191	M12	NA	4	4	4	3	6	4	6	5	6	19
Sly08g0268201	M12	NA	1	1	2	5	2	2	1	1	8	5
Sly08g0268211	M11	NA	4	5	6	1	1	9	7	7	1	1
Sly08g0268221	M1	NA	3	4	5	11	6	2	3	4	12	7
Sly08g0268231	M12	NA	3	3	4	3	2	7	6	6	4	3
Sly08g0268251	M9	NA	1	1	1	0	0	2	3	1	1	1
Sly08g0268261	M19	NA	3	3	2	3	1	3	2	2	2	2
Sly08g0268271	M12	NA	92	95	95	98	98	134	165	131	129	135
Sly08g0268361	M3	NA	31	28	15	18	11	19	23	14	10	11
Sly08g0268371	M1	NA	34	32	32	22	14	3	2	2	3	2
Sly08g0268381	M2	NA	19	17	20	22	27	17	19	18	26	30
Sly08g0268411	M12	NA	107	107	122	131	153	118	124	134	159	181
Sly08g0268441	M8	NA	60	61	57	67	65	61	63	57	81	86
Sly08g0268451	M2	NA	19	19	20	23	23	17	20	15	29	32
Sly08g0268501	M19	NA	14	16	18	15	12	12	11	15	9	6
Sly08g0268511	M9	NA	1	2	1	1	2	2	3	2	3	12
Sly08g0268571	M3	NA	25	24	17	12	9	21	23	13	8	7
Sly08g0268581	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0268591	M19	NA	39	45	42	61	49	42	38	38	33	30
Sly08g0268601	M3	NA	17	18	16	13	16	10	14	11	12	14
Sly08g0268621	M1	NA	6	7	6	15	88	2	4	4	11	27
Sly08g0268631	M9	NA	1	2	1	1	2	2	3	2	3	6
Sly08g0268651	M3	SIAux/IAA29	177	190	91	13	3	97	81	26	2	1
Sly08g0268671	M19	NA	18	24	17	16	13	19	14	19	10	15
Sly08g0268681	M19	NA	10	11	9	6	5	8	5	7	6	5
Sly08g0268691	M19	NA	7	11	9	10	7	9	6	7	5	6
Sly08g0268701	M19	NA	14	17	15	11	10	14	9	10	8	9
Sly08g0268711	M19	NA	16	21	17	14	12	17	13	14	13	11
Sly08g0268721	M3	NA	20	20	17	14	14	18	14	15	15	22
Sly08g0268751	M1	NA	3	3	3	4	4	2	3	3	4	5
Sly08g0268821	M12	NA	8	8	11	7	5	11	12	13	13	8
Sly08g0268831	M3	NA	3	2	2	1	2	2	2	2	4	5
Sly08g0268971	M11	NA	4	5	5	5	4	6	5	6	11	8
Sly08g0268981	M3	NA	13	14	13	13	12	13	14	12	13	14
Sly08g0268991	M3	NA	20	19	17	19	20	14	13	12	13	14
Sly08g0269011	M12	NA	1	2	2	4	3	4	5	5	12	10
Sly08g0269021	M12	NA	1	1	1	3	2	3	4	4	14	14
Sly08g0269031	M9	NA	1	1	1	1	1	1	3	1	1	1
Sly08g0269041	M12	NA	22	22	25	36	32	30	29	29	44	37
Sly08g0269051	M3	NA	33	34	29	27	23	25	29	25	28	32
Sly08g0269081	M9	NA	35	32	30	27	24	35	39	33	37	25
Sly08g0269091	M11	NA	101	85	106	176	376	90	85	102	172	375
Sly08g0269101	M12	PPR-like30	5	5	5	6	7	6	5	5	7	8
Sly08g0269111	M19	NA	30	33	35	35	37	33	29	33	27	28
Sly08g0269121	M3	NA	42	37	40	36	32	35	37	35	39	35
Sly08g0269131	M12	NA	11	9	12	13	15	14	16	15	17	21
Sly08g0269141	M11	NA	12	12	16	12	4	20	17	20	9	1
Sly08g0269151	M3	SITPL6	16	17	14	11	3	12	10	11	6	2
Sly08g0269161	M19	NA	9	9	9	8	3	8	5	6	4	1
Sly08g0269231	M3	SILOX8	1	1	1	0	0	1	1	1	0	0
Sly08g0269261	M12	NA	9	11	12	21	35	10	12	12	23	55
Sly08g0269421	M10	NA	10	23	11	1	1	20	35	6	1	1
Sly08g0269481	M12	NA	11	11	11	13	4	16	18	17	11	3
Sly08g0269491	M1	NA	24	22	24	14	6	1	2	2	1	0
Sly08g0269501	M11	NA	109	103	106	77	90	126	119	115	94	139
Sly08g0269541	M12	NA	2	3	2	5	6	3	3	4	8	7
Sly08g0269551	M7	NA	2	3	1	1	2	2	3	1	2	5
Sly08g0269561	M3	NA	9	10	7	8	7	7	9	7	12	10
Sly08g0269581	M1	NA	4	5	6	4	2	1	1	1	1	1
Sly08g0269601	M12	APx-R	14	14	17	16	19	19	19	20	27	31
Sly08g0269611	M18	NA	11	13	16	16	18	18	14	18	21	20
Sly08g0269661	M1	NA	10	10	8	3	2	4	4	2	1	1
Sly08g0269671	M9	NA	16	17	17	9	4	19	21	16	5	3
Sly08g0269681	M3	EBF1	209	178	144	209	180	187	163	114	203	219
Sly08g0269691	M11	NA	34	32	31	48	56	41	39	43	58	92
Sly08g0269701	M19	NA	36	40	39	51	54	49	38	50	45	56
Sly08g0269721	M1	NA	18	17	19	18	20	15	13	17	17	17
Sly08g0269741	M1	NA	58	60	77	47	79	42	52	42	132	410
Sly08g0269771	M3	NA	83	78	73	66	46	70	86	46	33	26
Sly08g0269811	M3	NA	23	37	13	1	1	13	10	3	1	1
Sly08g0269821	M1	NA	143	144	138	97	100	104	103	100	113	102
Sly08g0269831	M1	NA	3	1	4	1	0	1	1	1	0	0
Sly08g0269871	M22	NA	1	0	1	0	0	8	0	4	0	0
Sly08g0269881	M11	NA	34	31	35	40	34	35	34	38	44	37
Sly08g0269891	M22	NA	298	240	278	152	123	297	275	245	77	122
Sly08g0269921	M12	NA	5	9	9	59	61	7	9	10	94	72

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0333691	M11	NA	16	13	25	10	6	24	19	33	17	11
Sly02g0333701	M6	NA	28	33	25	20	29	29	33	23	20	37
Sly02g0333711	M11	NA	2	2	2	26	135	1	1	6	193	387
Sly02g0333731	M22	NA	1	0	1	0	0	2	1	1	0	0
Sly02g0333741	M22	NA	2	1	1	0	0	3	1	3	1	0
Sly02g0333761	M3	NA	23	33	19	2	1	9	10	2	1	0
Sly02g0333771	M12	NA	16	15	16	23	12	26	21	22	10	3
Sly02g0333781	M18	NA	8	8	10	8	19	10	8	13	3	7
Sly02g0333801	M11	NA	1162	879	1781	933	666	2193	1511	2917	558	639
Sly02g0333811	M12	RING1a-like	12	12	11	7	6	13	14	14	8	5
Sly02g0333821	M12	NA	35	38	39	56	73	41	44	44	65	75
Sly02g0333831	M11	NA	3	3	4	6	6	6	6	6	9	9
Sly02g0333841	M1	CNR	30	31	43	310	194	25	39	27	321	359
Sly02g0333851	M1	NA	43	52	49	111	88	32	39	37	86	170
Sly02g0333861	M1	NA	6	5	4	3	2	1	1	1	1	1
Sly02g0333871	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0333881	M23	NA	7	4	3	1	1	17	8	8	5	1
Sly02g0333891	M11	NA	2	2	2	1	0	4	5	5	2	1
Sly02g0333901	M11	NA	59	56	69	204	288	138	120	193	245	350
Sly02g0333911	M1	NA	20	17	18	16	18	13	11	13	21	28
Sly02g0333921	M9	NA	19	22	16	16	14	20	22	21	18	13
Sly02g0333931	M11	NA	15	15	19	45	62	20	17	22	28	38
Sly02g0333941	M3	NA	1	4	2	3	3	1	1	1	4	4
Sly02g0333951	M3	NA	80	120	75	168	198	54	70	61	254	240
Sly02g0333961	M12	NA	68	41	60	2	0	398	341	268	4	1
Sly02g0333971	M12	NA	1	1	1	1	1	5	4	3	1	0
Sly02g0334031	M1	NA	10	4	16	2	1	1	1	1	0	0
Sly02g0334041	M3	NA	167	166	130	120	100	114	127	97	98	90
Sly02g0334051	M3	NA	3	2	0	0	0	1	0	0	0	0
Sly02g0334061	M1	NA	27	26	24	32	60	15	18	17	51	54
Sly02g0334071	M11	NA	109	91	167	138	97	163	153	198	84	32
Sly02g0334081	M12	NA	69	63	82	223	158	159	168	144	75	99
Sly02g0334111	M3	NA	2	2	1	0	1	1	1	1	1	0
Sly02g0334121	M9	NA	5	6	5	4	6	7	9	8	7	6
Sly02g0334141	M3	NA	41	42	41	46	52	37	40	40	56	58
Sly02g0334151	M22	NA	29	26	28	17	11	37	21	31	16	15
Sly02g0334161	M22	NA	17	15	17	19	17	16	15	17	15	12
Sly02g0334171	M11	NA	6	7	10	8	8	22	18	26	3	2
Sly02g0334181	M11	NA	4	3	5	3	1	8	7	9	2	1
Sly02g0334201	M11	NA	75	66	77	65	85	92	72	89	65	92
Sly02g0334211	M18	NA	19	19	19	23	26	21	18	23	33	30
Sly02g0334221	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0334231	M1	NA	6	4	6	3	3	4	4	4	2	3
Sly02g0334241	M1	NA	9	10	13	7	5	10	10	10	8	8
Sly02g0334251	M1	NA	2	2	2	0	0	1	1	1	0	0
Sly02g0334271	M3	NA	32	28	27	24	21	23	23	24	29	22
Sly02g0334291	M3	NA	16	14	13	9	9	13	21	9	11	14
Sly02g0334301	M11	NA	8	8	7	6	7	10	8	10	8	8
Sly02g0334311	M12	NA	1	1	1	1	2	2	2	3	8	10
Sly02g0334321	M3	NA	4	4	4	3	4	3	3	3	3	4
Sly02g0334331	M1	NA	61	61	60	61	63	45	43	44	63	65
Sly02g0334341	M22	NA	1	1	1	13	17	1	1	3	33	17
Sly02g0334351	M11	NA	115	81	136	29	12	122	87	110	4	2
Sly02g0334361	M3	NA	11	10	9	6	5	9	8	9	7	4
Sly02g0334371	M12	NA	24	24	30	141	699	47	63	66	462	1085
Sly02g0334381	M9	NA	23	20	20	50	45	29	31	32	38	39
Sly02g0334411	M12	NA	26	25	26	26	25	28	28	27	29	30
Sly02g0334421	M11	NA	17	13	19	21	37	34	24	37	34	35
Sly02g0334431	M14	NA	30	25	44	47	71	25	21	38	69	53
Sly02g0334441	M12	NA	18	18	15	33	51	19	20	20	27	32
Sly02g0334451	M3	NA	102	137	22	2	11	52	57	12	5	5
Sly02g0334471	M11	NA	20	22	21	25	24	23	23	25	41	36
Sly02g0334481	M1	HUP54	9	8	11	4	2	6	4	7	2	1
Sly02g0334491	M21	NA	2	2	3	2	1	2	1	2	1	1
Sly02g0334501	M1	NA	2	3	4	2	2	3	2	2	1	0
Sly02g0334511	M19	NA	43	43	43	42	54	34	27	33	29	39
Sly02g0334521	M3	NA	16	28	17	2	2	9	8	3	1	1
Sly02g0334531	M2	NA	229	240	181	205	173	172	212	143	187	214
Sly02g0334541	M11	NA	16	17	16	23	33	20	18	21	29	31
Sly02g0334551	M1	NA	36	32	33	33	37	33	28	32	30	37
Sly02g0334561	M12	NA	82	55	94	54	32	269	197	249	5	4
Sly02g0334571	M3	NA	28	26	25	20	19	27	24	25	21	18
Sly02g0334581	M12	NA	11	10	18	7	3	37	38	42	12	6
Sly02g0334591	M12	NA	6	5	3	1	1	9	8	5	1	1
Sly02g0334601	M11	NA	58	57	60	50	60	67	58	68	71	65
Sly02g0334611	M10	NA	2	4	3	1	0	6	6	3	0	0
Sly02g0334621	M1	NA	12	10	17	24	19	7	5	6	13	16
Sly02g0334631	M12	NA	35	41	40	40	25	56	48	52	32	23
Sly02g0334651	M11	NA	7	9	11	2	1	55	45	71	8	4
Sly02g0334661	M11	NA	18	19	31	12	12	30	34	34	13	22
Sly02g0334691	M22	NA	2	2	1	1	0	3	1	2	0	0
Sly02g0334701	M12	NA	2	3	3	1	1	3	3	2	1	0
Sly02g0334721	M11	NA	3	2	4	2	1	3	3	3	2	3
Sly02g0334731	M12	NA	5	6	7	9	6	9	8	9	8	5
Sly02g0334741	M3	NA	5	6	3	1	2	4	4	2	18	19
Sly02g0334761	M1	NA	9	9	9	6	5	5	3	4	1	1
Sly02g0334771	M19	SUMJ14	32	35	33	38	40	34	29	36	45	47
Sly02g0334781	M1	NA	22	20	22	20	21	14	14	13	19	15
Sly02g0334791	M1	NA	7	7	5	5	7	2	3	2	2	5
Sly02g0334801	M1	NA	46	51	30	87	85	17	17	16	61	52
Sly02g0334811	M1	NA	62	58	51	36	44	41	41	37	42	50
Sly02g0334821	M8	NA	64	67	55	92	101	62	75	61	122	157
Sly02g0334831	M22	NA	3	2	2	1	0	3	1	2	1	1
Sly02g0334841	M11	NA	14	16	17	18	11	20	17	20	11	4
Sly02g0334851	M3	NA	80	71	12	3	2	28	28	11	6	3
Sly02g0334861	M3	NA	44	33	6	3	2	9	9	4	2	2
Sly02g0334871	M1	NA	47	45	43	29	40	44	39	42	42	51
Sly02g0334881	M3	NA	110	101	26	1	1	55	46	30	3	1
Sly02g0334891	M6	NA	97	102	76	55	79	141	127	43	45	53
Sly02g0334901	M12	NA	2	2	2	5	3	5	3	3	2	3
Sly02g0334911	M1	NA	27	29	30	36	16	25	26	25	14	5
Sly02g0334941	M11	NA	174	155	202	464	669	235	248	310	562	914
Sly02g0334951	M1	NA	6	5	7	2	2	3	3	3	1	1
Sly02g0334961	M3	NA	52	62	58	51	53	46	52	42	39	57
Sly02g0334971	M19	NA	37	35	33	29	36	34	30	33	33	42
Sly02g0334981	M12	NA	13	13	12	16	18	13	13	13	22	26
Sly02g0334991	M11	NA	37	37	39	53	68	42	41	47	68	75
Sly02g0335001	M19	NA	14	15	14	18	28	15	13	14	18	18
Sly02g0335011	M10	NA	5	9	7	12	59	13	20	5	1	10
Sly02g0335021	M1	NA	22	23	25	16	14	19	19	25	9	5
Sly02g0335031	M3	NA	9	8	5	5	5	5	4	3	3	2
Sly02g0335041	M5	NA	101	159	51	22	46	85	120	34	22	47
Sly02g0335051	M19	NA	11	10	11	9	8	11	9	11	12	7
Sly02g0335061	M3	NA	238	230	206	189	198	182	191	187	237	224
Sly02g0335091	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0335101	M3	NA	5	6	4	7	7	4	5	3	9	8
Sly02g0335111	M2	NA	75	82	76	126	142	60	72	61	143	164
Sly02g0335121	M3	NA	15	17	13	6	7	14	14	12	10	11
Sly02g0335141	M3	NA	22	21	19	20	17	18	18	17	24	18
Sly02g0335151	M22	NA	2	1	2	5	6	3	2	2	1	1
Sly02g0335161	M22	NA	2	2	1	5	4	2	1	2	1	1
Sly02g0335171	M3	NA	2	1	1	0	0	1	1	1	1	0
Sly02g0335181	M1	NA	2	3	2	7	1	1	0	1	1	1
Sly02g0335191	M3	NA	175	215	123	59	83	110	113	26	41	44
Sly02g0335201	M5	NA	8	11	3	1	1	10	10	1	1	1
Sly02g0335221	M11	SITIR1-like1	19	18	29	20	12	28	21	31	31	18
Sly02g0335231	M12	NA	5	5	5	4	3	14	15	18	8	15
Sly02g0335241	M1	NA	55	53	52	41	52	40	41	40	45	58
Sly02g0335251	M3	NA	84	89	34	1	1	30	26	8	1	1
Sly02g0335261	M12	NA	1	1	1	1	1	1	1	4	3	3
Sly02g0335271	M3	NA	60	69	38	26	29	48	48	37	38	45
Sly02g0335281	M11	NA	1	1	1	0	1	2	1	2	0	1
Sly02g0335291	M18	NA	11	9	10	10	20	11	10	13	12	23
Sly02g0335301	M1	NA	2	2	2	2	1	2	2	2	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0270041	M1	NA	3	2	3	5	3	3	1	2	3	3
Sly08g0270071	M6	NA	9	13	8	6	6	9	12	9	8	8
Sly08g0270091	M10	NA	28	28	22	22	13	31	30	24	8	4
Sly08g0270101	M1	NA	3	2	2	2	2	1	1	1	1	1
Sly08g0270111	M1	NA	17	19	8	5	4	1	1	1	0	1
Sly08g0270131	M12	NA	29	29	29	31	33	28	31	30	39	41
Sly08g0270141	M12	NA	6	7	6	6	8	10	13	8	9	14
Sly08g0270151	M12	NA	42	32	33	184	65	27	42	48	408	175
Sly08g0270181	M1	NA	2	1	2	1	1	0	1	1	1	1
Sly08g0270191	M3	NA	293	326	287	325	329	238	258	220	355	393
Sly08g0270211	M3	NA	7	8	8	6	4	7	7	7	7	7
Sly08g0270281	M1	NA	6	5	5	5	4	3	4	4	3	2
Sly08g0270311	M6	NA	79	99	58	59	22	87	97	33	79	47
Sly08g0270321	M11	NA	39	27	56	19	7	46	43	51	5	2
Sly08g0270331	M18	NA	17	18	22	23	23	21	17	23	24	18
Sly08g0270381	M22	NA	4	2	6	1	1	5	3	3	0	1
Sly08g0270391	M12	NA	4	3	2	1	1	15	14	8	1	1
Sly08g0270401	M11	NA	4	3	3	1	1	14	10	13	1	1
Sly08g0270411	M11	NA	64	51	71	37	35	106	89	126	82	66
Sly08g0270431	M3	NA	65	68	48	6	3	52	45	27	5	1
Sly08g0270481	M11	NA	5	5	6	8	6	11	11	14	4	3
Sly08g0270491	M1	NA	1	2	2	1	1	1	1	1	1	0
Sly08g0270501	M1	NA	4	3	3	2	1	3	2	2	1	1
Sly08g0270831	M12	NA	17	17	21	19	17	32	30	36	31	29
Sly08g0270841	M11	NA	51	47	62	54	46	76	65	81	59	55
Sly08g0270871	M1	NA	383	332	322	270	177	270	284	253	186	111
Sly08g0270881	M12	NA	5	7	8	10	10	7	6	8	16	19
Sly08g0270891	M19	NA	7	9	10	16	13	10	7	11	14	18
Sly08g0270901	M1	NA	4	3	4	2	1	2	1	1	1	1
Sly08g0270921	M11	SICKX1	1	1	2	1	1	2	1	1	0	1
Sly08g0270951	M2	NA	49	47	39	41	37	33	39	31	47	52
Sly08g0270971	M1	NA	18	20	12	4	13	5	6	5	5	14
Sly08g0270981	M1	NA	596	526	555	470	383	402	432	423	447	417
Sly08g0270991	M22	NA	5	3	4	0	0	7	1	10	1	0
Sly08g0271001	M11	NA	15	13	19	5	4	36	31	43	4	1
Sly08g0271131	M3	NA	24	34	15	8	12	20	35	12	10	41
Sly08g0271161	M3	NA	9	12	4	1	1	5	4	3	0	1
Sly08g0271171	M11	NA	49	50	48	68	79	56	55	57	55	66
Sly08g0271181	M22	NA	1	1	1	1	5	1	1	1	1	6
Sly08g0271211	M11	NA	9	6	5	2	1	31	21	28	1	1
Sly08g0271221	M1	NA	29	29	35	42	26	20	17	19	23	24
Sly08g0271231	M10	UDP-dependent glyco	8	10	5	1	4	20	26	7	12	6
Sly08g0271251	M19	NA	6	7	7	7	6	6	7	6	6	6
Sly08g0271261	M3	NA	25	31	11	1	1	12	13	3	1	1
Sly08g0271271	M4	NA	12	11	16	184	671	19	16	14	104	436
Sly08g0271281	M10	NA	4	5	3	1	1	12	16	6	1	1
Sly08g0271291	M1	NA	4	3	3	1	1	1	1	1	1	1
Sly08g0271321	M1	NA	2	5	2	1	1	1	1	1	1	0
Sly08g0271361	M3	NA	23	27	21	24	23	19	21	18	21	23
Sly08g0271401	M4	NA	8	5	16	49	311	20	12	15	29	402
Sly08g0271421	M12	NA	3	3	2	2	3	3	4	3	3	3
Sly08g0271441	M3	NA	4	6	2	1	1	2	3	2	1	1
Sly08g0271451	M5	NA	30	34	24	27	32	31	32	25	25	27
Sly08g0271511	M12	NA	2	5	4	7	2	5	5	6	11	7
Sly08g0271521	M1	NA	49	51	47	52	57	46	41	42	55	65
Sly08g0271531	M12	NA	1	1	2	2	2	3	4	4	9	5
Sly08g0271561	M12	NA	0	2	1	1	1	1	2	2	1	1
Sly08g0271581	M11	NA	36	38	48	72	100	77	74	88	77	109
Sly08g0271591	M3	NA	8	7	7	7	4	6	7	6	5	3
Sly08g0271601	M12	NA	59	62	63	75	83	71	69	72	61	62
Sly08g0271611	M12	SIPP2C7	23	23	21	25	17	26	26	23	21	15
Sly08g0271621	M12	NA	221	221	237	217	187	208	240	242	266	255
Sly08g0271631	M11	NA	48	48	50	85	56	60	54	70	121	75
Sly08g0271641	M3	NA	19	28	16	12	51	13	19	10	6	40
Sly08g0271651	M6	NA	29	50	28	19	97	26	30	18	9	37
Sly08g0271661	M1	NA	45	45	46	43	47	40	41	47	62	62
Sly08g0271671	M1	NA	1	1	2	2	1	1	1	1	1	0
Sly08g0271681	M3	NA	14	14	13	14	10	13	12	13	11	8
Sly08g0271791	M2	NA	102	99	88	75	62	74	87	70	82	72
Sly08g0271801	M12	NA	1	2	1	1	1	6	5	4	0	0
Sly08g0271811	M1	SILOG5	97	101	75	52	65	20	21	14	19	46
Sly08g0271841	M5	NA	21	28	19	11	11	23	23	19	15	16
Sly08g0271861	M3	NA	2	2	2	1	0	1	1	1	1	1
Sly08g0271871	M3	NA	2	2	2	1	1	2	2	1	1	1
Sly08g0271881	M3	NA	15	16	10	5	4	10	14	8	4	5
Sly08g0271901	M3	NA	294	291	273	192	143	243	259	205	141	126
Sly08g0271911	M1	NA	2	2	3	4	5	1	1	1	6	5
Sly08g0271921	M1	NA	438	436	467	316	217	308	328	288	201	139
Sly08g0271931	M11	NA	1	1	1	0	1	1	1	1	0	0
Sly08g0271961	M22	NA	1	1	1	1	0	1	1	1	0	0
Sly08g0271971	M1	NA	5	5	5	5	2	3	2	3	1	1
Sly08g0271981	M11	NA	45	32	85	142	160	210	145	281	250	307
Sly08g0271991	M1	NA	4	2	4	1	0	1	2	2	1	1
Sly08g0272011	M9	NA	20	20	17	17	4	31	37	25	10	2
Sly08g0272021	M12	NA	9	7	6	10	12	11	9	8	9	8
Sly08g0272031	M3	NA	10	11	11	17	9	7	9	9	16	12
Sly08g0272041	M12	NA	4	6	5	37	51	16	33	17	76	103
Sly08g0272051	M1	NA	49	46	48	57	62	40	36	40	49	54
Sly08g0272061	M12	NA	43	51	52	66	81	54	53	56	90	98
Sly08g0272071	M11	NA	55	57	67	141	181	84	83	99	172	217
Sly08g0272091	M11	NA	6	4	11	11	4	20	22	28	14	4
Sly08g0272101	M12	NA	1	2	1	2	2	5	9	6	19	30
Sly08g0272131	M1	NA	19	15	8	2	2	3	4	2	1	1
Sly08g0272141	M1	NA	11	8	14	5	3	8	10	6	2	1
Sly08g0272161	M1	NA	77	68	85	80	95	56	53	76	83	98
Sly08g0272171	M9	NA	42	53	26	58	98	54	69	47	194	130
Sly08g0272181	M3	NA	4	5	4	2	1	3	3	2	1	1
Sly08g0272191	M11	NA	61	59	68	65	68	92	83	90	39	42
Sly08g0272201	M3	NA	14	15	12	16	18	12	12	12	14	12
Sly08g0272211	M13	NA	16	12	22	43	40	19	17	33	26	22
Sly08g0272221	M3	NA	117	126	84	65	48	60	68	50	41	36
Sly08g0272231	M3	NA	112	133	79	66	44	66	61	51	35	26
Sly08g0272241	M3	GRL1	91	129	59	71	42	75	110	52	51	50
Sly08g0272251	M12	NA	7	7	8	10	11	23	19	28	24	21
Sly08g0272271	M1	SlHDA5	28	28	32	27	25	29	24	29	32	37
Sly08g0272281	M20	NA	19	17	24	16	16	18	15	16	9	14
Sly08g0272331	M1	NA	2	1	2	1	1	1	1	1	0	0
Sly08g0272341	M1	NA	19	12	13	3	3	8	8	4	1	2
Sly08g0272351	M1	NA	5	4	4	3	3	4	2	3	1	1
Sly08g0272381	M11	NA	25	22	24	29	29	26	28	28	37	32
Sly08g0272391	M3	NA	122	167	77	59	51	95	104	35	48	42
Sly08g0272401	M3	NA	49	51	45	43	60	28	33	28	38	47
Sly08g0272461	M22	NA	3	1	2	1	0	18	3	15	0	0
Sly08g0272481	M23	NA	1	0	1	0	0	1	1	1	0	0
Sly08g0272491	M22	NA	2	1	1	1	1	2	1	1	1	1
Sly08g0272501	M22	NA	2	1	1	0	0	3	2	1	1	2
Sly08g0272511	M1	NA	300	337	463	1180	2019	143	150	194	870	4117
Sly08g0272561	M1	NA	59	66	69	71	66	60	61	64	76	68
Sly08g0272661	M1	NA	69	67	63	46	51	41	43	39	38	40
Sly08g0272671	M22	NA	5	1	3	0	0	27	5	16	0	0
Sly08g0272681	M22	NA	13	3	10	0	0	167	10	92	1	0
Sly08g0272691	M1	NA	9	12	11	8	6	9	8	8	3	2
Sly08g0272701	M3	SIJMJ18	7	7	6	5	3	6	5	4	1	1
Sly08g0272711	M19	NA	4	5	4	3	2	5	2	4	1	1
Sly08g0272721	M19	NA	3	5	5	3	3	4	3	3	1	1
Sly08g0272731	M11	NA	31	22	35	51	48	37	33	50	35	33
Sly08g0272741	M9	NA	17	10	9	15	16	15	17	10	3	9
Sly08g0272751	M8	NA	21	19	19	19	20	21	25	17	19	13
Sly08g0272761	M1	NA	27	27	28	26	18	24	22	25	13	14
Sly08g0272771	M11	NA	125	103	124	141	289	131	127	143	219	301
Sly08g0272781	M12	NA	202	199	239	241	189	268	276	296	264	228

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0335321	M12	NA	6	7	6	6	7	9	8	9	8	10
Sly02g0335331	M3	NA	15	20	6	1	1	2	1	1	1	1
Sly02g0335341	M12	NA	20	18	16	7	4	22	23	34	7	2
Sly02g0335351	M12	SlJMJ13	9	10	10	13	11	11	12	11	15	10
Sly02g0335371	M1	NA	9	8	9	2	2	5	6	5	1	1
Sly02g0335391	M3	NA	7	9	8	2	1	6	8	8	3	1
Sly02g0335401	M1	NA	12	12	13	3	1	6	5	5	1	0
Sly02g0335421	M12	NA	1	1	1	1	0	2	2	1	1	1
Sly02g0335431	M1	NA	3	3	2	1	1	2	1	2	1	1
Sly02g0335441	M1	SlCycD6;3	1	2	1	1	1	1	1	1	1	1
Sly02g0335451	M1	NA	4	4	4	5	4	4	4	4	5	3
Sly02g0335461	M1	NA	14	14	11	3	2	5	4	4	2	2
Sly02g0335471	M2	NA	74	73	68	58	68	59	67	60	67	80
Sly02g0335481	M3	NA	42	45	32	32	37	33	39	31	41	50
Sly02g0335491	M1	NA	33	35	29	10	8	20	20	16	8	5
Sly02g0335501	M12	NA	2	1	2	1	1	3	3	2	0	0
Sly02g0335511	M23	NA	1	1	1	0	0	2	1	1	1	0
Sly02g0335521	M22	NA	1	0	1	0	0	4	1	3	0	0
Sly02g0335571	M1	NA	1653	1618	1904	114	114	34	9	8	1	1
Sly02g0335581	M1	NA	911	940	956	10	6	27	5	1	1	1
Sly02g0335591	M1	NA	7	8	2	1	0	1	1	1	0	0
Sly02g0335601	M3	NA	5	10	2	1	1	1	1	1	1	1
Sly02g0335611	M1	NA	10	19	10	7	5	1	1	1	0	0
Sly02g0335621	M1	NA	3	9	3	2	1	1	1	1	1	0
Sly02g0335641	M6	NA	6	12	5	1	1	11	13	2	1	1
Sly02g0335651	M3	NA	5	4	3	3	3	4	3	3	4	5
Sly02g0335661	M3	NA	121	136	59	24	26	47	61	13	11	22
Sly02g0335711	M1	NA	10	10	17	26	17	3	2	3	1	1
Sly02g0335751	M3	NA	5	6	5	6	2	3	3	1	1	0
Sly02g0335761	M1	NA	4	6	6	5	2	2	2	1	1	1
Sly02g0335781	M1	NA	15	16	15	26	28	14	12	16	26	23
Sly02g0335791	M12	NA	14	13	10	12	15	16	16	14	15	23
Sly02g0335801	M1	NA	96	102	86	329	276	55	26	33	43	126
Sly02g0335811	M1	NA	16	22	11	10	8	1	1	1	1	1
Sly02g0335821	M13	NA	64	64	72	131	189	68	68	91	136	157
Sly02g0335831	M11	NA	34	32	56	38	31	58	61	75	35	35
Sly02g0335841	M1	NA	6	3	7	1	1	5	4	2	1	1
Sly02g0335871	M3	NA	3	4	3	3	3	3	3	3	3	2
Sly02g0335881	M1	PPR-like36	11	9	11	13	17	8	9	8	15	17
Sly02g0335891	M9	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0335901	M12	NA	34	36	35	45	37	73	69	83	73	49
Sly02g0335911	M18	NA	6	8	5	10	7	11	9	12	13	9
Sly02g0335921	M3	NA	10	8	8	6	7	6	7	7	8	11
Sly02g0335931	M11	NA	113	120	127	140	122	133	125	154	131	123
Sly02g0335991	M1	NA	2	3	2	22	21	1	1	1	1	1
Sly02g0336001	M12	NA	69	51	105	290	371	184	160	191	210	592
Sly02g0336021	M11	NA	234	161	260	227	51	561	505	716	373	42
Sly02g0336031	M12	NA	155	148	162	116	96	339	306	365	216	167
Sly02g0336041	M12	NA	149	136	145	115	99	278	280	292	89	109
Sly02g0336051	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0336061	M3	NA	17	25	8	1	1	8	11	4	1	1
Sly02g0336081	M1	NA	5	13	11	3	1	1	1	1	1	1
Sly02g0336101	M3	NA	1	2	1	1	1	1	1	1	0	1
Sly02g0336111	M1	NA	36	80	48	28	20	7	6	2	1	2
Sly02g0336121	M1	NA	1	1	1	5	5	1	1	1	1	1
Sly02g0336131	M1	NA	33	48	30	67	37	11	10	5	2	1
Sly02g0336141	M5	NA	9	25	8	3	2	14	15	3	1	1
Sly02g0336151	M5	NA	6	17	4	2	1	9	9	2	1	1
Sly02g0336201	M6	NA	36	59	38	79	85	22	35	17	78	121
Sly02g0336211	M3	GA2ox7	1	1	1	1	0	0	0	0	0	0
Sly02g0336221	M2	NA	124	149	131	145	131	84	106	86	132	123
Sly02g0336231	M2	NA	50	48	49	56	64	44	47	50	61	81
Sly02g0336241	M1	NA	23	20	20	11	12	12	12	11	11	10
Sly02g0336251	M9	NA	7	7	5	1	2	16	19	15	4	4
Sly02g0336261	M12	PPR-like31	2	3	2	3	3	3	4	4	5	3
Sly02g0336271	M3	NA	2	2	2	5	4	2	2	2	2	2
Sly02g0336281	M1	NA	1	1	1	1	1	1	0	1	1	1
Sly02g0336291	M11	NA	1	1	1	0	0	2	1	2	0	0
Sly02g0336301	M3	NA	1	1	1	1	0	1	1	1	0	0
Sly02g0336311	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0336321	M23	NA	1	1	1	1	1	1	1	1	0	0
Sly02g0336341	M22	NA	2	2	2	1	2	3	1	2	1	1
Sly02g0336351	M9	NA	91	96	83	134	163	100	140	127	253	254
Sly02g0336361	M3	NA	9	8	9	11	16	7	8	7	13	16
Sly02g0336381	M1	NA	12	15	9	11	31	3	3	2	1	3
Sly02g0336391	M1	NA	6	8	7	10	12	3	3	3	3	1
Sly02g0336401	M11	NA	2	2	2	2	3	3	3	4	2	3
Sly02g0336411	M19	NA	9	10	10	9	13	10	10	9	10	11
Sly02g0336421	M22	NA	1	1	1	1	0	1	1	1	0	1
Sly02g0336431	M18	NA	5	6	5	6	7	8	7	5	3	2
Sly02g0336441	M12	NA	9	9	8	9	13	14	13	11	7	5
Sly02g0336451	M10	NA	3	3	3	3	3	3	3	3	3	3
Sly02g0336461	M22	NA	1	1	1	1	1	2	1	2	1	1
Sly02g0336481	M12	NA	140	145	137	88	74	498	524	490	250	225
Sly02g0336491	M11	NA	77	71	81	87	77	77	81	87	82	86
Sly02g0336501	M1	NA	1	1	1	0	1	1	1	1	0	0
Sly02g0336511	M22	NA	3	2	3	1	1	4	2	2	1	1
Sly02g0336521	M11	NA	144	129	122	123	143	145	148	154	161	184
Sly02g0336531	M1	NA	46	42	49	57	71	38	43	46	71	86
Sly02g0336541	M11	NA	27	24	28	39	95	38	35	48	75	129
Sly02g0336551	M3	NA	3	4	1	0	0	1	1	1	0	0
Sly02g0336561	M12	NA	1	1	1	1	1	4	3	6	1	2
Sly02g0336571	M1	NA	29	33	28	33	31	23	23	23	29	32
Sly02g0336581	M12	NA	9	8	9	2	1	106	89	80	1	1
Sly02g0336591	M11	NA	8	7	9	5	3	11	9	10	1	1
Sly02g0336601	M11	NA	17	16	24	16	14	26	25	28	10	11
Sly02g0336611	M11	NA	86	68	185	291	270	188	145	237	101	117
Sly02g0336621	M1	NA	3	2	4	11	25	2	1	1	1	1
Sly02g0336631	M11	NA	118	60	148	2	3	355	238	339	6	3
Sly02g0336641	M11	NA	54	48	69	52	9	128	111	151	28	2
Sly02g0336651	M11	NA	10	8	8	1	3	9	8	9	1	1
Sly02g0336661	M3	NA	34	34	22	6	4	16	23	10	5	1
Sly02g0336671	M18	STS4	13	16	19	44	72	21	19	24	39	44
Sly02g0336681	M11	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0336701	M9	NA	29	30	25	51	61	31	37	35	86	106
Sly02g0336711	M1	NA	5	3	6	3	2	1	1	2	1	1
Sly02g0336721	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0336741	M3	NA	10	13	6	3	1	2	3	1	1	1
Sly02g0336751	M11	NA	292	255	337	668	910	369	357	420	530	771
Sly02g0336761	M9	NA	18	24	17	135	74	63	65	45	266	83
Sly02g0336771	M5	NA	15	15	15	14	13	16	16	14	13	14
Sly02g0336781	M10	NA	8	8	8	10	9	9	9	8	5	5
Sly02g0336791	M23	NA	1	1	1	1	0	1	1	1	1	0
Sly02g0336841	M12	NA	1	1	1	1	0	1	1	1	0	0
Sly02g0336881	M1	NA	10	10	10	6	10	8	6	6	2	2
Sly02g0336901	M1	NA	46	50	46	35	40	25	28	22	35	31
Sly02g0336911	M11	NA	44	38	48	53	38	85	75	92	43	32
Sly02g0336921	M11	NA	32	27	27	36	43	33	30	35	36	46
Sly02g0336981	M22	NA	36	28	24	52	60	81	43	54	7	9
Sly02g0336991	M10	NA	3	7	9	6	20	16	17	5	2	9
Sly02g0337001	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly02g0337041	M12	NA	77	75	79	62	76	105	107	122	97	97
Sly02g0337051	M19	NA	6	7	6	5	5	6	5	6	6	4
Sly02g0337061	M22	NA	7	6	5	5	4	6	6	7	6	3
Sly02g0337071	M10	NA	36	41	31	40	42	43	56	36	54	49
Sly02g0337081	M11	NA	10	11	12	18	20	18	16	21	15	11
Sly02g0337101	M3	SlJMJ17	30	30	26	22	23	26	28	24	24	22
Sly02g0337121	M9	NA	139	200	101	47	61	271	411	231	39	138
Sly02g0337131	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0337141	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0337161	M12	NA	43	48	53	134	134	60	53	55	7	12
Sly02g0337171	M3	NA	37	33	27	23	29	30	36	31	32	28
Sly02g0337181	M21	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0337191	M22	NA	1	1	1	1	0	2	1	2	0	0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0272861	M11	NA	48	47	45	41	42	56	50	48	36	39
Sly08g0272871	M12	NA	35	34	33	31	34	34	34	36	39	40
Sly08g0272881	M18	NA	9	11	12	13	18	12	10	12	11	14
Sly08g0272891	M5	NA	33	48	14	7	4	24	24	7	3	1
Sly08g0272901	M20	NA	51	46	55	45	31	41	37	44	36	36
Sly08g0272911	M22	NA	7	4	5	4	4	12	6	17	4	5
Sly08g0272931	M3	NA	20	26	17	10	10	11	12	11	9	10
Sly08g0272941	M3	NA	12	15	10	7	5	7	6	4	6	7
Sly08g0272951	M1	NA	19	24	15	10	9	8	8	6	8	9
Sly08g0272961	M1	NA	24	28	17	15	11	12	8	6	11	13
Sly08g0272971	M11	NA	54	53	64	37	38	62	51	66	19	30
Sly08g0272991	M12	PFK6	39	47	48	42	11	64	70	86	35	7
Sly08g0273001	M1	NA	118	111	123	115	126	94	96	97	91	112
Sly08g0273011	M19	NA	26	25	30	34	33	23	20	27	25	30
Sly08g0273021	M22	NA	3	3	4	4	5	3	2	4	7	8
Sly08g0273031	M11	NA	85	71	73	68	73	81	72	90	102	111
Sly08g0273051	M1	NA	8	7	9	7	5	6	6	7	2	1
Sly08g0273071	M12	NA	1	1	1	0	0	1	2	1	0	0
Sly08g0273081	M19	NA	65	67	63	77	81	69	61	65	65	98
Sly08g0273091	M3	NA	23	28	19	12	15	17	21	6	2	3
Sly08g0273111	M12	NA	1	1	3	1131	1727	1	3	8	6629	5890
Sly08g0273151	M22	NA	1	1	1	0	0	1	1	1	0	1
Sly08g0273161	M12	NA	8	9	8	10	10	10	9	10	12	15
Sly08g0273181	M3	NA	7	9	5	1	1	2	2	1	0	1
Sly08g0273191	M1	NA	2	4	2	1	1	1	1	1	0	1
Sly08g0273201	M1	CDKA;1-3	43	30	39	9	3	27	20	22	2	1
Sly08g0273221	M1	NA	9	10	4	13	9	2	2	1	2	2
Sly08g0273231	M3	NA	4	3	3	2	3	2	2	2	5	7
Sly08g0273241	M3	NA	7	9	6	6	10	4	5	3	3	5
Sly08g0273251	M22	NA	1	1	1	0	0	2	1	2	0	0
Sly08g0273261	M4	NA	4	4	4	4	7	5	5	4	8	19
Sly08g0273271	M12	NA	1	1	1	2	1	1	1	2	1	1
Sly08g0273281	M9	NA	1	2	2	9	20	3	3	3	6	27
Sly08g0273291	M7	NA	42	66	36	27	45	54	77	34	23	47
Sly08g0273331	M1	NA	5	5	5	1	1	1	1	1	1	0
Sly08g0273351	M3	NA	5	7	3	1	1	2	2	1	1	0
Sly08g0273371	M3	NA	24	26	25	23	13	18	23	17	18	16
Sly08g0273381	M12	NA	2	1	2	1	1	4	3	3	1	1
Sly08g0273391	M11	NA	20	19	22	29	30	19	22	23	30	31
Sly08g0273411	M11	NA	12	11	16	21	25	20	14	21	16	22
Sly08g0273421	M11	NA	28	23	37	41	60	41	34	51	39	48
Sly08g0273431	M1	NA	41	41	38	31	29	38	35	35	33	33
Sly08g0273451	M1	NA	25	24	28	19	15	26	25	24	19	18
Sly08g0273461	M23	NA	1	1	1	1	1	1	1	1	1	0
Sly08g0273471	M12	NA	17	20	21	26	26	25	25	25	32	36
Sly08g0273481	M12	NA	16	19	17	20	27	21	23	21	37	51
Sly08g0273491	M12	NA	3	3	3	4	2	3	3	4	3	1
Sly08g0273511	M12	NA	7	7	7	5	7	7	9	8	5	4
Sly08g0273531	M3	SlERF.H8	1	2	1	0	1	0	0	0	0	0
Sly08g0273551	M1	NA	12	14	19	10	9	4	3	3	3	16
Sly08g0273561	M8	NA	49	54	49	56	61	50	56	51	82	114
Sly08g0273571	M12	NA	16	27	61	1589	1435	156	199	391	1699	1145
Sly08g0273581	M12	NA	17	27	36	676	659	67	95	198	1086	743
Sly08g0273591	M12	NA	1	1	2	90	55	3	7	13	282	44
Sly08g0273611	M11	NA	2	1	2	0	0	15	12	17	0	0
Sly08g0273621	M11	CCD9	3	2	3	1	1	22	16	20	1	1
Sly08g0273631	M18	NA	45	43	51	41	44	52	42	54	44	59
Sly08g0273641	M2	NA	11	14	15	5	5	13	15	12	3	4
Sly08g0273651	M9	NA	25	25	25	31	20	38	40	33	18	10
Sly08g0273661	M6	NA	3	6	4	2	2	5	6	4	1	1
Sly08g0273671	M7	NA	2	3	2	1	1	3	4	2	1	1
Sly08g0273681	M6	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0273701	M3	NA	28	28	16	14	14	9	11	7	14	11
Sly08g0273711	M14	NA	70	73	127	247	312	66	71	100	287	208
Sly08g0273721	M16	NA	1	1	1	3	4	1	1	1	5	4
Sly08g0273731	M1	NA	61	64	59	59	52	40	44	44	51	48
Sly08g0273751	M3	NA	5	5	5	2	1	3	4	2	1	1
Sly08g0273761	M11	NA	9	10	10	12	9	12	11	14	8	3
Sly08g0273771	M1	NA	2	2	1	1	2	1	1	1	1	1
Sly08g0273781	M3	NA	75	79	64	49	48	52	51	38	35	33
Sly08g0273811	M11	NA	33	37	41	26	24	41	38	39	35	32
Sly08g0273821	M19	NA	9	11	14	7	7	13	9	11	11	8
Sly08g0273831	M18	NA	3	3	5	3	2	5	4	5	3	2
Sly08g0273841	M19	NA	33	33	43	18	11	31	23	32	18	15
Sly08g0273851	M1	NA	1	2	2	1	1	2	1	1	1	1
Sly08g0273881	M1	NA	25	23	30	21	13	19	19	22	13	7
Sly08g0273891	M19	NA	17	17	19	21	28	17	15	19	20	20
Sly08g0273921	M5	NA	50	50	35	35	37	48	56	32	30	38
Sly08g0273931	M11	NA	1	1	1	1	0	1	1	2	1	0
Sly08g0273941	M9	NA	1	1	1	1	0	1	2	1	0	1
Sly08g0273951	M2	NA	255	246	260	353	341	218	296	216	317	346
Sly08g0273961	M20	NA	183	143	253	10	3	148	117	121	4	3
Sly08g0273971	M11	NA	30	30	34	32	35	38	34	38	30	34
Sly08g0273981	M1	SlPRMT7	14	14	13	4	2	12	11	12	3	1
Sly08g0273991	M19	PPR-like41	18	19	18	16	15	18	16	18	18	17
Sly08g0274001	M1	NA	13	14	13	13	16	10	11	11	12	15
Sly08g0274021	M19	NA	113	115	99	92	84	98	88	95	73	64
Sly08g0274031	M12	NA	54	52	44	40	28	234	251	305	92	40
Sly08g0274041	M1	NA	27	30	22	20	19	15	14	12	37	21
Sly08g0274051	M1	NA	26	27	22	13	8	7	6	6	3	1
Sly08g0274071	M1	NA	2	3	2	0	0	2	1	1	1	0
Sly08g0274081	M19	NA	5	5	5	3	3	5	4	4	3	3
Sly08g0274091	M20	DCL3	9	8	11	9	8	10	7	9	5	4
Sly08g0274131	M11	NA	7	8	9	6	6	8	7	9	3	2
Sly08g0274141	M11	NA	5	5	6	3	2	9	7	7	2	1
Sly08g0274151	M1	NA	150	137	239	288	173	12	5	7	2	1
Sly08g0274161	M12	NA	14	16	12	6	6	18	21	20	13	12
Sly08g0274171	M11	NA	12	11	11	8	7	17	14	17	9	6
Sly08g0274181	M3	NA	31	31	27	36	44	22	27	25	41	45
Sly08g0274231	M3	NA	1	1	1	1	8	1	1	1	0	2
Sly08g0274251	M3	NA	4	1	1	1	1	2	2	1	0	1
Sly08g0274261	M3	NA	9	2	2	0	0	3	3	3	0	0
Sly08g0274271	M3	NA	99	102	54	2	14	10	17	4	1	9
Sly08g0274281	M3	NA	37	38	16	0	0	4	6	1	1	1
Sly08g0274291	M1	NA	11	9	5	6	3	3	3	3	2	1
Sly08g0274301	M11	NA	2	2	2	2	1	2	3	2	2	1
Sly08g0274311	M3	NA	23	24	16	2	2	15	10	2	1	1
Sly08g0274351	M3	NA	158	189	99	2	1	25	34	7	1	1
Sly08g0274361	M19	NA	31	34	34	36	46	35	31	35	59	72
Sly08g0274371	M11	NA	33	28	31	45	77	46	42	51	69	123
Sly08g0274401	M3	NA	3	4	2	2	3	2	3	1	6	11
Sly08g0274411	M11	NA	20	19	21	20	26	22	23	25	34	48
Sly08g0274421	M9	NA	39	38	36	56	43	45	62	47	57	46
Sly08g0274451	M7	NA	1	2	1	1	9	2	4	3	3	56
Sly08g0274511	M9	NA	0	1	1	0	0	2	2	1	0	0
Sly08g0274531	M3	NA	2	4	3	4	5	2	3	2	3	5
Sly08g0274541	M12	NA	5	6	8	67	146	7	8	5	4	9
Sly08g0274551	M11	NA	5	4	5	53	107	7	5	6	4	6
Sly08g0274571	M3	NA	11	16	8	1	1	14	7	3	1	1
Sly08g0274591	M2	NA	9	7	8	3	5	5	5	2	1	1
Sly08g0274601	M22	NA	6	1	7	0	1	45	1	38	0	0
Sly08g0274621	M3	NA	2	2	1	1	1	2	2	1	1	1
Sly08g0274631	M3	NA	26	24	20	4	3	9	12	5	1	1
Sly08g0274641	M1	NA	14	16	10	3	2	4	4	2	1	1
Sly08g0274681	M11	NA	10	11	12	19	19	12	13	14	23	22
Sly08g0274711	M3	NA	66	85	52	46	63	52	69	42	44	64
Sly08g0274741	M1	NA	64	64	57	43	42	53	49	48	35	39
Sly08g0274751	M3	NA	1	2	1	2	2	1	1	0	0	1
Sly08g0274761	M15	NA	18	17	15	19	18	18	17	18	21	21
Sly08g0274771	M3	NA	44	44	38	37	48	37	40	35	60	61
Sly08g0274781	M1	NA	20	21	21	21	25	17

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0337201	M3	NA	93	94	63	49	47	43	53	35	54	65
Sly02g0337211	M20	NA	14	13	18	5	2	9	5	9	1	1
Sly02g0337221	M11	NA	219	199	236	243	216	241	237	251	267	269
Sly02g0337231	M2	NA	112	111	123	257	697	101	121	121	299	563
Sly02g0337251	M1	ACO4	109	99	49	17	13	27	18	16	2	3
Sly02g0337261	M3	NA	19	21	17	22	21	17	18	13	20	17
Sly02g0337271	M3	NA	5	4	4	1	1	4	4	3	1	1
Sly02g0337281	M1	NA	2	1	1	1	2	1	1	1	1	1
Sly02g0337291	M1	NA	2	2	2	2	3	1	1	1	1	1
Sly02g0337311	M18	NA	2	3	2	2	2	3	2	2	2	1
Sly02g0337321	M11	NA	4	4	3	3	3	4	4	4	3	4
Sly02g0337331	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0337351	M1	NA	3	5	4	3	4	3	3	2	3	3
Sly02g0337361	M1	NA	52	46	49	45	40	46	38	45	45	49
Sly02g0337371	M1	NA	2	2	2	2	3	1	1	1	2	2
Sly02g0337381	M1	NA	38	33	32	33	34	31	30	30	35	33
Sly02g0337391	M2	SISDG50	26	26	27	22	26	25	26	26	33	32
Sly02g0337401	M11	psy2	16	14	17	22	44	16	18	20	31	54
Sly02g0337421	M6	NA	16	13	10	1	1	17	17	3	1	1
Sly02g0337431	M6	NA	11	11	11	0	0	16	16	2	0	0
Sly02g0337441	M3	NA	24	23	20	1	1	21	18	4	1	1
Sly02g0337451	M3	NA	1	1	1	1	0	1	1	0	1	0
Sly02g0337461	M3	NA	77	72	53	45	51	44	48	41	54	58
Sly02g0337471	M3	NA	305	328	237	806	887	107	154	70	180	339
Sly02g0337481	M13	NA	99	101	125	352	395	94	102	112	167	326
Sly02g0337501	M1	NA	42	43	42	40	40	35	36	35	38	38
Sly02g0337511	M11	NA	4	4	5	11	10	7	6	8	23	13
Sly02g0337521	M3	NA	94	97	76	39	51	76	78	45	48	84
Sly02g0337531	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0337541	M1	NA	8	11	13	3	2	2	2	1	1	1
Sly02g0337551	M11	NA	13	13	14	13	14	14	13	14	12	11
Sly02g0337581	M1	NA	7	13	6	5	16	2	2	2	4	13
Sly02g0337591	M1	NA	30	46	20	2	2	6	6	2	1	1
Sly02g0337601	M1	NA	1	2	1	1	1	1	1	1	1	1
Sly02g0337611	M11	NA	16	15	18	19	26	17	16	20	21	31
Sly02g0337621	M11	NA	5	4	4	4	4	6	5	6	4	2
Sly02g0337641	M12	NA	3	4	3	13	62	4	3	4	7	62
Sly02g0337651	M3	NA	12	13	14	28	51	9	11	7	10	62
Sly02g0337661	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0337671	M17	NA	113	96	117	82	89	97	90	104	90	125
Sly02g0337681	M1	NA	68	68	66	66	95	51	49	56	67	90
Sly02g0337691	M1	NA	23	15	22	3	1	1	1	1	1	1
Sly02g0337701	M2	NA	10	10	9	14	14	10	13	8	14	13
Sly02g0337711	M3	NA	63	67	63	62	72	62	61	60	98	122
Sly02g0337731	M19	NA	35	39	41	43	53	37	37	42	67	67
Sly02g0337741	M12	NA	21	24	22	18	18	24	25	26	23	25
Sly02g0337751	M3	NA	23	26	21	14	16	15	16	12	18	17
Sly02g0337771	M1	NA	33	37	32	20	20	21	22	21	24	24
Sly02g0337781	M3	NA	2	2	1	2	1	1	2	1	1	0
Sly02g0337791	M2	NA	144	136	130	171	231	124	136	125	205	270
Sly02g0337821	M1	NA	12	10	10	6	5	7	8	7	5	2
Sly02g0337831	M22	NA	1	1	1	1	0	2	1	3	0	0
Sly02g0337841	M22	NA	1	1	1	0	0	2	0	2	0	0
Sly02g0337851	M22	NA	3	1	2	0	0	5	1	7	0	0
Sly02g0337871	M22	NA	1	1	1	0	0	2	1	2	0	0
Sly02g0337891	M1	NA	145	136	117	60	41	75	84	61	55	40
Sly02g0337911	M12	Solyc02g081830	25	26	37	204	87	42	68	151	476	86
Sly02g0337921	M8	NA	17	15	14	16	13	16	17	15	25	23
Sly02g0337931	M11	NA	11	13	17	17	7	14	14	15	8	10
Sly02g0337941	M1	NA	4	4	4	5	4	4	3	4	5	5
Sly02g0337951	M22	NA	1	1	1	1	0	1	1	1	0	0
Sly02g0337961	M13	NA	159	140	201	304	294	226	206	276	292	357
Sly02g0337971	M21	NA	5	4	6	4	2	8	1	6	0	1
Sly02g0337981	M11	NA	1	2	1	1	2	3	2	3	1	1
Sly02g0337991	M1	NA	10	11	10	11	13	6	5	6	7	6
Sly02g0338001	M11	SISDG42	17	18	24	37	34	33	27	34	27	26
Sly02g0338011	M1	NA	7	7	8	8	8	7	7	7	8	7
Sly02g0338021	M1	NA	23	25	25	20	25	20	16	21	20	22
Sly02g0338031	M3	NA	25	23	23	24	26	19	22	19	27	27
Sly02g0338041	M11	NA	34	32	38	37	44	44	36	48	59	65
Sly02g0338051	M1	NA	22	20	13	46	99	10	5	6	8	27
Sly02g0338061	M3	NA	17	14	14	2	2	8	17	9	3	5
Sly02g0338081	M16	NA	915	800	864	698	533	773	804	854	796	649
Sly02g0338091	M12	NA	9	10	9	14	15	11	10	10	12	17
Sly02g0338101	M3	NA	96	97	79	52	55	48	58	39	44	45
Sly02g0338111	M11	NA	28	29	28	37	62	28	30	29	41	59
Sly02g0338171	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0338181	M3	NA	67	91	60	42	29	23	31	13	6	6
Sly02g0338191	M10	NA	2	2	1	1	1	2	2	1	1	1
Sly02g0338201	M1	NA	77	73	68	62	46	50	56	53	37	41
Sly02g0338211	M22	NA	1	1	1	1	1	2	1	2	1	2
Sly02g0338231	M12	NA	6	9	6	5	6	10	14	8	5	5
Sly02g0338241	M19	NA	14	14	17	11	7	14	12	15	10	6
Sly02g0338251	M1	NA	3	3	3	3	2	2	2	2	1	1
Sly02g0338271	M1	NA	78	80	60	51	61	43	46	39	50	67
Sly02g0338281	M7	NA	59	75	55	19	37	81	93	49	13	18
Sly02g0338291	M7	NA	1	3	1	1	1	1	2	1	1	1
Sly02g0338301	M1	NA	4	4	4	3	4	3	3	3	4	5
Sly02g0338311	M22	NA	2	1	2	1	1	5	1	6	0	0
Sly02g0338321	M1	NA	32	27	29	9	9	13	16	13	5	3
Sly02g0338331	M18	NA	64	65	60	32	17	100	83	121	97	48
Sly02g0338341	M11	NA	65	55	67	123	226	66	69	90	210	356
Sly02g0338361	M11	NA	13	13	13	13	14	16	14	18	14	14
Sly02g0338371	M1	NA	76	81	75	79	84	71	67	69	64	91
Sly02g0338381	M10	NA	32	37	34	38	46	35	36	34	38	40
Sly02g0338391	M3	NA	7	13	4	1	1	3	2	3	0	0
Sly02g0338401	M3	NA	87	89	65	57	72	57	52	45	43	56
Sly02g0338411	M12	NA	59	51	68	12	27	796	614	693	18	33
Sly02g0338421	M1	NA	156	140	172	90	135	108	124	138	119	179
Sly02g0338431	M3	NA	28	27	23	19	14	26	26	25	18	16
Sly02g0338441	M11	NA	10	10	9	3	4	23	15	22	8	4
Sly02g0338451	M3	NA	5	4	4	2	2	3	3	2	4	3
Sly02g0338461	M18	NA	2	2	2	1	1	2	2	2	2	1
Sly02g0338481	M3	NA	3	6	3	6	8	3	3	3	6	8
Sly02g0338491	M11	NA	209	187	229	123	111	219	181	251	195	158
Sly02g0338501	M12	NA	22	25	23	25	20	29	32	29	25	29
Sly02g0338511	M1	NA	4	4	4	4	6	3	3	4	5	8
Sly02g0338541	M3	SlJMJ15	30	31	32	33	28	26	27	24	18	16
Sly02g0338551	M9	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0338571	M3	NA	17	15	13	8	6	11	13	11	4	6
Sly02g0338581	M3	NA	111	115	67	46	47	52	62	55	59	63
Sly02g0338591	M1	NA	26	31	18	5	6	2	2	1	1	1
Sly02g0338601	M3	SlPILS5	61	63	66	9	2	9	15	3	2	1
Sly02g0338611	M1	NA	53	57	52	49	46	43	36	38	37	44
Sly02g0338621	M12	NA	51	52	53	70	96	64	63	73	92	101
Sly02g0338631	M11	NA	19	18	21	16	10	25	25	24	14	11
Sly02g0338641	M10	NA	4	4	3	4	4	5	5	3	3	3
Sly02g0338651	M2	NA	59	53	45	37	33	39	48	36	48	34
Sly02g0338661	M3	NA	141	166	76	52	67	85	112	38	79	88
Sly02g0338691	M11	NA	67	74	78	77	61	85	80	84	65	65
Sly02g0338701	M6	NA	16	44	13	7	20	35	46	9	5	9
Sly02g0338711	M3	NA	14	20	13	11	26	11	15	11	27	54
Sly02g0338721	M2	NA	43	45	40	48	49	36	40	35	59	51
Sly02g0338741	M19	NA	8	9	8	8	10	8	8	9	13	18
Sly02g0338751	M11	NA	13	15	15	14	18	15	13	15	25	34
Sly02g0338761	M3	NA	4	5	5	3	6	4	7	4	3	19
Sly02g0338771	M3	NA	10	11	9	7	8	6	7	7	10	38
Sly02g0338781	M3	NA	10	14	10	8	12	9	9	10	12	39
Sly02g0338791	M12	NA	2	2	2	2	3	3	3	3	5	3
Sly02g0338801	M7	NA	3	5	2	3	9	3	7	4	4	35
Sly02g0338811	M12	NA	12	14	11	11	18	17	16	16	16	20
Sly02g0338821	M2	NA	178	212	154	169	97	179	212	156	155	103
Sly02g0338831	M1	NA	13	12	14	26	14	12	9	8	5	3
Sly02g0338841	M12	NA	24	33	38	75	35	128	155	159	127	138

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0274821	M11	NA	40	35	36	27	21	35	34	40	32	23
Sly08g0274831	M1	NA	57	53	49	53	50	47	43	52	64	53
Sly08g0274841	M12	NA	102	102	99	84	70	105	106	106	91	86
Sly08g0274851	M1	NA	21	23	20	23	20	18	16	17	16	15
Sly08g0274871	M22	NA	2	2	1	0	1	8	1	5	0	0
Sly08g0274891	M11	NA	197	174	197	149	122	219	215	283	275	276
Sly08g0274901	M1	NA	266	241	313	260	484	201	186	225	383	785
Sly08g0274911	M1	NA	12	8	8	9	9	5	4	4	5	6
Sly08g0274931	M22	NA	3	1	2	0	1	24	2	12	1	1
Sly08g0274981	M19	NA	11	13	13	15	16	14	11	13	12	14
Sly08g0274991	M11	NA	5	6	6	3	3	6	6	7	2	2
Sly08g0275011	M12	NA	29	24	26	22	22	25	32	29	25	23
Sly08g0275021	M13	2/2Hb3	39	34	40	42	56	32	33	43	53	67
Sly08g0275031	M12	HB3	5	5	6	10	9	7	7	7	11	12
Sly08g0275051	M11	NA	46	40	60	32	24	87	75	96	39	32
Sly08g0275061	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly08g0275071	M1	NA	1	2	1	1	1	1	1	1	0	1
Sly08g0275091	M1	NA	516	664	1011	1350	476	22	3	4	14	2
Sly08g0275111	M12	YUC6	1	1	1	0	0	9	8	7	1	1
Sly08g0275131	M16	NA	420	356	375	308	261	298	283	367	385	388
Sly08g0275151	M13	NA	26	21	33	40	63	30	26	38	42	57
Sly08g0275161	M11	NA	73	69	82	84	90	106	99	113	90	98
Sly08g0275171	M1	NA	68	56	50	58	58	44	40	48	59	78
Sly08g0275181	M12	NA	2	2	2	2	1	16	12	20	5	1
Sly08g0275201	M12	NA	1	1	1	1	1	1	1	1	2	1
Sly08g0275211	M11	NA	21	21	17	19	24	19	20	22	25	31
Sly08g0275231	M1	NA	213	218	166	225	97	105	114	105	45	18
Sly08g0275241	M12	NA	104	103	101	117	104	124	118	131	135	128
Sly08g0275251	M1	NA	101	103	104	70	71	83	81	88	77	71
Sly08g0275261	M3	NA	5	4	3	1	1	3	2	2	1	1
Sly08g0275271	M1	NA	57	57	72	232	275	50	53	56	126	141
Sly08g0275281	M1	NA	121	118	113	87	74	94	93	85	81	75
Sly08g0275291	M7	NA	12	14	9	8	10	14	17	13	6	9
Sly08g0275301	M3	NA	47	52	39	37	32	39	44	36	37	41
Sly08g0275321	M1	NA	3	4	3	3	2	3	3	2	1	1
Sly08g0275331	M1	NA	2	4	4	3	3	2	2	1	1	1
Sly08g0275341	M1	NA	3	3	3	3	3	2	2	2	1	1
Sly08g0275351	M1	NA	64	86	37	10	6	6	3	1	1	1
Sly08g0275361	M1	NA	100	117	49	14	7	8	7	2	1	1
Sly08g0275371	M3	NA	20	20	18	18	19	15	15	12	11	12
Sly08g0275381	M12	NA	1	1	1	1	2	3	3	3	3	4
Sly08g0275391	M1	NA	2	2	4	2	1	1	1	1	1	1
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Sly08g0275541	M1	NA	1	1	2	2	1	1	1	1	1	1
Sly08g0275551	M12	NA	3	4	4	6	4	5	5	5	11	5
Sly08g0275581	M11	NA	11	8	11	10	10	12	11	14	11	16
Sly08g0275591	M11	NA	7	6	8	8	6	8	7	10	6	6
Sly08g0275621	M11	NA	10	8	9	14	10	11	10	13	12	6
Sly08g0275631	M3	NA	20	23	20	19	21	22	21	20	19	17
Sly08g0275641	M12	NA	17	19	23	46	59	37	40	44	51	60
Sly08g0275651	M6	NA	13	52	20	5	9	44	53	13	1	1
Sly08g0275661	M10	NA	1	11	6	1	1	16	23	2	0	0
Sly08g0275681	M10	NA	1	2	2	1	1	4	5	1	0	0
Sly08g0275691	M10	NA	6	8	2	0	0	13	19	3	1	0
Sly08g0275701	M9	NA	1	1	1	1	1	12	13	3	0	0
Sly08g0275711	M9	NA	3	4	3	2	2	5	5	3	1	1
Sly08g0275721	M10	NA	7	8	2	1	1	18	22	4	1	1
Sly08g0275741	M6	NA	21	92	50	2	4	92	117	19	3	6
Sly08g0275751	M10	NA	314	603	292	45	30	715	996	374	30	82
Sly08g0275761	M12	NA	65	81	56	6	2	600	575	428	3	3
Sly08g0275771	M10	NA	11	20	7	1	0	118	97	7	1	0
Sly08g0275791	M3	NA	10	48	4	1	1	25	23	1	0	1
Sly08g0275841	M5	NA	6	20	6	0	1	19	20	2	0	0
Sly08g0275851	M3	NA	5	8	2	1	1	1	1	1	1	0
Sly08g0275861	M3	NA	6	11	5	4	11	5	5	2	3	16
Sly08g0275881	M3	NA	16	18	12	10	12	14	15	11	13	10
Sly08g0275891	M11	NA	12	11	13	21	33	16	16	18	21	41
Sly08g0275901	M9	NA	12	12	10	11	18	12	15	12	19	19
Sly08g0275911	M3	NA	5	3	2	1	1	2	2	1	1	1
Sly08g0275921	M10	NA	3	4	2	2	1	10	9	4	1	1
Sly08g0275931	M3	NA	5	4	2	1	1	4	3	3	1	1
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Sly08g0275951	M11	NA	13	15	13	16	15	18	16	17	15	10
Sly08g0275961	M18	NA	7	10	8	10	7	10	9	11	8	4
Sly08g0275971	M9	NA	16	15	15	19	18	16	21	15	19	17
Sly08g0275981	M9	NA	1	2	1	3	4	2	3	2	4	4
Sly08g0275991	M12	NA	2	3	2	4	9	4	4	3	6	12
Sly08g0276001	M1	NA	2	2	2	1	1	1	0	1	2	2
Sly08g0276021	M12	NA	1	1	1	1	1	3	2	2	2	1
Sly08g0276031	M22	NA	2	1	1	0	0	4	2	5	1	0
Sly08g0276051	M11	NA	21	26	20	20	13	33	32	28	18	12
Sly08g0276061	M11	PPR-like34	3	3	4	4	1	11	9	12	5	1
Sly08g0276071	M12	NA	1	1	1	2	1	3	2	3	2	2
Sly08g0276081	M11	NA	114	106	123	183	234	174	157	196	272	352
Sly08g0276091	M12	NA	3	2	2	3	3	11	6	10	5	3
Sly08g0276101	M3	NA	16	18	13	21	23	15	16	13	42	46
Sly08g0276111	M3	NA	77	109	62	161	216	50	66	27	416	548
Sly08g0276131	M15	NA	49	47	41	68	82	51	53	50	93	100
Sly08g0276151	M3	NA	10	10	8	11	10	8	8	9	7	7
Sly08g0276161	M1	NA	3	4	5	7	3	1	1	1	1	1
Sly08g0276171	M11	NA	27	25	29	27	34	33	28	37	46	64
Sly08g0276181	M12	NA	11	10	14	17	24	21	20	24	40	47
Sly08g0276191	M11	NA	11	9	11	10	9	20	17	24	13	13
Sly08g0276211	M1	NA	2	3	2	1	1	1	1	1	1	1
Sly08g0276231	M3	NA	13	14	13	16	16	12	12	11	15	14
Sly08g0276251	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0276291	M11	NA	4	4	5	1	1	8	7	7	1	0
Sly08g0276311	M11	NA	96	105	114	202	234	167	137	187	232	244
Sly08g0276321	M12	NA	15	15	12	21	18	15	17	18	31	27
Sly08g0276351	M17	NA	403	362	388	317	253	342	323	384	327	269
Sly08g0276371	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0276381	M11	NA	4	4	4	9	7	10	9	11	8	4
Sly08g0276391	M1	NA	20	18	20	17	19	17	16	15	9	10
Sly08g0276401	M1	NA	286	263	276	295	250	205	197	184	170	186
Sly08g0276471	M12	NA	1	1	2	1	2	2	2	2	2	2
Sly08g0276481	M12	NA	22	21	22	31	35	33	35	36	54	59
Sly08g0276491	M1	NA	33	35	30	33	37	22	22	20	28	33
Sly08g0276501	M1	NA	27	14	30	7	3	7	6	7	3	1
Sly08g0276531	M17	NA	72	71	74	83	97	69	64	81	92	109
Sly08g0276541	M1	NA	38	36	40	39	50	32	30	37	38	49
Sly08g0276551	M11	NA	64	58	59	55	80	61	49	66	45	54
Sly08g0276561	M12	NA	6	6	7	10	6	12	12	15	19	10
Sly08g0276581	M1	NA	919	860	1024	1441	667	121	135	69	66	269
Sly08g0276591	M22	NA	1	1	1	0	1	1	1	1	0	0
Sly08g0276601	M19	NA	19	23	21	20	18	21	18	21	17	17
Sly08g0276611	M3	NA	88	85	65	44	44	50	60	42	47	53
Sly08g0276621	M11	NA	12	14	16	28	26	33	30	43	29	28
Sly08g0276631	M11	NA	37	35	35	35	39	42	36	51	42	43
Sly08g0276641	M3	NA	40	40	38	37	48	28	34	32	44	70
Sly08g0276651	M1	NA	47	50	48	50	60	38	37	42	51	62
Sly08g0276661	M11	NA	10	11	12	10	9	13	10	14	11	6
Sly08g0276671	M3	NA	1	1	1	0	0	1	0	0	0	0
Sly08g0276701	M1	NA	1	1	2	1	1	1	0	1	0	0
Sly08g0276711	M1	NA	18	17	15	14	10	12	13	11	12	9
Sly08g0276731	M3	NA	2	4	1	0	0	1	1	1	0	0
Sly08g0276761	M9	NA	1	1	1	1	0	1	1	1	1	1
Sly08g0276771	M12	NA	1	1	1	1	1	1	4	2	1	6
Sly08g0276781	M10	NA	1	1	1	1	1	1	2	1	0	1
Sly08g0276801	M3	NA	3	4	4	3	3	3	4	3	3	5
Sly08g0276811	M1	NA	4	3	3	2	1	2	1	2	2	1
Sly08g0276821	M11	NA	99	75	93	122	174	145	133	167	169	190
Sly08g0276831	M3

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0338851	M3	NA	333	325	287	183	312	301	320	249	204	361
Sly02g0338861	M3	NA	27	28	24	26	28	20	21	19	29	32
Sly02g0338871	M12	NA	4	5	4	9	13	10	9	10	23	26
Sly02g0338881	M12	NA	29	28	26	28	29	34	35	35	33	42
Sly02g0338891	M1	NA	44	25	47	2	1	5	4	3	1	1
Sly02g0338911	M11	NA	24	22	24	31	32	54	43	56	23	39
Sly02g0338921	M12	NA	8	11	8	8	15	14	13	18	51	82
Sly02g0338931	M9	NA	19	22	18	18	43	26	29	33	160	295
Sly02g0338951	M3	NA	130	129	123	121	111	121	118	104	110	116
Sly02g0338961	M11	NA	11	10	9	8	10	12	10	10	7	7
Sly02g0338981	M8	NA	67	66	47	42	20	80	97	50	33	17
Sly02g0338991	M11	NA	30	33	41	35	29	49	43	54	27	22
Sly02g0339001	M12	NA	7	9	9	8	8	25	26	29	17	17
Sly02g0339011	M3	NA	23	21	18	20	23	18	21	19	34	30
Sly02g0339031	M3	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0339051	M12	NA	20	17	16	6	7	50	38	42	6	6
Sly02g0339061	M1	NA	11	13	4	1	1	1	1	1	0	1
Sly02g0339071	M3	NA	88	74	38	45	17	14	26	5	14	10
Sly02g0339081	M8	NA	22	29	17	53	26	31	61	17	82	29
Sly02g0339091	M12	NA	1	1	1	1	1	5	6	5	1	1
Sly02g0339101	M10	NA	11	17	6	3	2	18	26	9	6	3
Sly02g0339121	M3	PPR-like14	10	10	9	9	10	8	9	7	10	12
Sly02g0339131	M3	NA	2	3	1	1	1	0	0	1	0	0
Sly02g0339141	M12	NA	1	2	0	1	1	2	2	1	1	1
Sly02g0339151	M12	NA	2	2	1	1	1	3	4	3	2	1
Sly02g0339161	M18	NA	2	2	2	1	1	3	3	2	2	1
Sly02g0339291	M11	NA	23	18	27	13	7	36	30	40	15	9
Sly02g0339301	M1	NA	18	18	9	4	2	2	4	1	1	1
Sly02g0339311	M3	NA	43	41	35	9	9	42	40	36	7	5
Sly02g0339321	M11	NA	15	17	16	15	17	22	19	25	21	23
Sly02g0339331	M12	NA	21	22	20	30	37	21	24	22	29	30
Sly02g0339351	M12	NA	17	18	15	15	29	23	25	27	26	56
Sly02g0339361	M1	NA	59	56	63	60	87	53	44	54	43	65
Sly02g0339371	M1	NA	2	1	3	2	3	1	1	1	0	1
Sly02g0339391	M19	NA	15	19	13	15	13	14	11	13	14	12
Sly02g0339401	M19	NA	20	20	21	22	25	21	19	20	23	22
Sly02g0339411	M1	NA	25	22	23	21	28	22	19	21	26	29
Sly02g0339421	M11	NA	187	163	218	116	104	216	190	288	383	423
Sly02g0339441	M8	NA	20	19	20	21	19	19	22	19	20	19
Sly02g0339451	M1	NA	28	22	27	14	15	19	17	18	7	9
Sly02g0339471	M13	NA	5	3	6	1	1	5	5	5	1	2
Sly02g0339481	M13	NA	267	200	424	479	894	390	341	627	776	1520
Sly02g0339501	M12	NA	34	44	38	40	36	51	49	65	58	44
Sly02g0339541	M11	NA	97	69	83	16	17	153	114	213	11	8
Sly02g0339551	M11	NA	153	131	139	103	137	198	167	211	154	163
Sly02g0339561	M1	NA	14	15	22	5	3	7	7	7	16	9
Sly02g0339571	M18	NA	39	42	44	44	42	53	45	49	32	30
Sly02g0339581	M6	NA	10	13	12	9	13	12	12	9	14	20
Sly02g0339591	M3	NA	4	5	4	2	5	4	2	3	4	7
Sly02g0339601	M12	NA	11	13	13	46	126	25	17	32	111	427
Sly02g0339611	M6	SIP4H3	48	50	48	46	38	49	54	43	24	25
Sly02g0339621	M1	NA	37	46	31	18	28	13	17	12	12	35
Sly02g0339631	M11	NA	12	13	10	17	22	17	17	22	41	33
Sly02g0339651	M7	NA	43	54	38	47	59	46	57	34	30	44
Sly02g0339661	M12	NA	9	9	8	9	10	10	10	10	9	10
Sly02g0339681	M12	NA	2	2	2	2	1	6	4	4	2	1
Sly02g0339691	M3	NA	71	131	62	36	30	26	30	12	7	10
Sly02g0339701	M3	NA	41	41	30	21	23	23	27	17	27	23
Sly02g0339711	M22	NA	1	0	1	0	0	11	1	5	0	0
Sly02g0339731	M11	NA	30	29	36	66	156	38	38	43	67	129
Sly02g0339741	M12	NA	2	1	1	1	2	3	2	5	1	1
Sly02g0339801	M12	NA	7	5	9	15	10	24	21	29	18	10
Sly02g0339821	M2	NA	28	29	28	32	36	28	29	27	28	28
Sly02g0339831	M1	NA	8	8	7	10	6	1	1	1	1	1
Sly02g0339841	M3	NA	30	30	20	13	9	21	23	15	11	10
Sly02g0339851	M5	NA	89	95	78	127	146	106	114	58	101	155
Sly02g0339861	M3	NA	5	6	5	3	3	3	3	3	3	2
Sly02g0339871	M22	NA	2	2	1	2	3	2	1	2	10	11
Sly02g0339881	M12	SIAPx5	1	2	2	2	1	4	6	4	7	4
Sly02g0339891	M1	SIAPx	3	1	1	1	1	1	1	1	1	1
Sly02g0339911	M12	NA	53	50	51	97	143	63	67	78	131	163
Sly02g0339931	M11	NA	13	12	17	8	4	29	24	35	6	3
Sly02g0339941	M11	NA	8	6	10	3	2	17	15	15	2	1
Sly02g0339951	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0339961	M1	NA	70	73	75	88	21	55	54	42	7	2
Sly02g0339971	M1	NA	162	144	132	175	182	108	111	106	147	171
Sly02g0339981	M12	NA	1	1	1	1	1	2	2	2	1	0
Sly02g0339991	M22	NA	2	2	2	1	2	3	2	4	1	1
Sly02g0340001	M1	NA	3	2	2	1	1	1	1	1	0	0
Sly02g0340011	M12	NA	42	41	41	46	48	43	42	44	33	37
Sly02g0340021	M12	NA	10	8	19	15	7	31	30	39	6	2
Sly02g0340031	M12	NA	8	9	7	8	8	10	11	9	7	7
Sly02g0340041	M12	NA	9	10	7	8	9	10	11	12	7	6
Sly02g0340051	M11	NA	7	7	6	6	5	9	7	7	5	3
Sly02g0340061	M12	NA	4	4	3	3	5	6	6	5	4	5
Sly02g0340071	M12	NA	2	2	2	2	3	3	4	3	5	4
Sly02g0340081	M3	NA	24	19	18	25	34	19	17	19	24	48
Sly02g0340091	M11	NA	79	69	106	115	83	145	128	179	62	40
Sly02g0340101	M11	NA	10	11	13	14	20	13	15	14	13	21
Sly02g0340121	M22	NA	1	0	1	0	0	1	0	3	0	0
Sly02g0340131	M11	NA	203	129	269	351	339	243	182	306	118	167
Sly02g0340161	M3	NA	65	77	27	6	3	14	14	2	1	1
Sly02g0340171	M1	NA	40	56	42	938	486	3	2	3	1	1
Sly02g0340191	M3	NA	117	107	71	2	1	49	72	23	1	2
Sly02g0340211	M19	NA	22	25	29	32	31	31	24	30	16	18
Sly02g0340241	M9	NA	51	39	24	1	1	90	95	68	2	1
Sly02g0340251	M6	NA	14	19	12	10	17	15	15	14	10	17
Sly02g0340261	M3	NA	18	21	18	16	21	16	20	12	15	26
Sly02g0340281	M3	NA	11	12	8	7	12	6	7	6	9	11
Sly02g0340291	M11	NA	23	19	28	71	89	34	31	47	55	58
Sly02g0340301	M11	NA	3	3	4	5	7	5	4	5	6	8
Sly02g0340311	M11	NA	26	25	30	20	15	44	33	51	15	7
Sly02g0340321	M11	NA	17	16	20	29	31	46	44	60	28	28
Sly02g0340331	M1	SAUR33	9	13	11	3	1	6	6	6	2	1
Sly02g0340341	M15	NA	45	36	36	28	36	41	34	41	37	40
Sly02g0340351	M9	NA	26	27	26	27	22	29	39	31	25	19
Sly02g0340411	M9	NA	1	1	1	1	2	2	4	1	1	1
Sly02g0340421	M9	NA	1	1	1	1	1	3	7	2	1	6
Sly02g0340431	M9	NA	3	6	2	2	5	18	44	14	4	19
Sly02g0340471	M9	NA	2	2	1	2	2	3	11	4	2	5
Sly02g0340481	M9	NA	2	3	2	1	2	4	17	7	3	14
Sly02g0340491	M9	NA	1	2	1	1	1	3	7	3	2	6
Sly02g0340501	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0340511	M12	NA	2	1	1	1	1	2	2	2	1	1
Sly02g0340521	M12	NA	7	7	6	6	12	8	7	8	8	10
Sly02g0340531	M11	NA	65	60	83	98	118	92	84	104	136	181
Sly02g0340541	M11	NA	73	88	139	234	824	313	248	505	553	788
Sly02g0340591	M8	NA	4	5	2	2	1	4	6	3	3	13
Sly02g0340601	M12	NA	1	1	1	1	1	2	2	1	2	6
Sly02g0340611	M12	NA	2	1	1	2	1	3	3	2	4	9
Sly02g0340621	M4	NA	1	1	1	1	1	2	1	1	3	9
Sly02g0340631	M12	NA	2	1	1	2	2	3	3	2	7	20
Sly02g0340641	M11	NA	24	22	27	20	26	28	22	30	23	29
Sly02g0340651	M1	NA	1	1	1	1	0	1	0	0	0	0
Sly02g0340661	M12	NA	172	155	152	206	189	234	304	264	280	318
Sly02g0340681	M3	NA	31	34	32	34	45	23	24	23	44	55
Sly02g0340691	M1	NACK2-like	25	25	32	17	11	2	1	1	1	1
Sly02g0340701	M1	NA	6	3	5	1	3	3	3	2	1	1
Sly02g0340721	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0340731	M1	NA	6	3	5	10	26	2	2	2	4	7
Sly02g0340741	M11	NA	1339	1050	1520	1164	529	1581	1219	1901	1187	339
Sly02g0340751	M12	NA	4	3	4	3	4	5	5	5	5	4
Sly02g0340761	M12	NA	5	4	4	4	8	6	6	5	8	7
Sly02g0340781	M3	NA	8	9	4	4	3	3	4	2	2	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0276871	M19	NA	16	22	19	19	13	20	16	22	20	13
Sly08g0276881	M18	NA	20	22	22	21	12	23	16	24	18	15
Sly08g0276891	M12	NA	20	22	23	18	15	26	23	24	21	18
Sly08g0276901	M12	NA	12	10	12	12	11	15	17	16	20	18
Sly08g0276911	M12	NA	7	7	6	8	6	9	10	10	16	16
Sly08g0276921	M12	NA	9	8	8	12	8	15	16	13	19	21
Sly08g0276931	M3	NA	18	19	17	19	20	15	17	15	23	25
Sly08g0276961	M11	NA	1	1	1	1	0	2	2	3	1	1
Sly08g0276971	M9	NA	3	3	2	3	1	6	10	3	1	1
Sly08g0276991	M12	NA	1	1	1	4	2	8	5	8	20	10
Sly08g0277021	M12	NA	23	20	26	19	18	24	25	26	33	36
Sly08g0277041	M12	NA	3	3	3	2	2	3	5	4	5	5
Sly08g0277081	M12	NA	4	4	5	6	6	5	4	5	8	9
Sly08g0277111	M12	NA	23	14	17	133	67	145	67	149	1955	701
Sly08g0277131	M1	NA	1	1	2	2	2	1	1	1	9	10
Sly08g0277141	M1	NA	4	7	3	1	1	1	1	1	1	1
Sly08g0277181	M1	NA	2	2	2	2	3	2	1	2	2	2
Sly08g0277201	M12	NA	1	1	1	2	1	2	2	2	3	1
Sly08g0277211	M11	NA	10	10	10	12	13	9	9	11	18	15
Sly08g0277221	M1	NA	13	24	25	109	145	5	15	12	126	207
Sly08g0277271	M1	NA	13	13	12	14	12	10	8	9	11	7
Sly08g0277281	M23	NA	2	2	1	1	1	3	2	2	1	1
Sly08g0277291	M1	NA	165	157	161	98	72	117	124	109	105	78
Sly08g0277301	M11	NA	13	12	16	27	53	20	17	22	23	42
Sly08g0277321	M12	NA	14	14	16	11	4	29	26	29	4	2
Sly08g0277341	M1	NA	27	21	31	20	8	21	12	22	4	1
Sly08g0277351	M20	NA	25	23	27	23	28	20	17	21	19	19
Sly08g0277361	M11	NA	1	1	1	1	1	1	1	2	1	1
Sly08g0277391	M4	NA	3	2	2	2	6	3	3	3	6	18
Sly08g0277411	M12	NA	103	86	93	74	85	86	110	134	113	56
Sly08g0277421	M9	NA	3	2	2	1	1	2	3	2	2	1
Sly08g0277431	M1	NA	2	1	2	1	1	1	1	1	0	0
Sly08g0277471	M14	NA	65	43	103	179	323	38	36	62	195	262
Sly08g0277481	M1	NA	1	1	1	1	2	1	1	1	3	1
Sly08g0277491	M3	NA	16	15	15	25	28	11	12	10	24	24
Sly08g0277501	M3	NA	95	94	83	75	62	82	88	73	79	66
Sly08g0277511	M12	SICYP707A3	1	1	1	1	42	1	1	3	6	71
Sly08g0277521	M22	NA	1	0	1	0	0	6	0	5	0	0
Sly08g0277541	M3	NA	81	81	77	79	61	72	71	61	49	36
Sly08g0277551	M1	NA	3	2	3	2	2	2	2	2	2	1
Sly08g0277571	M22	NA	1	0	1	0	0	3	0	3	0	0
Sly08g0277591	M12	NA	3	3	2	2	2	4	3	5	6	2
Sly08g0277601	M8	NA	235	294	176	107	121	209	456	222	255	255
Sly08g0277611	M11	NA	69	65	77	73	72	77	74	86	82	95
Sly08g0277621	M11	NA	33	34	40	53	52	48	47	52	49	47
Sly08g0277631	M2	NA	46	44	39	26	32	25	32	25	34	41
Sly08g0277641	M2	NA	19	18	18	18	24	15	16	15	26	30
Sly08g0277651	M11	NA	54	45	79	40	46	75	55	94	40	50
Sly08g0277661	M1	ABCG14	7	7	7	20	18	2	2	2	1	1
Sly08g0277671	M3	NA	42	40	34	40	33	38	40	37	33	31
Sly08g0277681	M12	NA	3	3	3	1	1	8	6	6	1	1
Sly08g0277691	M11	NA	6	6	7	7	5	14	12	15	9	3
Sly08g0277701	M1	NA	10	9	8	5	2	9	8	7	3	1
Sly08g0277721	M1	CCD4-like1	26	14	44	2	1	1	1	1	1	1
Sly08g0277731	M1	NA	4	4	4	3	4	3	3	3	3	3
Sly08g0277741	M11	SUMJ23	9	7	8	8	6	8	9	9	7	5
Sly08g0277751	M11	NA	35	27	41	27	19	44	40	51	35	25
Sly08g0277761	M11	NA	47	44	60	36	31	63	52	68	41	33
Sly08g0277771	M11	NA	42	44	50	60	45	80	69	78	40	30
Sly08g0277781	M10	NA	63	68	48	21	128	96	126	51	48	85
Sly08g0277791	M3	NA	12	14	22	1	1	18	13	2	1	1
Sly08g0277801	M2	NA	103	105	111	91	74	98	125	81	116	105
Sly08g0277821	M1	NA	25	21	20	17	21	20	18	20	21	29
Sly08g0277881	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly08g0277891	M1	NA	2	3	2	1	1	1	1	1	1	1
Sly08g0277901	M1	NA	26	26	27	19	22	27	24	25	17	16
Sly08g0277911	M19	NA	14	13	16	10	6	14	12	16	8	6
Sly08g0277921	M11	NA	1	1	2	1	1	2	1	2	1	1
Sly08g0277931	M11	NA	382	324	388	586	476	344	343	380	425	447
Sly08g0277941	M1	NA	681	590	607	478	410	506	502	515	541	435
Sly08g0277951	M3	NA	61	76	44	31	29	47	50	30	22	26
Sly08g0277961	M1	NA	58	58	54	63	63	33	37	35	54	54
Sly08g0277971	M11	NA	111	112	117	159	143	120	127	133	161	155
Sly08g0277981	M2	NA	66	65	51	38	50	42	54	40	43	54
Sly08g0278001	M12	NA	57	58	54	205	313	54	64	63	262	280
Sly08g0278011	M1	NA	9	12	13	4	3	2	2	3	3	2
Sly08g0278021	M1	NA	30	24	27	22	26	22	21	25	19	18
Sly08g0278031	M11	NA	38	37	38	63	71	51	46	53	67	86
Sly08g0278051	M22	NA	5	3	2	1	1	21	5	12	1	1
Sly08g0278061	M3	NA	14	15	15	34	30	11	12	12	20	23
Sly08g0278071	M1	RDR6B	1	1	1	2	1	1	1	1	2	2
Sly08g0278081	M3	NA	2	1	1	2	2	1	1	1	3	3
Sly08g0278101	M11	NA	35	30	39	27	31	47	40	52	37	41
Sly08g0278111	M11	NA	35	32	37	50	58	35	32	39	54	55
Sly08g0278121	M12	NA	239	237	235	207	229	215	242	256	301	312
Sly08g0278141	M3	NA	267	331	181	170	97	158	283	152	247	224
Sly08g0278151	M1	NA	19	18	14	9	5	1	1	1	1	0
Sly08g0278161	M3	NA	179	194	179	138	136	165	168	167	215	188
Sly08g0278181	M11	NA	15	12	15	13	9	27	24	33	11	10
Sly08g0278191	M1	NA	20	19	23	6	3	7	4	5	1	1
Sly08g0278201	M3	NA	5	5	4	4	3	2	3	3	2	2
Sly08g0278211	M1	NA	23	25	32	20	11	20	19	27	7	3
Sly08g0278221	M11	NA	3	2	3	2	1	4	3	4	3	1
Sly08g0278231	M12	NA	146	121	123	100	91	160	178	194	205	184
Sly08g0278241	M2	NA	18	26	18	71	71	16	24	17	45	69
Sly08g0278251	M3	NA	16	21	15	56	53	13	18	14	31	40
Sly08g0278261	M11	NA	7	7	7	7	4	9	8	10	8	4
Sly08g0278271	M11	NA	5	7	6	6	4	8	6	11	5	3
Sly08g0278281	M1	NA	6	8	6	4	5	4	4	4	3	3
Sly08g0278291	M3	NA	8	10	5	3	5	5	4	4	3	4
Sly08g0278301	M7	NA	4	7	4	5	17	6	11	6	14	41
Sly08g0278311	M1	NA	18	18	17	14	20	16	14	15	14	20
Sly08g0278321	M12	NA	2	1	2	1	1	6	4	5	1	1
Sly08g0278331	M9	SITPL2	37	41	30	26	24	45	46	33	19	11
Sly08g0278391	M1	NA	3	5	4	7	4	1	2	2	2	2
Sly08g0278401	M11	NA	39	38	61	30	31	72	68	82	29	16
Sly08g0278421	M12	NA	1	1	1	6	7	2	2	3	55	61
Sly08g0278431	M12	NA	6	6	7	43	130	20	20	30	106	169
Sly08g0278441	M3	NA	75	74	56	42	45	41	44	40	47	41
Sly08g0278451	M3	NA	13	14	11	11	16	8	10	9	14	16
Sly08g0278461	M3	NA	24	23	19	25	36	16	16	19	31	33
Sly08g0278471	M1	NA	31	33	33	35	42	30	32	30	39	50
Sly08g0278481	M11	NA	3	3	4	2	1	7	6	6	3	3
Sly08g0278491	M14	NA	30	31	31	39	52	31	28	33	28	26
Sly08g0278501	M1	NA	9	6	15	36	14	2	2	2	2	1
Sly08g0278511	M1	NA	8	6	12	2	1	1	1	1	1	0
Sly08g0278521	M13	NA	16	13	17	19	16	14	13	17	25	19
Sly08g0278531	M11	NA	1	1	1	1	1	2	1	1	1	1
Sly08g0278541	M1	NA	210	214	215	152	177	168	155	156	187	224
Sly08g0278551	M2	NA	57	54	42	35	34	44	61	39	30	34
Sly08g0278561	M11	NA	61	53	63	47	10	84	73	91	12	3
Sly08g0278571	M14	NA	9	8	11	7	8	9	7	10	11	14
Sly08g0278601	M22	NA	9	2	6	0	1	20	2	27	0	0
Sly08g0278651	M11	NA	2	1	1	1	1	3	2	2	1	0
Sly08g0278661	M12	NA	8	9	8	9	7	10	9	10	11	5
Sly08g0278671	M12	NA	11	11	12	11	13	27	27	26	6	7
Sly08g0278681	M12	NA	35	45	44	62	56	96	115	96	114	86
Sly08g0278701	M16	NA	103	93	81	71	58	77	77	83	75	66
Sly08g0278711	M12	NA	1	1	1	0	1	3	2	2	1	0
Sly08g0278721	M12	NA	42	42	46	39	48	79	95	87	94	70
Sly08g0278731	M23	NA	1	1	1	1	1	1	1	1	1	0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0340791	M1	NA	27	26	23	14	7	16	16	14	7	8
Sly02g0340801	M19	NA	123	143	135	145	124	146	116	144	148	130
Sly02g0340811	M19	NA	58	60	56	58	65	62	53	63	74	77
Sly02g0340831	M11	NA	43	38	43	39	47	45	41	50	56	61
Sly02g0340841	M19	NA	10	14	12	15	15	13	11	14	16	10
Sly02g0340851	M11	NA	23	24	21	29	30	25	24	27	43	38
Sly02g0340861	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0340871	M1	NA	3	3	3	2	1	2	2	2	4	1
Sly02g0340881	M1	NA	59	56	55	54	63	47	48	46	54	73
Sly02g0340891	M1	NA	10	8	11	12	12	7	6	9	11	10
Sly02g0340901	M1	NA	16	36	26	25	10	14	6	16	2	1
Sly02g0340921	M22	NA	5	4	8	3	2	7	4	5	1	1
Sly02g0340951	M12	NA	5	6	11	7	3	14	14	17	3	3
Sly02g0340971	M1	NA	2	1	4	1	1	2	1	1	1	1
Sly02g0340981	M11	NA	15	13	18	13	15	17	14	18	9	10
Sly02g0340991	M1	NA	90	94	88	31	20	25	27	25	5	5
Sly02g0341001	M1	NA	30	33	56	102	24	13	10	7	1	1
Sly02g0341011	M3	NA	27	28	22	22	20	18	27	22	36	41
Sly02g0341021	M1	NA	27	22	25	20	26	15	16	17	17	24
Sly02g0341031	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0341041	M3	NA	2	2	2	1	2	1	2	1	1	2
Sly02g0341051	M11	NA	88	87	93	110	95	113	106	119	86	88
Sly02g0341061	M11	NA	53	54	58	56	69	58	56	59	73	82
Sly02g0341071	M8	NA	55	50	42	74	114	52	66	50	114	140
Sly02g0341081	M11	NA	45	36	57	23	23	58	52	52	37	22
Sly02g0341091	M1	NA	3	3	3	3	3	2	2	2	3	3
Sly02g0341111	M9	3-epi-6-deoxocathaste	9	12	10	4	11	13	14	11	2	14
Sly02g0341121	M11	NA	10	10	12	15	24	13	12	13	14	16
Sly02g0341131	M1	NA	103	90	91	82	84	51	53	54	84	103
Sly02g0341141	M12	NA	10	8	7	3	2	13	11	10	3	2
Sly02g0341181	M12	NA	12	14	13	16	16	15	16	15	17	16
Sly02g0341191	M12	NA	27	27	28	36	33	37	37	37	31	23
Sly02g0341201	M19	NA	6	7	7	7	6	6	6	7	8	5
Sly02g0341211	M12	NA	9	7	4	2	1	10	18	9	20	2
Sly02g0341221	M1	NA	4	5	3	1	1	3	2	2	1	0
Sly02g0341231	M22	NA	1	1	1	0	0	3	1	1	0	0
Sly02g0341251	M1	NA	50	59	55	172	109	26	31	25	104	61
Sly02g0341271	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly02g0341281	M7	NA	7	15	8	4	10	9	19	8	2	11
Sly02g0341291	M10	NA	19	18	16	7	9	20	23	17	9	9
Sly02g0341301	M18	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0341311	M11	NA	324	307	343	340	364	352	376	424	450	497
Sly02g0341321	M12	NA	2	1	2	1	1	12	10	12	1	1
Sly02g0341331	M1	SAM-METT-like4	5	6	9	17	14	1	1	1	1	1
Sly02g0341341	M1	NA	5	6	3	2	2	1	1	1	1	1
Sly02g0341351	M1	NA	6	7	3	4	4	2	2	1	1	1
Sly02g0341361	M22	NA	3	4	2	6	5	4	2	4	1	1
Sly02g0341371	M12	a-MAN	79	75	116	189	67	228	222	391	300	71
Sly02g0341381	M12	NA	28	36	29	69	71	52	60	65	135	74
Sly02g0341391	M1	NA	5	7	5	2	1	1	1	1	1	1
Sly02g0341401	M6	NA	16	40	16	3	8	42	35	11	1	4
Sly02g0341411	M12	NA	1	1	1	1	1	3	1	2	1	1
Sly02g0341421	M20	NA	8	9	14	12	9	6	3	8	4	3
Sly02g0341431	M11	NA	85	75	85	90	87	90	90	95	98	90
Sly02g0341441	M9	NA	63	63	49	40	60	64	81	67	91	115
Sly02g0341471	M11	NA	12	12	13	18	23	13	13	13	15	16
Sly02g0341491	M1	NA	19	15	18	18	12	16	15	15	6	2
Sly02g0341511	M1	NA	1	1	1	0	1	1	0	1	1	0
Sly02g0341521	M12	NA	3	3	3	4	2	11	13	18	13	3
Sly02g0341531	M3	NA	26	42	26	15	8	16	22	7	5	5
Sly02g0341551	M22	NA	2	2	2	2	2	3	2	2	2	1
Sly02g0341561	M1	NA	6	7	7	11	11	3	3	3	2	1
Sly02g0341571	M1	NA	30	37	44	41	14	16	12	14	7	3
Sly02g0341591	M12	NA	19	16	18	21	28	25	24	31	60	40
Sly02g0341601	M12	NA	2	3	2	3	3	6	4	5	4	2
Sly02g0341611	M1	NA	15	17	14	6	5	7	7	6	5	4
Sly02g0341621	M3	NA	5	4	4	5	2	3	4	4	4	2
Sly02g0341631	M1	NA	24	23	25	21	23	19	18	18	11	15
Sly02g0341661	M11	NA	69	63	74	67	51	87	96	110	94	87
Sly02g0341671	M18	NA	3	3	2	2	1	3	2	3	2	1
Sly02g0341681	M22	NA	4	5	4	2	1	5	3	4	2	1
Sly02g0341691	M1	NA	4	5	3	4	3	2	1	1	1	1
Sly02g0341701	M1	NA	93	74	82	72	134	65	68	71	128	116
Sly02g0341711	M3	NA	45	48	27	50	108	35	35	32	169	155
Sly02g0341731	M12	NA	19	15	16	2	2	25	21	21	2	1
Sly02g0341741	M12	NA	275	269	284	632	1097	340	368	363	1608	1774
Sly02g0341751	M1	SlCYP90B3	42	31	22	5	10	4	6	5	10	5
Sly02g0341761	M1	NA	13	11	14	13	17	12	11	12	11	12
Sly02g0341771	M12	NA	4	3	3	1	1	5	5	5	1	0
Sly02g0341791	M12	DDM1-like2	8	7	6	3	2	12	12	12	1	1
Sly02g0341801	M9	NA	2	4	1	1	1	3	12	4	1	4
Sly02g0341821	M19	NA	313	305	332	292	331	319	270	344	455	578
Sly02g0341831	M22	NA	2	1	1	1	1	2	1	2	1	1
Sly02g0341841	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0341851	M13	NA	6	5	6	5	5	5	6	6	5	4
Sly02g0341861	M2	NA	4	4	5	4	6	3	5	4	6	11
Sly02g0341871	M1	NA	6	4	6	6	9	4	5	5	8	12
Sly02g0341881	M11	NA	13	13	17	12	15	18	19	21	13	17
Sly02g0341891	M12	NA	7	6	4	4	2	21	29	21	26	7
Sly02g0341901	M12	NA	2	1	1	1	0	15	12	9	1	0
Sly02g0341911	M3	NA	2	3	2	7	15	2	3	2	3	8
Sly02g0341921	M11	NA	22	21	22	28	51	23	23	25	40	56
Sly02g0341931	M3	NA	2	2	1	1	1	1	2	1	1	1
Sly02g0341941	M11	NA	204	182	201	305	363	301	294	369	376	422
Sly02g0341961	M7	NA	13	16	15	14	20	16	16	14	23	23
Sly02g0341971	M19	NA	48	48	44	55	48	45	41	50	60	49
Sly02g0341981	M1	NA	111	111	101	111	116	95	93	96	167	156
Sly02g0341991	M3	NA	14	16	10	4	3	12	9	8	4	2
Sly02g0342001	M23	NA	12	4	6	1	1	35	10	18	2	1
Sly02g0342011	M1	NA	47	51	50	145	112	3	4	4	14	14
Sly02g0342021	M1	NA	27	28	27	20	18	23	21	24	22	11
Sly02g0342031	M22	NA	1	1	1	0	0	2	1	2	0	0
Sly02g0342041	M3	NA	86	68	27	1	1	25	27	10	2	2
Sly02g0342051	M3	NA	43	43	43	48	84	39	41	41	70	97
Sly02g0342071	M12	NA	1	2	4	29	69	11	14	23	49	30
Sly02g0342081	M12	NA	22	24	23	37	33	29	29	31	37	26
Sly02g0342091	M1	NA	9	8	7	3	4	5	3	3	2	1
Sly02g0342101	M9	NA	17	15	15	15	24	17	20	16	24	26
Sly02g0342111	M12	ggpps3	31	34	35	120	176	53	60	56	127	149
Sly02g0342121	M9	ggpps1/4	4	5	3	9	14	7	9	6	10	11
Sly02g0342141	M12	NA	1	2	1	1	3	2	2	2	1	2
Sly02g0342151	M12	ggpps5	3	2	2	2	2	4	4	3	1	1
Sly02g0342171	M9	NA	2	2	2	1	1	3	2	2	2	1
Sly02g0342181	M3	AOC3	992	1183	924	51	31	266	258	37	29	21
Sly02g0342191	M11	NA	20	19	20	22	26	23	24	23	24	23
Sly02g0342211	M11	NA	38	26	43	27	6	174	139	195	95	19
Sly02g0342221	M11	NA	33	29	33	29	29	34	28	36	22	25
Sly02g0342231	M11	NA	43	45	51	66	71	45	47	48	69	94
Sly02g0342251	M19	NA	23	27	24	21	20	24	22	23	15	16
Sly02g0342261	M1	NA	19	18	18	18	19	18	16	16	18	17
Sly02g0342271	M3	NA	25	43	21	43	13	6	9	3	55	11
Sly02g0342281	M1	NA	87	83	90	94	83	80	78	82	99	94
Sly02g0342291	M1	NA	12	14	17	29	11	11	11	12	8	7
Sly02g0342301	M1	NA	260	283	462	526	140	6	1	1	1	1
Sly02g0342311	M12	SlCYP735A2	2	3	1	1	0	4	4	3	1	0
Sly02g0342321	M12	SlCYP735A1	2	2	3	0	0	28	16	26	0	0
Sly02g0342331	M3	LBD41	30	34	11	19	16	12	11	13	20	45
Sly02g0342341	M11	NA	42	41	48	39	38	53	46	62	55	66
Sly02g0342351	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly02g0342361	M20	NA	10	7	9	3	1	8	5	7	1	1
Sly02g0342371	M12	NA	7	7	9	9	6	9	11	11	9	6
Sly02g0342381	M1	NA	7	7	7	1	1	2	1	2	1	1
Sly02g0342401	M22	NA	1	1	1	0	0	1	1	2	0	0
Sly02g0342411	M11	NA	2	3	4	4	6	3	4	5	6	12

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0278781	M5	NA	431	497	310	262	304	417	479	239	271	386
Sly08g0278791	M3	NA	18	20	17	15	18	15	16	15	22	27
Sly08g0278801	M3	NA	27	27	22	16	18	18	19	15	18	26
Sly08g0278811	M13	NA	37	33	48	85	208	42	41	51	105	251
Sly08g0278821	M15	NA	136	121	116	112	97	118	134	126	114	116
Sly08g0278831	M11	NA	17	20	17	40	44	23	22	25	27	35
Sly08g0278841	M11	NA	76	72	101	121	193	205	178	247	75	83
Sly08g0278851	M6	NA	22	31	19	14	11	18	22	16	13	10
Sly08g0278861	M3	NA	3	3	2	2	4	2	2	2	4	7
Sly08g0278881	M9	NA	18	18	17	29	45	23	23	17	39	69
Sly08g0278891	M1	NA	5	5	8	1	1	3	3	4	1	1
Sly08g0278901	M3	NA	31	28	20	13	7	25	26	18	25	15
Sly08g0278911	M12	NA	168	172	168	143	129	180	173	199	196	173
Sly08g0278961	M12	NA	12	13	11	15	14	15	15	14	16	15
Sly08g0278971	M3	NA	25	22	21	14	13	17	20	18	19	11
Sly08g0278981	M1	NA	2	2	2	2	2	2	1	1	1	1
Sly08g0278991	M14	NA	4	3	5	1	1	4	3	4	1	1
Sly08g0279031	M1	NA	11	13	8	0	0	1	1	1	0	0
Sly08g0279081	M11	NA	42	38	74	92	79	124	102	124	33	29
Sly08g0279091	M18	NA	37	35	40	33	32	40	33	42	27	30
Sly08g0279101	M3	NA	50	49	39	39	38	35	40	39	69	82
Sly08g0279121	M19	NA	12	12	13	10	11	12	10	13	9	12
Sly08g0279141	M22	NA	10	9	10	10	9	9	7	11	7	9
Sly08g0279171	M1	NA	88	93	177	20	24	8	4	4	3	3
Sly08g0279181	M1	NA	62	59	76	26	43	51	39	52	10	5
Sly08g0279191	M3	NA	47	46	40	54	59	34	41	34	54	71
Sly08g0279201	M1	NA	2	4	7	182	65	1	1	0	1	0
Sly08g0279211	M1	NA	11	11	18	272	167	1	1	1	1	1
Sly08g0279231	M1	NA	10	10	12	11	19	5	5	5	4	7
Sly08g0279241	M22	NA	1	1	2	0	0	2	1	1	1	0
Sly08g0279251	M1	NA	2	2	4	8	9	2	2	3	6	5
Sly08g0279261	M11	NA	13	13	19	37	39	15	14	18	32	28
Sly08g0279281	M3	NA	411	426	315	287	229	172	215	113	60	126
Sly08g0279291	M1	NA	8	6	8	2	1	7	4	5	1	1
Sly08g0279301	M1	NA	32	31	58	79	68	15	16	23	21	107
Sly08g0279321	M1	NA	44	29	29	2	5	1	1	1	0	1
Sly08g0279331	M1	NA	1	1	2	0	0	0	1	1	0	0
Sly08g0279341	M5	NA	19	21	14	8	10	19	19	12	7	6
Sly08g0279351	M2	NA	121	123	93	102	83	84	106	70	78	79
Sly08g0279361	M3	NA	135	152	73	82	153	86	92	50	42	96
Sly08g0279391	M1	NA	8	9	8	4	2	6	5	4	3	2
Sly08g0279401	M1	SlPYL5/PYR1	4	3	4	9	7	2	2	2	4	5
Sly08g0279411	M1	NA	274	271	330	79	61	4	2	2	1	2
Sly08g0279421	M1	NA	1	1	1	1	1	1	0	0	0	0
Sly08g0279431	M1	NA	73	70	72	82	91	56	62	59	68	84
Sly08g0279471	M12	NA	4	9	6	2	13	16	44	14	5	42
Sly08g0279481	M3	NA	32	34	28	23	22	25	27	18	23	22
Sly08g0279491	M3	glutathione peroxidas	29	29	22	25	26	21	21	20	25	23
Sly08g0279501	M11	NA	26	24	29	48	83	57	55	64	58	95
Sly08g0279511	M14	NA	182	103	225	9	3	129	92	122	2	2
Sly08g0279521	M13	NA	2	2	3	2	1	3	2	2	2	2
Sly08g0279541	M11	NA	13	13	14	19	17	14	14	14	19	19
Sly08g0279551	M22	NA	5	4	3	1	1	5	3	4	1	0
Sly08g0279561	M3	NA	11	8	4	3	2	7	5	6	1	1
Sly08g0279571	M1	NA	29	26	29	42	80	23	22	25	38	36
Sly08g0279581	M1	NA	50	48	44	70	154	40	41	38	69	82
Sly08g0279591	M3	NA	37	35	30	50	117	26	30	27	58	77
Sly08g0279601	M11	NA	12	11	14	22	18	20	19	21	24	18
Sly08g0279611	M21	NA	1	1	2	2	1	1	1	1	0	0
Sly08g0279621	M1	NA	27	25	28	40	44	22	25	22	38	41
Sly08g0279631	M9	NA	8	7	7	8	6	8	8	8	11	9
Sly08g0279641	M3	NA	14	15	13	19	22	11	12	10	23	23
Sly08g0279651	M3	NA	8	14	7	7	11	5	10	3	1	2
Sly08g0279661	M9	NA	92	91	89	92	111	99	115	92	95	138
Sly08g0279671	M12	SlPRR8	8	9	11	76	32	32	48	63	391	182
Sly08g0279691	M12	NA	176	179	198	161	106	255	282	241	86	89
Sly08g0279701	M13	NA	14	16	16	19	27	15	15	16	38	38
Sly08g0279711	M3	NA	46	40	39	36	43	40	45	37	60	79
Sly08g0279721	M3	NA	15	16	16	17	11	14	14	12	10	7
Sly08g0279731	M15	NA	30	25	24	29	27	25	26	26	34	31
Sly08g0279741	M3	NA	23	24	17	26	19	19	18	15	20	16
Sly08g0279761	M1	NA	17	18	22	52	107	2	2	3	14	96
Sly08g0279771	M19	NA	46	49	48	49	60	49	40	48	62	71
Sly08g0279781	M1	NA	2	3	3	2	2	2	2	2	3	2
Sly08g0279791	M1	NA	74	91	57	41	15	1	1	1	2	2
Sly08g0279801	M1	NA	6	6	6	4	2	7	7	6	5	3
Sly08g0279811	M12	NA	49	44	47	28	21	50	59	50	25	12
Sly08g0279821	M22	NA	2	2	2	1	1	5	3	5	1	1
Sly08g0279831	M10	NA	4	5	3	1	1	6	6	4	1	1
Sly08g0279851	M1	NA	13	13	11	9	8	8	9	7	8	6
Sly08g0279871	M12	NA	3	3	2	1	1	3	5	4	2	1
Sly08g0279881	M18	NA	24	25	31	33	35	40	31	42	28	31
Sly08g0279891	M11	NA	48	44	68	45	48	125	107	133	24	24
Sly08g0279901	M1	NA	269	271	151	87	101	85	84	94	82	98
Sly08g0279911	M11	NA	17	17	19	21	25	22	17	23	20	24
Sly08g0279921	M12	NA	58	48	97	263	120	49	69	88	228	109
Sly08g0279931	M3	NA	25	23	20	20	19	12	14	11	12	19
Sly08g0279941	M3	Solyc08g077480	78	63	67	27	15	36	49	31	30	27
Sly08g0279951	M19	NA	10	11	11	21	23	11	9	11	10	12
Sly08g0279961	M12	NA	65	60	61	156	137	62	74	74	108	91
Sly08g0279971	M11	NA	34	33	34	37	52	37	33	44	49	68
Sly08g0279981	M1	BAM3-like3	76	74	76	43	43	70	60	69	11	27
Sly08g0279991	M2	NA	15	15	12	18	18	13	15	15	31	31
Sly08g0280001	M1	NA	4	4	2	1	1	2	1	1	1	1
Sly08g0280011	M10	NA	25	35	14	7	17	39	57	27	28	51
Sly08g0280071	M2	NA	41	45	47	51	56	29	51	35	112	98
Sly08g0280081	M1	NA	22	23	25	30	20	17	17	18	40	21
Sly08g0280101	M16	NA	388	332	346	278	182	289	256	300	251	188
Sly08g0280111	M16	NA	415	359	351	289	200	314	271	342	278	180
Sly08g0280121	M1	NA	42	38	53	22	16	28	23	27	14	11
Sly08g0280131	M3	NA	4	6	2	1	1	1	1	1	1	1
Sly08g0280141	M1	NA	41	40	40	50	62	37	35	37	55	59
Sly08g0280151	M3	NA	25	43	15	3	2	11	30	8	1	4
Sly08g0280161	M3	NA	33	29	24	17	14	19	20	16	11	10
Sly08g0280171	M1	NA	182	192	99	45	26	33	37	19	90	41
Sly08g0280181	M3	NA	300	326	161	78	53	52	69	32	242	140
Sly08g0280201	M3	NA	87	74	49	22	13	35	41	28	14	14
Sly08g0280211	M3	NA	10	10	9	10	11	8	7	7	8	9
Sly08g0280251	M1	NA	31	31	30	32	35	28	26	29	34	43
Sly08g0280261	M12	NA	12	12	14	23	35	15	17	16	38	44
Sly08g0280271	M1	NA	10	13	12	7	8	10	9	9	8	7
Sly08g0280281	M12	NA	1	1	2	1	1	7	8	7	1	1
Sly08g0280291	M12	NA	22	18	22	4	1	202	207	204	18	2
Sly08g0280301	M12	NA	30	24	35	46	51	136	118	142	44	42
Sly08g0280311	M11	NA	102	91	110	177	230	152	139	169	160	225
Sly08g0280321	M1	NA	1	1	1	1	0	1	1	1	1	1
Sly08g0280331	M12	NA	1	1	1	0	1	1	0	2	1	1
Sly08g0280341	M2	NA	79	80	66	66	61	52	65	46	69	60
Sly08g0280351	M2	NA	73	75	72	89	98	64	68	64	82	85
Sly08g0280361	M22	SlSDG6	1	1	1	0	1	1	1	1	1	1
Sly08g0280371	M11	NA	17	12	15	11	13	21	17	22	28	19
Sly08g0280381	M1	NA	13	14	14	12	11	9	8	10	11	9
Sly08g0280391	M1	NA	11	12	8	6	3	5	4	4	9	14
Sly08g0280401	M3	NA	161	149	125	221	266	139	155	120	158	246
Sly08g0280411	M11	NA	2	2	2	1	1	3	3	2	1	1
Sly08g0280421	M12	NA	26	25	24	23	28	28	24	27	25	35
Sly08g0280431	M11	NA	13	13	14	25	35	18	17	17	13	17
Sly08g0280441	M1	NA	2	3	2	2	1	1	0	1	1	0
Sly08g0280451	M22	NA	1	1	1	0	0	2	0	1	0	0
Sly08g0280461	M3	NA	88	124	49	35	24	46	83	15	7	15
Sly08g0280471

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0342421	M1	NA	9	11	13	14	16	7	8	10	13	20
Sly02g0342431	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly02g0342441	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0342471	M12	NSY4/aba4	14	12	14	32	34	17	21	19	32	27
Sly02g0342481	M1	NA	28	27	23	22	26	16	20	17	33	35
Sly02g0342491	M1	NA	20	21	17	19	19	15	15	13	20	17
Sly02g0342501	M12	NA	6	6	7	13	6	7	8	8	15	9
Sly02g0342511	M11	NA	12	10	16	12	11	23	21	28	25	18
Sly02g0342521	M1	NA	19	19	18	10	7	13	11	14	14	9
Sly02g0342531	M1	NA	10	11	11	7	6	6	7	7	9	6
Sly02g0342541	M12	NA	1	1	1	1	1	1	2	1	1	0
Sly02g0342551	M1	NA	10	12	11	19	12	3	3	1	4	2
Sly02g0342561	M18	NA	20	22	24	23	14	24	24	23	11	8
Sly02g0342571	M7	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0342581	M11	NA	16	15	20	26	29	44	37	70	40	34
Sly02g0342591	M11	NA	48	44	54	80	67	58	53	70	47	45
Sly02g0342601	M12	NA	4	4	4	4	8	6	5	6	9	13
Sly02g0342611	M11	STE1-like2	5	3	11	1	1	15	8	10	1	1
Sly02g0342631	M18	NA	9	10	11	14	16	11	10	13	16	15
Sly02g0342641	M1	NA	10	23	11	2	1	2	4	1	1	1
Sly02g0342651	M1	NA	39	38	44	32	31	31	33	32	26	29
Sly02g0342661	M3	PPR-like48	5	4	4	3	4	3	4	3	3	3
Sly02g0342671	M1	NA	376	339	362	243	220	239	241	240	224	205
Sly02g0342681	M1	NA	7	6	7	2	1	6	5	5	2	1
Sly02g0342691	M12	NA	20	19	14	8	8	23	19	18	9	15
Sly02g0342701	M3	NA	17	29	20	4	2	18	16	4	1	1
Sly02g0342711	M6	NA	8	17	16	2	1	8	7	1	1	0
Sly02g0342721	M22	NA	1	1	1	1	0	2	1	1	0	0
Sly02g0342731	M3	NA	1	1	1	1	0	1	1	1	0	1
Sly02g0342741	M3	NA	170	285	121	28	31	29	43	12	5	11
Sly02g0342751	M11	NA	155	92	54	7	14	443	253	366	101	129
Sly02g0342761	M12	NA	68	71	70	82	79	82	111	94	119	105
Sly02g0342771	M12	NA	30	28	30	32	31	37	43	38	39	37
Sly02g0342781	M18	NA	19	25	23	24	20	27	25	29	26	20
Sly02g0342791	M1	NA	3	3	5	5	1	2	2	2	1	1
Sly02g0342801	M11	NA	13	14	16	13	17	18	17	19	19	21
Sly02g0342811	M12	NA	10	8	9	8	4	19	15	15	12	6
Sly02g0342821	M3	NA	16	15	9	6	7	13	14	9	8	7
Sly02g0342831	M10	NA	4	9	3	1	1	10	17	3	2	1
Sly02g0342851	M12	NA	1	1	1	1	1	3	2	1	1	3
Sly02g0342871	M12	NA	1	2	2	1	3	5	6	3	6	6
Sly02g0342881	M22	NA	1	1	1	0	0	2	0	1	0	0
Sly02g0342891	M18	NA	15	14	17	15	22	15	16	15	18	22
Sly02g0342901	M12	NA	1	1	1	1	1	3	2	1	0	1
Sly02g0342911	M1	NA	108	101	96	114	83	14	8	11	3	2
Sly02g0342921	M11	NA	2	2	2	1	1	3	3	2	1	1
Sly02g0342941	M22	NA	107	31	48	3	1	248	68	160	11	1
Sly02g0342951	M22	NA	13	13	14	12	18	15	13	13	10	11
Sly02g0342961	M3	NA	37	38	30	26	26	25	26	23	28	26
Sly02g0342971	M12	NA	35	33	34	37	29	39	41	41	54	49
Sly02g0342981	M3	NA	4	7	6	1	1	3	2	1	1	1
Sly02g0343001	M1	NA	23	24	23	18	12	16	16	16	4	5
Sly02g0343011	M17	NA	24	26	24	34	42	23	23	25	47	57
Sly02g0343031	M17	NA	2	2	2	2	3	2	2	2	1	2
Sly02g0343041	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0343081	M11	NA	8	7	10	30	81	8	9	12	43	124
Sly02g0343101	M3	NA	24	33	17	7	6	21	20	9	3	3
Sly02g0343111	M1	NA	20	21	19	14	20	17	15	15	19	23
Sly02g0343121	M1	NA	46	50	40	37	50	33	33	32	48	70
Sly02g0343131	M10	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0343141	M12	NA	5	5	4	7	8	11	11	10	16	16
Sly02g0343151	M12	NA	3	3	3	5	5	6	5	6	6	6
Sly02g0343161	M3	NA	19	20	16	22	27	17	17	15	43	45
Sly02g0343171	M3	NA	3	7	2	1	2	3	6	2	2	7
Sly02g0343181	M11	NA	33	29	34	30	41	48	40	51	39	42
Sly02g0343191	M12	BIN2	68	73	77	94	132	95	112	93	120	179
Sly02g0343201	M1	NA	19	18	21	21	41	18	18	19	24	44
Sly02g0343241	M12	NA	78	74	86	140	126	87	98	112	187	136
Sly02g0343261	M11	NA	50	41	53	79	90	111	94	127	90	114
Sly02g0343281	M11	NA	27	18	26	27	19	62	54	75	28	17
Sly02g0343291	M18	NA	34	34	35	48	58	41	34	42	56	64
Sly02g0343301	M11	NA	1	1	1	0	0	2	2	2	0	0
Sly02g0343331	M12	NA	2	1	1	1	1	4	4	2	1	1
Sly02g0343341	M6	NA	16	18	19	19	20	18	17	17	34	25
Sly02g0343361	M1	NA	49	50	44	50	57	36	34	34	42	43
Sly02g0343371	M3	NA	12	12	10	9	10	11	8	7	1	2
Sly02g0343381	M1	NA	15	12	14	9	8	4	4	2	1	1
Sly02g0343391	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0343401	M11	NA	33	27	31	33	95	32	31	37	36	90
Sly02g0343411	M12	NA	1	1	1	1	1	4	3	3	1	2
Sly02g0343431	M11	NA	17	14	17	16	14	19	19	21	12	11
Sly02g0343441	M11	NA	28	26	29	23	20	33	29	37	30	33
Sly02g0343451	M3	NA	572	710	548	362	406	296	368	264	293	293
Sly02g0343461	M11	NA	25	24	29	41	49	29	27	38	44	43
Sly02g0343471	M12	NA	17	20	19	18	13	22	26	21	14	20
Sly02g0343481	M11	NA	13	13	15	11	8	22	19	28	8	5
Sly02g0343501	M3	LeHb1	120	130	116	94	76	86	97	58	20	35
Sly02g0343511	M3	LeHb1	130	123	100	89	81	89	98	57	28	65
Sly02g0343521	M12	NA	10	11	11	7	6	14	16	12	5	6
Sly02g0343551	M11	NA	19	16	17	17	33	37	30	33	50	43
Sly02g0343561	M11	NA	8	8	7	10	15	14	11	14	18	15
Sly02g0343571	M12	NA	7	8	7	6	3	9	11	8	5	2
Sly02g0343581	M12	NA	18	17	22	12	3	83	83	75	19	5
Sly02g0343591	M1	NA	2	2	2	1	2	1	1	2	1	1
Sly02g0343611	M12	NA	2	3	2	2	2	4	4	5	6	7
Sly02g0343621	M1	NA	7	7	6	2	2	2	1	1	1	1
Sly02g0343631	M1	NA	5	5	6	2	1	5	4	4	1	1
Sly02g0343641	M1	NA	20	22	45	10	5	19	13	19	2	1
Sly02g0343651	M12	NA	1	1	1	0	1	2	2	1	0	0
Sly02g0343691	M1	NA	21	18	42	496	277	1	1	1	1	1
Sly02g0343711	M10	NA	53	58	44	42	58	71	78	49	50	70
Sly02g0343721	M11	NA	25	24	26	32	43	37	32	38	43	62
Sly02g0343731	M11	NA	18	17	22	36	49	42	35	54	39	46
Sly02g0343741	M2	NA	18	19	16	14	14	16	17	13	15	15
Sly02g0343751	M11	NA	18	17	19	15	13	24	24	26	31	25
Sly02g0343761	M12	NA	21	26	21	30	23	92	114	93	129	81
Sly02g0343771	M9	NA	9	9	10	6	4	14	18	11	11	12
Sly02g0343781	M7	NA	27	49	34	14	82	51	174	36	34	251
Sly02g0343791	M1	NA	18	15	16	22	21	14	13	15	30	34
Sly02g0343801	M11	NA	42	36	46	52	74	48	44	58	51	65
Sly02g0343811	M1	NA	136	134	132	206	194	123	123	123	149	152
Sly02g0343821	M19	NA	13	16	14	23	30	15	15	15	21	21
Sly02g0343841	M11	NA	71	63	71	64	52	82	77	94	39	26
Sly02g0343871	M11	NA	26	22	36	22	11	61	46	71	24	8
Sly02g0343881	M11	NA	2	2	2	1	1	2	2	2	1	1
Sly02g0343891	M12	NA	8	6	7	13	26	9	10	8	14	19
Sly02g0343901	M12	NA	20	19	20	38	67	29	26	22	44	38
Sly02g0343921	M3	NA	2	2	2	1	1	2	2	1	1	1
Sly02g0343931	M3	BIR3	35	36	33	21	24	31	35	25	16	24
Sly02g0343961	M3	NA	23	32	20	23	45	14	21	13	23	54
Sly02g0343971	M12	SIP4H6	1	1	1	0	0	2	1	1	1	1
Sly02g0343981	M12	NA	1	1	1	2	2	1	1	1	0	1
Sly02g0343991	M1	NA	3	3	3	3	4	2	3	2	2	2
Sly02g0344031	M6	NA	46	73	48	9	79	32	74	18	12	114
Sly02g0344041	M8	NA	50	50	43	60	35	54	56	46	36	27
Sly02g0344051	M11	NA	10	9	11	13	13	14	12	16	12	14
Sly02g0344071	M3	NA	4	4	3	1	0	3	3	2	1	1
Sly02g0344091	M11	NA	15	14	12	8	9	16	15	18	13	10
Sly02g0344101	M1	NA	3	4	3	3	3	2	3	3	3	2
Sly02g0344111	M11	NA	36	38	39	42	28	53	44	50	25	22
Sly02g0344121	M3	NA	49	50	38	46	60	37	43	38	74	92
Sly02g0344131	M1	NA	16	17	18	21	19	16	15	18	18	17
Sly02g0344151	M11	NA	20	17	22	33	33	24	24	31	39	35
Sly02g0344161	M11	SIPIN8	1	1	1	2	2	1	1	1	2	2

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0280541	M11	NA	28	27	24	28	39	26	23	27	38	44
Sly08g0280551	M22	NA	7	5	5	11	8	6	5	6	13	5
Sly08g0280561	M1	NA	12	12	10	12	15	9	9	8	10	15
Sly08g0280571	M23	NA	42	12	17	3	1	95	30	52	4	1
Sly08g0280581	M3	SIERF.A4	1	6	1	1	1	1	1	0	0	0
Sly08g0280591	M3	SIERF.A1	6	16	3	1	1	1	1	1	1	1
Sly08g0280601	M10	SIERF.B13	4	10	8	6	35	9	16	6	3	36
Sly08g0280621	M1	NA	14	13	27	8	13	4	3	6	4	5
Sly08g0280631	M11	NA	89	81	87	51	53	87	85	91	55	70
Sly08g0280641	M3	NA	1	1	1	1	0	1	1	1	0	0
Sly08g0280651	M19	NA	28	28	30	24	22	31	25	32	23	20
Sly08g0280661	M13	NA	78	69	81	105	112	71	71	82	107	145
Sly08g0280671	M11	NA	52	52	58	88	79	53	56	60	32	27
Sly08g0280691	M11	NA	35	31	31	31	34	39	40	39	40	43
Sly08g0280701	M11	PPR-like1	3	2	3	3	2	3	3	4	3	2
Sly08g0280711	M1	NA	5	5	5	3	3	1	1	2	1	1
Sly08g0280721	M12	NA	17	13	8	2	1	31	21	15	1	0
Sly08g0280731	M3	NA	24	26	13	7	4	17	14	13	13	5
Sly08g0280741	M18	NA	38	38	43	29	24	44	41	44	27	22
Sly08g0280761	M12	NA	21	19	20	9	8	60	58	38	5	6
Sly08g0280791	M11	NA	30	33	32	41	49	36	37	41	66	84
Sly08g0280801	M2	NA	8	8	8	9	9	8	8	7	9	8
Sly08g0280811	M3	OPC-8:CoA oxidase	309	346	265	114	84	136	140	90	65	55
Sly08g0280851	M13	NA	97	98	105	130	161	94	98	105	144	181
Sly08g0280861	M3	NA	29	32	22	22	30	21	24	20	20	27
Sly08g0280871	M12	NA	1	1	2	17	13	1	1	6	106	36
Sly08g0280881	M12	NA	1	3	7	331	461	3	19	68	1015	444
Sly08g0280891	M11	NA	3	3	4	5	5	5	3	5	19	2
Sly08g0280901	M3	NA	21	21	18	22	22	17	19	18	26	27
Sly08g0280911	M12	NA	3	4	4	8	6	5	4	5	7	6
Sly08g0280921	M1	NA	4	5	5	5	6	3	3	3	5	6
Sly08g0280931	M10	GEM-like5	118	169	76	72	283	176	232	84	94	384
Sly08g0280941	M10	NA	3	5	2	3	8	10	9	2	2	5
Sly08g0280951	M19	NA	58	62	61	83	94	59	49	59	53	58
Sly08g0280961	M12	NA	13	14	14	15	14	15	15	14	11	10
Sly08g0280971	M1	NA	2	2	2	14	10	1	1	1	1	1
Sly08g0280981	M1	NA	22	23	22	17	14	13	16	13	16	12
Sly08g0280991	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0281021	M13	NA	13	12	13	18	25	12	11	13	18	24
Sly08g0281031	M19	NA	30	30	32	28	38	29	25	29	39	69
Sly08g0281051	M12	NA	34	34	32	27	29	35	36	33	31	34
Sly08g0281071	M12	NA	12	22	38	89	21	58	106	101	166	58
Sly08g0281081	M1	NA	19	19	17	18	17	9	9	8	7	11
Sly08g0281091	M1	NA	94	112	87	5	4	42	42	19	2	4
Sly08g0281111	M12	NA	10	9	11	8	8	14	15	15	13	10
Sly08g0281121	M4	NA	9	6	21	50	371	21	12	15	129	478
Sly08g0281151	M3	NA	41	37	39	25	32	37	38	37	42	53
Sly08g0281171	M11	NA	8	10	10	13	15	13	12	16	20	20
Sly08g0281181	M1	NA	21	23	23	18	15	18	18	16	13	10
Sly08g0281191	M1	NA	8	11	12	13	3	3	3	3	1	1
Sly08g0281201	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0281211	M3	NA	9	14	10	9	7	8	7	4	4	5
Sly08g0281221	M22	NA	1	1	1	1	1	1	1	1	1	2
Sly08g0281231	M3	NA	14	13	12	16	16	14	15	11	18	20
Sly08g0281241	M11	NA	18	17	16	9	7	21	21	18	9	7
Sly08g0281251	M12	NA	111	110	123	305	430	150	173	232	646	762
Sly08g0281271	M12	NA	2	2	2	1	1	30	29	20	1	1
Sly08g0281281	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0281291	M3	LDH	9	10	3	2	3	5	5	6	1	2
Sly08g0281301	M11	NA	120	114	112	167	188	135	138	152	181	203
Sly08g0281311	M3	NA	22	64	7	12	86	15	29	14	171	137
Sly08g0281321	M3	NA	1	1	1	1	0	1	1	1	1	1
Sly08g0281331	M23	NA	15	4	3	1	1	36	11	4	1	1
Sly08g0281381	M1	NA	91	105	45	1	1	4	1	1	0	1
Sly08g0281391	M9	NA	20	36	17	9	4	32	44	26	26	10
Sly08g0281411	M3	NA	7	8	6	9	13	5	5	4	5	7
Sly08g0281421	M12	NA	2	1	1	1	0	4	4	2	1	0
Sly08g0281431	M12	NA	1	1	1	1	0	2	2	1	1	1
Sly08g0281441	M12	NA	30	29	35	34	38	45	41	53	52	47
Sly08g0281451	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0281471	M2	NA	21	17	19	20	17	17	18	18	15	11
Sly08g0281481	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0281491	M11	NA	1	1	1	1	0	3	1	2	1	0
Sly08g0281501	M11	NA	47	41	58	123	153	58	54	66	78	138
Sly08g0281511	M2	NA	1	1	1	1	1	1	1	1	0	0
Sly08g0281521	M12	NA	14	32	24	11	14	87	171	88	37	64
Sly08g0281531	M1	NA	10	10	8	6	3	1	1	1	0	0
Sly08g0281541	M11	NA	20	19	22	32	39	49	44	55	27	32
Sly08g0281581	M3	SAUR67	4	3	2	1	1	1	1	1	1	2
Sly08g0281591	M1	Solyc08g079150	1	1	1	1	1	1	1	1	0	0
Sly08g0281601	M23	NA	9	3	4	1	1	24	7	14	2	1
Sly08g0281611	M12	NA	166	147	172	214	448	218	190	247	301	756
Sly08g0281621	M18	NA	24	30	36	53	78	38	32	42	39	46
Sly08g0281631	M12	NA	1	0	0	0	0	3	3	1	0	0
Sly08g0281661	M12	NA	36	39	37	36	20	207	216	324	140	37
Sly08g0281671	M1	NA	3	2	2	1	0	2	1	2	1	1
Sly08g0281681	M12	NA	108	87	113	73	65	106	121	122	201	181
Sly08g0281691	M11	NA	189	176	210	224	347	236	213	256	292	435
Sly08g0281701	M22	NA	1	1	1	1	0	3	1	2	0	0
Sly08g0281711	M11	NA	8	6	12	9	19	10	7	13	7	6
Sly08g0281741	M12	NA	1	1	1	1	0	1	1	1	1	1
Sly08g0281781	M22	NA	1	1	1	0	0	3	1	2	0	0
Sly08g0281791	M22	NA	11	1	8	0	0	31	3	36	0	0
Sly08g0281801	M22	NA	5	1	4	0	0	10	2	11	0	0
Sly08g0281841	M22	NA	2	1	2	0	0	9	1	12	0	0
Sly08g0281851	M22	NA	5	2	3	0	0	12	1	10	0	0
Sly08g0281861	M22	NA	1	1	1	0	0	2	1	3	0	0
Sly08g0281871	M22	NA	7	1	5	0	0	17	2	18	0	0
Sly08g0281911	M1	NA	1	1	2	1	0	0	0	1	0	0
Sly08g0281921	M1	NA	33	40	15	1	0	2	1	1	0	1
Sly08g0281931	M14	NA	65	60	85	122	78	65	53	68	4	5
Sly08g0281941	M10	NA	10	9	9	5	7	11	12	9	4	7
Sly08g0281951	M12	NA	48	43	46	56	67	56	54	54	72	69
Sly08g0281961	M1	NA	15	18	18	11	6	2	2	2	1	1
Sly08g0281971	M12	NA	29	26	23	26	31	32	28	28	34	40
Sly08g0281981	M1	NA	6	5	5	10	17	3	2	4	25	29
Sly08g0281991	M12	NA	17	17	18	26	38	19	22	21	33	47
Sly08g0282001	M12	NA	81	82	84	128	171	87	87	93	148	196
Sly08g0282011	M7	NA	6	8	11	17	23	6	14	11	29	50
Sly08g0282021	M3	NA	51	66	50	32	31	33	36	29	27	30
Sly08g0282031	M1	NA	7	7	8	7	7	6	5	5	3	2
Sly08g0282041	M9	NA	2	1	1	0	1	2	2	1	0	0
Sly08g0282051	M11	NA	6	5	9	1	0	15	13	12	1	1
Sly08g0282081	M12	NA	13	12	10	13	11	15	13	13	8	5
Sly08g0282161	M10	NA	4	6	2	1	2	6	7	3	2	2
Sly08g0282171	M1	NA	20	16	7	3	1	4	2	2	1	1
Sly08g0282181	M2	NA	81	76	67	77	81	67	79	69	124	132
Sly08g0282191	M11	NA	60	56	63	112	188	74	79	86	127	209
Sly08g0282211	M1	NA	10	8	11	4	4	2	2	2	1	1
Sly08g0282221	M19	NA	3	4	3	2	2	3	2	3	1	2
Sly08g0282231	M1	NA	6	8	5	5	4	5	4	4	3	3
Sly08g0282241	M3	NA	5	5	5	3	4	4	4	4	3	2
Sly08g0282251	M22	NA	14	15	12	5	7	20	9	15	4	6
Sly08g0282261	M11	NA	24	24	26	48	70	32	36	37	58	87
Sly08g0282271	M11	NA	27	26	32	41	51	34	36	43	43	50
Sly08g0282281	M11	NA	3	3	4	2	2	4	4	6	1	1
Sly08g0282291	M1	NA	36	49	77	32	10	1	1	1	1	1
Sly08g0282301	M6	NA	32	39	30	20	159	33	49	28	21	289
Sly08g0282311	M22	NA	6	4	5	2	1	6	2	6	1	1
Sly08g0282341	M12	NA	12	10	14	4	1	137	147	189	8	2
Sly08g0282361	M12	NA	2	2	2

			Estimated Transcript Number								
			Pericarp					Gel			
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0344211	M1	SSRP1	92	104	83	64	82	67	73	61	49	74
Sly02g0344221	M3	NA	34	34	25	29	26	23	29	20	20	18
Sly02g0344231	M7	NA	31	37	26	31	43	28	35	32	48	65
Sly02g0344241	M9	PCO1	63	81	60	133	98	66	101	82	239	194
Sly02g0344251	M11	NA	187	188	211	230	240	183	174	248	246	273
Sly02g0344261	M12	NA	52	51	53	49	45	67	64	63	47	60
Sly02g0344271	M1	NA	91	82	106	52	21	16	15	15	8	7
Sly02g0344281	M1	NA	14	12	15	9	3	11	11	9	3	3
Sly02g0344301	M1	NA	17	19	15	4	1	6	5	4	2	1
Sly02g0344311	M1	NA	5	5	4	2	1	2	2	1	1	1
Sly02g0344341	M11	NA	2	1	2	1	1	5	4	4	1	1
Sly02g0344351	M11	NA	13	11	26	2	1	46	51	44	3	2
Sly02g0344361	M3	NA	27	42	23	6	14	34	31	16	1	3
Sly02g0344371	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly02g0344381	M1	NA	28	23	28	9	2	21	17	20	3	1
Sly02g0344391	M9	NA	3	3	3	12	19	6	7	7	35	21
Sly02g0344401	M3	NA	66	64	54	53	60	44	42	37	44	46
Sly02g0344411	M22	NA	38	9	26	1	1	71	15	91	1	1
Sly02g0344441	M17	NA	182	172	180	159	130	153	147	179	137	144
Sly02g0344451	M11	NA	39	40	46	51	46	48	52	56	60	55
Sly02g0344461	M3	NA	13	26	8	4	15	13	18	8	5	25
Sly02g0344471	M11	NA	4	4	6	4	5	7	7	7	11	12
Sly02g0344481	M15	NA	131	73	121	63	57	90	83	109	67	83
Sly02g0344491	M11	NA	6	5	6	1	1	10	7	8	1	1
Sly02g0344501	M9	NA	1	1	1	0	1	2	3	2	1	1
Sly02g0344511	M1	STS6	36	33	31	23	33	30	30	29	11	15
Sly02g0344521	M11	NA	27	28	27	28	32	28	27	31	31	37
Sly02g0344551	M1	NA	9	9	8	10	11	6	6	4	7	7
Sly02g0344581	M3	NA	8	7	6	2	3	5	5	4	7	9
Sly02g0344601	M10	NA	21	35	21	7	27	69	88	23	2	17
Sly02g0344611	M1	expansin precursor 5	64	54	92	17	5	33	29	37	4	2
Sly02g0344621	M14	NA	45	40	45	41	50	41	41	44	52	67
Sly02g0344631	M22	NA	3	2	3	2	1	4	3	3	2	1
Sly02g0344641	M12	NA	4	4	4	2	2	6	6	4	3	1
Sly02g0344661	M1	NA	7	8	6	69	56	2	4	2	9	7
Sly02g0344671	M11	NA	1	2	2	1	1	2	3	2	2	1
Sly02g0344681	M12	PPR-like45	2	2	1	2	2	3	3	3	2	1
Sly02g0344691	M12	NA	1	2	2	2	1	2	3	3	2	1
Sly02g0344701	M11	NA	6	6	6	6	6	6	6	7	6	6
Sly02g0344711	M1	NA	3	3	3	1	1	3	1	1	1	0
Sly02g0344721	M1	NA	14	9	18	36	37	1	1	1	1	3
Sly02g0344731	M12	NA	10	11	9	8	3	15	23	18	32	18
Sly02g0344741	M12	NA	15	16	14	13	6	26	34	31	51	23
Sly02g0344751	M1	NA	2	2	1	1	2	2	1	1	1	2
Sly02g0344761	M1	NA	10	12	14	8	5	3	2	2	1	1
Sly02g0344771	M1	NA	6	7	8	1	1	4	5	3	0	1
Sly02g0344781	M7	NA	12	16	11	4	4	15	31	15	8	21
Sly02g0344791	M7	NA	7	12	5	3	2	9	19	10	4	9
Sly02g0344801	M3	NA	283	285	232	267	348	215	235	189	314	394
Sly02g0344811	M12	NA	3	9	15	676	1630	9	29	39	1195	2459
Sly02g0344831	M3	NA	29	27	24	20	21	24	26	22	24	27
Sly02g0344841	M3	NA	22	26	22	29	24	21	19	20	24	21
Sly02g0344851	M18	NA	31	33	38	43	46	33	31	34	48	50
Sly02g0344861	M22	NA	2	1	2	2	3	2	1	2	3	3
Sly02g0344871	M22	NA	2	2	2	1	1	10	1	12	1	0
Sly02g0344881	M22	NA	6	2	5	1	1	20	2	24	1	1
Sly02g0344891	M3	NA	6	6	6	5	3	4	5	4	3	3
Sly02g0344901	M13	NA	22	22	40	63	79	34	35	60	33	20
Sly02g0344911	M11	NA	34	37	44	70	107	71	68	92	129	170
Sly02g0344921	M12	NA	4	5	3	2	6	8	17	8	13	39
Sly02g0344931	M9	NA	18	22	17	12	13	39	54	46	61	50
Sly02g0344941	M12	NA	8	8	11	10	16	12	11	13	28	37
Sly02g0344961	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0344981	M11	NA	1	1	1	1	1	1	1	2	1	1
Sly02g0345001	M11	NA	7	8	8	10	14	15	14	17	20	26
Sly02g0345011	M11	NA	3	4	4	5	7	7	8	9	9	5
Sly02g0345021	M12	NA	7	6	9	8	12	13	12	14	15	12
Sly02g0345031	M12	NA	2	2	3	3	11	5	7	7	7	6
Sly02g0345041	M3	NA	32	39	28	33	19	29	30	16	10	6
Sly02g0345051	M11	NA	4	4	6	5	6	8	7	13	4	4
Sly02g0345061	M12	NA	25	23	23	18	23	23	23	25	20	31
Sly02g0345081	M1	NA	64	46	51	23	39	37	33	42	40	56
Sly02g0345091	M11	NA	4	3	5	2	2	4	4	4	2	2
Sly02g0345101	M11	NA	13	12	15	30	22	23	21	28	35	32
Sly02g0345111	M12	NA	10	9	9	9	12	11	11	12	15	21
Sly02g0345121	M12	NA	69	73	71	94	104	73	72	72	75	81
Sly02g0345131	M3	NA	27	29	26	35	30	6	12	5	12	23
Sly02g0345141	M11	NA	30	27	27	29	25	36	36	40	38	35
Sly02g0345151	M4	NA	10	10	9	10	21	10	11	9	16	23
Sly02g0345161	M11	NA	28	24	30	29	29	33	32	38	36	33
Sly02g0345171	M14	NA	14	12	18	16	27	13	11	17	15	19
Sly02g0345181	M12	HSP110	21	20	31	224	669	60	50	63	147	389
Sly02g0345191	M3	NA	97	97	67	100	117	59	66	45	103	103
Sly02g0345201	M10	NA	34	57	23	7	11	58	112	20	5	23
Sly02g0345221	M1	NA	2	3	3	2	2	2	2	2	3	2
Sly02g0345231	M3	NA	19	20	18	23	26	19	20	18	27	28
Sly02g0345251	M7	NA	110	145	76	93	97	118	174	75	27	37
Sly02g0345261	M3	NA	156	169	139	172	162	140	161	128	172	153
Sly02g0345281	M18	NA	36	38	39	47	57	44	36	44	54	64
Sly02g0345291	M11	NA	32	29	33	38	32	34	37	41	43	18
Sly02g0345301	M3	NA	4	6	3	3	7	3	5	3	3	10
Sly02g0345311	M11	NA	1	1	1	0	0	1	1	1	1	0
Sly02g0345321	M11	NA	102	86	95	84	75	105	90	122	119	113
Sly02g0345331	M12	NA	5	5	5	4	5	6	5	5	7	10
Sly02g0345341	M1	NA	37	41	37	20	18	30	29	31	23	24
Sly02g0345361	M1	NA	54	48	43	47	72	41	41	44	79	108
Sly02g0345371	M3	NA	18	21	16	14	21	20	19	11	11	12
Sly02g0345391	M1	NA	1	1	1	1	0	1	0	1	0	0
Sly02g0345421	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0345471	M1	NA	3	2	2	2	1	1	1	1	1	0
Sly02g0345481	M11	NA	17	13	15	10	13	33	26	42	12	12
Sly02g0345491	M1	NA	15	18	15	10	8	9	12	8	3	2
Sly02g0345501	M3	NA	57	55	49	78	86	50	56	50	72	90
Sly02g0345511	M12	NA	23	33	21	18	26	33	39	29	45	47
Sly02g0345521	M12	NA	43	59	41	38	60	51	60	54	98	104
Sly02g0345531	M9	NA	54	61	48	39	68	63	84	66	139	166
Sly02g0345541	M3	NA	34	39	28	16	13	22	21	20	24	12
Sly02g0345551	M3	NA	39	40	36	17	17	25	26	26	31	18
Sly02g0345561	M3	NA	14	16	11	8	7	13	12	12	10	7
Sly02g0345571	M3	NA	27	33	25	15	15	28	31	21	20	27
Sly02g0345581	M8	NA	27	27	21	14	17	29	28	22	23	31
Sly02g0345591	M3	NA	17	21	11	8	9	17	19	10	10	17
Sly02g0345601	M1	NA	5	5	3	1	1	1	1	1	1	0
Sly02g0345621	M12	NSY1	2	2	1	1	1	3	2	2	1	1
Sly02g0345631	M3	NA	15	17	10	8	13	10	14	9	10	12
Sly02g0345641	M1	NA	1037	750	877	372	158	626	559	623	239	143
Sly02g0345651	M1	NA	96	100	92	69	64	70	78	71	71	61
Sly02g0345661	M12	NA	32	27	29	9	4	98	85	86	10	5
Sly02g0345671	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0345681	M1	NA	76	72	76	61	54	50	56	39	9	5
Sly02g0345691	M1	NA	57	54	56	50	57	37	39	36	44	45
Sly02g0345701	M3	NA	40	46	32	27	25	32	34	21	20	23
Sly02g0345711	M1	NA	17	16	22	33	38	8	6	7	5	12
Sly02g0345721	M22	NA	2	2	3	6	4	6	1	2	1	1
Sly02g0345731	M2	NA	1	1	1	1	0	1	1	4	0	1
Sly02g0345741	M12	NA	8	9	15	55	9	21	26	33	12	2
Sly02g0345751	M12	SIDWARF/SICYP85A1	16	26	9	34	49	15	24	22	27	66
Sly02g0345771	M3	NA	46	50	44	36	27	36	38	32	26	22
Sly02g0345791	M2	NA	672	708	627	503	366	485	604	447	481	513
Sly02g0345801	M1	NA	2	1	2	1	1	1	0	0	1	0
Sly02g0345811	M9	NA	7	8	8	10	15	8	8	8	10	14
Sly02g0345821	M18	NA	10	13	13	18	28	14	13	14	14	21
Sly02g0345831	M1	NA	21	21	19	17	17	17	17	18	19	18
Sly02g0345841	M11	NA	69	67	90	89	81	78	75	100	128	103

			Estimated Transcript Number								
			Pericarp					Gel			
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0282431	M1	NA	14	16	18	20	20	15	14	16	22	23
Sly08g0282441	M1	NA	25	33	33	48	52	17	25	23	26	44
Sly08g0282451	M12	SISOD4	33	31	32	79	234	35	35	40	112	259
Sly08g0282461	M21	NA	3	3	3	1	1	3	2	3	0	0
Sly08g0282471	M11	NA	1	1	1	1	0	1	1	1	0	0
Sly08g0282491	M1	NA	96	70	48	1	1	3	9	1	0	0
Sly08g0282501	M12	NA	1	1	1	7	9	3	1	2	1	1
Sly08g0282511	M3	NA	1	1	1	0	1	1	1	0	0	1
Sly08g0282531	M22	NA	1	0	1	0	0	1	0	1	0	0
Sly08g0282611	M3	NA	1	1	1	0	0	0	1	0	0	0
Sly08g0282631	M13	NA	1	1	1	2	3	1	1	2	2	3
Sly08g0282641	M1	NA	8	12	9	5	5	5	4	3	1	4
Sly08g0282651	M12	NA	1	1	2	1	1	6	6	6	2	1
Sly08g0282671	M11	NA	14	12	15	12	9	14	15	17	16	13
Sly08g0282681	M12	NA	7	7	6	4	5	15	10	12	3	6
Sly08g0282691	M12	NA	42	41	52	34	17	144	134	140	27	12
Sly08g0282701	M9	NA	1	1	1	0	0	1	2	1	0	0
Sly08g0282711	M9	NA	1	1	1	0	0	1	1	1	0	0
Sly08g0282721	M12	FZR2	12	11	13	25	29	25	27	23	73	76
Sly08g0282731	M12	SGR1	29	47	72	920	2449	47	83	128	1212	2865
Sly08g0282751	M1	NA	26	26	28	27	36	23	22	22	25	31
Sly08g0282771	M12	NA	58	50	51	53	59	77	82	93	82	93
Sly08g0282781	M5	NA	67	119	42	10	10	70	75	11	1	1
Sly08g0282791	M3	NA	171	139	146	31	11	142	147	126	25	8
Sly08g0282801	M1	NA	5	4	6	2	2	3	4	3	1	1
Sly08g0282811	M3	NA	12	8	7	3	2	5	6	3	2	1
Sly08g0282821	M1	NA	63	57	59	21	8	34	30	25	8	3
Sly08g0282831	M3	MOCOS-like2	3	3	3	1	1	2	2	1	1	1
Sly08g0282851	M1	NA	36	30	63	41	5	3	2	1	1	1
Sly08g0282861	M11	NA	41	44	50	62	66	42	44	51	64	70
Sly08g0282871	M22	NPRD1-like	5	5	4	7	11	6	5	5	8	12
Sly08g0282881	M12	NA	4	3	3	3	5	5	4	4	5	6
Sly08g0282891	M12	NA	50	43	49	83	75	65	68	72	100	90
Sly08g0282901	M13	NA	9	9	9	14	27	9	8	9	12	18
Sly08g0282911	M3	NA	41	42	33	28	28	24	28	20	22	21
Sly08g0282921	M22	NA	1	1	1	1	4	1	1	1	2	2
Sly08g0282941	M9	NA	1	1	1	1	1	2	7	1	1	3
Sly08g0282961	M2	NA	1	2	6	1	0	1	2	1	1	0
Sly08g0282971	M1	NA	1	1	2	1	1	1	1	1	1	0
Sly08g0282991	M1	NA	13	11	12	7	4	9	9	7	4	2
Sly08g0283001	M1	PP2-B1	54	49	34	18	27	18	18	16	18	34
Sly08g0283021	M14	NA	31	25	35	35	31	27	23	30	23	24
Sly08g0283031	M14	NA	17	14	28	18	11	18	14	23	5	2
Sly08g0283041	M11	NA	17	11	21	33	36	25	23	31	41	49
Sly08g0283051	M23	NA	1	1	1	3	3	1	1	1	2	2
Sly08g0283061	M3	NA	93	113	79	91	119	69	96	72	112	129
Sly08g0283071	M2	NA	80	84	75	85	94	75	79	78	105	130
Sly08g0283131	M9	NA	61	69	39	39	46	79	88	63	61	80
Sly08g0283151	M22	NA	28	9	14	1	1	77	24	49	8	1
Sly08g0283161	M22	NA	68	18	26	2	1	149	54	85	15	2
Sly08g0283171	M22	NA	1147	307	435	18	2	2360	603	1784	60	3
Sly08g0283181	M3	NA	228	226	111	85	83	148	196	124	121	145
Sly08g0283191	M3	NA	47	49	17	9	10	16	17	14	11	8
Sly08g0283201	M3	NA	20	21	18	20	21	16	14	14	17	20
Sly08g0283211	M9	NA	1	1	1	1	1	2	5	2	1	1
Sly08g0283221	M4	NA	6	7	7	5	21	15	14	9	5	20
Sly08g0283231	M14	NA	23	25	25	37	53	23	21	26	31	35
Sly08g0283241	M11	NA	3	3	1	2	2	5	6	2	1	1
Sly08g0283251	M11	NA	208	196	277	239	283	260	194	280	140	176
Sly08g0283261	M13	NA	5	4	5	3	2	5	4	4	2	2
Sly08g0283331	M7	NA	1	1	1	1	2	1	1	1	1	4
Sly08g0283341	M1	NA	30	29	35	12	152	2	1	1	3	3
Sly08g0283351	M1	NA	211	262	348	162	1008	4	3	3	83	61
Sly08g0283361	M1	NA	766	599	632	188	129	18	1	1	1	1
Sly08g0283381	M1	NA	2	3	1	0	1	0	0	0	0	0
Sly08g0283391	M2	NA	136	148	123	68	53	66	116	80	131	111
Sly08g0283401	M18	NA	27	30	33	30	30	39	31	43	25	25
Sly08g0283441	M1	NA	9	13	7	3	5	1	1	2	1	1
Sly08g0283451	M22	NA	2	1	2	0	0	23	1	13	0	0
Sly08g0283471	M16	NA	24	19	18	20	22	22	21	20	30	39
Sly08g0283481	M22	NA	2	1	2	1	1	3	2	3	1	0
Sly08g0283501	M22	NA	1	1	1	0	0	3	1	2	0	0
Sly08g0283511	M12	NA	8	11	9	2	4	27	19	25	1	2
Sly08g0283621	M11	NA	12	10	18	9	8	29	23	30	5	3
Sly08g0283691	M10	NA	12	14	13	7	5	14	15	12	3	2
Sly08g0283721	M1	NA	22	22	19	15	16	15	14	14	16	15
Sly08g0283731	M1	NA	5	4	5	6	10	1	1	1	4	3
Sly08g0283771	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly08g0283781	M3	NA	188	200	159	104	104	129	144	103	92	107
Sly08g0283791	M11	NA	37	39	37	39	30	39	37	39	41	30
Sly08g0283801	M2	NA	38	40	36	40	51	37	41	35	51	55
Sly08g0283831	M3	glutathione peroxidas	433	437	355	388	665	275	303	236	430	600
Sly08g0283851	M3	NA	20	19	20	56	71	9	11	7	30	37
Sly08g0283871	M1	NA	3	4	4	4	4	2	2	1	2	3
Sly08g0283881	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly08g0283891	M19	SIJMJ6	25	24	23	23	23	20	19	22	29	23
Sly08g0283901	M12	NA	77	75	81	386	621	98	106	130	586	655
Sly08g0283931	M3	NA	59	57	49	53	139	45	38	36	56	91
Sly08g0283941	M12	NA	2	1	2	1	2	3	3	2	1	0
Sly08g0283951	M18	NA	15	13	14	13	16	15	13	15	9	10
Sly08g0283961	M9	NA	5	5	5	5	2	8	9	5	1	1
Sly08g0283981	M20	NA	9	10	14	7	6	11	10	11	2	1
Sly08g0283991	M1	NA	17	17	21	27	34	14	14	16	24	31
Sly08g0284021	M12	NA	13	12	11	17	19	15	17	14	14	14
Sly08g0284031	M12	NA	10	10	11	13	13	12	11	13	8	7
Sly08g0284041	M19	NA	10	11	11	13	12	12	10	12	9	5
Sly08g0284051	M12	NA	29	26	27	34	35	30	31	33	45	54
Sly08g0284061	M11	NA	12	11	17	9	7	20	15	20	2	1
Sly08g0284071	M1	NA	74	69	67	16	8	35	37	33	14	10
Sly08g0284081	M11	NA	6	6	10	6	2	14	11	15	3	1
Sly08g0284091	M1	NA	13	12	15	43	35	11	11	13	32	18
Sly08g0284101	M1	NA	50	44	50	119	77	46	43	44	129	66
Sly08g0284111	M11	NA	1122	857	1125	1449	1673	1075	965	1190	904	1531
Sly08g0284121	M2	NA	44	42	46	53	29	38	43	47	72	59
Sly08g0284131	M1	NA	15	15	14	5	5	6	5	6	3	5
Sly08g0284141	M1	NA	35	17	78	1	1	3	2	3	1	1
Sly08g0284151	M6	NA	34	79	30	13	27	56	74	12	2	6
Sly08g0284161	M3	NA	118	130	70	35	39	57	68	32	23	36
Sly08g0284171	M1	NA	149	147	154	200	178	135	129	137	154	174
Sly08g0284181	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly08g0284191	M1	NA	13	12	13	20	23	10	11	13	21	23
Sly08g0284251	M2	CDKD;1	23	25	22	41	46	16	21	17	47	43
Sly08g0284261	M1	NA	16	16	15	14	15	13	13	13	8	11
Sly08g0284271	M2	NA	44	46	45	44	41	35	44	36	51	47
Sly08g0284281	M11	NA	37	26	45	12	33	38	35	38	16	45
Sly08g0284291	M12	NA	121	125	128	105	89	150	167	157	120	132
Sly08g0284301	M17	NA	90	79	87	71	97	82	71	86	84	90
Sly08g0284311	M11	NA	48	46	51	72	116	55	50	59	92	133
Sly08g0284321	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0284341	M12	NA	17	19	20	5	2	69	47	77	1	1
Sly08g0284351	M19	NA	9	9	13	8	6	9	8	8	5	4
Sly08g0284361	M3	NA	2	3	2	1	2	2	2	2	2	2
Sly08g0284371	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly08g0284381	M1	NA	13	12	18	19	12	4	3	3	2	3
Sly08g0284391	M11	NA	53	55	57	65	76	72	65	79	80	92
Sly08g0284401	M2	NA	17	15	17	10	5	18	16	14	5	2
Sly08g0284411	M3	NA	22	19	16	23	19	16	19	16	24	20
Sly08g0284431	M12	NA	7	5	7	13	75	9	8	11	27	148
Sly08g0284441	M12	NA	1	2	3	4	10	3	2	2	5	12
Sly08g0284451	M1	NA	2	2	3	1	1	1	0	0	0	0
Sly08g0284461	M3	NA	7	11	6

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0345851	M11	NA	2	2	3	1	1	4	4	4	1	0
Sly02g0345861	M3	NA	39	44	34	36	45	33	33	26	20	29
Sly02g0345871	M22	NA	12	9	12	9	9	11	9	11	21	21
Sly02g0345881	M3	NA	68	72	66	44	32	45	52	40	41	33
Sly02g0345891	M3	NA	44	54	35	40	46	33	42	29	44	52
Sly02g0345911	M13	NA	9	10	12	17	19	10	11	10	16	21
Sly02g0345921	M1	NA	16	16	15	13	10	7	8	8	9	7
Sly02g0345931	M19	NA	9	11	10	9	13	10	9	10	11	13
Sly02g0345941	M1	NA	15	18	17	16	22	15	14	13	23	27
Sly02g0345951	M1	NA	22	19	15	25	16	4	5	3	1	6
Sly02g0345961	M11	NA	31	30	36	43	43	35	30	37	43	36
Sly02g0345971	M19	NA	20	25	23	28	30	26	20	26	26	23
Sly02g0345981	M12	NA	38	41	40	48	56	42	45	47	55	64
Sly02g0345991	M3	NA	40	43	34	27	11	35	39	32	23	8
Sly02g0346001	M3	NA	8	8	6	6	7	6	7	6	7	8
Sly02g0346011	M12	NA	3	3	3	1	1	37	32	38	1	1
Sly02g0346021	M8	NA	61	68	39	23	17	69	89	43	13	12
Sly02g0346041	M12	NA	2	1	1	3	1	2	2	3	25	2
Sly02g0346051	M3	NA	2	3	1	1	1	1	1	1	1	1
Sly02g0346061	M12	NA	2	2	1	1	1	5	4	5	0	0
Sly02g0346071	M12	NA	11	13	13	16	58	20	24	34	59	265
Sly02g0346081	M12	NA	1	1	1	1	1	1	2	1	1	2
Sly02g0346091	M9	NA	1	1	1	1	1	1	2	1	1	2
Sly02g0346101	M12	NA	5	5	4	5	2	25	34	22	20	6
Sly02g0346111	M3	NA	17	18	16	16	16	15	15	14	12	11
Sly02g0346151	M1	NA	56	58	57	47	40	40	37	43	43	45
Sly02g0346161	M10	NA	105	110	48	18	185	223	425	90	52	494
Sly02g0346171	M12	NA	32	38	19	7	92	84	147	38	22	184
Sly02g0346181	M3	NA	38	23	32	38	56	28	35	21	31	68
Sly02g0346191	M12	NA	84	87	105	167	430	1243	1445	1031	274	346
Sly02g0346201	M9	NA	21	45	24	27	113	53	119	36	38	135
Sly02g0346211	M1	NA	4	5	3	3	2	1	2	1	1	1
Sly02g0346231	M11	NA	2	2	2	12	6	3	3	3	1	2
Sly02g0346241	M9	NA	1	1	1	1	0	1	1	1	1	1
Sly02g0346251	M5	NA	29	33	24	22	32	30	49	14	9	23
Sly02g0346261	M12	NA	7	7	7	2	2	42	46	45	5	1
Sly02g0346291	M3	NA	38	54	38	34	38	36	45	39	27	32
Sly02g0346301	M3	NA	3	8	4	1	1	2	3	1	1	1
Sly02g0346311	M12	NA	7	10	7	7	5	13	19	12	9	6
Sly02g0346321	M1	NA	8	10	16	237	228	1	1	1	1	1
Sly02g0346341	M19	SlHAC4	6	8	7	5	4	8	7	6	4	3
Sly02g0346351	M19	NA	32	36	40	38	43	30	29	35	35	38
Sly02g0346361	M3	NA	35	36	31	30	28	34	34	33	36	28
Sly02g0346371	M3	NA	107	96	96	130	173	90	97	95	153	190
Sly02g0346401	M12	NA	15	14	16	15	9	24	24	32	49	26
Sly02g0346411	M12	NA	14	16	17	15	9	23	29	30	50	28
Sly02g0346431	M11	NA	53	47	60	45	33	53	57	66	47	40
Sly02g0346441	M13	NA	16	16	18	21	6	14	15	17	4	1
Sly02g0346451	M12	NA	5	6	4	4	9	5	6	6	4	9
Sly02g0346461	M3	NA	32	67	27	7	21	21	31	7	4	14
Sly02g0346481	M3	NA	2	3	1	0	1	1	1	1	0	0
Sly02g0346491	M1	NA	31	29	25	19	20	16	9	14	3	3
Sly02g0346501	M21	NA	11	8	8	3	3	8	3	7	1	1
Sly02g0346511	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly02g0346521	M1	NA	3	3	3	4	2	1	1	1	1	1
Sly02g0346531	M12	SlSDG10	15	17	15	20	21	20	17	19	23	18
Sly02g0346541	M1	NA	17	18	20	9	7	15	14	13	7	6
Sly02g0346551	M9	NA	3	3	2	1	11	7	10	4	6	44
Sly02g0346561	M12	NA	14	12	10	12	16	14	15	16	15	18
Sly02g0346571	M11	NA	47	44	51	38	44	45	44	52	42	51
Sly02g0346581	M11	NA	18	17	26	10	11	43	34	61	17	17
Sly02g0346591	M11	NA	132	94	173	124	37	336	290	418	213	19
Sly02g0346611	M18	NA	8	7	10	16	15	13	10	14	28	19
Sly02g0346621	M12	NA	4	5	5	8	10	6	6	7	17	16
Sly02g0346631	M11	NA	12	11	13	6	4	16	15	15	6	4
Sly02g0346651	M13	NA	56	51	54	47	55	51	50	57	68	78
Sly02g0346661	M11	NA	23	18	22	25	34	31	28	36	28	45
Sly02g0346671	M3	NA	49	79	49	22	23	27	29	17	9	11
Sly02g0346681	M12	SRO5	7	7	9	8	8	8	8	35	51	34
Sly02g0346691	M12	NA	5	5	4	2	2	8	9	23	12	12
Sly02g0346701	M19	NA	14	17	15	15	17	17	13	14	12	11
Sly02g0346721	M12	NA	27	34	31	41	35	39	39	40	45	34
Sly02g0346731	M22	NA	1	1	1	1	1	4	2	3	1	1
Sly02g0346741	M3	NA	10	11	10	5	5	8	9	8	8	8
Sly02g0346751	M1	MOCOS-like1	23	24	28	37	41	20	19	20	22	27
Sly02g0346761	M1	NA	9	9	10	6	10	7	7	7	6	6
Sly02g0346781	M1	NA	2	2	1	1	0	1	0	1	0	0
Sly02g0346791	M1	NA	16	18	16	11	10	11	11	10	7	4
Sly02g0346801	M1	NA	3	3	3	4	4	3	3	3	4	3
Sly02g0346811	M11	NA	17	23	16	20	22	25	22	21	23	24
Sly02g0346821	M18	NA	3	6	4	5	4	5	5	4	4	3
Sly02g0346831	M12	NA	16	19	13	15	21	17	19	18	21	26
Sly02g0346841	M12	NA	25	29	20	24	36	28	30	23	33	64
Sly02g0346861	M2	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0346871	M3	NA	67	86	71	22	32	40	58	32	72	61
Sly02g0346881	M12	NA	8	8	8	6	11	10	9	10	12	19
Sly02g0346891	M1	NA	38	31	51	1	1	14	11	11	1	1
Sly02g0346901	M3	NA	248	226	95	1	1	160	128	35	1	1
Sly02g0346911	M7	NA	74	174	55	25	109	73	197	54	84	350
Sly02g0346921	M22	NA	14	5	7	1	0	37	8	24	5	1
Sly02g0346931	M5	NA	13	27	14	8	22	20	26	9	3	5
Sly02g0346941	M14	SlSnRK2.4	130	134	148	107	114	141	120	156	89	92
Sly02g0346951	M3	ARR13	3	5	3	1	1	1	2	1	1	1
Sly02g0346961	M22	NA	1	1	1	0	1	1	1	1	1	1
Sly02g0346971	M16	NA	60	54	58	44	55	52	51	55	62	83
Sly02g0346981	M18	NA	17	18	17	6	4	18	14	22	1	1
Sly02g0346991	M12	NA	8	8	5	11	6	10	12	10	8	2
Sly02g0347011	M1	NA	13	9	8	5	2	2	2	2	1	1
Sly02g0347031	M22	NA	3	3	3	2	1	5	3	4	1	1
Sly02g0347041	M3	NA	68	129	40	4	4	24	19	4	1	1
Sly02g0347051	M7	NA	5	9	4	2	5	5	9	6	2	6
Sly02g0347061	M7	NA	2	5	2	1	2	2	5	3	1	3
Sly02g0347071	M1	NA	3	2	4	1	1	2	2	2	1	1
Sly02g0347091	M3	NA	65	72	58	51	69	55	51	48	63	85
Sly02g0347111	M11	NA	2	1	1	1	1	2	2	2	0	1
Sly02g0347121	M3	NA	1	2	1	1	1	1	1	1	0	1
Sly02g0347131	M18	NA	40	48	46	44	38	47	47	44	26	29
Sly02g0347171	M6	NA	5	5	6	5	4	5	6	4	1	1
Sly02g0347211	M12	NA	9	7	5	1	1	55	58	36	1	1
Sly02g0347221	M9	NA	1	1	1	1	2	1	1	1	1	1
Sly02g0347231	M22	NA	2	1	1	2	4	2	2	2	5	6
Sly02g0347241	M11	NA	18	17	17	23	31	19	17	20	27	34
Sly02g0347271	M11	NA	40	37	39	67	78	51	47	62	68	82
Sly02g0347281	M1	NA	19	12	26	1	1	11	7	11	1	0
Sly02g0347291	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0347301	M12	NA	34	34	33	31	31	39	36	37	28	33
Sly02g0347331	M11	NA	21	22	15	8	11	28	23	26	13	21
Sly02g0347341	M12	NA	10	15	11	6	8	19	24	23	14	19
Sly02g0347351	M19	NA	43	49	39	40	39	39	36	36	23	23
Sly02g0347401	M11	NA	16	14	19	17	17	22	22	33	35	31
Sly02g0347411	M3	NA	123	147	75	92	184	56	69	29	83	205
Sly02g0347431	M1	NA	472	451	443	585	704	289	297	424	990	1082
Sly02g0347441	M11	NA	92	93	111	147	197	133	108	151	284	335
Sly02g0347451	M19	NA	67	68	66	69	58	62	59	67	63	57
Sly02g0347461	M12	NA	7	7	10	8	14	63	61	102	44	38
Sly02g0347471	M11	ZEP2/ABA1	30	23	57	42	73	75	62	100	13	8
Sly02g0347481	M11	NA	8	7	7	2	2	12	11	11	1	1
Sly02g0347491	M1	NA	91	87	77	70	102	67	64	68	82	121
Sly02g0347501	M1	NA	2	2	1	1	1	1	1	1	0	1
Sly02g0347511	M1	NA	438	409	308	2	1	71	92	35	4	1
Sly02g0347521	M3	NA	1	2	1	0	0	0	1	0	0	0
Sly02g0347551	M1	NA	2	1	3	0	0	1	1	1	0	0
Sly02g0347561	M3	NA	51	77	18	1	1	15	16	4	1	2
Sly02g0347571	M3	NA	16	20	6	1	1	3	3	1	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0284511	M12	NA	36	37	42	73	66	47	48	50	54	45
Sly08g0284521	M3	ACS1B	2	3	2	1	1	1	1	1	1	1
Sly08g0284531	M1	ACS1A	102	128	105	697	407	16	17	2	1	1
Sly08g0284551	M11	NA	29	25	32	53	57	42	41	49	65	59
Sly08g0284561	M14	NA	155	160	178	139	131	155	152	158	160	149
Sly08g0284601	M3	NA	2	7	3	0	1	1	1	1	1	1
Sly08g0284611	M12	cel5	5	3	5	103	32	11	7	8	45	40
Sly08g0284631	M19	NA	16	18	17	17	17	17	17	16	14	13
Sly08g0284641	M11	NA	3	3	3	2	1	4	4	4	1	1
Sly08g0284651	M12	NA	8	8	7	6	10	13	10	11	13	15
Sly08g0284661	M12	NA	14	14	13	12	12	19	17	17	15	14
Sly08g0284691	M10	NA	8	8	4	1	0	16	13	7	1	1
Sly08g0284701	M1	SlRbohG/SlRboh1	5	5	4	1	1	3	2	2	1	1
Sly08g0284711	M3	NA	1	2	1	1	0	1	0	1	0	1
Sly08g0284721	M22	NA	2	3	2	2	2	3	1	2	1	1
Sly08g0284741	M3	NA	3	3	1	1	1	2	1	1	1	1
Sly08g0284761	M3	NA	355	288	248	151	192	242	253	191	184	236
Sly08g0284771	M22	NA	1	1	1	1	1	2	1	1	1	1
Sly08g0284791	M3	NA	22	24	17	22	30	19	21	16	30	36
Sly08g0284811	M3	NA	204	200	162	114	128	190	187	151	109	129
Sly08g0284821	M11	NA	11	9	14	23	50	25	24	35	28	50
Sly08g0284841	M22	NA	4	1	2	1	10	25	2	16	1	3
Sly08g0284861	M23	NA	0	1	1	1	1	1	1	1	1	1
Sly08g0284871	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly08g0284881	M1	NA	9	9	10	12	15	6	5	6	5	4
Sly08g0284901	M18	NA	4	4	5	4	5	5	4	5	3	3
Sly08g0284911	M11	NA	5	5	7	5	7	7	4	7	5	5
Sly08g0284921	M12	NA	1	1	1	5	1	1	1	1	9	3
Sly08g0284951	M1	NA	19	21	25	85	29	2	1	1	20	32
Sly08g0284961	M11	NA	37	38	45	77	80	37	36	56	85	103
Sly08g0284971	M12	NA	141	128	156	294	278	193	219	197	264	213
Sly08g0284981	M11	NA	51	45	54	68	66	62	60	69	62	53
Sly08g0284991	M1	NA	53	53	53	52	26	48	37	42	34	33
Sly08g0285001	M1	NA	6	6	10	4	2	4	3	4	3	2
Sly08g0285011	M11	NA	759	660	748	623	380	884	797	1051	987	794
Sly08g0285061	M11	NA	19	17	21	13	16	31	29	32	18	27
Sly08g0285071	M18	NA	14	15	18	11	14	26	22	28	15	13
Sly08g0285081	M1	NA	13	11	10	8	9	9	8	9	9	9
Sly08g0285091	M1	NA	17	16	18	20	27	10	8	9	24	47
Sly08g0285101	M11	NA	42	39	45	64	83	46	38	56	101	117
Sly08g0285121	M1	NA	8	11	8	6	4	2	1	1	1	1
Sly08g0285141	M2	NA	19	18	15	7	2	12	15	11	3	1
Sly08g0285151	M22	NA	1	1	1	2	1	1	1	1	1	1
Sly08g0285161	M1	NA	23	26	29	93	41	17	19	25	109	57
Sly08g0285171	M3	NA	12	25	15	5	47	4	7	4	1	24
Sly08g0285181	M3	NA	23	25	24	23	22	21	22	20	25	23
Sly08g0285191	M1	NA	5	11	18	2	1	2	2	1	1	1
Sly08g0285201	M1	NA	11	11	16	33	13	1	1	1	1	1
Sly08g0285211	M1	NA	4	4	4	3	1	1	1	0	1	0
Sly08g0285241	M1	NA	6	9	4	1	1	1	1	1	0	1
Sly08g0285261	M11	NA	33	29	39	47	244	52	46	49	91	238
Sly08g0285271	M11	NA	34	31	50	30	66	109	79	110	39	90
Sly08g0285281	M1	NA	886	959	1031	1208	1058	19	17	16	19	20
Sly08g0285291	M13	NA	5	5	5	1	1	5	5	5	1	1
Sly08g0285301	M1	NA	45	74	78	88	118	8	11	13	5	19
Sly08g0285311	M3	NA	26	33	28	46	41	21	25	22	24	30
Sly08g0285321	M12	CEL8	82	116	62	38	31	250	217	355	69	43
Sly08g0285331	M12	SlPP2C10	1	1	1	1	1	1	2	1	1	1
Sly08g0285341	M9	NA	6	6	6	7	10	8	8	8	15	17
Sly08g0285351	M3	NA	68	84	59	18	25	57	53	41	12	13
Sly08g0285361	M2	NA	53	58	53	58	50	44	54	40	52	47
Sly08g0285371	M1	NA	13	16	15	15	14	13	13	12	13	11
Sly08g0285381	M1	NA	13	14	8	7	4	5	4	3	1	2
Sly08g0285391	M1	NA	24	22	20	21	23	14	13	12	14	18
Sly08g0285401	M3	NA	2	2	2	2	1	2	2	2	1	1
Sly08g0285411	M11	NA	45	41	49	51	50	56	54	61	49	51
Sly08g0285421	M22	NA	8	8	8	21	21	8	8	8	11	27
Sly08g0285431	M22	NA	2	2	2	2	2	3	1	3	1	2
Sly08g0285441	M1	NA	2	2	2	1	3	1	1	1	1	3
Sly08g0285461	M1	NA	18	23	36	6	1	4	3	3	1	1
Sly08g0285481	M1	NA	11	14	21	13	4	1	1	1	1	1
Sly08g0285501	M11	NA	37	30	49	37	27	71	57	90	43	26
Sly08g0285511	M19	NA	33	33	32	33	35	35	30	36	25	24
Sly08g0285521	M1	NA	58	56	46	36	43	35	39	40	41	54
Sly08g0285531	M1	NA	131	118	123	67	30	100	114	97	21	11
Sly08g0285551	M3	NA	65	67	61	63	65	46	54	57	45	63
Sly08g0285561	M7	NA	10	12	11	9	7	11	12	10	7	5
Sly08g0285571	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly08g0285581	M3	NA	5	6	5	9	12	4	5	4	8	10
Sly08g0285591	M11	NA	7	6	8	7	10	7	7	6	6	7
Sly08g0285611	M11	NA	2	1	2	1	1	2	2	2	1	2
Sly08g0285631	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly08g0285661	M18	NA	22	24	24	49	66	27	23	28	36	43
Sly08g0285671	M12	NA	7	9	10	26	26	15	19	17	36	19
Sly08g0285701	M2	NA	22	24	20	25	26	19	21	22	25	28
Sly08g0285711	M11	NA	19	16	19	13	12	32	25	35	15	13
Sly08g0285721	M1	NA	57	55	49	56	63	43	39	41	54	62
Sly08g0285731	M11	NA	1	1	1	1	1	1	1	1	1	0
Sly08g0285741	M3	NA	821	879	517	149	211	438	536	174	52	169
Sly08g0285751	M1	NA	6	3	4	1	1	1	1	1	0	0
Sly08g0285761	M22	SlARF9A	7	3	4	1	1	22	5	14	1	1
Sly08g0285771	M1	NA	1	1	1	11	3	1	1	1	1	1
Sly08g0285801	M1	NA	24	17	38	13	5	4	5	8	2	1
Sly08g0285811	M11	NA	32	27	35	65	84	52	51	71	74	94
Sly08g0285821	M3	NA	61	53	47	50	52	50	51	50	64	67
Sly08g0285831	M12	NA	106	95	102	114	139	100	105	110	156	200
Sly08g0285841	M1	NA	12	8	10	4	1	2	2	2	5	1
Sly08g0285851	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly08g0285861	M1	NA	51	49	52	64	75	40	41	42	40	59
Sly08g0285871	M2	NA	54	56	60	73	68	48	59	54	91	78
Sly08g0285881	M11	NA	21	20	21	25	36	24	22	21	20	18
Sly08g0285891	M1	NA	38	43	19	5	4	4	5	2	2	3
Sly08g0285901	M12	NA	53	50	46	58	63	61	67	53	66	72
Sly08g0285911	M20	NA	13	8	17	1	1	8	5	9	1	0
Sly08g0285921	M22	NA	6	3	5	3	1	18	4	14	2	1
Sly08g0285941	M3	NA	5	2	2	3	8	4	2	3	6	7
Sly08g0285951	M1	NA	22	19	18	18	25	15	14	15	18	22
Sly08g0285961	M2	NA	261	295	203	302	98	145	196	88	110	43
Sly08g0285971	M11	NA	13	14	16	30	41	16	15	18	61	50
Sly08g0285981	M1	NA	8	9	9	11	7	9	9	8	11	7
Sly08g0285991	M19	NA	135	138	141	100	84	122	102	134	83	71
Sly08g0286001	M1	NA	201	191	209	142	134	169	163	182	125	127
Sly08g0286021	M11	NA	6	6	7	7	4	6	6	6	4	2
Sly08g0286031	M1	NA	15	15	24	40	26	14	13	14	11	10
Sly08g0286041	M18	NA	48	49	50	42	52	53	46	56	58	70
Sly08g0286061	M12	NA	6	5	5	6	4	10	10	8	5	2
Sly08g0286071	M3	NA	7	6	6	3	2	4	5	4	3	4
Sly08g0286081	M9	NA	47	44	41	52	52	64	78	57	38	45
Sly08g0286091	M11	NA	8	7	11	20	19	11	11	15	7	8
Sly08g0286111	M3	NA	6	5	6	9	16	5	4	4	10	19
Sly08g0286121	M3	NA	55	55	49	65	82	53	53	52	70	79
Sly08g0286141	M1	NA	56	62	63	127	151	49	52	58	147	173
Sly08g0286151	M13	NA	4	4	7	68	61	3	4	11	84	110
Sly08g0286161	M11	NA	10	7	11	26	47	15	15	22	35	53
Sly08g0286171	M3	NA	20	21	19	23	32	16	18	15	19	27
Sly08g0286181	M1	NA	55	49	58	57	64	46	44	49	41	45
Sly08g0286191	M1	NA	37	38	34	39	44	32	31	29	30	37
Sly08g0286201	M9	HUP40	6	10	6	3	25	8	15	18	11	70
Sly08g0286211	M1	NA	36	29	52	17	12	4	3	3	1	1
Sly08g0286221	M9	NA	35	37	39	45	46	37	39	37	51	49
Sly08g0286231	M18	NA	11	10	13	14	16	11

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0347581	M3	NA	6	12	3	1	1	3	2	1	1	1
Sly02g0347591	M9	NA	35	41	30	32	17	74	105	98	137	50
Sly02g0347601	M3	NA	10	15	7	5	3	7	6	5	4	3
Sly02g0347611	M2	NA	10	18	8	5	3	5	6	4	4	2
Sly02g0347621	M3	NA	12	21	9	7	2	5	6	5	3	2
Sly02g0347631	M7	NA	47	53	36	23	21	50	59	46	42	22
Sly02g0347641	M1	NA	3	4	2	82	41	1	1	2	1	2
Sly02g0347661	M12	NA	1	1	1	1	2	10	10	10	2	2
Sly02g0347671	M9	NA	2	2	2	2	3	3	3	2	6	9
Sly02g0347681	M12	NA	9	8	7	9	11	11	10	10	11	13
Sly02g0347691	M3	NA	336	297	210	134	227	191	191	139	119	158
Sly02g0347701	M3	NA	10	11	9	5	8	7	8	7	8	10
Sly02g0347711	M1	NA	15	15	16	16	18	11	8	10	10	11
Sly02g0347721	M9	NA	3	4	3	5	6	6	6	7	11	8
Sly02g0347731	M5	SAM-METT-like10	12	20	13	25	52	16	18	11	7	14
Sly02g0347751	M5	NA	3	3	2	2	2	3	3	3	3	2
Sly02g0347761	M12	NA	2	4	5	4	86	5	13	11	8	221
Sly02g0347781	M11	NA	126	122	127	95	97	120	113	137	120	145
Sly02g0347801	M2	NA	50	51	51	38	35	42	45	41	31	41
Sly02g0347811	M1	NA	24	23	27	28	33	23	22	22	22	31
Sly02g0347831	M11	SIPILS2	48	46	66	71	70	54	53	56	33	50
Sly02g0347841	M6	NA	53	116	56	3	10	46	167	31	8	13
Sly02g0347851	M3	NA	5	10	4	0	0	2	1	1	0	0
Sly02g0347861	M1	NA	45	41	39	26	25	35	32	33	22	20
Sly02g0347871	M11	NA	64	61	73	145	254	85	81	104	174	236
Sly02g0347881	M11	NA	6	6	7	9	7	9	8	10	6	5
Sly02g0347911	M1	NA	16	16	13	14	17	8	10	11	16	15
Sly02g0347921	M1	NA	13	14	15	27	49	11	13	14	22	49
Sly02g0347931	M11	NA	7	7	9	16	28	8	7	8	13	22
Sly02g0347941	M1	NA	14	14	15	15	20	10	9	10	7	10
Sly02g0347971	M20	NA	4	4	5	3	2	4	3	3	1	1
Sly02g0347981	M1	NA	2	2	2	1	1	1	1	1	1	0
Sly02g0347991	M1	NA	1	1	1	1	1	1	0	1	1	0
Sly02g0348001	M1	NA	5	9	6	1	1	1	3	1	0	1
Sly02g0348011	M12	NA	1	1	1	1	1	2	3	2	2	1
Sly02g0348031	M19	NA	40	39	43	34	36	36	30	37	34	35
Sly02g0348051	M1	NA	57	44	82	42	37	36	34	47	47	29
Sly02g0348071	M14	NA	39	39	47	54	48	42	39	40	48	52
Sly02g0348091	M22	NA	2	2	2	1	1	2	1	2	1	0
Sly02g0348111	M2	NA	79	73	63	150	195	53	61	47	116	155
Sly02g0348121	M3	NA	7	15	9	9	57	4	9	5	6	84
Sly02g0348131	M3	NA	90	99	65	113	134	70	67	53	72	115
Sly02g0348141	M3	NA	51	83	56	66	122	42	50	49	45	97
Sly02g0348151	M12	NA	11	15	12	19	36	15	16	17	34	52
Sly02g0348161	M11	NA	1	1	1	1	1	1	1	1	2	1
Sly02g0348181	M11	NA	1	1	1	0	0	1	1	1	1	0
Sly02g0348191	M11	NA	211	181	212	69	22	245	197	249	23	7
Sly02g0348211	M1	NA	69	71	69	76	73	64	62	67	67	61
Sly02g0348221	M9	NA	1	1	1	1	1	3	3	1	1	1
Sly02g0348231	M12	NA	1	2	2	1	1	5	5	5	2	2
Sly02g0348241	M9	NA	7	9	5	4	4	10	12	7	5	7
Sly02g0348251	M9	NA	12	15	7	5	7	17	21	12	11	17
Sly02g0348261	M13	NA	25	26	26	30	44	24	24	28	46	48
Sly02g0348271	M3	NA	16	20	16	15	13	17	19	16	17	16
Sly02g0348281	M11	NA	18	22	15	22	25	20	21	18	14	21
Sly02g0348291	M12	NA	17	26	25	23	38	47	48	41	35	76
Sly02g0348301	M13	NA	12	11	13	35	26	11	13	12	13	10
Sly02g0348311	M12	NA	24	23	33	10	4	182	268	111	2	2
Sly02g0348321	M5	NA	61	86	44	84	51	73	108	41	5	4
Sly02g0348331	M1	NA	1	1	1	1	1	1	1	1	1	2
Sly02g0348341	M12	NA	38	37	36	39	41	38	38	40	35	49
Sly02g0348351	M7	NA	15	18	14	10	21	16	17	15	9	20
Sly02g0348361	M12	STS7	1	1	1	1	1	2	1	1	1	1
Sly02g0348371	M11	NA	2	1	1	1	1	2	2	2	1	1
Sly02g0348381	M12	NA	1	2	1	2	1	4	3	3	2	2
Sly02g0348391	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0348401	M12	NA	1	1	1	2	1	2	2	3	1	1
Sly02g0348411	M11	NA	4	4	4	6	5	5	5	6	11	4
Sly02g0348421	M12	NA	19	19	18	25	24	19	22	23	37	40
Sly02g0348431	M3	NA	1	1	1	1	1	1	1	1	0	0
Sly02g0348461	M12	NA	3	2	4	3	2	15	13	13	1	1
Sly02g0348471	M11	NA	151	145	247	364	213	409	345	375	104	94
Sly02g0348481	M1	NA	4	12	13	71	56	2	2	1	3	9
Sly02g0348491	M1	NA	28	19	23	3	1	12	7	10	1	1
Sly02g0348501	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly02g0348511	M10	NA	165	155	137	196	176	154	176	148	178	172
Sly02g0348521	M3	NA	24	22	23	10	4	21	21	14	3	2
Sly02g0348531	M11	NA	79	67	74	136	220	81	72	91	148	216
Sly02g0348551	M1	SIXTH7	30	16	55	1	1	1	1	1	0	0
Sly02g0348561	M1	NA	43	31	32	13	9	22	12	20	2	2
Sly02g0348571	M11	NA	11	10	10	10	10	10	10	11	9	11
Sly02g0348581	M11	NA	7	6	8	5	4	9	6	8	2	2
Sly02g0348591	M19	NA	35	36	39	40	41	36	33	36	34	30
Sly02g0348601	M11	NA	50	48	51	69	86	51	52	51	59	76
Sly02g0348621	M12	ACS3	1	1	1	1	1	1	7	1	1	1
Sly02g0348631	M7	NA	65	85	43	20	18	64	118	32	12	23
Sly02g0348641	M12	NA	35	32	30	44	65	35	32	32	42	46
Sly02g0348651	M12	NA	1	1	1	0	0	2	2	2	1	0
Sly02g0348671	M9	NA	3	4	3	1	1	4	6	4	2	1
Sly02g0348681	M1	NA	1	1	1	0	1	1	1	1	0	0
Sly02g0348701	M22	NA	2	1	1	1	1	4	1	2	1	1
Sly02g0348711	M3	NA	7	11	7	5	7	7	10	6	5	5
Sly02g0348731	M3	NA	8	10	8	4	5	6	7	5	4	3
Sly02g0348751	M3	NA	14	14	13	10	14	11	12	10	16	18
Sly02g0348761	M12	NA	27	18	30	22	15	39	58	85	37	6
Sly02g0348781	M2	NA	58	80	65	11	5	13	18	10	3	2
Sly02g0348791	M3	NA	13	19	17	11	4	3	2	2	1	1
Sly02g0348801	M15	NA	25	24	27	34	35	27	25	25	23	29
Sly02g0348811	M1	NA	5	5	5	15	28	3	4	5	38	44
Sly02g0348821	M1	NA	15	14	12	40	70	6	8	13	172	223
Sly02g0348831	M12	NA	31	29	36	38	52	45	45	45	47	76
Sly02g0348861	M1	NA	8	9	7	9	8	5	5	7	12	10
Sly02g0348871	M3	NA	4	6	4	7	2	3	4	5	9	4
Sly02g0348881	M11	NA	38	23	42	9	2	56	42	50	6	3
Sly02g0348891	M22	NA	14	10	15	4	1	17	14	16	3	2
Sly02g0348911	M9	NA	22	22	20	29	31	21	27	22	24	28
Sly02g0348921	M1	NA	8	10	7	12	21	3	5	6	21	43
Sly02g0348931	M1	NA	2	2	3	3	1	1	1	1	1	1
Sly02g0348941	M3	NA	26	27	21	12	10	18	18	12	5	3
Sly02g0348951	M12	NA	196	177	221	356	386	332	347	418	438	509
Sly02g0348971	M14	NA	16	15	17	18	29	15	14	17	20	20
Sly02g0348981	M3	NA	18	19	13	17	16	13	17	12	19	22
Sly02g0348991	M11	NA	9	9	11	20	28	18	16	24	28	37
Sly02g0349001	M11	NA	53	46	54	69	88	59	63	77	171	169
Sly02g0349011	M12	NA	1	1	1	1	1	1	1	1	2	3
Sly02g0349021	M12	NA	21	20	22	21	24	38	35	35	11	14
Sly02g0349031	M3	NA	1	1	1	1	1	1	1	1	0	0
Sly02g0349041	M3	NA	23	24	22	22	24	20	19	18	19	21
Sly02g0349051	M11	NA	12	9	12	7	10	14	13	14	6	6
Sly02g0349061	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0349071	M12	NA	3	3	4	2	2	13	10	16	6	3
Sly02g0349081	M12	NA	2	1	1	1	1	3	2	2	0	1
Sly02g0349091	M1	NA	178	162	158	79	35	92	93	85	51	33
Sly02g0349101	M12	NA	97	99	92	101	97	105	129	100	99	121
Sly02g0349111	M3	NA	4	8	2	1	1	1	2	1	1	1
Sly02g0349121	M11	NA	13	10	16	13	17	18	18	29	16	17
Sly02g0349131	M1	NA	8	7	6	4	3	4	3	3	1	2
Sly02g0349141	M3	NA	59	87	42	20	30	32	35	15	8	8
Sly02g0349151	M1	NA	241	195	74	14	52	14	4	10	1	2
Sly02g0349161	M1	NA	4	4	4	4	5	3	4	4	4	3
Sly02g0349171	M5	NA	11	12	10	7	6	12	12	9	16	7
Sly02g0349181	M19	NA	5	6	4	2	2	6	5	4	2	3
Sly02g0349191	M3	NA	8	10	6	3	3	8	8	5	3	5
Sly02g0349201	M5	NA	11	16	9	4	4	15	14	8	4	8

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly08g0286271	M1	NA	220	192	185	28	73	17	20	7	46	72
Sly08g0286281	M3	NA	187	158	135	123	109	95	109	84	105	82
Sly08g0286291	M1	NA	83	91	77	124	154	31	31	40	26	69
Sly08g0286301	M11	NA	13	11	11	23	31	12	11	12	17	18
Sly08g0286321	M1	NA	3	2	3	1	1	1	1	1	0	0
Sly08g0286341	M1	NA	13	12	7	0	0	1	1	1	0	0
Sly08g0286351	M1	NA	1	1	2	4	2	1	0	1	1	0
Sly08g0286361	M16	NA	25	19	19	20	19	18	19	17	19	14
Sly08g0286391	M11	NA	1	1	1	1	1	6	4	5	1	0
Sly08g0286401	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly08g0286411	M22	NA	1	1	1	1	0	5	1	1	1	0
Sly08g0286421	M11	NA	26	28	28	52	63	34	33	37	50	48
Sly08g0286431	M3	NA	28	31	26	17	24	21	23	19	22	29
Sly08g0286441	M11	NA	2	1	2	1	0	3	3	3	1	0
Sly08g0286451	M1	NA	7	6	4	1	1	2	1	2	1	1
Sly08g0286461	M19	NA	24	26	24	24	26	24	22	24	25	22
Sly08g0286471	M3	NA	49	51	44	54	51	45	42	40	49	47
Sly08g0286481	M12	NA	16	14	13	15	9	20	20	18	9	6
Sly08g0286491	M11	STS1	69	54	84	70	45	107	94	122	39	20
Sly08g0286501	M12	NA	308	359	300	235	338	677	622	924	960	978
Sly08g0286511	M3	NA	6	10	7	1	1	3	1	1	0	0
Sly08g0286521	M11	NA	28	21	24	38	61	35	30	43	36	58
Sly08g0286531	M11	NA	7	7	6	8	12	9	8	10	8	13
Sly08g0286541	M22	NA	1	1	1	0	0	1	1	1	0	1
Sly08g0286551	M3	NA	100	85	67	58	58	47	57	46	77	70
Sly08g0286571	M1	NA	1	1	1	1	1	1	1	0	1	1
Sly09g0076751	M1	NA	6	8	9	4	2	3	2	2	1	1
Sly09g0076761	M3	NA	74	66	62	23	18	34	36	24	15	13
Sly09g0076801	M3	NA	11	13	9	9	11	9	9	7	10	12
Sly09g0076831	M23	NA	1	1	1	1	1	2	1	1	2	1
Sly09g0076851	M3	NA	33	47	21	7	12	15	16	5	3	4
Sly09g0076871	M1	NA	6	6	3	1	1	1	1	1	1	1
Sly09g0076881	M12	NA	15	14	16	23	37	16	17	18	33	46
Sly09g0076891	M22	PDC2	2	1	1	2	2	2	1	2	1	1
Sly09g0076901	M4	NA	10	12	11	23	34	14	12	9	22	38
Sly09g0076911	M3	NA	20	21	20	16	14	20	20	18	13	11
Sly09g0076961	M1	NA	2	2	3	1	1	1	2	1	1	1
Sly09g0076971	M14	NA	2	1	3	1	1	1	1	1	0	0
Sly09g0077011	M1	NA	6	4	4	1	1	2	1	1	1	0
Sly09g0077031	M1	NA	6	5	8	13	7	1	1	1	1	1
Sly09g0077051	M22	NA	7	7	8	8	4	7	6	7	5	1
Sly09g0077071	M11	NA	12	12	12	24	25	15	13	16	31	21
Sly09g0077091	M1	NA	3	2	2	1	1	1	1	1	1	1
Sly09g0077111	M18	NA	16	16	17	17	21	17	15	17	22	23
Sly09g0077121	M1	NA	22	24	19	22	27	14	14	16	18	21
Sly09g0077131	M1	NA	3	4	3	2	2	2	1	1	1	1
Sly09g0077141	M3	NA	21	23	20	19	22	18	19	18	28	36
Sly09g0077151	M8	NA	43	45	40	45	39	46	52	40	37	35
Sly09g0077161	M12	NA	12	15	21	15	5	114	107	116	37	25
Sly09g0077171	M18	NA	45	46	52	47	51	53	43	53	39	43
Sly09g0077181	M12	NA	20	23	24	36	34	32	33	34	46	44
Sly09g0077191	M3	NA	35	33	33	29	31	28	30	27	26	31
Sly09g0077211	M22	NA	1	1	1	1	1	1	0	1	1	6
Sly09g0077221	M1	NA	52	49	46	55	48	33	36	38	67	53
Sly09g0077251	M3	NA	88	81	63	34	30	45	48	37	38	31
Sly09g0077261	M19	NA	4	6	5	4	2	5	3	4	1	1
Sly09g0077271	M1	NA	12	13	11	7	3	10	9	8	3	2
Sly09g0077311	M1	NA	1	1	1	1	1	1	1	1	2	3
Sly09g0077331	M1	NA	40	37	37	22	24	24	25	23	22	21
Sly09g0077341	M18	NA	5	9	7	10	10	11	8	10	12	11
Sly09g0077351	M11	NA	3	3	6	6	4	6	5	6	7	6
Sly09g0077361	M18	NA	4	4	5	7	7	7	5	7	7	8
Sly09g0077371	M18	NA	9	11	11	13	13	16	12	17	21	22
Sly09g0077381	M11	NA	13	14	17	20	22	21	17	22	29	32
Sly09g0077391	M12	NA	16	16	15	21	27	24	23	25	40	41
Sly09g0077401	M12	NA	53	53	53	46	42	61	63	63	53	41
Sly09g0077411	M6	NA	4	10	6	3	6	8	10	9	6	8
Sly09g0077421	M1	NA	22	25	22	3	4	2	2	1	1	2
Sly09g0077441	M1	NA	314	311	307	274	327	220	248	233	317	363
Sly09g0077451	M19	NA	23	24	24	26	31	24	22	24	24	28
Sly09g0077471	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly09g0077481	M12	NA	33	27	34	86	191	47	49	61	144	294
Sly09g0077501	M2	SCO1	30	34	31	28	24	24	25	21	28	27
Sly09g0077521	M12	NA	15	14	15	22	17	19	17	20	24	13
Sly09g0077551	M12	NA	4	4	4	2	2	20	16	24	6	7
Sly09g0077561	M11	NA	73	58	62	64	111	64	64	62	71	79
Sly09g0077571	M1	NA	249	235	272	171	125	160	179	182	140	97
Sly09g0077581	M1	NA	14	13	23	21	15	1	1	1	1	1
Sly09g0077591	M12	NA	22	22	22	32	42	24	24	22	32	33
Sly09g0077601	M12	NA	12	11	15	12	15	25	22	18	16	27
Sly09g0077611	M19	NA	65	68	75	43	41	70	58	65	41	42
Sly09g0077661	M12	NA	1	1	1	2	2	1	1	1	2	1
Sly09g0077691	M2	NA	9	10	8	12	11	8	10	8	18	15
Sly09g0077701	M3	NA	12	13	9	6	7	8	8	7	10	11
Sly09g0077741	M1	NA	2	2	2	2	1	1	1	1	0	1
Sly09g0077751	M1	NA	22	24	19	16	13	14	16	14	14	12
Sly09g0077761	M1	NA	14	13	14	11	11	12	12	12	17	14
Sly09g0077791	M22	NA	26	3	28	0	0	297	4	127	0	0
Sly09g0077801	M22	NA	1	0	2	0	0	18	0	7	0	0
Sly09g0077841	M9	NA	80	80	77	93	84	101	118	95	83	73
Sly09g0077871	M3	NA	1	3	4	1	1	1	1	1	0	1
Sly09g0077901	M1	SIPL	12	13	10	15	12	10	10	11	11	9
Sly09g0077911	M1	NA	25	38	28	9	7	5	4	2	1	1
Sly09g0077921	M2	NA	25	29	21	17	12	16	21	13	15	12
Sly09g0077931	M22	NA	1	1	1	1	0	1	1	1	0	0
Sly09g0077941	M8	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0077951	M3	NA	50	53	41	79	94	34	34	32	56	63
Sly09g0077961	M9	NA	44	41	41	66	60	45	49	43	47	44
Sly09g0077971	M1	NA	42	38	41	47	54	35	35	40	47	51
Sly09g0078001	M12	NA	25	24	24	31	43	25	25	28	47	53
Sly09g0078011	M22	NA	1	1	1	1	0	2	1	1	1	0
Sly09g0078021	M11	NA	73	74	74	83	123	100	85	122	157	156
Sly09g0078031	M3	NA	4	4	4	5	4	3	3	3	4	3
Sly09g0078041	M3	NA	29	25	26	17	8	23	23	22	21	11
Sly09g0078131	M1	NA	15	16	14	7	4	3	2	2	2	2
Sly09g0078141	M3	NA	2	2	2	2	2	2	2	1	1	1
Sly09g0078151	M1	NA	4	4	3	3	3	3	2	2	2	2
Sly09g0078161	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0078171	M9	NA	12	14	11	16	16	13	17	14	18	20
Sly09g0078181	M12	NA	29	30	24	29	34	83	75	95	31	28
Sly09g0078191	M3	NA	46	50	50	59	63	46	48	42	73	85
Sly09g0078201	M3	NA	28	30	27	27	24	25	29	29	16	21
Sly09g0078211	M12	NA	10	25	14	18	248	18	61	29	50	544
Sly09g0078221	M12	NA	4	4	4	2	1	7	7	6	2	1
Sly09g0078231	M1	NA	8	9	8	7	9	6	6	7	8	8
Sly09g0078241	M3	NA	28	34	17	14	10	19	18	13	13	9
Sly09g0078251	M1	NA	2	1	1	1	1	1	1	1	0	0
Sly09g0078261	M1	NA	42	41	43	11	3	12	15	9	2	1
Sly09g0078271	M12	NA	20	20	18	17	16	22	20	21	21	19
Sly09g0078281	M1	NA	40	40	39	31	30	33	28	28	29	24
Sly09g0078291	M3	NA	196	187	161	136	117	161	184	155	134	126
Sly09g0078301	M11	NA	22	16	27	34	55	29	22	34	25	50
Sly09g0078311	M18	NA	6	7	9	9	9	8	6	9	3	2
Sly09g0078321	M1	NA	54	52	55	38	33	43	42	48	39	40
Sly09g0078331	M3	NA	15	15	11	11	16	10	10	9	15	19
Sly09g0078341	M3	NA	111	110	107	113	120	89	90	91	132	126
Sly09g0078351	M1	NA	12	11	9	8	11	10	8	11	4	1
Sly09g0078361	M16	NA	334	285	270	217	205	251	245	251	241	237
Sly09g0078371	M11	NA	5	3	3	1	1	4	3	4	1	1
Sly09g0078381	M12	SIAPx	193	193	255	951	1854	305	360	521	1356	2861
Sly09g0078391	M12	NA	10	12	15	10	4	21	24	31	17	4
Sly09g0078401	M12	NA	93	94

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0349211	M3	NA	13	15	9	6	5	13	12	7	3	8
Sly02g0349221	M11	NA	6	6	8	7	6	10	9	9	9	12
Sly02g0349231	M1	NA	12	13	7	4	6	1	1	2	1	1
Sly02g0349241	M11	NA	25	23	37	23	30	74	62	97	75	91
Sly02g0349261	M10	NA	3	5	3	1	1	14	11	2	1	1
Sly02g0349271	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly02g0349281	M12	NA	15	13	17	27	68	18	23	24	160	286
Sly02g0349291	M12	NA	17	20	22	35	83	21	21	30	178	277
Sly02g0349301	M12	NA	16	17	21	33	83	22	21	30	150	204
Sly02g0349311	M18	NA	9	11	13	22	44	14	11	18	75	95
Sly02g0349321	M11	NA	69	63	78	158	246	103	92	127	308	502
Sly02g0349331	M12	NA	18	16	16	12	14	24	24	28	19	21
Sly02g0349341	M12	NA	10	11	10	10	14	28	27	24	15	19
Sly02g0349351	M12	NA	20	16	22	14	18	200	173	202	31	30
Sly02g0349361	M11	NA	24	19	26	22	23	54	51	62	31	21
Sly02g0349371	M12	NA	11	11	12	29	36	15	15	21	53	40
Sly02g0349381	M22	NA	2	1	2	1	1	3	2	2	2	1
Sly02g0349391	M11	NA	1	1	1	1	1	1	1	1	1	0
Sly02g0349401	M3	NA	9	9	7	6	7	8	10	7	7	9
Sly02g0349411	M1	NA	3	2	2	2	2	1	2	3	1	2
Sly02g0349421	M3	NA	42	57	26	14	23	19	26	15	9	12
Sly02g0349431	M3	NA	42	50	19	1	1	5	4	1	1	1
Sly02g0349441	M12	NA	2	2	2	6	9	6	8	8	20	21
Sly02g0349451	M11	NA	33	37	32	28	40	44	40	40	26	44
Sly02g0349461	M12	NA	63	117	71	26	63	213	403	174	99	256
Sly02g0349471	M1	NA	79	67	85	182	205	54	54	49	127	219
Sly02g0349481	M1	NA	11	10	9	6	8	5	1	3	1	3
Sly02g0349491	M9	SlGH3-4	7	7	3	1	1	42	22	24	1	1
Sly02g0349501	M1	NA	5	5	5	5	5	5	4	4	6	5
Sly02g0349511	M3	NA	61	53	33	12	7	27	27	18	10	4
Sly02g0349521	M3	NA	14	13	10	7	6	11	9	3	1	2
Sly02g0349531	M9	NA	8	9	8	14	10	11	12	12	15	6
Sly02g0349541	M12	NA	158	168	155	220	217	150	163	181	316	315
Sly02g0349551	M10	NA	1	2	3	0	0	3	4	1	0	0
Sly02g0349561	M8	NA	58	66	53	35	27	61	72	61	64	48
Sly02g0349571	M11	NA	24	24	30	21	26	34	30	34	18	25
Sly02g0349581	M3	NA	52	63	33	10	81	34	41	18	9	111
Sly02g0349591	M1	NA	21	24	17	17	5	10	8	8	2	1
Sly02g0349601	M9	NA	8	8	8	1	1	9	9	8	2	2
Sly02g0349631	M11	SlCycD3;4	9	8	10	4	3	11	8	10	3	3
Sly02g0349641	M9	NA	12	18	14	16	23	27	30	26	25	29
Sly02g0349651	M11	NA	18	18	18	24	22	21	21	21	21	15
Sly02g0349661	M12	NA	47	48	57	72	92	64	66	77	89	87
Sly02g0349671	M1	NA	29	31	20	2	2	3	2	2	1	1
Sly02g0349681	M11	NA	16	17	17	17	24	20	19	18	30	42
Sly02g0349691	M22	NA	1	1	1	1	1	2	1	1	1	1
Sly02g0349701	M3	NA	69	89	52	23	14	18	15	3	1	1
Sly02g0349711	M11	NA	27	24	32	52	63	34	33	37	58	81
Sly02g0349731	M11	NA	53	50	69	56	80	113	103	118	96	150
Sly02g0349741	M22	NA	6	4	4	0	0	24	6	24	1	1
Sly02g0349751	M1	NA	9	8	9	2	1	9	8	8	2	1
Sly02g0349761	M1	NA	143	141	123	94	116	83	86	85	135	153
Sly02g0349771	M22	NA	18	16	15	14	20	18	15	19	19	25
Sly02g0349781	M11	NA	7	5	6	5	8	7	6	8	9	12
Sly02g0349791	M12	NA	13	14	16	16	20	16	15	18	18	30
Sly02g0349801	M11	NA	17	11	15	15	25	20	18	21	23	35
Sly02g0349811	M12	NA	9	7	9	9	14	11	11	10	13	22
Sly02g0349821	M3	NA	3	3	2	2	1	2	2	1	3	3
Sly02g0349831	M11	CBSX1-like2	28	23	31	63	96	32	30	37	59	70
Sly02g0349841	M3	NA	68	63	37	16	8	47	53	32	17	7
Sly02g0349851	M3	NA	13	14	9	11	6	11	11	8	3	2
Sly02g0349861	M11	NA	10	9	11	12	7	22	21	30	27	9
Sly02g0349871	M1	NA	3	4	6	4	2	1	3	5	39	17
Sly02g0349881	M11	CLF-like	13	15	14	14	20	19	19	21	28	35
Sly02g0349891	M1	NA	10	8	9	15	7	3	2	2	1	1
Sly02g0349901	M11	NA	16	14	16	31	32	21	21	21	25	19
Sly02g0349911	M10	NA	20	41	9	4	2	68	73	7	1	1
Sly02g0349941	M10	NA	8	16	5	2	1	23	26	3	1	1
Sly02g0349951	M3	NA	112	157	75	8	2	175	137	26	2	1
Sly02g0349961	M1	NA	7	10	4	2	1	2	1	1	1	1
Sly02g0349971	M5	NA	78	82	61	45	82	79	74	53	41	41
Sly02g0349981	M11	NA	5	4	5	1	2	7	7	7	1	1
Sly02g0349991	M3	NA	52	52	22	2	1	33	35	11	1	2
Sly02g0350001	M22	NA	7	5	7	5	14	11	8	8	16	32
Sly02g0350011	M1	NA	9	13	7	4	6	1	1	2	2	8
Sly02g0350021	M1	NA	95	79	69	36	36	50	47	43	31	30
Sly02g0350031	M12	NA	6	6	6	8	9	8	9	10	10	7
Sly02g0350041	M3	NA	10	14	11	10	6	8	7	7	3	2
Sly02g0350051	M12	NA	145	138	149	117	83	179	188	182	123	70
Sly02g0350061	M1	NA	2	2	2	3	3	2	2	2	3	2
Sly02g0350071	M3	NA	32	35	31	42	46	24	25	22	48	48
Sly02g0350081	M1	NA	2	3	3	1	1	2	2	2	1	1
Sly02g0350091	M6	NA	27	33	20	15	17	27	26	17	8	12
Sly02g0350111	M1	NA	12	10	5	1	1	4	2	2	1	1
Sly02g0350121	M12	NA	16	22	17	18	32	30	36	57	117	110
Sly02g0350131	M12	NA	30	25	28	20	24	50	49	54	52	49
Sly02g0350141	M11	NA	21	20	22	17	16	21	20	23	18	20
Sly02g0350151	M11	NA	16	17	23	42	48	28	25	35	43	40
Sly02g0350161	M1	NA	54	48	44	31	21	21	16	18	8	5
Sly02g0350171	M1	NA	11	8	4	1	1	2	1	1	1	0
Sly02g0350181	M11	NA	39	36	46	51	73	50	46	65	73	97
Sly02g0350191	M1	NA	5	4	5	4	1	2	2	2	1	1
Sly02g0350201	M1	NA	19	20	17	19	18	14	14	14	11	9
Sly02g0350211	M3	NA	6	7	5	6	6	5	6	4	4	4
Sly02g0350221	M10	NA	65	107	78	153	175	89	119	85	209	194
Sly02g0350231	M1	NA	5	4	6	6	2	3	3	2	2	1
Sly02g0350241	M1	NA	51	44	52	54	75	12	9	10	9	35
Sly02g0350261	M11	NA	5	5	4	5	4	6	7	7	6	4
Sly02g0350281	M3	NA	12	12	8	9	9	10	9	10	11	10
Sly02g0350301	M12	SIPL	3	6	2	2	3	7	10	13	14	9
Sly02g0350311	M12	NA	11	9	11	8	2	28	26	31	11	1
Sly02g0350321	M12	NA	7	7	8	38	58	31	33	30	10	32
Sly02g0350331	M11	NA	2	3	2	1	1	3	3	3	1	1
Sly02g0350341	M11	NA	8	9	12	9	16	11	10	14	10	11
Sly02g0350351	M12	NA	144	144	159	195	194	208	212	196	149	160
Sly02g0350361	M1	NA	69	73	76	110	85	55	68	53	59	76
Sly02g0350381	M1	NA	1	1	1	0	1	1	1	1	1	0
Sly02g0350391	M1	NA	4	8	12	4	4	1	1	0	1	1
Sly02g0350401	M9	NA	155	162	154	244	266	163	223	172	258	258
Sly02g0350411	M2	NA	36	34	26	24	20	25	30	24	30	25
Sly02g0350421	M2	NA	15	14	9	18	5	5	10	6	9	3
Sly02g0350431	M3	NA	33	26	15	14	27	26	19	8	10	19
Sly02g0350441	M1	NA	1	1	1	1	1	1	0	1	0	1
Sly02g0350451	M12	NA	26	25	30	22	24	30	33	33	29	28
Sly02g0350471	M12	NA	10	10	11	12	11	15	14	14	6	10
Sly02g0350481	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0350491	M12	NA	25	25	26	28	27	63	61	53	15	13
Sly02g0350511	M12	NA	7	5	7	5	4	11	11	8	2	2
Sly02g0350521	M12	NA	47	43	40	31	32	49	46	43	37	33
Sly02g0350531	M18	NA	16	13	16	12	11	16	13	16	12	12
Sly02g0350541	M12	NA	78	75	79	83	107	83	84	94	142	188
Sly02g0350551	M3	NA	413	413	307	232	206	347	338	213	125	137
Sly02g0350561	M3	NA	26	27	20	14	13	24	23	20	17	14
Sly02g0350571	M12	NA	4	6	6	5	3	9	10	9	6	3
Sly02g0350581	M3	NA	79	193	52	9	2	62	65	22	6	14
Sly02g0350591	M3	NA	36	73	24	4	2	23	29	10	3	5
Sly02g0350601	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly02g0350611	M19	NA	44	44	45	58	87	41	35	45	64	70
Sly02g0350631	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly02g0350641	M11	NA	172	152	160	192	187	187	194	208	216	223
Sly02g0350651	M12	NA	11	10	10	11	11	15	15	21	17	14
Sly02g0350661	M3	NA	47	50	48	59	64	42	44	46	66	70
Sly02g0350671	M20	NA	4	3	4	1	1	4	2	3	1	1
Sly02g0350681	M11	NA	15	15	16	18	16	22	21	25	22	14

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0078431	M11	NA	10	10	12	16	19	13	13	14	14	15
Sly09g0078441	M11	NA	3	3	3	1	1	4	3	4	1	1
Sly09g0078451	M12	NA	6	6	6	7	6	7	7	8	9	9
Sly09g0078461	M12	NA	3	2	1	4	4	3	3	3	6	9
Sly09g0078471	M12	NA	3	3	3	2	1	3	3	3	1	1
Sly09g0078481	M1	NA	481	418	385	318	223	262	309	246	282	219
Sly09g0078491	M22	NA	1	1	1	1	1	3	1	1	0	1
Sly09g0078501	M12	NA	25	28	31	22	22	27	30	29	37	38
Sly09g0078511	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly09g0078521	M1	NA	29	29	28	28	33	18	21	21	33	40
Sly09g0078531	M1	NA	17	17	23	27	21	10	7	8	2	4
Sly09g0078541	M22	NA	1	1	1	0	1	4	1	3	1	1
Sly09g0078551	M1	NA	16	15	15	11	11	10	10	10	18	17
Sly09g0078571	M1	NA	30	34	31	23	33	25	26	26	27	32
Sly09g0078581	M3	NA	49	46	42	55	46	43	49	36	33	25
Sly09g0078591	M11	NA	1	1	1	1	1	2	1	1	1	1
Sly09g0078611	M1	NA	28	20	51	1	1	2	1	3	1	1
Sly09g0078621	M3	NA	106	106	98	114	131	94	96	91	109	157
Sly09g0078631	M12	NA	68	61	79	72	59	74	72	76	71	75
Sly09g0078641	M1	NA	21	18	23	9	8	12	9	12	1	3
Sly09g0078651	M1	NA	35	77	27	1	1	5	3	2	1	1
Sly09g0078671	M19	NA	34	37	36	59	75	30	27	32	81	99
Sly09g0078681	M18	NA	115	122	133	108	107	138	118	144	106	99
Sly09g0078691	M3	NA	22	13	12	2	1	13	15	11	3	5
Sly09g0078701	M11	NA	54	43	54	91	183	84	69	99	140	279
Sly09g0078711	M11	NA	4	4	5	4	3	8	7	7	8	8
Sly09g0078781	M1	NA	27	29	25	34	22	21	20	20	19	14
Sly09g0078791	M1	NA	7	7	7	5	4	5	4	5	3	3
Sly09g0078821	M19	NA	14	15	13	12	10	14	13	13	10	6
Sly09g0078831	M15	NA	24	23	19	15	15	22	22	24	15	15
Sly09g0078841	M13	NA	40	52	73	76	80	45	55	65	99	74
Sly09g0078851	M11	NA	80	80	97	83	117	100	108	128	180	214
Sly09g0078861	M12	NA	3	2	3	1	2	3	3	2	2	1
Sly09g0078871	M3	NA	6	6	7	4	3	6	6	5	2	2
Sly09g0078881	M3	NA	6	7	7	4	3	8	7	5	4	3
Sly09g0078891	M5	NA	14	30	14	4	4	19	27	5	2	2
Sly09g0078911	M1	NA	4	3	3	5	5	2	2	2	3	3
Sly09g0078921	M1	NA	14	10	10	1	0	2	2	2	0	1
Sly09g0078931	M1	NA	52	39	45	2	3	13	10	9	1	1
Sly09g0078941	M3	NA	59	100	30	1	3	11	27	11	1	10
Sly09g0078961	M12	NA	64	44	95	121	67	101	120	187	252	139
Sly09g0078971	M12	NA	15	15	16	21	21	16	19	21	32	31
Sly09g0078981	M1	SlARF16A	11	9	11	11	10	6	7	7	3	4
Sly09g0079001	M12	SlLOG2	1	1	1	0	0	2	1	1	0	0
Sly09g0079011	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0079021	M11	NA	191	139	260	396	401	337	252	472	289	287
Sly09g0079031	M12	NA	27	24	31	22	27	52	48	74	68	59
Sly09g0079041	M19	EIN2	62	60	68	59	51	60	54	68	43	43
Sly09g0079051	M12	NA	14	15	18	26	37	40	63	64	81	126
Sly09g0079061	M12	NA	1	1	1	1	2	1	1	1	1	1
Sly09g0079071	M6	NA	78	155	47	8	10	144	193	39	3	5
Sly09g0079081	M3	NA	174	286	78	316	134	181	159	13	1	1
Sly09g0079091	M11	NA	222	248	185	146	224	452	381	299	55	32
Sly09g0079101	M1	NA	4	5	3	1	1	1	1	1	0	0
Sly09g0079111	M3	NA	14	13	11	14	12	13	12	12	10	10
Sly09g0079131	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0079151	M1	NA	4	2	2	0	1	1	1	1	0	0
Sly09g0079161	M11	NA	18	19	23	36	39	25	23	27	61	55
Sly09g0079171	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0079181	M3	NA	64	75	43	25	30	31	41	25	18	33
Sly09g0079191	M3	NA	92	109	96	184	85	49	102	72	268	140
Sly09g0079201	M11	NA	8	8	9	6	5	14	14	17	5	4
Sly09g0079211	M13	NA	9	8	13	12	14	11	12	14	10	9
Sly09g0079221	M1	NA	31	28	30	29	24	14	14	12	8	8
Sly09g0079231	M1	NA	11	6	3	1	1	3	2	1	1	0
Sly09g0079241	M1	NA	3	2	3	2	1	1	1	1	1	0
Sly09g0079261	M13	NA	57	58	89	44	31	102	84	159	101	61
Sly09g0079271	M11	NA	5	6	8	6	5	11	8	11	13	5
Sly09g0079311	M1	NA	19	21	20	16	19	16	16	17	20	17
Sly09g0079321	M19	NA	20	20	22	21	17	17	16	20	23	19
Sly09g0079331	M11	NA	10	11	14	15	20	12	12	15	12	15
Sly09g0079341	M11	NA	5	5	12	8	10	7	6	11	6	7
Sly09g0079351	M3	NA	57	52	49	85	85	42	49	44	80	72
Sly09g0079361	M3	NA	12	13	10	16	10	9	9	8	10	9
Sly09g0079371	M13	NA	132	126	164	275	225	125	133	155	190	212
Sly09g0079381	M1	SAUR69	1	1	2	474	106	1	1	1	13	2
Sly09g0079391	M1	NA	14	23	21	247	99	1	1	2	52	41
Sly09g0079401	M12	NA	1	1	1	6	3	2	3	2	4	1
Sly09g0079411	M1	NA	34	33	37	129	74	17	20	22	79	37
Sly09g0079421	M1	NA	303	200	373	706	504	141	147	325	818	384
Sly09g0079431	M11	NA	2	2	1	1	1	4	5	4	1	1
Sly09g0079441	M11	NA	3	2	4	5	7	4	7	3	4	4
Sly09g0079451	M12	NA	1	1	1	2	3	2	2	2	4	6
Sly09g0079461	M1	NA	185	159	210	191	197	138	135	160	145	183
Sly09g0079471	M1	NA	34	33	27	7	3	32	25	28	1	1
Sly09g0079481	M1	NA	2	2	2	1	0	0	0	1	0	0
Sly09g0079491	M3	NA	10	8	9	4	3	9	10	6	4	2
Sly09g0079501	M22	NA	6	6	5	5	2	7	5	6	1	0
Sly09g0079511	M8	SAMS	644	818	387	233	154	561	973	322	192	261
Sly09g0079521	M11	NA	30	30	36	44	46	52	43	65	58	66
Sly09g0079531	M1	NA	3	4	4	3	2	3	2	3	2	1
Sly09g0079541	M1	NA	23	21	23	28	33	17	17	18	43	42
Sly09g0079551	M1	NA	28	24	37	4	3	1	1	1	1	1
Sly09g0079571	M19	NA	10	10	10	7	9	10	8	9	7	5
Sly09g0079581	M3	NA	137	126	125	120	122	97	115	107	116	120
Sly09g0079591	M11	NA	40	32	42	10	6	71	59	76	5	3
Sly09g0079611	M1	NA	4	4	2	5	5	1	1	1	11	7
Sly09g0079641	M12	NA	14	14	13	15	12	15	15	14	15	13
Sly09g0079651	M2	NA	53	59	50	58	46	36	43	35	55	54
Sly09g0079671	M1	NA	14	16	18	26	33	10	12	18	39	20
Sly09g0079681	M12	NA	1	1	1	1	5	1	2	3	3	4
Sly09g0079691	M1	NA	19	16	18	14	14	10	9	10	8	8
Sly09g0079701	M21	NA	16	13	17	7	2	16	12	13	2	1
Sly09g0079711	M1	NA	76	72	70	86	89	53	54	51	86	100
Sly09g0079721	M12	NA	58	51	44	30	30	76	89	53	21	19
Sly09g0079731	M18	NA	21	25	25	26	32	26	23	25	25	27
Sly09g0079761	M3	NA	40	41	25	13	12	26	28	22	17	18
Sly09g0079781	M12	NA	1	1	1	3	2	16	16	11	38	28
Sly09g0079801	M12	NA	9	8	8	14	8	9	9	10	10	4
Sly09g0079811	M3	gibberellin-A12 hydrat	93	117	47	2	1	14	14	8	1	1
Sly09g0079841	M3	NA	38	44	27	18	20	30	39	21	15	21
Sly09g0079851	M2	NA	83	86	92	108	89	84	93	77	65	65
Sly09g0079861	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0079871	M11	NA	10	10	10	8	7	10	10	10	8	5
Sly09g0079881	M11	NA	3	3	3	2	1	6	5	5	1	1
Sly09g0079891	M11	NA	7	8	8	3	2	15	11	15	4	1
Sly09g0079901	M1	NA	5	4	2	2	1	1	1	1	1	1
Sly09g0079911	M6	NA	9	16	17	1	1	15	30	6	1	1
Sly09g0079921	M11	NA	8	7	8	10	11	11	11	11	20	13
Sly09g0079931	M22	NA	2	1	2	1	2	4	1	7	1	2
Sly09g0079941	M11	NA	25	25	29	25	31	30	25	36	30	36
Sly09g0079951	M12	NA	4	3	4	4	3	14	18	17	58	38
Sly09g0079961	M14	NA	29	28	29	23	26	28	27	31	18	17
Sly09g0079981	M3	NA	3	4	1	1	0	1	1	0	0	1
Sly09g0079991	M1	NA	2	3	1	0	0	0	1	0	0	0
Sly09g0080001	M23	NA	5	3	2	1	1	9	5	6	6	1
Sly09g0080011	M12	NA	114	97	134	269	205	225	401	283	119	68
Sly09g0080021	M11	NA	32	29	50	22	16	54	39	65	10	6
Sly09g0080031	M1	NA	507	442	466	380	303	366	339	383	390	345
Sly09g0080051	M14	NA	18	19	20	20	29	18	15	24	29	45
Sly09g0080061	M12	HRA1	19	14	24	19	18	51	46	86	54	45
Sly09g0080

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly02g0350691	M1	NA	1	2	1	1	1	1	1	1	0	1
Sly02g0350711	M1	NA	7	8	5	2	2	2	2	1	1	1
Sly02g0350721	M1	NA	11	12	9	3	4	5	7	4	1	1
Sly02g0350731	M3	NA	5	8	3	1	1	6	6	2	1	1
Sly02g0350751	M12	NA	3	23	10	4	77	29	101	31	7	205
Sly02g0350781	M7	NA	2	7	2	0	1	6	20	2	1	5
Sly02g0350791	M9	NA	73	113	76	75	94	118	194	119	155	222
Sly02g0350811	M22	NA	1	1	1	1	0	5	1	2	0	0
Sly02g0350821	M11	NA	7	8	8	3	1	11	10	13	3	1
Sly02g0350851	M12	NA	77	80	83	88	77	94	100	94	81	78
Sly02g0350861	M11	NA	3	3	5	1	1	5	5	5	1	1
Sly02g0350881	M11	NA	254	231	278	336	480	484	426	537	649	728
Sly02g0350891	M11	NA	2	2	2	2	2	2	2	3	3	2
Sly02g0350901	M12	NA	425	402	523	597	595	851	880	1115	1273	1274
Sly02g0350911	M2	NA	42	46	40	36	35	31	38	30	42	39
Sly02g0350921	M2	NA	37	41	37	30	38	25	31	27	36	40
Sly02g0350931	M12	NA	12	14	14	28	50	21	21	23	34	65
Sly02g0350941	M11	NA	22	19	18	2	2	24	20	16	1	1
Sly02g0350951	M3	NA	33	37	33	38	51	31	35	31	55	64
Sly02g0350961	M12	NA	1	1	1	1	1	4	3	1	3	7
Sly02g0350971	M12	NA	1	2	1	1	1	2	3	2	1	1
Sly02g0350981	M12	NA	214	206	217	257	282	235	255	265	334	376
Sly02g0350991	M3	NA	3	2	2	1	2	2	1	1	1	1
Sly02g0351001	M1	NA	3	2	4	1	1	1	1	2	0	0
Sly02g0351011	M11	NA	30	23	29	44	36	30	33	31	26	25
Sly02g0351021	M11	NA	1	1	2	1	1	1	2	2	1	1
Sly02g0351031	M12	NA	2	2	2	2	1	2	2	3	2	1
Sly02g0351041	M13	NA	3	2	4	5	9	2	3	4	6	5
Sly02g0351051	M1	NA	4	2	3	2	2	1	0	1	2	5
Sly02g0351061	M3	NA	2	2	1	1	1	0	1	1	1	1
Sly02g0351071	M11	NA	17	17	18	17	19	18	16	18	24	25
Sly02g0351081	M11	NA	16	17	16	16	18	19	19	19	20	20
Sly02g0351101	M12	NA	71	74	57	69	73	125	129	92	43	51
Sly02g0351111	M1	NA	3	3	2	2	3	1	1	0	1	1
Sly02g0351121	M1	NA	2	3	2	2	3	1	1	1	1	1
Sly02g0351131	M1	NA	8	10	9	6	8	3	3	4	3	2
Sly02g0351141	M1	PPR-like16	4	4	5	4	3	3	3	4	4	3
Sly02g0351151	M11	NA	28	26	28	15	8	52	45	54	15	4
Sly02g0351161	M12	NA	11	6	14	4	2	56	59	63	5	5
Sly02g0351181	M3	NA	45	42	38	45	41	39	39	41	59	59
Sly02g0351191	M1	NA	26	32	30	35	35	20	19	20	26	32
Sly02g0351231	M9	NA	37	40	40	25	6	71	70	61	9	2
Sly02g0351241	M1	NA	62	63	68	81	162	36	56	53	177	633
Sly02g0351251	M10	NA	32	43	33	32	29	42	46	36	33	35
Sly02g0351261	M12	NA	16	15	14	24	14	17	20	21	24	26
Sly02g0351281	M11	NA	38	41	42	47	62	49	46	56	72	88
Sly02g0351301	M2	NA	275	273	250	249	191	191	234	162	195	177
Sly02g0351311	M1	NA	15	11	12	7	5	9	7	9	6	3
Sly02g0351321	M22	FUS3	2	1	1	1	1	7	2	3	1	1
Sly02g0351331	M2	NA	306	306	271	317	241	252	322	228	259	228
Sly02g0351341	M3	NA	11	13	9	12	12	11	13	10	11	13
Sly02g0351351	M3	NA	102	86	64	78	73	57	58	50	82	82
Sly02g0351361	M1	NA	43	44	39	42	40	39	35	37	49	43
Sly02g0351371	M12	NA	110	114	102	125	162	113	116	112	151	169
Sly02g0351381	M1	SISDGS	18	18	13	9	9	15	11	12	9	5
Sly02g0351391	M19	NA	47	48	45	50	56	44	42	45	56	52
Sly02g0351401	M11	NA	43	42	47	57	62	49	48	51	54	73
Sly02g0351411	M11	NA	6	7	7	5	6	8	6	6	3	2
Sly02g0351421	M11	NA	3	2	3	1	2	3	3	3	1	1
Sly02g0351431	M22	NA	4	4	4	4	2	6	4	5	2	1
Sly02g0351441	M11	NA	10	12	14	17	29	16	14	19	25	30
Sly02g0351451	M18	NA	23	26	24	30	31	26	24	23	27	35
Sly02g0351471	M11	NA	41	43	43	61	75	63	54	66	79	102
Sly02g0351481	M18	NA	17	21	20	26	34	29	23	32	43	43
Sly02g0351491	M12	NA	17	20	18	30	37	33	27	34	55	55
Sly03g0191011	M11	NA	16	16	20	25	22	23	21	29	27	26
Sly03g0191021	M11	NA	17	16	22	29	40	28	22	32	31	33
Sly03g0191031	M12	NA	14	24	30	477	627	43	78	68	180	122
Sly03g0191041	M13	NA	13	13	17	82	80	10	13	16	45	62
Sly03g0191051	M6	NA	1	3	2	0	1	3	4	3	1	1
Sly03g0191061	M1	NA	142	124	124	106	102	103	107	106	165	129
Sly03g0191071	M11	NA	2	1	2	1	1	2	2	2	1	1
Sly03g0191081	M12	NA	17	18	18	42	58	20	22	24	54	90
Sly03g0191091	M13	NA	38	38	46	87	114	49	46	59	115	151
Sly03g0191101	M1	NA	26	27	41	89	150	9	7	8	6	15
Sly03g0191111	M9	NA	14	13	13	19	21	15	17	13	18	20
Sly03g0191131	M12	NA	41	40	38	47	36	41	48	45	65	51
Sly03g0191141	M1	NA	12	9	13	21	18	7	4	5	5	4
Sly03g0191151	M3	NA	44	47	29	11	12	26	32	14	9	17
Sly03g0191191	M3	NA	16	17	15	20	17	13	13	12	13	12
Sly03g0191201	M12	NA	8	8	8	7	3	14	14	17	9	3
Sly03g0191241	M3	NA	1	7	2	1	1	0	0	0	0	0
Sly03g0191261	M12	NA	42	37	33	22	36	48	50	47	38	46
Sly03g0191271	M11	NA	94	91	96	141	139	133	116	129	147	155
Sly03g0191291	M12	NA	11	11	12	14	17	13	12	13	14	15
Sly03g0191301	M10	NA	42	43	34	52	71	53	46	36	73	77
Sly03g0191311	M3	NA	77	82	86	129	107	66	69	64	89	77
Sly03g0191331	M22	NA	2	1	1	1	0	3	1	2	1	1
Sly03g0191341	M23	NA	2	1	1	1	0	3	2	1	1	1
Sly03g0191351	M3	NA	37	35	27	27	25	31	33	27	31	28
Sly03g0191361	M11	NA	9	8	10	6	12	13	10	15	11	13
Sly03g0191371	M1	NA	2	3	2	2	1	2	1	2	1	0
Sly03g0191381	M11	NA	2	2	2	4	5	3	4	8	7	4
Sly03g0191401	M11	NA	31	32	40	63	58	39	36	49	66	68
Sly03g0191411	M13	NA	20	21	24	29	30	20	21	24	37	39
Sly03g0191441	M12	NA	11	10	12	14	15	13	13	14	16	14
Sly03g0191451	M12	NA	66	72	79	130	112	77	90	84	127	92
Sly03g0191461	M11	NA	46	45	51	51	47	57	55	59	51	52
Sly03g0191481	M1	NA	1	2	2	2	1	1	1	1	1	1
Sly03g0191491	M3	NA	1	2	1	1	1	1	1	1	0	0
Sly03g0191501	M18	NA	55	52	60	50	54	64	55	70	49	50
Sly03g0191511	M2	NA	9	10	9	8	7	9	9	9	13	7
Sly03g0191521	M1	NA	78	66	98	141	113	36	24	39	61	108
Sly03g0191531	M13	NA	2	1	2	0	0	1	1	1	0	0
Sly03g0191541	M11	NA	1	1	1	1	1	1	1	1	0	0
Sly03g0191551	M22	NA	1	1	1	0	1	1	1	1	1	1
Sly03g0191561	M6	NA	136	140	130	168	116	131	167	118	311	304
Sly03g0191571	M1	NA	6	6	6	4	2	1	1	1	4	2
Sly03g0191641	M10	NA	1	1	1	1	1	3	6	1	0	1
Sly03g0191651	M22	NA	1163	219	479	15	4	2806	507	1899	25	7
Sly03g0191661	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0191671	M2	NA	55	54	47	50	21	32	39	18	5	4
Sly03g0191691	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly03g0191701	M22	NA	1	1	1	1	1	1	0	1	0	1
Sly03g0191731	M1	NA	8	7	8	7	4	7	7	6	4	5
Sly03g0191741	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly03g0191751	M1	NA	57	53	44	37	23	26	23	22	21	22
Sly03g0191761	M2	NA	33	31	26	24	22	21	25	21	27	22
Sly03g0191771	M8	NA	24	27	22	10	8	25	32	20	14	11
Sly03g0191811	M11	NA	96	91	101	128	238	95	96	107	168	245
Sly03g0191831	M3	NA	167	151	137	160	138	126	131	126	174	139
Sly03g0191841	M13	NA	77	80	95	73	72	93	86	98	54	49
Sly03g0191851	M11	NA	209	85	345	97	42	682	543	972	131	18
Sly03g0191861	M11	NA	23	12	30	16	4	114	100	151	47	4
Sly03g0191871	M11	NA	7	3	8	2	1	38	32	58	5	1
Sly03g0191881	M11	NA	17	15	21	16	17	19	18	21	20	19
Sly03g0191891	M22	NA	2	1	1	3	4	2	1	2	1	1
Sly03g0191911	M11	NA	2	1	3	1	2	3	3	6	3	6
Sly03g0191921	M12	NA	13	13	15	25	22	19	20	19	26	29
Sly03g0191981	M11	NA	46	40	49	70	68	65	52	72	78	98
Sly03g0191991	M11	NA	2	2	2	2	7	3	3	3	3	4
Sly03g0192001	M12	NA	1	1	0	1	1	1	1	1	2	2
Sly03g0192031	M11	NA	17	17	17	30	30	29	25	29	40	39
Sly03g0192041	M12	NA	9	8	12	11	8	13	14	13	11	10

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0080151	M11	gppps6	64	60	76	129	137	78	79	89	89	93
Sly09g0080161	M13	NA	70	58	105	87	73	120	113	158	118	71
Sly09g0080171	M11	NA	13	9	19	6	16	14	9	18	2	3
Sly09g0080201	M4	NA	7	4	10	89	372	15	6	9	10	118
Sly09g0080221	M1	NA	6	4	2	0	1	1	1	1	0	0
Sly09g0080231	M16	ENO2	696	637	641	909	499	629	681	626	498	212
Sly09g0080251	M17	SlHDT1	163	151	158	96	81	134	116	139	129	102
Sly09g0080261	M1	NA	226	223	247	147	112	200	181	193	182	118
Sly09g0080271	M1	delta14-sterol reducta	36	27	35	16	7	19	19	20	10	4
Sly09g0080281	M3	SlDML1	28	28	21	10	7	27	20	21	3	2
Sly09g0080291	M3	CTR3	33	33	25	27	29	30	30	25	25	28
Sly09g0080301	M11	NA	48	36	55	27	54	49	39	44	28	46
Sly09g0080321	M3	NA	25	24	20	21	22	22	21	21	26	25
Sly09g0080331	M1	NA	218	272	119	14	21	12	12	5	4	4
Sly09g0080351	M12	NA	5	5	5	2	2	7	6	5	2	2
Sly09g0080361	M12	NA	1	1	1	1	1	2	1	2	1	1
Sly09g0080371	M23	NA	1	1	1	1	0	2	1	1	1	0
Sly09g0080381	M11	NA	26	24	31	42	55	35	33	38	32	24
Sly09g0080391	M11	NA	48	47	47	29	30	55	50	55	37	36
Sly09g0080401	M11	SBE1	17	17	26	26	27	24	18	28	10	16
Sly09g0080421	M11	NA	36	31	50	64	132	48	44	58	86	108
Sly09g0080431	M12	NA	2	2	1	5	3	2	3	2	9	6
Sly09g0080481	M2	NA	604	544	480	969	994	447	596	409	744	1161
Sly09g0080501	M3	NA	15	15	11	12	11	13	13	13	14	11
Sly09g0080531	M12	NA	20	21	26	53	85	21	23	27	64	79
Sly09g0080541	M12	NA	30	26	31	35	48	30	32	35	56	69
Sly09g0080581	M18	NA	10	10	11	6	6	12	9	12	5	4
Sly09g0080591	M19	NA	13	16	16	21	21	19	15	18	14	13
Sly09g0080601	M3	NA	2	2	2	2	3	2	2	2	2	4
Sly09g0080621	M11	NA	1	1	1	1	1	3	2	3	1	1
Sly09g0080631	M1	NA	338	312	269	270	327	120	109	91	125	210
Sly09g0080641	M3	NA	8	9	8	14	15	7	8	8	17	16
Sly09g0080651	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0080661	M1	NA	3	1	1	1	1	1	1	0	0	0
Sly09g0080671	M11	NA	29	28	39	83	103	43	35	53	62	83
Sly09g0080681	M11	NA	39	37	41	50	61	44	43	51	84	100
Sly09g0080691	M11	NA	13	11	14	16	15	17	19	19	18	19
Sly09g0080701	M11	NA	1	1	1	1	1	1	1	1	1	0
Sly09g0080711	M1	NA	11	12	13	4	1	4	2	4	2	1
Sly09g0080721	M12	SlABI5	1	1	1	1	1	1	1	1	2	2
Sly09g0080731	M3	NA	18	20	17	18	13	12	12	10	12	9
Sly09g0080741	M3	NA	44	48	42	50	39	31	37	33	38	36
Sly09g0080751	M12	NA	1	1	1	1	1	1	1	1	2	1
Sly09g0080761	M1	NA	64	45	106	108	64	28	23	39	22	21
Sly09g0080831	M1	NA	94	84	99	366	163	36	52	62	241	113
Sly09g0080841	M12	NA	1	1	1	2	1	3	1	2	1	1
Sly09g0080871	M3	NA	12	11	10	12	16	8	10	8	15	16
Sly09g0080881	M11	NA	93	81	90	86	93	93	91	109	106	112
Sly09g0080891	M3	NA	270	243	212	301	286	155	185	142	222	209
Sly09g0080901	M11	NA	4	4	5	3	2	8	7	9	7	7
Sly09g0080911	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly09g0080921	M3	NA	22	23	21	20	26	19	22	21	25	30
Sly09g0080931	M11	NA	79	69	85	71	76	99	83	115	86	82
Sly09g0080941	M3	NA	4	4	2	1	1	3	2	1	0	0
Sly09g0080951	M11	jasmonoyl-amino acid	14	8	8	0	1	20	16	20	1	0
Sly09g0080961	M11	jasmonoyl-amino acid	11	5	5	0	0	8	8	8	0	0
Sly09g0080971	M18	NA	5	4	6	2	4	5	4	5	2	2
Sly09g0080981	M11	NA	57	51	55	45	42	55	48	63	67	52
Sly09g0081001	M12	NA	1	1	1	10	9	1	1	2	291	173
Sly09g0081011	M1	NA	47	48	41	13	8	6	4	4	2	4
Sly09g0081021	M15	NA	10	10	9	11	11	10	9	10	15	16
Sly09g0081031	M11	NA	5	4	5	5	3	6	5	7	6	5
Sly09g0081041	M19	NA	12	12	12	11	14	12	10	12	11	12
Sly09g0081051	M1	NA	3	4	3	2	1	1	1	1	1	1
Sly09g0081061	M11	NA	13	12	16	15	23	16	14	17	5	6
Sly09g0081071	M1	NA	6	5	6	1	1	1	2	2	1	1
Sly09g0081081	M3	NA	26	34	20	12	13	14	12	6	12	16
Sly09g0081091	M1	NA	57	58	46	26	22	31	33	28	23	23
Sly09g0081111	M12	NA	49	50	52	61	63	53	59	51	49	61
Sly09g0081121	M15	NA	23	19	21	27	31	21	23	22	21	36
Sly09g0081131	M1	LIF2-like2	88	87	85	66	63	68	64	71	59	61
Sly09g0081141	M11	NA	7	5	6	1	1	7	7	7	1	1
Sly09g0081151	M12	NA	7	6	7	10	15	11	9	11	13	15
Sly09g0081161	M11	NA	13	12	16	13	13	17	18	19	13	11
Sly09g0081181	M11	NA	53	49	65	79	65	119	95	149	130	52
Sly09g0081191	M11	NA	4	4	4	4	3	4	4	5	5	2
Sly09g0081201	M9	NA	11	12	11	13	16	11	12	12	17	18
Sly09g0081211	M22	NA	3	3	3	1	1	5	1	4	1	1
Sly09g0081221	M3	SAUR70	2	2	1	1	1	1	1	1	0	0
Sly09g0081231	M20	NA	25	25	34	9	8	24	22	22	5	6
Sly09g0081241	M1	NA	21	37	27	9	3	2	1	1	1	1
Sly09g0081261	M1	NA	78	101	53	19	10	12	12	5	1	1
Sly09g0081271	M3	NA	30	32	30	26	24	24	24	22	22	19
Sly09g0081291	M3	NA	2	2	1	1	1	2	2	1	1	1
Sly09g0081301	M12	NA	2	2	2	1	1	3	3	2	1	0
Sly09g0081311	M3	NA	2	2	1	2	2	1	1	1	1	1
Sly09g0081321	M11	NA	4	3	5	3	7	3	6	7	1	2
Sly09g0081331	M2	NA	13	11	8	5	4	6	9	5	6	4
Sly09g0081351	M3	NA	11	12	7	4	3	7	9	6	5	3
Sly09g0081361	M1	NA	276	255	268	217	165	206	219	213	208	174
Sly09g0081381	M1	NA	47	48	56	151	320	33	33	44	175	362
Sly09g0081391	M11	NA	31	28	36	29	16	58	56	76	31	12
Sly09g0081401	M2	NA	73	75	61	60	58	45	56	48	67	66
Sly09g0081411	M1	NA	13	13	25	17	23	8	7	9	28	52
Sly09g0081421	M1	NA	7	7	9	8	12	2	2	2	6	23
Sly09g0081441	M1	NA	17	17	18	19	25	13	14	13	24	31
Sly09g0081451	M18	SPY	63	64	73	83	90	79	60	78	81	101
Sly09g0081461	M1	NA	30	27	31	27	29	25	22	27	33	33
Sly09g0081481	M12	CEL2	2	1	2	328	1299	2	4	7	2407	1995
Sly09g0081491	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly09g0081501	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0081511	M11	NA	5	5	6	2	3	8	7	5	3	2
Sly09g0081521	M5	NA	3	4	2	2	2	5	4	2	3	2
Sly09g0081541	M1	NA	49	56	50	111	137	49	47	47	65	76
Sly09g0081551	M12	NA	9	11	8	12	22	11	12	11	19	20
Sly09g0081561	M12	NA	25	24	28	32	38	30	33	34	39	54
Sly09g0081591	M12	NA	1	0	0	31	102	1	1	1	247	311
Sly09g0081601	M3	NA	7	9	7	14	14	6	8	7	12	10
Sly09g0081611	M12	NA	3	3	4	4	3	5	5	4	24	6
Sly09g0081621	M12	NA	6	7	8	13	9	12	11	14	51	15
Sly09g0081631	M1	NA	64	62	61	68	69	53	55	56	76	80
Sly09g0081651	M11	NA	20	18	29	22	21	35	30	42	22	21
Sly09g0081661	M1	NA	7	6	9	5	6	6	4	7	6	7
Sly09g0081671	M1	NA	140	135	143	100	78	109	126	120	113	105
Sly09g0081681	M1	NA	119	87	108	17	10	55	50	45	8	4
Sly09g0081691	M2	NA	37	36	31	22	24	25	30	20	29	24
Sly09g0081701	M11	NA	116	100	152	168	241	162	144	193	171	260
Sly09g0081711	M2	NA	71	67	59	48	57	58	59	51	56	54
Sly09g0081721	M3	NA	62	59	55	54	51	47	49	41	38	38
Sly09g0081731	M1	NA	29	30	32	40	10	3	1	1	1	1
Sly09g0081741	M1	NA	436	392	449	403	447	259	282	284	403	291
Sly09g0081751	M11	MEE40	5	5	5	7	8	6	5	6	5	5
Sly09g0081761	M19	NA	170	163	164	127	117	153	135	148	100	81
Sly09g0081771	M8	NA	3	3	3	6	4	3	3	3	10	12
Sly09g0081781	M12	NA	7	7	8	4	2	23	23	27	11	3
Sly09g0081791	M11	NA	5	3	4	3	1	7	5	7	1	1
Sly09g0081831	M17	NA	320	288	317	282	310	276	243	304	319	397
Sly09g0081841	M1	NA	8	7	7	6	5	4	4	4	5	7
Sly09g0081851	M12	NA	291	269	306	280	248	367	367	451	480	463
Sly09g0081871	M18	NA	8	8	8	4	4	12	9	11	4	6
Sly09g0081881	M18	NA	3	3	3	2

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0192051	M23	NA	12	5	5	1	1	19	15	15	7	1
Sly03g0192071	M1	NA	2	1	1	1	1	1	1	1	0	0
Sly03g0192081	M19	NA	3	3	4	4	6	3	3	4	7	10
Sly03g0192091	M23	Solyc03g005980	2	1	1	1	1	11	1	4	0	0
Sly03g0192101	M3	BEH4-like2	11	13	10	8	12	6	7	4	6	12
Sly03g0192111	M3	NA	30	34	28	30	82	17	19	16	22	63
Sly03g0192121	M12	NA	9	10	12	76	61	56	56	62	145	93
Sly03g0192131	M1	NA	13	10	13	23	20	10	10	11	22	27
Sly03g0192141	M22	NA	1	0	1	0	0	9	0	7	0	0
Sly03g0192151	M12	NA	2	4	2	1	1	3	3	3	1	1
Sly03g0192221	M9	NA	4	5	4	6	4	8	9	6	9	9
Sly03g0192231	M3	NA	7	8	6	8	8	6	5	5	6	4
Sly03g0192241	M2	BIN2	73	75	66	65	82	66	81	63	82	95
Sly03g0192251	M1	NA	11	16	7	2	1	3	2	2	1	1
Sly03g0192261	M11	NA	7	8	12	3	1	27	20	32	3	1
Sly03g0192271	M12	NA	1	1	1	1	1	1	1	2	4	4
Sly03g0192281	M11	NA	1	1	1	3	10	1	1	2	72	189
Sly03g0192291	M12	NA	33	51	50	46	55	77	102	109	105	130
Sly03g0192301	M9	NA	226	231	202	133	213	297	412	318	233	324
Sly03g0192341	M1	NA	14	14	14	9	11	13	13	13	16	17
Sly03g0192351	M19	NA	14	18	14	12	10	15	12	14	16	12
Sly03g0192371	M3	NA	7	14	3	1	0	1	0	0	0	0
Sly03g0192381	M1	NA	2	2	2	1	0	1	1	1	0	0
Sly03g0192401	M1	NA	3	2	4	1	0	1	0	1	0	0
Sly03g0192411	M12	NA	13	15	24	13	3	128	127	125	3	2
Sly03g0192421	M1	NA	3	2	2	1	1	1	1	1	1	0
Sly03g0192441	M2	NA	9	9	9	7	9	10	9	8	8	9
Sly03g0192451	M22	NA	1	1	1	3	5	2	1	1	1	0
Sly03g0192461	M22	NA	1	1	1	1	0	1	1	1	0	1
Sly03g0192481	M2	NA	40	40	35	22	17	27	33	24	23	16
Sly03g0192491	M16	SIERF.F7	6	4	4	1	1	5	5	5	1	1
Sly03g0192501	M12	NA	15	25	20	52	22	28	35	31	37	14
Sly03g0192511	M11	NA	16	16	17	17	16	18	18	20	16	16
Sly03g0192521	M12	NA	1	1	1	1	1	3	3	3	4	12
Sly03g0192531	M3	NA	3	3	2	1	7	2	3	1	3	5
Sly03g0192541	M11	NA	2	1	2	2	6	2	3	3	1	3
Sly03g0192561	M1	NA	6	6	6	7	9	5	4	5	10	10
Sly03g0192571	M1	NA	8	9	10	10	10	7	7	9	12	13
Sly03g0192581	M3	NA	22	25	14	29	31	6	9	14	48	27
Sly03g0192591	M1	NA	2	1	4	1	0	1	1	1	1	0
Sly03g0192621	M1	ORC1A	25	22	21	9	10	14	14	14	5	5
Sly03g0192631	M1	NA	11	12	12	9	9	10	10	9	4	4
Sly03g0192661	M11	NA	22	21	24	26	33	27	26	30	33	38
Sly03g0192711	M11	HUP54	441	309	502	97	36	593	463	723	131	58
Sly03g0192721	M8	NA	29	29	21	35	33	25	41	21	29	36
Sly03g0192731	M2	NA	91	97	72	76	79	61	71	57	88	84
Sly03g0192741	M18	NA	32	31	30	34	28	31	30	34	38	33
Sly03g0192761	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0192781	M1	NA	1	1	1	0	0	0	1	0	0	0
Sly03g0192791	M1	NA	22	26	19	18	16	9	10	8	11	10
Sly03g0192811	M3	NA	27	35	20	18	19	19	21	12	6	10
Sly03g0192821	M17	NA	30	28	28	31	27	28	27	29	15	9
Sly03g0192841	M1	NA	1	1	2	2	1	1	1	1	0	0
Sly03g0192851	M12	NA	3	4	7	11	16	10	17	21	154	188
Sly03g0192861	M3	NA	33	53	38	5	18	29	29	7	2	7
Sly03g0192871	M3	NA	18	20	18	16	16	12	14	14	44	43
Sly03g0192881	M2	NA	18	19	16	17	18	15	17	14	30	23
Sly03g0192891	M12	NA	2	1	1	1	2	16	13	20	7	10
Sly03g0192901	M3	NA	22	26	20	19	20	18	22	17	23	19
Sly03g0192921	M1	SlCycD6;2	1	1	1	0	1	1	1	1	1	1
Sly03g0192931	M11	NA	67	63	64	60	49	68	64	68	58	40
Sly03g0192941	M1	NA	1	1	1	0	0	1	1	1	0	1
Sly03g0192951	M1	NA	4	5	3	1	1	1	1	1	1	1
Sly03g0192961	M9	NA	1	0	1	0	0	2	4	1	0	0
Sly03g0193011	M1	NA	5	4	3	1	1	1	1	2	0	0
Sly03g0193021	M1	NA	5	6	4	1	1	1	1	1	0	0
Sly03g0193031	M1	NA	7	5	4	1	1	1	1	1	0	0
Sly03g0193041	M1	NA	5	5	4	1	1	1	1	1	0	1
Sly03g0193051	M1	NA	2	3	3	4	4	1	0	1	1	1
Sly03g0193081	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly03g0193091	M12	NA	2	1	2	1	2	1	2	2	2	3
Sly03g0193101	M2	NA	19	18	15	16	21	13	18	16	23	24
Sly03g0193111	M11	NA	5	5	5	4	3	8	9	12	6	7
Sly03g0193121	M21	NA	1	1	1	0	0	1	0	1	0	0
Sly03g0193131	M12	NA	12	12	12	16	13	14	14	15	15	11
Sly03g0193141	M10	NA	36	39	33	42	33	44	53	36	39	25
Sly03g0193151	M18	PGM1	17	14	16	9	8	18	13	17	3	2
Sly03g0193161	M12	GA20OX1	3	2	4	1	1	54	31	57	0	0
Sly03g0193181	M3	NA	1	1	1	1	1	0	0	0	0	0
Sly03g0193191	M1	NA	7	5	4	1	1	1	0	1	0	0
Sly03g0193201	M11	NA	1	1	1	2	2	1	1	1	3	6
Sly03g0193211	M1	NA	20	22	23	28	38	15	15	17	31	38
Sly03g0193221	M22	SIPP2C11	2	1	1	0	1	4	1	3	1	1
Sly03g0193231	M22	SIPP2C12	2	1	1	0	0	3	1	3	0	0
Sly03g0193241	M22	SIPP2C13	1	0	1	0	0	2	1	1	0	0
Sly03g0193251	M1	SIPP2C14	8	9	13	164	96	4	5	5	15	30
Sly03g0193261	M1	NA	3	1	3	4	2	1	1	1	0	1
Sly03g0193271	M1	NA	4	3	2	1	1	3	1	2	0	0
Sly03g0193281	M12	NA	4	5	4	4	4	5	5	4	4	3
Sly03g0193291	M9	NA	19	20	17	60	75	22	29	23	61	70
Sly03g0193301	M1	NA	11	10	11	6	6	8	7	9	4	3
Sly03g0193321	M11	NA	3	2	2	1	1	2	3	2	1	0
Sly03g0193331	M2	NA	26	25	23	20	11	20	21	18	18	10
Sly03g0193341	M21	NA	1	1	1	1	1	1	0	1	0	0
Sly03g0193351	M22	NA	2	3	3	2	1	3	2	3	2	1
Sly03g0193371	M11	ACS11	18	16	19	23	25	23	20	28	24	30
Sly03g0193381	M12	NA	1	3	1	1	1	3	3	2	2	2
Sly03g0193391	M9	NA	8	8	8	7	7	17	18	15	9	9
Sly03g0193401	M11	NA	23	24	28	22	25	35	28	34	24	29
Sly03g0193411	M11	NA	25	23	23	44	75	27	29	29	54	71
Sly03g0193421	M3	NA	48	45	38	28	28	38	44	28	29	21
Sly03g0193431	M1	NA	1	1	1	1	0	1	0	1	0	0
Sly03g0193441	M11	NA	13	12	15	11	8	16	17	18	12	9
Sly03g0193451	M3	NA	10	10	7	9	15	5	6	3	9	15
Sly03g0193471	M1	NA	50	52	43	13	9	33	28	25	8	4
Sly03g0193481	M1	NA	10	7	11	3	2	6	6	6	3	2
Sly03g0193491	M12	NA	62	64	61	101	113	65	69	74	120	114
Sly03g0193501	M11	NA	2	2	2	1	1	2	2	2	1	1
Sly03g0193511	M3	NA	35	49	29	23	28	34	42	25	17	23
Sly03g0193521	M5	NA	39	50	29	24	32	37	40	24	18	29
Sly03g0193531	M5	NA	50	61	34	7	1	45	70	20	5	1
Sly03g0193541	M12	SIPP2C8	99	78	107	157	96	147	184	367	495	279
Sly03g0193551	M1	NA	104	78	66	76	76	41	39	35	39	54
Sly03g0193561	M10	NA	37	35	23	18	29	48	48	31	18	36
Sly03g0193571	M12	NA	55	49	52	57	53	62	59	62	60	46
Sly03g0193581	M3	NA	29	29	22	21	25	24	20	18	18	18
Sly03g0193591	M22	NA	1	1	1	1	1	2	1	2	1	1
Sly03g0193611	M11	SIPYL10	28	20	26	22	32	29	22	29	15	22
Sly03g0193631	M3	NA	66	61	56	61	58	54	55	54	72	72
Sly03g0193641	M18	NA	21	22	24	16	11	33	29	37	16	9
Sly03g0193651	M12	NA	12	10	8	7	5	16	12	15	9	9
Sly03g0193661	M1	NA	3	3	3	4	3	2	2	2	3	2
Sly03g0193671	M1	NA	5	5	5	7	5	2	1	2	1	1
Sly03g0193681	M12	NA	6	4	6	9	49	11	12	12	25	48
Sly03g0193691	M1	NA	2	6	11	1	1	1	1	1	0	0
Sly03g0193701	M12	PPR-like43	6	6	6	8	8	7	7	8	13	12
Sly03g0193721	M11	NA	8	8	9	11	12	11	9	11	12	11
Sly03g0193731	M3	NA	36	33	32	71	97	23	25	23	92	94
Sly03g0193741	M3	NA	50	45	46	40	40	37	45	40	54	43
Sly03g0193761	M9	SIERF.G3	3	5	5	3	4	7	9	4	1	2
Sly03g0193771	M12	NA	236	236	253	246	158	283	364	361	447	300
Sly03g0193781	M12	NA	98	98	111	110	134	146	168	176	197	220
Sly03g0193791	M1	NA	3	3	3	1	1	1	2	1	1	1
Sly03g0193811	M3	NA	20	23	19	18	19	16	21	16	19	25

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0081951	M1	NA	2	2	2	1	1	1	1	1	2	2
Sly09g0081971	M12	NA	2954	2601	2806	1139	917	4457	4324	4949	3435	2686
Sly09g0081981	M7	NA	49	62	41	36	48	60	101	42	34	51
Sly09g0081991	M1	NA	21	18	17	24	17	11	14	13	34	45
Sly09g0082001	M1	NA	15	12	10	5	3	2	1	1	1	1
Sly09g0082011	M1	DPA	8	8	7	5	3	4	4	4	1	1
Sly09g0082021	M1	NA	5	5	4	4	4	1	1	1	1	1
Sly09g0082031	M3	NA	86	89	80	31	6	57	58	44	8	2
Sly09g0082041	M1	NA	4	3	4	1	1	2	1	1	1	1
Sly09g0082051	M19	NA	2	2	2	1	1	2	2	2	1	1
Sly09g0082091	M3	NA	79	85	63	49	44	69	71	64	65	66
Sly09g0082121	M12	NA	23	24	20	21	17	24	28	26	26	23
Sly09g0082131	M1	NA	9	20	8	2	2	4	3	3	1	2
Sly09g0082161	M1	MT2B	3469	3285	3843	5350	14853	3032	2804	3772	4142	4906
Sly09g0082171	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0082181	M3	NA	16	17	12	14	16	12	13	11	14	16
Sly09g0082191	M18	NA	22	27	31	49	55	39	34	47	52	68
Sly09g0082201	M1	NA	44	49	41	38	37	37	40	36	34	37
Sly09g0082211	M3	NA	45	72	35	12	9	25	32	10	3	5
Sly09g0082221	M1	expansin precursor 4	32	16	17	6	3	1	1	1	1	1
Sly09g0082231	M11	NA	17	18	19	29	45	21	18	24	33	44
Sly09g0082241	M12	NA	30	28	27	52	48	30	36	36	51	52
Sly09g0082261	M18	NA	3	3	4	4	4	4	3	5	3	3
Sly09g0082271	M11	NA	7	6	7	5	6	9	8	9	7	8
Sly09g0082281	M1	NA	12	11	7	6	7	5	5	4	11	8
Sly09g0082291	M11	NA	50	48	59	181	283	127	128	171	328	356
Sly09g0082301	M12	NA	245	217	209	64	94	225	253	270	266	447
Sly09g0082311	M19	NA	30	32	34	35	45	33	28	32	33	32
Sly09g0082331	M3	NA	27	26	22	42	49	16	16	10	16	35
Sly09g0082341	M6	NA	61	131	75	2	3	67	159	36	9	10
Sly09g0082381	M11	NA	24	17	24	15	18	55	48	54	29	16
Sly09g0082391	M11	NA	23	22	28	21	38	23	22	30	37	54
Sly09g0082411	M11	NA	62	68	79	238	476	154	141	206	391	631
Sly09g0082421	M12	NA	2	1	5	11	63	21	16	22	39	89
Sly09g0082441	M8	NA	2	2	1	1	0	2	2	1	1	1
Sly09g0082451	M3	NA	8	9	3	1	1	6	4	5	1	1
Sly09g0082461	M1	NA	3	3	2	1	1	1	1	1	1	1
Sly09g0082471	M12	NA	6	3	8	4	7	9	6	6	3	8
Sly09g0082491	M22	NA	1	0	1	0	0	7	0	2	1	0
Sly09g0082501	M22	NA	1	0	1	1	1	6	0	6	2	1
Sly09g0082531	M22	NA	1	1	1	1	0	3	0	1	2	2
Sly09g0082541	M12	NA	2	2	3	11	7	5	21	42	207	114
Sly09g0082571	M11	NA	30	29	46	2	1	44	41	35	1	0
Sly09g0082581	M4	NA	3	2	3	4	44	5	3	4	14	62
Sly09g0082591	M1	NA	48	52	48	8	5	12	11	10	2	1
Sly09g0082611	M12	NA	5	4	8	3	4	21	15	24	6	6
Sly09g0082641	M13	NA	17	16	25	30	51	25	25	34	29	42
Sly09g0082651	M11	NA	29	25	30	51	61	39	39	49	109	80
Sly09g0082661	M1	NA	20	16	15	15	13	11	13	12	13	11
Sly09g0082671	M3	NA	15	15	14	7	4	12	15	10	3	2
Sly09g0082681	M1	NA	5	6	7	9	9	6	6	6	9	5
Sly09g0082701	M3	NA	1	2	1	0	1	1	1	0	0	0
Sly09g0082721	M22	NA	1	0	1	0	1	2	1	2	1	1
Sly09g0082751	M11	NA	31	29	32	56	50	37	38	38	44	39
Sly09g0082761	M1	NA	2	2	3	6	2	1	1	1	3	1
Sly09g0082771	M2	NA	100	96	86	118	119	71	83	71	119	130
Sly09g0082791	M18	NA	26	26	25	27	30	26	25	27	29	30
Sly09g0082801	M12	NA	1	1	1	1	1	1	2	1	1	1
Sly09g0082811	M1	NA	44	37	36	40	26	35	33	33	18	8
Sly09g0082831	M3	NA	30	31	25	16	16	17	20	14	22	17
Sly09g0082841	M12	NA	35	31	27	36	36	38	37	39	51	53
Sly09g0082851	M1	NA	11	13	17	10	8	2	2	2	3	4
Sly09g0082861	M1	NA	24	49	11	1	1	2	2	1	1	0
Sly09g0082871	M3	NA	10	28	6	1	0	1	1	0	1	0
Sly09g0082881	M11	NA	12	12	14	25	56	18	15	21	43	72
Sly09g0082901	M3	NA	279	271	222	98	92	154	181	140	138	97
Sly09g0082921	M1	NA	71	69	73	74	122	59	59	62	90	126
Sly09g0082951	M3	NA	14	21	15	1	5	11	11	4	1	1
Sly09g0082971	M12	NA	52	64	68	306	344	77	111	130	785	659
Sly09g0083001	M14	NA	17	21	36	98	118	17	15	29	114	151
Sly09g0083011	M1	NA	4	5	4	1	2	1	2	1	0	0
Sly09g0083021	M10	NA	1	2	1	1	1	2	5	1	1	1
Sly09g0083041	M12	NA	1	1	1	0	2	3	6	1	0	0
Sly09g0083061	M5	NA	2	1	1	0	1	3	2	1	0	0
Sly09g0083071	M3	NA	5	9	4	4	41	2	2	1	1	0
Sly09g0083081	M1	NA	27	34	26	19	21	1	1	1	1	1
Sly09g0083091	M5	NA	4	6	2	1	1	5	5	1	0	0
Sly09g0083101	M3	NA	415	378	207	235	190	185	226	74	64	29
Sly09g0083111	M3	NA	10	15	11	9	24	3	6	1	1	1
Sly09g0083121	M1	NA	56	79	75	113	137	7	6	2	1	3
Sly09g0083131	M3	NA	1	2	1	1	3	1	1	0	0	1
Sly09g0083161	M3	NA	5	2	2	1	4	2	5	1	0	1
Sly09g0083181	M3	NA	85	81	48	12	9	27	36	22	11	12
Sly09g0083191	M6	NA	5	11	4	1	1	2	8	2	1	1
Sly09g0083201	M1	NA	22	21	13	1	1	5	4	3	1	1
Sly09g0083211	M3	NA	23	28	23	8	30	23	29	17	11	31
Sly09g0083231	M1	NA	166	178	149	188	132	3	5	6	189	199
Sly09g0083241	M1	NA	4	5	6	2	2	5	3	4	1	1
Sly09g0083251	M11	NA	16	14	17	19	27	23	21	23	25	32
Sly09g0083261	M10	NA	43	67	34	31	66	96	150	57	56	145
Sly09g0083271	M16	NA	10	9	8	9	11	8	8	9	8	9
Sly09g0083281	M13	NA	87	91	101	101	100	86	90	95	76	67
Sly09g0083291	M12	NA	7	6	5	11	5	10	9	9	4	1
Sly09g0083301	M3	NA	6	6	5	5	8	4	5	4	5	7
Sly09g0083351	M11	NA	14	14	23	31	11	36	33	44	8	1
Sly09g0083361	M12	NA	1	1	1	0	0	1	2	2	0	1
Sly09g0083371	M11	NA	18	15	21	30	46	37	30	43	42	50
Sly09g0083381	M12	NA	35	31	50	117	156	96	99	135	133	155
Sly09g0083391	M12	NA	20	22	21	43	57	22	20	24	59	62
Sly09g0083401	M6	NA	10	31	8	1	3	12	30	4	1	3
Sly09g0083411	M6	NA	14	33	20	1	1	21	27	5	1	1
Sly09g0083421	M3	NA	184	199	141	64	117	120	162	118	108	189
Sly09g0083461	M1	NA	8	8	6	3	2	2	2	2	1	1
Sly09g0083481	M3	NA	89	90	71	110	131	45	62	42	125	117
Sly09g0083491	M11	NA	57	59	63	83	98	66	60	69	130	151
Sly09g0083521	M1	NA	11	10	7	0	0	1	1	1	0	0
Sly09g0083531	M1	NA	2	2	3	1	1	1	1	1	0	0
Sly09g0083541	M1	NA	7	6	10	7	4	1	1	1	1	0
Sly09g0083591	M19	NA	2	2	2	2	1	2	2	2	1	1
Sly09g0083601	M12	NA	1	2	2	1	1	1	2	2	2	1
Sly09g0083621	M11	DET2-like	28	22	35	63	92	44	37	50	31	32
Sly09g0083631	M1	NA	123	130	134	444	487	94	100	92	228	310
Sly09g0083641	M11	NA	20	21	24	19	24	25	21	29	26	29
Sly09g0083651	M18	NA	18	19	21	36	54	23	20	27	33	31
Sly09g0083661	M3	NA	27	24	22	21	19	18	21	17	24	26
Sly09g0083671	M1	NA	42	38	43	32	29	40	36	40	32	38
Sly09g0083681	M1	NA	42	46	45	51	46	30	30	26	40	37
Sly09g0083691	M12	NA	16	14	13	17	18	21	20	20	39	41
Sly09g0083701	M9	NA	12	29	19	50	89	94	85	44	89	161
Sly09g0083711	M11	NA	1	1	1	1	0	1	1	1	1	1
Sly09g0083721	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly09g0083731	M1	NA	22	20	18	13	11	17	16	16	10	7
Sly09g0083741	M19	NA	4	5	5	4	3	5	4	5	4	2
Sly09g0083751	M11	NA	12	12	17	13	7	24	20	27	11	5
Sly09g0083761	M11	NA	1	1	1	0	1	1	1	1	1	0
Sly09g0083771	M23	NA	1	1	1	0	0	2	1	1	1	0
Sly09g0083781	M22	NA	3	2	2	0	0	7	4	9	0	0
Sly09g0083791	M12	NA	5	6	5	8	5	7	7	7	5	3
Sly09g0083811	M3	NA	368	357	108	96	36	146	134	59	86	25
Sly09g0083821	M1	NA	14	13	15	52	72	5	6	11	138	198

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0193821	M3	NA	50	48	44	50	63	28	34	29	70	60
Sly03g0193841	M12	NA	4	5	6	6	8	5	5	6	6	9
Sly03g0193851	M1	NA	167	145	151	77	99	98	94	103	98	130
Sly03g0193861	M1	NA	64	45	57	17	12	18	17	16	14	8
Sly03g0193871	M12	NA	6	6	5	14	20	7	8	8	18	30
Sly03g0193881	M11	NA	2	2	2	1	1	4	3	3	1	0
Sly03g0193891	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0193911	M18	NA	22	24	28	36	55	29	28	34	43	60
Sly03g0193921	M11	NA	34	32	52	77	108	53	46	79	118	152
Sly03g0193931	M1	NA	47	45	46	43	44	36	31	34	27	23
Sly03g0193941	M18	NA	26	25	29	43	49	30	29	35	43	47
Sly03g0193971	M11	NA	96	88	95	159	201	114	126	141	205	277
Sly03g0193981	M10	NA	111	105	93	68	103	120	129	100	76	129
Sly03g0193991	M12	NA	45	47	45	51	48	48	49	46	68	73
Sly03g0194001	M1	NA	2	2	3	2	2	2	2	2	2	1
Sly03g0194021	M12	NA	2	2	2	2	1	3	4	3	1	1
Sly03g0194031	M1	NA	2	2	3	1	2	1	2	2	1	5
Sly03g0194061	M11	NA	372	317	406	303	195	378	369	485	307	249
Sly03g0194071	M11	NA	469	373	423	342	256	417	418	505	354	318
Sly03g0194081	M16	NA	37	32	31	29	33	31	30	37	37	40
Sly03g0194091	M1	NA	26	23	10	3	3	4	3	3	1	1
Sly03g0194101	M9	NA	32	41	28	52	84	37	53	39	55	69
Sly03g0194131	M3	NA	9	12	5	1	1	2	1	1	1	1
Sly03g0194141	M13	NA	4	3	4	1	1	3	4	3	1	1
Sly03g0194151	M11	NA	95	96	123	216	270	129	118	139	140	194
Sly03g0194161	M12	NA	7	6	8	6	4	9	7	7	7	5
Sly03g0194171	M12	NA	9	7	8	15	34	9	10	11	32	53
Sly03g0194181	M3	NA	3	4	2	3	3	2	2	2	3	3
Sly03g0194191	M11	NA	4	4	5	3	2	5	5	5	2	2
Sly03g0194201	M11	NA	4	3	9	20	19	10	8	13	6	10
Sly03g0194211	M10	NA	58	117	77	112	255	108	190	58	53	231
Sly03g0194221	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0194231	M12	NA	9	6	12	54	175	30	18	27	59	168
Sly03g0194241	M3	NA	39	42	34	32	34	31	34	25	24	29
Sly03g0194261	M1	NA	62	49	51	16	7	20	19	16	3	1
Sly03g0194271	M12	NA	6	7	7	8	2	10	13	15	8	3
Sly03g0194281	M1	NA	1	1	1	0	1	1	1	1	1	0
Sly03g0194291	M3	crtrb2	46	52	26	84	208	26	31	15	40	203
Sly03g0194301	M12	NA	11	15	6	2	2	15	20	12	2	3
Sly03g0194311	M12	NA	9	9	9	21	45	11	11	12	39	64
Sly03g0194321	M12	NA	155	148	154	253	227	170	183	205	353	240
Sly03g0194331	M12	NA	231	202	205	381	341	233	244	285	553	457
Sly03g0194341	M7	NA	40	44	38	29	45	36	62	36	31	65
Sly03g0194351	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0194371	M12	NA	2	2	1	1	2	2	3	3	3	4
Sly03g0194381	M12	NA	1	1	2	2	2	2	2	2	3	4
Sly03g0194391	M12	NA	1	1	1	1	3	2	2	2	4	4
Sly03g0194401	M12	NA	1	3	1	2	3	2	2	2	2	5
Sly03g0194411	M12	NA	2	2	2	2	4	5	4	5	9	6
Sly03g0194421	M12	NA	1	1	2	2	2	3	2	2	4	3
Sly03g0194431	M12	NA	6	5	7	5	6	8	8	7	9	11
Sly03g0194441	M3	NA	37	41	33	48	47	32	29	28	27	32
Sly03g0194451	M3	NA	23	25	23	31	32	20	23	20	16	26
Sly03g0194471	M1	NA	39	40	51	74	89	30	33	26	35	75
Sly03g0194481	M1	NA	19	23	28	36	40	15	17	16	16	23
Sly03g0194501	M3	NA	11	10	9	8	4	10	11	6	2	1
Sly03g0194511	M3	NA	1	1	1	0	1	1	1	1	0	0
Sly03g0194521	M3	NA	21	15	9	2	2	5	5	4	4	3
Sly03g0194531	M14	NA	15	12	18	11	6	14	12	15	4	2
Sly03g0194571	M22	NA	1	1	1	4	9	1	1	1	1	1
Sly03g0194581	M15	NA	3	3	2	2	6	3	3	3	6	9
Sly03g0194591	M1	NA	295	274	235	103	82	160	175	141	116	97
Sly03g0194601	M19	NA	41	44	43	38	37	42	36	43	38	31
Sly03g0194611	M1	NA	28	32	34	27	25	20	20	22	17	19
Sly03g0194631	M11	NA	17	18	19	25	29	19	22	21	22	23
Sly03g0194641	M1	NA	197	161	269	39	11	17	10	12	7	10
Sly03g0194651	M1	NA	1	1	1	0	1	1	1	1	1	1
Sly03g0194661	M1	NA	168	167	162	213	274	151	151	143	141	258
Sly03g0194691	M1	NA	5	6	5	3	1	1	1	1	1	1
Sly03g0194701	M19	NA	30	30	32	28	26	28	23	30	18	20
Sly03g0194711	M1	NA	1	2	2	1	1	1	1	1	0	0
Sly03g0194721	M1	NA	34	165	61	8	2	2	1	1	1	1
Sly03g0194731	M1	NA	21	20	19	13	10	17	15	13	2	2
Sly03g0194741	M12	NA	30	30	27	32	32	32	30	32	38	43
Sly03g0194751	M1	NA	12	10	11	7	7	8	6	8	2	1
Sly03g0194761	M1	NA	25	23	24	16	19	21	20	22	18	20
Sly03g0194771	M11	NA	4	2	5	3	1	12	10	18	4	2
Sly03g0194781	M1	NA	30	30	33	23	23	27	23	27	19	24
Sly03g0194791	M1	NA	19	20	19	16	15	16	16	16	10	8
Sly03g0194801	M22	NA	2	1	1	1	0	9	3	8	0	1
Sly03g0194811	M22	NA	1	1	1	1	1	2	1	2	1	1
Sly03g0194821	M12	NA	16	14	15	20	27	16	19	18	23	24
Sly03g0194841	M12	SlP4H5	9	9	8	10	8	11	12	13	11	11
Sly03g0194851	M3	NA	46	46	41	55	77	40	38	39	114	143
Sly03g0194861	M1	NA	414	366	320	315	248	242	233	236	328	259
Sly03g0194871	M11	NA	56	59	63	75	74	104	89	120	79	69
Sly03g0194881	M12	NA	17	16	18	15	14	38	38	43	36	14
Sly03g0194891	M11	NA	52	49	51	63	52	52	51	52	44	43
Sly03g0194901	M2	NA	8	9	9	7	5	9	9	7	6	5
Sly03g0194911	M12	NA	9	10	16	16	56	71	51	65	8	9
Sly03g0194931	M14	NA	22	22	37	9	7	31	18	33	6	4
Sly03g0194941	M18	NA	38	41	58	29	36	71	53	75	24	25
Sly03g0194951	M11	NA	51	54	57	63	63	91	76	87	58	53
Sly03g0194961	M3	NA	1	3	3	1	0	1	1	1	0	1
Sly03g0195041	M13	NA	10	10	13	12	10	9	11	11	15	11
Sly03g0195051	M1	NA	2	2	2	3	7	2	1	2	3	3
Sly03g0195081	M9	NA	64	89	76	151	85	95	101	77	270	244
Sly03g0195091	M12	NA	34	39	43	76	72	92	120	106	322	291
Sly03g0195101	M3	NA	16	17	13	10	8	8	11	8	11	9
Sly03g0195111	M1	NA	4	3	4	1	1	1	1	1	1	0
Sly03g0195191	M14	NA	55	50	83	172	171	34	30	54	111	132
Sly03g0195201	M22	NA	1	1	1	2	1	2	1	2	2	1
Sly03g0195211	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0195221	M19	NA	2	2	3	7	2	2	2	3	15	2
Sly03g0195231	M11	NA	89	91	104	182	124	135	145	158	142	96
Sly03g0195241	M11	NA	242	223	299	314	400	292	299	406	400	649
Sly03g0195251	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0195261	M1	NA	5	4	4	1	1	3	3	3	0	0
Sly03g0195271	M2	NA	34	35	34	30	35	31	34	31	39	53
Sly03g0195281	M18	NA	20	21	23	32	30	25	22	27	44	39
Sly03g0195291	M3	NA	6	7	5	3	5	4	4	3	3	4
Sly03g0195301	M12	NA	85	74	75	135	128	86	93	93	112	124
Sly03g0195311	M12	NA	19	18	18	21	22	20	22	20	21	20
Sly03g0195321	M12	NA	39	37	41	44	54	44	53	51	105	103
Sly03g0195331	M11	NA	11	12	11	14	23	14	14	14	22	24
Sly03g0195361	M3	NA	30	35	22	21	23	24	25	21	27	28
Sly03g0195371	M1	receptor kinase regula	298	275	292	414	521	233	237	234	245	289
Sly03g0195381	M12	NA	5	5	3	9	16	7	6	4	1	3
Sly03g0195391	M22	NA	1	1	1	2	2	2	0	1	0	0
Sly03g0195401	M12	NA	18	19	17	55	74	30	22	28	69	60
Sly03g0195411	M11	NA	27	26	29	31	37	30	27	31	38	48
Sly03g0195421	M12	NA	13	14	14	21	21	18	18	21	21	22
Sly03g0195431	M13	NA	12	10	22	13	9	18	15	24	3	3
Sly03g0195441	M10	NA	10	8	7	6	5	9	10	8	6	6
Sly03g0195451	M12	NA	63	57	70	101	125	61	55	72	70	158
Sly03g0195471	M23	NA	1	1	1	0	0	1	1	0	0	0
Sly03g0195481	M11	NA	9	7	5	9	5	13	11	6	1	0
Sly03g0195491	M3	NA	27	32	24	12	10	24	23	16	6	7
Sly03g0195501	M1	NA	4	4	5	4	4	2	2	1	1	1
Sly03g0195511	M11	NA	1	1	1	1	1	3	2	3	1	1
Sly03g0195531	M1	NA	18	19	19	20	18	13	13	13	11	11
Sly03g0195541	M1	NA	16	14	25	25	11	10	9	8	4	2
Sly03g0195561	M23	NA	1	1	1	1	1	2	1	1	1	1
Sly03g0195571	M1	NA	8	6	9	12	4	6	6	7	4	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0083891	M14	NA	21	18	27	11	10	26	18	27	6	3
Sly09g0083901	M1	NA	30	29	24	23	22	25	21	25	27	29
Sly09g0083911	M12	NA	26	26	22	26	24	31	28	27	17	15
Sly09g0083921	M11	NA	65	59	62	120	172	66	60	91	203	232
Sly09g0083941	M1	NA	193	208	128	1	0	3	1	1	1	0
Sly09g0083951	M1	NA	2	2	2	1	1	2	1	1	0	0
Sly09g0083961	M11	NA	25	19	23	25	45	24	24	28	44	61
Sly09g0083971	M2	NA	27	28	25	30	35	24	27	25	34	40
Sly09g0083981	M11	NA	92	46	104	58	55	199	168	250	93	57
Sly09g0084021	M12	NA	1	1	1	1	1	2	2	3	2	1
Sly09g0084101	M9	NA	1	2	1	1	1	5	9	1	1	1
Sly09g0084111	M11	NA	159	144	173	243	343	198	187	237	380	515
Sly09g0084151	M12	NA	1	1	1	0	0	1	2	2	0	0
Sly09g0084271	M1	NA	3	4	3	2	1	2	2	2	2	1
Sly09g0084281	M3	NA	3	10	3	1	0	1	1	1	1	1
Sly09g0084301	M1	NA	7	7	11	6	2	1	1	1	1	1
Sly09g0084311	M22	NA	25	8	10	7	9	57	24	30	15	5
Sly09g0084321	M11	NA	50	47	54	94	145	66	67	73	84	103
Sly09g0084331	M1	NA	98	93	106	64	50	71	60	70	23	22
Sly09g0084341	M19	NA	49	54	47	53	57	46	43	44	38	44
Sly09g0084351	M3	NA	67	92	69	79	101	65	88	57	99	117
Sly09g0084421	M11	NA	1	2	2	3	1	3	2	4	2	1
Sly09g0084441	M1	NA	18	17	19	11	9	16	13	16	12	10
Sly09g0084451	M1	NA	23	35	26	26	10	12	14	13	12	12
Sly09g0084461	M2	NA	1	1	1	1	1	1	1	1	2	1
Sly09g0084471	M3	NA	3	4	3	2	3	3	3	3	3	3
Sly09g0084491	M1	NA	10	10	7	4	1	1	1	1	0	0
Sly09g0084521	M11	NA	16	15	12	12	17	17	15	14	15	21
Sly09g0084541	M3	NA	27	32	25	21	22	21	21	19	17	20
Sly09g0084551	M6	NA	17	64	27	1	1	42	65	8	1	1
Sly09g0084571	M9	NA	1	1	1	1	2	2	2	1	2	4
Sly09g0084581	M4	NA	8	9	15	166	629	11	9	15	31	1020
Sly09g0084591	M12	NA	4	4	5	52	202	9	5	6	11	118
Sly09g0084601	M11	NA	1	1	1	0	0	2	1	2	1	0
Sly09g0084621	M9	NA	33	41	31	58	93	43	49	40	37	108
Sly09g0084641	M11	NA	2	2	2	1	1	4	3	3	2	1
Sly09g0084651	M22	NA	5	3	5	1	1	8	4	3	1	0
Sly09g0084681	M22	NA	2	0	1	0	0	3	0	3	0	0
Sly09g0084701	M1	NA	19	19	17	14	15	16	15	15	21	19
Sly09g0084731	M3	NA	221	235	189	175	172	154	248	126	176	169
Sly09g0084741	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0084751	M12	NA	40	39	39	81	104	42	50	57	170	190
Sly09g0084971	M11	NA	24	26	26	41	40	36	37	41	59	49
Sly09g0084981	M12	NA	2	3	2	4	5	3	3	3	4	4
Sly09g0084991	M1	NA	2	2	2	1	0	1	1	1	0	0
Sly09g0085001	M3	SlPYL9	1	1	1	3	1	1	1	1	1	1
Sly09g0085031	M8	NA	3	4	4	3	3	4	4	3	4	6
Sly09g0085041	M12	NA	1	1	1	1	1	1	1	1	3	3
Sly09g0085051	M12	NA	1	1	1	1	1	2	1	2	1	1
Sly09g0085061	M2	NA	13	12	12	11	19	10	13	13	27	49
Sly09g0085101	M10	NA	1	1	1	1	1	1	1	1	1	2
Sly09g0085111	M11	NA	9	9	9	6	6	10	9	12	6	5
Sly09g0085131	M12	PPC	11	12	12	16	14	16	16	16	22	17
Sly09g0085161	M9	NA	2	2	3	13	8	3	4	3	14	7
Sly09g0085171	M3	NA	33	39	28	35	30	27	36	25	42	35
Sly09g0085341	M1	NA	188	187	183	133	177	90	83	103	119	140
Sly09g0085351	M3	NA	18	30	17	18	21	22	28	17	26	23
Sly09g0085361	M11	NA	117	111	116	138	147	143	134	150	123	129
Sly09g0085371	M18	NA	111	111	123	142	137	149	135	161	110	89
Sly09g0085381	M12	NA	1	1	1	5	4	1	1	2	8	7
Sly09g0085391	M11	NA	5	4	5	7	7	5	6	6	9	12
Sly09g0085401	M9	NA	7	8	6	4	4	8	8	8	7	15
Sly09g0085411	M1	NA	4	3	4	1	1	2	1	1	0	0
Sly09g0085441	M3	NA	516	503	303	51	179	144	207	82	55	415
Sly09g0085471	M1	NA	3	4	5	4	4	3	3	4	3	4
Sly09g0085481	M2	NA	125	120	91	84	93	84	98	78	102	134
Sly09g0085491	M12	NA	71	106	70	187	257	104	144	109	344	331
Sly09g0085501	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0085511	M18	NA	1	2	2	2	2	1	2	2	1	1
Sly09g0085571	M3	NA	46	49	42	51	61	42	45	41	74	78
Sly09g0085581	M2	NA	2	2	2	2	1	1	1	2	1	1
Sly09g0085591	M3	NA	27	32	23	27	26	21	22	18	27	21
Sly09g0085601	M19	NA	26	28	29	30	24	38	24	25	32	27
Sly09g0085611	M12	NA	25	27	26	26	26	32	30	27	37	43
Sly09g0085691	M1	NA	18	7	13	0	0	2	1	1	0	0
Sly09g0085711	M3	NA	11	13	9	5	2	6	7	5	1	1
Sly09g0085741	M1	NA	27	28	26	26	12	20	17	19	15	11
Sly09g0085751	M9	NA	2	2	1	9	3	2	4	3	34	15
Sly09g0085761	M12	NA	1	1	1	6	3	1	2	1	1	3
Sly09g0085831	M1	NA	10	10	10	14	14	8	8	8	10	11
Sly09g0085841	M1	NA	3	3	3	3	2	1	1	1	1	1
Sly09g0085881	M12	NA	2	2	2	2	2	3	3	3	4	6
Sly09g0085891	M7	NA	5	7	5	5	16	4	11	5	7	49
Sly09g0085921	M10	NA	3	4	3	3	2	4	4	3	1	1
Sly09g0085931	M10	NA	5	10	4	3	4	10	12	5	3	5
Sly09g0085951	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0085961	M10	NA	1	2	1	1	1	2	2	1	3	5
Sly09g0085981	M12	NA	3	3	5	4	3	4	4	8	6	2
Sly09g0086001	M11	NA	155	132	169	121	95	144	163	188	113	108
Sly09g0086011	M12	NA	4	5	5	7	6	5	6	5	10	14
Sly09g0086021	M12	NA	3	3	4	6	5	4	4	4	6	10
Sly09g0086031	M12	NA	4	4	4	4	4	4	5	6	10	9
Sly09g0086041	M19	NA	26	25	25	26	25	23	21	24	17	15
Sly09g0086071	M12	NA	29	31	28	24	29	34	34	31	25	36
Sly09g0086111	M1	NA	1	1	1	0	1	1	1	0	0	0
Sly09g0086121	M1	NA	81	81	74	59	56	50	44	42	34	32
Sly09g0086131	M1	NA	3	4	4	12	7	2	2	2	11	3
Sly09g0086161	M12	NA	3	1	3	2	2	7	8	7	8	5
Sly09g0086181	M3	NA	4	4	3	1	1	2	3	2	2	2
Sly09g0086201	M11	NA	40	33	43	35	30	50	46	51	29	35
Sly09g0086231	M3	NA	97	82	92	59	60	75	85	64	42	53
Sly09g0086241	M12	NA	5	6	6	6	24	6	11	7	12	51
Sly09g0086301	M11	NA	16	12	14	4	1	20	22	21	4	1
Sly09g0086311	M11	NA	14	17	19	8	2	23	24	19	3	1
Sly09g0086341	M1	NA	15	17	18	16	14	14	17	16	18	18
Sly09g0086351	M19	NA	11	14	14	16	14	14	12	13	14	15
Sly09g0086371	M1	NA	32	33	34	50	42	26	29	28	40	31
Sly09g0086381	M19	NA	11	12	11	11	9	11	10	11	10	7
Sly09g0086401	M18	NA	31	34	44	46	31	38	34	45	32	33
Sly09g0086411	M1	NA	61	63	68	59	62	55	57	64	66	79
Sly09g0086431	M14	NA	211	200	267	217	120	211	179	225	84	109
Sly09g0086451	M1	NA	13	13	15	16	13	11	9	12	15	11
Sly09g0086461	M1	NA	77	74	82	111	97	67	63	61	72	91
Sly09g0086481	M12	NA	1	1	1	1	1	2	1	1	1	1
Sly09g0086501	M11	NA	20	22	25	34	29	37	30	36	74	78
Sly09g0086511	M11	NA	18	24	25	37	30	33	35	37	82	121
Sly09g0086521	M22	NA	3	3	2	2	1	3	2	2	2	1
Sly09g0086551	M11	NA	1	1	1	1	1	2	1	2	1	1
Sly09g0086561	M12	NA	20	20	21	20	12	22	27	27	33	23
Sly09g0086571	M5	NA	53	54	41	44	37	56	54	44	44	39
Sly09g0086591	M12	NA	26	24	29	30	45	32	29	32	33	54
Sly09g0086601	M5	NA	22	21	13	8	3	20	27	11	4	5
Sly09g0086621	M12	NA	19	19	19	21	24	19	22	21	29	35
Sly09g0086631	M12	NA	18	18	20	25	32	23	20	22	31	42
Sly09g0086641	M12	NA	77	78	90	149	157	132	131	146	212	207
Sly09g0086651	M1	NA	195	185	184	160	145	145	144	142	137	130
Sly09g0086661	M3	NA	168	159	123	89	104	92	110	87	107	118
Sly09g0086671	M22	NA	6	5	6	5	4	6	5	6	2	2
Sly09g0086681	M1	NA	3	4	5	5	4	4	3	3	3	4
Sly09g0086721	M1	NA	58	55	63	118	84	39	39	46	85	86
Sly09g0086751	M22	ADH2-1	1699	397	689	24	2	4010	904	2645	70	3
Sly09g0086781	M1	NA	66	62	62	80

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0195581	M11	NA	7	8	7	2	1	9	8	8	2	1
Sly03g0195591	M11	NA	18	15	20	6	2	24	22	22	4	2
Sly03g0195601	M3	NA	1	1	1	0	0	1	0	0	1	0
Sly03g0195611	M11	NA	30	31	36	39	35	58	49	74	43	46
Sly03g0195621	M18	NA	36	35	37	44	47	39	34	40	41	42
Sly03g0195631	M11	NA	9	8	11	9	11	16	13	18	14	17
Sly03g0195641	M11	NA	19	17	23	7	3	22	16	19	3	3
Sly03g0195651	M3	NA	104	102	65	37	56	92	92	34	18	35
Sly03g0195661	M6	NA	8	20	9	1	1	9	12	5	1	1
Sly03g0195671	M17	NA	42	40	41	22	19	35	30	36	22	14
Sly03g0195681	M19	NA	19	22	22	11	11	18	14	19	11	8
Sly03g0195701	M12	NA	8	8	6	7	9	9	13	8	6	9
Sly03g0195711	M12	NA	1	1	1	1	14	1	4	2	1	22
Sly03g0195721	M12	NA	1	1	2	2	143	1	20	6	8	210
Sly03g0195731	M12	NA	1	2	1	2	43	1	17	4	3	127
Sly03g0195741	M2	NA	25	23	21	22	27	19	22	22	24	35
Sly03g0195751	M23	NA	9	7	7	7	9	8	7	8	7	10
Sly03g0195761	M3	NA	8	8	7	6	8	7	7	7	7	7
Sly03g0195771	M11	NA	36	36	38	66	105	48	45	50	80	102
Sly03g0195781	M14	NA	4	3	4	5	8	3	3	4	5	7
Sly03g0195791	M11	NA	55	50	60	47	59	66	56	65	42	52
Sly03g0195801	M3	NA	47	44	43	40	43	41	42	42	44	45
Sly03g0195811	M1	NA	1	2	3	3	1	1	0	1	0	0
Sly03g0195821	M1	NA	47	45	26	8	7	8	8	4	2	1
Sly03g0195901	M1	NA	18	25	17	10	5	6	5	4	1	2
Sly03g0195911	M1	NA	11	10	9	79	49	4	5	4	6	4
Sly03g0195921	M3	NA	7	11	7	60	40	4	6	4	4	4
Sly03g0195931	M7	NA	3	6	2	2	3	4	8	2	2	14
Sly03g0195941	M1	NA	1	2	2	1	1	0	0	0	0	0
Sly03g0195951	M1	PPR-like32	14	16	15	14	13	13	13	15	10	10
Sly03g0195961	M23	NA	1	1	1	1	1	3	1	2	1	1
Sly03g0196071	M11	NA	3	3	3	3	3	3	3	5	3	3
Sly03g0196111	M1	NA	163	138	129	61	21	101	99	86	26	6
Sly03g0196131	M9	NA	9	6	6	50	38	25	20	22	128	32
Sly03g0196141	M12	NA	0	1	1	0	0	1	1	5	1	1
Sly03g0196161	M11	NA	14	11	16	17	27	15	17	20	43	36
Sly03g0196181	M3	NA	56	61	51	49	54	39	43	34	28	38
Sly03g0196201	M1	NA	7	7	7	4	2	7	5	5	2	1
Sly03g0196211	M2	NA	81	72	83	110	139	70	80	78	132	162
Sly03g0196231	M11	NA	34	31	42	45	71	53	48	64	66	80
Sly03g0196251	M11	NA	204	206	212	172	143	207	217	223	212	185
Sly03g0196261	M1	NA	1	1	1	1	1	1	0	1	0	0
Sly03g0196271	M1	NA	1	1	1	2	1	1	0	0	0	1
Sly03g0196281	M6	NA	51	78	56	75	139	53	82	55	146	269
Sly03g0196291	M1	NA	2	2	2	1	1	2	1	1	1	0
Sly03g0196311	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0196321	M3	NA	120	110	113	107	96	80	90	80	79	83
Sly03g0196341	M12	NA	19	14	15	1	1	274	245	180	1	1
Sly03g0196361	M11	NA	11	11	15	15	24	16	15	18	23	32
Sly03g0196381	M8	NA	2	2	1	1	1	2	2	2	3	10
Sly03g0196401	M11	expansin	127	95	138	99	60	206	172	210	84	68
Sly03g0196411	M4	NA	8	8	8	23	19	8	8	9	20	18
Sly03g0196421	M12	psy1	72	122	138	4860	7549	149	299	531	11713	12445
Sly03g0196431	M3	NA	1	1	1	0	0	1	1	0	0	1
Sly03g0196451	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0196461	M11	NA	19	26	26	17	22	63	61	95	43	55
Sly03g0196501	M3	NA	18	20	3	1	1	8	17	3	1	2
Sly03g0196511	M3	NA	94	105	58	113	139	26	30	17	68	95
Sly03g0196531	M22	NA	1	1	1	0	0	2	1	4	0	1
Sly03g0196541	M1	NA	173	160	176	217	240	146	157	162	217	234
Sly03g0196561	M7	NA	3	3	2	1	2	3	8	2	3	6
Sly03g0196571	M18	SIARF8A	32	34	35	22	17	41	35	35	26	26
Sly03g0196581	M12	NA	92	91	96	53	48	102	109	94	73	78
Sly03g0196591	M3	NA	27	39	14	0	1	8	7	1	1	0
Sly03g0196601	M1	SlPILS3	3	3	3	1	1	1	1	1	1	0
Sly03g0196611	M6	NA	4	14	4	1	1	4	6	1	1	1
Sly03g0196621	M11	NA	38	31	35	32	33	37	36	36	33	36
Sly03g0196641	M8	NA	39	45	39	53	12	49	58	29	20	7
Sly03g0196661	M3	NA	67	77	56	92	31	59	59	36	45	15
Sly03g0196671	M1	NA	15	14	16	10	11	10	10	8	12	13
Sly03g0196681	M11	NA	21	21	37	45	45	36	33	33	38	19
Sly03g0196691	M4	NA	19	19	21	19	19	18	19	20	18	21
Sly03g0196701	M11	NA	25	22	31	49	39	41	32	43	18	21
Sly03g0196711	M11	NA	37	32	37	31	33	40	34	44	36	43
Sly03g0196721	M1	SlPILS7	1	2	1	2	2	1	1	1	0	1
Sly03g0196731	M12	NA	93	74	66	140	62	160	170	148	199	72
Sly03g0196741	M1	NA	13	14	13	13	13	10	12	10	15	13
Sly03g0196761	M11	NA	12	11	14	14	14	23	22	23	16	19
Sly03g0196771	M13	NA	552	539	685	582	611	646	607	853	541	689
Sly03g0196781	M3	NA	48	48	47	35	36	46	46	44	46	55
Sly03g0196791	M6	NA	80	110	62	33	43	67	100	41	21	48
Sly03g0196801	M14	NA	76	74	80	86	98	70	71	78	78	92
Sly03g0196811	M19	NA	13	14	14	15	16	13	11	12	11	12
Sly03g0196821	M22	SlCycB2;7	1	1	1	1	0	1	1	1	0	0
Sly03g0196851	M11	NA	7	8	10	3	2	12	11	13	1	1
Sly03g0196871	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly03g0196891	M12	NA	4	4	5	5	2	29	35	48	30	3
Sly03g0196921	M11	NA	4	4	4	4	2	7	6	7	3	1
Sly03g0196931	M12	NA	2	1	2	2	2	4	5	5	2	1
Sly03g0196941	M11	NA	4	3	5	6	3	6	8	8	3	1
Sly03g0196971	M1	NA	5	6	5	7	1	1	1	2	2	1
Sly03g0196991	M12	NA	66	65	71	72	80	104	111	133	156	130
Sly03g0197001	M12	SlP4H8	25	25	26	27	23	33	37	38	38	32
Sly03g0197011	M1	NA	52	60	55	2	6	22	20	27	16	27
Sly03g0197021	M3	NA	46	49	46	73	84	34	39	37	51	51
Sly03g0197031	M1	NA	3	3	3	2	2	3	3	3	1	1
Sly03g0197041	M1	NA	3	3	2	2	1	2	1	2	1	1
Sly03g0197051	M1	NA	7	8	6	4	3	5	5	5	2	2
Sly03g0197061	M11	NA	30	29	30	35	43	41	38	48	51	63
Sly03g0197071	M11	NA	10	8	8	1	1	14	11	10	1	1
Sly03g0197081	M3	NA	43	45	42	40	45	43	42	42	45	43
Sly03g0197091	M1	NA	4	5	3	7	5	0	1	1	1	1
Sly03g0197101	M12	NA	37	33	35	36	27	50	53	45	41	38
Sly03g0197141	M12	NA	29	31	33	37	40	33	37	37	62	62
Sly03g0197151	M10	NA	2	2	2	1	1	3	3	1	1	1
Sly03g0197161	M3	NA	6	6	3	2	1	3	4	3	5	2
Sly03g0197171	M12	NA	13	16	15	19	14	19	21	18	33	20
Sly03g0197181	M11	SEF	10	9	10	11	11	9	11	13	11	10
Sly03g0197191	M12	NA	3	3	4	5	4	7	5	8	4	6
Sly03g0197201	M3	NA	35	27	20	24	20	25	24	22	31	29
Sly03g0197211	M11	NA	4	6	8	7	3	16	16	28	5	2
Sly03g0197231	M11	NA	4	4	5	5	6	6	6	8	6	5
Sly03g0197251	M19	NA	6	6	6	7	10	5	5	6	8	14
Sly03g0197261	M10	NA	115	170	77	24	28	171	189	76	28	28
Sly03g0197271	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0197281	M13	NA	82	78	91	72	86	92	85	100	95	128
Sly03g0197301	M3	NA	28	30	25	28	29	26	28	25	34	37
Sly03g0197321	M1	NA	48	45	45	52	54	38	40	40	61	72
Sly03g0197331	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0197351	M11	NA	29	29	36	57	68	34	32	38	32	33
Sly03g0197361	M1	NA	37	37	35	28	30	27	26	28	26	25
Sly03g0197371	M12	NA	35	33	31	69	93	36	38	41	61	86
Sly03g0197381	M12	NA	28	27	31	38	49	34	33	40	53	75
Sly03g0197401	M1	NA	6	2	5	1	1	2	1	1	1	3
Sly03g0197421	M23	NA	2	2	2	1	1	13	4	7	1	1
Sly03g0197471	M3	NA	8	8	7	3	3	5	5	4	3	1
Sly03g0197481	M11	NA	3	2	3	1	1	4	3	3	1	1
Sly03g0197491	M23	NA	10	10	9	7	10	11	9	9	10	10
Sly03g0197541	M1	NA	2	2	2	1	1	1	1	0	0	0
Sly03g0197551	M1	NA	16	23	26	2	1	1	1	0	1	0
Sly03g0197561	M1	NA	7	8	10	6	6	5	7	9	8	10
Sly03g0197571	M3	NA	1	2	1	2	1	1	1	2	1	1
Sly03g0197581	M1	NA	7	8	6	5	4	5	5	4	7	7
Sly03g0197591	M3	NA	31	23	8	2	3	16	31	7	3	3

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0086811	M12	NA	13	14	16	20	17	33	34	32	34	37
Sly09g0086831	M12	NA	1	1	1	1	1	3	2	2	1	1
Sly09g0086901	M1	NA	2	2	3	1	0	1	1	1	0	0
Sly09g0086971	M1	NA	2	3	3	1	1	1	1	1	1	1
Sly09g0086981	M11	NA	9	10	11	12	11	13	14	16	21	10
Sly09g0086991	M3	NA	33	37	31	37	36	23	26	22	28	28
Sly09g0087491	M12	NA	4	3	3	1	1	7	9	8	1	0
Sly09g0087501	M12	NA	5	4	4	2	2	12	12	9	1	1
Sly09g0087511	M1	NA	2	2	2	6	7	1	0	1	0	0
Sly09g0087571	M11	NA	35	30	37	21	20	34	40	35	28	27
Sly09g0087581	M11	NA	4	4	5	6	3	6	6	7	6	3
Sly09g0087601	M1	NA	1	1	1	0	1	0	0	0	0	0
Sly09g0087611	M4	NA	3	2	3	3	4	3	2	3	4	7
Sly09g0087621	M1	NA	25	24	24	19	10	16	17	13	5	3
Sly09g0087631	M12	NA	51	59	61	114	101	67	83	76	163	126
Sly09g0087651	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0087661	M11	NA	19	18	25	52	65	36	37	45	55	72
Sly09g0087671	M12	NA	22	22	24	19	24	23	20	25	31	45
Sly09g0087701	M18	PHS-like2	52	49	48	41	26	55	46	53	20	10
Sly09g0087711	M1	NA	7	6	7	3	2	5	5	4	1	1
Sly09g0087731	M13	NA	15	13	18	17	16	17	14	18	14	13
Sly09g0087741	M12	NA	77	84	81	96	89	94	98	109	136	138
Sly09g0087761	M3	NA	41	47	31	16	35	22	51	22	21	105
Sly09g0087781	M3	NA	5	6	4	2	2	4	3	3	1	1
Sly09g0087811	M1	NA	10	11	7	1	0	1	1	1	0	0
Sly09g0087881	M7	NA	9	10	8	7	8	9	10	9	7	8
Sly09g0087891	M18	NA	72	73	71	90	111	79	70	80	78	86
Sly09g0087901	M9	NA	4	3	3	4	6	3	4	4	6	5
Sly09g0087921	M11	NA	17	17	25	27	44	30	24	34	24	34
Sly09g0087941	M11	NA	11	12	12	19	24	16	16	19	21	26
Sly09g0087951	M12	NA	15	15	14	19	19	15	21	17	23	22
Sly09g0087961	M19	NA	39	42	37	35	34	33	30	31	31	32
Sly09g0088001	M1	NA	17	18	19	23	23	16	16	17	17	13
Sly09g0088011	M11	NA	31	31	35	40	47	33	34	37	51	53
Sly09g0088021	M19	NA	24	26	28	24	25	28	23	29	28	26
Sly09g0088091	M14	NA	3	2	5	2	1	3	2	3	1	1
Sly09g0088111	M3	NA	10	10	9	9	9	9	11	9	11	11
Sly09g0088141	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0088151	M12	NA	2	2	2	2	2	2	2	2	4	3
Sly09g0088161	M3	NA	3	3	2	1	1	2	2	2	1	1
Sly09g0088181	M22	NA	2	1	1	1	1	1	2	1	3	1
Sly09g0088191	M12	NA	3	3	3	1	1	6	9	5	1	1
Sly09g0088201	M11	NA	35	39	36	30	32	77	82	88	19	24
Sly09g0088221	M12	NA	4	4	7	0	1	76	61	81	4	1
Sly09g0088251	M1	NA	2	2	3	6	2	1	1	1	1	1
Sly09g0088311	M3	NA	4	4	4	4	5	3	5	3	5	10
Sly09g0088321	M12	NA	3	5	2	1	4	6	11	5	3	16
Sly09g0088341	M19	NA	52	52	52	42	46	45	42	48	48	55
Sly09g0088361	M11	NA	7	6	7	6	7	6	7	7	4	6
Sly09g0088371	M22	NA	3	2	2	1	1	9	1	5	0	0
Sly09g0088381	M12	NA	18	19	20	17	15	18	22	21	18	22
Sly09g0088391	M12	NA	6	5	6	6	6	6	8	8	12	13
Sly09g0088401	M12	NA	15	14	14	9	10	17	16	19	10	6
Sly09g0088441	M11	NA	20	21	21	27	31	31	33	40	34	32
Sly09g0088451	M3	NA	6	6	5	4	6	6	5	6	4	4
Sly09g0088481	M2	NA	13	12	10	10	5	9	11	7	5	2
Sly09g0088501	M22	NA	4	3	4	3	2	4	3	4	3	2
Sly09g0088511	M23	NA	1	1	1	1	0	3	1	1	1	0
Sly09g0088521	M21	NA	1	1	1	0	0	1	1	1	0	0
Sly09g0088651	M3	NA	8	12	8	7	12	4	13	7	8	26
Sly09g0088661	M1	NA	13	16	16	16	22	2	2	3	3	8
Sly09g0088701	M14	NA	25	26	31	27	31	29	26	32	25	32
Sly09g0088731	M19	NA	23	26	26	30	35	25	22	24	24	28
Sly09g0088751	M12	NA	6	6	6	13	10	16	12	18	25	17
Sly09g0088791	M3	NA	42	43	39	43	48	36	38	35	35	35
Sly09g0088801	M12	NA	6	6	7	15	18	8	8	10	38	42
Sly09g0088821	M11	NA	39	37	42	38	42	52	48	50	38	38
Sly09g0088831	M11	NA	38	38	38	45	40	44	38	44	45	45
Sly09g0088971	M13	NA	1	2	2	2	2	1	1	2	3	3
Sly09g0089011	M22	NA	2	1	1	0	0	2	1	4	0	0
Sly09g0089021	M1	NA	3	2	2	1	1	1	1	1	1	1
Sly09g0089031	M1	NA	5	3	4	1	1	1	1	1	0	0
Sly09g0089041	M12	NA	12	12	16	16	14	18	17	19	27	30
Sly09g0089061	M3	NA	52	57	50	58	73	54	49	44	45	82
Sly09g0089071	M3	NA	2	2	2	1	2	1	1	1	2	2
Sly09g0089081	M3	NA	33	30	27	21	21	30	30	30	25	21
Sly09g0089101	M13	NA	7	7	13	6	10	6	8	11	6	14
Sly09g0089161	M1	NA	46	43	45	53	57	41	42	45	64	71
Sly09g0089211	M1	NA	63	67	66	57	48	60	60	58	49	42
Sly09g0089231	M3	NA	3	5	2	3	4	2	3	2	2	2
Sly09g0089261	M1	NA	115	103	113	62	35	98	92	105	55	39
Sly09g0089301	M12	NA	43	40	40	54	66	41	45	45	65	75
Sly09g0089321	M3	LOX1-like6	10	10	8	7	5	6	8	5	4	2
Sly09g0089331	M1	NA	18	16	15	14	6	11	11	11	5	3
Sly09g0089341	M1	LOX1-like7	3	3	3	3	3	2	2	2	1	1
Sly09g0089351	M11	NA	21	20	22	24	17	28	24	30	20	16
Sly09g0089361	M3	NA	8	9	7	7	8	9	7	7	5	5
Sly09g0089371	M1	NA	12	12	15	15	11	7	7	7	6	5
Sly09g0089381	M13	NA	34	37	54	58	62	41	33	58	51	54
Sly09g0089431	M18	NA	4	5	5	3	3	4	5	5	3	4
Sly09g0089481	M12	NA	17	15	27	25	14	36	36	26	42	51
Sly09g0089491	M2	NA	1	2	1	2	1	1	1	1	3	1
Sly09g0089531	M11	NA	12	11	15	7	5	27	24	31	12	10
Sly09g0089551	M3	NA	4	4	3	3	3	4	4	4	3	4
Sly09g0089571	M7	NA	1	2	1	1	1	1	2	1	1	1
Sly09g0089741	M1	NA	23	23	27	11	7	11	10	10	5	4
Sly09g0089751	M11	NA	51	47	57	81	120	73	65	82	108	148
Sly09g0089761	M21	NA	2	2	2	2	1	2	1	2	1	1
Sly09g0089791	M12	NA	2	3	2	5	9	2	4	3	5	16
Sly09g0089831	M1	NA	40	36	30	40	34	27	29	31	37	35
Sly09g0089841	M9	NA	11	16	12	11	21	12	27	15	23	60
Sly09g0089851	M3	NA	20	23	17	19	23	13	20	17	22	21
Sly09g0089911	M1	NA	57	52	60	49	58	47	44	48	73	111
Sly09g0089921	M11	NA	14	16	16	18	24	20	19	20	17	28
Sly09g0089931	M2	NA	8	8	9	11	11	8	9	8	12	12
Sly09g0090061	M12	NA	25	44	27	71	42	36	61	49	98	53
Sly09g0090071	M9	NA	30	35	26	30	32	44	57	33	24	34
Sly09g0090081	M8	NA	14	21	14	12	10	14	21	16	17	7
Sly09g0090111	M3	NA	41	88	18	2	2	14	25	3	1	1
Sly09g0090141	M10	NA	2	3	2	4	3	7	8	3	3	3
Sly09g0090151	M1	NA	13	12	13	9	7	11	10	10	14	11
Sly09g0090161	M1	NA	11	7	9	5	6	6	7	6	8	8
Sly09g0090181	M12	NA	15	18	17	19	105	22	48	25	71	163
Sly09g0090251	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0090361	M13	NA	3	4	4	5	4	2	4	4	4	4
Sly09g0090371	M11	NA	25	23	31	25	25	39	32	48	28	24
Sly09g0090401	M11	NA	1	1	1	1	1	2	2	3	3	4
Sly09g0090411	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly09g0090421	M3	NA	1	1	1	1	1	1	1	1	0	0
Sly09g0090431	M3	NA	14	14	4	3	3	9	9	3	2	2
Sly09g0090441	M9	NA	14	16	15	15	12	17	20	15	10	9
Sly09g0090451	M1	NA	424	367	357	289	224	267	252	283	274	230
Sly09g0090461	M20	NA	38	31	39	40	34	30	22	26	12	13
Sly09g0090471	M12	NA	196	204	216	234	198	222	251	238	272	220
Sly09g0090481	M22	NA	1	1	1	1	1	1	1	2	1	1
Sly09g0090501	M12	NA	13	12	14	16	13	22	23	19	20	18
Sly09g0090521	M5	NA	10	9	8	11	13	9	10	8	11	13
Sly09g0090531	M3	NA	4	6	5	12	11	4	5	4	4	3
Sly09g0090541	M3	NA	2	3	4	4	4	2	3	2	3	3
Sly09g0090721	M11	NA	15	13	15	13	11	17	15	20	13	12
Sly09g0090731	M11	NA	7	7	8	9	9	8	8	9	10	10
Sly09g0090791

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0197601	M3	NA	17	17	13	11	15	16	17	14	16	21
Sly03g0197671	M4	NA	3	2	3	2	2	3	2	2	3	5
Sly03g0197751	M18	NA	91	91	88	65	55	97	84	96	70	61
Sly03g0197771	M3	NA	37	36	34	22	15	29	32	26	12	15
Sly03g0197781	M3	NA	18	20	19	18	19	14	17	14	19	15
Sly03g0197791	M1	NA	1	1	3	2	1	1	1	1	0	0
Sly03g0197801	M1	NA	1	1	2	1	13	1	1	1	1	1
Sly03g0197811	M3	NA	22	25	9	3	3	12	15	4	3	3
Sly03g0197821	M11	NA	1	1	1	0	0	1	1	1	1	0
Sly03g0197841	M1	NA	14	11	13	11	15	8	8	10	13	15
Sly03g0197861	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0197871	M12	NA	3	4	2	2	1	6	6	4	2	1
Sly03g0197881	M19	NA	95	99	78	101	124	101	91	94	97	110
Sly03g0197891	M3	NA	9	8	9	7	8	8	9	5	9	10
Sly03g0197941	M12	NA	5	7	15	65	66	43	81	128	608	448
Sly03g0197961	M11	NA	3	3	3	4	4	5	4	5	5	5
Sly03g0197971	M11	NA	11	11	16	13	15	24	20	29	13	8
Sly03g0197981	M3	NA	79	87	62	74	73	60	63	61	86	98
Sly03g0197991	M11	NA	14	13	16	35	57	23	24	30	56	91
Sly03g0198001	M1	NA	84	87	81	66	60	61	59	54	60	56
Sly03g0198021	M11	NA	662	494	585	337	58	1274	1015	1414	102	18
Sly03g0198031	M1	NA	5	7	10	5	1	1	1	1	1	1
Sly03g0198041	M1	NA	2	3	5	2	1	1	1	1	0	1
Sly03g0198051	M3	NSY3	1	1	1	2	2	1	1	1	1	1
Sly03g0198061	M10	NA	17	31	16	17	18	37	50	19	18	23
Sly03g0198101	M12	NA	11	12	11	13	15	11	12	12	17	19
Sly03g0198131	M1	NA	2	1	2	1	1	1	1	1	1	1
Sly03g0198151	M12	NA	1	1	2	8	20	1	1	2	3	3
Sly03g0198161	M12	NA	2	3	2	1	1	16	8	12	5	3
Sly03g0198171	M22	NA	3	1	2	0	1	19	0	13	0	0
Sly03g0198201	M3	NA	7	3	0	0	0	1	1	0	0	0
Sly03g0198211	M1	NA	124	92	26	0	0	5	5	0	0	1
Sly03g0198221	M1	NA	1650	1442	1226	15	13	101	62	27	1	2
Sly03g0198261	M1	NA	8	7	6	3	2	6	4	4	4	1
Sly03g0198281	M1	NA	3	2	3	1	0	1	1	1	0	0
Sly03g0198291	M9	NA	1	1	1	1	2	3	8	2	3	4
Sly03g0198321	M2	NA	174	168	163	139	130	140	156	129	142	151
Sly03g0198331	M9	NA	134	147	136	163	196	218	244	199	210	321
Sly03g0198341	M12	NA	12	13	12	10	8	13	14	13	10	12
Sly03g0198351	M12	NA	2	1	2	2	2	2	3	2	2	1
Sly03g0198361	M12	NA	5	4	5	3	4	5	6	6	7	5
Sly03g0198431	M6	NA	6	24	9	1	1	15	14	1	0	0
Sly03g0198441	M6	NA	3	13	3	0	1	7	4	1	0	0
Sly03g0198511	M11	NA	21	19	23	26	43	24	20	24	25	45
Sly03g0198551	M1	NA	1	1	1	4	2	0	0	0	1	0
Sly03g0198581	M18	NA	38	41	43	54	60	51	45	56	70	94
Sly03g0198591	M1	NA	28	28	31	35	35	25	28	28	40	47
Sly03g0198601	M19	NA	2	2	3	3	4	2	2	2	3	2
Sly03g0198611	M1	NA	2	1	2	3	2	1	2	1	3	3
Sly03g0198631	M6	NA	7	16	9	2	3	7	10	3	1	2
Sly03g0198661	M11	NA	25	19	23	28	37	34	27	38	39	50
Sly03g0198671	M11	NA	4	4	4	3	4	6	6	7	8	7
Sly03g0198691	M12	NA	9	9	13	16	39	57	54	88	129	199
Sly03g0198701	M11	NA	15	14	20	56	123	24	22	29	89	159
Sly03g0198711	M11	NA	78	80	86	79	74	98	87	105	90	81
Sly03g0198721	M11	NA	1	1	2	0	0	8	5	8	0	1
Sly03g0198761	M12	NA	17	20	30	254	636	16	24	56	212	798
Sly03g0198781	M1	NA	4	3	4	4	2	1	1	2	1	1
Sly03g0198791	M22	NA	2	2	2	4	4	3	2	3	2	2
Sly03g0198811	M3	NA	19	32	18	37	33	6	8	9	16	17
Sly03g0198821	M1	NA	4	3	3	2	1	1	1	1	1	1
Sly03g0198831	M1	NA	2	1	1	1	1	0	1	1	1	0
Sly03g0198861	M3	NA	11	10	10	12	7	9	10	9	7	4
Sly03g0198871	M2	NA	10	12	14	36	36	8	14	9	20	29
Sly03g0198881	M3	NA	23	26	17	4	2	12	9	4	1	0
Sly03g0198891	M3	NA	28	28	26	20	31	23	21	17	13	21
Sly03g0198901	M12	NA	56	48	58	50	43	63	76	83	59	51
Sly03g0198941	M1	NA	693	644	692	539	347	434	463	477	417	322
Sly03g0198951	M2	NA	50	54	42	53	60	31	40	31	55	58
Sly03g0198961	M1	NA	2	2	2	1	1	2	2	2	1	1
Sly03g0198981	M3	NA	3	3	1	1	0	1	1	1	1	1
Sly03g0198991	M1	NA	5	4	4	2	1	3	3	3	2	1
Sly03g0199001	M3	NA	3	1	2	1	1	2	2	1	2	1
Sly03g0199011	M3	NA	10	9	8	11	11	9	10	7	5	4
Sly03g0199021	M3	NA	31	35	30	24	20	20	24	21	16	14
Sly03g0199031	M18	NA	4	4	5	1	1	6	6	7	3	1
Sly03g0199041	M1	NA	26	36	18	2	1	5	6	3	3	1
Sly03g0199051	M1	NA	9	8	7	3	2	4	4	3	2	1
Sly03g0199081	M12	NA	2	1	1	0	0	4	3	1	0	0
Sly03g0199091	M3	NA	1	1	1	0	0	0	0	0	0	0
Sly03g0199101	M1	NA	91	86	91	103	115	84	84	87	109	136
Sly03g0199111	M18	NA	49	51	62	5	4	70	54	53	1	1
Sly03g0199121	M3	NA	10	10	8	3	2	3	4	3	1	1
Sly03g0199131	M3	NA	13	18	12	6	12	5	8	4	13	16
Sly03g0199141	M10	NA	2	8	2	0	1	68	72	7	0	0
Sly03g0199161	M11	NA	38	34	44	69	74	52	46	54	43	77
Sly03g0199171	M14	ADH	32	32	43	66	87	31	32	32	43	61
Sly03g0199201	M3	NA	2	2	2	1	0	1	1	1	0	0
Sly03g0199211	M3	NA	18	20	16	8	7	15	18	10	6	4
Sly03g0199241	M2	NA	2	1	2	1	1	1	1	1	1	1
Sly03g0199251	M3	NA	76	65	63	72	86	48	56	50	60	67
Sly03g0199261	M14	NA	24	26	27	36	37	25	24	28	30	30
Sly03g0199291	M9	NA	2	1	2	2	1	1	2	2	1	1
Sly03g0199301	M1	AP2a	88	90	86	405	397	16	21	55	578	397
Sly03g0199311	M11	NA	212	195	226	175	56	235	194	278	257	84
Sly03g0199321	M12	NA	0	1	1	1	1	1	1	1	1	2
Sly03g0199331	M12	NA	1	2	2	1	3	1	3	2	1	5
Sly03g0199341	M2	NA	1	5	2	2	5	1	3	3	1	3
Sly03g0199351	M1	NA	12	12	13	13	14	10	9	10	11	12
Sly03g0199361	M1	EZ2	16	16	14	4	4	13	10	10	2	2
Sly03g0199391	M5	NA	3	2	2	2	3	3	3	2	2	3
Sly03g0199401	M3	NA	3	4	3	3	2	3	4	2	3	3
Sly03g0199411	M12	NA	14	13	15	28	32	20	20	22	27	25
Sly03g0199431	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly03g0199481	M12	NA	24	25	27	35	28	33	33	34	28	27
Sly03g0199501	M1	NA	2	2	4	1	1	1	1	1	0	0
Sly03g0199511	M22	NA	7	6	7	5	7	14	7	14	5	5
Sly03g0199581	M12	NA	2	1	2	7	14	8	7	10	34	119
Sly03g0199591	M1	NA	14	15	15	16	17	13	12	14	19	21
Sly03g0199601	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly03g0199661	M6	NA	23	24	19	16	17	22	28	19	22	12
Sly03g0199681	M11	NA	2	2	2	1	0	4	3	3	0	0
Sly03g0199721	M13	NA	8	8	9	8	8	8	7	9	4	5
Sly03g0199731	M11	NA	5	4	6	1	1	37	31	33	1	1
Sly03g0199761	M1	NA	13	11	11	11	14	10	8	7	12	18
Sly03g0199771	M1	NA	18	22	27	9	4	8	5	5	1	1
Sly03g0199781	M18	NA	1	1	1	1	1	1	1	1	0	1
Sly03g0199791	M1	NA	10	7	9	8	9	2	2	2	1	1
Sly03g0199821	M1	NA	7	7	7	7	5	3	3	3	4	2
Sly03g0199831	M1	NA	8	9	8	9	5	4	4	4	4	3
Sly03g0199861	M12	NA	1	1	0	0	1	4	5	1	1	1
Sly03g0199901	M11	NA	9	9	11	10	10	10	11	12	13	18
Sly03g0199911	M2	NA	33	32	24	28	15	19	24	20	29	18
Sly03g0199931	M6	NA	3	4	1	1	2	1	4	1	0	1
Sly03g0199941	M1	NA	177	149	143	19	26	28	28	29	14	23
Sly03g0199991	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly03g0200011	M1	NA	8	8	9	5	7	6	6	5	9	14
Sly03g0200081	M3	NA	63	72	48	44	54	42	43	38	34	39
Sly03g0200091	M1	NA	29	29	29	27	28	27	26	27	26	27
Sly03g0200101	M11	NA	2	2	2	1	0	5	5	7	1	0
Sly03g0200121	M11	NA	76	75	85	101	94	78	84	86	77	93
Sly03g0200131	M11	NA	5	4	7	4	1	12	9	13	2	1
Sly03g0200141	M12	NA	15	14	15	25	45	18	19	18	34	77
Sly03g0200161	M3	NA	13	14	10	10	11	9	9	9	13	14

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0090861	M1	NA	2	1	1	1	0	1	0	0	0	0
Sly09g0090881	M2	NA	2	1	2	1	1	1	1	1	1	1
Sly09g0090901	M3	NA	18	18	18	26	33	17	17	16	30	33
Sly09g0090931	M1	NA	3	2	2	1	1	1	1	1	0	1
Sly09g0090941	M11	NA	108	103	123	139	143	140	136	183	374	435
Sly09g0090951	M3	NA	315	340	260	247	220	293	267	173	286	267
Sly09g0091001	M11	NA	1	1	3	1	0	11	9	14	0	0
Sly09g0091021	M22	NA	2	1	1	2	1	3	1	1	2	1
Sly09g0091061	M12	NA	2	2	2	1	3	2	2	2	3	3
Sly09g0091071	M1	NA	2	3	5	85	49	1	1	1	1	1
Sly09g0091091	M11	NA	1	1	2	2	1	1	1	2	0	0
Sly09g0091101	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly09g0091141	M3	NA	4	2	1	0	0	1	1	1	0	0
Sly09g0091151	M8	NA	6	7	5	6	3	7	7	6	4	3
Sly09g0091161	M18	NA	5	6	5	6	2	6	6	5	3	2
Sly09g0091171	M19	NA	9	10	8	6	4	10	8	8	4	3
Sly09g0091191	M12	NA	101	102	117	140	138	145	161	154	140	138
Sly09g0091201	M11	NA	6	6	7	8	6	9	8	7	7	10
Sly09g0091211	M11	NA	10	9	11	12	10	13	10	10	12	19
Sly09g0091221	M12	NA	13	13	15	16	17	15	17	16	30	40
Sly09g0091231	M1	NA	69	74	69	64	45	57	56	52	55	49
Sly09g0091271	M12	NA	8	9	8	9	7	12	14	14	24	23
Sly09g0091291	M1	NA	18	17	20	26	26	11	9	9	13	18
Sly09g0091301	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0091331	M1	NA	58	74	45	13	3	12	10	4	2	2
Sly09g0091341	M11	NA	2	2	2	1	1	3	2	2	1	1
Sly09g0091361	M1	NA	46	51	46	36	38	41	39	42	37	37
Sly09g0091371	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly09g0091381	M12	NA	2	2	3	2	2	4	4	4	1	1
Sly09g0091391	M3	NA	45	40	39	38	44	39	41	39	40	49
Sly09g0091401	M3	NA	38	39	25	18	12	23	20	17	22	15
Sly09g0091411	M12	NA	4	5	4	4	3	6	5	5	3	3
Sly09g0091421	M1	NA	9	8	11	9	8	7	6	8	10	8
Sly09g0091431	M5	NA	32	43	23	21	27	32	40	20	24	28
Sly09g0091461	M11	NA	12	12	14	15	13	22	20	24	20	25
Sly09g0091481	M12	NA	1	1	1	1	1	1	1	1	3	1
Sly09g0091511	M3	NA	12	14	12	13	10	11	13	10	6	4
Sly09g0091521	M3	NA	3	3	3	2	2	2	2	2	3	3
Sly09g0091531	M12	NA	24	26	27	35	34	35	34	36	39	39
Sly09g0091541	M22	NA	23	4	16	0	0	166	11	164	0	0
Sly09g0091551	M1	NA	70	63	64	52	48	55	56	56	54	54
Sly09g0091561	M3	NA	2	1	1	1	1	1	1	2	1	1
Sly09g0091581	M4	NA	6	4	5	9	22	6	5	5	11	38
Sly09g0091601	M12	NA	13	15	16	16	7	35	36	37	18	7
Sly09g0091741	M1	NA	4	5	5	7	8	3	3	4	7	12
Sly09g0091751	M3	NA	5	6	4	6	10	4	5	3	15	28
Sly09g0091931	M12	NA	1	1	2	11	14	2	3	4	6	20
Sly09g0091941	M2	NA	36	36	33	36	31	33	36	32	32	26
Sly09g0091951	M1	NA	96	86	95	90	82	76	82	81	133	181
Sly09g0091971	M1	NA	3	3	6	2	1	4	3	4	1	1
Sly09g0092091	M1	NA	3	5	3	4	4	1	1	1	1	1
Sly09g0092101	M1	NA	2	2	2	2	2	1	1	1	1	1
Sly09g0092111	M1	NA	2	2	2	1	4	1	1	0	1	0
Sly09g0092151	M19	NA	12	13	14	13	13	13	12	14	13	16
Sly09g0092161	M1	NA	11	11	11	12	8	9	8	7	6	3
Sly09g0092171	M11	NA	2	2	3	4	4	5	3	4	2	2
Sly09g0092181	M22	NA	1	1	2	1	3	2	1	1	1	1
Sly09g0092211	M2	NA	8	8	8	9	10	7	8	7	14	23
Sly09g0092341	M1	NA	5	5	6	3	3	5	4	4	4	3
Sly09g0092351	M3	NA	4	4	3	2	2	4	3	2	4	3
Sly09g0092361	M9	NA	11	13	10	14	13	12	17	13	33	45
Sly09g0092371	M3	NA	51	52	48	51	29	43	55	40	45	33
Sly09g0092391	M11	NA	1	1	1	1	0	1	1	1	0	0
Sly09g0092411	M3	NA	12	14	11	7	8	12	12	12	10	12
Sly09g0092421	M3	NA	20	19	16	19	20	13	16	14	18	20
Sly09g0092431	M8	NA	10	15	9	11	12	13	21	12	36	20
Sly09g0092441	M1	NA	42	42	50	55	68	41	36	42	38	40
Sly09g0092451	M3	NA	103	95	79	105	131	57	53	43	80	113
Sly09g0092461	M3	NA	20	26	14	11	16	14	22	9	7	12
Sly09g0092481	M1	NA	10	10	12	10	9	9	9	10	12	8
Sly09g0092511	M1	NA	20	21	20	18	21	17	16	19	18	18
Sly09g0092531	M1	NA	6	6	6	8	6	3	1	2	1	1
Sly09g0092541	M11	NA	10	10	10	10	8	16	14	14	11	8
Sly09g0092561	M3	NA	117	123	91	53	47	62	70	46	50	43
Sly09g0092571	M11	NA	43	35	48	95	201	63	59	87	144	251
Sly09g0092781	M1	NA	2	2	1	8	6	1	1	1	1	0
Sly09g0092871	M10	NA	69	94	66	67	127	86	118	73	110	195
Sly09g0092901	M11	NA	36	35	33	28	43	41	40	45	32	32
Sly09g0092911	M9	NA	1	1	1	1	1	6	7	5	10	1
Sly09g0092921	M11	NA	35	34	29	30	40	40	37	42	48	64
Sly09g0092931	M1	NA	8	9	7	3	2	3	3	1	1	1
Sly09g0092941	M1	NA	4	5	3	3	2	1	2	1	1	1
Sly09g0092951	M12	NA	37	38	33	43	48	46	42	47	64	62
Sly09g0092961	M1	PPR-like28	3	3	3	2	2	2	2	2	2	2
Sly09g0092991	M1	NA	5	4	4	4	4	4	3	4	3	2
Sly09g0093001	M1	NA	4	6	6	23	91	1	1	1	1	1
Sly09g0093061	M4	NA	2	2	3	3	4	3	3	3	6	7
Sly09g0093071	M19	NA	2	2	3	2	3	3	2	2	4	7
Sly09g0093081	M3	NA	4	5	4	4	4	4	4	3	3	6
Sly09g0093091	M3	NA	701	813	556	12	10	257	385	79	11	4
Sly09g0093101	M3	NA	9	18	8	1	1	6	9	3	1	1
Sly09g0093111	M11	NA	16	13	19	8	6	17	18	17	9	7
Sly09g0093141	M3	SIPL	14	27	9	1	1	6	6	2	1	1
Sly09g0093181	M21	NA	5	4	6	8	8	5	2	4	1	1
Sly09g0093251	M12	NA	9	7	7	9	32	12	12	10	17	34
Sly09g0093261	M9	NA	13	12	10	15	16	13	14	11	14	21
Sly09g0093291	M11	NA	40	44	55	44	41	62	51	60	33	42
Sly09g0093321	M22	NA	6	5	6	0	0	12	3	7	1	0
Sly09g0093331	M11	NA	53	51	52	62	41	61	65	63	46	20
Sly09g0093351	M11	NA	168	119	202	106	25	457	391	584	228	49
Sly09g0093361	M11	NA	13	12	16	12	14	15	14	17	10	12
Sly09g0093371	M13	NA	89	76	91	29	14	82	85	81	9	8
Sly09g0093441	M12	NA	48	67	41	56	59	70	83	66	52	77
Sly09g0093461	M11	NA	11	12	12	12	12	16	13	16	14	11
Sly09g0093471	M11	NA	10	11	11	12	12	14	14	18	12	7
Sly09g0093481	M12	NA	7	6	6	4	2	8	8	8	3	1
Sly09g0093501	M1	NA	13	13	13	4	4	13	11	11	1	1
Sly09g0093521	M11	NA	9	9	9	10	10	15	14	15	11	9
Sly09g0093531	M22	NA	1	1	1	0	0	3	1	3	0	0
Sly09g0093571	M11	ADH	277	236	296	368	443	322	295	347	158	130
Sly09g0093581	M4	NA	17	16	17	28	53	16	19	13	43	96
Sly09g0093591	M4	NA	15	14	17	25	46	14	18	15	30	56
Sly09g0093601	M19	NA	2	2	2	2	6	2	1	1	3	3
Sly09g0093641	M11	NA	10	10	10	10	15	9	10	11	13	17
Sly09g0093651	M11	NA	20	19	25	32	27	53	48	74	50	27
Sly09g0093661	M3	NA	49	44	30	21	17	36	31	25	10	8
Sly09g0093671	M12	NA	113	116	123	172	157	138	149	144	161	159
Sly09g0093691	M3	NA	118	114	44	5	6	42	46	10	1	1
Sly09g0093711	M12	NA	13	13	13	13	5	32	32	34	9	4
Sly09g0093721	M10	NA	15	29	12	6	8	20	27	16	9	11
Sly09g0093731	M12	NA	2	2	3	3	1	7	6	6	2	2
Sly09g0093741	M12	SlAux/IAA12	10	7	8	8	23	62	36	65	3	4
Sly09g0093751	M11	NA	12	13	13	19	17	16	14	15	17	18
Sly09g0093801	M19	NA	70	71	76	75	82	76	63	74	90	125
Sly09g0093831	M3	NA	13	16	10	9	14	11	12	10	12	16
Sly09g0093841	M3	NA	11	13	8	7	10	11	10	11	10	10
Sly09g0093851	M5	NA	8	14	4	9	8	7	9	9	7	9
Sly09g0093861	M19	NA	8	12	8	8	9	11	10	10	8	6
Sly09g0093891	M9	NA	17	18	13	6	6	30	28	19	6	3
Sly09g0093921	M11	NA	137	127	136	105	79	145	130	154	124	93
Sly09g0093991	M1	NA	86	84	109	251	625	59	54	75	594	749
Sly09g0094011	M12	NA	2	2	3	4

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0200191	M12	NA	4	6	5	10	6	8	6	8	6	6
Sly03g0200201	M22	NA	1	0	2	0	0	3	1	4	0	0
Sly03g0200241	M11	NA	5	4	7	21	8	7	5	7	8	4
Sly03g0200271	M1	NA	1	1	1	0	0	0	0	0	0	0
Sly03g0200281	M3	NA	14	16	15	14	11	13	14	14	18	16
Sly03g0200291	M12	NA	10	9	11	13	12	13	15	15	11	9
Sly03g0200311	M11	NA	1	1	1	1	0	1	1	1	1	1
Sly03g0200321	M19	NA	5	6	4	3	3	5	4	5	2	2
Sly03g0200331	M19	NA	2	4	3	3	2	3	3	3	2	2
Sly03g0200381	M13	NA	11	11	12	24	27	12	11	12	13	10
Sly03g0200391	M14	NA	44	44	49	46	39	43	41	44	42	30
Sly03g0200421	M12	NA	5	6	4	2	2	13	38	14	5	19
Sly03g0200441	M3	NA	2	3	1	2	2	2	1	1	3	2
Sly03g0200451	M12	NA	4	5	4	5	4	4	4	5	6	5
Sly03g0200511	M19	NA	19	21	21	24	31	23	18	24	28	38
Sly03g0200521	M9	NA	16	17	20	17	13	19	21	15	8	10
Sly03g0200621	M1	NA	40	40	44	34	39	33	35	36	50	48
Sly03g0200641	M11	NA	20	21	21	19	15	25	24	25	16	15
Sly03g0200681	M1	NA	6	7	8	6	2	1	0	1	0	0
Sly03g0200721	M12	NA	13	13	16	14	13	13	16	19	34	55
Sly03g0200731	M22	NA	2	1	1	1	0	6	2	6	0	0
Sly03g0200761	M10	NA	1	1	1	1	0	1	1	1	1	0
Sly03g0200841	M12	NA	3	2	3	1	2	6	6	5	2	4
Sly03g0200851	M10	NA	4	3	3	4	5	4	6	3	5	7
Sly03g0200861	M1	NA	4	3	2	2	2	1	0	1	0	0
Sly03g0200871	M3	NA	7	7	7	8	8	7	7	7	9	7
Sly03g0200881	M18	NA	37	37	36	56	76	40	38	42	67	88
Sly03g0200891	M9	SIPL	12	11	11	11	16	15	17	12	12	18
Sly03g0200901	M22	NA	3	3	3	4	6	3	2	3	5	5
Sly03g0200911	M11	NA	28	30	31	32	19	64	53	67	37	17
Sly03g0200921	M11	NA	63	50	61	92	110	74	62	78	64	120
Sly03g0200941	M12	NA	1	1	1	1	1	1	1	1	0	1
Sly03g0200951	M18	NA	14	16	18	15	19	18	18	16	22	28
Sly03g0200981	M1	HB2	5	5	6	2	1	2	1	1	1	0
Sly03g0200991	M1	NA	3	2	3	1	1	1	1	1	1	1
Sly03g0201001	M1	NA	33	26	34	44	47	24	31	30	69	86
Sly03g0201011	M11	NA	10	9	12	9	11	18	16	17	12	18
Sly03g0201041	M3	NA	4	3	3	3	1	2	3	1	1	1
Sly03g0201431	M12	NA	34	37	38	48	49	40	46	46	39	42
Sly03g0201441	M1	NA	1	2	1	1	2	1	1	2	1	1
Sly03g0201451	M3	NA	45	45	33	29	19	36	39	27	17	18
Sly03g0201471	M11	NA	19	17	18	25	28	28	27	30	23	18
Sly03g0201501	M1	NA	33	36	36	20	19	26	23	25	14	13
Sly03g0201521	M11	NA	17	15	21	21	17	27	25	33	25	17
Sly03g0201531	M12	SISDG40	14	15	14	21	23	15	16	15	26	25
Sly03g0201541	M10	NA	8	9	7	6	7	9	14	6	5	6
Sly03g0201551	M10	NA	17	24	15	13	14	24	32	16	10	11
Sly03g0201571	M3	NA	89	88	83	86	96	82	84	79	94	106
Sly03g0201591	M2	NA	46	51	44	57	61	43	49	44	59	58
Sly03g0201601	M12	NA	11	12	13	25	35	17	27	24	61	100
Sly03g0201631	M11	NA	26	25	24	13	14	30	25	25	16	26
Sly03g0201661	M8	NA	1	1	1	1	1	1	2	1	1	2
Sly03g0201671	M11	NA	1	1	1	1	0	2	2	2	3	3
Sly03g0201681	M11	NA	13	13	17	17	20	17	17	19	14	18
Sly03g0201691	M12	NA	18	16	23	19	16	54	61	56	42	46
Sly03g0201701	M12	NA	32	25	35	44	16	85	96	104	85	34
Sly03g0201721	M12	NA	2	2	4	1	1	25	33	24	5	11
Sly03g0201731	M12	NA	1	1	2	4	5	9	18	14	68	83
Sly03g0201761	M9	NA	1	2	1	0	1	1	2	1	1	2
Sly03g0201771	M12	NA	46	47	51	71	93	148	147	152	70	113
Sly03g0202071	M23	NA	1	1	1	1	0	3	1	2	2	1
Sly03g0202091	M3	NA	54	49	41	36	37	42	42	42	43	34
Sly03g0202111	M19	NA	29	28	33	35	36	31	24	30	22	20
Sly03g0202141	M22	NA	3	1	2	0	0	4	1	5	0	0
Sly03g0202151	M19	NA	67	68	67	72	61	59	57	61	40	34
Sly03g0202201	M3	NA	5	5	3	1	1	4	4	2	1	1
Sly03g0202211	M13	NA	4	3	6	3	3	5	4	6	3	2
Sly03g0202251	M3	NA	13	15	12	12	14	12	11	11	14	13
Sly03g0202261	M18	NA	1	1	2	1	2	1	1	2	1	2
Sly03g0202271	M19	NA	10	11	10	10	11	10	8	8	10	8
Sly03g0202611	M12	NA	38	38	36	48	58	56	63	57	63	81
Sly03g0202621	M1	NA	25	27	27	26	30	19	19	18	22	26
Sly03g0202701	M12	NA	2	2	2	2	3	3	3	2	4	8
Sly03g0202711	M2	NA	91	93	77	67	40	62	80	50	56	33
Sly03g0202721	M11	NA	19	18	19	12	13	20	18	23	22	24
Sly03g0202731	M13	NA	16	17	18	8	11	16	14	19	13	16
Sly03g0202741	M1	NA	23	24	25	15	14	19	18	26	19	19
Sly03g0202781	M12	NA	15	15	14	13	5	52	55	48	27	6
Sly03g0202801	M12	NA	64	65	72	120	123	118	119	138	168	262
Sly03g0202841	M3	NA	23	21	19	17	19	16	15	14	18	17
Sly03g0202861	M12	NA	49	50	53	64	80	55	53	61	78	94
Sly03g0202881	M11	NA	3	1	3	2	1	6	3	3	2	3
Sly03g0202891	M1	NA	14	16	13	9	7	8	9	7	5	2
Sly03g0202911	M3	NA	41	38	27	20	16	29	32	25	16	17
Sly03g0202921	M11	NA	32	34	36	31	44	35	35	37	45	56
Sly03g0202931	M9	NA	15	15	16	13	16	24	34	21	25	53
Sly03g0202951	M12	NA	1	2	1	1	0	2	2	1	1	1
Sly03g0202961	M18	NA	8	8	9	8	13	12	9	11	12	12
Sly03g0202971	M18	NA	10	14	15	13	16	14	11	19	17	21
Sly03g0202981	M11	NA	13	15	15	17	22	19	16	24	28	29
Sly03g0202991	M11	NA	6	4	11	7	12	9	7	8	16	16
Sly03g0203001	M11	NA	13	15	16	17	23	18	19	21	29	41
Sly03g0203011	M11	NA	32	35	42	100	122	61	59	69	191	200
Sly03g0203021	M11	NA	22	25	28	73	87	44	37	52	123	117
Sly03g0203031	M23	NA	1	1	1	1	0	1	1	1	1	1
Sly03g0203061	M1	NA	22	27	23	16	14	8	8	10	3	2
Sly03g0203071	M7	NA	18	25	21	14	243	20	27	16	27	119
Sly03g0203081	M1	NA	3	2	2	1	1	1	0	0	0	0
Sly03g0203101	M12	NA	64	61	61	98	169	77	77	87	125	181
Sly03g0203111	M12	NA	9	9	11	8	8	11	12	12	15	16
Sly03g0203141	M3	NA	9	9	7	7	3	5	7	7	7	3
Sly03g0203151	M1	NA	6	7	6	5	3	5	4	4	3	3
Sly03g0203161	M1	NA	8	8	6	6	2	6	4	5	4	2
Sly03g0203171	M19	NA	6	6	7	4	3	6	4	7	5	3
Sly03g0203201	M1	NA	2	2	2	2	1	1	1	1	1	1
Sly03g0203211	M19	NA	21	25	23	24	27	22	20	22	22	22
Sly03g0203241	M11	NA	9	8	10	14	21	14	17	20	24	36
Sly03g0203261	M3	NA	28	32	25	25	31	26	30	20	19	31
Sly03g0203281	M11	NA	7	8	7	6	2	14	12	16	7	4
Sly03g0203321	M12	NA	2	2	2	2	2	3	3	3	1	1
Sly03g0203431	M12	NA	25	25	30	27	26	42	38	47	42	34
Sly03g0203491	M1	NA	11	11	11	13	16	10	8	9	11	12
Sly03g0203501	M11	NA	3	3	4	4	2	6	5	6	4	3
Sly03g0203511	M12	NA	23	24	25	15	14	35	31	32	14	22
Sly03g0203531	M12	NA	37	36	35	43	40	36	38	36	46	49
Sly03g0203551	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly03g0203561	M11	NA	3	3	3	1	0	9	7	10	0	0
Sly03g0203571	M11	NA	2	2	2	1	1	6	5	7	1	0
Sly03g0203581	M3	NA	24	24	24	14	12	19	19	15	10	7
Sly03g0203591	M1	NA	2	2	3	2	1	2	2	2	1	1
Sly03g0203601	M1	NA	1	1	2	1	1	1	1	1	1	0
Sly03g0203611	M12	NA	1	2	2	1	1	2	1	2	1	1
Sly03g0203651	M11	NA	20	17	21	25	35	54	47	60	29	29
Sly03g0203691	M3	NA	34	34	24	27	40	28	29	26	31	48
Sly03g0203701	M19	NA	14	17	13	13	15	14	14	16	15	17
Sly03g0203721	M11	SISOD2	129	124	123	275	342	173	176	196	345	362
Sly03g0203731	M1	NA	9	10	9	3	2	3	2	2	1	1
Sly03g0203741	M11	NA	9	10	10	12	14	14	13	14	14	18
Sly03g0203751	M11	NA	69	58	75	74	107	82	79	107	146	187
Sly03g0203761	M3	NA	6	5	3	4	5	4	3	4	8	4
Sly03g0203861	M1	NA	14	17	16	22	37	8	9	5	1	2
Sly03g0203871	M1	NA	11	14	12	15	29	5	7	5	1	1
Sly03g0203891	M11	NA	24	24	26	26	29	27	25	28	26	28
Sly03g0203961	M3	NA	1	1	1	1	1	1	1	1	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0094071	M11	ISA2	14	13	15	17	21	18	18	17	19	15
Sly09g0094081	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0094091	M1	NA	2	1	2	2	1	1	1	1	2	2
Sly09g0094101	M1	NA	7	5	3	1	2	1	1	1	1	1
Sly09g0094131	M19	NA	36	40	32	26	23	32	29	29	22	20
Sly09g0094141	M1	Glutathione peroxidas	25	25	33	30	29	19	20	26	44	36
Sly09g0094151	M11	NA	7	4	8	3	0	22	13	17	1	0
Sly09g0094161	M11	NA	104	91	110	96	113	111	100	129	131	158
Sly09g0094171	M22	NA	2	1	1	1	1	2	1	3	1	1
Sly09g0094181	M9	NA	17	19	17	16	13	19	20	17	20	19
Sly09g0094191	M10	NA	8	8	5	8	6	8	8	6	10	10
Sly09g0094211	M17	NA	18	15	16	12	20	16	14	16	19	30
Sly09g0094221	M11	NA	14	13	14	14	14	15	14	13	16	20
Sly09g0094231	M12	NA	52	55	62	73	73	76	76	79	79	96
Sly09g0094241	M12	NA	233	167	150	225	348	237	323	222	461	347
Sly09g0094331	M6	NA	7	9	8	11	8	8	11	6	9	12
Sly09g0094341	M11	NA	13	15	15	19	17	16	15	17	17	14
Sly09g0094351	M12	signal transducer (SLY	5	5	5	9	10	6	7	8	21	18
Sly09g0094361	M1	NA	12	16	13	21	9	8	7	8	8	9
Sly09g0094371	M7	NA	1	1	2	1	1	1	2	1	1	1
Sly09g0094421	M22	NA	3	2	2	1	1	14	5	11	1	1
Sly09g0094441	M1	NA	10	9	10	8	9	8	8	8	10	15
Sly09g0094451	M1	NA	50	56	64	57	56	48	47	49	51	58
Sly09g0094461	M4	NA	43	43	50	59	57	46	44	43	54	71
Sly09g0094481	M11	NA	22	20	27	24	19	42	35	47	28	22
Sly09g0094491	M18	NA	16	17	20	22	16	37	26	40	20	13
Sly09g0094511	M11	NA	25	25	28	28	7	50	45	56	11	6
Sly09g0094521	M11	NA	28	27	30	19	16	38	33	39	24	16
Sly09g0094531	M8	SlCycU3;1	32	35	27	27	15	30	39	25	13	8
Sly09g0094541	M2	NA	55	53	52	51	49	49	51	46	45	50
Sly09g0094571	M21	NA	15	10	19	2	1	10	5	10	1	1
Sly09g0094601	M22	NA	12	2	7	1	1	33	2	31	0	0
Sly09g0094611	M22	NA	3	1	1	0	1	3	1	4	1	1
Sly09g0094621	M11	NA	24	25	26	37	44	42	34	46	43	56
Sly09g0094631	M11	NA	87	74	84	81	94	82	76	93	101	126
Sly09g0094641	M11	NA	46	48	53	46	59	56	56	71	81	100
Sly09g0094651	M11	NA	8	8	10	14	15	12	12	14	16	18
Sly09g0094671	M1	NA	293	256	233	190	161	184	188	157	203	177
Sly09g0094681	M19	NA	19	17	16	14	10	19	16	17	8	5
Sly09g0094711	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0094721	M12	NA	29	29	31	26	24	48	56	55	48	43
Sly09g0094731	M12	NA	198	194	216	191	153	257	305	311	319	348
Sly09g0094741	M1	NA	29	30	52	57	28	14	16	19	23	29
Sly09g0094751	M8	NA	15	16	15	12	13	14	17	16	17	19
Sly09g0094791	M12	NA	1	1	1	1	0	2	1	1	0	1
Sly09g0094831	M23	NA	39	10	16	2	1	104	31	51	10	2
Sly09g0094841	M20	NA	4	5	6	5	1	5	4	4	1	1
Sly09g0094851	M11	NA	1	1	1	1	1	1	1	2	1	0
Sly09g0094881	M17	NA	39	32	36	30	30	36	25	36	30	28
Sly09g0094891	M2	NA	123	130	91	153	100	86	103	72	113	73
Sly09g0094901	M11	NA	74	70	102	84	100	126	108	163	125	124
Sly09g0094911	M19	NA	31	29	31	47	61	27	23	25	21	29
Sly09g0094921	M3	NA	92	148	138	203	72	40	37	9	3	1
Sly09g0094931	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0094941	M18	NA	6	6	7	7	8	7	6	7	7	9
Sly09g0094951	M19	NA	5	6	6	5	6	5	5	6	6	7
Sly09g0094961	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly09g0094971	M1	NA	20	19	21	14	11	11	13	11	16	8
Sly09g0094981	M7	NA	66	73	57	80	179	63	106	54	63	292
Sly09g0095001	M14	NA	5	5	8	9	10	5	5	7	7	6
Sly09g0095011	M19	NA	40	41	40	34	32	39	38	37	28	30
Sly09g0095021	M19	NA	10	12	12	24	32	11	11	12	15	27
Sly09g0095041	M19	NA	7	8	11	17	24	10	8	11	8	15
Sly09g0095061	M1	NA	1	1	1	9	39	0	0	0	0	2
Sly09g0095071	M12	NA	11	8	13	7	2	59	44	53	4	3
Sly09g0095091	M12	SlJMJ10	9	9	9	10	10	9	10	10	9	11
Sly09g0095101	M19	NA	20	23	21	16	18	21	16	21	15	15
Sly09g0095121	M1	NA	2	2	2	2	2	2	2	2	2	2
Sly09g0095161	M1	NA	44	45	50	46	45	40	37	44	54	51
Sly09g0095171	M1	NA	40	38	45	53	60	38	37	41	57	62
Sly09g0095181	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0095191	M1	NA	1	1	1	1	0	1	0	1	0	0
Sly09g0095201	M15	NA	242	209	216	201	177	244	215	243	222	263
Sly09g0095211	M1	NA	42	28	25	13	11	12	8	13	5	6
Sly09g0095241	M3	NA	2	2	1	2	3	1	1	1	1	2
Sly09g0095271	M1	NA	25	26	24	15	12	14	12	10	3	2
Sly09g0095281	M1	NA	45	56	45	29	29	29	29	28	14	21
Sly09g0095291	M11	NA	125	115	127	146	153	158	161	171	160	169
Sly09g0095301	M13	NA	14	9	16	10	8	13	12	19	11	7
Sly09g0095311	M7	SlAux/IAA3	64	103	45	76	263	94	198	50	179	687
Sly09g0095321	M12	NA	29	27	31	36	74	41	44	47	70	117
Sly09g0095331	M3	NA	82	89	61	43	41	79	75	50	45	52
Sly09g0095361	M11	NA	16	16	17	4	2	28	28	22	2	1
Sly09g0095371	M12	NA	9	15	5	1	1	43	44	23	1	1
Sly09g0095381	M13	NA	39	37	45	83	109	45	45	55	109	123
Sly09g0095391	M11	NA	259	150	299	171	76	402	328	558	256	60
Sly09g0095401	M11	NA	12	10	17	23	19	13	14	16	60	40
Sly09g0095411	M2	NA	20	19	19	20	23	18	21	18	27	22
Sly09g0095421	M11	NA	6	5	7	4	3	9	7	8	8	6
Sly09g0095431	M3	NA	29	32	23	29	31	25	30	20	38	39
Sly09g0095441	M3	NA	54	62	46	54	49	46	50	37	54	52
Sly09g0095451	M3	BMI-like1	17	20	16	25	26	15	16	13	14	24
Sly09g0095461	M3	NA	23	19	14	17	17	16	18	18	29	32
Sly09g0095481	M1	NA	6	5	6	5	4	2	1	2	1	2
Sly09g0095491	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0095511	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0095521	M12	NA	1	1	1	3	3	1	1	1	15	15
Sly09g0095531	M12	NA	3	3	3	5	6	7	8	10	21	14
Sly09g0095541	M11	NA	8	9	11	19	16	16	16	23	35	24
Sly09g0095571	M11	NA	41	36	47	39	47	73	70	81	36	47
Sly09g0095581	M12	NA	9	8	10	6	6	10	11	10	8	9
Sly09g0095591	M12	NA	10	10	10	6	8	11	11	10	9	12
Sly09g0095601	M13	NA	23	24	25	35	45	25	26	29	45	42
Sly09g0095611	M11	NA	6	6	7	8	8	8	8	9	10	8
Sly09g0095621	M12	NA	3	3	3	4	4	4	5	4	6	7
Sly09g0095631	M12	NA	31	23	35	537	1351	285	300	297	1000	1290
Sly09g0095691	M22	NA	9	7	7	4	5	8	6	7	3	3
Sly09g0095771	M12	NA	29	31	31	25	15	89	75	74	27	14
Sly09g0095781	M3	NA	15	16	14	14	18	14	14	12	17	19
Sly09g0095841	M10	SlERF.B12	1	4	1	0	0	3	4	0	1	0
Sly09g0095851	M3	SlERF.C3	72	62	19	4	3	13	10	2	2	4
Sly09g0095871	M3	NA	2	3	1	0	0	1	1	1	1	0
Sly09g0095881	M12	NA	1	1	1	1	1	2	2	1	3	4
Sly09g0095891	M1	NA	12	13	13	12	11	9	9	10	8	8
Sly09g0095901	M1	NA	478	453	450	316	230	313	337	325	337	217
Sly09g0095911	M3	NA	47	43	36	23	29	33	33	28	19	18
Sly09g0095931	M1	NA	105	69	84	21	22	18	18	14	13	12
Sly09g0095941	M3	NA	51	46	37	49	40	36	43	30	32	24
Sly09g0095951	M3	NA	29	34	23	15	17	21	20	18	13	11
Sly09g0095961	M8	NA	104	105	91	149	154	96	128	103	147	183
Sly09g0095971	M2	NA	155	150	125	109	104	102	121	95	127	149
Sly09g0096011	M22	NA	1174	276	378	22	2	2634	648	1273	50	3
Sly09g0096021	M1	NA	4	4	3	4	4	1	1	1	1	1
Sly09g0096031	M11	NA	54	55	58	74	84	64	59	70	72	84
Sly09g0096041	M12	NA	14	15	13	17	19	19	19	15	28	33
Sly09g0096051	M1	NA	48	47	39	50	53	29	27	32	57	54
Sly09g0096061	M12	NA	6	6	4	5	5	8	7	7	7	7
Sly09g0096081	M12	NA	1	1	1	2	3	1	1	1	1	3
Sly09g0096091	M1	NA	19	18	16	11	6	8	5	6	2	2
Sly09g0096111	M21	NA	1	1	1	1	1	1	1	1	0	0
Sly09g0096121	M11	NA	17	17	21	23	18	23	22	22

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0203971	M1	NA	1	2	1	15	3	0	1	0	1	0
Sly03g0204001	M1	AAD6	58	50	62	173	199	43	37	44	65	100
Sly03g0204031	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0204041	M1	NA	3	4	3	3	3	3	2	3	3	2
Sly03g0204091	M3	NA	39	38	33	38	43	30	33	33	40	69
Sly03g0204101	M11	NA	39	37	37	43	48	36	38	37	48	64
Sly03g0204141	M19	PIE	14	13	13	13	13	12	11	13	9	10
Sly03g0204151	M11	NA	29	29	38	61	102	40	37	55	81	103
Sly03g0204161	M14	NA	43	43	45	40	41	38	35	43	31	27
Sly03g0204171	M9	NA	19	17	17	28	17	20	30	25	33	39
Sly03g0204201	M12	NA	5	3	4	3	2	5	5	5	9	4
Sly03g0204211	M12	NA	3	3	3	4	1	4	4	4	4	1
Sly03g0204221	M11	NA	20	17	18	22	22	20	22	22	26	27
Sly03g0204241	M12	NA	43	41	50	74	100	53	57	62	95	146
Sly03g0204251	M1	NA	34	33	31	38	38	29	29	32	38	35
Sly03g0204261	M1	NA	46	50	44	46	44	39	40	41	51	47
Sly03g0204271	M1	NA	5	6	6	7	6	4	5	5	5	5
Sly03g0204451	M11	NA	53	58	60	71	84	103	77	94	45	50
Sly03g0204471	M12	NA	22	21	18	30	38	25	27	31	47	60
Sly03g0204491	M23	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0204511	M8	NA	12	12	11	17	19	12	14	11	15	15
Sly03g0204601	M3	NA	62	64	59	74	74	55	66	48	50	59
Sly03g0204711	M11	NA	20	21	22	22	18	29	23	26	23	17
Sly03g0204721	M3	NA	31	30	30	66	88	29	31	25	51	68
Sly03g0204751	M12	NA	8	8	9	15	9	48	54	52	78	36
Sly03g0204771	M11	NA	1	0	0	1	1	1	1	2	1	2
Sly03g0204781	M11	NA	1	1	1	1	1	2	2	2	1	1
Sly03g0204831	M1	NA	4	3	4	4	3	3	3	3	2	2
Sly03g0204841	M1	NA	4	4	5	2	1	4	3	3	1	1
Sly03g0204851	M3	NA	6	8	5	3	3	4	4	3	2	1
Sly03g0204861	M7	NA	14	18	10	9	16	12	17	14	11	20
Sly03g0204881	M8	NA	235	296	192	695	551	218	345	205	944	828
Sly03g0205271	M12	NA	2	1	2	1	1	2	3	2	1	1
Sly03g0205291	M12	NA	28	49	70	358	120	45	58	48	10	5
Sly03g0205321	M9	NA	0	0	1	0	1	1	3	1	5	5
Sly03g0205371	M11	PHS-like1	142	133	206	125	49	555	520	626	80	27
Sly03g0205431	M11	NA	4	3	6	1	1	11	9	11	1	0
Sly03g0205441	M12	NA	50	49	61	90	85	71	69	72	67	64
Sly03g0205471	M8	NA	11	12	8	10	8	10	12	9	9	5
Sly03g0206001	M11	NA	18	10	24	1	1	19	13	17	1	1
Sly03g0206011	M7	NA	1	5	1	1	0	1	9	2	1	5
Sly03g0206051	M12	NA	6	4	7	3	4	9	10	9	8	4
Sly03g0206061	M12	NA	2	2	2	1	2	5	4	3	2	2
Sly03g0206071	M1	NA	22	26	23	37	29	20	20	22	27	26
Sly03g0206081	M11	NA	12	11	15	11	25	23	21	25	11	8
Sly03g0206151	M1	NA	8	9	7	5	3	3	3	3	5	4
Sly03g0206161	M1	NA	129	80	30	1	1	4	5	1	1	0
Sly03g0206281	M12	NA	42	43	42	46	40	57	67	56	61	48
Sly03g0206331	M11	NA	6	6	8	4	1	12	11	11	3	1
Sly03g0206341	M1	NA	5	5	4	7	4	1	1	1	1	1
Sly03g0206351	M11	NA	1	1	1	2	1	2	2	2	2	1
Sly03g0206371	M11	NA	4	4	4	3	3	5	4	5	2	1
Sly03g0206381	M11	NA	40	40	48	51	49	61	53	66	65	65
Sly03g0206391	M19	NA	17	18	18	19	20	19	16	19	23	25
Sly03g0206401	M5	NA	9	10	8	9	11	8	11	8	14	22
Sly03g0206421	M11	NA	9	9	10	8	9	10	9	10	8	10
Sly03g0206431	M11	NA	30	30	42	53	58	47	41	57	53	47
Sly03g0206441	M3	NA	3	5	2	1	1	2	3	1	1	1
Sly03g0206451	M12	NA	7	7	7	6	7	9	12	9	5	6
Sly03g0206461	M3	NA	4	5	2	2	2	3	3	2	2	3
Sly03g0206471	M5	NA	88	98	57	32	37	87	105	58	42	54
Sly03g0206501	M12	NA	6	7	8	25	26	9	10	9	6	2
Sly03g0206511	M12	NA	17	13	13	6	8	20	23	22	6	5
Sly03g0206531	M22	NA	1	1	1	1	0	2	1	4	1	1
Sly03g0206541	M18	NA	2	3	3	3	3	4	3	4	3	3
Sly03g0206551	M2	NA	5	5	6	5	6	5	5	5	9	9
Sly03g0206561	M11	NA	6	6	5	5	4	6	6	8	4	2
Sly03g0206571	M12	NA	1	2	1	1	1	2	2	2	1	1
Sly03g0206631	M3	NA	177	166	158	145	107	144	155	126	132	111
Sly03g0206641	M1	NA	17	22	15	14	12	14	13	13	10	10
Sly03g0206651	M3	NA	8	10	7	6	6	6	7	5	5	5
Sly03g0206661	M9	NA	4	2	2	1	3	3	7	3	6	7
Sly03g0206671	M12	NA	4	2	2	1	3	3	4	5	6	6
Sly03g0206691	M1	NA	19	19	19	16	20	17	19	16	16	17
Sly03g0206701	M9	NA	12	15	14	41	59	22	32	18	67	83
Sly03g0206711	M3	NA	14	21	14	12	13	7	8	3	8	11
Sly03g0206721	M12	NA	53	55	65	118	160	83	101	138	226	277
Sly03g0206731	M1	NA	26	27	28	21	20	22	22	23	17	16
Sly03g0206741	M11	NA	988	826	1078	794	615	1087	1119	1287	1006	1132
Sly03g0206761	M11	NA	1	1	2	1	2	1	1	2	2	5
Sly03g0206801	M11	NA	1	1	2	0	1	2	2	2	1	0
Sly03g0206811	M12	NA	6	3	5	1	1	10	10	8	1	1
Sly03g0206841	M3	NA	1	2	2	1	1	1	1	1	1	1
Sly03g0206891	M1	NA	29	31	22	23	29	9	5	5	2	4
Sly03g0206931	M3	NA	4	4	4	3	2	3	3	3	4	3
Sly03g0206971	M11	NA	15	15	18	24	37	20	18	20	18	22
Sly03g0207001	M3	NA	50	45	21	19	24	17	19	11	28	60
Sly03g0207011	M8	NA	19	25	11	4	3	21	30	12	1	3
Sly03g0207021	M3	NA	4	5	2	1	1	1	1	1	0	0
Sly03g0207051	M11	NA	1	1	1	1	1	2	1	2	1	0
Sly03g0207061	M10	NA	2	2	2	1	1	2	2	2	0	0
Sly03g0207071	M11	NA	16	12	23	17	22	21	15	17	1	1
Sly03g0207081	M14	NA	13	11	19	14	21	14	12	13	1	1
Sly03g0207091	M1	NA	2	2	3	5	2	1	1	1	1	1
Sly03g0207101	M1	NA	10	15	6	10	8	1	1	2	5	13
Sly03g0207111	M1	NA	6	8	3	5	3	1	1	1	2	5
Sly03g0207121	M1	NA	3	3	4	6	5	3	2	3	4	7
Sly03g0207131	M18	NA	1	2	2	3	3	2	2	1	2	3
Sly03g0207141	M3	NA	2	2	2	6	7	2	2	2	3	5
Sly03g0207151	M1	NA	3	2	1	0	0	1	1	1	1	1
Sly03g0207161	M3	NA	3	2	1	1	0	1	1	1	1	0
Sly03g0207171	M22	UGT76C4-like	1	1	1	0	0	1	1	1	1	0
Sly03g0207181	M1	NA	6	5	5	4	5	4	4	4	4	5
Sly03g0207231	M2	NA	33	31	27	30	29	28	29	26	37	40
Sly03g0207261	M9	NA	8	9	7	9	10	10	11	9	14	16
Sly03g0207311	M3	NA	10	10	6	2	1	10	9	7	1	1
Sly03g0207321	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0207331	M3	NA	1	2	1	1	1	1	1	1	1	0
Sly03g0207341	M12	NA	14	14	15	15	17	15	14	15	19	26
Sly03g0207351	M3	NA	199	219	176	119	109	99	133	93	176	154
Sly03g0207361	M11	NA	192	176	205	177	217	253	233	284	290	338
Sly03g0207371	M14	NA	19	22	22	27	30	19	19	21	37	39
Sly03g0207391	M22	NA	1	1	1	1	0	2	1	2	1	1
Sly03g0207401	M8	NA	2	2	2	1	1	3	4	2	1	1
Sly03g0207421	M11	NA	11	11	14	11	9	22	17	23	14	9
Sly03g0207431	M18	NA	4	7	8	6	5	12	6	13	7	3
Sly03g0207441	M12	NA	7	9	9	50	64	18	23	25	91	62
Sly03g0207451	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly03g0207461	M1	NA	38	38	35	33	30	24	25	26	42	36
Sly03g0207471	M11	NA	42	36	70	37	12	53	56	67	21	10
Sly03g0207481	M22	NA	2	1	1	1	1	11	3	8	4	5
Sly03g0207491	M11	NA	26	20	26	5	4	80	52	100	3	2
Sly03g0207501	M3	NA	217	255	206	133	241	171	258	174	166	347
Sly03g0207521	M11	NA	124	69	140	144	88	124	152	263	486	141
Sly03g0207531	M9	NA	1	1	1	1	2	1	1	1	1	1
Sly03g0207541	M1	NA	27	30	16	44	12	2	1	1	1	1
Sly03g0207561	M1	HXK1	68	76	66	71	65	58	55	58	67	64
Sly03g0207581	M1	NA	275	271	286	206	176	212	210	248	266	323
Sly03g0207591	M3	NA	9	10	10	8	8	6	8	8	12	12
Sly03g0207601	M22	NA	17	15	15	2	3	46	9	37	1	2
Sly03g0207611	M3	NA	246	456	98	3	4	105	331	23	5	3
Sly03g0207621	M9	NA	12	12	11	10	13	12	15	12	14	17
Sly03g0207631	M9	NA	47	48	44	40	35	50	64	50	51	41
Sly03g0207641	M11	NA	1	1	1	1	1	1	1	1	2	2

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0096181	M1	NA	28	24	21	16	14	17	17	14	9	9
Sly09g0096241	M9	NA	6	7	5	8	3	9	10	10	8	4
Sly09g0096251	M1	NA	2	1	1	1	1	1	1	1	0	0
Sly09g0096261	M3	NA	3	7	2	1	0	1	2	1	0	0
Sly09g0096271	M22	NA	4	1	3	1	0	30	2	20	1	0
Sly09g0096281	M3	NA	44	45	40	48	45	35	38	35	52	48
Sly09g0096311	M11	NA	24	22	17	7	7	30	26	36	6	2
Sly09g0096321	M11	NA	3	4	5	3	4	11	10	9	3	1
Sly09g0096331	M16	NA	476	392	382	371	351	328	320	368	394	389
Sly09g0096341	M11	NA	6	6	7	5	5	8	7	9	5	4
Sly09g0096351	M18	SISDG13	9	9	12	11	10	15	11	16	10	8
Sly09g0096361	M17	NA	40	38	46	36	13	34	33	44	28	13
Sly09g0096391	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly09g0096461	M1	NA	42	37	35	41	40	30	32	35	46	45
Sly09g0096471	M22	NA	23	20	20	17	11	22	19	22	15	12
Sly09g0096481	M1	NA	46	43	51	43	53	42	42	45	73	57
Sly09g0096491	M2	NA	68	71	65	76	71	56	65	52	72	77
Sly09g0096541	M1	NA	14	21	12	15	12	1	1	1	1	1
Sly09g0096551	M3	NA	4	7	2	1	1	1	1	0	1	0
Sly09g0096561	M1	NA	8	9	9	5	3	1	1	1	1	1
Sly09g0096571	M12	NA	19	14	17	10	5	51	41	24	4	4
Sly09g0096581	M11	NA	98	94	102	122	122	153	140	162	144	184
Sly09g0096611	M3	NA	19	16	17	11	13	13	15	13	15	17
Sly09g0096621	M1	NA	9	10	11	12	13	9	7	9	9	16
Sly09g0096631	M19	NA	12	13	14	17	20	14	13	16	13	15
Sly09g0096691	M1	NA	4	2	2	2	2	2	2	2	2	2
Sly09g0096761	M3	NA	44	37	40	15	10	24	32	19	8	13
Sly09g0096781	M11	NA	18	23	31	38	32	31	37	57	66	32
Sly09g0096791	M10	NA	9	15	10	8	9	18	24	13	6	7
Sly09g0096801	M9	NA	7	7	7	3	3	12	12	9	18	13
Sly09g0096821	M9	GID1	5	13	7	26	48	12	20	11	26	68
Sly09g0096831	M12	NA	8	19	11	5	2	33	36	35	12	21
Sly09g0096851	M12	NA	8	7	5	1	1	11	10	6	1	2
Sly09g0096871	M12	NA	8	9	11	10	9	30	32	21	12	16
Sly09g0096881	M3	BSU1	75	88	75	71	66	70	71	65	70	84
Sly09g0096891	M18	NA	15	16	19	16	18	21	17	22	16	15
Sly09g0096901	M1	NA	4	5	3	2	2	2	1	1	1	1
Sly09g0096911	M6	NA	1	2	3	1	0	3	1	1	0	1
Sly09g0096921	M12	NA	14	14	12	11	13	17	17	15	18	27
Sly09g0096931	M2	NA	7	7	6	11	13	7	7	7	9	8
Sly09g0096941	M22	NA	3	2	3	2	3	4	2	3	2	2
Sly09g0096981	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0096991	M1	NA	94	91	90	101	105	78	75	85	103	113
Sly09g0097001	M14	NA	26	24	32	19	10	29	24	33	9	4
Sly09g0097011	M11	NA	24	24	29	32	25	46	36	49	30	26
Sly09g0097021	M21	YUC-like4	12	6	10	1	1	6	2	6	1	0
Sly09g0097041	M12	NA	8	6	11	23	10	20	24	27	16	5
Sly09g0097061	M11	NA	173	143	166	147	162	220	189	251	216	286
Sly09g0097071	M20	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0097081	M1	NA	3	5	4	6	24	1	1	1	2	3
Sly09g0097101	M3	NA	66	67	57	144	120	60	62	60	113	105
Sly09g0097111	M3	NA	1	1	1	0	1	1	1	1	1	1
Sly09g0097121	M11	SITIR1	42	31	57	21	23	75	56	79	25	40
Sly09g0097131	M3	NA	1	2	1	0	0	1	2	0	0	0
Sly09g0097141	M11	NA	51	23	23	6	3	126	71	170	2	1
Sly09g0097161	M1	NA	57	47	56	33	47	36	38	35	30	52
Sly09g0097171	M1	NA	1	1	1	1	0	1	0	0	0	0
Sly09g0097191	M1	NA	9	6	10	5	4	1	1	1	0	0
Sly09g0097201	M1	NA	3	3	2	1	1	1	0	0	0	1
Sly09g0097211	M11	NA	4	3	4	9	4	4	5	5	3	3
Sly09g0097221	M1	NA	10	7	18	6	3	2	1	2	1	1
Sly09g0097231	M11	NA	40	32	35	19	26	36	36	35	34	36
Sly09g0097241	M11	NA	19	17	23	40	81	21	18	32	61	101
Sly09g0097251	M11	NA	28	26	32	53	70	32	30	38	57	64
Sly09g0097261	M1	NA	22	26	20	19	19	18	19	18	16	23
Sly09g0097271	M1	NA	47	50	44	69	64	29	31	31	63	56
Sly09g0097281	M11	NA	15	16	16	17	19	17	16	19	17	16
Sly09g0097291	M19	NA	6	6	6	6	6	5	4	5	4	4
Sly09g0097301	M1	NA	14	15	15	17	19	13	11	12	14	17
Sly09g0097311	M12	NA	11	10	11	14	17	13	12	14	13	16
Sly09g0097341	M3	NA	2	2	2	1	1	1	1	2	2	3
Sly09g0097381	M3	WEE1	2	2	2	1	1	1	2	1	1	1
Sly09g0097391	M18	NA	22	24	31	31	36	41	31	48	46	63
Sly09g0097401	M11	NA	21	20	27	31	34	37	31	40	54	96
Sly09g0097411	M15	NA	19	17	17	28	29	17	18	19	34	31
Sly09g0097421	M15	NA	205	173	163	195	199	183	190	186	189	218
Sly09g0097441	M11	NA	9	11	10	14	11	16	16	18	7	3
Sly09g0097451	M10	NA	9	15	10	8	28	12	20	12	25	66
Sly09g0097461	M9	NA	26	27	27	31	32	27	33	28	38	39
Sly09g0097471	M2	TSPO-like	9	7	7	5	4	7	9	7	5	3
Sly09g0097481	M9	NA	9	12	10	10	8	11	12	10	14	12
Sly09g0097511	M1	NA	173	141	167	124	68	130	156	120	50	39
Sly09g0097521	M18	NA	53	56	61	64	45	72	63	77	58	43
Sly09g0097541	M12	NA	43	45	49	57	59	58	49	55	50	54
Sly09g0097561	M3	NA	7	9	6	3	2	3	4	2	2	2
Sly09g0097581	M1	NA	4	4	5	2	3	3	3	3	2	1
Sly09g0097591	M11	NA	40	37	39	34	39	41	41	41	48	54
Sly09g0097601	M1	NA	428	417	389	424	388	309	308	335	432	420
Sly09g0097611	M3	NA	69	84	45	23	11	80	73	26	4	3
Sly09g0097621	M1	NA	113	106	104	77	72	80	82	91	115	113
Sly09g0097631	M1	NA	4	4	4	4	4	3	3	3	1	2
Sly09g0097641	M1	NA	2	2	2	2	2	1	1	1	1	1
Sly09g0097651	M11	NA	2	2	2	1	1	2	1	2	1	1
Sly09g0097661	M1	NA	27	24	21	17	17	15	15	13	15	16
Sly09g0097671	M15	NA	204	180	180	152	174	203	170	192	198	244
Sly09g0097681	M2	NA	38	37	33	37	31	33	39	37	42	37
Sly09g0097691	M1	NA	758	708	522	58	29	173	173	86	60	31
Sly09g0097721	M1	NA	170	166	172	173	156	150	149	168	179	177
Sly09g0097731	M11	NA	8	11	14	21	7	15	21	20	33	10
Sly09g0097741	M11	NA	15	21	23	48	10	36	38	49	61	18
Sly09g0097751	M3	NA	162	148	144	153	120	114	123	121	189	146
Sly09g0097761	M12	NA	39	33	25	9	7	46	61	46	33	20
Sly09g0097771	M3	NA	5	5	4	5	3	3	3	3	5	3
Sly09g0097781	M11	NA	61	61	66	140	162	99	91	109	152	142
Sly09g0097791	M1	NA	11	12	12	10	10	9	10	10	9	9
Sly09g0097801	M1	NA	75	75	96	51	56	59	58	67	62	61
Sly09g0097811	M11	NA	28271	24930	31185	15482	4059	37643	32435	42498	12110	2719
Sly09g0097821	M2	NA	25	25	22	24	25	23	26	24	27	33
Sly09g0097831	M1	NA	32	28	31	24	37	21	24	19	21	39
Sly09g0097841	M3	NA	22	28	26	19	22	12	16	11	14	30
Sly09g0097851	M22	NA	2	1	1	3	2	3	2	3	14	9
Sly09g0097861	M9	NA	18	21	15	15	16	21	22	19	19	19
Sly09g0097871	M3	NA	302	284	226	171	133	209	216	179	229	145
Sly09g0097881	M1	NA	70	68	57	47	39	6	8	4	2	3
Sly09g0097891	M5	NA	4	4	3	2	4	4	4	2	1	2
Sly09g0097901	M3	NA	2	9	3	1	1	1	1	1	1	1
Sly09g0097931	M12	NA	1	1	1	1	1	11	10	11	2	1
Sly09g0097941	M2	NA	52	53	48	50	30	42	52	39	42	27
Sly09g0097951	M3	NA	11	12	8	10	8	9	9	8	12	11
Sly09g0097961	M11	NA	27	28	33	40	54	36	34	41	53	64
Sly09g0097971	M18	NA	19	21	25	31	40	29	24	32	36	36
Sly09g0097981	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly09g0098001	M9	SIERF.E1	53	83	43	26	36	82	134	86	111	360
Sly09g0098011	M1	NA	618	553	541	431	331	407	414	397	404	311
Sly09g0098021	M2	ETR3	196	221	153	729	708	82	123	78	692	803
Sly09g0098031	M2	NA	76	88	67	118	89	71	89	61	110	76
Sly09g0098041	M11	NA	69	78	107	94	19	190	191	268	259	62
Sly09g0098061	M21	NA	4	3	5	3	4	5	1	5	1	2
Sly09g0098071	M22	NA	3	2	4	2	3	4	1	4	1	1
Sly09g0098081	M12	NA	55	58	60	71	103	61	64	64	100	116
Sly09g0098091	M3	NA	12	10	9	7	9	7	7	6	8	9

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0207651	M14	SIPRR3	15	9	27	13	22	14	10	24	12	24
Sly03g0207681	M1	NA	14	13	18	8	7	2	2	2	1	1
Sly03g0207701	M22	NA	5	5	5	7	9	5	4	5	6	8
Sly03g0207711	M19	NA	4	4	4	5	6	4	3	4	3	5
Sly03g0207721	M11	NA	12	19	17	22	27	28	32	27	16	28
Sly03g0207731	M12	NA	18	17	13	16	15	18	18	17	19	17
Sly03g0207741	M11	NA	25	25	26	15	15	32	24	33	14	13
Sly03g0207751	M12	NA	7	8	6	4	6	18	25	19	7	17
Sly03g0207781	M11	NA	1	2	2	1	2	2	2	2	1	2
Sly03g0207801	M9	NA	31	101	92	62	350	164	263	171	117	776
Sly03g0207821	M12	NA	219	203	210	242	330	307	265	319	318	453
Sly03g0207831	M1	NA	43	41	39	31	32	34	35	34	20	21
Sly03g0207841	M1	NA	64	71	69	83	76	56	57	63	76	72
Sly03g0207851	M2	NA	12	9	11	12	24	9	10	8	16	17
Sly03g0207861	M12	SlHSP21	1	1	3	361	3336	6	4	6	135	1429
Sly03g0207881	M22	NA	1	1	1	1	0	2	1	1	1	0
Sly03g0207891	M9	NA	89	87	83	102	93	98	112	94	101	89
Sly03g0207901	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0207911	M1	NA	1	1	1	1	1	1	1	0	0	1
Sly03g0207921	M9	NA	31	34	28	25	19	30	33	33	44	25
Sly03g0207931	M18	NA	93	97	107	107	125	110	86	117	101	134
Sly03g0207941	M3	NA	32	45	25	24	36	26	30	16	19	34
Sly03g0207951	M3	SAUR35	2	4	2	1	1	1	1	1	1	1
Sly03g0207961	M6	SAUR36	4	7	6	1	1	5	10	6	1	4
Sly03g0207971	M7	SAUR37	10	22	15	2	28	18	29	24	5	53
Sly03g0207981	M1	NA	42	32	47	22	21	28	27	31	13	12
Sly03g0208011	M1	NA	3	2	3	2	1	1	1	0	1	2
Sly03g0208031	M11	NA	12	12	14	7	3	20	15	18	4	1
Sly03g0208041	M3	NA	272	261	225	156	114	167	192	173	189	158
Sly03g0208051	M11	NA	67	58	58	58	57	72	70	68	55	47
Sly03g0208061	M19	NA	35	31	37	53	60	36	28	42	94	69
Sly03g0208071	M11	NA	48	46	48	75	93	48	48	60	150	139
Sly03g0208081	M3	NA	725	647	490	261	287	448	467	378	390	478
Sly03g0208091	M3	NA	17	15	14	11	17	11	15	12	17	28
Sly03g0208101	M1	NA	124	108	72	17	24	8	6	4	2	2
Sly03g0208111	M1	NA	18	18	15	10	11	11	12	11	10	10
Sly03g0208121	M1	NA	13	15	15	4	2	4	4	4	3	7
Sly03g0208141	M12	NA	141	139	89	44	39	518	605	487	47	60
Sly03g0208151	M1	NA	6	4	7	15	13	5	3	5	18	17
Sly03g0208161	M12	NA	10	12	10	13	15	12	11	12	11	12
Sly03g0208181	M3	NA	51	55	28	5	2	13	13	5	1	1
Sly03g0208201	M14	NA	34	33	41	24	25	34	29	37	18	19
Sly03g0208211	M1	NA	172	159	215	216	403	88	95	101	83	167
Sly03g0208221	M1	NA	12	11	11	23	60	12	9	10	28	140
Sly03g0208231	M1	NA	11	14	13	22	56	13	10	11	30	125
Sly03g0208241	M12	NA	16	16	15	12	15	20	23	24	19	27
Sly03g0208271	M7	NA	2	3	2	1	1	2	9	2	1	12
Sly03g0208291	M12	NA	15	15	15	18	19	23	22	24	19	21
Sly03g0208301	M13	NA	4	4	4	7	12	4	4	5	7	9
Sly03g0208311	M1	NA	1	2	1	1	1	1	1	1	1	0
Sly03g0208321	M11	NA	29	28	30	25	23	33	33	38	28	26
Sly03g0208331	M11	SISDG27	3	3	3	1	1	3	3	3	1	1
Sly03g0208341	M1	NA	21	23	18	5	3	10	9	7	2	2
Sly03g0208351	M3	NA	5	4	5	5	4	3	5	3	8	11
Sly03g0208361	M9	NA	100	103	92	100	123	97	117	112	163	220
Sly03g0208371	M11	NA	26	23	34	50	73	42	37	53	50	105
Sly03g0208381	M11	NA	1	1	1	1	1	2	2	2	2	1
Sly03g0208391	M2	NA	58	51	53	54	47	47	54	47	51	44
Sly03g0208401	M3	NA	213	242	186	342	199	182	186	109	129	105
Sly03g0208411	M3	NA	76	74	68	59	77	62	70	63	66	86
Sly03g0208431	M11	NA	27	26	34	37	48	48	40	60	40	61
Sly03g0208441	M11	NA	22	20	21	45	71	25	20	28	36	65
Sly03g0208451	M12	NA	31	31	32	57	58	35	34	33	53	50
Sly03g0208461	M11	NA	6	7	9	5	4	13	10	14	5	4
Sly03g0208471	M13	NA	19	20	24	14	18	27	27	35	20	21
Sly03g0208481	M6	NA	36	61	20	7	8	21	24	10	8	9
Sly03g0208491	M1	NA	70	74	61	40	21	38	39	36	35	19
Sly03g0208501	M12	NA	31	56	36	156	101	94	132	124	212	120
Sly03g0208531	M21	NA	3	3	4	4	4	4	3	4	4	3
Sly03g0208581	M11	NA	21	16	23	20	22	24	23	31	21	24
Sly03g0208601	M13	STS2	67	66	107	397	738	89	76	129	163	198
Sly03g0208611	M20	NA	22	15	35	4	2	19	11	18	1	1
Sly03g0208631	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0208651	M19	NA	1	2	2	2	2	2	1	2	1	1
Sly03g0208661	M18	NA	15	17	19	20	30	20	16	21	28	39
Sly03g0208671	M11	NA	1	1	1	1	1	2	2	2	1	1
Sly03g0208681	M11	NA	2	1	1	1	1	1	1	3	1	0
Sly03g0208691	M11	NA	2	2	2	1	1	3	3	3	1	1
Sly03g0208701	M18	NA	10	9	12	8	9	15	11	13	9	9
Sly03g0208711	M11	NA	10	11	11	9	12	16	11	14	10	11
Sly03g0208721	M11	NA	7	6	7	6	8	9	7	8	9	12
Sly03g0208731	M11	DMS3-like	26	24	28	21	17	29	25	27	13	10
Sly03g0208751	M1	SlJMJ22	18	20	17	17	17	14	11	12	9	6
Sly03g0208761	M14	NA	42	39	50	130	196	43	38	51	66	72
Sly03g0208771	M1	NA	10	11	8	8	8	8	7	9	8	9
Sly03g0208781	M3	NA	10	11	7	7	7	8	8	6	8	9
Sly03g0208791	M12	NA	7	8	8	8	7	9	9	10	7	7
Sly03g0208801	M1	emb1796-like2	46	44	39	65	103	35	33	34	67	87
Sly03g0208811	M11	NA	11	11	12	12	10	12	11	12	13	12
Sly03g0208821	M1	NA	26	27	26	21	20	21	20	21	11	12
Sly03g0208831	M1	NA	29	27	28	30	44	22	24	24	35	49
Sly03g0208851	M2	NA	24	25	23	32	36	20	28	21	27	33
Sly03g0208871	M12	NA	24	24	28	28	39	42	38	45	50	84
Sly03g0208881	M1	NA	21	19	15	10	5	9	6	8	1	1
Sly03g0208921	M12	NA	180	176	202	227	292	247	261	340	425	535
Sly03g0208931	M11	NA	25	13	18	3	2	45	33	32	3	2
Sly03g0208941	M19	SISDG26	12	14	14	14	12	14	11	13	10	8
Sly03g0208951	M19	NA	21	20	21	19	19	21	21	21	19	18
Sly03g0208961	M11	NA	27	29	31	67	90	33	30	41	91	112
Sly03g0208971	M12	NA	32	31	32	67	98	34	37	44	103	156
Sly03g0208981	M11	NA	116	114	144	127	138	151	125	167	192	212
Sly03g0208991	M3	NA	31	29	16	9	8	19	13	29	35	18
Sly03g0209001	M1	NA	34	37	39	79	97	30	35	35	78	88
Sly03g0209011	M1	NA	15	18	13	16	7	4	5	2	3	2
Sly03g0209021	M6	NA	6	16	6	2	3	3	5	1	1	1
Sly03g0209031	M6	NA	4	22	6	1	1	6	14	2	0	1
Sly03g0209061	M23	NA	1	1	1	1	0	1	1	1	0	0
Sly03g0209071	M3	NA	80	80	66	67	69	64	69	60	85	107
Sly03g0209081	M16	NA	1294	1095	1058	686	385	1042	917	1096	956	692
Sly03g0209111	M1	NA	47	44	43	31	34	37	37	34	29	39
Sly03g0209121	M12	NA	3	4	3	6	4	4	4	4	9	5
Sly03g0209131	M12	NA	14	15	20	15	7	188	144	170	26	13
Sly03g0209141	M11	NA	8	8	10	24	37	19	16	24	36	41
Sly03g0209151	M11	NA	5	6	6	7	9	7	8	8	11	12
Sly03g0209161	M12	NA	2	2	1	3	2	2	1	2	1	1
Sly03g0209171	M4	NA	2	2	2	4	2	2	2	2	2	1
Sly03g0209181	M14	NA	27	28	35	44	37	27	25	31	29	34
Sly03g0209191	M12	NA	461	786	605	2779	2257	697	1243	1426	1721	1939
Sly03g0209201	M12	NA	234	388	223	1204	1141	317	560	619	873	1159
Sly03g0209241	M11	NA	4	4	6	68	170	6	13	24	177	170
Sly03g0209261	M3	NA	4	3	2	1	1	1	1	1	1	1
Sly03g0209271	M1	NA	7	8	8	0	0	0	1	0	0	0
Sly03g0209301	M6	NA	7	21	15	1	1	4	5	1	1	1
Sly03g0209311	M3	NA	2	11	3	1	0	1	2	1	0	0
Sly03g0209341	M6	NA	1	2	1	0	0	2	2	1	0	0
Sly03g0209351	M10	NA	20	72	27	1	3	98	181	28	3	6
Sly03g0209361	M1	NA	3	1	2	0	0	1	0	1	0	0
Sly03g0209471	M12	NA	26	48	29	40	30	51	97	89	107	78
Sly03g0209481	M1	FRUCT4	226	300	383	4018	8271	189	155	195	381	662
Sly03g0209501	M9	NA	2	2	2	2	3	3	3	2	1	7
Sly03g0209511	M12	NA	2	4	2	1	1	8	14	4	2	3
Sly03g0209521	M9	NA	69	62	60	69	67	110	106	104	129	86
Sly03g0209581	M11	NA	50	16	65	1	1	454	279	384	9	4
Sly03g0209711	M7	NA	42	121	36	20	94	82	216	74	24	115

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0098131	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly09g0098141	M1	NA	6	5	6	2	2	5	2	4	1	1
Sly09g0098151	M1	NA	22	20	26	16	16	16	18	20	45	25
Sly09g0098161	M1	NA	1	1	1	1	1	1	0	0	0	0
Sly09g0098181	M12	NA	7	6	11	15	19	12	15	14	5	10
Sly09g0098191	M18	NA	4	3	4	3	3	4	3	3	2	3
Sly09g0098211	M14	NA	9	8	11	8	8	11	8	11	5	6
Sly09g0098231	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0098251	M3	NA	2	3	3	0	0	2	2	1	1	1
Sly09g0098281	M12	NA	1	1	0	0	0	2	1	0	0	0
Sly09g0098301	M3	NA	3	3	2	9	17	2	2	2	51	52
Sly09g0098311	M2	NA	6	7	6	19	28	5	6	5	59	52
Sly09g0098331	M3	NA	1	1	1	1	0	1	1	1	0	0
Sly09g0098341	M3	SlCycT1;3	86	94	81	90	88	83	80	81	146	116
Sly09g0098351	M1	NA	1	1	1	3	1	1	1	1	1	1
Sly09g0098371	M11	NA	2	2	2	1	1	6	4	5	2	1
Sly09g0098381	M11	NA	3	3	4	2	1	9	8	9	2	1
Sly09g0098391	M6	NA	38	39	39	45	42	40	42	35	28	32
Sly09g0098401	M1	NA	16	10	16	1	1	3	2	2	1	0
Sly09g0098411	M3	NA	226	249	111	2	1	60	46	5	1	1
Sly09g0098421	M19	NA	112	111	102	121	132	110	97	108	120	129
Sly09g0098431	M11	NA	2	2	1	1	1	8	5	7	1	1
Sly09g0098451	M3	NA	26	29	30	34	36	19	23	20	26	32
Sly09g0098461	M1	SlLOX6	31	29	22	7	5	14	14	9	2	2
Sly09g0098491	M1	NA	104	97	97	19	15	10	15	11	2	8
Sly09g0098501	M1	NA	2	1	2	0	0	1	1	1	0	0
Sly09g0098511	M3	NA	29	47	20	5	2	5	4	1	1	0
Sly09g0098521	M1	NA	8	17	7	2	1	1	1	1	0	0
Sly09g0098531	M3	NA	4	10	2	1	0	1	1	1	0	0
Sly09g0098541	M1	NA	1	1	1	1	0	0	0	0	0	0
Sly09g0098551	M12	NA	6	6	10	91	293	14	11	16	58	412
Sly09g0098561	M1	NA	3	2	2	1	1	1	1	2	0	1
Sly09g0098571	M9	NA	1	2	2	1	6	1	2	3	4	14
Sly09g0098581	M20	NA	6	5	6	6	7	6	5	5	8	10
Sly09g0098591	M11	NA	9	9	10	10	8	13	15	18	15	13
Sly09g0098601	M19	NA	22	22	20	28	26	21	19	21	23	20
Sly09g0098611	M2	NA	31	32	31	55	61	30	33	30	41	47
Sly09g0098621	M12	NA	11	9	9	11	8	12	12	11	14	8
Sly09g0098631	M11	NA	54	52	58	77	138	72	57	77	68	125
Sly09g0098641	M1	NA	141	130	153	153	170	121	99	122	113	145
Sly09g0098651	M1	SISDG1	30	31	27	28	30	23	23	23	23	29
Sly09g0098661	M1	NA	244	206	271	123	40	170	155	160	75	37
Sly09g0098671	M11	NA	4	3	6	7	6	8	6	9	6	6
Sly09g0098701	M23	NA	3	2	1	1	1	4	2	3	6	1
Sly09g0098711	M7	NA	2	2	1	1	1	2	2	2	2	1
Sly09g0098721	M12	NA	87	78	99	67	52	166	189	217	73	33
Sly09g0098731	M12	NA	9	9	10	16	37	10	10	10	5	4
Sly09g0098741	M3	NA	25	21	21	18	24	23	22	20	20	24
Sly09g0098751	M12	NA	2	2	2	3	4	3	3	3	5	5
Sly09g0098761	M12	NA	13	12	14	18	29	14	14	15	24	31
Sly09g0098771	M2	NA	4	5	5	15	20	4	4	5	10	10
Sly09g0098801	M11	NA	20	19	20	32	39	21	23	24	38	35
Sly09g0098811	M11	NA	65	55	84	41	38	75	75	77	42	38
Sly09g0098821	M3	NA	1	2	1	1	0	1	1	0	0	0
Sly09g0098831	M3	NA	10	11	7	0	1	9	13	2	1	1
Sly09g0098841	M6	NA	55	99	42	3	7	89	126	29	3	4
Sly09g0098851	M10	NA	4	4	1	1	1	5	7	2	1	1
Sly09g0098871	M1	NA	14	11	12	1	2	3	5	4	3	3
Sly09g0098891	M3	NA	3	14	1	1	1	7	5	1	0	0
Sly09g0098951	M12	NA	100	98	97	139	186	95	105	101	155	214
Sly09g0098961	M23	NA	1	1	1	1	0	2	2	1	1	1
Sly09g0098971	M22	NA	578	199	201	19	2	1355	504	685	69	6
Sly09g0098981	M23	NA	3	1	1	1	1	10	2	1	1	1
Sly09g0098991	M3	NA	2	1	1	1	1	1	1	1	1	1
Sly09g0099001	M3	NA	6	7	5	8	7	5	6	5	20	16
Sly09g0099011	M1	NA	9	9	9	10	14	7	7	7	6	8
Sly09g0099021	M1	NA	4	4	4	3	3	4	3	4	4	3
Sly09g0099031	M12	NA	4	3	3	4	3	3	3	4	6	6
Sly09g0099071	M11	NA	3	3	3	5	7	4	4	5	8	9
Sly09g0099081	M12	NA	6	10	28	265	217	39	101	224	2483	631
Sly09g0099091	M9	NA	9	16	13	19	13	21	28	23	108	47
Sly09g0099111	M1	NA	15	14	14	15	16	11	13	11	16	16
Sly09g0099121	M18	NA	5	4	4	4	3	5	4	4	2	1
Sly09g0099131	M18	NA	20	22	24	11	10	27	22	22	5	3
Sly09g0099141	M3	NA	267	252	249	264	265	230	242	244	398	410
Sly09g0099161	M3	NA	49	49	47	36	33	43	47	45	56	47
Sly09g0099171	M1	NA	3	3	3	1	1	1	1	1	0	1
Sly09g0099191	M3	NA	1	1	1	1	1	1	1	1	0	0
Sly09g0099201	M1	NA	18	21	26	30	63	2	3	1	1	1
Sly09g0099211	M1	NA	6	5	13	1	0	1	1	1	0	1
Sly09g0099231	M22	chl3	1	0	1	0	0	1	1	4	0	0
Sly09g0099271	M11	NA	31	25	37	44	77	39	35	56	101	119
Sly09g0099291	M12	NA	595	605	692	1068	1667	708	795	862	1646	2380
Sly09g0099321	M12	NA	32	32	34	101	964	38	40	42	168	505
Sly09g0099351	M12	NA	113	89	80	76	77	130	124	106	82	91
Sly09g0099361	M12	NA	35	36	51	128	246	341	350	431	553	1201
Sly09g0099371	M12	NA	59	59	76	120	136	170	165	204	153	217
Sly09g0099391	M6	NA	1	1	1	0	0	1	1	1	1	1
Sly09g0099401	M9	NA	95	92	83	113	110	93	105	91	102	115
Sly09g0099411	M14	NA	180	140	217	120	78	155	149	200	71	30
Sly09g0099421	M11	NA	2	2	3	3	6	4	4	5	1	2
Sly09g0099431	M3	NA	28	29	25	21	20	22	23	19	18	18
Sly09g0099441	M22	NA	1	1	1	1	1	1	1	1	0	0
Sly09g0099451	M1	NA	8	7	6	3	11	5	1	6	9	21
Sly09g0099511	M22	NA	2	1	1	0	0	10	1	5	0	0
Sly09g0099541	M12	NA	11	10	10	58	43	35	30	33	154	226
Sly09g0099551	M7	NA	1	2	1	1	1	1	2	1	1	1
Sly09g0099571	M7	NA	3	8	1	1	2	3	8	2	1	2
Sly09g0099641	M13	NA	12	11	13	9	8	11	12	13	14	15
Sly09g0099661	M1	NA	4	2	3	4	4	2	3	2	3	5
Sly09g0099681	M9	NA	11	11	9	12	12	12	13	13	17	16
Sly09g0099691	M3	NA	74	69	63	60	63	58	64	58	81	101
Sly09g0099701	M11	NA	156	150	199	338	447	187	168	218	390	587
Sly09g0099711	M11	NA	128	103	241	101	136	315	330	458	127	115
Sly09g0099721	M11	NA	71	53	80	42	22	72	59	75	34	23
Sly09g0099731	M12	NA	45	42	48	46	52	48	52	55	56	74
Sly09g0099741	M1	NA	19	20	17	9	7	3	3	3	1	1
Sly09g0099751	M1	NA	445	353	301	71	40	60	58	30	7	4
Sly09g0099761	M1	NA	55	39	43	9	10	4	3	2	1	1
Sly09g0099771	M1	NA	2	2	2	1	2	1	1	1	1	0
Sly09g0099781	M1	NA	71	113	129	8	1	2	1	1	1	0
Sly09g0099791	M3	NA	57	64	31	10	10	37	50	19	4	4
Sly09g0099801	M9	NA	33	31	30	46	47	34	38	35	50	54
Sly09g0099811	M3	NA	199	190	173	90	72	121	132	106	96	68
Sly09g0099821	M3	NA	48	57	23	3	1	39	48	22	4	2
Sly09g0099831	M7	NA	35	60	25	68	52	42	56	31	52	45
Sly09g0099851	M1	PPR-like22	6	7	6	7	10	5	5	5	7	8
Sly09g0099861	M11	NA	4	4	6	5	2	7	6	6	3	1
Sly09g0099871	M11	NA	19	18	24	12	3	91	59	83	8	2
Sly09g0099881	M12	NA	37	35	31	26	27	35	35	36	37	44
Sly09g0099891	M11	NA	17	14	19	15	9	29	26	35	9	3
Sly09g0099961	M11	NA	20	23	23	8	1	43	37	46	3	1
Sly09g0099971	M1	NA	23	17	17	6	4	10	10	12	19	21
Sly09g0099981	M1	NA	183	195	120	19	13	48	45	27	22	17
Sly09g0099991	M14	NA	63	58	74	75	77	50	47	63	74	75
Sly09g0100001	M11	NA	11	12	14	17	15	17	15	18	23	16
Sly09g0100011	M12	NA	8	8	10	10	9	9	9	9	16	10
Sly09g0100021	M12	NA	17	16	16	19	17	18	20	23	34	28
Sly09g0100031	M1	NA	3	4	4	4	3	3	3	3	1	1
Sly09g0100041	M1	NA	23	23	23	19	18	17	16	17	18	15
Sly09g0100051	M5	SlAux/IAA

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0209731	M12	SlXTH3	3	19	7	3	18	20	70	22	9	33
Sly03g0209741	M12	NA	7	56	27	5	54	63	233	95	29	158
Sly03g0209751	M12	NA	3	22	22	3	30	35	149	73	17	69
Sly03g0209761	M1	NA	52	54	66	20	31	35	51	20	90	242
Sly03g0209771	M5	PPR-like15	7	9	7	7	6	8	8	7	7	5
Sly03g0209781	M19	NA	86	83	94	96	103	93	74	106	132	145
Sly03g0209801	M11	NA	1	1	1	1	0	4	2	4	1	0
Sly03g0209821	M8	NA	56	59	43	49	50	54	64	52	58	67
Sly03g0209831	M1	NA	12	12	11	8	4	10	10	10	12	7
Sly03g0209841	M11	NA	33	28	34	44	51	40	41	45	44	40
Sly03g0209861	M14	NA	22	18	20	28	30	15	12	18	16	16
Sly03g0209871	M11	NA	6	5	6	1	1	8	6	7	1	1
Sly03g0209911	M3	NA	19	19	17	16	22	17	15	16	24	30
Sly03g0209921	M21	NA	1	1	1	2	1	1	1	1	1	1
Sly03g0209951	M11	NA	2	1	2	0	0	7	5	7	0	0
Sly03g0210001	M11	NA	168	134	170	9	5	344	302	280	3	2
Sly03g0210031	M12	NA	2	3	3	3	2	3	4	3	3	1
Sly03g0210051	M1	NA	4	6	4	2	1	1	1	1	0	0
Sly03g0210091	M12	NA	35	33	38	38	70	39	40	45	60	99
Sly03g0210101	M11	NA	17	17	20	19	19	20	19	18	18	19
Sly03g0210111	M1	NA	8	9	7	6	5	2	3	2	2	1
Sly03g0210121	M1	NA	3	5	7	2	1	3	1	3	1	0
Sly03g0210131	M22	NA	7	6	9	12	11	9	7	8	9	9
Sly03g0210141	M1	NA	45	53	47	34	37	33	32	31	31	49
Sly03g0210151	M1	NA	4	3	3	2	1	2	2	2	1	1
Sly03g0210161	M5	NA	50	65	22	16	20	52	78	17	7	22
Sly03g0210171	M1	PFK	37	41	29	22	23	19	19	20	19	16
Sly03g0210181	M11	NA	15	15	21	9	5	20	17	20	2	3
Sly03g0210191	M6	SIERF.B4	13	39	12	5	6	18	31	7	1	4
Sly03g0210201	M10	SIERF.B5	11	31	14	8	14	26	42	10	2	16
Sly03g0210241	M10	SIERF.B2	23	67	22	22	82	86	144	50	17	218
Sly03g0210251	M11	NA	23	20	22	9	8	39	31	46	10	15
Sly03g0210261	M11	NA	8	8	9	2	1	17	14	17	1	1
Sly03g0210271	M3	SIERF.A2	17	28	5	2	2	7	15	2	1	1
Sly03g0210281	M3	NA	20	28	18	9	4	11	18	10	10	7
Sly03g0210301	M19	NA	3	3	3	3	3	3	3	3	3	2
Sly03g0210311	M18	EMF2	45	46	50	46	49	48	42	49	41	50
Sly03g0210321	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly03g0210341	M11	NA	79	64	64	75	74	83	81	91	78	71
Sly03g0210351	M11	NA	120	112	127	238	431	174	168	208	257	430
Sly03g0210361	M1	SISDG45	2	2	2	1	1	1	1	1	1	1
Sly03g0210371	M12	SISDG9	1	2	1	3	2	3	4	4	3	2
Sly03g0210421	M12	NA	1	1	1	1	1	1	1	1	9	5
Sly03g0210431	M12	SISDG8	1	1	1	5	6	2	2	5	33	23
Sly03g0210451	M12	NA	2	2	3	2	3	4	4	4	3	3
Sly03g0210471	M1	NA	27	23	45	26	8	8	5	9	6	2
Sly03g0210501	M12	NA	74	69	81	130	235	75	78	82	143	217
Sly03g0210511	M1	NA	4	4	4	3	5	4	4	4	3	4
Sly03g0210531	M1	NA	42	37	32	51	69	20	19	21	43	73
Sly03g0210541	M6	NA	15	21	15	1	1	13	24	5	1	1
Sly03g0210581	M3	NA	33	35	26	26	30	26	28	19	28	31
Sly03g0210591	M22	NA	2	2	1	3	1	2	1	2	0	0
Sly03g0210601	M11	NA	26	24	26	32	32	27	25	29	34	34
Sly03g0210621	M12	NA	8	8	6	8	8	11	10	8	4	3
Sly03g0210631	M9	NA	2	3	1	1	1	9	10	4	2	2
Sly03g0210641	M2	NA	17	21	17	20	22	13	17	14	21	19
Sly03g0210651	M11	NA	14	11	14	12	16	24	14	25	18	28
Sly03g0210661	M18	NA	6	7	6	5	7	6	6	8	7	9
Sly03g0210671	M1	NA	11	10	11	13	13	9	7	10	10	11
Sly03g0210681	M1	NA	12	10	13	11	11	8	10	11	11	12
Sly03g0210691	M11	NA	128	123	127	155	186	132	129	155	237	319
Sly03g0210721	M10	NA	1	1	1	1	1	2	3	1	1	1
Sly03g0210771	M7	NA	8	12	5	3	5	11	23	8	4	21
Sly03g0210781	M3	NA	26	60	23	15	37	10	14	5	2	6
Sly03g0210821	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0210851	M3	SISOD6	15	14	14	24	21	12	13	13	20	14
Sly03g0210861	M3	NA	38	34	34	24	17	28	30	28	28	18
Sly03g0210871	M1	NA	4	5	5	5	5	4	4	5	5	5
Sly03g0210891	M11	NA	104	102	104	98	82	113	116	116	123	100
Sly03g0210901	M11	NA	9	8	9	6	6	11	10	9	6	5
Sly03g0210911	M12	NA	6	6	6	4	2	9	9	8	6	1
Sly03g0210921	M1	NA	44	43	38	36	39	31	29	28	28	32
Sly03g0210941	M12	NA	25	25	30	46	72	34	34	34	46	59
Sly03g0210951	M1	NA	7	8	5	4	8	5	5	6	3	6
Sly03g0210961	M12	gibberellin modificatio	19	37	10	7	4	74	121	34	4	1
Sly03g0210971	M22	NA	5	5	5	5	6	5	5	5	4	6
Sly03g0211001	M11	NA	5	2	2	4	4	4	3	4	2	5
Sly03g0211011	M17	NA	4	3	2	3	4	3	2	4	2	2
Sly03g0211021	M1	NA	93	92	90	92	99	73	72	72	73	111
Sly03g0211041	M1	NA	8	6	6	3	1	1	1	1	1	1
Sly03g0211061	M19	NA	51	56	53	59	57	55	54	54	47	51
Sly03g0211111	M1	NA	10	12	11	12	14	8	9	9	14	12
Sly03g0211131	M3	NA	28	30	27	30	32	22	24	22	30	30
Sly03g0211141	M1	NA	3	3	2	1	1	1	1	1	1	1
Sly03g0211161	M3	NA	13	14	11	13	15	8	10	8	16	19
Sly03g0211231	M1	NA	12	11	11	1	2	9	8	9	2	1
Sly03g0211241	M1	NA	16	21	15	3	2	5	4	3	1	1
Sly03g0211251	M11	NA	25	25	28	59	130	35	31	44	62	93
Sly03g0211261	M22	NA	6	5	5	3	6	5	4	5	9	15
Sly03g0211281	M12	NA	1	1	1	1	0	4	3	4	1	0
Sly03g0211291	M11	NA	5	5	4	2	1	48	32	56	7	2
Sly03g0211301	M11	NA	3	4	4	2	0	52	37	65	7	2
Sly03g0211311	M19	NA	8	9	10	11	12	10	7	10	8	7
Sly03g0211321	M11	NA	11	11	13	15	17	12	11	13	12	15
Sly03g0211331	M1	NA	1	1	3	3	7	1	1	1	1	4
Sly03g0211341	M1	AMY1	22	21	25	40	59	17	14	20	38	35
Sly03g0211351	M3	NA	36	35	30	29	19	25	26	23	24	19
Sly03g0211361	M3	NA	161	145	111	117	87	124	142	119	123	101
Sly03g0211371	M23	NA	1	1	1	1	0	1	1	1	1	1
Sly03g0211401	M1	NA	15	13	14	11	11	12	8	9	3	2
Sly03g0211411	M1	NA	43	61	31	5	8	2	4	1	1	2
Sly03g0211421	M3	SIPYL4	2	3	1	1	1	1	1	1	0	1
Sly03g0211441	M1	NA	9	6	5	1	1	2	1	2	1	1
Sly03g0211481	M3	NA	108	104	102	93	81	87	93	90	113	105
Sly03g0211491	M12	NA	10	11	12	26	17	11	13	12	13	7
Sly03g0211501	M1	NA	4	4	6	55	35	2	3	5	29	10
Sly03g0211511	M1	NA	2	2	4	80	44	1	1	1	28	11
Sly03g0211521	M12	NA	3	9	31	2938	2659	20	131	366	4565	1793
Sly03g0211571	M1	NA	4	4	8	4	2	1	1	1	1	2
Sly03g0211581	M11	PPR-like26	6	4	7	5	9	9	9	10	15	14
Sly03g0211591	M23	NA	6	2	2	1	1	18	4	2	1	1
Sly03g0211621	M1	NA	2	4	7	2	1	2	1	3	1	1
Sly03g0211631	M11	NA	18	19	22	58	196	23	21	26	29	47
Sly03g0211641	M1	NA	3	8	8	68	302	3	3	6	4	9
Sly03g0211651	M12	NA	42	46	40	45	34	49	51	41	44	30
Sly03g0211681	M22	NA	1	1	1	0	0	4	1	2	0	0
Sly03g0211691	M23	PrxII	30	15	11	2	1	76	38	31	9	1
Sly03g0211701	M3	NA	24	30	10	5	8	2	4	3	9	11
Sly03g0211711	M3	NA	2	2	2	1	1	2	2	2	2	2
Sly03g0211721	M1	NA	6	6	4	3	2	3	2	2	1	1
Sly03g0211731	M11	NA	134	131	144	139	124	145	134	157	211	273
Sly03g0211741	M1	NA	9	8	10	6	5	8	7	9	4	5
Sly03g0211751	M1	NA	11	10	13	18	15	4	3	8	9	13
Sly03g0211781	M12	NA	2	5	4	3	4	2	5	8	3	7
Sly03g0211791	M13	NA	23	25	35	43	43	13	21	45	41	80
Sly03g0211811	M1	NA	6	12	12	10	12	4	11	11	9	21
Sly03g0211821	M1	NA	12	18	16	18	28	9	17	23	22	52
Sly03g0211841	M7	NA	1	1	1	0	1	1	1	1	0	0
Sly03g0211871	M11	NA	32	27	33	17	15	34	33	37	23	31
Sly03g0211911	M1	NA	33	25	40	52	59	24	19	23	48	68
Sly03g0211921	M11	NA	9	8	13	10	10	8	9	11	16	16
Sly03g0211941	M1	NA	166	177	91	3	1	9	13	3	0	1
Sly03g0211971	M1	NA	3	2	2	2	1	1	1	1	1	0
Sly03g0211981	M1	NA	310	275	241	230	174	187	196	184	218	170

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0100111	M9	NA	11	13	11	15	18	13	14	12	19	25
Sly09g0100121	M11	NA	17	18	22	34	42	20	19	26	22	18
Sly09g0100131	M3	NA	59	117	22	1	0	23	27	4	1	0
Sly09g0100141	M3	NA	41	50	36	28	24	35	40	33	33	24
Sly09g0100151	M11	NA	51	56	60	50	82	81	78	93	28	81
Sly09g0100171	M22	NA	1	1	1	1	4	3	1	3	6	18
Sly09g0100191	M1	NA	10	9	13	2	4	4	2	3	0	0
Sly09g0100201	M11	NA	61	56	67	104	100	79	79	83	84	80
Sly09g0100211	M11	NA	27	26	33	30	37	34	27	36	31	35
Sly09g0100231	M12	NA	1	1	1	0	0	1	2	1	1	0
Sly09g0100241	M1	NA	16	18	15	10	8	9	10	8	3	5
Sly09g0100251	M11	NA	65	41	94	1	1	966	797	930	1	1
Sly09g0100261	M11	NA	10	3	11	1	1	26	40	31	1	1
Sly09g0100278	M1	NA	2	2	2	0	0	1	1	0	0	0
Sly09g0100351	M11	NA	13	13	15	18	20	15	14	18	28	31
Sly09g0100361	M18	NA	21	22	27	23	27	34	29	45	45	34
Sly09g0100371	M3	NA	1	1	1	1	2	1	1	1	1	1
Sly09g0100411	M1	E8	536	557	854	12683	13944	126	358	885	22910	17662
Sly09g0100471	M3	ETR6	43	39	24	31	12	21	23	14	42	17
Sly09g0100491	M3	NA	13	9	8	9	12	9	10	11	13	18
Sly09g0100501	M3	NA	7	11	8	10	8	5	6	6	14	21
Sly09g0100511	M3	HUP39	20	19	17	14	12	16	15	16	9	13
Sly09g0100521	M19	NA	13	13	13	17	25	12	12	14	20	30
Sly09g0100531	M2	NA	70	79	57	47	23	44	67	33	25	18
Sly09g0100541	M1	NA	2	3	3	3	2	1	1	1	1	1
Sly09g0100551	M20	NA	15	17	23	10	4	16	15	18	5	2
Sly09g0100591	M1	NA	4	5	5	10	14	1	1	1	1	1
Sly09g0100601	M1	NA	10	14	7	10	5	1	1	1	1	1
Sly09g0100611	M1	NA	8	19	6	9	5	1	1	1	1	1
Sly09g0100681	M12	NA	1	1	0	1	0	1	1	1	1	1
Sly09g0100711	M3	NA	11	12	8	13	19	9	10	8	9	17
Sly09g0100721	M11	NA	1	1	1	1	1	1	1	1	1	2
Sly09g0100731	M11	NA	56	57	73	66	61	91	88	114	98	94
Sly09g0100741	M11	NA	46	51	48	47	46	47	49	51	45	51
Sly09g0100751	M22	NA	1	1	1	0	0	1	1	1	1	0
Sly09g0100781	M3	NA	16	18	5	0	0	6	7	1	0	0
Sly09g0100801	M3	SIERF.C4	79	128	34	3	1	19	16	5	1	1
Sly09g0100811	M3	NA	149	146	68	53	54	85	92	69	48	83
Sly09g0100821	M22	NA	31	1	35	0	1	295	3	211	0	0
Sly09g0100841	M22	NA	26	1	28	0	1	265	1	183	0	0
Sly09g0100851	M22	NA	3	1	1	0	0	7	0	3	0	0
Sly09g0100881	M3	NA	11	10	9	6	4	9	8	7	6	5
Sly09g0100891	M3	SISDG41	28	30	23	15	10	19	20	16	11	11
Sly09g0100901	M3	NA	75	75	69	21	19	43	38	18	2	5
Sly09g0100911	M14	NA	38	37	49	15	12	41	35	45	11	10
Sly09g0100921	M1	NA	37	38	38	26	32	28	31	31	25	28
Sly09g0100931	M3	NA	578	668	499	100	17	130	146	71	135	68
Sly09g0100941	M1	NA	6	6	10	4	7	1	1	1	1	2
Sly09g0100951	M12	NA	1	1	1	1	1	3	2	3	3	4
Sly09g0100961	M14	NA	64	64	78	63	69	66	54	67	44	49
Sly09g0100971	M3	NA	122	110	96	51	52	88	88	79	47	48
Sly09g0100981	M11	NA	23	20	26	17	18	24	20	25	16	21
Sly09g0100991	M12	NA	4	10	4	1	1	37	56	9	1	1
Sly09g0101001	M11	NA	646	511	559	578	439	598	671	619	358	340
Sly09g0101021	M22	NA	711	179	266	18	1	1621	385	871	40	2
Sly09g0101031	M1	NA	134	136	133	71	91	108	120	107	88	98
Sly09g0101051	M1	NA	5	4	4	1	1	1	1	1	1	0
Sly09g0101061	M8	NA	87	114	53	32	28	135	206	70	12	17
Sly09g0101071	M12	NA	82	94	86	103	90	104	112	107	123	99
Sly09g0101091	M19	NA	2	3	3	3	3	3	3	3	2	2
Sly09g0101101	M19	NA	4	4	4	4	4	4	3	4	3	3
Sly09g0101111	M1	NA	4	6	5	6	6	4	4	4	5	4
Sly09g0101121	M3	NA	36	39	30	21	22	27	26	21	19	19
Sly09g0101141	M11	NA	29	30	33	28	23	59	49	57	30	22
Sly09g0101151	M12	NA	1	1	1	4	3	4	3	5	69	46
Sly09g0101161	M1	NA	10	9	12	8	9	9	9	10	31	17
Sly09g0101181	M1	NA	2	2	3	5	3	1	1	1	1	0
Sly09g0101201	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0101211	M1	NA	31	32	31	55	180	25	28	31	61	151
Sly09g0101221	M3	NA	10	10	8	2	2	9	7	7	2	1
Sly09g0101231	M11	NA	3	2	4	2	2	41	28	51	20	24
Sly09g0101241	M12	NA	7	6	6	3	1	19	21	33	9	2
Sly09g0101271	M1	NA	21	23	22	24	28	20	19	21	33	36
Sly09g0101281	M10	NA	14	16	14	17	19	16	17	15	13	14
Sly09g0101301	M11	NA	7	7	8	4	4	9	9	9	5	4
Sly09g0101311	M11	NA	10	9	11	19	22	18	17	23	16	18
Sly09g0101321	M19	NA	26	29	27	27	31	25	23	25	20	21
Sly09g0101331	M11	NA	61	55	59	61	38	58	55	65	71	47
Sly09g0101341	M19	NA	5	6	5	5	4	5	4	6	5	5
Sly09g0101351	M1	NA	3	3	3	2	1	2	2	3	2	2
Sly09g0101371	M5	NA	29	34	23	26	42	33	30	26	30	48
Sly09g0101381	M1	NA	62	81	48	13	13	1	1	1	0	0
Sly09g0101411	M1	NA	1	1	1	1	1	1	0	0	0	0
Sly09g0101441	M18	NA	15	16	17	1	1	27	22	28	1	1
Sly09g0101451	M17	NA	126	110	120	113	127	109	97	117	104	127
Sly09g0101471	M3	NA	13	14	9	7	13	9	9	6	6	8
Sly09g0101481	M4	NA	1	1	1	1	1	2	2	1	1	1
Sly09g0101491	M6	NA	9	11	6	4	2	11	14	5	2	1
Sly09g0101501	M9	NA	22	29	35	7	17	48	61	22	14	9
Sly09g0101511	M17	NA	287	258	258	217	175	250	251	297	274	211
Sly09g0101531	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly09g0101541	M3	NA	192	170	147	89	55	122	133	112	106	65
Sly09g0101551	M9	NA	2	2	1	1	1	5	6	3	6	5
Sly09g0101561	M22	SISDG12	1	1	1	1	1	2	1	1	1	1
Sly09g0101571	M12	NA	25	31	30	72	176	64	81	74	86	132
Sly09g0101591	M19	NA	115	119	124	106	96	112	103	112	87	91
Sly09g0101601	M1	NA	4	3	3	2	2	2	2	2	1	1
Sly09g0101611	M12	NA	3	3	3	3	3	3	3	3	5	3
Sly09g0101621	M11	NA	1	1	2	1	1	2	1	9	4	3
Sly09g0101631	M9	NA	12	11	9	14	16	11	13	12	19	22
Sly09g0101641	M11	NA	93	91	96	108	97	98	91	110	91	93
Sly09g0101651	M2	NA	21	26	14	16	17	10	12	7	11	10
Sly09g0101671	M2	NA	95	91	89	61	59	73	84	63	77	74
Sly09g0101681	M3	NA	17	22	8	1	1	10	7	2	1	1
Sly09g0101691	M3	NA	31	34	27	21	19	21	23	19	18	19
Sly09g0101701	M11	NA	9	10	10	13	21	10	10	12	14	16
Sly09g0101721	M12	NA	4	3	4	12	43	9	13	9	10	35
Sly09g0101731	M11	NA	3	3	4	3	3	3	3	4	3	3
Sly09g0101741	M11	NA	3	3	3	5	5	3	3	4	5	4
Sly09g0101751	M11	NA	1	1	1	3	2	1	1	2	19	4
Sly09g0101761	M23	NA	7	2	2	2	1	7	7	4	9	1
Sly09g0101771	M11	SISDG4	17	17	24	18	10	21	18	25	6	5
Sly09g0101781	M12	NA	22	20	25	25	29	27	27	33	28	30
Sly09g0101791	M1	NA	13	9	10	8	6	9	8	9	10	8
Sly09g0101801	M9	NA	2	2	1	1	1	2	3	2	3	1
Sly09g0101821	M11	NA	14	14	16	28	38	16	16	19	39	40
Sly09g0101831	M12	NA	23	25	31	47	75	31	30	32	72	103
Sly09g0101851	M12	NA	19	18	16	18	19	19	18	19	17	22
Sly09g0101861	M18	NA	11	11	11	9	10	12	11	11	9	8
Sly09g0101881	M11	NA	3	4	5	4	4	6	6	5	4	2
Sly09g0101891	M12	NA	52	64	45	26	5	93	85	72	4	1
Sly09g0101901	M11	SlAux/IAA13	5	3	9	2	2	35	21	38	1	1
Sly09g0101921	M1	NA	16	15	18	25	21	11	11	13	6	2
Sly09g0101931	M1	NA	54	54	46	40	33	46	46	47	36	33
Sly09g0101951	M11	NA	34	30	36	45	61	40	38	52	84	67
Sly09g0101961	M1	NA	25	22	17	3	1	1	1	1	5	1
Sly09g0101971	M1	NA	3683	3186	4264	3511	1329	85	10	9	6	2
Sly09g0101981	M1	NA	75	85	64	2	1	5	1	1	0	1
Sly09g0101991	M1	NA	76	102	63	2	1	2	1	1	1	1
Sly09g0102021	M11	NA	34	30	34	20	5	34	35	37	16	2

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0212001	M1	NA	10	14	14	13	6	1	1	1	2	1
Sly03g0212011	M3	NA	33	44	20	16	14	21	24	10	7	10
Sly03g0212051	M3	NA	40	45	27	11	11	24	29	18	13	19
Sly03g0212061	M1	NA	12	9	13	1	1	2	1	1	0	0
Sly03g0212141	M3	NA	4	6	2	1	1	1	2	1	1	1
Sly03g0212161	M19	NA	4	6	5	6	3	5	4	4	4	3
Sly03g0212171	M11	NA	5	7	5	5	6	5	4	6	5	4
Sly03g0212181	M12	NA	6	6	5	7	8	7	7	7	8	9
Sly03g0212191	M4	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0212201	M11	NA	37	33	36	31	38	42	39	44	44	52
Sly03g0212231	M1	SIPP2C1	169	144	121	63	62	73	65	67	47	50
Sly03g0212251	M1	NA	4	4	4	6	4	2	3	2	3	1
Sly03g0212271	M1	NA	117	94	111	56	49	26	25	26	23	20
Sly03g0212281	M14	NA	17	14	22	14	15	11	11	14	21	35
Sly03g0212321	M1	NA	2	1	2	9	8	1	1	2	27	6
Sly03g0212331	M12	NA	4	4	3	39	26	9	7	12	174	52
Sly03g0212341	M1	NA	21	23	22	27	28	16	18	17	23	24
Sly03g0212351	M1	NA	5	5	6	2	1	3	2	2	1	1
Sly03g0212361	M3	NA	80	76	74	71	75	75	75	71	65	80
Sly03g0212371	M2	NA	29	29	27	19	16	26	26	20	12	5
Sly03g0212381	M14	NA	7	7	9	4	4	9	7	10	3	4
Sly03g0212391	M11	NA	158	106	163	42	37	311	248	281	19	28
Sly03g0212401	M11	NA	67	65	76	72	93	125	111	146	81	114
Sly03g0212411	M11	NA	45	40	53	70	63	54	54	67	104	111
Sly03g0212421	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0212431	M3	NA	25	26	21	19	17	17	17	15	10	10
Sly03g0212451	M11	NA	1	1	2	1	1	3	2	3	1	1
Sly03g0212461	M11	NA	10	9	11	6	3	25	16	22	4	1
Sly03g0212471	M1	NA	40	39	42	44	46	36	35	36	36	40
Sly03g0212481	M1	NA	84	94	89	87	71	71	73	70	73	67
Sly03g0212491	M9	NA	38	41	42	53	46	46	50	42	53	43
Sly03g0212501	M11	NA	38	32	37	50	70	57	51	66	81	76
Sly03g0212511	M11	NA	21	21	22	39	38	25	24	25	35	35
Sly03g0212521	M1	NA	71	68	62	53	50	49	48	46	62	62
Sly03g0212531	M12	NA	2	3	2	4	2	3	4	4	4	2
Sly03g0212541	M12	NA	34	30	40	34	16	53	53	49	19	5
Sly03g0212551	M12	NA	64	64	66	128	123	73	79	79	97	99
Sly03g0212561	M18	NA	8	9	10	9	10	11	10	13	10	9
Sly03g0212571	M11	NA	66	59	66	105	112	70	76	74	95	114
Sly03g0212581	M3	NA	32	37	23	20	21	21	25	12	17	17
Sly03g0212591	M1	NA	15	16	13	60	21	8	4	3	1	1
Sly03g0212611	M7	NA	6	25	8	18	121	13	61	17	34	112
Sly03g0212621	M12	NA	21	19	21	22	23	25	25	24	20	28
Sly03g0212631	M3	NA	205	220	145	131	137	126	145	110	124	149
Sly03g0212641	M11	NA	7	5	7	7	8	9	6	11	12	14
Sly03g0212671	M12	SIJMJ3	1	1	1	2	1	1	1	1	2	2
Sly03g0212681	M12	NA	4	6	5	15	12	6	6	7	12	7
Sly03g0212691	M2	NA	75	74	63	74	86	44	55	46	117	142
Sly03g0212701	M12	NA	49	46	47	113	120	51	50	51	106	135
Sly03g0212711	M11	NA	14	11	15	15	17	17	15	19	24	31
Sly03g0212721	M1	NA	24	28	29	33	40	25	25	26	31	37
Sly03g0212731	M15	NA	52	57	49	67	83	53	53	56	67	88
Sly03g0212741	M3	NA	14	13	13	10	5	11	13	11	9	5
Sly03g0212751	M1	NA	34	38	35	24	23	26	25	26	22	21
Sly03g0212761	M1	NA	25	50	49	178	19	3	4	2	4	2
Sly03g0212771	M6	NA	94	123	73	57	103	81	137	68	59	104
Sly03g0212781	M11	NA	35	33	37	20	12	41	39	35	13	8
Sly03g0212791	M11	NA	25	27	30	33	57	29	28	36	51	70
Sly03g0212801	M11	NA	32	30	35	68	108	43	36	52	75	121
Sly03g0212821	M9	NA	4	4	2	4	4	8	11	5	9	7
Sly03g0212831	M11	NA	22	23	30	16	18	27	24	35	17	17
Sly03g0212841	M11	NA	115	102	110	143	194	110	109	144	208	287
Sly03g0212851	M19	NA	31	37	34	38	39	36	34	37	61	45
Sly03g0212861	M3	NA	304	320	211	116	157	189	314	146	109	183
Sly03g0212871	M3	NA	25	27	23	20	20	21	20	16	15	16
Sly03g0212881	M19	NA	107	108	114	119	154	98	86	100	91	123
Sly03g0212891	M1	NA	30	30	29	28	29	20	21	22	21	25
Sly03g0212901	M3	NA	22	19	20	27	33	20	19	19	37	41
Sly03g0212911	M11	NA	2	2	3	3	1	3	3	4	2	1
Sly03g0212921	M22	NA	1	1	1	0	1	2	1	2	0	1
Sly03g0212931	M3	NA	33	38	31	33	35	34	33	30	31	39
Sly03g0212941	M1	NA	70	71	67	83	106	68	65	68	87	99
Sly03g0212951	M19	NA	59	69	63	75	88	65	57	62	67	71
Sly03g0212961	M1	NA	64	59	59	64	70	54	50	53	58	63
Sly03g0212971	M7	NA	12	15	14	26	93	14	17	12	38	72
Sly03g0212991	M22	NA	6	3	3	1	0	18	7	15	1	1
Sly03g0213001	M22	NA	6	3	4	1	1	16	7	12	1	1
Sly03g0213011	M22	NA	1	1	1	0	1	1	1	1	0	0
Sly03g0213021	M12	NA	5	4	5	5	5	5	6	6	8	10
Sly03g0213031	M9	NA	1	1	1	1	0	2	2	2	2	1
Sly03g0213041	M3	HVA22E-like2	1	2	1	0	0	2	1	1	0	0
Sly03g0213051	M1	NA	1	1	1	1	1	0	1	1	1	1
Sly03g0213061	M11	NA	4	2	3	78	308	6	7	14	404	713
Sly03g0213071	M22	NA	1	0	1	0	0	3	0	4	0	0
Sly03g0213081	M11	NA	12	12	13	13	13	14	11	16	10	8
Sly03g0213091	M18	NA	28	29	32	30	43	34	28	32	45	82
Sly03g0213101	M2	NA	45	50	45	249	263	40	49	45	190	219
Sly03g0213111	M3	NA	59	57	52	42	42	46	46	45	47	43
Sly03g0213121	M22	NA	2	1	1	2	1	13	2	8	1	1
Sly03g0213131	M3	SAUR38	1	2	1	0	1	1	0	1	1	1
Sly03g0213141	M18	NA	25	26	26	36	33	28	25	29	30	27
Sly03g0213151	M1	NA	2	2	2	1	0	1	1	1	1	1
Sly03g0213171	M11	NA	42	43	45	48	55	56	51	60	69	75
Sly03g0213181	M3	NA	4	3	3	1	5	1	4	1	1	2
Sly03g0213191	M3	NA	2	4	3	2	1	2	5	1	12	1
Sly03g0213201	M12	NA	146	148	259	17	2	3139	3699	4232	225	6
Sly03g0213211	M1	NA	18	17	11	1	0	3	1	1	1	0
Sly03g0213221	M1	NA	31	30	40	26	3	4	1	1	1	1
Sly03g0213231	M1	NA	1	1	1	1	0	0	1	0	0	0
Sly03g0213261	M3	NA	35	50	39	40	50	34	41	37	49	71
Sly03g0213271	M11	NA	16	17	16	11	4	22	21	24	9	6
Sly03g0213301	M3	NA	27	25	7	3	4	5	5	3	3	2
Sly03g0213341	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0213361	M2	NA	279	271	193	232	210	182	225	165	225	200
Sly03g0213391	M1	NA	3	4	3	3	4	2	2	2	1	1
Sly03g0213401	M1	NA	19	29	53	329	155	3	11	29	340	192
Sly03g0213411	M7	NA	12	18	9	40	63	7	30	11	90	232
Sly03g0213431	M11	NA	43	63	53	63	54	71	62	81	119	101
Sly03g0213441	M1	NA	2	2	3	0	0	0	0	0	0	0
Sly03g0213451	M22	NA	1	1	1	0	0	3	0	3	0	0
Sly03g0213461	M12	NA	15	17	20	24	18	44	42	48	29	21
Sly03g0213481	M22	NA	25	23	27	19	10	23	24	24	30	17
Sly03g0213491	M12	NA	1	1	1	1	1	3	2	3	1	1
Sly03g0213501	M12	NA	1	1	1	1	1	2	2	1	1	2
Sly03g0213511	M9	NA	24	26	22	34	38	32	38	27	32	50
Sly03g0213521	M9	NA	132	137	117	134	124	128	167	126	130	148
Sly03g0213541	M9	NA	3	3	2	1	1	8	9	3	1	1
Sly03g0213551	M3	NA	23	22	23	18	26	20	22	19	27	32
Sly03g0213561	M6	NA	15	28	18	3	1	41	38	6	2	1
Sly03g0213571	M1	NA	5	5	4	4	4	3	3	4	3	2
Sly03g0213581	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0213591	M1	NA	69	75	71	35	3	20	5	5	3	1
Sly03g0213601	M17	NA	586	482	544	303	204	479	459	531	307	229
Sly03g0213611	M11	NA	74	66	82	114	109	88	85	101	98	111
Sly03g0213621	M3	NA	56	59	33	14	9	29	33	22	8	16
Sly03g0213631	M1	NA	15	14	13	13	9	5	4	5	10	21
Sly03g0213641	M11	NA	19	17	20	31	34	27	26	33	37	53
Sly03g0213651	M11	NA	3	3	3	4	4	6	4	6	4	5
Sly03g0213661	M3	NA	163	138	128	134	157	107	137	119	152	165
Sly03g0213671	M1	NA	16	17	14	15	14	13	10	11	7	6
Sly03g0213681	M7	NA	27	29	23	13	19	22	35	24	14	18
Sly03g0213691	M1	NA	127	109	111	153	307	98	96	97	142	262
Sly03g0213701	M1	NA	3	2	4	1	1	1	1	1	2	3
Sly03g0213711	M1	NA	33	25	33	12	28	6	4	4	2	2

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0102081	M12	NA	19	19	21	59	127	20	25	25	70	118
Sly09g0102131	M6	YUC-like3	1	2	1	1	1	1	1	1	0	1
Sly09g0102141	M11	NA	13	13	14	17	24	21	16	20	19	19
Sly09g0102171	M11	NA	36	40	36	39	29	41	39	38	43	38
Sly09g0102181	M22	NA	6	0	4	0	0	53	1	27	0	0
Sly09g0102191	M22	NA	6	1	5	0	1	55	1	29	0	0
Sly09g0102221	M19	NA	11	16	11	10	14	13	14	12	14	16
Sly09g0102231	M5	NA	37	43	30	24	44	32	45	33	47	78
Sly09g0102241	M12	NA	112	106	102	167	210	143	156	172	207	264
Sly09g0102251	M8	NA	2	5	3	3	5	4	4	3	7	7
Sly09g0102261	M11	NA	120	113	122	178	182	152	174	185	192	190
Sly09g0102271	M3	NA	98	106	97	131	148	79	89	67	92	158
Sly09g0102291	M1	NA	27	27	30	33	43	20	22	20	37	48
Sly09g0102331	M3	NA	6	7	7	7	3	6	5	4	2	1
Sly09g0102341	M11	NA	16	15	21	38	49	24	25	29	25	33
Sly09g0102351	M1	NA	70	64	67	37	28	57	56	58	34	29
Sly09g0102361	M1	NA	4	3	3	1	1	3	2	2	2	1
Sly09g0102371	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0102381	M3	RBR1	30	30	30	21	19	28	28	24	17	13
Sly09g0102411	M22	NA	1	0	1	0	0	3	0	1	0	0
Sly09g0102421	M22	NA	3	0	3	0	0	31	1	15	0	0
Sly09g0102451	M22	NA	1	0	1	0	0	2	0	2	0	0
Sly09g0102461	M22	NA	1	0	1	0	0	4	0	2	0	0
Sly09g0102481	M22	NA	1	0	1	0	0	4	0	3	0	0
Sly09g0102591	M22	NA	2	0	1	0	0	9	1	7	0	0
Sly09g0102641	M1	NA	2	2	2	1	1	2	2	2	1	1
Sly09g0102651	M22	NA	6	1	4	1	0	11	2	21	1	0
Sly09g0102681	M22	NA	1	0	1	0	0	1	0	1	0	0
Sly09g0102701	M22	NA	1	1	1	4	8	3	2	2	1	3
Sly09g0102711	M1	NA	5	5	4	3	1	1	1	1	1	0
Sly09g0102721	M12	SIPL	3	10	2	478	157	7	8	7	105	72
Sly09g0102731	M1	SlHDA1	106	109	111	160	159	87	88	102	170	205
Sly09g0102741	M1	NA	56	57	67	79	82	51	50	55	76	73
Sly09g0102751	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0102761	M12	NA	232	235	258	1142	1682	330	367	378	884	1063
Sly09g0102771	M11	NA	22	19	21	18	15	20	19	22	16	15
Sly09g0102791	M1	NA	32	30	30	46	60	24	25	30	56	77
Sly09g0102801	M11	NA	2	3	3	1234	563	5	3	5	2	1
Sly09g0102821	M1	SAM-METT-like11	2	2	2	1	1	1	1	0	1	0
Sly09g0102841	M1	SAM-METT-like5	28	30	17	0	0	1	1	1	0	0
Sly09g0102851	M1	NA	38	40	22	17	11	11	12	5	2	2
Sly09g0102861	M11	NA	13	13	15	20	26	19	16	22	21	21
Sly09g0102871	M12	NA	33	31	38	51	71	50	46	52	65	82
Sly09g0102881	M11	NA	17	15	21	38	99	18	16	22	42	68
Sly09g0102891	M11	NA	23	24	23	31	27	33	31	33	38	34
Sly09g0102901	M9	NA	3	4	3	78	44	18	19	23	470	124
Sly09g0102971	M22	NA	2	1	2	1	1	7	1	5	1	1
Sly09g0102981	M11	NA	4	4	5	2	3	5	5	5	1	1
Sly09g0102991	M5	NA	98	201	75	14	9	147	152	20	1	2
Sly09g0103001	M5	NA	4	7	2	1	1	16	5	1	0	1
Sly09g0103031	M11	NA	28	21	30	33	25	37	31	40	19	15
Sly09g0103041	M12	NA	1	1	1	1	1	2	2	2	2	1
Sly09g0103051	M1	NA	39	36	34	33	31	30	29	26	22	26
Sly09g0103071	M22	NA	4	4	4	4	10	7	1	4	37	66
Sly09g0103081	M1	NA	244	227	219	166	138	182	187	176	194	189
Sly09g0103091	M3	NA	73	75	74	95	107	68	72	69	91	102
Sly09g0103131	M22	NA	21	19	17	16	19	21	17	18	16	15
Sly09g0103141	M11	NA	41	40	48	71	87	50	49	60	88	120
Sly09g0103151	M1	NA	33	23	39	4	1	2	0	1	0	0
Sly09g0103161	M22	NA	1	1	1	1	0	2	1	2	1	1
Sly09g0103171	M12	NA	230	231	249	319	274	264	311	267	291	253
Sly09g0103181	M11	NA	6	6	7	21	44	9	9	10	17	34
Sly09g0103191	M1	NA	143	148	156	128	92	88	80	89	117	103
Sly09g0103201	M19	NA	23	23	26	27	24	21	17	22	21	15
Sly09g0103211	M19	NA	10	10	13	9	7	10	6	9	4	3
Sly09g0103221	M12	YUC10-like3	1	1	1	0	0	2	2	1	1	0
Sly09g0103231	M22	NA	1	1	1	0	0	3	1	2	0	0
Sly09g0103241	M1	NA	1	2	2	1	1	1	1	1	0	3
Sly09g0103261	M8	NA	65	68	60	99	70	61	83	51	73	60
Sly09g0103271	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly09g0103301	M11	NA	16	16	17	18	15	20	19	22	24	18
Sly09g0103311	M16	NA	175	157	157	176	211	146	132	166	199	242
Sly09g0103331	M22	NA	2	1	2	1	1	3	1	2	0	0
Sly09g0103341	M1	NA	3	2	3	4	3	2	2	3	2	1
Sly09g0103351	M1	NA	90	83	88	62	69	60	57	68	59	57
Sly09g0103361	M3	NA	83	108	58	12	17	27	34	14	5	11
Sly09g0103411	M3	NA	23	23	22	24	31	20	22	20	32	37
Sly09g0103421	M1	NA	203	203	189	253	289	122	111	103	77	96
Sly09g0103431	M1	NA	3	3	3	3	3	2	2	3	3	3
Sly09g0103451	M12	NA	27	27	30	40	50	44	42	49	49	77
Sly09g0103461	M3	NA	59	62	48	20	12	36	42	32	21	16
Sly09g0103471	M3	NA	81	72	67	58	46	62	65	55	57	52
Sly09g0103481	M3	NA	8	9	7	6	7	6	6	6	6	5
Sly09g0103491	M11	NA	44	24	80	5	1	188	112	284	4	1
Sly09g0103501	M3	NA	53	48	45	35	33	44	46	43	66	51
Sly09g0103511	M11	NA	4	5	6	6	2	16	13	19	2	1
Sly09g0103551	M1	NA	39	41	41	43	43	36	36	36	43	41
Sly09g0103561	M22	NA	1	1	1	1	1	3	0	2	1	1
Sly09g0103571	M12	NA	1	2	2	2	2	1	2	2	2	2
Sly09g0103591	M22	NA	1	0	1	0	0	9	0	7	0	0
Sly09g0103601	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0103611	M11	NA	16	16	22	38	40	39	30	45	41	42
Sly09g0103621	M11	NA	1	1	1	0	0	1	1	2	1	0
Sly09g0103631	M13	NA	6	6	8	7	10	8	7	7	7	6
Sly09g0103641	M22	NA	3	1	2	1	1	12	3	6	0	0
Sly09g0103661	M22	NA	8	3	4	0	1	95	7	36	0	0
Sly09g0103671	M22	NA	9	3	4	0	1	104	6	42	0	0
Sly09g0103681	M22	NA	23	3	13	0	1	457	8	132	1	0
Sly09g0103691	M22	NA	3	1	1	0	0	33	3	15	0	0
Sly09g0103721	M18	NA	10	10	10	12	11	11	10	12	9	9
Sly09g0103731	M11	NA	2	2	2	2	3	2	2	3	4	6
Sly09g0103741	M12	NA	1	1	1	1	1	1	1	2	2	2
Sly09g0103751	M1	NA	2	2	2	1	1	1	1	1	0	0
Sly09g0103761	M19	NA	23	27	27	17	17	21	20	21	16	15
Sly09g0103791	M18	NA	35	35	39	35	42	40	33	42	46	51
Sly09g0103801	M11	NA	102	90	199	150	51	363	269	461	22	10
Sly09g0103831	M1	NA	33	58	83	210	67	2	1	1	1	0
Sly09g0103841	M1	NA	8	9	4	2	1	1	1	1	1	1
Sly09g0103851	M1	NA	8	11	6	2	1	1	1	1	1	1
Sly09g0103861	M1	NA	48	46	43	12	4	17	19	16	4	1
Sly09g0103871	M3	NA	126	131	65	19	10	66	75	46	26	8
Sly09g0103881	M14	NA	2	2	4	1	1	2	2	2	1	1
Sly09g0103901	M1	NA	31	30	27	34	27	21	21	25	36	29
Sly09g0103911	M22	NA	4	1	4	1	1	33	0	18	0	0
Sly09g0103921	M22	NA	1	0	1	1	1	5	0	2	1	1
Sly09g0103931	M12	HOG1-like3	1121	1109	1184	8805	9625	1227	1512	1709	17666	15885
Sly09g0103961	M1	NA	4	3	4	1	1	3	2	3	1	1
Sly09g0103971	M1	NA	113	74	162	10	3	34	19	43	2	1
Sly09g0103981	M1	NA	3	3	3	3	2	3	2	3	3	2
Sly09g0103991	M1	NA	22	25	35	21	12	9	7	9	6	7
Sly09g0104001	M12	NA	14	16	16	27	33	23	29	34	43	59
Sly09g0104021	M9	NA	3	5	4	4	10	8	11	4	2	2
Sly09g0104031	M2	NA	8	7	6	21	66	5	6	6	13	16
Sly09g0104041	M2	SlUGT75C1	100	116	134	705	1037	63	84	141	361	572
Sly09g0104051	M11	NA	3	2	3	1	1	4	3	4	1	1
Sly09g0104061	M9	SlXTH12/XET	3	7	2	3	5	9	8	2	2	2
Sly09g0104071	M1	NA	41	45	39	26	33	33	32	35	32	38
Sly09g0104091	M14	NA	21	19	26	22	22	22	19	21	11	10
Sly09g0104181	M1	NA	1	1	1	1	0	0	0	0	0	0
Sly09g0104201	M1	NA	1	1	1	1	0	0	0	0	0	0
Sly09g0104211	M20	NA	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0213721	M11	NA	1	1	1	0	0	2	1	1	0	0
Sly03g0213741	M3	NA	166	187	120	82	134	95	120	82	91	223
Sly03g0213761	M12	NA	3	3	2	1	1	4	4	4	2	3
Sly03g0213791	M12	NA	1	1	2	4	1	2	3	4	11	10
Sly03g0213801	M12	NA	22	22	35	56	7	101	142	163	752	98
Sly03g0213811	M11	NA	18	16	24	34	54	34	32	42	103	74
Sly03g0213821	M15	NA	17	14	15	18	14	14	14	16	10	12
Sly03g0213831	M1	NA	1	1	1	2	4	1	1	1	3	9
Sly03g0213841	M2	NA	22	22	20	22	24	20	21	22	27	32
Sly03g0213851	M12	NA	21	20	18	22	24	26	30	24	21	25
Sly03g0213861	M19	NA	32	35	30	33	30	29	27	27	24	24
Sly03g0213871	M1	NA	14	13	15	12	15	13	12	14	17	17
Sly03g0213881	M13	NA	40	39	46	42	48	43	39	50	32	56
Sly03g0213891	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly03g0213901	M1	NA	13	14	15	18	20	9	8	10	10	11
Sly03g0213911	M22	NA	1	1	2	0	0	3	1	3	1	0
Sly03g0213921	M1	NA	2	2	1	5	4	1	1	1	1	0
Sly03g0213931	M1	NA	59	54	37	22	21	20	21	16	11	11
Sly03g0213941	M10	NA	126	138	115	83	82	167	178	140	72	91
Sly03g0213951	M11	NA	64	62	70	146	176	90	91	105	173	244
Sly03g0213961	M12	NA	530	545	850	1664	1016	647	702	781	1014	998
Sly03g0213971	M1	NA	6	6	6	3	4	5	5	5	3	3
Sly03g0213981	M22	NA	1	1	1	0	0	3	1	2	0	0
Sly03g0213991	M19	NA	175	164	203	148	149	164	131	165	106	125
Sly03g0214001	M1	NA	2	3	3	34	62	1	1	1	1	2
Sly03g0214011	M5	NA	1	1	0	1	0	2	2	1	0	0
Sly03g0214031	M22	NA	2	1	1	0	0	3	1	4	0	0
Sly03g0214041	M11	NA	5	3	7	5	10	8	7	8	13	20
Sly03g0214051	M12	NA	11	12	11	9	19	12	12	11	14	19
Sly03g0214061	M11	NA	12	10	11	4	5	12	11	11	6	4
Sly03g0214121	M1	NA	20	20	16	11	4	14	14	15	9	5
Sly03g0214141	M12	NA	1	1	1	1	1	1	1	2	2	0
Sly03g0214161	M1	NA	59	55	53	62	82	46	49	48	71	112
Sly03g0214171	M19	NA	5	6	6	6	6	6	5	6	7	6
Sly03g0214181	M11	NA	7	7	8	7	8	9	7	8	12	12
Sly03g0214191	M11	NA	18	17	19	26	35	26	20	28	25	37
Sly03g0214201	M22	NA	2	2	2	1	2	3	1	2	1	1
Sly03g0214211	M11	NA	17	15	20	35	36	20	21	31	53	39
Sly03g0214221	M1	NA	54	53	52	51	51	45	45	48	66	67
Sly03g0214231	M12	NA	9	9	15	42	55	27	25	40	10	8
Sly03g0214301	M10	NA	2	1	1	1	1	1	2	1	1	1
Sly03g0214311	M3	NA	1	1	1	2	2	1	1	1	1	1
Sly03g0214331	M12	NA	1	1	2	2	1	3	3	5	3	1
Sly03g0214341	M11	NA	15	13	15	20	21	24	23	31	32	30
Sly03g0214351	M2	NA	86	86	76	77	67	72	83	61	61	57
Sly03g0214361	M12	NA	7	8	8	10	16	8	8	9	14	17
Sly03g0214371	M11	NA	31	31	33	40	50	40	35	44	55	80
Sly03g0214381	M1	NA	11	12	13	16	10	10	8	8	6	3
Sly03g0214391	M17	NA	20	20	20	12	18	19	17	19	14	14
Sly03g0214401	M11	NA	2	3	2	3	4	4	2	2	4	4
Sly03g0214411	M10	GEM-like12	11	29	12	1	7	24	33	7	1	3
Sly03g0214441	M9	NA	1	1	1	1	1	1	2	1	1	2
Sly03g0214451	M3	NA	1	2	1	1	1	1	2	1	2	2
Sly03g0214461	M3	NA	10	11	9	7	6	6	7	5	8	14
Sly03g0214471	M1	NA	1	1	3	1	0	0	0	0	0	0
Sly03g0214491	M1	NA	5	7	4	0	1	1	1	1	0	0
Sly03g0214501	M6	NA	21	48	43	12	4	12	16	7	3	4
Sly03g0214511	M6	NA	17	30	22	84	112	45	27	13	23	25
Sly03g0214531	M11	NA	74	86	106	79	32	73	77	132	105	42
Sly03g0214541	M1	NA	1	2	2	0	0	1	1	0	0	0
Sly03g0214581	M1	NA	28	35	44	3	2	15	25	17	1	1
Sly03g0214601	M1	NA	4	5	5	1	1	1	1	1	0	0
Sly03g0214611	M1	NA	6	10	19	1	0	6	1	2	0	0
Sly03g0214621	M1	NA	239	230	343	9	4	6	1	1	1	1
Sly03g0214631	M1	NA	21	24	22	1	1	1	1	1	0	0
Sly03g0214661	M18	NA	17	19	22	17	16	23	21	23	15	16
Sly03g0214671	M3	NA	5	3	2	1	2	1	1	1	0	1
Sly03g0214681	M9	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0214691	M7	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0214701	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0214731	M2	NA	6	6	6	3	3	5	5	5	4	3
Sly03g0214741	M2	NA	101	99	101	100	131	82	101	80	72	88
Sly03g0214751	M11	NA	26	23	28	43	59	34	31	42	39	44
Sly03g0214761	M11	NA	17	15	24	27	29	29	24	34	40	32
Sly03g0214771	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly03g0214781	M1	NA	38	39	40	38	34	34	35	38	42	46
Sly03g0214791	M1	NA	43	41	40	43	41	40	39	39	44	43
Sly03g0214801	M3	NA	34	32	22	3	2	13	16	11	4	2
Sly03g0214811	M11	NA	51	43	62	74	131	119	114	143	124	128
Sly03g0214821	M12	NA	1	1	1	0	0	1	1	1	0	1
Sly03g0214831	M15	NA	57	55	49	42	53	56	55	56	66	63
Sly03g0214841	M9	NA	43	46	42	57	65	48	45	43	85	88
Sly03g0214851	M3	NA	19	19	20	20	39	15	19	19	89	131
Sly03g0214871	M11	NA	27	13	15	12	3	75	37	67	76	15
Sly03g0214881	M11	NA	15	15	15	18	22	16	15	19	28	32
Sly03g0214891	M3	NA	36	36	28	21	18	23	23	21	13	14
Sly03g0214901	M1	NA	37	24	53	9	2	4	5	5	2	1
Sly03g0214911	M1	NA	531	490	528	306	223	406	407	404	315	229
Sly03g0214921	M1	NA	2	2	3	2	2	2	2	1	5	3
Sly03g0214931	M12	NA	23	33	45	66	25	40	46	45	29	39
Sly03g0214941	M11	NA	1	0	1	1	1	1	0	2	0	0
Sly03g0214961	M11	NA	21	23	24	31	40	23	24	24	41	56
Sly03g0214981	M12	NA	73	68	70	92	90	97	106	112	99	86
Sly03g0214991	M1	NA	12	21	32	101	105	1	1	1	3	11
Sly03g0215001	M21	NA	25	20	23	22	13	21	17	21	6	5
Sly03g0215031	M3	NA	50	56	43	39	38	43	47	35	39	37
Sly03g0215041	M3	NA	24	17	12	3	1	9	9	3	1	0
Sly03g0215051	M11	NA	10	9	13	19	43	18	18	26	20	29
Sly03g0215061	M14	NA	185	150	276	82	53	126	92	128	9	5
Sly03g0215071	M15	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0215191	M11	NA	28	26	31	25	18	42	38	51	31	20
Sly03g0215201	M2	NA	284	287	292	341	305	229	298	274	409	431
Sly03g0215211	M18	NA	22	23	29	28	37	40	30	40	26	39
Sly03g0215221	M22	NA	1	0	0	0	0	2	1	1	0	0
Sly03g0215231	M19	NA	97	94	96	139	122	94	85	96	117	100
Sly03g0215241	M1	NA	1	1	1	1	1	1	1	1	2	2
Sly03g0215251	M11	SlHAG14	64	59	63	49	57	61	56	67	55	69
Sly03g0215261	M12	HVA22K-like	18	18	20	26	28	22	23	23	32	42
Sly03g0215271	M1	NA	9	10	12	17	29	8	9	9	20	30
Sly03g0215281	M1	NA	9	9	8	7	5	7	8	8	7	4
Sly03g0215301	M12	NA	15	13	13	23	33	19	21	22	31	35
Sly03g0215311	M11	NA	8	8	7	8	6	9	8	8	5	4
Sly03g0215321	M11	NA	3	3	3	1	1	6	6	6	0	1
Sly03g0215341	M12	NA	1	0	1	5	3	1	3	5	53	41
Sly03g0215351	M12	NA	1	1	1	3	2	1	2	7	43	46
Sly03g0215361	M12	NA	162	167	166	658	1178	190	263	265	625	1360
Sly03g0215371	M1	NA	10	11	10	7	4	8	6	6	5	3
Sly03g0215391	M1	NA	29	31	33	52	67	27	27	30	48	45
Sly03g0215401	M12	NA	9	10	12	12	13	18	21	26	48	60
Sly03g0215411	M3	NA	100	99	78	59	70	86	85	81	79	86
Sly03g0215421	M12	NA	3	2	3	11	74	5	7	21	26	66
Sly03g0215431	M1	NA	5	6	6	2	0	4	2	3	3	2
Sly03g0215441	M12	NA	4	3	3	5	5	5	6	5	7	7
Sly03g0215461	M11	NA	3	2	1	2	4	3	3	4	6	5
Sly03g0215471	M1	NA	8	6	7	11	9	6	6	5	7	8
Sly03g0215481	M11	NA	33	33	30	56	96	49	49	56	58	72
Sly03g0215491	M3	NA	139	185	87	30	30	49	54	24	29	33
Sly03g0215501	M3	NA	52	55	54	89	89	41	46	44	57	49
Sly03g0215521	M5	NA	96	89	80	64	54	92	94	88	70	64
Sly03g0215531	M1	NA	4	4	3	5	7	3	2	3	4	4
Sly03g0215541	M3	NA	2	2	1	1	2	1	2	1	1	1
Sly03g0215551	M3	NA	925	894	867	655	455	726	818	779	704	536
Sly03g0215561	M2	SWP73B-like	25	26	22	36	58	19	21	18	40	54
Sly03g0215571	M11	NA	19	20	26	51	47	36	28	45	43	23

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly09g0104261	M22	NA	1	1	1	1	12	1	1	1	1	2
Sly09g0104281	M1	NA	29	81	102	15	9	3	1	3	0	0
Sly09g0104341	M22	NA	1371	650	909	3	2	6816	1831	7329	3	1
Sly09g0104351	M22	NA	201	106	132	1	1	1238	289	1173	2	1
Sly09g0104371	M22	NA	24	10	15	2	1	97	27	103	1	1
Sly09g0104381	M1	NA	86	63	65	11	5	15	2	11	2	3
Sly09g0104391	M1	NA	219	270	287	118	15	7	2	3	1	2
Sly09g0104401	M12	NA	121	108	127	95	54	1502	1394	1831	1010	554
Sly09g0104451	M11	NA	18	17	18	22	25	18	17	20	30	32
Sly09g0104461	M18	NA	44	45	57	61	73	62	55	74	70	82
Sly09g0104471	M3	NA	7	8	7	8	5	7	8	7	7	5
Sly09g0104481	M22	NA	133	85	103	198	352	163	56	136	147	135
Sly09g0104491	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0104501	M12	NA	35	59	38	32	22	60	84	94	93	49
Sly09g0104511	M11	NA	22	26	29	24	32	29	27	36	30	29
Sly09g0104531	M3	NA	25	24	22	14	9	12	18	10	8	3
Sly09g0104541	M11	NA	9	8	13	20	58	21	19	29	36	53
Sly09g0104551	M3	NA	14	14	13	18	22	11	12	13	17	21
Sly09g0104561	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly09g0104601	M7	NA	8	7	3	1	101	5	21	2	3	56
Sly09g0104611	M1	NA	7	7	8	7	2	3	2	2	1	1
Sly09g0104621	M1	NA	4	3	2	2	1	2	1	1	1	1
Sly09g0104641	M1	NA	1	1	1	0	1	1	1	1	0	0
Sly09g0104661	M1	NA	16	12	12	1	0	1	0	0	0	0
Sly09g0104671	M18	GWD3	53	52	72	106	123	82	70	93	66	73
Sly09g0104681	M3	NA	1	1	1	14	10	1	1	1	5	6
Sly09g0104701	M12	NA	57	78	77	111	113	90	112	77	51	63
Sly09g0104711	M3	NA	2	4	6	23	17	3	4	1	0	1
Sly09g0104721	M8	NA	10	11	10	11	9	12	12	9	4	3
Sly09g0104731	M1	NA	11	12	13	13	8	9	7	7	2	1
Sly09g0104741	M1	NA	20	26	18	10	3	14	12	11	8	7
Sly09g0104751	M1	NA	23	23	13	5	4	8	7	6	5	4
Sly09g0104771	M23	NA	28	11	11	3	1	61	32	33	11	1
Sly09g0104781	M11	NA	6	6	7	8	5	8	9	8	6	3
Sly09g0104791	M12	NA	40	37	38	60	64	34	40	41	72	85
Sly09g0104801	M2	NA	201	193	172	281	258	164	198	173	221	197
Sly09g0104811	M7	NA	10	16	6	1	1	19	15	7	3	2
Sly09g0104821	M12	NA	32	31	32	35	32	45	47	49	50	39
Sly09g0104831	M3	NA	2	4	1	1	1	2	1	1	1	0
Sly09g0104841	M1	NA	2	3	2	1	1	2	1	1	1	0
Sly09g0104851	M1	NA	2	3	3	2	1	2	2	2	1	1
Sly09g0104871	M12	NA	10	10	8	15	24	11	13	12	31	32
Sly09g0104881	M12	NA	7	7	8	10	12	14	14	15	36	23
Sly09g0104891	M1	NA	48	46	50	42	59	41	38	44	62	75
Sly09g0104901	M1	NA	114	120	119	83	62	87	88	74	48	48
Sly09g0104911	M18	SISDG44	15	16	17	19	17	18	15	17	16	18
Sly09g0104921	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly09g0104931	M3	NA	80	79	77	88	77	71	76	74	90	88
Sly09g0104941	M11	NA	16	11	18	3	1	40	40	39	3	2
Sly09g0104951	M9	NA	276	261	199	164	117	256	392	242	242	171
Sly09g0104961	M6	NA	623	650	320	229	258	505	902	328	323	407
Sly09g0104981	M3	NA	16	18	17	16	13	16	18	13	17	16
Sly09g0105011	M3	NA	34	32	27	18	21	22	22	21	16	17
Sly09g0105021	M1	NA	1	2	2	1	1	1	1	1	1	1
Sly09g0105031	M16	NA	312	287	299	202	148	274	261	283	274	208
Sly09g0105041	M3	NA	19	20	15	13	11	12	12	10	12	10
Sly09g0105061	M1	NA	10	10	11	11	10	10	9	9	10	7
Sly09g0105091	M22	NA	1	1	1	1	1	2	1	4	1	1
Sly09g0105101	M22	NA	1	1	1	4	2	1	1	1	1	1
Sly09g0105111	M12	NA	27	24	24	38	46	24	26	27	38	38
Sly09g0105121	M11	NA	29	29	30	24	19	35	29	38	19	17
Sly09g0105161	M1	NA	3	4	5	1	1	1	1	1	1	1
Sly09g0105171	M2	NA	10	11	10	17	13	8	10	8	10	8
Sly09g0105181	M22	NA	53	37	48	6	2	73	22	66	8	4
Sly09g0105201	M22	NA	21	14	21	2	1	38	7	51	3	1
Sly09g0105211	M3	NA	50	53	48	52	26	44	51	34	27	17
Sly09g0105221	M1	NA	450	312	466	100	117	265	221	242	100	110
Sly09g0105231	M20	NA	2789	2025	3202	491	369	1816	1351	1735	395	365
Sly09g0105241	M1	NA	91	85	101	89	90	80	74	78	92	93
Sly09g0105251	M1	NA	5	6	6	6	6	4	3	5	5	4
Sly09g0105271	M18	NA	20	23	24	28	33	28	26	32	24	21
Sly09g0105281	M11	NA	30	29	34	36	42	38	33	37	26	10
Sly10g0161731	M1	NA	2	2	2	1	1	1	1	1	0	0
Sly10g0161751	M22	NA	13	8	8	1	0	50	17	58	1	0
Sly10g0161761	M12	NA	1	1	1	1	1	2	2	2	1	0
Sly10g0161771	M14	SlPRR4	8	3	7	2	9	5	4	6	4	3
Sly10g0161781	M12	NA	10	10	13	38	9	9	15	20	137	33
Sly10g0161791	M11	NA	61	53	67	49	35	144	131	151	56	45
Sly10g0161801	M22	NA	3	3	3	2	3	4	2	3	1	1
Sly10g0161811	M22	NA	2	2	2	1	13	2	1	2	1	6
Sly10g0161821	M22	NA	2	2	2	2	18	3	1	3	2	13
Sly10g0161831	M11	NA	2	2	3	2	1	5	4	6	3	2
Sly10g0161841	M11	NA	291	313	477	740	816	726	691	985	1330	2034
Sly10g0161851	M11	NA	41	37	48	93	149	89	82	107	155	199
Sly10g0161871	M3	NA	26	32	26	14	16	25	25	21	11	13
Sly10g0161911	M22	NA	1	1	1	0	0	6	1	4	0	1
Sly10g0161921	M11	NA	55	50	62	85	40	92	90	116	84	34
Sly10g0161941	M9	NA	21	19	18	10	5	41	52	26	3	1
Sly10g0161951	M22	NA	4	2	4	1	0	4	2	5	0	0
Sly10g0161971	M11	NA	78	75	80	107	104	114	119	132	107	105
Sly10g0161991	M12	NA	1	1	1	1	2	2	2	2	3	2
Sly10g0162001	M11	NA	83	77	93	83	75	112	103	128	109	110
Sly10g0162021	M3	PPR-like5	24	26	18	16	13	19	18	16	16	15
Sly10g0162031	M3	NA	25	22	20	17	22	18	18	18	13	17
Sly10g0162041	M12	NA	10	9	8	9	5	21	18	25	9	3
Sly10g0162051	M1	NA	149	136	106	23	12	54	49	41	13	6
Sly10g0162061	M1	TSB-like6	370	285	182	1	1	11	13	2	1	0
Sly10g0162071	M1	NA	14	13	13	12	11	8	4	5	1	1
Sly10g0162081	M1	NA	6	6	6	9	7	2	2	2	5	9
Sly10g0162111	M1	GA2ox8	22	26	17	34	8	1	1	1	1	1
Sly10g0162121	M11	NA	67	62	73	107	180	82	73	92	131	212
Sly10g0162131	M22	NA	5	3	4	3	5	13	4	11	4	7
Sly10g0162191	M22	NA	1	0	1	0	0	3	0	2	0	0
Sly10g0162201	M3	NA	1	1	1	0	0	1	0	0	0	0
Sly10g0162211	M1	NA	2	1	2	0	0	2	1	1	0	0
Sly10g0162221	M3	NA	1	1	1	0	0	1	1	1	0	0
Sly10g0162231	M1	NA	4	3	4	2	1	3	3	3	1	0
Sly10g0162241	M10	NA	24	53	23	2	4	47	55	34	2	5
Sly10g0162251	M18	NA	24	26	26	27	31	34	28	34	31	33
Sly10g0162261	M11	NA	1	1	1	1	1	1	1	1	0	0
Sly10g0162271	M3	NA	150	147	118	103	48	135	155	101	32	9
Sly10g0162281	M3	NA	26	27	21	23	22	24	25	24	24	23
Sly10g0162291	M18	NA	48	48	57	51	56	68	55	72	50	59
Sly10g0162301	M11	NA	3	2	3	1	1	4	2	4	1	1
Sly10g0162311	M1	NA	4	13	4	1	0	0	1	0	0	0
Sly10g0162321	M11	NA	146	154	138	166	175	150	156	151	157	160
Sly10g0162331	M1	NA	16	14	20	12	13	10	9	8	6	7
Sly10g0162341	M1	NA	26	25	29	21	22	19	15	19	9	8
Sly10g0162351	M1	NA	139	136	142	103	96	117	108	114	107	118
Sly10g0162361	M1	NA	15	18	15	12	8	12	12	12	13	10
Sly10g0162381	M1	NA	7	8	8	3	2	2	2	1	1	1
Sly10g0162391	M6	NA	22	32	17	10	6	41	34	14	3	2
Sly10g0162401	M6	NA	52	72	40	15	23	55	62	36	12	23
Sly10g0162411	M22	NA	5	4	7	6	5	6	4	5	4	3
Sly10g0162421	M19	NA	89	91	92	109	118	91	87	96	120	125
Sly10g0162431	M2	NA	39	42	33	38	50	27	34	25	50	48
Sly10g0162441	M11	NA	81	69	76	123	141	94	99	99	111	159
Sly10g0162461	M11	NA	7	6	10	2	1	10	8	10	1	1
Sly10g0162471	M3	NA	27	28	25	19	16	26	24	23	12	8
Sly10g0162481	M1	NA	3	1	3	1	1	2	2	2	1	1
Sly10g0162491	M11	NA	52	45	58	47	31	63	54	61	33

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0215581	M11	NA	73	67	72	70	54	90	86	100	120	68
Sly03g0215591	M3	NA	19	27	6	1	1	15	17	5	1	1
Sly03g0215601	M3	NA	10	23	2	0	1	4	6	2	0	1
Sly03g0215611	M11	NA	463	452	570	427	333	642	567	913	380	296
Sly03g0215621	M7	NA	88	114	85	74	132	98	108	85	69	129
Sly03g0215631	M11	NA	23	19	24	27	31	30	27	38	35	38
Sly03g0215641	M3	NA	48	50	43	48	47	44	48	41	55	54
Sly03g0215651	M13	NA	6	5	7	1	2	5	6	5	2	3
Sly03g0215661	M12	NA	3	4	4	6	10	3	3	4	7	7
Sly03g0215671	M11	NA	35	33	37	36	27	37	36	41	43	28
Sly03g0215681	M11	NA	10	9	11	4	2	12	11	11	2	1
Sly03g0215691	M3	NA	48	51	41	27	18	36	37	33	28	17
Sly03g0215701	M23	NA	1	1	1	1	1	1	1	1	0	0
Sly03g0215711	M11	NA	10	9	10	14	20	12	10	12	24	26
Sly03g0215721	M3	NA	12	13	10	15	17	11	10	11	21	18
Sly03g0215731	M19	NA	12	14	14	19	21	13	12	14	21	18
Sly03g0215741	M19	NA	9	11	10	13	15	10	9	11	17	17
Sly03g0215751	M19	NA	11	14	12	17	18	13	10	12	15	14
Sly03g0215761	M12	NA	1	1	1	2	1	4	2	2	1	1
Sly03g0215821	M1	NA	5	6	6	6	4	4	3	3	3	2
Sly03g0215831	M3	NA	3	5	2	1	1	3	3	1	1	0
Sly03g0215871	M1	NA	55	46	96	920	414	7	3	4	2	2
Sly03g0215881	M3	NA	112	120	88	53	46	83	88	63	38	33
Sly03g0215891	M19	NA	62	64	61	69	69	64	60	64	56	55
Sly03g0215901	M19	SlREF6-1	19	22	23	48	83	21	19	24	61	93
Sly03g0215911	M12	NA	10	10	11	15	19	14	14	14	21	20
Sly03g0215921	M11	NA	14	12	14	15	8	25	21	24	4	1
Sly03g0215941	M2	NA	7	8	6	6	3	5	9	7	9	11
Sly03g0215951	M11	NA	24	23	26	32	22	25	25	38	36	22
Sly03g0215961	M19	NA	129	111	133	91	106	93	84	115	71	94
Sly03g0215971	M11	NA	8	8	12	13	10	14	12	16	7	6
Sly03g0215981	M3	NA	24	24	22	28	29	21	22	21	23	25
Sly03g0215991	M9	NA	16	14	11	8	5	29	30	25	8	6
Sly03g0216001	M11	NA	1	1	1	1	1	7	5	6	1	1
Sly03g0216011	M12	SlPL	21	40	107	2232	2557	189	360	1125	5000	1788
Sly03g0216021	M11	NA	26	26	36	21	4	68	61	81	18	2
Sly03g0216031	M3	NA	76	95	41	3	6	31	36	13	2	4
Sly03g0216041	M3	E4	505	447	366	1454	1119	172	294	235	2844	3032
Sly03g0216051	M22	NA	36	44	18	42	17	110	35	59	58	34
Sly03g0216061	M12	NA	18	21	20	22	26	22	24	24	25	30
Sly03g0216081	M11	NA	16	14	18	13	10	27	24	25	13	6
Sly03g0216111	M9	NA	18	19	18	28	39	21	23	21	43	56
Sly03g0216121	M3	NA	84	85	31	4	5	31	41	7	5	9
Sly03g0216131	M1	NA	6	3	4	0	1	1	1	1	0	0
Sly03g0216141	M1	NA	1	1	1	1	0	1	0	0	0	0
Sly03g0216151	M12	NA	9	7	9	12	20	9	9	11	16	26
Sly03g0216161	M11	NA	32	32	35	56	83	37	31	44	69	130
Sly03g0216171	M11	NA	60	56	62	94	156	88	79	102	128	172
Sly03g0216181	M13	NA	59	54	63	77	111	61	60	64	77	85
Sly03g0216191	M3	NA	12	17	6	3	5	6	7	4	4	2
Sly03g0216201	M1	NA	149	171	130	155	198	86	96	86	173	178
Sly03g0216231	M1	NA	1	1	1	1	1	1	1	0	2	1
Sly03g0216241	M12	NA	1	1	1	2	2	1	1	1	1	1
Sly03g0216251	M12	NA	2	1	1	13	70	9	3	7	96	60
Sly03g0216261	M11	NA	6	5	11	4	1	30	22	43	4	1
Sly03g0216311	M12	NA	14	23	34	551	768	80	94	140	817	800
Sly03g0216321	M22	NA	1	1	1	1	2	2	1	2	1	1
Sly03g0216351	M14	NA	1	1	2	4	28	1	1	1	8	32
Sly03g0216371	M3	NA	23	36	18	1	3	15	16	2	2	4
Sly03g0216391	M15	NA	260	242	225	276	323	260	239	247	405	402
Sly03g0216401	M3	NA	51	58	18	2	1	29	33	6	1	1
Sly03g0216411	M12	NA	47	49	50	64	107	61	62	63	77	91
Sly03g0216421	M9	NA	10	11	9	12	17	10	12	10	22	23
Sly03g0216451	M11	NA	1	2	2	1	1	2	2	2	1	1
Sly03g0216461	M1	NA	10	10	10	9	9	7	5	6	5	5
Sly03g0216471	M11	NA	47	43	46	74	124	59	54	73	104	155
Sly03g0216481	M1	NA	43	43	46	62	70	25	31	28	60	65
Sly03g0216501	M22	NA	1	0	1	1	1	3	0	2	2	0
Sly03g0216521	M1	BIR6-like	5	5	5	6	6	3	3	4	4	5
Sly03g0216531	M1	NA	32	35	40	78	36	1	2	1	2	1
Sly03g0216541	M1	NA	7	7	7	12	8	1	1	1	1	1
Sly03g0216551	M1	NA	28	32	25	28	11	2	2	2	1	1
Sly03g0216561	M11	NA	304	263	272	218	390	310	256	332	211	226
Sly03g0216571	M10	NA	1	2	1	0	0	2	1	1	0	1
Sly03g0216601	M11	NA	65	60	74	68	60	86	77	98	79	82
Sly03g0216611	M1	NA	3	3	2	5	8	1	1	1	2	3
Sly03g0216621	M12	NA	32	28	33	44	53	43	45	50	61	63
Sly03g0216631	M3	NA	7	10	5	7	6	6	8	4	4	6
Sly03g0216641	M3	NA	27	46	23	24	23	30	35	18	9	11
Sly03g0216661	M1	FRO05	10	8	6	2	2	2	2	2	2	1
Sly03g0216671	M12	NA	8	9	5	3	3	10	12	11	14	13
Sly03g0216681	M12	NA	21	36	41	133	179	93	99	113	116	152
Sly03g0216691	M11	NA	61	65	61	56	68	77	70	73	81	114
Sly03g0216701	M1	NA	526	447	408	260	163	302	340	286	212	151
Sly03g0216711	M3	NA	27	31	26	47	42	24	27	24	46	36
Sly03g0216721	M22	NA	18	11	9	1	1	17	8	18	1	1
Sly03g0216731	M3	SlHDA2	1	1	1	1	1	1	1	1	1	1
Sly03g0216741	M1	NA	5	5	4	4	5	4	4	4	4	3
Sly03g0216761	M22	NA	58	19	25	10	5	110	32	71	11	3
Sly03g0216771	M12	NA	34	32	38	41	46	35	39	40	50	55
Sly03g0216781	M23	TAA1-like4	3	2	2	2	1	4	2	2	1	1
Sly03g0216821	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly03g0216831	M3	NA	10	10	8	8	10	8	7	7	10	10
Sly03g0216841	M19	NA	45	44	46	41	40	41	34	41	41	39
Sly03g0216851	M1	NA	63	66	63	40	38	37	40	33	37	38
Sly03g0216871	M1	NA	7	6	6	3	5	5	5	6	5	6
Sly03g0216881	M11	PPR-like39	13	12	14	14	17	13	14	15	16	15
Sly03g0216891	M1	NA	9	9	11	15	61	8	8	9	32	142
Sly03g0216901	M11	NA	2	1	2	1	1	5	4	4	1	0
Sly03g0216911	M11	NA	16	17	24	30	15	65	50	83	40	11
Sly03g0216931	M1	SlJMJ11	13	12	12	11	11	10	10	11	15	13
Sly03g0216941	M1	NA	23	26	11	3	4	3	1	2	1	1
Sly03g0216951	M1	NA	10	11	5	2	2	2	1	1	1	0
Sly03g0216961	M1	NA	4	3	2	1	1	2	1	1	1	0
Sly03g0216971	M11	NA	19	18	19	33	49	18	17	21	31	37
Sly03g0216981	M9	NA	11	10	11	10	9	14	17	13	10	11
Sly03g0216991	M9	NA	19	19	17	16	19	23	30	22	19	21
Sly03g0217001	M11	NA	62	66	66	99	96	66	62	93	245	142
Sly03g0217011	M11	NA	35	35	33	36	35	41	40	46	41	33
Sly03g0217041	M3	NA	12	16	7	6	15	7	7	3	3	13
Sly03g0217061	M12	NA	9	7	9	4	5	13	13	11	5	6
Sly03g0217071	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0217101	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0217121	M11	NA	15	14	37	2	1	25	17	23	1	1
Sly03g0217131	M17	NA	50	48	46	51	58	44	41	54	51	43
Sly03g0217141	M3	NA	3	3	3	2	1	2	2	2	2	2
Sly03g0217151	M2	NA	1	1	1	1	1	1	1	1	1	0
Sly03g0217171	M11	NA	25	19	25	25	30	29	27	31	32	43
Sly03g0217181	M3	NA	36	38	31	21	19	25	26	21	20	19
Sly03g0217191	M11	NA	29	33	30	41	35	35	31	40	46	39
Sly03g0217201	M1	NA	1	1	1	1	1	1	1	0	0	0
Sly03g0217211	M16	NA	520	432	462	447	405	401	394	406	455	457
Sly03g0217221	M12	NA	11	12	10	15	28	15	15	14	27	32
Sly03g0217231	M3	NA	98	111	81	184	155	79	107	56	99	94
Sly03g0217241	M1	NA	8	5	3	1	1	3	2	1	1	1
Sly03g0217261	M11	NA	204	178	183	227	270	218	209	254	272	383
Sly03g0217271	M3	NA	70	73	61	53	45	60	52	49	46	38
Sly03g0217301	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly03g0217311	M1	NA	9	11	10	6	4	8	6	6	3	2
Sly03g0217321	M3	NA	8	10	6	4	2	6	9	4	2	2
Sly03g0217331	M3	NA	42	39	33	17	15	25	27	24	18	22
Sly03g0217351	M3	NA	28	30	26	33	37	26	26	27	33	34
Sly03g0217361	M11	NA	19	19	27	19	18	46	37	59	16	23
Sly03g0217371	M3	NA	89	89	90	133	182	66	77	75	135	180

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0162531	M1	NA	4	5	5	4	2	1	1	1	1	1
Sly10g0162561	M14	NA	60	61	85	101	98	62	56	67	52	94
Sly10g0162571	M3	NA	38	39	37	33	26	27	37	31	22	21
Sly10g0162581	M1	NA	8	6	10	7	3	5	5	5	1	1
Sly10g0162591	M11	NA	199	176	197	200	200	209	182	231	285	302
Sly10g0162601	M1	NA	8	7	9	11	7	2	2	2	2	2
Sly10g0162611	M11	NA	15	14	15	16	20	18	16	19	27	28
Sly10g0162621	M12	NA	21	19	22	26	38	31	28	30	46	70
Sly10g0162631	M1	NA	32	33	29	22	20	25	24	24	26	26
Sly10g0162641	M19	NA	17	18	14	12	9	17	12	13	13	14
Sly10g0162651	M12	NA	7	7	6	6	3	9	11	11	4	2
Sly10g0162661	M11	NA	4	4	4	3	1	6	5	6	3	1
Sly10g0162671	M11	UCK3	38	34	36	29	32	57	54	57	15	11
Sly10g0162681	M2	NA	73	77	69	86	83	50	55	51	94	98
Sly10g0162691	M1	NA	41	44	43	41	38	41	40	38	45	43
Sly10g0162721	M19	NA	3	4	3	4	4	4	3	4	4	3
Sly10g0162731	M11	NA	25	23	35	26	16	35	29	36	10	8
Sly10g0162741	M11	NA	27	23	33	52	63	35	33	46	57	55
Sly10g0162761	M3	NA	13	23	8	7	4	7	19	5	4	11
Sly10g0162771	M3	NA	17	16	14	1	1	9	9	4	1	1
Sly10g0162801	M1	NA	26	25	25	24	23	23	22	24	23	22
Sly10g0162811	M22	NA	2	2	2	1	1	4	1	2	1	1
Sly10g0162821	M3	NA	30	38	30	17	17	12	14	8	8	12
Sly10g0162831	M2	NA	58	62	51	44	47	31	41	30	58	47
Sly10g0162841	M11	NA	35	34	40	62	42	56	60	72	62	51
Sly10g0162851	M1	NA	6	4	5	6	4	3	3	3	35	26
Sly10g0162871	M12	NA	53	53	54	64	50	59	60	56	65	45
Sly10g0162881	M1	NA	403	363	373	268	209	279	273	290	261	226
Sly10g0162891	M23	NA	2	1	1	1	1	7	3	5	1	1
Sly10g0162901	M19	NA	17	19	20	27	36	18	14	19	28	37
Sly10g0162911	M8	NA	23	24	22	22	20	25	27	20	24	21
Sly10g0162931	M1	NA	1	1	1	1	2	1	1	1	1	4
Sly10g0162941	M1	NA	3	3	3	2	3	2	2	2	6	3
Sly10g0162951	M6	SlERF.F1	49	109	42	30	148	50	79	34	24	191
Sly10g0162961	M12	NA	51	50	51	33	34	55	57	60	46	54
Sly10g0162971	M3	NA	8	6	4	3	4	5	6	6	5	6
Sly10g0162981	M11	NA	1	2	1	3	8	2	2	3	12	13
Sly10g0162991	M12	NA	34	34	37	45	55	43	46	49	98	117
Sly10g0163001	M12	NA	20	27	24	36	36	30	34	31	61	58
Sly10g0163011	M11	NA	16	19	20	29	25	23	24	27	47	40
Sly10g0163021	M11	NA	18	16	22	22	28	22	20	24	38	52
Sly10g0163031	M11	NA	16	14	17	18	21	19	15	19	32	32
Sly10g0163041	M18	NA	10	12	13	15	18	13	10	14	25	22
Sly10g0163051	M18	NA	10	13	14	19	15	13	12	17	21	18
Sly10g0163061	M19	NA	16	18	20	21	21	18	15	20	29	25
Sly10g0163071	M11	NA	16	13	14	10	9	15	14	17	18	13
Sly10g0163081	M11	NA	183	109	231	196	41	518	456	686	230	17
Sly10g0163091	M11	NA	39	36	44	44	61	49	44	55	68	96
Sly10g0163101	M19	NA	77	67	86	53	48	89	60	103	53	44
Sly10g0163111	M19	NA	97	90	101	71	72	106	79	121	76	71
Sly10g0163141	M11	NA	129	109	124	118	114	126	117	156	146	128
Sly10g0163171	M11	NA	79	68	90	192	280	70	66	88	182	285
Sly10g0163181	M1	NA	2	3	2	2	3	2	1	2	1	1
Sly10g0163191	M3	NA	20	22	16	16	10	13	15	11	7	5
Sly10g0163201	M3	NA	36	33	32	40	51	31	31	29	47	60
Sly10g0163251	M3	NA	3	2	2	2	2	3	3	2	5	2
Sly10g0163261	M11	NA	7	8	11	15	6	21	18	21	6	1
Sly10g0163281	M11	NA	11	11	13	15	14	15	15	16	20	17
Sly10g0163291	M1	NA	7	7	4	10	15	3	2	2	14	13
Sly10g0163311	M11	NA	18	16	27	46	58	29	30	43	53	63
Sly10g0163321	M22	NA	1	1	1	1	0	2	1	1	1	1
Sly10g0163331	M19	NA	44	43	47	39	36	46	41	49	40	39
Sly10g0163341	M11	TSB-like2	35	32	35	53	94	38	38	40	55	62
Sly10g0163351	M13	NA	23	21	25	27	24	22	22	24	30	28
Sly10g0163381	M1	NA	2	2	2	1	1	1	1	1	0	1
Sly10g0163391	M3	NA	1	1	1	1	1	1	1	1	0	1
Sly10g0163401	M11	NA	61	55	58	62	79	58	49	67	60	74
Sly10g0163411	M8	NA	399	368	308	417	432	354	419	353	539	505
Sly10g0163421	M10	NA	1092	914	774	644	526	1082	1146	826	804	589
Sly10g0163431	M10	NA	562	528	442	347	277	620	651	446	430	251
Sly10g0163441	M11	NA	72	65	86	97	103	100	88	113	118	126
Sly10g0163451	M22	NA	1	1	1	0	1	6	1	4	0	0
Sly10g0163461	M2	NA	18	18	17	20	27	16	18	14	24	35
Sly10g0163471	M12	NA	9	8	9	8	8	10	11	10	8	8
Sly10g0163481	M11	NA	2	2	2	1	0	3	3	4	1	1
Sly10g0163501	M6	NA	37	54	31	28	27	28	34	22	18	18
Sly10g0163511	M12	NA	2	2	2	3	2	2	2	2	2	1
Sly10g0163521	M3	NA	51	46	42	76	89	42	46	37	50	76
Sly10g0163531	M12	NA	6	7	7	7	7	7	8	8	12	9
Sly10g0163541	M1	NA	392	327	312	215	180	224	228	207	203	189
Sly10g0163561	M1	NA	40	38	37	36	30	29	27	31	36	28
Sly10g0163571	M3	GH3-7	2	2	2	2	6	2	2	2	2	5
Sly10g0163601	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly10g0163611	M12	NA	84	92	97	148	198	100	113	134	274	347
Sly10g0163621	M10	NA	29	59	28	13	195	69	106	53	23	459
Sly10g0163631	M3	NA	5	7	4	2	4	4	5	2	3	5
Sly10g0163641	M3	NA	2	3	2	1	2	2	2	2	1	2
Sly10g0163651	M10	NA	27	55	26	18	164	50	84	43	14	268
Sly10g0163661	M3	NA	75	107	62	48	105	46	53	33	44	63
Sly10g0163671	M3	NA	2	4	2	1	1	1	1	1	1	1
Sly10g0163681	M9	NA	15	15	15	17	14	16	17	16	15	12
Sly10g0163691	M1	NA	9	9	6	1	6	1	2	2	1	2
Sly10g0163701	M2	NA	8	8	7	5	11	8	8	8	11	26
Sly10g0163721	M1	NA	71	62	55	48	52	44	42	37	40	42
Sly10g0163731	M12	NA	23	22	26	38	67	26	22	28	41	68
Sly10g0163741	M11	NA	19	20	21	25	26	23	22	24	29	26
Sly10g0163751	M3	NA	18	19	15	21	20	16	17	16	17	16
Sly10g0163761	M21	NA	2	1	1	1	1	1	1	1	1	1
Sly10g0163771	M3	NA	2	2	1	1	1	2	2	1	1	1
Sly10g0163791	M18	NA	16	18	19	22	10	23	21	22	16	8
Sly10g0163801	M3	NA	20	21	19	16	24	19	20	19	35	32
Sly10g0163811	M12	NA	33	31	28	28	44	30	32	32	64	71
Sly10g0163821	M12	NA	8	8	8	11	7	9	10	10	11	11
Sly10g0163831	M13	NA	19	14	19	35	125	13	16	19	49	57
Sly10g0163841	M12	NA	3	4	4	1	2	6	8	5	2	2
Sly10g0163851	M12	NOR	24	50	67	990	682	130	180	279	988	608
Sly10g0163861	M12	NA	24	28	24	64	26	34	29	31	30	21
Sly10g0163871	M11	NA	5	4	7	4	1	18	13	21	3	1
Sly10g0163891	M22	NA	2	1	1	0	0	2	1	2	1	0
Sly10g0163901	M12	NA	52	53	54	62	81	59	66	62	69	87
Sly10g0163921	M3	NA	11	11	7	9	18	7	8	8	6	10
Sly10g0163931	M1	NA	3	3	4	4	11	2	2	2	3	2
Sly10g0163941	M11	NA	20	15	19	35	62	24	23	33	39	68
Sly10g0163951	M9	NA	45	38	37	43	79	43	41	39	71	132
Sly10g0163961	M1	NA	44	45	47	49	49	35	37	37	47	48
Sly10g0163971	M1	NA	13	14	11	12	17	7	8	6	15	16
Sly10g0163981	M2	NA	34	38	24	25	30	22	30	23	31	30
Sly10g0163991	M12	NA	3	4	2	3	3	3	4	4	2	5
Sly10g0164001	M12	NA	48	34	40	18	9	77	79	78	20	16
Sly10g0164021	M12	NA	71	62	71	30	22	147	138	146	39	31
Sly10g0164031	M12	NA	1	1	1	16	38	4	6	14	188	210
Sly10g0164041	M11	NA	3	4	4	4	4	4	4	5	4	3
Sly10g0164051	M12	NA	3	4	4	3	4	6	5	5	3	3
Sly10g0164061	M1	NA	24	27	26	21	11	25	22	23	16	11
Sly10g0164071	M1	NA	121	113	117	51	8	19	14	15	8	2
Sly10g0164081	M1	NA	2	1	2	1	1	1	1	1	1	1
Sly10g0164091	M1	NA	2	1	2	1	1	1	1	1	1	0
Sly10g0164121	M1	NA	13	14	14	37	32	6	8	7	8	6
Sly10g0164141	M19	NA	1	1	1	1	1	1	1	1	1	0
Sly10g0164151	M11	NA	6	7	13	250	481	16	21	32	540	1170
Sly10g0164161	M11	NA	15	14	22	32	13	30	23	37	16

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0217381	M12	NA	34	36	65	223	306	160	159	223	553	633
Sly03g0217391	M3	NA	3	5	3	3	3	2	2	1	1	1
Sly03g0217411	M14	NA	20	19	33	22	13	17	12	19	4	2
Sly03g0217421	M10	NA	6	9	5	6	9	12	13	7	7	7
Sly03g0217431	M11	NA	1	1	2	0	0	4	2	3	1	1
Sly03g0217441	M9	NA	212	219	239	479	549	196	235	247	648	932
Sly03g0217461	M1	PCO2	17	17	14	3	2	4	4	5	2	3
Sly03g0217471	M1	NA	16	16	17	15	14	14	15	16	19	23
Sly03g0217511	M1	NA	1	1	1	2	1	0	1	1	1	0
Sly03g0217521	M3	NA	4	4	3	2	2	3	3	2	1	1
Sly03g0217541	M12	NA	1	1	1	1	1	3	2	1	1	1
Sly03g0217551	M10	NA	111	131	89	53	79	149	200	118	153	223
Sly03g0217581	M11	NA	63	57	62	43	41	105	96	123	72	44
Sly03g0217601	M11	NRT1.2	1	1	1	1	1	1	1	1	1	1
Sly03g0217611	M11	NA	4	3	4	5	6	6	5	6	10	16
Sly03g0217621	M1	NA	473	347	417	543	784	280	367	337	946	966
Sly03g0217631	M1	NA	5	4	5	7	4	3	3	3	4	2
Sly03g0217641	M1	NA	7	9	7	6	7	4	5	4	10	7
Sly03g0217681	M11	NA	15	15	17	33	28	20	19	20	22	18
Sly03g0217691	M11	NA	26	22	45	47	22	60	57	88	80	47
Sly03g0217701	M1	NA	19	18	16	3	3	7	6	4	1	1
Sly03g0217721	M11	NA	14	15	14	18	18	19	17	21	61	91
Sly03g0217731	M7	NA	23	35	22	21	45	25	33	19	45	70
Sly03g0217741	M2	NA	128	165	127	115	148	98	100	85	135	169
Sly03g0217751	M11	NA	47	41	48	34	22	70	63	86	25	23
Sly03g0217771	M2	NA	41	47	32	38	16	43	61	25	10	3
Sly03g0217781	M9	NRT1-2.9	62	155	76	52	14	132	352	188	67	13
Sly03g0217791	M12	NA	1	1	1	1	0	3	3	5	2	1
Sly03g0217801	M9	NA	4	4	3	3	2	7	8	4	1	1
Sly03g0217811	M11	NA	11	9	13	9	5	18	16	21	7	3
Sly03g0217831	M12	NA	7	23	19	112	80	28	40	64	111	25
Sly03g0217841	M12	NA	2	3	3	2	1	4	3	4	1	1
Sly03g0217851	M3	NA	35	38	31	30	29	29	28	25	24	21
Sly03g0217861	M12	NA	2	3	1	1	2	4	5	3	2	1
Sly03g0217871	M3	NA	10	13	7	5	8	8	11	6	5	10
Sly03g0217891	M3	NA	3	5	3	3	2	1	2	1	2	1
Sly03g0217911	M3	NA	1	1	1	2	1	1	1	1	0	1
Sly03g0217921	M8	NA	1	1	1	2	1	1	1	1	1	1
Sly03g0217961	M11	NA	61	54	62	75	93	81	68	88	107	128
Sly03g0217971	M12	NA	2	2	2	2	2	3	3	3	2	2
Sly03g0217981	M12	NA	21	17	20	15	20	31	27	30	19	22
Sly03g0217991	M12	NA	9	8	7	6	7	17	16	18	9	8
Sly03g0218001	M11	NA	242	120	297	8	10	255	219	314	10	12
Sly03g0218021	M11	NA	18	19	24	40	41	49	38	61	55	49
Sly03g0218031	M3	NA	34	37	30	24	26	26	27	27	23	25
Sly03g0218051	M11	NA	25	20	24	23	21	24	23	33	26	23
Sly03g0218061	M1	NA	18	15	16	20	21	12	11	15	18	16
Sly03g0218071	M12	NA	13	8	12	1	1	134	102	111	3	1
Sly03g0218081	M12	NA	1	1	1	1	1	4	3	3	1	1
Sly03g0218091	M11	NA	38	33	43	53	114	90	71	108	44	60
Sly03g0218101	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0218111	M5	SIRR2	4	4	2	1	3	4	3	3	1	1
Sly03g0218121	M11	NA	259	215	313	369	497	403	332	462	441	557
Sly03g0218131	M3	NA	13	14	14	11	12	12	13	13	13	11
Sly03g0218141	M11	OTP43-like	8	7	6	7	7	10	8	8	7	7
Sly03g0218151	M11	E2FD/DEL2-like1	1	1	1	1	1	2	1	1	1	1
Sly03g0218161	M11	NA	20	20	24	27	41	28	25	33	55	71
Sly03g0218171	M12	NA	26	28	26	36	31	46	42	45	28	19
Sly03g0218181	M3	NA	53	52	54	26	16	43	48	41	10	6
Sly03g0218191	M11	NA	186	161	188	181	177	193	188	192	111	134
Sly03g0218321	M1	NA	2	2	2	1	1	1	1	1	0	0
Sly03g0218331	M11	NA	1	2	2	2	2	2	3	2	2	1
Sly03g0218351	M22	NA	7	6	6	2	2	8	6	6	2	3
Sly03g0218361	M12	NA	2	1	2	1	3	3	3	2	1	1
Sly03g0218371	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly03g0218381	M12	NA	9	11	12	17	10	12	12	10	8	5
Sly03g0218391	M23	NA	1	1	1	0	1	1	1	1	1	0
Sly03g0218401	M1	NA	9	14	10	14	12	3	4	3	4	5
Sly03g0218411	M11	NA	1	2	5	240	739	1	2	11	47	356
Sly03g0218451	M12	NA	4	4	2	1	1	9	9	8	1	0
Sly03g0218461	M6	NA	8	18	7	3	5	6	11	4	2	9
Sly03g0218471	M11	NA	21	21	30	73	182	28	27	34	73	155
Sly03g0218481	M5	NA	96	111	63	37	27	83	95	55	16	19
Sly03g0218491	M12	NA	3	4	3	3	2	4	4	4	4	2
Sly03g0218501	M11	NA	25	23	27	10	7	51	42	52	5	8
Sly03g0218511	M1	NA	63	54	67	42	37	45	42	34	23	18
Sly03g0218521	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0218531	M15	NA	26	22	23	20	18	23	23	24	23	17
Sly03g0218541	M3	NA	63	77	56	65	62	58	52	48	63	57
Sly03g0218551	M1	NA	10	9	8	13	15	7	7	7	12	15
Sly03g0218571	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly03g0218581	M1	NA	109	86	77	35	13	88	73	81	20	21
Sly03g0218591	M11	NA	23	23	26	20	18	29	27	30	25	17
Sly03g0218601	M11	NA	21	18	23	21	23	38	31	42	42	34
Sly03g0218611	M1	NA	4	3	4	4	5	3	3	4	5	7
Sly03g0218621	M11	RDR2	25	22	28	27	42	32	25	35	24	43
Sly03g0218631	M11	NA	83	80	104	33	7	222	134	201	4	1
Sly03g0218641	M6	NA	2	4	2	4	12	2	3	2	1	3
Sly03g0218651	M12	NA	88	72	76	105	128	91	100	109	139	144
Sly03g0218661	M3	NA	38	55	28	4	1	17	17	3	1	1
Sly03g0218671	M3	NA	2	1	1	1	2	1	1	1	1	2
Sly03g0218691	M1	NA	4	4	3	1	1	1	1	1	1	0
Sly03g0218701	M1	NA	48	42	39	4	1	4	5	4	1	1
Sly03g0218721	M1	NA	4	4	5	0	0	1	1	0	0	0
Sly03g0218751	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0218761	M11	NA	11	11	12	10	6	19	18	20	9	2
Sly03g0218791	M5	NA	16	15	13	13	27	16	15	14	21	27
Sly03g0218801	M1	NA	11	10	9	7	6	4	6	5	6	5
Sly03g0218811	M12	NA	12	11	11	12	16	13	13	12	18	21
Sly03g0218821	M12	NA	1	1	1	1	0	2	2	2	1	0
Sly03g0218841	M12	NA	18	19	21	27	32	38	38	44	20	26
Sly03g0218851	M12	NA	11	11	13	15	22	52	46	59	16	16
Sly03g0218861	M12	NA	50	47	54	55	81	92	88	105	88	86
Sly03g0218871	M6	NA	4	6	2	1	1	5	5	2	2	3
Sly03g0218881	M7	SRO5	8	12	7	6	10	5	16	9	4	38
Sly03g0218891	M1	NA	96	98	90	55	45	67	69	62	61	47
Sly03g0218901	M22	NA	1	1	1	1	1	1	1	1	0	1
Sly03g0218911	M12	NA	4	4	4	4	7	7	6	6	8	10
Sly03g0218921	M12	NA	17	16	15	17	21	18	17	18	24	36
Sly03g0218931	M11	NA	28	29	30	33	43	36	30	38	42	42
Sly03g0218951	M3	NA	1	1	1	1	2	1	1	1	1	0
Sly03g0218971	M1	NA	1	1	1	1	1	1	1	0	1	0
Sly03g0218981	M11	NA	13	11	17	34	66	44	41	50	48	52
Sly03g0218991	M12	NA	33	33	33	61	98	49	42	47	54	94
Sly03g0219001	M12	NA	91	87	89	150	214	110	115	124	195	250
Sly03g0219011	M12	NA	7	7	8	17	14	14	15	13	12	16
Sly03g0219041	M9	ENOLASE	95	84	58	69	45	182	164	127	20	7
Sly03g0219051	M13	NA	39	36	49	56	65	45	41	58	53	68
Sly03g0219061	M11	NA	13	9	11	4	6	13	11	13	8	6
Sly03g0219081	M1	NA	1	1	2	2	1	0	0	0	0	0
Sly03g0219121	M11	NA	2	1	1	2	9	1	2	2	3	3
Sly03g0219131	M19	NA	3	2	3	5	4	2	3	2	5	4
Sly03g0219141	M13	NA	16	11	15	16	40	11	11	18	21	23
Sly03g0219151	M1	NA	22	21	27	25	60	20	17	23	37	32
Sly03g0219161	M14	NA	50	44	57	58	119	42	37	53	66	53
Sly03g0219171	M3	NA	45	42	27	27	30	28	34	23	31	39
Sly03g0219181	M6	NA	37	92	18	4	20	82	110	14	2	17
Sly03g0219231	M11	NA	9	9	11	20	35	13	12	15	15	26
Sly03g0219241	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0219251	M1	NA	9	10	8	8	8	8	6	8	8	8
Sly03g0219261	M11	NA	24	22	25	31	36	24	26	29	40	37
Sly03g0219271	M11	NA	36	33	32	41	45	40	36	44	43	46
Sly03g0219281	M11	NA	5	4	5	1	1	6	5	5	1	1
Sly03g0219301	M3	NA	46	62	27	83	56	28	39	13	22	26

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0164221	M22	NA	1	1	1	1	0	3	1	2	0	0
Sly10g0164241	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly10g0164251	M1	NA	125	114	127	118	177	93	96	104	138	180
Sly10g0164261	M2	NA	20	18	18	17	14	17	18	18	20	18
Sly10g0164271	M2	NA	23	23	24	36	34	22	30	19	28	30
Sly10g0164331	M2	NA	80	88	77	87	87	53	72	58	92	87
Sly10g0164351	M5	NA	113	181	105	1	1	154	190	24	1	1
Sly10g0164361	M3	NA	37	29	18	4	1	17	16	7	1	1
Sly10g0164371	M19	NA	8	8	8	7	6	7	7	6	6	9
Sly10g0164381	M12	NA	5	5	3	3	2	5	5	5	4	2
Sly10g0164391	M12	NA	202	200	267	512	386	272	381	364	1030	862
Sly10g0164401	M11	NA	21	21	26	53	56	34	29	37	57	51
Sly10g0164411	M1	NA	9	9	12	12	6	9	9	10	6	3
Sly10g0164421	M1	NA	25	27	27	25	29	24	24	24	25	31
Sly10g0164431	M11	NA	201	181	215	321	308	190	200	251	344	323
Sly10g0164441	M1	NA	7	8	10	21	25	7	7	8	34	60
Sly10g0164471	M2	NA	205	208	188	138	121	138	166	118	120	112
Sly10g0164481	M1	NA	8	8	8	5	6	6	6	7	4	3
Sly10g0164491	M1	NA	43	40	47	51	38	24	27	28	35	31
Sly10g0164501	M9	NA	3	3	3	3	2	3	4	3	2	2
Sly10g0164521	M1	NA	16	15	13	15	17	14	11	11	13	17
Sly10g0164541	M12	NA	8	8	8	9	9	9	9	9	10	9
Sly10g0164551	M19	NA	17	19	17	19	21	21	17	17	13	13
Sly10g0164561	M2	NA	233	236	242	187	178	207	241	212	256	301
Sly10g0164581	M11	NA	69	70	75	68	62	141	126	146	151	106
Sly10g0164601	M12	PPR-like19	7	7	7	7	6	8	8	9	10	6
Sly10g0164641	M1	NA	51	52	47	29	29	37	36	37	33	31
Sly10g0164651	M14	NA	23	16	25	10	11	20	16	21	22	26
Sly10g0164661	M13	GA2OX2-like5	25	16	28	10	15	17	21	21	26	26
Sly10g0164681	M12	NA	56	54	54	95	75	49	62	59	80	54
Sly10g0164691	M11	NA	953	1013	1735	4506	892	2495	1683	2646	405	68
Sly10g0164701	M5	NA	41	50	31	31	23	33	41	28	19	19
Sly10g0164741	M11	NA	1	1	1	0	0	6	4	7	0	0
Sly10g0164751	M3	NA	80	68	60	53	59	55	55	54	76	91
Sly10g0164761	M23	NA	2	1	1	1	1	4	2	1	1	1
Sly10g0164771	M11	NA	15	13	16	9	4	17	17	22	5	2
Sly10g0164781	M11	NA	7	6	8	9	10	17	15	21	11	10
Sly10g0164791	M11	NA	85	42	134	33	9	260	202	339	81	9
Sly10g0164801	M11	NA	48	47	57	76	69	63	64	83	157	187
Sly10g0164841	M3	NA	20	20	16	14	7	17	20	15	8	4
Sly10g0164851	M12	NA	7	7	7	11	13	7	8	8	16	17
Sly10g0164861	M1	NA	20	20	21	23	18	18	17	19	32	31
Sly10g0164881	M16	NA	144	126	131	129	163	124	118	140	158	234
Sly10g0164891	M14	NA	61	65	86	78	93	62	49	70	51	49
Sly10g0164901	M19	NA	20	16	17	14	10	17	15	17	7	4
Sly10g0164921	M23	NA	5	2	1	1	0	11	3	2	1	1
Sly10g0164931	M1	NA	14	14	15	12	12	12	12	12	11	11
Sly10g0164951	M11	NA	1	1	1	1	0	1	1	1	0	0
Sly10g0164961	M11	AMI1-like1	13	13	14	19	18	22	21	26	20	20
Sly10g0164971	M1	NA	46	48	54	74	55	44	45	45	60	50
Sly10g0165001	M3	NA	9	11	13	14	8	9	10	7	17	12
Sly10g0165021	M1	NA	5	4	3	1	1	1	0	0	0	0
Sly10g0165031	M1	NA	12	15	15	7	2	1	1	1	1	1
Sly10g0165041	M1	NA	2	2	1	1	1	1	1	1	1	1
Sly10g0165061	M1	NA	14	14	15	19	17	11	10	12	14	11
Sly10g0165071	M23	AOS-like2	1	1	1	0	0	4	3	1	0	0
Sly10g0165081	M12	NA	1	1	1	1	0	8	7	7	1	1
Sly10g0165091	M1	NA	296	274	253	249	200	201	216	203	263	222
Sly10g0165101	M11	NA	46	48	58	82	75	52	57	73	114	115
Sly10g0165121	M17	NA	105	94	100	136	165	100	88	107	120	145
Sly10g0165141	M11	NA	4	3	6	5	5	10	9	12	4	3
Sly10g0165161	M1	NA	2	2	1	1	1	1	1	1	1	0
Sly10g0165171	M11	NA	1	2	3	2	1	1	2	2	2	1
Sly10g0165181	M11	NA	6	4	5	6	7	7	6	7	6	5
Sly10g0165191	M12	NA	25	24	24	31	25	37	33	36	27	29
Sly10g0165211	M2	NA	1	1	2	0	1	1	2	1	0	0
Sly10g0165221	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0165231	M3	NA	17	14	9	4	2	8	7	6	2	2
Sly10g0165241	M1	NA	106	103	107	55	46	50	41	41	23	19
Sly10g0165261	M1	NA	1	1	1	0	0	0	1	1	1	0
Sly10g0165271	M12	NA	45	42	49	60	78	59	57	63	87	153
Sly10g0165281	M1	NA	174	177	167	144	144	121	135	123	172	171
Sly10g0165301	M1	NA	7	8	15	7	3	0	0	1	1	0
Sly10g0165311	M1	SlGLK2	12	12	23	11	5	1	0	0	1	1
Sly10g0165331	M12	NA	9	10	9	10	10	10	12	11	13	13
Sly10g0165341	M22	NA	3	2	2	1	1	3	2	2	1	1
Sly10g0165351	M22	NA	2	1	1	0	1	11	1	5	0	0
Sly10g0165371	M1	NA	34	35	22	14	19	3	4	2	3	6
Sly10g0165381	M1	NA	16	14	13	6	7	3	3	3	3	4
Sly10g0165391	M1	NA	16	15	12	8	13	7	7	8	6	8
Sly10g0165441	M6	NA	34	59	29	1	0	33	37	14	1	1
Sly10g0165481	M1	NA	1	1	1	0	0	0	0	0	0	0
Sly10g0165491	M6	NA	53	76	58	49	52	62	58	46	30	38
Sly10g0165541	M1	NA	39	43	51	31	22	37	40	36	27	22
Sly10g0165551	M2	NA	14	12	13	13	12	12	13	12	14	11
Sly10g0165561	M11	NA	8	6	6	2	4	9	9	7	3	5
Sly10g0165581	M3	NA	81	83	57	23	22	40	40	31	20	19
Sly10g0165601	M3	NA	35	53	48	3	13	16	42	15	4	20
Sly10g0165611	M1	NA	1	1	2	0	1	1	1	1	1	0
Sly10g0165621	M1	NA	3	4	4	1	1	2	1	1	1	1
Sly10g0165631	M3	NA	19	19	15	10	14	14	18	13	11	17
Sly10g0165641	M11	NA	158	100	203	68	138	313	284	435	100	248
Sly10g0165651	M20	NA	2	2	3	0	0	2	2	2	1	1
Sly10g0165661	M1	NA	29	27	28	27	35	25	22	22	37	49
Sly10g0165671	M19	NA	16	16	15	15	17	14	10	14	17	20
Sly10g0165681	M3	NA	1	2	1	1	1	1	1	1	0	1
Sly10g0165711	M1	NA	5	5	5	1	1	1	1	1	1	0
Sly10g0165721	M3	NA	12	13	8	4	2	6	5	4	2	1
Sly10g0165731	M12	NA	5	7	7	45	50	15	19	29	107	72
Sly10g0165741	M12	NA	9	11	9	13	16	10	11	13	35	27
Sly10g0165751	M7	NA	1	1	1	1	2	1	1	1	2	1
Sly10g0165761	M3	NA	33	38	34	72	87	28	35	30	104	109
Sly10g0165781	M12	NA	3	3	3	2	1	4	4	4	3	2
Sly10g0165791	M12	NA	2	2	2	1	1	2	2	2	3	2
Sly10g0165801	M3	GH3-10	10	8	6	1	1	5	5	3	1	0
Sly10g0165821	M1	NA	3	2	3	2	3	2	2	2	2	2
Sly10g0165851	M12	NA	95	116	114	98	73	106	138	120	107	95
Sly10g0165861	M11	NA	97	112	100	101	69	117	119	122	97	85
Sly10g0165871	M3	NA	5	5	4	5	5	3	3	3	3	3
Sly10g0165911	M3	NA	7	7	6	4	4	5	6	5	4	3
Sly10g0165921	M13	NA	2	2	2	2	3	2	2	2	2	2
Sly10g0165931	M12	NA	16	15	14	26	25	18	20	18	37	30
Sly10g0165961	M2	NA	29	35	19	20	29	16	22	14	73	119
Sly10g0165981	M12	NA	32	32	39	94	134	47	58	76	312	354
Sly10g0165991	M14	NA	57	56	73	62	60	58	56	71	69	83
Sly10g0166011	M1	NA	1	1	2	4	7	1	1	1	1	1
Sly10g0166021	M13	NA	5	3	9	18	46	6	5	7	2	8
Sly10g0166031	M1	NA	5	4	4	3	6	3	2	4	1	2
Sly10g0166041	M14	NA	3	3	5	4	5	3	2	4	2	2
Sly10g0166091	M10	NA	35	57	28	47	46	62	89	50	40	70
Sly10g0166101	M11	NA	33	28	45	96	43	106	98	151	109	35
Sly10g0166111	M11	NA	5	4	6	5	5	6	5	7	5	5
Sly10g0166121	M11	NA	24	21	27	27	16	35	31	36	31	30
Sly10g0166131	M1	NA	24	22	28	27	31	17	19	20	29	29
Sly10g0166151	M1	NA	39	43	41	34	34	19	15	19	11	7
Sly10g0166171	M19	NA	41	42	43	46	37	37	35	42	37	33
Sly10g0166211	M3	NA	10	8	8	7	7	6	7	6	7	11
Sly10g0166221	M3	NA	50	37	38	34	36	36	36	33	42	43
Sly10g0166231	M23	NA	1	1	1	1	0	2	1	1	1	0
Sly10g0166241	M1	NA	270	257	286	311	249	200	216	220	312	222
Sly10g0166251	M1	NA	29	31	29	18	19	13

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0219311	M3	NA	33	30	31	18	18	29	35	24	15	20
Sly03g0219321	M12	NA	62	51	27	3	2	79	76	67	7	4
Sly03g0219331	M9	NA	9	11	8	10	9	13	17	11	15	13
Sly03g0219341	M20	NA	4	4	10	194	166	4	4	6	34	13
Sly03g0219351	M12	NA	7	6	6	33	36	8	9	9	10	5
Sly03g0219371	M1	NA	12	14	14	7	8	9	9	9	9	7
Sly03g0219401	M11	NA	24	20	28	25	26	35	28	42	36	43
Sly03g0219411	M1	NA	7	5	6	4	1	1	1	1	0	0
Sly03g0219421	M3	NA	21	22	13	17	15	16	20	11	12	10
Sly03g0219431	M1	NA	2	3	1	1	0	1	1	0	0	0
Sly03g0219441	M12	FUL2	88	91	96	106	155	93	116	115	185	265
Sly03g0219451	M1	MADS1	108	109	104	50	18	20	15	14	3	2
Sly03g0219461	M1	NA	14	16	14	3	2	4	5	3	1	1
Sly03g0219481	M1	NA	43	60	23	3	1	3	4	1	1	1
Sly03g0219611	M3	NA	3	4	2	1	0	1	1	1	1	1
Sly03g0219621	M22	NA	1	1	1	1	1	3	1	3	1	1
Sly03g0219631	M12	NA	9	10	9	6	3	23	26	18	8	3
Sly03g0219641	M1	PNM1	25	25	23	27	30	19	19	20	18	20
Sly03g0219651	M11	NA	6	5	5	3	1	12	11	14	4	1
Sly03g0219661	M11	NA	1	1	1	0	0	3	1	2	0	0
Sly03g0219671	M1	NA	78	65	57	33	32	20	28	15	5	2
Sly03g0219681	M1	NA	18	19	18	32	26	14	11	11	13	7
Sly03g0219691	M11	NA	140	109	148	122	51	155	154	204	127	34
Sly03g0219701	M12	NA	14	14	13	12	16	16	16	15	23	25
Sly03g0219711	M22	NA	4	4	4	1	1	7	5	7	1	1
Sly03g0219761	M11	NA	166	123	149	139	144	216	186	278	158	191
Sly03g0219771	M3	NA	137	137	156	178	165	93	127	103	179	154
Sly03g0219781	M1	NA	2	4	2	1	1	1	1	1	1	1
Sly03g0219791	M11	NA	6	4	6	1	1	10	9	9	1	1
Sly03g0219801	M3	NA	3	5	2	2	2	3	3	3	2	2
Sly03g0219811	M3	NA	11	12	9	8	8	6	6	3	3	5
Sly03g0219821	M11	NA	12	8	10	12	11	10	10	12	9	10
Sly03g0219841	M18	NA	14	14	14	12	11	15	13	16	9	9
Sly03g0219851	M12	NA	189	183	181	203	191	208	226	207	193	179
Sly03g0219861	M11	NA	3	3	3	1	1	4	6	7	1	1
Sly03g0219871	M19	NA	23	22	25	19	18	20	19	23	21	20
Sly03g0219881	M13	SIHDA9	33	31	35	28	28	31	33	34	30	30
Sly03g0219891	M20	NA	3	2	5	1	1	3	2	2	1	0
Sly03g0219901	M11	NA	23	14	22	3	1	32	25	35	1	1
Sly03g0219911	M11	NA	7	6	7	5	4	9	8	8	7	7
Sly03g0219921	M9	NA	2	3	3	1	1	4	7	3	1	1
Sly03g0219931	M19	NA	8	8	9	5	6	7	5	9	9	14
Sly03g0219941	M1	NA	5	4	4	1	1	2	2	1	0	0
Sly03g0219951	M1	NA	3	3	6	186	87	1	1	2	3	3
Sly03g0219961	M4	NA	26	17	38	361	358	66	37	46	153	271
Sly03g0219971	M22	NA	67	67	60	63	72	71	60	67	56	65
Sly03g0219981	M19	NA	23	25	24	26	26	23	20	22	20	22
Sly03g0219991	M11	NA	4	4	7	3	4	7	6	7	7	5
Sly03g0220011	M12	NA	4	3	4	3	3	5	5	5	6	6
Sly03g0220021	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0220031	M22	NA	1	1	1	1	1	3	1	3	1	1
Sly03g0220051	M12	NA	5	5	6	4	3	6	6	6	5	3
Sly03g0220081	M16	NA	824	695	767	542	432	674	662	773	686	598
Sly03g0220091	M9	NA	40	58	33	47	75	72	120	55	40	105
Sly03g0220101	M3	NA	5	5	2	2	2	1	1	1	1	1
Sly03g0220111	M19	NA	19	20	19	19	18	19	16	17	17	16
Sly03g0220151	M3	NA	35	43	31	19	21	29	30	27	23	27
Sly03g0220161	M1	NA	13	12	12	8	5	7	8	8	6	4
Sly03g0220181	M10	NA	21	23	19	23	19	24	23	22	20	17
Sly03g0220191	M22	NA	1	1	1	1	1	3	1	3	1	0
Sly03g0220201	M3	NA	10	9	6	7	9	6	5	5	10	10
Sly03g0220211	M12	NA	1	1	1	1	4	2	1	1	2	2
Sly03g0220221	M11	NA	24	19	27	28	30	24	20	28	16	24
Sly03g0220241	M1	NA	43	40	45	65	62	34	34	39	69	64
Sly03g0220251	M1	NA	6	4	6	14	13	1	1	1	1	3
Sly03g0220261	M1	NA	13	15	13	24	27	11	11	11	15	16
Sly03g0220271	M1	NA	17	21	18	10	11	16	15	17	16	16
Sly03g0220291	M1	NA	14	13	20	15	21	12	11	11	11	11
Sly03g0220301	M1	NA	2	2	2	2	2	2	1	1	2	2
Sly03g0220311	M12	NA	14	13	16	12	20	15	15	16	18	25
Sly03g0220321	M11	NA	16	15	19	12	15	23	22	28	42	37
Sly03g0220341	M6	NA	38	72	32	9	5	69	80	27	9	10
Sly03g0220351	M7	NA	1	1	1	0	0	1	1	1	1	0
Sly03g0220361	M11	NA	135	138	141	135	106	139	136	151	116	86
Sly03g0220371	M11	NA	7	6	8	3	1	11	11	13	3	1
Sly03g0220381	M11	NA	557	489	518	339	331	710	636	948	884	888
Sly03g0220391	M1	NA	2	3	2	1	1	1	2	2	1	1
Sly03g0220401	M19	NA	25	28	29	40	27	30	26	35	35	27
Sly03g0220411	M12	NA	34	37	34	55	50	36	38	42	54	51
Sly03g0220421	M22	NA	6	4	4	1	1	22	8	22	1	1
Sly03g0220431	M11	NA	92	80	103	115	140	108	85	124	139	186
Sly03g0220441	M12	NA	1	1	1	2	4	1	2	2	4	3
Sly03g0220451	M11	NA	14	15	17	24	28	18	18	20	23	24
Sly03g0220461	M9	NA	14	13	11	11	16	18	20	17	16	25
Sly03g0220471	M7	NA	38	45	29	32	56	46	56	34	25	57
Sly03g0220491	M11	NA	181	171	214	191	228	205	220	251	277	377
Sly03g0220501	M12	SIPRR1	52	61	50	66	38	64	65	66	52	37
Sly03g0220521	M10	NA	1	1	1	1	1	2	2	1	1	1
Sly03g0220531	M14	NA	3	2	3	2	2	3	2	3	3	2
Sly03g0220541	M1	NA	1	1	2	1	1	1	2	1	1	1
Sly03g0220551	M11	SISAND	47	50	48	43	45	53	50	51	47	51
Sly03g0220561	M11	NA	78	69	81	111	140	171	155	182	117	150
Sly03g0220571	M11	NA	2	2	2	1	1	5	3	4	1	1
Sly03g0220581	M12	NA	18	19	19	19	18	22	22	20	13	14
Sly03g0220591	M23	NA	2	1	1	1	1	2	2	2	1	1
Sly03g0220601	M12	NA	12	13	13	41	32	33	43	42	60	44
Sly03g0220631	M12	ACTH	63	50	57	8	7	80	122	109	10	17
Sly03g0220651	M22	expansin 10	2	1	1	1	1	2	1	2	1	1
Sly03g0220661	M11	NA	19	9	30	13	3	108	92	128	21	2
Sly03g0220671	M12	NA	1	1	1	0	1	1	1	1	1	1
Sly03g0220691	M2	NA	42	55	40	6	60	15	34	13	18	45
Sly03g0220701	M2	NA	65	88	52	12	39	19	45	6	10	29
Sly03g0220711	M1	NA	26	14	23	4	6	6	5	9	1	3
Sly03g0220731	M1	NA	3	3	4	1	0	1	1	1	0	0
Sly03g0220761	M11	NA	25	15	33	74	92	92	70	123	64	53
Sly03g0220771	M8	NA	31	32	27	66	75	32	38	26	74	74
Sly03g0220781	M1	NA	3	3	3	3	2	2	2	3	2	2
Sly03g0220801	M17	NA	62	51	62	34	25	47	42	55	34	25
Sly03g0220811	M6	NA	30	41	22	17	21	23	30	19	19	17
Sly03g0220821	M1	NA	15	15	13	10	9	3	3	2	2	3
Sly03g0220841	M12	NA	1	1	1	1	0	1	1	1	0	0
Sly03g0220861	M1	NA	10	17	14	22	16	3	3	2	1	1
Sly03g0220871	M2	NA	107	105	91	113	270	74	82	60	158	236
Sly03g0220911	M1	NA	25	25	21	29	37	18	16	18	27	32
Sly03g0220921	M12	NA	13	12	13	19	19	14	14	14	18	17
Sly03g0220931	M11	NA	1	1	1	1	1	2	1	2	1	1
Sly03g0220941	M1	NRP2-like2	55	65	51	28	20	29	33	26	33	27
Sly03g0220951	M12	NA	16	18	19	10	7	37	37	38	5	3
Sly03g0220961	M11	NA	33	36	36	19	9	76	78	82	8	4
Sly03g0220971	M12	NA	5	6	5	4	10	7	7	8	21	31
Sly03g0220981	M12	NA	1	1	1	28	32	2	5	10	663	623
Sly03g0220991	M12	NA	504	474	813	389	239	15877	18006	16948	6833	5043
Sly03g0221001	M1	NA	2	3	2	1	2	2	2	2	1	1
Sly03g0221011	M12	NA	18	15	17	11	4	26	26	29	22	13
Sly03g0221021	M11	NA	17	15	18	13	5	25	23	29	20	8
Sly03g0221031	M3	NA	2	6	2	2	1	2	1	2	2	1
Sly03g0221061	M1	NA	2	1	4	0	0	0	0	1	0	0
Sly03g0221091	M14	NA	12	12	13	6	4	11	10	14	2	4
Sly03g0221101	M12	NA	16	15	18	12	6	23	24	26	6	3
Sly03g0221111	M11	NA	56	60	82	136	247	63	81	88	163	346
Sly03g0221121	M1	HVA22A-like2	50	41	62	64	71	42	40	47	51	77
Sly03g0221141	M12	NA	5	4	6	14	14	11	11	11	26	18
Sly03g0221151	M22	NA	1	1	1	1	1	1	1	1	0	1
Sly03g0221161	M1	NA	67	71	68	36	33	36	38	35	34	35

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0166341	M11	NA	212	175	258	132	68	322	255	339	70	37
Sly10g0166351	M1	NA	49	50	45	48	34	38	35	36	41	36
Sly10g0166361	M12	NA	13	13	12	9	6	14	14	16	22	22
Sly10g0166381	M1	NA	11	9	12	6	7	6	6	7	5	6
Sly10g0166391	M11	NA	22	18	32	18	7	53	51	64	17	10
Sly10g0166401	M11	NA	11	14	11	14	17	26	25	27	26	18
Sly10g0166411	M3	NA	11	11	11	15	17	10	11	9	17	24
Sly10g0166421	M10	NA	22	34	25	14	16	28	38	20	24	33
Sly10g0166431	M19	NA	34	35	41	23	17	36	31	38	15	14
Sly10g0166441	M1	NA	5	4	5	4	4	1	1	1	0	1
Sly10g0166451	M1	NA	4	4	4	2	1	1	1	1	1	0
Sly10g0166471	M3	SIERF.F5	504	370	177	11	117	100	115	47	10	145
Sly10g0166481	M3	NA	109	85	50	3	24	21	28	9	2	34
Sly10g0166491	M3	NA	8	8	6	4	3	8	7	6	4	3
Sly10g0166531	M12	NA	1	0	1	1	1	1	2	1	2	2
Sly10g0166541	M3	NA	17	15	15	13	10	16	15	15	16	16
Sly10g0166551	M23	NA	1	1	1	0	0	1	1	1	1	1
Sly10g0166561	M3	NA	125	115	108	68	77	94	96	85	67	81
Sly10g0166571	M1	NA	90	246	261	65	3	20	7	8	1	1
Sly10g0166581	M3	NA	43	49	38	43	52	29	33	25	51	52
Sly10g0166591	M5	NA	49	62	25	20	23	53	68	29	27	35
Sly10g0166601	M1	LIF2-like1	68	69	72	68	65	58	58	58	59	61
Sly10g0166611	M13	NA	7	6	9	13	19	7	6	7	15	16
Sly10g0166621	M1	NA	18	31	20	8	1	1	1	1	1	0
Sly10g0166641	M1	NA	3	4	3	2	1	1	1	1	1	1
Sly10g0166661	M3	NA	38	36	35	24	25	27	23	23	26	27
Sly10g0166671	M1	NA	48	48	13	1	1	2	1	1	0	0
Sly10g0166731	M12	NA	84	84	81	78	88	103	97	103	133	132
Sly10g0166741	M3	NA	10	9	6	4	3	8	10	5	2	3
Sly10g0166751	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0166781	M1	NA	2	2	2	1	1	0	1	0	0	1
Sly10g0166791	M1	NA	4	5	4	7	5	2	2	2	3	5
Sly10g0166801	M1	NA	16	15	14	1	1	5	7	4	4	4
Sly10g0166821	M1	NA	15	16	14	7	5	7	8	5	4	4
Sly10g0166831	M1	NA	338	354	221	10	6	133	46	63	6	9
Sly10g0166841	M12	NA	14	11	12	12	11	16	18	19	14	8
Sly10g0166851	M12	NA	1	1	1	7	23	3	3	3	62	66
Sly10g0166871	M22	NA	2	1	2	0	1	7	1	6	0	0
Sly10g0166921	M22	NA	1	0	1	0	0	2	0	1	0	0
Sly10g0166941	M1	NA	21	22	19	22	27	16	14	15	19	22
Sly10g0167001	M6	NA	7	21	10	1	9	9	17	4	1	6
Sly10g0167021	M11	NA	12	11	13	14	22	26	22	28	17	12
Sly10g0167031	M14	NA	5	3	7	1	1	4	3	4	1	1
Sly10g0167071	M22	GH3-12	1	0	1	1	1	1	1	1	0	1
Sly10g0167081	M19	GH3-14	19	21	24	19	12	21	16	22	14	15
Sly10g0167091	M11	NA	72	63	83	83	93	79	71	90	80	96
Sly10g0167101	M1	NA	1	1	1	0	1	1	1	1	0	1
Sly10g0167111	M18	NA	8	9	9	10	10	10	10	12	9	7
Sly10g0167121	M11	NA	10	10	10	12	12	12	12	14	15	13
Sly10g0167151	M11	NA	2	2	2	1	0	9	9	17	2	2
Sly10g0167161	M7	NA	122	212	93	47	119	157	336	128	75	360
Sly10g0167171	M12	NA	6	6	6	4	6	28	30	28	9	7
Sly10g0167181	M21	NA	2	1	2	1	1	2	1	1	1	1
Sly10g0167191	M11	NA	28	22	24	34	30	38	35	44	22	32
Sly10g0167211	M1	NA	62	60	52	47	43	38	39	33	43	44
Sly10g0167231	M6	NA	20	29	10	3	4	12	15	6	2	2
Sly10g0167241	M9	NA	6	5	4	2	1	11	14	12	6	2
Sly10g0167271	M2	NA	46	43	48	48	54	37	46	40	49	63
Sly10g0167281	M12	NA	4	6	3	4	2	7	8	7	4	2
Sly10g0167301	M7	NA	1	4	2	1	2	2	3	3	1	3
Sly10g0167351	M1	NA	1	1	1	3	2	1	1	1	1	1
Sly10g0167361	M21	NA	2	2	3	1	1	2	1	2	0	0
Sly10g0167371	M22	NA	4	3	4	1	1	12	5	15	1	1
Sly10g0167391	M3	NA	41	41	27	21	22	31	31	24	24	27
Sly10g0167401	M22	NA	2	1	1	1	0	2	1	2	1	0
Sly10g0167421	M19	NA	31	30	34	36	48	30	27	31	26	28
Sly10g0167431	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0167441	M11	NA	11	11	12	17	12	13	11	12	15	10
Sly10g0167451	M11	NA	116	114	118	104	101	130	129	137	129	129
Sly10g0167461	M10	NA	142	167	105	50	35	207	306	143	72	96
Sly10g0167471	M11	NA	1	1	2	1	1	7	6	10	6	3
Sly10g0167481	M11	NA	1	2	2	1	1	19	22	30	18	8
Sly10g0167491	M22	NA	8	1	8	1	0	63	1	35	1	0
Sly10g0167501	M22	NA	2	0	2	0	0	12	1	9	0	0
Sly10g0167511	M22	NA	5	1	3	0	0	33	1	20	0	0
Sly10g0167551	M3	NA	14	13	13	16	22	12	13	12	16	21
Sly10g0167561	M3	NA	31	40	25	38	45	16	19	16	99	81
Sly10g0167611	M12	NA	3	3	3	5	6	6	7	6	16	12
Sly10g0167681	M13	NA	115	111	172	531	834	171	159	262	277	317
Sly10g0167731	M3	NA	2	3	1	2	2	1	1	1	1	1
Sly10g0167751	M1	NA	4	3	4	3	4	2	1	2	2	4
Sly10g0167891	M3	NA	156	168	148	154	313	67	69	57	201	439
Sly10g0167921	M9	NA	4	5	4	5	3	4	5	4	3	3
Sly10g0167931	M18	NA	13	13	11	10	7	12	11	14	6	4
Sly10g0167941	M12	NA	56	55	53	68	76	63	65	62	83	93
Sly10g0167951	M3	NA	14	17	10	3	3	6	6	5	1	1
Sly10g0167961	M12	NA	6	5	6	4	5	6	6	7	9	11
Sly10g0167971	M2	NA	8	7	8	4	7	7	8	7	10	17
Sly10g0167991	M12	NA	1	1	1	5	6	4	3	3	12	17
Sly10g0168001	M12	NA	2	1	1	6	9	5	4	4	21	35
Sly10g0168021	M12	NA	1	1	1	1	1	1	1	2	1	1
Sly10g0168041	M11	NA	1	1	1	1	0	2	1	2	1	0
Sly10g0168071	M1	NA	93	94	88	92	79	82	81	80	81	72
Sly10g0168121	M3	NA	37	38	36	26	27	38	38	31	36	53
Sly10g0168141	M12	NA	12	14	13	18	17	15	16	15	18	15
Sly10g0168471	M12	NA	11	13	12	19	17	18	19	18	22	21
Sly10g0168481	M12	NA	1	1	1	0	0	1	1	1	0	1
Sly10g0168491	M8	NA	3	3	3	2	4	3	3	3	6	16
Sly10g0168501	M12	NA	65	59	70	94	46	264	302	264	287	139
Sly10g0168511	M11	NA	51	45	53	47	55	56	55	59	69	88
Sly10g0168641	M11	PP2-A11	17	21	28	56	50	45	53	94	89	66
Sly10g0168651	M12	NA	4	5	4	41	24	7	12	10	27	28
Sly10g0168661	M12	NA	27	43	51	425	77	138	360	199	1001	1174
Sly10g0168671	M12	NA	3	2	3	31	15	5	8	6	18	18
Sly10g0168701	M7	NA	14	22	17	16	37	16	25	18	29	111
Sly10g0168711	M1	NA	10	10	12	9	14	10	10	10	21	29
Sly10g0168811	M12	NA	3	3	4	3	3	4	4	4	3	4
Sly10g0168821	M19	NA	5	6	6	4	4	6	5	5	6	6
Sly10g0168831	M12	NA	6	5	6	5	4	6	6	5	6	8
Sly10g0168841	M1	NA	2	2	2	6	5	1	1	1	1	1
Sly10g0168861	M1	NA	1	2	3	30	44	1	1	0	1	2
Sly10g0168881	M2	NA	28	28	26	29	31	22	24	20	19	20
Sly10g0168931	M3	NA	1	3	1	1	0	1	1	0	0	0
Sly10g0168951	M15	NA	124	114	123	133	103	110	120	117	146	128
Sly10g0168961	M1	NA	3	2	3	1	1	1	1	1	0	1
Sly10g0168981	M11	NA	57	57	84	60	26	144	112	169	29	5
Sly10g0168991	M3	NA	3	3	3	2	2	2	2	2	1	2
Sly10g0169001	M12	NA	3	3	3	1	1	4	3	4	2	2
Sly10g0169031	M6	SAUR71	1	2	1	1	1	1	1	1	1	1
Sly10g0169041	M2	NA	35	36	33	22	16	24	26	20	18	10
Sly10g0169191	M19	NA	45	46	49	49	52	40	34	42	43	44
Sly10g0169231	M12	NA	7	7	8	6	7	11	9	9	10	6
Sly10g0169241	M19	NA	4	5	5	3	4	6	5	5	5	3
Sly10g0169271	M12	NA	10	12	11	22	43	18	19	18	31	54
Sly10g0169281	M12	NA	4	4	4	6	6	9	11	9	11	11
Sly10g0169291	M12	NA	39	39	41	48	57	48	55	52	40	44
Sly10g0169331	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0169411	M12	NA	2	3	3	2	1	4	4	4	2	1
Sly10g0169471	M12	NA	1	1	1	2	2	1	1	1	1	1
Sly10g0169481	M12	NA	5	4	7	16	11	4	6	14	37	17
Sly10g0169501	M1	NA	26	16	18	1	1	2	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0221171	M12	NA	37	28	13	3	3	113	103	78	23	31
Sly03g0221211	M1	NA	3	3	2	3	4	2	2	2	4	6
Sly03g0221221	M1	NA	14	17	15	10	16	10	11	11	16	32
Sly03g0221231	M3	NA	1	1	1	1	1	1	1	0	1	1
Sly03g0221241	M22	NA	1	0	1	1	1	1	1	3	1	0
Sly03g0221251	M13	NA	41	45	65	179	137	61	69	98	180	131
Sly03g0221261	M19	NA	1	2	2	4	2	2	1	2	10	4
Sly03g0221271	M11	NA	7	6	13	39	22	9	11	22	80	52
Sly03g0221281	M3	NA	44	56	46	47	39	32	39	35	56	83
Sly03g0221291	M22	NA	5	4	3	1	1	5	4	4	1	1
Sly03g0221301	M3	NA	125	200	113	45	33	98	96	41	5	7
Sly03g0221311	M3	NA	3	3	2	0	0	2	2	2	0	0
Sly03g0221321	M12	NA	24	23	25	34	73	27	32	32	19	33
Sly03g0221331	M19	NA	3	3	3	3	2	2	3	3	2	2
Sly03g0221341	M10	NA	26	26	19	16	16	30	32	22	18	19
Sly03g0221351	M11	NA	12	11	13	12	12	14	12	15	19	17
Sly03g0221361	M11	NA	27	24	23	51	157	29	27	32	87	201
Sly03g0221371	M22	NA	1	1	1	1	2	1	1	1	1	1
Sly03g0221381	M8	NA	161	200	152	154	272	143	335	126	254	462
Sly03g0221391	M8	NA	46	48	41	48	54	42	55	43	57	64
Sly03g0221411	M12	NA	1	1	1	1	1	1	2	1	2	1
Sly03g0221421	M12	NA	25	38	34	143	161	33	62	76	291	274
Sly03g0221431	M5	NA	20	16	18	12	18	18	21	15	30	25
Sly03g0221451	M12	NA	3	3	3	8	16	3	5	4	10	22
Sly03g0221461	M14	NA	234	226	286	137	114	216	168	278	36	49
Sly03g0221471	M11	NA	37	35	42	60	104	48	51	62	76	88
Sly03g0221481	M1	NA	8	9	8	1	0	1	2	1	1	0
Sly03g0221491	M3	NA	227	337	148	14	3	123	101	31	10	4
Sly03g0221501	M12	NA	12	13	13	7	13	11	14	13	11	30
Sly03g0221511	M8	SIPHP2	1	1	1	1	0	1	2	1	0	1
Sly03g0221531	M1	NA	31	27	11	1	1	5	4	2	1	0
Sly03g0221541	M1	NA	101	103	54	85	52	20	14	8	2	2
Sly03g0221551	M1	SITPL4	123	123	106	102	127	76	66	59	97	113
Sly03g0221561	M1	NA	65	66	69	51	65	45	48	36	41	71
Sly03g0221571	M1	NA	2	1	2	0	0	1	1	1	0	1
Sly03g0221581	M1	NA	88	84	84	74	88	69	73	67	82	82
Sly03g0221591	M3	NA	40	53	31	43	105	32	39	29	57	107
Sly03g0221601	M11	NA	11	9	12	10	13	23	21	29	18	24
Sly03g0221611	M2	NA	109	107	103	114	120	98	105	102	128	129
Sly03g0221621	M11	NA	36	31	42	45	56	43	47	46	50	61
Sly03g0221641	M18	NA	18	19	21	26	31	27	22	30	24	25
Sly03g0221651	M3	NA	10	11	7	4	4	7	8	4	4	3
Sly03g0221661	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0221691	M11	NA	12	12	18	34	19	31	28	43	17	8
Sly03g0221701	M11	NA	7	7	8	9	9	11	11	12	7	8
Sly03g0221711	M3	NA	181	300	55	4	8	60	94	10	2	6
Sly03g0221721	M1	NA	42	38	34	41	17	17	20	16	17	12
Sly03g0221731	M1	NA	3	2	2	4	14	1	1	1	1	2
Sly03g0221741	M22	NA	5	3	4	3	5	15	6	11	6	6
Sly03g0221751	M22	NA	3	1	2	2	2	10	3	8	3	4
Sly03g0221761	M4	NA	23	24	25	35	44	25	24	24	50	77
Sly03g0221791	M9	NA	1	2	1	2	2	2	2	1	3	3
Sly03g0221801	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0221811	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0221821	M2	NA	25	33	28	20	13	15	21	12	33	31
Sly03g0221831	M2	NA	31	32	26	29	22	25	28	22	24	25
Sly03g0221841	M11	NA	18	19	20	22	27	23	18	23	20	22
Sly03g0221851	M2	NA	91	94	79	110	86	69	73	59	66	63
Sly03g0221861	M1	NA	29	27	21	21	29	12	12	10	14	17
Sly03g0221871	M18	NA	136	120	144	114	110	173	143	187	108	110
Sly03g0221881	M9	NA	2	2	2	1	1	5	7	4	1	1
Sly03g0221891	M12	NA	17	15	18	10	9	49	51	43	8	8
Sly03g0221901	M11	NA	208	187	229	154	175	228	219	273	237	281
Sly03g0221911	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0221921	M2	NA	13	14	12	7	5	8	10	8	7	4
Sly03g0221931	M1	NA	18	15	16	11	17	11	9	11	12	13
Sly03g0221941	M9	NA	4	4	3	2	1	6	6	5	1	1
Sly03g0221951	M10	NA	65	64	46	45	60	62	80	56	79	108
Sly03g0221961	M1	NA	30	31	30	24	24	24	23	21	19	20
Sly03g0221981	M12	NA	1	1	1	2	3	1	1	1	1	3
Sly03g0221991	M12	NA	3	2	3	5	6	3	3	4	7	17
Sly03g0222011	M22	NA	6	5	6	4	3	7	7	6	2	2
Sly03g0222021	M12	NA	7	6	6	6	9	8	9	8	8	13
Sly03g0222031	M12	NA	24	23	21	31	39	28	28	28	38	50
Sly03g0222041	M3	NA	15	23	12	5	8	8	12	5	1	3
Sly03g0222091	M1	NA	43	45	10	0	0	1	1	0	0	0
Sly03g0222101	M1	NA	13	12	5	1	1	2	2	1	1	0
Sly03g0222111	M12	NA	39	40	39	77	138	79	86	84	155	225
Sly03g0222121	M12	NA	15	11	13	7	4	20	21	25	19	11
Sly03g0222131	M1	NA	14	10	15	4	2	3	3	3	1	1
Sly03g0222141	M12	NA	11	18	12	36	13	45	49	55	34	12
Sly03g0222151	M11	NA	59	54	60	54	71	54	53	66	60	66
Sly03g0222161	M3	NA	14	15	9	3	1	10	10	7	1	1
Sly03g0222171	M2	NA	6	5	4	3	3	5	5	5	4	1
Sly03g0222181	M10	NA	12	17	10	8	8	18	24	10	7	8
Sly03g0222191	M3	SITPL1	88	89	54	15	10	50	57	39	11	6
Sly03g0222201	M22	NA	7	8	7	6	6	8	7	7	7	6
Sly03g0222211	M3	NA	15	14	12	8	7	11	12	10	11	9
Sly03g0222221	M1	NA	10	11	10	5	6	9	9	9	14	7
Sly03g0222231	M3	NA	11	12	10	10	6	10	10	11	17	9
Sly03g0222241	M5	NA	13	13	10	9	10	14	13	11	16	15
Sly03g0222251	M11	NA	341	355	513	715	768	574	469	761	1038	1227
Sly03g0222261	M14	NA	170	132	246	203	350	152	126	181	137	226
Sly03g0222271	M11	NA	14	12	13	12	14	19	15	17	16	22
Sly03g0222301	M12	NA	43	40	38	47	51	49	49	49	65	68
Sly03g0222311	M11	NA	182	163	204	194	117	197	207	251	408	174
Sly03g0222321	M1	NA	34	31	47	25	12	16	10	18	2	2
Sly03g0222331	M12	NA	2	4	4	27	30	3	4	6	11	23
Sly03g0222341	M11	NA	9	8	11	7	9	13	8	13	12	11
Sly03g0222351	M11	NA	15	16	15	15	19	17	15	16	14	16
Sly03g0222361	M12	NA	8	8	9	7	9	11	11	11	14	11
Sly03g0222371	M1	NA	6	5	4	3	4	2	1	2	1	1
Sly03g0222381	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly03g0222391	M12	NA	6	6	6	5	4	8	8	6	7	5
Sly03g0222401	M18	PPR-like11	6	7	6	5	5	7	6	7	8	5
Sly03g0222411	M11	NA	57	49	47	61	56	75	68	71	84	73
Sly03g0222421	M11	NA	28	25	20	3	8	56	54	81	6	17
Sly03g0222431	M3	NA	111	88	37	57	39	21	14	6	1	1
Sly03g0222441	M3	NA	3	3	1	5	4	1	1	1	0	0
Sly03g0222461	M12	NA	2	3	3	97	231	5	3	6	22	160
Sly03g0222471	M3	NA	3	5	2	3	5	2	3	2	2	2
Sly03g0222481	M12	NA	21	23	21	24	25	23	22	23	24	32
Sly03g0222491	M1	NA	11	9	10	10	12	7	7	8	7	7
Sly03g0222501	M12	NA	59	55	65	129	132	68	67	81	128	145
Sly03g0222511	M11	NA	70	57	77	92	100	120	117	179	176	206
Sly03g0222521	M11	NA	2	1	2	3	1	2	2	2	2	1
Sly03g0222571	M1	NA	8	9	15	23	12	1	1	1	6	6
Sly03g0222591	M11	NA	24	21	23	23	21	22	24	24	27	21
Sly03g0222601	M1	NA	5	4	5	5	4	2	2	2	1	1
Sly03g0222611	M9	NA	24	27	21	27	32	38	38	41	31	41
Sly03g0222621	M12	NA	194	176	200	285	452	307	322	371	353	510
Sly03g0222631	M1	NA	58	59	57	66	71	49	53	53	84	91
Sly03g0222641	M22	NA	1	1	1	0	0	1	1	1	1	0
Sly03g0222651	M1	NA	38	91	116	134	8	1	1	1	1	0
Sly03g0222661	M1	NA	28	22	30	15	5	8	7	7	3	2
Sly03g0222671	M1	NA	7	7	7	6	6	6	7	6	4	6
Sly03g0222681	M12	NA	1	1	1	1	1	1	1	1	1	2
Sly03g0222691	M1	NA	40	26	18	3	4	8	5	5	1	1
Sly03g0222701	M12	NA	23	26	21	23	41	31	36	32	46	66
Sly03g0222711	M3	NA	340	291	134	2	14	50	64	15	21	10
Sly03g0222721	M10	NA	200	239	150	294	452	433	461	256	533	789
Sly03g0222741	M11	NA	69	61	106	280	326	102	103	149	381	454
Sly03g0222751	M11	NA	32	33	28	40	38	31	33	40	41	46
Sly03g0222761	M10	NA	1	1	1	1	1	1	1	1	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0169601	M11	NA	12	13	14	18	17	12	12	14	27	27
Sly10g0169621	M17	NA	9	8	9	9	8	8	9	9	9	10
Sly10g0169631	M11	NA	41	38	42	32	32	43	46	50	44	50
Sly10g0169641	M11	NA	27	27	30	22	21	32	30	39	27	22
Sly10g0169651	M4	NA	2	2	2	2	7	2	3	3	8	107
Sly10g0169671	M12	NA	10	10	9	12	12	12	10	11	17	18
Sly10g0169841	M1	NA	104	107	112	81	118	88	81	89	90	106
Sly10g0169851	M3	NA	2	2	2	1	1	1	1	1	1	1
Sly10g0169941	M7	NA	8	10	7	10	10	8	11	8	22	17
Sly10g0169991	M1	NA	2	1	2	2	3	1	0	1	4	5
Sly10g0170001	M2	NA	15	13	12	13	13	11	14	13	14	15
Sly10g0170081	M22	NA	2	1	2	0	0	5	1	10	0	0
Sly10g0170091	M22	NA	1	1	1	0	0	2	1	4	0	0
Sly10g0170101	M3	NA	13	11	10	8	5	8	9	7	5	4
Sly10g0170211	M1	NA	24	26	25	24	23	19	19	17	18	15
Sly10g0170291	M1	NA	1	2	2	4	2	1	1	1	1	1
Sly10g0170301	M1	NA	29	30	31	29	30	21	19	21	33	39
Sly10g0170311	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0170361	M11	NA	87	79	95	71	84	125	105	139	61	77
Sly10g0170371	M12	NA	7	11	15	316	318	61	75	115	731	700
Sly10g0170381	M12	NA	4	6	9	155	228	47	78	143	559	699
Sly10g0170391	M12	NA	2	2	4	67	151	15	24	55	645	577
Sly10g0170451	M1	LHP1-like2	39	40	40	43	39	28	29	27	27	27
Sly10g0170481	M22	NA	2	2	1	3	10	1	1	1	2	3
Sly10g0170521	M12	NA	13	11	14	14	16	21	19	20	29	32
Sly10g0170551	M22	NA	1	1	1	1	0	4	1	3	1	0
Sly10g0170641	M12	NA	4	3	5	4	3	7	7	6	8	7
Sly10g0170921	M11	NA	6	4	5	7	7	5	5	5	6	6
Sly10g0170971	M18	NA	27	28	29	34	41	34	29	35	31	37
Sly10g0171041	M11	NA	48	47	52	68	71	53	52	59	70	81
Sly10g0171071	M11	NA	27	25	30	52	46	31	33	37	44	39
Sly10g0171091	M9	NA	2	2	1	2	1	2	2	2	2	1
Sly10g0171101	M11	NA	23	22	28	26	29	30	28	34	37	44
Sly10g0171111	M12	NA	8	6	8	13	12	13	15	12	20	20
Sly10g0171161	M3	NA	14	13	10	7	8	9	12	9	10	9
Sly10g0171171	M2	NA	24	26	27	26	33	22	26	24	44	60
Sly10g0171191	M22	NA	8	6	7	3	2	7	6	6	3	2
Sly10g0171201	M12	NA	3	3	2	52	74	4	5	8	196	271
Sly10g0171241	M2	NA	83	88	87	115	96	71	84	74	113	101
Sly10g0171251	M3	NA	53	51	50	49	27	35	41	28	15	8
Sly10g0171271	M12	NA	1	0	1	1	0	1	1	1	2	1
Sly10g0171331	M3	NA	22	26	19	11	13	16	24	14	10	9
Sly10g0171341	M1	NA	47	47	49	26	26	35	32	34	24	24
Sly10g0171401	M12	NA	7	9	9	3	2	11	10	10	3	2
Sly10g0171421	M3	NA	1	2	1	1	2	1	2	1	1	5
Sly10g0171451	M11	NA	11	10	13	22	11	23	23	31	20	8
Sly10g0171461	M3	NA	40	39	32	21	14	33	35	32	16	15
Sly10g0171471	M5	NA	7	7	7	2	1	8	9	5	1	1
Sly10g0171481	M3	NA	3	3	3	2	1	2	2	3	3	2
Sly10g0171491	M5	NA	1	3	1	1	1	2	2	1	1	1
Sly10g0171501	M3	NA	10	8	5	3	3	4	6	5	4	2
Sly10g0171551	M9	NA	41	43	39	35	32	43	41	41	46	41
Sly10g0171581	M1	NA	29	26	28	27	34	23	24	25	38	38
Sly10g0171591	M2	NA	11	11	10	7	5	10	11	9	16	15
Sly10g0171611	M12	NA	0	1	1	0	0	1	1	1	0	0
Sly10g0171621	M3	NA	49	53	53	42	38	46	52	44	37	37
Sly10g0171691	M12	NA	4	3	3	2	1	7	6	6	2	1
Sly10g0171721	M22	NA	1	1	1	2	2	1	1	1	1	1
Sly10g0171891	M2	NA	30	28	26	22	24	27	29	25	24	28
Sly10g0171901	M3	NA	19	24	13	17	11	10	13	11	18	17
Sly10g0171911	M3	NA	29	28	24	22	23	18	23	19	29	18
Sly10g0171921	M2	NA	26	23	22	18	17	23	25	25	18	15
Sly10g0171931	M18	NA	7	7	7	5	1	7	9	6	1	2
Sly10g0172191	M18	NA	2	2	2	2	3	3	3	3	2	4
Sly10g0172211	M3	NA	10	11	7	2	3	6	6	2	2	1
Sly10g0172221	M19	NA	41	47	39	32	29	43	41	43	29	25
Sly10g0172231	M9	NA	16	17	15	16	14	19	21	18	18	18
Sly10g0172421	M19	NA	45	43	46	43	48	43	34	44	45	55
Sly10g0172441	M18	NA	27	28	30	42	46	33	28	36	31	28
Sly10g0172451	M11	NA	6	7	7	7	10	7	7	7	8	9
Sly10g0172461	M7	NA	6	8	5	7	13	6	10	6	5	18
Sly10g0172471	M7	NA	47	56	43	49	55	47	65	43	31	58
Sly10g0172481	M12	NA	82	89	83	92	69	95	108	93	82	71
Sly10g0172491	M11	NA	3	3	3	6	5	4	3	3	2	2
Sly10g0172501	M11	NA	127	84	146	89	138	277	265	345	133	219
Sly10g0172521	M1	NA	18	18	16	8	10	11	11	10	12	15
Sly10g0172631	M12	NA	29	30	29	31	32	40	37	35	27	31
Sly10g0172651	M19	NA	30	34	39	75	74	34	28	39	34	32
Sly10g0172661	M1	NA	2	1	4	2	1	1	1	1	1	1
Sly10g0172691	M11	NA	7	8	9	10	6	13	11	13	11	5
Sly10g0172701	M13	NA	14	14	16	16	16	14	14	15	24	19
Sly10g0172711	M1	NA	4	3	2	2	1	1	1	1	1	1
Sly10g0172731	M12	NA	24	25	24	26	24	29	31	28	25	19
Sly10g0172781	M12	NA	14	13	15	18	14	22	21	21	15	11
Sly10g0172791	M1	NA	12	8	11	8	5	8	7	10	6	7
Sly10g0172801	M1	NA	4	3	3	3	2	3	2	3	3	2
Sly10g0172831	M11	NA	7	7	8	6	3	11	9	10	3	2
Sly10g0172861	M11	NA	17	17	19	12	12	25	20	23	17	18
Sly10g0172871	M12	NA	29	30	31	42	46	40	42	39	48	60
Sly10g0172921	M1	NA	55	48	45	45	52	30	31	30	49	55
Sly10g0172961	M3	NA	23	22	17	11	6	11	12	7	5	3
Sly10g0173071	M12	NA	5	3	5	6	8	4	5	11	46	64
Sly10g0173091	M12	NA	25	23	24	30	33	30	32	31	32	32
Sly10g0173101	M11	RDM1-like1	60	53	68	45	45	73	71	82	73	84
Sly10g0173191	M18	NA	1	1	1	0	0	1	1	2	0	0
Sly10g0173221	M1	NA	5	5	5	2	2	3	3	3	2	1
Sly10g0173231	M1	NA	1	2	2	2	1	1	1	1	1	1
Sly10g0173251	M11	NA	27	23	26	22	17	26	28	28	20	17
Sly10g0173261	M11	NA	5	4	6	5	3	6	7	7	4	2
Sly10g0173271	M11	NA	7	5	8	6	4	12	8	13	6	6
Sly10g0173281	M3	NA	4	3	2	4	2	3	2	1	8	8
Sly10g0173291	M12	NA	6	4	6	4	6	9	8	11	12	14
Sly10g0173321	M1	NA	4	3	4	1	1	1	1	1	0	0
Sly10g0173331	M3	NA	3	4	2	2	1	2	2	1	1	1
Sly10g0173341	M1	SlHAG1	45	44	45	43	45	38	36	38	41	45
Sly10g0173351	M5	NA	33	74	26	7	9	41	52	15	6	8
Sly10g0173361	M3	NA	11	12	10	15	14	9	11	9	11	11
Sly10g0173371	M3	NA	7	8	5	5	4	4	8	5	6	7
Sly10g0173441	M3	NA	1	1	1	1	0	1	0	0	0	0
Sly10g0173461	M12	NA	5	5	4	3	2	6	6	5	2	1
Sly10g0173481	M11	NA	5	4	6	9	7	6	6	7	7	5
Sly10g0173531	M13	NA	33	32	34	53	68	33	33	33	48	83
Sly10g0173541	M3	NA	34	36	27	34	26	27	34	25	39	39
Sly10g0173561	M1	NA	5	4	8	4	1	1	0	0	1	0
Sly10g0173591	M12	NA	37	43	43	66	52	52	63	58	57	71
Sly10g0173611	M11	NA	2	1	2	3	3	3	3	3	4	4
Sly10g0173621	M11	NA	12	11	10	15	12	13	11	14	17	18
Sly10g0173631	M3	NA	63	59	54	75	96	54	58	60	80	93
Sly10g0173641	M12	NA	38	36	36	57	61	44	45	42	41	40
Sly10g0173801	M11	NA	6	6	7	5	3	6	6	6	5	3
Sly10g0173881	M1	NA	4	5	2	3	3	3	1	2	1	0
Sly10g0173901	M12	NA	3	3	3	1	0	7	6	6	1	0
Sly10g0173921	M19	NA	118	119	131	84	86	108	91	109	77	79
Sly10g0173971	M3	NA	71	73	52	51	49	48	50	39	45	57
Sly10g0173991	M11	NA	57	56	60	62	74	62	59	70	87	109
Sly10g0174021	M12	LeXYL1	1	1	1	2	24	2	1	2	20	37
Sly10g0174031	M2	NA	5	6	6	3	11	5	8	5	6	25
Sly10g0174041	M11	NA	18	18	19	16	13	25	22	24	11	9
Sly10g0174141	M3	NA	23	25	22	26	30	19	20	17	23	26
Sly10g0174151	M11	NA	29	27	32	25	25	38	34	47	42	38
Sly10g0174161	M5	SERK3A	58	60	35	26	22	69	68	36	17	21
Sly10g0174171	M3	NA	9

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0222771	M18	NA	11	10	12	11	13	13	12	15	15	15
Sly03g0222781	M1	NA	53	54	57	67	104	49	53	52	93	110
Sly03g0222791	M3	NA	104	140	68	117	193	74	82	64	161	187
Sly03g0222801	M3	NA	3	2	2	1	39	2	1	1	1	2
Sly03g0222811	M21	NA	12	11	14	10	11	12	10	12	9	8
Sly03g0222821	M3	SlRbohB/SlWfi1	128	255	104	10	6	64	64	11	1	1
Sly03g0222831	M12	NA	2	2	1	1	1	2	2	2	1	1
Sly03g0222841	M3	NA	6	11	3	3	6	7	5	3	6	7
Sly03g0222851	M1	NA	59	57	61	35	38	49	44	48	26	23
Sly03g0222861	M3	NA	236	242	220	249	141	204	196	177	122	81
Sly03g0222871	M1	AMI1-like5	37	37	39	36	36	33	33	32	28	36
Sly03g0222881	M3	NA	493	524	415	610	399	401	509	263	375	287
Sly03g0222901	M11	NA	5	3	2	2	10	9	8	8	2	6
Sly03g0222921	M20	NA	16	14	18	6	6	14	11	13	4	3
Sly03g0222931	M3	NA	6	5	4	4	4	4	4	4	4	3
Sly03g0222951	M3	NA	14	20	10	12	6	7	11	3	2	3
Sly03g0222961	M1	NA	3	4	4	18	5	1	1	0	1	1
Sly03g0222971	M11	NA	74	76	88	243	455	81	77	110	125	220
Sly03g0222981	M11	NA	11	7	12	1	1	16	14	18	1	1
Sly03g0222991	M12	NA	36	42	31	42	29	43	55	37	15	39
Sly03g0223001	M9	NA	12	13	14	22	19	12	16	14	13	12
Sly03g0223011	M1	NA	12	12	17	20	10	8	11	9	8	4
Sly03g0223031	M11	NA	58	55	59	67	68	64	62	69	58	62
Sly03g0223041	M3	NA	13	13	11	11	10	12	11	11	14	12
Sly03g0223051	M2	NA	1	1	2	2	1	1	2	2	5	5
Sly03g0223061	M1	SlERF.D7	4	9	5	6	2	1	1	1	5	3
Sly03g0223071	M12	NA	55	62	34	25	33	78	87	58	44	76
Sly03g0223081	M7	NA	9	12	6	5	7	12	13	8	7	12
Sly03g0223091	M3	NA	1	1	1	1	1	1	1	1	0	0
Sly03g0223121	M11	NA	18	16	24	40	35	62	53	81	69	31
Sly03g0223131	M14	NA	15	14	16	16	16	13	13	16	20	22
Sly03g0223141	M18	NA	4	4	4	4	5	5	4	4	4	4
Sly03g0223151	M3	NA	40	34	26	25	20	23	23	21	34	25
Sly03g0223161	M11	SlARF2A	108	112	147	347	297	217	197	267	421	361
Sly03g0223171	M12	NA	50	53	57	142	145	90	101	108	246	285
Sly03g0223181	M22	NA	2	1	2	1	1	4	1	4	0	1
Sly03g0223191	M3	NA	2	2	2	1	1	2	2	1	1	1
Sly03g0223201	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly03g0223211	M22	NA	1	1	2	1	1	1	1	1	1	0
Sly03g0223221	M2	NA	41	50	49	176	238	38	47	45	217	217
Sly03g0223231	M2	NA	28	27	27	33	26	26	28	26	31	26
Sly03g0223241	M19	NA	18	20	17	25	18	19	16	19	17	13
Sly03g0223261	M1	NA	2	1	2	1	1	1	1	1	0	0
Sly03g0223271	M11	NA	35	31	41	53	67	45	41	51	71	72
Sly03g0223281	M12	NA	49	56	47	72	74	59	65	57	70	66
Sly03g0223291	M11	NA	37	34	50	42	12	85	75	95	36	7
Sly03g0223301	M5	NA	59	51	46	31	42	56	59	42	44	51
Sly03g0223311	M19	NA	55	56	63	84	128	65	51	72	73	102
Sly03g0223321	M3	NA	1	3	1	1	1	1	1	1	1	1
Sly03g0223331	M3	NA	11	21	8	1	1	2	3	1	1	1
Sly03g0223341	M1	NA	12	23	18	7	92	2	8	2	1	84
Sly03g0223351	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly03g0223361	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0223371	M11	NA	18	17	20	22	24	23	20	24	28	22
Sly03g0223381	M11	NA	9	6	21	6	3	23	16	22	3	1
Sly03g0223391	M3	NA	86	86	73	81	71	65	68	56	69	71
Sly03g0223401	M2	NA	94	94	91	88	105	79	91	71	100	157
Sly03g0223411	M11	NA	31	35	38	49	38	72	69	90	60	51
Sly03g0223421	M12	JAI3-like	8	12	20	15	13	49	107	119	187	84
Sly03g0223431	M11	NA	42	38	43	43	45	50	42	48	29	44
Sly03g0223441	M11	NA	52	45	49	54	61	56	54	55	36	70
Sly03g0223461	M12	NA	22	25	26	35	41	31	29	32	59	69
Sly03g0223511	M9	NA	18	17	17	18	17	17	19	17	22	24
Sly03g0223521	M6	NA	16	20	17	16	20	16	19	16	17	26
Sly03g0223531	M1	NA	20	30	26	20	27	23	22	21	18	24
Sly03g0223541	M11	NA	3	4	4	2	2	5	5	5	1	1
Sly03g0223591	M11	NA	35	37	42	51	29	96	77	101	32	17
Sly03g0223601	M12	NA	35	33	42	84	99	55	63	75	129	132
Sly03g0223611	M3	NA	31	30	29	27	27	19	23	20	33	26
Sly03g0223621	M3	NA	58	55	53	61	50	54	57	53	46	36
Sly03g0223631	M1	NA	28	25	27	28	32	22	23	21	21	23
Sly03g0223641	M3	AMI1-like7	48	51	44	51	43	35	38	34	57	37
Sly03g0223651	M11	NA	7	6	6	5	6	7	6	8	10	8
Sly03g0223661	M1	NA	28	24	27	18	11	13	14	13	2	2
Sly03g0223671	M3	NA	49	54	34	34	42	40	51	38	66	79
Sly03g0223681	M3	SIPIN1	2	1	1	2	1	1	1	1	1	1
Sly03g0223691	M8	NA	24	25	23	34	17	24	27	22	14	12
Sly03g0223701	M1	NA	1	1	1	2	1	1	1	1	1	1
Sly03g0223711	M1	NA	3	2	1	1	1	1	1	1	0	0
Sly03g0223721	M23	NA	2	1	1	1	0	5	2	1	1	0
Sly03g0223731	M19	PPR-like25	4	6	6	7	7	7	6	7	7	7
Sly03g0223741	M11	NA	57	53	55	58	77	66	69	68	88	108
Sly03g0223751	M6	NA	86	122	39	9	106	75	178	56	28	128
Sly03g0223761	M2	NA	38	41	39	76	80	31	39	32	116	174
Sly03g0223771	M11	NA	13	13	14	15	14	23	23	30	25	23
Sly03g0223781	M11	NA	47	38	56	45	24	111	101	136	130	105
Sly03g0223791	M13	NA	18	17	24	26	31	22	18	24	26	25
Sly03g0223801	M1	NA	22	23	30	45	36	17	15	16	19	15
Sly03g0223811	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0223821	M7	NA	2	3	1	1	0	2	4	2	1	1
Sly03g0223831	M11	NA	38	39	43	40	45	51	46	59	67	77
Sly03g0223851	M13	NA	94	90	102	96	100	92	91	99	116	175
Sly03g0223861	M19	NA	38	42	40	42	49	34	32	35	45	42
Sly03g0223871	M12	NA	1	1	0	1	0	1	1	1	0	1
Sly03g0223901	M12	NA	1	1	1	0	0	2	2	1	0	0
Sly03g0223911	M6	NA	171	208	131	3	4	231	273	97	8	4
Sly03g0223921	M12	NA	7	7	8	8	12	8	9	8	19	20
Sly03g0223931	M11	NA	6	7	8	8	10	9	8	9	13	14
Sly03g0223951	M3	NA	13	10	9	9	10	8	9	7	13	11
Sly03g0223961	M11	NA	66	56	73	60	66	70	67	91	73	87
Sly03g0223971	M1	NA	36	35	35	32	34	29	30	30	24	25
Sly03g0223981	M1	NA	199	181	163	104	95	139	143	126	116	105
Sly03g0223991	M1	NA	16	18	14	8	7	13	11	11	10	7
Sly03g0224001	M1	NA	109	109	175	94	33	87	60	83	3	1
Sly03g0224011	M11	NA	2	1	2	1	1	3	3	3	0	0
Sly03g0224021	M1	NA	53	38	68	138	150	26	24	28	26	47
Sly03g0224031	M9	NA	63	62	62	73	68	64	69	62	61	65
Sly03g0224041	M22	NA	7	2	4	1	0	21	3	15	1	0
Sly03g0224051	M11	NA	8	7	9	5	3	13	13	12	4	4
Sly03g0224061	M1	NA	4	4	4	3	3	3	3	3	3	3
Sly03g0224071	M3	NA	126	136	115	114	105	116	122	95	88	92
Sly03g0224081	M3	NA	32	32	28	16	12	25	25	22	15	11
Sly03g0224091	M11	NA	19	14	28	21	6	44	32	60	8	2
Sly03g0224101	M8	NA	34	35	29	26	27	32	37	32	36	37
Sly03g0224111	M2	NA	53	54	50	40	42	42	42	38	39	41
Sly03g0224151	M11	NA	22	18	27	22	12	30	20	28	3	3
Sly03g0224161	M1	NA	25	25	11	1	1	1	1	1	0	0
Sly03g0224171	M22	NACK1	1	1	1	1	1	1	1	1	1	1
Sly03g0224181	M9	NA	2	3	3	2	1	9	11	9	7	3
Sly03g0224191	M9	NA	4	9	5	2	1	13	18	12	15	6
Sly03g0224201	M6	NA	65	211	55	23	63	44	79	16	2	11
Sly03g0224231	M12	NA	13	12	12	17	20	13	13	14	16	18
Sly03g0224241	M20	NA	13	12	15	34	40	12	11	14	33	30
Sly03g0224251	M19	NA	20	22	24	35	45	24	21	22	34	56
Sly03g0224261	M1	NA	9	9	12	13	7	8	6	7	8	5
Sly03g0224271	M21	NA	18	18	19	12	3	20	16	16	4	2
Sly03g0224281	M1	NA	12	8	22	11	8	6	6	8	2	1
Sly03g0224291	M3	NA	46	50	43	48	50	37	37	36	44	50
Sly03g0224301	M3	NA	6	7	6	6	6	5	7	5	7	9
Sly03g0224321	M1	NA	412	392	388	292	234	305	317	295	330	255
Sly03g0224331	M6	NA	7	16	6	1	0	11	13	5	1	1
Sly03g0224341	M2	NA	86	83	79	72	78	74	89	79	84	90
Sly03g0224361	M1	NA	6	4	3	1	1	2	2	1	0	0
Sly03g0224381	M18	NA	44	41	43	40	49	48	38	47	34	41

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0174231	M1	NA	80	76	77	76	80	63	60	68	88	98
Sly10g0174241	M1	NA	11	3	20	17	6	1	1	1	0	1
Sly10g0174251	M3	NA	24	20	18	8	3	18	23	16	6	2
Sly10g0174261	M11	NA	9	9	11	8	4	19	21	23	8	7
Sly10g0174271	M3	NA	18	21	18	23	21	18	20	17	15	14
Sly10g0174311	M3	NA	91	91	72	53	68	48	53	45	60	87
Sly10g0174321	M9	NA	11	13	11	5	2	17	25	14	8	5
Sly10g0174331	M3	AMI1-like3	33	33	25	17	23	27	31	19	20	29
Sly10g0174361	M1	NA	56	50	35	11	5	25	24	19	4	4
Sly10g0174371	M11	NA	1	1	2	0	0	3	3	6	1	0
Sly10g0174391	M12	SlHDMA3	10	11	10	15	15	11	11	13	19	17
Sly10g0174401	M12	NA	40	35	38	35	23	55	51	59	22	12
Sly10g0174411	M1	NA	25	23	25	22	22	21	22	21	19	20
Sly10g0174591	M12	NA	1	1	1	1	0	1	1	1	0	1
Sly10g0174681	M6	NA	8	12	9	4	2	11	15	7	5	2
Sly10g0174691	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0174711	M9	NA	61	69	61	72	65	67	70	66	63	65
Sly10g0174731	M17	NA	24	21	22	21	26	22	18	22	23	26
Sly10g0174741	M3	NA	278	230	188	282	373	167	200	164	352	396
Sly10g0174751	M1	NA	9	11	11	10	4	7	5	7	4	2
Sly10g0174761	M1	HVA22A-like1	40	41	36	20	19	27	29	27	20	12
Sly10g0174791	M3	NA	8	8	6	4	4	5	6	3	2	3
Sly10g0174801	M11	NA	6	5	8	8	11	7	6	8	7	5
Sly10g0175131	M11	NA	5	5	7	3	2	8	6	8	3	3
Sly10g0175161	M3	NA	4	4	4	3	2	3	2	2	2	1
Sly10g0175181	M11	NA	57	50	46	51	44	62	62	69	41	32
Sly10g0175211	M20	NA	45	34	45	32	36	30	24	29	10	6
Sly10g0175221	M11	NA	41	39	45	45	18	58	56	69	40	24
Sly10g0175291	M1	NA	1	1	1	1	1	1	1	0	1	0
Sly10g0175331	M11	NA	1	1	1	1	2	2	1	2	2	2
Sly10g0175441	M22	NA	1	1	1	0	0	2	1	2	1	1
Sly10g0175501	M11	NA	1	1	1	1	1	2	2	3	1	1
Sly10g0175531	M11	NA	22	25	28	26	16	28	25	33	16	10
Sly10g0175561	M12	NA	1	1	1	3	12	1	1	1	23	50
Sly10g0175591	M1	NA	16	12	21	16	13	18	9	11	11	10
Sly10g0175601	M1	NA	7	5	7	8	6	3	3	2	6	3
Sly10g0175611	M22	NA	1	1	1	22	4	1	1	2	2	3
Sly10g0175621	M12	NA	1	1	0	0	0	1	1	1	0	0
Sly10g0175701	M11	SlCycA3;6	29	28	29	28	24	31	31	35	31	23
Sly10g0175711	M22	NA	1	0	1	0	0	8	0	7	0	0
Sly10g0175781	M3	NA	5	3	1	1	0	1	1	1	1	0
Sly10g0175861	M12	NA	5	4	4	3	2	5	4	6	4	1
Sly10g0175881	M1	NA	2	1	2	1	1	1	1	1	1	1
Sly10g0175921	M11	NA	4	6	7	4	3	11	7	12	6	3
Sly10g0175931	M11	NA	7	7	8	8	7	7	7	8	7	6
Sly10g0175941	M1	NA	7	5	7	1	1	1	1	1	1	0
Sly10g0175961	M12	NA	58	52	54	91	116	89	94	92	115	188
Sly10g0175971	M7	NA	36	61	41	36	135	56	103	49	52	207
Sly10g0175981	M1	NA	4	4	3	1	1	3	2	2	1	1
Sly10g0175991	M1	NA	11	11	12	12	8	11	10	11	13	11
Sly10g0176021	M12	NA	1	2	1	1	1	3	3	3	1	1
Sly10g0176031	M12	NA	2	2	2	1	5	5	8	6	6	34
Sly10g0176041	M11	NA	120	126	143	404	691	151	160	192	458	646
Sly10g0176091	M22	NA	1	1	1	0	0	2	1	1	1	1
Sly10g0176101	M22	NA	1	0	1	1	0	2	1	1	1	1
Sly10g0176161	M2	NA	6	7	6	6	6	6	7	6	8	7
Sly10g0176301	M1	NA	2	1	1	2	1	1	1	1	1	1
Sly10g0176371	M1	SITIP41	72	67	65	77	83	53	56	56	69	84
Sly10g0176391	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly10g0176411	M8	NA	3	4	3	3	2	3	3	3	4	6
Sly10g0176421	M1	NA	3	3	3	2	2	1	1	1	1	1
Sly10g0176431	M9	NA	11	11	9	13	9	17	22	17	81	79
Sly10g0176481	M9	NA	25	23	22	25	32	23	26	23	46	56
Sly10g0176511	M11	NA	4	4	7	3	2	10	10	11	5	8
Sly10g0176521	M11	NA	2	3	2	2	1	6	4	7	3	4
Sly10g0176531	M22	NA	3	0	3	0	0	17	1	13	0	0
Sly10g0176551	M1	NA	244	217	209	57	77	50	52	30	4	4
Sly10g0176561	M8	NA	3	3	2	2	2	3	4	2	2	2
Sly10g0176591	M3	NA	3	2	3	1	1	3	3	2	1	1
Sly10g0176621	M6	NA	147	253	128	97	138	110	204	94	149	298
Sly10g0176671	M1	NA	41	24	70	1	0	9	5	7	1	1
Sly10g0176701	M3	NA	49	70	23	1	2	58	44	25	1	1
Sly10g0176711	M11	NA	58	57	60	61	66	58	56	62	64	77
Sly10g0176751	M12	NA	12	13	10	12	5	16	15	12	11	7
Sly10g0176771	M3	NA	30	25	24	24	27	23	25	23	24	21
Sly10g0176841	M19	NA	5	8	7	7	7	3	4	3	4	4
Sly10g0176851	M1	NA	4	6	6	6	7	3	2	3	5	6
Sly10g0176861	M1	NA	6	8	8	12	12	4	5	5	7	10
Sly10g0176871	M1	NA	12	14	16	18	23	8	8	9	18	25
Sly10g0176931	M11	NA	2	1	2	6	4	2	1	2	3	8
Sly10g0176951	M1	NA	5	4	6	3	3	3	2	3	1	1
Sly10g0176961	M11	NA	42	36	45	19	5	48	39	51	12	5
Sly10g0176971	M1	NA	1	2	2	2	2	1	1	1	1	1
Sly10g0177031	M11	NA	1	1	1	1	1	1	1	2	2	1
Sly10g0177051	M17	NA	2	2	3	1	1	2	1	3	1	1
Sly10g0177061	M1	NA	2	3	3	2	2	1	1	4	0	0
Sly10g0177081	M3	NA	2	4	1	0	0	1	0	0	0	0
Sly10g0177091	M1	NA	21	22	22	22	23	19	19	19	21	18
Sly10g0177151	M8	NA	2	3	1	2	0	1	3	2	1	1
Sly10g0177271	M9	NA	6	16	6	2	3	14	28	8	5	18
Sly10g0177281	M12	NA	4	10	4	2	3	11	20	7	3	12
Sly10g0177291	M7	NA	10	26	9	5	32	22	53	11	7	121
Sly10g0177351	M11	NA	8	7	10	9	9	12	11	13	12	13
Sly10g0177461	M12	NA	3	2	3	3	2	3	3	3	2	3
Sly10g0177471	M11	NA	54	56	61	85	84	84	84	87	74	79
Sly10g0177481	M1	NA	9	10	10	6	5	9	8	8	2	2
Sly10g0177491	M11	NA	214	212	229	143	134	227	207	234	104	102
Sly10g0177501	M6	NA	12	14	12	20	19	12	12	11	18	22
Sly10g0177511	M10	NA	2	2	1	1	1	16	13	2	1	1
Sly10g0177521	M3	NIR2	38	39	36	67	57	20	22	14	21	16
Sly10g0177541	M2	NA	9	9	10	8	11	7	9	9	20	28
Sly10g0177551	M3	NA	15	17	12	5	4	10	10	6	4	4
Sly10g0177561	M3	NA	23	28	22	11	10	10	13	5	6	6
Sly10g0177571	M1	NA	15	19	17	8	6	7	9	4	4	4
Sly10g0177581	M1	NA	17	20	19	8	6	7	9	4	4	3
Sly10g0177591	M5	NA	6	7	5	4	6	6	7	5	5	8
Sly10g0177621	M8	NA	5	6	1	0	1	7	13	2	0	1
Sly10g0177631	M9	SlERF.D4	4	7	2	1	2	12	21	7	1	3
Sly10g0177641	M12	NA	1	1	1	1	1	1	1	6	3	3
Sly10g0177651	M12	NA	3	2	4	2	3	8	10	65	138	136
Sly10g0177661	M19	NA	6	9	8	8	7	9	6	9	9	8
Sly10g0177671	M18	NA	7	7	7	7	7	8	6	7	8	9
Sly10g0177681	M22	NA	1	1	1	0	1	2	1	3	0	1
Sly10g0177691	M1	PPR-like27	3	3	3	3	3	3	2	3	2	3
Sly10g0177701	M9	NA	47	49	34	57	81	76	163	52	69	80
Sly10g0177711	M2	NA	29	26	21	23	15	19	20	12	9	7
Sly10g0177721	M1	NA	2	1	1	1	1	1	1	1	0	1
Sly10g0177741	M3	NA	2	3	2	2	1	2	2	1	1	2
Sly10g0177761	M7	NA	5	9	3	3	5	6	10	3	1	25
Sly10g0177791	M11	NA	28	28	32	21	18	48	43	50	18	5
Sly10g0177801	M1	NA	6	7	12	55	33	2	2	5	28	26
Sly10g0177841	M22	NA	2	1	2	1	1	2	2	2	1	1
Sly10g0177891	M11	NA	26	23	32	47	72	40	35	52	44	79
Sly10g0177911	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0177931	M1	NA	3	6	5	1	1	1	1	1	1	1
Sly10g0177941	M1	NA	4	6	6	1	1	1	1	1	1	1
Sly10g0177951	M1	NA	7	12	7	2	1	1	1	1	1	1
Sly10g0177961	M1	NA	4	7	5	2	1	1	1	1	1	1
Sly10g0177991	M3	NA	34	29	26	20	26	27	33	24	24	31
Sly10g0178001	M1	HVA22K	38	36	36	33	36	30	32	36	36	35
Sly10g0178011	M11	NA	57	51

			Estimated Transcript Number								
			Pericarp					Gel			
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0224401	M3	NA	34	35	29	28	34	28	30	27	32	33
Sly03g0224411	M11	NA	28	26	27	31	40	28	25	35	42	43
Sly03g0224421	M1	NA	34	34	23	18	17	12	12	10	5	6
Sly03g0224431	M18	NA	23	22	26	42	53	32	26	38	33	34
Sly03g0224441	M11	NA	109	99	130	116	115	134	122	159	193	185
Sly03g0224461	M6	NA	44	49	41	19	9	46	52	34	21	17
Sly03g0224471	M12	NA	4	4	3	1	1	6	6	5	1	1
Sly03g0224501	M2	NA	1	2	2	2	1	1	2	1	1	1
Sly03g0224511	M3	NA	142	117	113	42	48	103	114	105	40	63
Sly03g0224531	M12	LBD41	83	78	78	85	108	107	110	128	127	175
Sly03g0224551	M14	NA	13	5	19	2	1	9	6	9	1	0
Sly03g0224581	M1	NA	14	16	20	8	10	11	9	11	8	8
Sly03g0224591	M3	SICRF9	6	5	6	4	4	4	4	2	1	2
Sly03g0224601	M3	NA	6	5	1	0	0	1	2	1	0	1
Sly03g0224611	M1	NA	194	126	114	18	17	17	14	14	4	7
Sly03g0224621	M12	NA	3	2	6	5	4	6	10	8	5	16
Sly03g0224631	M1	NA	125	85	113	16	12	37	41	23	7	13
Sly03g0224651	M1	NA	3	2	2	2	2	1	1	0	0	1
Sly03g0224661	M19	NA	10	11	10	6	18	10	10	10	6	15
Sly03g0224671	M18	NA	62	64	67	70	68	83	70	80	39	39
Sly03g0224681	M1	NA	36	64	19	1	1	1	1	1	0	0
Sly03g0224691	M1	NA	15	25	12	5	8	7	7	9	6	8
Sly03g0224711	M1	NA	135	126	181	97	61	74	55	68	6	17
Sly03g0224721	M11	NA	42	35	53	38	73	80	68	100	60	87
Sly03g0224731	M3	NA	29	25	24	14	16	24	23	22	16	9
Sly03g0224741	M12	NA	45	43	42	47	42	53	58	63	72	47
Sly03g0224751	M11	NA	23	21	20	20	26	21	19	26	27	28
Sly03g0224761	M11	SIHDA8	18	18	20	14	17	21	18	21	22	26
Sly03g0224771	M13	NA	22	21	31	30	33	21	22	25	24	33
Sly03g0224781	M1	NA	20	20	20	10	6	19	18	17	5	2
Sly03g0224791	M11	NA	24	23	32	32	32	43	31	47	20	21
Sly03g0224821	M19	NA	37	36	35	31	36	31	26	31	27	32
Sly03g0224831	M1	NA	66	64	61	55	50	54	55	55	47	42
Sly03g0224861	M1	NA	39	68	55	4	1	4	1	2	1	1
Sly03g0224871	M23	NA	2	2	1	1	0	5	2	2	1	0
Sly03g0224881	M3	NA	4	3	4	5	6	3	3	2	5	6
Sly03g0224891	M12	NA	2	3	2	2	1	5	6	6	6	5
Sly03g0224901	M22	NA	4	1	2	1	1	8	1	7	1	1
Sly03g0224911	M11	NA	4	3	4	3	3	13	11	16	4	6
Sly03g0224921	M1	NA	25	24	25	24	29	20	20	21	24	28
Sly03g0224931	M23	NA	1	1	1	1	1	1	1	1	0	0
Sly03g0224941	M12	NA	12	11	11	11	18	15	15	15	23	27
Sly03g0224951	M22	NA	1	1	1	1	0	3	1	2	1	1
Sly03g0224981	M1	NA	10	9	11	7	8	10	7	8	4	5
Sly03g0224991	M1	NA	15	12	27	8	11	8	6	8	1	1
Sly03g0225001	M1	NA	1	1	1	1	1	1	0	1	1	0
Sly03g0225011	M11	NA	4	3	3	3	3	4	3	4	3	3
Sly03g0225021	M11	NA	3	2	2	2	1	4	4	4	1	1
Sly03g0225031	M1	NA	16	17	9	18	13	7	3	4	1	1
Sly03g0225041	M12	NA	14	17	9	38	19	33	23	17	3	3
Sly03g0225051	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly03g0225061	M11	NA	25	21	23	22	26	25	21	26	29	31
Sly03g0225071	M3	NA	240	236	212	199	185	218	223	215	305	254
Sly03g0225081	M12	NA	1	1	1	1	0	1	1	1	1	0
Sly03g0225101	M22	NA	9	8	8	6	7	9	7	8	9	12
Sly03g0225111	M12	SICYP734A7	2	1	1	0	1	9	5	6	1	1
Sly03g0225121	M12	NA	5	5	5	3	2	6	6	5	3	2
Sly03g0225131	M3	NA	35	37	26	15	14	23	24	18	15	15
Sly03g0225151	M4	NA	27	23	24	38	63	28	27	21	27	67
Sly03g0225171	M1	NA	3	4	4	4	1	1	1	1	1	1
Sly03g0225181	M1	NA	3	4	3	3	3	1	1	1	1	1
Sly03g0225191	M11	NA	14	14	17	16	18	18	17	19	24	20
Sly03g0225201	M2	NA	37	38	34	52	49	34	36	34	88	63
Sly03g0225211	M12	NA	27	26	28	43	63	35	46	47	78	83
Sly03g0225221	M11	NA	1	1	1	1	1	2	2	2	1	3
Sly03g0225231	M11	NA	2	2	2	1	1	8	6	9	1	2
Sly03g0225241	M11	NA	1	0	1	0	0	2	1	2	0	0
Sly03g0225251	M22	NA	1	1	1	0	0	2	1	2	1	1
Sly03g0225261	M19	NA	11	10	11	10	11	10	10	10	8	5
Sly03g0225271	M22	NA	1	1	1	1	1	2	0	2	1	3
Sly03g0225281	M11	NA	1	1	1	1	1	1	1	2	1	2
Sly03g0225311	M11	NA	5	5	8	8	11	10	8	11	6	4
Sly03g0225331	M2	NA	50	50	48	61	64	47	52	49	70	76
Sly03g0225341	M11	NA	1	1	1	2	2	2	1	2	2	1
Sly03g0225351	M3	NA	32	35	10	1	2	11	9	2	1	1
Sly03g0225361	M3	NA	126	135	124	129	108	116	122	102	81	80
Sly03g0225371	M1	NA	113	105	105	77	85	81	84	78	80	96
Sly03g0225381	M1	NA	2	1	1	0	0	1	1	1	0	0
Sly03g0225391	M14	NA	48	43	51	49	54	50	45	54	41	42
Sly03g0225401	M11	NA	19	14	23	41	38	28	24	26	37	25
Sly03g0225411	M11	NA	4	2	5	1	2	7	5	6	1	1
Sly03g0225421	M11	NA	2	2	1	1	2	3	2	3	2	1
Sly03g0225431	M1	NA	20	18	17	6	8	7	6	7	3	3
Sly03g0225441	M1	NA	63	64	62	62	57	63	60	59	53	45
Sly03g0225461	M1	SIAux/IAA19	25	11	11	0	0	1	1	1	1	0
Sly03g0225481	M1	SIAux/IAA15	867	793	662	215	175	468	421	381	196	126
Sly03g0225491	M12	NA	46	60	90	169	148	364	445	455	180	69
Sly03g0225501	M11	NA	14	14	17	22	27	29	31	35	16	17
Sly03g0225511	M3	SICycA2;1	1	1	1	1	1	1	1	1	1	1
Sly03g0225521	M11	NA	44	33	31	9	3	80	75	73	8	1
Sly03g0225531	M3	NA	7	8	7	6	6	6	7	7	6	6
Sly03g0225541	M1	NA	21	22	19	19	29	17	15	16	20	20
Sly03g0225551	M1	NA	88	73	32	1	3	5	4	1	1	1
Sly03g0225561	M1	NA	19	19	19	20	23	17	15	17	17	19
Sly03g0225571	M11	NA	47	41	46	52	59	53	58	59	75	76
Sly03g0225581	M1	SIAux/IAA27	130	87	177	22	9	72	60	74	8	3
Sly03g0225601	M11	NA	25	20	27	26	36	29	27	36	55	56
Sly03g0225611	M19	NA	2	2	3	1	1	3	2	2	1	1
Sly03g0225621	M12	NA	9	10	12	6	3	15	12	13	3	1
Sly03g0225631	M9	NA	33	32	31	25	18	36	48	33	28	20
Sly03g0225641	M9	NA	226	329	218	283	333	802	1261	701	372	460
Sly03g0225651	M11	NA	15	12	19	25	26	26	25	30	33	29
Sly03g0225661	M12	NA	1	1	1	65	445	1	1	1	268	339
Sly03g0225671	M12	NA	3	4	4	49	211	3	3	4	213	206
Sly03g0225691	M3	NA	28	27	26	32	35	23	24	23	40	43
Sly03g0225701	M21	NA	12	12	14	8	4	14	5	10	2	1
Sly03g0225711	M11	NA	32	31	40	47	50	45	47	59	45	59
Sly03g0225721	M11	NA	99	71	101	110	125	205	201	267	182	176
Sly03g0225741	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0225751	M11	NA	59	51	63	67	87	70	65	87	90	148
Sly03g0225761	M12	NA	4	4	4	7	6	6	5	6	6	3
Sly03g0225771	M12	NA	3	3	4	25	20	6	5	7	31	24
Sly03g0225781	M3	NA	22	23	19	36	47	21	24	18	33	35
Sly03g0225791	M3	NA	126	109	117	93	119	99	127	94	66	126
Sly03g0225801	M12	NA	52	68	60	135	94	64	82	91	165	97
Sly03g0225811	M1	NA	27	26	29	47	101	19	20	19	47	105
Sly03g0225821	M3	NA	18	17	13	20	23	13	14	14	22	32
Sly03g0225831	M2	NA	41	41	39	57	71	37	42	37	61	76
Sly03g0225841	M12	NA	14	14	15	9	8	16	15	17	11	8
Sly03g0225851	M3	NA	16	19	16	14	11	15	15	14	17	14
Sly03g0225861	M1	NA	177	168	154	116	90	112	115	111	122	82
Sly03g0225871	M1	NA	3	2	4	1	1	1	1	1	1	0
Sly03g0225881	M1	NA	1	1	1	1	1	1	1	0	0	0
Sly03g0225891	M3	NA	26	29	19	8	7	15	15	10	7	5
Sly03g0225901	M11	NA	13	12	12	11	12	16	13	19	13	17
Sly03g0225911	M11	NA	5	5	6	6	6	14	11	19	5	5
Sly03g0225921	M11	SIERF.H6	5	5	9	6	5	34	25	48	1	1
Sly03g0225931	M11	NA	61	58	61	107	137	159	126	154	95	131
Sly03g0225941	M22	NA	1	0	1	0	0	1	1	2	0	0
Sly03g0225961	M12	NA	86	83	98	67	74	93	93	101	130	142
Sly03g0225981	M11	NA	5	3	6	3	2	9	8	9	1	1
Sly03g0225991	M1	NA	13	12	13	13	12	12	10	10	4	1
Sly03g0226001	M18	NA	27	26	34	10	5	37	24	38	20	11
Sly03g0226021	M1	NA	9	7	6	5	6	1	1	1	3	3

			Estimated Transcript Number								
			Pericarp					Gel			
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0178101	M17	NA	334	237	329	332	361	215	174	251	256	299
Sly10g0178111	M17	NA	523	346	494	620	743	328	258	432	431	578
Sly10g0178171	M1	NA	16	17	21	133	94	2	2	3	80	48
Sly10g0178181	M3	NA	8	9	4	1	1	2	2	1	3	1
Sly10g0178191	M12	NA	5	6	6	13	13	6	7	6	16	17
Sly10g0178201	M22	NA	1	1	1	1	1	2	0	2	1	1
Sly10g0178341	M11	NA	12	8	11	2	1	17	10	18	2	1
Sly10g0178351	M3	NA	246	235	203	197	156	140	166	123	176	150
Sly10g0178421	M11	NA	18	16	18	21	19	18	17	21	24	30
Sly10g0178431	M22	NA	1	1	1	1	1	1	1	2	1	1
Sly10g0178461	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0178501	M22	NA	2	1	1	1	1	1	1	2	1	0
Sly10g0178511	M7	NA	1	2	1	1	1	1	2	1	1	4
Sly10g0178551	M3	NA	123	140	95	19	35	85	89	19	5	8
Sly10g0178561	M12	NA	12	13	15	12	11	14	15	16	20	24
Sly10g0178611	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0178621	M8	NA	51	54	45	42	38	51	52	43	40	39
Sly10g0178681	M3	NA	31	33	11	3	2	10	8	4	2	2
Sly10g0178691	M3	NA	29	35	22	18	24	22	21	17	17	23
Sly10g0178701	M3	NA	1	1	1	1	1	1	1	1	2	4
Sly10g0178711	M3	NA	10	10	8	14	12	7	7	6	11	11
Sly10g0178731	M22	NA	12	10	9	2	1	15	7	12	1	1
Sly10g0178751	M1	EDS5	5	5	4	3	2	2	2	1	1	1
Sly10g0178861	M3	NA	13	12	10	8	4	8	10	7	5	2
Sly10g0178901	M6	NA	35	48	28	16	18	40	46	21	26	26
Sly10g0178911	M11	NA	86	89	78	68	84	103	91	101	78	116
Sly10g0179001	M12	NA	3	4	2	3	3	3	3	4	4	5
Sly10g0179041	M1	NA	24	28	24	3	1	22	22	24	2	1
Sly10g0179051	M3	NA	607	880	393	39	46	404	466	95	13	15
Sly10g0179081	M3	NA	7	7	6	6	6	6	7	6	11	8
Sly10g0179091	M18	NA	9	10	8	9	8	10	10	10	12	8
Sly10g0179171	M5	NA	198	184	158	179	156	176	215	171	172	176
Sly10g0179191	M8	NA	114	109	86	95	95	102	132	99	101	117
Sly10g0179221	M15	NA	121	104	89	104	103	112	125	116	111	120
Sly10g0179261	M12	NA	18	19	25	38	80	25	27	31	53	71
Sly10g0179291	M22	NA	1	0	1	0	0	3	0	1	0	0
Sly10g0179311	M11	NA	2	2	3	2	2	2	2	3	2	2
Sly10g0179351	M1	NA	31	26	34	25	17	23	25	26	10	12
Sly10g0179361	M12	NA	1	1	1	3	2	3	3	3	1	0
Sly10g0179391	M1	NA	1	1	2	1	0	1	0	0	0	0
Sly10g0179401	M1	NA	50	28	74	4	1	3	2	2	1	0
Sly10g0179411	M12	NA	16	15	16	10	6	21	28	22	8	4
Sly10g0179421	M3	NA	16	19	15	10	10	14	14	12	12	10
Sly10g0179431	M1	TPI	2	3	1	1	0	1	1	1	1	0
Sly10g0179441	M2	NA	68	67	59	61	43	60	72	58	55	44
Sly10g0179451	M11	NA	21	10	6	0	0	50	16	35	1	1
Sly10g0179461	M12	NA	3	1	1	0	0	5	2	3	0	0
Sly10g0179471	M1	NA	17	15	16	19	34	6	6	6	13	57
Sly10g0179511	M3	NA	18	20	17	20	20	14	20	11	20	26
Sly10g0179851	M3	NA	33	58	12	1	1	38	28	1	1	1
Sly10g0179891	M20	NA	3	2	4	0	1	1	1	1	1	0
Sly10g0179901	M22	NA	2	1	1	0	0	3	1	2	0	0
Sly10g0180031	M1	NA	3	2	2	2	2	0	0	1	0	0
Sly10g0180061	M9	NA	2	3	3	5	7	2	4	3	7	12
Sly10g0180071	M1	NA	5	6	11	23	66	1	1	1	1	15
Sly10g0180081	M1	NA	5	5	6	4	5	3	3	3	3	9
Sly10g0180091	M1	NA	3	3	4	2	4	2	1	2	1	6
Sly10g0180101	M1	NA	41	34	46	15	5	37	27	28	1	1
Sly10g0180111	M22	NA	8	4	6	1	1	6	2	13	1	1
Sly10g0180121	M19	NA	49	54	50	65	66	54	45	51	42	44
Sly10g0180131	M22	NA	1	1	1	1	1	2	1	1	2	2
Sly10g0180141	M12	NA	3	2	2	2	2	3	3	3	2	2
Sly10g0180191	M1	NA	5	5	6	5	4	4	3	3	1	1
Sly10g0180211	M1	NA	3	3	4	3	3	2	2	2	1	1
Sly10g0180221	M1	NA	1	2	2	1	1	1	1	1	2	1
Sly10g0180231	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly10g0180241	M1	NA	2	2	1	0	0	1	1	1	0	0
Sly10g0180251	M1	NA	17	6	46	42	33	4	2	25	18	14
Sly10g0180261	M21	NA	1	1	2	2	3	1	0	1	1	1
Sly10g0180301	M11	NA	8	8	9	6	8	10	8	10	11	13
Sly10g0180311	M11	NA	6	6	7	6	8	8	7	10	9	16
Sly10g0180321	M1	NA	4	4	5	5	5	3	2	2	2	1
Sly10g0180331	M11	NA	9	5	11	14	29	20	17	24	20	23
Sly10g0180341	M11	NA	44	44	40	44	51	47	43	50	59	61
Sly10g0180351	M19	NA	12	11	13	13	11	13	11	13	12	9
Sly10g0180361	M12	NA	44	48	45	33	41	49	50	43	45	52
Sly10g0180371	M1	NA	4	5	2	1	1	1	1	1	1	1
Sly10g0180381	M1	NA	23	26	16	3	2	3	3	2	1	1
Sly10g0180391	M12	NA	62	61	71	87	45	78	89	93	75	68
Sly10g0180401	M10	SMT2-like1	5	5	4	2	2	9	8	2	1	1
Sly10g0180411	M18	NA	5	5	6	7	6	6	5	6	4	4
Sly10g0180421	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0180431	M1	NA	32	38	38	62	66	27	26	26	27	26
Sly10g0180471	M3	NA	2	3	2	1	0	2	3	2	1	0
Sly10g0180481	M3	NA	7	11	9	1	1	7	6	3	14	21
Sly10g0180521	M1	NA	46	66	49	43	37	11	13	8	2	5
Sly10g0180531	M3	NA	11	9	11	2	1	9	7	3	1	1
Sly10g0180561	M3	NA	172	158	104	8	9	36	38	12	4	2
Sly10g0180571	M1	NA	64	50	66	9	9	2	2	1	1	1
Sly10g0180581	M1	NA	2	2	1	0	0	1	1	1	0	1
Sly10g0180591	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly10g0180751	M11	NA	5	5	7	2	1	7	6	6	1	1
Sly10g0180761	M22	NA	1	1	1	0	0	4	1	3	0	0
Sly10g0180771	M6	NA	152	166	108	112	135	139	178	112	116	148
Sly10g0180781	M12	NA	5	4	5	4	4	6	6	6	5	4
Sly10g0180791	M12	NA	9	8	6	7	4	10	8	8	5	4
Sly10g0180801	M11	NA	7	6	8	6	4	7	6	7	6	3
Sly10g0180821	M12	NA	8	6	12	2	2	18	16	13	1	1
Sly10g0180831	M2	NA	21	28	24	15	12	14	18	12	11	12
Sly10g0180841	M10	NA	46	53	35	30	26	61	73	37	30	29
Sly10g0180851	M11	NA	26	27	28	49	117	46	43	54	91	157
Sly10g0180861	M11	NA	70	74	83	117	122	83	86	96	132	159
Sly10g0180871	M1	NA	8	10	11	13	20	9	8	9	17	29
Sly10g0180881	M18	NA	9	9	9	13	23	9	7	11	14	24
Sly10g0180911	M2	NA	31	30	28	36	42	26	32	24	37	43
Sly10g0180921	M11	NA	24	22	26	25	24	27	25	27	21	20
Sly10g0180951	M3	NA	74	78	71	76	84	57	63	56	91	95
Sly10g0180961	M1	NA	30	32	28	50	58	22	23	22	50	45
Sly10g0180971	M12	NA	29	28	25	22	11	33	34	29	14	8
Sly10g0180981	M9	CDKB1;1-1	6	4	3	1	1	6	6	4	1	1
Sly10g0180991	M12	NA	1	1	1	40	30	2	1	1	6	16
Sly10g0181001	M6	NA	108	154	64	87	165	89	130	50	163	373
Sly10g0181011	M3	NA	23	22	19	15	14	20	21	18	28	33
Sly10g0181021	M12	NA	40	54	44	41	40	47	54	44	46	58
Sly10g0181041	M11	SIPILS6	254	201	458	234	346	433	456	532	161	262
Sly10g0181051	M11	NA	2	1	1	1	1	5	5	3	1	1
Sly10g0181061	M22	NA	38	37	36	31	29	42	35	41	30	35
Sly10g0181071	M12	NA	5	6	6	4	2	8	9	7	2	1
Sly10g0181111	M11	NA	121	101	109	166	186	161	167	176	178	198
Sly10g0181121	M8	NA	43	49	37	51	38	41	50	42	62	33
Sly10g0181131	M3	NA	98	95	63	162	120	78	83	52	130	138
Sly10g0181141	M1	NA	8	10	9	5	3	5	4	4	2	2
Sly10g0181151	M19	NA	5	5	5	5	3	5	4	5	2	1
Sly10g0181161	M3	NA	29	30	21	24	32	21	18	18	28	32
Sly10g0181171	M1	NA	3	2	2	1	1	2	1	1	2	1
Sly10g0181181	M5	NA	74	84	49	35	37	75	81	60	52	72
Sly10g0181211	M12	NA	61	64	55	56	49	71	69	64	46	43
Sly10g0181221	M22	NA	3	3	5	5	4	6	3	5	1	1
Sly10g0181231	M11	NA	38	36	56	77	107	71	62	81	55	110
Sly10g0181241	M3	NA	336	346	327	261	200	308	349	266	153	112
Sly10g0181251	M11	NA	14	12	13	16	16	14	14	16	15

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0226041	M14	NA	70	62	86	103	107	61	55	67	78	102
Sly03g0226071	M3	NA	3	4	2	2	3	1	1	1	1	1
Sly03g0226081	M1	NA	56	123	78	282	430	10	8	10	58	124
Sly03g0226091	M6	NA	36	65	14	4	6	19	28	7	3	5
Sly03g0226121	M1	NA	19	18	21	27	26	12	14	15	19	18
Sly03g0226131	M12	NA	29	30	31	57	50	32	31	31	43	49
Sly03g0226141	M1	NA	27	29	28	28	28	27	24	23	23	19
Sly03g0226151	M1	NA	18	20	18	10	8	16	17	16	10	14
Sly03g0226161	M12	NA	27	26	33	199	133	39	40	59	339	216
Sly03g0226171	M14	NA	25	22	34	39	43	24	22	23	8	12
Sly03g0226181	M1	SlAux/IAA26	13	10	9	4	3	5	3	3	1	1
Sly03g0226191	M11	HXK	26	26	27	22	7	37	29	30	4	1
Sly03g0226201	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly03g0226211	M11	NA	111	107	94	12	47	132	123	123	10	42
Sly03g0226221	M3	NA	8	6	2	0	0	2	2	1	1	0
Sly03g0226231	M11	NA	10	11	11	9	9	12	11	11	10	11
Sly03g0226241	M18	NA	17	17	20	17	18	21	16	20	17	21
Sly03g0226251	M2	NA	64	72	50	40	41	42	51	39	43	52
Sly03g0226261	M1	NA	1	1	1	1	1	1	1	1	1	2
Sly03g0226291	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly03g0226301	M1	NA	172	175	262	26	2	15	7	5	1	1
Sly03g0226321	M1	NA	34	59	30	2	0	3	2	1	0	0
Sly03g0226341	M11	NA	33	33	31	44	55	35	35	42	57	73
Sly03g0226381	M11	NA	13	13	13	12	11	15	13	14	13	15
Sly03g0226391	M11	NA	13	12	14	17	16	15	14	16	15	13
Sly03g0226401	M18	NA	131	100	132	65	64	121	107	156	82	79
Sly03g0226411	M2	NA	15	14	14	11	11	13	15	13	10	15
Sly03g0226421	M3	NA	53	48	38	37	45	40	41	41	57	64
Sly03g0226431	M1	NA	17	19	22	33	18	8	8	17	66	32
Sly03g0226441	M11	NA	223	205	229	256	213	227	215	236	333	252
Sly03g0226451	M19	NA	12	11	12	12	11	11	10	12	11	11
Sly03g0226461	M1	NA	451	423	412	264	192	316	349	316	265	181
Sly03g0226471	M23	NA	4	2	2	1	1	9	4	5	1	1
Sly03g0226481	M9	NA	42	50	36	39	100	55	101	49	57	207
Sly03g0226491	M3	NA	48	43	47	50	45	41	44	40	53	51
Sly03g0226501	M19	NA	23	27	24	24	29	24	24	24	23	28
Sly03g0226521	M3	NA	4	6	4	8	24	2	3	2	5	29
Sly03g0226531	M2	NA	33	35	30	35	37	28	32	26	33	32
Sly03g0226541	M1	NA	1	2	1	4	5	1	1	1	1	1
Sly03g0226571	M18	NA	9	10	10	6	6	9	10	10	2	1
Sly03g0226581	M12	NA	27	28	27	29	33	29	31	30	40	49
Sly03g0226591	M9	NA	86	76	86	93	122	95	123	97	60	167
Sly03g0226601	M22	NA	2	2	2	2	3	6	3	4	4	4
Sly03g0226611	M11	NA	34	33	38	40	44	46	46	48	49	51
Sly03g0226621	M3	NA	20	18	14	13	12	14	14	13	12	12
Sly03g0226631	M1	NA	37	40	40	33	30	35	31	32	28	28
Sly03g0226651	M12	NA	11	11	10	9	11	13	14	11	9	10
Sly03g0226661	M1	NA	16	18	19	31	33	13	13	16	16	10
Sly03g0226671	M1	NA	85	127	190	626	893	60	91	159	1160	689
Sly03g0226681	M12	NA	1	1	1	1	1	1	1	2	3	1
Sly03g0226691	M12	NA	5	5	6	6	3	8	9	8	7	8
Sly03g0226701	M1	NA	36	34	37	29	25	18	14	15	7	6
Sly03g0226711	M1	MSI4	26	23	24	13	21	21	18	20	10	11
Sly03g0226721	M3	NA	230	244	207	159	122	149	163	117	93	94
Sly03g0226751	M1	NA	17	16	24	1	1	7	1	4	0	0
Sly03g0226761	M1	NA	9	10	11	7	4	2	2	2	1	1
Sly03g0226771	M3	NA	51	69	34	9	80	29	76	29	10	172
Sly03g0226781	M11	NA	13	12	13	14	16	16	12	17	13	14
Sly03g0226791	M1	NA	64	67	66	51	41	40	40	38	27	27
Sly03g0226801	M1	NA	13	13	14	14	16	11	11	12	13	18
Sly03g0226811	M12	NA	38	49	32	64	56	55	86	52	130	154
Sly03g0226821	M9	NA	7	9	8	14	20	9	10	8	14	21
Sly03g0226851	M3	NAP1;4	96	93	88	75	86	85	89	87	109	123
Sly03g0226861	M17	NA	57	58	52	55	71	48	44	55	63	79
Sly03g0226871	M11	NA	25	21	24	25	9	35	33	35	15	9
Sly03g0226881	M1	NA	61	57	62	56	69	52	52	58	81	136
Sly03g0226921	M12	NA	1	1	2	1	2	1	2	2	2	3
Sly03g0226931	M11	NA	4	4	4	5	4	4	4	4	5	4
Sly03g0226941	M2	NA	32	31	24	24	24	26	33	28	27	34
Sly03g0226951	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0226961	M5	NA	97	97	96	103	99	98	101	90	91	80
Sly03g0226971	M6	NA	48	44	30	9	5	58	46	28	3	2
Sly03g0226981	M3	NA	87	78	73	57	54	66	65	64	55	59
Sly03g0226991	M13	NA	39	37	47	65	103	46	45	59	121	132
Sly03g0227001	M14	NA	13	12	20	16	21	15	10	17	10	6
Sly03g0227011	M15	NA	68	64	54	48	47	60	59	71	82	89
Sly03g0227021	M12	NA	1	1	1	1	0	5	5	4	1	0
Sly03g0227031	M12	SlPP2C5	178	161	151	118	129	253	244	189	159	143
Sly03g0227041	M9	NA	13	20	13	29	56	31	44	31	46	62
Sly03g0227051	M12	NA	2	2	1	1	0	10	9	8	1	1
Sly03g0227061	M22	NA	63	48	48	15	21	56	52	53	15	23
Sly03g0227071	M11	Solyc03g121920	60	48	66	47	40	88	75	109	44	38
Sly03g0227081	M3	NA	10	10	7	6	6	4	5	4	2	5
Sly03g0227091	M12	NA	7	7	6	11	9	9	8	7	16	12
Sly03g0227101	M11	NA	92	86	103	88	102	99	83	103	89	103
Sly03g0227111	M12	NA	43	45	46	71	94	51	52	55	57	55
Sly03g0227121	M3	NA	8	7	7	2	1	5	11	5	1	1
Sly03g0227131	M1	NA	101	92	102	93	86	88	81	90	107	99
Sly03g0227141	M2	NA	37	39	37	37	56	34	45	35	50	77
Sly03g0227151	M2	NA	14	16	13	8	5	7	10	5	10	11
Sly03g0227181	M11	NA	24	22	25	25	29	27	26	30	34	35
Sly03g0227201	M3	NA	20	20	17	17	18	19	17	20	21	19
Sly03g0227211	M1	NA	42	41	32	12	8	27	22	20	5	4
Sly03g0227221	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly03g0227231	M12	NA	1	1	1	1	1	1	1	1	1	0
Sly03g0227241	M12	NA	55	59	59	83	74	56	65	62	117	97
Sly03g0227261	M3	NA	2	2	2	4	5	2	2	2	14	16
Sly03g0227271	M7	NA	45	61	44	98	142	52	71	45	61	87
Sly03g0227281	M12	NA	15	22	24	98	33	41	56	75	159	57
Sly03g0227321	M1	NA	7	6	7	8	6	2	2	2	2	2
Sly03g0227331	M11	NA	54	49	55	55	62	64	63	66	93	92
Sly03g0227341	M3	Salt responsive protei	321	361	90	11	12	84	100	30	6	8
Sly03g0227361	M3	NA	16	17	13	17	19	17	14	14	18	19
Sly03g0227371	M3	NA	23	22	21	5	2	24	23	16	2	1
Sly03g0227381	M9	NA	56	49	52	38	29	55	54	53	44	41
Sly03g0227391	M3	NA	117	108	115	243	255	103	110	101	168	155
Sly03g0227401	M1	NA	21	20	18	19	26	15	14	14	18	21
Sly03g0227411	M1	NA	82	85	80	71	144	25	29	26	72	162
Sly03g0227421	M11	NA	111	106	115	225	238	188	190	211	164	199
Sly03g0227451	M3	SlLOX4 (LOXD)	148	253	108	9	26	38	53	10	2	11
Sly03g0227461	M3	CYP71A1	479	545	237	376	554	167	292	56	32	158
Sly03g0227471	M1	CYP71A1-like	2	1	2	84	44	1	1	1	4	1
Sly03g0227481	M3	NA	22	23	19	16	16	19	21	16	18	16
Sly03g0227491	M5	NA	64	82	48	45	79	70	67	43	47	65
Sly03g0227501	M5	NA	1	1	1	1	1	1	1	1	0	1
Sly03g0227511	M21	NA	2	2	2	1	1	3	2	1	1	1
Sly03g0227521	M3	NA	2	3	1	1	1	1	1	1	0	0
Sly03g0227541	M9	NA	16	15	13	17	18	20	22	19	18	18
Sly03g0227551	M1	NA	5	6	5	2	1	1	1	1	0	0
Sly03g0227561	M12	SlDML4	6	8	8	10	7	11	10	10	6	4
Sly03g0227571	M7	NA	3	4	4	3	3	3	5	3	4	3
Sly03g0227581	M14	NA	42	34	45	41	38	28	30	36	16	72
Sly03g0227621	M19	NA	40	42	49	60	49	47	40	47	30	38
Sly03g0227631	M3	SIERF.E3	121	131	82	111	109	109	139	72	110	118
Sly03g0227651	M19	NA	41	53	50	45	40	47	46	44	35	40
Sly03g0227661	M1	NA	38	41	41	31	31	35	32	34	37	34
Sly03g0227671	M4	NA	1	1	2	3	26	2	1	1	1	29
Sly03g0227681	M12	SAUR39	1	2	1	5	14	7	4	6	1	3
Sly03g0227691	M12	NA	22	23	17	58	139	28	29	26	59	182
Sly03g0227711	M3	NA	37	53	35	46	47	24	29	22	34	45
Sly03g0227721	M11	NA	2	3	3	3	1	11	8	16	2	1
Sly03g0227731	M23	NA	2	1	1	1	1	2	2	1	1	1
Sly03g0227741	M12	NA	20	24	23	54	59	46	51	52	86	68
Sly03g0227751	M1	ALAAT1	97	96	92	114	116	68	69	73	96	90

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0181291	M10	NA	52	67	48	30	32	79	94	45	15	16
Sly10g0181301	M23	NA	6	2	2	1	1	14	6	2	1	1
Sly10g0181321	M1	NA	1295	1120	2346	1609	244	30	1	4	2	1
Sly10g0181341	M1	NA	211	249	281	234	106	6	2	1	1	1
Sly10g0181351	M1	NA	526	561	953	2163	628	33	13	16	2	1
Sly10g0181361	M1	NA	8	13	16	4	1	1	1	1	1	1
Sly10g0181401	M1	NA	1	6	4	126	12	0	3	1	2	1
Sly10g0181411	M1	NA	34	20	25	2	1	22	21	23	2	1
Sly10g0181541	M5	NA	79	168	99	3	3	143	186	8	1	3
Sly10g0181571	M11	NA	26	24	26	4	4	49	33	59	5	5
Sly10g0181581	M12	NA	17	21	18	24	25	27	25	28	44	31
Sly10g0181591	M1	NA	1	1	1	1	1	1	0	1	0	0
Sly10g0181601	M3	NA	14	16	5	5	8	8	9	6	4	6
Sly10g0181611	M12	NA	3	3	4	29	40	10	8	17	56	80
Sly10g0181651	M11	NA	104	84	89	108	117	108	117	118	104	115
Sly10g0181671	M6	NA	72	83	48	29	46	61	74	29	30	53
Sly10g0181691	M9	NA	2	1	1	1	2	2	3	2	6	3
Sly10g0181761	M11	NA	35	31	40	51	47	34	35	42	60	57
Sly10g0181791	M1	NA	2	2	2	2	2	2	2	2	1	1
Sly10g0181801	M12	NA	1	1	1	1	0	1	1	1	1	1
Sly10g0181831	M5	NA	36	58	16	6	2	38	39	6	1	1
Sly10g0181861	M3	NA	1	1	1	1	0	1	1	0	0	0
Sly10g0181871	M3	PDC1	470	459	368	128	155	239	223	242	269	241
Sly10g0181891	M12	NA	1	1	1	1	0	2	2	4	3	1
Sly10g0181901	M11	NA	1	1	1	1	1	2	2	3	2	1
Sly10g0181921	M1	NA	5	6	2	1	1	1	1	1	1	1
Sly10g0181951	M1	NA	17	18	22	19	20	15	18	13	14	14
Sly10g0181961	M1	NA	38	39	40	36	43	33	36	31	36	40
Sly10g0181971	M1	NA	42	43	55	253	293	38	31	47	75	70
Sly10g0182031	M2	NA	1	2	1	1	1	1	2	1	1	1
Sly10g0182041	M1	NA	26	39	33	8	8	10	9	18	24	2
Sly10g0182051	M2	NA	41	134	34	2	13	13	41	3	12	2
Sly10g0182061	M1	NA	31	27	27	27	28	12	10	6	4	8
Sly10g0182071	M11	NA	1	2	2	2	1	2	3	4	1	1
Sly10g0182081	M1	NA	13	10	16	2	1	4	4	3	1	1
Sly10g0182091	M1	NA	2	2	2	1	1	1	1	1	1	0
Sly10g0182111	M11	NA	44	44	51	38	33	66	61	71	57	63
Sly10g0182121	M12	NA	10	9	10	18	29	13	12	14	34	37
Sly10g0182141	M1	NA	9	10	11	10	15	8	6	9	5	4
Sly10g0182161	M5	NA	2	3	1	1	1	2	2	1	1	1
Sly10g0182171	M1	SlLAX4	1	2	2	1	1	1	1	1	1	0
Sly10g0182181	M12	NA	21	20	20	17	20	23	23	25	22	20
Sly10g0182191	M12	NA	5	4	5	6	6	6	5	5	3	5
Sly10g0182221	M1	NA	7	7	11	11	5	1	1	1	1	0
Sly10g0182231	M1	NA	2	2	2	1	1	0	0	0	0	0
Sly10g0182241	M11	NA	36	33	34	36	35	42	44	47	45	47
Sly10g0182251	M18	NA	49	55	54	50	54	60	53	54	44	53
Sly10g0182271	M12	NA	48	47	55	66	39	78	86	83	73	63
Sly10g0182281	M23	NA	1	1	1	1	0	2	1	1	1	0
Sly10g0182291	M19	NA	30	32	30	37	40	26	24	25	31	28
Sly10g0182301	M22	NA	13	13	14	16	15	15	13	15	9	4
Sly10g0182311	M1	NA	28	23	28	36	22	22	23	24	51	46
Sly10g0182331	M1	NA	19	13	27	6	3	5	6	6	6	2
Sly10g0182341	M11	NA	41	40	53	37	40	58	46	58	41	53
Sly10g0182351	M18	NA	15	17	18	20	18	22	18	22	13	14
Sly10g0182361	M11	NA	40	33	35	45	42	46	42	48	45	51
Sly10g0182371	M2	NA	288	284	273	280	192	180	245	159	151	172
Sly10g0182381	M3	NA	44	44	33	28	19	31	32	27	17	15
Sly10g0182391	M12	NA	49	46	46	71	84	51	52	55	95	100
Sly10g0182401	M11	NA	15	11	18	19	21	45	46	54	40	10
Sly10g0182411	M11	NA	27	26	32	57	62	43	41	49	59	64
Sly10g0182431	M19	SlSDG2	104	99	96	81	88	98	81	100	71	90
Sly10g0182441	M22	NA	2	1	1	0	0	14	3	8	1	0
Sly10g0182451	M12	NA	5	4	5	4	2	8	6	7	5	5
Sly10g0182461	M11	NA	1	1	1	1	2	2	2	2	1	1
Sly10g0182471	M3	NA	42	48	39	30	28	41	34	34	31	23
Sly10g0182481	M3	NA	60	58	51	39	37	50	49	38	46	41
Sly10g0182491	M11	NA	107	69	135	87	43	322	259	420	115	26
Sly10g0182501	M1	NA	39	45	40	11	11	25	23	18	4	19
Sly10g0182551	M14	NA	174	160	179	159	136	156	152	178	147	147
Sly10g0182561	M1	NA	8	7	13	3	1	4	2	3	1	1
Sly10g0182571	M11	NA	1	1	1	2	1	1	1	2	1	1
Sly10g0182581	M19	SlCycT1;1	90	92	91	84	91	74	66	79	86	76
Sly10g0182591	M1	SlDRM1-like1	21	20	23	22	48	15	12	19	13	24
Sly10g0182611	M1	NA	2	3	1	1	1	0	0	0	0	0
Sly10g0182621	M1	NA	4	7	4	1	1	1	0	0	1	0
Sly10g0182631	M10	NA	16	17	11	49	31	28	31	13	8	7
Sly10g0182641	M11	NA	14	13	14	15	2	37	31	39	10	2
Sly10g0182651	M11	NA	17	22	23	27	3	55	39	62	16	2
Sly10g0182661	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0182671	M11	NA	5	4	5	7	4	12	10	15	14	5
Sly10g0182681	M11	NA	6	6	9	9	7	18	16	24	21	13
Sly10g0182691	M3	NA	78	79	62	68	87	59	56	56	54	68
Sly10g0182701	M1	NA	312	295	378	313	291	262	252	287	227	185
Sly10g0182711	M1	NA	25	20	25	20	22	22	20	22	14	18
Sly10g0182721	M1	NA	12	13	12	10	11	6	7	7	10	13
Sly10g0182741	M12	NA	8	8	6	10	18	22	26	26	29	35
Sly10g0182751	M22	NA	1	1	1	1	0	1	1	1	1	1
Sly10g0182771	M11	SlPIN9	1	1	2	1	1	2	1	1	1	1
Sly10g0182791	M1	NA	70	67	89	44	22	11	9	9	3	2
Sly10g0182801	M12	NA	10	8	11	17	23	14	17	17	19	24
Sly10g0182811	M1	NA	5	3	15	1	1	1	1	1	1	0
Sly10g0182821	M3	NA	28	29	30	33	41	21	26	22	29	30
Sly10g0182831	M1	DPB	18	19	17	28	44	12	12	10	16	25
Sly10g0182841	M1	NA	61	51	56	24	16	5	8	3	5	10
Sly10g0182851	M1	NA	140	130	127	129	122	85	90	86	134	140
Sly10g0182881	M1	NA	1	2	1	1	1	1	0	1	0	1
Sly10g0182891	M3	NA	37	34	32	30	35	32	32	29	36	35
Sly10g0182901	M3	NA	55	58	33	18	17	34	35	23	14	16
Sly10g0182911	M9	NA	30	35	20	3	1	75	71	57	12	2
Sly10g0182921	M3	NA	3	5	2	2	1	2	2	2	1	0
Sly10g0182931	M12	NA	32	31	35	43	53	42	41	43	58	73
Sly10g0182941	M1	NA	108	109	52	7	10	8	9	4	1	1
Sly10g0182951	M1	NA	144	133	115	62	45	69	82	56	58	51
Sly10g0182961	M1	NA	32	32	26	16	8	5	5	4	1	1
Sly10g0182971	M1	NA	12	11	12	10	9	7	8	8	11	16
Sly10g0182981	M1	NA	6	5	5	3	2	2	1	1	1	0
Sly10g0182991	M9	NA	1	1	1	0	1	1	2	1	1	1
Sly10g0183021	M14	NA	166	145	254	289	262	119	101	180	234	235
Sly10g0183031	M1	NA	26	29	14	13	9	1	1	1	1	1
Sly10g0183061	M15	NA	962	853	839	724	670	854	881	921	1010	833
Sly10g0183071	M15	NA	718	492	499	475	468	596	521	688	485	504
Sly10g0183091	M1	NA	220	208	214	153	151	150	153	151	186	165
Sly10g0183101	M11	NA	1	1	1	1	2	2	2	2	1	6
Sly10g0183111	M22	NA	1	1	1	1	1	2	1	1	1	0
Sly10g0183121	M11	NA	200	172	199	292	288	218	205	247	309	320
Sly10g0183131	M14	NA	6	3	10	1	1	5	5	4	1	1
Sly10g0183141	M1	NA	28	27	31	27	21	18	23	22	23	17
Sly10g0183161	M1	NA	1	1	1	1	1	0	1	1	0	1
Sly10g0183171	M3	NA	14	15	14	6	8	11	13	11	10	10
Sly10g0183181	M1	NA	36	26	38	123	80	19	13	14	6	3
Sly10g0183191	M1	NA	40	34	34	24	29	27	26	30	26	31
Sly10g0183211	M23	NA	37	16	14	80	293	58	50	26	50	189
Sly10g0183231	M23	NA	2	1	1	1	1	3	2	2	1	1
Sly10g0183241	M3	NA	27	27	22	26	25	25	24	23	24	26
Sly10g0183281	M9	NA	60	63	57	69	68	63	73	63	80	99
Sly10g0183311	M1	NA	23	23	23	25	34	19	19	21	24	31
Sly10g0183321	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0183341	M3	NA	17	18	15	16	13	16	17	15	15	11
Sly10g0183351	M3	NA	32	37	27	12	7	28	34	17	3	2
Sly10g

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly03g0227761	M7	NA	12	31	9	2	7	12	38	12	3	12
Sly03g0227771	M1	PME1	307	214	343	5	2	12	6	7	1	2
Sly03g0227781	M11	NA	32	33	33	31	33	34	35	37	37	40
Sly03g0227791	M9	NA	2	2	1	1	3	2	2	1	4	5
Sly03g0227801	M2	NA	78	82	70	58	61	60	68	48	47	62
Sly03g0227811	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly03g0227821	M6	NA	6	12	9	1	1	13	15	4	1	1
Sly03g0227841	M11	NA	7	7	8	13	14	11	10	12	12	8
Sly03g0227851	M13	NA	25	19	32	106	325	20	16	28	19	82
Sly03g0227861	M3	NA	32	28	28	32	39	30	36	23	25	25
Sly03g0227871	M1	NA	38	36	34	48	79	31	31	28	40	51
Sly03g0227881	M16	NA	23	20	17	26	46	17	17	15	26	40
Sly03g0227891	M3	NA	30	27	16	5	5	17	16	10	4	7
Sly03g0227901	M11	NA	16	13	19	21	18	28	22	30	38	28
Sly03g0227911	M11	pds	51	54	68	190	336	95	92	133	296	409
Sly03g0227921	M12	NA	2	2	2	1	1	8	10	6	2	1
Sly03g0227931	M9	NA	2	2	1	1	1	4	6	3	1	1
Sly03g0227941	M1	NA	12	15	11	10	12	7	8	7	8	7
Sly03g0227951	M12	NA	31	37	37	25	18	42	47	38	24	39
Sly03g0227961	M3	NA	47	54	45	73	93	38	50	35	64	113
Sly03g0227991	M1	NA	93	91	163	132	28	37	37	23	7	1
Sly03g0228001	M11	NA	59	54	62	66	65	75	69	82	97	106
Sly03g0228011	M8	NA	18	20	12	4	5	25	23	11	2	4
Sly03g0228021	M3	NA	56	68	56	62	62	53	56	50	63	77
Sly03g0228031	M2	NA	56	57	58	103	112	49	56	56	125	128
Sly03g0228041	M11	NA	11	13	13	14	13	18	15	18	19	16
Sly03g0228051	M19	NA	83	88	91	88	75	81	77	84	66	63
Sly03g0228061	M11	HUP6	146	136	149	137	106	171	159	179	117	88
Sly03g0228071	M11	NA	35	32	43	37	36	54	47	59	38	45
Sly03g0228091	M1	NA	12	11	11	11	12	11	11	11	12	14
Sly03g0228111	M11	NA	28	28	30	27	25	33	32	37	37	31
Sly03g0228121	M22	NA	1	1	1	0	0	2	1	3	1	0
Sly03g0228131	M18	NA	48	48	55	72	84	51	44	55	67	76
Sly03g0228141	M1	NA	11	11	9	5	5	6	6	5	6	4
Sly03g0228151	M18	NA	14	17	16	18	18	21	17	21	23	17
Sly03g0228211	M11	NA	41	42	44	42	61	51	40	49	65	95
Sly03g0228221	M1	NA	37	37	31	15	16	27	26	24	9	7
Sly03g0228241	M11	NA	31	33	34	33	37	40	37	43	40	47
Sly04g0228261	M1	NA	5	5	6	8	12	4	4	4	6	8
Sly04g0228281	M12	NA	3	4	3	23	22	12	18	11	36	29
Sly04g0228291	M11	NA	51	53	51	61	71	66	59	65	61	68
Sly04g0228311	M6	NA	28	84	29	5	3	65	105	14	2	4
Sly04g0228331	M1	NA	11	8	13	2	1	2	1	1	1	1
Sly04g0228341	M1	NA	2	1	3	1	1	1	2	1	3	8
Sly04g0228351	M2	NA	56	56	57	63	60	54	59	53	63	57
Sly04g0228361	M11	NA	4	5	5	7	4	7	7	8	5	3
Sly04g0228371	M1	NA	108	128	163	201	248	95	93	101	14	38
Sly04g0228391	M11	NA	41	37	47	61	95	55	54	65	66	102
Sly04g0228401	M1	NA	4	4	5	5	2	4	3	3	1	2
Sly04g0228411	M11	NA	1	1	1	2	1	1	1	1	1	1
Sly04g0228421	M3	NA	147	224	107	89	101	136	167	59	50	91
Sly04g0228431	M1	NA	34	28	33	40	38	29	27	27	34	31
Sly04g0228461	M11	NA	2	2	3	2	2	4	3	5	2	1
Sly04g0228471	M11	NA	3	4	4	4	3	7	6	7	4	3
Sly04g0228531	M11	SIDRM1-like2	32	30	42	34	32	44	34	51	32	31
Sly04g0228541	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0228551	M11	NA	130	122	197	134	121	171	142	191	119	183
Sly04g0228561	M12	NA	23	25	25	25	32	25	30	30	35	50
Sly04g0228571	M1	NA	16	16	15	20	14	7	6	5	6	5
Sly04g0228581	M11	NA	20	18	21	35	40	28	27	35	67	68
Sly04g0228591	M1	NA	31	29	28	31	37	23	24	26	36	36
Sly04g0228601	M1	NA	1	1	2	1	1	1	0	0	0	0
Sly04g0228621	M11	NA	110	110	125	101	118	131	119	133	142	176
Sly04g0228631	M9	NA	345	322	314	230	148	343	466	357	322	286
Sly04g0228641	M11	NA	33	30	33	33	40	34	31	39	34	42
Sly04g0228671	M12	NA	19	9	10	2	1	30	27	23	1	1
Sly04g0228721	M9	NA	33	33	30	83	67	36	44	32	92	88
Sly04g0228731	M9	NA	14	16	13	19	18	16	18	14	23	27
Sly04g0228741	M1	NA	1	1	1	1	0	1	1	1	1	0
Sly04g0228751	M1	NA	89	90	97	95	66	81	80	79	48	42
Sly04g0228761	M12	NA	2	2	2	3	2	2	3	3	5	3
Sly04g0228781	M7	NA	49	98	35	14	84	69	216	54	30	215
Sly04g0228791	M5	NA	62	79	55	49	54	67	74	57	61	73
Sly04g0228801	M19	NA	19	19	18	33	38	17	15	18	30	26
Sly04g0228811	M2	NA	107	100	108	54	28	97	112	92	67	47
Sly04g0228821	M12	NA	9	9	5	2	1	10	12	10	5	2
Sly04g0228831	M11	NA	52	45	57	56	68	73	70	77	47	52
Sly04g0228841	M1	NA	33	31	27	19	22	14	10	8	1	1
Sly04g0228851	M3	NA	6	10	7	4	2	5	4	4	1	1
Sly04g0228861	M1	NA	2	1	3	2	1	1	1	1	1	0
Sly04g0228871	M11	NA	2	2	3	2	2	3	3	3	1	1
Sly04g0228881	M1	NA	18	17	18	14	4	15	14	15	4	1
Sly04g0228891	M11	NA	2	3	3	2	1	4	3	4	4	4
Sly04g0228901	M12	NA	47	39	47	49	61	52	60	64	65	91
Sly04g0228921	M1	SNAC9	7	7	8	3	2	6	4	2	1	1
Sly04g0228941	M13	NA	11	11	12	42	96	10	12	14	59	92
Sly04g0228971	M2	NA	123	128	121	130	165	106	121	105	130	160
Sly04g0228991	M6	NA	72	101	74	83	100	69	107	70	99	121
Sly04g0229001	M17	NA	326	294	313	268	281	276	262	330	302	327
Sly04g0229011	M19	NA	41	43	43	45	45	45	39	45	47	53
Sly04g0229051	M3	NA	14	13	13	8	8	9	10	9	8	7
Sly04g0229121	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0229131	M11	NA	2	2	2	2	2	2	2	2	2	2
Sly04g0229141	M1	NRT1.2	1	1	1	2	2	1	1	1	0	0
Sly04g0229151	M1	NA	1	2	2	1	1	1	1	1	1	0
Sly04g0229161	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0229171	M9	NA	16	14	13	16	19	16	18	14	14	23
Sly04g0229181	M22	NA	4	5	3	3	3	4	4	4	2	2
Sly04g0229211	M1	NA	123	140	114	125	103	68	63	50	26	34
Sly04g0229261	M3	NA	10	10	8	5	7	9	9	6	6	6
Sly04g0229271	M1	NA	9	11	9	10	8	1	1	2	1	1
Sly04g0229281	M1	NA	4	3	4	3	1	1	1	1	1	0
Sly04g0229331	M1	NA	11	10	12	7	3	8	7	7	4	1
Sly04g0229351	M1	NA	4	4	2	1	1	4	1	3	1	1
Sly04g0229371	M1	ABCG14	2	2	2	2	2	1	1	1	2	2
Sly04g0229381	M12	PPC4	148	148	197	142	45	640	507	609	23	17
Sly04g0229411	M22	NA	1	0	1	0	0	3	0	3	0	0
Sly04g0229441	M1	NA	1	1	1	2	2	1	1	1	1	1
Sly04g0229461	M1	NA	41	58	40	14	3	5	2	2	2	1
Sly04g0229491	M1	NA	168	149	153	66	73	68	74	62	78	69
Sly04g0229521	M1	NA	60	57	40	11	5	13	14	8	1	1
Sly04g0229531	M3	NA	83	72	35	3	2	18	20	7	1	1
Sly04g0229541	M1	NA	1	1	1	1	1	0	1	0	0	0
Sly04g0229571	M12	NA	11	9	10	11	12	13	12	13	11	10
Sly04g0229581	M11	NA	14	10	15	19	19	20	18	25	14	26
Sly04g0229601	M11	NA	116	103	133	185	179	116	120	138	169	169
Sly04g0229611	M9	NA	49	60	35	12	17	83	120	73	29	32
Sly04g0229621	M3	NA	68	56	6	0	0	3	5	1	1	1
Sly04g0229631	M12	NA	82	68	52	20	6	221	197	229	30	12
Sly04g0229641	M12	NA	117	105	76	30	10	301	323	311	47	21
Sly04g0229651	M1	NA	16	20	15	7	3	9	9	9	4	2
Sly04g0229661	M3	SICRF11	30	33	21	8	4	15	14	9	5	3
Sly04g0229701	M11	NA	27	19	33	20	4	68	55	83	17	4
Sly04g0229711	M1	NA	132	131	139	71	63	84	84	75	69	58
Sly04g0229721	M2	NA	50	50	46	39	38	38	48	37	46	41
Sly04g0229731	M12	SlIPT2	1	1	1	1	1	3	2	2	2	1
Sly04g0229751	M12	NA	1	1	2	2	5	3	3	3	6	14
Sly04g0229761	M9	NA	6	6	7	10	17	7	11	8	9	17
Sly04g0229771	M11	NA	42	37	47	34	39	50	42	54	30	27
Sly04g0229781	M19	NA	57	58	60	53	66	56	53	59	54	68
Sly04g0229811	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly04g0229821	M3	TIR-NBS11	11	18	5	2	1	3	3	2	1	1
Sly04g0229831	M1	NA	5	6	5	2	1	4	3	4	1	1
Sly04g0229841	M3	NA	26	27	20	20	12	21	22	17	11	9

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0183421	M1	NA	1066	995	975	700	604	761	819	858	792	637
Sly10g0183441	M12	NA	2	1	1	2	2	2	2	2	1	1
Sly10g0183461	M15	NA	31	27	22	27	30	31	33	32	37	43
Sly10g0183471	M19	NA	37	37	37	32	30	38	32	37	27	23
Sly10g0183501	M1	NA	3	3	4	12	49	2	1	1	88	203
Sly10g0183521	M20	NA	26	18	51	7	7	22	18	19	3	6
Sly10g0183531	M3	NA	128	120	108	123	149	102	117	103	178	222
Sly10g0183541	M1	NA	14	13	15	12	15	11	12	9	13	9
Sly10g0183551	M3	NA	75	101	51	17	24	59	111	46	32	44
Sly10g0183561	M6	NA	5	8	7	2	1	4	5	2	1	1
Sly10g0183571	M1	NA	9	9	8	4	1	6	5	4	1	1
Sly10g0183581	M1	NA	32	29	35	40	40	31	27	31	38	43
Sly10g0183591	M6	NA	54	103	46	23	28	71	86	37	12	17
Sly10g0183601	M12	NA	34	28	34	71	74	181	172	167	259	241
Sly10g0183611	M12	NA	1	1	1	1	1	4	4	2	7	2
Sly10g0183621	M1	NA	10	10	9	7	5	9	7	9	4	3
Sly10g0183631	M22	NA	2	1	1	1	1	5	1	5	1	1
Sly10g0183651	M11	NA	39	37	45	31	30	49	42	55	33	43
Sly10g0183661	M1	NA	7	8	5	4	3	5	4	3	1	1
Sly10g0183671	M22	sdl1-like1	1	1	1	1	1	2	1	2	1	0
Sly10g0183691	M12	NA	1	1	1	1	0	1	1	1	0	0
Sly10g0183701	M1	NA	3	2	3	1	1	1	2	1	2	1
Sly10g0183711	M11	NA	10	11	14	15	18	15	14	19	16	17
Sly10g0183721	M3	NA	56	58	58	65	69	39	47	38	44	45
Sly10g0183741	M1	NA	10	10	12	9	5	10	10	11	6	3
Sly10g0183751	M18	NA	9	8	10	8	9	13	11	13	12	10
Sly10g0183761	M11	NA	3	3	2	1	1	6	4	5	1	1
Sly10g0183771	M11	NA	13	15	13	10	10	14	16	16	12	10
Sly10g0183781	M3	NA	3	2	1	0	0	1	1	0	0	0
Sly10g0183831	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0183841	M11	NA	4	4	4	3	2	7	6	6	2	1
Sly10g0183851	M14	NA	159	148	207	136	216	141	127	161	41	35
Sly10g0183881	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0183891	M13	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0183901	M11	NA	4	4	7	2	1	14	10	11	1	1
Sly10g0183911	M10	NA	67	120	51	17	48	134	192	78	11	72
Sly10g0183921	M3	NA	62	65	48	27	30	38	42	32	35	36
Sly10g0183931	M11	NA	5	4	6	5	3	6	6	7	3	2
Sly10g0183941	M9	NA	21	23	20	30	26	26	29	24	22	22
Sly10g0183961	M11	NA	24	21	26	15	10	35	33	36	8	6
Sly10g0183971	M11	b-lcy2	2	1	2	1	1	7	5	7	1	1
Sly10g0183981	M11	NA	9	9	12	11	8	11	11	11	6	3
Sly10g0183991	M11	NA	97	86	106	120	124	109	93	132	128	149
Sly10g0184001	M11	NA	2	2	2	1	1	4	3	3	1	0
Sly10g0184061	M12	NA	3	2	3	2	1	5	5	5	1	1
Sly10g0184071	M13	NA	10	10	14	10	6	9	12	12	6	6
Sly10g0184081	M12	NA	1	1	2	57	104	1	3	10	391	164
Sly10g0184091	M9	NA	40	43	44	84	134	49	63	47	76	149
Sly10g0184101	M22	NA	1	1	1	0	1	3	1	2	1	0
Sly10g0184111	M11	SIRR5	32	22	27	12	30	36	27	38	7	13
Sly10g0184121	M13	NA	23	19	31	41	63	30	27	41	74	83
Sly10g0184131	M11	NA	6	4	7	7	19	17	11	15	11	13
Sly10g0184141	M11	NA	1	1	1	0	1	2	1	2	1	1
Sly10g0184151	M1	NA	65	53	49	1	2	14	14	8	2	1
Sly10g0184181	M3	NA	2	2	2	2	2	2	2	1	2	2
Sly10g0184201	M8	NA	142	164	50	178	40	126	203	51	274	46
Sly10g0184211	M1	SIRR4	2	2	3	4	3	2	2	2	15	14
Sly10g0184221	M12	NA	21	22	20	27	35	20	20	25	83	86
Sly10g0184231	M12	NA	33	31	31	55	64	40	39	43	86	82
Sly10g0184241	M22	NA	1	1	1	1	5	2	1	2	1	1
Sly10g0184251	M11	NA	29	27	29	32	37	36	31	39	39	45
Sly10g0184261	M1	NA	1	1	1	1	0	1	1	1	1	0
Sly10g0184281	M10	NA	105	110	103	54	128	148	176	74	36	137
Sly10g0184301	M11	NA	35	34	36	36	34	37	37	46	30	27
Sly10g0184311	M19	NA	40	37	34	35	43	39	33	47	31	24
Sly10g0184321	M1	NA	4	4	3	1	1	1	1	1	0	0
Sly10g0184341	M3	NA	39	35	17	6	7	12	13	3	24	27
Sly10g0184351	M12	NA	368	349	402	302	524	515	580	515	304	609
Sly10g0184361	M11	NA	24	21	26	25	24	38	30	41	29	39
Sly10g0184371	M11	NA	16	13	21	12	10	28	20	33	9	8
Sly10g0184381	M5	NA	22	25	20	24	23	23	24	21	31	27
Sly10g0184391	M7	NA	1	1	1	1	1	1	3	1	1	1
Sly10g0184401	M12	SlCKX7	1	1	1	2	2	19	20	7	17	7
Sly10g0184411	M1	NA	198	194	193	150	123	148	147	140	133	101
Sly10g0184421	M3	NA	140	173	95	111	138	98	146	94	137	223
Sly10g0184451	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0184461	M3	NA	27	33	22	22	23	25	30	21	16	14
Sly10g0184471	M3	NA	56	78	41	11	10	36	32	20	6	4
Sly10g0184481	M12	NA	5	6	7	4	7	15	18	19	10	4
Sly10g0184491	M12	NA	26	30	28	33	44	79	75	96	34	16
Sly10g0184501	M1	NA	24	23	22	16	14	20	18	19	12	11
Sly10g0184511	M22	NA	4	3	2	1	1	15	5	12	1	1
Sly10g0184521	M3	NA	49	48	35	18	9	35	32	37	24	24
Sly10g0184531	M3	NA	22	24	18	9	7	20	17	19	12	11
Sly10g0184541	M9	NA	11	21	11	3	3	20	33	19	12	8
Sly10g0184551	M12	NA	11	12	15	34	44	21	22	29	46	80
Sly10g0184561	M12	NA	4	4	2	1	1	16	8	13	4	2
Sly10g0184571	M11	NA	15	16	15	28	29	20	19	21	25	20
Sly10g0184601	M2	NA	20	18	17	12	15	12	13	12	19	23
Sly10g0184611	M11	NA	31	30	33	42	49	53	46	57	44	41
Sly10g0184621	M12	NA	14	14	12	14	14	24	25	24	25	18
Sly10g0184631	M3	NA	13	16	13	11	7	15	15	11	7	6
Sly10g0184641	M3	NA	17	17	17	17	21	13	15	15	21	27
Sly10g0184651	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0184661	M21	NA	5	5	5	3	3	5	3	5	2	1
Sly10g0184671	M1	NA	9	9	9	4	3	7	6	6	3	2
Sly10g0184691	M3	SMT1-like	6	6	5	3	2	6	6	5	3	2
Sly10g0184701	M12	NA	43	46	36	44	37	48	50	49	64	45
Sly10g0184721	M3	NA	43	43	34	28	26	26	28	21	27	23
Sly10g0184731	M12	NA	26	23	30	82	128	42	44	46	76	176
Sly10g0184741	M12	NA	5	5	6	5	8	7	8	5	7	9
Sly10g0184751	M1	PG2a/SlPG	2	29	18	10548	48217	1	1	1	40	583
Sly10g0184761	M1	NA	3	3	3	3	4	2	2	2	3	3
Sly10g0184771	M1	NA	45	41	42	45	48	22	27	23	13	36
Sly10g0184791	M2	NA	26	29	25	36	33	24	31	26	33	41
Sly10g0184811	M10	NA	26	33	23	21	30	37	34	22	23	37
Sly10g0184821	M1	NA	4	3	3	4	4	2	2	2	3	5
Sly10g0184831	M1	NA	89	83	91	76	76	65	71	64	72	74
Sly10g0184841	M11	NA	8	9	11	14	14	12	11	13	13	16
Sly10g0184861	M1	NA	33	39	36	20	23	20	22	18	17	21
Sly10g0184871	M22	NA	10	8	8	4	5	9	8	8	4	16
Sly10g0184881	M7	NA	157	222	83	30	194	168	355	178	105	485
Sly10g0184891	M12	NA	1	1	1	1	1	1	2	2	7	3
Sly10g0184901	M1	NA	17	13	16	3	1	8	6	8	1	1
Sly10g0184941	M11	NA	6	4	5	1	0	9	7	7	1	1
Sly10g0184951	M22	NA	3	1	2	1	1	7	2	6	1	1
Sly10g0184961	M1	NA	64	58	66	60	46	53	45	50	31	28
Sly10g0184971	M23	NA	1	1	1	0	0	1	1	1	0	0
Sly10g0184981	M3	NA	86	89	87	102	89	75	86	75	86	76
Sly10g0184991	M1	NA	45	40	28	17	11	18	19	16	21	13
Sly10g0185011	M3	NA	24	19	17	16	22	14	15	13	21	30
Sly10g0185021	M1	NA	26	25	17	14	17	13	15	13	16	17
Sly10g0185041	M12	NA	6	5	6	10	13	12	12	14	20	15
Sly10g0185051	M12	NA	19	17	17	18	17	20	21	19	16	17
Sly10g0185061	M1	NA	90	87	87	76	117	54	58	50	48	98
Sly10g0185071	M1	NA	5	6	7	1	1	4	4	4	1	1
Sly10g0185081	M1	NA	7	4	5	1	0	1	1	1	0	0
Sly10g0185091	M12	NA	4	2	4	6	12	11	5	10	3	4
Sly10g0185111	M1	NA	3	3	3	5	7	2	2	2	1	2
Sly10g0185121	M1	NA	1	2	1	1	1	0	1	0	0	1
Sly10g0185141	M1	NA	286	250	266	188	172	183

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0229851	M5	NA	17	20	12	18	27	17	16	15	22	28
Sly04g0229871	M3	NA	78	89	68	57	58	54	58	44	61	59
Sly04g0229881	M3	NA	2	3	1	0	0	1	1	1	0	1
Sly04g0229891	M6	NA	6	14	6	1	1	6	9	2	1	1
Sly04g0229901	M14	NA	5	5	8	2	1	5	5	5	2	3
Sly04g0229911	M11	NA	21	19	30	12	3	32	27	42	9	3
Sly04g0229921	M11	NA	9	7	10	5	4	9	8	11	5	2
Sly04g0229931	M11	NA	3	2	3	2	2	4	3	4	2	2
Sly04g0229961	M11	NA	12	13	15	20	18	13	12	17	22	23
Sly04g0229971	M1	NA	39	37	48	38	39	38	38	39	25	33
Sly04g0229981	M12	NA	19	25	19	45	8	32	34	27	62	12
Sly04g0229991	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly04g0230001	M1	NA	33	32	27	12	12	15	15	16	7	6
Sly04g0230011	M1	NA	395	389	318	37	157	82	81	88	33	130
Sly04g0230021	M18	NA	8	9	10	7	10	10	9	10	10	9
Sly04g0230031	M3	NA	19	20	17	13	10	14	14	12	8	10
Sly04g0230041	M9	NA	36	54	41	28	28	54	125	55	55	49
Sly04g0230051	M11	NA	21	19	31	21	11	39	39	39	8	3
Sly04g0230061	M2	NA	227	219	208	197	161	187	218	176	206	166
Sly04g0230071	M19	NA	51	47	49	55	85	48	43	46	46	59
Sly04g0230081	M22	NA	2	1	2	0	0	4	2	5	1	1
Sly04g0230091	M6	NA	17	41	43	1	18	22	34	9	1	28
Sly04g0230101	M1	NA	2	2	2	1	0	1	1	1	0	0
Sly04g0230111	M1	NA	21	20	26	33	27	17	20	18	12	10
Sly04g0230121	M3	NA	53	58	52	58	52	47	54	45	45	51
Sly04g0230131	M12	NA	2	6	3	1	9	5	24	9	5	54
Sly04g0230141	M12	NA	0	1	2	0	1	1	1	3	1	5
Sly04g0230151	M12	NA	10	10	14	26	20	21	22	30	63	45
Sly04g0230161	M1	NA	22	20	22	9	3	11	9	12	5	2
Sly04g0230181	M3	NA	27	31	20	17	13	22	26	18	18	19
Sly04g0230191	M22	NA	1	1	1	1	0	1	1	1	1	0
Sly04g0230211	M1	NA	2	2	1	1	1	3	1	1	0	1
Sly04g0230221	M3	SIPIN3	11	10	4	1	1	4	4	2	1	1
Sly04g0230231	M1	NA	43	37	37	39	36	33	29	32	31	33
Sly04g0230241	M1	NA	57	69	55	33	17	14	13	10	5	6
Sly04g0230251	M1	NA	6	7	7	5	4	4	3	4	2	2
Sly04g0230261	M2	NA	27	29	25	31	32	24	28	26	43	61
Sly04g0230311	M12	NA	2	2	5	457	2193	1	21	58	7723	34467
Sly04g0230331	M12	NA	9	5	9	8	28	38	33	37	33	99
Sly04g0230341	M12	NA	5825	5465	6071	5094	5856	23192	20934	26785	21505	11157
Sly04g0230351	M12	NA	47	58	54	37	24	214	388	429	22	5
Sly04g0230361	M12	NA	2	1	1	1	1	3	5	4	1	1
Sly04g0230371	M12	NA	1	1	1	0	0	16	11	14	1	1
Sly04g0230381	M1	NA	3	2	2	2	2	0	0	0	1	1
Sly04g0230431	M2	NA	31	30	27	33	22	26	33	28	35	28
Sly04g0230441	M3	NA	22	21	17	14	15	12	14	10	14	13
Sly04g0230451	M3	NA	108	112	95	102	84	90	103	81	95	83
Sly04g0230461	M3	NA	36	47	29	22	29	24	27	16	29	53
Sly04g0230471	M3	NA	91	159	64	52	149	41	66	34	141	254
Sly04g0230481	M3	NA	105	123	104	94	192	89	102	77	70	224
Sly04g0230491	M3	NA	49	66	47	24	19	34	38	23	4	4
Sly04g0230501	M1	NA	10	12	8	3	1	3	4	2	1	1
Sly04g0230511	M23	NA	1	1	1	0	0	2	1	1	1	0
Sly04g0230541	M11	NA	14	7	16	2	1	18	11	18	1	1
Sly04g0230551	M1	NA	2	2	2	5	7	1	1	1	1	1
Sly04g0230561	M11	NA	808	719	807	649	359	722	704	946	700	457
Sly04g0230571	M12	NA	114	111	113	182	222	111	127	129	158	244
Sly04g0230581	M3	NA	33	37	20	3	3	14	24	5	1	1
Sly04g0230601	M2	NA	29	30	26	30	27	25	27	22	29	24
Sly04g0230611	M11	NA	109	94	123	121	122	174	157	213	256	237
Sly04g0230621	M1	NA	10	9	10	9	8	7	6	6	8	7
Sly04g0230631	M20	NA	8	5	12	4	1	6	4	7	1	1
Sly04g0230641	M1	SIRR8	22	26	26	17	16	21	22	21	12	5
Sly04g0230661	M21	NA	3	2	2	1	1	2	1	2	2	2
Sly04g0230721	M3	NA	2	2	1	1	1	2	2	1	0	0
Sly04g0230731	M11	NA	15	12	14	11	12	14	13	17	20	22
Sly04g0230741	M6	NA	9	32	31	1	1	6	10	1	1	1
Sly04g0230751	M11	SIHK6	20	19	28	20	18	94	72	101	42	35
Sly04g0230761	M11	NA	2	2	3	2	3	5	5	7	6	9
Sly04g0230771	M12	NA	1	1	1	1	1	2	2	1	1	0
Sly04g0230871	M1	NA	1	1	1	1	1	0	0	0	1	1
Sly04g0230901	M22	NA	1	1	1	1	0	1	1	2	1	1
Sly04g0230911	M12	NA	10	11	5	2	1	15	18	11	5	3
Sly04g0230921	M12	NA	13	13	6	3	2	18	28	12	6	4
Sly04g0230931	M12	SIXTH8	8	15	24	48	48	72	87	103	165	260
Sly04g0230941	M3	NA	13	14	12	11	10	10	12	11	12	12
Sly04g0230951	M11	NA	1	1	1	2	2	1	2	2	3	3
Sly04g0230961	M3	NA	46	50	35	36	37	43	42	28	23	42
Sly04g0230971	M12	NA	1	1	1	3	2	1	2	2	21	14
Sly04g0230991	M3	NA	4	4	5	3	5	2	3	2	2	2
Sly04g0231011	M1	NA	145	123	124	132	125	97	114	116	131	126
Sly04g0231021	M19	NA	49	52	76	34	7	48	35	55	7	6
Sly04g0231031	M13	NA	17	15	21	29	33	20	19	26	35	38
Sly04g0231041	M1	UGT-like	60	54	42	31	24	36	31	33	14	9
Sly04g0231061	M1	NA	2	1	1	1	0	1	1	1	0	0
Sly04g0231081	M11	NA	65	63	73	103	98	77	74	80	92	104
Sly04g0231101	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly04g0231111	M3	NA	12	8	2	1	1	1	1	1	0	0
Sly04g0231121	M3	NA	76	77	66	79	73	69	70	68	107	101
Sly04g0231141	M1	NA	2	2	1	1	1	1	1	1	1	1
Sly04g0231151	M11	NA	4	5	5	5	6	7	6	7	5	5
Sly04g0231181	M1	BRI1-like 2	1	1	1	1	1	1	1	1	0	0
Sly04g0231201	M11	NA	2	3	3	4	1	6	5	6	2	1
Sly04g0231211	M1	NA	478	430	416	274	201	328	309	321	251	204
Sly04g0231241	M16	NA	95	82	81	107	103	75	74	85	90	92
Sly04g0231251	M11	NA	11	10	14	11	7	22	17	27	32	38
Sly04g0231261	M3	NA	41	44	41	36	39	43	40	38	40	53
Sly04g0231271	M11	NA	59	52	58	83	79	71	67	75	66	74
Sly04g0231291	M3	NA	47	44	48	46	46	45	44	42	31	45
Sly04g0231301	M3	NA	36	38	30	34	34	30	32	27	25	23
Sly04g0231311	M11	NA	17	14	16	14	16	16	16	18	16	20
Sly04g0231321	M11	NA	3	2	3	3	1	7	6	8	4	1
Sly04g0231331	M11	NA	24	19	27	29	31	33	30	36	38	48
Sly04g0231341	M1	NA	62	58	57	162	168	32	39	30	92	128
Sly04g0231351	M11	NA	3	2	3	1	0	5	4	5	1	1
Sly04g0231361	M19	SIHAC2	23	26	24	28	29	24	21	24	25	26
Sly04g0231371	M3	NA	54	64	29	32	47	29	29	23	35	34
Sly04g0231381	M1	NA	19	21	20	22	20	15	14	14	20	19
Sly04g0231391	M12	NA	36	38	38	39	35	44	44	41	40	41
Sly04g0231401	M3	NA	20	20	8	2	2	16	17	3	1	1
Sly04g0231411	M3	NA	27	29	25	29	28	26	26	23	26	28
Sly04g0231421	M22	GA2ox9	1	1	1	1	1	2	1	1	1	1
Sly04g0231431	M19	NA	47	51	53	48	52	41	34	41	32	36
Sly04g0231441	M11	NA	34	31	38	17	16	37	39	37	19	17
Sly04g0231451	M18	NA	18	20	24	21	24	22	19	21	23	27
Sly04g0231461	M1	NA	130	112	116	160	224	85	96	94	185	241
Sly04g0231471	M11	NA	4	4	6	6	8	6	4	6	7	8
Sly04g0231481	M1	NA	27	21	30	38	15	15	10	15	5	5
Sly04g0231491	M13	NA	207	197	225	280	256	197	212	225	257	297
Sly04g0231501	M11	NA	26	26	31	32	37	35	33	42	36	43
Sly04g0231511	M9	NA	11	12	11	15	20	18	18	17	22	34
Sly04g0231521	M3	NA	21	19	16	19	23	17	17	17	31	35
Sly04g0231531	M3	NA	4	5	4	4	4	3	3	3	5	6
Sly04g0231541	M3	NA	9	10	8	6	6	6	6	5	7	6
Sly04g0231551	M1	NA	49	47	43	50	52	43	43	47	68	59
Sly04g0231561	M3	NA	292	256	211	215	165	184	198	171	222	167
Sly04g0231571	M11	NA	11	8	9	1	1	12	11	10	1	1
Sly04g0231611	M11	NA	11	11	16	19	22	12	13	15	19	20
Sly04g0231621	M22	NA	1	1	1	1	1	2	1	1	0	1
Sly04g0231631	M1	SIPRMT2	20	18	19	23	30	18	19	18	28	32
Sly04g0231641	M1	NA	6	6	7	6	5	6	6	6	7	5
Sly04g0231651	M11	NA	2	1	2	1	1	3	2	2	1	1
Sly04g0231661	M1	NA	46	47	49	49	48	32	39	35	47	54
Sly04g0231671	M12	NA	4	3	4	4	6	3	4	4	6	8

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0185201	M19	NA	39	41	37	39	41	43	39	39	38	42
Sly10g0185241	M11	NA	181	168	191	161	205	191	157	203	161	283
Sly10g0185251	M13	NA	193	196	262	244	309	235	214	315	274	392
Sly10g0185261	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0185271	M12	NA	10	8	9	15	9	14	15	15	19	10
Sly10g0185281	M3	NA	11	13	2	1	1	5	7	5	3	3
Sly10g0185291	M11	NA	76	71	66	61	59	113	100	113	43	41
Sly10g0185301	M1	NA	159	148	166	154	176	125	125	140	189	298
Sly10g0185311	M11	NA	20	19	23	24	31	28	24	29	29	41
Sly10g0185321	M3	NA	21	19	15	9	5	16	18	15	6	3
Sly10g0185331	M19	NA	92	95	92	81	81	91	83	91	69	89
Sly10g0185351	M22	NA	4	4	4	4	2	5	3	5	2	1
Sly10g0185361	M5	NA	81	104	60	68	78	70	80	51	71	81
Sly10g0185411	M16	NA	30	30	30	31	33	28	30	30	43	48
Sly10g0185421	M2	NA	39	40	34	41	35	37	41	33	40	38
Sly10g0185431	M12	NA	1	2	1	1	0	3	2	2	0	1
Sly10g0185441	M12	NA	1	1	1	1	1	1	1	1	1	0
Sly10g0185451	M1	NA	29	27	76	422	285	1	1	1	21	18
Sly10g0185491	M1	NA	1	2	2	33	11	0	0	1	2	2
Sly10g0185501	M1	NA	1	3	2	64	22	0	0	0	3	5
Sly10g0185511	M1	NA	1	1	1	28	6	1	0	1	1	1
Sly10g0185521	M1	SIPIN7	2	2	2	18	26	1	1	1	1	3
Sly10g0185531	M12	NA	8	7	9	24	23	8	8	9	51	43
Sly10g0185541	M2	NA	79	83	106	2089	1135	37	72	106	6655	2891
Sly10g0185571	M1	NA	4	4	4	4	5	1	1	1	1	1
Sly10g0185581	M1	NA	34	39	34	40	46	24	25	33	65	59
Sly10g0185591	M11	NA	221	173	282	154	62	411	356	406	28	15
Sly10g0185611	M3	NA	1	1	2	1	2	1	2	1	1	3
Sly10g0185621	M1	NA	36	34	41	43	29	21	23	25	18	11
Sly10g0185631	M11	NA	2	2	2	1	1	2	2	2	1	1
Sly10g0185641	M1	NA	2	1	4	1	0	1	0	1	0	0
Sly10g0185651	M11	NA	72	62	85	48	42	90	85	110	72	77
Sly10g0185661	M1	NA	12	9	9	1	1	3	2	2	0	0
Sly10g0185671	M19	NA	62	64	74	68	65	81	65	81	46	44
Sly10g0185681	M1	NA	326	324	334	334	281	267	295	273	337	280
Sly10g0185691	M6	NA	17	26	18	10	63	15	25	13	8	94
Sly10g0185701	M6	NA	74	124	76	52	291	65	110	59	43	345
Sly10g0185711	M11	NA	18	17	18	18	18	19	18	18	20	17
Sly10g0185721	M12	NA	37	40	39	43	36	45	46	50	48	40
Sly10g0185731	M3	NA	78	80	70	75	67	74	73	70	68	66
Sly10g0185741	M11	NA	25	20	27	40	47	44	39	52	60	75
Sly10g0185751	M12	NA	17	17	22	8	3	37	47	52	25	14
Sly10g0185761	M11	NA	61	64	97	98	24	121	88	140	40	6
Sly10g0185771	M12	NA	67	68	76	95	108	72	74	78	100	114
Sly10g0185781	M3	NA	10	10	9	10	16	6	7	6	10	9
Sly10g0185791	M9	NA	45	51	40	47	82	49	67	49	89	132
Sly10g0185801	M11	NA	31	28	35	26	20	30	29	33	26	22
Sly10g0185811	M3	NA	1360	1682	813	472	789	1046	1714	808	787	1465
Sly10g0185821	M1	NA	245	242	192	150	135	122	136	110	118	131
Sly10g0185831	M1	NA	1249	1264	1131	711	706	553	563	525	456	501
Sly10g0185841	M18	NA	17	19	22	24	16	22	20	19	16	14
Sly10g0185851	M1	NA	5	4	4	3	3	4	4	4	2	2
Sly10g0185861	M11	NA	9	8	10	13	16	10	12	13	25	30
Sly10g0185871	M1	NA	18	21	17	19	18	14	11	13	15	16
Sly10g0185881	M19	NA	44	43	48	95	202	44	39	47	98	183
Sly10g0185891	M1	NA	10	11	12	7	10	9	8	8	6	6
Sly10g0185901	M1	NA	37	34	45	146	142	21	23	31	391	192
Sly10g0185911	M9	NA	30	28	28	27	33	28	31	29	40	40
Sly10g0185921	M11	NA	11	11	11	13	15	14	13	16	22	20
Sly10g0185931	M12	NA	7	7	5	9	10	9	9	9	18	16
Sly10g0185941	M22	NA	1	1	2	14	14	4	1	2	1	1
Sly10g0185951	M12	NA	357	317	390	227	100	536	565	661	292	115
Sly10g0185961	M1	NA	69	65	18	3	1	7	3	3	1	1
Sly10g0185971	M3	NA	83	78	70	49	32	67	64	66	51	41
Sly10g0185981	M11	NA	1	1	1	1	1	1	1	2	2	3
Sly10g0185991	M11	SIAREB3	12	13	11	11	11	23	21	29	13	13
Sly10g0186001	M8	NA	22	21	22	25	33	21	23	21	35	36
Sly10g0186011	M1	NA	168	176	176	162	186	109	132	104	152	149
Sly10g0186021	M2	NA	49	48	45	97	109	42	53	43	128	114
Sly10g0186031	M12	NA	1	1	1	1	1	2	2	5	7	4
Sly10g0186051	M12	NA	12	10	10	14	11	14	17	14	25	20
Sly10g0186061	M1	NA	3	3	4	5	6	1	1	1	2	4
Sly10g0186071	M11	NA	2	1	1	2	5	4	2	2	4	6
Sly10g0186081	M3	NA	134	124	125	265	243	116	123	99	151	181
Sly10g0186091	M1	NA	2	2	3	3	2	1	1	1	2	3
Sly10g0186101	M11	NA	182	168	211	179	183	288	287	299	238	241
Sly10g0186111	M11	NA	12	11	15	23	44	19	16	22	24	39
Sly10g0186121	M12	NA	141	120	137	179	181	165	169	205	325	322
Sly10g0186151	M3	NA	744	723	652	773	633	714	816	551	464	456
Sly10g0186171	M2	NA	268	270	274	400	452	235	285	240	384	416
Sly10g0186181	M2	NA	21	23	20	22	26	17	19	17	28	30
Sly10g0186231	M7	NA	154	274	80	67	168	173	403	130	47	308
Sly10g0186241	M2	NA	162	169	162	160	129	152	167	147	145	149
Sly10g0186251	M1	NA	20	17	20	11	10	12	11	11	8	5
Sly10g0186261	M1	NA	32	32	33	40	47	30	28	32	27	35
Sly10g0186281	M19	NA	75	81	80	94	85	74	64	69	61	60
Sly10g0186291	M11	NA	31	31	32	28	35	31	29	36	29	42
Sly10g0186301	M5	SIJMJ9	17	18	12	15	14	15	19	15	20	17
Sly10g0186311	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly10g0186321	M18	crtiso	39	49	45	186	337	41	40	52	193	311
Sly10g0186331	M12	NA	38	38	38	42	38	39	42	39	43	49
Sly10g0186371	M1	NA	13	11	12	8	8	6	4	3	3	9
Sly10g0186391	M1	NA	3	2	3	1	1	1	1	1	1	1
Sly10g0186401	M11	NA	75	70	75	99	98	84	74	89	102	111
Sly10g0186411	M1	NA	86	71	79	86	101	58	41	54	36	45
Sly10g0186421	M1	NA	82	66	86	21	20	36	31	31	13	17
Sly10g0186431	M5	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0186441	M2	NA	35	29	30	57	98	29	29	31	72	126
Sly10g0186451	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0186461	M1	NA	5	6	5	3	3	1	1	1	1	1
Sly10g0186491	M23	NA	4	1	2	1	0	10	3	6	1	1
Sly10g0186501	M23	NA	1	1	1	0	0	3	1	1	1	0
Sly10g0186511	M9	NA	46	44	42	39	38	68	76	65	49	51
Sly10g0186521	M11	RPA2B	5	5	5	3	2	7	5	7	3	2
Sly10g0186531	M11	NA	1	1	1	1	1	2	1	2	2	1
Sly10g0186541	M3	NA	24	40	22	11	9	11	8	6	2	2
Sly10g0186551	M12	NA	10	11	8	8	10	12	13	12	11	13
Sly10g0186561	M12	NA	14	11	11	10	10	15	13	14	12	10
Sly10g0186571	M18	NA	7	8	8	7	7	9	8	9	6	5
Sly10g0186591	M1	NA	39	45	41	58	111	34	36	38	52	85
Sly10g0186601	M11	NA	4	5	7	4	1	10	7	10	1	1
Sly10g0186611	M3	NA	68	70	62	32	23	33	44	25	30	20
Sly10g0186621	M8	NA	82	87	77	104	83	89	112	73	95	76
Sly10g0186631	M3	NA	7	4	4	2	6	4	4	3	7	6
Sly10g0186641	M22	NA	2	1	1	1	1	6	1	5	0	1
Sly10g0186651	M9	NA	1	1	1	1	1	1	3	1	1	1
Sly10g0186661	M1	NA	506	356	477	23	5	154	142	154	5	1
Sly10g0186671	M10	NA	2	12	11	1	5	14	23	11	2	8
Sly10g0186681	M7	NA	14	32	22	7	47	25	53	30	15	159
Sly10g0186701	M1	NA	1	1	1	1	0	1	1	1	0	0
Sly10g0186721	M11	SlLOG7	1	1	1	1	1	1	1	1	1	1
Sly10g0186731	M11	PrxII	86	83	88	106	84	125	137	148	78	76
Sly10g0186781	M1	NA	1	1	1	2	4	1	1	1	1	4
Sly10g0186821	M2	NA	82	76	79	45	36	71	76	81	66	53
Sly10g0186831	M3	NA	109	103	103	168	166	81	92	85	139	167
Sly10g0186841	M1	NA	13	13	20	53	64	10	3	7	1	2
Sly10g0186851	M11	NA	47	47	38	47	44	52	46	51	45	46
Sly10g0186861	M9	NA	44	45	44	42	46	46	44	43	44	60
Sly10g0186871	M1	NA	139	130	128	101	67	97	99	104	97	84
Sly10g0186891	M11	NA	3	2	3	2	1	4	4	4	1	1
Sly10g0186901	M12	NA	17	15

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0231701	M22	NA	1	1	1	2	2	1	1	1	0	1
Sly04g0231711	M22	GEM-like13	3	2	4	3	5	2	2	3	1	1
Sly04g0231721	M1	GEM-like14	3	3	4	5	5	3	2	3	1	1
Sly04g0231731	M1	GEM-like8	6	4	9	9	8	5	4	6	1	1
Sly04g0231741	M11	GEM-like6	3	2	4	2	2	6	3	7	1	1
Sly04g0231751	M12	GEM-like10	9	4	8	4	3	33	26	39	1	1
Sly04g0231761	M14	NA	87	62	105	43	47	75	65	95	61	92
Sly04g0231771	M11	NA	6	6	7	6	5	6	6	7	6	5
Sly04g0231781	M1	NA	5	6	4	4	3	3	3	3	3	3
Sly04g0231791	M3	NA	31	30	26	25	27	27	32	24	30	35
Sly04g0231801	M11	NA	6	5	8	7	4	22	19	29	12	1
Sly04g0231811	M11	NA	141	113	142	124	43	221	181	230	39	6
Sly04g0231831	M11	NA	28	16	22	7	33	22	22	18	18	31
Sly04g0231841	M14	NA	49	49	55	55	70	47	47	55	62	66
Sly04g0231941	M1	NA	16	14	15	11	11	10	10	10	14	14
Sly04g0231951	M1	NA	3	3	4	4	4	2	3	3	3	4
Sly04g0231961	M3	NA	10	9	9	7	9	8	10	8	9	10
Sly04g0231971	M19	NA	15	13	14	12	13	14	13	16	15	13
Sly04g0231981	M22	NA	5	4	3	3	4	5	3	4	3	2
Sly04g0231991	M3	NA	8	8	7	4	2	7	6	5	1	1
Sly04g0232001	M2	NA	25	28	25	23	28	18	22	19	26	37
Sly04g0232011	M11	NA	56	48	51	64	63	100	84	98	42	21
Sly04g0232021	M1	NA	5	6	5	5	4	4	4	5	4	3
Sly04g0232031	M18	PPR-like2	4	5	4	4	4	5	4	5	3	3
Sly04g0232041	M2	NA	46	47	41	74	140	37	47	41	96	190
Sly04g0232061	M3	NA	1	1	1	1	1	0	0	1	2	2
Sly04g0232071	M11	NA	6	7	8	8	2	12	11	13	16	3
Sly04g0232081	M12	NA	1	0	0	1	1	1	2	2	4	11
Sly04g0232091	M12	NA	2	3	2	4	12	26	22	17	41	120
Sly04g0232101	M12	NA	2	2	1	3	6	12	11	9	18	35
Sly04g0232111	M11	NA	16	16	23	26	31	21	18	26	18	14
Sly04g0232141	M6	NA	4	6	5	9	6	5	5	4	49	20
Sly04g0232151	M10	NA	23	23	19	28	24	23	25	22	31	28
Sly04g0232161	M1	NA	12	13	13	17	15	8	8	9	10	8
Sly04g0232171	M11	AUR3	12	13	13	9	5	16	14	19	13	10
Sly04g0232181	M11	NA	21	21	23	32	41	24	22	26	41	43
Sly04g0232191	M11	NA	25	25	30	36	40	28	30	29	20	15
Sly04g0232201	M12	NA	8	8	9	9	14	10	10	12	11	15
Sly04g0232211	M11	NA	9	8	11	16	39	17	16	22	15	23
Sly04g0232221	M3	NA	33	32	27	32	40	21	20	20	34	33
Sly04g0232241	M5	NA	3	3	3	2	2	3	3	3	3	2
Sly04g0232251	M13	NA	149	132	143	147	174	124	135	149	191	260
Sly04g0232261	M11	NA	9	6	11	7	2	12	10	13	3	1
Sly04g0232271	M9	SISRT2	11	10	10	13	24	12	12	10	21	29
Sly04g0232281	M6	NAC1	160	248	69	5	9	168	206	43	13	26
Sly04g0232291	M22	NA	3	2	3	2	2	4	2	3	4	4
Sly04g0232321	M11	NA	23	22	29	28	30	41	34	44	41	51
Sly04g0232331	M12	NA	22	21	24	23	39	31	28	32	43	56
Sly04g0232361	M1	NA	52	57	42	29	28	33	34	30	32	29
Sly04g0232371	M12	NA	28	26	38	19	16	59	49	63	31	19
Sly04g0232381	M3	NA	4	5	3	2	3	3	3	3	2	2
Sly04g0232391	M12	NA	13	15	16	17	6	24	24	26	17	6
Sly04g0232401	M11	NA	25	25	33	71	59	42	46	59	81	57
Sly04g0232411	M12	NA	19	18	18	10	9	26	26	25	12	9
Sly04g0232421	M11	NA	34	35	41	46	41	90	82	102	113	96
Sly04g0232431	M2	NA	26	25	24	20	21	17	23	18	30	30
Sly04g0232441	M1	NA	22	21	22	22	22	14	13	14	10	14
Sly04g0232461	M3	NA	6	8	7	4	3	6	9	5	5	2
Sly04g0232471	M12	NA	4	4	5	4	3	5	5	6	3	3
Sly04g0232481	M5	NA	13	15	11	16	16	15	15	12	18	19
Sly04g0232491	M19	NA	5	9	6	5	8	10	7	7	7	11
Sly04g0232501	M1	NA	92	91	74	58	48	31	35	29	24	22
Sly04g0232511	M3	NA	17	23	6	4	3	2	3	1	1	3
Sly04g0232521	M1	NA	32	32	33	44	52	26	28	28	45	43
Sly04g0232531	M1	NA	2	2	2	1	1	0	1	1	0	1
Sly04g0232581	M3	NA	21	20	20	18	13	14	20	16	16	15
Sly04g0232601	M11	NA	10	9	12	11	12	15	12	17	11	9
Sly04g0232621	M11	NA	64	54	70	49	34	66	53	71	63	48
Sly04g0232641	M12	NA	497	447	517	393	560	506	462	543	655	804
Sly04g0232661	M12	NA	43	33	19	8	3	60	44	60	10	5
Sly04g0232671	M6	NA	127	167	86	62	77	128	145	78	150	163
Sly04g0232681	M2	NA	38	38	31	22	15	25	30	23	40	32
Sly04g0232691	M1	NA	11	7	9	4	1	3	2	2	1	1
Sly04g0232711	M12	NA	10	10	9	14	12	10	10	11	20	14
Sly04g0232721	M3	NA	8	11	8	10	4	4	5	4	3	2
Sly04g0232731	M1	NA	7	11	6	4	2	1	1	1	1	1
Sly04g0232741	M3	NA	149	182	108	15	11	61	88	47	25	12
Sly04g0232761	M1	NA	17	25	15	2	1	1	1	0	1	0
Sly04g0232791	M3	NA	11	10	6	8	11	9	7	6	22	11
Sly04g0232801	M22	NA	20	7	10	1	1	90	17	51	1	0
Sly04g0232811	M12	Phosphoenolpyruvate	25	23	29	35	6	106	139	253	122	32
Sly04g0232821	M3	NA	42	48	33	45	42	36	44	34	50	47
Sly04g0232851	M12	NA	31	30	30	56	77	34	39	33	80	81
Sly04g0232861	M19	NA	62	61	66	57	54	64	54	63	59	55
Sly04g0232871	M22	NA	21	17	22	85	141	23	17	20	568	545
Sly04g0232881	M1	NA	17	17	16	13	15	13	13	12	14	14
Sly04g0232901	M12	SUMJ7	27	32	28	28	29	34	35	40	43	39
Sly04g0232911	M3	NA	27	30	25	24	32	23	25	23	34	44
Sly04g0232921	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0232931	M3	NA	62	67	59	62	63	47	54	52	81	82
Sly04g0232941	M12	NA	1	1	1	2	3	1	1	1	2	2
Sly04g0232951	M11	NA	1	1	1	2	1	1	2	2	3	1
Sly04g0232961	M3	NA	9	9	7	5	3	4	4	2	1	1
Sly04g0232971	M11	NA	5	6	7	8	6	11	10	15	17	6
Sly04g0232981	M3	NA	68	73	64	78	81	54	56	48	72	72
Sly04g0232991	M13	NA	25	24	30	35	40	29	26	31	29	37
Sly04g0233001	M2	NA	29	29	34	34	32	27	32	31	40	44
Sly04g0233011	M12	NA	44	42	44	60	54	42	42	49	73	85
Sly04g0233021	M12	NA	7	9	8	12	15	9	9	11	13	15
Sly04g0233031	M18	NA	3	4	3	3	3	4	4	3	3	2
Sly04g0233041	M12	NA	14	14	14	21	28	15	17	16	23	32
Sly04g0233051	M12	NA	36	36	42	53	66	44	46	51	61	74
Sly04g0233061	M19	NA	2	3	2	2	2	2	2	2	1	1
Sly04g0233071	M19	NA	2	2	2	3	2	2	1	2	1	1
Sly04g0233081	M1	NA	2	3	2	3	2	2	2	2	1	1
Sly04g0233091	M1	NA	3	4	3	3	3	2	2	2	2	1
Sly04g0233101	M3	NA	7	6	6	5	7	5	4	4	3	3
Sly04g0233171	M3	NA	31	38	25	31	34	32	29	29	30	27
Sly04g0233181	M11	NA	13	11	15	25	75	26	23	30	31	97
Sly04g0233191	M3	NA	3	4	3	65	30	2	3	2	1	1
Sly04g0233201	M12	NA	1	1	1	1	1	4	5	6	2	1
Sly04g0233211	M11	NA	38	38	43	51	61	44	41	46	50	55
Sly04g0233231	M11	SIPL	28	25	30	33	41	31	31	34	33	45
Sly04g0233241	M3	NA	461	416	340	262	174	247	295	228	222	137
Sly04g0233251	M11	NA	175	145	231	5	1	204	163	198	3	1
Sly04g0233261	M19	NA	50	52	51	48	42	51	45	50	35	36
Sly04g0233281	M11	NA	3	2	6	9	12	6	6	7	14	18
Sly04g0233291	M12	NA	7	9	10	17	24	12	14	16	32	46
Sly04g0233321	M14	NA	20	17	22	21	25	19	18	20	12	10
Sly04g0233331	M3	NA	32	39	25	25	26	29	29	22	17	19
Sly04g0233361	M9	NA	1	1	1	1	1	1	1	1	1	2
Sly04g0233371	M12	NA	1	1	1	1	1	4	3	3	1	1
Sly04g0233381	M1	NA	12	15	16	36	45	5	5	5	7	8
Sly04g0233391	M13	NA	133	126	132	155	260	121	125	138	211	273
Sly04g0233401	M2	NA	74	70	68	71	63	50	61	54	76	71
Sly04g0233421	M18	NA	30	34	34	34	47	40	36	42	53	62
Sly04g0233431	M11	NA	61	45	40	2	2	92	77	70	2	2
Sly04g0233451	M3	NA	480	408	359	268	195	312	346	281	257	242
Sly04g0233471	M3	NA	19	18	18	28	27	14	20	18	31	31
Sly04g0233481	M12	NA	19	19	17	23	20	27	27	24	18	23
Sly04g0233491	M12	NA	607	580	718	1062	1106	737	788	1009	1323	1803
Sly04g0233511	M4	NA	79	60	73	229	448	152	126	73	208	644
Sly04g0233531	M1	NA	76	80	57	68	48	50	49	48	46	37
Sly04g0233551	M3	NA	1	4	1	0	0	1	1	0	0	0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0186941	M1	NA	9	8	6	33	14	1	1	1	16	14
Sly10g0186951	M14	NA	52	52	54	60	61	47	47	57	63	66
Sly10g0186971	M1	NA	27	19	24	16	11	20	18	23	18	4
Sly10g0186981	M11	NA	20	15	22	25	29	21	17	23	30	36
Sly10g0186991	M3	NA	294	259	242	212	166	209	207	192	214	183
Sly10g0187001	M1	NA	20	32	12	1	1	2	1	1	0	1
Sly10g0187021	M11	NA	1	1	1	1	1	2	2	2	1	1
Sly10g0187041	M9	NA	4	3	4	1	1	6	5	3	1	0
Sly10g0187051	M1	NA	3	2	2	1	1	1	1	1	1	1
Sly10g0187071	M11	NA	10	10	10	16	20	18	16	19	14	19
Sly10g0187091	M12	NA	45	40	24	17	52	202	172	113	103	233
Sly10g0187101	M11	NA	16	16	18	23	18	35	29	35	41	23
Sly10g0187111	M11	NA	58	56	69	60	53	86	89	97	123	80
Sly10g0187121	M11	NA	26	29	28	28	25	43	42	45	65	46
Sly10g0187141	M1	NA	14	10	13	41	134	3	3	5	50	174
Sly10g0187161	M11	NA	1	0	1	0	1	3	1	2	1	1
Sly10g0187171	M11	NA	1	1	0	1	0	1	2	2	1	0
Sly10g0187181	M1	NA	24	24	55	129	56	3	2	2	1	1
Sly10g0187201	M11	NA	33	23	46	22	24	79	70	105	32	33
Sly10g0187211	M22	NA	15	15	11	13	18	18	14	15	18	23
Sly10g0187221	M1	NA	37	36	32	34	31	34	30	33	31	32
Sly10g0187231	M11	NA	19	16	18	33	36	22	18	23	19	16
Sly10g0187241	M12	NA	10	9	10	7	12	15	13	13	3	3
Sly10g0187251	M23	NA	1	1	1	1	0	1	1	1	0	1
Sly10g0187261	M20	NA	22	20	32	23	17	17	13	19	18	16
Sly10g0187271	M22	NA	1	1	1	1	1	2	1	1	1	2
Sly10g0187321	M1	NA	1	1	1	1	0	0	0	0	0	0
Sly10g0187331	M2	NA	279	273	259	611	404	205	319	200	323	254
Sly10g0187351	M1	NA	102	130	197	814	435	21	42	49	265	133
Sly10g0187361	M12	NA	14	14	13	16	17	14	15	15	18	14
Sly10g0187371	M3	NA	105	113	81	64	56	60	67	50	75	68
Sly10g0187381	M3	CTR1	134	156	74	69	57	50	61	33	72	57
Sly10g0187391	M12	SlDML2	105	117	140	684	342	105	117	161	559	167
Sly10g0187401	M19	NA	203	192	199	216	191	175	147	188	241	262
Sly10g0187411	M13	PrxII	51	46	72	550	716	57	59	86	261	229
Sly10g0187431	M1	NA	26	14	31	1	1	2	1	1	1	0
Sly10g0187451	M11	NA	36	27	20	65	55	45	32	44	5	1
Sly10g0187461	M12	NA	5	5	3	1	1	15	16	15	1	1
Sly10g0187471	M11	NA	14	13	18	12	25	19	16	24	21	50
Sly10g0187481	M12	NA	96	97	93	333	744	109	173	285	1653	1141
Sly10g0187501	M11	NA	20	16	20	19	16	33	27	42	38	36
Sly10g0187511	M17	NA	89	79	77	48	34	77	71	88	72	55
Sly10g0187531	M1	NA	122	112	147	94	103	56	42	60	96	108
Sly10g0187561	M3	NA	46	46	42	42	46	35	40	37	55	62
Sly10g0187571	M11	CYP97C1	8	8	10	8	6	12	11	13	4	2
Sly10g0187581	M11	NA	6	6	4	1	1	7	5	9	2	2
Sly10g0187591	M22	NA	2	0	2	0	0	11	0	6	0	0
Sly10g0187601	M19	NA	16	18	18	23	22	22	20	22	23	21
Sly10g0187611	M12	NA	20	22	22	26	28	27	27	26	36	40
Sly10g0187641	M13	NA	15	16	19	40	17	18	17	20	31	17
Sly10g0187671	M1	NA	6	7	18	4	2	1	1	1	1	0
Sly10g0187691	M11	NA	74	70	82	69	57	80	78	88	78	77
Sly10g0187701	M11	NA	1	1	1	21	15	2	3	4	47	23
Sly10g0187731	M11	NA	29	28	30	34	31	33	36	36	40	36
Sly10g0187741	M11	NA	34	34	42	33	22	69	61	86	41	24
Sly10g0187751	M1	NA	23	22	26	33	34	24	20	24	19	23
Sly10g0187761	M1	NA	2	3	2	27	59	1	1	1	1	1
Sly10g0187771	M1	NA	7	7	8	6	5	7	5	6	2	1
Sly10g0187781	M11	NA	6	7	8	8	7	10	7	10	2	1
Sly10g0187791	M6	SAMS	327	347	170	103	49	331	463	118	42	55
Sly10g0187821	M12	NA	12	11	8	15	32	13	12	15	20	49
Sly10g0187831	M12	NA	2	8	7	2	6	14	52	34	10	52
Sly10g0187861	M9	NA	1	1	1	0	0	1	4	1	0	0
Sly10g0187911	M12	NA	17	18	21	99	112	38	39	45	58	82
Sly10g0187921	M12	NA	3	3	3	4	4	4	5	4	5	5
Sly10g0187931	M12	NA	3	4	5	4	5	5	6	6	5	7
Sly10g0187941	M1	NA	148	141	143	168	229	96	103	93	172	178
Sly10g0187971	M1	NA	3	2	2	1	1	1	1	1	1	1
Sly10g0187981	M12	NA	7	9	14	172	169	25	54	63	193	280
Sly10g0187991	M1	NA	6	4	3	1	1	2	2	2	1	1
Sly10g0188001	M11	PPR-like46	4	4	4	6	5	4	5	5	5	4
Sly10g0188011	M19	NA	6	7	7	7	7	6	6	7	7	6
Sly10g0188021	M12	NA	4	4	5	7	7	6	5	6	8	7
Sly10g0188031	M11	NA	2	3	3	2	4	4	3	3	4	5
Sly10g0188071	M13	NA	3	3	3	7	7	3	2	3	2	4
Sly10g0188081	M9	NA	126	119	128	137	159	123	131	128	129	191
Sly10g0188091	M1	NA	4	4	5	5	4	3	3	5	3	4
Sly10g0188121	M1	NA	59	58	53	38	38	43	48	43	42	46
Sly10g0188131	M10	NA	6	5	5	9	24	8	8	4	5	17
Sly10g0188141	M10	NA	33	36	32	10	6	36	52	28	16	8
Sly10g0188181	M2	NA	72	70	64	80	96	59	71	58	97	125
Sly10g0188191	M18	NA	16	17	18	20	21	18	15	19	19	25
Sly10g0188211	M1	NA	1	1	1	2	1	1	1	1	0	0
Sly10g0188221	M3	NA	1	2	1	0	0	1	1	1	0	0
Sly10g0188231	M1	NA	17	14	19	6	1	6	5	4	1	0
Sly10g0188241	M1	NA	32	29	31	28	26	22	26	29	23	21
Sly10g0188261	M1	NA	24	25	26	22	27	18	14	17	19	23
Sly10g0188271	M12	NA	34	37	29	17	10	78	80	58	23	18
Sly10g0188281	M22	NA	1	1	1	1	0	2	1	2	0	0
Sly10g0188301	M16	NA	295	239	261	172	162	216	206	233	198	203
Sly10g0188311	M1	NA	20	15	17	2	2	5	5	3	1	1
Sly10g0188331	M11	NA	2	2	3	1	1	6	6	9	3	1
Sly10g0188351	M1	NA	189	155	170	127	151	150	147	150	166	168
Sly10g0188361	M1	NA	3	1	2	1	16	2	2	2	3	14
Sly10g0188371	M22	NA	2	1	1	0	0	6	3	5	1	1
Sly10g0188381	M22	NA	1	1	1	0	0	4	2	3	1	1
Sly10g0188401	M12	NA	21	22	29	98	479	59	82	110	269	319
Sly10g0188411	M12	NA	0	1	1	1	0	1	1	1	1	1
Sly10g0188421	M22	NA	1	1	1	1	1	3	1	2	0	0
Sly10g0188441	M12	NA	8	8	7	9	14	11	10	11	12	22
Sly10g0188461	M1	NA	12	11	8	3	2	5	3	3	3	6
Sly10g0188471	M9	NA	102	91	92	153	141	139	182	138	149	117
Sly10g0188481	M12	NA	1	1	2	4	3	5	8	9	24	14
Sly10g0188491	M11	NA	1	1	1	2	1	2	1	2	2	2
Sly10g0188501	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0188511	M12	NA	8	7	11	11	5	10	11	19	5	3
Sly10g0188521	M12	NA	57	45	72	47	58	446	470	556	71	44
Sly10g0188591	M4	NA	1	1	1	4	72	1	1	1	50	153
Sly10g0188601	M1	NA	42	38	34	23	18	21	25	19	31	19
Sly10g0188611	M1	NA	42	40	34	36	33	27	30	31	42	30
Sly10g0188621	M2	NA	44	48	43	37	46	31	37	30	51	49
Sly10g0188631	M11	NA	42	32	56	43	39	66	60	92	31	27
Sly10g0188641	M18	NA	27	29	32	46	60	31	29	31	44	55
Sly10g0188651	M12	NA	4	3	6	5	3	6	7	11	5	3
Sly10g0188661	M1	NA	12	14	11	5	2	5	6	5	3	1
Sly10g0188671	M11	NA	6	5	5	4	3	9	6	9	3	1
Sly10g0188681	M3	NA	5	4	3	3	1	2	2	2	1	1
Sly10g0188691	M9	NA	15	16	12	12	5	23	25	17	11	7
Sly10g0188721	M3	NA	33	28	25	30	29	21	23	19	30	30
Sly10g0188771	M11	NA	26	23	31	25	28	33	25	34	37	48
Sly10g0188801	M12	NA	43	46	48	76	92	63	51	59	62	73
Sly10g0188811	M3	NA	27	29	18	8	3	23	27	16	4	2
Sly10g0188841	M6	NA	90	106	75	67	87	88	105	65	88	101
Sly10g0188851	M11	NA	4	3	4	2	1	5	5	6	3	2
Sly10g0188861	M9	NA	12	10	10	13	14	13	15	13	14	15
Sly10g0188871	M2	NA	6	8	6	3	1	5	6	4	2	1
Sly10g0188891	M16	NA	40	40	34	24	27	37	33	38	25	20
Sly10g0188921	M1	NA	2	3	2	2	1	1	1	1	2	1
Sly10g0188931	M7	NA	7	22	12	9	31	26	54	26	4	32
Sly10g0188971	M12	NA	19	16	16	19	19	18	20	18	19	21
Sly10g0188991	M1	NA	24	24	22	41	36

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0233571	M11	NA	15	11	16	12	14	15	15	14	14	17
Sly04g0233581	M11	NA	112	97	127	154	193	162	160	195	164	204
Sly04g0233601	M3	TPI	453	414	384	262	205	343	391	334	186	172
Sly04g0233611	M3	NA	38	40	25	21	47	13	16	12	26	56
Sly04g0233621	M11	NA	30	29	28	32	39	31	31	34	45	48
Sly04g0233631	M12	NA	3	4	5	14	40	9	11	19	105	205
Sly04g0233641	M21	NA	50	40	52	59	84	46	30	36	28	51
Sly04g0233651	M11	NA	21	17	24	18	24	27	23	29	28	43
Sly04g0233661	M11	NA	21	19	21	23	25	21	19	24	24	22
Sly04g0233671	M11	NA	21	20	32	28	13	47	35	51	10	3
Sly04g0233701	M22	NA	31	27	26	28	24	29	25	30	23	24
Sly04g0233711	M12	NA	90	89	95	117	141	94	103	101	137	147
Sly04g0233731	M1	NA	13	10	7	16	4	3	1	1	1	1
Sly04g0233751	M1	NA	22	22	28	28	29	19	18	20	23	24
Sly04g0233761	M1	NA	25	29	33	56	51	19	16	21	35	27
Sly04g0233771	M11	NA	19	20	20	8	4	29	26	25	3	2
Sly04g0233821	M2	NA	14	14	15	13	13	14	15	14	16	12
Sly04g0233861	M1	NA	32	30	27	10	4	2	1	1	0	1
Sly04g0233881	M3	NA	3	13	2	0	0	2	3	1	0	0
Sly04g0233901	M3	NA	15	24	10	1	1	18	15	3	0	2
Sly04g0234011	M11	NA	9	9	10	9	4	16	15	18	9	3
Sly04g0234021	M23	NA	1	1	1	3	1	2	1	1	1	0
Sly04g0234081	M18	NA	23	22	26	36	52	29	24	31	31	46
Sly04g0234091	M8	NA	7	8	4	2	1	9	11	5	2	1
Sly04g0234111	M2	NA	23	26	25	26	31	17	22	17	21	24
Sly04g0234121	M3	GLABRA2-like1	57	55	53	77	80	52	52	52	82	95
Sly04g0234151	M3	PFK	31	32	28	22	22	27	26	23	16	17
Sly04g0234281	M3	NA	2	3	1	0	0	1	1	0	0	0
Sly04g0234291	M1	NA	55	53	58	42	21	28	25	23	13	12
Sly04g0234311	M10	NA	2	4	2	0	1	2	10	3	0	0
Sly04g0234321	M11	NA	110	95	119	127	145	132	125	153	195	245
Sly04g0234331	M1	NA	3	2	2	2	1	1	1	1	1	1
Sly04g0234381	M22	NA	1	1	2	2	1	1	1	1	0	0
Sly04g0234391	M3	NA	255	259	221	204	257	223	224	200	286	380
Sly04g0234411	M12	NA	21	19	35	187	774	56	45	76	168	1091
Sly04g0234421	M9	NA	119	109	112	148	146	114	143	121	151	139
Sly04g0234431	M3	NA	100	99	75	200	134	82	80	74	259	173
Sly04g0234451	M1	NA	5	4	5	1	1	2	2	3	1	1
Sly04g0234461	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0234481	M1	SIERF.C2	4	2	5	1	0	1	0	0	0	0
Sly04g0234491	M1	NA	27	26	26	25	16	19	20	18	31	27
Sly04g0234511	M11	NA	66	61	63	67	72	72	61	76	79	85
Sly04g0234521	M8	NA	126	126	105	90	70	141	171	117	76	59
Sly04g0234531	M12	HRU1-like	33	33	69	297	633	190	229	180	378	1148
Sly04g0234541	M1	NA	4	5	6	3	3	4	3	4	2	2
Sly04g0234571	M3	NA	4	6	2	1	0	1	1	1	0	0
Sly04g0234611	M1	NA	42	42	40	68	57	37	39	43	49	46
Sly04g0234621	M20	NA	29	25	32	13	10	25	18	20	4	3
Sly04g0234641	M11	NA	4	4	11	5	7	18	16	21	11	11
Sly04g0234651	M22	NA	18	17	20	22	31	21	16	22	18	29
Sly04g0234661	M11	NA	41	35	45	42	51	48	45	50	36	41
Sly04g0234671	M1	NA	3	3	3	4	5	1	2	2	1	0
Sly04g0234681	M1	NA	337	311	293	223	167	272	283	270	290	202
Sly04g0234701	M1	NA	2	1	2	1	1	1	1	1	1	1
Sly04g0234711	M1	NA	44	46	54	32	14	19	25	20	45	22
Sly04g0234721	M12	NA	14	13	13	13	9	17	16	16	17	17
Sly04g0234731	M22	NA	1	1	1	1	0	2	1	1	1	0
Sly04g0234741	M12	NA	10	10	10	15	13	11	12	15	24	22
Sly04g0234761	M22	NA	3	0	2	0	0	15	1	9	0	0
Sly04g0234781	M22	NA	4	1	3	0	0	11	1	12	1	0
Sly04g0234791	M1	NA	14	14	18	9	5	1	0	1	1	1
Sly04g0234801	M11	NA	22	20	27	32	30	19	21	29	40	32
Sly04g0234811	M1	NA	61	56	43	7	2	10	8	6	1	1
Sly04g0234821	M14	NA	27	16	32	1	1	26	17	24	1	1
Sly04g0234841	M1	NA	1	1	1	0	1	1	1	1	1	0
Sly04g0234861	M1	RDR6A	15	18	15	16	17	12	9	12	10	14
Sly04g0234901	M1	NA	15	15	8	2	1	1	1	1	1	1
Sly04g0234911	M1	NA	9	11	6	1	1	1	1	1	0	0
Sly04g0234921	M19	NA	9	10	8	8	7	7	6	6	6	5
Sly04g0234941	M1	NA	32	35	30	23	25	20	20	19	23	25
Sly04g0234961	M19	NA	7	10	10	8	8	9	7	10	7	9
Sly04g0234971	M19	NA	8	11	13	10	10	13	7	11	9	12
Sly04g0234981	M3	NA	9	10	9	7	10	11	7	7	9	12
Sly04g0234991	M2	NA	8	9	10	8	10	10	9	8	11	18
Sly04g0235011	M1	NA	2	1	2	1	1	1	0	0	1	1
Sly04g0235021	M1	NA	38	42	36	14	3	5	4	5	1	1
Sly04g0235051	M22	NA	1	1	1	1	1	3	2	2	1	1
Sly04g0235061	M12	NA	259	207	200	240	163	498	495	553	383	285
Sly04g0235071	M20	NA	1	1	1	1	4	1	1	1	15	67
Sly04g0235081	M11	NA	12	10	14	21	17	26	23	28	10	7
Sly04g0235091	M15	NA	47	42	44	61	60	43	46	47	63	65
Sly04g0235111	M6	NA	53	66	27	13	9	42	44	20	7	4
Sly04g0235121	M12	NA	12	11	13	13	14	12	14	14	17	21
Sly04g0235131	M3	NA	5	4	3	4	7	3	4	3	7	11
Sly04g0235141	M13	NA	57	57	62	159	240	52	54	65	354	392
Sly04g0235161	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0235171	M12	NA	53	53	45	39	36	62	64	52	23	37
Sly04g0235181	M12	NA	21	22	20	17	15	28	24	25	10	15
Sly04g0235191	M3	NA	5	4	3	6	9	4	4	4	37	48
Sly04g0235201	M1	NA	13	14	15	26	24	7	9	8	7	6
Sly04g0235211	M3	NA	31	33	12	5	3	7	6	3	1	1
Sly04g0235221	M2	NA	36	36	30	32	33	29	31	28	36	37
Sly04g0235231	M11	NA	47	45	50	57	68	51	47	50	67	95
Sly04g0235241	M2	NA	22	23	23	19	18	24	23	21	10	9
Sly04g0235251	M12	PFK	17	15	18	52	57	38	42	72	102	62
Sly04g0235261	M12	NA	1	1	1	1	1	1	1	2	2	1
Sly04g0235271	M3	NA	12	11	7	4	4	6	7	6	3	3
Sly04g0235311	M22	NA	1	0	1	0	0	1	1	2	0	0
Sly04g0235321	M12	NA	46	48	53	55	49	64	67	68	51	46
Sly04g0235331	M11	NA	5	4	5	4	3	5	5	5	1	1
Sly04g0235341	M2	NA	33	34	29	30	29	26	28	24	31	29
Sly04g0235351	M1	NA	14	14	14	15	15	13	12	14	11	11
Sly04g0235371	M14	NA	9	10	12	16	15	9	9	12	16	21
Sly04g0235381	M3	NA	39	38	35	152	215	30	32	28	49	30
Sly04g0235411	M1	NA	29	32	29	35	45	26	25	26	40	50
Sly04g0235421	M7	NA	9	15	12	8	100	14	36	13	13	162
Sly04g0235431	M12	NA	73	69	78	102	101	86	94	114	109	127
Sly04g0235451	M1	NA	2	2	3	1	1	1	1	1	1	0
Sly04g0235461	M3	NA	11	10	8	15	17	7	9	8	17	22
Sly04g0235471	M11	NA	1	1	1	3	2	1	1	1	3	3
Sly04g0235481	M18	NA	9	8	11	14	13	12	10	15	12	10
Sly04g0235491	M18	NA	30	33	35	42	61	45	39	48	47	64
Sly04g0235501	M1	NA	6	7	5	1	1	1	1	1	1	1
Sly04g0235511	M11	NA	5	4	5	3	1	6	6	6	2	1
Sly04g0235521	M13	NA	22	19	32	80	145	27	26	46	74	105
Sly04g0235531	M11	NA	10	11	14	38	39	22	18	25	20	15
Sly04g0235551	M11	NA	20	17	22	21	25	27	24	36	33	35
Sly04g0235571	M1	NA	37	38	37	19	26	1	1	1	4	2
Sly04g0235581	M12	NA	1	2	4	19	6	3	13	29	293	50
Sly04g0235601	M11	NA	46	39	66	48	39	80	72	87	25	19
Sly04g0235611	M11	NA	1	1	1	1	1	2	2	2	1	2
Sly04g0235621	M12	NA	8	8	9	8	6	10	10	10	7	7
Sly04g0235631	M1	NA	6	7	6	6	6	5	4	4	2	1
Sly04g0235641	M2	NA	117	119	93	168	125	82	111	78	187	125
Sly04g0235651	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0235661	M21	NA	3	3	4	4	2	3	2	3	1	1
Sly04g0235681	M11	NA	5	4	7	9	10	25	22	31	57	66
Sly04g0235691	M1	NA	3	2	3	1	1	2	2	2	1	1
Sly04g0235701	M19	NA	2	2	2	1	1	2	2	2	1	1
Sly04g0235711	M12	NA	102	106	114	132	119	134	132	165	164	162
Sly04g0235721	M1	NA	47	53	34	15	14	14	12	7	3	4
Sly04g0235731	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0235741	M19	NA	2	1	2	1	1	2	2	2	1	1
Sly04g0235771	M12	NA	13	11	14	10	8	22	17	19	6	2

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0189041	M11	NA	17	18	22	7	3	70	51	61	3	2
Sly10g0189061	M1	NA	4	4	5	2	2	4	3	4	4	4
Sly10g0189071	M9	signalling protein kina	30	35	25	9	14	58	57	43	7	14
Sly10g0189081	M6	NA	115	276	209	21	43	155	334	180	15	68
Sly10g0189091	M6	NA	157	181	141	84	49	162	186	110	52	61
Sly10g0189101	M12	NA	16	31	15	45	196	28	32	23	91	241
Sly10g0189111	M19	NA	16	18	19	34	37	17	17	18	24	24
Sly10g0189121	M12	NA	1	1	1	1	1	3	3	2	1	1
Sly10g0189131	M12	NA	2	3	3	3	1	8	9	8	7	2
Sly10g0189141	M22	NA	2	1	1	1	0	8	3	8	1	1
Sly10g0189151	M18	NA	9	9	13	11	17	10	9	12	25	52
Sly10g0189181	M1	NA	10	11	14	13	16	3	3	3	7	18
Sly10g0189191	M1	NA	20	35	28	15	44	2	2	2	4	28
Sly10g0189201	M1	NA	9	11	8	6	5	7	7	8	4	3
Sly10g0189211	M11	NA	47	51	48	51	54	49	49	54	61	60
Sly10g0189231	M2	NA	25	28	21	31	32	16	20	17	28	33
Sly10g0189241	M7	NA	1	2	1	0	0	2	4	1	0	0
Sly10g0189251	M19	NA	41	48	52	73	52	42	37	45	22	22
Sly10g0189261	M11	NA	1	1	1	2	1	1	1	1	1	1
Sly10g0189271	M15	NA	68	57	57	68	83	76	62	97	99	118
Sly10g0189281	M12	NA	4	4	3	8	5	5	5	6	15	10
Sly10g0189291	M1	NA	15	14	14	12	5	9	11	7	5	2
Sly10g0189301	M12	SlUGT76E1	6	9	19	1194	1673	27	48	80	1944	1442
Sly10g0189311	M11	NA	1	1	1	18	24	1	1	2	100	17
Sly10g0189321	M3	NA	1	1	1	2	1	1	1	1	2	1
Sly10g0189331	M20	UGT-like2	6	5	8	17	6	6	6	5	2	1
Sly10g0189341	M3	NA	4	4	3	1	2	3	4	2	2	4
Sly10g0189351	M1	NA	44	39	45	36	43	33	33	35	39	48
Sly10g0189361	M14	NA	1	1	1	0	0	1	1	1	0	0
Sly10g0189391	M5	NA	78	81	63	38	53	71	79	67	56	76
Sly10g0189401	M3	SlPYL7	7	8	3	1	1	6	6	3	2	2
Sly10g0189411	M1	NA	29	23	23	16	12	14	15	15	7	2
Sly10g0189421	M11	NA	6	5	8	9	15	10	8	12	9	10
Sly10g0189431	M1	NA	7	5	2	0	0	1	1	1	0	0
Sly10g0189461	M3	NA	1	2	1	1	1	1	1	1	1	0
Sly10g0189471	M1	NA	14	14	17	9	6	15	10	13	3	4
Sly10g0189481	M1	NA	17	17	16	14	15	15	13	14	19	20
Sly10g0189491	M5	NA	187	304	79	6	8	89	206	33	5	14
Sly10g0189501	M11	NA	139	133	161	151	187	187	193	213	211	257
Sly10g0189511	M3	NA	28	27	23	22	27	22	26	19	32	38
Sly10g0189521	M1	NA	16	13	16	6	5	8	6	8	3	2
Sly10g0189531	M1	NA	2	1	2	0	0	0	0	0	0	0
Sly10g0189541	M1	NA	335	296	312	310	259	217	217	237	333	278
Sly10g0189551	M11	NA	17	17	17	18	20	19	17	22	30	27
Sly10g0189561	M1	NA	19	17	24	5	1	1	1	1	0	0
Sly10g0189601	M22	NA	1	0	1	0	0	1	0	1	0	0
Sly10g0189611	M22	NA	2	1	2	0	0	13	1	11	1	0
Sly10g0189631	M12	NA	23	26	25	83	37	43	46	46	74	21
Sly10g0189651	M1	SlHDT2	115	110	104	61	54	86	85	88	73	59
Sly10g0189661	M3	CTR4	20	21	17	16	16	16	14	15	16	16
Sly10g0189671	M1	NA	33	33	32	25	33	24	25	25	25	29
Sly10g0189681	M7	NA	16	27	18	23	124	22	51	26	42	253
Sly10g0189691	M11	NA	5	5	6	6	6	6	5	6	4	4
Sly10g0189711	M1	NA	7	7	6	6	5	1	1	1	1	1
Sly10g0189721	M2	NA	25	25	25	29	27	25	26	24	24	21
Sly10g0189761	M11	NA	22	19	24	16	16	26	23	29	23	27
Sly10g0189781	M1	NA	1	1	1	1	0	1	1	0	1	0
Sly10g0189791	M18	NA	13	12	15	20	31	19	18	24	24	20
Sly10g0189801	M11	NA	11	9	11	16	28	11	10	15	18	24
Sly10g0189821	M3	NA	55	58	42	40	39	40	42	35	40	34
Sly10g0189831	M7	NA	16	23	16	16	26	17	21	18	22	30
Sly10g0189851	M22	NA	4	1	2	0	0	5	2	7	1	1
Sly10g0189861	M22	NA	1	1	1	2	1	3	1	3	2	1
Sly10g0189881	M3	NA	83	79	82	108	129	71	74	77	162	192
Sly10g0189901	M12	NA	3	2	3	19	13	9	13	28	260	142
Sly10g0189911	M9	NA	63	84	54	87	115	132	211	129	293	337
Sly10g0189921	M14	NA	35	25	40	38	81	30	26	35	38	62
Sly10g0189931	M1	NA	25	27	39	265	567	16	13	19	181	619
Sly10g0189951	M1	NA	15	21	15	9	7	8	4	7	3	3
Sly10g0189961	M12	UGT73D1	1	1	1	1	0	3	2	1	0	1
Sly10g0189971	M11	UGT73C3-like	1	1	1	1	1	1	1	1	1	1
Sly10g0189981	M12	NA	105	154	389	5433	7512	1322	1512	2779	9673	9761
Sly10g0189991	M12	NA	21	28	72	1148	1250	279	275	584	1689	1380
Sly10g0190001	M12	NA	9	9	13	176	232	20	28	49	321	277
Sly10g0190011	M12	NA	25	23	28	28	29	50	60	65	27	50
Sly10g0190021	M3	NA	3	3	2	1	1	3	2	1	1	1
Sly10g0190041	M11	NA	13	14	14	18	23	19	15	19	28	32
Sly10g0190061	M12	NA	3	2	3	2	1	35	36	44	12	3
Sly10g0190071	M2	NA	7	5	7	8	11	5	7	5	16	19
Sly10g0190081	M11	NA	77	77	84	98	143	78	81	95	135	196
Sly10g0190091	M11	NA	8	9	10	11	14	15	12	18	10	10
Sly10g0190101	M3	NA	38	39	32	34	34	34	39	33	38	43
Sly10g0190111	M1	SlPRR6	35	31	38	29	25	27	27	29	23	18
Sly10g0190121	M1	NA	152	138	136	118	104	91	94	85	93	89
Sly10g0190131	M1	NA	427	385	397	267	196	267	285	302	273	236
Sly10g0190141	M22	NA	7	3	5	2	2	32	9	37	18	17
Sly10g0190151	M3	NA	50	52	39	52	62	30	36	25	60	66
Sly10g0190161	M11	NA	35	33	36	19	10	53	53	58	9	3
Sly10g0190171	M8	NA	108	102	85	115	97	98	121	95	139	118
Sly10g0190181	M3	NA	26	29	24	28	33	17	19	16	26	27
Sly10g0190211	M22	NA	1	1	1	1	1	4	1	2	1	0
Sly10g0190231	M13	NA	23	20	22	17	12	18	22	23	19	14
Sly10g0190261	M12	NA	1	1	1	1	1	1	1	1	0	0
Sly10g0190271	M13	NA	104	106	104	121	58	90	91	104	80	21
Sly10g0190291	M11	AMI1-like4	5	4	9	18	7	23	21	34	57	15
Sly10g0190301	M12	NA	9	13	4	144	44	47	44	21	466	128
Sly10g0190311	M5	NA	81	88	73	23	11	86	102	54	12	6
Sly10g0190331	M12	NA	24	22	21	15	18	24	25	23	17	16
Sly10g0190341	M12	OPR2-like3	12	15	22	7	2	26	28	22	2	1
Sly10g0190361	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly10g0190401	M10	NA	76	225	106	14	88	326	360	121	7	50
Sly10g0190441	M1	NA	2	2	1	1	1	1	1	2	1	1
Sly10g0190451	M1	NA	5	4	3	1	1	3	2	3	1	1
Sly10g0190481	M1	NA	159	160	139	127	103	92	105	85	121	99
Sly10g0190491	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0190501	M1	NA	134	136	132	94	86	84	91	77	67	78
Sly10g0190511	M9	NA	111	111	104	105	113	115	131	125	162	181
Sly10g0190521	M3	GAI-like3	1	1	1	1	1	1	1	1	1	0
Sly10g0190531	M1	GAI-like2	8	9	7	2	1	1	1	1	1	1
Sly10g0190541	M12	NA	1	1	1	1	0	1	1	1	1	0
Sly10g0190551	M11	NA	214	187	209	147	118	256	231	305	231	194
Sly10g0190561	M3	NA	187	145	110	20	21	160	147	96	52	59
Sly10g0190571	M6	NA	85	93	61	39	28	89	103	61	38	27
Sly10g0190581	M3	NA	1	1	1	1	1	1	0	1	1	0
Sly10g0190591	M1	NA	2	2	1	2	3	1	1	1	1	1
Sly10g0190621	M11	NA	5	6	6	6	6	7	5	7	6	6
Sly10g0190631	M11	NA	4	4	5	5	3	7	6	5	2	1
Sly10g0190641	M3	NA	1	3	1	3	2	1	1	1	1	0
Sly10g0190651	M3	DET2	43	49	23	5	4	11	15	2	2	2
Sly10g0190661	M2	NA	96	98	78	85	71	54	62	49	75	60
Sly10g0190671	M9	expansin 6	20	22	17	7	9	23	32	17	5	22
Sly10g0190681	M9	NA	1	1	1	1	1	1	1	1	1	1
Sly10g0190691	M1	NA	17	16	16	12	14	9	9	9	9	11
Sly10g0190701	M3	NA	54	59	57	81	85	42	45	41	79	70
Sly10g0190711	M3	FHL	124	114	108	87	52	94	107	87	105	31
Sly10g0190721	M11	NA	16	17	23	18	8	62	46	77	23	20
Sly10g0190731	M11	NA	136	117	170	130	98	273	227	271	60	48
Sly10g0190781	M1	NA	32	31	38	16	5	2	2	2	1	0
Sly10g0190791	M22	NA	2	1	1	1	0	9	1	8	1	0
Sly10g0190821	M1	NA	2	2	2	1	1	1	1	1	1	0
Sly10g0190

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0235781	M11	NA	6	3	10	43	179	14	11	15	49	139
Sly04g0235791	M12	NA	17	16	17	21	24	26	23	28	38	29
Sly04g0235881	M11	NA	59	63	62	39	45	88	88	84	74	142
Sly04g0235891	M1	NA	3	3	2	1	0	1	0	1	1	1
Sly04g0235921	M1	NA	206	226	223	161	132	194	190	186	134	143
Sly04g0235941	M1	NA	26	21	47	11	5	11	9	14	3	7
Sly04g0235961	M19	NA	21	22	22	12	11	21	19	21	13	11
Sly04g0235971	M18	NA	9	10	12	12	12	14	13	16	9	7
Sly04g0235981	M3	NA	2	2	2	2	3	1	2	1	2	3
Sly04g0235991	M3	NA	33	33	24	17	14	28	25	17	16	12
Sly04g0236001	M3	NA	2	2	1	1	1	1	1	1	0	0
Sly04g0236021	M3	NA	3	10	4	1	1	6	7	1	5	1
Sly04g0236031	M11	NA	7	8	9	9	6	11	10	13	13	11
Sly04g0236041	M12	NA	9	8	9	9	6	13	11	13	15	16
Sly04g0236051	M11	NA	4	3	5	6	6	5	5	7	13	16
Sly04g0236101	M11	NA	10	9	9	8	8	10	9	11	8	8
Sly04g0236171	M11	NA	31	30	32	37	50	33	32	34	46	60
Sly04g0236201	M3	NA	10	9	7	2	2	6	7	4	2	1
Sly04g0236221	M3	NA	7	9	4	1	1	5	4	1	1	1
Sly04g0236231	M2	NA	9	12	8	7	9	8	10	10	9	12
Sly04g0236241	M3	NA	2	3	1	1	0	1	1	1	1	0
Sly04g0236261	M1	NA	2	2	3	1	1	1	1	1	1	1
Sly04g0236271	M12	NA	3	3	3	2	1	8	7	7	2	3
Sly04g0236281	M11	NA	46	38	53	13	4	74	69	65	17	7
Sly04g0236291	M6	NA	28	27	10	1	1	57	49	4	1	0
Sly04g0236311	M1	NA	24	29	25	18	9	4	5	3	2	2
Sly04g0236321	M18	NA	41	40	46	35	40	48	40	45	32	37
Sly04g0236331	M9	NA	1	1	1	2	2	1	2	1	1	3
Sly04g0236341	M3	NA	93	124	41	6	6	53	45	13	1	3
Sly04g0236351	M3	NA	32	30	9	2	2	11	12	3	1	1
Sly04g0236371	M11	NA	4	4	6	3	2	9	7	8	2	1
Sly04g0236381	M3	NA	16	23	16	22	20	11	14	13	28	33
Sly04g0236411	M1	NA	36	29	40	17	6	24	18	22	2	1
Sly04g0236441	M11	NA	161	145	173	194	164	207	201	216	157	167
Sly04g0236451	M19	INO80	16	18	17	21	22	19	14	17	18	19
Sly04g0236461	M3	NA	101	103	82	55	59	41	54	33	58	55
Sly04g0236471	M5	NA	15	20	13	21	15	16	17	13	21	16
Sly04g0236481	M1	NA	26	24	25	15	11	13	14	15	15	14
Sly04g0236491	M18	NA	17	19	19	19	18	19	19	20	14	14
Sly04g0236501	M12	NA	7	11	5	6	3	12	10	12	14	10
Sly04g0236511	M7	SICKX5	1	1	1	1	1	1	1	1	1	1
Sly04g0236521	M3	NA	4	4	5	4	2	3	4	3	3	1
Sly04g0236541	M12	NA	59	59	73	110	30	205	241	175	73	22
Sly04g0236551	M13	NA	5	4	5	4	3	5	4	5	12	6
Sly04g0236561	M11	NA	1	1	2	1	1	3	2	2	1	1
Sly04g0236581	M11	NA	46	42	62	48	54	55	51	64	64	83
Sly04g0236591	M2	NA	77	80	68	85	69	71	81	61	52	47
Sly04g0236601	M11	NA	11	11	16	20	26	14	14	16	17	18
Sly04g0236611	M1	NA	9	16	12	18	22	10	11	10	16	8
Sly04g0236621	M18	NA	5	5	5	6	7	6	5	5	4	4
Sly04g0236631	M18	NA	14	13	15	15	19	14	12	15	15	16
Sly04g0236641	M19	NA	7	8	10	9	10	7	7	8	7	6
Sly04g0236651	M19	NA	5	6	7	6	4	6	5	7	5	4
Sly04g0236691	M20	NA	1	1	2	1	1	1	1	1	1	1
Sly04g0236701	M22	NA	1	1	2	1	1	2	1	1	1	1
Sly04g0236741	M19	NA	23	26	21	23	26	26	26	22	30	37
Sly04g0236751	M19	NA	16	18	14	20	25	19	16	13	24	34
Sly04g0236761	M5	NA	38	39	29	38	53	36	40	31	60	96
Sly04g0236791	M12	NA	18	20	18	23	20	20	22	20	33	20
Sly04g0236801	M23	NA	1	1	1	1	2	1	1	1	1	2
Sly04g0236811	M1	NA	27	24	25	27	33	23	23	22	38	36
Sly04g0236821	M12	NA	402	355	321	429	322	539	579	469	573	517
Sly04g0236831	M11	NA	6	6	8	8	9	7	6	7	5	6
Sly04g0236841	M17	NA	80	73	76	60	61	71	65	74	71	95
Sly04g0236861	M9	NA	1	1	1	3	21	2	2	1	1	2
Sly04g0236881	M11	NA	1	2	1	2	1	2	2	2	2	2
Sly04g0236891	M1	NA	28	32	36	56	44	17	16	24	76	64
Sly04g0236911	M10	NA	1	2	1	0	1	14	14	2	1	0
Sly04g0236921	M1	NA	40	47	34	22	12	16	14	11	3	2
Sly04g0237021	M12	NA	25	17	34	25	30	31	40	47	64	72
Sly04g0237031	M12	NA	10	8	12	9	7	12	17	20	26	20
Sly04g0237041	M10	NA	4	6	3	3	2	5	6	5	6	6
Sly04g0237051	M12	NA	26	27	29	29	30	41	44	55	51	40
Sly04g0237061	M11	NA	2	2	3	2	2	3	2	4	3	4
Sly04g0237071	M11	NA	3	3	4	3	2	4	3	4	3	1
Sly04g0237081	M10	NA	106	165	84	107	207	172	255	104	126	315
Sly04g0237091	M3	NA	6	8	5	9	22	4	7	4	12	30
Sly04g0237101	M3	NA	6	7	5	7	17	5	6	4	11	17
Sly04g0237111	M3	NA	7	8	7	7	5	6	7	6	11	10
Sly04g0237121	M2	NA	6	7	6	8	9	5	7	5	16	23
Sly04g0237141	M1	NA	1	2	3	2	1	1	1	1	1	1
Sly04g0237151	M1	NA	4	3	5	2	4	1	1	1	2	3
Sly04g0237221	M3	NA	8	11	2	4	4	6	12	1	10	4
Sly04g0237261	M11	NA	2	3	3	4	4	4	2	3	3	3
Sly04g0237271	M12	NA	1	1	1	3	2	2	2	2	5	6
Sly04g0237311	M1	NA	1	1	1	1	0	1	1	0	0	0
Sly04g0237321	M3	NA	115	122	75	45	61	24	66	32	12	46
Sly04g0237331	M12	NA	49	45	50	29	32	59	58	57	31	41
Sly04g0237341	M12	b-lcy1	15	11	13	11	17	17	17	17	6	2
Sly04g0237351	M10	NA	440	463	298	274	175	607	828	404	592	450
Sly04g0237361	M1	NA	24	23	24	23	23	18	20	19	28	30
Sly04g0237371	M11	NA	8	8	11	9	2	24	23	23	7	1
Sly04g0237381	M11	NA	15	12	17	10	4	38	30	35	11	1
Sly04g0237411	M1	NA	63	71	25	1	0	3	2	1	1	1
Sly04g0237421	M1	NA	6	6	3	1	1	1	1	0	0	0
Sly04g0237431	M14	NA	6	6	9	5	5	7	5	8	4	2
Sly04g0237451	M3	NA	13	12	11	9	14	9	10	10	17	34
Sly04g0237521	M12	NA	15	13	11	9	11	21	20	19	15	18
Sly04g0237531	M1	NA	8	10	5	2	2	2	1	1	1	1
Sly04g0237541	M1	NA	7	8	5	1	1	1	1	1	1	1
Sly04g0237571	M19	NA	40	46	36	40	50	35	33	31	39	40
Sly04g0237581	M18	NA	4	4	5	4	3	4	4	5	3	3
Sly04g0237591	M12	OPR2-like4	2	1	1	1	2	2	2	2	2	2
Sly04g0237671	M19	NA	4	4	3	5	7	4	4	4	2	3
Sly04g0237681	M18	NA	17	13	23	19	71	20	20	30	8	43
Sly04g0237701	M22	NA	17	18	17	18	40	16	19	25	6	17
Sly04g0237711	M12	NA	2	2	2	8	17	3	3	3	1	8
Sly04g0237861	M11	NA	9	9	10	19	19	15	14	17	28	31
Sly04g0237881	M9	NA	11	11	8	3	1	16	19	11	2	1
Sly04g0237891	M3	NA	14	11	11	16	23	8	13	10	14	23
Sly04g0237901	M18	NA	4	4	4	4	4	4	4	5	3	3
Sly04g0237911	M1	NA	18	17	19	25	31	16	18	17	21	27
Sly04g0237931	M12	NA	0	1	1	1	0	1	1	1	1	0
Sly04g0237951	M3	NA	6	7	6	5	3	5	6	5	3	2
Sly04g0237961	M3	NA	7	7	7	5	4	5	7	4	3	3
Sly04g0237971	M1	NA	2	2	1	1	0	1	1	1	0	0
Sly04g0237981	M1	NA	6	7	5	3	1	4	4	4	1	1
Sly04g0237991	M1	NA	12	12	11	11	11	6	6	6	7	4
Sly04g0238001	M3	SIERF.D5	14	57	6	1	1	15	25	3	1	9
Sly04g0238011	M1	NA	13	11	15	5	5	11	11	9	3	2
Sly04g0238081	M3	NA	257	234	190	265	346	171	205	164	357	392
Sly04g0238091	M11	NA	5	7	8	11	8	9	8	9	7	8
Sly04g0238101	M3	NA	22	35	18	105	40	11	10	11	12	20
Sly04g0238111	M1	SlSnRK2.8	129	155	127	327	214	27	34	26	152	168
Sly04g0238121	M19	NA	34	36	36	41	52	33	30	35	45	48
Sly04g0238131	M9	NA	67	69	65	64	66	62	72	70	87	97
Sly04g0238161	M19	SlJMJ21	8	9	8	9	10	7	6	8	7	6
Sly04g0238241	M6	NA	1	1	1	0	1	2	2	1	0	0
Sly04g0238261	M1	NA	29	28	29	17	7	27	30	25	14	8
Sly04g0238291	M12	NA	6	5	5	5	5	5	6	5	7	6
Sly04g0238301	M22	NA	2	1	2	2	2	2	2	2	3	3
Sly04g0238371	M3	NA	30	28	23	30	24	28	30	22	33	23
Sly04g0238381	M7	NA	22	25	24	29	20	22	28	23	23	12
Sly04g0238391	M1	NA	168	167	165	147	135	136	147	144	139	133

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly10g0190911	M12	NA	7	9	7	8	7	10	12	8	9	9
Sly10g0190921	M2	NA	5	14	19	6	14	4	9	13	13	62
Sly10g0190941	M11	NA	49	42	62	24	9	57	46	62	25	11
Sly10g0190971	M9	NA	21	20	17	15	8	29	34	24	11	9
Sly10g0191001	M3	NA	20	23	17	17	12	20	22	15	15	11
Sly11g0286581	M15	NA	91	76	74	72	49	81	94	82	64	43
Sly11g0286591	M9	NA	31	32	27	33	28	33	36	31	36	35
Sly11g0286601	M18	NA	29	33	35	41	56	35	29	36	32	32
Sly11g0286611	M3	NA	30	29	25	27	24	27	26	25	25	23
Sly11g0286621	M2	NA	98	99	95	115	73	90	110	91	81	61
Sly11g0286631	M11	NA	37	41	44	47	47	54	55	63	59	49
Sly11g0286641	M1	NA	8	14	6	3	5	3	2	1	1	1
Sly11g0286651	M11	NA	24	25	31	22	19	77	63	111	26	11
Sly11g0286661	M22	SlCycA1;1	1	1	1	1	1	1	1	1	1	1
Sly11g0286671	M3	NA	1	1	1	0	1	1	1	1	1	0
Sly11g0286681	M12	NA	31	32	31	36	45	37	35	40	67	84
Sly11g0286701	M12	NA	0	1	1	1	1	1	1	1	3	3
Sly11g0286711	M1	NA	25	27	24	21	22	19	17	18	20	19
Sly11g0286721	M3	PPR-like13	29	27	22	23	20	20	22	18	16	15
Sly11g0286731	M9	NA	14	26	16	2	6	50	99	55	11	32
Sly11g0286751	M11	NA	134	135	137	157	190	143	127	149	235	279
Sly11g0286781	M12	NA	1	1	1	2	1	3	2	2	2	1
Sly11g0286791	M11	NA	6	6	8	32	14	30	26	34	46	22
Sly11g0286801	M12	SlP4H9	25	23	25	53	51	83	86	105	182	139
Sly11g0286821	M12	NA	142	139	146	146	133	174	182	181	162	168
Sly11g0286831	M12	NA	1	1	1	1	0	1	2	2	1	1
Sly11g0286841	M9	NA	2	3	1	1	1	4	12	3	2	4
Sly11g0286851	M18	NA	49	48	49	63	76	52	46	50	72	78
Sly11g0286861	M19	NA	32	32	34	43	47	35	26	36	37	31
Sly11g0286871	M2	NA	11	10	10	9	14	9	10	10	14	19
Sly11g0286881	M11	NA	1	1	1	1	1	7	5	10	1	1
Sly11g0286891	M3	NA	4	5	2	1	1	3	3	5	1	0
Sly11g0286901	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly11g0286911	M1	NA	3	2	2	1	1	1	1	1	0	0
Sly11g0286931	M1	NA	2	1	1	0	1	1	0	1	0	0
Sly11g0286941	M3	NA	867	823	855	642	486	724	785	764	676	646
Sly11g0286951	M11	NA	1	1	1	1	0	2	2	2	1	0
Sly11g0286961	M1	NA	10	8	4	3	1	1	1	1	0	1
Sly11g0286971	M1	NA	48	45	45	75	95	38	39	44	66	84
Sly11g0286981	M3	NA	117	104	108	97	80	95	102	94	108	91
Sly11g0286991	M3	NA	41	76	71	71	111	37	44	49	29	95
Sly11g0287001	M12	NA	1	1	1	1	1	3	2	4	2	3
Sly11g0287011	M2	NA	18	18	15	17	23	12	16	11	21	20
Sly11g0287021	M22	NA	1	1	1	0	0	4	1	3	1	0
Sly11g0287031	M1	NA	1	2	2	1	1	1	1	1	1	1
Sly11g0287041	M1	NA	2	2	2	0	0	1	0	1	0	0
Sly11g0287051	M3	NA	9	10	8	5	4	5	5	4	4	3
Sly11g0287061	M12	NA	173	167	180	130	89	220	226	252	154	90
Sly11g0287071	M12	NA	22	22	22	15	12	24	25	22	11	7
Sly11g0287091	M1	NA	22	33	15	18	4	1	1	1	1	0
Sly11g0287121	M22	NA	2	1	1	0	0	4	1	3	0	0
Sly11g0287141	M12	NA	19	18	17	22	28	22	22	26	31	40
Sly11g0287161	M3	NA	24	29	23	26	10	18	20	14	6	6
Sly11g0287171	M1	NA	49	51	47	51	51	38	41	42	75	77
Sly11g0287181	M11	NA	10	10	12	10	14	14	12	15	13	16
Sly11g0287191	M12	NA	52	49	47	53	56	53	50	55	85	93
Sly11g0287201	M1	NA	47	49	49	64	62	46	45	45	64	60
Sly11g0287221	M3	NA	43	42	34	35	16	30	31	28	24	13
Sly11g0287231	M1	NA	27	35	26	24	17	6	5	2	4	10
Sly11g0287241	M17	NA	16	17	17	33	62	14	10	18	33	72
Sly11g0287251	M1	NA	17	20	26	43	65	16	14	17	33	59
Sly11g0287261	M1	NA	16	18	21	35	55	14	12	15	24	44
Sly11g0287271	M12	NA	183	240	221	151	322	408	423	457	289	384
Sly11g0287281	M12	NA	380	445	418	279	663	753	839	870	629	1208
Sly11g0287301	M11	NA	781	732	755	627	489	755	799	826	796	660
Sly11g0287331	M1	BRU1-like	6	6	6	2	1	3	3	3	1	1
Sly11g0287341	M12	NA	2	2	2	1	1	4	5	2	1	0
Sly11g0287351	M12	NA	10	11	9	15	12	33	38	29	11	9
Sly11g0287361	M12	NA	1	1	1	1	1	2	2	2	2	1
Sly11g0287371	M3	NA	22	33	12	16	19	17	20	12	8	12
Sly11g0287381	M3	SlSDG28	10	11	7	20	18	9	10	8	15	11
Sly11g0287391	M12	NA	2	1	1	1	1	7	7	7	4	1
Sly11g0287401	M12	NA	1	1	1	1	1	2	2	2	1	2
Sly11g0287411	M12	NA	11	7	7	1	1	66	32	67	5	1
Sly11g0287421	M12	NA	9	9	9	5	2	21	13	16	3	1
Sly11g0287441	M22	NA	6	7	6	3	2	7	6	6	2	1
Sly11g0287451	M11	FAS2	9	9	9	3	2	9	10	9	2	2
Sly11g0287461	M19	NA	28	29	28	45	63	25	26	29	51	70
Sly11g0287471	M1	NA	4	3	2	1	1	2	1	1	0	0
Sly11g0287491	M1	NA	13	26	17	0	0	1	1	1	0	1
Sly11g0287511	M6	NA	1	6	2	1	1	3	5	1	1	1
Sly11g0287521	M12	NA	8	7	7	10	12	9	9	9	12	13
Sly11g0287531	M11	NA	40	34	37	62	69	49	45	52	79	78
Sly11g0287551	M11	NA	11	10	8	12	13	11	11	11	15	15
Sly11g0287561	M19	NA	39	46	41	47	39	41	38	41	40	34
Sly11g0287571	M1	NA	158	141	134	88	98	98	92	94	107	96
Sly11g0287591	M1	PPR-like44	16	17	12	12	12	11	9	10	10	9
Sly11g0287601	M18	NA	14	13	15	12	9	14	12	14	6	5
Sly11g0287611	M1	NA	2	2	2	2	2	1	2	2	1	1
Sly11g0287621	M5	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0287651	M22	NA	2	1	1	1	6	7	2	5	1	1
Sly11g0287661	M7	NA	83	94	66	91	111	83	110	63	116	159
Sly11g0287671	M12	NA	1	1	1	1	1	1	2	2	1	1
Sly11g0287681	M18	NA	14	11	14	4	1	13	9	14	1	1
Sly11g0287691	M6	NA	2	7	9	1	0	3	4	1	1	1
Sly11g0287701	M11	NA	1	1	2	1	1	3	3	3	1	1
Sly11g0287721	M11	NA	34	28	47	88	115	63	52	96	90	86
Sly11g0287731	M3	NA	213	175	164	74	56	112	130	93	93	74
Sly11g0287741	M11	NA	23	21	26	19	20	24	21	29	19	20
Sly11g0287771	M11	NA	7	8	8	17	33	12	12	16	29	37
Sly11g0287781	M1	NA	2	2	2	2	2	1	1	1	1	2
Sly11g0287791	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly11g0287801	M22	NA	1	2	2	1	1	3	1	3	1	1
Sly11g0287811	M1	NA	3	5	4	3	2	2	2	2	1	2
Sly11g0287831	M19	NA	18	16	18	14	15	16	15	18	10	16
Sly11g0287841	M3	ETR5	8	9	7	8	8	6	6	4	6	6
Sly11g0287851	M11	NA	23	23	22	27	33	29	25	33	30	43
Sly11g0287861	M11	NA	25	22	27	28	34	28	25	37	34	39
Sly11g0287871	M1	NA	20	22	21	14	17	13	13	13	13	15
Sly11g0287881	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0287891	M1	NA	17	7	34	1	0	1	1	1	0	0
Sly11g0287911	M11	NA	19	19	19	20	19	22	19	21	22	22
Sly11g0287921	M1	NA	210	54	333	1	1	2	1	1	1	0
Sly11g0287941	M11	enoyl-CoA reductase-l	33	32	56	161	59	50	63	104	567	124
Sly11g0287971	M1	SRD5A-like	5	5	8	8	7	1	2	1	6	3
Sly11g0287981	M1	enoyl-CoA reductase-l	1	1	3	1	20	1	1	1	2	17
Sly11g0288001	M1	NA	53	56	51	51	50	37	35	37	39	37
Sly11g0288031	M1	NA	17	17	21	28	47	13	12	15	21	22
Sly11g0288051	M1	NA	30	28	29	21	15	24	25	27	23	22
Sly11g0288061	M11	NA	56	45	79	97	71	132	95	183	130	136
Sly11g0288071	M11	NA	75	71	134	143	101	172	147	265	155	120
Sly11g0288081	M11	NA	47	53	59	88	74	63	61	64	103	80
Sly11g0288091	M3	NA	29	29	23	24	19	18	21	16	19	15
Sly11g0288101	M18	NA	41	39	45	29	26	44	42	43	28	30
Sly11g0288111	M11	NA	27	23	25	28	39	27	27	28	42	52
Sly11g0288121	M3	NA	23	26	24	35	34	20	22	24	20	23
Sly11g0288131	M11	NA	3	3	3	2	1	5	5	6	1	1
Sly11g0288171	M12	NA	2	1	1	1	1	5	5	3	1	1
Sly11g0288181	M11	NA	1683	1556	1717	1466	1587	2782	2510	3279	3323	3259
Sly11g0288191	M1	NA	51	42	45	49	33	44	40	43	51	42
Sly11g0288201	M

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0238411	M11	NA	2	2	2	2	1	2	2	3	3	1
Sly04g0238481	M12	NA	3	3	3	3	3	4	4	4	4	2
Sly04g0238491	M10	NA	40	43	44	51	46	44	46	40	40	41
Sly04g0238511	M19	NA	2	4	4	4	4	5	4	5	3	2
Sly04g0238521	M18	NA	4	5	5	8	9	5	6	6	10	16
Sly04g0238531	M18	NA	11	12	12	16	16	14	12	15	17	22
Sly04g0238551	M18	NA	13	12	12	11	10	14	12	15	12	12
Sly04g0238641	M1	NA	1	2	1	1	1	1	1	1	1	2
Sly04g0238651	M3	NA	8	9	7	6	15	6	9	7	8	34
Sly04g0238671	M1	NA	1	1	1	1	1	1	1	1	1	2
Sly04g0238681	M1	NA	2	1	2	1	1	1	1	1	1	0
Sly04g0238701	M1	NA	274	221	216	192	150	154	163	165	205	146
Sly04g0238801	M12	NA	24	23	24	27	27	31	40	34	59	39
Sly04g0238831	M1	NA	1	1	1	0	0	0	0	0	0	0
Sly04g0238901	M18	NA	52	49	51	30	22	53	45	52	19	13
Sly04g0238951	M19	NA	48	44	46	33	36	42	36	50	36	34
Sly04g0238991	M23	NA	1	1	1	1	2	2	1	2	1	2
Sly04g0239011	M2	NA	28	34	31	30	24	28	35	28	26	26
Sly04g0239111	M9	NA	1	1	1	1	1	1	1	1	1	2
Sly04g0239151	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly04g0239191	M5	NA	23	27	16	17	16	25	28	17	20	21
Sly04g0239241	M11	NA	90	82	104	77	70	100	88	102	52	54
Sly04g0239251	M12	NA	96	87	91	81	68	108	106	106	60	65
Sly04g0239261	M3	NA	58	112	22	4	2	15	19	4	1	1
Sly04g0239311	M12	NA	5	5	5	10	10	8	12	10	32	27
Sly04g0239351	M22	NA	6	7	6	5	2	7	6	6	2	1
Sly04g0239361	M11	NA	2	2	1	2	1	2	2	2	1	1
Sly04g0239371	M12	NA	3	3	3	3	4	4	5	4	4	10
Sly04g0239381	M1	NA	3	4	3	3	2	2	3	3	4	5
Sly04g0239391	M1	NA	23	24	25	36	53	21	20	22	37	47
Sly04g0239401	M3	GAD4	26	52	29	1	1	22	17	4	1	1
Sly04g0239481	M1	NA	8	8	7	8	4	6	6	6	6	3
Sly04g0239501	M1	NA	4	5	5	5	5	5	4	4	5	4
Sly04g0239511	M19	NA	3	3	3	3	3	3	3	3	3	2
Sly04g0239531	M12	NA	1	1	1	1	1	1	1	1	2	2
Sly04g0239631	M1	NA	1	1	2	4	4	1	1	1	2	6
Sly04g0239651	M1	NA	11	7	12	15	6	4	4	8	8	6
Sly04g0239661	M9	NA	8	8	8	8	10	8	9	7	12	23
Sly04g0239671	M12	NA	7	5	6	7	9	6	6	7	9	18
Sly04g0239701	M19	NA	56	57	65	71	80	54	48	60	60	65
Sly04g0239711	M11	NA	28	26	28	45	78	34	31	41	55	84
Sly04g0239751	M3	NA	27	27	26	29	23	23	24	23	12	10
Sly04g0239761	M1	NA	15	16	15	8	5	8	9	7	4	5
Sly04g0239811	M11	NA	19	15	21	15	18	23	18	25	21	31
Sly04g0239831	M3	NA	21	26	17	14	14	13	14	10	10	7
Sly04g0239841	M19	NA	6	7	6	9	6	6	6	7	7	5
Sly04g0239851	M11	NA	4	5	6	6	5	6	6	7	7	6
Sly04g0239861	M3	NA	19	20	14	12	12	15	14	13	12	11
Sly04g0239871	M11	NA	28	27	33	53	77	45	38	48	51	62
Sly04g0239901	M11	NA	24	21	22	35	67	31	31	38	40	62
Sly04g0239911	M12	NA	1	1	1	1	1	6	4	4	2	1
Sly04g0239951	M1	NA	132	144	133	161	64	4	3	4	2	1
Sly04g0239971	M11	NA	18	20	20	24	23	22	19	22	28	28
Sly04g0239981	M19	NA	13	14	16	17	16	14	11	15	16	13
Sly04g0239991	M19	NA	13	17	16	20	16	17	12	17	13	18
Sly04g0240001	M19	NA	11	14	14	15	13	15	9	14	13	12
Sly04g0240011	M19	NA	10	13	11	11	9	11	9	12	9	11
Sly04g0240021	M19	NA	10	14	10	14	7	10	8	12	8	8
Sly04g0240031	M19	NA	7	9	6	7	5	8	4	6	7	6
Sly04g0240111	M1	NA	14	11	15	7	6	11	14	11	5	7
Sly04g0240121	M11	NA	21	20	20	20	22	23	21	22	25	32
Sly04g0240231	M1	NA	5	5	14	4	11	2	1	1	1	1
Sly04g0240241	M1	NA	2	1	1	1	1	1	1	1	0	0
Sly04g0240261	M5	NA	5	9	3	1	1	5	8	2	1	1
Sly04g0240281	M12	NA	8	7	7	6	6	9	9	9	8	9
Sly04g0240311	M3	NA	24	24	20	19	20	21	24	21	21	27
Sly04g0240411	M12	NA	46	44	47	61	69	58	61	67	75	94
Sly04g0240481	M2	NA	45	48	41	43	39	37	44	34	45	42
Sly04g0240491	M12	NA	8	8	8	5	5	8	8	10	5	4
Sly04g0240501	M12	NA	50	47	46	49	56	51	51	48	60	70
Sly04g0240561	M11	NA	69	53	83	52	39	79	68	98	51	47
Sly04g0240571	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly04g0240581	M1	NA	21	21	23	34	39	14	15	15	19	17
Sly04g0240591	M12	NA	2	3	3	3	3	3	4	4	3	3
Sly04g0240631	M3	NA	35	35	32	38	45	30	35	32	49	61
Sly04g0240641	M1	NA	12	11	12	11	14	10	9	10	17	26
Sly04g0240711	M11	NA	2	2	3	2	1	5	3	4	3	2
Sly04g0240731	M12	NA	13	8	8	13	15	14	11	11	12	13
Sly04g0240741	M11	NA	260	242	282	280	320	276	290	317	223	294
Sly04g0240811	M11	NA	40	37	46	51	66	49	49	59	82	91
Sly04g0240821	M9	NA	2	1	1	1	1	2	2	1	1	2
Sly04g0240831	M12	NA	1	1	1	1	1	2	2	2	2	2
Sly04g0240841	M12	NA	1	1	1	1	1	2	2	1	3	4
Sly04g0240861	M12	NA	16	17	16	20	21	24	24	23	18	20
Sly04g0240871	M12	NA	25	27	27	31	29	26	28	28	29	27
Sly04g0240881	M2	NA	18	20	19	22	20	17	22	18	22	22
Sly04g0240891	M11	NA	3	3	4	3	4	5	4	6	6	5
Sly04g0240901	M18	NA	2	2	2	1	1	3	2	2	2	2
Sly04g0240911	M10	NA	9	9	7	2	1	10	10	8	1	1
Sly04g0240961	M3	NA	5	5	4	3	2	3	4	2	1	1
Sly04g0240971	M12	NA	3	2	2	3	8	4	4	3	4	10
Sly04g0240981	M11	NA	17	16	17	35	51	24	23	30	43	60
Sly04g0240991	M12	NA	2	1	2	5	7	9	14	16	46	50
Sly04g0241001	M12	NA	1	1	2	4	5	7	12	12	34	30
Sly04g0241011	M1	NA	17	17	17	23	22	14	14	17	36	26
Sly04g0241021	M12	NA	38	43	43	16	5	115	121	83	19	9
Sly04g0241031	M11	NA	18	20	23	7	2	54	46	43	8	4
Sly04g0241041	M12	NA	74	67	65	95	92	79	85	83	102	111
Sly04g0241051	M1	NA	31	30	30	28	29	25	23	24	29	36
Sly04g0241061	M3	NA	19	18	18	8	3	15	17	14	7	4
Sly04g0241081	M12	NA	19	17	18	20	23	18	19	18	17	16
Sly04g0241091	M12	NA	11	13	14	16	13	17	17	17	17	8
Sly04g0241111	M1	NA	12	12	13	12	9	10	9	9	5	4
Sly04g0241131	M12	NA	2	3	3	4	7	2	2	3	5	4
Sly04g0241141	M2	NA	119	129	109	125	103	100	127	88	97	98
Sly04g0241161	M11	NA	32	29	32	38	39	35	39	41	48	48
Sly04g0241181	M9	NA	190	191	187	168	176	213	230	209	310	336
Sly04g0241261	M11	NA	8	7	9	4	2	22	18	26	6	5
Sly04g0241311	M12	NA	5	5	12	1	2	137	143	151	6	6
Sly04g0241331	M3	NA	664	652	371	36	17	130	137	55	20	23
Sly04g0241371	M3	NA	30	27	20	13	9	16	16	14	10	6
Sly04g0241441	M11	NA	31	31	39	44	50	39	33	44	49	63
Sly04g0241461	M1	NA	74	72	68	86	76	55	60	53	58	52
Sly04g0241471	M1	NA	19	18	14	12	10	2	2	2	1	1
Sly04g0241481	M23	NA	1	1	1	1	0	1	1	1	1	0
Sly04g0241501	M19	NA	52	56	49	48	46	52	43	51	36	33
Sly04g0241511	M11	NA	1	1	1	2	1	1	1	1	1	1
Sly04g0241521	M11	NA	20	20	22	32	41	25	20	25	26	32
Sly04g0241531	M19	SIJMJ19	29	34	29	25	26	28	29	27	20	20
Sly04g0241541	M3	NA	17	19	13	23	13	12	18	11	13	16
Sly04g0241551	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly04g0241561	M12	NA	31	32	31	41	43	48	48	44	50	44
Sly04g0241591	M12	NA	50	46	51	51	43	65	73	74	52	46
Sly04g0241651	M3	NA	10	8	6	9	8	3	5	5	4	4
Sly04g0241661	M11	NA	8	7	9	10	11	10	9	11	13	18
Sly04g0241811	M12	NA	1	2	3	3	11	21	39	23	30	158
Sly04g0241821	M11	NA	529	429	554	1016	1578	645	672	826	1168	2170
Sly04g0241831	M12	NA	73	72	89	143	248	86	113	109	173	342
Sly04g0241841	M10	NA	151	168	128	148	176	205	204	116	118	164
Sly04g0241851	M3	NA	27	28	25	22	19	23	23	21	25	19
Sly04g0241871	M11	NA	21	21	23	37	39	40	34	39	36	24
Sly04g0241891	M12	NA	3	2	2	10	5	5	4	3	8	10
Sly04g0241901	M12	NA	18	17	17	23	22	20	24	25	28	29
Sly04g0241931	M12	NA	62	61	69	91	62	78	75	73	33	24

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0288241	M1	NA	15	16	15	19	21	13	11	12	16	23
Sly11g0288281	M10	NA	11	15	10	10	15	29	34	9	3	7
Sly11g0288291	M12	NA	105	106	113	169	115	107	116	118	129	139
Sly11g0288311	M11	NA	3	3	5	4	3	5	5	5	5	3
Sly11g0288321	M12	NA	1	1	1	1	1	2	2	1	2	2
Sly11g0288331	M11	NA	10	9	11	10	6	15	15	14	7	5
Sly11g0288341	M14	NA	2	1	4	1	0	2	2	2	1	0
Sly11g0288361	M1	NA	45	45	47	55	76	43	43	47	56	79
Sly11g0288371	M1	NA	5	4	5	3	1	3	2	3	1	1
Sly11g0288381	M1	NA	3	3	3	2	2	1	1	1	1	1
Sly11g0288391	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly11g0288401	M1	NA	52	50	51	49	41	40	42	39	46	45
Sly11g0288411	M11	NA	5	4	7	3	3	21	16	20	1	1
Sly11g0288421	M11	NA	2	2	4	1	1	10	9	12	0	1
Sly11g0288441	M11	PPR-like18	11	12	15	19	19	29	23	32	20	15
Sly11g0288451	M1	NA	499	462	477	389	253	363	390	368	421	284
Sly11g0288461	M1	NA	3	4	4	3	4	3	3	3	4	3
Sly11g0288471	M12	NA	4	4	3	4	1	17	11	11	3	1
Sly11g0288481	M12	NA	54	46	45	28	54	51	60	66	74	103
Sly11g0288491	M3	NA	1	1	1	1	1	0	1	1	2	2
Sly11g0288501	M1	NA	5	3	5	3	3	4	2	4	5	3
Sly11g0288511	M1	NA	31	28	31	28	72	33	28	28	73	107
Sly11g0288521	M11	NA	37	34	40	162	271	43	50	59	120	303
Sly11g0288531	M11	NA	59	53	49	50	55	55	51	62	64	74
Sly11g0288541	M1	NA	42	44	46	97	90	40	39	41	102	100
Sly11g0288551	M1	NA	68	66	72	95	123	61	63	65	77	124
Sly11g0288561	M11	NA	1	1	1	1	1	11	4	7	1	0
Sly11g0288591	M3	NA	2	2	2	2	2	2	2	2	2	3
Sly11g0288641	M16	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0288651	M9	NA	10	13	11	22	18	15	19	16	18	15
Sly11g0288661	M1	NA	51	57	48	39	35	40	39	35	32	33
Sly11g0288671	M1	NA	3	3	4	3	2	2	1	1	1	1
Sly11g0288681	M9	NA	14	18	13	21	9	17	21	18	23	15
Sly11g0288691	M12	NA	1	1	1	16	14	3	6	2	62	75
Sly11g0288701	M3	NA	27	26	22	31	32	24	24	25	36	40
Sly11g0288721	M1	NA	6	5	6	4	2	2	2	2	1	1
Sly11g0288731	M1	NA	5	6	6	5	4	4	5	5	5	3
Sly11g0288751	M23	NA	3	1	1	1	2	6	2	2	1	2
Sly11g0288761	M19	NA	47	61	49	60	67	54	54	52	55	68
Sly11g0288781	M11	NA	246	236	356	380	662	378	386	452	217	397
Sly11g0288791	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly11g0288801	M12	NA	48	78	90	232	145	146	158	258	316	183
Sly11g0288811	M2	NA	10	12	10	13	11	7	9	7	13	12
Sly11g0288821	M3	NA	22	22	20	12	10	17	17	16	11	10
Sly11g0288841	M3	NA	123	130	75	62	42	39	46	22	21	14
Sly11g0288851	M10	NA	3	3	1	1	1	9	6	1	1	1
Sly11g0288861	M10	NA	11	11	10	19	27	11	13	10	19	15
Sly11g0288871	M22	NA	1	0	1	0	0	6	1	6	1	0
Sly11g0288881	M11	NA	22	20	27	28	30	29	26	33	35	35
Sly11g0288891	M1	NA	17	18	19	28	44	14	16	18	28	47
Sly11g0288911	M3	NA	25	23	18	22	30	21	23	18	29	47
Sly11g0288921	M11	NA	14	14	15	20	35	17	15	18	23	39
Sly11g0288931	M3	NA	82	81	66	71	86	58	60	53	81	84
Sly11g0288941	M13	NA	22	21	27	40	59	21	25	24	48	53
Sly11g0288951	M1	NA	37	37	58	60	90	32	25	35	31	50
Sly11g0288961	M1	NA	5	7	9	19	12	3	4	4	10	5
Sly11g0288981	M11	NA	5	5	7	5	3	8	6	7	2	1
Sly11g0288991	M11	NA	173	170	199	210	267	197	192	212	241	310
Sly11g0289011	M1	NA	3	4	3	7	4	0	1	1	0	1
Sly11g0289021	M3	NA	30	28	19	71	200	22	15	24	40	96
Sly11g0289061	M1	NA	3	4	3	4	3	2	2	2	2	1
Sly11g0289081	M22	NA	1	1	2	0	0	2	1	1	1	0
Sly11g0289091	M11	NA	24	23	24	27	42	28	27	28	33	39
Sly11g0289131	M12	NA	6	6	5	4	4	9	9	7	6	5
Sly11g0289141	M11	NA	33	34	40	45	63	44	43	48	52	66
Sly11g0289161	M11	NA	29	26	36	31	29	31	27	39	84	90
Sly11g0289171	M11	NA	8	9	8	9	8	11	9	11	11	9
Sly11g0289201	M1	NA	3	8	4	27	20	1	1	1	2	2
Sly11g0289211	M1	NA	30	43	25	5	1	2	1	1	1	1
Sly11g0289221	M1	NA	8	8	4	1	1	1	1	1	0	0
Sly11g0289281	M12	NA	3	3	3	3	2	4	4	4	5	5
Sly11g0289291	M12	NA	3	3	5	3	3	9	10	6	6	4
Sly11g0289301	M5	NA	30	34	20	6	4	32	38	20	4	2
Sly11g0289341	M11	NA	1	1	2	1	1	11	8	14	1	1
Sly11g0289351	M1	SlCYP77A1	8	6	18	0	0	1	1	1	0	1
Sly11g0289361	M3	NA	3	4	2	2	2	2	2	2	2	2
Sly11g0289371	M12	NA	3	4	4	4	6	5	6	7	6	9
Sly11g0289381	M11	NA	1	1	1	1	1	1	1	1	2	1
Sly11g0289391	M3	NA	3	3	3	2	1	2	3	2	1	1
Sly11g0289401	M1	SlDML3	36	38	29	23	22	15	12	11	7	10
Sly11g0289431	M12	NA	31	30	30	43	98	41	39	38	58	99
Sly11g0289451	M3	NA	26	28	22	13	7	15	17	13	9	4
Sly11g0289461	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly11g0289481	M3	NA	3	3	3	1	1	2	3	3	1	1
Sly11g0289491	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0289501	M5	NA	49	82	31	13	13	36	47	16	4	7
Sly11g0289511	M18	NA	18	19	22	22	28	20	20	24	30	27
Sly11g0289521	M12	NA	27	23	28	62	131	28	29	38	77	234
Sly11g0289531	M17	NA	17	15	22	26	31	16	12	18	8	8
Sly11g0289551	M1	NA	21	18	19	15	19	15	13	15	24	27
Sly11g0289561	M13	NA	13	13	14	16	13	12	12	14	16	11
Sly11g0289571	M12	NA	51	52	51	72	71	58	60	57	75	66
Sly11g0289581	M22	NA	2	1	1	1	1	1	1	2	1	1
Sly11g0289591	M3	NA	25	27	24	19	21	18	21	16	28	27
Sly11g0289601	M3	NA	5	7	4	4	4	4	4	3	4	3
Sly11g0289611	M3	NA	15	19	14	16	13	13	16	9	9	8
Sly11g0289621	M10	NA	21	25	20	73	60	52	46	22	67	39
Sly11g0289641	M1	NA	45	43	47	90	107	24	25	32	92	133
Sly11g0289661	M19	NA	16	17	15	11	12	17	14	16	15	16
Sly11g0289671	M1	NA	14	14	14	12	17	14	12	14	16	19
Sly11g0289681	M3	NA	1	1	1	0	1	1	1	1	1	1
Sly11g0289701	M13	SEX4	77	67	89	146	184	89	78	119	90	80
Sly11g0289711	M3	NA	8	8	7	7	6	7	6	6	6	3
Sly11g0289721	M1	NA	46	45	48	75	139	37	37	39	75	125
Sly11g0289731	M1	NA	78	64	78	98	93	55	51	62	64	79
Sly11g0289751	M22	NA	1	1	1	0	0	1	1	1	1	2
Sly11g0289761	M3	gibberellin-A12 hydrat	3	4	1	0	0	1	1	0	0	0
Sly11g0289771	M11	NA	6	11	13	12	13	12	10	15	8	7
Sly11g0289781	M19	NA	24	26	24	24	26	26	22	25	23	20
Sly11g0289791	M12	NA	171	157	165	207	336	186	184	182	198	366
Sly11g0289801	M12	NA	8	8	9	26	44	27	36	44	82	143
Sly11g0289811	M12	NA	14	14	13	24	15	14	16	15	15	8
Sly11g0289831	M12	NA	75	72	70	53	33	78	81	80	45	29
Sly11g0289861	M1	NA	1	1	1	0	1	1	0	0	0	0
Sly11g0289881	M11	NA	149	136	162	138	55	286	266	286	84	23
Sly11g0289891	M3	NA	114	111	86	88	104	64	70	55	106	106
Sly11g0289901	M1	NA	220	191	197	122	91	112	116	79	70	73
Sly11g0289911	M13	NA	35	32	39	71	53	32	28	41	28	37
Sly11g0289921	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0289931	M11	LDA	3	4	4	4	3	7	5	6	1	1
Sly11g0289951	M3	NA	5	12	2	1	1	1	1	1	1	1
Sly11g0289961	M18	NA	14	14	13	7	7	15	12	14	11	10
Sly11g0289971	M2	NA	36	36	27	19	22	22	24	18	24	29
Sly11g0289981	M19	NA	25	27	26	26	30	23	20	22	22	26
Sly11g0289991	M1	NA	42	41	40	40	50	33	34	35	37	54
Sly11g0290011	M1	SIPL	10	8	9	1	1	7	6	6	1	1
Sly11g0290021	M18	SPT5	45	45	58	52	46	71	48	74	38	34
Sly11g0290051	M18	NA	19	19	17	17	21	21	18	21	25	27
Sly11g0290061	M19	NA	17	22	17	16	15	17	17	17	17	13
Sly11g0290071	M19	NA	14	14	15	13	14	15	12	15	15	13
Sly11g0290131	M18	NA	10	9	10	15	34	11	9	10	14	18
Sly11g0290141	M11	N

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0241981	M2	NA	74	82	65	74	68	61	69	55	70	73
Sly04g0242051	M3	NA	19	18	18	32	36	17	17	17	30	35
Sly04g0242061	M3	NA	43	42	40	23	22	29	29	23	18	14
Sly04g0242091	M11	NA	23	23	24	32	33	29	26	30	28	28
Sly04g0242141	M12	NA	4	4	4	3	2	4	4	4	3	1
Sly04g0242151	M3	NA	29	31	24	17	17	16	18	13	13	11
Sly04g0242161	M13	SIPRR5	196	200	258	197	241	261	218	324	190	195
Sly04g0242171	M18	NA	90	94	123	95	107	113	90	150	76	70
Sly04g0242181	M8	NA	42	47	40	45	52	43	46	40	58	70
Sly04g0242211	M11	NA	32	32	35	33	31	32	31	37	44	48
Sly04g0242221	M11	NA	18	18	20	27	16	23	22	23	19	9
Sly04g0242251	M19	NA	46	48	46	52	54	46	36	45	42	49
Sly04g0242261	M2	NA	19	18	17	18	22	18	19	18	21	25
Sly04g0242301	M12	NA	3	4	4	4	4	15	12	15	6	4
Sly04g0242331	M19	NA	8	8	8	6	5	9	7	8	8	4
Sly04g0242341	M11	NA	28	28	31	35	50	34	33	41	45	53
Sly04g0242351	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly04g0242401	M12	NA	1	1	2	4	5	10	12	15	79	84
Sly04g0242511	M11	NA	6	6	7	7	8	7	5	7	7	7
Sly04g0242551	M13	NA	18	17	18	15	14	16	18	20	18	19
Sly04g0242571	M1	NA	42	45	42	50	45	35	31	34	35	34
Sly04g0242581	M11	NA	2	1	1	1	0	4	3	2	1	0
Sly04g0242591	M1	NA	23	23	24	21	14	16	21	17	11	8
Sly04g0242631	M1	NA	20	19	22	18	22	17	17	17	28	45
Sly04g0242661	M19	NA	15	17	21	17	15	14	10	18	7	7
Sly04g0242671	M12	NA	2	3	3	13	9	9	9	14	20	12
Sly04g0242791	M5	NA	15	20	10	5	5	14	15	7	5	5
Sly04g0242801	M19	NA	17	20	19	20	20	18	14	19	17	19
Sly04g0242811	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0242821	M2	NA	45	41	43	35	31	41	44	39	48	46
Sly04g0242831	M12	NA	21	20	23	23	24	29	27	27	18	14
Sly04g0242911	M7	NA	2	6	1	1	2	2	6	4	1	5
Sly04g0242921	M1	NA	20	22	19	12	12	17	15	14	7	7
Sly04g0242931	M9	NA	72	78	71	93	126	77	98	81	119	160
Sly04g0242941	M12	NA	18	18	19	15	16	22	22	21	26	29
Sly04g0242981	M11	NA	38	39	45	58	62	47	48	60	69	80
Sly04g0242991	M11	NA	2	4	2	3	1	3	3	3	2	1
Sly04g0243001	M19	NA	2	5	2	2	2	4	4	4	1	1
Sly04g0243011	M11	NA	23	22	32	36	44	36	31	44	50	53
Sly04g0243031	M1	NA	15	22	42	13	2	0	0	1	1	0
Sly04g0243201	M11	NA	27	23	30	57	63	35	33	40	59	63
Sly04g0243211	M11	NA	14	13	14	15	14	13	14	16	18	13
Sly04g0243221	M1	NA	14	16	22	8	2	2	1	1	0	0
Sly04g0243231	M19	NA	36	43	41	39	28	34	30	30	18	16
Sly04g0243331	M11	NA	15	16	19	32	24	25	22	30	26	17
Sly04g0243351	M19	NA	15	17	17	17	14	17	13	19	15	12
Sly04g0243361	M11	NA	25	28	26	27	29	25	25	29	30	30
Sly04g0243371	M12	NA	1	2	1	1	1	3	3	2	1	1
Sly04g0243391	M14	NA	88	56	74	4	1	61	44	60	2	1
Sly04g0243401	M22	NA	1	0	2	0	0	12	0	10	0	0
Sly04g0243541	M1	NA	4	4	3	2	2	1	1	1	1	1
Sly04g0243551	M1	NA	4	6	7	2	2	1	1	1	1	1
Sly04g0243561	M1	NA	4	4	4	3	3	3	3	3	3	3
Sly04g0243611	M12	NA	2	2	2	2	2	3	3	3	4	4
Sly04g0243621	M19	NA	16	18	18	15	18	19	16	17	25	32
Sly04g0243651	M22	NA	1	1	1	0	0	7	1	4	0	1
Sly04g0243661	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly04g0243671	M1	NA	1	1	2	1	1	0	1	1	0	0
Sly04g0243681	M1	NA	4	2	3	2	1	2	1	1	1	1
Sly04g0243821	M1	NA	38	32	41	15	6	28	23	24	5	3
Sly04g0243831	M12	VDE	11	14	16	41	28	47	47	66	73	42
Sly04g0243861	M12	NA	6	6	5	2	1	5	7	7	2	1
Sly04g0243871	M11	NA	20	18	25	20	17	22	18	26	12	11
Sly04g0243911	M1	NA	5	4	4	5	4	1	1	1	1	1
Sly04g0243921	M3	NA	12	15	10	21	13	11	13	12	20	18
Sly04g0244051	M12	NA	22	19	25	15	20	22	27	24	27	37
Sly04g0244061	M12	NA	4	5	4	4	6	5	4	5	9	18
Sly04g0244071	M19	NA	3	4	3	2	4	5	3	3	6	15
Sly04g0244081	M12	NA	23	21	24	41	58	24	25	25	55	77
Sly04g0244121	M9	NA	6	7	4	4	4	8	8	6	6	8
Sly04g0244181	M18	CYP97A3	16	17	19	23	24	18	18	20	17	14
Sly04g0244191	M3	NA	55	53	43	49	68	49	57	41	48	58
Sly04g0244211	M12	NA	5	5	6	7	7	6	7	8	19	22
Sly04g0244251	M22	NA	15	9	11	44	41	30	9	21	10	4
Sly04g0244271	M2	NA	2	1	1	1	1	1	1	1	1	1
Sly04g0244281	M5	NA	90	127	68	36	27	96	114	57	35	41
Sly04g0244321	M8	NA	64	57	52	58	52	58	66	57	99	99
Sly04g0244331	M11	NA	13	13	16	4	4	18	16	15	4	2
Sly04g0244341	M6	SIERF.D1	27	46	9	1	1	22	40	7	1	2
Sly04g0244351	M1	NA	140	142	140	133	136	119	124	124	149	176
Sly04g0244391	M3	NA	4	4	2	1	2	1	2	1	1	1
Sly04g0244421	M1	NA	6	5	4	4	4	3	3	3	2	1
Sly04g0244431	M12	NA	4	3	5	1	0	26	20	25	0	0
Sly04g0244451	M3	NA	12	12	12	7	7	11	10	9	9	9
Sly04g0244461	M1	NA	1	1	1	1	1	0	0	0	0	0
Sly04g0244471	M1	NA	9	5	18	7	32	3	2	5	5	19
Sly04g0244491	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0244501	M9	NA	5	4	3	1	8	3	8	4	6	6
Sly04g0244511	M3	NA	45	47	33	21	20	34	37	16	9	10
Sly04g0244531	M12	SIBRI1	33	35	28	9	7	57	51	39	2	2
Sly04g0244551	M19	NA	13	16	16	16	18	14	12	15	11	11
Sly04g0244561	M11	NA	16	15	15	11	8	19	16	17	3	1
Sly04g0244581	M1	NA	19	19	17	18	21	15	15	17	22	26
Sly04g0244591	M19	NA	7	7	9	8	11	8	8	7	6	9
Sly04g0244611	M3	NA	2	3	2	3	1	2	2	2	2	1
Sly04g0244621	M11	NA	4	4	4	4	2	4	4	4	3	2
Sly04g0244631	M1	NA	17	16	17	14	13	12	11	13	12	8
Sly04g0244641	M1	NA	37	37	37	26	24	25	26	24	21	22
Sly04g0244661	M3	NA	15	23	7	1	1	1	2	1	0	1
Sly04g0244671	M3	NA	34	39	27	17	18	26	32	19	15	16
Sly04g0244681	M15	NA	34	29	30	21	21	34	33	36	42	45
Sly04g0244701	M12	NA	2	1	1	1	1	1	1	2	7	10
Sly04g0244721	M12	NA	10	9	9	11	8	22	25	30	18	15
Sly04g0244731	M12	NA	1	1	1	1	0	2	2	3	1	1
Sly04g0244741	M12	NA	0	1	1	1	0	3	3	2	1	1
Sly04g0244751	M11	NA	25	24	31	31	28	41	41	51	43	47
Sly04g0244761	M11	NA	41	30	62	59	253	62	55	86	102	145
Sly04g0244771	M12	NA	84	84	73	32	84	210	242	201	45	151
Sly04g0244781	M3	NA	45	42	43	36	38	35	38	34	40	43
Sly04g0244791	M11	NA	115	109	124	131	160	127	129	176	187	197
Sly04g0244801	M12	NA	23	23	16	30	31	37	34	21	29	28
Sly04g0244811	M11	NA	20	16	26	17	14	36	30	43	22	18
Sly04g0244821	M12	NA	1	1	1	1	1	1	1	1	2	1
Sly04g0244991	M12	NA	1	1	1	16	8	2	2	2	1	1
Sly04g0245021	M7	NA	29	78	33	12	100	71	235	48	28	313
Sly04g0245031	M7	NA	1	2	1	1	1	2	7	1	1	2
Sly04g0245061	M11	NA	257	241	280	302	304	410	382	531	781	705
Sly04g0245101	M1	NA	2	2	1	2	1	0	1	1	0	0
Sly04g0245111	M11	DPE	30	24	34	22	16	61	50	59	6	4
Sly04g0245121	M12	NA	206	187	257	786	1619	229	251	282	770	3020
Sly04g0245181	M1	NA	10	11	8	4	3	3	2	2	1	1
Sly04g0245191	M1	NA	2	1	2	2	3	2	1	1	2	7
Sly04g0245201	M12	NA	2	2	3	2	5	2	2	2	5	13
Sly04g0245231	M3	NA	46	50	40	35	33	32	36	26	29	27
Sly04g0245241	M1	NA	1	1	1	1	1	0	0	0	0	1
Sly04g0245251	M3	NA	25	27	22	16	17	21	23	21	19	16
Sly04g0245261	M1	NA	44	50	42	24	23	27	30	22	28	23
Sly04g0245281	M18	NA	14	12	20	21	87	30	22	28	30	49
Sly04g0245291	M12	NA	16	15	17	23	15	16	17	18	40	18
Sly04g0245351	M12	NA	2	2	6	1	0	15	8	4	1	0
Sly04g0245361	M12	NA	1	1	1	1	0	1	1	1	1	0
Sly04g0245371	M1	NA	13	12	7	6	4	2	2	2	1	1
Sly04g0245391	M11	NA	3	3	4	5	6	5	4	5	5	5
Sly04g0245411	M18	NA	3	3	4	4	3	3	3	4	4	3

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0290181	M9	NA	20	19	19	28	27	20	21	20	36	35
Sly11g0290191	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0290201	M2	NA	76	78	70	84	87	52	69	55	114	107
Sly11g0290211	M18	SlHDMA1	18	18	16	21	22	19	17	19	19	20
Sly11g0290231	M12	NA	43	50	48	58	55	57	54	53	51	56
Sly11g0290241	M12	NA	14	16	18	51	97	23	26	45	199	154
Sly11g0290251	M11	NA	35	33	42	80	158	46	41	55	113	186
Sly11g0290261	M1	NA	9	9	8	15	19	3	3	3	7	11
Sly11g0290271	M1	NA	16	18	14	27	33	5	5	5	15	16
Sly11g0290281	M3	NA	56	59	46	33	34	54	53	51	49	43
Sly11g0290311	M9	NA	4	4	3	5	9	6	7	6	16	11
Sly11g0290321	M3	NA	96	91	84	86	102	72	79	80	102	118
Sly11g0290351	M3	NA	50	72	69	158	127	20	36	14	49	32
Sly11g0290361	M9	NA	17	20	17	24	28	19	23	18	42	45
Sly11g0290371	M19	NA	73	65	67	54	65	68	52	73	53	55
Sly11g0290381	M11	NA	3	2	4	1	1	8	7	9	1	0
Sly11g0290401	M1	NA	15	13	14	13	11	12	13	13	11	8
Sly11g0290411	M1	NA	528	510	533	369	266	373	417	350	363	259
Sly11g0290431	M3	NA	55	59	45	4	31	24	29	13	14	11
Sly11g0290441	M3	NA	244	257	133	4	23	79	113	24	11	20
Sly11g0290451	M12	NA	18	18	20	27	42	20	22	22	25	35
Sly11g0290471	M12	NA	13	12	15	20	19	16	16	15	14	14
Sly11g0290481	M18	NA	81	75	83	76	106	83	65	88	99	95
Sly11g0290491	M9	NA	12	12	13	12	10	16	16	14	9	6
Sly11g0290501	M1	NA	4	3	5	2	16	1	1	1	4	30
Sly11g0290511	M9	NA	8	7	5	4	5	10	11	8	8	7
Sly11g0290521	M12	NA	25	26	26	41	31	38	39	38	33	20
Sly11g0290531	M1	NA	37	17	66	11	2	1	1	1	1	0
Sly11g0290571	M11	FAS1	10	10	12	5	4	13	11	12	4	5
Sly11g0290581	M12	AAD6	13	14	15	100	123	18	15	19	21	32
Sly11g0290601	M22	NA	1	1	2	1	1	1	1	2	2	1
Sly11g0290611	M11	NA	30	29	32	40	43	33	28	34	34	45
Sly11g0290621	M1	NA	30	33	29	34	35	23	25	24	31	33
Sly11g0290631	M2	BG1	4	5	6	178	29	2	4	7	389	93
Sly11g0290651	M12	NA	16	16	16	22	31	16	15	18	28	38
Sly11g0290661	M19	NA	44	48	48	52	54	51	45	50	42	46
Sly11g0290671	M10	NA	1	1	1	2	1	1	1	1	1	2
Sly11g0290681	M12	NA	3	3	4	17	12	3	5	7	31	18
Sly11g0290691	M1	NA	37	39	38	43	39	26	26	26	30	29
Sly11g0290701	M11	NA	8	7	9	4	4	14	9	12	3	1
Sly11g0290711	M12	NA	5	6	6	5	5	8	8	9	6	5
Sly11g0290721	M11	NA	43	46	38	36	46	75	67	69	36	37
Sly11g0290731	M12	NA	8	7	7	1	1	36	30	23	1	1
Sly11g0290741	M12	NA	32	26	28	12	9	189	210	205	36	16
Sly11g0290771	M1	NA	17	17	18	11	11	15	16	14	16	14
Sly11g0290791	M10	NA	105	99	75	88	64	116	143	84	89	70
Sly11g0290801	M11	NA	1	1	1	0	1	1	1	1	1	1
Sly11g0290811	M1	NA	129	118	118	95	78	62	74	60	63	72
Sly11g0290821	M1	NA	33	31	37	43	51	25	24	25	57	62
Sly11g0290831	M9	NA	10	8	10	9	11	10	12	8	11	14
Sly11g0290841	M1	NA	1	1	1	0	1	1	1	0	0	0
Sly11g0290851	M1	NA	7	8	7	11	17	5	5	5	11	11
Sly11g0290871	M1	NA	36	34	32	64	75	6	6	6	48	80
Sly11g0290891	M1	NA	4	5	5	6	5	5	4	4	6	5
Sly11g0290901	M11	NA	32	27	31	49	59	32	35	36	53	83
Sly11g0290921	M11	NA	50	48	53	108	180	62	62	66	121	172
Sly11g0290931	M11	NA	35	37	47	106	102	50	54	83	154	97
Sly11g0290961	M12	NA	28	29	50	97	93	41	53	76	167	106
Sly11g0290981	M11	NA	5	5	5	1	1	11	9	12	1	1
Sly11g0290991	M11	NA	12	10	10	9	9	14	12	15	14	15
Sly11g0291011	M1	NA	16	12	22	28	22	8	4	7	6	4
Sly11g0291021	M1	NA	17	14	23	26	23	8	4	7	7	6
Sly11g0291031	M11	NA	3	3	4	6	7	4	3	3	3	3
Sly11g0291041	M22	NA	6	6	8	12	10	8	6	6	6	5
Sly11g0291051	M12	NA	12	12	13	20	21	13	14	15	17	15
Sly11g0291061	M11	NA	140	118	176	274	285	270	236	329	257	286
Sly11g0291071	M9	NA	102	101	102	96	114	119	126	114	153	182
Sly11g0291081	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly11g0291091	M3	NA	54	54	46	46	39	39	49	41	39	45
Sly11g0291101	M1	NA	37	39	42	29	34	34	26	32	24	24
Sly11g0291111	M11	NA	7	4	9	1	1	31	16	29	1	1
Sly11g0291151	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0291161	M1	NA	43	34	31	10	19	15	16	15	6	11
Sly11g0291171	M1	NA	49	47	45	41	44	40	40	44	47	49
Sly11g0291181	M2	NA	113	113	105	115	124	75	90	75	117	120
Sly11g0291191	M3	NA	204	198	161	54	15	79	109	77	35	11
Sly11g0291201	M1	NA	5	7	6	4	2	1	1	1	1	1
Sly11g0291211	M1	NA	3	3	4	2	1	2	2	2	1	1
Sly11g0291221	M12	NA	285	275	327	486	692	435	493	539	993	1309
Sly11g0291231	M22	NA	30	26	29	27	34	29	28	28	30	43
Sly11g0291241	M10	NA	29	66	66	2	2	76	164	46	2	7
Sly11g0291251	M3	NA	3	3	3	2	2	3	2	2	2	2
Sly11g0291261	M1	NA	211	222	249	109	55	103	126	74	16	15
Sly11g0291271	M1	NA	1	1	1	1	0	1	0	1	0	0
Sly11g0291281	M11	NA	13	13	15	27	49	14	15	16	74	78
Sly11g0291291	M11	NA	14	14	16	36	43	18	16	23	42	36
Sly11g0291301	M12	NA	2	2	3	8	5	4	4	6	9	9
Sly11g0291311	M3	NA	120	151	96	106	117	70	101	68	81	116
Sly11g0291321	M1	NA	1	1	2	0	0	1	1	1	0	0
Sly11g0291331	M1	NA	3	2	4	6	2	2	1	1	1	0
Sly11g0291351	M3	NA	22	24	18	11	9	8	11	6	5	6
Sly11g0291361	M10	NA	237	196	194	48	53	275	302	173	86	50
Sly11g0291401	M12	NA	13	13	18	18	18	24	31	29	27	31
Sly11g0291411	M1	NA	51	43	40	46	72	20	23	19	22	32
Sly11g0291421	M12	GLABRA2-like2	56	59	55	34	27	73	76	75	41	41
Sly11g0291431	M12	PFK	43	43	54	132	167	44	50	49	82	108
Sly11g0291441	M11	SlCycD4;1	1	1	2	1	1	3	2	2	1	1
Sly11g0291451	M22	NA	245	233	220	152	165	245	232	234	183	173
Sly11g0291461	M2	NA	67	66	62	55	94	45	49	42	61	83
Sly11g0291471	M12	NA	18	23	19	27	30	25	28	25	42	37
Sly11g0291481	M7	NA	112	221	132	73	125	177	260	133	55	90
Sly11g0291501	M12	NA	12	12	12	24	31	21	24	27	39	33
Sly11g0291511	M19	NA	18	1	2	10	6	1	8	5	18	3
Sly11g0291521	M1	NA	7	0	0	9	7	0	0	0	2	1
Sly11g0291541	M9	NA	8	10	9	15	13	10	10	8	12	10
Sly11g0291551	M11	NA	27	26	32	20	25	39	29	34	20	20
Sly11g0291561	M12	NA	2	2	2	1	1	3	2	3	1	1
Sly11g0291571	M1	NA	38	34	30	30	21	20	22	18	13	10
Sly11g0291591	M11	NA	210	170	213	64	44	216	203	187	95	93
Sly11g0291601	M3	NA	53	51	40	37	46	36	35	29	30	35
Sly11g0291621	M1	NA	161	146	54	30	14	20	13	17	5	3
Sly11g0291631	M1	NA	1	1	1	2	3	1	1	1	5	11
Sly11g0291641	M1	NA	34	30	40	57	48	15	17	15	12	8
Sly11g0291651	M12	NA	30	33	34	53	73	43	40	42	38	66
Sly11g0291661	M10	NA	93	189	58	10	20	167	344	93	6	27
Sly11g0291671	M15	NA	58	55	50	50	54	54	51	60	73	92
Sly11g0291681	M1	NA	6	6	11	6	2	5	2	3	1	1
Sly11g0291691	M1	NA	12	12	13	7	3	6	6	6	4	2
Sly11g0291711	M1	NA	17	20	12	80	41	7	4	4	12	5
Sly11g0291721	M1	NA	19	18	15	25	21	15	13	13	10	14
Sly11g0291731	M12	NA	11	14	15	18	13	36	56	134	236	41
Sly11g0291761	M12	NA	2	2	3	28	22	4	4	5	12	16
Sly11g0291771	M10	NA	2	2	2	2	1	6	5	1	0	1
Sly11g0291781	M1	NA	3	4	4	1	1	1	1	1	0	0
Sly11g0291791	M1	NA	3	2	4	2	1	2	2	2	1	1
Sly11g0291811	M1	NA	26	17	31	4	1	11	11	9	1	1
Sly11g0291821	M1	NA	2	2	3	1	1	2	1	2	1	1
Sly11g0291841	M1	NA	35	36	38	38	37	27	26	27	35	32
Sly11g0291851	M1	NA	33	26	21	2	1	2	2	1	1	1
Sly11g0291871	M9	NA	9	9	8	6	7	13	14	10	9	18
Sly11g0291881	M11	NA	1	1	1	2	2	1	1	1	1	0
Sly11g0291891

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0245431	M12	NA	17	17	23	121	148	49	54	77	362	326
Sly04g0245441	M12	NA	13	14	13	11	11	17	18	17	13	12
Sly04g0245461	M3	NA	6	5	4	5	8	5	6	4	3	27
Sly04g0245471	M12	NA	30	27	29	32	32	29	30	31	30	31
Sly04g0245481	M11	HUP9	28	19	39	6	5	88	67	130	8	8
Sly04g0245491	M11	NA	21	17	34	12	5	87	70	137	12	3
Sly04g0245511	M12	NA	16	16	17	27	35	18	20	20	71	36
Sly04g0245521	M12	NA	12	13	13	16	16	13	13	14	19	19
Sly04g0245551	M13	NA	16	12	24	49	67	20	20	31	36	51
Sly04g0245571	M3	NA	1	1	1	1	1	0	1	0	0	1
Sly04g0245591	M11	NA	30	25	29	44	71	29	31	34	60	70
Sly04g0245611	M1	NA	40	42	44	57	53	36	40	40	46	43
Sly04g0245621	M1	NA	97	88	96	26	9	31	27	22	1	1
Sly04g0245631	M1	NA	5	5	6	6	3	2	2	2	1	1
Sly04g0245641	M12	NA	20	12	9	2	2	31	37	10	1	1
Sly04g0245651	M2	NA	22	24	20	17	16	14	19	11	25	23
Sly04g0245661	M11	NA	6	6	6	4	2	11	9	12	3	1
Sly04g0245671	M22	NA	7	1	3	1	0	9	1	15	1	0
Sly04g0245781	M10	NA	17	80	31	1	1	112	194	31	1	2
Sly04g0245791	M1	NA	41	41	48	41	47	36	33	39	42	65
Sly04g0245801	M10	NA	88	90	77	101	94	110	115	75	72	72
Sly04g0245821	M1	NA	6	6	6	5	2	1	1	1	1	1
Sly04g0245841	M22	NA	18	6	13	7	26	24	8	23	11	29
Sly04g0245851	M3	NA	8	6	5	5	9	3	3	2	5	6
Sly04g0245861	M19	NA	10	13	11	10	12	11	10	12	9	10
Sly04g0245871	M19	NA	8	9	9	7	8	8	7	7	8	11
Sly04g0245881	M23	NA	2	2	2	1	1	2	2	2	1	1
Sly04g0245891	M9	NA	745	869	656	1097	998	760	1264	919	1658	1476
Sly04g0245901	M3	NA	37	40	24	30	36	24	30	18	39	56
Sly04g0245911	M12	NA	1	1	1	1	5	1	1	4	10	27
Sly04g0245971	M20	NA	14	13	18	20	15	12	10	13	12	10
Sly04g0245981	M12	NA	25	27	27	82	99	44	50	57	108	82
Sly04g0245991	M3	NA	6	8	7	5	3	6	6	4	4	3
Sly04g0246001	M3	SIERF.H10	220	328	223	131	137	186	233	107	29	58
Sly04g0246021	M11	NA	20	20	17	18	16	20	23	20	12	11
Sly04g0246041	M11	NA	16	15	19	20	12	57	53	59	26	15
Sly04g0246051	M3	NA	17	25	6	1	0	4	4	1	1	1
Sly04g0246081	M11	NA	635	552	636	406	177	976	811	1006	187	96
Sly04g0246091	M11	NA	63	47	66	11	4	108	95	91	3	2
Sly04g0246101	M1	NA	2	2	2	1	1	1	1	1	1	2
Sly04g0246111	M22	NA	31	30	33	32	37	32	28	30	53	58
Sly04g0246121	M23	NA	3	1	2	1	0	4	3	2	1	1
Sly04g0246131	M11	NA	3	1	1	1	1	4	4	2	1	1
Sly04g0246141	M1	NA	14	13	16	16	16	1	1	1	1	2
Sly04g0246151	M7	NA	2	2	2	2	4	2	2	2	3	8
Sly04g0246161	M3	NA	16	15	5	1	1	11	15	6	1	1
Sly04g0246191	M23	NA	1	1	1	1	0	2	1	1	0	0
Sly04g0246201	M12	NA	24	25	23	41	34	26	29	31	41	51
Sly04g0246211	M19	NA	53	62	63	95	83	54	48	53	64	53
Sly04g0246261	M12	NA	11	8	10	11	3	40	43	44	73	18
Sly04g0246271	M12	NA	368	348	373	163	78	576	581	567	223	113
Sly04g0246291	M11	NA	33	30	34	33	37	49	45	61	50	62
Sly04g0246301	M12	NA	14	15	16	23	17	21	23	20	20	15
Sly04g0246311	M3	NA	36	38	34	30	38	32	34	30	32	47
Sly04g0246351	M12	NA	7	7	5	3	4	14	14	6	3	8
Sly04g0246361	M1	NA	7	6	5	0	0	1	1	1	0	0
Sly04g0246371	M1	SAM-METT-like8	10	13	6	0	0	1	1	1	0	0
Sly04g0246381	M1	NA	5	4	3	1	1	1	1	1	1	1
Sly04g0246391	M5	NA	126	172	95	64	75	147	139	84	50	68
Sly04g0246401	M1	CDKC;1-2	32	30	29	23	24	20	19	20	23	25
Sly04g0246411	M1	NA	14	14	17	19	16	14	13	13	14	15
Sly04g0246441	M3	NA	35	39	33	12	9	27	29	17	7	5
Sly04g0246451	M5	NA	10	9	8	4	3	10	9	7	3	5
Sly04g0246461	M5	NA	53	70	35	9	12	52	62	24	16	17
Sly04g0246471	M3	NA	153	147	146	173	161	113	132	121	194	196
Sly04g0246491	M13	NA	22	20	22	32	35	19	19	24	32	33
Sly04g0246501	M12	NA	3	3	2	1	1	6	6	4	1	2
Sly04g0246511	M11	NA	131	123	141	343	855	165	163	187	366	785
Sly04g0246521	M19	NA	2	2	2	1	1	3	2	2	1	1
Sly04g0246531	M11	NA	2	2	2	1	2	3	2	3	1	1
Sly04g0246551	M11	NA	11	9	10	13	12	14	11	14	14	14
Sly04g0246751	M11	NA	3	1	3	2	3	3	2	5	5	4
Sly04g0246761	M11	NA	7	6	6	11	10	6	7	8	14	15
Sly04g0246781	M11	NA	10	10	12	29	36	16	16	19	33	37
Sly04g0246821	M3	NA	116	99	98	53	56	75	77	75	62	73
Sly04g0246841	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly04g0246861	M12	NA	52	51	56	57	15	111	109	114	60	9
Sly04g0246871	M9	NA	21	25	19	32	30	21	28	23	55	73
Sly04g0246881	M1	NA	41	39	39	49	51	34	33	36	43	41
Sly04g0246891	M19	NA	21	23	19	27	25	19	16	19	20	18
Sly04g0246901	M3	NA	29	28	26	41	41	20	24	21	36	34
Sly04g0246931	M11	NA	41	37	55	54	61	61	58	71	44	34
Sly04g0246941	M12	NA	4	3	4	1	1	5	5	4	1	1
Sly04g0246951	M12	NA	28	29	27	39	57	35	36	35	45	66
Sly04g0246961	M5	NA	11	20	3	1	1	14	12	2	1	1
Sly04g0247001	M1	NA	2	3	3	4	1	3	2	2	2	1
Sly04g0247031	M22	NA	2	0	1	1	1	2	1	3	2	1
Sly04g0247101	M22	NA	1	0	1	0	0	1	0	2	0	0
Sly04g0247131	M11	NA	7	7	8	9	11	8	8	10	10	13
Sly04g0247141	M12	NA	6	7	6	8	3	12	11	12	16	8
Sly04g0247151	M12	NA	8	8	7	11	17	14	14	14	16	15
Sly04g0247161	M3	NA	8	20	6	1	0	1	2	1	1	0
Sly04g0247201	M22	NA	1	1	1	1	1	3	1	4	1	1
Sly04g0247221	M1	NA	3	3	3	2	1	1	1	1	1	1
Sly04g0247231	M11	NA	41	38	43	76	77	46	45	58	57	57
Sly04g0247241	M3	SISDG33	15	19	16	21	22	16	16	15	24	21
Sly04g0247251	M12	NA	42	37	51	84	104	63	72	81	155	166
Sly04g0247271	M22	NA	11	1	7	0	0	68	1	43	0	0
Sly04g0247281	M3	NA	63	59	45	71	51	36	36	14	53	40
Sly04g0247291	M1	NA	3	4	3	1	1	1	1	1	1	0
Sly04g0247301	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0247311	M18	NA	23	22	28	25	23	34	27	36	20	27
Sly04g0247321	M11	NA	8	9	11	11	10	13	10	16	10	11
Sly04g0247331	M11	NA	9	8	8	3	1	15	12	16	1	1
Sly04g0247341	M19	NA	18	21	19	21	25	21	17	20	20	22
Sly04g0247351	M2	NA	335	305	321	225	165	252	312	245	210	161
Sly04g0247361	M3	NA	103	91	98	65	50	75	86	74	69	55
Sly04g0247371	M3	NA	78	59	59	42	36	48	52	53	45	43
Sly04g0247381	M22	NA	2	2	3	1	3	4	2	3	1	1
Sly04g0247391	M1	NA	4	4	3	4	2	2	1	1	1	2
Sly04g0247411	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly04g0247421	M22	NA	1	1	1	0	0	1	1	1	0	1
Sly04g0247431	M22	NA	1	2	2	1	1	2	1	2	1	1
Sly04g0247451	M11	NA	1	1	1	0	1	3	2	3	0	0
Sly04g0247461	M12	NA	18	19	18	25	24	31	32	29	30	29
Sly04g0247481	M1	NA	64	58	65	50	56	52	51	50	57	62
Sly04g0247511	M1	NA	9	11	9	4	1	3	2	1	1	1
Sly04g0247531	M19	HXK2-like	21	20	20	19	25	20	18	23	21	21
Sly04g0247541	M19	NA	31	28	30	31	39	29	27	31	35	38
Sly04g0247551	M1	MT2B	363	270	305	164	90	159	127	118	14	10
Sly04g0247571	M6	NA	5	14	4	2	12	8	12	3	1	11
Sly04g0247581	M11	NA	5	6	8	13	11	10	8	9	3	3
Sly04g0247591	M3	NA	7	7	6	5	5	6	6	6	4	5
Sly04g0247601	M11	NA	11	12	14	14	17	14	11	14	12	14
Sly04g0247641	M1	NA	45	44	29	5	1	2	1	1	0	1
Sly04g0247671	M3	NA	108	84	70	38	23	80	90	45	6	4
Sly04g0247681	M11	NA	13	11	14	9	8	14	15	15	7	4
Sly04g0247691	M1	NA	1	1	3	1	0	2	1	1	0	0
Sly04g0247701	M1	NA	2	2	4	2	1	2	2	1	0	0
Sly04g0247711	M1	NA	2	2	2	2	2	1	2	2	2	1
Sly04g0247721	M3	NA	171	182	151	105	100	150	175	134	113	127
Sly04g0247731	M3	NA	396	366	294	255	200	229	263	210	250	206
Sly04g0247741	M3	NA	2	2	2	2	3	2	2	2	2	2
Sly04g0247751	M3	NA	8	8	8	5	7	6	6	6	7	11

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0291921	M1	NA	12	11	13	13	16	11	10	11	13	12
Sly11g0291951	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly11g0291961	M12	NA	15	13	21	36	38	72	81	98	141	159
Sly11g0291971	M22	NA	2	1	1	0	0	3	1	4	1	0
Sly11g0291981	M1	NA	23	25	26	26	26	20	22	23	27	25
Sly11g0291991	M1	ADH	137	54	205	6	2	10	3	4	1	0
Sly11g0292011	M1	NA	5	5	3	0	0	1	0	0	0	0
Sly11g0292041	M11	NA	22	17	20	12	6	31	28	32	10	6
Sly11g0292051	M12	NA	6	6	8	8	5	11	12	12	11	9
Sly11g0292061	M1	JAI3-like	110	117	77	1	1	5	4	2	1	0
Sly11g0292071	M5	NA	59	51	41	38	55	50	60	42	58	91
Sly11g0292081	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly11g0292091	M3	NA	22	21	15	11	8	20	13	16	9	7
Sly11g0292101	M3	NA	20	26	15	10	5	19	18	12	6	3
Sly11g0292111	M3	NA	12	15	10	12	14	12	11	9	11	16
Sly11g0292121	M22	NA	1	1	1	1	3	7	2	3	1	1
Sly11g0292131	M1	NA	1	1	1	1	2	1	0	1	3	5
Sly11g0292141	M3	NA	88	98	55	45	26	55	70	35	81	61
Sly11g0292151	M3	NA	291	295	182	106	127	160	184	113	155	148
Sly11g0292171	M2	NA	73	67	62	58	47	48	64	50	47	49
Sly11g0292181	M19	NA	9	8	10	11	9	8	8	10	11	6
Sly11g0292191	M11	NA	16	18	22	22	31	20	16	23	26	47
Sly11g0292201	M11	NA	31	30	32	36	92	34	29	33	24	48
Sly11g0292211	M1	NA	24	38	33	10	3	1	1	1	1	1
Sly11g0292231	M1	NA	53	49	42	17	11	15	18	10	7	7
Sly11g0292241	M2	NA	52	63	48	53	47	39	55	45	55	39
Sly11g0292251	M12	NA	18	30	12	245	255	56	67	91	918	424
Sly11g0292261	M9	NA	95	95	86	107	81	179	174	167	75	67
Sly11g0292271	M11	NA	15	12	19	21	7	29	29	40	9	4
Sly11g0292281	M1	ggpps1	1	3	2	1	1	1	1	1	1	1
Sly11g0292291	M11	NA	25	28	28	45	64	34	36	38	55	62
Sly11g0292301	M11	DELLA	46	45	50	50	40	84	84	96	62	57
Sly11g0292321	M8	NA	1	1	1	0	0	1	2	1	1	1
Sly11g0292331	M8	NA	3	5	1	1	1	4	8	2	1	1
Sly11g0292361	M22	NA	6	4	4	18	80	28	7	21	115	189
Sly11g0292371	M22	NA	1	1	1	0	0	3	1	2	1	1
Sly11g0292391	M3	NA	1	1	2	1	1	1	1	1	0	0
Sly11g0292401	M3	NA	13	14	20	1	2	6	6	1	1	1
Sly11g0292411	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly11g0292421	M3	NA	6	10	2	1	0	1	1	1	0	0
Sly11g0292431	M22	NA	3	3	3	1	1	4	3	3	1	1
Sly11g0292441	M1	NA	274	271	333	1397	988	75	74	122	1091	362
Sly11g0292451	M11	NA	25	25	28	30	36	29	30	35	38	39
Sly11g0292461	M12	NA	82	78	97	106	58	84	125	133	281	131
Sly11g0292471	M11	NA	23	25	28	21	13	45	42	53	29	21
Sly11g0292481	M12	NA	36	35	35	49	53	34	35	38	56	55
Sly11g0292501	M12	NA	55	54	68	9	48	109	112	100	4	4
Sly11g0292511	M1	NA	7	7	7	12	10	5	7	7	11	11
Sly11g0292521	M3	NA	13	14	11	11	9	10	10	9	10	8
Sly11g0292531	M11	NA	132	124	142	179	194	166	158	180	165	182
Sly11g0292541	M1	NA	35	35	34	43	46	28	25	29	34	39
Sly11g0292551	M1	NA	23	22	21	20	24	19	18	20	27	30
Sly11g0292571	M5	NA	5	11	3	1	1	10	12	1	1	0
Sly11g0292591	M22	NA	3	2	3	2	1	3	2	3	1	1
Sly11g0292601	M3	NA	8	7	7	6	3	6	6	5	3	1
Sly11g0292611	M18	NA	6	7	8	8	7	7	7	8	8	6
Sly11g0292621	M18	NA	8	10	10	11	9	10	10	10	10	7
Sly11g0292631	M18	NA	9	10	10	9	10	11	10	11	12	12
Sly11g0292641	M12	NA	16	16	16	15	16	15	16	17	23	27
Sly11g0292651	M1	NA	23	23	20	19	17	17	15	15	16	12
Sly11g0292661	M1	NA	10	9	9	8	11	7	6	7	9	12
Sly11g0292671	M1	NA	6	5	7	5	2	4	3	3	1	1
Sly11g0292681	M12	NA	6	6	7	5	4	7	7	7	4	4
Sly11g0292691	M12	NA	7	6	7	6	6	8	8	7	6	6
Sly11g0292711	M22	NA	3	4	3	4	3	4	3	4	2	4
Sly11g0292721	M22	GEM-like11	6	4	8	8	7	6	5	7	1	1
Sly11g0292731	M22	GEM-like7	5	3	7	8	6	8	4	9	1	1
Sly11g0292741	M22	NA	2	1	4	4	2	2	1	3	0	1
Sly11g0292751	M12	GEM-like9	2	2	3	3	3	7	2	5	1	1
Sly11g0292761	M1	NA	51	65	32	58	17	4	8	2	4	2
Sly11g0292771	M1	NA	197	242	175	253	84	29	41	24	25	14
Sly11g0292781	M1	NA	196	263	204	291	112	20	44	17	30	22
Sly11g0292791	M1	NA	14	15	11	6	2	3	2	1	1	2
Sly11g0292801	M13	Solyc11g011630	1	1	1	1	1	1	1	1	1	1
Sly11g0293041	M11	NA	199	175	236	125	150	478	418	479	135	144
Sly11g0293051	M1	NA	5	5	8	15	17	2	1	1	1	1
Sly11g0293061	M2	NA	57	53	50	62	89	44	51	42	87	124
Sly11g0293071	M12	NA	1	2	2	2	4	2	2	2	4	7
Sly11g0293111	M12	NA	11	9	10	12	27	21	20	23	32	41
Sly11g0293121	M9	NA	35	40	36	51	60	58	55	49	48	49
Sly11g0293131	M1	NA	2	3	3	7	8	2	2	2	4	5
Sly11g0293141	M3	NA	3	5	2	1	1	4	5	2	1	1
Sly11g0293161	M3	NA	7	10	5	2	2	8	8	2	1	1
Sly11g0293171	M12	NA	8	8	9	6	7	12	14	15	11	15
Sly11g0293181	M1	NA	2	2	3	1	1	1	1	1	0	1
Sly11g0293201	M12	NA	94	99	107	126	101	106	115	106	85	81
Sly11g0293211	M1	NA	491	497	461	30	14	178	174	128	21	10
Sly11g0293221	M2	NA	84	98	98	211	212	63	89	76	220	217
Sly11g0293231	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly11g0293241	M14	NA	444	404	486	270	167	437	460	450	259	199
Sly11g0293251	M1	NA	73	68	103	68	47	50	58	55	89	86
Sly11g0293261	M1	NA	3	4	5	3	3	1	1	1	1	1
Sly11g0293271	M11	NA	34	29	45	118	208	39	40	60	151	195
Sly11g0293281	M1	NA	16	15	14	17	13	8	10	8	13	13
Sly11g0293291	M22	NA	2	1	2	0	0	6	1	11	0	0
Sly11g0293311	M1	NA	1	1	1	1	0	1	1	1	1	0
Sly11g0293331	M1	NA	2	1	2	1	0	2	1	1	0	0
Sly11g0293341	M21	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0293351	M1	NA	12	13	13	7	6	6	6	4	1	1
Sly11g0293361	M1	NA	21	17	14	19	10	12	10	11	4	3
Sly11g0293371	M1	NA	92	88	100	128	126	68	77	74	112	136
Sly11g0293381	M3	NA	3	3	3	3	4	2	3	2	1	2
Sly11g0293391	M11	NA	14	13	13	16	18	16	16	16	20	20
Sly11g0293401	M1	NA	467	417	415	329	228	278	307	262	294	210
Sly11g0293421	M3	NA	3	2	2	1	2	2	2	1	1	2
Sly11g0293461	M11	NA	107	104	122	110	83	146	126	148	95	80
Sly11g0293471	M1	NA	52	51	49	104	98	42	44	49	79	63
Sly11g0293481	M1	NA	70	75	81	267	215	35	37	42	95	89
Sly11g0293501	M12	NA	13	13	14	19	15	19	21	23	31	11
Sly11g0293511	M2	NA	14	12	12	8	4	12	14	12	2	1
Sly11g0293521	M3	NA	7	5	4	4	4	4	3	3	1	1
Sly11g0293541	M3	NA	1	1	1	0	1	1	1	1	1	0
Sly11g0293561	M5	NA	3	5	1	1	1	4	5	1	0	1
Sly11g0293581	M10	NA	33	55	37	60	50	78	92	34	22	29
Sly11g0293591	M12	NA	8	9	9	6	2	17	14	12	4	1
Sly11g0293601	M3	NA	105	101	94	83	92	91	90	89	92	103
Sly11g0293611	M19	NA	35	32	40	25	28	35	27	34	13	17
Sly11g0293631	M3	NA	3328	2916	3257	3463	1991	2102	3120	2458	4103	4262
Sly11g0293671	M12	NA	3	3	2	3	18	7	3	6	1	3
Sly11g0293681	M22	NA	6	1	6	0	0	60	0	43	0	0
Sly11g0293711	M1	NA	45	38	53	45	22	27	27	36	65	50
Sly11g0293721	M1	NA	50	48	52	76	66	43	48	47	54	38
Sly11g0293731	M12	NA	68	73	73	138	174	125	152	135	269	286
Sly11g0293751	M1	NA	65	60	75	86	42	34	42	44	68	46
Sly11g0293761	M1	NA	36	38	48	51	16	8	5	10	7	5
Sly11g0293771	M11	NA	37	32	44	44	38	66	54	84	49	42
Sly11g0293781	M11	NA	64	49	59	41	35	76	65	86	45	31
Sly11g0293791	M12	NA	17	15	17	22	38	18	19	16	28	35
Sly11g0293801	M1	NA	1	1	1	2	1	1	1	1	1	2
Sly11g0293811	M6	NA	1	1	1	0	0	1	1	1	1	1
Sly11g0293821	M10	NA	50	90	34	12	11	83

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0247771	M1	NA	3	4	4	4	3	3	3	3	3	3
Sly04g0247781	M1	NA	40	32	37	68	94	18	11	27	213	182
Sly04g0247791	M11	NA	28	32	31	44	46	35	31	38	46	31
Sly04g0247801	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0247811	M11	NA	33	23	32	31	61	54	39	61	43	80
Sly04g0247831	M2	NA	16	16	13	14	15	10	14	11	14	14
Sly04g0247911	M1	NA	13	17	17	34	14	14	15	14	22	13
Sly04g0247921	M11	NA	17	17	16	17	14	18	18	18	20	17
Sly04g0247941	M19	NA	23	23	24	21	17	21	20	22	18	16
Sly04g0247951	M2	NA	24	23	19	21	18	19	26	18	14	16
Sly04g0247961	M1	NA	105	105	94	103	119	67	74	77	123	150
Sly04g0247971	M7	NA	82	82	77	122	163	74	83	81	135	229
Sly04g0247981	M12	NA	6	7	6	7	7	7	7	7	8	7
Sly04g0247991	M3	NA	54	71	47	11	4	43	50	25	4	3
Sly04g0248001	M12	NA	1	1	1	0	0	1	1	1	0	1
Sly04g0248011	M6	NA	37	48	41	28	38	42	45	36	21	39
Sly04g0248021	M1	NA	20	21	21	22	18	14	15	14	18	15
Sly04g0248031	M1	NA	92	86	95	78	88	76	79	84	89	91
Sly04g0248041	M1	NA	28	37	23	10	6	13	12	8	1	1
Sly04g0248051	M22	NA	10	3	5	0	0	19	4	20	0	0
Sly04g0248061	M12	NA	1	2	3	17	12	13	27	44	138	76
Sly04g0248071	M1	NA	4	3	5	1	1	2	2	1	1	1
Sly04g0248081	M23	NA	1	1	1	0	1	2	1	1	0	1
Sly04g0248091	M3	NA	3	2	3	5	5	2	2	2	2	5
Sly04g0248101	M3	NA	4	5	3	4	6	3	2	2	3	5
Sly04g0248111	M19	NA	2	2	2	2	3	2	2	2	2	2
Sly04g0248121	M19	NA	5	7	6	5	6	6	6	6	5	5
Sly04g0248131	M11	NA	14	12	16	12	15	21	20	19	19	20
Sly04g0248141	M9	NA	35	41	38	36	39	39	53	40	44	76
Sly04g0248151	M12	NA	13	17	16	16	16	16	19	18	19	34
Sly04g0248161	M8	NA	43	67	23	2	22	55	187	29	12	82
Sly04g0248171	M3	NA	79	83	70	57	63	69	71	63	44	58
Sly04g0248191	M11	ADH1	4	4	3	1	1	11	7	7	3	1
Sly04g0248201	M1	NA	18	18	22	14	5	15	14	17	4	1
Sly04g0248221	M3	NA	1	1	1	1	2	1	1	1	1	2
Sly04g0248231	M3	NA	4	4	4	4	4	4	4	4	5	4
Sly04g0248241	M19	NA	3	4	4	4	4	4	3	4	4	3
Sly04g0248251	M22	NA	2	1	2	2	1	9	2	7	1	1
Sly04g0248261	M19	NA	72	74	71	73	77	64	60	66	69	72
Sly04g0248271	M1	NA	31	31	31	37	32	28	31	28	28	23
Sly04g0248281	M1	NA	24	27	23	25	27	22	20	21	23	24
Sly04g0248291	M3	NA	112	122	90	76	74	77	100	60	63	75
Sly04g0248301	M2	NA	19	20	19	17	16	18	21	18	18	15
Sly04g0248311	M11	NA	10	10	13	14	14	14	15	20	17	24
Sly04g0248331	M19	NA	15	14	16	40	46	14	13	17	61	66
Sly04g0248341	M2	NA	6	5	5	1	1	3	5	2	1	2
Sly04g0248361	M1	NA	3	4	3	1	2	2	2	2	1	1
Sly04g0248371	M3	NA	74	70	33	15	26	36	39	10	34	31
Sly04g0248381	M3	NA	41	47	28	3	2	12	15	3	7	2
Sly04g0248391	M1	NA	38	31	70	12	3	22	21	22	2	1
Sly04g0248401	M1	NA	7	4	9	2	1	3	4	4	1	0
Sly04g0248411	M11	NA	9	7	15	4	1	18	13	24	2	1
Sly04g0248421	M11	PRX_like1	10	11	14	18	31	23	20	25	21	47
Sly04g0248431	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0248441	M1	NA	1	1	1	1	1	0	1	1	1	1
Sly04g0248461	M1	NA	2	3	4	4	4	1	0	1	0	0
Sly04g0248471	M1	NA	4	8	5	3	2	1	1	1	1	0
Sly04g0248491	M18	NA	48	48	46	16	8	56	48	48	7	2
Sly04g0248501	M3	NA	37	36	31	38	41	27	28	26	37	35
Sly04g0248511	M9	NA	1	1	1	1	1	1	2	1	1	1
Sly04g0248521	M11	NA	27	27	29	37	53	34	35	38	41	50
Sly04g0248551	M6	NA	21	40	28	12	34	15	21	8	3	17
Sly04g0248561	M11	NA	38	45	31	24	25	61	51	53	20	21
Sly04g0248571	M15	NA	27	25	24	25	24	24	26	26	32	26
Sly04g0248581	M22	NA	3	1	2	1	1	6	2	5	1	1
Sly04g0248591	M3	NA	6	9	4	6	13	5	1	1	1	1
Sly04g0248611	M12	NA	1	1	1	1	0	4	1	1	1	1
Sly04g0248621	M12	NA	1	2	1	1	0	5	4	1	2	0
Sly04g0248631	M12	NA	1	1	1	0	1	2	1	1	0	1
Sly04g0248651	M22	NA	6	3	4	3	3	19	5	10	1	2
Sly04g0248661	M1	NA	16	17	31	21	15	8	5	11	11	12
Sly04g0248691	M11	NA	31	27	37	31	22	32	32	38	28	23
Sly04g0248701	M11	NA	163	130	256	238	175	535	420	801	386	219
Sly04g0248711	M13	NA	9	9	18	103	248	8	11	17	162	176
Sly04g0248721	M11	NA	43	41	43	47	54	41	39	46	61	69
Sly04g0248741	M1	NA	29	26	24	24	20	18	19	20	16	17
Sly04g0248851	M14	PPR-like37	8	7	11	10	14	9	7	10	8	9
Sly04g0248861	M12	NA	5	6	5	7	7	7	6	6	10	9
Sly04g0248871	M11	NA	5	5	5	6	5	5	5	5	11	11
Sly04g0248891	M12	NA	7	5	5	4	6	6	7	6	16	9
Sly04g0248921	M11	NA	26	24	24	21	23	29	27	29	27	26
Sly04g0248931	M3	NA	30	32	29	40	39	28	28	24	30	32
Sly04g0248941	M9	NA	26	29	25	31	39	29	28	26	44	69
Sly04g0248951	M11	NA	39	40	38	25	8	88	65	99	30	7
Sly04g0248961	M3	NA	70	74	63	65	64	58	60	51	52	52
Sly04g0248971	M11	NA	17	17	26	31	32	27	22	24	13	25
Sly04g0249001	M1	NA	5	4	3	0	0	1	0	1	0	0
Sly04g0249041	M11	NA	19	17	23	24	16	25	21	30	10	8
Sly04g0249061	M1	NA	37	34	31	30	34	25	26	24	31	36
Sly04g0249071	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly04g0249081	M11	NA	11	10	13	10	9	15	13	15	7	3
Sly04g0249091	M7	NA	20	33	30	19	191	34	69	27	29	313
Sly04g0249111	M22	NA	1	1	1	0	1	1	1	1	1	0
Sly04g0249121	M3	NA	15	15	15	16	15	14	13	14	16	15
Sly04g0249131	M23	NA	1	1	1	6	6	1	1	1	1	1
Sly04g0249141	M23	NA	1	1	1	3	3	1	1	1	2	5
Sly04g0249151	M5	NA	7	7	5	16	30	7	7	6	16	17
Sly04g0249161	M1	NA	25	24	22	12	6	14	13	12	8	4
Sly04g0249171	M9	NA	16	16	15	27	27	20	21	22	49	61
Sly04g0249181	M11	NA	8	9	11	12	8	15	15	17	15	11
Sly04g0249191	M1	NA	132	126	108	22	12	41	34	39	21	11
Sly04g0249201	M6	SIASR3	3	6	11	0	1	10	8	3	1	1
Sly04g0249221	M6	NA	1	5	4	1	1	5	5	1	1	1
Sly04g0249241	M11	SIASR1	10765	9566	11853	21141	55995	13728	14240	21631	44973	52849
Sly04g0249251	M3	NA	1146	1500	1375	492	77	525	1329	883	173	59
Sly04g0249261	M12	NA	10	9	10	16	11	13	16	18	27	21
Sly04g0249291	M3	NA	123	68	54	5	2	44	46	26	2	3
Sly04g0249301	M11	NA	3	3	3	1	1	4	3	3	1	1
Sly04g0249311	M3	NA	4	6	3	2	2	2	3	2	1	1
Sly04g0249321	M3	NA	3	3	1	1	1	2	1	1	1	1
Sly04g0249351	M11	NA	4	4	6	7	5	6	5	7	7	4
Sly04g0249371	M2	NA	68	67	53	52	61	46	62	43	66	70
Sly04g0249381	M2	NA	36	37	33	35	36	32	37	31	49	49
Sly04g0249401	M3	NA	51	50	43	26	8	43	42	41	25	14
Sly04g0249421	M3	SIERF.D6	101	137	45	19	12	30	46	30	83	67
Sly04g0249431	M12	NA	5	4	4	3	7	5	5	8	9	17
Sly04g0249441	M12	NA	10	9	11	6	2	40	38	79	26	3
Sly04g0249451	M12	NA	1	1	1	1	1	1	1	2	1	1
Sly04g0249471	M13	NA	38	28	87	19	7	63	34	53	1	1
Sly04g0249541	M3	NA	63	59	42	13	21	43	44	34	14	16
Sly04g0249551	M3	NA	52	62	26	10	12	28	36	13	9	16
Sly04g0249561	M3	NA	100	105	83	71	43	72	78	53	21	16
Sly04g0249571	M1	NA	628	593	473	30	8	11	6	3	1	1
Sly04g0249581	M1	peroxidase	220	179	190	7	11	9	5	6	1	1
Sly04g0249601	M1	NA	15	18	7	2	2	3	4	2	1	0
Sly04g0249621	M11	NA	18	14	14	17	18	29	29	30	15	12
Sly04g0249631	M12	aba2	21	23	24	42	32	34	33	34	66	47
Sly04g0249651	M11	NA	1	1	1	1	1	3	3	3	1	0
Sly04g0249661	M3	NA	50	62	35	18	7	40	50	36	22	14
Sly04g0249671	M2	NA	47	44	38	48	34	30	45	31	59	51
Sly04g0249681	M13	NA	89	98	119	159	142	110	88	135	87	101
Sly04g0249691	M1	NA	41	61	20	6	1	2	2	1	1	0
Sly04g0249701	M1	NA	33	36	35	34	35	26	27	25	25	29
Sly04g0249711	M3	NA	56	79	31	10	24	10	10	4	8	24

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0293871	M1	NA	13	12	11	10	11	11	8	11	12	13
Sly11g0293881	M1	NA	5	4	5	4	3	4	4	3	3	2
Sly11g0293891	M1	NA	2	3	3	2	1	1	1	0	0	0
Sly11g0293921	M1	NA	3	2	3	1	1	2	2	2	1	1
Sly11g0293931	M1	NA	8	7	8	8	8	7	6	7	9	8
Sly11g0293941	M11	NA	6	6	6	6	2	14	14	17	5	1
Sly11g0293951	M22	NA	2	0	1	0	0	6	1	1	0	0
Sly11g0293971	M1	NA	13	14	15	34	48	13	11	13	25	26
Sly11g0293981	M21	NA	11	10	13	3	2	9	5	10	3	4
Sly11g0293991	M22	NA	1	1	1	2	2	2	1	2	1	0
Sly11g0294001	M1	NA	99	103	98	259	226	73	75	73	75	72
Sly11g0294011	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly11g0294021	M1	NA	7	7	8	12	10	6	4	5	3	3
Sly11g0294031	M11	NA	8	7	8	10	12	9	7	10	13	14
Sly11g0294041	M12	NA	52	50	56	65	50	80	103	89	100	66
Sly11g0294051	M11	NA	42	40	48	37	37	43	42	50	36	40
Sly11g0294061	M23	NA	2	1	1	1	2	1	1	1	1	1
Sly11g0294071	M1	NA	13	14	13	18	17	11	11	12	12	9
Sly11g0294081	M19	NA	44	51	55	61	64	51	43	51	34	36
Sly11g0294091	M5	NA	46	53	30	31	49	38	44	31	43	67
Sly11g0294111	M1	NA	49	43	37	21	25	26	24	19	7	11
Sly11g0294121	M19	NA	14	14	15	12	9	15	12	15	6	4
Sly11g0294131	M11	NA	22	21	21	24	41	22	22	26	37	58
Sly11g0294141	M11	NA	58	53	67	80	104	81	72	94	135	185
Sly11g0294151	M1	NA	51	42	50	54	79	32	35	41	60	82
Sly11g0294161	M11	NA	8	5	11	20	31	23	25	33	75	66
Sly11g0294171	M1	NA	9	7	13	5	3	6	5	6	4	2
Sly11g0294181	M11	NA	13	12	15	13	10	15	15	13	17	14
Sly11g0294191	M12	NA	7	7	6	9	9	7	8	8	13	11
Sly11g0294201	M12	NA	42	52	53	74	65	51	61	58	88	72
Sly11g0294211	M9	NA	91	84	80	73	86	87	90	86	113	154
Sly11g0294221	M11	NA	30	29	30	41	32	39	40	42	36	23
Sly11g0294231	M12	NA	24	25	26	25	27	32	34	39	24	22
Sly11g0294241	M1	NA	11	11	14	28	14	11	8	9	2	1
Sly11g0294251	M15	NA	21	19	16	21	16	18	20	20	18	18
Sly11g0294261	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly11g0294271	M11	NA	38	36	49	62	76	59	56	63	38	38
Sly11g0294281	M12	NA	1	2	1	1	11	2	6	4	3	19
Sly11g0294301	M3	NA	67	72	59	76	53	35	46	31	58	46
Sly11g0294311	M1	NA	11	11	14	21	11	9	9	10	5	5
Sly11g0294321	M11	NA	36	29	40	40	35	39	37	48	41	36
Sly11g0294331	M1	NA	32	34	26	20	22	17	16	14	16	22
Sly11g0294341	M11	NA	9	11	11	18	47	13	12	13	21	24
Sly11g0294351	M1	NA	4	4	4	3	4	4	3	4	3	4
Sly11g0294361	M12	NA	103	105	108	259	415	125	153	160	390	602
Sly11g0294371	M1	NA	127	160	193	2993	1593	3	2	4	65	47
Sly11g0294381	M1	NA	37	43	40	30	28	31	29	30	23	14
Sly11g0294411	M1	NA	102	98	117	38	7	34	28	30	3	1
Sly11g0294421	M1	NA	5	5	4	2	1	1	1	1	1	1
Sly11g0294431	M1	NA	6	6	12	6	4	2	2	2	1	2
Sly11g0294451	M3	NA	119	130	89	95	55	53	66	42	62	50
Sly11g0294471	M22	NA	25	25	21	23	22	31	23	21	9	12
Sly11g0294481	M3	NA	119	122	74	59	66	73	69	52	69	77
Sly11g0294491	M1	NA	8	8	8	10	11	6	6	6	11	10
Sly11g0294521	M3	NA	6	7	4	1	1	4	3	2	1	1
Sly11g0294541	M1	NA	104	98	102	102	111	76	86	85	110	144
Sly11g0294551	M11	NA	4	3	6	1	1	18	14	17	1	1
Sly11g0294561	M11	NA	44	44	53	58	68	71	67	70	59	68
Sly11g0294571	M18	NA	25	26	33	37	36	47	37	50	34	28
Sly11g0294591	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0294601	M1	SILAX3	77	90	88	97	23	2	1	1	1	1
Sly11g0294631	M1	NA	19	25	25	64	27	7	10	11	34	17
Sly11g0294641	M11	NA	17	11	18	18	25	22	18	25	24	37
Sly11g0294651	M12	NA	11	11	11	15	19	10	14	12	19	21
Sly11g0294661	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0294681	M11	NA	28	30	34	62	77	37	33	41	76	73
Sly11g0294691	M11	NA	9	9	10	17	16	15	14	17	17	23
Sly11g0294701	M11	NA	5	6	9	12	10	11	9	15	8	9
Sly11g0294721	M13	BSH1-like	80	79	97	77	81	91	90	106	75	80
Sly11g0294751	M22	NA	1	1	1	0	0	2	1	2	0	0
Sly11g0294761	M3	NA	98	94	78	72	63	68	76	61	56	58
Sly11g0294771	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly11g0294781	M12	NA	27	27	26	40	46	29	32	36	74	76
Sly11g0294791	M1	SIARF17	6	8	10	39	45	5	6	7	26	29
Sly11g0294801	M3	NA	40	39	43	33	48	24	33	29	27	25
Sly11g0294811	M2	NA	8	12	7	19	10	2	4	3	3	3
Sly11g0294821	M13	SIHAM1	41	34	49	41	49	52	43	57	49	61
Sly11g0294831	M19	NA	33	37	34	39	42	31	26	30	27	28
Sly11g0294841	M12	NA	28	25	24	27	40	34	33	34	37	44
Sly11g0294941	M19	NA	15	16	16	16	11	16	14	16	15	11
Sly11g0294961	M2	NA	24	25	22	22	23	18	21	17	22	22
Sly11g0294971	M9	NA	17	18	14	17	19	21	27	22	26	30
Sly11g0294991	M6	NR	72	106	50	33	50	68	82	107	242	312
Sly11g0295001	M19	NA	24	25	26	37	51	24	23	26	41	56
Sly11g0295011	M9	NA	16	17	16	19	17	20	23	19	20	16
Sly11g0295021	M2	NA	7	9	9	9	8	7	8	8	9	9
Sly11g0295051	M1	NA	30	31	30	28	30	19	19	15	7	6
Sly11g0295061	M11	NA	6	6	12	7	2	15	15	18	7	1
Sly11g0295081	M9	NA	1	1	1	0	1	3	3	2	2	1
Sly11g0295141	M10	NA	15	38	31	3	1	29	46	14	4	3
Sly11g0295151	M6	NA	6	13	9	1	1	7	11	4	2	1
Sly11g0295161	M6	NA	1	3	2	1	1	1	2	1	1	1
Sly11g0295171	M11	NA	37	37	37	39	29	40	38	43	42	35
Sly11g0295181	M11	NA	10	8	12	12	12	11	13	13	15	11
Sly11g0295191	M9	NA	13	14	14	17	17	13	16	13	13	13
Sly11g0295221	M23	NA	1	1	1	1	1	1	1	1	2	2
Sly11g0295251	M11	NA	21	21	25	26	31	25	22	25	28	44
Sly11g0295261	M6	NA	37	50	34	30	22	39	40	29	19	21
Sly11g0295271	M2	NA	201	258	190	182	98	138	165	78	31	20
Sly11g0295291	M19	NA	41	43	42	35	36	36	34	38	31	34
Sly11g0295301	M1	NA	9	10	8	9	10	7	7	7	9	9
Sly11g0295311	M22	NA	3	3	3	3	5	5	2	4	8	14
Sly11g0295321	M3	NA	156	162	128	137	163	98	116	89	152	151
Sly11g0295341	M11	NA	1	1	1	1	1	1	1	1	1	0
Sly11g0295351	M12	NA	55	54	51	44	42	60	60	66	56	53
Sly11g0295371	M1	NA	14	16	16	17	16	11	9	10	7	8
Sly11g0295391	M3	NA	15	18	15	17	19	11	11	9	8	12
Sly11g0295401	M11	NA	22	20	23	50	63	32	30	41	62	63
Sly11g0295411	M11	NA	1	2	1	1	3	1	1	2	1	4
Sly11g0295421	M12	NA	1	1	1	2	3	2	2	2	2	4
Sly11g0295431	M12	NA	7	7	6	8	9	8	8	8	9	10
Sly11g0295441	M1	NA	20	17	19	28	39	12	14	16	23	24
Sly11g0295461	M3	NA	54	50	43	107	120	35	40	33	84	100
Sly11g0295471	M3	NA	160	203	84	14	10	52	65	16	4	7
Sly11g0295481	M3	NA	2	3	1	1	1	1	1	0	1	0
Sly11g0295491	M1	NA	2	2	1	1	1	1	1	1	0	1
Sly11g0295501	M1	NA	5	5	4	4	3	3	2	3	3	2
Sly11g0295511	M3	NA	3	4	3	3	3	3	2	3	2	1
Sly11g0295521	M3	NA	57	54	54	42	36	52	52	49	49	49
Sly11g0295531	M11	NA	3	3	3	3	3	4	4	4	4	3
Sly11g0295541	M11	NA	1	1	1	2	2	2	1	2	2	1
Sly11g0295551	M18	NA	3	4	5	4	4	5	4	5	4	3
Sly11g0295561	M18	NA	3	3	4	3	3	5	3	5	4	3
Sly11g0295571	M18	NA	6	7	7	6	5	8	5	8	5	2
Sly11g0295581	M11	NA	4	6	5	5	3	5	6	6	4	2
Sly11g0295591	M22	NA	5	5	5	5	4	6	4	6	4	3
Sly11g0295611	M3	NA	5	4	4	3	2	3	4	3	3	3
Sly11g0295621	M3	NA	3	4	4	2	1	3	3	2	2	2
Sly11g0295661	M1	NA	3	2	2	3	2	3	2	2	1	1
Sly11g0295671	M1	NA	2	2	2	2	2	2	2	2	1	1
Sly11g0295691	M3	NA	5	5	5	6	5	3	4	3	5	3

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0249741	M1	NA	1	1	1	1	1	0	1	0	0	0
Sly04g0249751	M11	NA	46	44	48	64	66	49	53	60	74	82
Sly04g0249761	M12	NA	42	45	40	42	31	44	59	47	69	51
Sly04g0249771	M6	NA	8	21	3	0	0	16	32	3	1	1
Sly04g0249801	M3	NA	7	7	5	6	5	6	7	6	7	7
Sly04g0249811	M3	NA	9	8	5	5	6	6	6	5	7	8
Sly04g0249831	M11	NA	18	20	20	17	18	18	18	19	19	21
Sly04g0249841	M11	NA	4	4	4	5	4	5	4	5	5	5
Sly04g0249851	M12	NA	11	10	13	47	150	18	17	19	101	295
Sly04g0249861	M19	NA	3	3	4	3	3	3	2	3	2	3
Sly04g0249871	M1	NA	7	7	10	9	4	3	3	3	1	1
Sly04g0249881	M3	NA	7	7	6	4	2	7	7	6	4	3
Sly04g0249891	M3	NA	8	10	8	5	4	8	7	6	5	4
Sly04g0249901	M1	NA	17	16	16	10	9	13	10	10	6	5
Sly04g0249911	M1	NA	55	61	54	37	38	40	40	36	28	31
Sly04g0249921	M14	NA	10	10	13	22	45	11	8	12	21	38
Sly04g0249931	M17	NA	16	14	18	51	109	15	12	17	39	59
Sly04g0249941	M11	NA	3	3	1	1	1	3	6	4	7	1
Sly04g0249951	M19	NA	12	15	15	9	7	11	10	11	5	4
Sly04g0249961	M3	NA	4	7	2	1	1	2	2	1	1	1
Sly04g0249971	M9	NA	44	50	47	55	50	47	49	47	60	54
Sly04g0249991	M1	NA	3	2	3	1	0	2	1	2	1	1
Sly04g0250081	M3	NA	3	7	1	1	0	1	2	1	0	0
Sly04g0250091	M3	NA	79	95	42	1	1	17	22	9	1	1
Sly04g0250101	M1	NA	4	4	5	2	1	2	2	2	1	1
Sly04g0250111	M3	NA	53	60	44	37	32	26	30	20	28	26
Sly04g0250121	M11	NA	29	29	42	142	446	37	37	48	150	381
Sly04g0250131	M11	NA	57	43	46	57	56	60	54	58	57	68
Sly04g0250171	M1	NA	65	65	68	59	84	50	41	51	62	108
Sly04g0250181	M11	NA	30	26	37	14	8	110	87	130	29	15
Sly04g0250191	M12	NA	7	6	5	2	1	8	16	12	17	1
Sly04g0250231	M9	NA	7	6	5	11	13	6	7	6	11	13
Sly04g0250241	M1	NA	9	8	8	6	13	6	6	6	7	12
Sly04g0250251	M22	NA	1	1	1	1	0	7	0	3	0	0
Sly04g0250261	M3	NA	18	16	15	16	20	12	14	11	14	17
Sly04g0250271	M3	NA	11	11	10	11	12	9	11	10	17	19
Sly04g0250281	M12	NA	4	4	4	6	6	4	5	4	8	8
Sly04g0250291	M1	NA	8	8	9	9	8	5	5	5	6	5
Sly04g0250301	M11	NA	4	4	4	4	4	4	5	5	3	2
Sly04g0250311	M3	NA	71	80	66	57	71	58	82	51	62	77
Sly04g0250321	M1	BAK1	20	19	17	6	3	8	4	5	1	1
Sly04g0250341	M3	NA	8	9	8	6	7	6	7	6	6	7
Sly04g0250351	M6	NA	5	7	5	4	5	6	7	5	7	8
Sly04g0250361	M6	NA	25	57	33	1	3	35	91	12	7	2
Sly04g0250371	M10	NA	4	19	16	1	4	18	58	9	6	5
Sly04g0250381	M10	NA	1	1	1	0	1	3	3	1	1	1
Sly04g0250391	M1	NA	16	17	15	9	4	11	10	9	2	2
Sly04g0250401	M3	NA	40	43	31	28	29	15	22	18	25	22
Sly04g0250421	M3	NA	218	199	194	134	97	158	205	152	150	96
Sly04g0250431	M11	NA	109	119	119	105	100	125	116	131	137	134
Sly04g0250451	M11	NA	6	8	9	13	13	12	10	12	10	15
Sly04g0250461	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly04g0250511	M1	NA	3	2	1	2	2	1	1	1	1	1
Sly04g0250521	M3	NA	2	2	1	2	1	2	1	1	3	1
Sly04g0250531	M11	NA	15	15	17	24	37	21	19	23	33	41
Sly04g0250551	M13	NA	112	75	168	83	82	103	104	109	17	8
Sly04g0250561	M12	NA	2	2	1	0	0	4	3	3	1	0
Sly04g0250571	M5	NA	25	28	9	25	8	58	42	7	4	2
Sly04g0250581	M12	NA	27	18	22	11	8	26	31	26	12	5
Sly04g0250591	M12	NA	23	21	23	11	8	23	26	27	11	3
Sly04g0250601	M3	NA	30	27	28	57	56	23	26	21	78	66
Sly04g0250611	M19	NA	18	20	18	40	36	16	14	16	38	27
Sly04g0250621	M1	NA	15	11	15	1	1	9	4	8	1	1
Sly04g0250631	M11	NA	3	2	3	2	2	3	3	4	3	2
Sly04g0250651	M2	SlCycH1;2	28	30	27	49	69	27	27	28	60	77
Sly04g0250661	M1	NA	128	111	114	190	220	50	57	52	59	162
Sly04g0250671	M1	SlERF.H12	230	261	143	143	148	48	65	26	29	87
Sly04g0250681	M3	NA	109	117	96	98	84	78	86	73	67	67
Sly04g0250691	M3	NA	5	9	3	6	5	2	8	3	2	4
Sly04g0250701	M5	NA	22	26	19	16	16	26	20	22	11	12
Sly04g0250711	M7	NA	2	3	2	2	2	2	3	3	1	1
Sly04g0250721	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly04g0250731	M1	NA	26	27	26	39	131	3	3	2	7	19
Sly04g0250741	M12	NA	5	8	6	8	12	9	11	9	7	13
Sly04g0250751	M3	NA	29	28	27	27	17	26	24	20	9	11
Sly04g0250761	M22	NA	1	1	1	2	2	1	1	1	2	2
Sly04g0250771	M12	NA	964	925	1048	733	435	1770	1835	1925	1254	663
Sly04g0250781	M1	NA	3	2	2	2	1	1	1	1	1	1
Sly04g0250801	M1	NA	1	1	1	1	1	1	0	0	0	0
Sly04g0250811	M1	NA	1	1	1	1	1	1	0	0	0	0
Sly04g0250821	M11	NA	120	113	111	111	128	135	124	143	148	191
Sly04g0250831	M1	NA	3	3	2	1	1	1	0	1	1	1
Sly04g0250861	M1	NA	62	52	71	50	22	8	4	4	1	0
Sly04g0250871	M1	NA	33	35	31	22	21	20	20	20	19	19
Sly04g0250881	M3	NA	166	142	94	72	47	108	121	77	66	62
Sly04g0250891	M12	NA	7	5	4	3	1	11	7	5	1	1
Sly04g0250901	M1	NA	3	3	3	2	3	3	3	3	1	2
Sly04g0250911	M11	NA	6	7	7	7	6	10	8	10	3	2
Sly04g0250921	M11	NA	42	39	51	69	62	76	74	91	111	114
Sly04g0250931	M3	NA	58	51	42	31	30	24	33	22	36	40
Sly04g0250941	M19	NA	6	6	6	6	6	5	5	6	6	6
Sly04g0250961	M19	NA	16	15	22	37	54	14	11	16	44	50
Sly04g0250971	M22	NA	6	6	6	10	18	9	5	10	15	22
Sly04g0250981	M3	NA	3	3	2	4	1	2	2	1	1	1
Sly04g0250991	M1	NA	227	204	189	867	584	162	171	170	630	321
Sly04g0251001	M14	NA	95	86	115	123	117	85	83	97	99	90
Sly04g0251011	M19	NA	4	4	4	4	4	4	3	4	3	2
Sly04g0251031	M7	NA	26	33	20	18	35	41	67	33	95	100
Sly04g0251041	M3	NA	5	5	5	7	6	5	5	5	7	8
Sly04g0251061	M10	NA	66	93	52	44	41	91	101	62	35	37
Sly04g0251081	M1	NA	511	468	427	320	218	343	350	327	286	233
Sly04g0251101	M12	NA	1	1	2	1	1	7	8	8	1	1
Sly04g0251121	M12	NA	1	1	1	0	0	1	1	1	1	0
Sly04g0251131	M12	NA	6	3	5	1	0	78	68	62	1	0
Sly04g0251141	M12	NA	1	2	1	1	1	7	6	6	1	1
Sly04g0251151	M9	UGT-like5	1	2	1	0	0	5	5	2	1	1
Sly04g0251181	M3	UGT-like6	1	2	1	0	0	1	1	1	1	1
Sly04g0251201	M12	NA	3	13	16	3	20	35	110	39	9	36
Sly04g0251211	M9	EXL1	19	53	32	5	11	192	401	140	7	30
Sly04g0251221	M12	EXL1	5	16	10	2	15	24	54	23	1	17
Sly04g0251231	M12	EXL1	6	30	26	6	90	32	147	66	25	142
Sly04g0251241	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly04g0251261	M3	NA	495	474	246	102	42	391	362	142	47	14
Sly04g0251271	M7	SlJMJ12	42	49	32	40	139	41	67	42	64	183
Sly04g0251281	M3	SlSnRK2.7	24	22	19	21	21	14	16	15	35	28
Sly04g0251291	M2	NA	218	213	180	92	38	169	216	158	87	47
Sly04g0251301	M1	NA	23	29	20	15	14	12	15	14	13	16
Sly04g0251311	M11	ADH	13	13	17	11	5	14	12	16	5	5
Sly04g0251321	M12	NA	1	1	1	2	1	1	1	1	2	1
Sly04g0251331	M2	NA	212	190	201	206	165	181	211	184	174	143
Sly04g0251341	M1	NA	105	101	86	69	64	68	65	64	78	87
Sly04g0251351	M12	NA	204	207	225	305	478	322	391	381	756	1020
Sly04g0251361	M1	NA	13	12	12	13	20	12	11	12	15	18
Sly04g0251371	M11	SlAPx	7	6	6	3	2	16	15	17	3	3
Sly04g0251381	M11	NA	10	11	10	9	9	11	11	12	13	13
Sly04g0251391	M1	NA	37	34	37	16	17	28	23	27	17	17
Sly04g0251401	M10	NA	10	33	21	1	1	22	42	11	1	3
Sly04g0251411	M3	NA	34	36	30	29	23	26	29	26	27	32
Sly04g0251421	M3	NA	32	34	13	1	2	16	14	14	3	3
Sly04g0251431	M3	NA	3	5	1	1	1	1	1	1	0	0
Sly04g0251441	M12	NA	16	19	14	12	9	25	24	19	3	2
Sly04g0251451	M9	NA	151	215	211	88	116	289	412	328	263	362
Sly04g0251461	M22	NA	5	5	2	1	0	13	2	8	1	0
Sly04g0251471	M11	NA	1	1	1	1	1	2	1	2	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0295731	M2	NA	23	28	21	19	9	14	17	13	4	2
Sly11g0295741	M1	NA	9	9	9	9	7	6	6	6	5	4
Sly11g0295751	M23	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0295761	M22	NA	1	1	1	0	0	7	0	5	0	0
Sly11g0295771	M19	NA	17	16	22	15	13	19	14	19	19	14
Sly11g0295781	M9	NAC4	140	161	112	452	247	249	312	227	794	467
Sly11g0295801	M12	NA	1	1	1	5	1	7	10	15	43	7
Sly11g0295811	M1	NA	7	6	13	6	5	6	5	6	4	6
Sly11g0295821	M11	NA	10	10	10	9	10	11	11	10	9	10
Sly11g0295851	M11	SlAPx6	15	16	17	22	8	29	21	29	8	2
Sly11g0295861	M1	NA	1	2	2	2	1	1	1	1	0	1
Sly11g0295871	M3	NA	30	28	26	21	20	19	22	17	19	20
Sly11g0295891	M11	NA	49	48	58	95	130	80	95	81	57	127
Sly11g0295901	M12	NA	2	2	2	4	5	9	12	9	15	25
Sly11g0295921	M1	NA	22	20	10	1	1	5	4	3	1	1
Sly11g0295931	M11	NA	7	7	7	9	13	10	8	11	9	10
Sly11g0295981	M11	NA	37	36	40	42	48	41	37	46	58	64
Sly11g0295991	M1	NA	28	26	26	10	5	12	9	13	2	2
Sly11g0296011	M1	NA	5	5	5	14	33	4	4	3	2	3
Sly11g0296041	M11	NA	8	5	9	2	1	10	7	7	1	1
Sly11g0296061	M3	NA	17	19	17	24	23	19	17	16	23	17
Sly11g0296071	M1	NA	4	4	3	3	1	1	1	1	1	1
Sly11g0296091	M1	NA	16	21	18	17	21	15	16	16	16	17
Sly11g0296131	M3	NA	3	7	2	1	1	1	1	0	1	1
Sly11g0296151	M11	NA	10	12	13	9	13	12	14	13	11	16
Sly11g0296161	M11	NA	6	8	8	7	6	8	8	11	6	7
Sly11g0296301	M22	NA	18	13	10	1	0	27	8	11	0	0
Sly11g0296311	M1	NA	11	14	14	16	14	10	9	8	12	10
Sly11g0296321	M11	NA	37	36	41	54	54	46	48	50	69	58
Sly11g0296341	M12	NA	25	25	29	39	36	32	36	36	53	50
Sly11g0296351	M8	NA	15	17	15	17	15	15	18	14	19	19
Sly11g0296361	M11	NA	12	13	12	13	13	16	15	15	15	16
Sly11g0296431	M12	NA	21	27	42	171	1161	62	53	74	163	1273
Sly11g0296441	M1	NA	5	3	7	3	2	3	4	3	2	2
Sly11g0296451	M12	NA	30	36	31	89	53	61	66	54	117	95
Sly11g0296471	M12	NA	6	7	8	9	10	8	11	10	20	27
Sly11g0296491	M18	NA	6	8	9	5	2	8	7	8	3	1
Sly11g0296541	M11	NA	12	9	11	26	46	10	8	14	25	54
Sly11g0296621	M11	NA	65	70	69	61	76	80	73	86	92	123
Sly11g0296651	M12	NA	7	7	7	6	6	11	11	11	8	7
Sly11g0296681	M1	NA	2	4	4	2	1	2	2	1	1	1
Sly11g0296721	M1	NA	68	64	57	16	5	41	33	32	1	1
Sly11g0296731	M11	NA	24	21	30	11	5	30	33	28	8	3
Sly11g0296741	M11	NA	19	21	21	12	6	34	29	29	6	3
Sly11g0296751	M11	NA	73	74	82	119	167	81	91	89	127	151
Sly11g0296811	M22	NA	27	17	32	675	1616	35	22	32	35	273
Sly11g0296831	M8	NA	19	19	18	24	22	16	22	17	25	29
Sly11g0297481	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0297491	M12	NA	1	1	1	0	0	2	9	2	1	1
Sly11g0297511	M12	NA	23	22	23	32	34	30	36	34	46	50
Sly11g0297531	M11	NA	6	5	6	6	5	6	5	7	6	5
Sly11g0297591	M1	NA	48	51	66	60	136	28	27	37	79	152
Sly11g0297621	M1	NA	12	11	11	15	16	10	11	12	19	23
Sly11g0297631	M1	NA	12	13	26	44	28	10	10	12	17	26
Sly11g0297641	M18	NA	6	7	8	7	5	9	7	8	7	5
Sly11g0297651	M1	NA	47	43	41	34	46	39	39	40	41	61
Sly11g0297661	M3	NA	88	100	75	58	64	57	62	48	48	49
Sly11g0297671	M1	NA	25	25	21	18	18	19	19	16	16	15
Sly11g0297701	M12	NA	1	1	1	1	1	4	6	5	3	1
Sly11g0297731	M1	NA	35	38	36	39	40	26	31	27	48	50
Sly11g0297741	M3	NA	232	214	206	150	90	138	207	147	156	109
Sly11g0297751	M1	NA	12	12	11	12	15	10	9	9	13	12
Sly11g0297761	M12	NA	6	6	8	9	10	10	12	12	78	66
Sly11g0297781	M2	NA	5	5	5	4	6	5	5	5	9	13
Sly11g0297801	M1	NA	22	24	31	40	23	5	4	4	2	3
Sly11g0297831	M1	NA	2	2	1	2	1	1	1	1	1	1
Sly11g0297901	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0297921	M1	NA	3	2	9	0	0	0	0	0	0	0
Sly11g0298101	M1	NA	5	5	6	8	13	4	5	4	2	4
Sly11g0298111	M19	NA	4	4	4	6	11	4	3	4	2	4
Sly11g0298121	M22	NA	3	4	4	6	9	4	3	4	2	4
Sly11g0298131	M19	NA	3	3	4	5	8	3	3	3	2	3
Sly11g0298141	M1	NA	17	19	18	22	26	13	13	13	15	24
Sly11g0298151	M22	NA	3	4	5	6	6	4	4	4	3	4
Sly11g0298171	M18	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0298191	M19	NA	2	3	3	3	3	3	2	3	1	2
Sly11g0298231	M1	NA	2	3	2	2	3	2	2	2	1	1
Sly11g0298321	M3	NA	2	2	2	2	5	2	2	1	1	1
Sly11g0298361	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0298811	M1	NA	1	1	1	2	1	1	1	1	1	1
Sly11g0298821	M11	NA	13	11	11	5	1	11	9	11	1	1
Sly11g0298851	M18	NA	22	21	25	32	37	30	27	32	34	34
Sly11g0298861	M11	NA	21	21	22	23	29	23	21	25	29	35
Sly11g0298871	M11	NA	11	10	13	13	8	18	14	19	10	9
Sly11g0298941	M18	NA	3	3	4	2	1	5	3	3	1	1
Sly11g0298951	M11	NA	13	11	18	7	2	16	11	13	3	1
Sly11g0298961	M12	NA	37	31	41	104	154	42	47	47	133	169
Sly11g0298971	M11	NA	26	22	34	88	110	36	34	40	91	90
Sly11g0298981	M1	NA	2	1	2	2	2	1	1	1	1	4
Sly11g0299001	M3	NA	43	42	36	36	43	37	33	36	40	46
Sly11g0299031	M12	NA	3	4	5	24	39	24	26	38	101	120
Sly11g0299041	M2	NA	113	126	105	118	92	97	130	83	86	80
Sly11g0299081	M12	NA	13	29	40	3	2	131	169	107	11	5
Sly11g0299091	M19	NA	11	15	12	8	6	12	12	12	8	9
Sly11g0299101	M19	NA	13	16	15	12	5	16	13	19	10	13
Sly11g0299111	M19	NA	16	17	17	14	8	17	16	17	14	14
Sly11g0299121	M12	NA	20	21	20	20	16	24	25	25	24	28
Sly11g0299131	M14	NA	15	14	17	12	13	14	13	18	12	15
Sly11g0299141	M12	NA	3	3	4	6	5	3	4	5	6	9
Sly11g0299241	M3	NA	2	5	1	2	1	2	5	1	1	1
Sly11g0299271	M1	NA	3	3	3	2	1	1	1	1	1	1
Sly11g0299491	M1	NA	3	2	3	1	2	1	1	1	1	1
Sly11g0299521	M1	NA	12	13	12	14	14	10	11	15	18	20
Sly11g0299571	M22	NA	2	1	2	0	0	4	1	7	0	0
Sly11g0299581	M1	NA	3	4	3	3	2	1	1	1	0	1
Sly11g0299601	M8	NA	2	2	1	1	2	2	2	1	2	5
Sly11g0299631	M12	NA	1	1	1	0	0	5	3	4	1	1
Sly11g0299671	M5	NA	3	3	1	2	2	3	2	1	2	1
Sly11g0299701	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly11g0299711	M22	NA	2	1	1	0	0	4	1	6	0	0
Sly11g0299791	M1	NA	1	2	2	2	4	1	1	2	1	4
Sly11g0299831	M1	NA	104	113	154	249	822	48	48	67	50	287
Sly11g0299991	M1	NA	2	3	3	3	3	2	2	3	7	9
Sly11g0300001	M22	NA	1	1	1	0	0	2	1	3	0	0
Sly11g0300011	M2	NA	11	12	10	11	13	11	13	9	16	15
Sly11g0300021	M11	NA	15	15	19	10	3	32	28	34	7	2
Sly11g0300031	M11	NA	6	5	9	4	2	13	8	17	2	1
Sly11g0300071	M16	NA	80	67	60	108	105	60	60	62	94	119
Sly11g0300081	M1	NA	38	28	31	6	5	16	14	11	1	1
Sly11g0300121	M18	NA	1	1	2	3	1	2	2	2	1	1
Sly11g0300131	M12	NA	8	9	10	10	7	9	9	10	14	11
Sly11g0300151	M11	NA	1	1	1	4	2	3	1	3	4	3
Sly11g0300371	M12	NA	37	33	36	27	24	48	46	36	33	32
Sly11g0300391	M11	NA	142	128	142	156	232	140	142	168	240	248
Sly11g0300401	M12	NA	8	6	9	2	3	92	76	90	16	28
Sly11g0300431	M1	NA	3	3	6	1	0	1	1	1	0	0
Sly11g0300441	M15	NA	37	28	35	22	24	32	32	36	29	29
Sly11g0300451	M18	NA	28	30	37	42	29	50	47	64	39	39
Sly11g0300471	M11	NA	244	222	258	162	123	237	251	256	183	138
Sly11g0300791	M22	NA	1	2	3	2	2	3	1	3	5	5
Sly11g0300881	M12	NA	9	10	10	14	11	12	12	12	21

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0251481	M11	NA	9	8	9	10	6	12	11	14	10	6
Sly04g0251491	M1	NA	4	3	3	1	3	2	1	2	1	1
Sly04g0251501	M3	NA	10	7	3	0	0	2	1	1	0	1
Sly04g0251521	M1	NA	4	5	5	2	3	2	2	2	3	2
Sly04g0251531	M1	NA	57	59	61	66	97	52	53	60	85	120
Sly04g0251541	M12	NA	1	1	1	1	0	2	2	1	1	1
Sly04g0251551	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly04g0251561	M7	NA	2	5	3	67	22	5	20	5	112	52
Sly04g0251571	M12	NA	1	1	1	1324	423	1	5	4	2480	474
Sly04g0251581	M12	NA	49	54	78	340	234	105	115	158	366	204
Sly04g0251591	M12	NA	12	12	15	18	10	23	27	32	19	10
Sly04g0251601	M13	NA	24	23	33	14	14	35	32	42	5	6
Sly04g0251631	M3	NA	3	1	1	1	0	1	1	1	0	0
Sly04g0251641	M9	NA	2	3	2	2	1	3	3	2	2	2
Sly04g0251651	M15	NA	181	156	169	163	144	163	173	199	227	223
Sly04g0251661	M23	NA	1	1	1	0	0	1	1	1	0	1
Sly04g0251681	M3	NA	21	23	19	30	30	20	19	16	23	31
Sly04g0251691	M3	NA	140	203	51	3	4	75	78	17	2	7
Sly04g0251701	M2	NA	38	39	28	44	41	24	33	21	35	43
Sly04g0251711	M11	NA	6	6	7	6	7	9	8	9	8	8
Sly04g0251731	M3	SITIR1-like2	24	25	19	19	19	23	24	17	17	19
Sly04g0251741	M1	NA	4	2	2	1	0	1	1	1	0	0
Sly04g0251751	M1	NA	7	9	4	2	1	2	2	1	1	1
Sly04g0251771	M1	NA	271	197	255	162	232	122	142	127	60	117
Sly04g0251781	M18	NA	21	22	25	31	41	23	22	25	31	46
Sly04g0251791	M3	NA	157	173	147	106	87	105	119	80	111	119
Sly04g0251801	M1	NA	104	124	103	72	52	77	78	57	71	62
Sly04g0251811	M12	SlCycD5;1	16	17	17	5	4	24	22	16	6	4
Sly04g0251821	M12	NA	51	46	59	166	285	88	92	109	168	294
Sly04g0251831	M9	NA	131	131	119	117	85	128	131	126	137	109
Sly04g0251841	M1	PPR-like3	13	13	15	12	15	12	11	13	12	14
Sly04g0251851	M2	NA	22	22	24	24	20	22	22	24	27	23
Sly04g0251861	M1	PGI1A	44	42	48	103	108	31	31	35	45	57
Sly04g0251871	M22	NA	2	1	2	1	1	4	2	3	1	0
Sly04g0251881	M3	NA	90	89	77	72	77	73	81	74	98	122
Sly04g0251901	M11	NA	3	3	3	2	2	4	3	4	3	3
Sly04g0251911	M12	NA	2	2	2	2	1	5	4	4	3	1
Sly04g0251931	M19	NA	28	28	26	19	21	26	22	23	8	9
Sly04g0251951	M11	NA	77	74	84	131	166	103	106	134	204	235
Sly04g0251961	M3	NA	62	65	49	47	52	46	38	34	31	30
Sly04g0251971	M1	NA	11	17	9	22	25	3	2	2	1	1
Sly04g0251981	M3	NA	106	102	99	110	98	89	95	85	87	81
Sly04g0252001	M12	NA	3	3	4	15	18	7	6	6	1	3
Sly04g0252011	M11	NA	6	5	6	6	5	5	5	6	5	5
Sly04g0252021	M22	NA	67	61	58	44	43	62	56	62	51	58
Sly04g0252031	M1	NA	1	1	1	1	1	0	0	1	0	0
Sly04g0252041	M11	NA	17	17	22	19	16	30	29	29	11	10
Sly04g0252051	M1	NA	25	28	20	5	2	10	9	9	3	2
Sly04g0252061	M1	NA	1	1	1	1	0	1	1	1	1	0
Sly04g0252071	M1	NA	34	34	34	27	27	21	22	22	19	12
Sly04g0252081	M3	NA	3	4	2	2	2	3	2	2	2	1
Sly04g0252091	M1	NA	20	14	23	15	15	15	11	12	9	7
Sly04g0252101	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0252111	M2	NA	11	13	13	11	14	12	12	11	11	10
Sly04g0252121	M11	PPR-like10	4	4	4	5	4	5	4	5	3	3
Sly04g0252131	M11	NA	186	176	211	141	116	209	182	216	137	105
Sly04g0252141	M11	NA	18	18	18	15	14	22	20	24	12	9
Sly04g0252151	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0252161	M3	NA	14	14	12	16	16	14	13	12	17	15
Sly04g0252171	M12	NA	24	23	20	31	36	25	25	26	47	51
Sly04g0252181	M3	NA	27	27	22	22	24	20	22	19	21	23
Sly04g0252191	M9	NA	2	1	1	1	1	3	1	1	1	1
Sly04g0252201	M12	NA	45	50	45	51	34	75	88	92	48	29
Sly04g0252211	M12	NA	25	31	28	32	20	45	47	59	26	14
Sly04g0252221	M1	NA	23	18	18	15	21	8	9	8	13	22
Sly04g0252231	M23	NA	2	1	2	1	1	3	2	2	1	1
Sly04g0252241	M19	NA	29	33	28	24	22	23	21	21	18	20
Sly04g0252251	M3	NA	58	68	49	36	48	39	39	28	30	42
Sly04g0252261	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly04g0252271	M11	NA	30	33	35	40	54	46	45	53	53	76
Sly04g0252281	M19	NA	41	43	40	52	71	44	39	37	25	35
Sly04g0252291	M1	NA	75	74	70	53	65	55	52	56	65	78
Sly04g0252301	M1	NA	19	14	12	6	8	6	5	4	5	5
Sly04g0252311	M1	NA	16	15	17	23	29	12	14	14	31	47
Sly04g0252331	M3	HVA22C-like	74	86	25	17	17	14	24	8	5	5
Sly04g0252341	M3	NA	37	44	13	7	6	8	12	4	3	2
Sly04g0252351	M19	NA	71	79	72	67	70	65	57	62	41	46
Sly04g0252361	M21	NA	1	1	1	5	4	1	1	1	1	1
Sly04g0252381	M12	NA	2	1	1	1	1	5	3	3	5	2
Sly04g0252391	M12	NA	9	10	9	8	7	12	13	10	5	7
Sly04g0252401	M1	NA	96	97	102	96	97	81	85	89	77	85
Sly04g0252411	M1	NA	19	19	17	13	15	15	16	19	13	12
Sly04g0252421	M1	NA	9	9	10	15	25	5	6	6	10	13
Sly04g0252431	M1	NA	6	6	5	4	2	3	3	3	1	1
Sly04g0252451	M6	NA	4	13	36	0	1	15	23	3	1	0
Sly04g0252461	M11	NA	26	23	32	27	20	35	35	40	23	22
Sly04g0252501	M11	NA	30	21	18	1	1	127	59	135	1	0
Sly04g0252511	M14	NA	49	64	67	9	4	59	42	55	1	1
Sly04g0252521	M11	NA	78	68	83	174	167	121	103	116	88	80
Sly04g0252531	M11	NA	4	4	7	4	4	10	10	15	4	3
Sly04g0252541	M12	NA	65	68	58	52	40	65	66	82	93	48
Sly04g0252551	M14	NA	121	113	150	225	227	113	97	170	205	180
Sly04g0252561	M2	NA	32	35	32	50	60	26	34	32	107	158
Sly04g0252571	M1	NA	49	51	56	87	90	48	49	52	150	193
Sly04g0252591	M12	SlAux/IAA9	434	392	401	455	490	2312	2209	2353	1098	699
Sly04g0252611	M1	NA	37	62	19	11	4	2	1	1	1	1
Sly04g0252621	M11	NA	63	51	81	42	53	90	80	111	49	28
Sly04g0252631	M12	NA	256	298	371	335	554	499	564	593	1979	734
Sly04g0252641	M1	NA	102	98	104	114	123	79	85	86	119	128
Sly04g0252651	M3	NA	21	23	21	22	22	19	19	18	19	21
Sly04g0252661	M5	NA	27	29	20	15	15	27	28	21	12	10
Sly04g0252671	M11	NA	11	11	14	11	10	22	20	27	20	13
Sly04g0252681	M3	NA	2	1	1	1	1	1	1	1	1	1
Sly04g0252691	M1	NA	9	10	9	16	9	5	6	5	5	4
Sly04g0252701	M3	NA	3	4	2	1	1	2	1	1	0	1
Sly04g0252711	M5	NA	168	200	106	25	29	172	166	69	12	18
Sly04g0252721	M2	NA	8	8	9	8	13	7	8	7	12	19
Sly04g0252731	M12	NA	11	9	12	6	7	31	40	42	3	1
Sly04g0252741	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0252751	M12	NA	1359	1324	1372	662	214	1948	2189	1842	455	142
Sly04g0252761	M1	NA	11	12	14	26	28	7	6	10	15	13
Sly04g0252771	M1	NA	13	12	13	14	15	10	9	10	9	11
Sly04g0252781	M3	NA	629	803	297	45	15	87	135	27	4	3
Sly04g0252791	M11	NA	29	29	35	33	36	36	33	38	32	36
Sly04g0252841	M19	NA	4	4	5	8	6	5	3	5	5	5
Sly04g0252851	M1	NA	5	7	8	11	7	3	4	3	8	4
Sly04g0252861	M14	NA	11	9	15	5	12	7	8	11	8	22
Sly04g0252871	M11	NA	28	21	22	35	52	39	30	42	34	54
Sly04g0252881	M12	NA	3	2	1	1	1	3	4	4	1	1
Sly04g0252891	M12	NA	21	18	18	21	21	17	22	23	22	23
Sly04g0252901	M1	NA	43	40	44	23	5	33	39	35	3	2
Sly04g0252911	M12	NA	1	1	1	2	1	2	3	6	2	2
Sly04g0252921	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly04g0252931	M23	NA	3	2	2	1	1	5	2	2	1	1
Sly04g0252971	M12	NA	35	36	30	17	30	68	83	97	51	48
Sly04g0252981	M3	NA	70	96	39	8	3	12	12	7	3	3
Sly04g0252991	M12	NA	7	7	4	1	1	7	14	10	4	2
Sly04g0253031	M3	NA	19	50	14	1	2	14	17	6	1	3
Sly04g0253041	M1	NA	4	5	3	1	1	2	1	1	0	0
Sly04g0253051	M12	NA	12	14	12	12	9	13	14	14	9	7
Sly04g0253061	M3	NA	2	6	1	1	1	1	1	1	1	1
Sly04g0253071	M3	NA	4	9	2	1	2	2	2	1	1	1
Sly04g0253081	M3	NA	10	12	12	8	7	10	10	9	10	13
Sly04g0253111	M12	NA	3	3	5	5	7	7	9	9	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0301381	M13	NA	30	26	34	39	65	29	28	35	46	63
Sly11g0301391	M5	NA	19	20	16	17	16	18	19	18	24	19
Sly11g0301401	M10	NA	5	6	4	1	1	13	14	5	1	1
Sly11g0301591	M22	NA	1	1	1	0	0	5	1	3	0	0
Sly11g0301621	M12	NA	3	3	3	9	8	15	13	19	41	63
Sly11g0301661	M21	NA	2	1	1	1	1	1	1	1	1	0
Sly11g0301681	M22	NA	1	0	1	1	1	6	1	3	0	1
Sly11g0301731	M12	NA	5	4	5	1	1	68	59	67	3	1
Sly11g0301741	M1	NA	6	6	4	4	3	1	1	1	1	0
Sly11g0301751	M1	NA	1	1	1	1	1	1	0	1	0	0
Sly11g0301761	M1	NA	3	3	3	3	2	1	1	1	1	1
Sly11g0301771	M11	NA	1	1	2	1	0	4	5	4	1	0
Sly11g0301811	M3	OPR1-like2	42	46	31	28	36	38	43	30	38	73
Sly11g0301901	M12	NA	19	25	24	30	46	21	28	26	53	89
Sly11g0301911	M11	NA	14	13	15	12	23	17	16	16	15	26
Sly11g0301961	M1	NA	22	20	21	21	18	10	10	12	11	6
Sly11g0301971	M11	NA	47	47	62	57	56	97	76	104	55	52
Sly11g0301981	M3	NA	62	61	52	58	63	49	51	48	73	87
Sly11g0301991	M2	NA	182	184	188	185	161	158	173	152	198	169
Sly11g0302041	M15	NA	53	42	36	28	22	42	40	45	24	25
Sly11g0302071	M3	NA	33	33	28	31	25	32	31	26	21	19
Sly11g0302081	M1	NA	21	26	24	8	4	7	10	4	1	1
Sly11g0302091	M12	NA	26	27	27	68	88	38	37	44	80	96
Sly11g0302101	M11	NA	181	166	165	215	214	194	191	184	176	205
Sly11g0302121	M11	NA	5	4	4	6	8	6	5	6	7	9
Sly11g0302151	M11	NA	10	11	11	9	9	11	11	13	13	10
Sly11g0302171	M2	NA	10	12	13	8	3	10	12	10	4	1
Sly11g0302201	M1	NA	9	10	11	8	6	4	4	5	5	2
Sly11g0302241	M1	NA	11	12	13	9	12	9	9	9	21	33
Sly11g0302251	M3	NA	4	5	4	3	4	2	3	2	4	7
Sly11g0302261	M1	NA	2	1	2	1	0	1	1	1	0	0
Sly11g0302281	M12	NA	27	30	29	29	35	34	34	33	44	60
Sly11g0302291	M12	NA	19	19	18	18	16	19	21	21	18	20
Sly11g0302301	M19	NA	9	10	9	9	9	10	8	10	8	7
Sly11g0302321	M1	NA	3	2	2	2	1	1	1	1	1	0
Sly11g0302371	M22	NA	1	1	1	0	0	2	1	2	0	0
Sly11g0302451	M12	NA	12	13	13	19	22	17	16	18	23	31
Sly11g0302471	M11	NA	32	30	30	32	29	36	32	36	26	27
Sly11g0302481	M11	NA	17	16	18	20	21	18	17	20	17	19
Sly11g0302531	M1	NA	16	18	15	11	11	13	13	13	16	15
Sly11g0302551	M11	NA	8	8	8	8	9	9	9	10	9	8
Sly11g0302571	M12	NA	6	6	10	7	6	34	26	35	18	10
Sly11g0302581	M22	NA	1	1	1	1	0	1	1	1	1	1
Sly11g0302591	M14	NA	10	11	13	15	22	10	9	13	17	20
Sly11g0302601	M3	NA	35	33	32	19	28	32	33	27	25	53
Sly11g0302611	M11	NA	14	13	16	32	50	18	17	22	32	45
Sly11g0302621	M19	NA	12	13	12	17	17	15	12	15	13	14
Sly11g0302661	M3	NA	158	200	121	120	152	102	159	88	97	176
Sly11g0302671	M3	NA	44	43	40	29	68	37	33	31	31	76
Sly11g0302681	M1	NA	6	5	4	4	3	2	1	3	1	1
Sly11g0302691	M1	NA	10	10	12	11	11	10	9	10	11	9
Sly11g0302731	M1	NA	9	8	9	12	11	8	6	7	6	5
Sly11g0302741	M11	NA	7	5	6	3	2	7	6	6	2	1
Sly11g0302751	M18	NA	7	9	9	7	6	9	7	10	4	3
Sly11g0302761	M5	NA	3	3	2	3	3	2	3	2	2	3
Sly11g0302771	M1	NA	2	1	2	1	1	1	1	1	1	0
Sly11g0302781	M11	NA	21	22	33	17	11	94	63	101	17	5
Sly11g0302791	M12	NA	8	7	10	6	2	27	22	28	10	4
Sly11g0302811	M11	NA	11	29	53	414	102	46	51	86	159	66
Sly11g0302821	M14	NA	30	29	31	39	49	29	28	33	45	46
Sly11g0302841	M3	NA	33	38	34	31	25	38	35	33	21	22
Sly11g0302851	M11	NA	24	22	27	29	27	31	26	32	20	21
Sly11g0302871	M3	NA	2	2	2	0	1	1	1	0	0	0
Sly11g0302911	M3	NA	20	17	13	7	7	17	13	13	6	5
Sly11g0302931	M3	NA	33	31	30	25	19	24	27	24	27	26
Sly11g0302941	M12	NA	1	1	2	1	0	22	16	21	1	0
Sly11g0303111	M12	ABF3-like2	153	141	144	82	76	152	153	143	31	43
Sly11g0303121	M11	NA	25	21	27	45	44	31	29	37	27	31
Sly11g0303141	M11	NA	9	10	9	8	3	13	14	13	2	1
Sly11g0303161	M18	NA	18	18	19	16	13	19	19	20	13	11
Sly11g0303171	M11	NA	19	15	22	20	14	26	20	30	11	8
Sly11g0303191	M11	NA	45	45	53	47	52	58	52	58	48	52
Sly11g0303201	M1	NA	64	66	55	27	10	8	9	5	4	3
Sly11g0303221	M1	NA	7	4	6	1	0	2	2	1	0	0
Sly11g0303291	M11	NA	7	7	8	9	4	15	13	16	12	7
Sly11g0303321	M18	NA	11	11	11	10	9	13	11	11	6	4
Sly11g0303331	M2	NA	6	6	6	5	4	5	6	6	5	5
Sly11g0303341	M12	NA	21	24	23	47	56	24	24	27	58	67
Sly11g0303351	M17	NA	31	29	32	44	45	28	25	30	34	23
Sly11g0303361	M12	NA	21	22	22	32	39	24	26	28	31	41
Sly11g0303391	M12	NA	20	19	20	26	43	26	27	28	35	67
Sly11g0303401	M10	NA	13	12	11	10	15	14	13	11	10	10
Sly11g0303411	M12	NA	162	145	162	213	143	159	172	190	295	211
Sly11g0303431	M1	NA	70	73	74	72	62	68	67	65	68	58
Sly11g0303451	M2	NA	13	14	13	9	7	13	14	12	14	9
Sly11g0303461	M12	NA	45	39	45	43	47	56	59	58	50	50
Sly11g0303481	M18	NA	25	27	28	36	31	35	30	33	23	21
Sly11g0303491	M22	NA	19	5	17	1	0	41	9	64	2	0
Sly11g0303611	M8	NA	61	67	59	56	55	59	69	61	60	64
Sly11g0303641	M11	NA	16	17	15	7	1	27	23	26	2	1
Sly11g0303651	M13	NA	320	295	323	282	280	298	297	317	296	284
Sly11g0303661	M9	NA	11	11	10	9	7	12	12	10	10	5
Sly11g0303721	M23	NA	1	1	1	0	0	1	1	1	1	0
Sly11g0303731	M19	NA	47	52	51	41	44	57	50	56	59	63
Sly11g0303741	M12	NA	56	57	60	46	54	67	64	59	75	97
Sly11g0303761	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly11g0303781	M11	NA	1	1	1	1	1	1	2	1	1	0
Sly11g0303841	M11	NA	15	10	17	20	26	22	20	25	15	9
Sly11g0303871	M11	NA	33	31	38	62	118	51	44	64	88	194
Sly11g0303881	M3	NA	52	60	52	35	28	37	40	34	38	33
Sly11g0303891	M3	NA	1	2	1	1	0	1	1	1	0	1
Sly11g0303901	M7	NA	1	2	1	1	0	1	2	1	0	1
Sly11g0303941	M19	NA	4	5	4	4	4	5	4	5	4	4
Sly11g0303951	M19	NA	3	4	3	3	3	4	3	4	2	3
Sly11g0303961	M11	NA	11	12	12	11	10	14	13	16	14	13
Sly11g0303971	M1	NA	9	8	10	6	15	9	8	6	11	19
Sly11g0303991	M8	NA	14	15	14	13	9	14	19	12	13	7
Sly11g0304001	M11	NA	19	18	25	23	27	22	20	22	27	21
Sly11g0304011	M1	NA	1	2	1	1	1	1	1	2	1	2
Sly11g0304041	M3	NA	2	1	1	1	2	1	1	1	1	2
Sly11g0304081	M14	NA	37	42	45	73	97	42	38	43	46	58
Sly11g0304111	M19	NA	145	146	127	130	123	138	128	134	154	135
Sly11g0304121	M1	NA	1	1	1	0	1	1	0	1	0	0
Sly11g0304131	M1	NA	2	3	2	3	2	1	1	1	1	1
Sly11g0304161	M11	NA	18	13	16	18	15	27	22	27	20	22
Sly11g0304171	M11	NA	14	13	13	13	9	18	13	23	15	12
Sly11g0304191	M1	NA	3	3	3	3	3	2	2	2	3	4
Sly11g0304201	M11	NA	14	15	16	18	20	21	19	21	27	31
Sly11g0304211	M1	NA	4	4	5	4	2	3	4	4	3	1
Sly11g0304231	M11	NA	12	11	14	15	14	17	16	18	17	12
Sly11g0304241	M11	NA	7	8	8	10	7	12	9	11	10	6
Sly11g0304251	M19	NA	4	6	6	5	3	8	6	9	6	3
Sly11g0304261	M18	NA	6	7	9	11	4	16	10	12	8	3
Sly11g0304271	M18	NA	3	3	4	3	2	5	3	5	3	1
Sly11g0304281	M18	NA	4	2	4	4	2	6	5	5	3	1
Sly11g0304301	M11	NA	45	39	48	37	40	45	43	47	38	49
Sly11g0304311	M18	NA	28	30	36	30	29	34	30	36	23	25
Sly11g0304361	M1	NA	24	26	22	10	2	7	5	4	2	1
Sly11g0304371	M12	NA	1	1	1	2	1	1	1	1	1	0
Sly11g0304381	M2	NA	28	29	26	52	47	26	33	28	63	55
Sly11g0304391	M1	NA	45	42	52	33	49	35	37	38	19	16

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0253121	M1	NA	1	2	2	4	9	1	1	1	0	1
Sly04g0253161	M3	NA	6	8	3	1	1	1	1	1	0	0
Sly04g0253171	M3	NA	1	1	1	0	1	1	1	1	1	0
Sly04g0253191	M12	NA	21	22	23	34	31	29	31	29	25	22
Sly04g0253201	M3	NA	25	27	20	22	22	20	18	16	22	20
Sly04g0253211	M11	SQE1-like	52	44	74	17	20	105	103	124	51	49
Sly04g0253221	M12	NA	3	3	3	1	2	5	4	4	2	2
Sly04g0253231	M7	NA	4	6	4	4	3	5	7	4	5	4
Sly04g0253241	M11	NA	9	11	19	28	35	13	19	18	36	33
Sly04g0253251	M11	NA	7	5	8	5	3	9	8	9	6	4
Sly04g0253261	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0253271	M11	NA	11	8	10	11	23	17	17	20	22	41
Sly04g0253281	M11	NA	18	15	21	22	45	30	30	45	39	59
Sly04g0253291	M20	NA	5	2	5	1	1	5	3	3	1	1
Sly04g0253301	M19	NA	12	12	13	14	17	12	12	13	16	18
Sly04g0253311	M1	NA	6	5	5	3	4	4	4	4	3	3
Sly04g0253351	M1	NA	2	2	1	1	1	1	1	1	1	1
Sly04g0253371	M1	NA	2	2	2	2	3	1	1	1	1	1
Sly04g0253381	M11	NA	27	29	31	34	38	31	31	37	41	48
Sly04g0253391	M12	NA	2	1	2	4	2	1	1	4	92	58
Sly04g0253401	M12	NA	2	2	1	0	0	7	13	7	1	1
Sly04g0253411	M12	NA	18	17	15	16	18	30	29	30	10	10
Sly04g0253421	M12	NA	30	32	30	33	28	30	32	34	33	30
Sly04g0253431	M1	NA	17	20	18	16	17	14	13	11	8	9
Sly04g0253441	M12	NA	2	4	2	1	1	3	3	7	1	3
Sly04g0253461	M11	NA	1	1	1	12	43	1	1	2	16	47
Sly04g0253471	M12	NA	46	54	90	654	853	146	204	295	1954	1671
Sly04g0253481	M18	NA	15	15	21	25	22	26	18	25	11	16
Sly04g0253491	M14	NA	22	21	32	22	7	25	21	22	2	1
Sly04g0253501	M3	NA	47	46	41	32	30	35	34	30	37	31
Sly04g0253511	M3	NA	7	7	2	0	0	2	1	1	0	1
Sly04g0253571	M11	NA	4	2	2	5	10	6	4	6	8	15
Sly04g0253581	M12	NA	3	4	3	7	9	4	4	5	8	14
Sly04g0253601	M11	NA	12	11	12	20	20	15	15	18	23	21
Sly04g0253611	M14	NA	162	127	229	116	48	120	100	134	74	31
Sly04g0253621	M3	NA	38	37	34	40	43	31	33	30	39	42
Sly04g0253631	M1	NA	1	1	1	24	39	1	1	1	6	16
Sly04g0253641	M12	NA	14	14	14	33	38	14	14	20	74	52
Sly04g0253651	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0253671	M1	NA	11	13	12	16	16	4	6	6	20	20
Sly04g0253681	M5	NA	19	18	11	8	12	18	18	14	16	27
Sly04g0253691	M1	NA	50	52	69	111	28	6	8	10	6	3
Sly04g0253701	M3	NA	11	12	10	18	9	11	11	9	7	6
Sly04g0253751	M6	NA	81	98	72	79	121	78	107	67	159	202
Sly04g0253761	M18	NA	18	18	19	21	24	22	19	24	24	22
Sly04g0253771	M18	NA	20	22	24	19	17	25	23	26	18	20
Sly04g0253781	M3	NA	1	1	1	1	0	1	1	1	1	0
Sly04g0253791	M12	NA	530	495	527	791	814	738	788	889	1306	1538
Sly04g0253801	M6	NA	34	85	40	8	109	42	89	18	5	172
Sly04g0253811	M1	NA	17	16	14	7	4	5	6	7	3	1
Sly04g0253821	M22	NA	4	4	3	4	8	5	3	4	3	4
Sly04g0253831	M23	NA	1	1	1	1	0	3	1	1	0	0
Sly04g0253861	M12	NA	2	2	1	1	1	2	2	2	1	1
Sly04g0253871	M19	NA	22	25	25	30	30	25	22	24	28	24
Sly04g0253881	M11	NA	6	4	7	15	13	12	8	15	21	18
Sly04g0253891	M15	NA	389	319	339	414	587	361	339	417	649	778
Sly04g0253921	M1	NA	43	48	55	102	111	34	38	60	299	145
Sly04g0253931	M12	NA	1	1	1	1	2	3	2	2	4	2
Sly04g0253941	M12	NA	3	3	4	6	6	14	10	9	6	8
Sly04g0253951	M1	NA	16	16	15	8	6	9	10	10	7	4
Sly04g0253961	M3	NA	39	39	36	30	31	36	39	34	36	43
Sly04g0253971	M11	NA	6	5	6	10	18	9	7	10	16	21
Sly04g0253981	M11	NA	7	6	8	8	10	10	9	11	10	13
Sly04g0254011	M22	NA	6	5	5	2	3	9	3	6	2	2
Sly04g0254021	M1	NA	67	47	118	28	5	16	7	21	1	1
Sly04g0254071	M9	NA	27	25	20	18	16	30	28	25	15	13
Sly04g0254081	M12	NA	4	4	4	3	4	6	6	7	10	6
Sly04g0254091	M3	NA	59	72	40	3	2	12	16	5	1	1
Sly04g0254101	M3	NA	39	50	27	3	1	10	11	3	1	1
Sly04g0254111	M22	NA	1	1	1	1	1	3	1	2	1	1
Sly04g0254121	M1	SlCycA3;2	1	1	1	1	1	1	1	1	0	0
Sly04g0254131	M18	NA	41	42	48	50	67	52	40	58	63	72
Sly04g0254151	M22	NA	6	6	4	1	1	29	8	16	1	1
Sly04g0254161	M12	NA	3	2	4	5	8	27	26	41	17	51
Sly04g0254171	M12	NA	1	1	1	1	1	1	1	1	2	2
Sly04g0254191	M22	NA	18	13	4	0	1	41	4	22	1	1
Sly04g0254201	M9	NA	89	86	77	91	94	88	99	83	85	104
Sly04g0254211	M7	NA	2	6	3	5	5	4	5	2	1	6
Sly04g0254221	M11	NA	50	55	65	69	65	85	70	99	75	147
Sly04g0254231	M11	NA	27	23	31	51	79	38	32	42	63	99
Sly04g0254241	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly04g0254251	M1	NA	170	165	84	38	88	38	38	31	26	95
Sly04g0254291	M12	NA	38	36	38	191	38	187	230	317	1209	350
Sly04g0254301	M1	SlCycD3;3	1	1	1	0	0	1	0	1	1	1
Sly04g0254311	M1	NA	15	16	15	17	26	13	13	14	17	20
Sly04g0254321	M1	NA	45	44	39	44	35	40	37	40	38	43
Sly04g0254331	M8	J18	5	6	3	7	5	5	6	4	16	8
Sly04g0254341	M3	NA	128	135	112	139	126	125	141	108	143	181
Sly04g0254351	M11	NA	3	3	6	4	2	8	8	10	4	3
Sly04g0254371	M3	NA	31	31	18	11	17	11	8	4	11	110
Sly04g0254381	M6	NA	41	77	64	37	86	26	34	14	5	39
Sly04g0254401	M22	NA	1	1	1	1	0	4	2	5	0	0
Sly04g0254411	M12	NA	38	33	48	127	242	64	57	69	117	280
Sly04g0254421	M3	NA	59	81	44	44	34	41	38	29	27	35
Sly04g0254431	M1	NA	28	23	22	31	24	23	21	24	26	18
Sly04g0254441	M3	NA	10	13	7	5	3	8	8	3	2	2
Sly04g0254451	M12	NA	66	73	76	148	167	95	145	197	236	368
Sly04g0254461	M1	NA	1	1	1	1	0	0	0	0	0	0
Sly04g0254471	M6	NA	4	6	6	3	2	6	7	2	2	1
Sly04g0254481	M3	NA	11	10	10	5	11	11	10	9	7	10
Sly04g0254491	M3	NA	80	123	67	43	47	71	81	45	30	42
Sly04g0254501	M3	NA	10	9	8	5	2	8	6	5	3	2
Sly04g0254511	M22	NA	11	9	9	8	4	16	10	16	3	2
Sly04g0254521	M3	NA	1	1	1	1	0	1	1	1	1	0
Sly04g0254541	M12	NA	1	1	1	0	1	1	1	2	0	0
Sly04g0254551	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly04g0254561	M12	NA	19	26	13	17	38	51	74	34	18	65
Sly04g0254571	M3	NA	38	34	32	37	52	31	30	30	51	61
Sly04g0254591	M23	NA	1	1	1	0	0	1	1	1	1	1
Sly04g0254601	M1	NA	37	36	32	24	21	22	24	20	15	16
Sly04g0254621	M3	NA	10	14	15	1	0	6	6	4	1	1
Sly04g0254631	M12	NA	10	11	11	71	56	15	17	21	64	34
Sly04g0254651	M1	NA	4	4	4	12	18	2	2	3	13	24
Sly04g0254661	M3	NA	125	132	112	97	123	113	135	99	106	154
Sly04g0254671	M1	NA	49	50	44	27	21	31	32	29	15	14
Sly04g0254681	M19	ABF3-like4/SlABF2/SlA	36	33	37	16	17	33	31	32	15	23
Sly04g0254691	M11	NA	9	8	10	14	22	10	9	12	19	22
Sly04g0254701	M1	NA	3	3	3	2	2	2	2	2	2	1
Sly04g0254711	M1	NA	38	35	40	35	34	20	22	17	15	21
Sly04g0254721	M13	NA	42	36	57	71	80	31	44	44	39	62
Sly04g0254731	M12	NA	11	12	11	15	17	10	12	12	18	17
Sly04g0254741	M1	SlCYP707A1	10	8	7	5	4	3	2	3	0	0
Sly04g0254751	M12	NA	11	13	12	26	11	25	28	31	25	14
Sly04g0254761	M3	NA	101	111	122	405	392	83	124	81	153	205
Sly04g0254771	M11	NA	5	3	4	9	6	5	5	4	4	2
Sly04g0254781	M11	NA	6	5	6	10	6	5	8	7	5	1
Sly04g0254791	M1	NA	2	2	2	1	1	2	2	2	1	1
Sly04g0254801	M11	NA	4	4	5	6	10	12	10	14	12	14
Sly04g0254811	M12	NA	1	2	2	1	1	8	9	9	2	1
Sly04g0254821	M22	NA	2	1	1	1	1	6	1	6	1	0
Sly04g0254831	M11	NA	25	22	28	46	83	29	27	34	59	79
Sly04g0254861	M11	NA	1	1	1	1	0	1	1	1	1	0
Sly04g0254881	M12	NA	2	2	4	4	2	13	11	15	5	2
Sly04g0254891	M12	NA	5	4	8	10	4	31	30	36	13	3

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0304481	M11	NA	36	30	32	25	32	37	31	37	34	44
Sly11g0304491	M11	NA	2	2	3	4	3	4	4	4	2	2
Sly11g0304551	M3	NA	27	25	19	19	22	15	21	11	18	21
Sly11g0304561	M3	NA	23	24	19	17	18	19	19	18	19	23
Sly11g0304601	M3	NA	108	105	89	72	65	78	79	75	73	70
Sly11g0304621	M19	NA	14	15	16	15	15	16	12	14	11	11
Sly11g0304651	M12	NA	621	613	648	977	1034	650	740	766	1082	1432
Sly11g0304661	M1	NA	92	94	84	87	83	56	59	57	61	66
Sly11g0304771	M3	NA	8	9	8	12	8	5	7	3	5	4
Sly11g0304811	M10	NA	13	17	13	16	31	18	22	12	12	24
Sly11g0304901	M2	NA	176	191	163	131	120	123	152	104	107	121
Sly11g0305001	M1	NA	14	14	13	5	4	6	9	4	3	3
Sly11g0305011	M12	NA	1	1	1	2	2	1	2	1	1	0
Sly11g0305021	M11	NA	15	15	23	7	4	30	24	45	1	1
Sly11g0305241	M3	NA	7	8	5	3	7	2	3	1	1	1
Sly11g0305251	M3	NA	10	14	8	5	11	3	3	1	1	1
Sly11g0305271	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly11g0305281	M11	NA	5	3	4	5	11	7	5	7	2	4
Sly11g0305321	M1	NA	56	42	145	52	25	16	18	20	15	23
Sly11g0305371	M22	NA	2	1	1	1	0	10	1	5	0	0
Sly11g0305401	M3	NA	5	5	6	3	2	6	5	2	1	1
Sly11g0305431	M8	NA	22	22	19	15	14	22	29	17	25	19
Sly11g0305441	M12	NA	58	55	56	108	105	64	74	74	172	191
Sly11g0305751	M11	NA	1	0	1	0	0	2	1	2	1	0
Sly11g0305801	M1	NA	3	3	3	1	0	1	1	1	0	0
Sly11g0305821	M12	NA	1	0	1	1	2	1	2	2	7	6
Sly11g0305841	M9	NA	7	7	7	8	15	8	11	8	14	28
Sly11g0305851	M19	SPD	45	53	54	59	59	48	40	48	38	36
Sly11g0305911	M3	NA	36	36	33	37	63	36	33	30	34	46
Sly11g0305921	M12	NA	13	13	15	15	24	29	31	36	67	89
Sly11g0305931	M12	NA	16	16	17	19	33	34	38	39	83	130
Sly11g0305961	M11	NA	5	4	5	8	10	13	11	14	8	13
Sly11g0305971	M11	NA	28	27	31	34	46	34	29	35	38	46
Sly11g0305991	M1	NA	4	5	5	5	6	2	1	2	1	2
Sly11g0306011	M1	NA	6	5	5	5	6	2	2	1	1	3
Sly11g0306021	M1	NA	8	8	5	7	11	2	2	3	1	4
Sly11g0306031	M11	NA	1250	1161	1139	1020	819	1501	1572	1627	1090	946
Sly11g0306051	M12	NA	530	504	453	370	213	577	662	562	405	268
Sly11g0306061	M1	NA	5	4	8	6	3	2	3	3	5	3
Sly11g0306071	M19	NA	30	33	34	35	36	29	23	31	22	17
Sly11g0306081	M1	NA	14	16	17	15	16	10	12	10	11	10
Sly11g0306091	M19	NA	56	50	49	54	66	48	39	50	45	47
Sly11g0306101	M1	NA	3	3	3	4	2	3	3	2	3	2
Sly11g0306111	M12	NA	5	5	5	4	3	6	7	6	8	6
Sly11g0306121	M1	NA	63	62	61	79	85	58	56	58	79	83
Sly11g0306131	M11	NA	29	27	26	18	23	29	22	32	17	13
Sly11g0306141	M11	NA	1	2	2	2	1	2	1	2	1	1
Sly11g0306151	M19	NA	20	21	21	20	22	20	16	19	15	14
Sly11g0306181	M1	NA	2	2	4	1	1	1	1	1	0	1
Sly11g0306191	M2	NA	7	7	7	9	8	6	8	6	6	5
Sly11g0306201	M1	NA	36	34	29	20	11	25	19	20	8	3
Sly11g0306211	M1	NA	12	15	8	1	1	4	3	3	1	1
Sly11g0306221	M11	NA	58	54	61	37	32	56	58	61	62	74
Sly11g0306241	M11	NA	32	31	41	37	44	46	41	57	44	44
Sly11g0306261	M12	NA	47	42	33	1	1	257	201	178	1	1
Sly11g0306461	M3	NA	57	72	61	91	66	54	56	48	53	39
Sly11g0306471	M22	NA	1	1	1	2	2	2	1	2	1	2
Sly11g0306481	M12	NA	67	65	64	76	75	98	102	95	100	96
Sly11g0306491	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly11g0306501	M12	NA	24	25	37	119	120	144	160	197	344	277
Sly11g0306511	M11	NA	8	9	10	14	17	11	10	10	12	11
Sly11g0306521	M3	BSK3	115	120	96	74	74	89	102	81	86	95
Sly11g0306541	M11	NA	18	18	23	15	24	20	16	21	7	8
Sly11g0306561	M5	NA	58	65	46	41	49	48	54	39	34	50
Sly11g0306571	M1	NA	8	7	9	10	17	6	7	7	15	29
Sly11g0306621	M1	NA	91	81	85	61	51	73	73	65	28	20
Sly11g0306651	M5	NA	15	21	14	6	3	19	16	13	3	1
Sly11g0306661	M3	NA	22	29	19	7	3	23	23	14	4	2
Sly11g0306671	M1	NA	8	8	8	9	6	6	6	6	7	2
Sly11g0306711	M1	NA	50	45	46	71	89	17	15	12	40	90
Sly11g0306721	M1	NA	21	19	20	16	9	13	11	14	6	6
Sly11g0306731	M7	NA	30	33	33	40	51	30	34	31	51	62
Sly11g0306741	M3	NA	1	2	1	1	0	1	1	1	0	0
Sly11g0306761	M11	NA	68	64	73	84	94	74	70	83	104	122
Sly11g0306771	M3	NA	22	23	20	25	21	16	17	16	22	16
Sly11g0306781	M1	NA	13	14	12	14	10	8	8	8	8	6
Sly11g0306791	M12	NA	11	8	9	11	15	10	11	12	15	16
Sly11g0306801	M19	NA	24	25	27	28	27	27	21	27	19	18
Sly11g0306811	M11	NA	28	29	33	28	30	28	28	33	32	39
Sly11g0306821	M1	NA	2	3	2	1	1	1	2	1	1	1
Sly11g0306831	M12	NA	5	5	5	6	6	7	7	7	6	4
Sly11g0306841	M1	NA	19	19	18	15	12	16	15	18	12	9
Sly11g0306851	M21	NA	4	3	5	2	2	4	3	4	1	1
Sly11g0306871	M11	NA	9	9	11	21	25	13	12	14	15	14
Sly11g0306881	M18	NA	2	2	4	2	2	3	2	4	1	1
Sly11g0306891	M19	NA	26	25	27	17	15	30	21	30	13	11
Sly11g0306901	M1	NA	42	40	40	42	53	31	31	32	42	51
Sly11g0306911	M22	NA	6	1	5	1	0	46	1	38	0	1
Sly11g0306951	M1	NA	24	17	48	8	5	17	12	16	3	3
Sly11g0306961	M1	NA	2	2	3	3	4	1	1	1	1	1
Sly11g0306971	M1	NA	58	56	81	162	124	4	2	2	1	1
Sly11g0306991	M12	NA	1	1	1	1	1	1	1	1	0	1
Sly11g0307001	M22	NA	21	21	18	27	32	22	18	20	31	37
Sly11g0307061	M19	NA	21	23	23	15	14	18	16	18	17	17
Sly11g0307131	M11	NA	105	94	103	113	121	125	116	121	89	90
Sly11g0307141	M11	NA	4	3	5	3	7	7	6	5	3	4
Sly11g0307161	M12	NA	30	32	47	442	493	53	68	105	424	172
Sly11g0307181	M11	NA	374	352	400	291	138	429	443	514	437	208
Sly11g0307221	M1	NA	8	6	8	9	5	7	6	7	19	10
Sly11g0307231	M12	NA	75	69	74	159	90	91	96	88	266	106
Sly11g0307241	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0307251	M12	NA	18	18	17	17	19	22	22	22	26	27
Sly11g0307271	M3	NA	22	24	16	9	9	15	14	9	6	2
Sly11g0307281	M3	NA	111	107	91	76	62	61	69	53	70	54
Sly11g0307291	M11	NA	11	11	17	16	8	15	13	22	8	5
Sly11g0307301	M15	NA	53	52	48	59	69	50	55	56	65	73
Sly11g0307311	M12	NA	38	33	37	34	70	40	40	45	61	120
Sly11g0307341	M22	NA	1	1	1	1	1	1	0	1	1	0
Sly11g0307351	M3	NA	64	61	57	55	57	53	51	54	53	67
Sly11g0307361	M12	NA	13	12	12	18	22	12	15	16	26	23
Sly11g0307371	M2	NA	82	79	84	63	62	74	78	82	84	92
Sly11g0307381	M11	NA	12	8	11	1	0	14	10	13	1	1
Sly11g0307391	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly11g0307401	M3	NA	7	10	6	7	6	6	6	6	7	6
Sly11g0307411	M3	NA	8	12	6	8	7	8	9	6	6	9
Sly11g0307421	M3	NA	11	13	6	8	10	8	8	9	8	11
Sly11g0307431	M3	NA	8	15	8	8	8	8	9	6	9	13
Sly11g0307441	M3	NA	15	18	11	12	12	12	15	11	15	17
Sly11g0307451	M1	NA	4	5	6	7	7	1	1	2	1	2
Sly11g0307461	M3	NA	21	18	18	40	68	17	20	17	48	61
Sly11g0307491	M22	NA	1	0	1	0	0	4	0	2	0	0
Sly11g0307511	M11	NA	13	12	18	25	40	20	15	24	19	23
Sly11g0307521	M1	NA	46	46	44	34	40	23	23	21	28	30
Sly11g0307531	M1	NA	2	3	3	3	4	1	1	1	1	1
Sly11g0307551	M12	NA	40	41	41	38	38	44	50	47	53	56
Sly11g0307571	M18	XDH1	76	83	92	188	190	120	110	146	153	178
Sly11g0307581	M19	XDH1-like	22	22	22	18	17	21	20	20	25	19
Sly11g0307591	M1	NA	53	49	58	36	32	24	18	23	9	7
Sly11g0307601	M1	NA	21	19	25	26	39	17	16	21	28	34
Sly11g0307611	M12	NA	6	7	7	10	7	8	7	7	11	6
Sly11g0307621	M1	NA	29	27	29	23	24	24	24	25	28	24

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0254911	M1	NA	2	1	2	1	0	1	1	1	1	0
Sly04g0254921	M12	NA	77	77	98	93	42	140	152	147	24	4
Sly04g0254931	M11	NA	22	14	28	1	1	33	32	30	1	0
Sly04g0254941	M1	NA	18	14	12	5	6	4	5	5	1	0
Sly04g0254961	M1	NA	2	1	1	1	1	0	1	1	0	0
Sly04g0254981	M11	NA	31	31	32	22	16	32	33	38	23	14
Sly04g0254991	M12	NA	23	26	30	23	17	43	47	52	31	17
Sly04g0255001	M3	BKI1	6	9	8	6	2	6	7	6	2	1
Sly04g0255011	M9	NA	20	31	19	28	30	26	52	36	71	71
Sly04g0255031	M1	NA	24	22	29	32	21	22	23	24	24	14
Sly04g0255041	M3	PPR-like7	3	4	3	2	3	2	3	2	3	3
Sly04g0255051	M2	NA	12	14	18	21	16	12	15	14	18	12
Sly04g0255061	M11	NA	1	1	1	1	1	1	1	1	1	2
Sly04g0255071	M12	NA	117	113	127	207	277	162	181	189	231	266
Sly04g0255081	M12	NA	21	18	21	26	42	56	49	58	22	5
Sly04g0255091	M2	NA	136	129	124	150	146	113	132	122	166	189
Sly04g0255101	M3	NA	8	10	4	7	1	2	1	1	1	1
Sly04g0255111	M3	NA	5	5	3	5	1	2	1	1	1	0
Sly04g0255121	M3	NA	6	8	3	7	1	2	1	1	1	0
Sly04g0255131	M3	NA	1	1	1	1	0	1	1	0	1	1
Sly04g0255161	M1	NA	1	3	1	1	1	0	1	0	0	0
Sly04g0255181	M3	NA	66	61	56	69	69	55	61	63	73	69
Sly04g0255191	M19	NA	6	7	6	5	4	7	6	7	7	4
Sly04g0255201	M11	NA	5	5	5	8	4	5	5	6	5	2
Sly04g0255211	M3	NA	22	29	15	9	6	22	23	15	5	5
Sly04g0255221	M12	NA	1	1	0	1	1	3	1	1	1	1
Sly04g0255231	M3	NA	80	76	56	15	5	59	57	45	7	4
Sly04g0255241	M12	NA	64	55	57	41	63	70	71	70	65	81
Sly04g0255261	M21	NA	3	3	5	1	1	4	2	2	1	1
Sly04g0255271	M3	NA	16	20	16	46	131	16	15	6	34	84
Sly04g0255281	M3	NA	16	21	3	2	2	5	7	3	1	4
Sly04g0255291	M3	NA	3	3	1	0	0	1	1	1	1	0
Sly04g0255301	M2	NA	28	32	29	33	32	19	22	19	30	32
Sly04g0255311	M11	NA	10	10	11	13	14	12	10	11	10	8
Sly04g0255321	M3	NA	13	23	12	7	11	5	6	3	2	3
Sly04g0255331	M3	NA	48	48	39	33	32	35	36	33	42	39
Sly04g0255341	M3	NA	135	173	90	50	49	36	50	15	11	14
Sly04g0255351	M3	NA	274	297	203	97	138	123	163	72	75	169
Sly04g0255361	M3	NA	98	95	65	44	41	40	54	37	39	36
Sly04g0255371	M3	NA	2	2	1	0	1	1	1	1	0	1
Sly04g0255381	M3	NA	2	3	1	0	1	1	1	1	1	1
Sly04g0255391	M3	NA	46	59	14	3	8	5	14	3	1	2
Sly04g0255401	M1	NA	5	6	4	5	3	1	1	1	1	0
Sly04g0255431	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0255441	M1	NA	2	1	2	73	211	1	1	1	1	8
Sly04g0255451	M12	NA	11	10	13	16	14	14	17	16	18	17
Sly04g0255461	M10	NA	126	156	114	145	168	160	211	107	124	152
Sly04g0255471	M1	NA	10	7	23	1	1	2	1	1	1	0
Sly04g0255481	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly04g0255491	M12	KO	4	3	4	1	1	40	28	29	2	1
Sly04g0255501	M11	NA	15	15	19	20	20	19	18	20	19	19
Sly04g0255551	M13	NA	88	89	108	66	90	99	96	100	44	29
Sly04g0255561	M12	NA	3	3	3	8	8	12	17	17	17	8
Sly04g0255571	M12	NA	1	1	1	1	1	2	3	2	1	1
Sly04g0255581	M1	NA	3	3	7	6	6	3	3	3	1	1
Sly04g0255591	M12	NA	1	1	1	1	0	2	2	2	1	0
Sly04g0255621	M12	NA	1	1	1	1	1	5	4	6	0	0
Sly04g0255641	M3	NA	7	8	4	2	1	3	3	2	1	1
Sly04g0255651	M1	NA	87	86	77	46	38	72	70	58	26	23
Sly04g0255661	M3	AOS-like3	140	249	69	2	3	80	85	11	3	3
Sly04g0255671	M3	NA	13	15	10	12	21	10	12	8	21	23
Sly04g0255681	M3	NA	21	22	14	14	24	19	21	14	20	26
Sly04g0255691	M3	NA	21	38	31	1	6	18	19	4	3	8
Sly04g0255701	M19	NA	17	17	15	14	10	16	15	16	14	10
Sly04g0255711	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0255721	M11	NA	56	54	56	164	327	83	87	102	220	367
Sly04g0255731	M9	NA	20	22	18	18	18	22	26	20	18	16
Sly04g0255741	M6	NA	1	3	3	1	0	3	3	1	1	0
Sly04g0255751	M1	NA	4	4	4	2	1	1	1	1	1	1
Sly04g0255761	M2	NA	22	30	22	11	13	15	20	13	9	17
Sly04g0255771	M18	PPR-like17	10	12	11	9	9	12	10	11	12	10
Sly04g0255781	M10	NA	19	20	8	1	1	25	19	15	1	1
Sly04g0255801	M5	NA	12	12	8	5	4	10	15	9	4	5
Sly04g0255821	M11	NA	58	53	83	41	25	94	75	106	6	5
Sly04g0255831	M3	NA	1	1	1	0	0	1	1	1	1	1
Sly04g0255841	M12	NA	43	41	39	36	35	45	43	43	61	55
Sly04g0255851	M12	NA	16	15	21	18	12	19	20	22	21	12
Sly04g0255861	M3	NA	146	150	105	46	23	77	95	63	31	25
Sly04g0255871	M12	NA	7	8	7	8	14	11	11	12	13	15
Sly04g0255891	M1	gggps2	9	8	9	60	67	6	6	8	60	69
Sly04g0255901	M12	NA	417	398	493	563	557	497	528	614	645	799
Sly04g0255911	M3	SIBES1 (BZR1)	27	33	27	23	20	24	31	25	33	34
Sly04g0255921	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly04g0255931	M12	NA	25	22	23	25	35	23	24	28	36	48
Sly04g0255941	M1	NA	18	16	15	27	23	3	2	2	1	1
Sly04g0255951	M12	NA	27	29	34	49	52	61	61	67	69	76
Sly04g0255961	M12	NA	9	12	11	8	5	17	19	17	8	6
Sly04g0255971	M11	NA	1	1	1	1	1	1	1	1	2	1
Sly04g0255981	M8	NA	22	25	19	23	18	22	27	18	22	20
Sly04g0255991	M12	NA	9	8	8	9	13	13	11	13	14	17
Sly04g0256001	M12	NA	2	1	1	2	2	1	1	2	1	2
Sly04g0256011	M2	NA	38	35	37	32	21	35	38	34	18	15
Sly04g0256021	M12	NA	1	1	1	1	1	3	2	2	1	1
Sly04g0256031	M11	NA	25	23	26	34	32	27	25	32	31	34
Sly04g0256041	M2	NA	5	6	5	4	6	5	5	4	5	5
Sly04g0256051	M19	NA	4	4	4	4	4	4	3	4	3	3
Sly04g0256061	M3	NA	13	19	11	1	1	6	5	2	1	1
Sly04g0256071	M11	NA	22	21	29	30	38	40	33	46	39	51
Sly04g0256081	M1	NA	34	38	40	50	58	32	34	38	72	65
Sly04g0256091	M1	NA	15	16	22	25	13	5	5	6	9	6
Sly04g0256101	M3	NA	30	27	28	28	23	22	22	18	13	13
Sly04g0256111	M1	NA	10	13	14	11	8	9	8	7	6	4
Sly04g0256121	M3	NA	54	57	46	34	27	36	38	35	27	21
Sly04g0256131	M3	NA	10	9	7	3	3	5	6	4	2	2
Sly04g0256151	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0256171	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly04g0256181	M3	NA	88	100	63	34	51	35	42	31	19	37
Sly04g0256201	M18	NA	53	59	63	97	91	63	60	75	173	80
Sly04g0256211	M12	NA	1	1	1	31	25	1	3	5	196	59
Sly04g0256221	M12	NA	1	1	1	7	12	2	6	8	37	21
Sly04g0256231	M12	NA	1	1	1	5	13	2	3	9	31	19
Sly04g0256251	M1	NA	11	9	9	16	15	4	6	5	8	10
Sly04g0256271	M22	NA	1	1	1	0	0	1	0	1	0	0
Sly04g0256281	M12	NA	1402	1381	1457	1602	2383	1891	1845	2058	3758	5622
Sly04g0256301	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly04g0256311	M3	NA	201	177	130	30	32	151	145	88	21	16
Sly04g0256321	M1	NA	39	37	36	22	43	31	29	32	35	45
Sly04g0256331	M9	NA	23	33	22	6	5	48	67	42	35	31
Sly04g0256361	M1	NA	60	59	52	65	89	46	46	43	74	83
Sly04g0256371	M1	NA	29	28	30	21	25	25	20	27	26	28
Sly04g0256381	M1	NA	52	52	57	53	48	25	24	23	9	17
Sly04g0256391	M1	NA	33	34	33	20	19	20	23	21	18	15
Sly04g0256401	M11	NA	22	22	36	67	73	48	40	67	140	148
Sly04g0256451	M1	NA	1	1	1	1	0	0	0	0	0	0
Sly04g0256461	M12	NA	11	10	11	29	49	19	18	19	22	24
Sly04g0256481	M12	NA	40	44	41	54	61	46	49	47	54	63
Sly04g0256491	M12	NA	25	22	27	46	46	99	78	117	200	204
Sly04g0256501	M1	NA	13	12	10	3	2	1	1	1	1	0
Sly04g0256521	M12	NA	14	14	14	13	17	16	16	17	19	18
Sly04g0256541	M23	NA	1	1	1	0	0	1	1	1	0	0
Sly04g0256601	M1	NA	2	1	1	1	1	1	1	1	0	0
Sly04g0256621	M1	RGAT1	40	36	46	21	29	9	5	11	6	10
Sly04g0256631	M3	NA	70	92	64	64	37	28	23	28	98	59
Sly04g0256651	M1	NA	56	55	51	30	26	37	40	35	16	7

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0307681	M3	NA	21	21	18	13	10	17	18	14	14	13
Sly11g0307691	M1	NA	4	3	3	1	1	1	1	1	1	0
Sly11g0307701	M3	NA	664	557	361	257	136	177	162	62	113	105
Sly11g0307711	M11	NA	36	37	41	52	48	42	39	47	56	62
Sly11g0307721	M12	NA	3	5	3	3	8	7	10	5	5	21
Sly11g0307731	M12	NA	7	7	7	6	5	8	9	8	9	8
Sly11g0307741	M4	NA	20	16	26	253	452	40	24	31	134	434
Sly11g0307751	M11	NA	47	40	53	85	143	74	60	87	100	150
Sly11g0307761	M11	NA	2	2	4	3	7	2	3	4	3	5
Sly11g0307771	M12	NA	26	17	23	7	9	51	42	44	4	4
Sly11g0307801	M1	NA	9	8	8	16	21	3	1	3	2	1
Sly11g0307811	M11	NA	7	5	5	2	5	11	10	11	5	6
Sly11g0307831	M12	NA	4	4	5	6	5	6	8	8	6	5
Sly11g0307841	M22	NA	5	3	4	1	1	64	8	23	1	1
Sly11g0307851	M3	NA	15	16	12	12	13	12	12	11	11	14
Sly11g0307861	M12	SIXTH6	9	14	4	1	1	11	13	10	1	0
Sly11g0307871	M1	NA	68	62	66	31	27	51	50	49	19	21
Sly11g0307881	M1	NA	112	104	94	75	64	52	63	55	40	50
Sly11g0307891	M18	NA	5	5	6	6	10	8	7	9	9	12
Sly11g0307901	M12	NA	7	7	7	6	5	12	12	12	10	8
Sly11g0307921	M12	NA	60	63	99	55	29	125	112	154	30	19
Sly11g0307931	M14	NA	18	24	32	12	2	15	17	27	2	1
Sly11g0307941	M1	NA	7	7	8	4	6	6	7	7	6	6
Sly11g0307961	M12	NA	79	96	89	148	179	184	278	284	247	196
Sly11g0307971	M11	NA	31	31	29	25	26	32	31	33	27	17
Sly11g0307981	M11	NA	8	7	11	10	6	14	11	14	16	8
Sly11g0307991	M12	SISOD3	68	64	75	108	82	137	149	150	122	97
Sly11g0308001	M18	NA	2	2	2	1	1	2	1	2	1	1
Sly11g0308011	M11	NA	28	32	34	58	72	70	53	94	74	93
Sly11g0308021	M1	NA	1	2	2	1	1	1	1	1	0	1
Sly11g0308031	M11	NA	30	23	25	47	82	43	40	35	32	82
Sly11g0308041	M12	NA	55	54	65	259	300	60	67	89	302	320
Sly11g0308051	M12	NA	24	25	29	29	33	27	30	35	31	37
Sly11g0308061	M3	NA	11	11	11	15	21	10	9	10	18	23
Sly11g0308071	M9	NA	61	63	61	92	46	61	68	60	32	16
Sly11g0308081	M19	NA	33	33	33	35	33	37	27	37	34	30
Sly11g0308091	M1	NA	1	1	1	0	0	0	1	1	0	0
Sly11g0308101	M3	NA	33	33	24	39	44	21	23	15	25	34
Sly11g0308111	M11	NA	4	5	9	18	12	16	14	23	8	28
Sly11g0308121	M22	NA	1	0	1	1	1	2	1	2	0	1
Sly11g0308141	M12	NA	22	24	22	24	22	25	23	22	21	21
Sly11g0308151	M18	NA	22	24	23	25	29	23	22	26	31	32
Sly11g0308171	M12	NA	1	1	1	0	0	2	1	1	1	0
Sly11g0308181	M1	NA	12	8	4	1	1	1	0	0	0	0
Sly11g0308201	M2	NA	17	16	14	16	19	14	16	16	26	31
Sly11g0308211	M9	NA	41	57	41	220	221	114	157	112	709	501
Sly11g0308221	M1	NA	53	52	56	30	19	22	22	23	23	15
Sly11g0308241	M1	NA	13	14	14	13	14	10	9	9	9	14
Sly11g0308271	M11	NA	25	23	30	23	22	43	35	39	12	6
Sly11g0308281	M22	NA	14	9	13	16	12	15	10	12	1	1
Sly11g0308291	M11	NA	9	8	8	11	11	14	11	11	3	4
Sly11g0308301	M11	NA	2	3	2	1	1	3	3	2	1	1
Sly11g0308321	M22	NA	3	1	2	0	0	7	1	5	1	1
Sly11g0308331	M3	NA	114	105	86	24	8	50	72	37	10	4
Sly11g0308341	M12	NA	3	3	3	4	4	4	4	5	4	3
Sly11g0308351	M12	NA	18	17	18	33	36	19	19	24	34	36
Sly11g0308361	M3	NA	29	32	23	17	15	24	26	18	12	12
Sly11g0308371	M3	NA	12	13	10	10	11	9	9	8	8	7
Sly11g0308381	M1	NA	7	7	7	4	3	6	6	5	4	2
Sly11g0308391	M9	NA	1	1	1	1	1	5	5	2	1	1
Sly11g0308401	M11	NA	1	2	2	3	3	3	3	4	3	1
Sly11g0308411	M1	NA	124	101	152	188	80	37	58	111	362	129
Sly11g0308441	M12	NA	46	39	53	81	147	70	65	77	194	313
Sly11g0308451	M1	SlHDT3	665	610	595	202	89	409	428	386	223	114
Sly11g0308461	M3	NA	40	47	22	21	9	14	12	14	12	10
Sly11g0308471	M1	NA	282	265	154	113	15	48	49	31	45	15
Sly11g0308481	M18	NA	39	36	42	39	36	44	38	50	34	31
Sly11g0308511	M5	NA	17	24	11	395	443	38	39	5	9	9
Sly11g0308521	M12	NA	8	8	10	12	6	25	21	27	5	5
Sly11g0308531	M12	NA	32	33	32	26	23	37	40	42	29	24
Sly11g0308541	M1	NA	4	3	3	5	4	3	3	3	5	4
Sly11g0308551	M9	NA	20	30	27	75	36	23	54	39	139	88
Sly11g0308561	M1	NA	6	8	6	46	6	1	2	5	30	5
Sly11g0308571	M1	NA	5	2	2	1	1	3	1	1	1	0
Sly11g0308581	M12	SlIPT5	6	6	8	6	7	10	10	11	9	10
Sly11g0308601	M1	NA	35	37	32	34	26	27	24	27	26	25
Sly11g0308611	M3	NA	1	2	1	0	1	1	1	0	1	0
Sly11g0308621	M11	NA	39	35	44	43	64	51	45	63	67	90
Sly11g0308641	M12	SlHDA4	24	23	30	28	33	29	31	32	36	36
Sly11g0308651	M1	NA	3	3	4	2	3	2	2	2	3	2
Sly11g0308661	M12	NA	23	23	23	30	29	28	26	23	23	22
Sly11g0308671	M11	NA	27	25	27	86	85	32	34	44	99	133
Sly11g0308681	M1	NA	9	10	12	20	44	8	8	9	38	51
Sly11g0308691	M1	NA	15	16	18	34	15	11	14	12	16	6
Sly11g0308701	M1	CYP71	32	34	32	27	26	29	29	33	27	30
Sly11g0308711	M1	NA	629	563	593	388	269	469	492	479	434	339
Sly11g0308721	M14	NA	8	8	12	6	6	9	7	11	2	1
Sly11g0308731	M1	NA	6	7	7	8	10	5	5	5	7	7
Sly11g0308741	M12	NA	23	21	32	188	406	44	44	55	276	518
Sly11g0308781	M1	NA	5	7	5	10	6	1	1	1	1	1
Sly11g0308791	M1	NA	3	7	4	5	1	1	1	1	1	3
Sly11g0308801	M11	HIRA	24	23	25	40	38	23	22	26	41	37
Sly11g0308811	M1	NA	3	4	4	3	3	3	3	3	3	2
Sly11g0308821	M2	NA	65	68	60	65	48	50	56	45	44	47
Sly11g0308831	M3	NA	58	62	49	61	56	47	60	42	55	65
Sly11g0308841	M23	NA	4	2	1	1	1	10	4	2	1	1
Sly11g0308851	M11	NA	77	78	103	155	117	163	167	201	185	181
Sly11g0308871	M1	NA	79	78	66	59	61	38	43	36	67	86
Sly11g0308891	M1	NA	4	5	5	4	3	4	4	4	5	3
Sly11g0309001	M19	NA	3	2	4	1	1	3	2	3	1	1
Sly11g0309011	M12	NA	1	1	1	1	1	2	2	2	0	1
Sly11g0309021	M3	NA	3	6	1	1	2	1	1	0	1	1
Sly11g0309041	M3	NA	127	125	103	155	125	97	105	93	155	125
Sly11g0309061	M1	NA	319	300	304	212	177	221	222	218	217	169
Sly11g0309081	M2	NA	106	128	90	92	78	80	125	102	135	145
Sly11g0309091	M6	NA	121	185	182	84	146	160	281	98	106	207
Sly11g0309101	M12	NA	18	19	15	19	19	21	21	24	31	46
Sly11g0309111	M9	NA	23	28	25	32	38	43	46	36	60	96
Sly11g0309121	M3	NA	8	8	7	7	6	6	6	6	6	4
Sly11g0309131	M1	NA	21	18	22	16	28	16	18	20	23	24
Sly11g0309141	M11	NA	45	37	45	60	66	51	44	67	68	113
Sly11g0309151	M11	NA	29	29	34	41	28	40	39	39	23	21
Sly11g0309161	M11	NA	65	59	65	85	97	78	80	85	92	70
Sly11g0309171	M16	NA	87	86	59	28	19	84	70	73	29	19
Sly11g0309181	M23	NA	8	9	8	6	5	9	8	8	2	2
Sly11g0309191	M11	NA	72	66	79	109	83	93	90	101	103	99
Sly11g0309201	M1	NA	40	36	33	22	19	34	33	35	10	24
Sly11g0309261	M2	NA	34	39	32	25	24	23	31	23	33	34
Sly11g0309271	M1	NA	2	3	2	6	6	1	1	0	0	1
Sly11g0309281	M11	NA	27	17	9	1	1	89	26	58	1	0
Sly11g0309291	M12	NA	59	60	58	60	55	72	69	66	50	55
Sly11g0309301	M2	NA	25	26	22	30	33	19	21	20	38	36
Sly11g0309321	M7	NA	45	47	43	44	56	47	46	44	52	56
Sly11g0309331	M1	NA	77	75	75	75	51	39	35	38	49	38
Sly11g0309341	M13	NA	8	7	11	19	13	11	10	14	12	5
Sly11g0309351	M1	NA	22	23	22	12	9	17	17	17	14	13
Sly11g0309361	M3	NA	41	130	55	5	27	30	52	12	1	15
Sly11g0309371	M6	NA	44	106	47	5	23	27	43	13	1	21
Sly11g0309381	M1	NA	2	2	3	3	1	1	1	1	1	0
Sly11g0309411	M11	NIT-like	31	25	36	81	155	45	35	50	88	234
Sly11g0309421	M11	MBD5	45	38	39	39	36	40	40

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0256661	M11	NA	78	68	90	84	49	123	95	145	63	47
Sly04g0256671	M15	NA	95	84	79	102	147	90	93	93	128	162
Sly04g0256681	M22	NA	2	2	1	1	1	3	2	2	1	1
Sly04g0256691	M12	NA	38	35	36	34	55	39	40	40	50	56
Sly04g0256711	M11	NA	56	48	60	62	74	86	79	112	65	80
Sly04g0256721	M1	NA	9	8	9	5	3	2	2	2	1	1
Sly04g0256751	M12	NA	20	18	19	16	17	22	23	21	24	23
Sly04g0256761	M3	NA	5	4	4	5	21	3	3	2	7	15
Sly04g0256771	M3	NA	1	1	1	1	2	1	1	1	1	1
Sly04g0256781	M14	NA	156	127	175	147	381	133	119	153	161	435
Sly04g0256791	M1	NA	1	1	1	1	1	1	0	1	0	0
Sly04g0256801	M1	NA	1	1	1	1	1	0	0	0	0	0
Sly04g0256811	M1	NA	53	49	57	47	33	29	31	28	17	15
Sly04g0256821	M9	NA	133	123	103	195	133	120	138	127	200	133
Sly04g0256831	M1	NA	2	3	3	8	1	1	1	1	0	0
Sly04g0256851	M11	NA	24	23	25	34	57	30	27	37	41	54
Sly04g0256871	M22	NA	3	3	2	3	2	4	2	4	3	3
Sly04g0256881	M12	NA	10	10	12	17	18	13	14	14	23	27
Sly04g0256891	M1	NA	51	47	48	68	73	25	34	28	58	52
Sly04g0256901	M3	SICKX4	45	31	10	1	1	23	9	14	1	1
Sly04g0256911	M11	NA	5	5	8	6	4	14	11	19	6	3
Sly04g0256931	M3	NA	687	677	404	239	327	358	489	347	322	473
Sly04g0256941	M11	NA	40	33	48	81	127	57	53	71	103	114
Sly04g0256951	M1	NA	26	24	20	22	12	3	2	2	1	1
Sly04g0256971	M12	NA	11	9	8	6	5	12	12	10	8	6
Sly04g0256981	M11	NA	3	4	4	6	6	5	4	5	6	4
Sly04g0256991	M12	NA	2	2	1	1	0	3	3	4	1	0
Sly04g0257001	M12	NA	2	1	2	1	0	19	14	14	1	0
Sly04g0257011	M11	NA	30	28	28	30	31	33	32	33	34	39
Sly04g0257031	M1	NA	3	2	3	1	0	1	1	1	0	0
Sly04g0257041	M23	NA	2	2	1	1	1	2	1	2	1	1
Sly04g0257051	M12	NA	11	10	9	11	15	10	13	12	13	16
Sly04g0257061	M14	NA	703	637	1055	1680	2400	491	437	704	500	551
Sly04g0257081	M3	NA	104	105	92	98	84	86	93	70	62	65
Sly04g0257101	M1	NA	67	66	84	111	87	49	47	54	47	58
Sly04g0257121	M2	NA	15	20	18	4	2	14	23	12	2	1
Sly04g0257131	M3	NA	61	64	48	32	32	38	43	31	34	36
Sly04g0257161	M11	NA	22	18	24	27	26	26	21	28	24	27
Sly04g0257171	M11	NA	1	2	2	2	2	2	2	2	2	2
Sly04g0257181	M13	NA	21	18	27	33	72	27	21	31	34	49
Sly04g0257201	M12	NA	336	292	281	419	371	428	450	431	387	412
Sly04g0257211	M19	SlHDMA6	14	14	14	15	15	13	11	13	12	11
Sly04g0257261	M1	NA	101	93	78	66	55	46	45	40	61	65
Sly04g0257271	M11	NA	20	19	20	12	4	20	21	24	8	3
Sly04g0257281	M11	NA	60	63	69	66	67	70	63	77	62	58
Sly04g0257301	M12	NA	28	38	36	107	51	67	72	111	184	65
Sly04g0257311	M1	NA	45	49	39	27	22	23	27	19	26	20
Sly04g0257321	M11	NA	35	34	54	42	49	55	46	61	28	37
Sly04g0257331	M1	NA	25	21	25	32	24	17	19	14	30	18
Sly04g0257341	M11	NA	31	33	41	57	58	54	48	59	24	19
Sly04g0257351	M12	SlARF5	6	10	16	16	17	59	96	94	66	33
Sly04g0257361	M1	SAUR51	10	19	51	89	19	1	2	2	2	1
Sly04g0257371	M22	NA	7	6	13	10	6	11	8	7	1	1
Sly04g0257381	M1	SAUR52	8	8	16	27	9	1	1	1	1	1
Sly04g0257391	M19	NA	36	38	37	41	35	34	29	35	26	22
Sly04g0257401	M3	SlLOG3	25	24	9	6	5	11	23	6	2	4
Sly04g0257411	M1	NA	46	34	55	25	18	30	21	27	1	1
Sly04g0257421	M1	NA	19	17	19	10	11	14	15	13	15	14
Sly04g0257441	M11	NA	19	18	22	28	26	24	22	31	33	21
Sly04g0257451	M11	NA	63	45	55	41	65	82	77	84	58	103
Sly04g0257461	M12	HVA22-like2	28	25	29	39	39	27	32	34	34	37
Sly04g0257471	M3	E2FC	5	6	5	3	5	3	5	3	3	7
Sly04g0257481	M3	NA	22	23	19	17	17	14	17	14	15	17
Sly04g0257491	M1	NA	8	6	9	5	3	4	1	3	1	3
Sly04g0257521	M9	plastidic hexokinase	27	27	22	38	40	43	46	36	40	28
Sly04g0257531	M2	NA	64	64	59	69	65	53	69	55	71	68
Sly04g0257541	M12	NA	12	12	14	61	79	23	22	23	51	103
Sly04g0257551	M13	NA	27	28	28	35	36	25	27	31	31	30
Sly04g0257561	M11	NA	363	322	338	168	164	384	355	447	280	250
Sly04g0257571	M13	NA	7	6	8	6	7	7	6	7	8	10
Sly04g0257581	M1	NA	15	15	14	15	10	1	1	1	1	1
Sly04g0257591	M1	NA	16	14	15	10	13	11	12	14	19	17
Sly04g0257621	M2	NA	9	9	12	4	5	8	10	10	8	9
Sly04g0257641	M11	NA	201	169	282	289	164	275	302	305	132	76
Sly04g0257651	M12	NA	24	23	25	24	41	31	33	32	37	58
Sly04g0257671	M3	NA	20	28	17	9	7	11	10	8	3	2
Sly04g0257681	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly04g0257721	M12	NA	59	49	46	27	19	81	107	106	31	34
Sly04g0257731	M11	NA	11	10	10	21	28	16	15	19	24	24
Sly04g0257741	M3	NA	49	54	28	9	10	18	21	14	6	13
Sly04g0257751	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly04g0257761	M3	NA	528	537	367	383	201	394	442	226	107	88
Sly04g0257771	M3	NA	57	64	50	36	37	34	36	30	38	36
Sly04g0257781	M1	NA	4	5	5	13	9	1	1	1	1	1
Sly04g0257791	M17	NA	32	29	31	36	46	30	27	35	39	60
Sly04g0257801	M4	NA	2	2	1	1	0	3	2	2	0	0
Sly04g0257811	M5	NA	193	252	102	78	122	162	194	82	92	146
Sly04g0257821	M2	NA	90	99	74	84	141	56	73	48	49	111
Sly04g0257831	M12	NA	118	114	112	157	179	128	130	135	185	216
Sly04g0257841	M1	NA	28	30	68	38	35	1	1	0	1	0
Sly04g0257851	M1	NA	51	39	59	12	6	1	1	1	0	0
Sly04g0257871	M1	NA	3	2	2	1	0	1	0	0	0	0
Sly04g0257891	M12	NA	2	2	1	0	0	7	4	5	0	0
Sly04g0257911	M3	NA	65	69	56	48	49	43	47	38	56	46
Sly04g0257931	M12	NA	1	1	1	1	3	1	1	1	1	2
Sly04g0257941	M11	NA	14	9	13	8	11	15	15	19	16	19
Sly04g0257961	M3	NA	6	7	4	0	1	5	5	3	1	1
Sly04g0257971	M1	NA	333	334	339	369	481	223	191	238	612	995
Sly04g0257981	M12	NA	12	12	17	31	326	57	61	89	398	1108
Sly04g0257991	M3	NA	236	243	271	267	567	120	162	152	355	645
Sly04g0258001	M12	NA	148	140	97	16	15	130	156	172	66	34
Sly04g0258011	M12	NA	17	17	13	12	10	19	20	20	19	19
Sly04g0258021	M2	NA	24	22	20	25	34	21	19	25	26	38
Sly04g0258031	M12	NA	12	12	12	9	10	12	11	14	15	14
Sly04g0258041	M2	NA	11	10	9	9	8	9	10	8	11	11
Sly04g0258071	M2	NA	30	43	24	2	5	13	20	9	5	16
Sly04g0258081	M1	NA	109	95	116	97	142	66	79	78	108	84
Sly04g0258091	M3	NA	10	10	8	6	5	8	9	7	8	8
Sly04g0258101	M12	NA	2	1	2	5	6	3	2	3	1	1
Sly04g0258111	M12	NA	1	1	1	1	1	2	2	1	0	0
Sly04g0258121	M12	NA	1	2	1	1	1	3	3	1	1	1
Sly04g0258131	M11	NA	34	26	39	40	71	122	111	159	68	82
Sly04g0258141	M12	NA	24	23	26	45	132	38	46	53	106	259
Sly04g0258151	M3	NA	68	88	27	10	4	40	39	5	2	1
Sly04g0258161	M7	NA	10	14	8	4	2	12	15	10	2	1
Sly04g0258171	M11	NA	253	177	431	333	157	796	722	1113	475	437
Sly04g0258181	M1	NA	20	17	23	9	9	15	12	16	8	14
Sly04g0258191	M3	NA	41	38	33	22	18	28	28	27	19	18
Sly04g0258221	M12	AMY2	27	29	26	40	44	40	45	47	98	74
Sly04g0258241	M1	NA	1	1	1	1	1	1	0	1	0	0
Sly04g0258251	M12	NA	2	3	2	2	1	3	3	3	1	1
Sly04g0258261	M22	NA	3	4	4	18	43	8	3	5	17	27
Sly04g0258271	M1	NA	28	28	28	21	15	18	17	19	20	9
Sly04g0258281	M1	NA	16	17	17	11	9	11	11	10	10	4
Sly04g0258291	M1	NA	12	13	13	13	8	7	7	8	8	2
Sly04g0258301	M3	NA	173	197	74	4	3	64	110	32	2	9
Sly04g0258311	M1	NA	18	16	15	15	14	12	12	14	15	16
Sly04g0258321	M19	NA	82	79	78	70	87	82	74	86	95	121
Sly04g0258371	M3	NA	3314	3535	1970	1356	2331	2344	4275	1931	1858	2803
Sly04g0258381	M12	NA	65	47	65	43	40	118	112	144	65	49
Sly04g0258391	M5	NA	15	11	7	5	9	12	13	8	5	3
Sly04g0258411	M15	NA	98	71	74	148	164	102	93	116	162	189
Sly04g0258431	M11	NA	42	37	50	124	203	96	83	112	110	142
Sly04g0258441	M2	BSK1	103	108	94	103	102	84	97	81	98	93

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0309461	M1	NA	8	8	15	8	3	2	3	5	1	0
Sly11g0309471	M3	NA	74	111	39	49	33	51	86	35	92	82
Sly11g0309481	M23	NA	2	2	1	0	1	4	2	2	1	1
Sly11g0309491	M12	NA	22	24	23	45	68	24	26	30	81	106
Sly11g0309501	M3	E2FA-like2	18	16	13	10	9	17	16	14	14	9
Sly11g0309511	M11	NA	31	30	30	28	35	35	36	40	47	57
Sly11g0309521	M11	NA	133	114	126	181	242	246	232	270	269	321
Sly11g0309531	M14	NA	84	73	91	95	86	81	71	78	55	47
Sly11g0309541	M11	NA	35	34	45	62	79	51	46	64	86	128
Sly11g0309551	M11	NA	2	2	2	3	4	3	3	3	3	4
Sly11g0309571	M1	NA	7	7	8	5	6	4	4	5	4	6
Sly11g0309591	M3	NA	17	18	15	14	12	15	15	13	10	7
Sly11g0309601	M6	NA	9	24	17	1	1	11	9	5	1	3
Sly11g0309611	M1	NA	461	450	504	205	120	296	358	293	295	213
Sly11g0309621	M1	NA	88	64	71	20	10	42	33	51	8	5
Sly11g0309641	M1	NA	29	28	20	22	15	11	14	10	19	15
Sly11g0309651	M2	NA	41	42	43	31	31	30	37	33	43	36
Sly11g0309661	M11	NA	130	127	140	145	166	141	132	164	210	227
Sly11g0309671	M1	NA	49	45	38	20	10	18	20	15	7	2
Sly11g0309681	M1	NA	2	3	2	1	1	1	0	1	1	0
Sly11g0309701	M1	NA	82	76	85	63	34	77	79	72	49	27
Sly11g0309711	M11	NA	81	73	100	77	64	95	82	95	50	39
Sly11g0309731	M3	NA	16	26	5	1	1	4	6	1	1	0
Sly11g0309741	M11	NA	36	34	40	47	55	44	43	48	65	62
Sly11g0309751	M1	NA	1307	1261	1340	676	454	938	785	867	486	418
Sly11g0309781	M2	NA	312	306	285	219	156	196	271	182	179	153
Sly11g0309801	M2	NA	118	103	88	73	60	66	91	61	72	65
Sly11g0309821	M1	NA	5	6	5	5	6	5	5	5	7	9
Sly11g0309831	M3	NA	5	6	5	5	7	4	6	5	5	6
Sly11g0309841	M4	NA	6	5	6	10	17	5	6	7	18	22
Sly11g0309851	M12	NA	5	5	6	12	19	5	6	7	20	39
Sly11g0309861	M11	NA	118	109	115	174	222	108	119	124	200	242
Sly11g0309871	M18	NA	104	105	109	121	137	112	97	116	141	147
Sly11g0309881	M13	NA	20	17	24	27	41	21	22	25	24	27
Sly11g0309891	M11	NA	22	20	22	4	4	22	22	22	3	2
Sly11g0309901	M11	SlARF4	77	54	81	27	19	205	161	169	10	2
Sly11g0309951	M11	NA	5	5	7	5	5	6	5	8	3	2
Sly11g0309961	M22	NA	1	1	1	0	0	2	1	1	1	0
Sly11g0309981	M11	NA	9	8	9	12	15	9	10	10	10	11
Sly11g0309991	M1	NA	48	55	55	49	76	29	14	24	14	19
Sly11g0310001	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0310011	M13	NA	35	27	28	39	52	27	28	29	40	51
Sly11g0310021	M3	NA	74	74	55	67	78	51	59	40	75	62
Sly11g0310031	M22	NA	34	32	34	62	65	35	31	36	38	38
Sly11g0310041	M1	NA	543	499	367	165	112	144	161	139	103	68
Sly11g0310051	M1	NA	53	51	51	35	40	38	35	40	42	46
Sly11g0310061	M1	NA	36	43	45	39	25	11	8	15	49	55
Sly11g0310071	M3	NA	34	39	31	22	35	24	24	21	22	40
Sly11g0310081	M19	NA	28	31	31	41	57	27	27	31	48	85
Sly11g0310091	M14	NA	137	128	134	198	379	136	121	136	165	257
Sly11g0310101	M22	NA	2	2	1	2	1	1	1	2	0	1
Sly11g0310111	M1	NA	94	96	95	86	72	84	81	82	51	53
Sly11g0310121	M11	NA	39	34	38	63	70	38	39	48	82	84
Sly11g0310131	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0310141	M11	NA	525	459	784	282	503	930	752	1039	489	1700
Sly11g0310151	M1	NA	183	170	185	178	157	119	128	128	137	108
Sly11g0310161	M1	NA	145	113	197	80	52	19	14	29	13	30
Sly11g0310171	M1	NA	15	18	13	6	3	5	5	4	1	1
Sly11g0310181	M1	NA	21	18	23	13	17	17	15	17	12	13
Sly11g0310191	M12	NA	63	55	56	55	51	62	60	66	54	60
Sly11g0310201	M1	NA	82	87	84	96	102	70	66	68	83	94
Sly11g0310211	M11	SlARF10A	19	20	34	43	31	25	18	25	17	21
Sly11g0310221	M11	NA	20	19	22	14	15	24	23	27	17	20
Sly11g0310231	M12	NA	20	20	23	27	25	25	23	28	31	28
Sly11g0310241	M19	NA	32	31	39	39	51	31	23	32	29	24
Sly11g0310251	M22	NA	3	1	2	0	0	12	3	11	0	0
Sly11g0310271	M3	NA	17	16	14	15	17	16	14	13	10	12
Sly11g0310281	M22	NA	1	1	1	0	0	1	1	2	0	0
Sly11g0310291	M1	SlLOG1	10	7	7	1	2	2	2	3	1	1
Sly11g0310311	M1	NA	4	4	5	4	7	2	2	3	2	4
Sly11g0310321	M21	NA	27	17	38	74	29	25	10	26	1	1
Sly11g0310331	M1	NA	10	11	12	4	5	5	2	4	1	1
Sly11g0310341	M22	NA	10	8	9	8	10	10	9	9	10	13
Sly11g0310351	M19	NA	13	15	15	12	12	13	11	13	10	11
Sly11g0310361	M1	NA	2	1	2	2	1	1	1	1	1	1
Sly11g0310371	M1	NA	3	2	2	2	2	1	1	1	1	1
Sly11g0310391	M3	NA	1	2	1	0	1	1	1	1	0	0
Sly11g0310411	M12	NA	2	2	3	2	1	6	5	5	1	1
Sly11g0310421	M11	NA	1	1	2	1	1	2	2	2	1	1
Sly11g0310441	M3	NA	27	27	22	21	18	21	23	14	16	14
Sly11g0310451	M3	NA	110	89	44	2	30	40	50	26	19	10
Sly11g0310461	M18	NA	8	7	13	9	5	10	7	10	2	1
Sly11g0310471	M1	NA	92	85	100	100	120	68	65	69	65	74
Sly11g0310531	M12	NA	9	8	8	8	8	16	15	16	9	10
Sly11g0310551	M1	NA	2	2	3	1	1	1	1	2	1	1
Sly11g0310561	M12	NA	14	13	10	8	11	30	24	29	7	6
Sly11g0310571	M11	NA	136	116	157	399	1317	197	183	209	649	992
Sly11g0310581	M3	AOS	81	66	44	10	7	18	22	10	18	10
Sly11g0310591	M3	NA	16	17	15	12	8	11	14	11	5	10
Sly11g0310601	M5	NA	1	1	1	1	2	1	1	1	1	1
Sly11g0310611	M1	NA	7	9	9	8	10	7	8	8	10	11
Sly11g0310621	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly11g0310631	M18	NA	2	2	3	3	6	4	3	3	3	3
Sly11g0310641	M12	NA	2	3	3	5	7	3	3	3	4	5
Sly11g0310651	M12	NA	55	57	67	112	113	73	83	86	148	151
Sly11g0310691	M1	NA	11	9	12	2	1	3	2	2	1	0
Sly11g0310711	M11	NA	47	39	47	55	68	48	42	50	78	96
Sly11g0310721	M1	NA	3	3	3	2	2	1	1	1	1	1
Sly11g0310731	M1	NA	10	8	13	6	4	2	3	2	1	1
Sly11g0310741	M1	NA	6	6	4	3	3	1	1	2	1	0
Sly11g0310751	M1	NA	105	77	89	13	16	21	16	18	10	20
Sly11g0310761	M1	NA	41	43	44	50	60	33	31	33	42	48
Sly11g0310771	M12	NA	1	1	1	0	1	1	2	1	0	1
Sly11g0310791	M11	NA	1	2	2	1	1	3	3	3	1	1
Sly11g0310801	M11	NA	7	8	8	5	2	11	10	10	4	1
Sly11g0310811	M11	NA	1	1	1	0	1	1	1	1	1	0
Sly11g0310821	M3	NA	12	12	11	18	12	10	10	9	15	8
Sly11g0310831	M12	NA	196	185	230	319	428	269	293	338	366	475
Sly11g0310841	M11	NA	4	4	5	4	5	5	4	5	4	6
Sly11g0310851	M6	NA	40	40	36	43	57	42	42	35	44	58
Sly11g0310861	M7	NA	19	18	16	19	50	18	20	16	20	54
Sly11g0310871	M3	NA	7	13	8	4	4	6	9	5	6	6
Sly11g0310901	M3	NA	35	36	30	28	21	30	34	29	27	20
Sly11g0310911	M2	NA	12	14	12	22	21	10	14	12	31	31
Sly11g0310921	M11	NA	20	21	25	37	46	30	27	39	53	57
Sly11g0310931	M11	NA	414	377	424	410	352	395	361	461	469	436
Sly11g0310941	M22	CDKA;1-2	2	2	2	1	1	3	2	2	1	1
Sly11g0310961	M11	NA	10	9	11	13	10	11	12	14	15	14
Sly11g0310971	M3	NA	24	25	20	8	5	15	16	11	6	3
Sly11g0310981	M12	NA	3	2	3	4	5	4	3	4	9	11
Sly11g0310991	M12	NA	5	4	4	5	8	4	5	4	8	13
Sly11g0311001	M12	NA	2	2	3	16	21	2	2	3	17	36
Sly11g0311011	M12	NA	17	15	16	14	17	16	20	18	18	27
Sly11g0311041	M11	NA	8	8	9	9	13	9	9	9	10	14
Sly11g0311071	M23	NA	1	1	1	1	1	1	1	1	1	0
Sly11g0311081	M2	NA	36	34	31	23	39	33	33	34	33	51
Sly11g0311091	M12	NA	30	30	32	30	39	36	37	40	30	46
Sly11g0311101	M9	NA	33	35	32	57	56	33	39	39	55	58
Sly11g0311141	M1	NA	5	5	5	2	1	4	4	3	1	1
Sly11g0311151	M21	NA	3	2	2	1	1	3	2	1	1	1
Sly11g0311161	M1	NA	10	11	11

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly04g0258451	M7	NA	2	4	2	1	1	3	7	3	1	1
Sly04g0258461	M3	NA	2	2	2	3	1	1	1	1	1	1
Sly04g0258471	M11	NA	13	8	13	2	8	32	23	33	1	2
Sly04g0258481	M11	NA	27	25	29	20	21	29	27	30	24	23
Sly04g0258491	M11	NA	26	24	28	43	43	30	30	33	43	46
Sly04g0258501	M11	NA	6	6	7	8	10	8	7	9	11	14
Sly04g0258511	M1	NA	51	54	43	31	26	31	32	27	30	25
Sly04g0258521	M3	NA	26	22	19	19	20	23	25	17	17	16
Sly04g0258541	M5	NA	7	8	6	8	7	7	8	6	10	6
Sly04g0258551	M3	NA	13	12	10	5	6	8	9	5	2	2
Sly04g0258561	M9	NA	29	28	31	39	42	30	36	29	45	45
Sly04g0258571	M11	SBE2	25	27	34	84	235	46	42	50	86	190
Sly04g0258581	M11	NA	51	53	100	153	366	70	55	109	134	364
Sly04g0258601	M22	SlCycB2;4	1	1	1	0	1	1	1	1	0	1
Sly04g0258621	M11	NA	26	22	28	28	55	38	32	51	48	59
Sly04g0258631	M11	Catalase 3	40	35	55	127	192	198	182	237	221	252
Sly04g0258641	M1	NA	44	43	44	42	39	35	33	39	39	41
Sly04g0258651	M9	NA	7	7	6	4	3	8	9	6	2	1
Sly04g0258661	M1	NA	19	28	29	14	10	19	14	15	7	3
Sly04g0258671	M3	NA	28	54	26	9	17	24	29	3	1	3
Sly04g0258681	M12	NA	8	10	9	35	46	8	10	14	129	136
Sly04g0258701	M3	NA	9	17	3	3	5	4	7	4	4	7
Sly04g0258731	M3	NA	58	62	57	48	43	58	60	50	36	36
Sly04g0258741	M3	NA	32	36	18	12	14	19	22	14	10	14
Sly04g0258751	M1	NA	10	9	9	9	5	3	1	2	1	1
Sly04g0258761	M1	NA	7	8	8	16	8	4	4	4	2	1
Sly04g0258771	M1	NA	38	38	37	39	50	34	34	32	29	43
Sly04g0258781	M11	NA	12	13	13	7	5	17	14	16	3	2
Sly04g0258791	M12	NA	27	28	25	23	21	30	28	29	21	18
Sly04g0258801	M11	NA	89	66	94	80	16	280	251	287	84	8
Sly04g0258811	M15	NA	93	77	86	163	127	79	84	87	134	130
Sly04g0258821	M11	NA	6	5	5	7	7	10	7	8	6	4
Sly04g0258831	M11	NA	2	2	1	1	2	2	2	2	1	1
Sly04g0258841	M2	NA	92	88	88	89	79	85	99	74	77	71
Sly04g0258851	M11	NA	43	39	41	48	59	46	46	51	94	103
Sly04g0258861	M12	NA	9	8	9	43	42	20	19	27	228	105
Sly04g0258871	M13	NA	23	21	28	52	41	21	24	26	50	36
Sly04g0258881	M1	NA	3	1	2	1	1	1	1	1	1	1
Sly04g0258891	M12	NA	15	15	21	57	88	20	23	20	50	112
Sly04g0258901	M11	NA	2	4	4	4	2	7	7	8	8	4
Sly04g0258911	M11	NA	5	4	5	5	3	11	8	11	9	5
Sly04g0258931	M1	NA	7	5	7	3	3	5	4	5	2	1
Sly04g0258941	M3	NA	27	27	22	31	40	20	20	20	29	35
Sly04g0258951	M12	NA	92	101	91	104	102	103	110	103	141	130
Sly04g0258961	M11	NA	84	77	90	170	244	138	138	156	141	195
Sly04g0258971	M2	NA	53	62	52	55	63	42	54	39	51	59
Sly04g0258981	M3	NA	29	24	22	26	26	20	24	20	31	34
Sly04g0258991	M9	NA	8	12	8	11	7	14	15	12	19	18
Sly04g0259001	M12	NA	29	31	32	45	61	33	32	38	66	66
Sly04g0259011	M12	SlPILS4	24	30	28	68	48	37	49	50	105	79
Sly04g0259021	M21	CDKB1;1-2	1	1	1	1	1	1	1	1	1	1
Sly04g0259031	M12	NA	3	4	4	3	3	4	4	4	6	5
Sly04g0259041	M12	NA	1	1	1	3	3	1	1	1	1	1
Sly04g0259051	M1	NA	3	3	2	3	2	2	2	2	2	2
Sly04g0259061	M11	NA	63	59	69	175	116	68	79	75	111	115
Sly04g0259071	M10	NA	202	197	165	134	169	218	288	186	171	214
Sly04g0259081	M3	NA	10	11	7	9	7	8	12	7	10	12
Sly04g0259091	M11	NA	17	13	21	10	7	23	14	28	6	6
Sly04g0259101	M11	NA	21	17	22	33	83	26	25	33	58	95
Sly04g0259111	M11	NA	2	2	3	5	5	4	3	3	6	5
Sly04g0259121	M12	NA	3	3	4	4	5	6	6	6	10	10
Sly04g0259131	M6	NA	20	36	25	5	26	30	41	11	4	30
Sly04g0259141	M22	NA	3	2	2	1	1	4	2	2	1	1
Sly04g0259151	M19	NA	16	17	20	26	27	19	14	20	26	26
Sly04g0259171	M12	NA	12	10	14	17	24	13	16	13	26	32
Sly04g0259181	M1	NA	5	3	4	5	2	4	2	3	2	2
Sly04g0259191	M11	NA	32	29	35	66	143	38	33	43	62	96
Sly05g0133371	M11	NA	34	30	51	20	11	62	55	59	12	10
Sly05g0133381	M1	NA	2	2	2	1	1	1	1	1	0	0
Sly05g0133391	M18	GWD1	59	62	75	123	127	89	76	99	83	87
Sly05g0133421	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly05g0133431	M6	NA	8	23	11	2	1	14	11	4	1	2
Sly05g0133441	M20	NA	372	262	358	19	4	350	268	253	5	1
Sly05g0133451	M12	NA	1	1	1	1	0	1	1	1	1	0
Sly05g0133471	M3	NA	18	16	15	19	19	12	14	10	5	7
Sly05g0133491	M3	NA	11	12	10	16	16	9	11	11	24	22
Sly05g0133501	M19	NA	7	8	7	8	9	7	5	7	8	8
Sly05g0133521	M19	NA	4	5	4	6	6	4	3	5	7	6
Sly05g0133531	M11	NA	3	2	6	1	1	7	5	6	1	1
Sly05g0133541	M10	NA	12	32	9	2	1	65	95	13	1	1
Sly05g0133551	M3	NA	140	139	85	56	20	94	97	48	18	7
Sly05g0133571	M11	NA	16	15	16	13	3	33	29	34	9	1
Sly05g0133581	M3	NA	340	324	292	262	238	308	341	290	258	272
Sly05g0133591	M3	NA	203	214	131	85	148	111	127	108	159	254
Sly05g0133601	M1	NA	18	20	17	24	36	14	14	13	22	31
Sly05g0133641	M1	NA	35	37	32	78	60	28	27	29	59	52
Sly05g0133651	M3	NA	43	76	49	8	36	22	30	11	4	40
Sly05g0133661	M1	SRO5	3	4	2	15	10	1	1	0	1	1
Sly05g0133671	M1	SRO5	30	27	23	9	50	12	11	13	27	33
Sly05g0133681	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0133691	M12	NA	6	6	5	6	5	6	6	6	7	6
Sly05g0133701	M12	NA	15	10	10	8	4	72	80	85	50	21
Sly05g0133711	M1	NA	9	9	11	7	5	2	1	1	1	1
Sly05g0133721	M11	NA	3	2	2	2	2	3	3	4	2	1
Sly05g0133731	M22	NA	6	3	5	1	0	16	5	17	1	0
Sly05g0133741	M22	NA	4	2	3	0	0	10	3	11	0	0
Sly05g0133751	M22	NA	3	1	2	0	0	5	2	6	1	0
Sly05g0133761	M22	NA	8	2	4	0	0	17	3	22	0	0
Sly05g0133791	M22	NA	3	1	2	0	0	6	1	5	0	0
Sly05g0133851	M22	NA	6	2	3	0	0	14	2	12	1	1
Sly05g0133871	M3	NA	94	85	32	8	12	13	12	8	2	5
Sly05g0133891	M11	NA	28	22	38	59	238	62	56	69	39	47
Sly05g0133901	M12	NA	241	290	300	796	905	378	434	610	1752	2110
Sly05g0133921	M1	NA	102	112	119	166	146	66	72	82	153	161
Sly05g0133931	M1	NA	1	1	1	4	5	1	0	1	0	0
Sly05g0133951	M1	NA	2	1	2	1	0	1	1	1	0	0
Sly05g0133961	M1	NA	254	232	367	10	4	7	2	3	1	0
Sly05g0133971	M1	PGE1	886	840	1579	286	86	250	154	222	2	1
Sly05g0133981	M1	NA	16	20	25	4	2	19	13	9	1	1
Sly05g0134011	M11	NA	15	12	17	19	34	20	18	23	19	30
Sly05g0134031	M1	NA	7	6	7	7	6	3	3	4	3	2
Sly05g0134041	M19	NA	92	95	96	84	59	99	76	100	105	111
Sly05g0134061	M11	NA	16	17	18	20	19	21	19	22	25	27
Sly05g0134071	M19	NA	14	17	17	19	20	17	15	19	14	17
Sly05g0134101	M23	NA	1	1	1	1	0	1	1	1	0	0
Sly05g0134121	M1	NA	200	167	128	75	49	84	86	73	61	33
Sly05g0134131	M1	NA	424	409	474	274	152	83	67	85	14	3
Sly05g0134141	M1	NA	338	336	355	199	109	55	49	67	13	2
Sly05g0134151	M1	NA	292	292	331	182	93	59	44	59	9	3
Sly05g0134161	M1	NA	251	229	256	190	239	149	153	162	188	281
Sly05g0134171	M1	NA	65	68	62	81	94	40	43	44	39	58
Sly05g0134181	M1	NA	84	88	95	64	54	70	69	79	65	56
Sly05g0134191	M1	NA	9	8	10	3	1	4	6	4	1	1
Sly05g0134201	M3	NA	63	72	62	47	45	52	57	65	30	29
Sly05g0134211	M11	NA	8	8	10	6	3	15	14	12	2	1
Sly05g0134221	M12	NA	16	14	17	18	18	17	15	18	22	17
Sly05g0134231	M9	NA	70	72	72	62	56	72	87	69	62	52
Sly05g0134241	M11	NA	4	4	5	12	9	7	8	10	25	18
Sly05g0134251	M11	NA	88	87	97	102	101	91	88	104	117	107
Sly05g0134261	M1	NA	5	4	5	1	1	1	1	1	1	1
Sly05g0134291	M11	NA	0	1	1	0	0	3	2	4	1	0
Sly05g0134311	M11	NA	7	7	8	13	7	9	10	10	8	3
Sly05g0134331	M11	NA	27	31	23	5	1	56	36	44	2	1
Sly05g0134341	M11	NA	24	21	29	38	57	42	40	56	51	95

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0311211	M22	NA	1	1	1	1	0	1	1	1	1	0
Sly11g0311231	M11	NA	44	39	47	56	63	58	52	73	60	75
Sly11g0311241	M3	NA	30	32	22	43	45	19	24	18	46	37
Sly11g0311251	M1	NA	20	19	18	23	19	15	14	16	39	28
Sly11g0311271	M1	NA	4	4	4	7	11	4	3	4	8	9
Sly11g0311291	M1	NA	2	1	3	1	1	0	1	1	0	0
Sly11g0311301	M1	NA	5	4	6	2	1	2	1	2	1	1
Sly11g0311311	M1	NA	3	2	3	1	1	1	1	1	1	0
Sly11g0311321	M1	NA	9	7	11	4	2	1	1	1	1	1
Sly11g0311341	M1	NA	5	5	6	6	3	2	2	1	1	1
Sly11g0311351	M1	NA	13	16	12	13	9	4	4	4	3	1
Sly11g0311361	M1	NA	10	8	9	8	2	8	7	8	2	1
Sly11g0311371	M3	NA	9	10	10	1	0	4	5	1	0	0
Sly11g0311391	M1	NA	110	100	84	66	54	67	68	62	59	51
Sly11g0311401	M12	NA	2	2	4	4	7	2	4	4	8	9
Sly11g0311411	M22	NA	7	7	8	11	11	11	7	11	17	22
Sly11g0311421	M12	NA	39	31	39	48	55	46	49	52	81	130
Sly11g0311441	M1	NA	13	11	11	11	10	11	10	10	12	12
Sly11g0311451	M3	NA	23	24	21	39	34	20	20	21	54	59
Sly11g0311461	M1	NA	15	17	13	6	1	8	7	10	2	1
Sly11g0311471	M1	NA	8	8	5	2	1	3	2	4	1	0
Sly11g0311481	M1	NA	6	5	5	2	2	6	4	5	2	1
Sly11g0311531	M1	AAO4-like3	1	1	1	1	1	0	1	0	0	0
Sly11g0311541	M1	AAO1-like2	1	1	1	1	1	1	1	1	1	1
Sly11g0311551	M1	AAO4-like5	9	13	12	9	4	1	1	1	1	1
Sly11g0311571	M12	NA	7	12	12	49	33	9	11	25	74	34
Sly11g0311591	M11	NA	72	67	69	57	57	76	67	81	79	81
Sly11g0311611	M11	NA	4	3	4	3	2	4	3	4	3	3
Sly11g0311621	M11	TSL	17	18	18	25	24	20	17	21	22	17
Sly11g0311631	M11	NA	64	58	79	46	34	79	67	89	56	51
Sly11g0311641	M1	NA	60	67	68	69	70	57	56	57	62	59
Sly11g0311651	M11	NA	18	19	26	31	21	25	27	27	22	14
Sly11g0311661	M11	NA	3	2	3	4	2	4	3	3	2	1
Sly11g0311671	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly11g0311681	M12	NA	2	2	2	1	3	3	10	12	3	17
Sly11g0311691	M3	NA	22	21	16	13	12	17	16	15	16	14
Sly11g0311701	M11	NA	3	2	3	1	1	3	2	3	1	1
Sly11g0311711	M12	NA	79	61	64	132	85	76	87	94	154	86
Sly11g0311721	M14	NA	24	19	37	39	14	25	18	24	3	1
Sly11g0311731	M1	NA	46	46	71	216	112	1	1	1	1	1
Sly11g0311741	M11	NA	22	20	36	48	39	37	39	37	2	1
Sly11g0311751	M4	NA	19	17	24	74	85	36	25	30	79	121
Sly11g0311761	M12	NA	17	15	16	20	13	25	24	25	22	15
Sly11g0311771	M12	NA	23	17	19	20	14	25	25	22	19	11
Sly11g0311781	M2	NA	49	47	46	72	78	44	50	45	109	104
Sly11g0311791	M8	NA	12	14	11	9	8	13	17	11	26	19
Sly11g0311811	M11	NA	5	4	6	6	6	5	5	5	4	2
Sly11g0311831	M1	NA	80	76	64	64	65	47	46	43	43	47
Sly11g0311841	M3	protein phosphatase (	39	40	34	39	47	38	32	34	35	36
Sly11g0311851	M1	NA	36	36	40	53	64	35	34	37	61	74
Sly11g0311871	M11	NA	25	19	26	22	26	22	20	25	23	30
Sly11g0311881	M1	NA	13	12	12	12	10	8	8	9	10	10
Sly11g0311891	M11	NA	3	4	5	4	1	8	7	8	1	1
Sly11g0311901	M3	NA	2	4	2	1	1	1	1	1	1	1
Sly11g0311911	M1	NA	6	6	8	5	2	4	4	5	1	1
Sly11g0311921	M12	NA	32	29	32	55	90	37	36	35	62	103
Sly11g0311941	M1	NA	36	38	31	15	4	7	5	4	1	1
Sly11g0311951	M10	NA	3	4	4	3	1	7	8	4	2	2
Sly11g0311961	M16	NA	30	26	24	22	23	26	25	27	18	16
Sly11g0311971	M22	NA	1	1	1	1	1	3	1	2	0	0
Sly11g0311981	M2	NA	30	31	30	34	42	29	30	26	42	48
Sly11g0311991	M11	NA	3	3	3	3	1	4	4	4	3	1
Sly11g0312001	M3	NA	31	30	27	23	22	27	28	28	29	30
Sly11g0312011	M12	NA	9	9	11	19	25	14	16	15	17	23
Sly11g0312021	M1	NA	41	34	32	35	19	22	20	21	22	16
Sly11g0312031	M1	NA	34	37	44	43	25	31	33	36	52	30
Sly11g0312041	M1	NA	4	4	3	4	1	2	2	2	3	1
Sly11g0312061	M3	NA	12	13	12	13	14	10	10	11	14	18
Sly11g0312071	M19	NA	16	14	14	23	27	13	12	16	31	39
Sly11g0312081	M11	NA	7	8	9	15	14	10	9	12	10	10
Sly11g0312091	M1	NA	21	20	22	17	15	16	15	15	5	3
Sly11g0312101	M1	NA	641	572	576	349	227	460	505	495	370	299
Sly11g0312131	M12	NA	8	9	8	9	9	11	12	12	15	14
Sly11g0312151	M1	NA	48	37	38	72	46	25	24	26	63	46
Sly11g0312171	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly11g0312181	M1	NA	88	76	68	55	54	45	51	40	62	59
Sly11g0312191	M9	NA	55	52	44	66	56	50	66	56	82	86
Sly11g0312201	M1	NA	6	5	5	2	2	5	4	5	3	3
Sly11g0312211	M2	NA	39	36	30	38	38	25	31	23	44	53
Sly11g0312221	M11	NA	18	15	17	23	22	22	20	25	26	22
Sly11g0312231	M11	GA20OX3	6	5	11	81	115	58	52	142	427	318
Sly11g0312241	M11	NA	37	47	56	147	104	68	56	99	222	152
Sly11g0312251	M11	SlRR14	11	11	12	13	17	18	16	21	25	26
Sly11g0312261	M17	NA	259	243	239	249	295	246	217	255	291	362
Sly11g0312271	M23	NA	31	9	12	2	2	78	24	35	4	1
Sly11g0312281	M1	NA	23	25	20	15	14	9	8	7	7	5
Sly11g0312291	M1	NA	2	2	2	3	4	2	2	2	2	2
Sly11g0312301	M3	NA	36	36	36	47	52	26	28	26	63	76
Sly11g0312311	M12	NA	25	28	25	41	60	30	29	30	45	57
Sly11g0312321	M1	NA	24	22	23	47	49	20	20	24	46	43
Sly11g0312331	M9	NA	224	235	209	392	355	237	304	253	358	301
Sly11g0312341	M1	NA	13	15	15	17	14	13	12	14	14	12
Sly11g0312351	M12	NA	82	86	101	223	221	170	226	284	754	540
Sly11g0312361	M1	NA	59	63	40	5	6	9	7	7	6	12
Sly11g0312371	M11	NA	14	9	25	3	3	52	35	59	5	3
Sly11g0312381	M1	NA	8	8	5	1	1	4	3	3	1	1
Sly11g0312391	M11	NA	21	17	22	7	2	24	22	28	7	3
Sly11g0312401	M3	NA	22	24	22	30	35	24	21	21	20	28
Sly11g0312421	M3	NA	29	30	22	18	13	23	25	15	10	10
Sly11g0312431	M11	NA	49	43	60	79	94	70	61	86	80	96
Sly11g0312441	M3	NA	130	152	86	85	146	83	111	60	86	158
Sly11g0312471	M1	NRT	1	1	1	1	1	1	1	0	1	1
Sly11g0312481	M11	NA	72	76	84	71	69	97	89	96	72	69
Sly11g0312491	M3	NA	83	86	27	1	1	28	28	7	1	1
Sly11g0312511	M12	NA	5	4	4	5	5	6	7	6	4	3
Sly11g0312521	M3	NA	5	4	2	1	1	1	1	1	1	1
Sly11g0312531	M3	NA	2	2	1	0	0	1	2	1	0	0
Sly11g0312551	M2	NA	71	80	71	28	13	31	38	31	56	17
Sly11g0312561	M5	NA	34	31	33	53	117	36	31	31	30	66
Sly11g0312571	M22	NA	1	0	1	0	0	3	1	2	0	0
Sly11g0312581	M3	NA	35	39	33	37	47	17	23	17	22	28
Sly11g0312591	M1	NA	5	4	5	5	4	4	3	3	4	4
Sly11g0312601	M2	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0312611	M12	NA	26	23	25	21	14	28	30	23	14	7
Sly11g0312631	M14	NA	97	96	179	119	47	114	93	128	54	23
Sly11g0312641	M1	NA	7	6	7	9	6	3	3	3	1	3
Sly11g0312651	M1	NA	8	9	10	10	12	8	7	8	8	9
Sly11g0312661	M2	NA	29	31	22	22	27	17	21	15	32	32
Sly11g0312671	M19	NA	2	3	2	3	2	3	2	2	3	3
Sly11g0312681	M3	NA	3	2	3	3	3	3	2	2	5	5
Sly11g0312751	M12	SlRbohH	1	1	1	1	1	1	1	1	1	1
Sly11g0312761	M19	NA	33	34	32	34	33	30	27	29	27	26
Sly11g0312771	M18	NA	17	17	18	10	4	22	19	23	4	2
Sly11g0312781	M12	NA	3	4	2	1	1	5	6	5	2	1
Sly11g0312791	M11	NA	12	9	14	2	1	26	20	23	6	2
Sly11g0312801	M1	ARR5-like1	7	5	5	1	1	0	1	0	1	0
Sly11g0312811	M11	NA	48	31	32	2	1	95	81	77	1	1
Sly11g0312831	M7	NA	111	128	108	140	175	134	134	105	94	147
Sly11g0312841	M12	NA	24	21	39	71	167	37	41	47	196	245
Sly11g0312851	M12	NA	1	1	1	1	1	1	1	1	2	2
Sly11g0312861	M11	NA	19	19	26	18

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0134351	M11	NA	6	7	7	6	7	7	6	7	5	4
Sly05g0134361	M1	NA	11	13	15	13	12	11	10	13	9	8
Sly05g0134371	M23	NA	1	1	1	1	4	2	1	1	1	1
Sly05g0134381	M1	NA	1	1	2	8	28	1	1	1	1	1
Sly05g0134411	M1	NA	55	47	45	12	6	25	24	21	3	1
Sly05g0134421	M1	NA	42	38	34	6	3	19	19	15	1	1
Sly05g0134431	M1	NA	48	35	64	36	25	31	26	33	1	2
Sly05g0134441	M14	NA	45	29	46	3	2	33	34	37	1	1
Sly05g0134451	M12	NA	44	30	39	7	5	82	81	92	3	2
Sly05g0134461	M12	NA	1	1	1	1	0	1	1	1	0	0
Sly05g0134471	M1	NA	8	8	9	2	1	8	6	7	1	1
Sly05g0134481	M1	NA	22	22	19	25	25	15	15	11	3	5
Sly05g0134491	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly05g0134501	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0134511	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly05g0134531	M3	NA	114	111	74	73	61	46	61	32	11	19
Sly05g0134551	M1	SlCycD1;1	23	37	27	5	1	9	7	7	1	1
Sly05g0134571	M11	NA	8	11	11	19	26	9	10	11	21	23
Sly05g0134581	M3	NA	76	77	63	74	63	64	81	63	63	61
Sly05g0134591	M12	NA	16	15	14	23	25	18	17	15	18	20
Sly05g0134601	M12	NA	10	10	10	15	20	12	11	12	22	31
Sly05g0134611	M20	NA	5	3	5	6	4	4	4	3	3	1
Sly05g0134621	M12	NA	2	2	2	2	2	3	3	3	3	3
Sly05g0134631	M11	NA	15	16	16	11	13	17	16	16	12	10
Sly05g0134651	M21	NA	2	2	2	1	1	2	1	1	2	1
Sly05g0134661	M11	NA	31	33	39	62	110	52	44	54	56	163
Sly05g0134691	M11	NA	20	19	20	20	24	19	18	20	18	21
Sly05g0134701	M1	NA	3	2	2	1	1	1	1	1	1	1
Sly05g0134711	M3	NA	61	55	43	40	35	29	34	28	33	35
Sly05g0134721	M3	NA	210	230	122	1	1	48	51	15	1	1
Sly05g0134741	M1	NA	74	75	87	52	55	51	51	56	65	74
Sly05g0134771	M1	NA	2	3	3	0	1	1	1	0	0	0
Sly05g0134781	M11	NA	56	52	50	35	32	55	50	61	48	45
Sly05g0134791	M1	NA	41	40	47	51	58	29	32	27	6	5
Sly05g0134801	M1	NA	77	95	95	76	104	10	12	13	8	7
Sly05g0134831	M3	NA	1	2	1	1	1	1	1	0	1	2
Sly05g0134841	M9	NA	2	1	1	0	0	2	3	1	1	5
Sly05g0134851	M12	NA	1	1	1	1	1	1	1	1	5	2
Sly05g0134861	M10	NA	11	31	27	7	103	23	51	27	10	135
Sly05g0134891	M11	NA	61	57	74	124	199	93	84	100	98	166
Sly05g0134901	M11	NA	7	6	9	6	9	9	8	9	8	10
Sly05g0134911	M1	SlRR1	111	102	89	12	12	84	70	105	9	9
Sly05g0134921	M1	NA	2	2	1	2	1	1	1	1	1	1
Sly05g0134931	M11	NA	32	28	46	40	19	79	67	92	17	5
Sly05g0134941	M11	NA	3	3	3	3	3	3	3	3	3	3
Sly05g0134951	M19	NA	2	2	2	3	2	2	2	2	2	1
Sly05g0134961	M22	NA	1	0	2	0	0	5	0	3	0	0
Sly05g0134971	M12	NA	29	26	22	30	29	33	32	32	36	42
Sly05g0134981	M1	NA	22	23	23	21	26	16	17	16	23	25
Sly05g0134991	M19	NA	59	70	75	82	65	57	53	67	47	50
Sly05g0135011	M3	NA	3	3	2	1	2	2	2	1	1	1
Sly05g0135021	M12	NA	99	96	85	72	58	148	165	151	181	126
Sly05g0135031	M11	NA	8	7	9	6	9	13	10	15	8	12
Sly05g0135041	M18	NA	29	32	36	32	40	45	43	52	41	45
Sly05g0135051	M1	NA	6	5	5	1	1	4	3	3	1	0
Sly05g0135061	M10	NA	16	21	14	11	23	25	30	17	8	18
Sly05g0135071	M12	BIR3	1	1	1	1	1	3	2	3	1	0
Sly05g0135081	M9	NA	21	20	21	24	31	21	26	25	22	34
Sly05g0135091	M3	PP2AC1	56	58	44	55	65	48	55	37	61	71
Sly05g0135111	M1	NA	2	3	2	2	1	1	1	0	0	0
Sly05g0135121	M12	NA	24	26	27	31	14	39	41	40	40	12
Sly05g0135131	M12	NA	15	15	16	8	4	20	18	15	4	2
Sly05g0135141	M3	NA	35	42	22	22	23	33	36	26	23	32
Sly05g0135151	M1	NA	24	19	30	24	6	6	7	4	3	2
Sly05g0135161	M3	NA	43	47	32	34	35	14	19	16	36	32
Sly05g0135191	M12	NA	9	8	9	13	15	11	11	10	9	11
Sly05g0135201	M3	NA	1	1	1	1	2	1	1	1	1	2
Sly05g0135211	M1	NA	3	2	3	1	1	1	1	1	1	0
Sly05g0135221	M19	NA	9	11	9	9	8	9	10	10	9	7
Sly05g0135231	M3	NA	21	22	22	20	21	20	23	18	23	24
Sly05g0135251	M1	NA	131	122	125	69	31	23	18	28	14	7
Sly05g0135271	M11	NA	15	15	20	15	22	27	22	33	21	29
Sly05g0135281	M1	NA	5	3	6	7	4	5	4	4	2	1
Sly05g0135291	M1	NA	58	75	61	91	160	21	22	15	17	110
Sly05g0135311	M1	NA	7	7	7	14	26	6	6	7	15	19
Sly05g0135321	M1	NA	4	5	4	6	6	4	4	3	4	6
Sly05g0135381	M22	NA	1	0	1	0	0	4	1	3	0	0
Sly05g0135391	M11	NA	13	11	17	22	28	20	18	23	33	41
Sly05g0135401	M1	NA	10	9	10	3	1	1	1	1	1	1
Sly05g0135431	M1	NA	30	34	36	39	20	1	1	1	2	1
Sly05g0135451	M1	NA	17	19	12	14	8	2	2	2	1	1
Sly05g0135461	M1	NA	66	57	65	40	36	47	41	49	34	26
Sly05g0135471	M1	NA	18	18	24	19	25	4	1	3	1	4
Sly05g0135481	M12	NA	52	48	88	69	44	349	376	422	83	23
Sly05g0135491	M1	NA	3	3	2	3	3	2	2	2	2	2
Sly05g0135501	M11	NA	22	22	25	42	69	27	25	33	47	73
Sly05g0135511	M8	NA	52	58	50	80	76	53	58	51	87	88
Sly05g0135521	M9	NA	19	16	13	6	19	24	25	19	20	25
Sly05g0135531	M12	NA	16	11	12	6	14	20	21	18	15	13
Sly05g0135541	M12	NA	58	47	55	14	21	77	79	59	11	7
Sly05g0135561	M1	NRT1.2	2	2	2	2	1	1	1	1	0	1
Sly05g0135571	M22	NRT1.2	1	1	1	1	1	1	1	1	1	1
Sly05g0135591	M22	NA	1	0	1	1	1	1	1	1	2	1
Sly05g0135601	M14	NA	80	75	107	127	167	80	64	122	169	186
Sly05g0135611	M12	NA	44	48	50	43	38	48	52	49	50	44
Sly05g0135621	M23	NA	3	3	2	0	0	25	6	11	1	1
Sly05g0135631	M12	NA	25	23	19	2	1	174	70	118	2	1
Sly05g0135641	M3	NA	41	43	34	14	13	35	33	34	13	9
Sly05g0135651	M12	NA	192	204	225	556	533	258	300	367	703	604
Sly05g0135661	M12	AMY3	233	259	308	699	744	400	402	619	1310	1465
Sly05g0135671	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0135681	M11	NA	3	2	4	4	3	8	7	8	4	2
Sly05g0135691	M1	NA	18	19	20	18	26	16	15	16	17	24
Sly05g0135711	M22	NA	51	34	57	6	3	62	41	47	2	1
Sly05g0135721	M11	NA	11	9	12	9	6	16	12	14	4	2
Sly05g0135781	M10	NA	47	56	30	10	21	97	111	34	7	15
Sly05g0135801	M3	NA	39	43	27	32	15	29	43	15	13	8
Sly05g0135811	M1	NA	39	49	41	5	3	13	13	8	5	2
Sly05g0135821	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0135841	M12	NA	19	15	19	1	1	63	64	30	2	1
Sly05g0135851	M3	NA	42	43	29	18	17	34	38	29	11	10
Sly05g0135861	M12	NA	43	45	42	52	60	60	65	76	70	100
Sly05g0135901	M22	NA	32	35	27	48	43	36	31	38	29	41
Sly05g0135911	M3	NA	1	1	1	1	0	1	1	1	0	1
Sly05g0135921	M1	NA	63	42	82	128	161	21	16	31	97	110
Sly05g0135931	M3	NA	316	313	247	213	172	190	226	160	187	129
Sly05g0135941	M11	NA	71	65	67	106	119	76	80	75	92	113
Sly05g0135951	M1	NA	37	36	33	28	27	16	18	11	12	18
Sly05g0135961	M12	NA	9	12	12	17	20	22	22	21	16	14
Sly05g0135991	M6	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0136101	M12	NA	4	4	5	5	4	7	7	8	5	3
Sly05g0136111	M11	NA	57	56	72	66	79	67	68	79	78	94
Sly05g0136121	M11	ORC6	4	3	3	1	1	5	5	5	1	0
Sly05g0136131	M3	NA	36	39	33	12	7	30	33	27	11	8
Sly05g0136141	M1	NA	13	16	14	3	3	5	4	3	1	1
Sly05g0136151	M11	NA	17	17	19	11	10	54	46	55	1	1
Sly05g0136161	M1	NA	16	14	10	3	2	5	4	3	1	1
Sly05g0136171	M11	NA	13	12	13	18	24	17	18	19	13	11
Sly05g0136181	M1	RDR1-like	90	61	63	32	31	37	32	34	17	21
Sly05g0136221	M1	NA	425	358	281	216	152	233	231	209	226	162
Sly05g0136231	M1	NA	6	6	7	10	10	2	1	2	1	1
Sly05g0136241	M1	NA	6	9	4	1	1	2	1	2	1	1
Sly05g0136251	M11	NA	13	13	18	9	8	28	22	34	16	21
Sly05g0136261	M11	NA	6	6	9	5	5	16	12	21	7	8

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly11g0312901	M1	NA	39	42	42	46	51	38	37	35	41	46
Sly11g0312921	M11	NA	23	23	31	33	31	35	31	37	42	49
Sly11g0312941	M1	NA	29	51	40	15	5	2	1	1	1	0
Sly11g0312961	M1	NA	1	1	1	1	4	1	1	1	1	1
Sly11g0313021	M3	NA	46	55	45	39	32	37	43	29	23	27
Sly11g0313031	M3	NA	4	15	20	1	11	3	9	3	0	8
Sly11g0313041	M7	NA	1	2	2	0	1	1	3	2	1	2
Sly11g0313071	M10	NA	8	33	36	1	7	32	55	11	1	8
Sly11g0313081	M10	NA	12	46	36	1	5	42	63	18	1	11
Sly11g0313091	M10	NA	19	36	11	3	4	40	44	16	4	4
Sly11g0313101	M1	NA	2	2	2	2	2	1	1	1	1	1
Sly11g0313111	M3	NA	3	5	2	1	1	1	1	1	0	1
Sly11g0313121	M1	NA	10	7	16	12	8	4	3	4	3	2
Sly11g0313131	M11	NA	10	8	11	1	1	33	28	35	4	1
Sly11g0313141	M17	NA	1	2	2	4	12	1	1	2	2	0
Sly11g0313151	M12	NA	1	1	1	2	3	1	1	1	1	1
Sly11g0313161	M11	NA	7	9	10	18	16	14	12	15	9	3
Sly11g0313171	M11	NA	1	1	1	3	2	1	1	1	1	1
Sly11g0313181	M1	NA	22	21	22	26	21	14	15	16	13	10
Sly11g0313191	M1	NA	48	36	46	39	35	24	23	30	44	34
Sly11g0313201	M11	NA	1	1	1	1	0	1	1	1	1	1
Sly11g0313211	M11	NA	2	2	2	2	2	2	2	3	2	1
Sly11g0313221	M3	PPR-like50	4	4	4	5	5	4	4	4	6	4
Sly11g0313231	M1	NA	40	42	42	64	52	32	36	28	63	50
Sly11g0313241	M3	NA	110	110	110	153	177	79	91	80	171	201
Sly11g0313251	M12	NA	105	92	83	128	115	138	154	111	85	109
Sly11g0313261	M22	NA	3	1	2	1	1	2	2	2	0	0
Sly11g0313271	M11	NA	5	7	7	7	5	9	8	9	11	4
Sly11g0313281	M17	NA	69	60	63	50	49	61	58	68	56	61
Sly11g0313291	M9	NA	52	53	51	54	67	57	63	53	75	107
Sly11g0313351	M19	NA	2	3	3	3	3	2	2	2	1	1
Sly11g0313571	M1	NA	3	3	5	5	5	2	3	2	2	4
Sly11g0313581	M1	NA	3	4	4	4	4	3	2	3	1	4
Sly11g0313591	M1	NA	2	3	2	3	4	2	1	2	1	3
Sly11g0313621	M1	NA	2	2	2	1	2	1	1	1	1	1
Sly11g0313641	M1	NA	5	5	6	6	6	5	4	5	3	3
Sly11g0313651	M1	NA	5	6	6	6	6	4	5	6	2	4
Sly11g0313671	M12	NA	1	1	1	1	1	1	2	2	2	1
Sly11g0313691	M12	NA	1	2	1	2	4	3	2	3	4	1
Sly11g0313701	M7	NA	2	3	3	4	3	2	3	3	2	1
Sly11g0313711	M1	NA	2	3	3	2	3	2	2	3	1	1
Sly11g0313731	M22	NA	2	2	2	3	2	2	2	3	2	2
Sly11g0313741	M1	NA	3	3	3	2	3	3	2	3	1	1
Sly11g0313751	M1	NA	2	2	2	2	2	2	1	2	1	2
Sly11g0313761	M1	NA	2	2	2	2	2	2	2	2	1	1
Sly11g0313801	M3	NA	2	3	2	3	4	2	2	1	1	2
Sly11g0313811	M1	NA	1	2	2	2	2	1	1	1	1	2
Sly11g0313881	M11	NA	1	1	1	2	2	2	1	1	2	2
Sly11g0313901	M1	NA	2	2	2	3	4	2	1	2	1	2
Sly11g0313941	M1	NA	1	2	2	2	1	1	1	1	1	1
Sly11g0314031	M1	NA	3	4	6	5	8	4	3	4	3	6
Sly11g0314051	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0314141	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0314171	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0314221	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0314241	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly11g0314251	M1	NA	2	3	3	3	3	2	2	2	1	2
Sly12g0048561	M12	NA	12	13	12	18	23	15	14	16	19	21
Sly12g0048571	M2	NA	127	126	128	155	149	103	110	99	150	157
Sly12g0048581	M1	NA	1	2	2	2	1	1	1	1	1	1
Sly12g0048591	M13	NA	21	18	21	67	93	17	17	22	54	102
Sly12g0048601	M11	NA	5	5	6	6	6	6	6	5	5	8
Sly12g0048611	M1	CPK21	118	83	122	29	20	55	56	81	40	23
Sly12g0048621	M1	CPK9	74	58	92	24	13	44	34	63	28	14
Sly12g0048631	M1	NA	27	11	29	1	1	2	1	1	0	0
Sly12g0048641	M11	NA	23	22	24	14	12	26	20	24	11	12
Sly12g0048651	M1	NA	3	3	3	1	1	3	1	2	1	0
Sly12g0048661	M1	NA	6	6	7	6	4	5	5	6	5	2
Sly12g0048671	M1	NA	11	11	11	17	23	6	5	5	6	7
Sly12g0048681	M3	NA	12	13	8	9	8	9	11	8	12	10
Sly12g0048691	M1	NA	81	59	86	43	44	54	40	52	36	30
Sly12g0048711	M12	NA	1	1	1	0	0	1	1	1	1	0
Sly12g0048721	M11	NA	42	41	50	73	50	64	57	73	45	30
Sly12g0048731	M1	NA	1	1	1	1	0	1	0	1	1	1
Sly12g0048741	M1	NA	23	24	22	22	13	15	15	14	10	4
Sly12g0048761	M1	NA	42	43	40	58	65	24	29	27	50	72
Sly12g0048771	M3	NA	9	9	7	4	3	6	7	5	2	1
Sly12g0048781	M1	NA	4	4	4	4	3	2	2	2	1	1
Sly12g0048791	M1	NA	6	6	5	4	1	2	3	4	1	0
Sly12g0048801	M3	NA	12	11	11	2	1	12	11	9	2	1
Sly12g0048811	M12	NA	130	116	131	218	310	162	157	176	174	269
Sly12g0048821	M22	NA	6	6	6	12	10	6	5	6	7	4
Sly12g0048831	M6	NA	10	16	10	9	11	9	11	8	9	15
Sly12g0048841	M3	chl4	1	2	1	2	2	1	1	1	0	1
Sly12g0048851	M1	GH3-15	1	1	2	1	1	1	1	1	1	1
Sly12g0048871	M16	NA	501	440	482	337	299	406	394	415	310	341
Sly12g0048881	M6	NA	39	91	43	21	108	52	80	27	15	113
Sly12g0048891	M11	NA	14	13	15	23	14	33	25	32	4	5
Sly12g0048941	M1	NA	81	82	79	54	76	9	5	7	6	16
Sly12g0048951	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly12g0048961	M12	NA	15	12	12	16	11	17	15	14	13	6
Sly12g0048971	M23	NA	1	1	1	1	0	2	1	1	1	1
Sly12g0048981	M1	NA	61	48	18	2	1	2	3	1	0	0
Sly12g0049001	M3	NA	7	18	6	0	0	5	7	1	0	0
Sly12g0049031	M12	NA	13	13	14	25	39	18	14	17	24	51
Sly12g0049041	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0049101	M3	NA	3	3	1	1	0	1	1	1	0	1
Sly12g0049111	M22	NA	2	1	2	1	1	3	1	1	1	1
Sly12g0049121	M9	NA	144	153	131	150	117	132	185	152	140	115
Sly12g0049141	M1	NA	30	34	30	32	34	23	24	22	32	32
Sly12g0049161	M1	NA	1	1	1	1	0	0	0	0	0	0
Sly12g0049171	M11	NA	86	70	80	59	36	121	100	120	40	20
Sly12g0049181	M11	NA	50	47	58	39	21	77	79	86	22	8
Sly12g0049191	M3	NA	7	14	2	0	0	1	1	0	0	0
Sly12g0049221	M11	NA	6	4	5	2	4	7	4	7	1	3
Sly12g0049251	M11	NA	2	1	1	1	0	3	2	3	0	0
Sly12g0049291	M1	NA	6	10	4	1	0	1	1	1	0	0
Sly12g0049301	M2	NA	16	19	21	28	29	9	14	23	57	47
Sly12g0049311	M1	NA	5	4	4	1	1	1	1	1	0	0
Sly12g0049321	M3	NA	13	7	3	1	0	5	3	1	0	0
Sly12g0049331	M9	NA	28	23	29	20	40	36	39	32	23	42
Sly12g0049341	M3	NA	17	17	15	18	22	16	15	16	22	27
Sly12g0049361	M19	NA	9	10	9	10	9	8	7	11	10	11
Sly12g0049371	M11	NA	52	49	53	66	90	54	51	57	78	95
Sly12g0049441	M1	NA	82	92	86	10	3	22	22	21	2	3
Sly12g0049471	M22	NA	1	1	1	0	0	3	1	2	0	0
Sly12g0049481	M11	NA	20	19	20	2	1	24	28	23	7	3
Sly12g0049491	M6	NA	70	71	53	51	25	80	92	44	75	40
Sly12g0049501	M11	NA	219	200	237	232	122	356	335	480	523	320
Sly12g0049511	M11	NA	31	33	40	50	58	58	48	80	81	81
Sly12g0049521	M11	NA	12	12	20	15	8	32	27	30	7	5
Sly12g0049551	M1	NA	11	11	10	9	10	9	8	8	13	12
Sly12g0049561	M7	NA	64	84	37	16	18	48	134	37	22	45
Sly12g0049571	M7	NA	1	1	1	0	1	1	1	1	1	0
Sly12g0049581	M14	NA	18	18	23	100	178	18	17	18	27	71
Sly12g0049591	M12	ACO2	2	2	2	1	4	7	9	3	4	22
Sly12g0049601	M11	NA	30	30	43	39	60	40	35	53	73	102
Sly12g0049611	M12	SIERF.F6	7	8	8	10	12	16	13	16	18	20
Sly12g0049621	M19	NA	9	10	10	8	7	10	8	8	4	2
Sly12g0049641	M4	NA	38	36	44	61	127	38	35	37	84	214
Sly12g0049651	M12	NA	21	20	25	19	17	25	24	26	15	18

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0136341	M12	NA	51	51	46	47	52	77	84	78	75	88
Sly05g0136351	M1	NA	64	59	60	69	68	54	52	63	92	70
Sly05g0136361	M11	NA	3	4	4	2	2	5	4	5	3	2
Sly05g0136401	M3	NA	14	12	11	13	11	10	10	11	12	10
Sly05g0136411	M3	NA	20	22	17	18	17	15	16	15	20	20
Sly05g0136421	M1	NA	8	9	10	5	5	7	8	8	5	5
Sly05g0136441	M3	NA	102	118	63	65	29	43	45	44	134	118
Sly05g0136451	M11	NA	14	16	12	10	1	20	18	23	15	2
Sly05g0136461	M12	NA	5	4	2	2	1	4	4	4	3	1
Sly05g0136471	M8	SIPL	44	56	40	94	65	48	59	47	146	98
Sly05g0136481	M1	NA	69	70	72	97	91	64	58	63	89	84
Sly05g0136491	M3	NA	38	38	33	30	29	26	28	24	26	25
Sly05g0136511	M3	NA	38	31	7	1	1	3	4	2	1	1
Sly05g0136521	M12	NA	8	9	8	15	13	9	10	12	35	21
Sly05g0136531	M12	NA	3	3	4	5	6	5	5	6	17	16
Sly05g0136561	M12	NA	3	3	3	1	4	11	9	10	1	4
Sly05g0136571	M1	NA	3	2	2	2	2	1	1	1	0	1
Sly05g0136581	M12	NA	14	8	18	15	31	25	19	31	15	31
Sly05g0136591	M11	NA	6	6	8	5	4	8	8	9	7	6
Sly05g0136611	M3	NA	4	5	3	3	10	4	3	3	2	8
Sly05g0136621	M23	NA	1	1	1	7	8	2	1	1	1	2
Sly05g0136631	M1	NA	22	56	22	1	1	6	3	3	1	1
Sly05g0136641	M11	NA	22	21	27	29	31	28	24	30	41	50
Sly05g0136651	M11	NA	46	47	49	49	50	45	47	52	48	60
Sly05g0136661	M22	NA	1	1	1	0	1	1	1	1	1	1
Sly05g0136671	M18	NA	13	15	13	16	19	14	13	16	26	30
Sly05g0136681	M1	NA	6	7	8	3	2	1	1	1	1	0
Sly05g0136691	M16	NA	456	359	343	321	284	284	250	318	353	466
Sly05g0136711	M18	NA	7	6	7	7	5	10	9	12	7	3
Sly05g0136721	M22	NA	1	0	1	0	0	2	1	1	0	0
Sly05g0136731	M12	SIPIN4	22	30	19	8	5	73	100	27	4	9
Sly05g0136741	M1	NA	3	4	3	2	2	1	1	1	1	1
Sly05g0136751	M1	NA	2	2	1	1	1	1	0	0	1	1
Sly05g0136761	M1	NA	46	48	48	7	4	24	19	21	5	6
Sly05g0136771	M11	NA	36	36	46	38	43	39	49	70	124	158
Sly05g0136781	M1	NA	222	230	220	665	470	133	168	233	755	656
Sly05g0136791	M3	NA	8	6	4	4	10	6	4	3	3	4
Sly05g0136801	M2	NA	44	44	47	66	70	44	39	42	42	51
Sly05g0136811	M3	NA	34	36	25	21	12	27	33	9	3	5
Sly05g0136821	M7	NA	7	13	6	2	5	19	30	6	6	22
Sly05g0136841	M22	NA	1	0	1	1	0	4	1	2	0	0
Sly05g0136871	M6	NA	31	31	29	22	28	35	32	27	14	12
Sly05g0136881	M1	NA	46	44	45	30	29	28	32	29	34	32
Sly05g0136891	M1	NA	89	93	87	106	119	41	42	38	116	140
Sly05g0136901	M5	NA	9	16	10	1	1	26	17	2	1	1
Sly05g0136911	M10	NA	15	24	16	3	1	48	39	16	20	6
Sly05g0136921	M1	NA	12	13	8	1	0	1	1	1	1	1
Sly05g0136931	M13	NA	23	23	35	34	25	36	34	46	22	19
Sly05g0136961	M3	NA	22	26	23	28	26	24	23	22	19	14
Sly05g0136971	M11	NA	8	7	9	18	24	12	12	15	14	15
Sly05g0136991	M1	NA	23	25	47	37	44	14	8	14	6	14
Sly05g0137001	M22	NA	2	1	2	1	1	3	1	3	1	0
Sly05g0137011	M1	NA	11	22	16	14	10	6	6	4	2	1
Sly05g0137031	M1	NA	6	6	7	7	6	5	6	6	6	5
Sly05g0137041	M1	NA	15	14	11	10	7	6	7	6	7	6
Sly05g0137051	M22	NA	45	42	43	35	23	54	39	47	7	9
Sly05g0137061	M1	NA	2	7	3	1	1	1	0	0	0	0
Sly05g0137081	M3	NA	103	130	44	27	14	25	34	13	11	9
Sly05g0137091	M1	NA	42	51	37	44	155	11	15	14	82	387
Sly05g0137101	M1	NA	104	105	141	149	103	9	6	7	4	3
Sly05g0137111	M11	NA	25	22	33	23	23	45	44	48	30	20
Sly05g0137131	M11	NA	18	17	20	13	10	20	17	22	13	6
Sly05g0137141	M5	NA	47	66	38	49	65	55	64	37	52	85
Sly05g0137151	M11	NA	89	79	105	60	63	120	102	144	85	83
Sly05g0137161	M11	NA	123	115	130	380	559	141	148	177	361	457
Sly05g0137171	M3	NA	337	331	302	378	296	302	332	284	272	232
Sly05g0137201	M3	NA	12	10	9	2	2	8	8	8	2	2
Sly05g0137221	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0137251	M3	NA	32	36	20	27	28	13	17	8	17	17
Sly05g0137261	M2	NA	35	36	39	39	49	32	36	37	66	73
Sly05g0137271	M14	NA	68	56	62	74	136	51	46	63	79	116
Sly05g0137281	M11	ORC4	4	5	5	2	2	5	6	4	1	1
Sly05g0137301	M18	PPR-like35	11	12	12	12	14	13	11	13	12	13
Sly05g0137321	M1	NA	17	18	17	21	32	5	4	4	12	47
Sly05g0137331	M2	NA	51	52	40	47	43	33	43	30	42	32
Sly05g0137341	M12	NA	326	313	369	549	463	366	406	383	544	502
Sly05g0137351	M1	NA	39	36	41	35	39	35	34	37	40	35
Sly05g0137361	M11	NA	2	2	3	1	0	5	5	4	1	0
Sly05g0137371	M18	NA	48	46	47	63	72	64	54	67	67	58
Sly05g0137381	M3	NA	5	6	4	27	16	4	4	3	27	17
Sly05g0137501	M2	NA	27	27	24	43	43	22	29	28	83	74
Sly05g0137511	M1	NA	23	22	22	17	7	18	16	17	23	22
Sly05g0137521	M12	NA	29	34	28	33	23	40	46	35	20	21
Sly05g0137531	M11	NA	17	18	21	32	45	20	18	22	41	52
Sly05g0137551	M11	NA	12	13	13	21	12	22	21	22	15	11
Sly05g0137561	M1	NA	79	96	110	32	45	68	57	48	9	21
Sly05g0137571	M1	NA	27	32	23	13	9	5	4	4	1	1
Sly05g0137581	M12	NA	57	50	67	56	69	101	103	118	70	84
Sly05g0137611	M3	NA	14	15	12	9	4	10	11	9	11	5
Sly05g0137621	M11	NA	13	14	16	26	43	19	17	21	24	43
Sly05g0137641	M1	NA	3	2	2	0	0	1	1	0	0	0
Sly05g0137651	M1	NA	52	45	50	29	14	40	32	39	12	4
Sly05g0137661	M11	NA	1	1	1	0	0	2	1	2	0	0
Sly05g0137681	M11	NA	57	55	64	185	225	55	60	76	245	234
Sly05g0137691	M1	NA	25	34	16	13	24	7	9	6	7	8
Sly05g0137701	M1	NA	2	3	2	4	3	1	1	1	1	1
Sly05g0137711	M1	NA	1	1	1	1	0	1	0	0	0	0
Sly05g0137721	M3	NA	3	3	2	1	1	1	1	1	0	0
Sly05g0137741	M3	NA	3	3	1	1	0	1	1	1	0	0
Sly05g0137751	M1	NA	2	2	2	1	1	1	1	1	0	0
Sly05g0137761	M1	NA	23	34	24	8	13	4	6	2	1	2
Sly05g0137771	M3	NA	10	11	11	12	11	10	10	10	11	10
Sly05g0137781	M2	NA	56	52	49	79	119	51	53	53	92	147
Sly05g0137801	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0137811	M3	NA	10	15	8	4	1	5	4	3	1	1
Sly05g0137821	M9	NA	30	33	27	21	21	34	43	28	15	13
Sly05g0137831	M11	NA	5	4	8	6	5	11	10	12	4	1
Sly05g0137851	M23	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0137861	M10	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0137871	M9	NA	27	62	85	22	32	131	147	82	81	101
Sly05g0137881	M1	NA	5	4	3	5	10	3	2	3	5	11
Sly05g0137891	M3	NA	37	38	30	48	48	20	21	18	34	40
Sly05g0137901	M18	NA	24	25	29	35	35	31	27	32	25	19
Sly05g0137911	M2	NA	31	31	24	29	37	22	26	22	33	37
Sly05g0137921	M1	NA	10	8	4	2	1	1	1	1	1	1
Sly05g0137931	M3	NA	1	1	1	1	1	1	1	1	0	0
Sly05g0137941	M1	NA	79	82	72	50	38	57	55	53	42	28
Sly05g0137961	M1	NA	4	4	4	3	1	2	2	1	0	0
Sly05g0137971	M1	NA	82	81	81	81	75	59	54	53	57	56
Sly05g0137981	M3	NA	4	7	3	1	1	2	1	1	0	0
Sly05g0137991	M1	NA	8	7	7	6	5	4	2	2	1	1
Sly05g0138001	M1	NA	5	4	5	5	5	4	4	4	4	4
Sly05g0138011	M11	NA	4	5	6	3	1	7	5	7	3	1
Sly05g0138021	M11	NA	8	6	8	4	3	10	10	10	6	2
Sly05g0138031	M12	NA	1	1	1	3	3	2	2	2	14	18
Sly05g0138041	M1	NA	1	1	1	3	3	0	0	0	1	0
Sly05g0138061	M1	NA	70	67	81	72	83	56	55	66	103	116
Sly05g0138071	M13	NA	72	50	108	40	18	100	86	139	54	18
Sly05g0138081	M14	NA	14	11	25	3	1	13	10	18	1	1
Sly05g0138091	M22	NA	10	4	5	1	1	30	11	26	1	0
Sly05g0138111	M12	NA	25	22	27	6	2	39	40	38	3	2
Sly05g0138121	M3	NA	4	9	2	1	1	1	2	1	5	2
Sly05g0138131	M18	NA	20	20	25	13	16	22	18	23	15	18
Sly05g0138141	M18	NA	3	3	4	5	5	4	4	4	7	11

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0049691	M11	NA	18	19	21	16	19	22	22	22	23	25
Sly12g0049711	M1	NA	12	14	10	21	17	2	3	2	16	17
Sly12g0049721	M3	NA	6	12	7	1	1	4	13	4	2	1
Sly12g0049731	M12	NA	8	8	12	13	22	11	13	15	21	25
Sly12g0049741	M12	NA	2	2	1	3	4	3	3	2	10	8
Sly12g0049821	M22	NA	2	1	1	0	0	17	1	10	0	0
Sly12g0049831	M22	NA	6	5	6	10	9	6	5	6	4	3
Sly12g0049851	M11	NA	4	2	4	3	1	23	20	34	5	1
Sly12g0049871	M12	NA	57	52	71	98	112	68	69	81	140	141
Sly12g0049881	M1	NA	30	33	30	44	46	28	27	29	33	33
Sly12g0049891	M3	NA	41	40	36	41	39	36	31	29	23	17
Sly12g0049921	M3	NA	3	3	2	1	1	2	2	1	1	0
Sly12g0049931	M1	NA	13	8	14	40	27	8	7	8	28	22
Sly12g0049941	M13	NA	7	9	10	18	23	9	8	13	11	15
Sly12g0049951	M12	NA	9	9	10	10	10	11	12	12	12	14
Sly12g0049961	M1	NA	113	91	202	138	40	69	65	75	101	374
Sly12g0049971	M1	NA	2	1	3	1	0	1	1	1	0	0
Sly12g0049981	M1	NA	2	2	3	1	0	1	1	1	0	0
Sly12g0050001	M13	NA	46	42	51	61	63	56	51	63	45	49
Sly12g0050021	M1	NA	4	4	5	5	5	4	2	4	4	4
Sly12g0050031	M9	NA	18	21	18	25	24	24	26	23	32	23
Sly12g0050061	M11	NA	140	142	162	281	295	253	217	276	416	439
Sly12g0050081	M3	SlARF6A	21	30	20	11	8	18	17	13	6	8
Sly12g0050091	M3	NA	16	22	13	10	7	12	10	8	8	7
Sly12g0050101	M22	NA	1	1	1	0	1	6	2	4	1	1
Sly12g0050111	M3	NA	23	30	24	60	118	14	23	16	47	105
Sly12g0050121	M3	NA	114	70	35	1	1	30	41	5	1	1
Sly12g0050161	M6	NA	55	83	52	51	94	54	81	37	31	84
Sly12g0050181	M11	NA	11	9	8	2	1	13	13	17	4	1
Sly12g0050191	M1	NA	41	42	30	66	19	14	13	11	74	21
Sly12g0050201	M14	KAO2-like2	7	7	16	15	5	8	9	8	1	1
Sly12g0050211	M11	NA	46	28	65	11	2	87	76	82	11	1
Sly12g0050221	M18	NA	27	31	35	29	28	38	34	38	30	28
Sly12g0050231	M2	NA	22	21	18	28	22	15	20	13	18	12
Sly12g0050241	M3	NA	30	28	26	24	17	27	27	20	10	7
Sly12g0050251	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly12g0050261	M1	NA	10	6	21	1	1	2	2	2	1	1
Sly12g0050271	M1	NA	24	20	42	29	9	1	1	1	1	1
Sly12g0050281	M3	NA	209	201	211	269	231	161	174	161	227	202
Sly12g0050291	M11	NA	172	167	213	151	163	200	175	225	252	298
Sly12g0050301	M1	NA	3	2	2	1	0	1	1	2	1	1
Sly12g0050311	M12	NA	2	2	3	1	1	4	8	5	1	1
Sly12g0050321	M11	NA	4	5	5	7	5	6	5	6	6	4
Sly12g0050331	M1	NA	31	31	28	47	20	1	1	1	1	1
Sly12g0050341	M1	NA	1	2	2	26	13	1	0	0	0	1
Sly12g0050361	M22	NA	2	2	2	1	1	2	2	2	1	1
Sly12g0050371	M1	NA	9	11	20	4	2	2	1	2	1	1
Sly12g0050381	M11	NA	5	3	8	0	1	7	6	7	0	0
Sly12g0050391	M11	NA	1	1	1	0	1	1	1	2	0	0
Sly12g0050401	M11	NA	19	18	18	17	18	19	18	20	24	27
Sly12g0050411	M1	NA	3	3	5	2	1	2	1	2	1	1
Sly12g0050421	M1	NA	22	22	23	28	36	19	19	21	33	31
Sly12g0050441	M22	NA	3	2	2	1	0	4	1	6	1	0
Sly12g0050451	M12	NA	1	1	1	1	1	3	3	2	1	1
Sly12g0050461	M1	NA	136	119	106	77	74	97	94	97	83	84
Sly12g0050471	M3	NA	12	12	11	11	10	9	9	8	11	10
Sly12g0050531	M1	NA	1	2	3	20	10	1	1	1	1	1
Sly12g0050551	M23	NA	1	1	1	0	1	1	1	1	0	0
Sly12g0050561	M1	NA	8	8	8	7	4	1	1	1	1	1
Sly12g0050571	M11	NA	2	1	2	3	4	2	3	2	3	2
Sly12g0050591	M15	NA	47	41	38	44	39	38	45	46	57	54
Sly12g0050601	M3	NA	8	18	5	1	1	4	5	1	1	1
Sly12g0050611	M3	NA	59	106	46	4	7	12	9	2	1	3
Sly12g0050621	M12	SlCYP734A8	1	1	1	1	2	6	2	2	14	14
Sly12g0050631	M11	NA	71	66	71	91	115	69	69	75	107	150
Sly12g0050641	M2	NA	20	20	19	30	36	13	18	15	65	79
Sly12g0050651	M2	NA	21	22	18	18	18	16	18	16	18	19
Sly12g0050661	M1	NA	2	4	5	28	10	1	0	0	1	1
Sly12g0050671	M1	NA	15	20	14	28	23	4	4	2	2	2
Sly12g0050681	M1	NA	67	73	107	110	77	67	79	55	87	85
Sly12g0050691	M1	NA	26	27	26	20	21	25	24	25	17	18
Sly12g0050721	M7	NA	42	61	35	114	240	47	81	59	218	255
Sly12g0050731	M12	NA	6	11	6	17	25	10	18	10	36	31
Sly12g0050741	M7	NA	7	12	8	10	22	12	25	10	28	29
Sly12g0050751	M7	NA	92	137	73	134	353	127	247	118	265	394
Sly12g0050761	M7	NA	4	6	4	5	15	6	10	5	14	17
Sly12g0050771	M10	NA	70	76	62	54	52	86	94	76	57	56
Sly12g0050791	M11	NA	80	84	104	133	126	105	111	136	159	145
Sly12g0050801	M12	NA	73	59	76	93	111	84	96	94	131	149
Sly12g0050811	M11	NA	23	21	24	31	16	41	34	42	23	5
Sly12g0050831	M3	NA	38	49	39	36	36	29	28	27	52	40
Sly12g0050851	M3	NA	1	1	1	0	1	1	1	1	0	0
Sly12g0050861	M3	NA	52	55	32	4	1	33	19	17	3	2
Sly12g0050871	M12	NA	1	1	1	2	3	1	1	2	19	27
Sly12g0050891	M10	NA	44	125	104	3	4	150	195	62	3	4
Sly12g0050901	M1	NA	88	53	119	92	86	11	7	12	11	34
Sly12g0050931	M1	NA	36	26	36	158	105	18	15	19	41	53
Sly12g0050971	M13	NA	25	18	32	78	181	34	29	52	94	135
Sly12g0050981	M12	NA	16	22	18	21	24	28	40	22	23	24
Sly12g0050991	M10	NA	40	51	40	34	50	50	60	39	24	40
Sly12g0051001	M11	NA	10	9	10	25	26	12	13	13	27	23
Sly12g0051011	M2	NA	155	152	124	62	60	86	126	65	84	83
Sly12g0051031	M12	NA	27	28	32	39	43	31	36	35	37	41
Sly12g0051041	M1	NA	9	10	9	7	3	6	6	5	2	1
Sly12g0051051	M1	NA	1	1	1	1	0	1	1	1	1	1
Sly12g0051061	M23	NA	1	1	1	0	1	2	1	1	1	1
Sly12g0051071	M1	NA	233	222	197	100	96	94	103	67	62	67
Sly12g0051081	M12	NA	15	15	13	33	53	20	19	23	94	167
Sly12g0051091	M18	NA	6	7	6	16	19	7	7	10	26	32
Sly12g0051101	M12	CDKF;1	51	53	61	67	51	63	64	77	68	63
Sly12g0051141	M1	SlAux/IAA8	24	19	15	9	5	15	13	11	2	1
Sly12g0051151	M1	NA	1	1	1	1	0	1	1	1	1	0
Sly12g0051191	M18	NA	101	104	99	86	85	105	94	103	72	75
Sly12g0051201	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0051211	M2	NA	6	4	5	13	25	4	4	5	35	41
Sly12g0051221	M11	NA	48	49	60	169	213	65	66	85	153	198
Sly12g0051241	M22	NA	1	1	1	1	13	2	1	1	1	3
Sly12g0051251	M1	NA	40	40	39	25	27	28	34	32	25	47
Sly12g0051261	M1	NA	31	34	36	24	22	28	30	29	22	35
Sly12g0051271	M3	NA	16	14	11	8	5	10	10	9	6	4
Sly12g0051281	M1	NA	19	22	16	6	6	6	7	2	1	1
Sly12g0051291	M3	NA	206	177	178	121	89	97	120	88	71	62
Sly12g0051301	M1	NA	186	172	176	116	74	97	107	89	59	47
Sly12g0051311	M18	NA	122	108	130	105	106	128	103	144	122	184
Sly12g0051321	M9	NA	2	3	4	2	1	7	11	4	1	1
Sly12g0051331	M3	NA	39	41	41	48	42	40	40	37	48	43
Sly12g0051341	M1	NA	2	2	3	1	1	1	1	1	1	0
Sly12g0051351	M1	NA	22	26	38	15	6	8	5	7	4	2
Sly12g0051361	M1	NA	27	31	42	18	7	10	9	7	6	2
Sly12g0051371	M1	NA	1	1	1	19	153	1	1	1	5	75
Sly12g0051391	M2	NA	13	13	12	15	13	11	13	11	22	27
Sly12g0051401	M1	NA	6	5	6	4	4	1	1	1	1	1
Sly12g0051411	M1	NA	32	24	30	28	22	24	21	31	17	11
Sly12g0051421	M12	NA	2	2	1	1	1	1	1	2	1	1
Sly12g0051451	M12	NA	7	8	9	11	8	26	31	28	52	49
Sly12g0051471	M3	NA	70	113	43	6	2	17	18	5	1	1
Sly12g0051481	M11	HXK3	2	2	2	1	1	5	4	7	2	1
Sly12g0051491	M1	NA	2	1	1	0	1	1	1	1	0	0
Sly12g0051501	M1	NA	3	3	3	1	2	3	2	2	1	1
Sly12g0051511	M12	NA	3	2	3	3	1	3	4	3	2	1
Sly12g0051521	M12	NA	5	5	6	6	3	7	6	7	4	2
Sly12g0051531	M11	NA

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0138151	M3	NA	105	120	76	162	97	62	80	61	88	58
Sly05g0138161	M11	NA	27	26	27	102	134	42	38	49	112	120
Sly05g0138171	M1	NA	1	1	1	1	1	1	0	0	0	0
Sly05g0138181	M3	NA	90	100	72	15	17	31	30	14	19	11
Sly05g0138191	M3	NA	3	5	3	3	2	3	3	3	3	2
Sly05g0138201	M9	SIIPT1	3	3	2	1	1	10	10	5	3	5
Sly05g0138221	M3	NA	175	222	81	173	147	94	110	61	86	87
Sly05g0138231	M22	NA	2	1	1	3	3	4	1	4	4	2
Sly05g0138251	M3	SIERF.J3	38	37	19	12	14	20	25	13	14	17
Sly05g0138261	M3	NA	21	20	11	8	8	11	17	8	7	8
Sly05g0138271	M11	NA	22	25	38	35	17	66	66	91	36	7
Sly05g0138281	M3	NA	10	7	3	1	0	1	1	1	0	1
Sly05g0138291	M2	NA	47	48	26	2	10	11	17	5	3	23
Sly05g0138301	M1	NPF3	5	3	3	1	1	0	0	1	1	1
Sly05g0138321	M12	NA	6	6	7	9	19	15	25	21	57	96
Sly05g0138331	M7	NA	29	35	31	80	55	31	38	28	58	35
Sly05g0138341	M19	NA	28	29	26	28	27	30	26	30	35	36
Sly05g0138351	M12	NA	108	235	122	78	104	284	386	206	176	184
Sly05g0138361	M10	NA	14	25	12	8	15	27	42	20	21	39
Sly05g0138371	M11	NA	17	15	19	19	3	28	27	31	18	4
Sly05g0138401	M12	NA	172	172	169	172	170	170	173	174	151	174
Sly05g0138411	M3	NA	3	2	1	1	1	1	1	1	1	1
Sly05g0138421	M3	NA	96	138	56	4	4	19	17	3	1	3
Sly05g0138431	M6	NA	1	2	2	1	0	1	2	1	0	0
Sly05g0138441	M1	NA	35	31	27	13	13	10	9	10	3	4
Sly05g0138461	M6	NA	27	88	54	7	3	18	40	6	1	2
Sly05g0138471	M6	NA	5	13	5	1	1	3	4	1	0	1
Sly05g0138481	M11	NA	15	15	16	8	4	17	15	19	4	1
Sly05g0138491	M12	NA	11	9	11	10	4	15	15	17	10	2
Sly05g0138501	M3	NA	154	137	122	72	73	125	153	97	87	87
Sly05g0138511	M1	NA	12	11	6	16	5	3	1	2	1	1
Sly05g0138521	M11	NA	25	24	28	22	26	29	28	34	34	47
Sly05g0138531	M1	NA	10	9	16	10	12	7	4	9	1	1
Sly05g0138551	M1	NA	12	13	10	12	9	7	7	6	2	2
Sly05g0138561	M6	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0138571	M1	NA	17	16	11	5	2	6	7	6	4	3
Sly05g0138591	M13	NA	22	22	29	35	40	30	23	32	21	17
Sly05g0138601	M3	NA	36	69	24	3	2	9	14	4	1	1
Sly05g0138611	M12	NA	19	30	25	67	52	22	24	26	61	36
Sly05g0138631	M1	NA	6	5	3	1	1	2	1	1	1	1
Sly05g0138641	M3	NA	76	64	36	5	4	21	26	12	2	2
Sly05g0138661	M7	NA	46	53	35	17	21	44	56	31	20	24
Sly05g0138671	M11	NA	32	34	32	32	42	38	37	41	41	56
Sly05g0138681	M21	NA	4	2	4	1	1	5	2	1	0	0
Sly05g0138691	M21	NA	4	1	4	0	1	5	1	1	0	0
Sly05g0138701	M11	NA	26	22	33	85	90	40	41	64	229	219
Sly05g0138721	M1	NA	2	1	3	1	0	1	1	1	0	0
Sly05g0138731	M23	NA	2	2	1	0	0	3	2	1	0	0
Sly05g0138751	M2	NA	80	74	73	114	266	70	74	78	163	316
Sly05g0138771	M12	NA	0	0	1	0	0	1	3	1	1	1
Sly05g0138781	M11	NA	13	14	20	38	37	26	21	32	29	27
Sly05g0138791	M18	NA	39	45	48	43	43	50	44	55	30	29
Sly05g0138801	M11	NA	17	18	18	28	43	20	19	23	21	27
Sly05g0138811	M1	NA	21	12	19	2	1	10	8	8	1	0
Sly05g0138841	M11	NA	295	301	384	294	272	488	460	522	275	257
Sly05g0138851	M12	NA	1	1	1	0	0	13	14	9	1	1
Sly05g0138861	M3	NA	2	3	2	0	0	3	2	1	0	0
Sly05g0138871	M1	NA	1	3	1	0	0	1	1	1	0	0
Sly05g0138881	M1	NA	63	57	65	61	67	48	51	51	51	56
Sly05g0138891	M3	NA	2	2	1	1	0	1	1	0	0	0
Sly05g0138921	M12	NA	11	10	13	9	7	21	23	27	9	8
Sly05g0138931	M22	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0138941	M22	NA	28	25	26	27	32	45	25	39	43	61
Sly05g0138961	M18	NA	21	24	28	34	32	31	24	34	32	31
Sly05g0138971	M6	NA	11	23	15	22	12	20	22	10	6	3
Sly05g0138981	M11	NA	1	1	1	1	1	1	1	1	2	0
Sly05g0138991	M12	NA	18	19	20	16	18	45	40	38	20	31
Sly05g0139001	M8	NA	12	12	11	16	19	12	13	10	16	17
Sly05g0139031	M12	NA	1	1	1	2	2	1	2	2	2	2
Sly05g0139041	M2	NA	3	4	4	3	3	3	3	4	2	3
Sly05g0139051	M1	NA	40	42	39	22	23	33	34	29	21	20
Sly05g0139091	M11	crtiso2	4	4	7	20	28	5	6	6	13	14
Sly05g0139111	M22	NA	0	0	1	0	1	2	1	2	1	0
Sly05g0139181	M11	NA	19	17	19	24	17	29	26	31	22	17
Sly05g0139191	M3	NA	72	69	59	81	61	58	58	43	50	51
Sly05g0139201	M23	NA	1	1	1	1	1	1	1	1	1	2
Sly05g0139211	M3	NA	38	36	36	40	53	30	35	33	40	73
Sly05g0139221	M1	NA	14	15	15	25	25	11	13	12	16	18
Sly05g0139231	M1	NA	41	39	41	39	43	34	33	37	57	48
Sly05g0139251	M12	NA	19	20	24	6	2	87	96	106	25	4
Sly05g0139271	M12	NA	7	9	12	28	9	18	28	51	363	117
Sly05g0139281	M11	NA	6	6	6	5	4	7	7	7	5	3
Sly05g0139391	M12	NA	14	12	17	16	21	16	14	17	30	54
Sly05g0139421	M1	NA	7	4	7	3	2	2	1	2	1	0
Sly05g0139441	M3	NA	2139	2185	1701	8386	6807	1054	1464	953	2442	1950
Sly05g0139451	M2	NA	1763	2027	1708	7604	4817	957	1274	876	1946	1191
Sly05g0139461	M2	NA	45	41	41	56	58	40	41	43	56	65
Sly05g0139471	M12	NA	6	8	8	8	5	8	9	10	8	4
Sly05g0139481	M1	NA	27	27	23	23	22	23	22	21	18	18
Sly05g0139491	M2	NA	60	60	58	53	53	45	58	41	41	44
Sly05g0139511	M2	NA	28	41	29	39	58	14	27	16	17	45
Sly05g0139531	M1	NA	7	8	8	16	10	6	5	6	7	12
Sly05g0139541	M3	NA	50	48	42	27	32	34	36	29	31	36
Sly05g0139571	M12	NA	1	1	3	6	4	1	4	8	38	36
Sly05g0139601	M3	NA	9	14	6	2	2	5	5	4	3	2
Sly05g0139621	M4	NA	4	4	4	2	1	5	4	5	2	1
Sly05g0139631	M3	NA	4	3	2	2	1	3	2	2	2	2
Sly05g0139641	M1	NA	3	4	3	2	1	3	2	2	3	1
Sly05g0139651	M3	NA	4	5	2	2	2	3	3	2	2	2
Sly05g0139661	M3	NA	12	13	7	4	4	7	7	6	9	8
Sly05g0139671	M3	NA	3	6	2	3	2	3	3	3	4	3
Sly05g0139681	M3	NA	6	7	5	4	2	6	5	6	6	3
Sly05g0139691	M10	NA	2	2	1	0	0	1	3	1	0	0
Sly05g0139701	M6	NA	20	25	4	1	1	15	46	10	1	1
Sly05g0139721	M12	NA	55	51	64	66	77	72	74	81	83	89
Sly05g0139731	M22	NA	2	0	2	0	0	13	1	15	0	0
Sly05g0139741	M22	NA	7	1	8	0	0	72	1	51	0	0
Sly05g0139781	M22	NA	1	0	1	0	0	5	0	5	0	0
Sly05g0139811	M12	NA	8	8	8	7	8	16	16	13	4	2
Sly05g0139831	M11	NA	7	7	8	6	5	8	6	8	5	5
Sly05g0139841	M19	NA	3	4	4	4	3	3	3	3	3	2
Sly05g0139851	M1	NA	3	3	3	3	2	3	2	2	2	2
Sly05g0139861	M1	NA	1	1	1	0	0	1	1	1	0	0
Sly05g0139871	M1	NA	29	29	30	18	18	25	24	23	18	18
Sly05g0139881	M12	NA	133	125	135	262	539	164	147	140	251	366
Sly05g0139901	M11	NA	2	1	2	0	1	3	3	2	1	1
Sly05g0139911	M20	NA	15	7	15	1	2	11	10	11	1	1
Sly05g0139931	M10	NA	3	3	2	2	2	4	5	2	2	2
Sly05g0139991	M3	NA	13	13	10	9	8	12	12	11	11	11
Sly05g0140001	M19	NA	13	14	13	10	8	14	11	12	11	9
Sly05g0140111	M19	NA	7	11	8	6	5	10	8	10	7	5
Sly05g0140031	M12	NA	128	120	173	591	466	218	209	299	678	496
Sly05g0140091	M12	NA	16	18	17	15	13	19	21	21	24	22
Sly05g0140101	M12	NA	2	2	3	2	1	3	3	3	2	1
Sly05g0140121	M1	NA	18	21	23	62	51	10	10	11	52	57
Sly05g0140181	M22	NA	1	0	1	0	0	2	0	3	0	0
Sly05g0140211	M11	steroid sulphotransfer	7	5	7	8	56	7	8	8	44	154
Sly05g0140221	M22	NA	1	1	1	0	0	3	1	4	0	0
Sly05g0140241	M10	NA	17	27	16	7	8	27	27	22	14	16
Sly05g0140251	M18	NA	17	20	18	14	13	19	16	20	17	16
Sly05g0140271	M9	NA	18	27	12	11	29	39	32	18	42	105
Sly05g0140291	M10	NA	25	34	12	12	35	42	45	21	49	141
Sly05g0140311	M13	NA	81	50	64	38	23	53	56	74	79	50
Sly05g0140321	M1	NA	36	39	35	24	24	22	24	21	28	28

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0051561	M15	NA	355	334	332	372	308	324	372	377	444	414
Sly12g0051571	M12	NA	4	4	3	4	4	9	16	11	8	18
Sly12g0051581	M12	NA	2	2	2	2	2	2	2	2	3	2
Sly12g0051591	M13	NA	47	43	54	64	77	50	47	54	56	67
Sly12g0051601	M2	NA	242	253	243	315	251	212	248	215	234	212
Sly12g0051611	M11	NA	73	63	121	185	258	202	185	280	343	379
Sly12g0051621	M1	NA	32	19	16	2	1	12	1	6	1	0
Sly12g0051631	M11	NA	27	16	28	2	8	215	154	203	10	4
Sly12g0051651	M12	NA	3	2	2	1	1	3	3	2	1	1
Sly12g0051661	M12	NA	1	1	1	1	1	3	3	2	1	1
Sly12g0051671	M11	NA	20	15	22	41	43	26	27	33	31	28
Sly12g0051681	M16	NA	340	270	232	205	156	182	187	166	201	148
Sly12g0051691	M12	NA	28	29	29	48	49	33	31	33	43	49
Sly12g0051701	M1	NA	556	500	450	357	269	377	378	370	333	237
Sly12g0051721	M12	NA	112	110	118	151	119	117	140	145	176	142
Sly12g0051741	M18	NA	80	80	84	95	115	86	76	87	94	111
Sly12g0051751	M3	SlPRMT8	88	92	71	46	43	52	60	44	62	58
Sly12g0051761	M11	NA	36	33	35	21	11	33	34	39	22	15
Sly12g0051771	M1	NA	41	41	45	65	68	36	34	36	46	52
Sly12g0051781	M11	NA	13	14	13	14	18	16	14	16	13	14
Sly12g0051791	M1	NA	3	4	7	4	3	1	1	1	1	1
Sly12g0051801	M1	NA	46	50	41	35	38	28	32	30	29	35
Sly12g0051811	M1	NA	60	65	51	49	47	41	40	44	41	46
Sly12g0051831	M11	TBG4	18	23	41	557	732	49	38	73	130	139
Sly12g0051851	M2	NA	59	56	55	73	65	44	60	42	60	52
Sly12g0051861	M11	NA	28	28	31	39	43	43	39	45	43	44
Sly12g0051871	M18	NA	14	13	16	19	21	22	18	28	18	19
Sly12g0051881	M18	NA	15	16	19	27	25	25	19	29	21	15
Sly12g0051891	M12	SlCKX6	20	17	20	1	1	275	290	274	1	1
Sly12g0051901	M12	NA	46	41	45	51	46	43	53	49	60	46
Sly12g0051931	M3	NA	3	4	1	0	0	2	1	1	0	0
Sly12g0051941	M3	NAP1;2	165	184	154	73	76	143	190	134	88	133
Sly12g0051951	M3	NA	12	14	10	6	2	10	10	7	2	1
Sly12g0051961	M1	NA	6	10	8	3	1	1	1	1	1	1
Sly12g0051971	M10	NA	56	70	45	44	38	83	96	56	53	67
Sly12g0051981	M11	LCY-E	4	3	5	6	1	19	14	21	3	1
Sly12g0051991	M9	NA	2	3	2	2	1	3	3	3	2	2
Sly12g0052001	M7	NA	35	107	44	25	182	56	140	73	88	368
Sly12g0052021	M12	NA	3	5	3	5	2	12	16	29	16	8
Sly12g0052031	M3	NA	61	65	40	25	33	25	29	12	19	70
Sly12g0052041	M1	NA	29	24	25	24	29	20	21	23	24	31
Sly12g0052051	M23	NA	1	1	1	1	2	1	1	1	1	1
Sly12g0052061	M23	NA	2	1	1	3	9	4	1	1	4	19
Sly12g0052071	M3	NA	87	93	70	103	155	65	76	70	129	188
Sly12g0052091	M11	NA	16	7	20	7	2	36	28	49	14	2
Sly12g0052101	M11	NA	7	4	7	3	1	16	13	16	3	2
Sly12g0052111	M11	NA	38	37	39	43	39	47	44	52	55	58
Sly12g0052121	M11	NA	26	24	29	29	30	32	31	38	30	32
Sly12g0052131	M11	NA	14	15	18	27	36	20	19	22	36	43
Sly12g0052141	M1	NA	1	1	1	14	16	1	1	1	3	3
Sly12g0052151	M16	NA	44	36	37	81	77	36	35	36	64	78
Sly12g0052181	M3	NA	153	148	146	182	214	128	147	131	176	185
Sly12g0052191	M3	NA	58	57	47	83	54	45	52	27	21	11
Sly12g0052201	M7	NA	13	18	11	8	6	16	24	14	16	12
Sly12g0052211	M12	NA	2	2	1	1	0	7	5	6	1	1
Sly12g0052221	M2	NA	112	108	90	67	27	79	91	65	27	10
Sly12g0052241	M11	NA	2	3	3	3	1	8	7	11	5	1
Sly12g0052251	M12	NA	33	34	27	38	63	35	35	33	36	47
Sly12g0052261	M3	JAZ1	211	267	184	1	2	126	166	26	1	3
Sly12g0052271	M11	NA	18	21	19	20	23	22	20	22	24	21
Sly12g0052281	M6	NA	5	25	11	3	38	5	13	6	1	55
Sly12g0052291	M11	NA	240	216	212	234	330	280	260	267	133	271
Sly12g0052301	M11	NA	5	3	3	4	5	4	5	5	8	10
Sly12g0052311	M3	NA	4	4	4	5	4	4	4	3	5	4
Sly12g0052321	M1	NA	68	55	53	52	31	4	2	3	1	2
Sly12g0052371	M1	SuSy (SUS4)	242	124	345	10	5	62	14	42	1	1
Sly12g0052381	M11	NA	1	1	1	1	0	1	1	1	0	0
Sly12g0052411	M3	NA	47	50	37	29	34	23	26	20	25	30
Sly12g0052451	M3	NA	45	44	43	45	42	35	40	40	48	47
Sly12g0052461	M1	NA	16	17	11	16	18	6	6	5	19	23
Sly12g0052471	M12	NA	68	66	65	224	242	63	70	73	147	249
Sly12g0052481	M1	NA	103	96	90	220	262	71	75	72	155	304
Sly12g0052501	M1	NA	5	6	5	2	2	5	2	3	1	1
Sly12g0052511	M1	NA	12	10	13	11	11	11	12	11	6	7
Sly12g0052521	M13	NA	39	30	51	80	97	45	40	69	85	82
Sly12g0052531	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0052551	M13	NA	37	34	45	63	90	38	39	48	71	114
Sly12g0052561	M1	NA	24	21	29	8	6	8	7	11	15	40
Sly12g0052571	M1	NA	7	2	13	0	0	0	0	1	0	0
Sly12g0052581	M12	NA	7	8	6	4	5	9	9	8	6	11
Sly12g0052591	M3	NA	20	36	14	1	1	6	7	1	0	1
Sly12g0052611	M3	NA	2	8	2	0	0	2	3	1	0	0
Sly12g0052621	M3	NA	2	5	2	0	0	2	3	1	0	0
Sly12g0052631	M3	EBF2	218	252	109	172	91	157	181	61	207	127
Sly12g0052641	M1	NA	12	13	13	8	9	8	7	8	4	5
Sly12g0052661	M18	NA	19	21	21	39	52	21	20	21	19	34
Sly12g0052671	M11	NA	11	12	15	14	3	36	33	46	21	1
Sly12g0052681	M20	NA	123	106	134	81	137	101	83	115	169	223
Sly12g0052701	M1	NA	30	29	30	27	33	22	23	24	32	36
Sly12g0052711	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly12g0052721	M1	NA	37	36	37	42	39	29	29	29	29	30
Sly12g0052731	M12	NA	1	1	1	1	1	4	5	3	3	3
Sly12g0052761	M1	NA	13	16	25	35	16	4	2	3	1	1
Sly12g0052801	M1	NA	5	5	8	1	1	1	0	0	0	0
Sly12g0052821	M10	NA	1	1	1	1	0	1	1	0	0	0
Sly12g0052841	M1	NA	27	29	25	12	6	16	15	11	2	1
Sly12g0052851	M1	NA	24	24	21	11	4	10	13	9	2	2
Sly12g0052861	M1	NA	17	12	25	3	1	7	5	7	1	0
Sly12g0052871	M11	NA	51	43	60	54	72	75	74	105	99	122
Sly12g0052881	M3	NA	11	15	14	3	2	9	12	7	2	1
Sly12g0052891	M12	NA	28	26	32	35	38	34	40	37	55	54
Sly12g0052901	M3	NA	14	14	9	5	3	7	8	6	2	1
Sly12g0052931	M1	NA	78	75	71	46	36	53	49	51	35	32
Sly12g0052951	M1	NA	21	15	23	10	7	11	11	13	4	5
Sly12g0052961	M12	NA	32	36	32	37	27	42	46	43	34	28
Sly12g0052991	M11	NA	4	3	4	1	1	19	14	22	1	1
Sly12g0053001	M11	NA	13	10	16	1	1	20	23	21	1	0
Sly12g0053011	M12	NA	6	6	6	6	5	6	6	6	7	5
Sly12g0053031	M11	NA	241	238	247	214	166	273	248	267	205	158
Sly12g0053041	M10	NA	18	19	14	11	12	22	21	16	10	13
Sly12g0053051	M13	NA	54	47	56	73	92	55	50	64	76	87
Sly12g0053061	M3	NA	186	192	153	141	157	125	122	104	95	110
Sly12g0053091	M1	NA	111	115	98	61	76	40	39	39	30	45
Sly12g0053101	M3	NA	70	78	56	2	1	15	20	3	1	1
Sly12g0053111	M1	NA	19	25	14	1	1	3	6	1	1	1
Sly12g0053121	M3	NA	1	1	1	0	0	1	1	0	0	0
Sly12g0053131	M13	NA	218	203	259	343	345	248	236	276	294	326
Sly12g0053141	M1	NA	2	2	2	1	1	1	1	1	0	1
Sly12g0053161	M12	NA	882	813	854	600	655	898	955	1048	696	756
Sly12g0053201	M12	NA	1	1	1	0	0	1	1	1	1	0
Sly12g0053211	M12	NA	18	20	18	28	27	41	51	43	71	39
Sly12g0053221	M3	NA	17	17	15	22	21	14	16	12	22	26
Sly12g0053231	M7	NA	170	199	129	132	144	189	193	172	846	787
Sly12g0053241	M1	NA	3	4	5	4	1	1	1	1	1	1
Sly12g0053251	M1	NA	16	18	16	21	20	14	14	16	27	22
Sly12g0053261	M1	NA	3	4	4	4	5	2	3	2	5	3
Sly12g0053271	M3	NA	1	1	1	1	1	1	1	1	2	1
Sly12g0053281	M11	NA	18	15	17	32	62	26	21	29	48	73
Sly12g0053291	M3	NA	3	2	2	1	1	1	1	2	2	1
Sly12g0053301	M12	NA	4	3	4	16	37	14	9	20	157	129
Sly12g0053321	M3	NA	13	13	11	11	13	12

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0140341	M3	NA	22	23	23	34	24	17	20	19	36	16
Sly05g0140351	M1	NA	85	86	141	96	55	2	1	1	1	1
Sly05g0140361	M12	RIN	9	16	36	929	1459	10	48	109	1623	1394
Sly05g0140391	M3	NA	18	18	15	17	18	12	14	12	17	16
Sly05g0140411	M19	NA	4	4	6	3	3	4	4	4	1	1
Sly05g0140421	M1	NA	70	69	68	66	54	37	45	31	36	34
Sly05g0140431	M2	NA	32	31	25	35	22	20	26	19	32	23
Sly05g0140441	M1	NA	10	11	10	9	10	8	8	7	9	7
Sly05g0140451	M14	NA	20	21	24	47	77	17	18	23	72	80
Sly05g0140461	M11	NA	53	33	76	25	29	74	57	100	37	27
Sly05g0140471	M11	NA	15	15	16	17	18	19	16	19	24	17
Sly05g0140481	M11	NA	43	36	34	31	42	45	40	47	47	62
Sly05g0140491	M18	NA	29	31	24	16	22	29	24	37	16	16
Sly05g0140501	M12	NA	14	15	13	18	25	17	18	19	37	41
Sly05g0140511	M11	NA	312	241	257	242	194	357	305	337	163	193
Sly05g0140581	M22	NA	1	0	1	0	0	7	0	3	0	0
Sly05g0140591	M3	NA	16	24	16	1	1	15	15	5	1	1
Sly05g0140611	M1	NA	24	23	24	14	14	18	20	19	16	15
Sly05g0140621	M1	NA	28	28	26	19	24	21	21	19	27	33
Sly05g0140641	M1	NA	17	13	7	1	1	3	2	1	1	1
Sly05g0140651	M1	NA	12	12	11	11	13	9	10	11	11	13
Sly05g0140661	M1	NA	1	1	1	2	5	1	1	1	1	1
Sly05g0140671	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0140681	M11	PPR-like23	8	8	7	8	6	8	10	9	7	6
Sly05g0140691	M1	NA	44	41	43	51	44	39	37	38	26	18
Sly05g0140701	M1	NA	40	42	36	110	163	34	35	39	118	122
Sly05g0140731	M1	NA	33	27	27	9	9	17	18	15	6	6
Sly05g0140741	M1	NA	12	12	11	12	11	7	9	8	12	15
Sly05g0140751	M1	NA	33	42	40	29	28	23	22	20	19	14
Sly05g0140761	M3	NA	5	7	3	2	2	2	3	2	2	1
Sly05g0140771	M1	NA	2	2	2	0	0	1	1	1	0	0
Sly05g0140791	M12	NA	45	44	43	38	36	46	44	44	32	30
Sly05g0140801	M18	NA	15	19	19	18	14	24	16	18	9	10
Sly05g0140811	M22	NA	1	1	1	0	0	1	1	1	1	0
Sly05g0140821	M22	NA	1	1	1	1	1	2	1	1	1	1
Sly05g0140831	M11	NA	5	6	6	4	1	8	5	8	2	1
Sly05g0140841	M1	NA	23	20	16	5	2	9	6	4	1	1
Sly05g0140851	M2	NA	40	40	37	38	37	33	35	30	37	34
Sly05g0140861	M1	NA	45	46	45	43	48	38	36	36	50	68
Sly05g0140871	M22	NA	1	0	1	0	0	2	1	3	0	1
Sly05g0140891	M3	NA	3	4	2	1	1	1	2	1	1	1
Sly05g0140901	M12	NA	22	23	18	12	10	37	46	37	14	8
Sly05g0140911	M12	NA	24	28	28	81	49	50	62	81	107	52
Sly05g0140921	M1	NA	21	21	23	23	27	19	17	20	21	29
Sly05g0140941	M8	NA	46	46	40	70	119	47	54	42	57	62
Sly05g0140971	M1	NA	46	59	48	54	80	19	20	18	28	58
Sly05g0140981	M11	NA	51	41	74	68	11	63	47	72	11	1
Sly05g0141001	M1	NA	2	2	2	1	3	1	1	1	1	1
Sly05g0141011	M1	NA	4	6	6	7	6	1	1	2	1	1
Sly05g0141021	M12	NA	1	1	2	1	1	2	2	2	1	2
Sly05g0141031	M11	NA	2	2	2	2	2	3	2	3	1	2
Sly05g0141041	M12	NA	2	2	3	1	2	3	2	2	2	3
Sly05g0141051	M1	NA	74	60	95	63	67	59	62	67	51	73
Sly05g0141061	M1	NA	1	1	1	0	0	0	0	1	0	0
Sly05g0141071	M3	NA	725	714	704	189	307	285	536	240	76	290
Sly05g0141091	M3	NA	43	42	31	25	25	28	35	27	37	43
Sly05g0141101	M11	NA	12	14	17	21	5	27	27	38	9	1
Sly05g0141111	M11	NA	40	41	49	53	72	69	63	72	69	99
Sly05g0141121	M11	NA	25	23	30	34	51	52	46	57	45	42
Sly05g0141131	M11	NA	3	3	3	3	2	3	3	3	2	1
Sly05g0141141	M1	NA	12	12	12	11	14	10	10	9	9	7
Sly05g0141151	M11	NA	10	10	12	10	12	15	14	15	11	11
Sly05g0141161	M12	NA	1	2	2	1	1	3	2	2	2	1
Sly05g0141171	M1	NA	1	1	1	1	1	1	1	1	0	1
Sly05g0141181	M12	NA	4	4	5	1	1	8	6	5	1	1
Sly05g0141191	M2	NA	30	35	28	46	60	26	32	25	72	66
Sly05g0141201	M11	NA	31	36	42	65	86	51	51	70	84	141
Sly05g0141211	M12	NA	15	15	15	25	37	18	18	17	32	45
Sly05g0141221	M5	NA	7	6	5	5	6	7	7	6	6	5
Sly05g0141261	M1	NA	21	22	13	14	22	2	3	2	7	11
Sly05g0141271	M12	NA	1	2	2	1	1	2	2	2	1	1
Sly05g0141281	M11	NA	13	13	21	4	1	44	33	43	1	1
Sly05g0141291	M12	NA	5	5	6	5	3	8	8	8	5	5
Sly05g0141301	M12	NA	13	12	17	14	8	20	22	18	8	5
Sly05g0141311	M3	NA	2	4	3	2	2	3	2	3	3	2
Sly05g0141321	M12	NA	6	6	8	20	15	15	22	29	63	45
Sly05g0141341	M3	NA	36	73	53	35	41	25	38	39	128	85
Sly05g0141351	M12	NA	0	1	1	1	1	1	1	2	4	8
Sly05g0141381	M5	NA	3	7	1	1	1	4	4	1	1	1
Sly05g0141391	M5	NA	8	13	2	1	1	11	11	2	1	0
Sly05g0141401	M3	NA	1	1	1	1	1	1	1	0	0	1
Sly05g0141421	M3	NA	11	11	10	8	7	8	9	8	6	7
Sly05g0141431	M2	NA	21	25	21	20	20	21	23	20	32	33
Sly05g0141441	M12	NA	7	7	7	28	17	13	12	17	49	21
Sly05g0141451	M12	NA	2	2	1	4	3	2	3	3	9	4
Sly05g0141521	M3	NA	125	122	111	125	105	100	118	106	140	111
Sly05g0141531	M1	NA	14	15	14	29	37	13	12	15	20	25
Sly05g0141541	M11	NA	50	43	44	57	66	57	51	65	77	89
Sly05g0141551	M12	NA	8	10	12	26	65	18	15	23	48	85
Sly05g0141561	M12	NA	12	10	7	19	70	16	14	24	55	112
Sly05g0141571	M3	NA	153	169	117	109	110	106	123	83	133	148
Sly05g0141641	M8	NA	45	41	38	41	25	43	48	39	20	6
Sly05g0141651	M8	NA	11	13	10	13	10	13	12	10	6	3
Sly05g0141661	M11	SISDG51	3	3	5	3	2	7	6	7	1	2
Sly05g0141691	M11	SISDG53	9	9	13	38	41	23	20	29	36	36
Sly05g0141711	M1	NA	18	18	14	8	8	9	10	7	11	10
Sly05g0141721	M1	NA	3	3	2	2	2	1	1	1	1	2
Sly05g0141731	M18	NA	4	4	4	4	4	4	4	5	3	2
Sly05g0141741	M11	NA	5	7	6	8	5	9	8	10	9	5
Sly05g0141751	M1	NA	25	25	20	37	9	9	8	9	8	7
Sly05g0141771	M1	NA	62	56	57	48	22	49	50	43	22	7
Sly05g0141781	M12	NA	1	1	1	1	2	1	2	2	2	2
Sly05g0141791	M1	NA	4	4	5	3	2	4	3	3	2	2
Sly05g0141821	M3	NA	12	14	11	8	4	11	11	9	4	2
Sly05g0141831	M5	NA	16	19	14	13	10	17	17	12	17	11
Sly05g0141851	M11	NA	8	8	9	7	5	10	9	12	6	5
Sly05g0141861	M11	NA	26	27	33	22	14	35	30	36	21	20
Sly05g0141871	M19	NA	27	33	43	30	16	39	30	43	21	14
Sly05g0141881	M11	NA	3	3	4	2	1	3	4	3	1	0
Sly05g0141891	M12	NA	1	1	2	1	1	3	4	5	4	2
Sly05g0141901	M12	NA	116	119	117	125	128	114	120	118	122	139
Sly05g0141941	M11	NA	56	58	67	39	23	116	113	125	43	26
Sly05g0141951	M12	NA	4	3	4	1	1	8	13	7	2	0
Sly05g0141961	M12	NA	22	21	21	25	32	33	39	31	44	67
Sly05g0141971	M18	NA	14	17	16	19	20	25	21	23	25	30
Sly05g0141981	M9	NA	8	11	7	3	5	39	112	21	4	13
Sly05g0142021	M12	NA	40	40	43	76	83	68	66	75	81	72
Sly05g0142031	M11	NA	2	2	3	4	1	8	4	5	1	1
Sly05g0142051	M1	NA	15	15	17	12	7	13	12	11	2	1
Sly05g0142071	M11	NA	34	27	45	83	198	52	44	83	182	301
Sly05g0142081	M19	NA	39	42	42	44	46	41	37	42	56	56
Sly05g0142091	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly05g0142101	M12	NA	24	26	29	57	72	44	42	44	47	64
Sly05g0142111	M1	NA	8	7	9	7	14	2	2	3	19	71
Sly05g0142121	M12	SIERF.F9	1	1	1	2	2	1	1	1	1	1
Sly05g0142131	M11	NA	1	1	2	1	1	3	2	5	1	1
Sly05g0142141	M12	NA	12	8	7	1	1	36	24	30	1	1
Sly05g0142161	M6	NA	17	21	21	21	33	16	20	14	21	48
Sly05g0142221	M1	NA	43	38	40	158	87	1	1	1	2	1
Sly05g0142231	M1	NA	79	93	90	111	53	11	11	4	4	4
Sly05g0142251	M1	NA	29	27	21	11	5	12	10	10	3	2
Sly05g0142261	M11	NA	12	12	16	18	19	22	18	23	17	13
Sly05g0142271	M12	NA	1	1	1	1	1	2	2	1	1	1
Sly05g0142281	M22	NA	2	1	1	0	0	5	2	4	0	0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0053361	M19	NA	4	5	5	5	4	6	5	7	4	4
Sly12g0053371	M19	NA	9	9	11	11	8	10	8	10	15	12
Sly12g0053381	M18	NA	7	8	9	10	7	9	8	10	11	9
Sly12g0053391	M22	NA	6	4	5	5	4	7	5	6	5	6
Sly12g0053401	M18	NA	3	5	5	4	4	7	5	6	5	5
Sly12g0053411	M12	NA	8	8	9	10	11	12	11	12	16	18
Sly12g0053421	M12	TIL	126	153	164	1155	1766	316	467	580	4077	4234
Sly12g0053431	M18	SIRR22	19	20	22	26	29	21	20	23	44	48
Sly12g0053441	M3	NA	56	56	54	66	74	38	47	42	76	98
Sly12g0053451	M1	NA	111	102	92	85	62	75	79	73	87	60
Sly12g0053481	M11	NA	16	15	20	27	31	24	22	31	32	27
Sly12g0053491	M3	NA	198	187	119	103	89	134	175	88	77	78
Sly12g0053501	M12	NA	198	149	138	109	78	258	292	269	280	397
Sly12g0053511	M3	NA	17	27	23	12	6	16	27	13	15	30
Sly12g0053521	M12	NA	5	8	4	2	22	10	43	9	5	87
Sly12g0053531	M12	NA	1	2	1	1	1	2	2	4	3	4
Sly12g0053541	M12	NA	22	22	20	19	36	31	37	36	36	81
Sly12g0053551	M10	NA	11	21	8	4	11	29	39	13	6	14
Sly12g0053561	M3	NA	11	9	5	4	9	8	9	5	11	26
Sly12g0053591	M3	NA	1	1	1	1	1	1	1	1	0	0
Sly12g0053641	M3	NA	105	104	75	61	51	70	75	55	54	52
Sly12g0053661	M7	NA	8	16	8	7	58	9	23	10	19	112
Sly12g0053691	M22	NA	1	1	1	0	0	1	1	1	1	1
Sly12g0053721	M1	NA	5	4	8	0	0	1	0	0	0	0
Sly12g0053741	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly12g0053751	M12	NA	1	1	1	0	0	2	2	2	1	0
Sly12g0053771	M12	NA	19	19	20	24	32	23	24	26	36	45
Sly12g0053781	M3	NA	8	9	7	7	9	6	7	6	9	8
Sly12g0053791	M18	NA	1	1	1	2	1	1	1	2	2	1
Sly12g0053801	M18	NA	1	2	1	1	1	2	1	1	2	1
Sly12g0053811	M1	NA	1	1	1	1	1	1	1	1	2	1
Sly12g0053821	M11	NA	1	1	1	1	1	1	1	1	2	2
Sly12g0053831	M10	NA	5	6	5	1	1	6	8	5	1	1
Sly12g0053841	M1	NA	24	23	27	23	29	17	18	18	28	27
Sly12g0053861	M9	NA	14	16	13	14	9	36	44	30	20	13
Sly12g0053881	M3	NA	30	64	45	1	1	26	35	7	1	1
Sly12g0053901	M1	NA	119	102	76	66	84	27	26	40	15	10
Sly12g0053911	M11	NA	218	218	334	294	315	748	636	973	438	682
Sly12g0053921	M22	NA	6	3	4	1	1	8	3	6	1	1
Sly12g0053971	M3	NA	82	87	74	59	59	74	88	74	75	85
Sly12g0053981	M12	NA	2	2	3	10	4	13	21	22	67	36
Sly12g0054001	M22	NA	1	0	1	0	0	1	0	1	0	0
Sly12g0054041	M23	NA	5	3	2	2	2	12	6	6	4	3
Sly12g0054051	M11	NA	21	23	26	28	35	34	34	46	54	49
Sly12g0054061	M11	NA	137	128	155	150	143	186	154	188	116	86
Sly12g0054071	M1	NA	9	8	10	8	4	8	8	9	4	5
Sly12g0054081	M3	NA	108	109	104	149	131	81	96	90	151	120
Sly12g0054091	M11	NA	14	12	16	29	35	14	14	19	26	22
Sly12g0054111	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0054121	M12	NA	26	24	24	18	18	31	29	28	17	24
Sly12g0054131	M11	NA	23	20	27	14	15	35	33	38	9	10
Sly12g0054141	M1	NA	27	19	14	1	1	16	14	14	1	1
Sly12g0054161	M23	NA	80	29	37	4	1	192	67	103	12	2
Sly12g0054171	M1	NA	274	238	227	136	91	185	197	189	145	112
Sly12g0054181	M3	NA	8	16	5	3	2	4	7	2	1	2
Sly12g0054191	M13	NA	58	58	58	50	65	44	61	70	172	124
Sly12g0054201	M1	NA	101	115	61	1	1	13	12	1	1	1
Sly12g0054211	M3	NA	36	29	14	0	0	13	12	1	0	0
Sly12g0054231	M3	NA	2	3	1	1	1	1	1	1	1	1
Sly12g0054241	M2	NA	178	196	171	229	154	125	165	109	134	113
Sly12g0054251	M21	NA	7	2	3	1	0	5	2	1	1	0
Sly12g0054261	M11	NA	5	4	5	6	10	5	5	6	8	8
Sly12g0054271	M12	SIXTH9	2	4	3	2	6	8	14	7	4	16
Sly12g0054281	M9	NA	3	5	9	2	8	12	26	23	10	24
Sly12g0054291	M1	SlLOX10	60	44	32	1	1	1	1	1	0	1
Sly12g0054301	M11	NA	25	22	27	30	41	32	29	37	30	38
Sly12g0054311	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly12g0054341	M1	NA	28	76	15	0	0	3	1	1	0	0
Sly12g0054371	M12	NA	16	17	17	28	56	18	18	20	37	81
Sly12g0054381	M1	NA	1	1	1	1	0	1	1	1	1	0
Sly12g0054401	M1	NA	73	75	62	175	98	52	40	29	12	8
Sly12g0054411	M1	NA	1	1	1	1	1	1	0	1	1	1
Sly12g0054421	M3	NA	35	48	41	47	61	28	32	27	48	59
Sly12g0054431	M1	NA	20	24	20	27	32	15	15	16	25	26
Sly12g0054441	M3	NA	16	15	14	15	14	15	15	15	17	15
Sly12g0054481	M1	NA	6	6	6	3	3	1	2	2	3	3
Sly12g0054511	M1	NA	44	43	47	45	41	36	39	38	37	38
Sly12g0054521	M11	NA	5	4	5	3	1	20	19	29	4	1
Sly12g0054531	M1	NA	2	2	2	2	2	1	1	1	1	1
Sly12g0054551	M11	NA	2	1	3	186	1192	2	3	2	27	280
Sly12g0054561	M1	NA	24	20	26	20	20	7	7	9	6	3
Sly12g0054571	M3	ETR1	41	42	38	31	31	36	38	37	27	26
Sly12g0054581	M12	NA	51	47	52	92	113	56	59	48	121	127
Sly12g0054591	M6	NA	5	13	4	0	1	4	6	1	0	0
Sly12g0054611	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0054621	M3	NA	17	16	11	8	10	10	8	7	4	7
Sly12g0054631	M1	NA	4	4	3	1	1	0	1	0	0	0
Sly12g0054651	M3	NA	4	5	4	5	5	3	4	3	4	4
Sly12g0054661	M1	NA	19	5	27	1	1	1	1	1	0	0
Sly12g0054671	M1	NA	13	4	19	1	1	1	1	1	0	0
Sly12g0054681	M11	NA	39	38	58	143	154	83	81	120	130	134
Sly12g0054691	M12	NA	13	13	15	28	27	27	30	35	59	65
Sly12g0054701	M11	NA	64	54	73	36	24	85	68	91	31	29
Sly12g0054711	M11	NA	24	9	47	3	5	65	45	89	4	3
Sly12g0054721	M12	NA	45	39	44	62	118	56	59	56	94	166
Sly12g0054751	M4	NA	28	27	31	64	94	32	32	31	67	117
Sly12g0054761	M3	NA	19	19	15	14	21	15	23	10	13	29
Sly12g0054771	M3	NA	2	3	1	1	2	2	3	1	2	3
Sly12g0054781	M11	NA	47	39	62	68	58	53	52	65	71	94
Sly12g0054791	M11	NA	47	50	47	48	47	53	50	63	47	43
Sly12g0054801	M11	NA	89	85	96	159	209	101	106	115	179	274
Sly12g0054811	M11	NA	3	4	4	9	4	4	4	4	13	4
Sly12g0054831	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0054841	M12	NA	16	18	20	33	27	53	55	69	69	52
Sly12g0054851	M1	NA	1	1	1	1	1	0	1	1	0	0
Sly12g0054861	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly12g0054871	M6	NA	2	2	2	1	0	3	3	1	0	0
Sly12g0054881	M3	NA	165	171	105	118	145	105	89	122	259	287
Sly12g0054911	M1	NA	5	5	5	10	7	3	1	2	1	1
Sly12g0054961	M12	NA	154	181	168	1020	2129	290	479	594	4665	3960
Sly12g0054971	M12	HUP54	26	22	45	847	898	31	51	186	3459	1557
Sly12g0054981	M11	NA	8	4	13	4	4	25	20	30	13	6
Sly12g0055001	M3	NA	3	2	1	1	0	1	0	0	0	0
Sly12g0055021	M1	NA	67	69	62	27	30	27	31	22	15	20
Sly12g0055031	M1	NA	115	127	105	42	50	51	52	40	26	28
Sly12g0055061	M3	NA	22	20	20	24	29	18	18	19	32	32
Sly12g0055071	M12	NA	26	24	26	22	24	46	45	51	35	32
Sly12g0055081	M11	NA	70	50	61	61	105	97	87	115	92	175
Sly12g0055091	M3	NA	25	30	17	14	38	28	15	19	39	106
Sly12g0055121	M11	NA	6	6	9	11	20	9	9	9	13	21
Sly12g0055131	M11	NA	1	1	1	1	2	1	1	1	1	2
Sly12g0055161	M11	NA	21	23	25	28	31	23	23	26	38	39
Sly12g0055171	M12	ORC3	7	7	8	4	4	26	22	20	7	6
Sly12g0055181	M11	NA	26	23	32	30	20	38	32	45	24	14
Sly12g0055201	M3	NA	100	147	49	26	21	14	25	5	2	2
Sly12g0055211	M1	NA	18	20	19	7	4	9	10	6	3	5
Sly12g0055221	M9	NA	16	17	16	21	17	18	24	18	18	14
Sly12g0055231	M11	NA	65	55	80	78	107	88	82	101	85	142
Sly12g0055261	M19	NA	27	26	29	24	23	27	24	28	25	24
Sly12g0055271	M1	NA	23	32	14	8	7	4	3	3	5	6
Sly12g0055281	M19	NA	5	5	5	3	2	5	4	5	1	1
Sly12g0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0142301	M22	NA	61	53	50	58	60	64	50	58	73	75
Sly05g0142311	M6	NA	2	2	3	2	5	3	2	1	1	1
Sly05g0142321	M11	NA	47	47	53	80	62	85	69	76	24	22
Sly05g0142331	M3	NA	31	32	27	28	22	27	29	23	14	17
Sly05g0142341	M18	NA	26	26	30	25	25	30	25	30	24	26
Sly05g0142351	M5	NA	45	76	35	8	4	44	57	13	3	3
Sly05g0142371	M2	NA	37	37	36	39	35	37	36	34	39	35
Sly05g0142381	M3	NA	47	50	39	27	30	44	41	35	27	24
Sly05g0142391	M12	NA	16	19	18	19	21	18	18	18	20	22
Sly05g0142401	M11	NA	4	4	5	3	2	4	5	4	2	1
Sly05g0142411	M3	NA	18	18	13	37	11	10	12	5	10	2
Sly05g0142421	M3	NA	23	25	16	44	10	13	11	6	11	3
Sly05g0142431	M1	NA	146	136	141	186	282	121	124	126	202	276
Sly05g0142471	M1	NA	6	3	4	1	0	1	1	1	1	0
Sly05g0142481	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly05g0142491	M11	NA	10	10	11	9	5	13	14	16	8	4
Sly05g0142521	M12	NA	1	1	1	1	0	1	1	1	0	0
Sly05g0142541	M15	NA	77	65	58	93	85	65	70	69	98	106
Sly05g0142551	M22	NA	3	1	3	1	1	6	2	9	1	1
Sly05g0142561	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly05g0142571	M12	NA	23	27	26	33	31	33	38	31	54	45
Sly05g0142591	M11	NA	13	15	20	30	34	30	27	31	35	33
Sly05g0142601	M1	NA	19	19	17	12	9	13	11	13	10	10
Sly05g0142611	M1	NA	22	21	17	14	12	13	11	14	11	13
Sly05g0142621	M3	NA	1	1	1	1	0	1	1	1	1	1
Sly05g0142631	M1	NA	259	263	285	319	298	194	209	201	251	293
Sly05g0142641	M20	SIPL	49	29	52	1	1	38	28	28	1	0
Sly05g0142661	M18	NA	73	75	82	90	106	79	67	83	108	123
Sly05g0142681	M1	NA	36	36	39	58	87	30	26	32	43	51
Sly05g0142701	M18	NA	29	31	39	35	31	42	32	39	27	28
Sly05g0142711	M12	NA	37	40	46	46	49	51	47	47	42	58
Sly05g0142721	M12	NA	19	22	34	125	144	42	53	56	135	150
Sly05g0142731	M19	NA	19	17	20	10	9	17	16	19	15	10
Sly05g0142741	M22	NA	1	1	1	0	0	3	1	2	0	0
Sly05g0142781	M22	NA	1	1	1	0	0	4	1	4	0	0
Sly05g0142791	M1	NA	18	20	16	10	9	12	11	9	4	3
Sly05g0142821	M1	NA	6	9	6	4	3	4	4	3	1	1
Sly05g0142851	M11	NA	3	2	3	4	1	5	4	6	4	1
Sly05g0142861	M19	NA	18	18	19	20	15	18	19	19	15	12
Sly05g0142871	M1	NA	1	1	1	1	0	1	1	1	0	1
Sly05g0142891	M1	NA	3	4	3	2	1	1	1	1	1	1
Sly05g0142901	M19	NA	7	7	7	7	6	7	6	7	4	2
Sly05g0142911	M1	NA	6	6	12	8	4	1	1	1	1	0
Sly05g0142921	M1	NA	3	4	4	4	3	1	0	0	0	0
Sly05g0142931	M20	SIRR21	22	18	24	9	2	19	13	17	4	1
Sly05g0142941	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly05g0142991	M9	NA	6	3	4	6	20	11	26	9	40	20
Sly05g0143001	M11	NA	63	62	82	96	114	121	110	149	156	144
Sly05g0143011	M12	NA	5	6	7	10	19	8	11	8	14	26
Sly05g0143031	M3	NA	32	39	24	21	21	19	20	13	13	14
Sly05g0143041	M13	NA	4	4	6	7	6	5	4	4	5	5
Sly05g0143061	M1	NA	5	5	5	6	6	3	4	4	8	8
Sly05g0143081	M1	NA	53	57	56	226	166	4	3	2	2	2
Sly05g0143091	M11	NA	5	6	6	3	3	7	6	6	5	3
Sly05g0143131	M10	NA	972	891	783	703	536	988	1202	846	655	511
Sly05g0143141	M12	NA	7	8	6	6	3	10	10	9	9	3
Sly05g0143151	M12	NA	6	8	6	5	4	9	10	9	8	3
Sly05g0143161	M19	NA	12	13	12	11	10	12	10	11	9	9
Sly05g0143171	M3	NA	22	22	18	18	19	19	19	16	14	19
Sly05g0143181	M22	NA	5	4	5	4	7	5	4	4	6	8
Sly05g0143191	M3	NA	10	9	7	1	2	8	9	5	1	2
Sly05g0143221	M11	NA	7	6	7	2	2	8	8	7	1	1
Sly05g0143231	M12	NA	2	3	3	5	4	12	18	29	49	28
Sly05g0143241	M1	NA	2	2	3	2	1	1	1	1	1	0
Sly05g0143291	M1	NA	202	372	75	1	1	9	15	2	3	1
Sly05g0143321	M1	NA	3	4	3	5	4	2	2	2	1	1
Sly05g0143331	M1	NA	12	14	12	10	9	9	9	7	4	5
Sly05g0143341	M3	NA	18	15	14	8	11	12	12	10	10	13
Sly05g0143371	M22	NA	2	2	2	1	1	2	2	2	1	1
Sly05g0143401	M22	NA	1	1	1	1	1	3	1	1	1	0
Sly05g0143411	M11	NA	3	4	3	2	2	5	4	4	1	1
Sly05g0143431	M12	NA	103	126	101	100	179	121	125	118	136	307
Sly05g0143441	M1	SILOX11	37	33	38	58	63	19	20	17	16	12
Sly05g0143591	M1	NA	2	1	1	4	7	1	1	1	19	5
Sly05g0143611	M18	NA	29	31	34	37	26	36	33	38	29	18
Sly05g0143621	M3	NA	49	48	38	54	26	39	37	30	19	8
Sly05g0143701	M18	NA	18	19	20	21	21	21	18	20	16	19
Sly05g0143721	M15	NA	10	7	8	8	7	8	8	8	5	6
Sly05g0143731	M22	NA	43	37	44	31	26	49	37	50	32	23
Sly05g0143741	M3	NA	2	2	1	1	3	1	1	1	1	1
Sly05g0143751	M3	NA	25	30	22	12	8	8	12	7	2	3
Sly05g0143761	M12	NA	6	6	6	5	4	7	8	6	3	3
Sly05g0143781	M13	NA	4	4	8	8	9	7	5	7	2	1
Sly05g0143811	M11	NA	17	18	16	15	14	20	19	21	12	12
Sly05g0143821	M3	NA	29	29	29	33	28	26	27	24	21	18
Sly05g0143831	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0143841	M19	NA	21	22	25	26	19	18	20	21	13	9
Sly05g0143901	M11	NA	10	9	12	18	40	14	11	18	21	45
Sly05g0143911	M3	NA	1	1	1	0	1	1	1	1	0	0
Sly05g0143921	M12	NA	3	2	3	1	1	4	5	4	1	0
Sly05g0143961	M2	NA	1	2	2	128	520	1	2	2	16	111
Sly05g0144011	M11	NA	362	274	463	692	1111	442	428	563	684	1401
Sly05g0144021	M11	NA	11	11	13	16	23	15	17	17	10	9
Sly05g0144031	M11	NA	5	5	8	9	9	8	7	9	5	4
Sly05g0144041	M11	NA	9	11	15	16	17	16	14	18	9	7
Sly05g0144051	M11	NA	14	13	20	21	26	18	18	25	43	60
Sly05g0144081	M1	NA	64	58	35	39	43	16	16	13	13	18
Sly05g0144101	M7	NA	4	6	3	3	7	5	6	4	8	21
Sly05g0144131	M1	NA	3	6	5	19	17	1	1	1	17	59
Sly05g0144151	M10	NA	16	17	15	18	14	17	24	17	68	38
Sly05g0144181	M12	NA	6	6	7	6	10	7	7	8	14	22
Sly05g0144191	M1	NA	6	7	9	10	5	5	5	4	4	1
Sly05g0144201	M1	NA	100	109	141	220	64	16	2	6	1	0
Sly05g0144211	M1	NA	3	4	2	1	1	3	1	2	0	0
Sly05g0144231	M12	NA	3	4	4	6	9	3	3	4	16	18
Sly05g0144241	M12	NA	1	1	1	1	1	2	1	2	10	2
Sly05g0144251	M11	NA	157	140	158	151	139	176	167	202	217	219
Sly05g0144261	M11	NA	33	34	39	56	65	38	43	42	57	55
Sly05g0144271	M11	NA	39	38	45	93	163	41	40	54	99	103
Sly05g0144281	M8	NA	199	197	150	235	184	181	216	164	201	192
Sly05g0144321	M22	NA	3	2	3	1	1	7	4	7	2	1
Sly05g0144331	M3	NA	4	4	4	5	8	3	3	2	6	9
Sly05g0144371	M1	SIHK5	79	82	96	90	82	55	54	69	65	66
Sly05g0144391	M12	NA	40	35	49	117	196	53	62	65	129	159
Sly05g0144401	M18	NA	34	34	32	29	28	40	32	36	24	27
Sly05g0144431	M1	NA	107	113	105	87	77	79	89	97	70	69
Sly05g0144441	M11	NA	2	2	3	3	2	4	4	5	3	3
Sly05g0144451	M11	NA	4	3	7	4	4	6	6	8	6	4
Sly05g0144461	M2	NA	334	331	320	280	194	262	298	239	193	154
Sly05g0144481	M3	NA	3	3	1	0	0	1	1	1	1	0
Sly05g0144511	M11	NA	2	3	3	2	7	3	4	4	3	10
Sly05g0144521	M1	NA	45	46	38	37	39	27	29	25	39	36
Sly05g0144541	M3	NA	2	2	1	1	2	1	1	1	1	2
Sly05g0144551	M3	NA	6	10	4	2	1	1	1	1	0	1
Sly05g0144561	M3	NA	9	16	7	1	1	6	8	1	2	1
Sly05g0144571	M12	NA	68	75	74	131	141	71	74	77	134	146
Sly05g0144611	M1	NA	3	4	4	11	15	3	3	4	1	6
Sly05g0144661	M3	NA	6	6	4	2	2	4	5	3	2	1
Sly05g0144671	M3	NA	2	2	2	2	1	2	3	2	1	1
Sly05g0144701	M23	NA	2	1	1	1	3	5	2	2	5	3
Sly05g0144711	M3	NA	1	1	2	1	1	1	1	1	1	1
Sly05g0144731	M18	NA	32	32	35	34	30	43	34	45	33	30
Sly05g0144741	M18	NA	43	44	49	46	41	58	47	60	40	42
Sly05g0144751	M1	NA	26	29	33	18	2	1	0	1	1	0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0055321	M20	NA	2	1	2	1	1	2	1	1	0	1
Sly12g0055331	M20	NA	2	2	4	1	1	2	2	2	1	1
Sly12g0055341	M1	NA	1	1	2	1	1	2	1	1	0	1
Sly12g0055351	M11	NA	30	31	37	65	67	39	34	48	58	68
Sly12g0055361	M1	NA	50	56	52	36	43	42	40	45	58	62
Sly12g0055381	M11	NA	38	37	47	46	52	50	42	61	59	68
Sly12g0055391	M3	NA	61	61	48	54	41	45	52	37	54	53
Sly12g0055401	M19	NA	13	11	13	11	12	13	11	13	14	18
Sly12g0055411	M11	NA	58	56	80	95	104	96	89	125	103	147
Sly12g0055421	M1	NA	29	32	26	21	20	7	5	6	10	28
Sly12g0055431	M12	NA	21	20	21	11	9	29	32	25	11	12
Sly12g0055451	M22	NA	4	2	3	1	1	18	4	16	0	0
Sly12g0055461	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly12g0055471	M11	NA	8	9	9	7	7	15	13	15	9	6
Sly12g0055481	M1	NA	30	33	29	32	37	30	27	29	26	29
Sly12g0055491	M3	NA	22	20	17	12	10	14	15	12	5	2
Sly12g0055501	M11	IPT9	13	13	14	14	19	18	17	20	21	25
Sly12g0055511	M22	NA	1	1	1	0	0	5	1	4	0	0
Sly12g0055521	M3	NA	39	36	31	37	37	33	33	32	37	40
Sly12g0055531	M11	NA	9	9	10	10	7	15	13	18	12	7
Sly12g0055541	M3	NA	79	79	62	39	56	43	48	38	60	79
Sly12g0055561	M14	NA	60	55	90	79	36	71	56	77	35	20
Sly12g0055571	M1	NA	5	4	6	4	1	3	2	3	2	3
Sly12g0055581	M1	NA	4	4	4	3	2	3	2	2	1	1
Sly12g0055591	M1	NA	17	18	16	19	16	14	14	13	15	12
Sly12g0055601	M11	NA	155	144	160	187	190	161	154	203	238	256
Sly12g0055621	M1	NA	3	3	3	2	1	1	1	1	1	1
Sly12g0055631	M3	NA	17	17	15	7	4	14	15	14	9	5
Sly12g0055641	M1	PPR-like21	4	4	5	4	3	4	4	4	4	3
Sly12g0055661	M1	NA	53	58	65	59	34	28	26	38	34	21
Sly12g0055671	M1	NA	5	2	3	0	0	2	1	1	0	0
Sly12g0055691	M11	NA	88	91	104	158	150	116	120	138	150	149
Sly12g0055701	M11	NA	62	55	66	105	89	91	85	110	120	144
Sly12g0055721	M14	NA	104	102	113	122	118	95	92	104	118	129
Sly12g0055741	M3	NA	27	27	30	20	12	19	24	20	13	8
Sly12g0055761	M1	NA	20	33	16	2	1	3	2	2	1	0
Sly12g0055771	M1	NA	11	8	12	4	1	3	3	3	2	1
Sly12g0055781	M11	NA	38	35	45	38	29	44	39	43	29	18
Sly12g0055801	M13	NA	30	29	38	26	20	36	35	46	26	11
Sly12g0055811	M12	NA	17	17	19	23	35	19	21	22	27	40
Sly12g0055821	M11	NA	8	7	10	7	9	11	11	14	11	18
Sly12g0055831	M12	NA	18	21	25	13	5	45	39	50	5	2
Sly12g0055841	M1	IAMT1-like	2	1	1	1	0	1	1	1	1	0
Sly12g0055851	M5	NA	20	28	14	6	8	28	26	9	3	4
Sly12g0055861	M18	NA	26	28	30	23	24	36	33	38	26	26
Sly12g0055901	M12	NA	3	3	3	3	2	5	4	5	3	2
Sly12g0055911	M12	NA	3	3	3	3	2	5	6	6	3	1
Sly12g0055921	M12	NA	3	2	3	1	1	44	40	39	3	1
Sly12g0055931	M12	NA	0	0	1	0	1	2	1	1	0	1
Sly12g0055941	M12	NA	1	1	1	1	1	3	2	2	1	1
Sly12g0055951	M3	NA	45	49	37	43	17	37	43	26	25	6
Sly12g0055961	M1	NA	14	14	18	9	6	8	5	7	2	2
Sly12g0055991	M23	NA	25	17	15	7	5	20	21	18	6	2
Sly12g0056001	M1	NA	18	18	18	19	21	13	12	14	12	7
Sly12g0056011	M3	NA	7	7	6	5	7	5	5	4	4	5
Sly12g0056021	M1	NA	9	9	9	5	6	8	8	8	9	7
Sly12g0056031	M11	NA	25	21	22	25	31	20	23	28	27	36
Sly12g0056041	M11	NA	7	4	9	3	1	15	15	17	1	1
Sly12g0056061	M11	NA	13	13	17	27	35	22	19	26	33	33
Sly12g0056071	M11	NA	5	7	7	7	8	8	7	9	12	10
Sly12g0056081	M2	NA	24	23	20	42	45	20	29	18	26	22
Sly12g0056111	M1	NA	9	7	13	7	3	5	5	2	1	1
Sly12g0056121	M1	NA	41	45	41	25	21	26	31	26	24	20
Sly12g0056141	M22	NA	3	1	1	0	0	17	1	9	0	0
Sly12g0056161	M12	NA	20	20	22	53	90	21	23	26	49	59
Sly12g0056171	M1	NA	4	2	4	6	10	2	4	3	9	17
Sly12g0056181	M12	NA	9	9	11	4	2	128	147	128	23	6
Sly12g0056191	M3	NA	125	144	93	111	55	71	93	51	116	127
Sly12g0056201	M3	NA	66	64	55	57	46	52	57	52	78	73
Sly12g0056211	M3	NA	341	280	245	127	158	159	137	100	162	177
Sly12g0056241	M14	NA	14	14	16	35	60	14	13	16	36	52
Sly12g0056261	M17	NA	75	56	85	58	34	58	48	72	51	30
Sly12g0056521	M19	NA	31	27	29	36	36	28	28	30	38	36
Sly12g0056541	M12	NA	1	1	1	1	2	1	1	2	2	3
Sly12g0056551	M11	NA	32	32	33	27	26	34	33	36	36	38
Sly12g0056571	M7	NA	1	2	1	1	1	1	2	1	1	2
Sly12g0056581	M10	NA	1	2	1	1	1	2	2	1	1	3
Sly12g0056591	M19	NA	11	12	16	12	6	8	6	9	5	3
Sly12g0056601	M1	NA	24	25	30	23	12	17	14	16	10	8
Sly12g0056611	M1	NA	23	27	32	23	12	14	14	16	10	9
Sly12g0056621	M1	NA	15	15	18	44	105	11	8	14	40	77
Sly12g0056631	M9	SIXTH11	31	64	60	63	405	57	157	70	104	657
Sly12g0056641	M12	NA	21	24	61	425	791	84	88	159	576	1161
Sly12g0056651	M3	NA	57	60	55	65	57	54	54	54	69	39
Sly12g0056661	M11	NA	2	2	2	4	3	2	3	3	2	2
Sly12g0056671	M1	NA	6	5	7	8	10	4	3	3	5	5
Sly12g0056681	M11	NA	13	15	15	28	38	17	14	17	30	34
Sly12g0056751	M1	NA	4	3	3	3	3	1	1	1	1	1
Sly12g0056761	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly12g0056791	M13	NA	34	31	36	38	42	34	32	34	46	52
Sly12g0056801	M11	NA	35	38	40	43	42	49	44	56	36	37
Sly12g0056811	M12	NA	15	18	16	18	18	28	27	25	24	27
Sly12g0056821	M9	NA	28	29	28	35	21	48	48	39	24	18
Sly12g0056831	M3	NA	50	48	19	1	1	7	11	2	0	1
Sly12g0056841	M1	NA	4	4	4	3	4	4	3	3	2	2
Sly12g0056851	M6	NA	1	2	1	1	1	1	1	1	1	1
Sly12g0056861	M3	NA	2	5	3	1	1	1	1	0	0	0
Sly12g0056871	M11	NA	10	12	11	23	38	13	13	13	23	32
Sly12g0056881	M12	NA	2	1	1	1	1	2	2	2	2	2
Sly12g0056891	M3	NA	76	120	33	41	14	33	60	16	59	32
Sly12g0056901	M19	NA	27	27	25	28	29	27	24	25	28	25
Sly12g0056911	M11	NA	141	139	148	150	157	143	151	150	166	205
Sly12g0056921	M2	NA	1	4	2	2	3	1	3	2	5	6
Sly12g0056941	M2	NA	6	8	8	6	7	6	7	7	10	11
Sly12g0056951	M19	NA	1	1	1	2	1	1	1	1	1	1
Sly12g0056961	M12	NA	6	5	5	6	5	6	7	6	8	8
Sly12g0056971	M1	NA	55	55	49	18	15	37	38	29	10	8
Sly12g0056991	M13	NA	17	15	22	13	20	20	18	27	19	23
Sly12g0057011	M3	NA	2	1	1	1	0	1	1	1	1	0
Sly12g0057171	M19	NA	25	32	29	26	18	27	27	28	16	11
Sly12g0057181	M18	NA	73	81	76	71	51	81	85	77	55	42
Sly12g0057281	M12	NA	13	12	12	30	22	16	18	21	45	25
Sly12g0057311	M18	NA	15	17	16	18	21	18	16	19	20	21
Sly12g0057371	M18	NA	73	75	81	78	70	78	76	72	44	50
Sly12g0057381	M11	NA	12	12	11	11	11	14	13	16	12	16
Sly12g0057391	M3	NA	23	23	14	1	0	17	15	8	0	0
Sly12g0057401	M3	NA	5	6	3	1	1	2	2	1	1	1
Sly12g0057411	M12	NA	73	74	75	139	145	141	158	142	146	142
Sly12g0057421	M3	NA	56	50	42	34	37	35	36	35	32	30
Sly12g0057431	M11	NA	23	20	25	48	44	32	31	44	91	111
Sly12g0057481	M8	NA	1	2	2	2	2	1	2	1	2	8
Sly12g0057501	M12	NA	1	1	1	1	2	1	2	1	3	6
Sly12g0057511	M19	NA	39	35	46	42	43	29	25	31	26	34
Sly12g0057541	M11	NA	7	9	10	17	20	14	12	14	14	14
Sly12g0057631	M12	NA	1	1	1	0	0	1	1	1	1	0
Sly12g0057721	M1	NA	41	44	38	38	39	29	29	25	29	30
Sly12g0057731	M14	NA	26	26	30	55	67	26	25	37	52	56
Sly12g0057741	M3	NA	14	13	6	0	0	16	18	2	1	0
Sly12g0057801	M3	NA	7	11	4	3	2	2	3	1	1	1
Sly12g0057841	M1	NA	60	65	63	40	26	32	33	28	11	7
Sly12g0057851	M11	NA	28	25	23	22	23	25	26	29	30	31
Sly12g0057891	M21	NA	1	1	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0144771	M1	NA	37	41	37	88	73	25	26	25	43	45
Sly05g0144781	M1	NA	2	1	2	2	2	1	1	1	1	1
Sly05g0144791	M9	NA	44	48	33	43	37	58	69	56	52	63
Sly05g0144841	M1	NA	5	3	4	4	6	5	1	1	4	2
Sly05g0144851	M1	NA	5	6	5	2	1	2	3	2	2	1
Sly05g0144861	M1	NA	2	3	3	1	1	1	1	1	2	1
Sly05g0144871	M3	NA	24	25	20	17	12	18	17	15	10	6
Sly05g0144911	M3	NA	162	214	114	29	18	68	87	54	15	21
Sly05g0144991	M12	NA	17	16	16	13	19	21	20	17	42	62
Sly05g0145011	M11	NA	31	31	35	47	64	33	29	37	51	66
Sly05g0145021	M1	NA	73	72	79	82	79	65	61	69	77	85
Sly05g0145031	M12	NA	12	11	12	11	13	18	19	18	19	17
Sly05g0145041	M3	NA	13	17	14	8	5	16	17	10	6	2
Sly05g0145051	M3	NA	22	28	17	10	6	18	21	12	8	6
Sly05g0145071	M22	NA	1	1	1	0	0	1	1	1	1	0
Sly05g0145081	M11	NA	1	1	1	0	0	2	1	1	1	1
Sly05g0145111	M10	NA	6	13	18	9	20	20	30	14	5	5
Sly05g0145131	M11	CYP97B3	13	12	15	23	13	21	19	24	10	4
Sly05g0145151	M12	NA	4	4	3	3	2	4	7	6	6	2
Sly05g0145161	M3	NA	9	11	10	17	19	10	9	8	7	12
Sly05g0145181	M1	NA	2	2	2	1	2	2	1	1	1	1
Sly05g0145191	M11	NA	119	120	126	126	154	135	119	138	152	208
Sly05g0145241	M18	NA	26	30	28	37	32	33	29	31	26	22
Sly05g0145441	M12	NA	1	1	1	1	0	1	2	2	1	1
Sly05g0145491	M5	NA	3	6	1	1	0	7	4	1	0	0
Sly05g0145521	M1	NA	1	2	1	1	1	1	1	1	1	1
Sly05g0145531	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0145621	M9	NA	104	107	100	118	85	139	162	124	93	71
Sly05g0145651	M5	NA	7	8	6	6	5	6	8	5	7	9
Sly05g0145681	M12	NA	4	4	3	2	2	4	5	5	3	2
Sly05g0145711	M1	NA	4	5	6	6	11	3	4	4	6	18
Sly05g0145731	M3	NA	31	34	30	34	36	31	31	29	32	38
Sly05g0145821	M19	NA	25	25	26	26	30	28	22	26	18	22
Sly05g0145841	M1	NA	5	5	5	8	6	3	2	2	1	1
Sly05g0145851	M12	NA	20	20	21	12	10	25	28	26	16	11
Sly05g0145861	M1	NA	1	2	2	1	1	1	1	1	0	0
Sly05g0145871	M1	NA	4	3	5	4	6	2	1	2	1	1
Sly05g0145891	M9	NA	124	124	98	123	98	172	191	146	139	73
Sly05g0145901	M1	NA	20	15	19	12	9	7	5	5	3	2
Sly05g0145911	M11	NA	2	2	2	1	1	4	3	5	1	1
Sly05g0145921	M11	NA	40	40	42	34	24	53	48	47	39	28
Sly05g0145931	M11	NA	36	32	33	45	52	38	33	41	70	83
Sly05g0146071	M3	NA	7	11	5	12	3	4	5	1	1	1
Sly05g0146101	M11	NA	12	13	14	30	56	21	22	31	67	153
Sly05g0146121	M2	NA	55	57	50	62	53	38	49	40	68	52
Sly05g0146151	M1	NA	6	7	6	5	4	5	5	6	4	4
Sly05g0146161	M11	NA	2	2	3	2	4	3	2	3	3	2
Sly05g0146171	M12	NA	2	1	2	2	3	3	2	2	3	2
Sly05g0146211	M11	NA	2	1	2	1	0	4	3	3	0	1
Sly05g0146221	M1	NA	25	30	24	17	27	17	18	16	15	30
Sly05g0146251	M1	NA	32	33	40	44	60	27	26	29	36	56
Sly05g0146271	M12	NA	1	0	1	2	1	1	2	2	3	2
Sly05g0146291	M1	NA	8	6	7	5	6	4	2	3	3	9
Sly05g0146301	M14	NA	17	17	18	28	51	16	14	19	31	44
Sly05g0146311	M11	NA	18	19	19	26	24	23	21	21	16	17
Sly05g0146331	M3	NA	64	60	56	44	40	56	54	57	35	36
Sly05g0146361	M3	NA	68	64	53	56	57	59	55	56	70	80
Sly05g0146371	M1	NA	18	19	15	23	28	14	13	14	27	27
Sly05g0146381	M22	NA	4	1	3	0	0	27	1	17	0	0
Sly05g0146391	M3	VIN3-like	17	16	14	20	18	15	15	14	18	18
Sly05g0146431	M11	NA	16	16	18	20	20	20	19	24	27	28
Sly05g0146461	M12	NA	7	8	8	9	8	8	9	12	10	12
Sly05g0146481	M12	NA	6	5	7	6	1	8	8	8	4	2
Sly05g0146541	M1	NA	17	10	14	19	15	4	2	5	2	2
Sly05g0146571	M12	NA	67	69	65	69	65	70	71	71	69	63
Sly05g0146581	M11	NA	12	14	13	12	12	14	14	14	18	19
Sly05g0146591	M1	NA	23	31	27	12	9	16	18	17	9	11
Sly05g0146601	M1	NA	18	15	35	5	3	6	3	5	1	1
Sly05g0146641	M12	NA	60	56	67	104	127	77	80	83	95	115
Sly05g0146691	M1	NA	116	111	112	108	114	98	102	102	132	134
Sly05g0146721	M13	NA	111	106	116	125	149	101	112	112	140	175
Sly05g0146731	M18	NA	63	62	69	76	84	67	60	72	78	77
Sly05g0146751	M2	SUF3	14	14	13	15	13	13	15	14	16	13
Sly05g0146761	M3	NA	56	55	42	51	50	46	49	38	49	49
Sly05g0146781	M20	NA	73	60	64	57	123	67	55	63	63	142
Sly05g0146791	M11	NA	118	104	139	126	143	175	162	188	117	133
Sly05g0146801	M11	NA	97	97	127	119	119	174	142	211	96	93
Sly05g0146811	M18	NA	99	103	123	129	113	176	137	193	97	87
Sly05g0146831	M12	NA	3	4	5	2	1	7	6	6	2	0
Sly05g0146841	M11	NA	2	1	2	2	1	3	4	4	1	1
Sly05g0146851	M11	NA	55	52	77	77	26	88	81	88	18	6
Sly05g0146901	M12	NA	3	3	2	2	1	4	4	4	2	1
Sly05g0146951	M3	NA	18	21	16	17	15	12	15	11	15	17
Sly05g0146961	M1	NA	30	30	31	17	15	19	18	20	14	14
Sly05g0146971	M3	NA	15	17	15	22	17	13	15	14	36	27
Sly05g0147041	M11	NAP1;2-like	351	342	392	355	359	383	349	417	601	569
Sly05g0147051	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0147061	M1	NA	5	5	5	3	3	3	3	2	2	2
Sly05g0147081	M1	NA	7	5	8	46	80	5	4	4	9	8
Sly05g0147101	M12	NA	2	2	2	2	1	3	3	2	2	3
Sly05g0147111	M11	NA	1	1	1	1	0	3	2	3	1	0
Sly05g0147121	M1	NA	4	3	4	2	1	2	2	2	3	2
Sly05g0147161	M12	NA	1	1	1	0	0	2	1	1	0	0
Sly05g0147241	M13	NA	13	13	19	11	11	14	13	15	19	27
Sly05g0147271	M12	NA	34	33	36	27	18	34	35	35	25	21
Sly05g0147381	M11	NA	39	38	40	50	51	47	45	50	59	57
Sly05g0147391	M22	NA	1	1	1	1	0	1	1	1	0	0
Sly05g0147411	M12	NA	6	5	8	5	2	10	7	9	5	2
Sly05g0147621	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0147641	M12	ADH	8	9	9	8	9	10	10	11	18	18
Sly05g0147651	M19	NA	22	25	26	24	20	24	20	27	50	51
Sly05g0147661	M19	NA	13	17	14	14	12	14	12	13	12	11
Sly05g0147671	M19	NA	9	9	11	9	7	11	6	9	9	7
Sly05g0147681	M19	NA	14	18	16	14	8	12	9	13	10	11
Sly05g0147691	M19	NA	13	15	11	12	7	10	7	10	10	7
Sly05g0147701	M19	NA	5	7	5	6	4	6	4	4	4	4
Sly05g0147851	M12	NA	26	20	36	42	21	29	27	31	19	20
Sly05g0147861	M22	VIM1-like	4	3	3	1	1	5	3	4	1	1
Sly05g0147871	M1	NA	32	37	33	33	31	21	24	20	20	25
Sly05g0147961	M11	NA	55	58	77	90	63	89	84	94	150	79
Sly05g0147971	M9	NA	35	39	42	39	43	58	59	54	39	63
Sly05g0147981	M11	NA	4	4	5	3	3	7	6	7	3	3
Sly05g0147991	M11	NA	18	20	21	18	10	21	21	22	9	4
Sly05g0148011	M2	NA	353	358	356	459	582	310	347	362	543	626
Sly05g0148031	M12	NA	29	29	27	24	27	30	30	31	31	36
Sly05g0148041	M1	NA	74	41	94	39	68	31	36	31	32	53
Sly05g0148051	M1	NA	11	10	16	11	10	6	7	7	10	12
Sly05g0148061	M1	NA	7	7	11	8	7	3	6	5	7	8
Sly05g0148091	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0148141	M3	NA	3	3	3	3	3	3	3	3	3	2
Sly05g0148291	M1	NA	122	100	113	81	92	53	50	66	164	149
Sly05g0148311	M11	NA	18	15	23	26	34	18	15	21	40	109
Sly05g0148321	M11	NA	18	17	21	24	25	18	14	21	31	70
Sly05g0148331	M14	NA	30	28	32	34	30	25	25	27	22	26
Sly05g0148441	M1	NA	32	29	31	25	28	16	17	18	36	48
Sly05g0148481	M1	NA	5	4	4	4	2	5	2	3	1	1
Sly05g0148521	M12	NA	1	1	1	1	1	2	2	3	2	2
Sly05g0148531	M3	NA	4	9	1	0	0	4	9	0	1	0
Sly05g0148571	M12	NA	61	56	57	86	81	56	66	60	59	57
Sly05g0148591	M12	NA	92	90	174	410	355	97	197	381	866	299
Sly05g0148601	M1	NA	72	74	59	53	51	43	44	38	27	35
Sly05g0148651	M22	NA	3	0	3	0	0	33	1	24	0	0
Sly05g0148711	M12	NA	0	1	1	7	4	1	2	5	48	22
Sly05g0148721	M2	NA	5	5	5	5	5	4	5	5	6	8

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0057921	M11	NA	7	4	8	2	1	15	12	20	3	1
Sly12g0057931	M1	NA	13	16	16	17	14	11	8	8	5	4
Sly12g0058041	M12	NA	0	1	1	16	31	1	1	2	125	86
Sly12g0058051	M1	NA	42	33	40	42	24	26	30	33	35	23
Sly12g0058061	M3	NA	135	160	124	17	69	71	111	70	48	386
Sly12g0058131	M7	NA	22	26	26	16	23	22	30	24	23	65
Sly12g0058141	M11	NA	131	106	134	65	48	137	107	161	62	43
Sly12g0058161	M2	NA	25	23	23	25	29	23	24	23	25	35
Sly12g0058171	M18	NA	17	15	20	20	20	18	16	17	17	21
Sly12g0058181	M19	NA	19	18	20	20	22	21	15	19	18	23
Sly12g0058301	M12	NA	48	52	50	78	78	50	51	54	82	86
Sly12g0058361	M9	NA	9	13	10	12	15	12	15	12	10	9
Sly12g0058451	M3	NA	88	87	64	65	58	68	68	58	57	47
Sly12g0058461	M11	NA	8	9	9	10	8	12	10	12	10	7
Sly12g0058471	M19	NA	88	89	85	92	121	86	76	87	108	147
Sly12g0058561	M1	NA	63	65	63	44	41	46	45	42	38	36
Sly12g0058571	M1	NA	7	7	5	2	2	5	4	4	1	1
Sly12g0058591	M2	NA	4	4	5	3	2	4	5	4	3	1
Sly12g0058611	M1	NA	4	3	4	3	5	4	3	3	7	14
Sly12g0058621	M11	NA	34	32	37	30	29	44	41	50	32	29
Sly12g0058631	M22	NA	1	0	1	0	0	2	1	4	0	0
Sly12g0058641	M22	NA	2	1	2	0	0	3	1	4	0	0
Sly12g0058651	M11	NA	26	21	37	20	13	26	23	37	24	11
Sly12g0058661	M11	NA	18	18	21	26	30	30	27	36	46	46
Sly12g0058671	M11	NA	24	27	26	28	25	28	25	30	22	27
Sly12g0058741	M1	NA	36	33	32	16	11	23	23	20	11	8
Sly12g0058751	M18	NA	40	44	49	70	55	53	48	57	80	55
Sly12g0058801	M11	NA	12	11	14	19	36	18	15	21	21	27
Sly12g0058841	M12	NA	34	35	36	51	81	46	46	47	66	90
Sly12g0058851	M6	NA	1	1	1	1	3	1	1	1	1	2
Sly12g0058861	M12	NA	20	26	25	36	45	31	30	30	42	42
Sly12g0058871	M11	NA	38	35	45	59	63	68	61	82	74	65
Sly12g0058901	M11	NA	28	32	30	30	18	42	41	44	28	20
Sly12g0058931	M19	NA	3	5	4	9	6	4	4	3	3	1
Sly12g0058941	M11	NA	11	13	13	28	37	14	12	11	16	16
Sly12g0058961	M11	NA	5	6	5	6	7	6	5	6	5	4
Sly12g0058971	M3	NA	10	10	8	10	8	7	9	9	7	8
Sly12g0059011	M1	NA	13	14	14	6	6	3	3	3	3	5
Sly12g0059041	M1	NA	61	60	59	57	58	49	41	50	43	50
Sly12g0059071	M18	NA	16	14	15	15	15	16	14	18	17	17
Sly12g0059131	M12	NA	10	9	10	11	13	12	11	11	18	29
Sly12g0059141	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0059161	M12	NA	1	1	1	1	1	1	1	1	1	2
Sly12g0059171	M12	NA	20	19	20	20	15	19	22	21	11	13
Sly12g0059221	M12	NA	1	1	1	3	6	5	5	6	2	1
Sly12g0059231	M12	NA	1	1	2	2	3	5	4	5	2	1
Sly12g0059241	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly12g0059251	M11	NA	1	1	1	0	0	1	1	1	0	0
Sly12g0059271	M1	NA	18	17	17	15	9	15	13	13	9	5
Sly12g0059281	M11	NA	38	37	44	45	52	43	39	45	53	52
Sly12g0059311	M3	NA	11	12	8	7	9	7	8	6	7	11
Sly12g0059321	M11	NA	29	30	33	44	53	30	29	31	31	47
Sly12g0059331	M1	NA	10	10	10	8	8	7	6	6	9	10
Sly12g0059341	M3	NA	7	7	6	8	8	5	5	6	10	13
Sly12g0059391	M12	NA	1	1	1	2	5	1	1	4	11	19
Sly12g0059401	M1	NA	25	35	51	29	10	19	15	32	7	5
Sly12g0059441	M18	NA	18	17	19	13	7	27	21	26	6	2
Sly12g0059451	M8	NA	3	3	2	1	2	3	3	2	3	6
Sly12g0059551	M11	NA	26	27	29	30	33	30	31	37	44	57
Sly12g0059571	M3	NA	21	19	18	16	12	15	16	15	16	21
Sly12g0059581	M12	NA	10	10	8	15	20	11	11	13	20	25
Sly12g0059591	M18	NA	1	1	2	1	1	2	1	1	1	1
Sly12g0059601	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0059621	M11	NA	6	8	8	14	19	9	8	10	17	19
Sly12g0059641	M2	NA	54	58	56	42	52	52	56	52	57	79
Sly12g0059651	M1	NA	5	5	4	4	3	3	2	4	2	3
Sly12g0059661	M18	CDKE;1	43	43	43	35	39	43	40	46	41	43
Sly12g0059721	M1	NA	23	19	28	8	6	6	6	8	6	8
Sly12g0059731	M1	NA	42	42	49	33	18	14	12	14	14	15
Sly12g0059751	M11	NA	3	3	3	13	11	5	5	10	42	63
Sly12g0059761	M1	NA	50	51	49	37	40	35	35	35	33	37
Sly12g0059791	M12	NA	14	22	20	58	23	48	69	107	152	44
Sly12g0059811	M12	NA	7	9	7	4	3	9	11	8	5	5
Sly12g0059851	M1	NA	70	65	68	34	29	48	58	46	22	30
Sly12g0059861	M11	NA	16	18	18	21	27	24	22	24	19	20
Sly12g0059891	M1	NA	9	9	13	9	7	5	6	7	9	11
Sly12g0059921	M3	NA	1	2	1	0	0	0	0	0	0	0
Sly12g0059931	M11	LSF1	10	11	15	27	18	23	22	30	14	6
Sly12g0059971	M1	NA	57	55	51	58	65	35	37	33	45	65
Sly12g0059981	M12	NA	28	27	30	25	27	44	52	53	57	95
Sly12g0060011	M12	NA	1	1	1	10	8	3	7	8	117	98
Sly12g0060021	M12	NA	1	1	1	1	0	2	2	2	1	1
Sly12g0060031	M12	NA	4	4	5	4	4	4	5	5	5	5
Sly12g0060091	M12	NA	6	5	7	3	3	11	9	9	6	8
Sly12g0060101	M11	NA	6	9	10	5	2	15	12	13	8	8
Sly12g0060111	M12	NA	7	7	9	6	3	16	15	13	11	10
Sly12g0060121	M12	NA	9	7	11	5	4	16	15	13	11	20
Sly12g0060131	M9	NA	2	2	2	2	4	2	2	2	5	21
Sly12g0060151	M3	NA	18	17	12	7	5	7	10	6	4	4
Sly12g0060161	M3	NA	23	23	17	14	12	19	20	15	14	19
Sly12g0060241	M22	NA	1	1	1	0	0	2	1	2	0	0
Sly12g0060311	M23	NA	7	6	5	6	7	7	7	6	6	6
Sly12g0060331	M19	NA	6	6	6	6	7	8	6	6	5	5
Sly12g0060551	M1	NA	4	5	6	1	1	1	1	0	0	0
Sly12g0060731	M1	NA	3	4	3	1	0	1	1	1	0	0
Sly12g0060801	M12	NA	6	5	7	8	8	7	7	8	14	19
Sly12g0060821	M12	NA	80	76	85	173	246	109	117	129	220	338
Sly12g0060831	M12	BIN2	187	202	203	247	258	219	247	222	287	314
Sly12g0061041	M1	NA	2	2	3	5	2	1	1	1	1	0
Sly12g0061071	M18	NA	11	12	17	9	6	22	16	28	13	10
Sly12g0061081	M18	NA	11	12	14	13	12	14	12	13	15	17
Sly12g0061091	M12	NA	8	9	9	7	6	10	10	8	10	8
Sly12g0061131	M5	NA	24	23	17	16	18	24	25	19	17	24
Sly12g0061141	M19	NA	54	56	54	53	62	60	50	55	60	70
Sly12g0061221	M12	NA	1	1	2	1	1	7	10	6	2	4
Sly12g0061251	M1	NA	56	51	53	59	57	48	47	47	53	47
Sly12g0061421	M1	NA	10	11	13	11	8	11	10	10	12	9
Sly12g0061431	M1	NA	14	11	13	13	11	12	9	9	12	12
Sly12g0061441	M1	NA	13	11	12	11	8	9	8	9	9	13
Sly12g0061481	M11	NA	1340	1167	1379	1063	876	1858	1535	2094	1742	1414
Sly12g0061501	M11	PPR-like47	8	10	9	7	6	11	12	14	16	19
Sly12g0061541	M1	NA	5	5	7	11	4	2	1	1	1	1
Sly12g0061581	M11	NA	41	40	47	53	56	44	55	53	71	79
Sly12g0061621	M11	NA	9	9	10	7	7	10	9	12	11	12
Sly12g0061631	M1	NA	23	24	22	21	16	17	17	19	17	11
Sly12g0061681	M19	NA	15	15	15	16	17	15	13	15	16	14
Sly12g0061721	M11	NA	0	0	0	0	0	1	1	3	1	0
Sly12g0061761	M18	NA	8	11	12	13	11	11	9	13	16	16
Sly12g0061771	M12	NA	14	19	20	21	22	21	19	20	33	31
Sly12g0061781	M12	NA	10	9	12	14	15	12	13	13	22	31
Sly12g0061821	M12	NA	7	7	7	7	9	9	8	8	8	9
Sly12g0061861	M12	NA	13	14	14	19	15	20	18	20	14	13
Sly12g0061881	M18	NA	31	37	28	38	38	39	34	37	35	25
Sly12g0061971	M1	NA	5	4	5	4	3	4	4	5	4	2
Sly12g0061991	M3	NA	17	18	15	15	15	14	17	14	20	16
Sly12g0062011	M1	NA	30	28	26	17	20	24	22	25	16	16
Sly12g0062031	M18	NA	16	17	19	19	24	20	17	22	16	19
Sly12g0062041	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly12g0062571	M11	NA	2	3	3	3	2	7	5	6	1	1
Sly12g0062601	M1	NA	6	5	7	9	9	5	6	5	14	17
Sly12g0062611	M11	NA	9	9	7	3	1	18	19	17	1	1
Sly12g0062631	M9	NA

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0148741	M9	NA	3	3	3	3	2	3	5	3	2	1
Sly05g0148761	M11	nitrile-specifier protei	89	68	92	153	136	153	131	200	149	151
Sly05g0148791	M11	NA	26	19	27	22	9	59	66	59	24	8
Sly05g0148871	M1	NA	11	11	14	10	5	11	11	9	6	3
Sly05g0148881	M11	NA	63	60	60	53	56	92	76	102	70	75
Sly05g0148891	M1	NA	14	12	13	3	2	9	8	8	4	2
Sly05g0148951	M12	NA	1	1	2	1	1	2	2	2	1	1
Sly05g0148991	M11	NA	5	4	5	5	6	6	5	5	7	8
Sly05g0149001	M12	NA	10	10	16	15	8	53	49	73	31	20
Sly05g0149061	M11	NA	66	46	70	40	7	231	201	297	62	7
Sly05g0149071	M3	NA	7	8	6	8	9	6	6	6	7	7
Sly05g0149081	M12	NA	6	5	6	4	3	8	7	7	6	4
Sly05g0149151	M11	NA	1	1	1	0	0	1	1	1	1	0
Sly05g0149171	M3	NA	18	20	16	21	24	14	18	17	27	35
Sly05g0149191	M12	SlRbohC	2	2	1	4	2	13	11	13	38	14
Sly05g0149251	M1	NA	2	2	1	1	1	1	1	1	1	0
Sly05g0149281	M1	NA	45	47	46	41	28	41	41	38	27	21
Sly05g0149351	M1	NA	5	5	5	4	5	4	4	4	6	5
Sly05g0149361	M1	NA	4	8	6	3	1	3	3	2	2	0
Sly05g0149371	M1	NA	9	9	12	4	2	7	6	6	2	1
Sly05g0149381	M3	NA	2	4	2	1	1	1	1	1	1	0
Sly05g0149391	M22	NA	1	1	1	1	2	2	1	3	1	1
Sly05g0149451	M11	NA	61	60	70	63	58	74	80	95	87	73
Sly05g0149461	M1	NA	18	19	16	11	9	10	8	9	7	5
Sly05g0149681	M11	NA	3	4	3	2	2	6	6	6	3	4
Sly05g0149701	M1	NA	1	1	2	12	12	1	1	1	5	22
Sly05g0149771	M12	NA	23	21	19	18	18	25	27	22	26	29
Sly05g0149791	M8	NA	18	19	17	14	12	21	20	16	17	17
Sly05g0149801	M3	NA	11	10	9	7	7	5	6	5	9	10
Sly05g0149851	M12	NA	18	19	19	19	19	25	26	25	22	22
Sly05g0149861	M22	NA	1	1	1	0	1	3	1	1	1	0
Sly05g0149871	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0149971	M7	NA	86	94	60	75	74	82	107	70	95	129
Sly05g0149981	M12	NA	12	13	13	17	18	19	17	19	22	22
Sly05g0150021	M10	NA	39	38	34	41	40	39	43	36	46	44
Sly05g0150031	M11	NA	16	18	20	20	21	25	21	26	21	20
Sly05g0150071	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0150081	M3	NA	14	13	14	10	12	10	12	10	18	24
Sly05g0150091	M3	NA	19	21	24	5	1	17	20	12	2	1
Sly05g0150101	M9	NA	1	1	1	1	1	1	2	1	1	1
Sly05g0150141	M9	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0150151	M12	NA	27	26	25	51	59	29	30	30	55	59
Sly05g0150211	M12	NA	29	25	23	12	11	26	31	27	24	28
Sly05g0150221	M12	NA	1	1	1	1	0	1	1	1	1	1
Sly05g0150241	M3	NA	17	16	15	10	12	12	12	9	17	22
Sly05g0150261	M19	NA	46	48	49	60	56	48	43	46	49	44
Sly05g0150271	M2	NA	154	155	127	83	72	106	114	92	83	83
Sly05g0150281	M11	NA	24	23	26	28	11	44	40	46	17	10
Sly05g0150311	M14	NA	32	31	34	48	66	31	29	34	30	31
Sly05g0150321	M12	NA	10	13	13	8	3	33	35	41	15	2
Sly05g0150381	M2	NA	44	43	43	47	52	40	41	41	45	47
Sly05g0150411	M19	NA	39	40	43	44	38	37	34	40	35	32
Sly05g0150451	M1	NA	32	28	31	28	26	21	20	21	19	20
Sly05g0150461	M18	NA	27	26	28	27	26	34	27	34	25	29
Sly05g0150491	M1	NA	12	10	6	1	1	1	0	1	0	0
Sly05g0150531	M1	NA	27	20	29	26	7	1	1	1	1	0
Sly05g0150541	M1	NA	25	19	25	21	6	1	0	1	1	0
Sly05g0150551	M9	NA	29	28	29	35	27	34	36	30	43	41
Sly05g0150561	M12	NA	26	28	24	31	26	40	46	40	24	20
Sly05g0150631	M1	NA	3	4	5	3	1	1	1	1	0	0
Sly05g0150641	M1	NA	1	1	2	2	1	1	1	1	1	0
Sly05g0150651	M1	NA	4	3	3	3	2	1	1	1	1	1
Sly05g0150711	M12	NA	4	3	5	6	12	6	5	4	5	22
Sly05g0150721	M11	NA	10	7	10	5	5	14	14	17	9	7
Sly05g0150741	M3	NA	3	3	3	2	1	4	3	2	1	1
Sly05g0150751	M3	NA	9	8	8	6	3	7	8	6	4	3
Sly05g0150771	M23	NA	3	1	3	3	4	3	2	2	4	6
Sly05g0150861	M3	NA	13	13	12	11	10	12	11	10	9	9
Sly05g0150901	M12	NA	1	1	1	0	0	3	3	2	0	0
Sly05g0150921	M11	NA	1	1	1	0	0	2	1	2	0	0
Sly05g0150931	M12	NA	8	8	6	4	5	8	9	9	4	4
Sly05g0150941	M12	NA	13	12	11	8	5	15	14	14	12	7
Sly05g0150961	M1	NA	4	3	9	1	1	3	2	3	1	1
Sly05g0150971	M1	NA	3	3	4	4	5	3	2	4	6	7
Sly05g0150981	M12	NA	6	6	7	6	10	7	8	7	13	25
Sly05g0151071	M11	NA	105	111	136	207	241	122	133	193	272	412
Sly05g0151211	M3	NA	4	5	4	4	1	4	4	4	4	2
Sly05g0151281	M11	NA	16	15	18	20	23	22	22	24	37	39
Sly05g0151291	M11	NA	16	15	18	18	6	24	23	26	18	3
Sly05g0151301	M1	NA	5	4	3	1	1	1	1	1	1	0
Sly05g0151311	M1	NA	5	4	3	1	1	1	1	1	0	1
Sly05g0151361	M11	NA	19	20	24	15	5	43	37	49	13	5
Sly05g0151371	M1	NA	16	21	15	2	1	12	7	4	1	1
Sly05g0151401	M12	NA	7	5	7	11	11	10	10	11	13	22
Sly05g0151421	M3	NA	2	1	1	1	1	1	1	1	1	0
Sly05g0151551	M8	NA	27	34	25	15	16	25	41	26	39	79
Sly05g0151611	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0151631	M19	NA	3	6	6	8	5	5	4	5	7	3
Sly05g0151641	M1	NA	2	1	3	3	3	1	1	1	1	1
Sly05g0151651	M11	NA	16	13	16	17	17	18	16	17	23	24
Sly05g0151661	M19	NA	1	1	1	1	2	1	1	1	1	1
Sly05g0151671	M12	NA	2	3	4	3	3	3	4	3	4	4
Sly05g0151681	M11	NA	4	4	7	5	6	6	6	9	5	7
Sly05g0151691	M13	NA	25	28	34	29	36	25	27	30	41	47
Sly05g0151731	M5	NA	615	927	340	85	88	576	652	203	68	104
Sly05g0151821	M11	NA	61	57	69	51	51	66	57	71	57	59
Sly05g0151831	M3	NA	7	7	6	7	7	6	6	6	7	7
Sly05g0151841	M3	NA	17	19	13	12	12	14	15	12	14	16
Sly05g0151861	M11	NA	3	3	3	4	5	3	4	4	5	5
Sly05g0151871	M11	NA	4	4	5	4	5	4	4	5	5	4
Sly05g0151911	M1	NA	55	48	59	41	55	50	46	48	72	107
Sly05g0151921	M18	NA	14	13	18	14	16	16	15	15	23	28
Sly05g0151971	M11	NA	21	23	21	17	19	27	27	30	16	21
Sly05g0152011	M11	NA	4	4	4	3	2	6	6	7	4	3
Sly05g0152021	M11	NA	3	2	3	2	1	3	4	4	4	2
Sly05g0152171	M7	NA	2	2	2	1	2	2	3	2	2	7
Sly05g0152211	M23	NA	1	1	0	1	0	1	1	1	1	1
Sly05g0152261	M1	NA	11	12	30	30	13	2	1	1	0	0
Sly05g0152271	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0152281	M12	NA	23	26	25	28	26	33	33	28	31	31
Sly05g0152311	M10	NA	3	3	3	3	3	3	3	3	6	8
Sly05g0152321	M3	NA	23	17	16	15	10	12	11	8	12	11
Sly05g0152331	M1	NA	8	9	7	2	2	4	4	2	2	2
Sly05g0152351	M12	NA	7	6	8	6	4	7	11	9	8	7
Sly05g0152361	M12	NA	6	7	8	7	6	8	9	10	8	6
Sly05g0152371	M19	NA	8	8	8	7	3	8	8	10	6	5
Sly05g0152381	M19	NA	4	10	8	8	4	10	7	9	5	5
Sly05g0152391	M19	NA	3	6	5	6	4	6	3	7	5	4
Sly05g0152401	M11	NA	6	7	6	5	3	6	7	8	6	6
Sly05g0152431	M11	NA	136	117	152	239	318	266	247	308	319	390
Sly05g0152531	M11	NA	6	6	6	8	10	6	6	7	10	7
Sly05g0152541	M1	NA	11	11	15	8	7	12	7	11	3	3
Sly05g0152571	M11	NA	1	1	1	1	1	2	1	2	1	0
Sly05g0152651	M7	NA	4	6	4	4	6	5	8	4	6	25
Sly05g0152671	M1	NA	21	17	24	16	17	19	15	19	27	30
Sly05g0152681	M12	NA	14	13	14	19	29	15	15	17	33	76
Sly05g0152691	M3	NA	7	7	5	7	6	6	6	5	8	9
Sly05g0152701	M2	NA	14	15	17	16	17	13	17	15	28	36
Sly05g0152711	M19	NA	58	66	63	71	70	70	63	72	95	83
Sly05g0152721	M1	NA	30	25	20	24	25	9	12	10	20	51
Sly05g0152731	M11	NA	22	18	18	23	15	34	30	36	20	7
Sly05g0152741	M3	NA	4	4	3	1	1	2	3	2	1	0
Sly05g0152761	M11	NA	1	1	1	0	0	3	5	4	1	1
Sly05g0152771	M22	NA	6	4	4	3	1	11	6	9	5	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0062681	M11	NA	35	34	40	35	37	41	44	48	58	54
Sly12g0062711	M1	NA	4	3	4	2	1	4	2	2	2	3
Sly12g0062721	M1	NA	3	4	4	3	2	4	2	3	2	2
Sly12g0062731	M1	NA	4	3	4	3	2	4	2	3	2	3
Sly12g0062751	M11	NA	18	19	19	22	19	19	17	21	23	22
Sly12g0062761	M1	NA	6	7	7	4	2	3	3	3	3	2
Sly12g0062771	M1	NA	7	7	6	2	1	1	1	1	0	0
Sly12g0062781	M3	NA	11	13	6	1	1	5	3	2	1	1
Sly12g0062791	M3	NA	12	12	12	8	10	11	10	10	15	25
Sly12g0062851	M12	NA	3	4	3	3	1	6	6	8	3	1
Sly12g0062861	M3	NA	1	2	1	1	1	1	2	1	1	1
Sly12g0062901	M18	NA	16	18	18	15	14	21	19	22	16	12
Sly12g0062951	M3	NA	13	12	13	9	5	12	14	10	8	6
Sly12g0062961	M1	NA	11	15	12	9	8	11	12	11	8	6
Sly12g0062971	M3	NA	1	3	1	0	0	1	1	0	0	1
Sly12g0063031	M1	NA	3	3	4	2	2	1	1	1	1	1
Sly12g0063061	M1	NA	5	4	3	3	2	3	3	3	2	2
Sly12g0063071	M12	NA	2	1	1	1	1	4	3	2	1	1
Sly12g0063221	M10	NA	11	17	11	4	2	25	25	16	6	3
Sly12g0063361	M12	NA	1	1	1	1	0	5	9	5	10	10
Sly12g0063371	M12	NA	2	1	2	2	2	3	3	4	6	7
Sly12g0063381	M11	NA	3	3	6	4	3	9	10	12	8	8
Sly12g0063391	M1	NA	1	1	1	1	1	1	1	1	2	1
Sly12g0063431	M11	NA	185	155	163	224	191	228	211	234	195	201
Sly12g0063441	M1	NA	13	12	19	4	4	5	5	4	2	1
Sly12g0063451	M1	NA	10	8	15	2	3	4	5	3	1	2
Sly12g0063461	M1	NA	12	10	14	3	4	3	5	3	2	1
Sly12g0063481	M9	NA	2	2	1	2	1	2	3	2	1	0
Sly12g0063531	M12	NA	4	5	7	6	3	8	8	8	5	7
Sly12g0063541	M12	NA	1	1	1	1	1	2	3	1	1	1
Sly12g0063611	M1	NA	3	3	4	4	3	3	2	3	3	3
Sly12g0063621	M1	NA	1	1	2	1	1	1	1	1	1	1
Sly12g0063631	M1	NA	12	8	7	1	0	1	1	1	0	0
Sly12g0063691	M11	NA	19	21	20	41	72	21	22	25	53	76
Sly12g0063701	M1	ARP4	60	61	64	76	93	56	57	57	89	108
Sly12g0063801	M12	NA	2	2	2	1	1	3	3	3	2	1
Sly12g0063851	M1	NA	5	5	8	4	4	4	4	5	4	5
Sly12g0063871	M11	NA	31	24	31	10	11	32	33	36	8	10
Sly12g0063971	M12	NA	30	27	29	28	33	40	37	41	37	43
Sly12g0063981	M11	NA	0	1	1	0	0	2	1	2	0	0
Sly12g0064001	M12	NA	1	1	2	1	1	2	3	3	6	18
Sly12g0064011	M12	NA	1	2	2	2	1	5	4	5	10	23
Sly12g0064021	M1	NA	21	20	20	17	20	14	15	14	20	21
Sly12g0064051	M11	NA	59	63	50	47	35	77	70	68	31	30
Sly12g0064071	M9	NA	6	7	6	5	8	7	8	6	12	29
Sly12g0064081	M1	NA	8	10	10	12	16	7	7	8	14	17
Sly12g0064101	M12	NA	1	1	2	1	2	27	33	31	2	7
Sly12g0064111	M12	NA	26	26	27	28	25	38	41	34	39	55
Sly12g0064181	M19	NA	15	16	17	14	15	14	13	15	12	12
Sly12g0064191	M11	NA	1	1	1	1	1	1	1	2	3	2
Sly12g0064201	M1	NA	4	4	4	4	1	0	0	1	1	0
Sly12g0064211	M3	NA	47	49	33	16	14	28	30	22	23	26
Sly12g0064221	M1	NA	10	7	10	4	3	5	4	3	1	1
Sly12g0064231	M1	NA	15	17	16	18	19	14	14	14	20	18
Sly12g0064241	M1	NA	5	4	6	4	5	3	3	4	3	2
Sly12g0064251	M1	NA	7	5	6	5	7	4	4	5	4	3
Sly12g0064261	M16	NA	18	19	17	23	19	17	19	18	22	19
Sly12g0064301	M2	NA	80	86	59	50	34	47	56	33	40	43
Sly12g0064321	M3	NA	4	4	2	1	1	3	4	2	4	4
Sly12g0064341	M11	NA	20	21	25	23	16	36	29	38	25	18
Sly12g0064431	M1	NA	5	3	7	5	4	2	1	1	1	0
Sly12g0064441	M1	NA	3	5	9	11	12	2	1	5	4	4
Sly12g0064451	M1	NA	3	4	7	5	8	2	2	2	2	2
Sly12g0064461	M13	NA	40	36	40	29	25	37	35	41	39	50
Sly12g0064481	M1	NA	4	3	3	3	2	2	1	3	1	1
Sly12g0064541	M12	NA	20	20	23	13	10	25	28	25	14	12
Sly12g0064591	M12	NA	34	34	35	45	59	39	38	39	65	88
Sly12g0064601	M1	NA	150	131	137	80	64	83	83	80	65	56
Sly12g0064731	M12	NA	13	10	14	32	34	14	16	16	31	37
Sly12g0064741	M11	NA	16	17	21	48	55	21	18	25	42	44
Sly12g0064751	M18	NA	7	10	11	25	20	11	9	12	18	11
Sly12g0064771	M3	NA	214	191	177	130	101	158	166	151	161	133
Sly12g0064811	M1	NA	8	10	11	31	22	6	7	16	57	42
Sly12g0064841	M1	NA	56	54	53	42	41	49	46	46	31	30
Sly12g0064951	M22	NA	3	4	3	4	3	4	3	3	2	2
Sly12g0065031	M1	NA	2	1	2	1	1	1	1	1	1	1
Sly12g0065051	M12	NA	3	2	3	3	3	3	3	3	3	2
Sly12g0065111	M14	NA	12	10	18	12	8	9	8	13	9	7
Sly12g0065131	M12	NA	3	1	1	0	0	13	4	11	1	0
Sly12g0065141	M12	NA	9	10	11	11	11	10	12	10	13	15
Sly12g0065161	M22	NA	1	1	1	1	1	2	2	2	1	1
Sly12g0065171	M11	NA	13	13	15	17	15	15	15	15	17	16
Sly12g0065181	M2	NA	43	43	37	29	21	31	36	30	29	28
Sly12g0065191	M3	NA	3	3	2	1	1	2	2	1	2	1
Sly12g0065341	M1	NA	14	8	16	1	0	1	0	1	0	0
Sly12g0065361	M3	NA	61	75	48	35	54	47	69	38	32	75
Sly12g0065371	M1	NA	7	3	5	5	7	4	3	4	13	25
Sly12g0065381	M12	NA	3	3	3	6	10	4	4	5	13	27
Sly12g0065391	M22	NA	1	0	1	1	1	1	1	1	1	1
Sly12g0065411	M3	NA	1	2	1	1	1	1	1	1	0	0
Sly12g0065451	M23	NA	1	1	1	1	0	1	1	1	1	0
Sly12g0065461	M23	NA	5	2	2	1	1	15	5	2	1	1
Sly12g0065471	M23	NA	2	1	1	1	0	12	3	1	1	0
Sly12g0065491	M11	NA	1	1	1	1	1	3	3	3	1	1
Sly12g0065501	M12	NA	88	77	71	15	6	142	125	100	15	5
Sly12g0065511	M12	NA	61	61	58	68	64	73	69	70	94	113
Sly12g0065541	M11	NA	1	1	1	1	0	2	2	2	1	0
Sly12g0065551	M23	NA	2	1	1	1	0	3	2	1	1	0
Sly12g0065561	M11	nxd	32	30	31	31	18	46	46	45	36	27
Sly12g0065581	M11	NA	1	1	1	1	1	1	1	1	2	1
Sly12g0065591	M11	NA	2	1	1	1	1	2	2	2	1	1
Sly12g0065601	M11	NA	1	1	1	1	1	2	1	2	1	1
Sly12g0065611	M11	NA	1	1	1	1	1	1	1	2	1	1
Sly12g0065621	M11	NA	2	2	2	2	1	2	2	3	1	2
Sly12g0065631	M11	NA	2	1	2	1	1	2	2	2	1	1
Sly12g0065651	M3	NA	32	33	26	32	37	28	29	29	33	41
Sly12g0065671	M22	NA	23	26	23	27	30	25	21	25	25	32
Sly12g0065701	M1	NA	40	38	35	12	4	2	3	2	5	6
Sly12g0065831	M11	NA	288	277	340	537	885	416	344	476	481	761
Sly12g0065841	M11	SlARF2B	94	95	102	75	98	105	98	99	102	108
Sly12g0065851	M19	NA	68	71	71	58	63	80	61	80	56	59
Sly12g0065891	M1	NA	526	423	440	290	202	347	314	355	275	232
Sly12g0065901	M18	NA	3	3	3	2	3	6	4	7	3	2
Sly12g0065911	M11	NA	4	5	6	3	3	7	5	6	4	3
Sly12g0065921	M12	NA	4	3	4	2	2	6	6	6	3	2
Sly12g0065941	M12	NA	7	9	8	6	4	17	18	16	6	2
Sly12g0065951	M11	NA	7	8	8	6	3	16	12	15	5	1
Sly12g0065961	M1	NA	12	13	12	14	11	10	11	11	12	12
Sly12g0066021	M11	NA	7	6	9	3	1	17	15	16	4	1
Sly12g0066081	M3	NA	2	3	2	1	1	1	1	1	1	0
Sly12g0066091	M1	NA	3	3	3	1	1	2	2	2	1	1
Sly12g0066131	M8	NA	38	42	35	30	28	45	56	33	20	23
Sly12g0066151	M1	NA	156	154	189	133	414	115	89	109	97	200
Sly12g0066171	M1	NA	2	2	2	2	2	2	2	2	2	1
Sly12g0066181	M3	NA	42	36	25	10	8	19	20	9	4	3
Sly12g0066191	M11	NA	33	30	35	29	35	30	30	38	42	42
Sly12g0066201	M1	NA	11	19	5	1	0	5	2	4	1	1
Sly12g0066211	M1	NA	21	22	30	2	1	14	11	12	1	1
Sly12g0066221	M1	NA	61	56	48	35	16	7	4	1	1	1
Sly12g0066231	M10	NA	4	3	3	1	2	4	5	3	1	2
Sly12g0066241	M11	NA	1	1	1	1	0	2	2	2	0	1
Sly12g0066251	M11	NA	39	39	53	7	5	149	114

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0153241	M12	NA	1	1	1	0	0	3	2	2	1	1
Sly05g0153261	M12	NA	2	3	3	7	4	2	3	3	5	3
Sly05g0153271	M1	NA	3	2	3	1	1	1	1	1	0	0
Sly05g0153291	M12	NA	10	12	9	18	19	20	23	26	42	51
Sly05g0153451	M11	NA	7	6	9	5	6	15	12	20	6	6
Sly05g0153461	M1	NA	3	4	4	4	3	3	2	3	2	2
Sly05g0153471	M1	NA	4	4	4	4	4	4	4	3	3	3
Sly05g0153481	M1	NA	2	2	3	2	3	2	2	2	3	3
Sly05g0153491	M1	NA	1	1	1	1	2	1	1	1	1	1
Sly05g0153511	M14	NA	58	47	63	47	74	53	47	55	27	34
Sly05g0153521	M4	NA	8	7	10	31	51	11	9	10	34	53
Sly05g0153531	M12	SAUR55	2	2	2	1	1	4	3	3	1	1
Sly05g0153541	M3	NA	79	76	74	58	36	71	82	65	48	34
Sly05g0153551	M12	NA	1	1	1	1	1	1	1	2	1	3
Sly05g0153601	M9	NA	2	1	1	1	1	2	4	1	1	1
Sly05g0153631	M11	NA	148	124	121	202	196	193	181	202	218	208
Sly05g0153641	M3	NA	39	33	29	27	24	22	26	21	34	38
Sly05g0153671	M14	NA	32	30	39	22	21	30	27	35	25	27
Sly05g0153691	M12	NA	52	48	48	58	79	49	50	55	67	88
Sly05g0153701	M1	SIARF7B	25	21	31	20	35	19	16	19	13	13
Sly05g0153741	M22	NA	1	1	1	0	0	2	0	2	0	0
Sly05g0153781	M22	NA	2	1	2	0	0	6	1	7	0	0
Sly05g0153791	M19	NA	43	46	47	44	48	47	39	43	44	47
Sly05g0153801	M2	NA	3	3	2	2	2	2	3	5	1	1
Sly05g0153811	M18	NA	5	5	6	3	2	11	8	11	5	2
Sly05g0153821	M11	NA	10	10	13	7	4	20	15	18	10	3
Sly05g0153831	M12	NA	3	3	4	3	2	10	10	10	4	2
Sly05g0153851	M1	NA	1	1	1	1	1	1	1	0	0	0
Sly05g0153861	M1	NA	6	5	12	1	1	1	1	1	1	0
Sly05g0153871	M11	NA	11	13	23	27	19	27	20	28	2	1
Sly05g0153881	M12	NA	20	18	22	21	23	22	24	26	18	23
Sly05g0153901	M3	NA	1	1	1	0	0	1	1	0	0	0
Sly05g0153911	M17	NA	76	66	70	86	98	63	63	72	123	133
Sly05g0153921	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0153931	M11	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0153971	M14	NA	99	89	114	73	68	91	84	93	71	80
Sly05g0154001	M2	NA	67	66	63	73	74	55	62	53	57	61
Sly05g0154011	M11	NA	9	8	10	10	10	12	10	13	9	12
Sly05g0154091	M13	NA	55	51	59	42	43	50	49	61	40	46
Sly05g0154111	M12	NA	24	21	22	18	20	24	22	22	14	14
Sly05g0154161	M1	NA	9	8	8	7	7	8	8	8	8	9
Sly05g0154171	M2	NA	100	86	84	75	75	75	85	76	100	114
Sly05g0154191	M12	NA	7	6	7	16	15	9	8	10	19	19
Sly05g0154201	M19	NA	15	15	14	14	16	13	14	15	15	18
Sly05g0154211	M22	NA	8	3	7	36	22	13	3	13	12	29
Sly05g0154221	M1	NA	26	23	25	6	2	15	14	15	5	1
Sly05g0154231	M3	NA	11	12	8	21	41	6	7	5	17	41
Sly05g0154241	M1	ACS4	5	4	6	266	320	1	1	1	51	103
Sly05g0154261	M11	NA	5	4	7	6	11	7	5	6	7	6
Sly05g0154301	M11	NA	2	1	2	1	5	2	2	3	2	4
Sly05g0154371	M11	NA	17	14	25	4	1	44	35	63	11	2
Sly05g0154391	M12	NA	1386	1508	970	290	161	2011	1871	1622	480	190
Sly05g0154401	M1	NA	41	18	14	10	3	4	7	1	1	1
Sly05g0154451	M2	NA	308	282	315	344	355	247	289	285	390	373
Sly05g0154461	M12	NA	2	1	1	1	1	3	9	2	1	1
Sly05g0154471	M12	NA	4	4	4	11	12	4	14	8	38	42
Sly05g0154481	M3	NA	321	290	297	414	414	240	280	278	584	672
Sly05g0154531	M3	SlGH3-5	54	54	47	30	21	51	67	22	117	143
Sly05g0154561	M19	NA	17	20	20	21	24	20	17	19	49	23
Sly05g0154571	M3	NA	10	9	8	11	14	7	8	9	40	23
Sly05g0154581	M1	NA	35	46	19	8	3	4	4	2	7	4
Sly05g0154591	M6	NA	2	6	1	0	0	2	2	1	1	0
Sly05g0154601	M1	NA	2	4	2	1	0	1	1	0	0	0
Sly05g0154611	M1	NA	3	4	2	1	1	1	1	0	0	0
Sly05g0154621	M20	NA	10	9	13	6	3	10	8	11	4	3
Sly05g0154631	M23	NA	9	7	10	4	2	12	7	7	2	2
Sly05g0154641	M3	NA	24	51	15	3	2	4	6	1	0	1
Sly05g0154651	M1	NA	65	68	68	62	71	60	58	65	75	94
Sly05g0154831	M11	NA	46	43	57	44	54	52	48	62	51	72
Sly05g0154841	M22	NA	1	0	1	1	2	4	1	3	0	0
Sly05g0154871	M1	NA	15	14	19	23	22	15	14	14	12	16
Sly05g0154881	M1	NA	2	2	3	2	3	2	2	2	2	2
Sly05g0154911	M3	NA	42	47	16	8	10	12	13	9	7	7
Sly05g0154931	M1	NA	2	3	3	4	6	2	2	3	3	4
Sly05g0154941	M13	NA	35	31	45	50	51	38	37	50	44	42
Sly05g0154961	M3	NA	86	86	73	81	71	42	54	40	68	75
Sly05g0154971	M18	NA	10	11	13	10	6	21	17	23	4	2
Sly05g0155021	M2	NA	75	73	61	70	62	52	60	49	68	64
Sly05g0155041	M11	NA	3	3	4	3	1	7	7	9	6	2
Sly05g0155051	M11	NA	7	9	12	10	3	22	20	26	15	6
Sly05g0155061	M11	NA	13	13	14	15	14	16	14	18	19	19
Sly05g0155091	M1	NA	8	9	14	16	18	7	8	10	17	14
Sly05g0155101	M19	NA	1	1	1	2	3	1	1	1	2	2
Sly05g0155111	M19	NA	1	1	1	2	3	1	1	1	2	2
Sly05g0155121	M1	NA	2	2	3	5	7	2	2	3	7	5
Sly05g0155131	M19	NA	1	2	2	2	3	1	1	2	2	1
Sly05g0155141	M12	NA	1	1	1	3	4	1	1	1	3	2
Sly05g0155151	M11	NA	1	1	3	4	5	3	1	4	7	4
Sly05g0155161	M9	NA	3	3	2	3	2	7	7	6	5	3
Sly05g0155191	M3	NA	855	884	318	28	48	496	675	161	19	28
Sly05g0155201	M1	NA	3	7	6	5	6	2	3	4	3	2
Sly05g0155211	M1	NA	4	5	4	3	5	3	2	3	3	3
Sly05g0155231	M1	SIERF.H5	8	4	16	3	2	1	1	0	0	1
Sly05g0155241	M1	NA	5	5	8	4	6	2	2	2	6	7
Sly05g0155251	M3	NA	322	295	209	317	270	223	253	215	359	348
Sly05g0155261	M2	NA	3	3	3	4	4	2	4	2	4	4
Sly05g0155271	M2	NA	62	56	53	39	29	54	59	59	36	31
Sly05g0155321	M1	NA	9	8	10	7	2	4	4	3	1	1
Sly05g0155331	M1	NA	13	12	13	11	7	9	10	10	10	10
Sly05g0155341	M1	NA	10	11	11	10	7	8	10	9	9	9
Sly05g0155351	M3	NA	95	82	58	14	3	49	67	22	5	2
Sly05g0155361	M3	NA	35	36	33	33	40	28	33	30	38	43
Sly05g0155371	M11	NA	18	17	19	32	40	23	21	24	40	44
Sly05g0155381	M14	NA	4	3	3	1	2	3	3	3	1	1
Sly05g0155401	M1	NA	110	92	101	164	203	46	36	42	41	53
Sly05g0155411	M11	NA	13	13	17	28	18	25	22	22	6	2
Sly05g0155421	M9	NA	6	5	5	8	6	7	8	7	6	4
Sly05g0155431	M3	NA	157	136	105	93	66	79	99	64	86	62
Sly05g0155441	M1	NA	5	4	5	1	1	1	1	1	1	1
Sly05g0155451	M1	NA	83	76	81	67	52	65	69	73	59	49
Sly05g0155461	M9	NA	34	35	35	35	30	35	38	34	39	32
Sly05g0155471	M12	BIN2	30	36	45	30	24	56	49	57	31	24
Sly05g0155481	M1	NA	38	38	34	20	10	9	10	6	3	3
Sly05g0155491	M19	NA	42	39	42	44	44	38	34	45	48	41
Sly05g0155691	M1	SIERF.C1	22	21	11	2	10	1	1	0	1	1
Sly05g0155711	M3	NA	2	3	2	5	7	2	2	2	1	3
Sly05g0155721	M11	NA	63	57	60	50	50	68	67	72	74	88
Sly05g0155731	M1	NA	16	21	27	32	30	4	9	3	9	19
Sly05g0155741	M22	NA	1	1	1	1	0	1	1	1	1	0
Sly05g0155751	M22	NA	4	0	2	0	0	11	5	12	0	0
Sly05g0155771	M1	NA	20	22	10	1	1	2	1	1	0	0
Sly05g0155781	M1	NA	14	15	14	14	14	8	9	8	6	8
Sly05g0155791	M11	NA	7	4	8	5	6	16	11	14	5	5
Sly05g0155831	M3	NA	3	4	2	1	1	1	2	1	0	0
Sly05g0155851	M14	NA	10	10	12	12	7	9	9	11	8	7
Sly05g0155861	M18	NA	10	12	14	17	12	17	14	20	9	6
Sly05g0155871	M11	NA	5	5	6	6	5	7	7	8	5	5
Sly05g0155901	M11	NA	7	8	10	9	9	9	7	8	7	7
Sly05g0155911	M22	NA	2	1	1	0	1	5	1	2	1	1
Sly05g0155941	M5	NA	59	88	41	10	32	69	65	34	5	14
Sly05g0155951	M12	NA	4	4	3	1	1	15	14	10	1	1
Sly05g0155961	M1	SlCyD4;2	2	2	2	1	1	1	1	1	1	0
Sly05g0155981	M4	NA	4	3	5	3	9	5	4	5	9	26
Sly05g0156031	M3	NA	3	2	1	1	0	1	1	0	0	0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0066301	M1	NA	3	2	4	1	1	1	1	1	0	0
Sly12g0066311	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly12g0066331	M3	NA	36	40	32	23	16	23	21	19	16	10
Sly12g0066351	M1	NA	3	4	2	0	1	1	0	0	0	0
Sly12g0066361	M3	UGT73C1-like	18	7	4	1	0	3	4	1	0	0
Sly12g0066391	M1	NA	378	330	322	198	156	226	217	216	205	172
Sly12g0066401	M22	NA	1	1	1	0	0	6	0	5	0	0
Sly12g0066411	M2	NA	19	17	16	14	16	15	19	16	18	19
Sly12g0066421	M11	NA	40	37	40	29	25	39	38	41	44	36
Sly12g0066491	M22	NA	1	0	1	0	0	3	1	3	0	0
Sly12g0066521	M18	NA	31	34	41	36	30	34	33	41	30	24
Sly12g0066531	M11	NA	15	15	15	13	15	14	15	15	17	19
Sly12g0066541	M1	NA	2	3	2	1	1	1	2	2	3	6
Sly12g0066551	M3	NA	47	49	45	46	47	42	44	40	52	48
Sly12g0066581	M13	NA	84	69	107	125	121	83	76	120	92	89
Sly12g0066611	M12	NA	14	13	17	16	18	21	22	22	34	42
Sly12g0066621	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0066631	M12	NA	3	3	7	478	456	11	9	10	26	160
Sly12g0066681	M12	NA	1	1	1	1	2	1	1	2	2	4
Sly12g0066691	M11	NA	1	1	1	1	2	2	1	2	2	2
Sly12g0066701	M1	NA	7	4	3	1	1	1	1	0	0	1
Sly12g0066711	M3	NA	238	237	169	112	100	133	155	126	120	119
Sly12g0066721	M11	NA	3	4	4	16	13	4	5	4	11	8
Sly12g0066731	M12	NA	26	25	21	26	39	40	47	43	32	31
Sly12g0066741	M6	NA	1	2	1	1	1	1	1	1	2	1
Sly12g0066751	M14	NA	143	136	148	152	136	114	108	138	186	167
Sly12g0066761	M9	NA	1	1	1	1	2	1	2	1	1	1
Sly12g0066771	M12	NA	1	1	1	1	3	1	1	1	2	1
Sly12g0066821	M1	NA	31	31	28	27	24	25	25	26	25	23
Sly12g0066861	M3	NA	92	98	92	108	90	95	97	88	76	69
Sly12g0066871	M11	NA	73	69	88	131	112	127	99	151	88	53
Sly12g0066881	M3	NA	10	10	8	5	9	9	9	7	7	14
Sly12g0066891	M9	NA	5	6	5	6	6	8	9	7	7	6
Sly12g0066901	M12	NA	26	36	25	26	27	36	39	32	28	27
Sly12g0066921	M4	NA	48	45	47	49	48	47	48	46	49	46
Sly12g0066931	M11	NA	6	7	7	7	7	10	8	11	9	9
Sly12g0066941	M4	NA	121	113	127	145	211	128	120	131	139	266
Sly12g0066951	M1	NA	74	73	78	107	132	55	53	51	99	157
Sly12g0066961	M12	NA	1	1	2	1	1	9	8	15	4	2
Sly12g0066971	M6	NA	1	1	1	1	0	1	1	1	0	0
Sly12g0066981	M11	NA	845	820	984	1211	1009	837	815	971	1039	990
Sly12g0067031	M1	NA	26	28	28	25	9	10	11	8	2	2
Sly12g0067041	M1	NA	16	17	18	18	6	7	7	6	2	1
Sly12g0067051	M1	NA	10	7	10	1	1	3	2	2	1	0
Sly12g0067061	M1	NA	7	7	7	1	1	2	1	1	0	1
Sly12g0067071	M11	NA	26	30	32	44	53	33	28	34	53	76
Sly12g0067081	M1	NA	21	20	19	5	2	7	6	7	1	2
Sly12g0067091	M3	NA	185	213	88	25	15	68	123	24	13	10
Sly12g0067111	M1	NA	42	46	45	36	17	24	17	24	10	7
Sly12g0067121	M1	NA	1	2	1	2	1	1	1	1	1	1
Sly12g0067131	M11	NA	2	2	2	1	1	2	2	2	1	0
Sly12g0067141	M12	NA	1	2	2	1	1	5	5	3	5	1
Sly12g0067151	M11	NA	1	1	1	1	1	4	4	6	6	1
Sly12g0067161	M11	NA	6	5	6	1	1	25	21	29	2	0
Sly12g0067171	M1	NA	32	31	43	31	39	21	17	20	19	15
Sly12g0067181	M1	NA	32	29	40	26	36	17	13	17	16	15
Sly12g0067201	M11	NA	1	1	1	0	1	1	1	1	0	0
Sly12g0067211	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly12g0067221	M11	NA	5	3	6	0	1	14	8	17	0	0
Sly12g0067231	M11	NA	8	8	10	7	7	11	11	11	8	5
Sly12g0067251	M1	NA	12	13	12	9	10	7	5	7	5	5
Sly12g0067261	M11	NA	8	7	11	11	8	12	11	13	11	6
Sly12g0067281	M7	NA	1	2	1	1	1	1	3	1	1	1
Sly12g0067291	M18	NA	28	31	34	41	60	38	33	40	36	39
Sly12g0067301	M7	NA	16	19	17	11	17	17	21	15	11	12
Sly12g0067311	M1	NA	5	3	3	1	1	1	1	1	1	0
Sly12g0067341	M3	NA	4	3	3	5	5	4	2	2	7	4
Sly12g0067361	M22	NA	2	2	2	1	1	2	1	3	0	0
Sly12g0067371	M3	NA	7	7	7	3	4	5	6	6	3	4
Sly12g0067381	M1	NA	8	9	8	4	4	6	5	6	3	3
Sly12g0067391	M22	NA	2	1	1	0	0	4	1	3	0	0
Sly12g0067401	M2	NA	5	4	5	7	10	5	6	4	17	44
Sly12g0067451	M12	NA	348	316	398	605	954	522	514	495	966	1443
Sly12g0067461	M19	NA	7	7	10	5	2	6	5	7	2	1
Sly12g0067471	M2	NA	2	2	2	2	1	1	2	1	1	1
Sly12g0067481	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly12g0067491	M1	NA	41	40	48	45	43	36	38	43	54	67
Sly12g0067611	M3	NA	2	4	3	2	4	2	3	1	2	9
Sly12g0067621	M11	NA	3	3	3	3	3	3	3	4	6	7
Sly12g0067631	M9	NA	4	6	4	6	17	7	11	7	9	44
Sly12g0067691	M10	NA	16	18	12	14	11	17	17	15	16	14
Sly12g0067711	M1	NA	655	600	639	442	270	538	542	610	399	330
Sly12g0067721	M12	NA	8	9	7	5	3	11	10	9	5	3
Sly12g0067731	M1	NA	119	119	120	154	181	108	110	122	167	223
Sly12g0067751	M12	NA	1	2	1	1	1	2	3	3	2	1
Sly12g0067811	M3	NA	54	52	48	53	52	50	51	47	45	40
Sly12g0067831	M1	NA	12	12	16	2	1	11	8	10	1	0
Sly12g0067851	M18	NA	1	1	1	1	1	1	1	1	0	0
Sly12g0067861	M12	NA	68	52	55	43	37	64	63	72	55	62
Sly12g0067871	M12	NA	48	50	50	61	82	52	54	53	65	96
Sly12g0067881	M13	NA	10	10	14	31	20	10	10	12	48	20
Sly12g0067891	M12	NA	5	4	5	4	1	9	9	8	8	2
Sly12g0067901	M12	NA	2	2	2	2	1	4	3	3	4	2
Sly12g0067921	M8	NA	49	49	35	42	26	54	70	43	38	25
Sly12g0067931	M1	NA	3	4	3	1	1	1	1	1	1	1
Sly12g0067941	M1	NA	73	69	55	16	13	25	25	14	6	3
Sly12g0067951	M3	NA	216	250	104	25	43	184	186	55	8	10
Sly12g0067961	M4	NA	7	6	6	3	7	7	6	6	6	15
Sly12g0067971	M1	NA	3	3	2	0	0	1	1	2	0	0
Sly12g0067981	M1	NA	5	6	8	1	1	1	1	2	0	1
Sly12g0068021	M3	NA	1	1	2	1	1	1	1	1	1	1
Sly12g0068031	M1	NA	6	6	5	3	1	3	4	3	2	2
Sly12g0068051	M1	NA	32	36	35	10	4	10	8	8	5	4
Sly12g0068061	M1	NA	30	28	29	8	5	9	6	8	5	3
Sly12g0068071	M1	NA	10	14	6	0	0	1	1	1	0	0
Sly12g0068081	M1	NA	10	16	6	1	0	1	1	0	0	0
Sly12g0068091	M3	NA	349	404	189	7	3	98	86	25	1	2
Sly12g0068111	M1	NA	27	25	16	0	0	2	1	1	1	0
Sly12g0068121	M3	NA	5	3	1	1	0	1	2	1	0	1
Sly12g0068171	M22	NA	1	1	2	3	1	2	1	2	0	0
Sly12g0068311	M17	NA	47	42	40	36	33	38	34	46	45	49
Sly12g0068321	M3	NA	69	75	59	56	55	42	48	42	61	54
Sly12g0068371	M11	NA	39	39	47	80	126	47	47	58	86	159
Sly12g0068381	M12	NA	4	3	4	9	13	7	7	6	5	5
Sly12g0068391	M3	NA	47	44	31	26	26	26	29	21	26	22
Sly12g0068401	M23	NA	1	1	1	4	3	1	1	1	1	0
Sly12g0068411	M13	NA	27	24	25	40	50	23	24	27	43	60
Sly12g0068421	M23	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0068431	M3	NA	15	16	14	13	13	12	14	16	20	17
Sly12g0068461	M3	NA	1	2	1	0	0	1	0	1	0	0
Sly12g0068471	M3	NA	29	28	28	25	19	28	25	22	13	9
Sly12g0068491	M12	NA	19	17	23	15	7	23	22	22	3	2
Sly12g0068501	M1	JAZ1-like1	178	167	80	1	1	5	7	1	1	3
Sly12g0068511	M19	NA	32	33	35	27	25	31	28	31	29	28
Sly12g0068521	M1	NA	24	24	26	20	25	15	13	14	19	28
Sly12g0068541	M18	NA	1	3	2	2	1	2	2	3	2	1
Sly12g0068551	M22	NA	2	2	2	2	2	2	2	2	2	1
Sly12g0068561	M11	NA	4	4	4	4	4	4	4	4	4	4
Sly12g0068581	M11	NA	3	3	4	2	1	5	3	4	1	1
Sly12g0068601	M12	NA	25	28	26	22	21	29	30	31	24	25
Sly12g0068611	M12	NA	2	2	1	1	1	1	1	2	6	5
Sly

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0156041	M3	NA	47	33	11	1	1	9	10	5	2	2
Sly05g0156061	M3	NA	2	2	1	1	0	0	0	0	0	0
Sly05g0156071	M1	NA	10	16	5	1	1	1	1	0	0	0
Sly05g0156081	M7	NA	20	22	18	23	26	20	22	20	27	26
Sly05g0156091	M1	NA	92	82	90	107	149	79	70	86	131	156
Sly05g0156101	M22	NA	2	1	2	1	4	3	2	2	2	2
Sly05g0156111	M3	NA	10	10	7	7	8	6	8	4	12	10
Sly05g0156121	M1	NA	32	31	34	24	19	27	25	27	21	14
Sly05g0156131	M3	NA	2	2	1	0	0	1	0	0	0	0
Sly05g0156151	M11	NA	1	1	1	1	0	2	2	2	1	0
Sly05g0156181	M12	NA	5	4	6	3	5	12	11	12	5	5
Sly05g0156191	M12	NA	116	115	112	88	36	122	139	130	54	34
Sly05g0156201	M1	NA	2	1	2	0	1	1	1	1	1	1
Sly05g0156211	M11	NA	24	21	27	29	31	26	25	26	33	32
Sly05g0156221	M1	NA	3	3	4	3	1	1	1	1	2	3
Sly05g0156251	M12	NA	8	8	9	10	16	14	14	13	10	12
Sly05g0156261	M11	NA	10	11	12	12	12	11	11	12	11	13
Sly05g0156271	M22	NA	1	1	1	1	0	1	1	1	0	0
Sly05g0156301	M1	NA	55	50	37	8	7	38	21	22	2	3
Sly05g0156321	M14	NA	23	22	28	16	19	24	20	26	26	21
Sly05g0156331	M2	NA	20	19	16	16	11	12	15	10	6	3
Sly05g0156341	M13	NA	63	57	75	222	430	55	56	73	161	240
Sly05g0156351	M11	NA	4	2	4	6	9	4	4	3	8	12
Sly05g0156391	M1	NA	6	4	6	1	1	0	1	1	0	0
Sly05g0156401	M1	NA	48	50	70	20	43	1	1	1	1	1
Sly05g0156431	M13	NA	15	15	15	16	11	12	13	18	12	8
Sly05g0156451	M12	NA	12	16	17	19	7	18	17	19	10	2
Sly05g0156461	M3	NA	91	87	88	72	67	76	83	77	77	94
Sly05g0156471	M3	NA	21	20	14	11	10	13	13	11	9	7
Sly05g0156481	M11	NA	92	76	96	28	16	121	103	172	110	84
Sly05g0156491	M1	NA	1	1	2	1	0	1	1	1	0	1
Sly05g0156531	M3	NA	27	27	20	34	27	17	18	16	23	28
Sly05g0156551	M11	NA	150	129	197	183	72	152	223	166	21	5
Sly05g0156571	M1	NA	3	2	2	1	1	0	0	0	0	0
Sly05g0156611	M2	NA	36	37	31	25	18	24	31	26	10	5
Sly05g0156631	M1	NA	7	10	7	1	1	1	0	0	1	0
Sly05g0156671	M1	NA	2	2	2	3	3	1	1	1	1	1
Sly05g0156691	M1	NA	6	6	4	2	2	3	3	3	2	1
Sly05g0156721	M12	NA	16	16	16	18	22	18	20	17	34	39
Sly05g0156731	M12	NA	15	15	15	18	19	17	17	16	27	32
Sly05g0156741	M1	NA	42	40	46	37	37	38	35	43	34	33
Sly05g0156751	M1	SIERF.B3	60	73	59	9	6	29	21	30	3	7
Sly05g0156761	M6	SIERF.B1	28	85	45	28	166	48	88	22	5	48
Sly05g0156771	M3	SIERF.A3/SlPti4	139	172	84	32	48	66	73	46	31	46
Sly05g0156781	M22	NA	1	1	1	0	0	3	1	2	0	0
Sly05g0156791	M12	NA	102	107	111	104	82	101	111	111	99	91
Sly05g0156821	M12	NA	15	13	18	14	6	26	24	31	17	3
Sly05g0156851	M1	NA	1	2	1	1	1	1	1	0	0	0
Sly05g0156861	M9	NA	204	205	197	304	256	199	250	209	277	274
Sly05g0156871	M13	NA	26	26	31	33	34	30	30	36	33	37
Sly05g0156881	M18	NA	17	17	19	18	25	19	15	20	19	22
Sly05g0156891	M3	NA	37	36	32	27	28	25	26	24	38	43
Sly05g0156901	M11	NA	21	17	22	30	37	22	18	26	38	38
Sly05g0156911	M12	NA	55	58	66	50	43	59	61	59	45	46
Sly05g0156921	M1	NA	38	39	23	22	26	13	12	11	19	27
Sly05g0156931	M22	NA	23	23	22	31	33	22	20	25	35	36
Sly05g0156961	M1	NA	4	5	5	381	289	2	1	2	1	1
Sly05g0156991	M3	NA	62	62	60	92	154	52	61	59	114	215
Sly05g0157011	M3	NA	58	60	57	45	51	59	54	57	54	87
Sly05g0157021	M1	NA	9	12	5	1	0	1	1	1	0	1
Sly05g0157031	M1	NA	31	76	33	5	1	6	5	1	1	0
Sly05g0157051	M9	NA	1	1	1	1	0	2	2	1	1	0
Sly05g0157061	M1	NA	68	62	64	79	76	57	58	69	106	119
Sly05g0157071	M3	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0157101	M11	NA	4	4	5	4	4	4	4	4	2	2
Sly05g0157111	M1	NA	3	4	3	5	6	2	2	1	2	3
Sly05g0157121	M12	NA	2	2	1	1	1	13	5	9	1	1
Sly05g0157141	M11	SIERF.H14	4	3	6	15	35	6	5	9	21	45
Sly05g0157151	M12	NA	1	1	1	1	0	1	1	2	1	0
Sly05g0157181	M1	NA	10	19	14	16	14	3	2	2	1	1
Sly05g0157191	M3	NA	9	8	8	10	9	8	8	7	7	6
Sly05g0157201	M12	NA	79	78	89	106	149	81	82	92	104	163
Sly05g0157211	M1	NA	14	13	14	27	48	9	9	9	16	33
Sly05g0157221	M3	NA	18	22	14	13	7	17	18	16	7	3
Sly05g0157241	M12	NA	15	13	11	10	9	14	15	13	6	5
Sly05g0157261	M3	NA	182	210	201	214	179	198	211	175	121	113
Sly05g0157271	M3	NA	20	22	14	13	40	12	19	10	6	21
Sly05g0157311	M6	NA	84	246	121	62	421	131	271	62	30	336
Sly05g0157321	M3	NA	35	40	30	34	30	19	26	16	18	28
Sly05g0157331	M1	NA	4	4	3	1	1	1	1	1	1	1
Sly05g0157341	M11	NA	53	41	62	63	57	83	60	93	17	9
Sly05g0157361	M11	NA	30	29	41	37	28	43	37	57	23	25
Sly05g0157371	M11	COI	25	23	31	84	68	26	26	29	20	21
Sly05g0157381	M13	NA	94	82	138	155	175	116	109	143	124	118
Sly05g0157391	M1	NA	34	37	47	63	77	28	30	34	81	114
Sly05g0157401	M1	NA	24	26	19	4	1	1	1	1	1	1
Sly05g0157411	M1	NA	45	72	19	1	1	2	3	1	1	1
Sly05g0157421	M3	NA	47	56	32	15	1	8	13	3	3	1
Sly05g0157431	M1	NA	35	35	36	27	20	26	24	27	13	9
Sly05g0157441	M12	NA	15	18	14	18	21	41	50	45	27	25
Sly05g0157451	M11	NA	22	20	25	38	40	33	31	39	21	44
Sly05g0157461	M15	NA	55	41	52	49	58	64	53	79	91	126
Sly05g0157471	M11	NA	21	20	23	30	49	32	32	41	36	45
Sly05g0157491	M10	NA	37	57	33	9	17	79	101	29	15	20
Sly05g0157501	M12	NA	108	105	137	115	174	221	231	267	171	255
Sly05g0157531	M2	NA	96	91	84	66	45	71	91	70	54	40
Sly05g0157541	M5	NA	70	80	45	43	43	59	82	47	45	54
Sly05g0157551	M16	NA	182	150	155	104	91	132	106	134	110	132
Sly05g0157561	M3	NA	134	111	87	80	65	78	83	62	89	79
Sly05g0157571	M11	NA	6	6	9	5	2	10	8	10	2	1
Sly05g0157601	M10	NA	6	8	4	3	1	7	8	6	4	2
Sly05g0157611	M3	NA	13	11	7	6	4	7	6	5	4	3
Sly05g0157621	M12	NA	8	9	10	12	6	73	89	102	52	18
Sly05g0157631	M12	NA	3	3	5	2	1	53	58	72	14	3
Sly05g0157681	M1	NA	7	7	5	4	2	1	1	1	1	1
Sly05g0157691	M12	NA	65	65	53	68	73	77	84	68	82	101
Sly05g0157711	M12	NA	27	26	23	19	19	34	41	31	24	27
Sly05g0157721	M12	NA	8	9	7	5	5	11	11	10	4	4
Sly05g0157731	M11	NA	1	1	1	1	8	1	1	1	1	10
Sly05g0157741	M11	NA	36	34	34	36	42	37	35	39	43	45
Sly05g0157751	M12	NA	27	27	31	36	26	49	49	46	23	21
Sly05g0157761	M12	SIPP2C2	148	109	146	138	243	134	115	148	115	251
Sly05g0157771	M2	NA	21	20	18	13	6	16	17	13	2	3
Sly05g0157781	M3	NA	1	2	1	1	1	1	1	1	1	2
Sly05g0157801	M12	NA	8	14	5	2	2	20	20	14	2	1
Sly05g0157811	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly05g0157821	M22	NA	4	2	2	0	0	20	7	14	1	1
Sly05g0157831	M12	NA	45	41	52	54	68	57	56	63	58	72
Sly05g0157861	M3	NA	742	891	378	99	384	476	1016	456	654	929
Sly05g0157871	M1	NA	20	25	19	23	26	8	9	7	13	19
Sly05g0157881	M11	NA	30	28	38	38	23	50	38	59	12	8
Sly05g0157901	M23	NA	1	1	1	0	0	3	1	1	0	0
Sly05g0157911	M11	NA	32	31	33	32	37	35	34	37	39	45
Sly05g0157921	M1	NA	49	46	50	39	36	34	39	31	34	38
Sly05g0157941	M23	NA	4	1	2	1	0	7	4	3	3	1
Sly05g0157961	M1	NA	4	3	2	1	1	1	0	1	1	0
Sly05g0157971	M11	NA	9	8	10	15	17	14	12	16	18	20
Sly05g0157981	M11	NA	4	5	5	4	2	6	5	6	4	2
Sly05g0157991	M11	NA	299	365	412	629	429	784	798	1225	1435	882
Sly05g0158001	M1	NA	65	65	58	38	40	40	38	38	40	44
Sly05g0158011	M3	NA	75	74	54	48	35	55	53	44	43	34
Sly05g0158021	M1	NA	41	40	44	29	29	31	28	29	20	19
Sly05g0158031	M3	NA	65	63	55	52	73	36	42	32	57	78
Sly05g0158041	M11	NA	10	11	12	16	19	16	12	17	16	22

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0068651	M19	NA	10	12	12	15	13	11	11	12	19	17
Sly12g0068661	M18	NA	63	62	64	53	49	68	68	69	43	38
Sly12g0068671	M1	NA	18	17	18	14	15	13	12	12	13	19
Sly12g0068681	M3	NA	10	10	8	9	9	6	7	6	7	8
Sly12g0068691	M11	NA	1	1	2	2	4	2	2	2	3	2
Sly12g0068701	M11	NA	1	1	1	1	2	2	1	1	2	3
Sly12g0068721	M12	NA	1	1	1	1	2	2	1	1	1	2
Sly12g0068731	M4	NA	1	1	1	1	1	1	1	1	1	2
Sly12g0068761	M2	NA	1	1	1	1	2	1	1	1	1	3
Sly12g0068781	M3	NA	2	6	4	2	3	3	4	2	2	4
Sly12g0068791	M11	NA	29	29	36	22	22	35	31	46	19	23
Sly12g0068811	M19	NA	41	52	50	37	36	46	36	52	43	47
Sly12g0068821	M11	NA	22	20	24	11	15	27	26	27	25	31
Sly12g0068831	M15	NA	10	6	7	4	6	8	7	8	10	13
Sly12g0068841	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly12g0068931	M6	NA	1	2	1	1	1	1	3	1	0	1
Sly12g0068941	M11	NA	56	51	70	55	57	68	61	65	54	78
Sly12g0068961	M12	NA	22	26	26	30	24	28	29	26	13	13
Sly12g0068971	M5	NA	33	37	18	22	27	29	38	18	19	39
Sly12g0068981	M11	NA	199	167	180	335	328	243	269	256	233	255
Sly12g0069001	M11	NA	31	31	32	34	42	41	33	45	34	47
Sly12g0069011	M11	NA	477	454	525	647	491	585	575	597	414	374
Sly12g0069021	M1	NA	2	2	2	1	1	1	2	2	1	1
Sly12g0069031	M1	NA	20	22	21	24	19	13	16	14	22	17
Sly12g0069041	M2	NA	272	237	212	137	96	174	210	166	117	88
Sly12g0069051	M11	NA	27	22	46	8	3	137	114	132	2	1
Sly12g0069061	M11	NA	15	13	19	13	8	23	21	29	16	7
Sly12g0069071	M2	NA	137	133	121	115	99	92	136	96	115	102
Sly12g0069081	M23	NA	1	1	1	1	0	2	1	1	1	1
Sly12g0069121	M1	NA	11	12	14	13	13	9	7	9	7	8
Sly12g0069141	M7	NA	16	24	14	18	33	26	45	15	34	51
Sly12g0069151	M11	NA	30	29	39	29	18	74	62	87	34	23
Sly12g0069171	M3	NA	16	16	15	18	22	12	16	15	22	29
Sly12g0069191	M12	NA	1	2	1	1	0	4	2	3	0	0
Sly12g0069201	M11	SlPYL1/2	29	32	32	49	36	40	39	41	61	73
Sly12g0069241	M1	NA	62	66	71	70	87	56	64	65	85	103
Sly12g0069291	M19	NA	54	54	58	57	55	54	50	60	54	51
Sly12g0069301	M12	NA	15	17	15	17	17	14	16	17	18	20
Sly12g0069321	M12	NA	440	422	536	712	814	518	522	644	762	841
Sly12g0069331	M12	NA	42	43	46	42	29	47	60	52	45	30
Sly12g0069341	M18	NA	71	60	77	116	100	75	67	81	86	90
Sly12g0069351	M12	NA	11	11	13	17	18	17	16	19	30	27
Sly12g0069361	M12	NA	5	5	6	7	9	9	8	9	13	10
Sly12g0069401	M1	NA	5	5	6	6	3	5	4	6	2	2
Sly12g0069411	M12	NA	2	2	2	2	1	4	3	3	2	2
Sly12g0069431	M1	NA	26	24	20	14	17	19	16	18	14	13
Sly12g0069441	M3	ACS13	5	8	3	0	0	1	1	1	0	0
Sly12g0069461	M1	NA	9	6	14	1	0	8	6	5	1	0
Sly12g0069471	M3	NA	244	234	155	111	151	169	209	147	187	221
Sly12g0069481	M11	NA	179	123	228	82	27	295	227	300	42	7
Sly12g0069511	M1	Glutathione peroxidas	159	150	168	158	149	99	107	139	122	106
Sly12g0069521	M12	Glutathione peroxidas	32	34	37	28	16	35	42	42	24	24
Sly12g0069531	M3	NA	254	300	316	200	147	156	218	188	171	83
Sly12g0069561	M3	NA	2	2	2	1	1	1	2	1	1	1
Sly12g0069581	M12	NA	11	12	11	30	44	19	16	17	29	50
Sly12g0069591	M12	NA	5	7	7	8	14	10	10	10	16	21
Sly12g0069601	M11	NA	10	13	15	16	20	18	17	25	27	31
Sly12g0069621	M1	NA	9	11	14	11	4	9	8	8	3	2
Sly12g0069671	M3	NA	22	23	19	13	14	15	16	13	14	14
Sly12g0069681	M1	NA	5	4	6	8	2	2	2	2	1	0
Sly12g0069691	M1	NA	4	4	4	1	1	2	1	2	1	1
Sly12g0069701	M3	NA	27	57	26	6	2	14	24	5	1	1
Sly12g0069731	M1	NA	2	2	1	1	1	1	1	1	0	0
Sly12g0069741	M12	NA	9	13	11	19	33	11	13	12	31	32
Sly12g0069751	M12	PP2-A11	27	26	32	39	61	46	50	48	85	81
Sly12g0069781	M9	NA	22	26	25	31	26	30	35	26	29	20
Sly12g0069791	M22	NA	1	0	1	0	0	3	1	2	0	0
Sly12g0069821	M1	NA	9	9	8	11	8	3	3	2	2	1
Sly12g0069851	M3	NA	9	15	19	1	0	5	4	1	0	0
Sly12g0069861	M1	FZR2-like	2	2	2	1	2	1	2	2	2	2
Sly12g0069881	M11	NA	19	17	26	21	14	31	27	35	11	6
Sly12g0069891	M18	NA	6	6	6	8	8	8	7	9	18	13
Sly12g0069901	M12	NA	79	83	83	184	258	116	127	139	288	329
Sly12g0069911	M11	NA	6	4	3	1	0	8	7	5	1	1
Sly12g0069921	M1	NA	1	1	1	2	1	0	0	0	0	0
Sly12g0069941	M3	NA	18	17	16	9	9	15	15	14	7	9
Sly12g0069951	M22	NA	10	8	9	4	6	8	7	10	5	6
Sly12g0069961	M22	NA	1	1	1	0	0	1	1	1	1	1
Sly12g0069971	M3	NA	45	46	33	12	8	37	46	27	5	10
Sly12g0070011	M5	SlERF.D2	45	60	21	12	9	27	45	12	18	22
Sly12g0070021	M3	NA	47	52	25	74	63	10	20	2	436	120
Sly12g0070051	M3	NA	2	1	1	4	10	1	1	1	1	1
Sly12g0070061	M12	NA	2	3	3	4	3	3	4	3	5	7
Sly12g0070071	M19	NA	3	2	3	3	4	3	2	3	4	9
Sly12g0070081	M1	NA	6	6	6	7	10	5	5	5	8	20
Sly12g0070091	M3	NA	89	89	86	110	115	53	72	64	144	130
Sly12g0070101	M8	NA	55	52	41	52	32	49	62	45	48	26
Sly12g0070111	M14	NA	163	168	217	226	215	155	146	175	103	110
Sly12g0070121	M11	NA	9	8	10	8	7	10	9	11	5	2
Sly12g0070131	M3	NA	12	13	9	8	4	11	10	6	5	3
Sly12g0070141	M5	NA	1	1	1	1	1	1	1	1	1	0
Sly12g0070231	M11	NA	29	26	32	34	53	36	33	41	42	49
Sly12g0070261	M21	NA	2	2	2	1	1	2	1	2	1	1
Sly12g0070271	M1	NA	28	26	26	15	12	22	24	26	17	15
Sly12g0070281	M1	NA	15	13	14	51	104	10	10	11	64	137
Sly12g0070291	M10	NA	94	111	90	59	52	119	134	84	72	72
Sly12g0070301	M11	NA	17	13	15	10	4	17	16	15	5	3
Sly12g0070321	M23	NA	1	1	1	0	0	2	1	1	1	0
Sly12g0070331	M11	NA	85	78	107	91	29	151	132	192	49	12
Sly12g0070341	M10	NA	30	30	29	34	28	31	35	27	34	25
Sly12g0070351	M11	NA	13	12	14	34	86	14	13	16	36	73
Sly12g0070361	M1	NA	23	25	24	16	7	8	6	8	3	1
Sly12g0070381	M12	NA	5	5	5	3	3	5	5	5	3	3
Sly12g0070391	M12	NA	47	48	49	58	69	49	54	54	72	90
Sly12g0070401	M15	NA	36	36	38	45	40	37	35	40	60	57
Sly12g0070411	M11	NA	0	0	1	1	1	1	1	1	1	1
Sly12g0070421	M1	NA	5	4	4	2	1	1	1	1	1	1
Sly12g0070431	M1	NA	32	42	50	141	82	10	9	13	44	35
Sly12g0070441	M1	NA	7	5	10	22	45	4	4	4	2	2
Sly12g0070451	M1	NA	3	3	2	1	1	1	1	1	0	0
Sly12g0070471	M1	NA	6	6	5	1	2	4	3	4	2	2
Sly12g0070481	M1	NA	2	2	1	1	1	1	0	0	0	0
Sly12g0070501	M18	NA	10	13	15	12	11	12	11	14	17	26
Sly12g0070511	M1	NA	5	6	5	2	1	1	1	1	1	1
Sly12g0070551	M11	NA	32	28	50	15	6	88	73	107	11	2
Sly12g0070581	M3	NA	21	34	11	1	2	12	16	9	3	4
Sly12g0070611	M9	NA	1	2	1	0	0	4	6	3	1	0
Sly12g0070621	M12	NA	2	2	1	1	1	5	6	4	0	0
Sly12g0070631	M1	NA	1	1	1	1	1	1	0	1	0	0
Sly12g0070651	M1	NA	1	1	1	1	1	1	1	1	0	0
Sly12g0070661	M8	NA	79	76	72	22	7	87	122	69	14	7
Sly12g0070671	M12	NA	46	50	44	80	125	60	67	60	70	175
Sly12g0070681	M10	NA	1	3	1	0	0	18	22	2	0	0
Sly12g0070691	M3	NA	1	2	2	1	1	1	1	1	0	0
Sly12g0070711	M3	NA	14	48	35	2	2	11	14	4	1	2
Sly12g0070721	M12	NA	14	53	36	12	155	50	165	88	34	182
Sly12g0070731	M7	NA	24	78	65	15	243	41	144	56	20	312
Sly12g0070741	M11	NA	28	29	39	55	63	37	39	47	62	71
Sly12g0070751	M1	NA	59	57	69	122	114	46	48	64	106	117
Sly12g0070761	M9	NA	1	1	1	3	8	1	1	1	1	1
Sly12g0070801	M1	NA	1	1	1	1	1	1	0

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0158051	M11	NA	15	14	19	34	39	24	21	23	23	28
Sly05g0158061	M3	NA	36	42	29	30	61	26	35	23	38	57
Sly05g0158071	M2	NA	73	77	67	103	119	58	67	55	98	99
Sly05g0158081	M12	NA	74	66	65	84	23	109	117	91	18	3
Sly05g0158091	M2	NA	13	15	8	6	3	8	11	5	2	2
Sly05g0158111	M11	GA2ox1	1	1	1	1	0	1	1	1	0	0
Sly05g0158121	M11	NA	13	11	11	9	13	13	18	15	9	11
Sly05g0158131	M20	NA	25	26	38	28	40	22	33	29	22	40
Sly05g0158141	M1	NA	31	30	40	37	45	23	27	26	26	35
Sly05g0158151	M1	NA	3	2	3	2	2	1	2	2	1	1
Sly05g0158161	M5	NA	4	6	2	1	1	4	4	1	1	1
Sly05g0158171	M11	NA	44	33	43	44	40	51	48	55	47	59
Sly05g0158181	M19	NA	3	3	4	6	3	3	2	3	8	4
Sly05g0158201	M19	NA	5	5	8	16	17	5	4	7	20	17
Sly05g0158221	M2	NA	13	12	11	10	10	12	14	11	14	12
Sly05g0158231	M1	NA	362	326	313	228	135	227	223	229	216	137
Sly05g0158251	M22	NA	2	0	1	0	0	7	0	6	0	0
Sly05g0158261	M22	NA	1	0	1	0	0	7	1	5	0	0
Sly05g0158281	M22	NA	2	0	2	0	0	12	0	10	0	0
Sly05g0158301	M22	NA	1	1	1	0	0	4	0	3	0	0
Sly05g0158321	M22	NA	3	1	2	0	0	22	1	13	0	0
Sly05g0158351	M1	NA	142	144	147	196	240	89	90	79	156	193
Sly05g0158361	M12	NA	7	8	8	11	11	10	11	13	10	10
Sly05g0158371	M9	NA	10	11	9	21	24	10	13	11	17	19
Sly05g0158381	M6	NA	13	20	16	20	26	12	20	6	5	25
Sly05g0158421	M17	NA	39	39	41	126	103	38	35	40	51	53
Sly05g0158431	M1	NA	26	22	79	1346	1035	3	2	3	2	1
Sly05g0158471	M21	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0158491	M11	NA	45	46	59	67	56	57	50	63	31	32
Sly05g0158501	M3	NA	17	43	15	9	17	27	20	3	1	1
Sly05g0158511	M3	NA	23	39	6	1	1	3	2	1	1	0
Sly05g0158521	M3	NA	158	129	84	22	28	100	88	114	150	77
Sly05g0158531	M23	NA	6	3	4	1	1	53	10	24	1	0
Sly05g0158541	M23	NA	11	6	5	0	1	101	16	44	1	0
Sly05g0158551	M1	NA	88	92	89	80	80	71	69	75	55	46
Sly05g0158571	M1	NA	368	337	342	254	188	251	271	251	237	155
Sly05g0158591	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly05g0158611	M11	NA	22	20	24	25	28	28	24	29	30	40
Sly05g0158621	M3	NA	38	40	31	34	28	36	37	30	28	25
Sly05g0158631	M15	NA	66	55	58	67	59	61	62	65	93	71
Sly05g0158641	M3	NA	10	11	12	7	9	8	9	7	10	9
Sly05g0158661	M3	NA	22	23	18	21	54	19	16	26	18	50
Sly05g0158671	M3	NA	20	18	16	18	18	16	16	14	15	13
Sly05g0158681	M1	NA	580	568	557	486	420	313	378	348	461	507
Sly05g0158701	M18	NA	26	29	35	54	52	30	28	36	38	38
Sly05g0158711	M12	NA	117	103	109	101	77	143	160	129	55	26
Sly05g0158721	M11	NA	25	25	30	64	51	40	41	48	55	43
Sly05g0158731	M3	NA	147	156	132	118	94	125	140	112	88	92
Sly05g0158741	M1	NA	191	210	169	149	152	120	123	106	103	123
Sly05g0158761	M11	NA	50	45	110	65	14	142	142	224	17	3
Sly05g0158781	M23	NA	16	14	12	5	2	19	17	11	2	1
Sly05g0158791	M2	NA	18	17	13	7	6	11	13	9	10	8
Sly05g0158801	M5	NA	1	1	1	2	1	2	1	1	1	1
Sly05g0158811	M12	NA	7	5	7	17	12	48	48	59	86	53
Sly05g0158841	M3	NA	75	85	43	15	3	17	27	10	3	1
Sly05g0158851	M2	NA	158	166	155	175	170	136	168	143	214	224
Sly05g0158861	M11	NA	21	21	23	45	40	33	34	42	51	35
Sly05g0158871	M11	NA	2	1	1	1	1	2	1	2	2	1
Sly05g0158881	M1	NA	28	29	27	38	25	13	15	13	29	25
Sly05g0158891	M3	NA	7	8	6	5	3	6	6	5	3	2
Sly05g0158901	M1	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0158931	M2	NA	7	6	7	7	7	6	8	6	2	2
Sly05g0158951	M2	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0158961	M3	NA	3	3	3	3	3	2	2	1	3	4
Sly05g0158981	M1	NA	220	194	188	181	168	125	135	112	177	177
Sly05g0158991	M12	NA	30	32	33	58	87	41	47	45	76	113
Sly05g0159001	M22	NA	371	194	339	13	12	624	311	667	6	3
Sly05g0159011	M15	NA	118	102	111	126	119	104	109	106	113	118
Sly05g0159021	M11	NA	1	1	1	1	1	2	2	2	1	0
Sly05g0159031	M12	NA	8	9	7	2	2	11	11	9	2	1
Sly05g0159041	M11	NA	32	29	35	25	26	54	44	58	33	36
Sly05g0159051	M3	NA	38	37	39	27	27	26	33	27	32	30
Sly05g0159071	M1	NA	23	25	23	10	3	10	9	8	2	1
Sly05g0159091	M10	NA	46	71	29	15	23	77	74	51	10	11
Sly05g0159111	M3	NA	52	58	37	24	28	32	34	26	14	20
Sly05g0159121	M21	NA	3	2	3	1	1	3	1	1	0	1
Sly05g0159131	M11	NA	16	17	20	17	15	27	23	24	14	18
Sly05g0159151	M11	NA	40	37	53	40	19	59	54	43	4	4
Sly05g0159161	M1	NA	30	31	37	48	43	13	13	15	17	18
Sly05g0159171	M1	NA	4	4	6	5	4	2	1	2	1	1
Sly05g0159181	M22	SIPRMT3	24	22	28	16	14	27	23	26	15	14
Sly05g0159191	M7	NA	1	3	3	1	1	2	6	2	3	4
Sly05g0159201	M9	NA	35	38	35	37	23	39	42	39	29	22
Sly05g0159241	M1	NA	29	30	31	25	21	25	26	25	19	14
Sly05g0159251	M3	NA	62	53	52	46	46	51	49	43	46	36
Sly05g0159261	M1	NA	20	23	24	24	7	19	21	17	5	2
Sly05g0159271	M1	NA	45	46	80	67	27	3	1	2	1	1
Sly05g0159281	M11	NA	16	16	22	34	26	37	34	38	29	30
Sly05g0159291	M11	NA	387	314	508	492	335	620	521	814	599	179
Sly05g0159311	M10	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0159321	M11	NA	64	61	76	49	25	114	96	116	44	23
Sly05g0159341	M5	NA	18	24	13	1	0	54	38	2	1	0
Sly05g0159351	M2	SIRR9	72	75	55	19	19	39	58	32	30	59
Sly05g0159361	M3	NA	38	34	32	20	17	29	31	24	15	17
Sly05g0159371	M3	NA	15	16	13	7	5	6	7	5	2	3
Sly05g0159381	M1	NA	57	53	61	44	18	52	47	55	20	9
Sly05g0159391	M1	NA	9	10	10	16	11	9	8	8	4	3
Sly05g0159401	M1	NA	10	9	10	6	4	9	8	8	5	3
Sly05g0159421	M12	NA	11	10	13	12	9	20	17	19	8	8
Sly05g0159441	M3	NA	41	41	33	33	32	35	40	33	38	37
Sly05g0159451	M3	NA	5	4	3	5	1	3	4	2	7	2
Sly05g0159461	M1	NA	75	71	88	99	62	42	44	47	30	24
Sly05g0159471	M11	NA	63	61	69	58	67	80	74	97	83	100
Sly05g0159491	M3	NA	29	28	27	33	33	24	25	24	43	50
Sly05g0159501	M12	NA	2	1	2	2	1	3	3	3	2	2
Sly05g0159511	M12	NA	42	41	49	55	63	65	64	66	60	70
Sly05g0159521	M12	NA	32	28	28	22	19	40	44	36	22	24
Sly05g0159531	M9	NA	136	125	106	131	52	204	244	146	103	49
Sly05g0159541	M9	NA	86	83	71	86	61	90	114	71	103	88
Sly05g0159571	M3	NA	762	710	636	464	310	492	542	407	365	248
Sly05g0159581	M22	NA	11	10	11	25	23	47	13	30	24	44
Sly05g0159591	M11	NA	8	8	9	9	10	11	10	11	5	4
Sly05g0159601	M11	NA	12	10	9	1	1	25	19	20	1	1
Sly05g0159611	M11	NA	55	38	92	44	38	171	146	237	31	23
Sly05g0159621	M19	NA	25	25	24	22	22	24	21	25	20	19
Sly05g0159641	M3	NA	206	220	187	138	93	120	138	108	90	65
Sly05g0159651	M9	NA	1	2	1	1	1	4	3	2	2	5
Sly05g0159671	M1	NA	4	3	5	8	15	2	2	2	4	5
Sly05g0159681	M12	NA	2	2	2	2	1	5	4	4	1	1
Sly05g0159691	M7	NA	2	1	1	1	1	1	1	1	0	1
Sly05g0159751	M18	NA	20	18	21	22	18	22	20	20	18	20
Sly05g0159761	M3	NA	41	41	36	26	26	38	36	36	25	30
Sly05g0159771	M11	NA	72	68	80	148	255	106	98	118	156	238
Sly05g0159781	M1	NA	18	16	24	27	26	15	12	16	9	11
Sly05g0159791	M11	NA	18	19	22	22	15	29	26	27	13	7
Sly05g0159821	M13	NA	215	223	258	209	258	202	233	251	319	206
Sly05g0159831	M3	NA	36	44	22	11	13	23	29	12	12	14
Sly05g0159841	M3	NA	1	1	1	0	1	1	1	1	1	1
Sly05g0159851	M3	NA	1	2	1	1	1	1	1	1	1	1
Sly05g0159861	M3	NA	2	2	1	1	1	1	2	1	1	1
Sly05g0159871	M3	NA	195	245	147	107	139	138	173	94	87	147
Sly05g0159881	M1	NA	438	417	419	315	210	269	324	271	275	183
Sly05g0159901	M5	NA	134	166	83	35	51	146	163	82	35	53
Sly05g0159911	M12	NA	7	7	8	10	9	12	12	12	12	11

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0070871	M3	NA	2	2	1	0	0	2	1	1	0	0
Sly12g0070891	M23	NA	2	1	1	0	0	4	1	1	0	0
Sly12g0070901	M3	NA	80	123	50	10	27	24	48	19	8	52
Sly12g0070911	M3	NA	35	48	29	36	47	33	38	31	43	74
Sly12g0070921	M13	NA	16	18	19	19	21	17	17	19	21	24
Sly12g0070931	M1	NA	42	35	45	38	21	2	1	1	1	1
Sly12g0070941	M3	NA	13	13	11	8	8	7	8	7	8	9
Sly12g0070961	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0070971	M2	NA	14	13	11	17	14	12	13	14	17	18
Sly12g0070981	M1	NA	59	54	52	38	39	37	39	35	37	48
Sly12g0070991	M1	NA	1	2	1	1	1	1	1	1	1	1
Sly12g0071001	M1	NA	29	27	20	4	1	10	9	8	6	2
Sly12g0071021	M12	NA	11	11	13	13	13	13	15	15	21	17
Sly12g0071131	M3	NA	7	8	4	1	1	2	3	2	1	1
Sly12g0071151	M12	NA	33	32	34	41	44	47	63	59	53	79
Sly12g0071161	M11	NA	19	21	22	37	27	25	23	25	68	55
Sly12g0071171	M12	NA	1	2	14	1065	1686	2	25	114	6392	5899
Sly12g0071181	M8	NA	168	247	169	170	139	158	285	184	114	145
Sly12g0071191	M12	NA	9	16	10	15	14	8	11	19	9	6
Sly12g0071201	M22	NA	1	1	1	0	0	2	0	1	0	0
Sly12g0071241	M14	NA	3	2	4	1	0	3	2	3	1	0
Sly12g0071281	M1	NA	53	54	54	48	44	51	46	50	46	40
Sly12g0071291	M12	NA	1	1	1	1	2	1	1	1	2	2
Sly12g0071301	M18	NA	6	6	8	14	22	13	11	15	18	12
Sly12g0071311	M11	NA	3	1	3	2	1	3	4	3	1	1
Sly12g0071331	M11	NA	55	55	59	50	45	57	56	64	51	44
Sly12g0071341	M7	NA	14	18	7	3	24	14	23	11	7	52
Sly12g0071351	M3	NA	24	23	14	12	20	17	21	12	37	32
Sly12g0071371	M3	NA	4	12	4	1	2	2	2	1	0	0
Sly12g0071381	M3	NA	2	5	3	1	1	1	1	1	1	1
Sly12g0071391	M3	NA	2	2	1	3	3	2	2	2	4	5
Sly12g0071401	M2	NA	10	11	9	49	61	7	10	8	29	39
Sly12g0071411	M1	NA	10	8	7	4	3	4	3	3	1	0
Sly12g0071421	M6	NA	40	49	30	29	37	31	34	26	32	37
Sly12g0071431	M11	NA	6	7	9	12	18	9	9	12	18	24
Sly12g0071441	M13	NA	2	2	3	51	165	2	2	3	3	5
Sly12g0071451	M1	SlCycA3;4	2	2	2	2	2	1	2	2	2	1
Sly12g0071461	M11	NA	16	14	18	12	12	17	14	18	13	11
Sly12g0071471	M3	NA	2	2	1	1	2	1	2	1	2	4
Sly12g0071481	M11	SlCycA3;5	1	1	1	1	0	1	1	1	1	1
Sly12g0071501	M11	SlCycA3;3	1	2	2	1	1	2	2	2	1	1
Sly12g0071511	M11	SlCycA3;1	13	11	18	1	1	21	17	19	1	1
Sly12g0071581	M22	NA	1	1	1	0	0	1	0	1	0	0
Sly12g0071621	M1	SlCycD3;2	3	3	2	2	1	3	1	1	1	0
Sly12g0071631	M9	NA	26	28	25	29	26	28	34	28	21	20
Sly12g0071641	M1	NA	47	60	94	62	27	3	1	1	2	1
Sly12g0071651	M11	NA	4	5	5	9	16	6	6	8	18	18
Sly12g0071661	M12	NA	6	6	5	2	0	10	10	9	1	0
Sly12g0071671	M11	NA	11	12	11	3	1	24	19	20	3	1
Sly12g0071691	M1	NA	480	470	496	395	351	340	318	314	345	340
Sly12g0071701	M2	NA	56	55	48	63	66	44	47	42	61	70
Sly12g0071711	M1	NA	23	22	22	29	33	14	12	16	28	38
Sly12g0071721	M1	NA	9	8	10	6	4	6	4	5	1	1
Sly12g0071771	M12	NA	1	1	1	1	1	2	1	2	1	0
Sly12g0071781	M1	NA	12	12	12	12	19	9	8	10	10	15
Sly12g0071791	M1	NA	3	4	5	2	2	3	3	3	1	3
Sly12g0071801	M11	NA	16	22	25	38	25	33	31	44	72	81
Sly12g0071821	M1	NA	36	35	30	36	36	2	1	1	1	1
Sly12g0071881	M3	NA	6	5	5	2	1	5	4	4	1	2
Sly12g0071891	M2	NA	6	5	6	5	5	5	6	5	6	5
Sly12g0071901	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0071911	M1	NA	41	39	35	31	27	24	26	23	28	25
Sly12g0071921	M1	NA	9	9	6	2	1	2	2	2	1	1
Sly12g0071931	M12	NA	18	18	17	15	20	36	28	29	14	20
Sly12g0071941	M1	NA	1	1	1	1	1	0	1	0	0	0
Sly12g0071951	M1	NA	4	7	3	1	1	1	1	1	0	1
Sly12g0071971	M1	NA	52	55	59	72	58	39	43	45	58	46
Sly12g0072001	M3	NA	51	53	48	45	39	49	51	43	40	41
Sly12g0072011	M1	NA	56	57	55	72	94	41	39	47	80	93
Sly12g0072021	M3	NA	12	13	6	3	3	5	4	3	2	3
Sly12g0072031	M3	NA	16	15	8	4	4	7	7	5	5	5
Sly12g0072041	M1	NA	47	43	45	34	38	19	16	16	31	46
Sly12g0072051	M10	BZR1-like/BZR1-1D	45	47	47	45	69	43	59	46	70	115
Sly12g0072061	M1	NA	1	1	1	1	1	1	1	0	1	0
Sly12g0072071	M11	NA	23	20	25	18	12	24	23	24	9	7
Sly12g0072101	M3	NA	37	39	32	27	25	26	26	26	25	27
Sly12g0072111	M1	NA	3	3	3	2	1	3	1	1	1	1
Sly12g0072131	M1	NA	597	587	706	536	661	479	514	529	509	1081
Sly12g0072141	M2	NA	13	14	14	19	23	12	13	14	37	38
Sly12g0072151	M1	NA	111	105	86	61	62	50	49	62	56	55
Sly12g0072161	M12	NA	89	85	89	82	89	85	90	95	67	73
Sly12g0072181	M3	NA	30	37	24	16	11	18	18	9	5	6
Sly12g0072201	M22	NA	2	0	2	0	0	3	1	7	0	0
Sly12g0072211	M11	NA	26	31	37	47	41	66	68	95	37	24
Sly12g0072241	M12	NA	4	4	4	5	4	5	6	6	7	6
Sly12g0072251	M11	NA	30	26	36	44	778	79	74	106	46	230
Sly12g0072261	M11	NA	37	30	65	106	194	50	56	130	176	253
Sly12g0072271	M1	NA	1	2	2	2	1	1	0	1	0	1
Sly12g0072281	M1	NA	39	54	71	189	367	8	33	70	237	321
Sly12g0072301	M12	NA	1	1	1	0	0	2	2	1	1	0
Sly12g0072311	M5	NA	20	20	18	15	15	19	20	19	20	14
Sly12g0072331	M1	NA	31	34	30	22	22	24	23	22	19	18
Sly12g0072351	M12	HVA22-like1	5	6	7	8	5	28	34	30	29	11
Sly12g0072361	M12	NA	4	3	2	4	2	56	59	52	49	18
Sly12g0072371	M12	NA	21	26	34	71	63	357	462	476	498	368
Sly12g0072391	M3	NA	24	24	21	22	22	25	24	22	20	21
Sly12g0072411	M11	NA	26	27	29	57	98	30	29	31	67	110
Sly12g0072461	M3	NA	3	2	1	0	0	1	0	0	0	0
Sly12g0072471	M11	NA	116	108	146	99	106	139	148	167	99	111
Sly12g0072481	M12	NA	56	46	122	102	25	276	312	484	287	58
Sly12g0072491	M11	ATL23	186	116	189	56	28	163	159	243	56	27
Sly12g0072501	M3	NA	13	26	12	1	2	10	14	2	1	1
Sly12g0072511	M23	NA	1	1	1	2	2	1	1	1	1	1
Sly12g0072531	M1	NA	11	11	14	35	44	10	11	12	39	49
Sly12g0072541	M11	NA	64	53	74	128	136	86	74	100	94	103
Sly12g0072551	M11	NA	4	3	3	7	10	4	4	4	7	6
Sly12g0072561	M22	NA	2	1	2	1	0	7	1	6	0	0
Sly12g0072591	M1	NA	53	57	58	66	36	21	27	21	17	10
Sly12g0072611	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0072631	M11	NA	6	6	8	5	3	7	7	7	1	1
Sly12g0072641	M11	NA	23	22	32	25	27	36	28	41	30	36
Sly12g0072651	M1	ADH	23	20	20	18	23	15	14	13	5	2
Sly12g0072661	M3	NA	26	37	22	17	15	19	21	21	13	12
Sly12g0072671	M3	OPC-8:CoA synthetase	235	239	120	52	76	67	77	23	17	46
Sly12g0072691	M12	NA	41	41	38	36	30	42	46	41	27	32
Sly12g0072701	M12	NA	20	24	22	31	49	29	32	35	21	20
Sly12g0072721	M11	NA	11	10	9	8	6	16	14	14	5	2
Sly12g0072731	M1	NA	21	21	23	27	30	16	16	19	21	18
Sly12g0072751	M1	NA	3	3	5	8	4	1	1	1	1	1
Sly12g0072761	M1	Catalase	1425	1624	2247	6694	5462	206	86	252	180	488
Sly12g0072771	M11	NA	88	65	100	109	162	134	109	165	103	139
Sly12g0072781	M11	NA	22	28	15	2	1	41	35	47	1	1
Sly12g0072791	M3	NA	38	42	13	2	1	6	7	3	1	1
Sly12g0072801	M3	NA	40	55	17	2	1	8	10	3	1	1
Sly12g0072811	M1	NA	13	12	8	6	3	1	1	1	1	1
Sly12g0072841	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0072851	M1	NA	1	1	1	0	0	0	1	0	0	0
Sly12g0072861	M3	NA	51	52	44	46	46	42	41	39	62	65
Sly12g0072871	M11	NA	5	4	4	3	1	4	3	5	1	1
Sly12g0072881	M1	NA	3	7	6	18	3	0	0	1	1	0
Sly12g0072961	M23	SlPILS8	1

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0159931	M3	NA	34	40	19	23	19	22	21	11	5	12
Sly05g0159941	M3	NA	8	7	6	5	8	5	4	4	4	6
Sly05g0159951	M3	NA	8	11	3	3	1	4	3	2	1	1
Sly05g0159971	M3	NA	46	49	42	43	49	39	41	38	53	48
Sly05g0159981	M11	NA	381	356	381	298	241	425	381	525	446	443
Sly05g0159991	M1	NA	2	1	1	1	1	1	1	1	1	1
Sly05g0160001	M11	NA	20	19	27	42	65	32	33	40	54	68
Sly05g0160011	M12	NA	21	22	21	32	34	23	25	21	31	43
Sly05g0160021	M3	NA	102	103	94	97	118	82	87	82	114	148
Sly05g0160031	M19	NA	63	65	69	60	49	69	59	69	41	42
Sly05g0160041	M3	NA	49	50	44	45	41	44	43	43	40	37
Sly05g0160051	M2	NA	29	31	25	22	21	22	24	20	26	21
Sly05g0160061	M11	NA	28	27	32	64	137	37	41	48	81	145
Sly05g0160071	M4	NA	18	17	22	52	86	29	25	29	71	128
Sly05g0160081	M22	NA	1	1	1	0	0	1	1	1	0	0
Sly05g0160101	M10	NA	4	4	2	0	1	9	9	1	0	0
Sly05g0160111	M3	NA	23	23	19	14	12	22	21	20	10	11
Sly05g0160131	M12	NA	58	60	64	61	55	74	75	78	72	55
Sly05g0160141	M3	ETR7	40	46	32	38	32	18	19	16	31	23
Sly05g0160151	M6	NA	1	5	5	0	3	3	7	2	0	3
Sly05g0160161	M1	NA	54	55	54	49	40	43	41	40	33	28
Sly05g0160171	M22	NA	1	1	1	0	0	1	1	2	0	0
Sly05g0160181	M11	NA	43	43	47	24	22	46	46	44	27	25
Sly05g0160211	M11	NA	2250	2173	2574	2187	2098	2198	1775	2615	3381	3276
Sly05g0160221	M3	NA	59	59	50	45	25	43	43	40	51	35
Sly05g0160241	M11	NA	1	1	1	0	0	5	3	5	1	0
Sly05g0160261	M1	NA	1	1	1	1	0	1	1	1	0	0
Sly05g0160271	M14	NA	102	96	122	125	136	104	98	119	125	134
Sly05g0160291	M1	NA	216	194	203	137	123	152	160	146	127	94
Sly05g0160301	M12	NA	36	36	34	47	69	38	38	43	53	73
Sly05g0160311	M11	NA	23	20	24	46	47	28	30	34	40	34
Sly05g0160321	M1	NA	203	193	170	141	120	84	82	85	107	86
Sly05g0160331	M6	NA	14	27	19	0	0	18	18	2	0	0
Sly05g0160341	M2	NA	47	46	39	59	53	27	39	29	40	33
Sly05g0160361	M3	NA	20	20	16	16	16	17	19	15	16	18
Sly05g0160371	M1	NA	82	70	86	115	122	43	38	47	47	39
Sly05g0160391	M1	NA	5	7	11	14	8	1	0	1	1	1
Sly05g0160401	M18	NA	21	19	28	22	22	22	18	26	35	43
Sly05g0160411	M13	NA	19	18	22	41	56	21	19	23	44	66
Sly05g0160421	M1	NA	29	28	32	30	30	26	26	29	35	48
Sly05g0160441	M3	NA	28	29	22	21	23	17	17	15	21	22
Sly05g0160451	M12	NA	10	10	11	14	17	15	15	15	19	21
Sly05g0160461	M1	SICYP77A2	123	101	235	15	1	5	2	2	1	1
Sly05g0160491	M12	NA	14	16	17	14	14	19	22	19	12	13
Sly05g0160501	M22	NA	1	1	1	1	1	2	1	2	1	1
Sly05g0160511	M11	NA	6	5	5	6	7	8	6	8	5	5
Sly05g0160521	M1	NA	145	131	132	234	344	113	99	100	76	247
Sly05g0160531	M3	NA	96	104	83	79	95	63	77	56	51	52
Sly05g0160551	M3	NA	71	72	53	67	76	46	50	34	68	71
Sly05g0160561	M12	NA	30	24	26	12	19	44	40	41	24	26
Sly05g0160591	M1	SIPL	8	8	6	7	3	2	1	1	1	1
Sly05g0160601	M3	NA	8	8	7	4	3	6	7	6	2	1
Sly05g0160621	M14	NA	16	19	29	29	9	17	14	17	6	2
Sly05g0160641	M21	NA	4	2	3	2	1	3	1	1	0	0
Sly05g0160651	M23	NA	1	1	1	1	1	1	1	1	0	0
Sly05g0160661	M22	SlHDMA2	1	1	1	1	1	1	1	1	1	0
Sly05g0160671	M11	NA	53	53	63	77	89	69	62	68	84	98
Sly05g0160681	M19	Met-10+ like protein	22	23	24	21	16	22	22	23	15	14
Sly05g0160711	M1	NA	3	4	5	1	0	1	0	0	0	0
Sly05g0160721	M3	NA	15	15	18	24	30	12	13	11	18	23
Sly05g0160731	M16	NA	89	78	71	55	36	57	57	56	47	30
Sly05g0160761	M13	NA	1	1	1	1	1	1	1	1	1	0
Sly05g0160781	M1	NA	6	6	8	63	28	2	2	1	1	1
Sly05g0160801	M3	NA	2	1	1	1	1	1	1	1	0	1
Sly05g0160831	M1	NA	70	67	58	41	13	25	26	28	7	4
Sly05g0160841	M2	NA	328	325	312	342	354	266	312	260	296	296
Sly05g0160851	M1	NA	16	15	13	6	6	8	9	7	8	9
Sly05g0160861	M19	NA	11	12	10	21	24	9	8	13	29	37
Sly05g0160871	M5	NA	23	25	10	3	2	22	21	8	2	1
Sly05g0160881	M12	NA	4	4	3	2	2	5	6	4	2	3
Sly05g0160901	M1	NA	14	13	13	14	16	11	11	14	16	15
Sly05g0160911	M12	NA	9	10	10	8	1	15	17	15	6	1
Sly05g0160921	M11	NA	12	12	14	20	12	21	19	22	16	8
Sly05g0160931	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly05g0160941	M12	NA	93	78	58	14	18	90	120	93	45	30
Sly05g0160951	M1	NA	6	9	8	5	2	3	3	2	1	1
Sly05g0160961	M12	NA	33	29	30	26	21	30	33	34	31	30
Sly05g0160981	M1	NA	76	74	55	21	4	19	20	18	4	1
Sly05g0161011	M11	NA	36	35	47	43	28	59	58	69	38	19
Sly05g0161051	M11	NA	5	5	5	5	3	7	6	8	5	2
Sly05g0161061	M1	NA	1	1	1	0	1	1	1	0	0	1
Sly05g0161071	M11	NA	100	110	116	193	201	147	149	156	111	122
Sly05g0161081	M11	NA	16	16	17	21	26	20	17	22	13	14
Sly05g0161091	M12	NA	38	36	35	97	96	55	58	62	56	60
Sly05g0161101	M12	NA	47	48	63	94	76	230	217	343	353	127
Sly05g0161111	M12	NA	3	3	3	7	3	17	19	25	53	10
Sly05g0161121	M5	SIARF24	66	80	41	15	6	67	81	38	10	10
Sly05g0161141	M11	NA	10	6	9	5	1	62	57	81	14	1
Sly05g0161151	M1	NA	35	29	28	20	23	27	26	23	11	11
Sly05g0161161	M11	NA	52	30	64	30	8	182	158	237	30	3
Sly05g0161171	M5	NA	14	28	9	4	6	19	22	4	1	1
Sly05g0161191	M2	NA	26	27	25	26	27	19	24	16	24	24
Sly05g0161201	M1	NA	50	50	40	38	58	41	36	41	43	46
Sly05g0161211	M11	NA	36	35	44	35	35	48	41	56	41	58
Sly05g0161221	M12	NA	12	13	13	17	13	26	36	24	6	8
Sly05g0161231	M1	NA	126	126	112	86	58	65	72	53	44	35
Sly05g0161241	M3	NA	7	10	5	5	2	3	3	2	1	1
Sly05g0161251	M3	NA	7	8	5	7	9	6	6	6	7	7
Sly05g0161261	M14	NA	132	117	124	155	194	115	123	119	142	201
Sly05g0161271	M3	NA	18	16	4	2	1	9	7	1	1	1
Sly05g0161291	M12	NA	8	6	8	13	9	9	11	10	13	6
Sly05g0161301	M12	NA	9	8	9	17	11	12	13	12	21	10
Sly05g0161311	M19	NA	51	52	51	48	55	50	42	55	43	48
Sly05g0161321	M18	NA	42	44	56	50	59	61	48	73	62	74
Sly05g0161331	M3	NA	284	262	233	154	153	195	208	151	87	115
Sly05g0161341	M15	NA	183	158	159	166	182	167	182	176	193	292
Sly05g0161351	M11	NA	125	115	121	110	99	127	126	136	152	147
Sly05g0161361	M11	NA	47	46	47	100	140	63	58	70	115	137
Sly05g0161371	M11	NA	15	13	19	69	183	24	21	25	62	154
Sly05g0161381	M1	NA	79	81	71	63	67	49	49	49	53	53
Sly05g0161391	M1	NA	54	53	56	153	151	42	48	41	77	66
Sly05g0161401	M11	NA	26	18	35	20	51	34	25	38	34	62
Sly05g0161411	M14	NA	142	141	156	181	288	148	139	154	194	281
Sly05g0161421	M1	NA	104	112	110	83	136	110	98	88	92	119
Sly05g0161431	M2	NA	7	7	5	6	5	5	6	5	6	5
Sly05g0161441	M19	NA	65	65	62	64	73	64	59	62	66	67
Sly05g0161451	M1	NA	126	125	122	111	111	91	93	85	69	68
Sly05g0161471	M1	NA	18	20	23	13	12	2	2	3	1	1
Sly05g0161481	M3	NA	5	16	11	1	1	2	2	1	0	0
Sly05g0161491	M2	NA	77	75	77	85	110	56	60	43	91	167
Sly05g0161501	M22	NA	1	1	1	2	2	2	1	2	3	11
Sly05g0161511	M3	NA	1	2	1	1	0	1	1	1	0	1
Sly05g0161521	M3	NA	2	3	1	1	1	1	1	1	0	0
Sly05g0161531	M1	SAUR56	2	3	2	1	1	1	1	1	1	0
Sly05g0161551	M11	NA	41	37	46	46	57	50	41	58	65	81
Sly05g0161561	M23	NA	1	1	1	0	0	1	1	1	0	0
Sly05g0161571	M22	NA	4	1	4	0	0	36	1	20	0	0
Sly05g0161581	M11	NA	3	2	2	1	0	6	3	7	1	1
Sly05g0161601	M11	NA	2	1	1	1	0	4	2	3	1	1
Sly05g0161611	M12	NA	21	23	38	40	30	43	48	58	30	20
Sly05g0161621	M12	NA	24	25	26	75	86	40	41	47	105	108
Sly05g0161631	M3	NA	2	3	2	1	1	1	2	1	1	0
Sly05g0161641	M12	NA	53	55	54	58	62	55	58	53	65	71
Sly05g0161651	M11	NA	7	7	9	9	7	8	7	8	6	5

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0073001	M8	NA	49	50	39	53	43	57	78	37	37	37
Sly12g0073011	M9	NA	56	61	53	55	35	78	81	77	66	74
Sly12g0073021	M22	NA	2	1	1	2	1	3	1	2	1	1
Sly12g0073031	M9	NA	18	17	19	15	15	15	23	19	16	15
Sly12g0073041	M19	NA	96	91	91	102	98	92	77	92	85	83
Sly12g0073051	M12	NA	13	14	13	17	20	14	13	14	17	25
Sly12g0073061	M12	NA	8	9	10	4	3	54	53	69	19	4
Sly12g0073071	M1	CDKA;1-1	75	70	65	48	53	52	56	55	70	81
Sly12g0073081	M3	AUR2	10	11	8	8	6	7	7	7	7	5
Sly12g0073091	M2	PFK6	51	55	53	78	88	38	46	38	62	74
Sly12g0073101	M3	NA	56	62	52	44	46	53	50	52	59	56
Sly12g0073111	M11	NA	17	17	23	26	23	27	26	37	26	21
Sly12g0073121	M13	NA	160	130	191	262	269	174	159	235	225	241
Sly12g0073131	M11	NA	34	28	38	21	19	41	37	40	31	30
Sly12g0073141	M1	NA	43	40	37	21	19	27	26	22	19	17
Sly12g0073151	M3	NA	29	25	22	20	18	21	25	21	25	21
Sly12g0073161	M11	NA	460	439	514	363	356	482	414	529	421	473
Sly12g0073181	M3	NA	6	5	4	1	1	6	6	2	1	1
Sly12g0073191	M2	NA	456	459	413	375	341	349	416	354	437	442
Sly12g0073201	M2	NA	341	343	327	363	293	296	338	341	355	304
Sly12g0073211	M1	NA	7	6	8	7	5	7	6	6	5	4
Sly12g0073221	M1	SlPP2C6	36	33	35	28	35	24	24	24	21	26
Sly12g0073231	M22	Solyc12g096030	13	12	12	11	9	14	12	12	8	7
Sly12g0073241	M12	NA	20	18	20	15	20	31	31	36	43	43
Sly12g0073251	M3	NA	30	31	24	26	25	22	20	18	19	19
Sly12g0073261	M2	NA	29	32	35	70	75	27	34	33	62	90
Sly12g0073271	M12	NA	7	8	7	23	21	10	10	12	21	25
Sly12g0073281	M23	NA	2	2	1	1	1	7	5	4	1	1
Sly12g0073291	M11	NA	11	8	14	15	32	14	13	15	14	38
Sly12g0073301	M11	NA	7	7	10	9	2	22	20	26	3	1
Sly12g0073321	M12	NA	88	81	81	113	117	86	94	88	69	55
Sly12g0073341	M2	PPR-like42	72	70	54	35	39	49	60	39	50	44
Sly12g0073351	M3	NA	313	308	242	231	167	165	204	136	229	156
Sly12g0073361	M12	NA	24	23	24	32	29	31	31	29	22	24
Sly12g0073371	M11	NA	7	7	8	3	2	7	8	7	2	1
Sly12g0073401	M11	TSB-like4	130	132	174	188	127	202	176	217	85	73
Sly12g0073431	M22	NA	3	3	3	3	3	4	3	3	6	8
Sly12g0073441	M3	NA	2	1	1	1	1	1	1	1	1	1
Sly12g0073451	M16	NA	756	666	721	557	512	633	605	698	664	646
Sly12g0073461	M3	NA	10	10	9	7	7	8	9	9	8	8
Sly12g0073491	M3	NA	3	3	2	3	3	2	2	2	2	2
Sly12g0073501	M18	NA	2	3	1	4	2	3	2	2	2	2
Sly12g0073511	M6	NA	32	35	27	23	22	30	36	26	21	31
Sly12g0073521	M11	NA	10	8	11	12	13	13	12	13	16	14
Sly12g0073531	M3	NA	11	11	10	7	4	8	10	7	5	3
Sly12g0073541	M1	NA	485	424	411	357	271	364	359	340	345	251
Sly12g0073551	M12	NA	18	24	41	225	108	322	415	633	1343	435
Sly12g0073561	M12	NA	8	7	10	19	6	34	31	38	19	5
Sly12g0073571	M11	NA	14	13	15	14	14	22	18	24	20	22
Sly12g0073581	M9	NA	84	98	80	120	155	107	125	97	191	266
Sly12g0073591	M3	NA	12	21	12	6	7	7	7	6	1	2
Sly12g0073601	M1	NA	12	13	13	12	9	13	12	12	8	5
Sly12g0073621	M11	NA	22	18	24	25	22	22	20	30	22	25
Sly12g0073631	M11	NA	3	3	4	2	1	11	11	15	5	2
Sly12g0073641	M12	NA	60	55	56	71	60	75	71	89	92	65
Sly12g0073651	M22	NA	1	1	1	1	4	1	1	1	1	2
Sly12g0073681	M3	NA	38	40	34	36	58	27	29	26	41	52
Sly12g0073691	M1	NA	27	31	26	24	19	19	17	19	19	18
Sly12g0073701	M1	NA	45	42	44	47	55	33	33	40	42	45
Sly12g0073711	M12	NA	2	2	4	10	6	2	3	3	16	13
Sly12g0073721	M14	NA	5	5	9	1	1	5	4	6	1	1
Sly12g0073731	M14	NA	163	128	164	19	17	114	90	140	5	7
Sly12g0073741	M11	NA	4	4	6	4	3	8	5	9	3	2
Sly12g0073751	M8	NA	95	102	93	118	144	95	103	95	123	168
Sly12g0073771	M1	NA	309	263	232	198	175	202	201	207	204	198
Sly12g0073781	M11	NA	29	20	31	40	103	47	36	41	36	33
Sly12g0073791	M12	NA	149	140	146	123	92	218	213	208	124	98
Sly12g0073801	M3	NA	36	76	19	35	6	7	14	3	16	5
Sly12g0073811	M1	NA	27	28	28	25	21	17	19	20	31	23
Sly12g0073821	M3	NA	21	19	15	13	12	16	15	14	11	12
Sly12g0073831	M1	NA	18	16	9	5	6	5	5	3	4	7
Sly12g0073841	M1	NA	16	15	8	4	5	3	5	4	3	6
Sly12g0073861	M12	NA	6	6	8	1	1	91	83	101	2	1
Sly12g0073871	M12	NA	1	1	2	1	1	14	12	15	3	6
Sly12g0073881	M2	NA	53	54	54	56	56	50	53	56	59	55
Sly12g0073891	M18	NA	1	2	2	2	2	2	1	2	2	2
Sly12g0073901	M11	NA	2	2	2	2	4	2	2	2	2	3
Sly12g0073911	M1	NA	87	93	79	106	74	56	63	52	82	68
Sly12g0073921	M1	NA	14	17	10	7	3	2	3	2	3	2
Sly12g0073931	M3	NA	87	88	72	64	91	54	58	50	65	75
Sly12g0073941	M2	NA	397	392	348	276	236	256	309	250	315	222
Sly12g0073951	M1	NA	17	33	22	41	49	4	5	2	1	2
Sly12g0073961	M1	NA	3	5	3	7	10	1	1	1	1	1
Sly12g0073971	M22	NA	2	3	2	2	1	4	1	5	1	1
Sly12g0074001	M1	NA	131	114	156	191	184	110	99	112	124	188
Sly12g0074011	M1	NA	50	39	14	1	0	2	1	1	1	0
Sly12g0074021	M1	NA	4	4	3	1	0	1	1	0	0	0
Sly12g0074031	M1	NA	4	4	3	1	0	1	1	1	0	0
Sly12g0074041	M1	NA	1	1	1	0	0	1	1	0	0	0
Sly12g0074051	M1	NA	22	18	18	8	9	9	10	8	8	8
Sly12g0074061	M1	NA	9	8	9	4	1	4	3	3	1	1
Sly12g0074071	M11	NA	30	27	36	29	18	43	40	51	24	16
Sly12g0074101	M9	NA	1	1	1	0	0	2	2	1	1	1
Sly12g0074111	M11	NA	3	3	7	1	1	6	3	7	0	0
Sly12g0074121	M1	NA	4	6	2	1	0	1	1	1	0	0
Sly12g0074131	M1	NA	42	45	41	11	2	5	2	3	0	0
Sly12g0074141	M1	NA	1	3	2	1	1	1	1	1	0	1
Sly12g0074151	M23	NA	24	7	9	1	0	59	16	32	3	1
Sly12g0074161	M1	NA	4	4	3	2	1	2	1	1	1	1
Sly12g0074171	M3	NA	7	11	5	1	3	7	8	4	2	2
Sly12g0074181	M3	NA	31	47	20	1	1	8	9	3	1	1
Sly12g0074221	M12	SlSDG3	10	10	9	8	6	12	12	12	10	5
Sly12g0074231	M6	NA	26	39	13	3	2	14	24	11	5	2
Sly12g0074241	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly12g0074251	M11	NA	13	14	14	17	16	19	16	21	18	19
Sly12g0074261	M15	NA	14	11	12	27	35	10	11	13	26	32
Sly12g0074281	M1	NA	1	2	2	1	1	1	1	1	0	0
Sly12g0074291	M9	NA	9	9	10	13	14	11	14	12	19	17
Sly12g0074391	M23	NA	19	5	4	1	0	31	13	8	4	1
Sly12g0074411	M12	NA	61	65	66	112	85	66	72	74	51	22
Sly12g0074421	M1	NA	17	20	17	15	14	13	12	12	10	10
Sly12g0074441	M8	NA	2	3	2	2	2	2	4	3	6	4
Sly12g0074451	M9	NA	28	34	28	33	38	30	42	36	77	68
Sly12g0074481	M1	NA	5	5	7	5	8	6	4	5	3	4
Sly12g0074501	M1	NA	1	2	2	1	0	1	0	0	0	0
Sly12g0074511	M1	NA	185	174	327	61	7	7	1	2	0	0
Sly12g0074591	M21	NA	36	29	39	27	28	35	22	31	16	16
Sly12g0074601	M1	NA	2	2	2	13	3	1	0	0	1	1
Sly12g0074611	M3	NA	271	245	198	158	131	140	158	117	139	120
Sly12g0074621	M12	NA	58	42	89	48	10	127	163	137	43	9
Sly12g0074631	M11	NA	33	33	42	65	90	42	38	53	81	113
Sly12g0074641	M12	NA	7	7	7	6	7	10	12	10	8	5
Sly12g0074651	M12	NA	13	14	14	8	4	22	21	22	8	7
Sly12g0074661	M19	NA	31	30	31	23	28	29	25	32	23	24
Sly12g0074671	M3	NA	6	5	5	4	6	6	5	5	5	7
Sly12g0074701	M3	NA	72	72	64	83	77	64	64	60	78	78
Sly12g0074721	M12	NA	22	22	23	30	32	26	27	24	35	37
Sly12g0074731	M12	NA	41	41	37	46	37	41	48	43	49	31
Sly12g0074741	M22	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0074761	M3	NA	21	21	21	19	17	21	20	19	20	14
Sly12g0074771	M9	NA	1	1	1	1	1	3

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly05g0161661	M1	NA	5	5	5	4	3	4	3	4	2	1
Sly05g0161671	M11	ADH	62	66	99	72	83	88	66	119	91	79
Sly05g0161681	M1	SlSnRK2.1	1	1	1	2	1	1	1	1	1	1
Sly05g0161691	M1	NA	9	8	10	13	14	5	7	6	10	16
Sly05g0161701	M1	NA	39	38	29	28	24	20	21	18	26	18
Sly05g0161711	M3	NA	216	231	204	225	170	196	219	173	165	173
Sly05g0161721	M11	NA	20	20	21	22	26	20	19	22	28	32
Sly06g0351631	M11	NA	8	9	12	5	2	14	14	17	4	2
Sly06g0351661	M2	NA	3	3	3	2	2	3	3	3	2	2
Sly06g0351671	M2	NA	1112	1041	1061	853	596	1049	1128	1029	895	664
Sly06g0351691	M11	NA	1	1	1	0	0	3	3	4	1	0
Sly06g0351701	M11	NA	60	62	66	64	73	68	62	68	61	72
Sly06g0351721	M6	NA	16	26	14	13	26	12	13	9	15	25
Sly06g0351731	M11	NA	21	21	21	13	20	24	23	26	16	28
Sly06g0351751	M1	NA	1	1	1	0	0	1	0	1	0	0
Sly06g0351761	M11	NA	19	20	23	16	19	21	19	22	19	22
Sly06g0351771	M12	SlApx2	196	169	172	136	146	233	228	211	221	286
Sly06g0351781	M3	SlApx1	519	369	394	519	530	412	430	320	375	507
Sly06g0351791	M6	NA	85	265	60	17	56	99	186	32	6	28
Sly06g0351811	M3	NA	57	59	52	45	53	53	50	49	47	58
Sly06g0351821	M2	NA	9	10	9	10	12	9	10	9	14	16
Sly06g0351831	M3	NA	7	7	5	4	3	5	5	5	4	4
Sly06g0351841	M11	NA	4	5	5	6	3	5	5	7	5	2
Sly06g0351851	M12	NA	13	10	12	17	16	37	34	33	13	12
Sly06g0351871	M12	NA	37	35	33	23	7	68	72	82	48	17
Sly06g0351881	M3	NA	406	367	272	260	443	238	254	252	370	437
Sly06g0351901	M12	NA	4	6	6	4	5	10	8	8	2	3
Sly06g0351911	M11	NA	3	4	4	3	2	6	4	4	1	2
Sly06g0351941	M3	NA	28	30	25	22	23	27	28	24	18	25
Sly06g0351951	M2	NA	1	1	1	1	6	0	1	1	2	22
Sly06g0351981	M11	NA	1	1	1	1	0	4	3	3	0	1
Sly06g0351991	M12	NA	526	483	478	537	652	472	553	541	759	958
Sly06g0352011	M1	NA	33	31	32	36	49	22	21	23	35	38
Sly06g0352021	M11	NA	10	10	10	10	12	11	10	10	16	18
Sly06g0352041	M22	NA	1	0	1	0	0	5	1	3	0	0
Sly06g0352051	M12	NA	3	4	4	12	17	6	6	7	21	19
Sly06g0352081	M12	NA	22	21	19	18	26	21	22	22	25	30
Sly06g0352091	M12	NA	15	14	15	14	20	17	14	15	16	25
Sly06g0352101	M12	NA	27	19	24	17	25	37	36	37	27	32
Sly06g0352111	M1	NA	1	1	2	0	0	1	1	1	0	0
Sly06g0352131	M1	NA	15	16	12	7	6	5	7	5	4	3
Sly06g0352141	M2	NA	21	23	17	16	10	12	15	12	8	7
Sly06g0352211	M12	NA	55	44	65	151	127	82	79	84	144	155
Sly06g0352221	M6	NA	20	36	20	11	20	23	32	11	11	20
Sly06g0352231	M12	TPI	63	58	76	231	478	193	181	225	216	475
Sly06g0352241	M3	NA	103	136	79	30	30	107	108	29	2	5
Sly06g0352251	M10	NA	12	15	9	2	1	31	33	21	10	3
Sly06g0352321	M3	NA	14	28	8	5	2	4	3	4	1	1
Sly06g0352331	M19	NA	53	51	53	48	48	48	44	55	53	62
Sly06g0352351	M11	NA	16	15	17	18	18	19	20	19	19	17
Sly06g0352361	M11	NA	32	31	36	25	28	33	30	38	31	39
Sly06g0352381	M22	NA	1	1	1	0	0	2	1	1	0	0
Sly06g0352431	M12	NA	13	10	8	12	18	28	23	29	20	35
Sly06g0352441	M12	NA	9	10	8	10	9	11	10	10	13	14
Sly06g0352451	M6	NA	69	131	76	47	142	81	139	64	39	162
Sly06g0352471	M1	NA	107	106	108	199	186	83	79	92	116	123
Sly06g0352481	M11	NA	26	21	25	40	30	36	29	51	29	15
Sly06g0352491	M12	NA	1	1	1	1	1	1	1	1	2	1
Sly06g0352501	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0352511	M1	NA	3	3	2	3	3	2	2	2	2	2
Sly06g0352521	M11	NA	10	9	14	8	2	20	16	24	6	2
Sly06g0352531	M18	NA	2	3	3	4	3	4	4	5	4	3
Sly06g0352541	M11	NA	1	1	1	2	1	2	2	2	1	1
Sly06g0352551	M11	NA	1	2	1	1	1	2	2	3	1	2
Sly06g0352561	M18	NA	1	2	1	2	1	2	2	2	1	1
Sly06g0352571	M11	NA	9	9	11	22	19	23	20	22	18	21
Sly06g0352611	M12	NA	15	12	6	0	1	59	38	40	2	2
Sly06g0352621	M12	NA	16	11	8	1	1	99	28	57	3	2
Sly06g0352641	M1	NA	36	31	32	32	35	30	29	34	51	44
Sly06g0352651	M3	NA	37	37	30	25	20	26	29	23	19	19
Sly06g0352661	M8	NA	18	22	15	9	7	25	36	18	24	23
Sly06g0352681	M12	NA	3	4	5	297	173	13	10	21	240	143
Sly06g0352701	M3	NA	15	16	13	8	7	11	14	10	12	10
Sly06g0352711	M12	NA	5	4	8	22	14	8	10	10	31	23
Sly06g0352721	M3	NA	13	14	12	8	8	11	12	11	14	12
Sly06g0352731	M2	NA	21	25	19	16	17	17	19	16	20	20
Sly06g0352741	M1	NA	3	3	1	1	1	1	0	1	1	1
Sly06g0352751	M1	NA	2	2	1	1	0	1	0	1	1	0
Sly06g0352771	M1	NA	2	2	2	1	1	1	1	1	1	1
Sly06g0352801	M1	NA	71	59	57	35	14	33	31	31	13	6
Sly06g0352811	M11	NA	1	1	1	1	1	1	1	1	1	0
Sly06g0352831	M12	NA	148	196	182	641	445	215	222	200	376	313
Sly06g0352841	M11	NA	37	36	46	60	58	45	38	53	48	39
Sly06g0352861	M11	NA	13	13	18	51	14	25	24	34	28	7
Sly06g0352871	M12	NA	1	1	1	1	1	2	2	2	2	2
Sly06g0352881	M18	NA	18	20	21	28	28	25	22	25	26	21
Sly06g0352891	M13	NA	45	33	79	71	20	69	49	103	15	1
Sly06g0352901	M3	NA	2	1	1	0	0	1	0	0	0	0
Sly06g0352941	M3	NA	1	1	1	1	1	1	1	0	0	0
Sly06g0352991	M14	NA	159	107	340	125	51	110	79	153	29	19
Sly06g0353011	M14	NA	36	21	61	25	16	16	12	21	9	5
Sly06g0353021	M1	NA	7	3	11	3	1	2	2	2	1	0
Sly06g0353031	M11	NA	108	117	159	929	1136	200	199	254	611	631
Sly06g0353051	M11	NA	1	1	1	1	0	2	1	1	1	1
Sly06g0353061	M1	NA	22	22	24	22	35	12	10	10	15	25
Sly06g0353081	M1	NA	35	20	12	4	2	4	3	3	1	1
Sly06g0353091	M20	NA	5	4	6	2	1	5	3	4	1	1
Sly06g0353101	M1	NA	9	7	7	22	86	4	6	7	144	213
Sly06g0353121	M11	NA	12	12	13	16	17	13	12	13	18	17
Sly06g0353131	M12	NA	1	1	1	0	0	1	1	1	0	0
Sly06g0353151	M22	NA	1	1	2	1	1	4	1	3	0	0
Sly06g0353161	M12	NA	4	3	2	1	1	19	7	8	1	2
Sly06g0353181	M7	NA	4	13	7	2	31	13	37	8	1	37
Sly06g0353191	M14	NA	126	116	126	93	81	117	111	119	88	76
Sly06g0353201	M1	NA	289	251	240	232	166	206	217	200	214	150
Sly06g0353211	M1	NA	218	175	156	128	85	125	122	109	133	69
Sly06g0353231	M22	NA	6	3	6	1	1	6	1	5	1	0
Sly06g0353251	M1	NA	25	22	21	23	24	20	18	18	21	18
Sly06g0353261	M12	NA	6	6	7	6	7	9	8	8	10	11
Sly06g0353271	M11	NA	5	6	6	6	5	8	8	7	6	7
Sly06g0353281	M18	PPR-like51	7	7	8	7	6	10	8	10	8	8
Sly06g0353301	M11	NA	5	5	6	4	5	7	6	8	7	8
Sly06g0353311	M11	NA	18	19	20	35	41	28	23	30	32	37
Sly06g0353321	M2	NA	74	74	69	85	92	55	63	49	68	75
Sly06g0353351	M22	NA	9	8	11	16	15	9	10	9	18	21
Sly06g0353361	M3	NA	88	81	78	99	119	49	55	52	77	88
Sly06g0353401	M11	NA	6	6	8	13	19	12	12	16	30	32
Sly06g0353411	M12	NA	10	11	10	21	28	20	22	23	44	46
Sly06g0353421	M11	NA	76	73	81	59	54	71	77	80	77	89
Sly06g0353431	M11	NA	1	1	1	1	0	1	1	1	0	0
Sly06g0353471	M11	NA	80	76	87	48	42	130	111	136	36	52
Sly06g0353481	M1	NA	79	83	30	3	4	10	8	5	2	3
Sly06g0353491	M1	NA	3	3	3	2	1	1	1	1	1	0
Sly06g0353501	M1	NA	815	787	866	579	406	626	625	700	510	435
Sly06g0353511	M12	NA	26	24	29	27	37	25	28	29	42	54
Sly06g0353521	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly06g0353551	M11	NA	1424	1301	1620	1703	1429	1729	1532	2141	1861	2343
Sly06g0353561	M3	NA	393	354	316	336	302	220	263	195	336	309
Sly06g0353571	M1	NA	11	10	11	7	5	7	7	7	5	4
Sly06g0353581	M9	NA	139	131	113	191	186	130	176	133	210	223
Sly06g0353621	M8	NA	1	1	1	1	0	1	1	1	1	1
Sly06g0353631	M3	NA	144	140	121	151	144	114	124	115	196	181
Sly06g0353641	M11	NA	24	17	31	12	5	62	60	109	172	115
Sly06g0353651	M12	NA	21	23	20	25	37	25	25	28	30	38

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0074811	M11	NA	80	74	93	57	67	124	116	146	92	96
Sly12g0074821	M11	NA	14	12	18	13	12	21	19	25	18	21
Sly12g0074831	M11	NA	11	6	9	1	1	59	42	82	5	1
Sly12g0074841	M11	NA	1	1	1	1	0	2	2	3	2	0
Sly12g0074851	M11	NA	1	1	2	0	0	6	2	5	0	0
Sly12g0074871	M12	NA	31	42	40	25	12	64	79	74	39	17
Sly12g0074881	M12	NA	2	5	5	3	1	4	11	11	18	9
Sly12g0074901	M11	NA	17	17	20	4	1	48	39	47	2	1
Sly12g0074911	M11	NA	1	1	1	1	1	2	1	2	3	9
Sly12g0074921	M23	NA	2	1	1	1	1	3	2	1	1	0
Sly12g0074931	M12	NA	1	1	1	3	19	1	1	2	34	69
Sly12g0074941	M12	NA	1	1	1	1	1	2	1	1	3	2
Sly12g0074951	M12	NA	59	52	51	33	15	57	61	51	15	7
Sly12g0074971	M1	NA	4	4	5	7	3	4	3	3	2	1
Sly12g0074981	M11	NA	73	71	78	98	109	93	91	100	105	122
Sly12g0074991	M11	NA	291	272	320	170	126	285	284	311	192	151
Sly12g0075001	M12	NA	55	54	55	39	62	52	60	66	82	95
Sly12g0075011	M18	NA	30	32	33	45	68	35	31	39	71	97
Sly12g0075021	M12	ziso	43	40	48	876	2973	43	57	67	1599	2454
Sly12g0075031	M3	NA	11	11	8	5	6	7	7	7	7	8
Sly12g0075041	M9	NA	31	30	29	45	41	32	39	32	58	48
Sly12g0075061	M11	NA	173	171	178	99	59	198	198	199	111	95
Sly12g0075151	M12	NA	9	7	13	38	35	16	13	16	15	26
Sly12g0075161	M3	NA	87	92	79	69	56	45	51	49	49	57
Sly12g0075171	M1	NA	57	63	75	165	194	46	40	51	81	90
Sly12g0075181	M1	NA	2	1	3	1	2	1	1	0	1	1
Sly12g0075191	M11	NA	145	119	247	414	197	569	384	607	230	57
Sly12g0075201	M11	NA	16	16	18	11	13	20	16	20	17	21
Sly12g0075231	M11	NA	24	22	26	30	30	52	47	62	32	36
Sly12g0075241	M12	NA	3	2	1	2	1	8	5	6	8	3
Sly12g0075251	M3	NA	6	7	3	1	1	2	2	1	1	1
Sly12g0075261	M11	NA	14	12	15	12	30	17	16	16	12	15
Sly12g0075281	M1	NA	573	545	595	587	514	398	388	484	553	535
Sly12g0075291	M11	NA	66	65	64	46	44	91	77	89	70	72
Sly12g0075301	M3	NA	31	35	20	4	2	28	25	11	1	1
Sly12g0075311	M3	NA	80	81	69	81	79	57	61	58	90	92
Sly12g0075321	M1	NA	15	12	12	11	11	12	10	14	11	9
Sly12g0075331	M3	SAMS	398	380	255	221	106	209	268	144	238	170
Sly12g0075341	M3	NA	12	14	11	16	19	11	10	11	17	16
Sly12g0075351	M1	NA	196	186	197	158	123	125	144	143	174	158
Sly12g0075381	M11	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0075391	M11	NA	216	204	231	198	230	204	216	258	279	387
Sly12g0075401	M3	NA	51	54	48	58	56	38	40	37	48	44
Sly12g0075411	M3	NA	130	131	87	55	41	72	88	49	42	30
Sly12g0075421	M22	NA	1	0	2	0	0	10	0	7	0	0
Sly12g0075431	M1	NA	30	30	27	48	74	15	18	16	43	37
Sly12g0075441	M1	NA	16	32	14	5	1	2	1	2	1	1
Sly12g0075451	M1	NA	74	85	58	11	2	2	1	1	2	2
Sly12g0075461	M1	NA	16	22	8	5	3	4	3	3	6	5
Sly12g0075481	M1	NA	176	161	120	75	41	19	21	14	2	1
Sly12g0075491	M1	NA	14	12	12	11	15	10	9	11	12	16
Sly12g0075501	M3	NA	2	2	2	4	3	2	2	1	3	4
Sly12g0075511	M1	NA	20	19	17	6	5	12	8	9	14	7
Sly12g0075521	M1	NA	282	263	462	193	226	75	62	98	167	184
Sly12g0075541	M12	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0075561	M1	NA	103	87	81	92	76	68	66	71	94	97
Sly12g0075571	M1	NA	21	25	24	5	4	8	9	9	4	2
Sly12g0075581	M5	NA	44	48	26	11	3	47	50	26	13	2
Sly12g0075591	M11	NA	52	48	61	58	38	108	85	112	107	69
Sly12g0075601	M19	NA	17	16	17	8	6	15	12	15	9	7
Sly12g0075611	M21	NA	11	9	9	6	9	10	7	7	3	3
Sly12g0075631	M1	NA	159	151	151	256	214	115	109	127	210	183
Sly12g0075641	M11	NA	36	36	39	41	45	38	36	41	36	38
Sly12g0075651	M1	NA	177	159	157	135	91	116	127	122	117	87
Sly12g0075661	M19	NA	81	91	85	86	57	83	82	93	68	36
Sly12g0075671	M11	NA	7	5	9	3	1	9	7	10	1	1
Sly12g0075681	M13	NA	138	123	206	341	433	203	186	277	159	246
Sly12g0075691	M3	NA	33	33	27	12	10	28	32	25	6	8
Sly12g0075721	M3	NA	92	82	83	39	70	75	86	63	38	74
Sly12g0075741	M1	NA	164	124	69	18	24	24	25	19	18	26
Sly12g0075761	M1	NA	19	19	17	13	11	18	15	17	14	9
Sly12g0075771	M1	NA	146	121	189	76	27	74	75	82	31	6
Sly12g0075781	M13	NA	230	222	268	493	508	250	239	319	349	417
Sly12g0075791	M12	NA	1	1	1	1	1	2	2	2	1	1
Sly12g0075811	M10	NA	17	37	13	4	3	31	60	11	2	4
Sly12g0075821	M10	NA	68	67	59	54	49	68	74	61	72	54
Sly12g0075851	M12	NA	91	95	77	91	97	114	123	113	128	119
Sly12g0075861	M7	NA	49	86	42	16	36	56	109	42	27	56
Sly12g0075871	M2	NA	34	33	30	33	30	29	32	28	33	29
Sly12g0075881	M11	NA	2	2	2	1	1	3	3	3	1	1
Sly12g0075901	M18	NA	27	26	27	25	31	28	25	29	28	30
Sly12g0075911	M21	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0075921	M1	NA	14	17	10	5	2	4	3	3	1	1
Sly12g0075931	M1	SlPRMT9	15	14	14	6	3	6	5	6	1	1
Sly12g0075941	M3	NA	43	42	33	37	29	34	37	32	33	29
Sly12g0075951	M1	NA	1	1	1	1	1	0	0	0	0	1
Sly12g0075971	M11	NA	12	10	10	8	24	18	16	20	8	9
Sly12g0076001	M1	NA	2	2	2	2	2	1	2	1	2	1
Sly12g0076011	M1	NA	7	7	7	4	3	5	5	4	1	1
Sly12g0076021	M3	NA	2	2	1	1	1	1	2	1	1	0
Sly12g0076031	M11	NA	31	17	36	14	2	106	85	142	26	2
Sly12g0076041	M12	NA	65	69	71	98	79	69	73	68	86	71
Sly12g0076071	M3	NA	25	25	24	55	63	22	23	23	38	47
Sly12g0076081	M3	NA	64	58	43	56	60	35	40	30	48	46
Sly12g0076111	M11	NA	12	12	14	14	16	14	14	18	20	21
Sly12g0076121	M2	NA	32	34	30	48	50	27	28	27	82	78
Sly12g0076131	M2	NA	162	154	126	100	111	110	183	133	183	208
Sly12g0076161	M3	NA	2	2	1	1	1	1	1	1	1	1
Sly12g0076171	M3	NA	2	2	2	3	5	2	2	2	4	5
Sly12g0076181	M1	NA	21	22	22	43	53	15	19	18	52	51
Sly12g0076191	M12	NA	7	7	5	30	57	7	9	10	85	107
Sly12g0076201	M2	NA	33	31	28	27	26	22	26	21	31	29
Sly12g0076211	M1	BSK3-like	18	16	18	3	2	10	8	9	1	1
Sly12g0076221	M3	NA	12	10	8	6	7	6	7	5	6	5
Sly12g0076231	M11	NA	4	4	4	5	4	5	4	6	6	5
Sly12g0076241	M11	NA	4	3	3	3	3	4	3	4	2	3
Sly12g0076251	M3	NA	6	5	2	0	0	1	1	1	0	0
Sly12g0076271	M1	NA	63	64	53	40	32	37	38	34	35	26
Sly12g0076281	M1	NA	39	36	35	20	12	25	27	25	26	6
Sly12g0076291	M19	NA	50	54	48	54	59	42	40	46	69	63
Sly12g0076301	M11	NA	21	20	22	32	35	23	21	27	37	38
Sly12g0076311	M11	NA	48	52	77	38	7	86	57	89	22	3
Sly12g0076321	M1	NA	49	53	55	49	53	44	41	51	41	45
Sly12g0076331	M10	NA	1	1	1	1	1	4	5	1	1	0
Sly12g0076341	M11	NA	22	21	25	10	3	38	38	40	17	6
Sly12g0076351	M11	NA	108	95	132	57	50	177	136	219	77	72
Sly12g0076361	M3	NA	36	33	33	46	44	26	30	26	33	42
Sly12g0076371	M3	NA	46	56	42	44	42	42	42	32	37	44
Sly12g0076381	M3	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0076401	M3	NA	39	58	23	1	1	3	7	1	1	0
Sly12g0076411	M3	HRA1	22	22	21	19	16	19	19	18	16	14
Sly12g0076421	M17	NA	31	25	30	22	21	24	23	28	17	20
Sly12g0076431	M11	NA	349	287	357	195	163	434	365	559	209	201
Sly12g0076441	M3	NA	11	12	11	12	10	8	10	9	11	12
Sly12g0076501	M11	NA	11	9	22	31	33	16	15	19	5	2
Sly12g0076511	M3	NA	22	23	14	15	15	18	23	13	14	16
Sly12g0076521	M1	NA	18	18	25	5	3	19	18	16	2	2
Sly12g0076541	M11	NA	25	22	28	53	61	45	39	57	31	33
Sly12g0076551	M3	NA	3	6	2	2	4	1	1	1	1	1
Sly12g0076561	M1	NA	1	1	1	1	1	1	1	1	1	1
Sly12g0076581	M12	NA	14	13	18	17	16	21	22	24	20	12
Sly12g

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly06g0353661	M22	NA	4	4	3	3	2	6	2	6	1	1
Sly06g0353671	M22	NA	2	1	1	1	1	4	1	4	1	0
Sly06g0353681	M12	NA	43	48	46	38	48	114	155	101	57	84
Sly06g0353691	M12	NA	52	45	42	70	72	55	57	62	77	76
Sly06g0353701	M1	NA	119	122	112	77	73	83	80	69	59	57
Sly06g0353721	M13	NA	27	25	30	24	27	33	28	37	38	41
Sly06g0353731	M1	NA	630	585	548	455	377	400	436	385	526	402
Sly06g0353741	M11	NA	9	10	12	12	9	14	14	15	11	9
Sly06g0353751	M9	NA	4	3	4	4	4	4	4	3	5	5
Sly06g0353761	M3	NA	302	295	204	152	159	228	234	185	159	191
Sly06g0353771	M1	NA	79	80	72	75	69	50	61	48	79	78
Sly06g0353781	M18	NA	2	3	3	2	1	3	2	3	2	1
Sly06g0353791	M11	NA	3	3	3	2	2	4	4	4	2	1
Sly06g0353801	M11	PPR-like52	4	4	4	4	4	4	4	5	3	2

			Estimated Transcript Number									
			Pericarp					Gel				
Locus	Module	Symbol	33DPA	35DPA	36DPA	Br	Br+4	33DPA	35DPA	36DPA	Br	Br+4
Sly12g0076651	M1	NA	9	4	3	1	1	1	1	1	1	1
Sly12g0076681	M3	SISDG35	9	11	8	4	5	8	8	6	3	4
Sly12g0076701	M1	NA	70	72	78	68	83	62	58	65	67	72
Sly12g0076711	M12	NA	19	19	20	24	19	23	25	24	31	27
Sly12g0076721	M11	SlCMT3-like1	55	54	57	26	18	64	58	57	25	21
Sly12g0076741	M19	NA	31	36	33	34	31	33	27	33	27	25

Supplementary Table 2. List of primers used in this study.

Primers	Sequence (5' -> 3')	Purpose	Constuction	Vector
Sl-ERF_E_1_F	GTTCCTCTCAACCCCAAACG	RT-qPCR		
Sl-ERF_E_1_R	TTCATCTGCTCACCACCTGTAGA			
Sl-ERF_E_2_F	ACTTCGTGAGGAAACCCTGAAC	RT-qPCR		
Sl-ERF_E_2_R	GTTACTAATATAAGTCATGTTGGGCTGAA			
Sl-ERF_E_3_F	GCATTTGCGATCTGAAGTTGTT	RT-qPCR		
Sl-ERF_E_3_R	CAAATGGCTTGACATCGACTTG			
Sl-ERF_E_4_F	AGGCCAAGGAAGAACAAGTACAGA	RT-qPCR		
Sl-ERF_E_4_R	CCAAGCCAAACGCGTACAC			
ERF.E2_AttB_F	AAAAAGCAGGCTTCATGTGTGGTGGTGCAATTATCT	RNAi	35S-SlERF.E2-RNAi	pHellsgate12
ERF.E2_AttB_R	CAAGAAAGCTGGGTCTTAGTAGGCACCTCC			

Supplementary Table 3. Report of the counts of reads that map to a single location and summarized at the gene level. Total read count is associated with a gene (meta-feature) which correspond to the sum of reads associated with each of the exons (feature) that belong to that gene.

[a]Assigned: Number of reads or fragments that were assigned to features (exon)

[b]Unassigned multiMapping : Number of alignment records that were not assigned because corresponding reads mapped to multiple locations (genome coordinates)

[c]Unassigned noFeatures: Number of reads or fragments not assigned to any features of the gene model

[d]Unassigned Ambiguous: Number of reads or fragments not assigned because they overlap multiple features (exons) or meta-features (genes)

Normal ripening

ID	Tissue	Stage	Replicate	Assigned	Unassigned MultiMapping[b]	Unassigned NoFeatures[c]	Unassigned Ambiguous[d]	Total	Total Unassigned	% Assigned	% Unassigned
N_1A	Pericarp	33 DPA	R1	21,782,908	1,198,762	791,005	50,393	23,823,068	2,040,160	91.44	8.56
N_1B	Gel	33 DPA	R1	20,529,790	2,668,654	816,973	47,622	24,063,039	3,533,249	85.32	14.68
N_2A	Pericarp	35 DPA	R1	18,280,973	970,522	719,270	35,662	20,006,427	1,725,454	91.38	8.62
N_2B	Gel	35 DPA	R1	20,318,061	1,684,035	749,528	46,820	22,798,444	2,480,383	89.12	10.88
N_3A	Pericarp	36 DPA	R1	20,810,432	1,269,812	739,645	48,877	22,868,766	2,058,334	91.00	9.00
N_3B	Gel	36 DPA	R1	22,355,294	2,310,885	780,733	58,468	25,505,380	3,150,086	87.65	12.35
N_4A	Pericarp	Br	R1	20,773,386	1,178,085	754,678	56,776	22,762,925	1,989,539	91.26	8.74
N_4B	Gel	Br	R1	21,028,911	1,015,798	1,016,163	49,982	23,110,854	2,081,943	90.99	9.01
N_5A	Pericarp	Br+4	R1	22,344,032	1,000,847	825,992	71,100	24,241,971	1,897,939	92.17	7.83
N_5B	Gel	Br+4	R1	21,281,120	864,052	859,014	83,085	23,087,271	1,806,151	92.18	7.82
N_6A	Pericarp	33 DPA	R2	20,091,482	1,608,748	874,600	46,797	22,621,627	2,530,145	88.82	11.18
N_6B	Gel	33 DPA	R2	19,973,619	3,881,480	897,416	47,638	24,800,153	4,826,534	80.54	19.46
N_7A	Pericarp	35 DPA	R2	18,448,110	1,140,667	727,645	43,654	20,360,076	1,911,966	90.61	9.39
N_7B	Gel	35 DPA	R2	19,686,595	1,936,331	855,134	45,318	22,523,378	2,836,783	87.41	12.59
N_8A	Pericarp	36 DPA	R2	21,410,534	1,350,931	781,682	52,390	23,595,537	2,185,003	90.74	9.26
N_8B	Gel	36 DPA	R2	22,292,094	2,252,261	921,629	54,748	25,520,732	3,228,638	87.35	12.65
N_9A	Pericarp	Br	R2	21,242,150	1,091,226	705,684	55,405	23,094,465	1,852,315	91.98	8.02
N_9B	Gel	Br	R2	21,425,782	970,386	911,686	53,232	23,361,086	1,935,304	91.72	8.28
N_10A	Pericarp	Br+4	R2	20,441,387	1,046,583	718,615	57,585	22,264,170	1,822,783	91.81	8.19
N_10B	Gel	Br+4	R2	18,784,228	907,564	935,145	47,177	20,674,114	1,889,886	90.86	9.14
N_11A	Pericarp	33 DPA	R3	21,177,421	1,603,806	631,550	55,120	23,467,897	2,290,476	90.24	9.76
N_11B	Gel	33 DPA	R3	21,063,423	2,167,929	886,882	48,565	24,166,799	3,103,376	87.16	12.84
N_12A	Pericarp	35 DPA	R3	19,709,784	1,561,615	871,151	45,375	22,187,925	2,478,141	88.83	11.17
N_12B	Gel	35 DPA	R3	20,649,252	2,135,328	916,344	49,024	23,749,948	3,100,696	86.94	13.06
N_13A	Pericarp	36 DPA	R3	21,842,764	1,442,004	888,677	56,629	24,230,074	2,387,310	90.15	9.85
N_13B	Gel	36 DPA	R3	19,743,751	4,231,959	910,855	47,830	24,934,395	5,190,644	79.18	20.82
N_14A	Pericarp	Br	R3	21,146,235	1,146,793	727,233	56,791	23,077,052	1,930,817	91.63	8.37
N_14B	Gel	Br	R3	23,679,489	994,711	1,104,603	55,725	25,834,528	2,155,039	91.66	8.34
N_15A	Pericarp	Br+4	R3	21,453,802	795,460	705,156	55,566	23,009,984	1,556,182	93.24	6.76
N_15B	Gel	Br+4	R3	19,254,101	852,204	947,039	47,895	21,101,239	1,847,138	91.25	8.75