Molecular Characterization of Carotenoid Accumulation in Light Signalling Mutants and Wild Relatives of Tomato

Thesis submitted for the award of the degree of

Doctor of Philosophy

By

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2017

Enrol. No. 10LPPH22

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DECLARATION

I hereby declare that the work described in this thesis entitled "**Molecular Characterization of Carotenoid Accumulation in Light Signalling Mutants and Wild Relatives of Tomato**" has been carried out by me under the supervision of Dr. Y. Sreelakshmi, Department of Plant Sciences, School of Life Sciences, University of Hyderabad, Hyderabad-500046, and this work has not been submitted for any degree or diploma of any other University.

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CERTIFICATE

This is to certify that the thesis entitled "**Molecular Characterization of Carotenoid Accumulation in Light Signalling Mutants and Wild Relatives of Tomato**" is based on the results of the work done by Ms. Himabindu Vasuki Kilambi for the degree of Doctor of Philosophy under my supervision. The work presented in this thesis is original and plagiarism free. No part of this thesis has been submitted for any degree or diploma of any other University.

Dr. Y. Sreelakshmi

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CERTIFICATE

This is to certify that this thesis entitled "**Molecular Characterization of Carotenoid Accumulation in Light Signalling Mutants and Wild Relatives of Tomato**" submitted by Himabindu Vasuki Kilambi, bearing registration number 10LPPH22 in partial fulfillment of the requirements for award of Doctor of Philosophy in the School of Life Sciences is a bonafide work carried out by her under my supervision and guidance.

This thesis is free from plagiarism and has not been submitted previously in part or in full to this or any other University or Institution for award of any degree or diploma.

Parts of this thesis have been:

A. Published in the following journals:

1. Plant Physiology (1 publication)
2. Frontiers in Plant Science (1 publication)

B. Presented in the following conference:

1. SOL 2015- International Solanaceae Conference

Further, the student has passed the following courses towards fulfillment of coursework reqirements for Ph. D.

Course Code	Name	Credits	Pass/Fail
1. PL 802	Research Ethic & Managment	2	Pass
2. PL 803	Lab Work	4	Pass
3. PL 804	Biostatistics	2	Pass
4. PL 805	Analytical Techiques	3	Pass
5. PL 806	Seminar	1	Pass

Supervisor **Head of Department** **Dean of School**

Dedicated to

My beloved Parents & Family

Acknowledgements

It gives me immense pleasure to thank all the people without whom this thesis might not have been written and I am greatly indebted to all.

Firstly, I express my deep sense of gratitude to my supervisor, ***Dr. Y. Sreelakshmi****, who gave me this wonderful opportunity to work with her. Her inexhaustible energy, patience, valuable guidance and encouragement to pursue new experiments helped me to develop not only in scientific arena but also on a personal level. Her enthusiasm, constant support, immense knowledge and constructive criticism assisted me to develop my writing, presentation and communication skills. I have no words to tell about her unfailing care and support in every aspect of my educational and personal life that led me to successfully groom my skills and complete this Ph. D programme.*

With great pleasure, I want to extend my heartfelt thanks to ***Prof. R. P. Sharma*** *for his constant support and encouragement throughout the course of work. Thank you Sir, for your insightful comments and motivation.*

My sincere thanks to ***Prof. P. Reddanna*** *(Dean, School of Life Sciences),* ***Prof. A. S. Raghavendra, Prof. R. P. Sharma, Prof. Aparna Dutta Gupta, Prof. M. Ramanadham*** *(Former Deans, School of Life Sciences);* ***Prof. Ch. Venkata Ramana*** *(Head, Dept. of Plant Sciences), and* ***Prof. A. R Reddy****,* ***Prof. Appa Rao Podile****,* ***Prof. G. Padmaja*** *(Former Heads, Dept. of Plant Sciences) for providing me the opportunity to utilize the facilities of the School and Department.*

I also would like to thank ***Prof. R. P. Sharma*** *and* ***Prof. A. R. Reddy****, my doctoral committee members for their support throughout the research work.*

I am highly thankful to ***Dr. Gopinath Kodetham*** *and* ***Prof. Klaus Appenroth*** *for their encouragement and support throughout the course of work.*

I thank all the faculty members of the Department of the Plant Sciences and School of Life Sciences for extending their lab facilities and giving me valuable support needed for my research.

I would like to thank UGC-CAS, DST-FIST and DBT-CREBB for providing the facilities to the Department and the School.

*I thank **Prof. Madhuchhanda Bhattacharjee**, School of Mathematics and Statistics for her help in analysing iTRAQ proteome data.*

*My sincere thanks to **Dr. Guy Houlne** for his generous gift of bell pepper PAP antibody.*

I also would like to thank AIRF, JNU, New Delhi for extending their TEM facility.

*I would like to thank **Prof. Ch. Venkata Ramana** for allowing me to use HPLC-PDA with fluorescence detector and **Dr. Mujahid** for helping me in using the above instrument.*

*My heartfelt thanks to **Dr. Brad Till**, Plant Breeding and Genetics Labaratory, Austria for his help in NGS experiment and **Prateek** for analysis of NGS data.*

*I want to extend my heartfelt thanks to all the lab members of RTGR for their help, support and for the friendly environment in the lab. My sincere thanks to **Dr. Sulabha, Dr. Chaitanya Charkana, Dr. Suresh Gupta, Dr. Soni Gupta, Dr. Vijee and Dr. Sapana** for their timely discussions and suggestions. I extend my gratitude to **Dr. Sherin, Dr. Pallawi, Dr. Rakesh Gupta, Dr. Kapil Sharma, Dr. Supriya Sarma, Dr. Reddiah, Dr. Alka, Dr. Vineet and Dr. Rahul** for their help and support. Iam thankful to **Hemalatha, Kalyani, Anusha, Prateek and Sumona** for their help during my research period.*

*I extend my thanks to field assistants (**Narsimha, Jamir and Yadagiri**) for maintenance of plants and lab accountants, **Venkat Reddy** and **Anil** for clearance of bills.*

*I have no words to express my love and gratitude towards all my friends from school and college. I would like to mention **Lalitha, Sarada, Rachana, Supriya, Paparao, Mastan and Latha** whose care and support helped me to focus on my Ph. D.*

*Most importantly, none of this would have been possible without the love and support from my family members. I would like to thank **my mother** for her constant encouragement, patience, postive energy and moral support. My special thanks to my better-half **Kamal**, my brother **Raghava**, my uncle **Mr. Krishna**, my auntie **Ms. Krishna Veni**, my mother-in-law **Ms. Maya Devi** and all my **in-laws** for supporting me in all phases of my educational life.*

*I would like to thank **DBT** and **DST** for their funding to the lab.*

*I thank the financial support provided by **UGC** in the form of **JRF** and **SRF.***

*I would also extend my thanks to **UPE2** and **DBT** for the financial support provided to attend the SOL 2015 conference at Bordeaux, France..*

Finally, Iam highly grateful to the almighty for blessing me with the best opportunities in life and for giving the physical and mental strength which helped me to successfully achieve this goal.

Himabindu Vasuki Kilambi

2017

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List of abbreviations

AGC	Automatic gain control
bp	Base pair
BZR1	Brassinazole-resistant 1
cDNA	Complementary DNA
crtB	Bacterial carotenoid biosynthetic gene for *phytoene synthase*
crtE	Bacterial carotenoid biosynthetic gene for *geranyl geranyl pyrophosphate synthase*
crtI	Bacterial carotenoid biosynthetic gene for *phytoene desaturase*
cry2	*cryptochrome2*
DNA	Deoxyribonucleic acid
DNase	Deoxyribonuclease
dNTP	Deoxyribonucleotide triphosphate
dpa	Days post anthesis
EMS	Ethyl methyl sulfonate
ERF	Ethylene response factor
ETR3	Ethylene receptor 3
FTMS	Fourier transform mass spectrometry
GeLCMS	1D SDS-PAGE followed by in-gel digestion and identification of proteins through liquid chromatography tandem mass spectrometry

h	hours
hp2	*high pigment 2*
hp3	*high pigment 3*
HPLC	High performance liquid chromatography
Hsp70	Heat shock protein 70
Ip	*Intense pigment*
iTRAQ	Isobaric tag for relative and absolute quantification
kV	Kilo volt
LED	Light-emitting diode
LOV2	Light, oxygen or voltage 2
m RNA	Messenger RNA
mA	Milli ampere
min	Minute
NGS	Next generation sequencing
Nr	*Never ripe*
PCR	Polymerase chain reaction
PHOT1	Phototropin 1
PHOT2	Phototropin 2
phy	*Phytochrome*
PIF1a	Phytochrome interacting factor 1a
q-PCR	Quantitative real-time PCR
RNA	Ribonucleic acid

RNase	Ribonulcease
SE	Standard error
sec	second
SIFT	Sorting intolerant from tolerant
SNP	Single nucleotide polymorphism
UHPLC	Ultra-high performance liquid chromatography
UV	Ultra-violet light
UVR8	UV-B resistance protein 8, UV-B receptor
V	Volt
v/v	volume/volume
w/v	weight/volume
WT	Wildtype

Chapter 1

Introduction

Fruit ripening is the final stage of fruit development and is accompanied by changes in fruit texture, flavor, taste and color that enhance its sensory quality (Giovannoni, 2004; Vogel et al., 2010). The biochemical, physiological and structural alterations (Bouzayen et al., 2010; Palma et al., 2011; Seymour et al., 2013) associated with fruit ripening are tightly regulated at the genetic level thereby facilitating the appearance, flavor and texture of the fruit for attracting seed dispersing organisms including humans (Ronen et al., 2000). In view of the socio-economic importance, the fruit biology has been widely studied at biochemical, physiological and genetic levels. From early 1980's, tomato has been extensively used for exploring the molecular basis of fleshy fruit development (Pirrello et al., 2009). Tomato is considered as model species for fleshy fruit ripening because of the availability of both spontaneous and induced mutants; whole genomic sequence (The Tomato Genome Consortium, 2012; Aoki et al., 2013); resources for reverse genetics, and feasibility for transcriptomics, proteomics, metabolomics approaches (Alba et al., 2004; Rose et al., 2004; Fernie et al., 2004; Moore et al., 2005). The availability of tomato genome sequence has opened the opportunity to examine the effect of novel transcription factors, phytohormones and other associated factors on carotenoid metabolism (The Tomato Genome Consortium, 2012).

Among the various attributes that contribute to the fruit ripening, texture modifications, volatile synthesis and increase in pigment production are well studied in tomato (Klee and Giovannoni 2011). Carotenoids are the red, orange and yellow colored pigments that accumulate in high amounts in the chromoplasts of fully ripe tomato fruits (Egea et al., 2011). The characteristic red color of tomato fruit is caused by increase in lycopene (Tadmor et al., 2005) along with decrease in chlorophyll during chloroplast to chromoplast transition. Carotenoids are also important sources of vitamin A and antioxidant compounds that prevent cancer, eye diseases and cardio-vascular diseases in humans (Fraser and Bramley 2004; Krinsky and Johnson, 2005; Ford and Erdman 2012). Carotenoid biosynthesis is a complex pathway involving several enzymes acting in a concerted fashion via the renowned non-mevalonate pathway or methylerythritol 4-phosphate pathway that operates exclusively in plastid (Eisenreich et al., 2001; Milborrow and Lee 1998). The genes involved in carotenoid biosynthesis have been cloned (Cunningham and Gantt 1998; Hirschberg 2001), and regulation of carotenoid production was studied during fruit ripening (Bramley, 2002). The characterization of mutants with altered carotenoid content such as *yellow-flesh (r)* which has mutation in

psy1 gene (Fray and Grierson 1993), the *delta*, with a mutation in *lcye* gene (Ronen et al., 1999), the *Beta*, with a mutation in *cycb* gene (Ronen et al., 2000), and the *tangerine*, with a mutation in *crtiso* gene (Isaacson et al., 2002) led to the better understanding of the carotenoid biosynthesis. The mutants and transgenics for transcriptional regulators such as *rin* (Vrebalov et al., 2002), *nor* (Tigchelaar et al., 1973), *Cnr* (Manning et al., 2006), *ful1* (Bemer et al., 2012), *ful2* (Shima et al., 2014), *glk2* (Powell et al., 2012), *aprr2-like* (Pan et al., 2013), *bzr1-1D* (Liu et al., 2014) display positive effects and *ap2a* (Chung et al., 2010), *tagl1* (Itkin et al., 2009; Vrebalov et al., 2009), *erf6* (Lee et al., 2012), *sgr1* (Luo et al., 2013) show negative effects on carotenoid accumulation.

The carotenoid metabolism is modulated by several factors (Matas et al., 2009) including environment [light (Schofield and Paliyath 2005; Liu et al., 2004), temperature (Dumas et al., 2003; Cocaliadis et al., 2014)], abiotic stress [Neta-Sharir et al., 2005], genetic [transcription factors (Yuan et al., 2015)], epigenetic [Kachanovsky et al., 2012; Zhong et al., 2013] and hormones [ethylene (Marty et al., 2005), auxin (Jones et al., 2002), ABA (Sun et al., 2012; Weng et al., 2015; Galpaz et al., 2008), jasmonate (Liu et al., 2012), brassinosteroids (Vardhini and Rao 2002); Liu et al., 2015]. Light plays an important role in modulation of carotenoid content in tomato (Bramley 2002; Romer and Fraser 2005). Light in the form of radiation is perceived by photoreceptors (Christie et al., 2015). Six different classes of photoreceptors were recognized in plants including phytochromes (Chen and Chory 2011), cryptochromes (Chaves et al., 2011), phototropins (Christie 2007), UVR8 (Rizzini et al., 2011), zeitlupe and FKF receptors (Suetsugu and Wada 2013). Phytochromes are red light photoreceptors that regulate the extent of lycopene accumulation in tomato (Alba et al., 2000). Phytochromes regulate carotenoid levels by acting singly or in combination and determine the transition intervals between different developmental stages during tomato fruit ripening (Gupta et al., 2014). Similarly, overexpression of *cryptochrome2* resulted in accumulation of lycopene and flavonoids in tomato (Giliberto et al., 2005). The role of phototropins and other photoreceptors like UVR8 in regulation of carotenoid metabolism in tomato is still unknown.

Apart from photoreceptors, mutation in the genes from light signaling pathway including *ddb1* (*hp1*; Lieberman et al., 2004; Liu et al., 2004), *det1* (*hp2*; Mustilli et al., 1999) and RNAi mediated repression of *cop1like* increased carotenoid content in the

fruits whereas silencing of *hy5* decreased carotenoid levels in the fruits (Davuluri et al., 2004; Liu et al., 2004; Davuluri et al., 2005). The tomato high pigment mutant, *hp3*, has mutation in *zeaxanthin epoxidase* (*zep*) gene from carotenoid pathway (Galpaz et al., 2008). Another high pigment mutant, *Ip* also shows exaggerated photomorphogenesis similar to *hp1* and *hp2* but the information on the chromosomal location and association of the *Ip* gene with the carotenoid regulation has not been understood till now (Lavi et al., 2009). The enhanced level of carotenoids in the high pigment mutants, *hp1*, *hp2* and *hp3* is associated with increase in plastid (both chloroplast and chromoplast) number and size that enables the accumulation and storage of the high levels of carotenoids in these mutants (Kolotilin et al., 2007; Galpaz et al., 2008; Azari et al., 2010; Enfissi et al., 2010).

In addition to mutants, wild relatives of tomato display vast diversity in fruit color ranging from green, orange and red (Bauchet and Causse 2012). Based on morphological and phylogenetic studies, the wild species along with cultivated tomato are grouped into 13 species (Peralta et al., 2005; Spooner et al., 2005). The fruit color of majority of the wild species is green, except *S. pimpinellifolium* which produces red fruits that are rich in lycopene and *S. cheesmanie* and *S. galapagense* that produce orange colored fruits which accumulates β-carotene. The molecular mechanisms involved in regulation of fruit color in tomato and its wild species is still not known. It is proposed that the green color of fruits is the result of down-regulation of *psy1* (Melendez-Martinez et al., 2010; Bolger at al., 2014). Using the inter-specific crossing between wild species and tomato, several quantitative trait loci (QTL) are identified that influence fruit color and carotenoid content (Liu et al., 2003). The analysis of introgression lines (ILs) generated from *S. pimpinellifolium* led to the identification of QTLs that are associated with lycopene content (Chen et al., 1999). The study of ILs and backcrossed lines generated from *S.parviflorum* and *S. pennellii* aided in identification of QTLs associated with red, orange and yellow fruit colors (Fulton et al., 2000; Frary et al., 2004; Rousseaux et al., 2005). Based on transcriptome analysis in *S. pennellii*, enhanced expression of photosynthetic genes along with absence of *psy1* expression, are considered as underlying factors responsible for green fruit color in this species (Bolger et al., 2014). Based on the above, an integrated analysis involving the comparison of data at transcript, protein and metabolite level is required to understand the regulation of fruit color in tomato and its wild species.

Since chromoplasts are the sites for carotenoid synthesis and accumulation, chromoplast biogenesis also influences carotenoid metabolism (Li and Yuan 2013). The mutation in *Or*, the only gene known to be related to chromoplast biogenesis increases storage capacity of plastids by converting proplastids into chromoplasts in cauliflower, potato and melon (Lu et al., 2006; Tzuri et al., 2015; Lopez et al., 2008). In *Arabidopsis*, OR proteins influence carotenoid biosynthesis through posttranscriptional regulation of *psy1* (Zhou et al., 2015). Carotenoid sequestration and storage is also crucial for enhanced carotenoid accumulation in chromoplasts. Plastoglobules are lipid containing carotenoid sequestering structures associated with thylakoids and contain carotenoid biosynthesis enzymes (Austin et al., 2006; Brehelin and Kessler 2008). In *crtE*, *crtB* and *crtI* carotenogenic lines of tomato, the increased accumulation of carotenoids boosted the development of membranous structures in chromoplasts (Nogueira et al., 2013). In the above lines, the accumulation of carotenoid precursors and biosynthetic enzymes in different compartments in chromoplasts has been identified as an efficient method to sequester and stabilize carotenoids within tomato fruits (Nogueira et al., 2013, Fraser et al., 1994; Fraser and Bramley 2004).

It is now evident that the carotenoid metabolism is regulated at various levels by several factors including environmental cues, developmental signals and phytohormones. But the complete information on the function and underlying molecular mechanisms of the above factors in regulating carotenoid metabolism is still lacking (Liu et al., 2015). A combination of "omics" technologies such as phenomics, genomics, proteomics and metabolomics has been considered as an essential means to understand the molecular events that trigger the carotenoid biosynthesis and degradation (Ricroch et al., 2011; Pirrello et al., 2009). The combination of transcript, protein and metabolite data in fruits of ripening inhibitor mutants such as *rin*, *nor* and *Nr* recognized several interactions that control fruit ripening (Osorio et al., 2011). The correlation of transcript profiles with metabolite abundances led to the identification of regulatory networks of fruit ripening (Rohrmann et al., 2011; Lee et al., 2012). Proteomics is one of such "omics" technologies, which is a large scale study on identification, function and interactions of thousands of proteins present in the organism (Katam et al., 2015). While the genome of an organism is more or less constant, proteome always changes with time and environmental factors (Holman et al., 2013; Smith et al., 2013).

Proteomics has been used as an excellent technique to understand tomato fruit development (Saravanan and Rose 2004; Rocco et al., 2006; Faurobert et al., 2007; Xu et al., 2013), chloroplast to chromoplast differentiation (Barsan et al., 2012), fruit softening (Pan et al., 2014), effect of transcription factors such as RIN (Qin et al., 2012), NOR (Yuan et al., 2016), BZR1 (Liu et al., 2016) during fruit ripening. Proteomic analysis of chromoplasts from six crop species including tomato revealed species specific accumulation of proteins related to chromoplast biogenesis and development (Wang et al., 2013). The increased accumulation of Acetyl Coenzyme A carboxylase D (ACCD) protein during early fruit ripening stages in tomato Micro Tom mutant provides storage matrix for carotenoids thereby assisting in carotenoid accumulation in this mutant (Barsan et al., 2012). Further, an ubiquitin conjugating enzyme, UBC32 detected in the nuclear proteome of *rin* mutant modulates fruit coloration by directly binding with RIN (Wang et al., 2014).

In this study, we examined the *high pigment* mutant (*hp1*), three wild species of tomato and high carotenoid accumulating *phototropin1* mutant, *Nps1* with emphasis on proteomic analysis, to uncover the diversity in the regulation of fruit coloration. To unravel the mechanisms underlying altered carotenoid accumulation in the above species, the following objectives were defined:

1. To decipher the molecular basis of enhanced carotenoid accumulation in *hp1* mutant of tomato.
2. To understand the molecular basis for diversity in fruit coloration in the tomato clade.
3. To examine the influence of *phototropin1* on tomato fruit quality and shelf life.

Chapter 2

Review of literature

2.1 Fruit types in Angiosperms

Fruit represents the mature ovary developed after fertilization and is required for plant adaptation and reproduction (Coombe 1976, Giovannoni 2004). Fruits that develop from extracarpellary tissues other than ovary are known as false fruits (Perkins Veazie, 1995; Velasco et al., 2010). Based on the hardness of the pericarp, angiosperm fruits can be divided into two main groups-dry and fleshy fruits. Dry fruits can be further classified into dehiscent fruits that release seeds on maturity and indehiscent fruits which do not disseminate seeds (Fahn 1967; Knapp, 2002). Fleshy fruits have thick and fleshy pericarp which gives juicy nature to the fruit that help in attracting seed dispersing insects or animals (Fahn 1967; Rodriguez et al., 2013). Tomato is an example of fleshy fruit which is a berry that contains many seeds in the pulp.

2.2 Tomato as a model system for fruit ripening

Tomato (*Solanum lycopersicum*), a vegetable species from Solanaceae, grown as annual crop, is a model plant for studying climacteric fruit ripening (Giovannoni 2007). According to FAO statistics, 2014, Asia is the major producer of tomato with 52% share in total world production. India ranks third in tomato production after China and United States of America. Tomato is consumed both in fresh and processed form of ketchup, sauces, puree and canned whole (Vegetables and Pulses Outlook, USDA ERS, 2015). In addition, tomato offers more advantages such as relatively small genome size (950 Mb), diploid genome (n=12), short reproductive cycle (3-4 generations per year), efficient transformation, flexibility for inbreeding, variability in secondary metabolism and availability of fully sequenced genome (app. 35000 protein coding genes). All these features make tomato as a model system for studying molecular and genetic machinery regulating fruit ripening (Pesaresi et al., 2014; The Tomato Genome Consortium, 2012). The availability of several single gene mutants, gene banks with variety of accessions (Tomato Genetics Resource Centre, tgrc.ucdavis.edu), mutagenized populations (zamir.sgn.cornell.edu/mutants) and application of transcriptomics, proteomics, metabolomics led researchers to characterize the molecular mechanisms underlying fruit development and ripening in tomato (Alba et al., 2004; Moore et al., 2005; Osorio et al ., 2011; Osorio et al., 2012).

2.3 Fruit development and ripening in tomato

Fruit development in tomato is divided into five main stages (Gillaspy et al., 1993). Immediately after fertilization, the first stage (2 weeks after fertilization) begins and is characterized by rapid cell division resulting in increase in cell number. During the second stage, which last for 3-4 weeks, massive cell expansion and end reduplication occurs leading to increase in fruit weight. The third phase known as mature green stage (MG) where the fruit attains its final size (Bergervoet et al., 1996; Giovanonni 2004). After MG stage, initiation of several metabolic changes occur in the fruit together and are described as ripening process. During ripening, two stages such as breaker (BR) and red ripe (RR) are characterized that involve conversion of chloroplasts to chromoplasts, degradation of chlorophylls, and accumulation of red, orange, yellow pigments which give color to the fruits (Ho and Hewitt 1986, Grotewold 2006). A climacteric fruit such as tomato, exhibits an increase in respiration and induction of gaseous hormone ethylene during onset of ripening (Alexander and Grierson 2002). Instead, in non-climacteric fruits such as strawberry and grape, the above phenomenon was not observed (Kumar et al., 2014; Fig. 2.1).

2.4 Nutritional aspects of tomato fruit

Tomato fruit is the major dietary source of lycopene which is the most abundant carotenoid present in tomato. It also contains considerable amounts of β-carotene, potassium, iron, riboflavin, thiamine and fiber (Lenucci et al., 2006; Guil-Guerrero and Rebolloso-Fuentes 2009). β-carotene is the precursor for vitamin A and tomato fruit also provides vitamin C (Liu et al., 2004). Lycopene and β-carotene are potential antioxidants and consumption of these compounds reduces the risk of cancer and cardio-vascular diseases (Agarwal and Rao 2000; Giovannucci 1999). Tomato also contains very low levels of saturated fats and sodium (Liu et al., 2004; Azari et al., 2010). Eating tomato in processed form has more benefits since cooking or heating breaks the cell walls and increases bioavailability of lycopene (Beecher et al., 1998).

2.5 Ripening associated changes in tomato fruits

Tomato fruit ripening is a complex phenomenon that brings in color, flavor and aroma to the fruit and assists in reproduction by attracting seed dispersing organisms (Ronen et al., 2000). Several biochemical changes occur during ripening including, changes in color, texture, alterations in acid and sugar content and increased susceptibility to pathogens (Seymour et al., 2013). Among various modifications that occur during

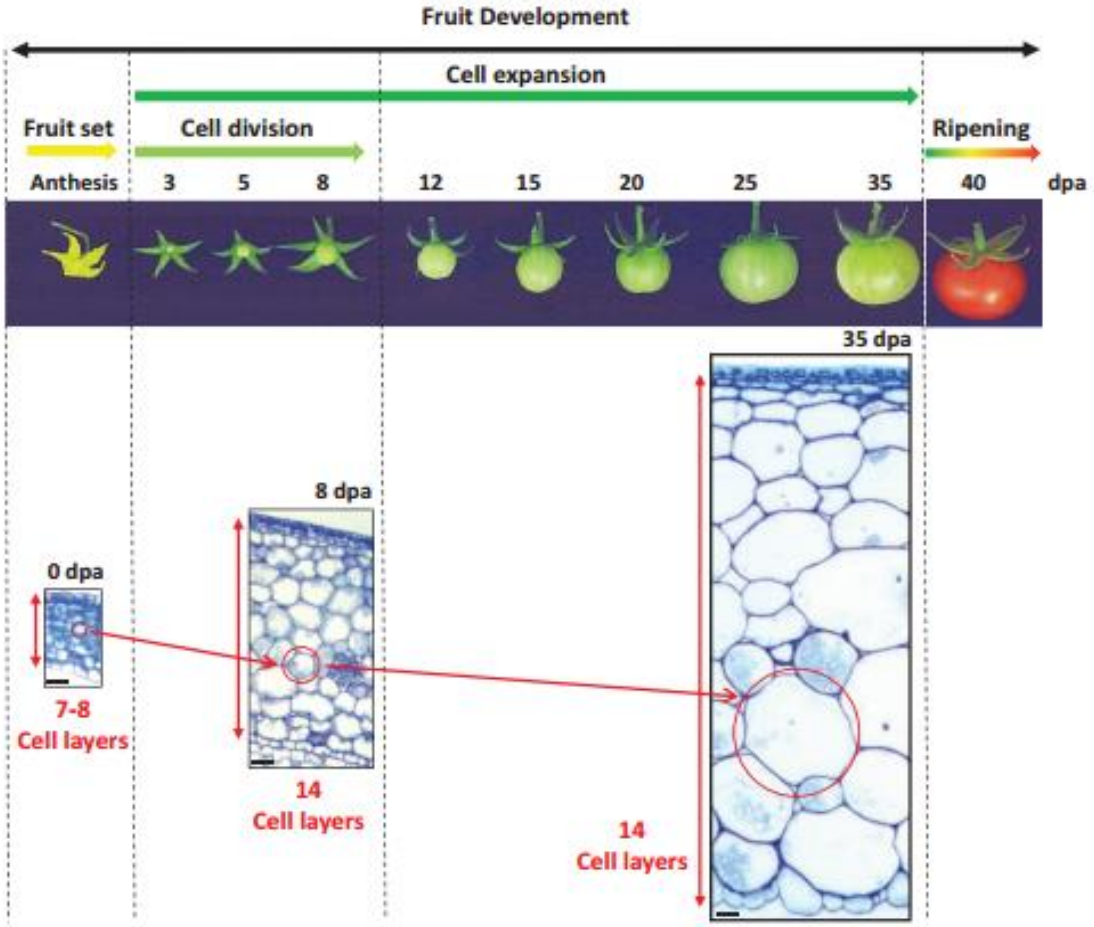


Figure 2.1. Fruit development in tomato. The fruit originates from the development of the ovary. Following fertilization (concomitant with anthesis) and fruit set, fruit growth starts with a period of very active cell division inside the ovary that lasts for 8–10 days post-anthesis (dpa). After anthesis and in <8–10 d, the number of cell layers across the pericarp has doubled compared with that at anthesis and becomes fixed until the end of development. Fruit growth then proceeds into the cell expansion phase and continues until ripening (~35 dpa). Cell enlargement starts concomitantly with cell division as early as 1 or 2 dpa and contributes to the increase in fruit size. Adapted from Azzi et al., 2015.

ripening, the changes that resulted in the enhancement of fruit nutritional and sensory qualities such as pigment accumulation, texture modifications and generation of volatiles have been well studied in tomato (Klee and Giovannoni 2011). Considering the health promoting role of several secondary metabolites such as carotenoids and anthocyanins, various studies have been initiated on the synthesis and accumulation of these compounds. The genes and enzymes involved in the above changes were characterized to identify the regulatory mechanisms governing these processes (Vicente et al., 2007; Ruiz-May and Rose, 2013).

2.5.1 Fruit color development

The accumulation of red pigment is the most evident change that occurs during ripening. The characteristic accumulation of red color during tomato fruit ripening is due to accumulation of lycopene. This is accompanied by degradation of chlorophyll during conversion of chloroplast into chromoplast that brings about organoleptic qualities to the fruit (Bramley, 2002). Other than the typical red color, tomato fruits can be orange because of β-carotene accumulation and yellow due to xanthophylls or flavonoid pigment accumulation (De Jong et al., 2004). More information regarding fruit color is given from section 2.7-2.10.

2.5.2 Fruit softening

Fruit softening and texture are the important factors that contribute to the commercial value of the fruits. While the desirable changes in texture contributes to integrity of the fruit for industrial processing, the reduced softening influences shelf-life, post-harvest deterioration, and decreases transportation time and storage costs. Tomato fruit softening has been considered as a consequence of alterations in cell wall assembly caused by action of various cell wall modifying enzymes (Fig. 2.2). The cell wall is a rigid, inextensible matrix consisting of cellulose microfibrils held together by extensive networks of pectins, glycans and glycoproteins (Carpita and Gibeaut, 1993; McCann and Roberts, 1992). During ripening, modifications occur in cell wall structure and in the polysaccharides associated with the cell wall. The cell wall pectins change their cohesive bonding as a result of which the cells will be separated from one another (Jarvis, 1984). In tomato, the reduction in cell-to-cell adhesion results in dissolution of pectin containing middle lamella. This softening process occurs early in ripening in tomato (Crookes and Grierson, 1983), whereas it occurs during late stages of ripening in apple (Ben-Arie et al.,

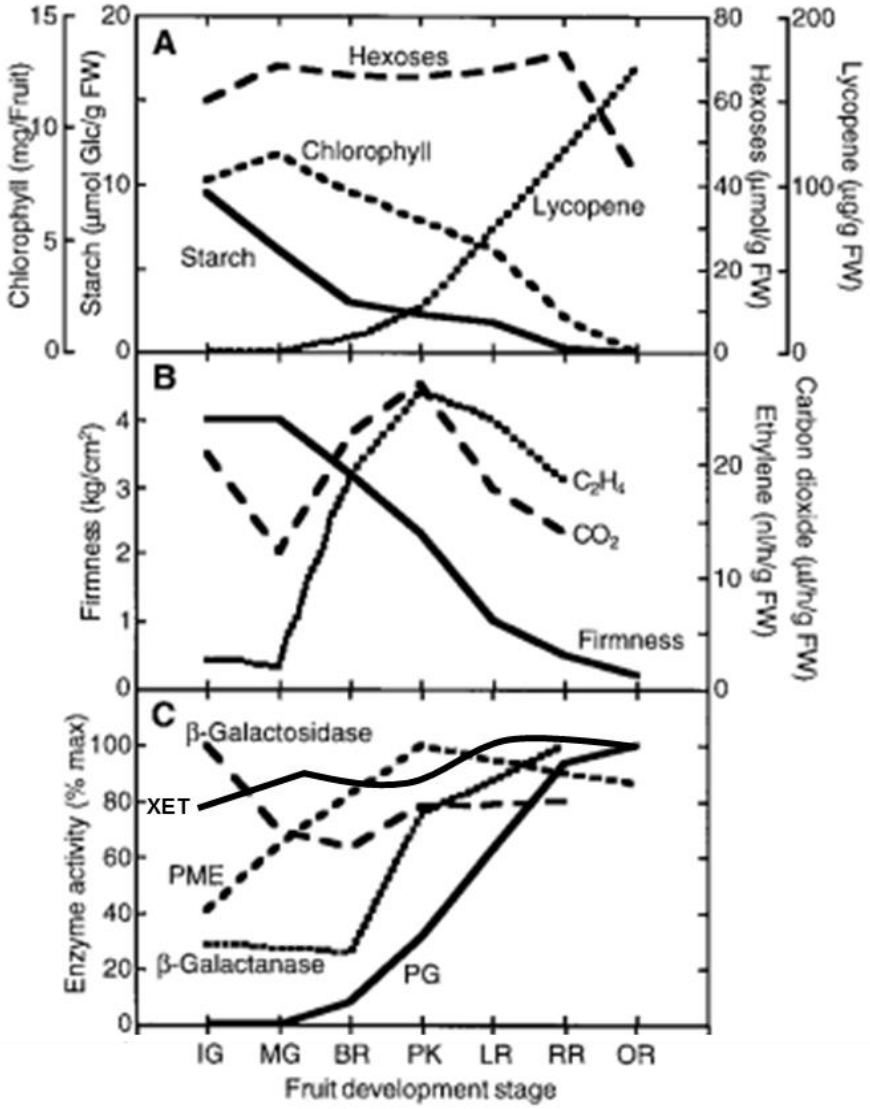


Figure 2.2. Changes in ripening parameters and cell wall polysaccharide-modifying enzyme activities during tomato fruit development. A. Pigments and sugars. Chlorophyll (a+b), McMahon et al. (1990); lycopene, Smith et al. (1988); hexoses (Glc+Fru) and starch, Yelle et al. (1988). B. Firmness and climacteric. Firmness, Maclachlan and Brady (1994); ethylene and carbon dioxide, Rothan and Nicolas (1989). C. Pectin-modifying enzymes. Polygalacturonase (PG), Smith et al. (1990); pectin methylesterase (PME), Harriman et al. (1991); β-galactanase and β-galactosidase, Carey et al. (1995). Matrix glycan-modifying enzymes. xyloglucan endotransglycosylase (XET), Maclachlan and Brady (1994). Data redrawn from sources indicated. Abbreviations of ripening stages: IG, immature green (expanding, not full size); MG, mature green (full size, locules developing); BR, breaker (first sign of red coloration on outside of fruit); PK, pink (30–70% light red); LR, light red (100% light red); RR, red ripe (100% dark red and edibly soft); OR, over ripe (senescing). Adapted from Brummel and Harpster 2001.

1979). The regulation of expression of cell wall modifying proteins has been investigated by characterizing ripening impaired mutants such as *rin*, *nor* and *Nr*. The fruits of *rin* and *nor* does not produce climacteric ethylene, do not accumulate lycopene and other carotenes, and soften very slowly (Tigchelaar et al., 1973). In *rin*, depolymerized xyloglucan (Maclachlan and Brady, 1994) and polyuronides are present at minimum levels (Giovannoni et al., 1989; DellaPenna et al., 1990). In addition, the activities of polygalacturonase and pectinesterase are barely detectable in *rin* fruits (Buescher and Tigchelaar, 1975; Poovaiah and Nukaya, 1979).

Polygalacturonase (PG)

PGs are enzymes that catalyze the cleavage of 1→4-α-D-galacturonide linkages. The substrate for PG is mainly de-esterified homogalacturonan that is secreted into the cell wall (Jarvis, 1984, Carpita and Gibeaut, 1993). The ripening fruits of tomato, peach and avocado possess high level of PG activity, but in tomato, the PG activity is 50 times higher than peach (Pressey and Avants, 1978) and the activity continues to be high at overripe stage (Tucker et al., 1980). The *pg* mRNA accumulates at breaker stage while the activity increases from early ripening stage suggesting that PG protein and activity is regulated by translational or posttranslational mechanisms (Sitrit and Bennett 1988). The suppression of *pg* transcript by antisense *pg* transgene resulted in reduced depolymerization of polyuronides with no effect on fruit lycopene and ethylene levels (Smith et al., 1990). Fruits with suppressed *pg* mRNA were slightly more firm than controls (Kramer et al., 1992; Langley et al., 1994). In *rin* fruits, *pg* mRNA accumulates at low levels (Knapp et al., 1989), and both PG activity (Buescher and Tigchelaar, 1975) and polyuronide solubilization (Seymour et al., 1987a) were reduced. The Flavr Savr tomato developed through suppression of endogenous *pg* also possess reduced PG activity (Sheehy et al., 1988) but lost consumer attraction due to poor taste and also because of high production and distribution costs. On the whole, it was shown that PG influences textural properties of fruit which are important for processing industry with less effect on fruit softening (Brummel and Harpster, 2001).

In tomato fruit, PG protein is present in three forms, the high molecular weight PG1 along with a combination of PG2A or PG2B and a glycoprotein, PG-β subunit (Pressey and Avants, 1973; Pogson et al., 1991). It was proposed that the function of PG-β is to localize PG2 to cell wall or to modify its activity (Pogson et al., 1991; Moore and

Bennett, 1994; Knegt et al., 1991). The mRNA and protein of *pg-β* are present before *pg* mRNA and activity appears in the fruit (Pogson and Brady 1993; Zheng et al., 1992, 1994). In the *pg-β* transgenic lines expressing antisense *β*-gene, slightly higher amounts of PG activity, increased polyuronide depolymerization are observed. This activity was present only for PG2 because of lack of PG-β protein in these lines. Fruits with suppressed *β*-subunit protein amounts have similar firmness to control fruits at mature green stage, but as ripening progressed, fruit show more softening than control fruits (Chun and Huber 2000). In these lines, the middle lamella lost cohesion due to which the tissue integrity is reduced. Since β-subunit protein accumulated before PG protein, it was proposed that this β-protein directs the diffusion of PG into cell wall which would control PG mediated pectin degradation (Brummel and Hapster, 2001).

Pectin methylesterase (PME)

PME is another pectin degrading enzyme that catalyzes the de-esterification of polyuronides from galacturonic acid and makes polyuronides available for PG mediated degradation (Pressey and Avants, 1982; Carpita and Gibeaut, 1993). The activity and protein abundance of PME increases in young fruit, before mature green stage and then declines afterwards (Tieman et al., 1992) while mRNA accumulates at mature green stage, thereafter decreases later in ripening (Harriman et al., 1991). In fruits of *Nr* and *nor*, the PME activity, protein and mRNA levels are not different from wildtype whereas in *rin*, all of these declined suggesting that *rin* mutation influences PME expression (Harriman et al., 1991). Antisense suppression of PME activity reduced the mRNA and protein amounts to trace levels but minimum activity of PME is present in the fruits (Tieman et al., 1992; Hall et al., 1993). In these fruits, the pectin methyl esterification was high and the fruit ripening in terms of ethylene and lycopene levels was not affected compared to control fruits. However, the suppression of PME resulted in increase of soluble solids in raw and processed fruits (Tieman et al., 1992; Thakur et al., 1996a). In PME antisense lines, an increase in levels of cations such as Ca^{+2}, Mg^{+2} and Na^{+2} and loss of tissue integrity without any change in fruit firmness has been observed. This suggests that PME is involved maintaining tissue integrity by influencing cation binding to the cell wall (Tieman and Handa 1994).

Pectate lyase (PL)

PLs are another class of pectin degrading enzymes that catalyze the cleavage of de-esterified pectin (Carpita and Gibeaut, 1993). PL has been initially considered to be secreted by pathogenic bacteria, where it causes depolymerization of pectin from cell walls in higher plants (Henrisaat et al., 1991). *Pectate lyase* gene was isolated from strawberry fruit and its mRNA showed ripening specific accumulation (Medina-Escobar et al., 1997). Antisense suppression of *pl* in tomato resulted in increased firmness without any effect on ethylene content, total solids, size, weight and color of fruits. The increase in cell wall homogalactouronans (HG) levels in fruits of *pl* suppressed lines suggests reduced breakage of HG that resulting in decreased availability of pectic polysaccharides for PG enzymes (Uluisik et al., 2015).

β-galactosidase (β-GAL)

In tomato fruit, loss of galactose residues from the cell wall starts early in ripening and occurs throughout the ripening (Gross and Wallner 1979; Gross 1983). The galactose that is present in the cell wall is in the form of (1→4) β-D-galactan and is degraded by the enzyme, β-D-galactosidase (Carpita and Gibeaut, 1993). Three isoforms of β-GAL were extracted from tomato, named β-GAL I, β-GAL II and β-GAL III of which β-GAL II were shown to react with β-D-galactan isolated from tomato cell wall (Pressey, 1983). The activity of β-GAL II is low at mature green stage and increases during ripening whereas the activities of β-GAL I and β-GAL III are high in green fruit and decrease during ripening (Pressey, 1983; Carrington and Pressey, 1996). In tomato, β-GAL is encoded by seven genes, *tbg1-tbg7*. β-GAL II is encoded by *tbg4* and its mRNA levels increase at turner stage and decline at the late ripening stages. In *rin* and *nor* mutants, mRNA abundance of *tbg4* is reduced but the activity does not increase during ripening (Carey et al., 1995; Smith and Gross, 2000). Antisense suppression of *tbg4* in early ripening stage resulted in decreased levels of free galactoside in fruits and also reduced fruit softening. This result suggests that β-GAL help in reducing the mechanical strength of cell wall and thereby allowing other hydrolases for depolymerization of cell wall polysaccharides (Brummel and Harpster, 2001).

Xyloglucan endotransglycosylase (XET)

XET cleaves the internal (1→4) β-D-glucan linkages of cell wall xyloglucan (Fry et al., 1992). In tomato, XET activity is high in very young fruit, decreases during ripening and slightly increases during late ripening (Percy et al., 1996). In *rin* fruits,

reduced XET activity is present compared to wildtype (Maclachlan and Brady, 1994). In tomato two XET genes are present, *Lexgt1*, that is expressed in young fruit and *Lextb1* which is expressed in ripening fruit. Analysis of transgenic lines with over expression of *Lexgt1* revealed increased fruit size. In addition, a negative correlation is observed for fruit size and soluble solid content in the fruits of these lines (Asada et al., 1999). However, in antisense lines of *Lextb1*, no correlation was observed between mRNA abundance and fruit softening. This suggests that for suppression of XET activity, multiple *xet* genes have to be silenced in fruit in order to identify the role of XET in fruit softening. In tomato, XET is believed to have a maintenance role that introduces new xyloglucans into cell walls (Brummel and Harpster, 2001).

Expansin (Exp)

Expansins are identified originally as the enzymes that cause cell wall loosening in *invitro* experiments (McQueen-Mason et al., 1992). The enzymatic action of expansin is through the reversible cleaving of hydrogen bonds between cellulose microfibrils and xyloglucan, leading to loosening and slippage of microfibrils present in the cell wall (McQueen-Mason et al., 1995; Cosgrove et al., 2000). In tomato, six expansin genes were identified with overlapping pattern of mRNA accumulation during ripening (Brummel et al., 1999a; Catala et al., 2000). The mRNAs of *exp2*, *exp4* accumulate at earlier stages of fruit development before immature green stage, *exp5*, *exp6* at immature and mature green stages and *exp3* accumulate throughout fruit development and ripening stages. The mRNA and protein of *exp1* accumulate higher than other isoforms and persist in high levels after ripening (Rose et al., 1997; 2000). In addition, mRNA of ripening related *exp1* is positively regulated by ethylene and the expression levels are at very low levels in fruits of *rin* and *nor* (Rose et al., 1997). Antisense suppression of *exp1* resulted in reduced fruit softening, polyuronide depolymerization, but did not modify matrix xyloglucan degradation. In overexpression lines of *exp1*, an opposite effect of increased fruit softening and depolymerization of xyloglucan observed (Brummel et al., 1999c).

α-Mannosidase (α-MAN) and β-D-*N*-hexosaminidase (β-HEX)

α-MAN and β-HEX are glycosyl hydrolases that break glycosidic bonds between carbohydrate substrates (Jagadeesh et al., 2004). These are N-glycan processing enzymes and α-MAN cleaves α-mannosidic linkages (Hossain et al., 2009) whereas β-HEX cleaves N-acetyl-β-*D*-hexosamine residues of N-glycans in the cell wall (Strasser et al., 2007).

The injection of N-glycans into green tomato induced red coloration indicating the important role of these compounds in fruit ripening (Priem and Gross 1992). RNAi mediated suppression of α-MAN and β-HEX in tomato resulted in fruits with increased firmness and enhanced shelf life, whereas overexpression resulted in excessive fruit softening (Meli et al., 2010). The decreased accumulation of free glycans in these transgenic lines suggests the requirement of N-glycans for fruit softening in tomato. In *rin* and *Nr* fruits, the mRNA abundances of *α-man* decreased compared to control fruits. Similarly, the transcript abundances of *β-hex* in *rin*, *nor* and *Nr* are lower compared to wildtype control fruits. In addition, the transcripts of other cell wall modifying enzymes are also down-regulated in *α-man* and *β-hex* RNAi lines, suggesting the involvement of N-glycans in regulating the action of these enzymes (Meli et al., 2010).

β-mannosidase (β-MAN)

β-MAN is an enzyme that hydrolyzes glucomannans, galactomannans present in the hemicellulose component of cell walls. In tomato fruit, the *β-man* mRNA accumulates throughout the ripening from immature green fruit. Both the protein accumulation and activity of *β-man* increases from mature green stage to the overripe stage with barely undetectable levels before mature green stage (Bewley et al., 2000). The β-MAN protein isolated from tomato fruit exhibits both hydrolase and transglycosylase activity (Schroder et al., 2006). In *rin*, *nor* and *Nr* fruits, which remain firm, the activity of *β-man* increases (Bewley et al., 2000). In tomato fruits, the suppression of *β-man* through RNAi resulted in reduced firmness at turning, orange and red ripe stages (Wang et al., 2009). The absence of correlation between fruit firmness and β-MAN activity in the transgenic lines indicates the involvement of this enzyme in cell wall rearrangement by transferring glycosyl residues and also in supply of substrates for other cell wall modifying enzymes rather than directly causing hydrolysis of cell wall components (Wang et al., 2009). Further studies are needed to confirm the precise role of this enzyme in the fruit ripening and softening.

Deoxyhypusine synthase (DHS)

DHS is an enzyme involved in catalyzing the formation of deoxyhypusine from *eIF-5A*, the step required for posttranslational activation of eIF-5A protein (Wang et al., 2003). In tomato fruits, the enhanced abundance of *dhs* mRNA at the onset of senescence is also associated with up-regulation of *eIF-5A*, suggesting the role of DHS in fruit

softening (Wang et al., 2001). Antisense suppression of *dhs* in tomato resulted in delayed onset of senescence, indicating the crucial role of DHS in regulation of fruit senescence (Wang et al., 2005).

2.6 Chloroplast to chromoplast transition

Plastids are a class of cell organelles that are involved in several pathways, including starch metabolism, fatty acid synthesis, pigment metabolism and nitrate assimilation (Bian et al., 2011). Based on the functional properties, plastids can be autotrophic such as chloroplasts and heterotrophic such as chromoplasts, amyloplasts, eliaoplasts (Siddique et al., 2006). Chromoplasts are carotenoid storing plastids present in fruits and flowers of plants and are the sites for synthesis of vitamins, amino acids, hormones, fatty acids as indicated by the presence of proteins related to above pathways in tomato chromoplast proteome (Barsan et al., 2012). In tomato, chromoplasts originate from chloroplasts through binary fission, budding and fragmentation (Cookson et al., 2003; Forth and Pyke 2006). After chromoplasts are formed, cell division stops or reduces. This is supported by the presence of only few members of FtsZ proteins which are required for plastid maintenance and division in the chromoplast proteome (Barsan et al., 2012).

Chromoplasts store carotenoids in specialized structures such as globular, membranous, tubular, reticulo-tubular, crystalloid bodies and more than one type of structure can be present in chromoplasts (Ljubesic et al., 1991). In tomato at mature green stage, chloroplasts exhibit red auto florescence because of chlorophyll. After this stage, there is a loss of thylakoid integrity and decrease in chlorophyll content in the chromoplasts of ripening fruits. This is supported by the decrease in the abundance of a thylakoid binding protein, MFP1 which participates in synthesis of thylakoid membrane (Jeong et al., 2003). At breaker stage, a heterogenous population of chloroplasts and chromoplasts exists since chloroplast to chromoplast transition is not uniform throughout the fruit. Chromoplasts at red ripe stage are smaller in size, exhibit green auto fluorescence due to high carotenoid content with oblong and needle like appearance in outer mesocarp and large and ovoid shape in inner mesocarp regions of fruit (Waters et al., 2004; Egea et al., 2010). In tomato fruits, carotenoids are accumulated in the form of lycopene crystalloids in membranous structures (Harris and Spurr, 1969). In red pepper, the chromoplasts contain carotenoid-protein bodies associated with tocopherols and quinones in center surrounded by polar lipid layer, finally surrounded by a layer of

plastoglobulin, fibrillin (Deruere et al., 1994). The high level of fibrillin in ripening fruits allows sequestration of carotenoids in the form of crystals. This sequestration helps in protecting carotenoids from oxygenation, degradation and also prevents the otherwise harmful effects of excess of carotenoids on cellular functioning (Barsan Ph.D. thesis, 2010, University of Toulouse, France).

An increase in the size and number of plastoglobuli is observed during chloroplast to chromoplast transition (Harris and Spurr, 1969). Plastoglobuli arise from highly curved margins of thylakoid membrane at stromal side (Austin et al., 2006). Antisense suppression of *chrc* (Chromoplast specific carotenoid associated protein), a plastoglobulin in tomato resulted in 30% reduction of carotenoids in flowers suggesting the role of CHRC in chromoplast differentiation and carotenoid metabolism (Leitner-Dagan et al., 2006a). Both RNAi and antisense mediated suppression of *chrdc/i*, a protein from Yjgf family, resulted in reduced accumulation of carotenoids in corollas of tomato flowers indicating the functional role of *chrdc/i* in carotenoid accumulation (Leitner-Dagan et al., 2006b). In addition, overexpression of a pepper fibrillin resulted in increase of carotenoids and carotenoid derived volatiles indicating the role of fibrillins in thylakoid disorganization (Simkin et al., 2007). Analysis of plastoglobule proteome in red pepper revealed the presence of carotenoid biosynthetic enzymes, including ζ-carotene desaturase, lycopene-β-cyclase and β-carotene hydroxylase in them (Ytterberg et al., 2006). In tomato chromoplast proteome, majority of carotenoid pathway enzymes have been detected, such as PSY1, PDS, ZDS, CRTISO and CYCB (Barsan et al., 2012; Fig. 2.3).

The significance of chromoplast differentiation is further comprehended by the isolation of *Or* gene from cauliflower which conferred orange color to the curd due to accumulation of β-carotene (Lu et al., 2006). *Or* is also associated with increase in carotenoid accumulation in potato and melon (Lopez et al., 2008; Tzuri et al., 2015). The *Or* gene encodes a DNAJ-like co-chaperone lacking J domain but consists of cysteine rich domain. DNAJ proteins interact with Hsp70 chaperones and modulate protein assembly, folding and translocation. The action of *Or* gene is through creation of a metabolic sink by inducing the chromoplast differentiation (Li and Van-Eck 2007). In *Arabidopsis*, OR proteins influence carotenoid biosynthesis through posttranscriptional regulation of *psy1* (Zhou et al., 2015).

2.7 Carotenoids and carotenoid derived metabolites

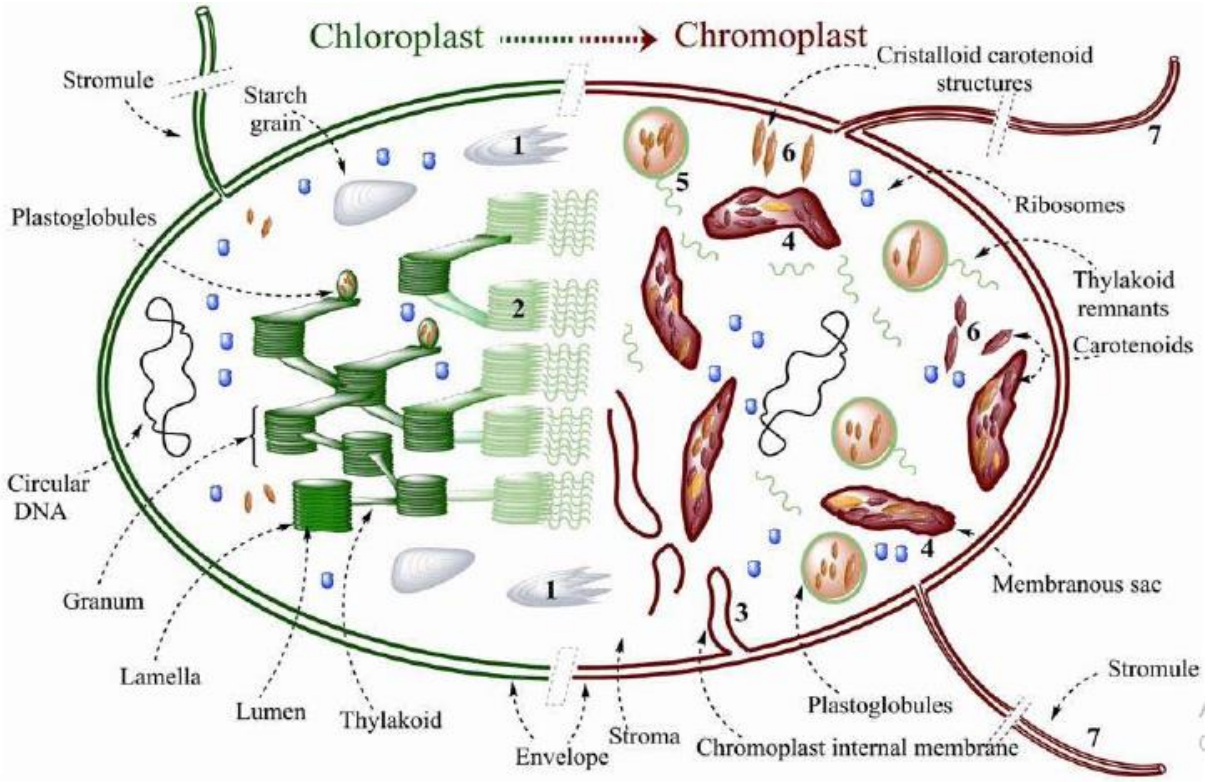


Figure 2.3. Schematic representation of the chloroplast-chromoplast transition. The scheme shows the breakdown of starch granules (1), and of grana and thylakoids (2), the synthesis of new membrane structures form the inner membrane envelope of the plastid (3), leading to the formation of carotenoid-rich membranous sacs (4), the increase in the number and size of plastoglobules (5), the appearance of carotenoid-containing crystalloids (6), and the increase in the number of protrusions emanating from the plastid envelope, called stromules (7). Taken from Egea et al., 2010.

Carotenoids are naturally occurring colored compounds responsible for red, yellow and orange colors of fruits, flowers, seeds and roots (Grotewold 2006). Carotenoids are synthesized in plastids of higher plants, photosynthetic algae, also by some bacteria, fungi and aphids (Cuttriss et al., 2011; Velayos et al., 2000; Iniesta et al., 2008; Moran and Jarvik 2010). Animals and humans cannot synthesize carotenoids and acquire them through diet (Krinsky et al., 1994). Carotenoids are the second most abundant group of natural pigments widely distributed in the world with 750 different types of structurally diverse compounds (Nisar et al., 2015). Carotenoids are C_{40} tetraterpenoids containing eight isoprene units connected in a head-to-tail fashion with central unit in reverse orientation (Alvarez et al., 2013). Based on the presence or absence of oxygen in the hydrocarbon backbone, carotenoids can be divided into two major groups: carotenes which are hydrocarbon carotenoids and xanthophylls which are oxygenated hydrocarbons containing oxygen in the form of epoxy, methoxy, keto, hydroxyl or carboxyl groups (Armstrong, 1994). Carotenoids occur in free form or in esterified form in conjugation with fatty acids. This esterification helps in sequestration of carotenoids into lipid layer of plastoglobules and prevents them from degradation (Howitt and Pogson, 2006; Cazzonelli and Pogson, 2010). In nature, carotenoids mainly exist in *trans* isomeric form rather than *cis* form (Britton 1995). The light absorption function of carotenoids is because of the presence of polyene chromophore in the carotenoid structure. The conjugated double bonds present in the chromophore absorbs light in the wavelength range of 400-500 nm and reflects light from other wavelengths (Britton 2008).

A number of carotenoid derived metabolites that are identified in plants are involved in diverse physiological functions. Apocarotenoids are derived from oxidative cleavage of carotenoids through the action of carotenoid cleavage dioxygenases (CCDs). The phytohormone, ABA is produced from xanthophylls and is involved in seed dormancy and stress regulation (Raghavendra et al., 2010). Strigolactones are a new class of hormones that convert β-carotene to lactone (Alder et al., 2012); act as signaling molecules and regulate shoot branching thus controlling plant architecture (Umehara et al., 2008). In addition, the pigment from seed arils of *Bixa*, bixin; saffranal from flower stigmas of *Crocus* (Rosati et al., 2009) and volatile compounds such as β-ionone, α-ionone are also examples of apocarotenoids, signifying the role of these carotenoid derived compounds in imparting flavor (Auldridge et al., 2006). Apocarotenoids also provide defense against biotic and abiotic stresses (Salt et al., 1986; Fester et al., 1999).

2.8 Carotenoid biosynthetic pathway

Carotenoids are built from five carbon compound, isopentenyl pyrophosphate (IPP) through cytosolic mevalonic acid (MVA) pathway and the plastidic methylerythritol 4-phosphate (MEP) pathway (Lichtenthaler et al., 1997; Eisenreich et al., 2004; Fig. 2.4). In cytosolic MVA pathway, IPP is generated from acetyl coA through the formation of MVA. IPP is converted to dimethylallyl pyrophosphate (DMAPP) by the action of IPP isomerase (IDI). DMAPP acts as a substrate for the production of sesquiterpenes (C_{15}) and triterpenes (C_{30}) (Hsieh and Goodman 2005). One molecule of DMAPP condenses with a molecule of IPP to produce geranyl pyrophosphate (GPP). In plants, the plastidial MEP pathway is the major source for IPP and DMAPP required for carotenoid biosynthesis (Bramley 2002, Eisenreich et al., 2004). Along with carotenoids, different varieties of metabolites including gibberellins, tocopherols, and chlorophylls are generated from IPP and DMAPP in plastids (Rodriguez-Concepcion 2010). The synthesis of carotenoids occurs on plastid membrane through the action of nuclear encoded enzymes and it is suggested that the location of these enzymes is crucial for its activity (Cunningham and Gantt 1998; DellaPenna and Pogson, 2006; Cuttriss et al., 2011). The organization of enzymes as protein complexes has been confirmed through in-vivo channeling studies and identification of high molecular weight complexes with carotenoid biosynthesis enzymes (De la Guardia et al., 1971; Candau et al., 1991; Al-Babili et al., 1996).

The plastidial MEP pathway generates IPP through a series of steps of which the reaction between pyruvate and glyceraldehyde-3-phosphate is the first step catalyzed by the enzyme DXP (1-deoxy-D-xylulose 5-phosphate) synthase (DXS) that generates DXP. MEP is formed from DXP through intramolecular rearrangement and reduction by DXP reductoisomerase (DXR). It has been shown that DXS is the rate limiting enzyme that regulates flux through the pathway (Lois et al., 2000; Pulido et al., 2013). IPP formed from MEP through a series of phosphorylations and reductions thus condenses with DMAPP by the action of isopentenyl diphosphate isomerase (IPI), generating GPP. Two molecules of IPP are added to GPP to form a C_{20} compound, geranylgeranyl pyrophosphate (GGPP), which is catalyzed by the enzyme, GGPP synthase (GGPPS; Bramley 2002; Fraser and Bramley 2004). The condensation of two GGPP molecules into 15-cis phytoene catalyzed by the enzyme phytoene synthase (PSY1, chromoplast specific), is the first committed step in the pathway (Cunningham and Gantt 1998; Fraser

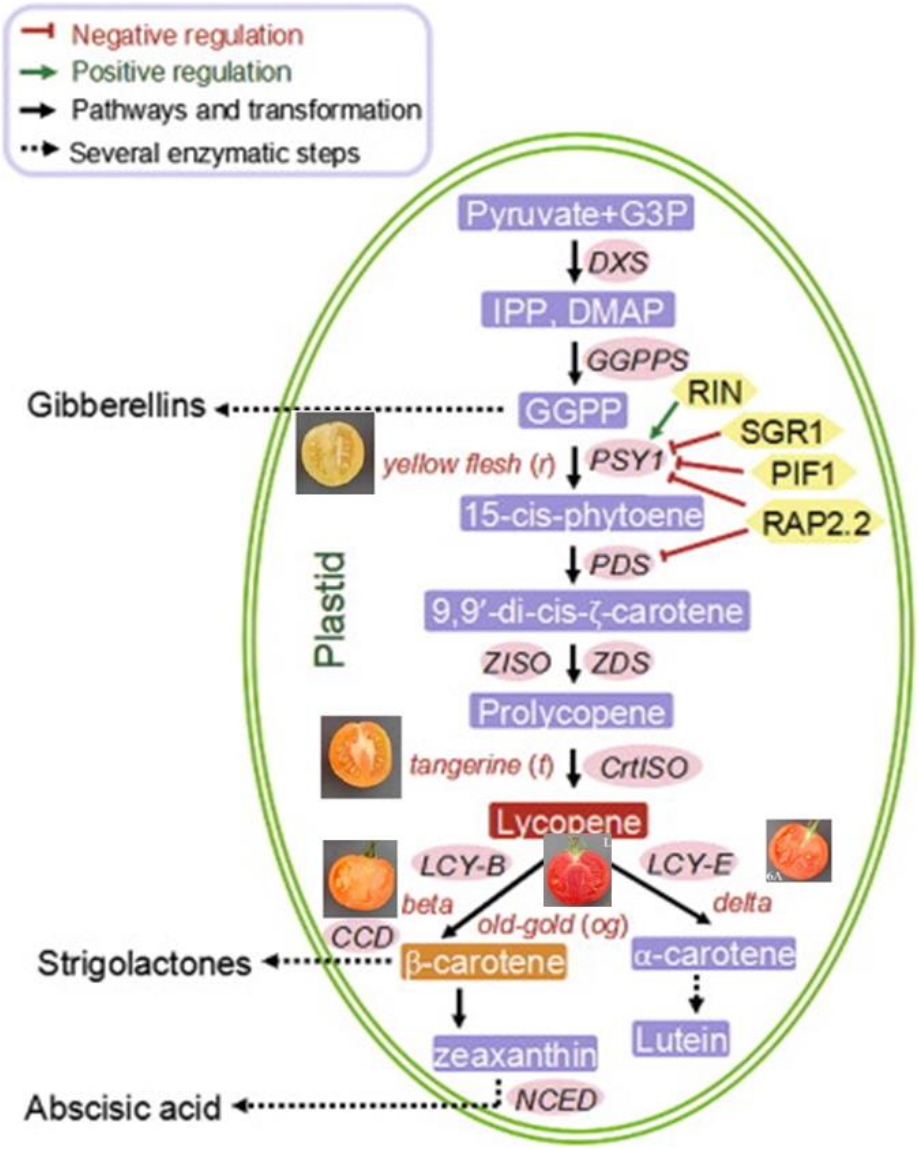


Figure 2.4. Carotenoid biosynthesis pathway with associated enzymes and regulatory genes. Mutants related to carotenoid biosynthesis are indicated in italic red type. The rounded rectangles represent the substrates involved in carotenoid biosynthesis. The pink ellipses represent carotenoid pathway genes localized in plastids. The hexagons represent transcription factors regulating carotenoid biosynthesis. *CCD*, *carotenoid cleavage dioxygenases*; *CrtISO*, *carotene isomerase*; DMAPP, dimethylallyl diphosphate; *DXS*, *1-deoxy-d-xylulose 5-phosphate synthase*; G3P, glyceraldehyde 3-phosphate; GGPP, geranylgeranyl diphosphate; *GGPPS*, *geranylgeranyl pyrophosphate synthase*; IPP, isopentenyl diphosphate; *LCY-B*, *lycopene β-cyclase*; *LCY-E*, *lycopene ε-cyclase*; *NCED*, *9-cis-expoxycarotenoid dioxygenases*; *PDS*, *phytoene desaturase*; PIF1, phytochrome interacting factor 1; *PSY1*, *phytoene synthase*; RAP2.2, related to ap2; RIN, ripening inhibitor; SGR1, stay-green; *ZDS*, *ζ-carotene desaturase*; *ZISO*, *ζ-carotene isomerase*. Adapted from Liu et al., 2015.

et al., 2002). In plants, the synthesis of lycopene from phytoene involves four reactions of successive dehydrogenations and isomerizations. These desaturation steps are catalyzed by the enzymes, phytoene desaturase (PDS) and ζ-carotene desaturase (ZDS) which introduce double bonds into the chromophore, converting the colorless phytoene into red colored lycopene. Phytoene is converted into tri-*cis*-ζ-carotene by the action of enzyme, PDS via formation of phytofluene. ζ-carotene isomerase (ZISO) catalyzes the *cis*-*trans* isomerization of 9,15,9'-tri-*cis*-ζ-carotene into 9,9'-di-*cis*-ζ-carotene (Li et al., 2007). This isomerization step can occur in the presence of light but the analysis of mutants in Arabidopsis revealed that ZISO is required even in light conditions (Ruiz-Sola and Rodriguez-Concepcion 2012). Desaturation of 9,9'-di-*cis*-ζ-carotene into 7,9, 9',7' tetra-*cis*-lycopene (pro-lycopene) is through the action of enzyme ζ-carotene desaturase (ZDS) via formation of 7,9,9'-tri-*cis*-neurosporene. The reaction catalyzed by the enzyme, carotenoid isomerase (CRTISO) is the last step in the lycopene synthesis and this enzyme converts *cis*-lycopene into all-*trans*-lycopene (Isaacson et al., 2004). The above conversion of pro-lycopene to all-*trans*-lycopene can occur in green tissues without any enzymatic action in the presence of light (Isaacson et al., 2002; Park et al., 2002). In bacteria and fungi, all these reactions of lycopene formation are carried out by single enzyme, CRTI (Sandmann 1994; Armstrong 1997) which generates *trans* intermediates in contrast to *cis* forms in plants. The *cis*-forms generated in higher plants acts as regulators of various signaling pathways (Kachanovsky et al., 2012).

Lycopene is the substrate for two cyclase enzymes that insert β or ε-ionone rings into the isoprenoid backbone. LCYB (lycopene β-cyclase) catalyzes the formation of γ-carotene which undergoes cyclization at one end and forms β-carotene after cyclization at the other end (Pecker et al., 1996). LCYE (lycopene ε-cyclase) catalyzes the introduction of ε-ring into lycopene to generate δ-carotene and subsequent cyclization of other end by LCYB produces α-carotene (Cunningham and Gantt 2001). The chromoplast specific *lcyb* expressed in flowers and fruits of tomato known as *cycb* regulates tissue specific regulation of carotenoid composition (Ronen et al., 2000). The expression of *lcyb* and *lcye* affects cyclase activities by regulating β-carotene and α-carotene ratio in tomato and Arabidopsis (Yu and Beyer 2012; Giorio et al., 2013).

Xanthophylls, the oxygenated hydrocarbons are produced from hydroxylation of α- and β-carotenes. β-carotene is converted by β-carotene hydroxylases (BCH) to zeaxanthin while lutein is produced by hydroxylation of ε- and β-ionone rings of α-carotene by

cytochrome P450 hydroxylases, CYP97A3 and CYP97C1 (Kim et al., 2009). Zeaxanthin is epoxidised by zeaxanthin epoxidase (ZEP) to produce antheraxanthin and then to violaxanthin, which is a reversible reaction catalyzed by violaxanthin de-epoxidase (VDE). All these reactions together constitute xanthophyll cycle (Niyogi et al., 1998). The epoxidation and de-epoxidation reactions in xanthophyll cycle are light-dependent and are involved in dissipation of excess light energy and assist in acclimation of plants to varying light intensities (Latowski et al., 2004; Jahns et al., 2009). In addition to violaxanthin cycle, the reversible de-epoxidation of lutein epoxide to lutein also occurs in young tomato fruits, known as lutein epoxide cycle (Rabinowitch et al., 1975; Garcia-Plazaola et al., 2007). The final step in the carotenoid pathway is the synthesis of neoxanthin from violaxanthin (Parry and Horgan 1991). Both neoxanthin and violaxanthin act as precursors for ABA, while in tomato, violaxanthin alone is enough for producing ABA *invivo* (Neuman et al., 2014). In tomato, the gene responsible for neoxanthin synthesis is identified through molecular analysis of neoxanthin deficient mutation (*nxd1*). However, no neoxanthin activity has been shown by purified NXD1 in functional complementation assay in *E.coli* (Neuman et al., 2014). This could be due to the high similarity of violaxanthin and neoxanthin at spectral level that limits its identification in transformed *E.coli* during functional analysis study (Rosas-Saavedra and Stange 2016).

2.9 Biological role of carotenoids

In humans, carotenoids play a prominent role as health promoting nutrients. β-carotene or provitamin A is precursor for retinoids (retinal, retinol and retinoic acid), the deficiency of which causes xerophthalmia and keratomalacia (Sommer and Vyas 2012). The presence of lycopene and β-carotene in regular human diet has been shown to reduce the incidence of several diseases such as macular degeneration, cancer, neurodegenerative and heart diseases (Delcourt et al., 2006; Zu et al., 2014; Lu et al., 2010; Karppi et al., 2013). In plants, carotenoids impart distinct colors to flowers and fruits that aid in pollination and seed dispersal (Kevan and Baker, 1983). Carotenoids such as β-carotene in the seeds of maize have been used for bio-fortification of cereal crops (Vallabhaneni and Wurtzel 2009; Wurtzel et al., 2012). Carotenoids also play an important role in photoprotection by detoxifying free radicals, prevents damage to membrane lipids from reactive oxygen species, dissipates excess light energy in the form of heat (DellaPenna and Pogson 2006; Li et al., 2008; Havaux 2014). Carotenoids present in photosystems act

as antenna, harvest light energy and transfer it to the chlorophylls present at reaction centres (Grotewold 2006; Walter and Strack 2011). Carotenoid derivatives, such as ABA and strigolactones are hormones involved in stress regulation and rhizosphere signaling (Messing et al., 2010; Walter and Strack 2011).

2.10 Tomato mutants with altered carotenoid content

A considerable amount of information exists on tomato mutants which show differential accumulation of carotenoids. This knowledge has provided appropriate means to understand the synthesis and function of genes associated with carotenoid production in plants (Hirschberg 2001; Fraser and Bramley 2004; Ruiz-Sola and Rodriguez-Concepcion 2012). Since PSY1 is the rate limiting enzyme that regulates flux through the pathway, many studies have been focused on the genetic manipulation of *psy1* for manipulation of carotenoid levels. The null mutation in *psy1* (*r mutant*) resulted in yellow flesh with reduced levels of carotenoids in fruits (Rick and Butler 1956). Fruit specific overexpression of *psy1* in tomato increased carotenoid content, reduced gibberellic acid (GA1) and chlorophyll levels (Fray et al., 1995). In a similar way, fruit specific expression of a bacterial *crtB* gene in tomato increased PSY1 activity, phytoene levels and also total carotenoid content (Fraser et al., 2002). Moreover, a large increase in carotenoid content has been observed in cases of using plant *psy1* rather than bacterial *crtB* which might be due to the less efficiency of bacterial enzyme to interact within protein complexes in contrast to plant PSY1 (Rosas-Saavedra and Stange 2016). In addition to *psy1*, two other mutants, including *apricot* (*at;* Jenkins and Mackinney 1955) and *sherry* (*sh*; Zscheile et al., 1962) also gives yellow fruits at young stage which turn pinkish-red at maturity. The accumulation of colorless phytoene in the tomato fruit resulted in white fruit in the *ghost* (*gh*) mutant (Josse et al., 2000). *gh* possess mutation in *immutans* gene that codes for plastid terminal oxidase (PTOX) which regulates chloroplast redox balance and acts as a cofactor for desaturation of phytoene (Josse et al., 2000; Carol and Kuntz 2001).

In tomato, lycopene accumulates in *trans* form, but the *tangerine* (*t*) mutant accumulates *cis*-lycopene (pro-lycopene) because of a mutation in *crtiso* and the fruits are orange in color (Isaacson et al., 2002). Since *cis* isomers are more available than *trans* forms (Boileau et al., 2002), significant interest has been aroused to analyze the regulatory mechanisms behind carotenoid accumulation in this mutant. In tomato, the expression of *lcye* decreases during ripening. But, in dominant *Delta* (*Del*) mutant, which

has mutation in *lcye*, the expression of *lcye* increases to about 30 fold and the fruit color changes to orange instead of red because of accumulation of δ-carotene (Ronen et al., 1999). The constitutive expression of *lcye* gene in tomato resulted in high lutein and δ-carotene levels in the fruits suggesting the diversion of the flux to the other branches of the pathway in these transgenic lines (Giorio et al., 2013). In addition, two other color mutants exist in tomato, *Beta* and *old-gold* which have mutation in *Beta* gene that encodes CYCB, a chromoplast specific lycopene β-cyclase. *Beta* is partially dominant mutation in which the fruit accumulates β-carotene because of the enhanced transcription of *Beta* gene. On the contrary, *old-gold* carries a null mutation in *Beta* gene, resulting in increased accumulation of lycopene and low levels of β-carotene (Ronen et al., 2000). More information regarding other mutants with altered carotenoid content is given in section 2.12.

2.11 Tomato wild species

The cultivated tomato has been originated from South America and the initial domestication took place in the central American region, Mexico (Giordano and Silva, 2000). A wild tomato species, *S. lycopersicum var. cerasiformae*, also called cherry tomato is referred as the ancestor to the cultivated tomato (Rick et al., 1994). The presence of less exerted stigmas has been considered as favorable feature for self-pollination that was accidentally selected and this trait was introduced into modern cultivars through breeding (Rick and Chetelat 1995). Tomato was initially known as *Lycopersicum esculentum*, but the genus *Lycopersicum* has been changed to *Solanum* based on genetic and molecular evidences (Spooner et al., 1993; Peralta et al., 2005). The cultivated tomato and its wild species are grouped on the basis of geographic distribution, morphology and phylogeny into 13 species (Peralta et al., 2005; Peralta and Spooner 2001; Spooner et al., 2005). Tomato domestication resulted in drastic reduction of genetic diversity in cultivated tomato compared to that observed in closest wild species (Sim et al., 2010; Tanksley and McCouch 1997). The economically important traits such as fruit color, weight, size, sugar content and shelf life have been used for human selection.

Fruits of tomato wild species exhibit diverse colors ranging from green, orange and red (Bauchet and Causse 2012). The green fruit color has been considered as ancient and colored fruits originated later in the evolution (Peralta and Spooner 2001; Alvarez et al., 2001; Miller and Tanksley 1990). In the wild species, *S. pimpinellifolium* produces red berries and accumulates lycopene, while *S. galapagense* and *S. cheesmanie* produce

orange berries and accumulate β-carotene. Except the above three species, fruits of all other wild species including *S. chimielewskii*, *S. habrochaites*, *S.pennellii*, *S. arcanum*, *S. chilense*, *S. corneliomulleri*, *S. huaylasense*, *S. parviflorum* and *S. peruvianum* are green in color. The regulation of fruit color in the tomato and wild species is not known. The genes responsible for fruit color such as *r*, *B* and *Del* were identified based on different interspecific crosses between wild tomato and modern tomato. In addition to the genes from carotenoid biosynthesis pathway, several quantitative trait loci (QTL) are identified that influence fruit color and carotenoid content (Liu et al., 2003). The study of ILs and backcrossed lines generated from *S. pimpinellifolium*, *S. parviflorum* and *S. pennellii* aided in identification of QTLs associated with lycopene and β-carotene content in the fruits (Foolad 2007). It is proposed that the green color of fruits is the result of down-regulation of *psy1* (Melendez-Martinez et al., 2010; Bolger at al., 2014). The primary metabolite profiling in leaves and fruits of wild species revealed that the fruit metabolome of *S. habrochaites* is closer to cultivated tomato. In case of leaf, *S. pimpinellifolium* is closer to cultivated tomato while that of *S. habrochaites* is distinct (Schauer et al., 2006). Transcriptome analysis in *S. pennellii* revealed higher expression of photosynthetic genes and lack of *psy1* expression in the fruits which might be associated with green color of the fruits in this species (Bolger et al., 2014). More comprehensive analyses at systems biology level are required to unveil the regulation of fruit color in the tomato and its wild species.

2.12 Factors influencing carotenoid metabolism

In tomato, carotenoid metabolism is regulated by many factors.

Light: In plants, light acts not only as a source of energy but also involved in many aspects of plant life cycle including photomorphogenesis, phototropism, germination and circadian rhythms (Jiao et al., 2007). To perceive quality, quantity, direction and duration of light, plants use photoreceptors (Moglich et al., 2010). Six different classes of photoreceptors are recognized in plants including phytochromes (Chen and Chory 2011), cryptochromes (Chaves et al., 2011), phototropins (Christie 2007), UVR8 (Rizzini et al., 2011), zeitlupe and FKF receptors (Suetsugu and Wada 2013). Phytochromes are red and far red receptors that exist in two forms, the inactive Pr form that absorbs light at 660 nm and active Pfr form which absorbs light at 730 nm (Rockwell et al., 2006). In tomato, five genes for phytochromes are identified and include *phyA*, *phyB1*, *phyB2*, *phyE* and *phyF* (Pratt et al., 1997). It has been shown by Alba et al. (2000) that fruit localized

phytochromes regulate the extent of lycopene accumulation in tomato independent of ethylene. The carotenoid content and PSY1 activity increased in pericarp discs from breaker stage tomato fruit that were kept in darkness and interrupted with red or far red light (Schofield and Paliyath, 2005). Phytochromes influence carotenoid levels by acting in single or in combination and determine the transition intervals during different ripening stages of tomato ripening process (Gupta et al., 2014). PIF1a, a member of phytochrome interacting factor family, adjusts tomato to actual ripening process by binding to *psy1* promoter. PIF1a represses *psy1* at green stage and then PIF1 gets degraded by active phytochromes during ripening process, which in turn derepresses *psy1* and promotes carotenoid accumulation in the tomato fruit (Llorente et al., 2016).

Cryptochromes are UV A/blue light photoreceptors that absorb light in blue (400-500 nm) and UV-A (320-390 nm) region (Llorente et al., 2016). In tomato, four genes of cryptochrome are identified, namely, *cry1a*, *cry1b*, *cry2* and *cry3* (Perrotta et al., 2000, 2001). The reduction of *cry1a* transcript did not influence fruit carotenoid content (Ninu et al., 1999) while overexpression of *cry2* resulted in accumulation of lycopene and flavonoids in tomato (Giliberto et al., 2005). Phototropins are a special class of blue light receptor kinases in plants that mediate root and hypocotyl phototropism (Sakai et al., 2001), chloroplast movement (Kagawa et al., 2001), stomatal opening (Kinoshita et al., 2001) and leaf expansion (Tokutomi et al., 2008). These are plasma membrane associated serine/threonine kinases containing two LOV (light-oxygen-voltage) domains in the N-terminal and a kinase domain in the C-terminal end (Briggs et al., 2001; Briggs and Christie, 2002; Christie et al., 2012). Two members exist in the phototropin family, PHOT1 and PHOT2 and they have different photosensitivities as determined by their N-terminal domains. PHOT1 mediates low fluence blue light responses (<0.1-1 μ mol $m^{-2}s^{-1}$) whereas PHOT2 mediates high fluence blue light responses (≥ 1μ mol $m^{-2}s^{-1}$; Sakai et al., 2001; Higa et al., 2014). On exposure to light, phototropins undergo blue light induced autophosphorylation which is the first step in phototropic signal transduction pathway (Inoue et al., 2008a; Inoue et al., 2011; Boex-Fontvieille et al., 2014; Deng et al., 2014). Until now, three phosphorylation targets for PHOT1 were identified including Blue Light Signaling1 (BLUS1; Takemiya et al., 2013a), ATP-binding cassette B19 (ABCB19; Christie et al., 2011) and Phytochrome Kinase Substrate4 (PKS4; Demarsy et al., 2012; Kami et al., 2014). In Arabidopsis, along with autophosphorylation, PHOT1 undergoes ubiquitination which requires Non-Phototropic Hypocotyl3 (NPH3; Roberts et

al., 2011; Wan et al., 2012). The role of NPH3 and other related proteins such as Root Phototropism Protein2 (RPT2; Sakai and Haga 2012) has to be further elucidated in order to understand their involvement in phototropic signaling.

Tomato has two phototropin genes-*phototropin1*, *phototropin2* and *Nps1* is a non-phototropic seedling mutant of tomato with mutation in *phot1* that resulted in disruption of protein function by regulating protein degradation (Sharma et al., 2014). This mutant displayed loss of both low and high blue light responses, no chloroplast accumulation under low intensity but avoidance under high light intensity, inability of stomata to respond to blue light and inhibition of opening of cotyledons. But, the role of phototropins in regulation of fruit pigmentation remains to be unveiled.

UVR8 is a UV-B photoreceptor that absorbs light in the wavelength region of 280-315 nm with the help of tryptophan residues that constitute potential chromophore (Rizzini et al., 2011). It was shown that both UVR8 and PHYB together function in sensing and adapting plant to different wavelengths of light, particularly under canopy conditions (Mazza and Ballare 2015). The diverse roles of UVR8 in regulating other plant processes, such as controlling fruit pigment accumulation is not known. The association of other classes of blue light photoreceptors such as Zeitlupe (ZTL), Lov Kelch Protein2 (LKP2) and Flavin binding, Kelch repeat, F-Box1 (FKF1) proteins (Suetsugu and Wada 2013) with fruit carotenoid metabolism has to be revealed in future.

In addition, previous reports indicate that manipulation of light signaling components also affects fruit carotenoid levels in tomato. The mutation in the genes from light signaling pathway including *ddb1* (*hp1*; Lieberman et al., 2004; Liu et al., 2004), *det1* (*hp2*; Mustilli et al., 1999) and RNAi mediated repression of *cop1like* increased carotenoid content in the fruits whereas silencing of *hy5* decreased carotenoid levels in the fruits (Davuluri et al., 2004; Liu et al., 2004; Davuluri et al., 2005). Another high pigment mutant, *Ip* also shows exaggerated photomorphogenesis similar to *hp1* and *hp2* but the information on the chromosomal location and association of the *Ip* gene with the carotenoid regulation has not been understood till now (Lavi et al., 2009). The enhanced level of carotenoids in the high pigment mutants, *hp1*, *hp2* and *hp3* (*zep*; Galpaz et al., 2008) is associated with increase in plastid (both chloroplast and chromoplast) number and size that enables the accumulation and storage of the high levels of carotenoids in these mutants (Kolotilin et al., 2007; Galpaz et al., 2008; Azari et al., 2010; Enfissi et al., 2010; Fig. 2.5; Fig. 2.6).

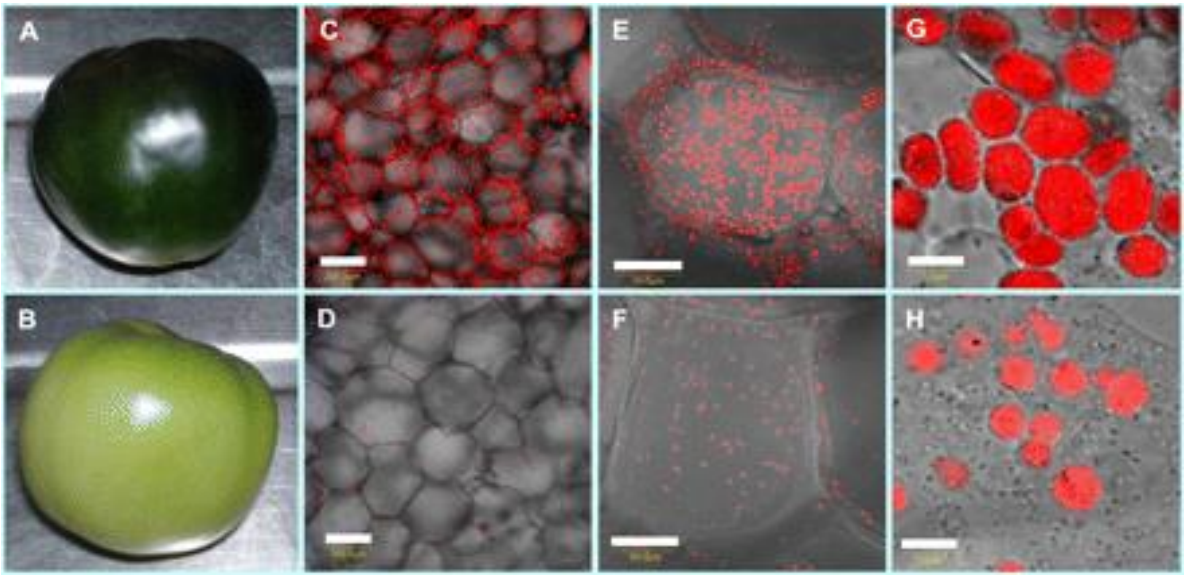


Figure 2.5. Visual display of the effects of *hp-2dg* mutation on chloroplast biogenesis in mature-green fruits compared to their normal controls. Images of *hp-2dg*/*hp-2dg* mutant fruits (A, C, E, and G) are shown relatively to their normal counterparts (B, D, F, and H). Whole fruits (A and B), pericarp tissue (C and D), single cells (E and F), and chloroplasts inside cells (G and H). Scale bars: C and D = 100 μm, E and F = 50 μm, G and H = 5 μm. Taken from Kolotiln et al., 2007.

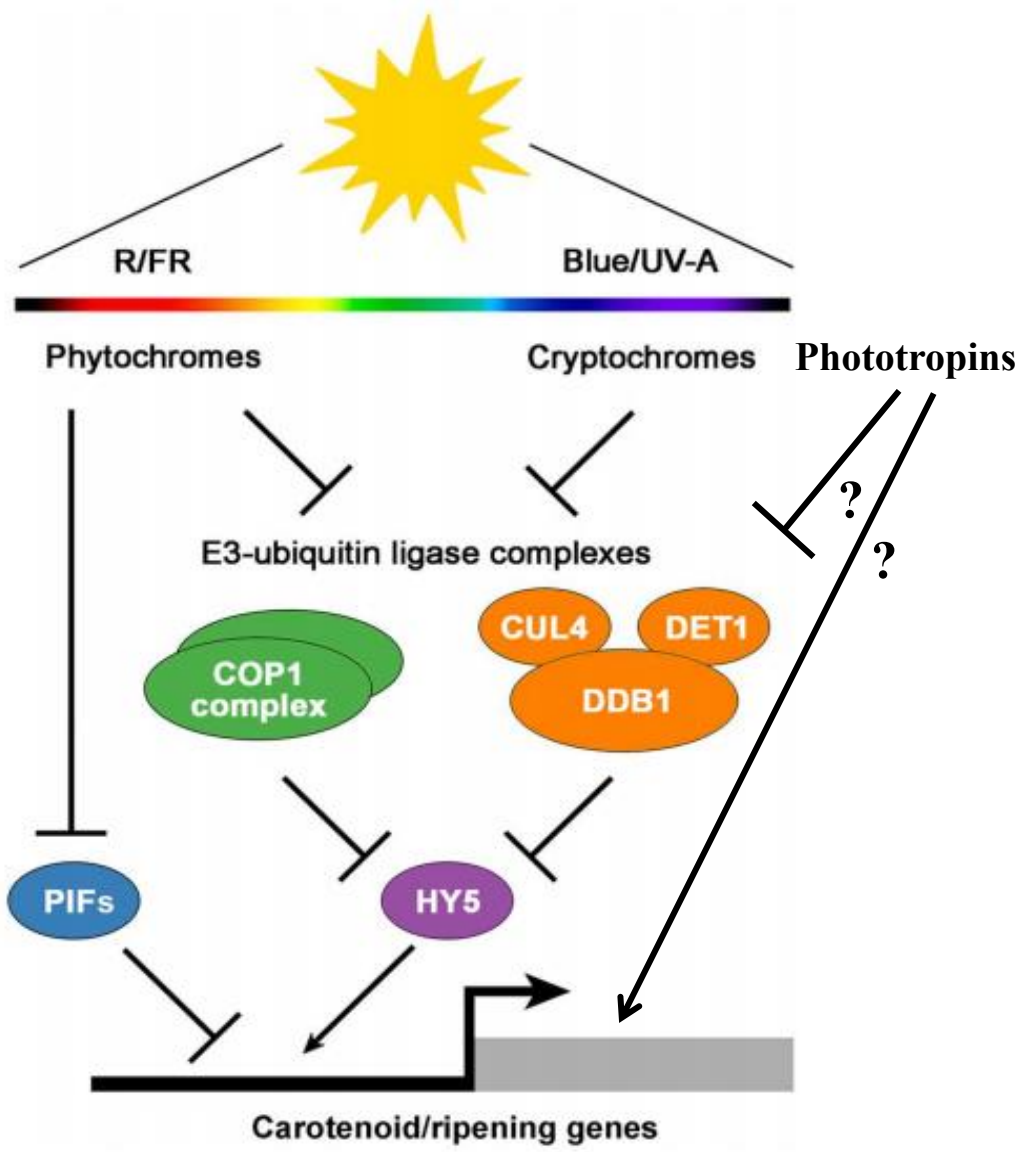


Figure 2.6. A simplified model of light signaling components involved in the regulation of tomato fruit pigmentation and ripening. Fruit-localized phytochrome and cryptochrome photoreceptors regulate the activity of the downstream E3-ubiquitin ligase COP1 and CUL4-DDB1-DET1 complexes, which in turn mediate the degradation of the transcriptional activator HY5. In addition, active phytochromes reduce the activity of transcriptional repressors such as PIFs. The mode of action of blue light receptors, phototropins in regulation of carotenoid gene expression is not known. The balance between activators and repressors finally modulates the expression of carotenoid and ripening-associated genes. R, red light; FR, far-red light; Blue, blue light; UV-A, ultraviolet-A light. Adapted from Lloronte et al., 2016.

Temperature: Temperature is one of the factors that affects fruit carotenoid accumulation. In tomatoes that are exposed to low temperatures below 12°C, the lycopene content was reduced and when exposed to high temperatures above 32°C, lycopene synthesis was completely inhibited (Dumas et al., 2003). High temperatures result in bleaching of tomato fruits, the effect more prominent in the shoulders of the fruits (Cocaliadis et al., 2014). During heat stress, the transcript of a small heat shock protein *hsp21* is induced which is involved in the prevention of aggregation of PSII components and assists in their refolding. The transgenic lines with high levels of HSP21 accumulated 10 times more carotenoids in developing fruits but not in mature green fruits indicating a secondary role of HSP21 in regulating carotenoid content in tomato fruits (Neta-Sharir et al., 2005).

Regulatory genes: Along with the biosynthetic genes that are directly involved in production of carotenoids, a complex network of transcription factors have been identified that regulate carotenoid accumulation in tomato fruits. The mutants and transgenics for transcriptional regulator genes such as *rin* (Vrebalov et al., 2002), *nor* (Tigchelaar et al., 1973), *Cnr* (Manning et al., 2006), *ful1* (Bemer et al., 2012), *ful2* (Shima et al., 2014), *glk2* (Powell et al., 2012), *aprr2-like* (Pan et al., 2013), *bzr1-1D* (Liu et al., 2014) display positive effects and *ap2a* (Chung et al., 2010), *tagl1* (Itkin et al., 2009; Vrebalov et al., 2009), *erf6* (Lee et al., 2012), *sgr1* (Luo et al., 2013) show negative effects on carotenoid accumulation. The study of ripening impaired mutants such as *rin* (*ripening inhibitor*), *nor* (*non-ripening*) and *Cnr* (*Colorless non-ripening*) revealed the ethylene independent mechanisms of fruit ripening. The genes mutated in *rin*, *nor* and *Cnr* encode transcription factors, MADS-RIN, NAC-NOR and SPB-CNR respectively that are involved in various ripening related processes such as fruit color and cell wall modification (Vreblov et al., 2002; Manning et al., 2006; Giovannoni et al., 2007). The exogenous application of ethylene does not induce ripening in the fruits of *rin* and *nor* (Vreblov et al., 2002; Tigchelaar et al.,1978). RIN regulates the expression of target genes by binding to its promoter at CArG sites and RIN binding sites are identified through Chromatin Immunoprecipitation (ChIP). RIN activates the expression of *psy1*, *ziso*, *crtiso*, and represses the expression of *lcyb* and *lcye*. RIN also regulates the expression of *nor*, *Cnr* and *rin* itself by binding to these promoters (Martel et al., 2011; Fujisawa et al., 2013).

The genes responsible for silique development and valve dehiscence in *Arabidopsis* are also identified in the tomato including *tagl1*, *ful1* and *ful2*. *tagl1* (*tomato agamous-like1*) is an orthologue of *shatterproof* (*shp*) gene of *Arabidopsis* which is involved in seed dispersal (Liljegren et al., 2004). In tomato, *tagl1* is evolved to function in fruit color formation along with regulating the seed dispersal. The transcript expression of *tagl1* increases in young fruits and at the onset of ripening. The overexpression lines of *tagl1* yield yellow fruits with decreased lycopene and ethylene levels. In these lines, the transcript levels of *psy1*, *lcyb* and *cycb* are also down-regulated, correlating with the low carotenoid levels. In addition, the expression of *tagll* is not influenced by the *rin* mutation (Itkin et al., 2009; Vrebalov et al., 2009). In tomato, *fruitful1* (*ful1*) and *fruitful2* (*ful2*) are homologous of *Arabidopsis* MADS box transcription factor genes, previously called, *tdr4* and *mbp7*. Both FUL1 and FUL2 interact with RIN and their gene expression increases during ripening. The single knock-down lines of *ful1* or *ful2* display less alterations in fruit pigmentation whereas the double-knock down lines exhibit reduced carotenoid levels with orange fruits suggesting the redundant function of FUL1 and FUL2 (Bemer et al., 2012). FUL1 and FUL2 together with RIN affect ethylene levels and contribute to the fruit softening (Shima et al., 2014).

ap2 (*apetala2*) is a homeotic gene that regulates floral development in Arabidopsis (Kunst et al., 1989). *ap2* is from *ap2*/*erf* (*ethylene response element*) family, also known as *ap2*/*erebp* (*ethylene responsive element binding protein*) family (Kim et al., 2006; Riechmann and Meyerowitz, 1998). *ap2a* has been identified in a microarray expression profiling study as the gene associated with fruit development (Alba et al., 2005). The mRNA levels of *ap2a* are low in immature green fruit but increases at breaker and breaker+3 stages and decreases afterwards. Suppression of *ap2a* through RNAi resulted in fruits that produce excess ethylene, which ripen early and are in orange color due to reduced lycopene and increased β-carotene content (Chung et al., 2010). Tomato *erf6* belongs to group VII of *ap2*/*erf* family of transcription factors containing conserved ERF domain (Nakano et al., 2006). This gene is identified to be associated with fruit ripening on the basis of its high expression in the ripening fruit and also because of its strong negative correlation with lycopene and β-carotene obtained from a large scale carotenoid and transcription factor correlation network analysis (Lee et al., 2012). The transcript levels of *erf6* is reduced in the fruits of ripening impaired mutants, *rin*, *nor* and *Nr*. Suppression of *erf6* through RNAi resulted in elevated ethylene and carotenoid levels in

the fruits. ERF6 binds to the promoters of genes from carotenoid pathway (*dxs*), *hsp21* and ethylene biosynthesis related genes such as *acs2*, *aco1* and *aco3* and negatively regulates their expression (Lee et al., 2012).

aprr2-like (*Arabidopsis pseudo response regulator2-like*) is another transcription factor identified through artificial neural network analysis on the basis of its enhanced expression at breaker stage of wildtype tomato fruits. In the overexpression lines of *aprr2-like*, enhanced chlorophyll content in green fruits and increased lycopene and β-carotene levels in red fruits along with increase in plastid number and area was observed (Pan et al., 2013). In tomato, uniform ripening trait is acquired by presence of *uniform ripening* (*u*) gene which codes for Golden2-Like (GLK) transcription factor that regulates the pattern and distribution of plastids in fruits (Powell et al., 2012). The loss of function of *u* gene confers uniform pale colored fruits in tomato. In tomato, two genes exists, *glk1* and *glk2* in which *glk1* is expressed in cotyledons and leaves whereas *glk2* is expressed in green fruit. Modifying *glk2* expression through constitutive promoter or through the use of promoters which express before ripening results in more chloroplasts, high starch and chlorophyll levels at green stage followed by increased abundance of carotenoids and sugars at red ripe stage in the fruits (Powell et al., 2012).

sgr (*stay-green*) gene code for chloroplast targeted protein that regulates senescence and chlorophyll degradation in plants (Hortensteiner, 2009). A mutation in *sgr1* in tomato resulted in *green-flesh* (*gf*) mutant with ripe fruits that consist of both chloroplasts and chromoplasts. As a result, *gf* fruit is in green-red color (Barry et al., 2008). Suppression of *sgr1* in tomato lessened chlorophyll degradation in fruits and leaves enhanced accumulation of lycopene and β-carotene in the fruits (Hu et al., 2011; Luo et al., 2013). SGR1 interacts with PSY1 in the nucleus and reduces *psy1* expression and enzyme activity.

Hormonal regulation: The regulation of carotenoid metabolism is linked with several developmental processes that are influenced by phytohormones such as ethylene, auxin, abscisic acid (ABA), jasmonate and brassinosteroids (Fig. 2.7). Ethylene is the major plant hormone that increases during ripening. As tomato is a climacteric fruit, two systems have been proposed for ethylene biosynthesis including system 1, which is autoinhibitory stage of ethylene production and system 2, which involves autocatalytic induction of ethylene (Barry et al., 2000). Ethylene is synthesized from methionine in three steps, known as Yang cycle (Yang and Hoffmann, 1984). In the first step, S-

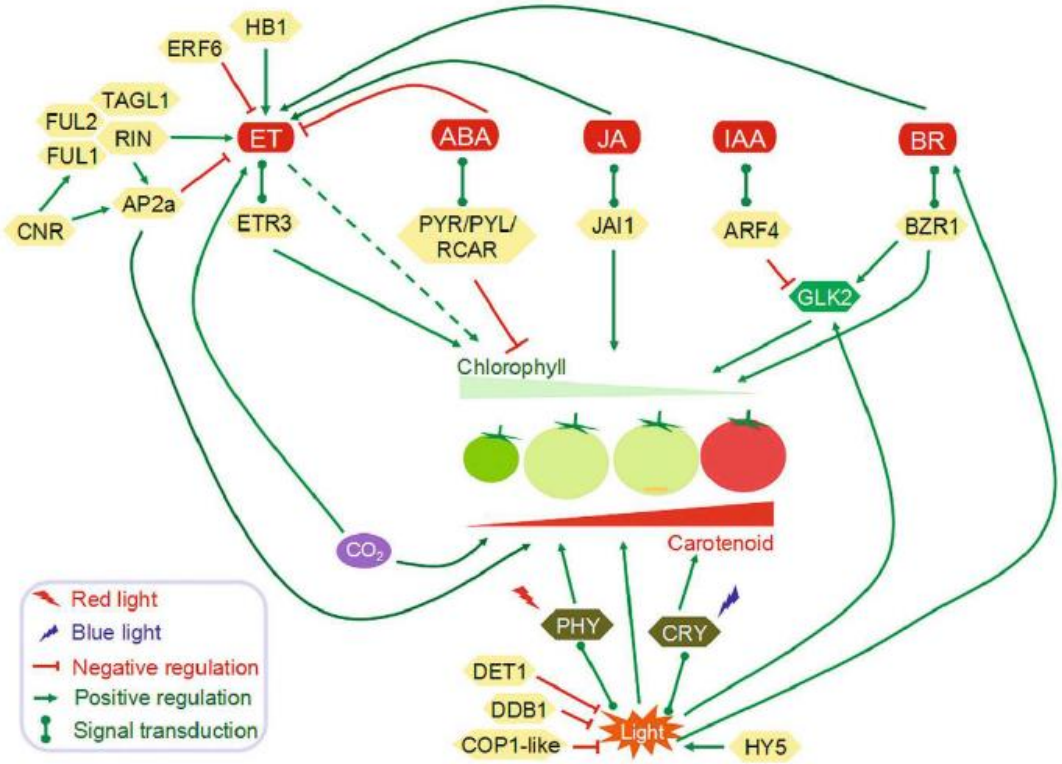


Figure 2.7. Roles of plant hormones, CO_2, light, and their interplay in carotenoid accumulation during tomato fruit ripening. The hexagons represent transcriptional factors and signaling components. ABA, abscisic acid; AP2a, apetala2; ARF4, auxin response factor 4; BR, brassinosteroids; BZR1, brassinazole resistant1; CNR, colorless non-ripening; COP1, constitutively photomorphogenic 1; CRY, cryptochrome; DDB1, UV-damaged DNA-binding protein 1; DET1, de-etiolated1; ERF6, ethylene response factor 6; ET, ethylene; ETR3, ethylene receptor 3; FUL1, fruitfull1; FUL2, fruitfull2; GLK2, golden2-like; HB1, an HD Zip homeobox protein; HY5, hypocotyl 5; IAA, indole-3-acetic acid; JA, jasmonic acid; JAI1, jasmonic acid-insensitive-1 (Li et al., 2003b); PHY, phytochrome; PYR/PYL/RCAR, pyrabactin resistance1/pyr1-like/regulatory components of ABA receptors; RIN, ripening inhibitor; TAGL1, tomato agamous-like. Taken from Liu et al., 2015.

adenosyl methionine (SAM) is synthesized from methionine through the action of SAM synthethase. In the second reaction, SAM is converted into 1-aminocycloproane 1-carboxylic acid (ACC) by the enzyme, ACC synthase (ACS) and in this reaction, 5′-methylthioadenosine (MTA) also formed as minor product which is recycled to methionine. In the third step, ethylene is synthesized from ACC by the activity of ACC oxidase (ACO). The fruits of antisense *acs2* transgenic lines produce less ethylene and exhibit longer shelf-life compared to wildtype fruits (Sobolev et al., 2014). In a similar way, antisense suppression of *aco* resulted in reduced fruit lycopene content and the fruits show longer post-harvest shelf life (Picton et al., 1993). The master regulator RIN also regulates the expression of ethylene related genes such as *acs2*, *acs4* and an ethylene receptor, *etr3*, also known as *Nr* (Martel et al., 2011; Fujisawa et al., 2013). The fruits of *rin* mutant, does not exhibit both climacteric ethylene production and lycopene accumulation (Vreblov et al., 2002). Similarly, the lycopene accumulation is not observed in the fruits of *Nr* mutant which is deficient in ETR3 and is perturbed in ethylene signaling (Lanahan et al., 1994). The expression of *aco1* is induced by transcription factor HB1, which is a HD-Zip homeobox protein that stimulate ethylene biosynthesis followed by color development in the fruits (Lin et al., 2008).

Along with ethylene, auxin is another phytohormone that regulates fruit ripening in tomato. Auxin is involved in delaying ripening process when applied exogenously on the fruits (Cohen 1996). During ripening, the levels of free auxin decreases and the abundances of IAA-amino acid conjugates increases which are necessary for inducing ripening (Bottcher et al., 2010). Auxin response factors (ARF) bind to the Auxin response elements (ARE) present in the promoters of auxin regulated genes and promote or repress their expression (Ulmasov et al., 1999). In the *arf4* antisense and cosuppressed lines of tomato, the mature green fruits show dark green color with more chlorophyll content and increased number of chloroplasts (Jones et al., 2002). This increase in plastid number in these lines is regulated by GLK1, as *glk1* consists of ARF binding motif in its promoter region (Sagar et al., 2013). The plant senescence hormone ABA is also implicated in enhancing plastid number. In the ABA deficient mutants of tomato including *hp3*, *flacca* and *sitiens*, the increase in chloroplast and chromoplast number is associated with enhancement of carotenoid levels (Galpaz et al., 2008). Suppression of *nced1* which is an ABA biosynthetic gene, resulted in increase in expression of *psy1*, with high ethylene levels and increased lycopene, β-carotene abundances in the fruits (Sun et al., 2012).

Silencing of *zfp2* (zinc *finger protein2*) resulted in enhanced accumulation of lycopene and β-carotene levels in fruits. *zfp2* negatively regulates ABA abundance by suppressing ABA biosynthetic genes in the fruits of *flacca*, *sitiens* and *notabilis* (Weng et al., 2015).

Jasmonate (JA) and methyl jasmonate (MeJA) are lipid derived plant growth regulators, which are involved in disease resistance, synthesis of volatiles and also influences fruit carotenoid content (Chen et al., 2006; Saniewski and Czapski 1983). In the fruits of jasmonate deficient mutants, such as *spr2* (suppressor of pro-systemin responses2) and *def1* (defective in octadecanoid synthesis pathway), the carotenoid content and ethylene levels are reduced whereas in constitutive jasmonate producing *35S::prosystemin* lines, the carotenoid and ethylene levels are increased. The application of MeJA to *Nr* fruits resulted in increased lycopene levels suggesting the independent action of JA on fruit carotenoid metabolism (Liu et al., 2012).

Brassinosteroids (BR) are another group of plant hormones that regulate seed germination, flowering and senescence. The application of brassinosteroids to the tomato fruit pericarp discs resulted in enhanced lycopene content (Vardhini and Rao, 2002). Similarly, the application of brassinosteroids to the *Nr* fruit discs elevated carotenoid content indicating that BR mediated fruit carotenoid accumulation is not influenced by *Nr* (Liu et al., 2014). *brassinozole resistant1-1D* (*bzr1-1D*) is a brassinosteroid (BR) gene involved in BR signaling which codes for BZR1 transcription factor. BZR1 regulates BR mediated cellular responses through a phosphorylation signaling pathway that affects stability and localization of BZR1 (Wang et al., 2002). The overexpression of *bzr1-1D* in tomato resulted in enhanced carotenoid content and increased sugar levels in the fruits during ripening. Consistent with high carotenoid levels, the expression of carotenoid biosynthetic genes such as *dxs*, *psy1* and *ggpps* also increased in these transgenic lines (Liu et al., 2014).

Epigenetic control: Epigenetic changes are heritable or non-heritable modifications that occur beyond the nucleotide sequences in the organisms. Various types of epigenetic modifications can occur in plants including methylation, phosphorylation and acetylation and ubiquitination of histones. These epigenetic changes are implicated in flowering, heterosis and a range of abiotic and biotic stresses (Dowen et al., 2012; King 2015; Schnable and Springer 2013). The hyper-methylation in the gene *Cnr* inhibits fruit color development. This is further confirmed with the appearance of red sectors on the fruits when treated with an inhibitor of methylation, azacytidine (Manning et al., 2006; Zhong

et al., 2013). In a similar way, silencing of *dml2* (*Demeter like DNA methylase2*) resulted in inhibition of initiation and advancement of fruit ripening due to hyper-methylation of ripening related genes (Liu et al., 2015).

Feedback inhibition: Feedback regulation has been considered as one of the regulatory mechanisms that influences carotenoid metabolism in tomato fruits. The tomato *tangerine* locus, *t* is epistatic over *yellow flesh*, *r* locus. The *cis*-carotene produced by *t* causes feedback regulation in tomato, whereas this regulation is ruled out in *tangerine* mutant as a result of which *psy1* expression is partially recovered in this mutant (Kachanovsky et al., 2012). In a recent study, when bacterial *crtI* is overexpressed in *tangerine* and *old gold crimson* mutants, it resulted in the accumulation of β-carotene. Metabolomic characterization of *crtI* lines revealed feedback regulation at the level of *psy1* and feedforward regulation of cyclases in the transgenic lines (Enfissi et al., 2017).

Carotenoid sequestration: Carotenoid sequestration and storage is also crucial for enhanced carotenoid accumulation in chromoplasts. Plastoglobules are lipid containing carotenoid sequestering structures associated with thylakoids and contain carotenoid biosynthesis enzymes (Austin et al., 2006; Brehelin and Kessler 2008). In *crtE*, *crtB* and *crtI* carotenogenic lines, the increased accumulation of carotenoids boosted the development of membranous structures in chromoplasts (Nogueira et al., 2013). In the above lines, the accumulation of carotenoid precursors and biosynthetic enzymes in different compartments in chromoplasts has been identified as an efficient method for sequestering and stabilizing carotenoids within tomato fruits (Nogueira et al., 2013, Fraser et al., 1994; Fraser and Bramley 2004).

Posttranscriptional and posttranslational regulation: Since chromoplasts are the sites for carotenoid synthesis and accumulation, chromoplast biogenesis also influences carotenoid metabolism (Li and Yuan 2013). The mutation in *Or*, the only gene known to be related to chromoplast biogenesis increases storage capacity of plastids by converting proplastids into chromoplasts in cauliflower, potato and melon (Lu et al., 2006; Tzuri et al., 2015; Lopez et al., 2008). In *Arabidopsis*, overexpression of *Or* resulted in increased PSY1 enzyme activity and phytoene accumulation whereas *Or* mutants exhibited reduction in PSY1 activity suggesting that OR proteins regulate carotenoid biosynthesis through posttranscriptional mechanisms (Zhou et al., 2015).

The carotenoid biosynthetic enzyme, DXS is recruited to Hsp70 proteins after interacting with plastidial J20 and this process is required for delivery of DXS to Hsp70 chaperone system. The HSp70 chaperone assists in proper folding of DXS that is essential for its enzyme activity (Pulido et al., 2013).

2.13 Systems biology approaches

The complete information on the function and molecular mechanisms of the above factors in regulating carotenoid metabolism is still lacking (Liu et al., 2015). A combination of "omics" technologies such as phenomics, genomics, proteomics and metabolomics has been considered as an essential means to understand the molecular events that trigger the carotenoid biosynthesis and degradation (Ricroch et al., 2011; Pirrello et al., 2009). The comparison of transcript or transcription factor profiles with metabolite abundances disclosed the regulatory networks of fruit ripening (Rohrmann et al., 2011; Osorio et al., 2011; Lee et al., 2012).

Proteomics is one of such "omics" technologies, which is a large scale study on identification, function and interactions of thousands of proteins present in the organism (Katam et al., 2015). While the genome of an organism is more or less constant, proteome always changes with time and environmental conditions (Holman et al., 2013; Smith et al., 2013). Proteomics has been used as an excellent technique to understand tomato fruit development (Saravanan and Rose 2004; Rocco et al., 2006; Faurobert et al., 2007; Xu et al., 2013), chloroplast to chromoplast differentiation (Barsan et al., 2012), fruit softening (Pan et al., 2014), effect of transcription factors such as RIN (Qin et al., 2012), NOR (Yuan et al., 2016), BZR1 (Liu et al., 2016) during fruit ripening. Proteomic analysis of chromoplasts from six crop species including tomato revealed species specific accumulation of proteins related to chromoplast biogenesis and development (Wang et al., 2013). Proteomic studies revealed that the increased accumulation of acetyl coenzyme A carboxylase D (ACCD) protein during early mature green stage in tomato Micro Tom mutant provides storage matrix for carotenoids thereby assists carotenoid accumulation in this mutant (Barsan et al., 2012). Further, an ubiquitin conjugating enzyme, UBC32 detected in the nuclear proteome of *rin* mutant modulates fruit coloration by directly binding with RIN (Wang et al., 2014).

Chapter 3

To decipher the molecular basis of enhanced carotenoid accumulation in *hp1* mutant of tomato

3.1 Introduction

Tomato high pigment mutants *hp1* (*hp1*, *hp1^{w}*), *hp2* (*hp2*, *hp2^{j}* , *hp2^{dg}*), *hp3*, and *intense pigment* (*Ip*) not only share characteristically high lycopene content but also exhibit an increased number and size of chloroplasts in leaves as well as in green fruits. This leads to a higher number of chromoplasts when the fruits ripen (Azari et al., 2010). *hp1* has a lesion in DNA Damage-Binding Protein1 (DDB1; Lieberman et al., 2004; Liu et al., 2004), while *hp2* encodes the Arabidopsis (*Arabidopsis thaliana*) homolog of Deetiolated1 (DET1; Mustilli et al., 1999) and the *hp3* mutant has a lesion in zeaxanthin epoxidase (Galpaz et al., 2008). However, the gene product for *Ip* is still unknown (Lavi et al., 2009). Similar to *hp1* and *hp2* mutants, *Ip* also shows exaggerated photomorphogenesis (Lavi et al., 2009). Due to their high lycopene, flavonoid, and vitamin C contents, *hp1* and *hp2* mutations have been introgressed into various breeding populations. One such introgression from *hp2^{dg}* resulted in a 3.5-fold increase in lycopene content in tomato fruits (Levin et al., 2003). Both DDB1 and DET1 seem to interact with Cullin4 (CUL4) and were found to be components of a CUL4-based E3 ubiquitin ligase complex (Wang et al., 2008). CUL4-DDB1 complexes have been shown to affect overall plant development (Bernhardt et al., 2006) and flowering (Chen et al., 2010), where they may affect the epigenetic control of flowering. Analysis of double mutants of *ddb1a* and *ddb1b* showed that DDB1 is critical for embryo development in Arabidopsis (Bernhardt et al., 2010).

Manipulation of light signalling components appears to be a good strategy to improve tomato fruit quality, as shown by fruit-specific RNA interference (RNAi) mediated suppression of *DET1* and repression of *LeCOP1LIKE* genes, which resulted in increased carotenoid levels (Liu et al., 2004; Davuluri et al., 2005). Similarly, repression of *cul4* and fruit-specific repression of *hp1*/*ddb1* by RNAi resulted in increased plastid compartment size and enhanced pigmentation of tomato fruits (Wang et al., 2008). Disrupting the function of all or any of these light signaling components seems to affect plastid biogenesis, leading to an increased number of plastids with greater storage capacity for the carotenoids and/or pigments (Liu et al., 2004; Kolotilin et al., 2007). Likewise, the deficiency of abscisic acid (ABA) also seems to result in a similar high-pigment phenotype (Galpaz et al., 2008). In all the above cases, the efficient conversion of chloroplasts to chromoplasts is necessary to accumulate the high amount of synthesized carotenoids.

A number of changes occur during the conversion of chloroplasts to chromoplasts. The first is the disintegration of thylakoid membranes, followed by loss of chlorophyll, increase in the number of plastoglobules, accumulation of lycopene, and increase in the number of stromules, etc. (Bian et al., 2011). Plastoglobules, besides accumulating lipids, also accumulate carotenoids either in the crystalline form, as seen in tomato (Klee and Giovannoni, 2011), or the fibrillar form, as observed in bell pepper (*Capsicum annuum*; Pozueta-Romero et al., 1997). In addition, these plastoglobules also appear to be involved in regulating carotenoid metabolism, as enzymes such as ζ-carotene desaturase, lycopene β-cyclase, and β-carotene hydroxylases are present in them (Ytterberg et al., 2006). Furthermore, proteins called plastoglobulins are associated with plastoglobules and help in the accumulation of carotenoids. These include fibrillin, also known as CHRB or plastid lipid-associated protein (PAP) from pepper chromoplast fibrils, and chromoplast-associated carotenoid binding protein (CHRC) and CHRD from petals of cucumber (*Cucumis sativus*; Vishnevetsky et al., 1999). The expression of plastoglobulin genes appears to be under strict spatial and temporal regulation and well-coordinated with the expression of carotenoid biosynthetic genes like *psy1* in tomato fruits (Giuliano et al., 1993; Vishnevetsky et al., 1999).

All the plastoglobulins share a hydrophobic domain of 17 to 19 amino acids, and this region seems to be important for carotenoid-protein interactions (Vishnevetsky et al., 1999). The significance of the above-mentioned plastoglobulins in the sequestration and storage of carotenoids was elegantly exemplified in two studies (Leitner-Dagan et al., 2006; Simkin et al., 2007). Overexpression of a pepper *fibrillin* gene in tomato resulted in a 2-fold increase in carotenoid levels as well as carotenoid-derived volatiles (Simkin et al., 2007), whereas down-regulation of *CHRC* in tomato led to a 30% reduction of carotenoids in the flowers (Leitner-Dagan et al., 2006). Moreover, a delayed loss of thylakoids was observed during chromoplastogenesis in *fibrillin*-overexpressing tomato (Simkin et al., 2007). In addition, the *Or* gene of cauliflower (*Brassica oleracea*), which encodes a DnaJ Cys-rich zinc finger domain-containing protein, is also targeted to plastids and seems to control carotenoid accumulation by stimulating the formation of chromoplasts (Lu et al., 2006; Zhou et al., 2008; Li et al., 2012). All these studies suggest that manipulation of carotenoid sequestration and storage by stimulating chromoplastogenesis to create a metabolic sink might be an alternative strategy to increase carotenoid levels in food crops.

Currently, using systems biology approaches, efforts are being made to understand the complex interplay of ripening-related pathways wherein transcriptome, proteome, and metabolome are examined and attempts are made to interlink them (Osorio et al., 2011). Such a study in *rin*, *nor*, and *Nr* mutants led to a comprehensive understanding of ethylene-regulated processes during ripening and also reinforced the need for the integration of transcript, proteome, and metabolite analyses (Osorio et al., 2011). In the *hp1* mutant, transcription factor profiling was combined with microarray and metabolite analyses, and that study revealed that the secondary metabolism is controlled at the transcriptional level (Rohrmann et al., 2011). Using fruit-specifically down-regulated *DET1* tomato lines, Enfissi et al. (2010) showed the significance of posttranscriptional regulation in modulating carotenoid and isoprenoid biosynthesis.

On the other hand, several proteomics studies have been carried out in tomato (Rocco et al., 2006; Faurobert et al., 2007; Manaa et al., 2011; Osorio et al., 2011) as well as other fruits like strawberry (*Fragaria* spp.; Bianco et al., 2009), grape (*Vitis vinifera*; Zhang et al., 2008), and *Citrus* spp. (Zeng et al., 2011) and also in isolated chromoplasts (Siddique et al., 2006; Barsan et al., 2010). This led to global understanding of the changes in protein profiles accompanying ripening. Several recent studies examining the linkage between gene expression and the metabolite levels during tomato fruit ripening also highlighted the need for more comprehensive network approaches (Carrari and Fernie, 2006; Mounet et al., 2009; Rohrmann et al., 2011). Considering this, and given the importance of the *hp1* mutant for improving the phytonutrient quality, we undertook a proteomic approach to decipher the role of DDB1 in tomato fruit ripening, as information on the proteome complement of *hp1* is lacking. In this study, the proteome profiles of outer pericarp in both wildtype and *hp1* fruits were compared at different stages during ripening.

3.2 Materials and methods

3.2.1 Plant material and experimental design

Fruits of tomato photomorphogenic mutant, *high pigment1* (*hp1*) and its isogenic wildtype Ailsa Craig (AC, Srinivas et al., 2004) were obtained from the Tomato Genetics Resource Centre (University of California, Davis) and used for proteomic analysis in this study. Tomato seeds were surface sterilized with 4% (v/v) sodium hypochlorite (Qualigens) solution for 10 min, washed thoroughly with distilled water, and kept in dark

on blotting paper for germination. Germinated seeds were transferred to vermiculite (Karnataka Explosive Ltd.) and after 15 days of growth, seedlings were transferred to pots in the greenhouse, and were maintained till maturity under natural photoperiod at 28±1°C during day and ambient temperature at night. Plants of both the wildtype and *hp1* were grown in three randomized blocks, (each block constituting one biological replicate) with each block consisting of three rows, with five plants each for the wildtype and *hp1* per row (Fig. 3.1). To minimize variation, fruits developed on the first and second truss only were used for experiments. The flowers were tagged at the time of anthesis for chronological monitoring of fruit developmental stages (Fig. 3.2A). The fruits were harvested at different ripening stages, mature green (MG, 35 DPA), breaker (BR, 40 DPA) and red ripe (RR, 49 DPA). From each block, (biological replicate), 30 to 35 fruits per ripening stage per genotype were harvested, and the outer pericarp was pooled separately at every ripening stage for both the wildtype and *hp1* (Fig. 3.1), flash frozen in liquid nitrogen, stored at -80°C until use.

3.2.2 Plant material used for protein, transcript and carotenoid analysis

Fruits of both wildtype and *hp1* were collected at different ripening stages as described above. Since a temporal difference in the synthesis of carotenoids in the outer and inner pericarp was observed in the *hp1* mutant, an independent study was initiated on both outer and inner pericarp. The outer pericarp is the outer layer of the fruit including skin, (Fig. 3.2B); its thickness is measured with Vernier callipers and varies from 0.5 ± 0.1 mm in MG and BR to 0.3 ± 0.1 mm in RR (Fig. 3.2B, C). The outer pericarp was carefully excised from fruits at different ripening stages and from all biological replicates using a scalpel, pooled, flash frozen in liquid nitrogen, and stored at -80°C until further use. This tissue was used for proteome, transcript and carotenoid analyses.

3.2.3 Protein extraction

Proteins were extracted from fruit outer pericarp tissue using the protocol previously described (Isaacson et al., 2006) with slight modifications. About 1 g of tissue was homogenized in liquid nitrogen and suspended in 7 mL of extraction buffer containing 0.7 M sucrose, 0.1 M KCl, 0.5 M Tris pH 7.5, 50 mM EDTA, 50 mM dithiothreitol (DTT), 1 mM phenylmethylsulfonyl fluoride (PMSF) and 25 µL protease inhibitor cocktail (Sigma-Aldrich). To this, an equal volume of Tris-saturated phenol was added and the sample was mixed thoroughly by shaking at 4ºC for 30 min. The mixture

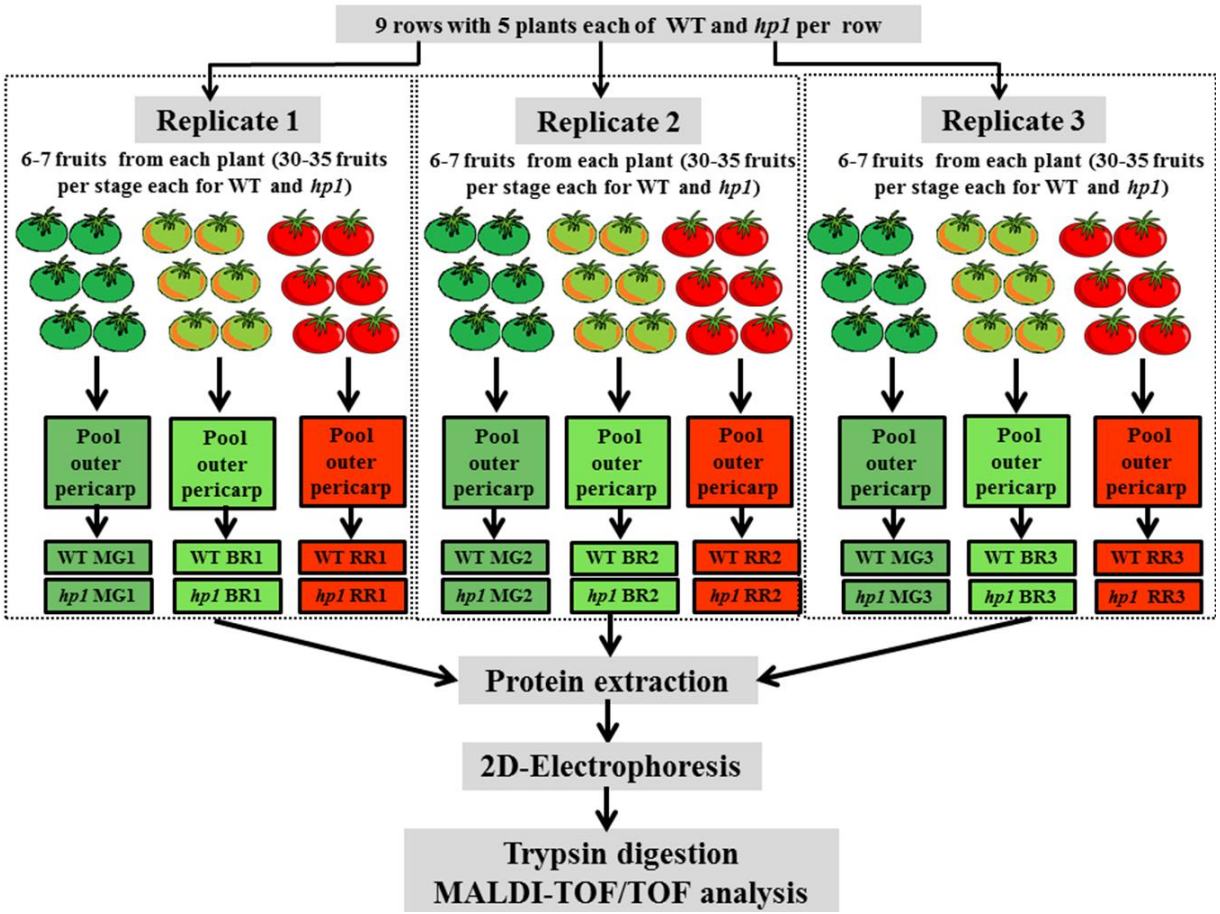


Figure 3.1. Randomized block design describing growth of plant material, collection of fruit tissue at different stages of ripening in three biological replicates for 2D electrophoresis and protein identification.

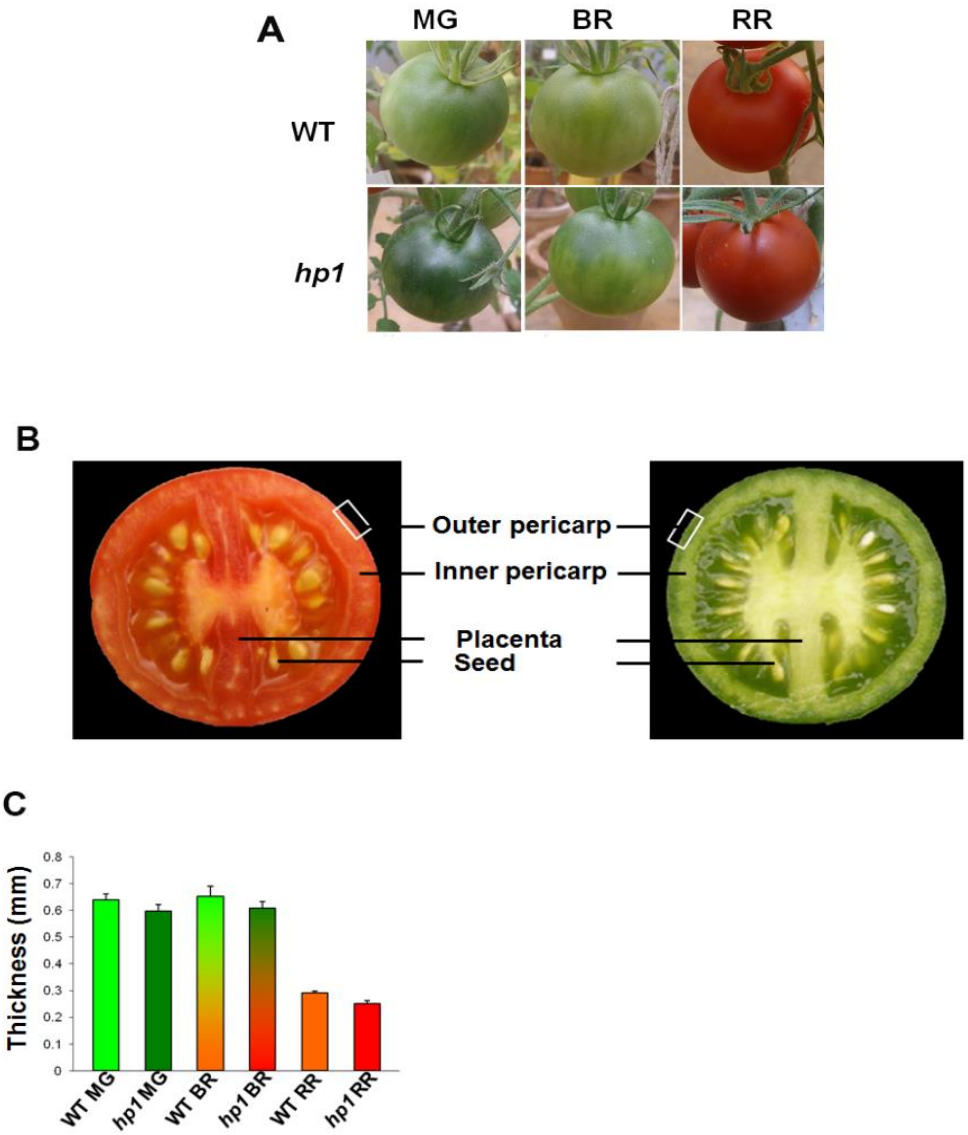


Figure 3.2. A, Phenotypes of wildtype (WT) and *hp1* fruits at MG, BR and RR stages during ripening. B, Visualization of outer pericarp in green and red fruits of tomato. C, Outer pericarp thickness was measured using Vernier Caliper.

was centrifuged at 20,000*g* for 30 min at 4°C. The upper phenolic phase was collected and reextracted two times as described above. The protein in the phenolic phase was precipitated at -80°C by adding 5 volumes of 0.1 M ammonium acetate containing 50 mM DTT and the protein was pelleted by centrifugation at 26,200*g* for 30 min at 4°C. The protein pellet was washed twice with methanol containing 10 mM DTT and once with acetone with 10 mM DTT, and finally dissolved in lysis buffer (7 M urea, 2 M thiourea, 4% [w/v] 3-(3-cholamidopropyl) dimethylammonio-1-propanesulfonate (CHAPS)). The protein was quantified using Amido Black method (Goldring and Ravaioli, 1996). For each developmental stage, at least three biological replicates were used in three independent extractions.

3.2.4 Two dimensional gel electrophoresis

Proteins (500 µg) were dissolved in 250 µL rehydration buffer (7 M urea, 2 M thiourea, 4% [w/v] CHAPS, 50 mM DTT and 1% [v/v] ampholytes [pH 4-7]) and applied to 13 cm Immobiline dry strips, pH 4 to 7 (GE Healthcare) by passive rehydration overnight. Isoelectric focusing was carried out at 20°C in Ettan IPGPhor 3 (GE Healthcare) and the settings used were as follows: 150 V for 1 h, 250 V for 1 h, 500 V for 1 h, 1,000 V for 30 min, 8,000 V for a total of 40,000 V h with a maximum current of 50 μA per strip. After isoelectric focusing, the strips were equilibrated first in buffer containing 6 M urea, 0.075 M Tris, 2% (w/v) SDS, 30% (v/v) glycerol, and 2% (w/v) DTT for 20 min. In the second step, 2.5% iodoacetamide was used instead of DTT in the same buffer for another 20 min. Then the strips were layered on 13% (w / v) acrylamide gels and sealed with agarose (0.65% [w/v] in 1X electrode buffer) for separation in the second dimension using Ruby SE600 electrophoresis set up (GE Healthcare). SDS-PAGE was carried out at 20 mA for initial 1 h and 30 mA for next 3.5 h or until bromophenol blue dye reached the end of the gel. Following SDS-PAGE, the gels were rinsed with MilliQ water two or three times, fixed for 1 h in methanol:water:acetic acid (5:4:1, v/v/v) and stained for 16 to 18 h in colloidal Coomassie stain (0.08% [w/v] Coomassie Brilliant Blue G-250, 20% [v/v] ethanol, 8% [w/v] ammonium sulphate and 0.35 M phosphoric acid). Gels were destained for 24 h in deionised water with several changes on a shaker and after completion of destaining, gels were stored in 20% (v/v) methanol.

3.2.5 Image visualization and analysis

A total of 18 gels (two genotypes, three ripening stages and three biological replicates at every ripening stage) were scanned using Image Scanner (GE Healthcare) and images were analysed with Image Master 2D Platinum Software 6.0 (GE Healthcare) as per manufacturer's instructions. About 800 spots were detected and matched. Spots that matched automatically on all the gels in both the wildtype and *hp1* were also manually verified. The percentage spot volumes were statistically analysed using one-way ANOVA (Sigmaplot version 11.0) and the spots showing two fold differences (up- and down-regulation in at least one of the stages during ripening) in all three biological replicates with $P \leq 0.05$ were considered for identification by mass spectrometry. The power of the test was determined as 0.9 to 0.99 using one-way ANOVA from the percentage spot volumes.

3.2.6 Trypsin digestion

The spots selected for further identification by MALDI-TOF/TOF analysis were manually excised and digested with trypsin (sequencing grade; Promega) as described in Shevchenko et al., 2006. Briefly, the gel pieces were washed with 50 mM ammonium bicarbonate and 50% [v/v] ACN. The gel pieces were then completely dried with 100% ACN for 20 min after removing 50% [v/v] ACN. The dried gel pieces were kept for overnight digestion with trypsin (1:50; enzyme: protein) in 50 mM ammonium bicarbonate at 37°C. The peptides were eluted twice with 2:1 [v/v] ACN: water, added with 0.1% TFA for 30 min using sonication. Eluted peptide fragments were concentrated in 5 µL of 1:1 (v/v) acetonitrile and 1% (v/v) trifluoroacetic acid.

3.2.7 Mass spectrometry

Peptide fragments (2 µL) obtained after trypsin digestion were mixed with 2 µL of *α*-cyano-4-hydroxycinnamic acid matrix (freshly made in 50% [v/v] ACN and 1% [v/v] trifluoroacetic acid (1:1 [v/v]), spotted onto MALDI target plate and dried. Tandem mass spectrometry (MS/MS) analyses were carried out using AutoFlex III smartbeam MALDI TOF mass spectrometer (Bruker Daltonics). TOF spectra within the range of 500 to 4000 mass-to-charge ratio (*m/z*) were obtained using Flex Control software 3.0 (Bruker Daltonics) in the reflector mode with a laser intensity of 6,000 V and an average of 2,000 shots per spectrum. The mass spectra obtained were calibrated with external standards with masses ranging from 757.399 to 3147.4710 *m/z*. Trypsin autolysis peaks were used for internal calibration and they are as follows: trypsin (108-115; *m/z* 842.509400),

trypsin (98-107; *m/z* 1,045.563700), trypsin (58-77; *m/z* 2,211.104000), trypsin (78-97; *m/z* 2,283.180200), trypsin (58-72; *m/z* 1,713.808400), trypsin (62-77; *m/z* 1,774.897500) and trypsin (58-76; *m/z* 2,083.009600). A range of two to ten precursor ions were selected for MS/MS analysis. Monoisotopic mass was attributed using Bruker's Sophisticated Numerical Annotation Procedure by collecting data from an average of 5,000 laser shots at a threshold intensity of 2,500 over the mass range. Peak lists from mass spectrometry and MS/MS analyses were generated using Flex Analysis software 3.0 (Bruker Daltonics). Proteins were identified using MASCOT (http:// www.matrixscience.com; Matrix Science) with the help of Biotools software (Bruker Daltonics). The following parameters were set for searches against target databases such as National Centre for Biotechnology Information nonredundant (downloaded on October 1, 2012; 20,543,454 sequences, 7,050,788,919 residues), SwissProt (downloaded on October 1, 2012; 537,505 sequences, 190,795,142 residues) and Plant EST (downloaded on October 1, 2012; 157,988,786 sequences, 27,903,646,510 residues): (1) tryptic cleavage with a maximum of two missed cleavages; (2) mass tolerance of 30-100 ppm; (3) peptide mass tolerance of 0.1 to 1.0 D; (4) a minimum of two peptides matching the protein; (5) fixed and variable modifications like carbamidomethylation of Cys and Met oxidation respectively. In addition, the peak lists were also searched in SGN (offline from Mascot) at the link ftp://ftp.solgenomics.net/genomes/Solanum_lycopersicum/annotation/ITAG2.3_release/ITAG2.3_proteins.fasta. The false discovery rate for the statistically significant proteins was found to be 5% using the Benjamin and Hochberg method (Benjamini and Hochberg, 1995; Eravci et al., 2009).

3.2.8 Hierarchical clustering

PermutMatrix software version 1.9.3 was used to generate hierarchical clustering (Pearson's algorithm; Caraux and Pinloche, 2005). The data file with all identified proteins together with their expression profiles were given as input and a cluster map along with protein expression profile was generated.

3.2.9 RNA isolation and quantitative real time PCR

RNA was isolated from wildtype and *hp1* fruits at three ripening stages, MG, BR and RR (each with three biological replicates) using TRI reagent (Sigma-Aldrich) according to manufacturer`s protocol. The isolated RNA was treated with RQ1 RNase Free DNase (Promega) according to manufacturer's recommendations to remove DNA.

Reverse transcription was performed with 2 μg of RNA using Superscript III RT First Strand Synthesis Kit (Invitrogen) according to manufacturer's protocol. Quantitative real-time PCR was performed with around 4 ng of total RNA in 10 μL reaction volume using SYBR Green PCR Master Mix (Takara) on a 7300 Fast Real Time PCR System (Applied Biosystems; http://www.appliedbiosystems.com/). Gene specific primers were designed from the sequences obtained from SGN database using Primer 3 software and represented in Annexure1. The relative fold differences for each sample were determined by normalizing cycle threshold (Ct) values of each gene to the mean expression of both *β-Actin* and *Ubiquitin* genes and were calibrated using the equation $2^{-\Delta Ct}$, which gives the relative expression of each gene. Mean ± SE (Sigmaplot version 11.0) cycle threshold values obtained from three biological replicates were used for calculation of expression levels.

3.2.10 Determination of ethylene evolution

Ethylene was measured form the fruits using the protocol as described in Santisree et al., 2011. Briefly, after harvesting, the fruits were enclosed in air tight boxes (250 mL). After 4 hours, 1 mL of head space gas was removed from the boxes and injected into a Porapak T column connected to a gas chromatograph (GC-17A; Shimadzu) equipped with flame ionization detector. The column and detector temperature was set at 110°C and 135°C respectively. As a standard, 20 µL of pure ethylene (Chemtron science Laboratories Pvt. Ltd) was injected. The area of chromatogram from the ethylene standard was used for estimating the ethylene present in the sample. For every sample, ethylene in the headspace gas was measured at least three times using a minimum of three biological replicates at each ripening stage.

3.2.11 Estimation of carotenoids

Carotenoids were extracted from fruits and estimated using a previously described procedure (Barba et al., 2006). Carotenoids were separated and analysed by HPLC (Shimadzu) on a C-18 column (250 x 4.6 mm, 5 μm; Phenomenex) using a 60 min isocratic gradient of methanol: acetonitrile (90:10, v/v) plus trimethylamine (9 µM) as mobile phase. Carotenoids were identified and quantified based on the retention times and peak areas of the standards (lycopene [L-9879] from tomato, β-carotene [C-4582] and lutein [X-6250]; Sigma-Aldrich), and β-carotene, lutein and lycopene contents were

determined by monitoring A_{475} (Barba et al., 2006) using a UV-visible detector (SPD 20 A; Shimadzu).

3.2.12 Isolation of Plastoglobules

Plastoglobules were isolated from tomato fruits at the RR stage using a method adapted from two protocols: the procedure of Besagni et al. (2011) and that of Lundquist et al. (2012). About 400 g of fruit tissue was ground in 400 mL of cold homogenization buffer (450 mM sorbitol, 20 mM Tricine-KOH, pH 8.4, 10 mM EDTA, 10 mM $NaHCO_3$, 1 mM $MnCl_2$, 5 mM sodium-ascorbate, 0.05% [w/v] bovine serum albumin fraction V and 1 mM PMSF). The homogenate was filtered immediately through four layers of 20 µm Miracloth and the filtrate was distributed equally into eight 50 ml tubes and then centrifuged for 10 min at 1,200*g*. Each chromoplast membrane pellet was gently resuspended in 4 to 5 ml of 0.6 M Sucrose/1X TrE (10X stock solution has 50 mM Tricine-KOH, pH 7.5, 2 mM EDTA and 2 mM DTT) and these were pooled into 50 ml falcon tube. The membrane fraction was then sonicated five times for 40 s each on ice at an amplitude of 23% with a 3 min interval between sonications (Sonics and Materials; Vibracell VCX 130PB). The samples were disbursed in 5 to 6 ml aliquots into the required number of UltraClear SW28 tubes and then carefully overlaid with the Sucrose/1X TrE solutions in the following order: 6ml of 38% (w/v) Sucrose, 6 ml of 20% (w/v) Sucrose, 4 ml of 15% (w/v) Sucrose and finally 8 ml of 5% (w/v) Sucrose to the top of the tube. These gradients were centrifuged for 16h in a Beckman Coulter Optima L-90K centrifuge at 100,000*g*. The plastoglobule rich fraction was then collected from the top layer.

The plastoglobule fraction thus obtained was dialyzed against 1X TrE buffer using a 3500 MWCO membrane (Thermo Scientific) and the protein was precipitated from the plastoglobule fraction using methanol-chloroform as essentially described by Besagni et al. (2011). After precipitation, the protein was resuspended in sample buffer, boiled and then separated by 12% SDS-PAGE followed by western blotting with CHRC antibody (Western blot experiment was performed by Mr. Rakesh).

3.2.13 Western blotting

The outer pericarp of tomato fruit (from each genotype, three biological replicates were used) was homogenized in extraction buffer (200 mM Tris, pH 8.0, 150 mM NaCl, 2.5 µL of protease inhibitor cocktail per 1 mL of extraction buffer [Sigma], 1 mM PMSF,

and 0.125% [v/v] Triton X-100) and centrifuges at 13000g at 4°C for 15 min, and the supernatant was collected. The protein content was quantified by the method of Bradford (1976). After 12% SDS-PAGE (Laemmli, 1970), proteins were electro blotted onto a polyvinylidene difluoride membrane (Millipore; Towbin et al., 1979). The blots were incubated with a 1:2500 dilution of antibodies raised against bell pepper (Capsicum annuum) PAP protein followed by anti-rabbit IgG alkaline phosphatase conjugate (1:80000 dilution; Sigma-Aldrich). The blots were finally developed using chromogenic substrate for alkaline phosphatase, 66 µL of nitro blue tetrazolium (50 mg mL^{-1}) and 33 µL of 5-bromo-4-chloro-3-indolyl phosphate (50 mg mL^{-1}) in 10 mL of buffer (100 mM Tris-HCl, 100 mM NaCl and 5 mM MgCl2, pH 9.5; Sreelakshmi, 2000). This experiment was performed by Mr. Rakesh.

3.2.14 Confocal microscopy of isolated plastoglobules

Confocal images of purified plastoglobules were obtained with a laser scanning confocal microscope (Carl Zeiss; LSM710 NLO) coupled to an inverted microscope (with non-descanned detector multiphoton laser). Freshly isolated plastoglobules were placed on a glass slide and covered with a cover slip. The carotenoid autoflourescence from the isolated plastoglobules was examined by measuring the emission between 500 and 510 nm (green) and chlorophyll emission was measured between 740 and 750 nm (red) after excitation with a laser at 488 nm.

In addition, the absorption spectrum for carotenoids from the plastoglobule fraction was obtained as follows. To about 100 *µ*l of freshly isolated plastoglobule fraction, an equal volume of *n*-hexane was added and mixed thoroughly. The mixture was centrifuged at 12,000*g* for 5 min and the supernatant was dried in a SpeedVac. After drying, the sample was dissolved in 6 µl of *n*-hexane and the absorption spectra for 1.5 µl were recorded three times in a Nanodrop spectrophotometer (ND1000; Thermo Scientific) from 350 to 700 nm.

3.3 Results

3.3.1 Proteome analysis in wildtype and *hp1* fruits

hp1 fruits are characteristically different from wildtype fruits, they are dark green in colour at the mature green (MG) stage (Fig. 3.2A) and dark red at the red-ripe (RR) stage (Fig. 3.2A). In view of this, the proteome profiles at both these stages were characterized. An intermediary breaker (BR) stage where the fruit makes transition, marking the onset of

the ripening process was also included. Consistent with the earlier reports, loss of function of DDB1 led to an enhanced accumulation of lycopene in tomato fruits (Fig. 3.3A). But no statistically significant change in β-carotene was observed in *hp1* fruits. In addition, the RR fruits of *hp1* displayed 3-fold higher levels of lutein (Fig. 3.3B). In contrast, ethylene, an important regulator of fruit ripening, although elevated in *hp1* at the MG stage, declined considerably at the BR stage of fruit development (Fig. 3.3C).

A randomized block design was used to grow the tomato plants. The fruit sampling for all three biological replicates was independently carried out according to the scheme shown in Fig. 3.1. For proteome profiling, the proteins extracted from the outer pericarp of wildtype and *hp1* fruits (Fig. 3.2) were analysed. Representative two-dimensional gel electrophoresis images comparing the above three stages in wildtype and *hp1* fruits are shown in Fig. 3.3D. Image analysis of the gels (n=3) with the Image Master Platinum software revealed about 800 proteins on each gel. Seventy two proteins were found to be differentially expressed by at least two fold (overexpression or underexpression; statistically significant expression based on ANOVA with $P \leq 0.05$) in both mutant and wildtype fruits in at least one stage during ripening, representing about 9% of spots on the gel. Notwithstanding the distinct phenotype of *hp1* fruits, we did not find any proteins specific to the wildtype or the mutant alone. This indicates that the subtle changes in proteome profile may be responsible for the specific phenotype of *hp1* fruits. To ascertain this, we identified the molecular nature of differentially expressed proteins to reveal any development-specific fine-tuning in the expression of specific proteins in both the mutant and the wildtype. The differentially expressed protein spots (Figs. 3.3D and 3.4) were excised from the gel and after digestion with trypsin, subjected to matrix-assisted laser-desorption ionization (MALDI)-time of flight (TOF) analysis. Of the 72 spots, 51 were successfully identified using Matrix Science's Mascot search engine. For 17 spots, no firm identity could be assigned. For the remaining four spots, only a single peptide match was obtained that appeared to be statistically significant (Table 3.1). On comparing these differentially expressed proteins with the proteins identified from cherry tomato (Faurobert et al., 2007), tomato ecotypes (Rocco et al., 2006) and the *rin* mutant (Qin et al., 2012), our study revealed 14 additional proteins (Table 3.2) that were not detected in any of the above studies. Nevertheless, such variations between different studies are expected, considering the diversity in the genotypes of different cultivars and mutants, sampling tissue and stages, the methods used for protein extraction, etc.

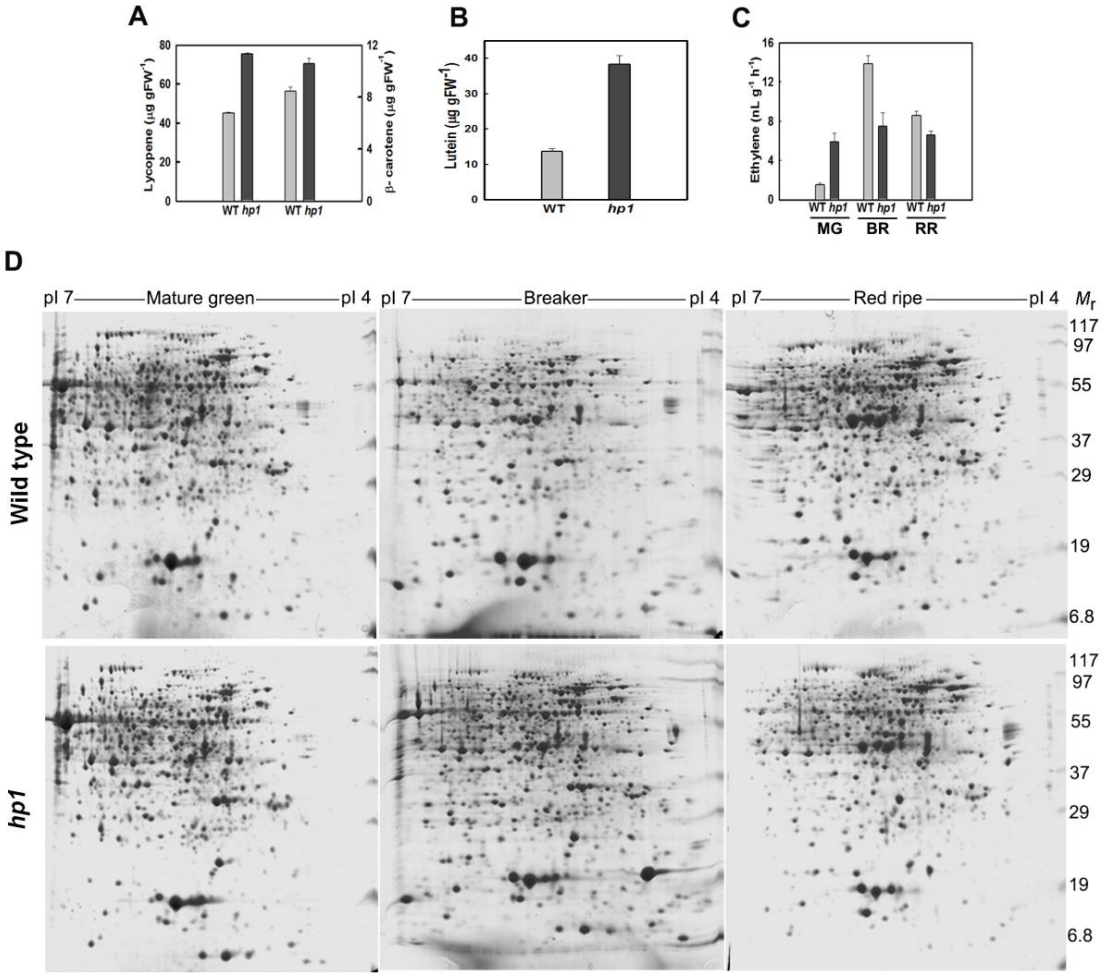


Figure 3.3. Characterization of the phenotypic and metabolic differences between wildtype and *hp1* fruits. A, Levels of lycopene (left) and β-carotene (right) in fruits of the wildtype (WT) and *hp1* (n > 3). B, Lutein levels in fruits of *hp1* and the wildtype (WT; n > 3). C, Ethylene emission from wildtype (WT) and *hp1* fruits at different stages of ripening (n > 3). FW, Fresh weight. Error bars indicate SE. D, Comparison of pericarp proteome profiles isolated from wildtype and *hp1* fruits at MG, BR, and RR stages. Representative images from two-dimensional gel electrophoresis are shown.

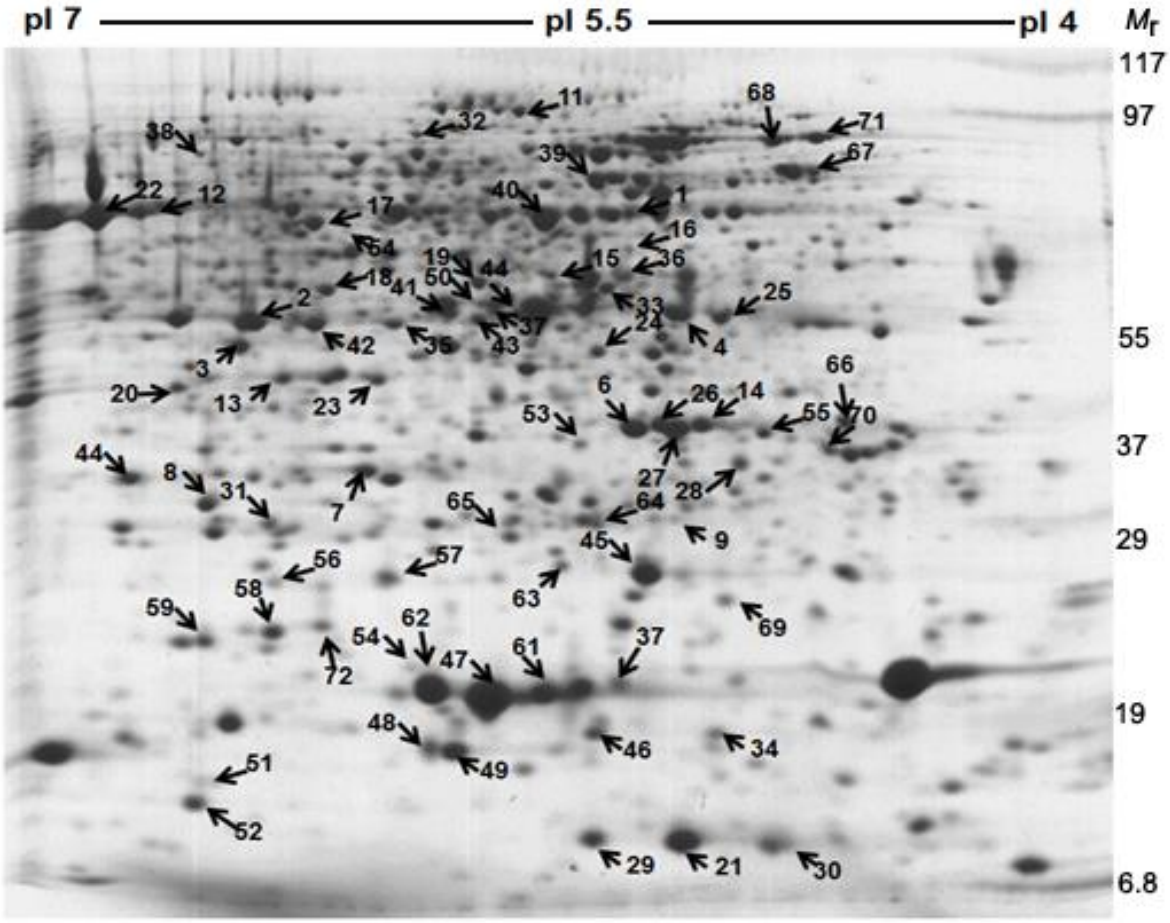


Figure 3.4. A representative two dimensional gel electrophoresis colloidal Coomassie blue-stained gel showing the profile of proteins extracted from *hp1* fruits at the stage. The numbers indicate differentially expressed proteins that were later identified by mass spectrometry, and the arrows indicate their relative positions on the gel.

3.3.2 Functional classification of differentially expressed proteins

Functional distribution of the identified proteins was performed according to the FunCat annotation as shown in Fig. 3.5. The differentially expressed proteins were distributed across 12 different categories, with nearly half of the proteins being involved in carbon metabolism (46%), in accordance with the massive up-regulation of metabolic processes such as respiration during fruit ripening. Among the remaining categories, stress response (14%) was maximally represented, followed by detoxification (7%), protein fate modification/ degradation (6%), transport (6%), amino acid and hormone metabolism (4%), cell cycle regulation (3%), secondary metabolism (3%), replication (1%), protein synthesis and storage (1%), transcription (1%) and unclassified (8%).

3.3.3 Hierarchical clustering of identified proteins

To reveal patterns of protein expression, the above differentially expressed proteins were grouped. These proteins were clustered based on the unweighted pair group method with arithmetic mean (Caraux and Pinloche, 2005) using the differences in protein spot intensity at different ripening stages of both wildtype and *hp1* fruits. The above analysis distinguished three main clusters of proteins, hereafter named clusters I, II and III (Fig. 3.6A). As expected in all three clusters, proteins involved in carbohydrate metabolism were most abundant (Fig. 3.6B).

Cluster I (30.55% of all protein spots) included three different sub clusters reflecting protein expression patterns. In the first sub cluster, the expression patterns of proteins remained nearly uniform during fruit development. This sub cluster included 14 spots, of which the identity of six (spot nos. 3, 10, 37, 47, 4 and 70) was not known. The remaining eight spots (2, 8, 11, 12, 13, 42, 43 and 52) belonged to proteins involved in carbohydrate metabolism. The second sub cluster consisted of proteins whose level was similar at the MG and RR stages but varied at the BR stage. This cluster consisted of five proteins, of which two were unidentified proteins (34 and 44) and the remaining three were involved in carbohydrate metabolism (5, 9 and 17). The third sub cluster comprised three proteins that declined during fruit development (1, 6 and 7). While the majority of these proteins belonged to housekeeping functions, cluster I also included proteins regulating protein fate modification and degradation (11), detoxification (7), replication (52) and transport (1; Fig. 3.6B).

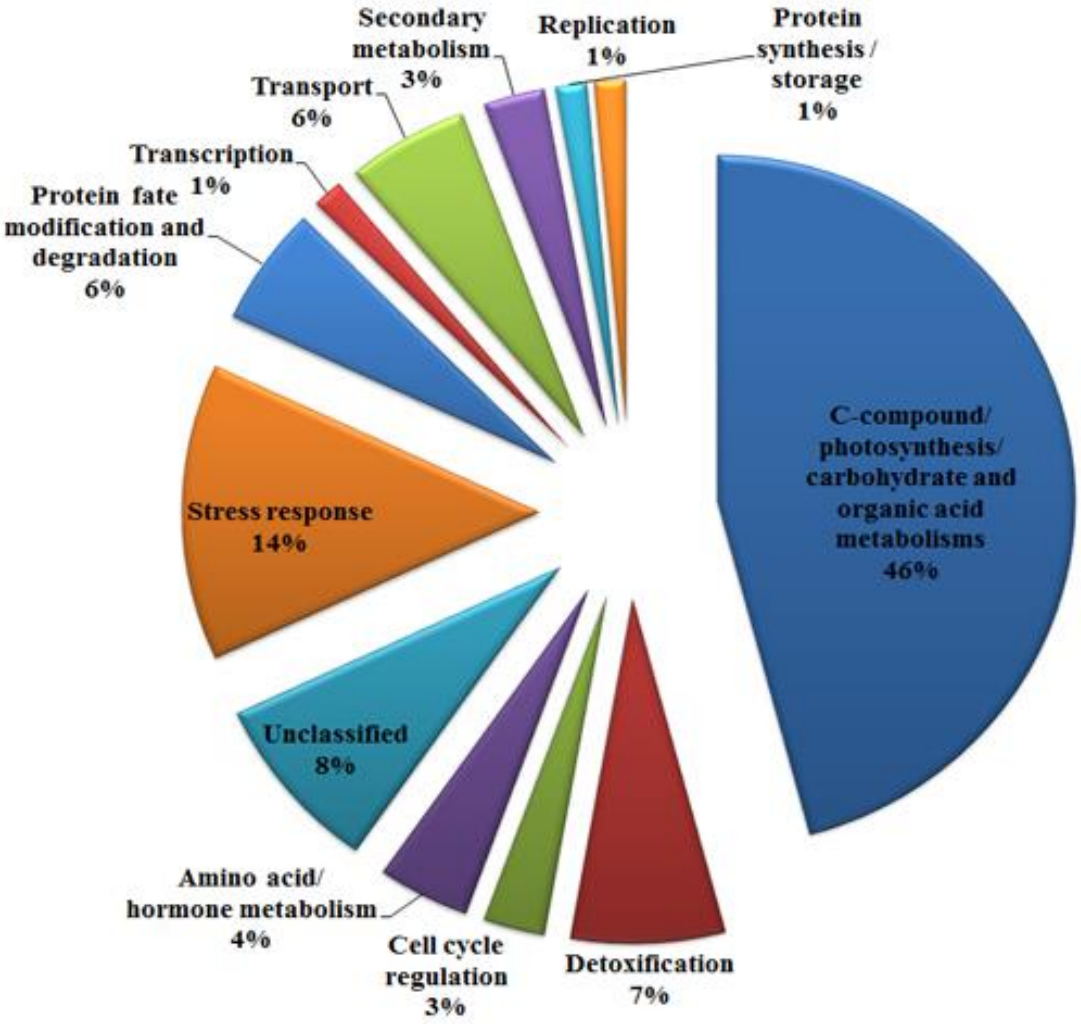


Figure 3.5. Functional classification of differentially expressed proteins isolated from outer pericarp of tomato fruits. Proteins were assigned to 12 different functional categories using the FunCat scheme (http://mips.helmholtzmuenchen.de/proj/funcatDB/) and relative percentage of proteins belonging to each category is indicated.

Similar to cluster I, cluster II (33.33% of proteins) also included three sub clusters. Sub cluster 1 included proteins most of which were down-regulated at the BR stage in the wildtype (but with almost similar expression levels at MG and RR) but were up-regulated in *hp1* and were specifically involved in carbohydrate metabolism (21, 23, 25, 29, 30 and 45). The proteins that showed higher expression in the BR stage of *hp1*, with reduced but similar expression levels at MG and RR, were classified in sub cluster 2 (15, 19, 22, 28, 36, 38, 50 and 51). While most of these proteins were part of the photosynthesis machinery, this also included a small heat shock protein17.7 (50). Sub cluster 3 consisted of proteins that shared almost constant expression levels in both the wildtype and *hp1* (16, 18, 20, 24, 32, 33 and 63) during ripening. These proteins belonged to carbon metabolism (24 and 32), amino acid/ hormone metabolism (18 and 33), cell cycle regulation (16), secondary metabolism (20), transport (40) and detoxification (63; Fig. 3.6B).

Cluster III (36.12% of proteins) comprised proteins with diverse biological functions showing similar expression patterns in either the wildtype or *hp1* across different developmental stages during ripening. In wildtype fruits, this cluster included proteins modulating stress (60, 62, 65 and 68), detoxification (49), hormone metabolism (41), secondary metabolism (58) and unknown functions (54, 57, 71 and 72; Fig. 3.6B). The spots that were specifically modulated in *hp1* fruit consisted of proteins involved in protein fate modification/ degradation (46 and 56), detoxification (49), stress response (61) and a few of unknown function (39, 57 and 71; Fig. 3.6B). One of the spots (66) showed a diametrically different expression pattern in the wildtype and *hp1*. It had higher expression in the wildtype at the MG stage and declined at subsequent BR and RR stages, while in *hp1*, its expression progressively increased from MG to RR stages (Fig. 3.6A).

The metabolic assignment of variably expressed proteins during fruit ripening revealed three main pathways. The first pathway comprised proteins that are involved in the Calvin-Benson cycle, glycolysis, the tricarboxylic acid cycle and the interconnecting pathways (Fig. 3.7). Reactions related to photosynthetic electron transport in the plastids constituted the second pathway (Fig. 3.8). The third pathway (Fig. 3.9) is a model showing the probable mode of action of differentially expressed heat shock proteins detected in our study.

3.3.4 Expression profiling of genes involved in carotenoid precursor and carotenoid biosynthesis

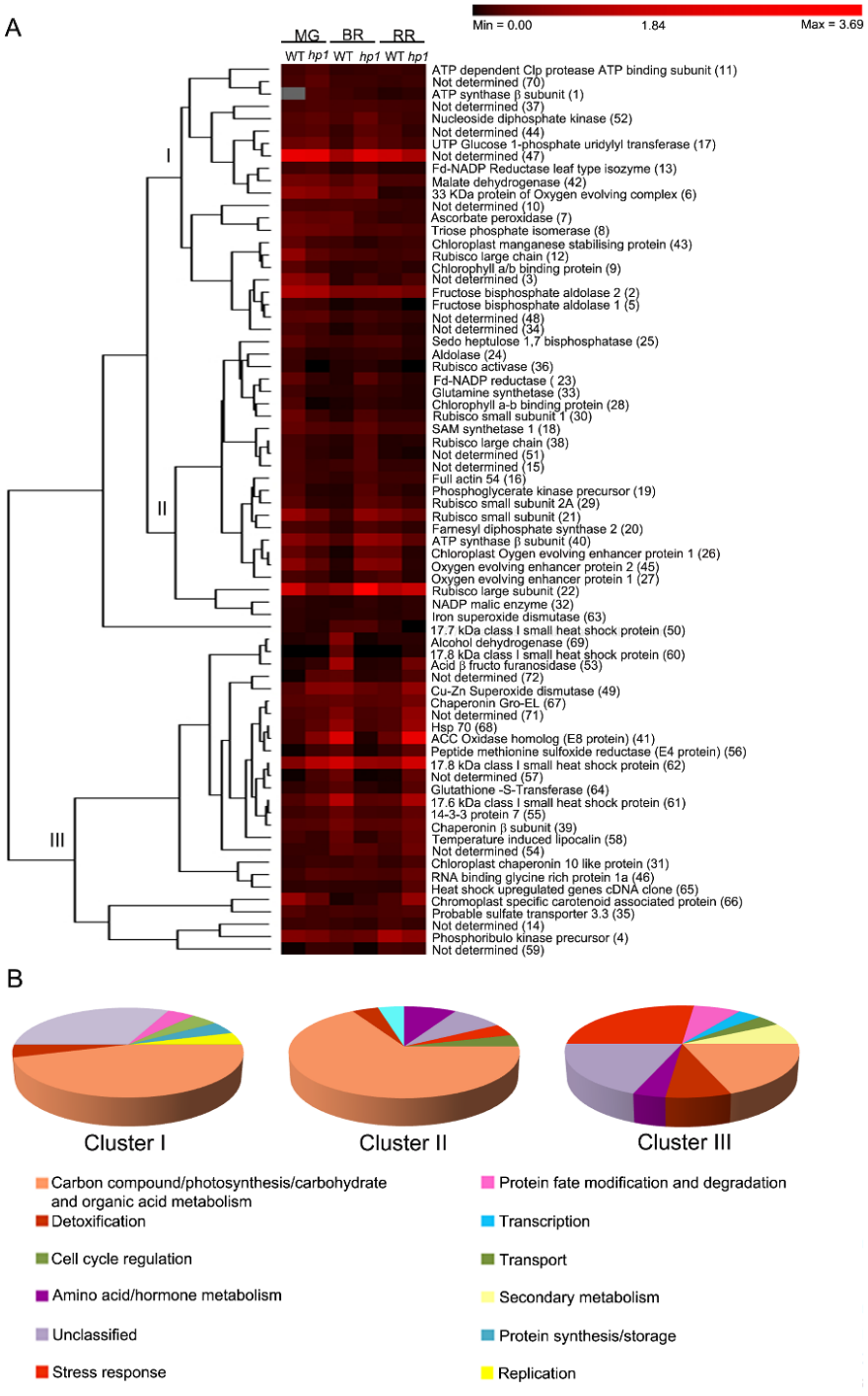


Figure 3.6. Hierarchical clustering analysis of differentially expressed proteins in wildtype (WT) and *hp1* fruits during ripening. A, Using Permut Matrix 1.9.3, proteins were clustered into three clusters based on their percentage spot volumes. A color bar corresponding to the relative levels of expression is given at the top of the heat map. The identity of each protein (spot no.) is indicated to the right of the rows. The columns represent levels of proteins at MG, BR, and RR stages of wildtype and *hp1* fruits. B, Pie diagram showing the relative distribution of different functional classes of proteins in each cluster.

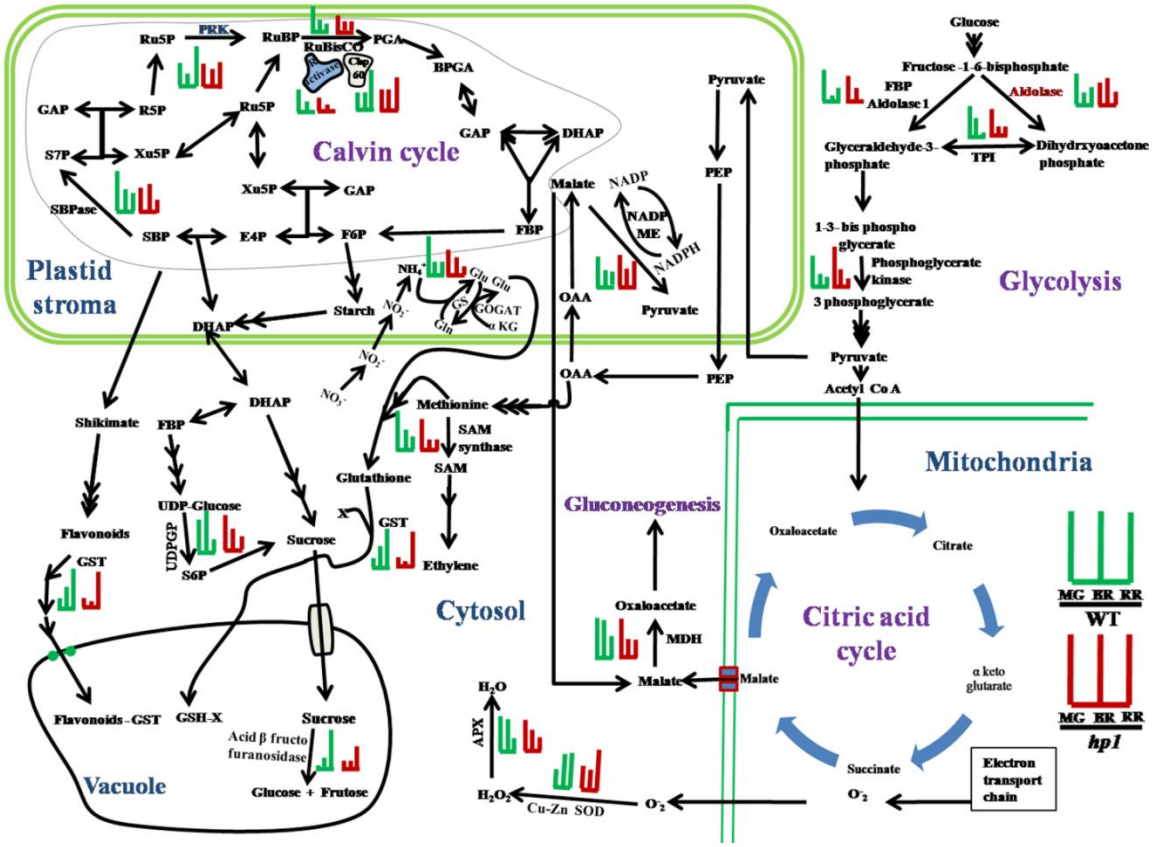


Figure 3.7. Schematic representation of metabolic pathways depicting the exchange of metabolites between different subcellular compartments and organelles in tomato fruits. The differentially expressed proteins in WT (green) and *hp1* (red) are shown at relevant places in the pathway. The relative abundance of proteins is depicted in bar diagram (with height of bar denoting extent of expression) sequentially at MG, BR and RR stages of ripening in both WT (green) and *hp1* (red) fruits.

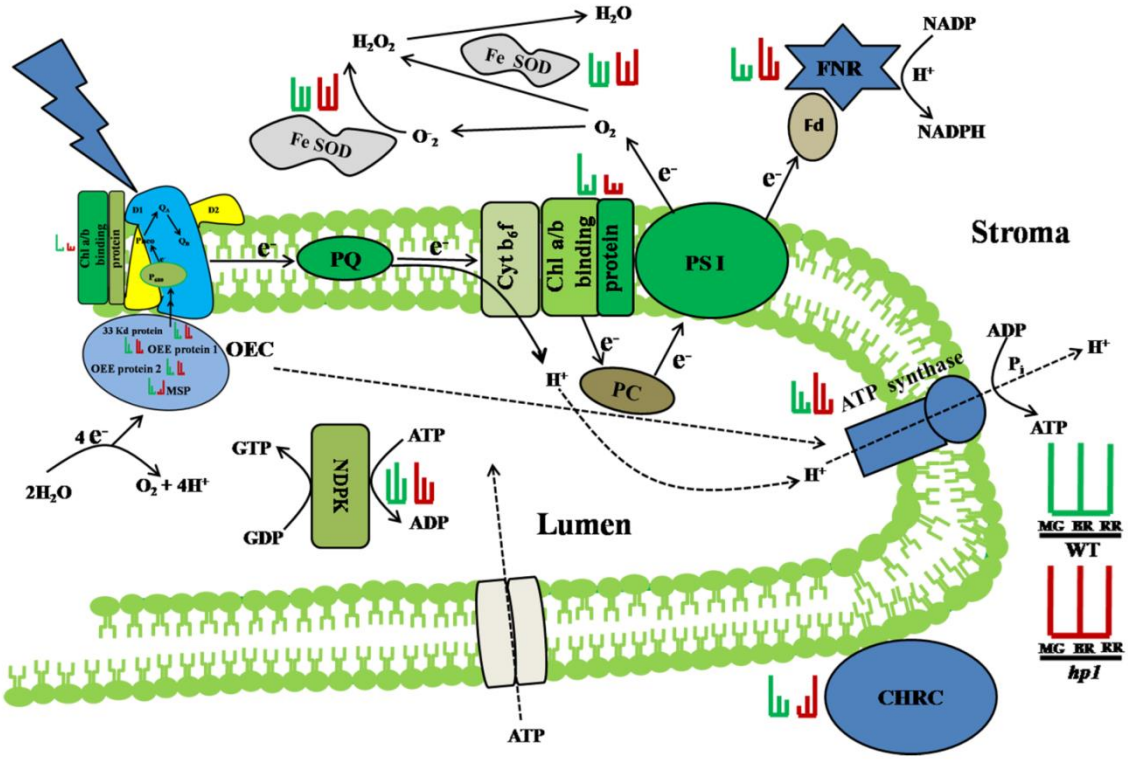


Figure 3.8. Schematic representation of electron transport chain operating in the thylakoid membranes of chloroplasts. The electrons produced by splitting of water molecule in the lumen are transported through PSII to PSI to generate proton motive force necessary for production of ATP and NADPH. Chromoplast specific carotenoid associated protein is also present in the membrane and binds to carotenoids. Fe-SOD participates in detoxification of superoxide free radicals generated from light reactions. The abundance of proteins at different stages is depicted (Fig. 7) for WT (green) and *hp1* (red).

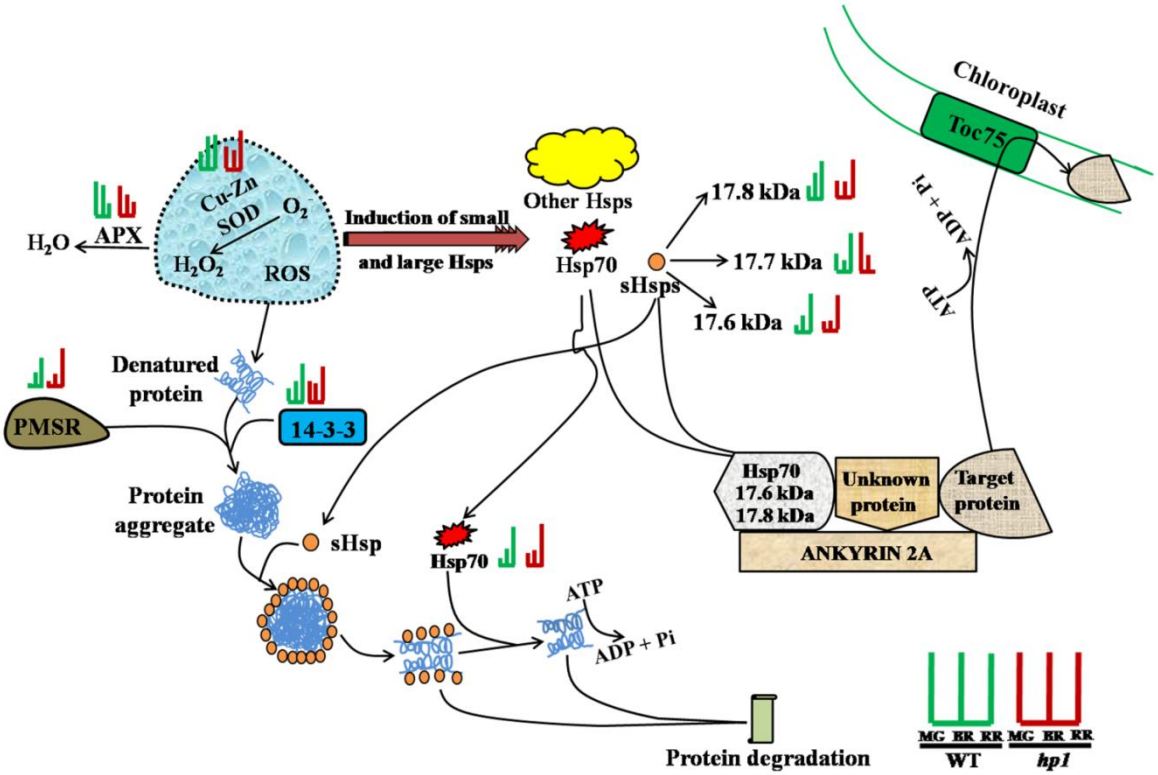


Figure 3.9. Hypothetical model representing the induction of Hsps during fruit ripening and their probable role in tomato fruits. The pool of Reactive Oxygen Species (ROS) produced from various metabolic processes is detoxified by ascorbate peroxidase and superoxide dismutase. ROS also induces the production of both large and small heat shock proteins which together with the help of 14-3-3 proteins and peptide methionine sulfoxide reductase (PMSR) may participate in preventing the denaturation of proteins and the formation of insoluble protein aggregates. Heat shock proteins may also interact with ankyrin 2A and 2B proteins and may aid in targeting of chloroplast proteins to outer membranes (Kim et al., 2011). The abundance of proteins at different stages is depicted (Fig. 3.6) for WT (green) and *hp1* (red).

Although it is logically expected that high carotenoid levels in *hp1* fruits should be reflected in up-regulation of enzymes of the pathway, our proteome analysis did not reveal any differentially expressed protein spots for any of the carotenoid biosynthetic enzymes. Apparently, the levels of these enzymes in both the wildtype and *hp1* were below the detection limits of colloidal Coomassie blue staining, and it is believed that the flux in the carotenoid biosynthetic pathway is mainly modulated by posttranscriptional, translational or posttranslational regulation. To ascertain the influence of the *hp1* mutation on transcript level, we examined the expression of genes encoding the entire carotenoid biosynthetic pathway. Figure 3.10 shows the expression profiles of 20 genes involved in carotenoid synthesis using quantitative real time PCR analysis, including genes contributing to the formation of the first precursor phytoene. Despite the accumulation of higher levels of lycopene in *hp1* fruits, the transcripts of genes belonging to the carotenoid pathway, regulating the formation of phytoene and its desaturation to lycopene, did not show any concerted up-regulation at the BR and RR stages when compared with the wildtype. The absolute levels of different transcripts varied distinctly and could be classified into two groups. In wildtype fruit at the MG stage, *lcyb1*, *lcyb2*, *zep* and *nced1* were the most abundant transcripts (greater than 1.0-8.0), whereas other genes were expressed at a lower level (0.0-1.0). A comparison of wildtype gene expression with *hp1* fruit at the MG stage indicated that the expression of most genes was significantly down-regulated in the mutant, except *cyp97a29, cyp97c11*, *crtrb1* and *crtrb2* which were up-regulated.

In the wildtype, *ggds2* and *lcyb2* were the most abundant transcripts (greater than 1.0-13.0) at the BR stage, whereas other genes were expressed at a lower level. While the expression levels of *dxs*, *idi*, *ggds2*, *psy1*, *zds* and *vde* were nearly similar, other transcripts such as *psy2*, *zis*, *crtiso*, *lcyb2*, *cycb*, *lcye* and *crtrb2* were down-regulated in *hp1* compared with the wildtype. At the BR stage, the level of *pds*, *zep*, *cyp97a29*, *cyp97c11* and *crtrb1* transcripts were significantly higher in the *hp1* mutant than in the wildtype.

At the RR stage, *dxs* and *zep* were the most abundant transcripts (greater than 1.0-24.0) in the wildtype, whereas other genes were expressed at a lower level. In RR fruits, transcript levels of *dxs*, *psy2*, *lcyb1*, *lcye* and *nced1* were nearly similar in the wildtype and *hp1*, whereas *idi*, *ggds2*, *psy1*, *zis*, *crtiso*, *lcyb2*, *crtrb2* and *zep* were down-regulated in *hp1*. In contrast, expression levels of *pds*, *zds*, *cycb*, *vde*, *cyp97a29*, *cyp97c11* and

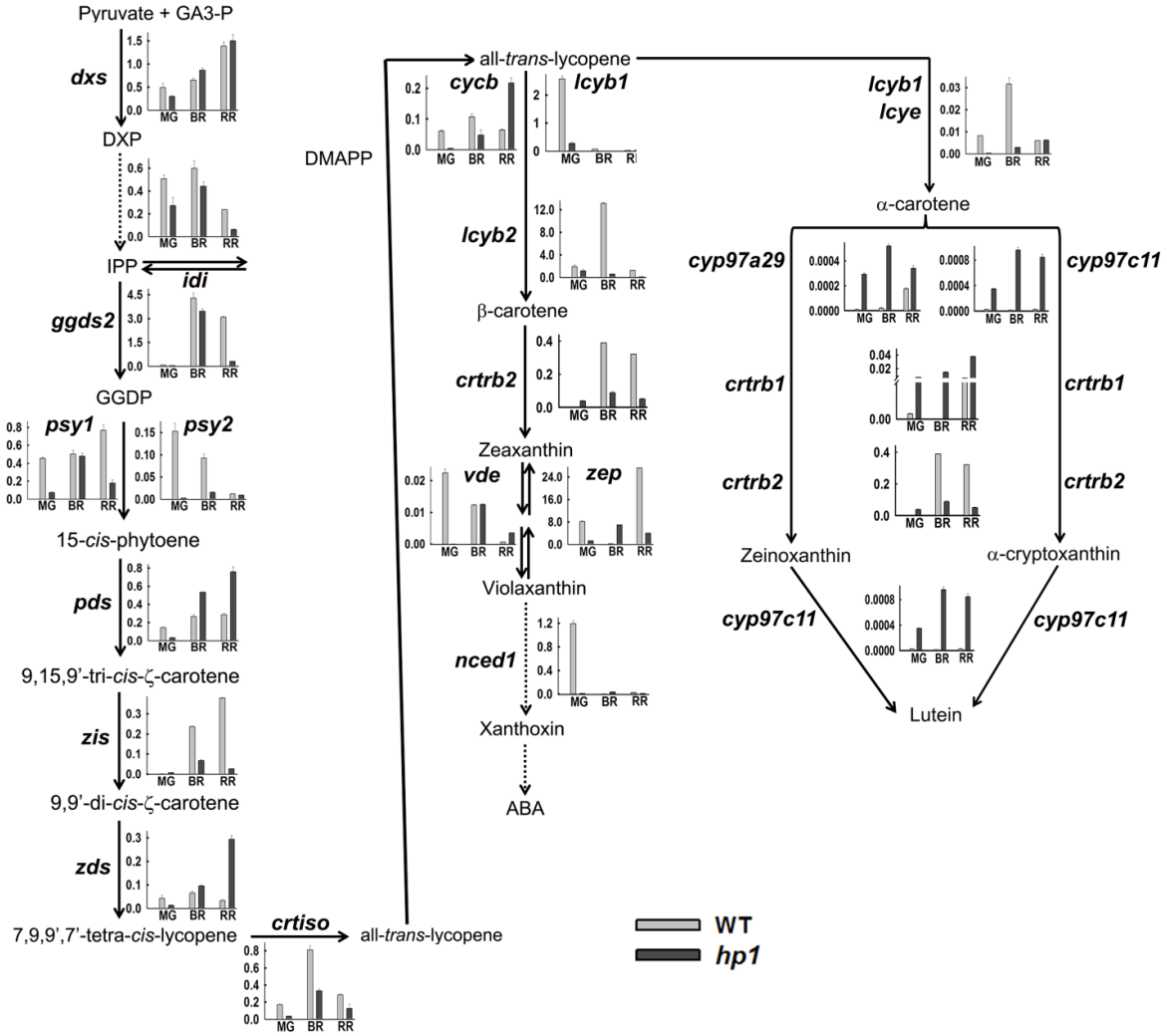


Figure 3.10. The biosynthetic pathway of carotenoids depicting the expression profiles of enzymes catalyzing different steps beginning from the precursors. Dotted arrows indicate multiple steps in the pathway. The transcripts were quantified in the wildtype and *hp1* at MG, BR, and RR stages of fruit development using real-time PCR. The transcripts were expressed after normalization with two internal controls, *β-actin* and *ubiquitin*.

crtrb1 were higher in the *hp1* mutant. Among these seven transcripts, the gene products of only *pds* and *zds* contribute to lycopene, whose levels are elevated in the *hp1* mutant. The slight accumulation of β-carotene level in *hp1* fruits may be related to an up-regulation of *cycb* transcript at the RR stage. Similarly, the gene products of *cyp97a29*, *cyp97c11* and *crtrb1* seem to contribute to the higher lutein levels found in RR fruits of *hp1*, as their transcripts are up-regulated. These results are in agreement with the study of Stigliani et al., (2011) reporting higher expression of *cyp97a29*, *cyp97c11* and *crtrb1* during tomato ripening.

Of interest was the opposite expression patterns of *zep* and *vde* transcripts, with down-regulation of *zep* and up-regulation of *vde* in the *hp1* mutant. While the gene product of *zep* converts zeaxanthin to violaxanthin, the gene product of *vde* reconverts violaxanthin to zeaxanthin. The reduced expression of *zep* and the enhanced expression of *vde* in *hp1* appear to be in agreement with the characteristic increase in chloroplast number and size, which could be correlated to reduced ABA levels in *hp1* (Carvalho et al., 2011). A similar phenotype was also observed in the ABA deficient *hp3* mutant, which has a lesion in *zep* (Galpaz et al., 2008). A link between *HP1* transcript levels and ABA level is also apparent from observations that the application of external ABA stimulates the expression of *DDB1* mRNA in wildtype tomato seedlings (Wang et al., 2008).

3.3.5 Correlation of protein, transcript and metabolite levels

The emergence of "omics" has highlighted the need for a systems biology approach for deciphering the links between coexpressed genes and pathways and identifying master regulatory points governing a biological response (Saito et al., 2008). The expression of a metabolome phenotype during the development of an organism results from a complex interaction between multiple responses at several levels, from the expression of genes regulating the pathway until the final synthesis of metabolites. In order to understand the complexities of the regulation of metabolic networks during fruit development in tomato, it is essential to correlate data from protein, transcript and metabolite experiments. In view of this, the proteome data obtained in this study was correlated with the transcript data available at www.ted.bti.cornell.edu and metabolite data from Rohrmann et al. (2011). Out of 72 differentially expressed proteins that varied during fruit development, transcripts for only 18 proteins were available on the TOM1 microarray. Furthermore, a detailed examination of the gene expression data revealed that in the TOM1 microarray,

the transcript profiles obtained at 7 DPA of fruit development were used for normalizing all other data at the different stages (7-57 DPA). However, we obtained proteome data only at three different ripening stages, MG, BR and RR. Since we did not include a time point corresponding to 7 DPA in our study, a direct correlation to this data set was ruled out. As an alternative, the transcript profiles for five carotenoid pathway genes obtained were compared with the corresponding metabolite data obtained earlier in the wildtype and *hp1* at the RR stage (Cookson et al., 2003). These transcript-metabolite pairs include *psy1*-phytoene, *zis*-ζ-carotene, *zds*-lycopene, *crtiso*-lycopene and *cycb*-β-carotene. The above pairs were correlated using the Pearson correlation algorithm with XLSTAT 2012 software (Fig. 3.11A). The correlation coefficient values indicated a negative correlation between transcripts and metabolites in the wildtype. Despite the high expression of *psy1* and *crtiso* in the wildtype, low lycopene levels were observed at the RR stage. On the contrary, a poor correlation was observed in the mutant, where *zds* was up-regulated but *crtiso* was down-regulated, yet resulted in higher lycopene levels in *hp1* fruits. A similar lack of correlation was also observed between the transcript profiles of *cyp97a29*, *cyp97c11*, *crtrb1*, and *crtrb2* and the lutein levels in wildtype and *hp1* fruits (Fig. 3.11B). Similarly, the protein data (for five differentially expressed proteins) and the corresponding metabolite data across different developmental stages were correlated in both the wildtype and *hp1* (Rohrmann et al., 2011). The protein-metabolite pairs, acid invertase (spot 53)-Glucose, UDP-Glucose pyrophosphoylase (spot 17)-Sucrose, SAM synthetase (spot 18)-ethylene, E8 protein (spot 41)-ethylene, and malate dehydrogenase (spot 42)-malate were analysed by XLSTAT (Fig. 3.11C and D). Analysis of the correlation data revealed that a negative correlation was observed between the proteins and metabolites at MG and BR stages whereas at RR stage, weak or no correlation was observed in both the wildtype and *hp1*.

3.3.6 Tomato CHRC is a plastid lipid associated protein (PAP) that assists in carotenoid sequestration and storage

CHRC was first discovered in cucumber corollas (Smirra et al., 1993) and was found to be a lipid binding protein. A survey of the literature revealed that this protein was extensively studied in bell pepper (Deruere et al., 1994) and was named as PAP. Comparison of protein sequences of bell pepper PAP and tomato CHRC revealed 89% homology (Fig. 3.12A and C). Also, tomato CHRC protein showed 100% sequence similarity to the tomato PAP protein sequence, suggesting that these two proteins are

A

WT RR

Variables	Transcript	Metabolite
Transcript	1	-0.436
Metabolite	-0.436	1

***hp1* RR**

Variables	Transcript	Metabolite
Transcript	1	0.280
Metabolite	0.280	1

B

WT RR

Variables	Transcript	Metabolite
Transcript	1	0.342
Metabolite	0.342	1

***hp1* RR**

Variables	Transcript	Metabolite
Transcript	1	0.559
Metabolite	0.559	1

C

WT MG

Variables	Transcript	Metabolite
Transcript	1	-0.771
Metabolite	-0.771	1

WT BR

Variables	Transcript	Metabolite
Transcript	1	-0.552
Metabolite	-0.552	1

WT RR

Variables	Transcript	Metabolite
Transcript	1	0.189
Metabolite	0.189	1

D

***hp1* MG**

Variables	Protein	Metabolite
Transcript	1	-0.595
Metabolite	-0.595	1

***hp1* BR**

Variables	Protein	Metabolite
Transcript	1	-0.720
Metabolite	-0.720	1

***hp1* RR**

Variables	Protein	Metabolite
Transcript	1	0.129
Metabolite	0.129	1

Figure 3.11. Comparison of protein, transcript and metabolite levels in WT and *hp1* fruits during ripening. Primary metabolite data were obtained from Rohrmann et al., (2011), phytoene, ζ-carotene contents were obtained from Cookson et al., (2003) and lycopene, β-carotene and lutein amounts are from the present study (Fig. 3.3 A, B). A, The transcript-metabolite pairs used for correlation analysis by Pearson correlation algorithm using XLSTAT 2012 software include PSY1-phytoene, *zis*-ζ-carotene, *zds*-lycopene, *crtiso*-lycopene and *cycb*-β-carotene. Table indicates the correlation coefficient values for both WT and *hp1* at RR stage. B, The transcript-metabolite pairs used for correlation analysis by Pearson correlation algorithm include *cyp97a29*-lutein, *cyp97c11*-lutein, *crtrb1*-lutein and *crtrb2*-lutein C, D, The absolute abundances of five protein-metabolite pairs (Acid invertase-glucose, UDP glucose pyrophosphorylase-sucrose, SAM synthetase-ethylene, E8 protein-ethylene and Malate dehydrogenase-malate) in both WT (C) and *hp1* (D) at MG, BR and RR stages during ripening were correlated as mentioned above. Tables indicate the correlation coefficient (R) values thus obtained.

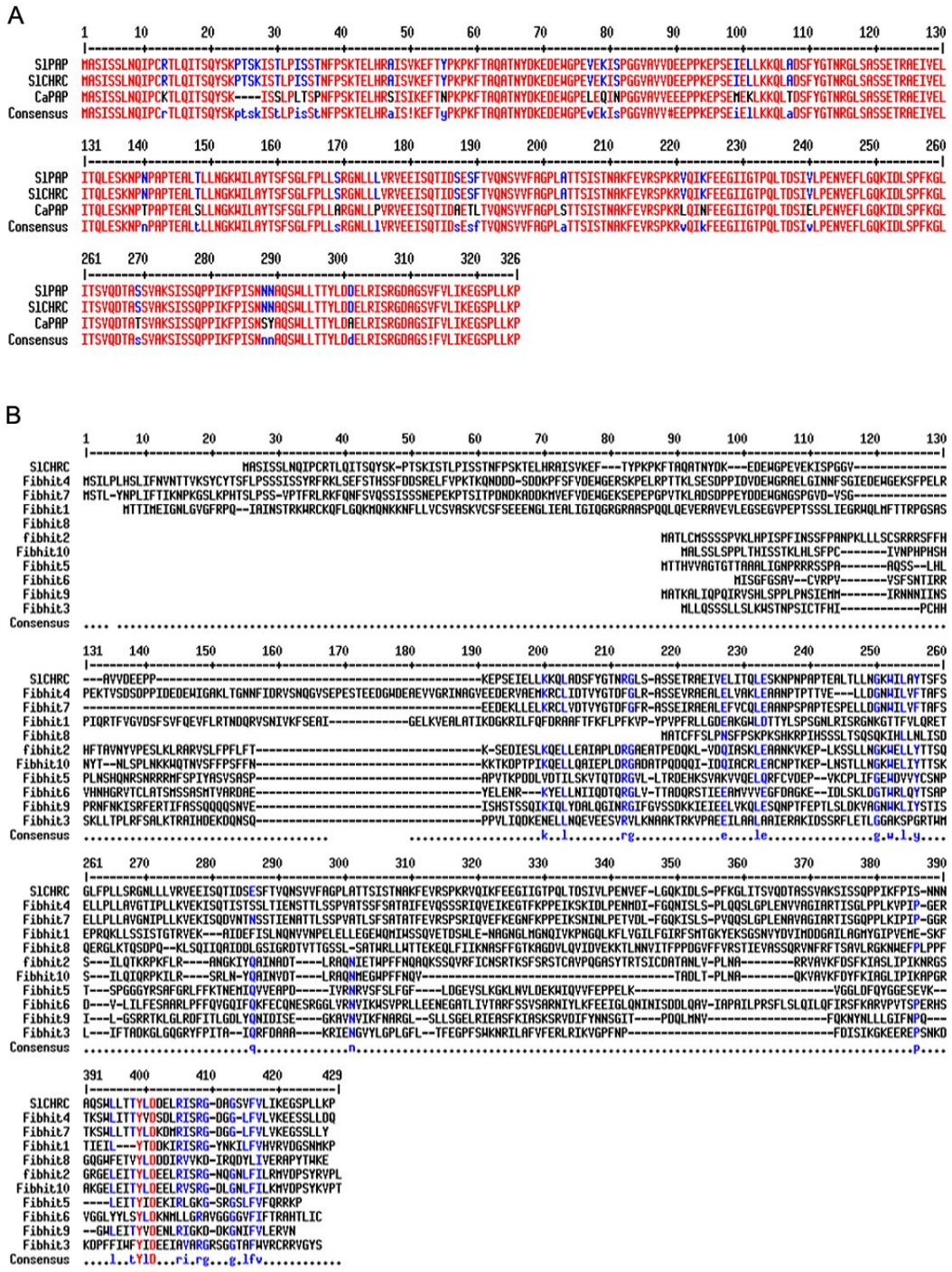
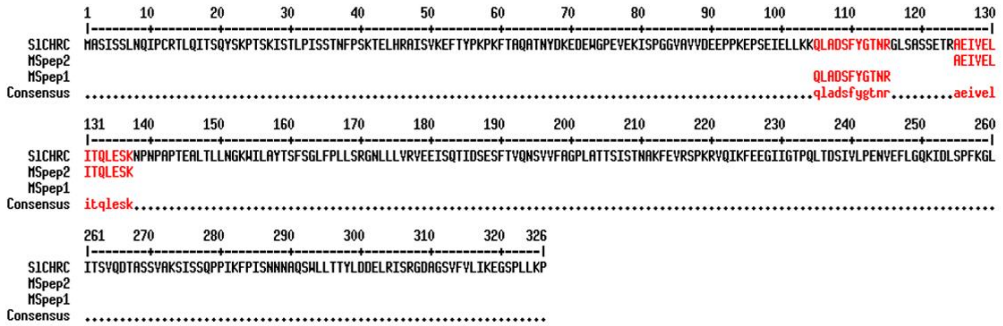


Figure 3.12. Homology between sequences of different chromoplast associated fibrillin and CHRC proteins. A, Comparison of amino acid sequences of chromoplast associated carotenoid binding protein (CHRC), plastid lipid associated protein (PAP) from tomato with PAP from bell pepper (Capsicum annum). B, Amino acid sequence homology between tomato CHRC and ten fibrillin accessions obtained from SGN database (http://solgenomics.net/).

C

Name of the protein	Accession numbers	Homology to CHRC (%)	M_r	No. of amino acids
S. *lycopersicum* PAP/ CHRC	Solyc02g081170.2	100	35.66	326
C. *annum* PAP	CAA10373	89	35.27	322
S. *lycopersicum* FIBRILLIN hit 1	Solyc01g006330.2.1	19	44.61	398
S.*lycopersicum* FIBRILLIN hit 2	Solyc01g104320.2.1	26	31.92	284
S. *lycopersicum* FIBRILLIN hit 3	Solyc06g069030.2.1	18	28.12	248
S. *lycopersicum* FIBRILLIN hit 4	Solyc08g005220.2.1	41	46.14	418
S. *lycopersicum* FIBRILLIN hit 5	Solyc08g006160.2.1	16	26.76	241
S. *lycopersicum* FIBRILLIN hit 6	Solyc08g068590.2.1	21	30.51	274
S. *lycopersicum* FIBRILLIN hit 7	**Solyc08g076480.2.1**	**50**	**37.48**	**344**
S. *lycopersicum* FIBRILLIN hit 8	Solyc10g018590.1.1	18	23.43	206
S. *lycopersicum* FIBRILLIN hit 9	Solyc11g005340.1.1	27	28.97	256
S. *lycopersicum* FIBRILLIN hit 10	Solyc11g044530.1.1	28	26.46	234

D



E

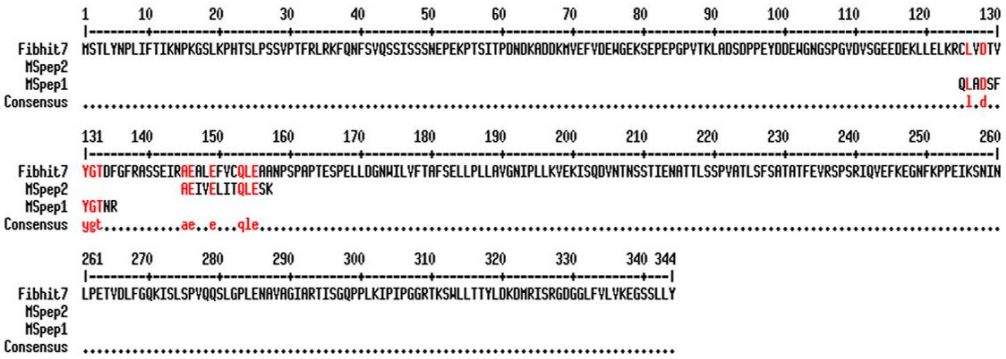


Figure 3.12. Homology between sequences of different chromoplast associated proteins. C, Table shows the accession numbers for PAP/CHRC and different FIBRILLIN hits obtained from SGN database, their homology to CHRC, molecular weights and the number of amino acids present in each protein. Note that only Fibrillin hit 7 has the molecular weight closest to CHRC, but showed less homology. D, E, Alignment of peptide sequences obtained for spot 66 after trypsin digestion followed by MALDI with that of tomato CHRC (D) and fibrillin hit 7 (E). Note that Fibrillin hit 7 showed very poor homology to the two tryptic peptides obtained for CHRC.

similar (Fig. 3.12A). On the contrary, alignment of tomato CHRC/PAP with tomato fibrillin family members (10 members based on BLAST search in the Solanaceae Genome Network [SGN] database; Fig. 3.12B) revealed a high degree of mismatches except for two sequences (Solyc08g005220.2.1 and Solyc08g076480.2.1), where homology of 41% and 50% respectively found (Fig. 3.12B). The divergence in CHRC sequence with fibrillin indicated that while these two proteins are different, the occurrence of PAP domains in fibrillin protein sequences led to their classification as PAP family proteins. Nevertheless, both CHRC and fibrillin appear to play major roles in the storage of carotenoids in chromoplasts (Vainstein et al., 1994; Pozueta-Romero et al., 1997). The specific role of CHRC in chromoplasts is also supported by the observation that a down-regulation of tomato CHRC using an RNAi strategy led to a 30% reduction of total carotenoids in tomato flowers (Leitner-Dagan et al., 2006). Since RNAi suppression of CHRC reduced the carotenoid level, overexpression should increase its level. Although there are no reports of CHRC overexpression of a related protein, fibrillin from pepper, which shares the PAP domain with CHRC in tomato, resulted in almost a doubling of carotenoid levels and carotenoid derived aroma compounds in tomato fruits (Simkin et al., 2007). Evidence is emerging for additional roles for plastoglobulin proteins like CHRC, which not only participate in the sequestration of carotenoids but also appear to influence chromoplastogenesis as well as carotenoid metabolism (Brehelin and Kessler, 2008; Li et al., 2012). Taken together, the up-regulation of CHRC in chromoplasts supports the role of this protein in chromoplast-specific carotenoid storage (Leitner-Dagan et al., 2006).

3.3.7 *chrc* is regulated posttranscriptionally in *hp1*

A comparison of the protein profiles in wildtype and *hp1* fruits revealed an increase in the abundance of CHRC (spot 66) at the RR stage of *hp1*, whereas its level declined in the wildtype at the same stage. A detailed chronological analysis revealed an interesting pattern of abundance of CHRC, with the wildtype and *hp1* following dramatically opposite patterns. Based on the intensity of spot volumes, in the wildtype, CHRC level was highest at MG, followed by a decline to nearly similar levels in both BR and RR. In contrast, in *hp1*, CHRC level increased from MG to RR, with maximal level at the RR stage (Fig. 3.13A). Analysis of *chrc* transcript levels (Fig. 3.13B) corroborated the above pattern of CHRC protein levels, albeit with a few differences. In the MG stage, the wildtype exhibited a slightly higher *chrc* expression (1.7 fold) than *hp1*. At the BR stage,

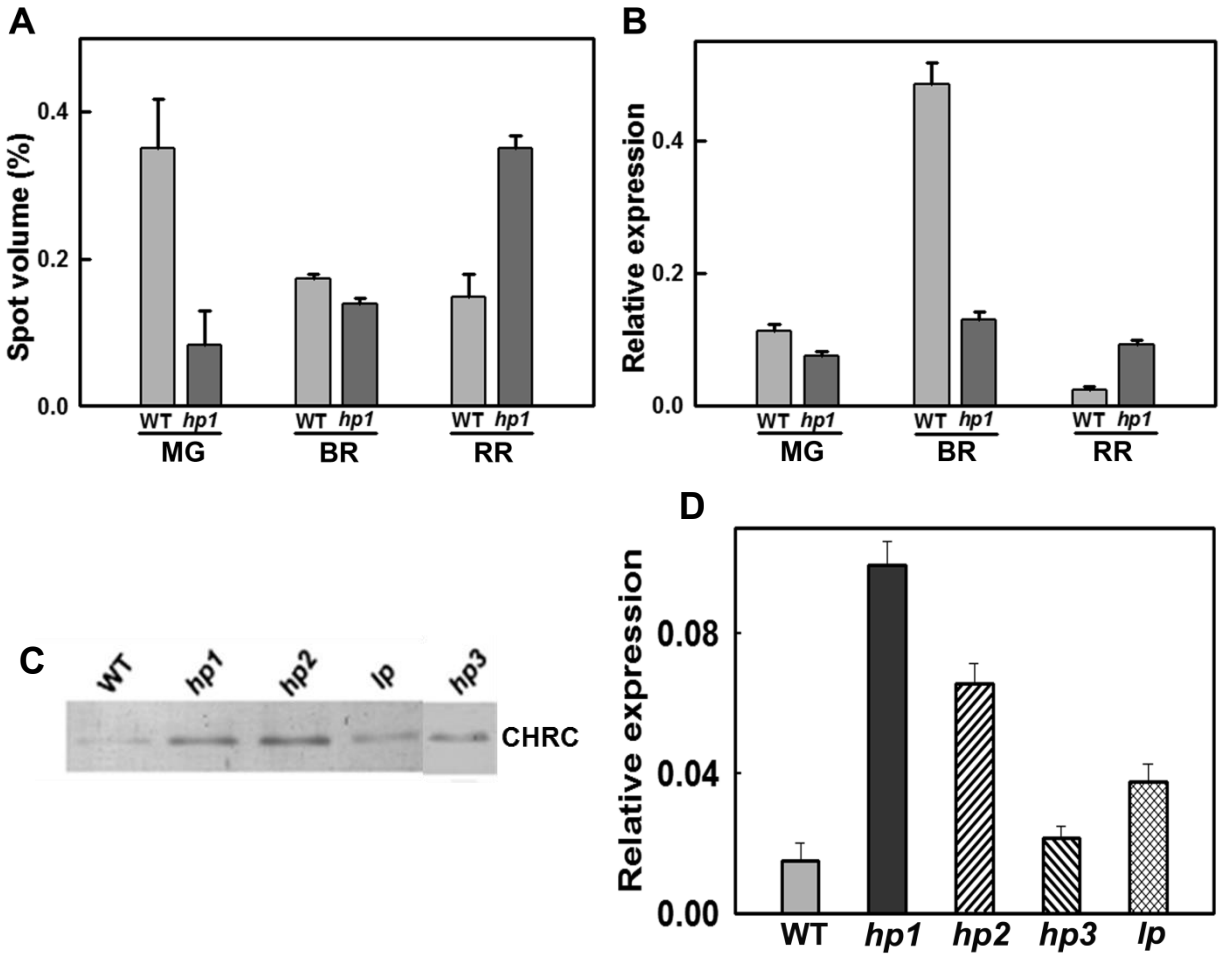


Figure 3.13. Comparison of CHRC levels in wildtype (WT) and *hp1* fruits. A, Relative spot volume of CHRC protein in wildtype and *hp1* fruits at different stages of ripening. B, Real-time PCR quantification of CHRC transcript in wildtype and *hp1* fruits at different stages of ripening. C, Analysis of CHRC levels in fruits of the wildtype, *hp1*, *hp2*, *Ip* and *hp3*. D, Comparison of CHRC transcript levels in RR fruits of *hp1*, *hp2*, *hp3*, and *Ip* in relation to the wildtype.

the wildtype showed a 3 fold higher *chrc* expression than *hp1*, but at RR stage, *hp1* showed around 6.35 fold higher expression than the wildtype. *hp1* showed highest *chrc* expression in BR followed by RR (Fig. 3.13B). But the protein profile revealed the opposite, with high abundance at the RR stage, suggesting posttranscriptional regulation of *chrc*.

3.3.8 Loss of function of *ddb1* enhances the abundance of CHRC

A comparison of CHRC protein levels in both wildtype and *hp1* fruits at the RR stage revealed at least 2-fold higher CHRC level in *hp1* than in the wildtype (Fig. 3.13C). Since mutation in *det1* (*hp2*; Mustilli et al., 1999) also leads to a high-pigment phenotype, it was of interest to examine whether this mutant too exhibits high levels of CHRC protein. Analysis of CHRC levels from *hp2* mutant fruits at RR stage (Fig. 3.13C) revealed an abundance level similar to *hp1*, suggesting an overlap in the action of *hp1* and *hp2* loci in regulating CHRC levels. Although *ddb1* (*hp1*) and *det1* (*hp2*) are diverse loci, the observed overlap may have emanated from their coaction as part of the CUL4-DDB1-DET1 complex (Wang et al., 2008), where loss of function of either of these proteins may contribute to higher CHRC and also pigment levels. Consistent with the enhanced expression of CHRC protein in *hp2*, Enfissi et al. (2010) showed increases in the number and size of plastoglobules in fruits of *det1* down-regulated lines. Similarly, it was reported earlier that the chloroplast-to-chromoplast transition in tomato is accompanied by an increase in the number and size of plastoglobules (Harris and Spurr, 1969). Taken together with the above observations, the increased levels of CHRC protein in both *hp1* and *hp2* fruits may be linked to an increase in the abundance of plastoglobules, where higher CHRC levels in chromoplasts assist in the sequestration and stabilization of carotenoids, thus boosting their levels.

Similar to *hp1* and *hp2* mutants, the *Ip* mutant exhibits high lycopene content in fruits and also has similar increases in the number and size of chloroplasts, but the gene responsible for this phenotype is not yet identified (Jones, 2000; Lavi et al., 2009). Kendrick et al. (1997) reported that *Ip* displayed photomorphogenic responses intermediate between *hp1* and normal genotypes. In view of its high pigment phenotype, we examined whether *Ip* also exhibits a high level of CHRC protein in ripened fruits. Western analysis revealed that, similar to *hp1* and *hp2*, *Ip* also up-regulates CHRC protein but has levels intermediate between those in the wildtype and *hp1* and *hp2* fruits (Fig. 3.13C). Consistent with the intermediate CHRC level, the RR fruits of the *Ip* mutant

also showed intermediate levels of lycopene and β-carotene between those of the wildtype and *hp1* (Jones, 2000). This suggests that increases in chloroplast number, size, and lycopene level in *Ip* are likely regulated by a mechanism similar to that in high-pigment mutants and thus shows an intermediate increase in CHRC level.

Since a deficiency in could also lead to a high-pigment phenotype (*hp3*), it was of interest to examine the CHRC levels in this mutant. Monitoring of CHRC levels by western blotting in the RR fruits of the *hp3* mutant revealed a lower abundance of CHRC compared with that in *hp1*; nonetheless, it was higher than that of the wildtype (Fig. 3.13C). This result is corroborated by the observation that the deficiency of ABA in *hp3* is accompanied by an increase in plastid compartment size due to increased plastid division (Galpaz et al., 2008). This could result in a higher storage capacity for the carotenoids similar to *hp1* and *hp2* mutants. Although *hp3* is not a member of the CUL4-DDB1-DET1 complex (Wang et al., 2008), this mutation may affect the carotenoid levels through feedback regulation (Galpaz et al., 2008).

In view of the observed differences in the CHRC abundance in *hp1*, *hp2*, *hp3*, and *Ip*, it was of interest to examine the transcript levels of CHRC in the RR fruits of these four mutants (Fig. 3.13D). In comparison with the wildtype, *hp1* showed the highest expression of CHRC (6.35-fold), followed by *hp2* (4.12-fold), *Ip* (2.37-fold), and *hp3* (1.37-fold; Fig. 3.13D). These transcript profiles appear to be consistent with the protein profiles determined by western blotting, except in the case of *hp2*. Nevertheless, all four mutants exhibited high transcript as well as protein levels for CHRC compared with the wildtype, which is consistent with their high-pigment phenotype, where this protein might have a major role in sequestering the elevated carotenoids.

3.3.9 Plastoglobules are enriched in carotenoids

The transition from chloroplasts to chromoplasts during ripening is accompanied by an increase in osmiophilic bodies associated with the thylakoids named plastoglobules. The chromoplasts of the *hp1* mutant show a 1.3 fold increase in size compared with the wildtype (Cookson et al., 2003). Likewise, down-regulation of *DET1* leads to an increase in plastoglobule number in the chromoplasts (Enfissi et al., 2010). Biochemical analysis of plastoglobules revealed that these are enriched in lipids and also contain several proteins, including enzymes participating in carotenoid metabolism (Austin et al., 2006; Brehelin and Kessler, 2008). Based on the enrichment of lipids in the plastoglobules, it is

assumed that carotenoids are also present in them. Since CHRC has been implicated as a protein that assists in the sequestration and storage of carotenoids, and it may be localized in plastoglobules, the presence of carotenoids and CHRC were examined in the isolated plastoglobules. The plastoglobules were purified from RR fruits of tomato by taking advantage of their lower density compared with other membranous fractions on Suc density gradients (Fig. 3.14A) by adapting the procedures of Besagni et al. (2011) and Lundquist et al. (2012). The purity of the plastoglobule fraction and fluorescence emission from globuli were examined by confocal microscopy (Fig. 3.14, B-D), which revealed the presence of intact globules (Fig. 3.14D). Moreover, the purified plastoglobules exhibited a bright green autoflourescence on exposure to a 488 nm argon laser, indicating the enrichment of carotenoids (emission in the range of 500-510 nm; Fig. 3.14, B and E), whereas they exhibited only a trace level of red autoflourescence (740-750 nm; Fig. 3.14C), indicating a near absence of chlorophylls. Since the plastoglobules were isolated from RR fruits, the absence of chlorophyll was expected, akin to an earlier observation for the isolated chromoplasts (Egea et al., 2011). In addition, carotenoids were extracted from the plastoglobule fraction and the absorbance spectrum of the extract showed a distinct peak in the 440 to 475 nm range, which is characteristic of carotenoids (Fig. 3.14F). From the foregoing observations, it is evident that the plastoglobules isolated from RR fruits are enriched in carotenoids.

3.4 Discussion

3.4.1 *hp1* mutant fruits accumulate proteins related to carotenoid sequestration and metabolism

High pigmentation of fruits in tomato appears to be regulated by a diverse set of genes encoded by distinct genetic loci: *hp1*, *hp2*, *hp3* and *Ip* (Azari et al., 2010). At the RR stage, fruits of all these mutants possess elevated levels of lycopene and β-carotene, signifying commonality in the up-regulation of carotenoids. In view of this, we specifically examined the 72 differentially abundant proteins for the presence of specific enzymes or proteins that may have assisted in carotenoid accumulation by regulating biosynthesis, sequestration or degradation. We found three such proteins, lipocalins, alcohol dehydrogenase and CHRC. Lipocalins are lipid-associated transporter molecules helping in the transport of certain lipids and small molecules (Frenette Charron et al., 2002). They also include enzymes like violaxanthin deepoxidase and zeaxanthin epoxidase (Hieber et al., 2000), which play roles in carotenoid degradation. During

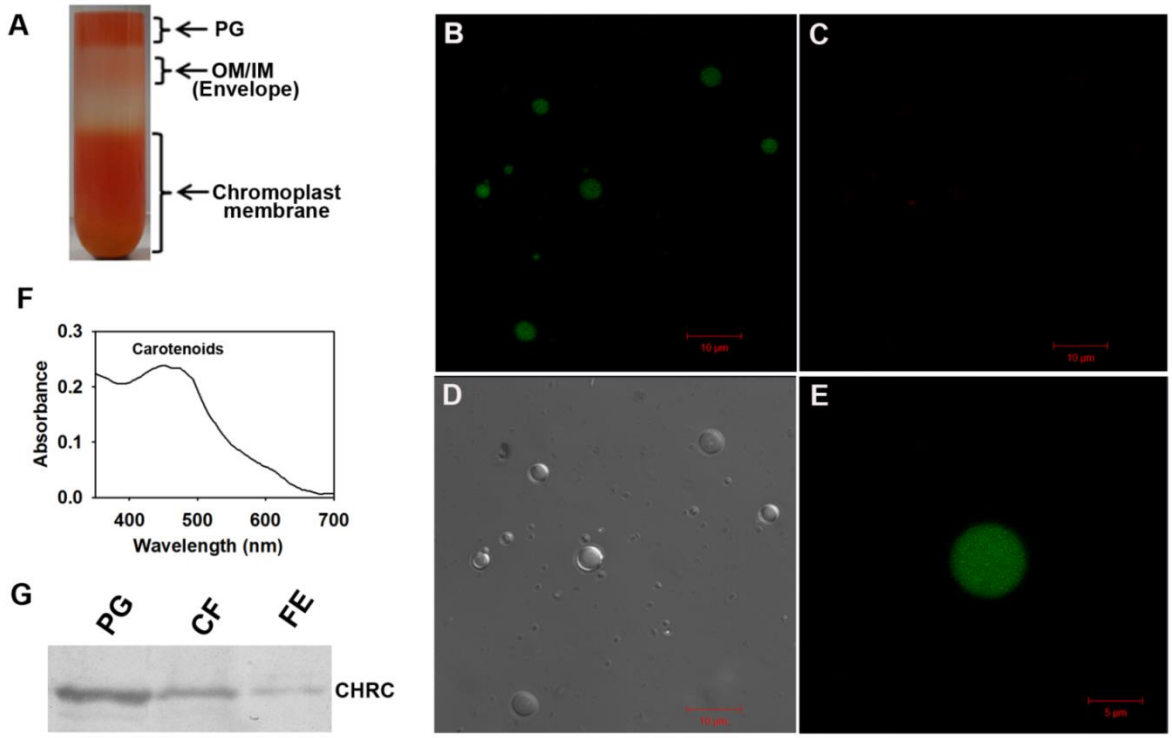


Figure 3.14. Confocal microscopy imaging and western blotting of isolated plastoglobules. A, Suc density gradient purification of plastoglobules (PG). Note that the distinct upper layer of purified plastoglobules is well separated from the underlying chromoplast membranous fractions. OM/IM indicate outer and inner membranes of chromoplasts. B to D, Purified plastoglobules were visualized using a confocal microscope. On excitation with a 488-nm laser, the plastoglobules exhibit strong green fluorescence (emission between 500 and 510 nm; B) but show negligible red fluorescence (emission between 740 and 750 nm; C). D shows a bright-field image of the plastoglobules. E, Enlarged view of a single plastoglobule. F, Absorption spectrum of the extract obtained from purified plastoglobules showing characteristic carotenoid peaks at 440 to 475 nm. G, Western analysis of CHRC levels in the purified plastoglobule fraction (PG; 0.33 μg) in comparison with the chromoplast membrane fraction (CF [the chromoplast fraction prior to sonication]; 2.5 μg) and total protein from the outer pericarp of RR fruits of *hp1* (FE, fruit extract; 2.5 μg).

ripening, the abundance of temperature-induced lipocalins increased in both the wildtype and *hp1*, although expression at the BR stage was less in the wildtype and thereafter increased at the RR stage. Similar increases in levels of lipocalins were also observed in other tomato proteomics studies (Faurobert et al., 2007; Osorio et al., 2011). It is known that alcohol dehydrogenase is an important enzyme in the biosynthesis of volatiles in tomato (Speirs et al., 1998). Alcohol dehydrogenase was up-regulated in both the wildtype and mutant at the RR stage, but the protein level was much higher in the wildtype. The observed increase in alcohol dehydrogenase and lipocalins at the RR stage may be related to increases in the levels of compounds contributing to volatile / flavour formation in tomato fruits.

One protein that showed an interesting expression pattern is CHRC. This protein showed a gradual decline in abundance during ripening in the wildtype. On the other hand, in *hp1*, the protein showed an opposite trend; it progressively increased, attaining a peak at RR (Fig. 3.13). This protein was also found in chromoplast proteome studies of tomato, bell pepper and *Citrus* spp. (Siddique et al., 2006; Barsan et al., 2010; Zeng et al., 2011) and it is assumed that it plays a role in carotenoid storage.

Moreover, none of the carotenoid biosynthetic enzymes were detected in our proteomics studies, either because their levels were below the detection limits or they were regulated at the protein translation level.

3.4.2 Carotenoid biosynthesis pathway in *hp1* fruits is regulated at posttranscriptional level

Despite the distinctive increase in lycopene level in *hp1* fruits, the transcript levels of most enzymes of the carotenoid biosynthesis pathway were lower than those of the wildtype at all stages of fruit ripening. The predominant down-regulation of transcripts in *hp1*, barring a few such as *pds*, *zds*, *cycb* and *vde* that show up-regulation at the RR stage, indicates that the enhanced carotenoid formation in the *hp1* mutant is most likely regulated at the posttranscriptional level. Similar to this study, Enfissi et al. (2010) also suggested the posttranscriptional regulation of the carotenoid biosynthesis pathway, as they did not find a correlation between transcript profiles of carotenoid biosynthetic genes and changes in the carotenoid levels in *DET1* down-regulated tomato fruits. One of the enzymes that may regulate flux into the carotenoid biosynthesis pathway is phytoene synthase 1. It is believed that an increase in phytoene level has a feed-forward effect on

carotenoid biosynthesis (Fraser et al., 2007). It was also reported that the activity of the PSY1 enzyme in *hp1* was up-regulated by 2 fold, although there was no corresponding increase in the transcripts of *psy1* and *pds* (Cookson et al., 2003). Transcript profiling of carotenoid pathway genes revealed overall up-regulation of the pathway in the wildtype rather than in *hp1*, except the desaturation steps catalysed by *pds* and *zds*, suggesting posttranscriptional control of the pathway. However, the transcript levels of *cytochrome P450 carotenoid β-* and *ε- hydroxylases* responsible for the conversion of α-carotene to lutein were up-regulated in the *hp1* mutant but not in the wildtype, consistent with the elevated lutein levels found in the mutant. Compared with the wildtype, transcript levels for ABA biosynthetic genes were down-regulated in *hp1*, suggesting a relation between low ABA levels and increases in chloroplast number and size, as reported previously in the *hp3* mutant (Galpaz et al., 2008).

3.4.3 A systems biology approach is required to uncover the contribution of *hp1* to fruit ripening

A lack of correlation between transcript and metabolite profiles leading to lycopene formation was observed in our study. A similar result was also reported in case of *DET1* down-regulated tomato lines (Enfissi et al., 2010) and also in *PSY1* overexpressing tomato lines (Fraser et al., 2007). At the same time, in *DET1* down-regulated tomato lines (Enfissi et al., 2010), a strong correlation between ripening associated transcripts and specific metabolites was observed, underlining the diversity in the regulation of metabolic networks in fruit ripening. The negative correlation between carotenoid pathway transcripts and carotenoids indicates the importance of posttranscriptional regulation in elevating carotenoid levels in *hp1* fruits. This view is supported by the observation that although there was no corresponding increase in the transcripts of *psy1* and *pds*, the activity of the PSY1 enzyme in *hp1* was up-regulated by 2 fold (Cookson et al., 2003). A similar lack of correlation was also observed between the transcript profiles of *cyp97a29*, *cyp97c11*, *crtrb1* and *crtrb2* and the lutein levels in the wildtype and *hp1* fruits (Fig. 3.12B). Although the correlation coefficient values obtained were higher in *hp1* compared with the wildtype, they do not indicate a strong correlation between the transcripts and the lutein levels. The absence of correlation between transcript levels and their respective metabolites (lutein and lycopene) indicate that alternative mechanisms like posttranscriptional regulation might be controlling the carotenoid pathway.

The resulting correlation coefficient value between five protein-metabolite pairs suggested a negative correlation between proteins and metabolites at MG and BR stages for both the wildtype and the mutant. On the contrary, at the RR stage, the correlation coefficient values were very low, indicating weak or no correlation between proteins and metabolites in both the wildtype and *hp1*. On the whole, these results highlight the need for a comprehensive systems approach, including posttranslational regulation, feedback regulation, metabolite turnover and portioning between different organelles and/ or locations in the cell, to uncover the linkage between metabolic networks regulating fruit ripening (Fernie and Stitt, 2012).

3.4.4 Both carotenoids and CHRC are present in the plastoglobules

Since the isolated plastoglobules are enriched in carotenoids, it was assumed that CHRC may be associated with the plastoglobules. To ascertain the presence of CHRC in the purified plastoglobules, the proteins were extracted from the plastoglobule fraction and resolved by SDS-PAGE, followed by western blotting. Figure 3.14G shows the presence of CHRC protein in purified plastoglobules. The comparison of CHRC levels in plastoglobules with other fractions indicated a substantial enrichment of the CHRC protein in the plastoglobules over the chromoplast membrane fraction (prior to its sonication to release the plastoglobules) is also in conformity with an earlier transmission electron microscopy observation that the plastoglobules are associated with chromoplast membranes in the ripe fruits (Harris and Spurr, 1969).

3.4.5 Loss of DDB1 up-regulates CHRC protein that helps in carotenoid sequestration and storage

The up-regulation of CHRC in the fruits of *hp1* mutant suggests an interrelationship between carotenoid accumulation and CHRC levels. Several studies have indicated that the CHRC and related proteins, fibrillins enhance the sequestration of carotenoids into plastoglobules (Brehelin and Kessler, 2008). The importance of carotenoid sequestration and storage is highlighted in studies where attempts to enhance the carotenoid levels were mitigated by the absence of a proper sink. In potato tubers, a massive loss of carotenoids occurs during long-term storage due to enzymatic or nonenzymatic oxidation of carotenoids. However, such loss can be prevented by expression of the cauliflower *Or* gene, which stimulates the formation of plastoglobule like structures storing carotenoids in potato tubers. The sequestration of carotenoids in the above structures prevents the

oxidation of carotenoids and ensures the continued formation of carotenoids during the storage of tubers (Li et al., 2012). It is likely that higher CHRC levels function to abet the storage of carotenoids and protect them from degradation in *hp1* mutant. However, it remains to be investigated whether the up-regulation of CHRC by genetic or transgenic means would improve the storage capacity of carotenoids in tomato fruits. In summary, this study revealed that CHRC likely regulates carotenoid sequestration and storage, which seems to be important for the enhanced accumulation of carotenoids in *high pigment 1* tomato fruits.

Chapter 4

Optimization of shotgun proteomics method for proteome profiling in tomato fruits

4.1 Introduction

Tomato is a good model for fleshy fruit ripening due to the availability of a high quality genome sequence, mutant collections, well characterized wild relatives, ease of transformation, etc. It is extensively used for deciphering the molecular basis for fruit ripening at transcriptome and metabolome levels (Gapper et al., 2014; Pesaresi et al., 2014). Proteome is an essential link that connects transcriptome and metabolome (Gapper et al., 2014). As proteins functionally represent the genome, proteome profiling identifies the regulatory components mediating diverse pathways, as well as the proteins that can serve as markers for improving nutritional quality, flavor, disease resistance/tolerance, shelf life, etc.

To capture the complete repertoire of the proteins present in plant tissue, a robust extraction protocol coupled with efficient peptide fractionation and identification by MS is essential. The major challenge underlying proteome profiling is the sheer number and the wide dynamic range of proteins constituting the protein complement. Moreover, plant tissues pose additional challenges owing to high level of proteases, and presence of primary and secondary metabolites that interfere with protein extraction (Saravanan and Rose, 2004). Though several protocols are available for protein extraction (Issacson et al., 2006; Wang et al., 2008) from fruit tissues like apple, banana (Carpentier et al., 2005; Amoako-Andoh et al., 2014), grape (Vincent et al., 2006), tomato (Saravanan and Rose, 2004) for 2DE based proteomics, very few exist for shotgun proteomics. Currently, shotgun proteomics is the most preferred method for proteome profiling (McCormack et al., 1997). For profiling complex mixtures of proteins, 2DLC in combination with MS/MS, MudPIT (Multidimensional Protein Identification Technology) is used (Washburn et al., 2001; Motoyama et al., 2008). Although several labeling techniques are available for proteome profiling, their inherent limitations including high costs and incomplete labeling have made label free quantification a more feasible choice for researchers (Patel et al., 2009).

In tomato fruits, shotgun proteomics for obtaining proteome profiles was used in few studies wherein, GeLCMS using purified chromoplast proteins (Barsan et al., 2012; Wang et al., 2013) or SCX (strong cation exchange chromatography) using proteins from fruit pericarp (Osorio et al., 2011) were employed prior to separation on nanoLCMS. However, no rationale was given for selecting any of these methods. Considering the difficulties involved in protein extraction and the effect of various LC conditions

(Peterson et al., 2009; Xu et al., 2009) and MS parameters (Wong et al., 2009; Zhang et al., 2009; Andrews et al., 2011; Kalli and Hess, 2012) on proteome coverage, sample preparation protocols were optimized for proteome profiling of tomato fruits. In this study, various protein extraction, fractionation protocols were evaluated and their effect on final proteome profiles were assessed. Based on the results, the protocol that had a significant impact on proteome coverage was validated across two cultivars.

4.2 Materials and methods

4.2.1 Plant material

Tomato cultivars, Arka Vikas (AV) and Ailsa Craig (AC) were grown in a green house at 25 ± 2°C. Flowers were tagged at anthesis and fruits were collected at red ripe stage. Each fruit was cut into four halves, deseeded, frozen in liquid nitrogen and stored at -80°C until use. For all experiments, AV fruit tissue was used whereas; AC and AV fruit tissue were used for validation experiments.

4.2.2 Protein extraction

With buffer saturated phenol

Proteins were extracted following the protocol described by Kilambi et al., 2013 and the protocol was given in Chapter 3.

With trichloroacetic acid (TCA)

Proteins were extracted using the protocol described by Ippoushi et al. 2015 with slight modifications. Briefly, 100mg of frozen tissue was homogenized and suspended in 1 ml of 10% (w/v) TCA in 80% (v/v) acetone containing 2% (w/v) DTT. The mixture was incubated overnight at -20°C. Thereafter, the mixture was centrifuged at 14,000 *g* at 4°C for 30 min and the supernatant was discarded. The pellet was rigorously washed with 10 ml of 80% (v/v) acetone and centrifuged at 14,000 *g* for 10 min at 4°C. The resulting supernatant was discarded and the acetone wash of the pellet was repeated as described above. Protein pellet obtained after two acetone washes was stored at -80°C until further use.

With SDS

A. Proteins were extracted with 1 ml of SDS buffer[a] (0.5 M Tris pH 6.8, 50% (v/v) glycerol, 10% (w/v SDS), 0.2 M DTT) using an earlier protocol (Mora et al., 2013).

Briefly, 1 g of homogenized tissue was suspended in 1 ml of SDS buffer[a], boiled at 95°C for 30 min. the resulting mixture was centrifuged at 5000 g for 5 min. The supernatant was precipitated with 80% (v/v) acetone by incubating at -80°C for 3 h. The protein pellet obtained after centrifugation at 20,000 *g* for 20 min was washed with 100% acetone and stored at -80°C until further use.

B. Proteins were extracted with SDS buffer[b] (4% (w/v) SDS, 100 mM Tris-HCl, pH 7.6, 0.1 M DTT) following the protocol described in (Wisniewski et al., 2009). Briefly, 0.7 g of homogenized tissue was suspended in 7 ml of SDS buffer and boiled at 95°C for 30 min. The resulting mixture was centrifuged at 5000 *g* for 5 min and the supernatant was precipitated with 80% (v/v) acetone by incubating at -80°C for 3 h. The protein pellet obtained after centrifugation at 20,000 *g* for 20 min was washed with 100% (v/v) acetone and solubilized in 50 mM ammonium bicarbonate (ABC). The protein solution was dialyzed for 16-18 h against 20 mM Tris-HCl pH 8.0. The protein solution was further used for digestion with trypsin and peptide fractionation.

C. Proteins were extracted with SDS buffer[c] (20 mM Tris-HCl pH 8.8, 2% (w/v) SDS) following the protocol described in Tanca et al., 2013. About 1 g of homogenized tissue was suspended in 1 ml of SDS buffer (20mM Tris-HCl pH 8.8, 2% (w/v) SDS) boiled at 95°C for 30 min. The resulting mixture was centrifuged at 20,000 *g* for 20 min and the supernatant was diluted to a final concentration of 0.2% (w/v) SDS and precipitated with 80% (v/v) acetone by incubating at -80°C for 3 h. Protein pellet obtained after centrifugation at 20,000 *g* for 20 min was washed with 100% (v/v) acetone and stored at -80°C further use.

With FASP (Filter Aided Sample Preparation)

100 mg homogenized fruit tissue was solubilized in 1 ml of SDS buffer[b] and proteins were extracted by FASP protocol described in Wisniewski et al., 2009. Briefly, 100 mg of homogenized tissue was solubilized in 1 ml of SDS buffer and sonicated for 5 min. Sample was centrifuged at 16,000 *g* for 5 min. The supernatant was transferred to filter unit (Millipore, YM30) and 200 µL of UA (8 M urea in 0.1 M Tris-HCl pH 8.5) was added and centrifuged at 14,000 *g* for 15 min. This step was repeated twice and the flow through was discarded. Then 100 µL of 50 mM iodoacetamide (IAA) was added and mixed at 600 rpm in thermomixer for 1 min at room temperature followed by incubation without mixing for 20 min. The filter units were then centrifuged at 14,000 *g* for 10 min

followed by addition of 100 µL of UA. This was followed by centrifugation at 14,000 *g* for 15 min. this step was repeated twice. Then 100 µL of 50 mM ABC was added and the samples were centrifuged at 14000 *g* for 10 min. This step was repeated twice. Trypsin (Promega) was added to the filter in the ration of 1: 100 (enzyme: protein) and mixed at 600 rpm on a thermomixer for 1 min. The filter units were then incubated in a wet chamber at 37°C for 16 h. After incubation, the filter units were transferred to new collection tubes and centrifuged at 14,000 *g* for 10 min. Peptides were eluted using 50 µL of 0.5 M sodium chloride and centrifuged at 14,000 *g* for 10 min. The eluate was acidified with 0.1% (v/v) formic acid, desalted using C18 spin columns (Pierce) and dried under vacuum. These samples were stored at -80°C until further use.

With FASP after phenol extraction

Proteins were extracted using phenol extraction protocol as described above and precipitated with ammonium acetate. This protein pellet was dissolved in UA (8 M urea in 0.1 M Tris-HCl pH 8.5) and processed as per FASP protocol discussed above.

4.2.3 Protein estimation

For all the discussed protocols, protein estimation was done using amido black method (Goldring and Ravaioli 1996). The amount of protein considered for further downstream processing is 100 µg unless stated otherwise.

4.2.4 Peptide fractionation

After obtaining pellets using extraction protocols descried in the previous section, proteins were digested with trypsin at specific conditions using DTT, IAA as the common reagents. The concentrations of these components and the processing conditions varied according to the fractionation method employed and are described below.

In-gel digestion-SDS-PAGE (GeLCMS)

Protein (100 µg) obtained after phenol and TCA extraction was dissolved in 2D lysis buffer and then separated on SDS-PAGE according to Laemmli, 1970. After destaining, the gel was cut into 36 slices and six slices were pooled in a single fraction (total 6 fractions were obtained). The proteins were reduced with 10 mM DTT, alkylated with 55 mM IAA and subjected to trypsin digestion (1:25, enzyme: protein) for 16 h at 37°C. Peptides from each fraction were separately extracted by addition of 60% (v/v) acetonitrile (ACN) containing 0.1% (v/v) formic acid and sonicated in ice for 30 min.

This step was repeated thrice and peptides obtained from each extraction step were pooled. The pooled peptides for each fraction were then concentrated using speed vacuum concentrator (Thermo Scientific), desalted using C18 spin columns and then subjected to LCMS analysis.

In-solution digestion

A. Phenol-extracted proteins (100 µg) were dissolved in 2D lysis buffer (7 M urea, 2 M thiourea, 4% (w/v) CHAPS), reduced with 10 mM DTT, alkylated with 40 mM IAA. Urea concentration in the solution was reduced to 2 M by the addition of 50 mM ABC. This solution was then subjected to trypsin digestion (added in the ratio of 1: 50, enzyme: protein) at 37°C for 16 h. Peptides were extracted, concentrated and desalted prior to LCMS analysis.

B. Phenol-extracted proteins (100 µg) were dissolved in 10% (w/v) SDS buffer[a], boiled at 95°C for 30 min. Samples were reduced with 10 mM DTT, alkylated with 40 mM IAA. SDS buffer concentration in the solution was reduced to 0.2 % (w/v) SDS by the addition of 50 mM ABC. The solution was then subjected to trypsin digestion (added in 1: 50, enzyme: protein) at 37°C for 16 h. Peptides were extracted, concentrated, desalted and then subjected to LCMS analysis.

C. Phenol-extracted proteins (100 µg) were dissolved in 6 M Guanidium hydrochloride buffer and boiled at 95°C for 30 min (Yeats et al., 2010). Samples were reduced with 10 mM DTT, alkylated with 40 mM IAA. Guanidium hydrochloride concentration in the solution was reduced to 0.6 M by the addition of 50 mM ABC and subjected to trypsin digestion (added in 1: 50, enzyme: protein) at 37°C for 16 h. Peptides obtained were concentrated, desalted and then subjected to LCMS analysis.

D. TCA-extracted proteins (100 µg) were digested as per the protocol descried in Ippoushi et al., 2015. Extracted peptides were concentrated, desalted prior to LCMS analysis.

E. Proteins (100 µg) obtained after extraction with SDS buffer[a] were solubilized in 1X Invitrosol (Life Technologies)/0.1% (v/v) Rapigest (Waters) in 50 mM ABC. The resulting solution was vortexed for 5 min, reduced with 10 mM DTT, incubated at 60°C for 30 min (until the pellet was completely dissolved). After the samples were cooled to room temperature, 25 mM IAA was added and incubated in dark for 30 min. Trypsin was added to the samples in the ratio of 1: 20 (enzyme: protein) and subjected to digestion at

37°C for 16 h. Formic acid (0.1% v/v) was added to the samples to stop digestion. Samples were centrifuged, supernatant was collected and peptides in the supernatant were concentrated, desalted and then subjected to LCMS analysis.

F. Proteins (100 µg) obtained after extraction with SDS buffer[b] were digested after dialysis for 16-18 h. Trypsin was added to the sample in the ratio of 1: 40 (enzyme: protein) and subjected to digestion at 37°C for 16 h. Formic acid (0.1% v/v) was added to the samples to stop digestion. Samples were centrifuged; peptides in the supernatant were concentrated, desalted and subjected to LCMS analysis.

G. Proteins (100 µg) obtained after extraction with SDS buffer[c] were solubilized in 8 M urea and incubated at room temperature for 30 min. The sample was then diluted with MilliQ water to reduce the final urea concentration to 2 M and subjected to digestion at 37°C for 16 h with trypsin. In the method where precipitation was not adopted, the concentration of SDS was reduced to 0.2% (w/v) by desalting. Protein samples were then reduced with 10 mM DTT by incubating at 56°C for 30 min. Samples were cooled to the room temperature, 25 mM IAA was added and incubated in dark for 30 min. Trypsin was added to the sample (1: 20, enzyme: protein) and subjected to digestion at 37°C for 16 h. formic acid (0.1% v/v) was added to the samples to stop digestion. Samples were centrifuged; peptides in the supernatant were concentrated, desalted and subjected to LCMS analysis.

H. Phenol-extracted proteins (100 µg) were dissolved in UA and processed as per FASP protocol discussed previously. Peptides obtained after digestion were desalted, dried and subjected to LCMS analysis.

Separation based on charge

Strong Anion Exchange (SAX)

Phenol extracted proteins (100 µg) were reduced with 10 mM DTT followed by alkylation with 40 mM IAA. The concentration of urea was reduced to 2 M using 50 mM ABC and then subjected to trypsin digestion for 16 h at 37°C (1: 50, enzyme: protein). The obtained tryptic peptides were desalted, dried and reconstituted in Tris buffer (20 mM Tris-HCl, pH 8.0) and then loaded onto SAX column (2 ml of Q-Sepharose (GE Healthcare) packed in 5 ml syringe). Fractionation was done using step gradients of 0.1 M, 0.25 M and 0.5 M NaCl, with 5 column volumes of each salt gradient. Each fraction was dialyzed for 16 h in Tris buffer (20 mM Tris-HCl pH 8.0) and thereafter desalted

prior to LCMS analysis. Similar steps were carried out for peptides obtained from FASP protocol after phenolic extraction of proteins for FASP-SAX and also for peptides obtained from TCA extracted protein.

Peptide IEF (PEP-IEF)

Peptide IEF was carried out based on the protocol developed by Atanassov and Urlaub, 2013. Peptides obtained from phenol extraction (250 µg and 500 µg), phenol-FASP protein extraction (100 µg) and TCA extraction (100 µg) were dissolved in 8 M urea and 0.2% (v / v) IPG (immobilized pH gradient) buffer (GE Healthcare). This peptide solution was applied to 4-7 pH/3-10 pH IPG strips and passively rehydrated overnight at 25°C followed by separation on IPGphor (GE Healthcare) at maximum of 50 µA per strip using the following conditions: 150 V for 1 h, 250 V for 1 h, 500 V for 30 min, 1750 Vh at a gradient of 500 V to 3000 V, then 27750 Vh at 8000 V at 20°C. After peptide IEF, IPG strips were cleaned by immersing them in n-hexane for 10 sec followed by slicing the gel into 12 pieces (1 cm each). Peptides were then extracted by incubating the gel slices for 30 min each with 1% (v / v) FA; 50% (v / v) ACN, 1% (v / v) FA; and 99% (v / v) ACN, 1% (v / v) FA. Extracted peptides were desalted, dried and subjected to LCMS analysis.

4.2.5 LCMS analysis for peptide separation

Separation of peptides was carried out on Easy nanoLC-II coupled with LTQ Velos Pro mass spectrometer (Thermo Scientific). Tryptic peptides (350 ng) were loaded onto a trap column (Integrafrit 100 µm x 2.5 cm, 5 µm, New Objective, USA) using solvent A (95/5-water/ACN with 0.1% (v/v) formic acid) and solvent B (95/5-ACN/water with 0.1% (v/v) formic acid) at a flow rate of 350 nl/min. Different gradients were employed for samples obtained from various extraction protocols based on the complexity of the sample, fractionation technique employed and the number of fractions collected and the details of the gradients are listed in Table 4.1. Column eluate was connected to nanospray ionization source operated at a voltage of 1.7 kV and a capillary temperature of 260°C. Mass spectra were obtained through data dependent acquisition in positive mode. MS scans were performed in Orbitrap at a resolution of 60,000 within a scan range of 350-2000. Data dependent MS/MS scans were performed in ion trap using CID as the fragmentation technique. The activation energy of 35% and activation time of 10 ms was used for fragmentation. Dynamic exclusion of 30 sec was enabled with a

repeat count of 1 and a lock mass of 445.120030 was used for mass accuracy. An isolation window of 2 *m/z* was applied. Automatic gain control targets of 500 ms and 500000 ions for FTMS and 100 ms and 10000 ions for MS/MS were applied respectively.

4.2.6 Validation of protein preparation and fractionation

To check the consistency of the sample extraction/solubilization/fractionation conditions, proteome profiling of ripe tomato fruits from two different cultivars-Arka Vikas (AV) an Indian cultivar grown predominantly in South India, and Ailsa Craig (AC), a popular European cultivar was carried out. Phenol extraction followed by in-gel digestion (GeLCMS for all the cultivars) was employed for sample preparation in three biological replicates.

4.2.7 Data analysis

Data analysis was done using Proteome Discoverer (version 1.4, Thermo Scientific). S. lycopersicum iTAG2.3 proteome sequence (ftp://ftp.solgenomics.net/tomato_genome/annotation/ITAG2.3_release/ITAG2.3_proteins.fasta, downloaded on February 5, 2013, 26705 sequences and 9322189 residues) was used as the database against which the searches were done. Peptide mass tolerance and fragment mass tolerance were set to 5 ppm and 0.8 Da respectively. Sequest was used as the search engine with the following search parameters- trypsin as the protease, a maximum of two missed cleavages were allowed, carbamidomethylation of cysteine and oxidation of methionine were selected as fixed and variable modifications respectively. Peptides were filtered for high confidence and these were used for assigning protein IDs. Percolator tool was used to assess peptide confidence; peptides with q value ≤ 0.05 were selected (false discovery rate (FDR) of 1%), which was estimated based on the number of decoy hits. Proteins that passed the criteria of high confidence with XCorr threshold greater than 2.0 and a minimum number of two matched peptides were considered. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium (Vizcaino et al., 2014) via the PRIDE partner repository with the dataset identifier PXD003920.

4.2.8 Gene Ontology analysis

Proteins identified in this study were annotated based on their molecular function, biological process and cellular component with Gene Ontology (GO) annotation using ProteinCenter (Version 1) in Proteome Discoverer 1.4.

4.2.9 Label-free quantitation

The raw data obtained from the mass spectrometer were analyzed using Scaffold software (version 4.4.8, Proteome Software) using the parameters and the database as mentioned above in data analysis. Peptides were filters for high confidence (95% protein and peptide probabilities, assigned through Protein Prophet algorithm; Nesvizhskii et al., 2003) and these were used for assigning protein IDs. An FDR cut off of 1% which was estimated through a local FDR database was used to filter the peptides on the basis of number of decoy hits. Label-free quantification was performed by spectral counting method in Scaffold. The protein abundances were calculated through normalized spectral abundance factor (NSAF), which divides the weighted spectrum count for each protein by the length of the same protein and the results are then normalized across all samples (Zybailov et al., 2006). Fisher's exact test was applied on the proteins with a match of minimum two peptides and FDR of 0.1% to identify the statistically significant proteins based on their P Values. The proteins which have passed the criteria of minimum two peptides, two-fold up- or down-regulation and a P Value of less than or equal to 0.05 were considered as significantly different between AC and AV cultivars.

4.2.10 Carotenoid profiling

Carotenoid content in the red ripe fruits of AV and AC was determined using a previously published protocol (Gupta et al., 2015). Briefly, the fruit tissue was homogenized into powder and extracted with 1 ml of chloroform and 0.5 ml of dichloromethane. The samples were then incubated for 20 min on a thermomixer at 1000 rpm, 4°C. 0.5 ml of NaCl saturated water was added and the samples were mixed and centrifuged at 5000*g* for 10 min at 4°C. The carotenoid-rich lower phase was collected and aqueous phase obtained was re-extracted with 0.5 ml chloroform and 0.25 ml dichloromethane to separate the phases. Both the carotenoid phases were pooled and dried in a speed vac and were then dissolved in 1 ml of MeOH: MTBE (25:75). A final volume of 20 µl was injected into HPLC. The samples were separated on a C30, 3 µm column (250 x 4.6 mm) coupled to a 20 x 4.6 mm C30 guard column using mobile phases consisting of 5% aqueous methanol (A), 2% aqueous methanol (B) and tert-methyl butyl ether (C) at a flow rate of 1 ml per min and column temperature was maintained at 20°C. The gradient method used with this column was 70% A, 30% C at 0 min, followed by linear gradient to 60% A, 40% C at 2.00 min, a step to 60% B, 40% C at 2.01 min followed by a linear gradient to 100% C by 12 min and return to initial conditions by

13.00 min. A re-equilibration for 7 min was then used to condition the column to the initial concentrations of mobile phases A and C. The carotenoid amounts were calculated after comparing the peak areas with standard areas using Xcalibur software.

4.3 Results

Ideally, the protein extraction protocol should reproducibly capture most of the protein repertoire from a given biological matrix with minimal protein degradation and minimal contamination of extraneous components. The presence of high levels of soluble sugars, cell wall polysaccharides, organic acids and the aromatic ring containing secondary metabolites in tomato fruits interferes and leads to suboptimal protein extraction (Saravanan and Rose, 2004). Few studies (Wang et al., 2008; Saravanan and Rose, 2004; Wu et al., 2014) have critically reviewed phenol and TCA/acetone for protein extraction and precipitation in a variety of plant tissues for proteome profiling using 2DE. However, their applicability to shotgun proteomics remains to be established. In this study, the suitability of sample preparation protocols on final proteome coverage using shotgun proteomics approaches was examined. Additionally, efforts were made to simplify the protocol by altering the components, using filter aids and consequential differences in protein identification were examined.

4.3.1 Comparison of protein extraction protocols

Among the extraction methods tested, protein extraction with buffer-saturated phenol followed by precipitation with ammonium acetate in methanol and subsequent fractionation (either by in-gel/in solution-IEC) yielded highest number of proteins (3220) compared to proteins obtained with TCA/acetone (2907) (Fig. 4.1). Replacing phenol with SDS buffer[a] (Fig. 4.1), SDS buffer[b] or SDS buffer[c] (Table 4.2) resulted in total loss of proteins. Precipitation with chilled acetone after extraction with SDS buffer[a] yielded only 114 proteins.

For animal and bacterial tissues, FASP is widely used as it is a simple and efficient method (Wisniewski et al., 2009). In plants, only few studies used FASP after extraction of protein using TCA/phenol (Zhang et al., 2015, Wang et al., 2014). In the present study, the applicability of FASP to tomato fruit tissue was examined with an aim to simplify and reduce the number of steps involved in sample preparation. After lysis of the homogenized fruit tissue in the SDS buffer[b] on micron filters, followed by washing and digestion as per FASP protocol, no proteins were detected by LCMS analysis. In

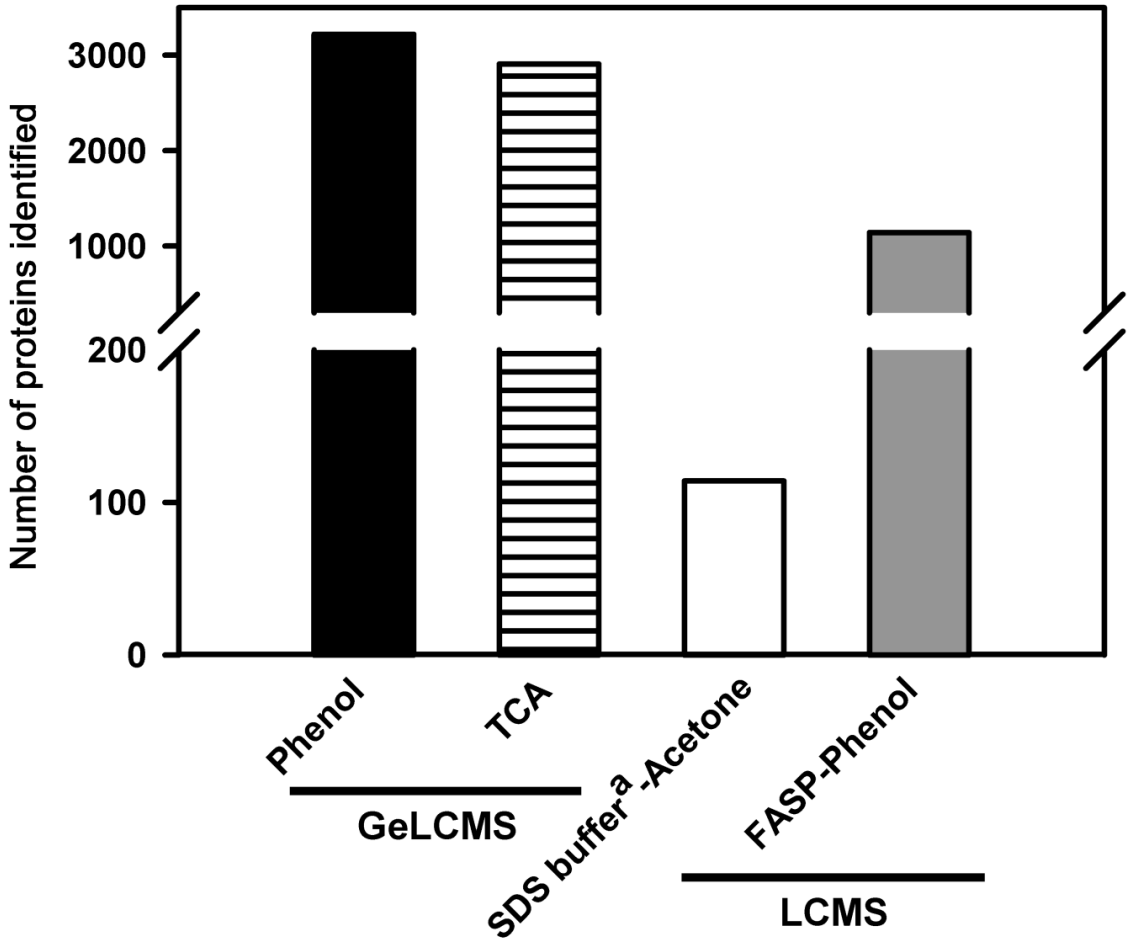


Figure 4.1. Effect of different extraction and precipitation reagents on protein identification. Only the proteins identified with ≥2 peptide matches are shown. The details of the buffer composition, reagent concentrations, and conditions are described in methods.

contrast, repetition of the same procedure with protein obtained after phenol extraction and ammonium acetate precipitation followed by digestion on micron filters identified 1141 proteins (Fig. 4.1).

4.3.2 Addition of surfactants has no appreciable impact on protein identification

Solubilization of proteins is essential to untangle the complex structural organization to simpler polypeptide chains by breaking the non-covalent interactions. Incomplete solubilization results in loss of proteins and a range of compounds such as chaotropes like urea, thiourea, detergents such as SDS, CHAPS (Molloy, 2000), and reducing agents like DTT or 2-mercaptoethanol (Mechin et al., 2003) are used in combination to assist protein solubilization. Recently, Chen et al. (2007) reported the usage of Invitrosol and Rapigest for improving the total proteome coverage in shotgun proteomics. Table 4.2 shows an evaluation of both conventional chaotropes that are used in buffers as well as MS compatible surfactants for protein solubilization in in-solution digested samples. Usage of 8 M urea for solubilization of protein obtained after boiling with SDS buffer and precipitation with 80% acetone yielded 610 proteins on separation on nanoLCMS. In contrast, use of 50 mM ammonium bicarbonate and/or guanidium hydrochloride/Invitrosol/Rapigest for dissolving proteins dissolving proteins identified a total of 0, 233, 888, and 402 proteins respectively. The addition of Invitrosol though increased the number of proteins but not appreciably. The addition of Rapigest decreased the number of identified proteins (Table 4.2). Notwithstanding the inadequacy of Rapigest for tomato fruits, it has been used for microsomal protein in tomato roots (Mbeunkui and Goshe, 2011). The solubilization of proteins obtained after phenol/TCA extraction in 2D lysis buffer/SDS buffer and a combination of both was also inefficient, resulting in very few proteins (9, 8, 10, and 0 proteins) respectively (Table 4.2). Above results indicated that irrespective of the methods used for protein extraction and precipitation, the solubilization of proteins is a very critical step for obtaining good proteome coverage.

4.3.3 Fractionation is necessary for increased protein identification

Protein fractionation helps in reducing the inherent complexity of the sample and helps in improving the proteome coverage as well as the visibility of low abundance proteins. Various fractionation techniques were evaluated using the protein isolated from tomato fruits (Fig. 4.2). Post-fractionation, peptides were separated on LC using different

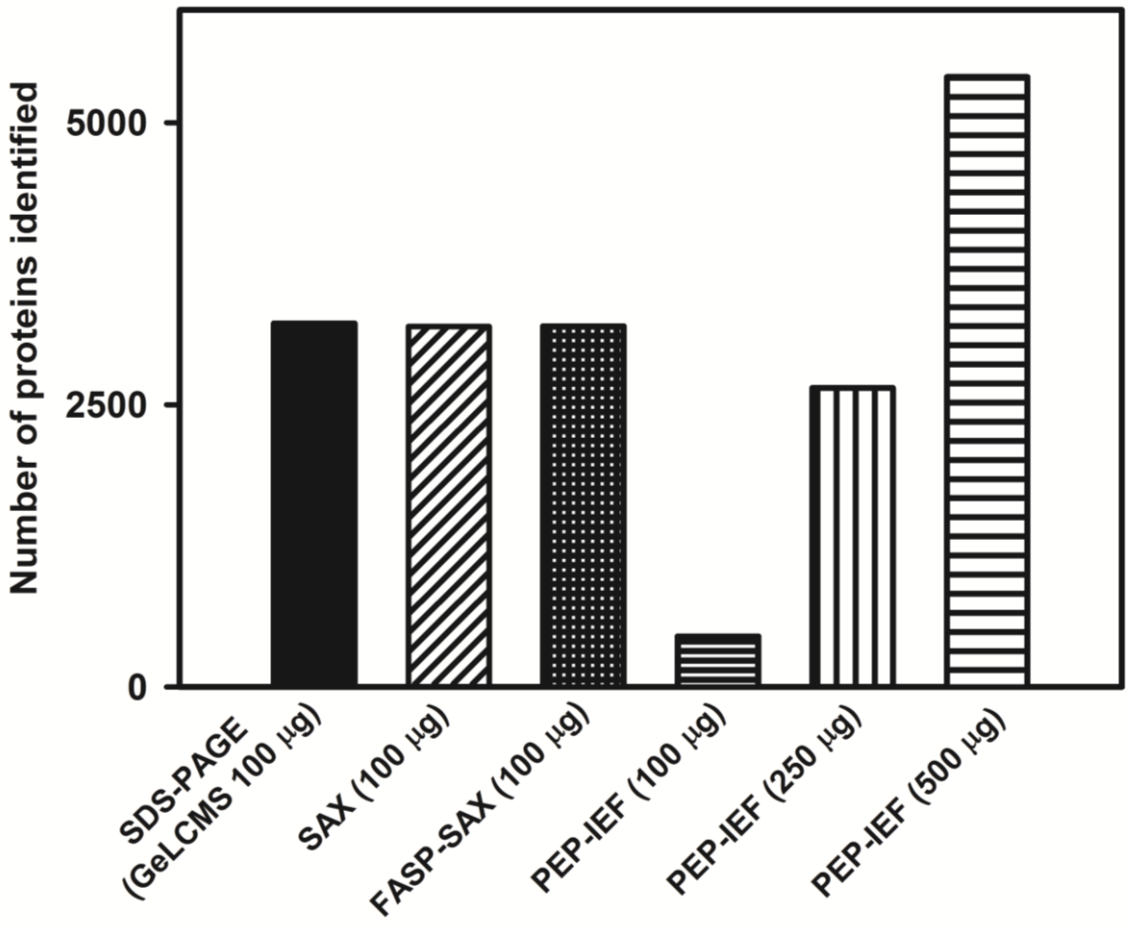


Figure 4.2. Effect of different fractionation techniques on proteome coverage. Only the proteins identified with ≥2 peptide matches are shown. The details of the buffer composition, fractionation conditions, etc. are described in methods.

gradients based on the complexity of the sample and fractionation technique employed (Table 4.1). The size fractionation of proteins (100 µg) on SDS-PAGE followed by tryptic digestion resulted in the identification of 3220 (Phenol; Figs. 4.1 and 4.2) and 2907 (TCA; Fig. 4.1) proteins after LCMS. Treatment of proteins obtained after phenol extraction with 6 M Guanidium hydrochloride followed by tryptic digestion and further fractionation based on the charge by strong anion exchange chromatography (SAX) resulted in the identification of 3100 proteins (Fig. 4.2). However, when SAX was carried out using protein obtained from TCA/acetone, no proteins were identified. Similarly, FASP followed by separation of peptides on SAX resulted in 3195 proteins (Fig. 4.2). FASP, when used alone, did not yield any protein identification. Fractionation of peptides obtained after digestion of 500 µg and 250 µg protein (obtained after phenol extraction) by peptide IEF (PEP-IEF) yielded about 5404 and 2649 proteins (Fig. 4.2). On the contrary, PEP-IEF using an initial protein concentration of 100 µg (which was used for the previously mentioned in-gel and in-solution preparations) identified only 447 proteins. However, when PEP-IEF was performed using peptides obtained after digestion of 100 µg TCA-extracted protein, no proteins could be identified.

4.3.4 Functional annotation of the proteins identified from different extraction and fractionation techniques

We investigated whether the GeLCMS approach was biased for proteins based on their molecular function, the biological processes they mediate or to the cellular component they belong. All the peptide fractionation techniques such as GeLCMS, SAX, FASP-SAX and PEP-IEF (250 µg) that resulted in the identification of a similar number of proteins were considered for GO analysis. Overall, GO analysis revealed that none of the categories were significantly different between the peptide fractionation techniques employed in this study. However, membrane proteins were enriched marginally in SAX (33%) and FASP-SAX (36%) compared to GeLCMS (23%) (Fig. 4.3). Moreover, for all the GO categories, the proportion of un-annotated proteins was lowest for GeLCMS than any other fractionation technique employed in this study.

4.3.5 Validation of the peptide fractionation protocols using different tomato cultivars

To check the consistency of the results obtained through GeLCMS protocol, the in-gel samples from two different tomato cultivars were subjected to LCMS analysis. The

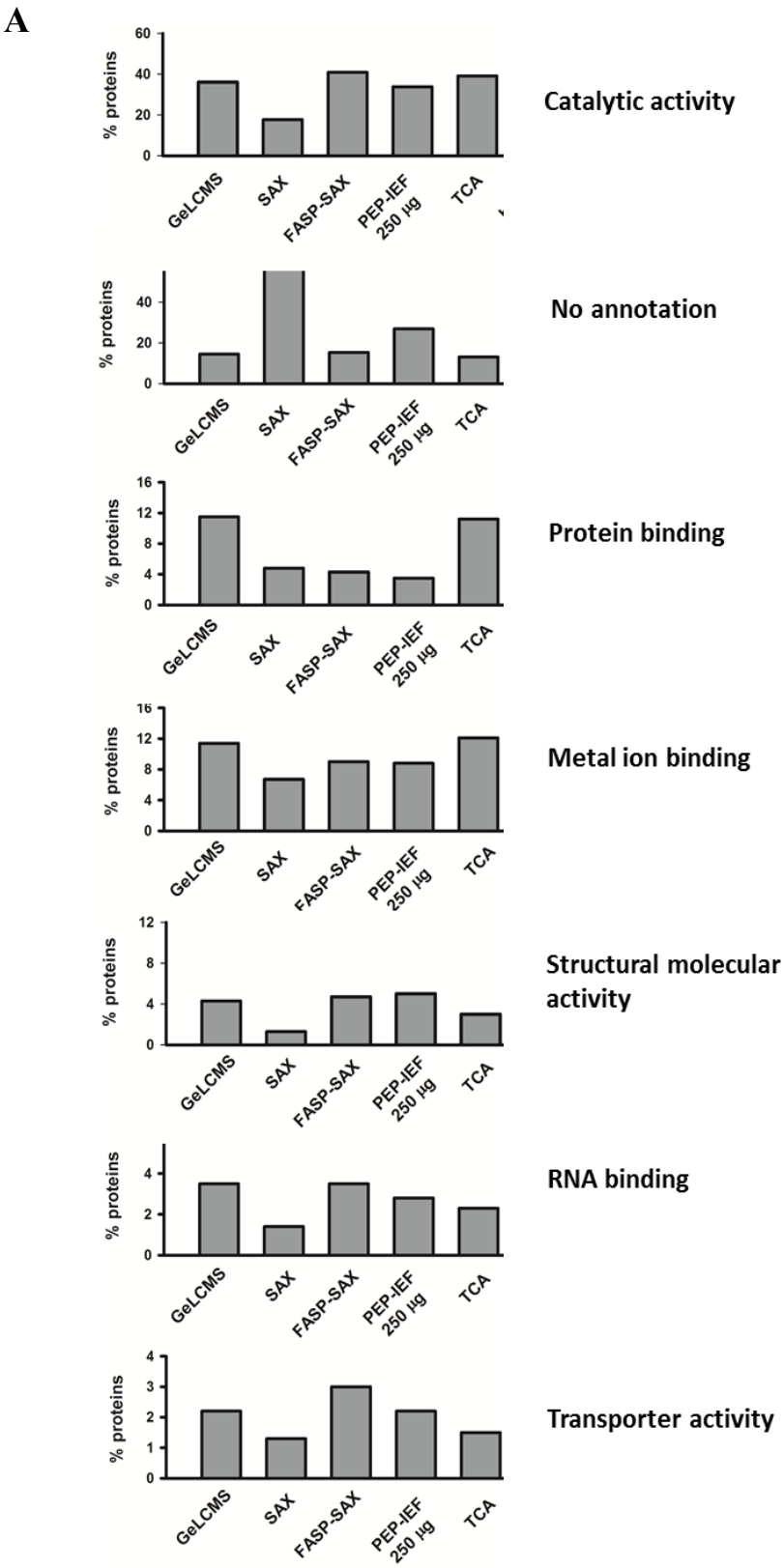


Figure 4.3. GO annotation of the proteins identified using different fractionation methods. A, based on molecular function.

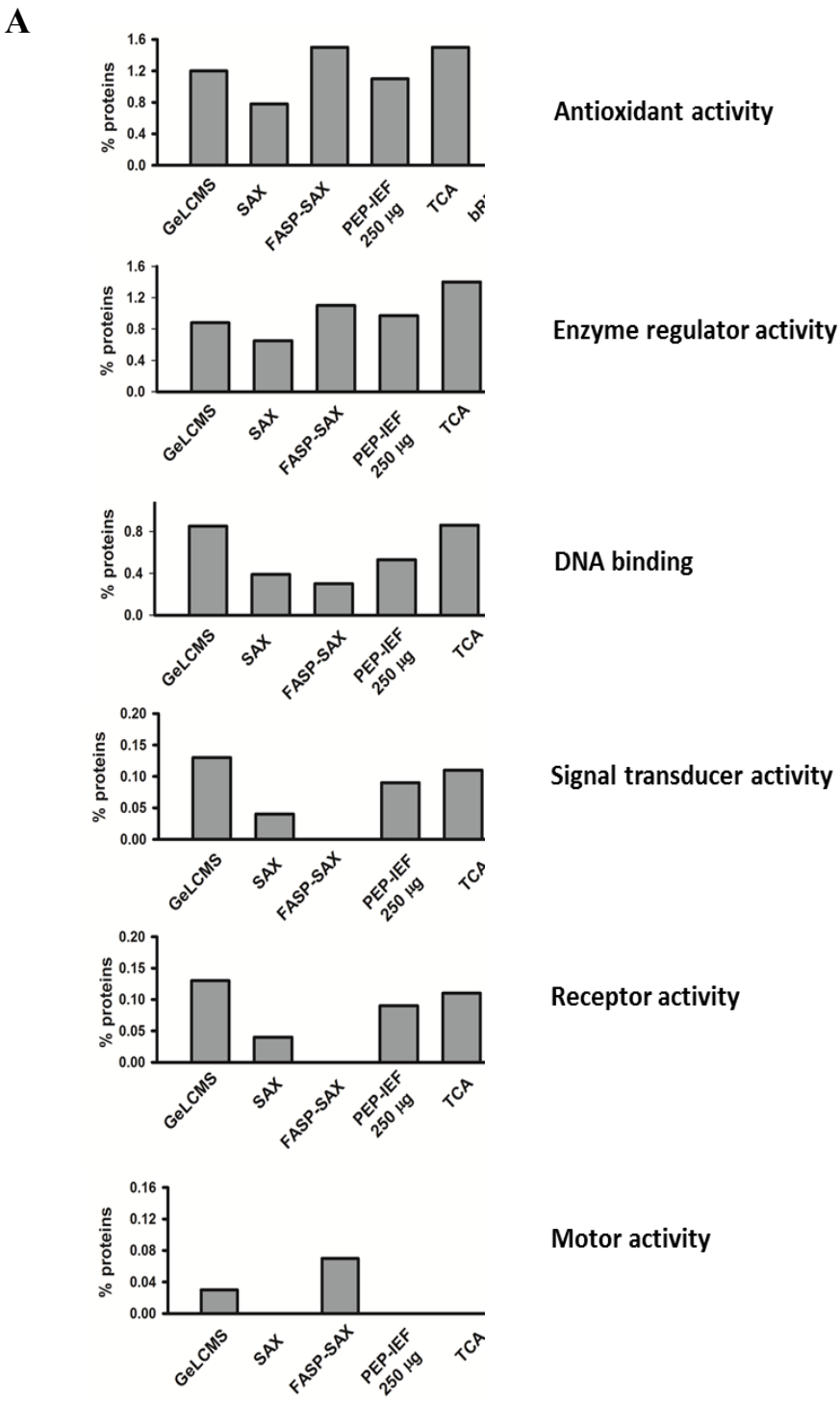


Figure 4.3. GO annotation of the proteins identified using different fractionation methods. A, based on molecular function.

B

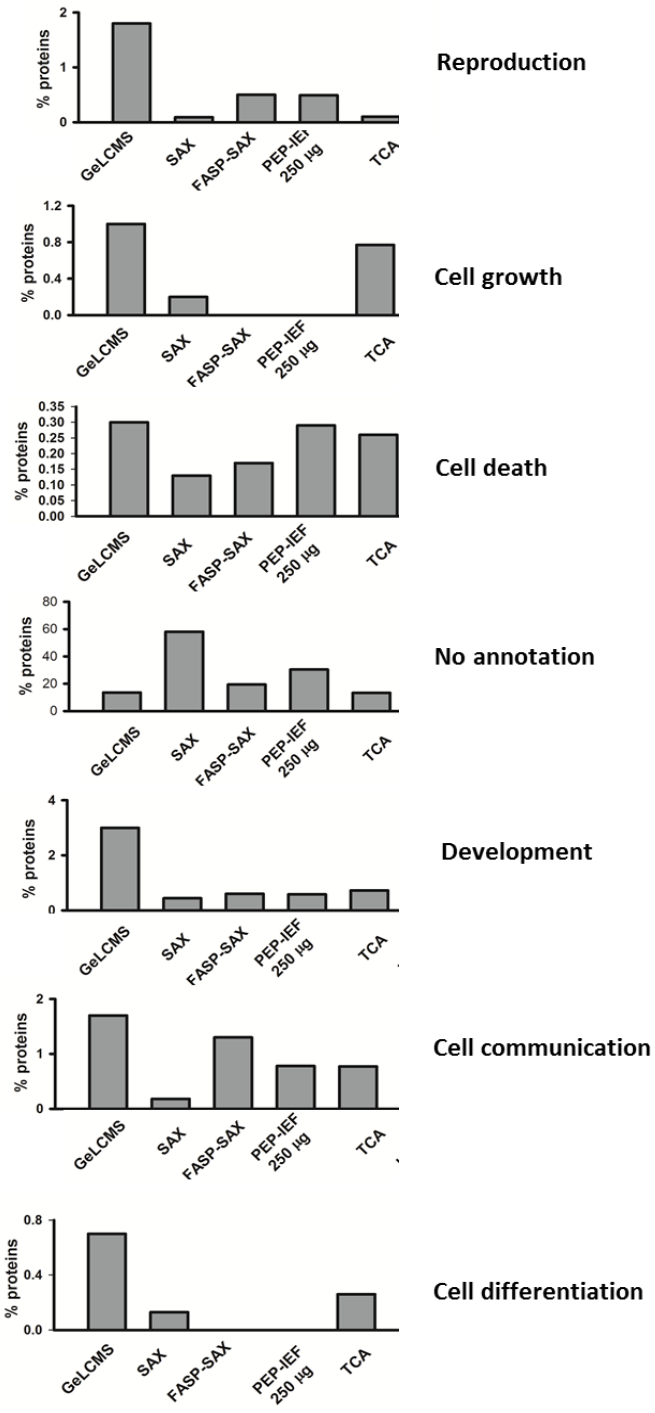


Figure 4.3. GO annotation of the proteins identified using different fractionation methods. B, based on biological process.

B

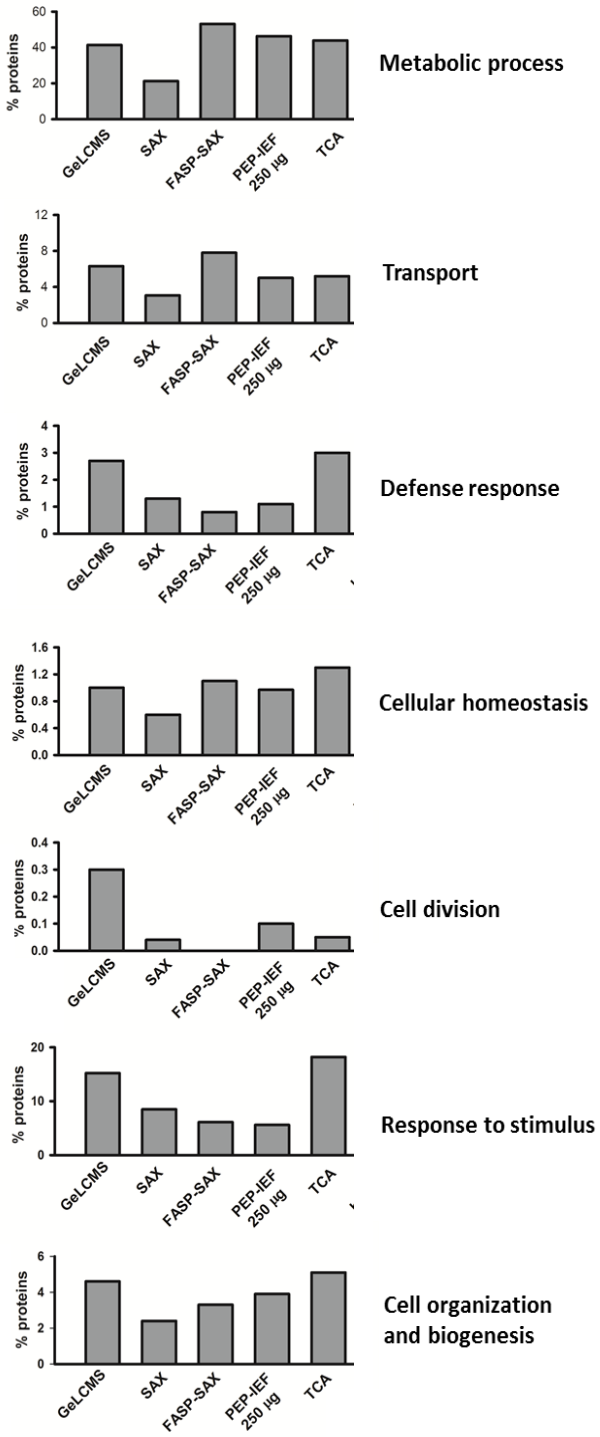


Figure 4.3. GO annotation of the proteins identified using different fractionation methods. B, based on biological process.

B

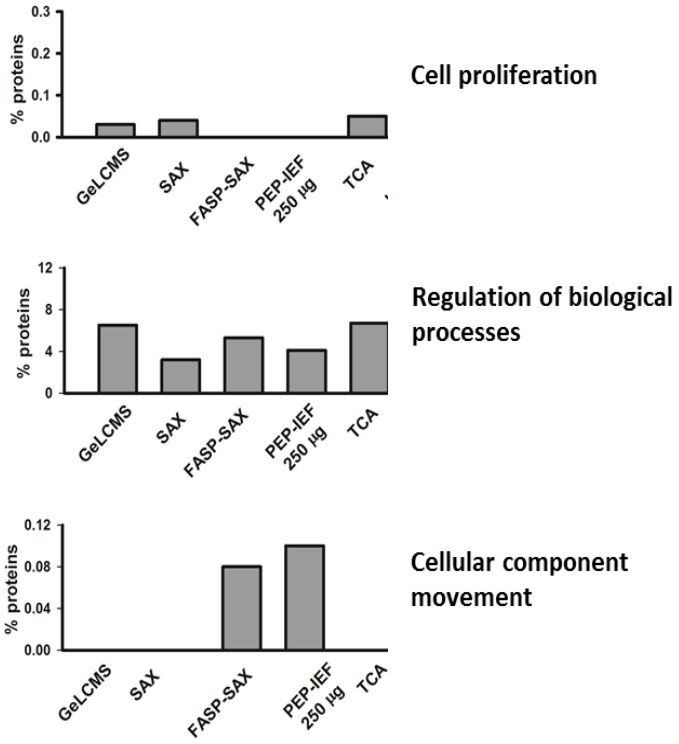


Figure 4.3. GO annotation of the proteins identified using different fractionation methods. B, based on biological process.

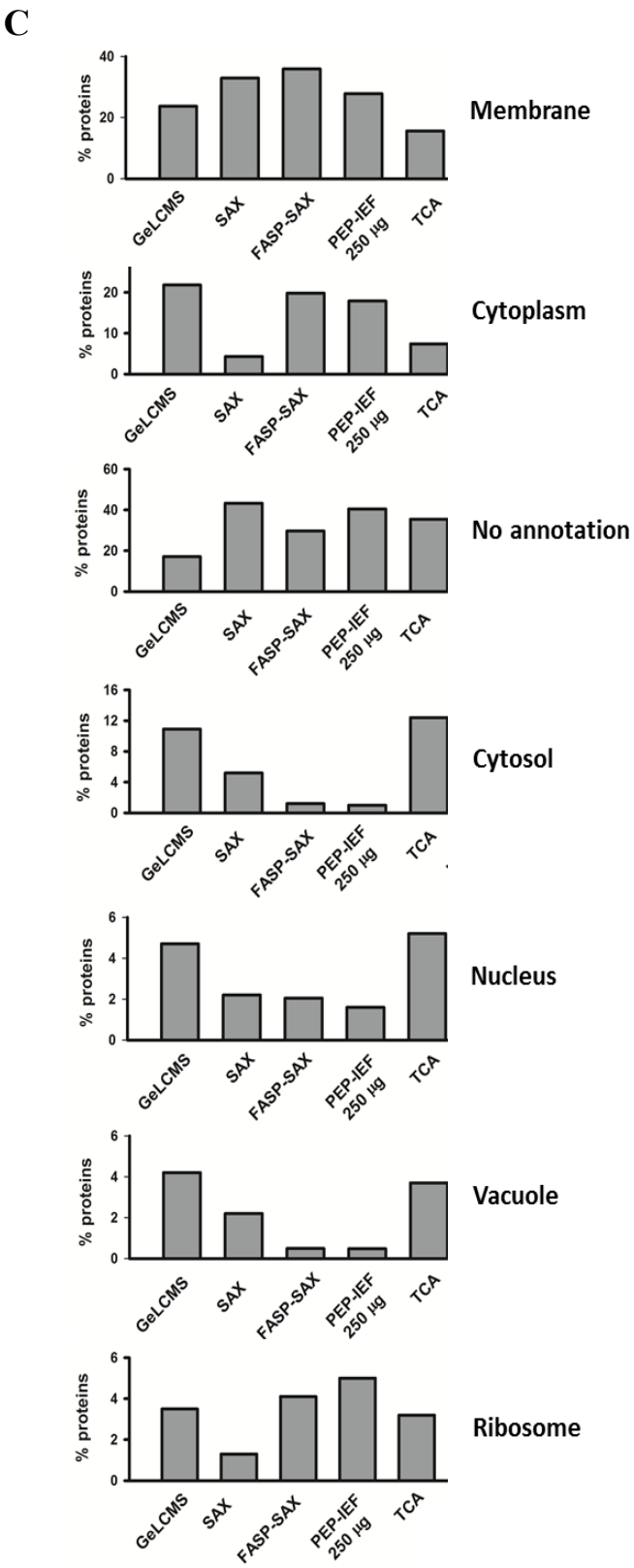


Figure 4.3. GO annotation of the proteins identified using different fractionation methods. C, based on cellular component.

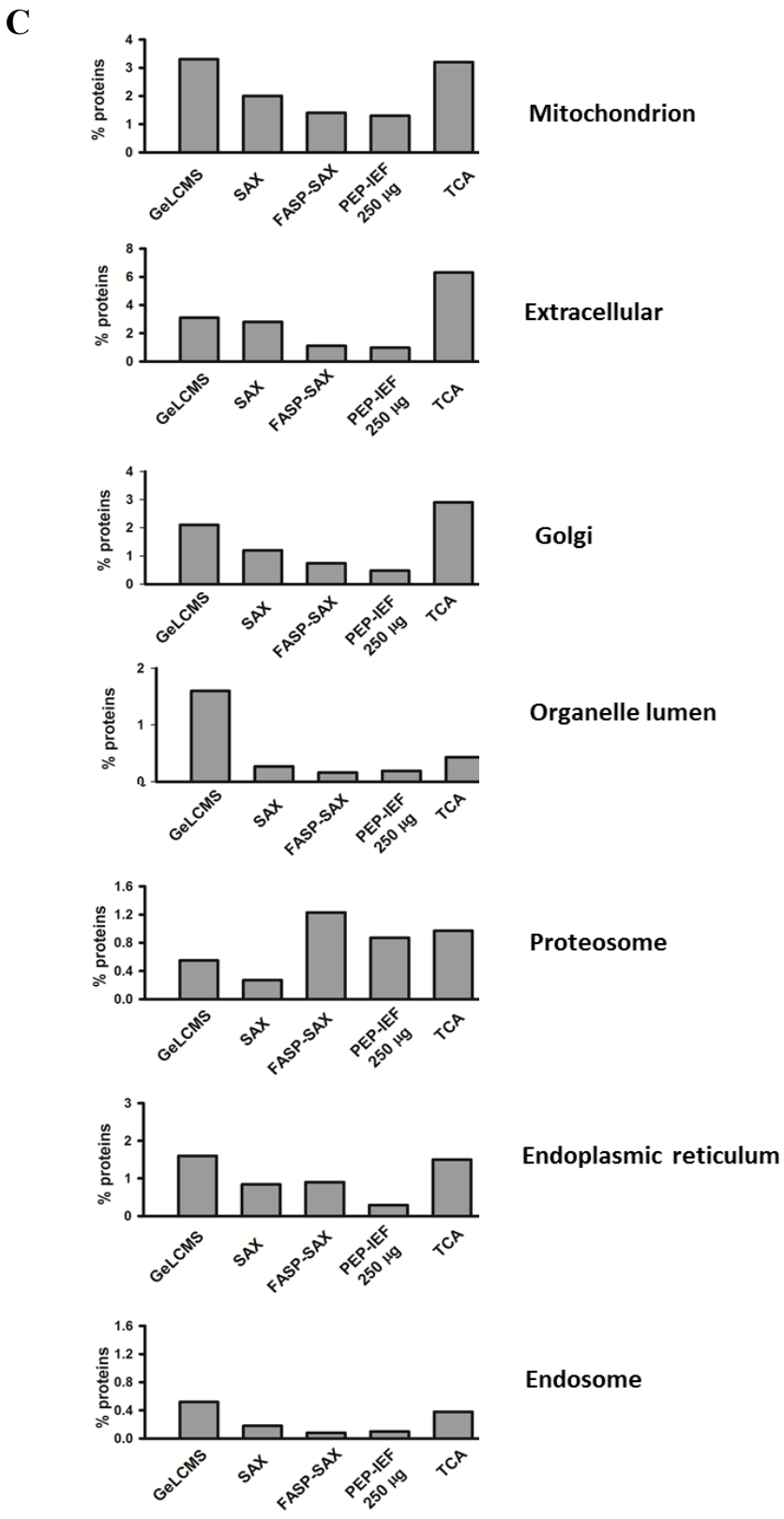


Figure 4.3. GO annotation of the proteins identified using different fractionation methods. C, based on cellular component.

C

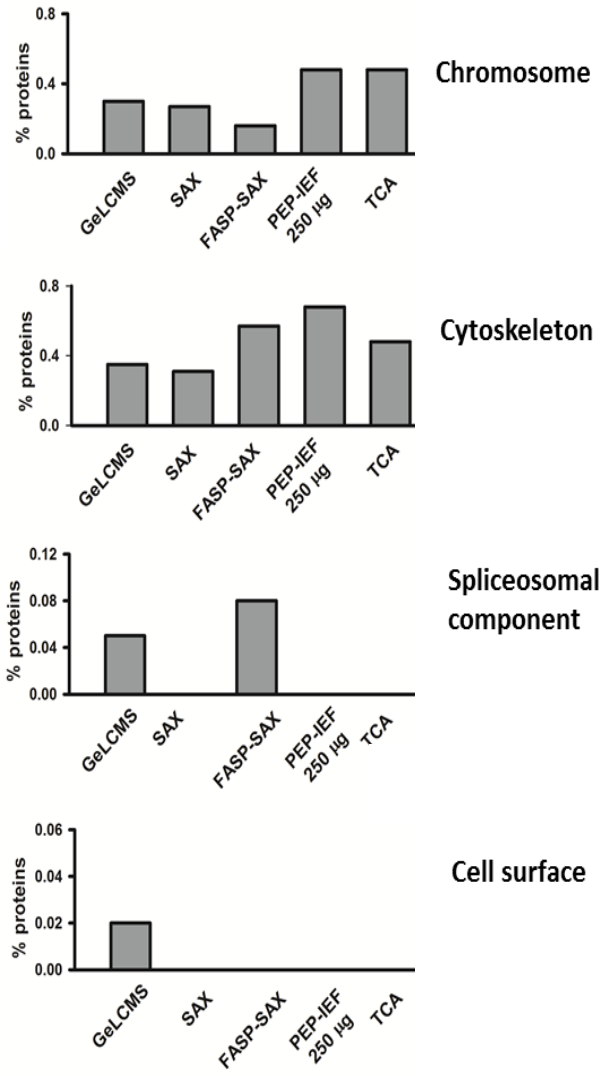


Figure 4.3. GO annotation of the proteins identified using different fractionation methods. C, based on cellular component.

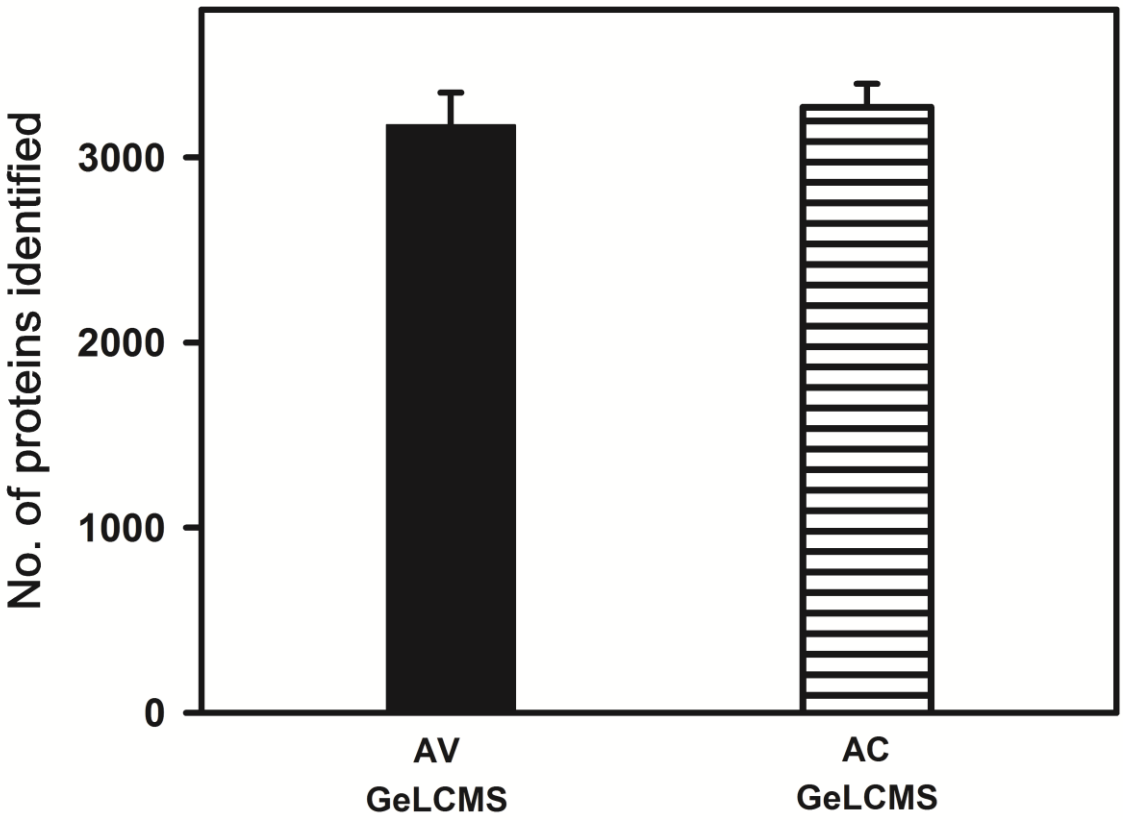


Figure 4.4. Validation of optimized sample preparation and data dependent acquisition method using two tomato cultivars. Proteins/peptides obtained after extraction with phenol and fractionation using GeLCMS from ripe fruits of tomato cultivars (AV and AC) were used for validation. Only the proteins identified with ≥2 peptide matches are shown (n=3±SE).

number of proteins identified were consistent in both the cultivars with CV<10% suggesting the reproducibility and the robustness of the method (Fig. 4.4). It is to be noted that the proteome coverage obtained in our study is much higher (3220 proteins) than reported earlier in tomato fruits using MUDPIT (Shah et al., 2012; 588 proteins) and 2D electrophoresis followed by protein identification by nLCMS (Xu et al., 2013; 506 proteins). As expected, subcellular fractionation and enrichment of chromoplasts from tomato fruits yielded good proteome coverage with GeLCMS (1932 proteins-Barsan et al., 2012; 953 proteins-Wang et al., 2013). However, chromoplast isolation is time consuming and requires large quantities of fruit tissue (a minimum of 250 g), whereas our protocol uses only 1 g of fruit tissue as starting material. Also, the protocol can be scaled up depending upon the experimental goals to obtain even better proteome coverage as PEP-IEF with 500 µg protein identified 5404 proteins.

4.3.6 GO analysis for the proteins identified in AC and AV

We next examined the variation in the fruit proteome between two cultivars, AC and AV using spectral counting of the proteins identified by GeLCMS. GO analysis revealed a similar proportion of functional categories based on their molecular function, biological process and cellular component in case of AC and AV suggesting no major differences in protein function in these two cultivars (Fig. 4.5).

4.3.7 Identification of differentially expressed proteins between AC and AV fruits using label-free quantification

Of the total proteins identified in red ripe fruit samples of AV (3220) and AC (3278) (Fig. 4.4), a total of 2664 and 2734 proteins were quantified in a label-free manner using spectral counting in Scaffold. The above quantification resulted in the identification of 292 differentially expressed proteins of which 186 proteins were up-regulated and 106 proteins were down-regulated in AV in comparison to AC (Table 4.3). In addition, 113 proteins were detected only in AC whereas 234 proteins were detected only in AV (Table 4.4). Proteins detected only in AC or only in AV were not represented as single peptide hits in the cultivars.

4.3.8 Functional classification of differentially expressed proteins

The differentially expressed proteins were classified into functional categories using Mapman (Usadel et al., 2009). All the up-regulated proteins were classified into 36 functional categories and 33 functional classes were identified in down-regulated

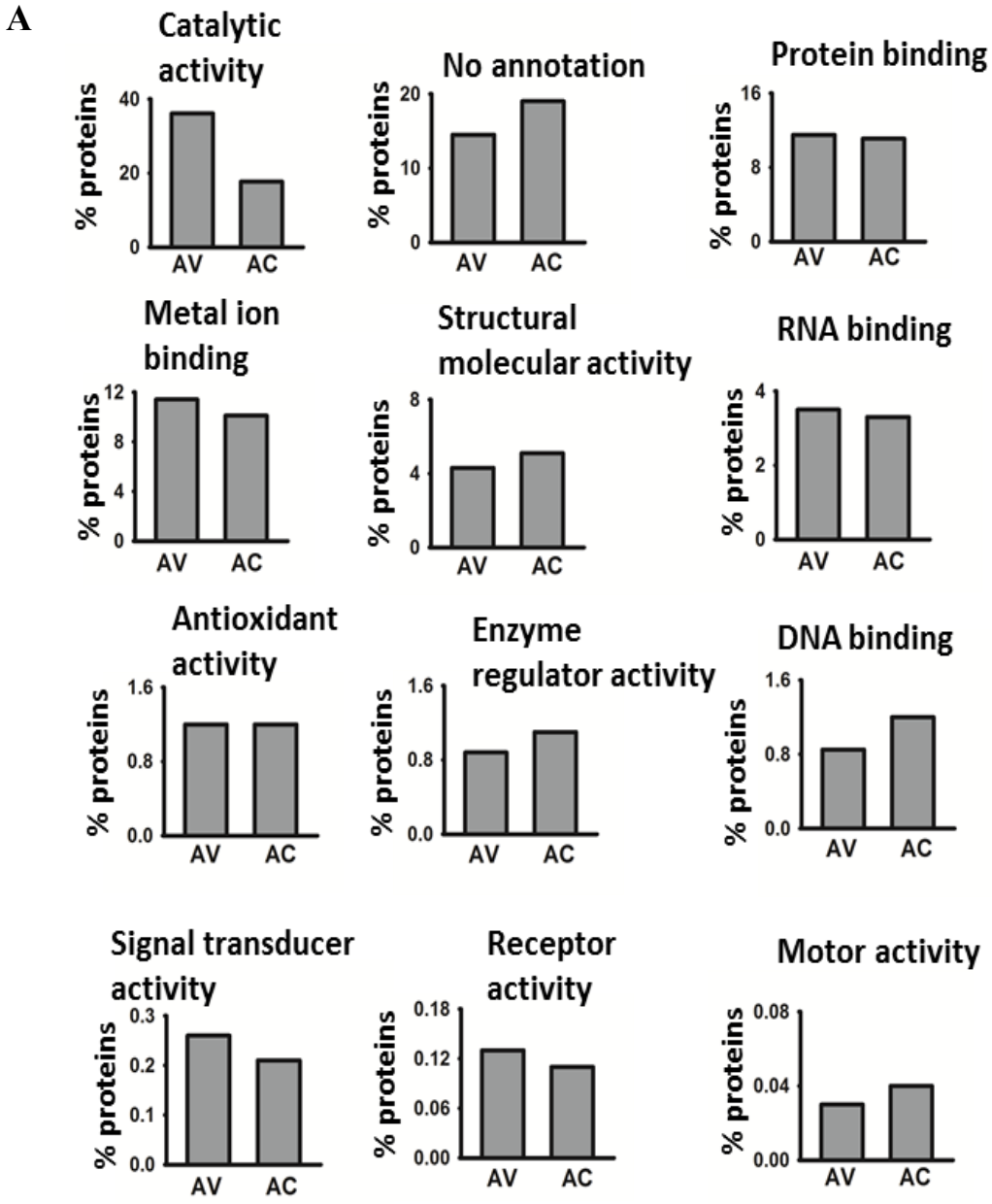


Figure 4.5. GO annotation of the proteins identified in AC and AV cultivars. A, based on molecular function.

B

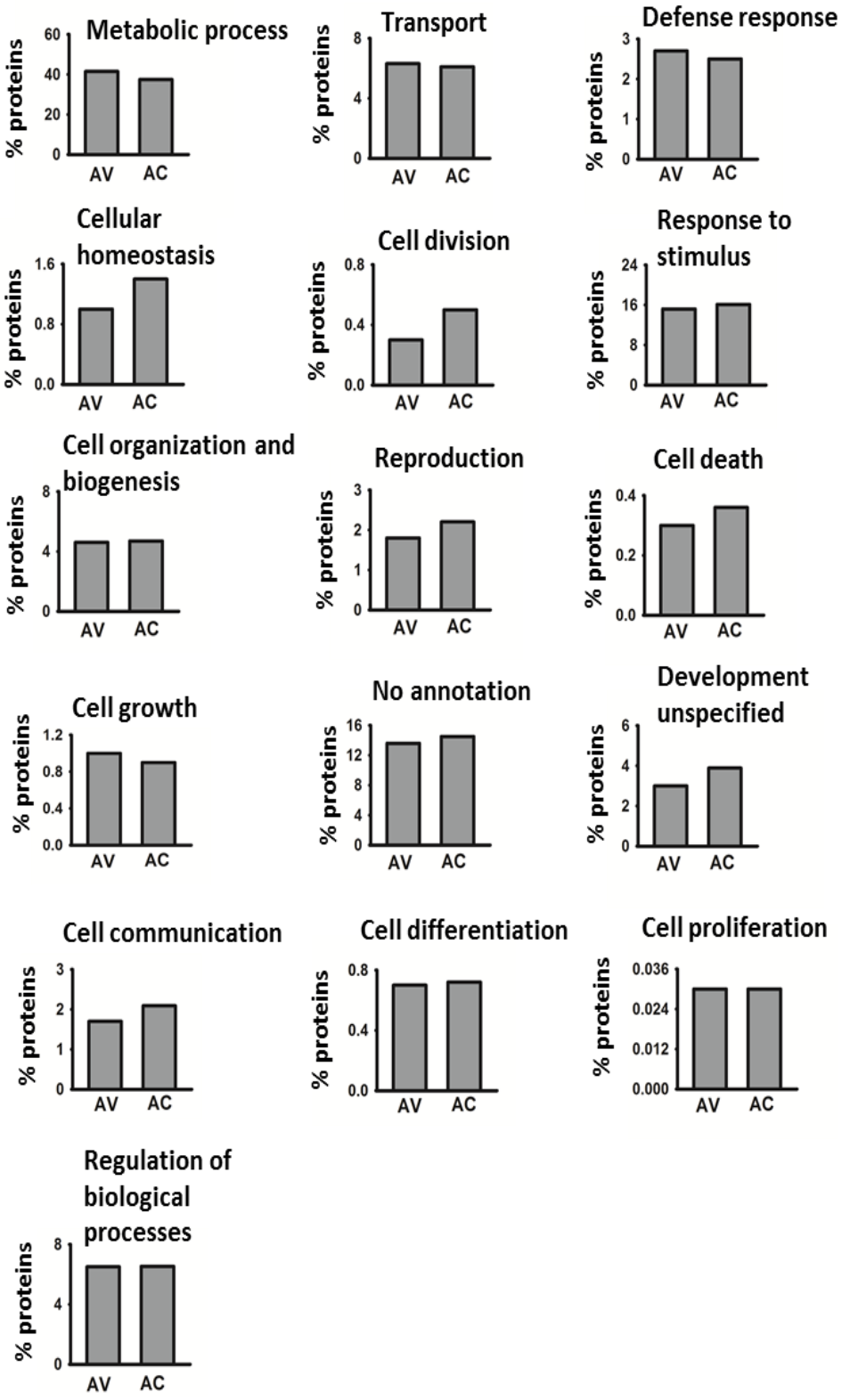


Figure 4.5. GO annotation of the proteins identified in AC and AV cultivars. B, based on biological process.

C

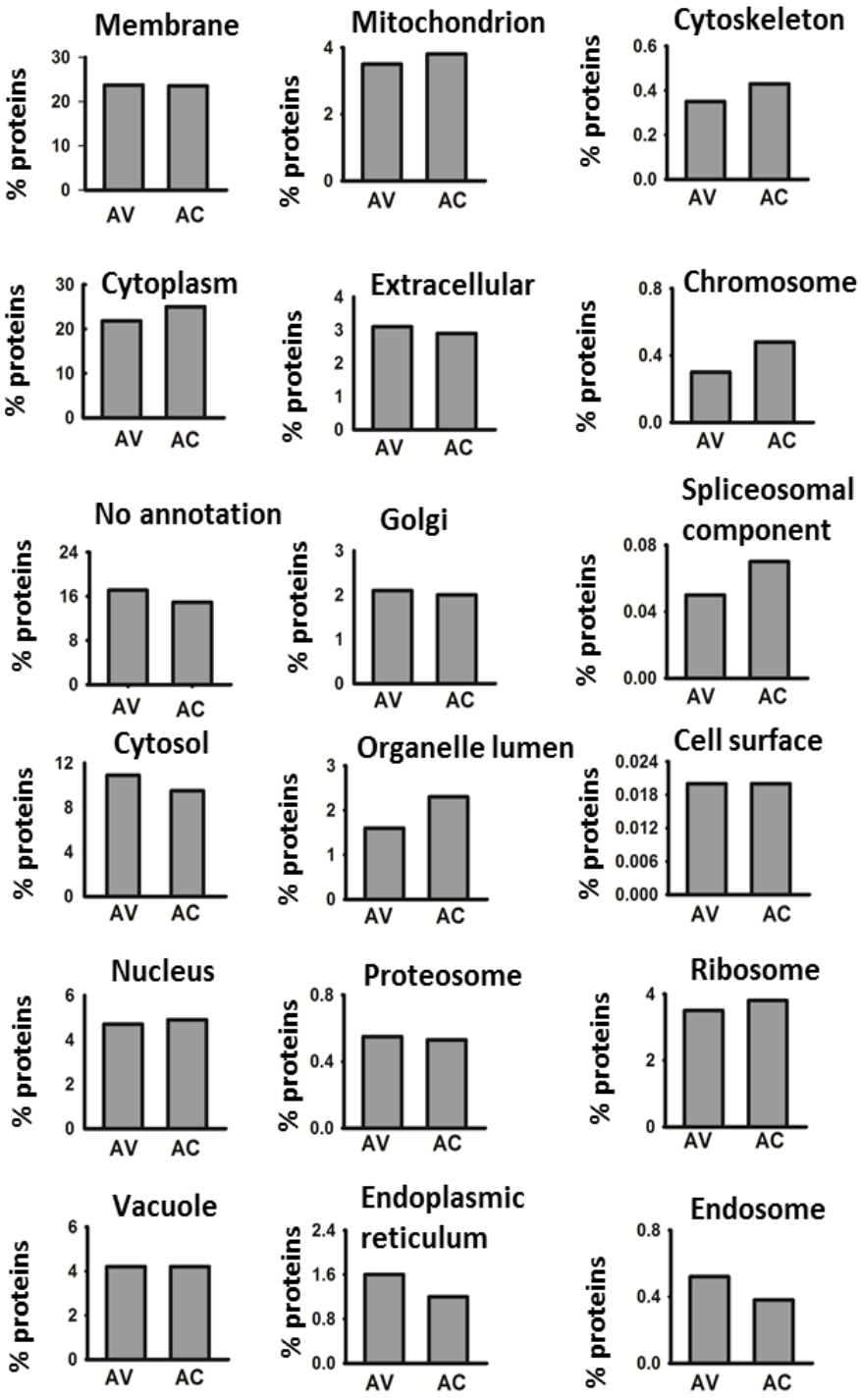


Figure 4.5. GO annotation of the proteins identified in AC and AV cultivars. C, based on cellular component.

A

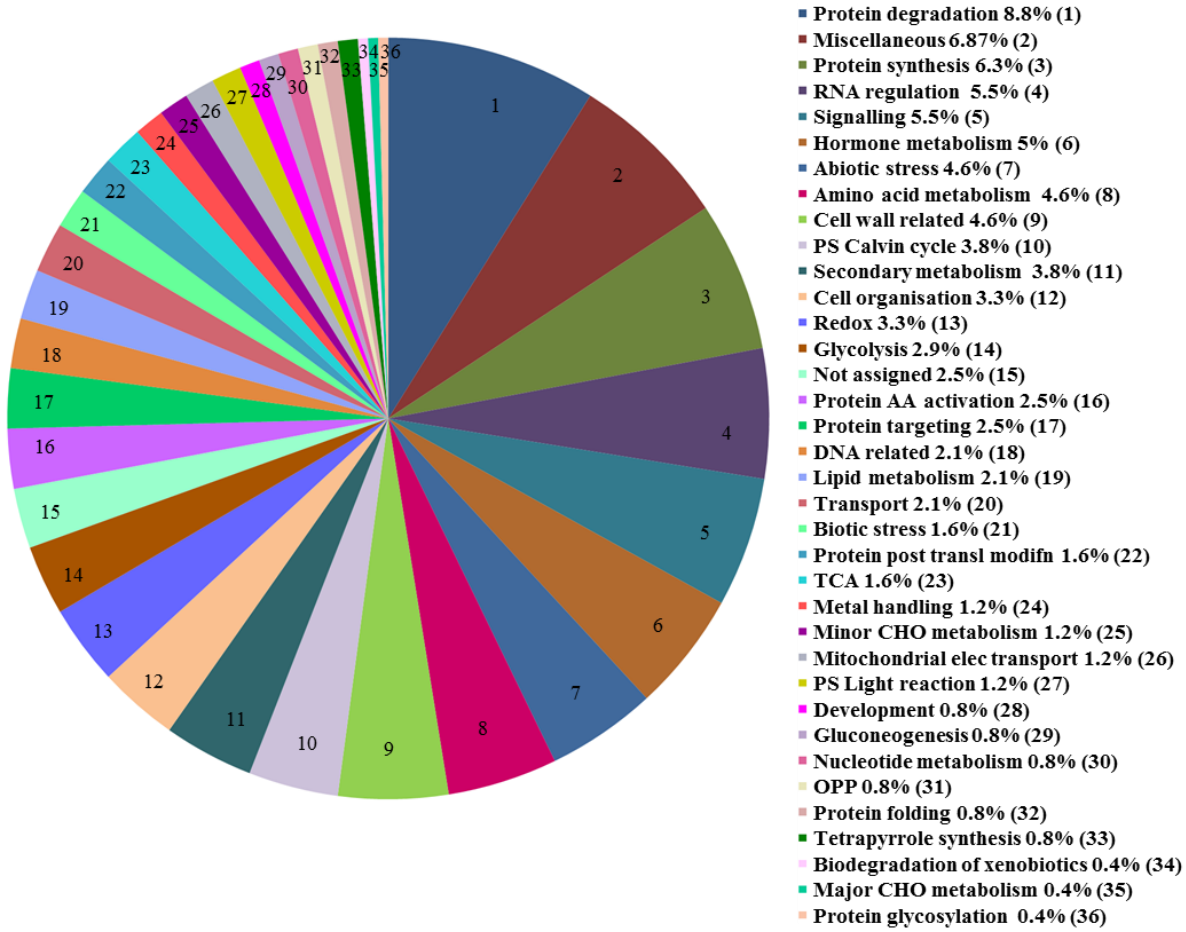


Figure 4.6. Functional classification of differentially expressed proteins in AV in comparison to AC. A. Proteins up-regulated in AV in comparison to AC.

B

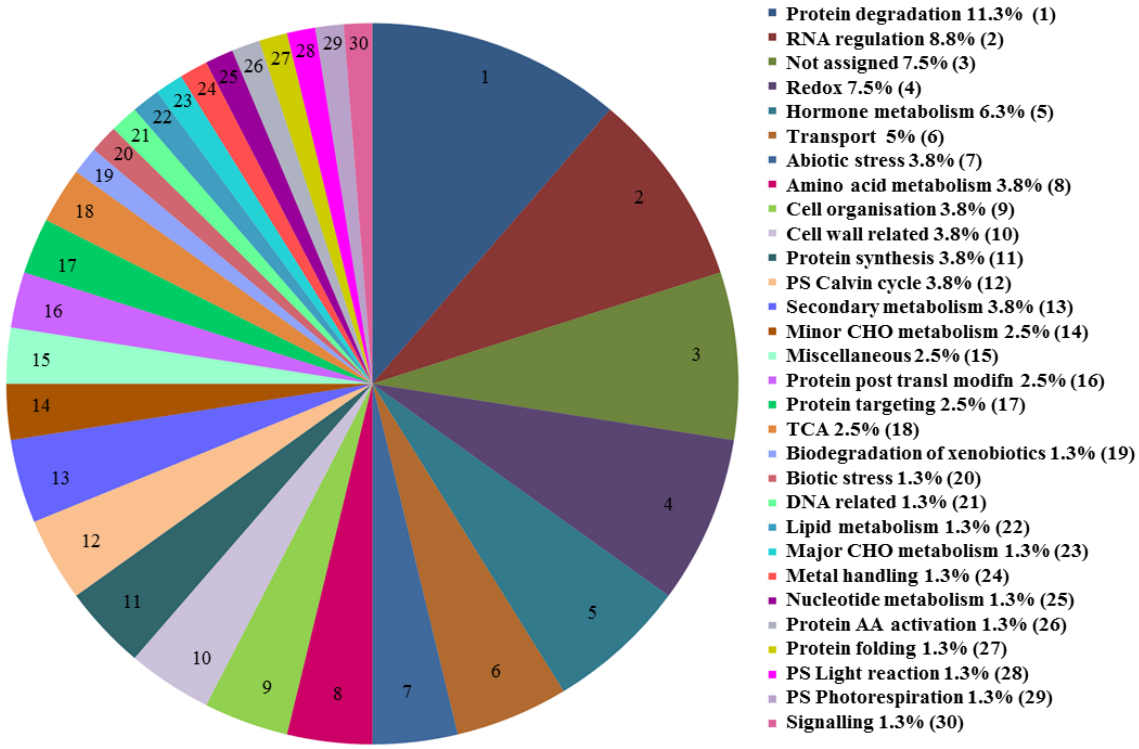


Figure 4.6. Functional classification of differentially expressed proteins in AV in comparison to AC. B. Proteins down-regulated in AV in comparison with AC

A

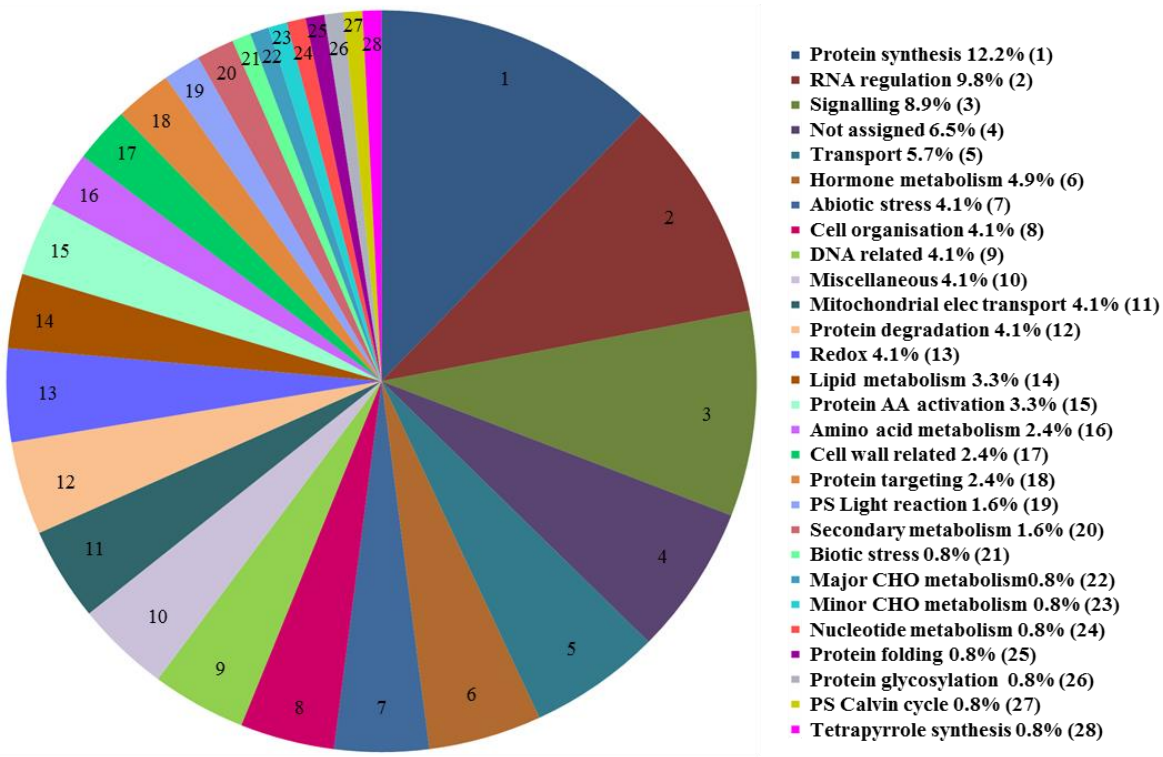


Figure 4.7. Functional classification of proteins identified in only one cultivar.
A. Proteins identified only in AC.

B

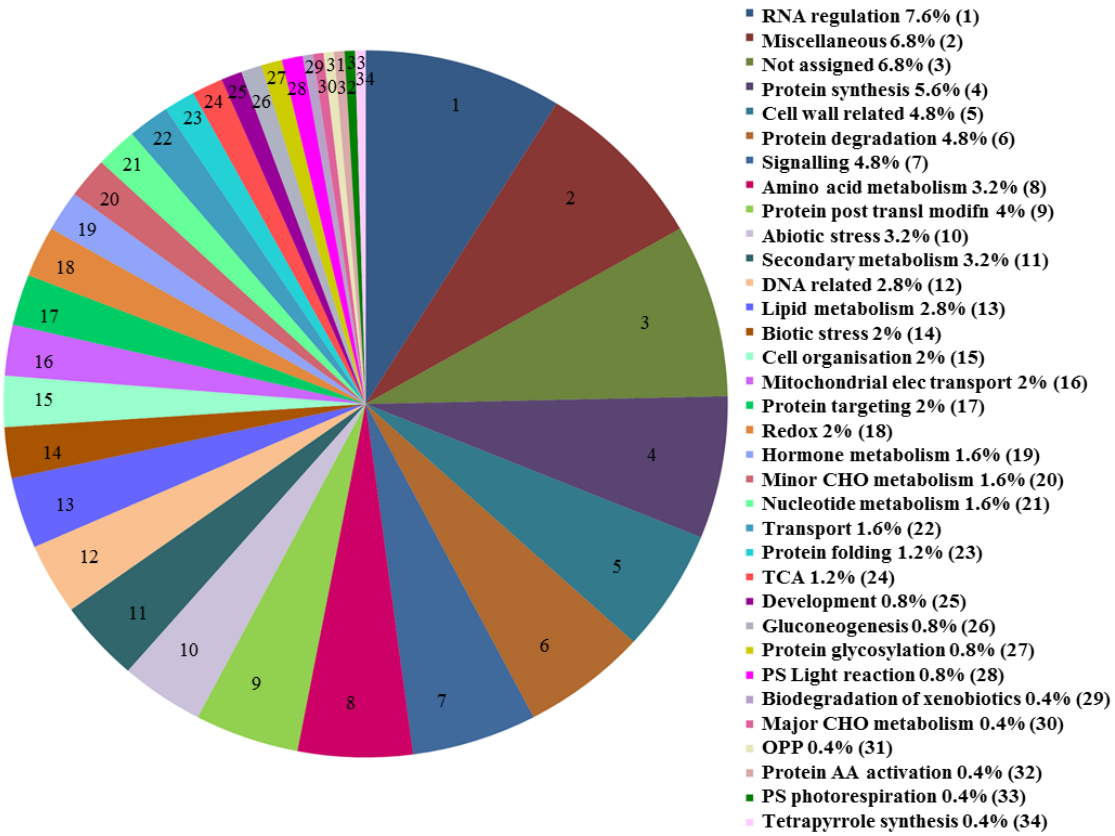


Figure 4.7. Functional classification of proteins identified in only one cultivar.
B. Proteins identified only in AV

proteins. In up-regulated proteins, protein degradation was the major category (9.6%). In down-regulated proteins, both protein degradation and miscellaneous were major categories, comprising of 9.6% and 9.4% of the proteins respectively (Fig. 4.6). Interestingly, 32 categories were observed in the proteins present only in AC and 35 categories among proteins present only in AV. In case of proteins that were identified only in AC, proteins belonging to "not assigned" and abiotic stress categories formed the major class (11.5%) followed by proteins from protein synthesis category (9.7%) (Fig. 4.7). In AV, RNA regulation was the major category comprising of 7.6% of the proteins.

4.3.9 Increased abundance of carotenoid biosynthesis pathway proteins in AV

As tomato fruit is rich in carotenoids like lycopene and β-carotene, it was of interest to examine the carotenoid metabolism related proteins in the proteomes of AV and AC. Spectral counting revealed the presence of many of the carotenoid metabolism related proteins in AV proteome in our study. Phytoene desaturase (PDS; 2.1-fold) and ζ-carotene isomerase (ZISO; 10-fold), two of the enzymes involved in carotenoid biosynthesis were up-regulated in AV and carotenoid cleavage dioxygenase 1B (CCD1B), a carotenoid degradation enzyme was 2.5-fold down regulated (Table 4.3). Interestingly, two of the carotenoid pathway enzymes including 1-deoxy-D-xylulose-5-phosphate reductoisomerase (DXR) and ζ-carotene desaturase (ZDS) were identified only in AV but not in AC (Table 4.4).

4.3.10 AV fruits are enriched in carotenoids

To elucidate the correlation between the abundance of proteins related to carotenoid metabolism and carotenoid content, carotenoid profiles in the fruits of both AC and AV cultivars were determined and compared. Out of eight carotenoids identified in AC and AV, only four carotenoids, phytofluene, ζ-carotene, lycopene, β-carotene were significantly different between both the cultivars (Fig. 4.8). Among all the carotenoids, lycopene is the major carotenoid which was 1.96 fold higher in AV compared to AC fruits. Phytofluene (2.5 fold), ζ-carotene (1.5 fold) and β-carotene (1.95 fold) also accumulated in AV compared to AC, contributing to the high carotenoid content in AV fruits.

4.4 Discussion

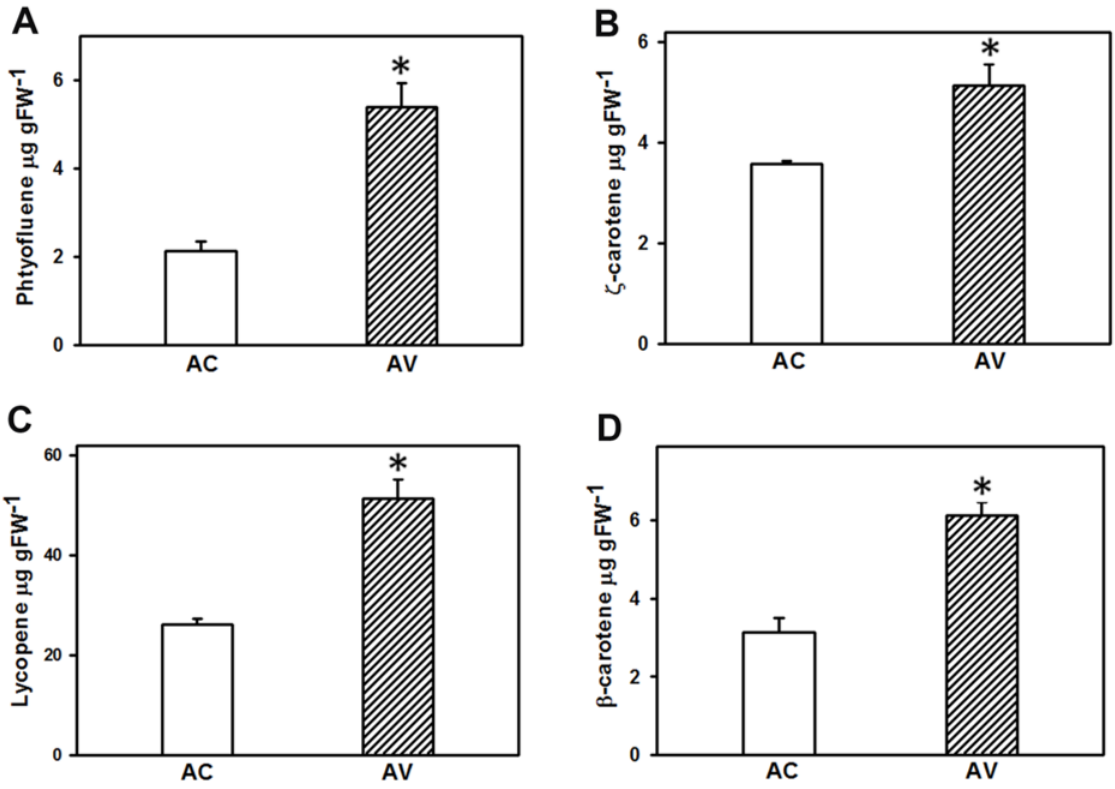


Figure 4.8. Carotenoid profiling in the ripe fruits of AV and AC cultivars. Carotenoid content was determined in the red ripe fruits of both AC and AV using the method described in Gupta et al., 2015 (n=3±SE). **A**, phytofluene; **B**, ζ-carotene; **C**, lycopene; **D**, β-carotene. *indicates significant differences with $P \leq 0.05$.

4.4.1 Protein extraction with buffer-saturated phenol followed by precipitation is optimal for sample preparation from tomato fruit

Highest number of proteins was obtained with phenol based protein extraction method followed by precipitation with ammonium acetate in methanol. Though both phenol and TCA/acetone extraction show well resolved protein profiles on 2DE (Saravanan and Rose, 2004), our results revealed that phenol is better suited for extracting protein from tomato fruits for shotgun approaches. The efficacy of phenol likely resulted from the efficient partitioning of interfering substances into the aqueous phase while proteins were retained in phenol (Issacson et al., 2006). In contrast, TCA reportedly precipitates polysaccharides along with proteins (Wu et al., 2014). While protein extraction with SDS buffer[a], SDS buffer[b] or SDS buffer[c] yielded no proteins, and precipitation with chilled acetone after extraction with SDS buffer[a] resulted in less number of proteins. Above results indicated that precipitation of proteins after extraction in an ideal reagent is a crucial step, as in addition to efficient extraction of proteins, the reagent should also effectively eliminate the common contaminants. Similarly, using FASP protocol also resulted in total loss of proteins. However, performing FASP with protein obtained after phenol extraction and ammonium acetate precipitation followed by digestion on micron filters yielded significant number of proteins. The above difference in protein identification emphasized the importance of phenolic extraction and precipitation prior to any subsequent treatments.

4.4.2 Fractionation is an essential step in proteome profiling of tomato fruits

In order to reduce the complexity of the sample, protein isolated from tomato fruits were subjected to various fractionation techniques such as SDS-PAGE, SAX and PEP-IEF. From the results, it was evident that GeLCMS and SAX (±FASP) using phenol-extracted sample resulted in higher proteome coverage, whereas, a 3-10 fold higher initial protein amount was required for a similar proteome coverage using PEP-IEF. In essence, our results suggest that protein fractionation is essential for obtaining better proteome coverage, especially from tomato fruit tissue.

4.4.3 Functional annotation of proteins revealed that GeLCMS is an unbiased technique

The proteins identified from peptide fractionation techniques were classified as per GO annotation to analyze whether the above technique was suitable only for

selective/preferential categories of proteins. Although, the membrane proteins were slightly higher in SAX and FASP-SAX compared to GeLCMS, the number of un-annotated proteins was lowest for GeLCMS. Earlier reports indicate that FASP protocol extracts low abundance proteins (Wisniewski et al., 2009). In this study, GeLCMS approach resulted in identification of low abundance classes comparable with that of FASP. From the foregoing, it is evident that GeLCMS is essentially unbiased as it did not lead to preferential extraction of proteins based on MW, charge etc. (Schirle et al., 2003) and for any specific GO category.

4.4.4 Increased proteome coverage with GeLCMS is validated through label-free proteome analysis

GeLCMS is a robust and reproducible technique and resulted in the identification of consistent number of proteins in two cultivars, AC and AV. The proteome coverage obtained in this study is much higher than reported earlier in the literature. Proteome coverage obtained in our study is also comparable to the data obtained in GeLCMS profiling of six human cell lines, wherein using 50 µg protein, 1785 proteins were identified (Schirle et al., 2003). Moreover, GeLCMS is very simple to use and cost effective compared to chromatography based approaches and can efficiently capture proteome encompassing a wide dynamic range.

4.4.5 Enhanced accumulation of carotenoid proteins and carotenoid metabolites in AV fruits

In AV, an increase in the abundances of carotenoid biosynthesis proteins was observed along with down-regulation of carotenoid degradation enzymes. The accumulation of DXR and ZDS only in AV but not in AC could be due to the low abundance of these proteins in AC fruits. Our observation is supported by a previous report where spectral counting was unable to detect the differences when the protein abundances are low (Liu et al., 2004, Old et al., 2005). The up-regulation of carotenoid biosynthesis and down-regulation of carotenoid degradation enzymes in AV proteome highly correlates with the elevated carotenoid levels in AV fruits and also explains the dark red fruit phenotype of AV in comparison to AC fruits.

Chapter 5

To understand the molecular basis for diversity in fruit coloration in the tomato clade

5.1 Introduction

Diversity in form and function signifies the resilience of plants to survive in nature and compete with other species. Members of Solanaceae comprising of nearly 10,000 species show very diverse morphology. The genomes of plants belonging to Solanaceae such as tomato, potato, tobacco and pepper show high degree of synteny in their organization (Tomato genome consortium 2012; Potato genome consortium, 2011; Sierro et al., 2014; Kim et al., 2014). Currently, efforts are being made to understand the molecular basis of diversity between closely related species in Solanaceae (Aflitos et al., 2014; Bolger et al., 2014). The comparison of genomes and transcriptomes indicate that the phenotype differences between species reflect differences in the regulation of gene expression in conjunction with variation in genome sequences (Khaitovich et al., 2005; Bolger et al., 2014).

Of all the diversity observed in form and function, the diversity in fruit coloration has attracted considerable attention. The wide range of fruit colours encompassing red, yellow, purple and black are imparted by two pigments; carotenoids and/or anthocyanins (Seymour et al., 2013). The selection of carotenoids or anthocyanins for fruit colouration for a given species shows wide diversity even within a family. In Solanaceae, anthocyanins impart fruit coloration in eggplant and carotenoids contribute to coloration of tomato (Dhar et al., 2014). At the same time many Solanaceous plants have green fruits that do not accumulate these pigments (Knapp, 2002). It is not known why few species in a family acquire fruit coloration. Ecologists propose that the acquisition of a particular fruit trait in a species is likely driven by need for the seed dispersal by frugivores (Lomascolo et al., 2010).

In vegetative tissues, carotenoids and anthocyanins mainly function to protect the plants from light stress. Among the two, carotenoids are most essential for protection of the photosynthetic machinery from photooxidation. The biochemical steps leading to the formation of carotenoids in green tissue are well characterized and conserved across species (Ruiz-Sola and Rodriguez-Concepcion, 2012). The carotenoid accumulation in organs such as flowers, roots and fruits involved modifications of the carotenoid biosynthesis for organ-specific expression. In the greening leaf, light induces carotenoid accumulation along with chlorophyll leading to acquisition of photosynthesis (Giuliano et al., 1993). In contrast, light suppresses the carotenoid formation and differentiation of chromoplasts (Stange et al., 2008; Fuentes et al., 2012) in carrot root. It is believed that in

carrot, root carotenoid biosynthesis is modified at several levels to enhance preferential accumulation of carotenoids (Rodriguez-Concepcion and Stange 2013).

In general, two major modifications pave the way for accumulation of carotenoids in non-green organs. The first modification is the acquisition of a storage sink for carotenoids and involves differentiation of plastids to chromoplasts. Molecular analysis of orange cauliflower gene revealed that the expression of the *Orange* (*Or*) gene assists in the accumulation of carotenoids by transforming non green plastids to chromoplasts (Lu et al., 2006). The formation of chromoplasts is also associated with increase in number and size of plastoglobules that act as major loci for carotenoid storage. Plastoglobules are composed of lipids and several proteins, of which plastoglobulin and chromoplast-specific carotenoid-associated protein (CHRC) are believed to assist in the storage of carotenoids (Nogueira et al., 2013; Kilambi et al., 2013).

The second modification involves the alteration of carotenoid biosynthesis pathway. In tomato fruits, two critical steps of carotenoid biosynthesis are mediated by fruit-specific isoforms of phytoene synthase (*psy1*) and lycopene-β-cyclase (*cycb*), distinct from the leaf specific isoforms. Moreover, the fruit-specific regulation of these isoforms is coupled with climacteric induction of ripening. The evolution of ethylene, while stimulating the expression of *psy1* gene, inhibits *cycb* expression, leading to preferential accumulation of lycopene in fruits (Alba et al., 2005). In addition, increase in chromoplast numbers and size in tomato fruits enhances carotenoid accumulation (Azari et al., 2010; Pan et al., 2013; Powell et al., 2012). Furthermore, the accumulation of carotenoids in tomato fruits is strictly regulated by ripening, consequently, mutations leading to non-ripening phenotypes block the carotenoid biosynthesis (Tigchelaar et al., 1978; Thompson et al., 1999; Klee and Giovannoni, 2011). It is now believed that carotenoid accumulation in tomato is governed by a combination of factors regulating fruit ripening and ethylene formation.

Currently, little information is available about the diversity in regulation of carotenogenesis across species. Comparison of gene expression between ripe fruits of tomato, pepper and eggplant revealed stronger similarities between tomato and pepper than with eggplant. While both climacteric tomato and non-climacteric pepper fruits accumulate carotenoids, ethylene-mediated carotenogenesis is restricted to tomato (Moore et al., 2005; Kim et al., 2014). At the same time ripening-stimulated up-regulation of *psy1* and ζ-*carotene desaturase* (*zds*) in pepper was similar to tomato (Osorio et al.,

2011), whereas, *β-carotene hydroxylase* and other downstream genes from lycopene were up-regulated only in pepper (Moore at al., 2005).

Members of the tomato clade display a wide diversity in fruit coloration making it an excellent model group for examining the molecular basis of carotenogenesis (Bauchet and Causse, 2012). Most members of the tomato clade are green-fruited, excepting *S. galapagense* and *S. cheesmaniae* with orange fruits and *S. pimpinellifoilum* and tomato with red fruits. It is presumed that the "green-fruitedness" in tomato clade may be due to underexpression of key carotenogenic genes like *psy1* (Melendez-Martinez et al., 2010; Bolger at al., 2014). Recent availability of genome sequences (Aflitos et al., 2014) and application of high-throughput methods have aided efforts to understand the molecular basis of diversity in tomato clade (Ichihashi et al., 2014; Koenig et al., 2013). Comparing the primary metabolome in tomato clade, Schauer et al. (2006) reported that the metabolome of *S. pimpinellifoilum* leaves was closer to tomato, while that in *S. habrochaites* was most distinct. Contrarily, fruit metabolome of *S. habrochaites* was closer to tomato than other wild relatives.

Currently, systems approaches are increasingly used to decipher the key steps regulating a metabolic pathway in greater detail. Majority of such studies focused on transcript/transcription factor profiling coupled with metabolite analysis to understand the intricacies of regulation of metabolism (Rohrmann et al., 2011; Enfissi et al., 2010; Osorio et al., 2011). Correlation of carotenoid contents and the transcriptome in introgression lines of led to identification of *ethylene response factor* (*erf6*) transcription factor as a key regulator of fruit ripening and carotenoid accumulation (Lee et al., 2012). So far, only a lone study, combining, transcripts, proteins and metabolites in tomato and its non-ripening mutants uncovered novel interactions that regulate fruit ripening (Osorio et al., 2011).

Given that the regulation of fruit coloration in tomato clade is incompletely understood, we used a systems approach using the information acquired at carotenoid, proteome and transcript levels to understand the molecular basis of diversity in carotenogenesis. In this study, *S. habrochaites* was used as a representative for green fruited species, along with *S. pimpinellifoilum*, *S. galapagense* and *S. lycopersicum*.

5.2 Materials and methods

5.2.1 Plant material and experimental design

Tomato (*Solanum lycopersicum* cv. Ailsa Craig (LA2838; SL)) and its wild relatives, *S. pimpinellifoilum* (LA1589; SP), *S. galapagense* (LA0483; SG) and *S. habrochaites* (LA1777; SH) were used in this study. Plants of SL, SP, SG and SH were grown in the open field in pots during October-January at the University of Hyderabad (day 30 ± 2°C, night 18 ± 2°C) in a randomized design in 12 rows with five plants of each genotype per row (Fig. 5.1). Four rows constituted one biological replicate, and fruits formed on first and second trusses were used in all the experiments to minimize the size variations. In the open field, SL ripened 9-10 days earlier than when grown in the greenhouse (Kilambi et al., 2013). We also observed higher fruit set in all the wild species when grown in the open field than in the greenhouse. The flowers were tagged on the day of anthesis, fruit growth was periodically monitored (Fig. 5.2), and fruits were collected, pooled separately at every stage, snap frozen in liquid nitrogen, and were stored at -80°C till use.

Seedlings were grown in coconut peat (Sri Balaji Agro Services, India) in a growth room maintained at 25 ± 1°C with 16 h light/8 h dark cycle (100 µmole m^{-2} sec^{-1}). The first and second leaves of 15 day old seedlings were used for analyses (Fig. 5.2).

5.2.2 Determination of ethylene evolution

The ethylene emission from the harvested fruits at 15, 20, 26, 29 and 39 dpa was measured described in chapter 3 and in Kilambi et al., (2013).

5.2.3 Carotenoid profiling

The carotenoid profiles were analysed using Accela UHPLC coupled to a PDA detector (Thermo Fisher Scientific) as per the protocol described in chapter 4 and in Gupta et al. (2015). Chlorophylls were determined spectrophotometrically as described by Wellburn (1994).

5.2.4 RNA isolation and transcript analysis

Total RNA was isolated using TRI reagent (Sigma-Aldrich; T9424) following manufacturer's instructions. q-PCR was carried out as described in chapter 3 (for primer details, see Annexure 1) and in Kilambi et al. (2013).

5.2.5 Transmission Electron Microscopy (TEM)

Fruits collected at 39 dpa from SL, SP, SG and SH were sliced using a sharp scalpel into 2 mm pieces and fixed overnight in 2.5% (v/v) glutaraldehyde in 0.1M

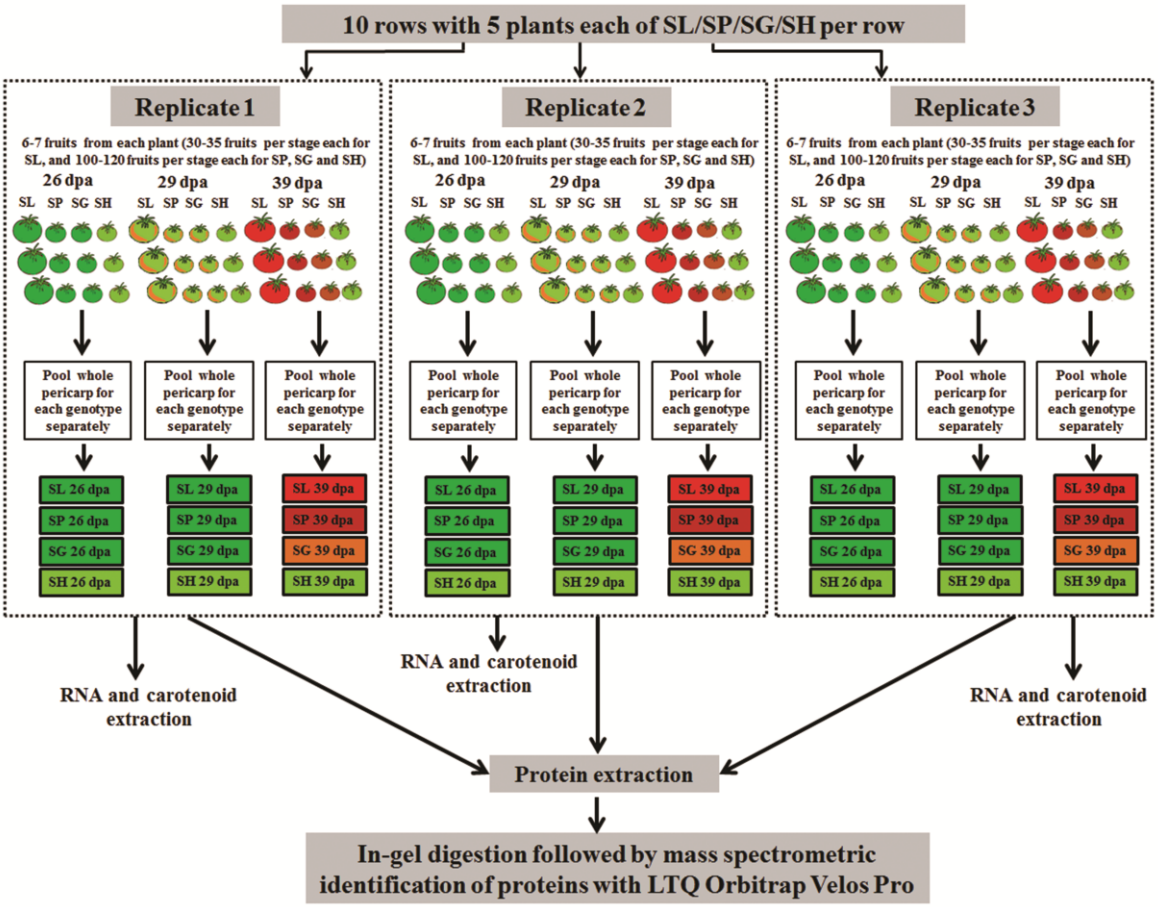


Figure 5.1. Experimental design describing the growth of plant material, collection of fruit tissue at different stages of ripening in tomato and wild relatives for carotenoid, RNA and protein extraction.

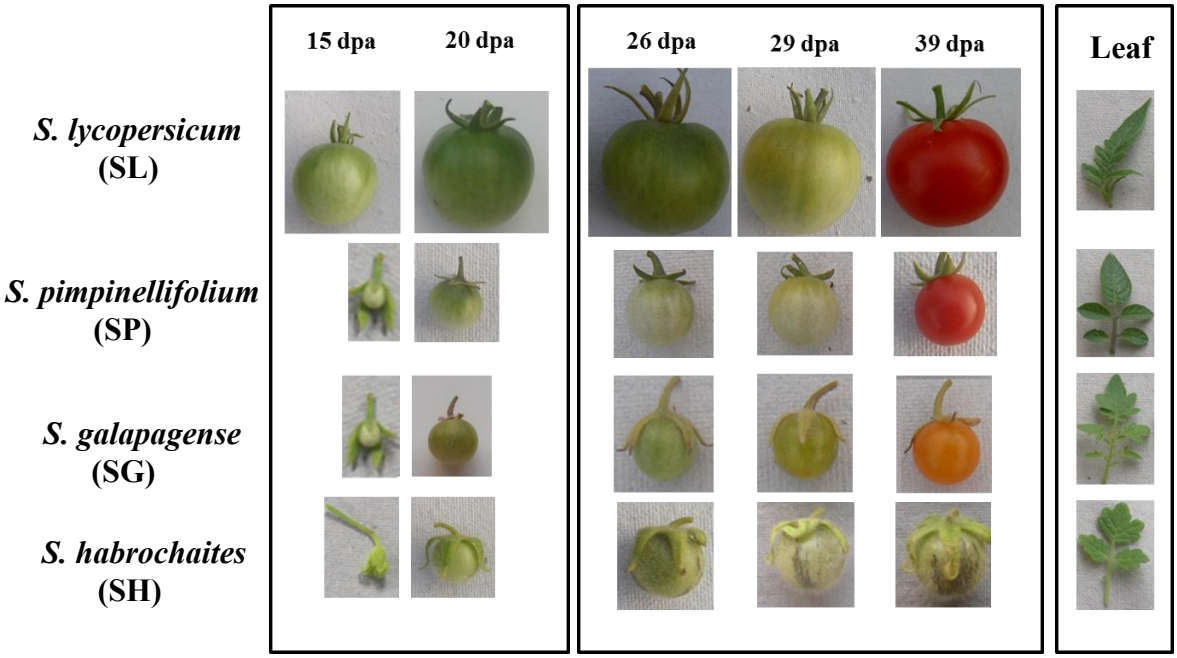


Figure 5.2. Fruit phenotypes of tomato and wild relatives at different time points during development and leaf phenotypes of 15 day old seedlings used in the study.

sodium phosphate buffer (SB buffer), pH 7.2 at 4°C. Thereafter, tissue was rinsed in ice-cold SB buffer (10 min x 2) followed by fixation in 1% (w/v) osmium tetroxide in SB buffer for 2 h. at 4°C. Tissue was washed with SB buffer (3 x 2 h.) at 4°C. Tissue was then dehydrated at room temperature using graded series of acetone (50 to 100%) with 1 h. incubation at each concentration and finally dehydrated for 2 h. in dry acetone. Thereafter, the tissue was cleared in toluene (2 x 1 h.) followed by infiltration with Araldite CY212 resin (TAAB laboratories equipment ltd, UK) in toluene: resin ratio of 3:1, 2:2, 1:3 with each step for 2 h at room temperature and finally in pure resin for 2 h at 50°C. The tissue was then transferred to embedding moulds and polymerised overnight at 50°C followed by incubation for 48 h at 60°C. Ultrathin sectioning of the polymerised blocks was performed using Leica EM UC6 ultramicrotome and sections were collected on 300 mesh copper grids. Counterstaining of the sections was carried out using saturated uranyl acetate in 50% (v/v) alcohol for 15 min followed by three washes with MQ water and further incubation with lead citrate for 12 min followed by washes with MQ water (3 times). Sections were viewed in JEM-2100F Transmission Electron Microscope (JEOL, USA) at 120 KV. The images for respective species were obtained from three biological replicates.

5.2.6 Protein extraction

Proteins from fruit tissue were extracted using the protocol described in chapter 3 and in Kilambi et al., (2013). For the fruit samples of SL, SP and SG, 70 µg protein was solubilized in lysis buffer (7 M urea, 2 M thiourea, 4% CHAPS (w/v)) and subjected to SDS-PAGE (12% w/v). In SH fruits, on the addition of extraction buffer post-homogenization, the homogenate became viscous. This viscous material interfered with protein extraction. The protein extraction protocol for SH and corresponding SL consisted of one additional step. The homogenized fruit powder obtained after grinding in liquid N_2 was washed with acetone on a sintered funnel till the green colour disappeared. Thereafter, the powder was air dried and used for extraction using the protocol described in Kilambi et al. (2013). Dried protein (70 µg) from SH and SL samples was solubilized in lysis buffer (7 M urea, 2M thiourea, 2% (w/v) $C7B_ZO$, 2% (w/v) CHAPS) and subjected to SDS-PAGE (12% w/v).

5.2.7 MUDPIT approach (GeLCMS)

For proteome profiling, a corresponding sample from SL was extracted and analysed in parallel with respective wild species right from the protein extraction to LC-MS separation. Proteins after separation on SDS-PAGE were stained with Colloidal coomassie blue stain (Kilambi et al., 2013). Each lane (70 µg of protein) using a grid cutter (The Gel Company) was cut into 36 equal pieces and pooled into six fractions (6 pieces in each fraction) as illustrated in Fig. 5.3. In-gel digestion was carried out following the protocol of Barsan et al. (2012). In brief, the gel pieces were washed with water, destained and dried by adding 100% ACN (v/v). Thereafter ACN was removed and pieces were incubated in 10 mM DTT at 60°C for 30 min. After discarding DTT, pieces were incubated in 55 mM iodoacetamide at 25°C for 30 min in dark. Thereafter, pieces were treated with 100% ACN (v/v) for 30 min and dried using speedvac (Thermo Scientific).

Proteins were digested by incubating pieces with 0.5 µg trypsin (Trypsin Gold, Promega) (1 µg trypsin per 25 µg of protein) as described in Shevchenko et al. (2006). Eluted peptides after concentration in speedvac were desalted through C18 spin columns (Thermo Scientific) and after aliquoting and drying, the peptides were stored at -80°C.

5.2.8 Mass spectrometry

The trypsin digests were analysed using Easy-nLC II coupled To LTQ Orbitrap-Velos Pro mass spectrometer (Thermo Scientific). For separation on nano-LC-MS/MS, an aliquot of dried peptides was re-suspended in solvent A (5% ACN + 95% water (v/v)) and 300 ng of peptides were loaded onto a trap column (Integra Frit 100 µm x 2.5 cm, 5 µm, New Objective, USA) and eluted on a Biobasic C18 Pico frit column (75 µm x 10 cm, 5 µm, New Objective, USA) at a flow rate of 350 nL/min using solvent A (water/ACN (95/5) with 0.1% formic acid) and solvent B (ACN/water (95/5) with 0.1% formic acid). For SH-SL samples, the gradient was-5%-15% B (0-5 min), 15%-95% B) (6-80 min), 95% B hold (81-83 min), 95%-5% B (84-86 min), 5% B hold (87-90 min). For SP-SL and SG-SL fruit samples, the gradient was- 5%-30% B (0-100 min), 30%-95% B (101-103 min), 95% B hold (104-106 min), 95%-5% B (107-113 min), 5% B hold (114-118 min). The column eluate was connected to nanospray ionization source operated at a voltage of 1.7 kV and a capillary temperature of 260°C.

Mass spectra were acquired using a data dependent method in positive mode with Xcalibur (version 2.2, Thermo Scientific). The mass spectrometer was

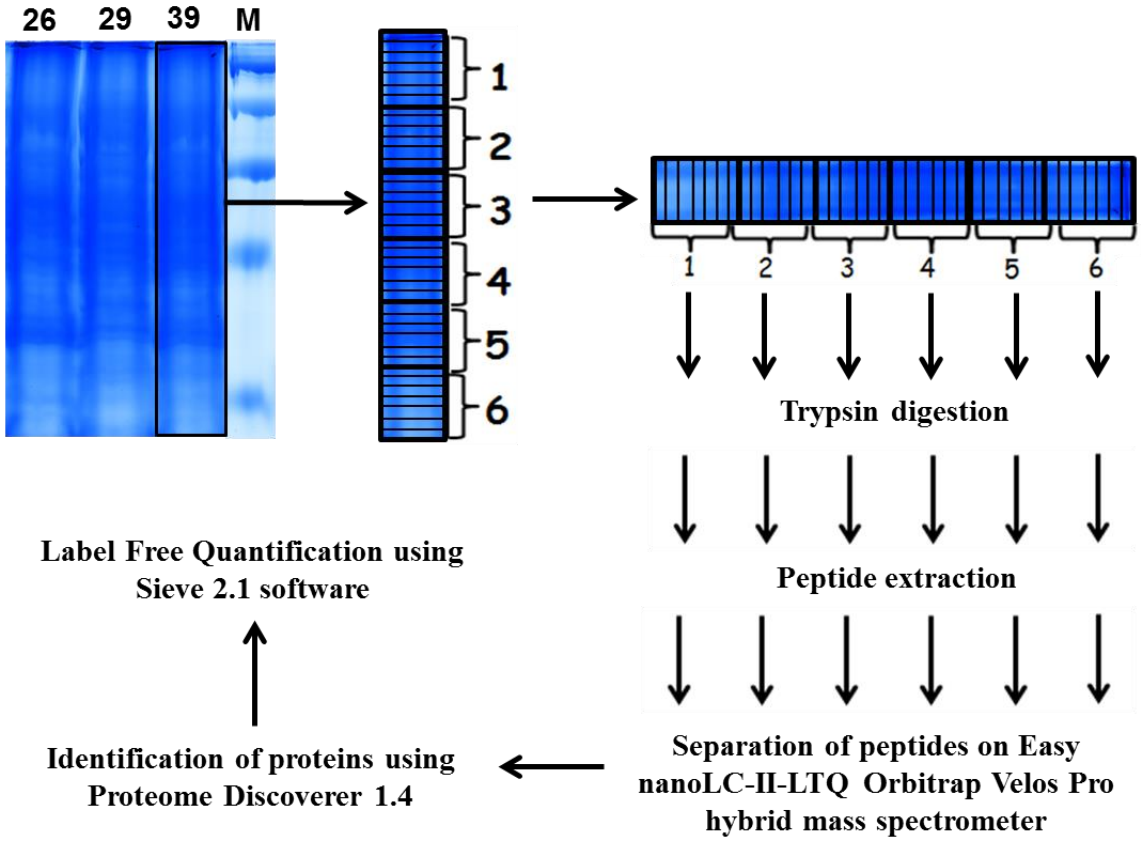


Figure 5.3. GELC-MS scheme used for proteome analysis in the fruits and leaves of wild species and tomato.

calibrated for both positive and negative modes with Pierce LTQ Velos positive and negative calibration solutions (Thermo Scientific). The survey scans were performed in Orbitrap at a resolution of 60,000 using a mass range of 350-2000. MS/MS spectra were obtained in ion trap (IT) using collision induced dissociation (CID) for top 20 peaks resulting from each survey scan. A 30 sec dynamic exclusion period was enabled with a repeat count of 1 and a lock mass of 445.120030 was used for mass accuracy. The top 20 peaks were fragmented by CID using normalized collision energy of 35% with an isolation window of 2 *m/z*. Automatic gain control targets (AGC) for full MS and MSn were set at 1,000,000 (Orbitrap) and 10,000 (IT) for SH-SL. For SG-SL and SP-SL the values were set at 500,000 (Orbitrap) and 10,000 (IT). Full MS data were acquired in profile mode while the MS/MS data were acquired in centroid mode.

5.2.9 Data analysis

Data were analyzed using Proteome Discoverer (PD version 1.4, Thermo Scientific). Independent searches were performed for each fraction of an individual sample. Data obtained from SL were searched against the *S. lycopersicum* iTAG 2.3 proteome sequence (ftp://ftp.solgenomics.net/tomato_genome/annotation/ITAG2.3_release/ITAG2.3_proteins.fasta, downloaded on February 2013, 26705 sequences and 9322189 residues). For SP and SG, data were searched against the S. lycopersicum iTAG 2.3 proteome sequence (ftp://ftp.solgenomics.net/genomes/Solanum_pimpinellifolium/annotations/Spimpinellifolium_genome_protein_anno.fa) containing 32,715 sequences, 11112863 residues, downloaded on April 25, 2013). For SH, data were searched against protein database generated from SH RNA-Seq data obtained from Julin Maloof's lab (14,369 sequences, 6321576 residues, downloaded on March 26, 2015). Peptide mass tolerance and fragment mass tolerance were set to 5 ppm and 0.8 Da respectively. In Sequest search engine, trypsin was selected as a protease and a maximum of two missed cleavages were allowed. Carbamidomethylation of cysteine and oxidation of methionine, deamidation of aspargine and glutamine were selected as fixed and variable modifications respectively. Peptides were filtered for high confidence and a minimum number of two matched peptides were considered for assigning protein IDs. Percolator tool was used to assess peptide confidence; peptides with q value ≤ 0.01 (equivalent to a power of 1 at a $P < 0.05$) were selected, which was estimated based on the number of decoy hits. Label-free quantitation (Sieve 2.1 software, Thermo Scientific) was used to identify the differentially expressed

proteins in SH-SL, SP-SL, SG-SL pairs after passing stringent selection criteria (P value ≤ 0.05, minimum 2-fold change (either up-or down-regulation), minimum two peptides for identification, FDR=1%). The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium (Vizcaíno et al., 2014) via the PRIDE partner repository with the dataset identifier PXD003817.

5.2.10 Targeted peptide monitoring (TPM) for carotenoid proteins in fruits and leaves

Total proteome data of fruit at 39 dpa and leaf from 15 day old seedlings was examined for the presence of the carotenoid pathway proteins. Peptides pertaining to the carotenogenic proteins were chosen for TPM taking the following into consideration – (i) the peptide must be unique to the protein of interest, (ii) the peptide must be devoid of modifications, (iii) the peptide should not contain methionine, cysteine or tryptophan residues and (iv) the peptide length should be preferably between 8 and 25 amino acids (Lange et al., 2008; Taylor et al., 2014). A list of such proteotypic peptides with precursor m/z values and the expected retention times that were present consistently in all three biological replicates in fruits and leaves of wild species was generated manually. Manual identification was superior to the usage of Pinpoint software (Thermo Scientific) which resulted in the identification of very few proteotypic peptides. Based on the above, the numbers of peptides chosen for TPM in fruit were as follows- 96 for SH-SL, 97 for SP-SL and 116 for SG-SL comparisons (Table 5.1). Similarly, the number of proteotypic peptides (for 22 proteins) chosen for TPM in leaf for each genotype were-121 for SH-SL, 119 for SP-SL and 124 for SG-SL comparisons (Table 5.2).

Use of synthetic labelled peptides was not practically possible for the current study due to the high costs involved, as the number of peptides monitored for each genotype was very high. In the absence of labelled peptides, data normalization with inherent protein controls and validation of the data with retention time standards is recommended for achieving high confidence results (Carr et al., 2014). Keeping this in view, we used Pierce retention time calibration mixture (Thermo Scientific, Product No. 88321, 15 heavy isotope labelled peptides in the mass range of 843.4582-1600.8084) at 50 fmol/sample to optimize LC-MS runs. In addition, we chose few housekeeping proteins whose abundance remained constant in SL and the wild relatives to serve as inherent controls. Because these internal control proteins undergo similar treatment to the

carotenogenic proteins during sample preparation, chromatography and ionization, they compensate for any ion suppression effects (Table 5.3, Sherrod et al., 2012).

For TPM, the column specifications were the same as described under mass spectrometry with the only difference in the data-dependent settings. For TPM, data-independent settings were used with first four selected ion monitoring (SIM) scans in Orbitrap at a resolution of 30,000 with m/z scan range for each event- 450-650, 650-850, 850-1050 and 1050-1250; the last scan event was MS/MS in ion trap for the inclusion list of peptides representing the carotenoid proteins (Thermo Application note 500; Hewel et al., 2013) (Fig. 5.4) outlines setup of TPM experiment). A retention time (RT) window tolerance of RT ± 2 was used with an isolation width of one. Ions detected in the defined RT window were isolated and fragmented with normalized collision energy of 35%. The AGC targets for Orbitrap and ion trap analyzers for SIM scans were set at 100,000 and 10,000 respectively. Three biological replicates were run for all the samples. Statistical significance was determined by t-test using the abundances of carotenoid proteins in SP-SL, SG-SL and SH-SL comparisons.

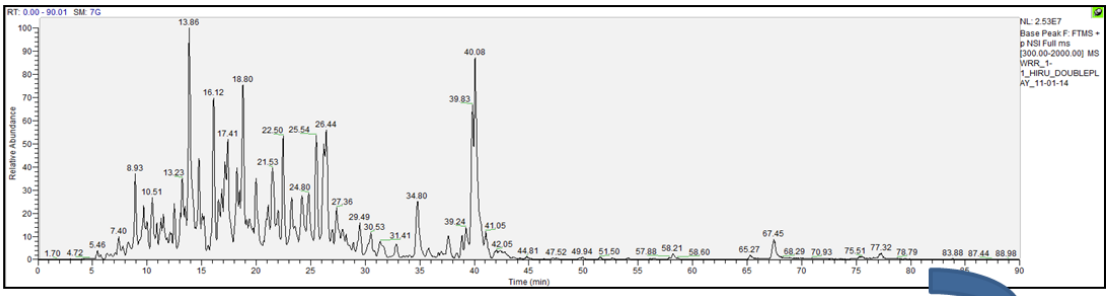
5.2.11 Label-free quantitation of targeted peptides

The raw files obtained after TPM were analysed in PD 1.4 using the same search and selection criteria as described above. The peptide identity was confirmed by matching its fragmentation spectrum with that of precursor fragmentation spectrum obtained from proteome profiles using Xcalibur software (Fig. 5.4). The area under the curve (AUC) was measured for the matched peaks. Three peptides were considered for every protein and the peptide with the best peak shape was quantified, the other two were used for confirmation. Similarly, AUC values for internal reference peptides fulfilling the outlined criteria were noted. Abundance of each protein was represented as:

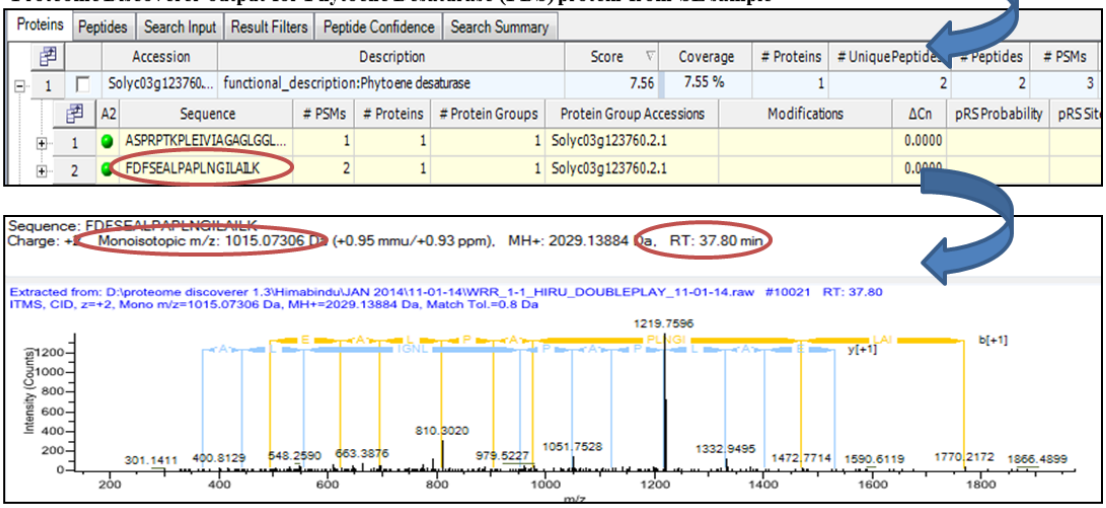
$$\text{Abundance} = \frac{\text{Mean AUC of targeted peptide}}{\text{Mean AUC of internal reference peptide}}$$

For stringency and consistency in results, each protein was normalized using at least, three internal reference proteins (Table 5.3). Out of 20 proteins selected for TPM, only consistently identified peptides were considered for quantification. Statistical significance was determined by t-test using the abundances of carotenoid proteins in SP-SL, SG-SL and SH-SL comparisons.

Workflow for Targeted Peptide Monitoring -



Proteome Discoverer output for Phytoene Desaturase (PDS) protein from SL sample



Pictorial representation of a typical TPM experiment -

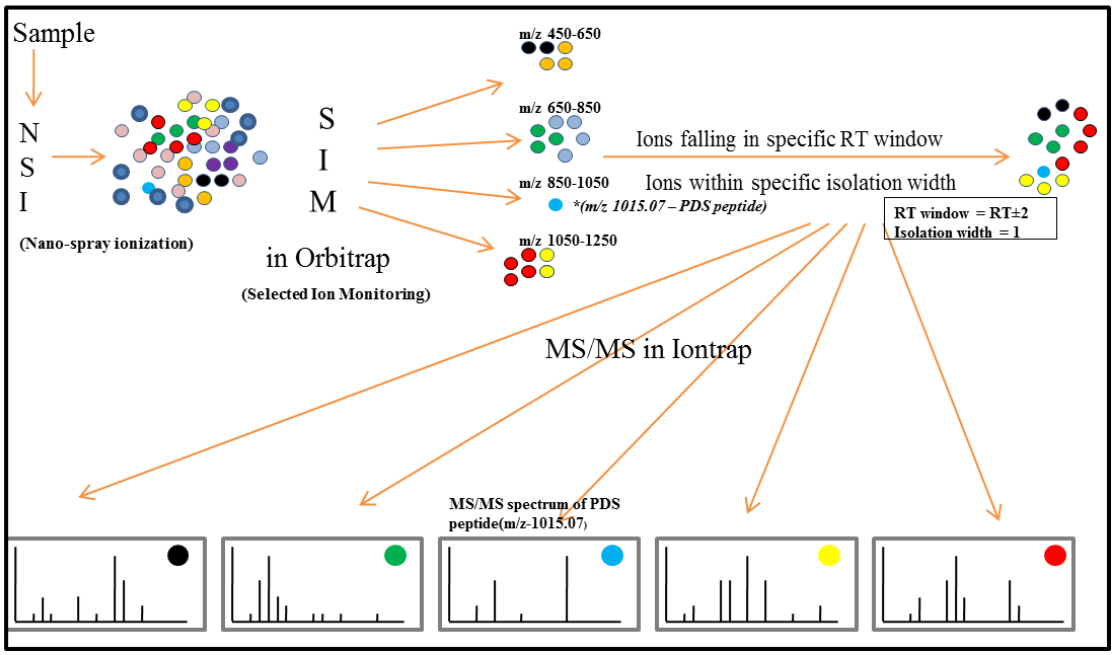
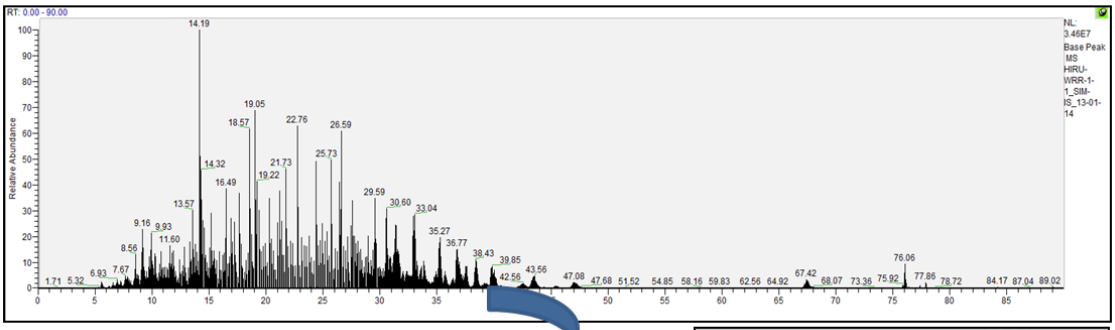
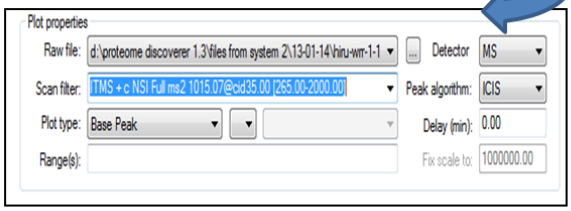


Figure 5.4. Contd.

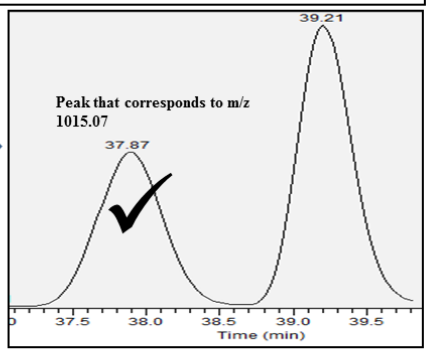
TPM raw file processing -



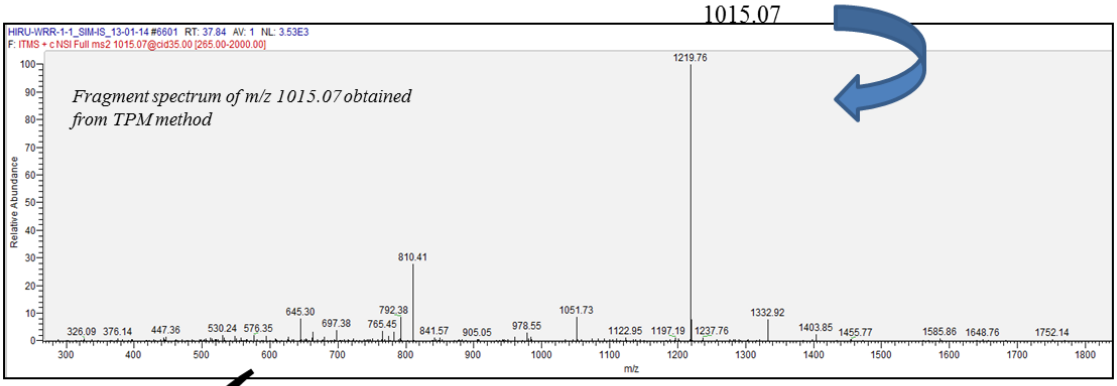
Total Ion Chromatogram of SL sample



Tab displaying the extraction of m/z 1015.07

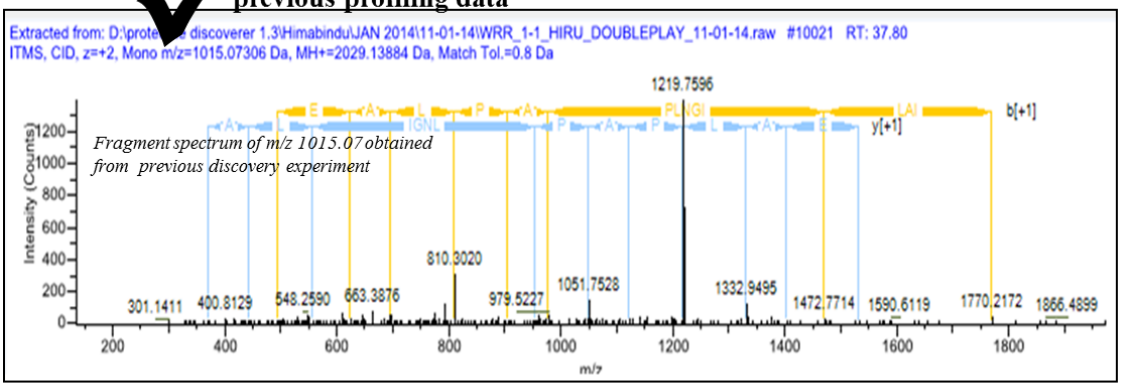


XIC of peak pertaining to m/z 1015.07



Confirming MS/MS with previous profiling data

F D F S[E[A[L[P[A[P[L N G I[L[A[I]L K



(Similar procedure was carried out for internal reference control proteins)

Figure 5.4. Contd.

Calculation of ratio of peak areas –

- Abundance of each pathway protein was represented as a ratio of mean of area under the curve (AUC) of three replicates of peptide of interest and mean of AUC of three replicates of internal reference peptides.

Mean of AUC of peptide = (AUC of 1st replicate+ AUC of 2nd replicate+ AUC of 3rd replicate)/3

Mean of AUC internal reference peptide = (AUC of 1st replicate+ AUC of 2nd replicate+ AUC of 3rd replicate)/3

$$\text{Abundance} = \frac{\text{Mean of AUC of peptide of interest}}{\text{Mean of AUC of internal reference control peptide}}$$

Figure 5.4. Methodology and workflow for setting up targeted peptide monitoring for quantification of proteins.

5.2.12 Photosystem II activity

The activity of PSII was determined using Hill reaction (Bregman 1990). About 1 g of pericarp tissue (26 and 39 dpa fruits of SL, SP, SG and SH) was homogenized in a chilled mortar and pestle with 4 ml of ice cold extraction buffer containing 0.3 M sucrose, 0.2 M Tris, 5 mM $MgSO_4$, pH 7.5 (Tris-sucrose buffer-TSB). The homogenate was filtered through two layers of cheese cloth and centrifuged at 2000*g* at 4°C for 5 min. The chloroplast pellet was suspended in 2 ml of TSB. An aliquot from it was used for estimating chlorophyll concentration (Bregman 1990). The PSII activity was measured in 5 ml total reaction volume by adding chloroplast suspension (equivalent to 20 µg chlorophyll) to 0.04 mM DCPIP (2,6-dichlorophenol indophenol, Sigma) in TSB. The mixture was irradiated with 200 µmole m^{-2} sec^{-1} light at 25°C for 3 min with a heat sink between the reaction tubes and the light source. The photoreduction of DCPIP was measured at 30 sec intervals at 600 nm and ΔA was calculated. As a control, Hill reaction was carried out in the presence of 0.01 mM DCMU (3-(3,4-dichlorophenyl)-1,1-dimethyl urea, Sigma; Trebst, 2007), an electron transport inhibitor and also in the dark incubated samples. The activity of PSII was expressed as ΔDCPIP $min^{-1}gFW^{-1}$. All the assays were performed in three biological replicates for each genotype.

5.2.13 PAO/RCCR activity

The enrichment of PAO and RCCR from fruit tissue was carried out as described earlier (Hortensteiner et al., 1995, Christ et al., 2012). Briefly, 1 g of the pericarp tissue from fruits of SL and SH (39 dpa) was homogenized in a chilled mortar and pestle with 5 ml of extraction buffer containing 0.4 M sorbitol, 25 mM Tricine-KOH pH 8, 2 mM Na-EDTA, 1 mM $MgCl_2$, 0.1% (w/v) BSA, 5 mM polyethylene glycol and 5 mM ascorbic acid. The homogenate was filtered through two layers of cheese cloth and centrifuged at 6000g, 4°C for 5 min. The thylakoid pellets after washing with 25 mM Tris-MES pH 8 were suspended in 100 µl of the same buffer containing 1% (w/v) Triton X-100 and mixed by shaking at 4°C for 30 min in the dark. The solubilized thylakoid membranes were centrifuged at 40000g at 4°C for 90 min, and the supernatant was used for PAO/RCCR enzyme assay (Hortensteiner et al., 1995, Rodoni et al., 1997, Pruzinska et al., 2003).

The assay mixture consisting of 40 µl of PAO/RCCR extract, 2 mM of pheophorbide a (isolated from spinach leaf, Hortensteiner et al., 1995), 10 µg of

ferredoxin (Sigma), 2 mM glucose-6-phosphate (Sigma), 1 mM NADPH (Sigma), 50 milliunits of glucose-6-phosphate dehydrogenase (Sigma) and 10 milliunits of ferredoxin-NADPH-oxidoreductase (Sigma) was incubated at 25°C for 1 h. The reaction was terminated by addition of methanol to a final concentration of 70% (v/v). The samples were then vacuum dried and stored at -80°C until further use. The samples were reconstituted in 100 µl of methanol and the fluorescent chlorophyll catabolites (FCCs) were separated and analysed by HPLC (Shimadzu) on a C-18 column (250 x 4.6 mm, 5 µm, Phenomenex) with 40 mM potassium phosphate and methanol (2:3, v/v) (solvent A) and 100% methanol (solvent B) as mobile phases. The following step-up gradient was used: 20-60% B (0-30 min), 60% B hold (30.01-40 min), 100% B (40.01-42 min), 100 % B hold (43-60 min). FCCs were identified by comparing their fluorescence (320/450 nm) and absorption spectra (320 and 360 nm). The peak areas of FCCs were compared in SL and SH samples, and the ratio of peak areas in SL and SH was used as a measure of estimating PAO/RCCR activity. The lack of commercial standards for FCCs precluded the identification of individual catabolites.

5.2.14 Estimation of Jasmonate

Jasmonate (JA) from fruit tissues of tomato and wild relatives was extracted in five biological replicates based on the protocol described by Pan et al. 2010. Waters Acquity UPLC coupled with Thermo Exactive Plus (Thermo Fisher Scientific) was used for LCMS analysis. JA was separated on a Hypersil Gold C18 column (50 x 2.1 mm, 1.9 µ particle size) using 0.1% (v/v) formic acid in water (mobile phase A) and 0.1% (v/v) formic acid in acetonitrile (mobile phase B) employing a 9 min gradient with following parameters – 5% B from 0-1 min followed by a linear increase to 80% B within the next five mins and a minute hold at 80% B followed by re-equilibration to 5% B in the next two minutes. The column was run at room temperature while the tray temperature was set to 4°C to avoid sample degradation. Column eluate was connected to a heated electrospray ionization source (HESI) operated at a voltage of 4.5 kV in positive mode and 3.2 kV in negative mode at a capillary temperature of 350°C. Sheath gas and auxiliary gas flow rates were set to 35 and 10 respectively. Auxiliary gas heater temperature was set to 300°C. Full scans (MS) were acquired at a resolution of 70,000 followed by all-ion fragmentation (AIF) using stepped collision energies of 18, 20 and 25. Fragment ions were scanned at a resolution of 35,000. 445.12003 was used as the lock mass. AGC target of 1E+06 was set for both MS and AIF modes. Jasmonic acid eluted at

a retention time of 3.87 min and exhibited a m/z of 209.1180 in the negative mode with a normalised collision energy of 20. 1 µg/µL stock solution of jasmonic acid (Sigma) was prepared in methanol and stored at -20°C. External calibration was used with a total of 8 concentrations in the range of 1 pg to 400 pg/µL to assess the linearity and to plot calibration curve. JA levels in the fruits of tomato and wild relatives were calculated using the standard curve.

5.2.15 Statistical Analysis

Unless otherwise mentioned a minimum of three biological replicates were used for every experiment. Based on the samples, either Student's t-tests or one way ANOVA followed by Holm-Sidak test were performed to determine significant differences using Sigmaplot (version 11.0). Wherever required, the P values <0.05, <0.01, <0.001, <0.0001 were indicated by one, two, three or four asterisks respectively. Hierarchial clustering was performed using Gene-E. The heat maps were generated using either Gene-E or R. Pearson's Correlation algorithm (XLSTAT 2013 software) was used to perform a pairwise correlation based on the ratio of the abundance values for protein, transcript, and carotenoid data of each wild species with SL ($n = 3$, $Pvalue \leq 0.05$).

5.3 Results

5.3.1 Wild species emit higher ethylene than tomato

Tomato, being a climacteric fruit, carotenoid accumulation during ripening is preceded by the emission of ethylene; consistent with this, an ethylene insensitive mutant, *Nr* does not accumulate carotenoids. Taking into account the integral role of ethylene in fruit ripening and associated carotenoid accumulation, we examined ethylene emission in the wild species. The wild species emitted much higher ethylene compared to SL at all the time points. In SL, ethylene emission was low at 15 dpa and moderately increased till 29 dpa and remained at that level even at 39 dpa. SP fruits emitted high ethylene from 15 to 26 dpa and then emission declined at 29 dpa, thereafter remained at the same level. In SG, the ethylene emission gradually increased from 15 to 39 dpa. In the green-fruited SH, ethylene emission gradually increased from 15 to 26 dpa and declined thereafter. The time point for peak ethylene emission was different for each species. Also, the accumulation of carotenoids in SP fruits does not coincide with the peak ethylene (Fig. 5.5A). A similar lack of correlation is also observed in SG where ethylene emission progressively increased till 39 dpa. These results on ethylene emission from wild

relatives' fruits are at variance from other reports. This is likely related to the different growth conditions (Dal Cin et al., 2009) and the accession used (SP-LA1633, SG-LA455, SH-LA1775, Grumet et al., 1981).

The divergence between ethylene emission and fruit coloration of wild relatives suggest that the carotenoid formation in the wild species is most likely not coupled with ethylene emission. Considering this, we examined fruits of SP, SG, and SH with reference to ripening stages of SL, i.e., green stage at 26 dpa, transitional stage at 29 dpa and orange/red stage at 39 dpa (26→39 dpa) (Fig. 5.2). Though SH fruits lack color transitions, we used above time points for SH too.

5.3.2 Expression pattern of genes mediating ethylene biosynthesis varies in wild species

In SL, ethylene emission is reportedly preceded by up-regulation of *1-aminocyclopropane-1-carboxylate synthase 2* and *4* (*acs2*, *acs4*), *1-aminocyclopropane-1-carboxylic acid oxidase 1* and *3* (*aco1*, *aco3*) transcripts (Barry et al., 2000). The expression profiles and the relative levels of these transcripts were distinctly different in wild species. In SL and SP, *acs2* peaked at 29 dpa, whereas in SH and SG it continually increased. The expression profile of *acs4* was similar in wild species with a peak at 29 dpa, whereas in SP, it continually declined and in SG showed a dip at 29 dpa. Expression of *aco3* in SL showed a peak at 29 dpa and in SG followed a reverse pattern. In SP and SH, *aco3* levels declined after 29 and 26 dpa respectively (Fig. 5.5B).

5.3.3 Carotenoid profiling

In orange/red-fruited species, increase in carotenoid levels (26 to 39 dpa) was associated with decline in chlorophylls. However, SH fruits retained similar level of carotenoids and chlorophylls (Table 5.4). The initiation of ripening led to preferential accumulation of lycopene/β-carotene and appearance of phytoene and phytofluene at 39 dpa in all species, except SH. In addition, lycopene/β-carotene ratios revealed a shift from high β-carotene to high lycopene from SH (0.0), SG (0.05), SL (5.25) to SP (22.8). Among the carotenoids present at 26 dpa, only violaxanthin and lutein were retained at 39 dpa in all species, whereas neoxanthin was retained in SH. The examination of ratios between β-carotene and α-carotene pathways revealed that β-carotene pathway was predominant in SP at 26 dpa (SP>SL>SG>SH) and in SG at 39 dpa (SG>SL>SP>SH). The Chl/Car ratio in fruits showed continual decline (26 to 39 dpa) except in SH. In leaf,

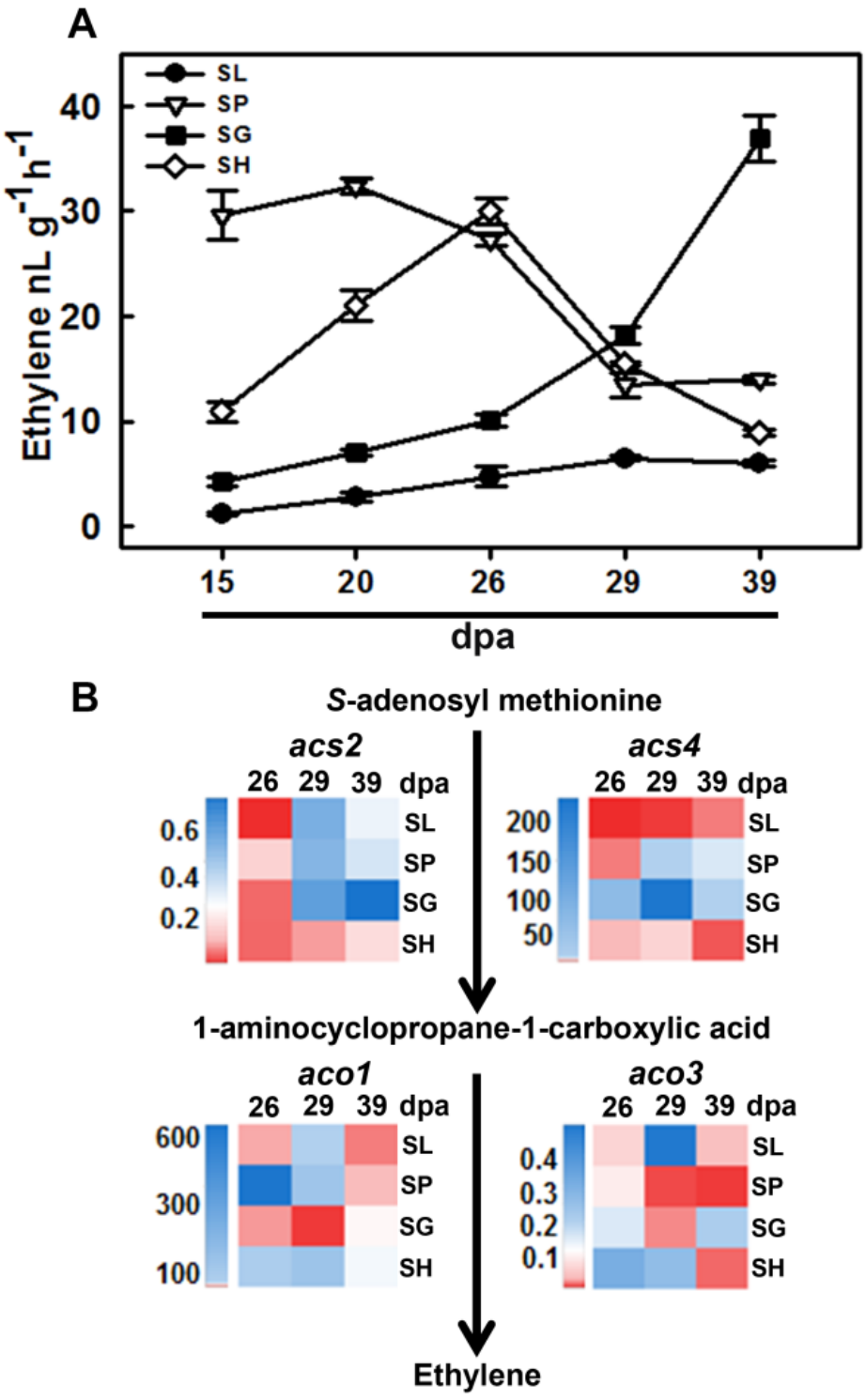


Figure 5.5. Ethylene emission in tomato and wild species fruits. The fruits were harvested at the indicated time points, and ethylene emission was measured (Data are means ± SE (n = 3), P ≤ 0.05)

Table 5.4. Carotenoid and chlorophyll contents in the fruits and leaves of wild species and tomato

Metabolite	*S. lycopersicum*				*S. pimpinellifolium*				*S. galapagense*				*S. habrochaites*			
(µg gFW^{-1})	26 dpa	29 dpa	39 dpa	Leaf	26 dpa	29 dpa	39 dpa	Leaf	26 dpa	29 dpa	39 dpa	Leaf	26 dpa	29 dpa	39 dpa	Leaf
Phytoene	0.0 ± 0.0	0.0 ± 0.0	13.16 ± 0.97	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	**66.86 ± 2.31*** **	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	**34.35 ± 1.2*** **	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
Phytofluene	0.0 ± 0.0	0.0 ± 0.0	2.47 ± 0.12	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	**7.08 ± 0.50*** **	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	2.55 ± 0.23	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
Lycopene	0.0 ± 0.0	0.0 ± 0.0	64.59 ± 9.3	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	**189.24 ± 11.31*** **	0.0 ± 0.0	0.0 ± 0.0	**0.29 ± 0.004*** **	1.54 ± 0.05***	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
α-Carotene	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	**3.11 ± 0.48*** **	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
β-Carotene	2.21 ± 0.09	3.85 ± 0.17	12.31 ± 0.3	11.77 ± 2.3	2.08 ± 0.30	2.36 ± 0.28	8.30 ± 0.50	20.61 ± 3.27	**3.96 ± 0.54*** **	5.27 ± 1.04	**30.13 ± 3.13** **	11.19 ± 0.8	**3.76 ± 0.08*** **	2.75 ± 0.17	**4.42 ± 0.27** **	14.49 ± 1.3
Lutein	3.1 ± 0.11	3.56 ± 0.21	4.62 ± 0.6	18.13 ± 4.4	3.82 ± 0.33	3.75 ± 0.61	5.08 ± 0.13	37.76 ± 13.2	**7.46 ± 0.88*** **	**6.41 ± 0.96** **	5.07 ± 0.48	26.53 ± 6.6	**6.57 ± 0.52*** **	3.88 ± 0.26	5.36 ± 0.40	29.47 ± 6.9
Zeaxanthin	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	**1.22 ± 0.17*** **	**1.13 ± 0.21*** **	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0
Violaxanthin	1.64 ± 0.12	2.49 ± 0.29	1.19 ± 0.01	4.69 ± 0.3	**3.0 ± 0.18*** **	1.82 ± 0.12	1.22 ± 0.03	5.35 ± 0.76	**3.16 ± 0.36*** **	3.37 ± 0.57	**1.73 ± 0.14***	3.73 ± 0.3	2.08 ± 0.12	2.47 ± 0.23	**2.22 ± 0.2*** **	4.48 ± 0.3
Antheraxanthin	1.09 ± 0.01	2.13 ± 0.06	0.0 ± 0.0	0.0 ± 0.0	**1.43 ± 0.04*** **	2.26 ± 0.08	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	2.48 ± 0.27	0.0 ± 0.0	0.0 ± 0.0	**1.21 ± 0.02** **	2.19 ± 0.18	0.0 ± 0.0	0.0 ± 0.0
Neoxanthin	1.12 ± 0.02	0.90 ± 0.08	0.0 ± 0.0	7.56 ± 2.94	**1.64 ± 0.05** **	1.23 ± 0.07	0.0 ± 0.0	13.93 ± 1.8	**1.73 ± 0.21** **	**2.83 ± 0.51*** **	0.0 ± 0.0	8.33 ± 0.64	1.01 ± 0.07	1.33 ± 0.027	**0.99 ± 0.12*** **	9.52 ± 0.96
Total CAR	9.16 ± 0.37	12.93 ± 0.52	101.62 ± 8.5	42.15 ± 5.13	**11.97 ± 0.44** **	11.42 ± 0.41	**277.78 ± 25.3*** **	77.65 ± 9.5	**17.53 ± 1.04*** **	21.78 ± 0.7	**78.48 ± 5.4*** **	49.78 ± 4.25	**14.63 ± 1.03*** **	12.62 ± 0.41	**12.99 ± 0.99*** **	57.96 ± 4.25
Chlorophyll *a*	73.25 ± 1.27	44.9 ± 0.93	24.6 ± 0.81	191 ± 3.54	**108.5 ± 5.7*** **	**57.5 ± 0.5*** **	**23.32 ± 0.19***	**160 ± 2.7*** **	**124.47 ± 13.2*** **	**97.7 ± 3.8*** **	**25.4 ± 0.31***	**146 ± 4.5*** **	**74.75 ± 2.4***	**65.9 ± 1.3*** **	**67.74 ± 5.04*** **	**153 ± 0.49*** **
Chlorophyll *b*	46.1 ± 0.61	43.2 ± 1.42	38.28 ± 0.87	63 ± 4.1	**59.8 ± 0.52*** **	**44.2 ± 1.25***	**36.8 ± 0.59***	**51.5 ± 0.91*** **	**69.5 ± 4.4*** **	**59.9 ± 5.3*** **	**38.45 ± 0.67***	**45 ± 1.9*** **	**49.7 ± 1.08***	**46 ± 0.23***	**49.23 ± 0.87*** **	**62 ± 0.23***
Chl *a*: Chl *b*	1.59 ± 0.009	1.04 ± 0.09	0.64 ± 0.006	3.03 ± 0.13	**1.81 ± 0.06***	**1.3 ± 0.025*** **	0.63 ± 0.01	3.1 ± 0.01	**1.79 ± 0.07***	**1.64 ± 0.08*** **	0.66 ± 0.005	**3.25 ± 0.05***	**1.5 ± 0.02***	**1.43 ± 0.02*** **	**1.37 ± 0.04*** **	**2.47 ± 0.001*** **

Metabolite (µg gFW^{-1})	*S. lycopersicum*				*S. pimpinellifolium*				*S. galapagense*				*S. habrochaites*			
	26 dpa	**29 dpa**	**39 dpa**	**Leaf**	**26 dpa**	**29 dpa**	**39 dpa**	**Leaf**	**26 dpa**	**29 dpa**	**39 dpa**	**Leaf**	**26 dpa**	**29 dpa**	**39 dpa**	**Leaf**
Total Chl	119.35 ± 0.1	88.1 ± 2.54	62.88 ± 1.25	254 ± 3.62	**168.3 ± 2.34***	**101.7 ± 0.75****	**60.12 ± 0.6***	**211.5 ± 1.1*****	**193.97 ± 10.22***	**157.6 ± 5.4*****	63.85 ± 0.75	**191 ± 2.8*****	**124.45 ± 2***	**111.9 ± 0.7*****	**116.97 ± 3.5*****	**215 ± 0.3*****
CHL:CAR	13.2 ± 8.45	6.81 ± 0.073	0.61 ± 0.032	6.02 ± 0.25	**14 ± 0.654*****	**8.9 ± 0.76****	**0.216 ± 0.019*****	2.72 ± 0.32	11.06 ± 0.12	**7.23 ± 0.79****	**0.81 ± 0.08*****	3.83 ± 0.26	**8.5 ± 0.83*****	**8.86 ± 0.9*****	**9.00 ±0.79*****	3.7 ± 0.23

Carotenoid and chlorophyll contents are presented as µg/g fresh weight. Chl, chlorophyll; CAR, carotenoid. Holm-Sidak test was used to determine the significant differences in the metabolites between the wild species and tomato. Values in bold indicate where significant differences have been found. The P values < 0.05, < 0.01 and < 0.001 were indicated by one, two or three asterisks respectively.

only four carotenoids accumulated i.e. β-carotene, violaxanthin, neoxanthin and lutein and all four were also present in fruits at 26 dpa.

5.3.4 Expression profiles of carotenogenic genes in the fruit

The geranylgeranyl diphosphate (GGPP) required for phytoene formation is derived from the plastid localized methylerythritol-4-phosphate pathway (MEP) pathway. The genes [*dxs*, *dxr*, *4-hydroxy-3-methylbut-2-enyl diphosphate reductase* (*hdr*), *isopentenyl diphosphate isomerase 5g* (*idi5g*), *ggpp synthase 2* (*ggpps2*)] leading to GGPP formation were up-regulated in all wild species compared to SL barring a few exceptions (Fig. 5.6). Relative to SL, only a few genes were down-regulated (*dxs*, 26 dpa-SP, 29 dpa-SH; *hdr*, 39 dpa-SG, SH; *ggpps2*, 29 dpa-SG; *idi5g*, 26 dpa-SP, SH; 29 dpa-SG).

In tomato, PSY1 and PSY2 reportedly contribute to fruit (Fray and Grierson 1993) and leaf-specific (Fraser et al., 1999) carotenoid formation respectively. Consistent with this, *psy1* expression in orange/red fruits was much higher than *psy2* with high levels in SP and SG at 39 dpa. Conversely in leaf, *psy2* showed higher expression than *psy1*. Though SH is green fruited, yet showed high level of *psy1* compared to *psy2* (66, 158, 860 folds high 26-39 dpa respectively). However, *psy1* level declined after 26 dpa in SH compared to other species. The conversion of phytoene to lycopene is contributed by four genes, *phytoene desaturase* (*pds*), *ζ-carotene isomerase* (*ziso*), *ζ-carotene desaturase* (*zds*) and *carotenoid isomerase* (*crtiso*). The *pds* and *ziso* expression profile was similar in all species except *ziso* in SG. Compared to SL, expression of *zds* was immensely up-regulated in wild species. The expression of *crtiso* was different in each species.

Out of three lycopene β-cyclases (*lcyb1*, *lcyb2*, *cycb*) in tomato, only *cycb* drives the β-carotene formation in fruits. Consistent with this, *cycb* expression in fruits was higher than *lcyb1* and *lcyb2*; its expression declined in wild species while it increased in SL (26 to 39 dpa). Though SH formed little β-carotene, it had higher *cycb* expression than orange/red fruited species. The expression profile of *lcyb1* was similar to *cycb*, whereas *lcyb2* expression gradually declined in SP and SG and remained constant in SL and SH.

The expression profile of *β-carotene hydroxylase 2* (*crtrb2*) was different in each wild species and SL. The expression profiles of *zeaxanthin epoxidase* (*zep*) and *violaxanthin deepoxidase* (*vde*) at different stages were opposite to each other. Among four species, SG showed very high *neoxanthin synthase* (*nxs*) expression at 26 dpa, thereafter, its expression declined. The *lycopene ε-cyclase* (*lyce*) expression was lowest in

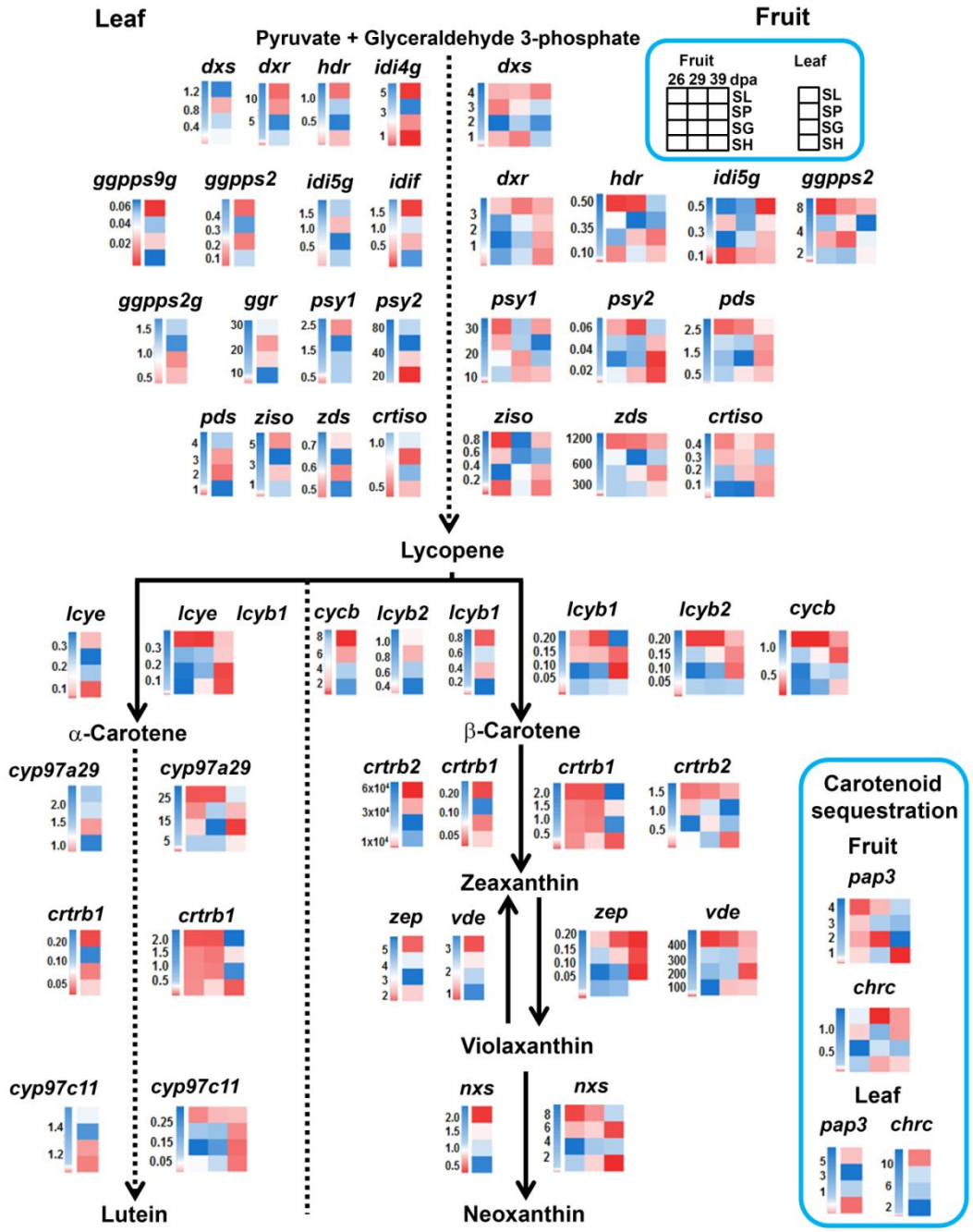


Figure 5.6. Relative expression of genes mediating carotenoid biosynthesis and sequestration in tomato and wild species fruits (Data are means ± SE (n = 3), P≤ 0.05). See primer at top right corner of the figure for time points and species depicted on heat maps. Dotted arrows indicate multiple steps in the pathway. The genes mediating carotenoid sequestration are enclosed in the rectangle. The heat maps depict data obtained after normalization with *β-actin* and *ubiquitin*. The vertical scale on left of heat map represents relative range (Red-low; Blue-high).

SL fruits. In contrast, SH fruits showed higher expression of *lyce* at 26 dpa. The genes leading to lutein synthesis, *cytochrome P450 carotenoid β-hydroxylase A29* (*cyp97a29*), *β-carotene hydroxylase 1* (*crtrb1*), and *cytochrome P450 carotenoid β-hydroxylase C11* (*cyp97c11*) showed variable expressions.

In conjunction with carotenoid biosynthetic genes, the expression of sequestration genes, i.e., *chrc* and *pap3* was also examined. The orange/red fruited species showed high expression of *pap3* at 39 dpa, whereas, in SH, it peaked at 29 dpa. The *chrc* expression in SL, SG, SH dipped at 29 dpa and increased thereafter, while SP showed a peak at 29 dpa.

The relationship between metabolites and the transcripts was examined by using stringent pairwise correlation analysis ($r \geq 0.80$). The *dxs* expression positively correlated with most abundant carotenoids viz. lutein-SH, β-carotene-SG and lycopene-SP (Table 5.5). Contrarily, *psy1* expression negatively correlated with lutein-SH, β-carotene-SG and lycopene-SP. The *psy2* expression in fruits positively correlated with lutein, violaxanthin in SH, lutein in SG and negatively correlated with lycopene in SG. Accumulation of β-carotene in fruit is specifically mediated by *cycb*, whose expression correlated with β-carotene positively in SG and negatively in SP and SH.

Notwithstanding the differences in their relative expression, transcript profiles of the carotenogenic genes revealed common patterns. The majority of the genes had similar expression patterns in all the three wild species when compared to SL (Table 5.6). The expression patterns were more similar between SG-SH than SP-SG and SP-SH. The commonality of gene expression progressively declined from 26 to 39 dpa.

5.3.5 Expression profiles of carotenogenic genes in the leaf

In case of leaf, additional transcripts, *idif*, *idi4g*, *ggpps9g*, *ggpps2g* and *geranylgeranyl reductase* (*ggr*) were included as their respective proteins were detected in the proteome profiles of leaf. The expression level of carotenogenic transcripts in leaf was higher than fruits and in general, wild species showed higher expression levels than SL (Fig. 5.6). Intriguingly *cycb* expression in leaf was higher than the fruit. Majority of genes contributing to α-/β- carotene pathway were up-regulated in wild species compared to SL. In addition, both *chrc* and *pap3* genes were up-regulated in all wild species. Unlike fruit, *dxs* expression did not correlate with the most abundant carotenoid in leaf (Table 5.5). The *psy2* expression correlated to different carotenoids in a species-specific fashion.

The analysis revealed positive correlation of *cycb* and *lcyb1* in SH and *lcyb2* in SP with β-carotene, whereas in SG, no correlation was observed.

5.3.6 Expression profiles of ripening regulators

We also examined whether the green fruited nature of SH resulted from the lack/subdued expression of transcription factors regulating fruit ripening. In general, the expression levels of most transcription factors were higher in wild species including SH than SL, the exception being *erf6* and *HD-Zip homeobox protein1* (*hb1*) (39 dpa) (Fig. 5.7A). The expression of *colorless nonripening* (*cnr*) increased in red/orange fruited species whereas in SH it declined (26 to 39 dpa). In addition, the expression of *phytochrome interacting factor1* (*pif1*), *related to apetala2.2* (*rap2*.2), *Arabidopsis pseudo response regulator 2-like* (*aprr2*) and *golden 2-like* (*glk2*) were examined in leaf (Fig. 5.7B). *rap2*.2 and *aprr2* showed higher expression in all wild species compared to SL, while *pif1* showed species-specific expression with high expression in SG and low expression in both SP and SH in comparison to SL.

5.3.7 Transmission electron microscopy (TEM) reveals intact grana in SH fruits

The chloroplast to chromoplast transformation is accompanied by several changes in the plastid ultrastructure. At 39 dpa, the fruits of SL, SP and SG showed a reduction in the granal membranes and the higher number of plastoglobules (Fig. 5.8A-C, E). Consistent with high carotenoid levels in SP, the plastoglobules were larger in size compared to SL whereas in SG, plastoglobules were many and smaller in size than SL. Consistent with green-fruited nature, the thylakoid membranes were intact in SH fruits (Fig. 8D). Though SH had fewer plastoglobules than SL, these were similar in size to SL. Distinct differences in staining were observed for the plastoglobules in SP and SG. Lycopene crystalloids were predominant in SP corroborating with high lycopene levels in fruits. Also, crystalloid remnants of lycopene associated with undulating internal membranes could be seen in SL, SP and SG but not in SH.

5.3.8 Proteome analysis in fruit and leaf

Using shotgun proteomics approach, a much wider spectrum consisting of 3250-3500 proteins were detected in orange/red fruited species than a previous report in tomato (Barsan et al., 2012) (Fig. 5.9A, B). In SH, usage of a modified protocol reduced the yield, nevertheless, 2188 and 1777 proteins were identified in SL and SH fruits respectively (Fig. 5.9C). Comparison with SL revealed large number of differentially

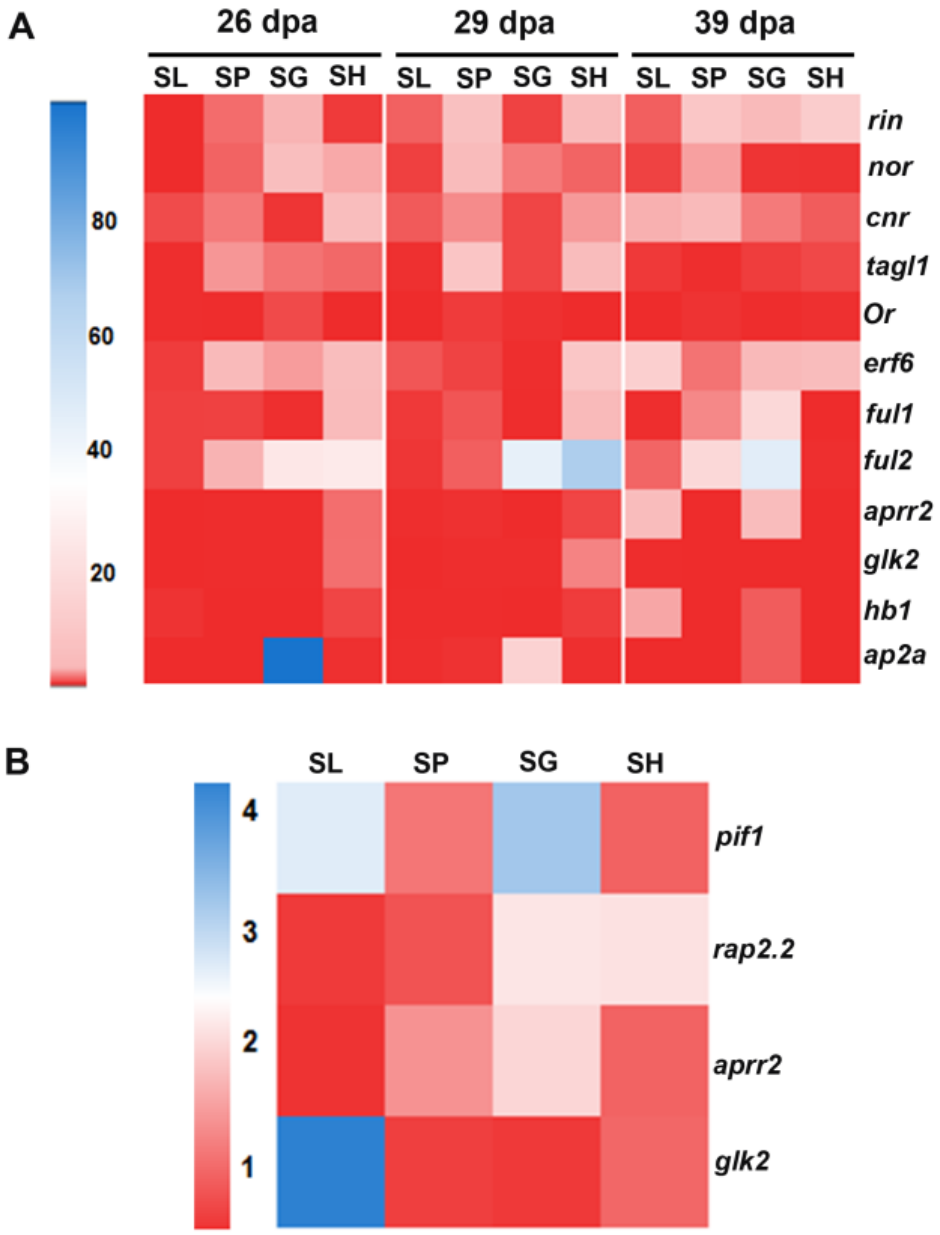


Figure 5.7. Relative expression levels of regulatory genes in fruits and leaves of tomato and wild species. **A**, Fruits. **B**, Leaves. The heat maps depict data obtained after normalization with β-actin and ubiquitin ($n \geq 3 \pm SE$, $P \leq 0.05$). The vertical scale on left of heat map represents relative range (Red-high; Blue-low).

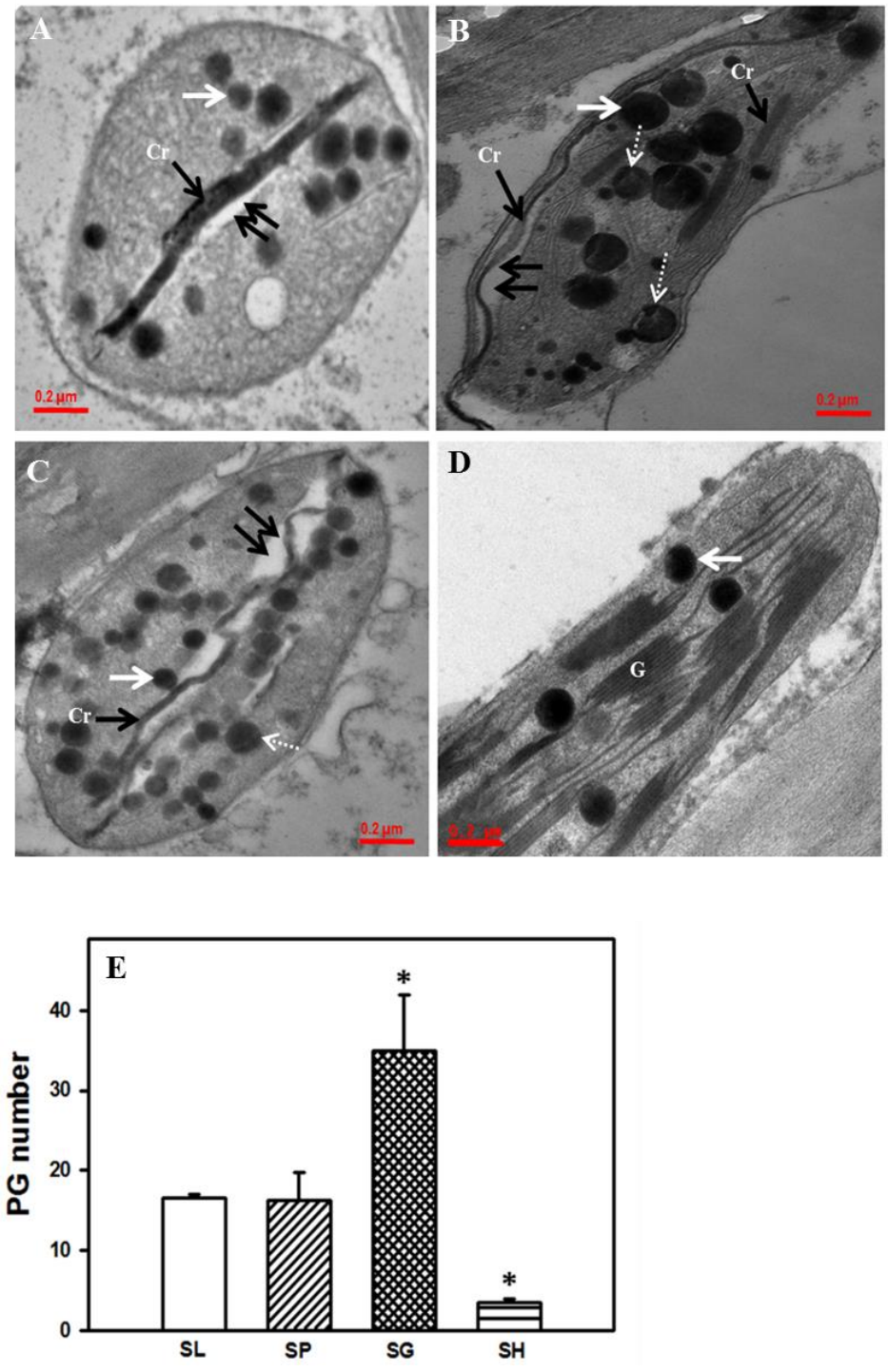


Figure 5.8. Transmission electron micrographs of chromoplasts/chloroplasts present in the 39 dpa fruits of tomato and wild relatives. **A,** SL; **B,** SP; **C,** SG and **D,** SH. Double arrows show an enlarged granal compartment, black arrows show lycopene crystalloid, Cr indicates lycopene crystal, G indicates granum, white arrows indicate plastoglobules, and dashed white arrows show morphologically distinct plastoglobules. **E,** Relative number of plastoglobules present in chloroplast/chromoplasts of tomato and wild species. Data are means ± SE (n = 3), * = $P \leq 0.05$.

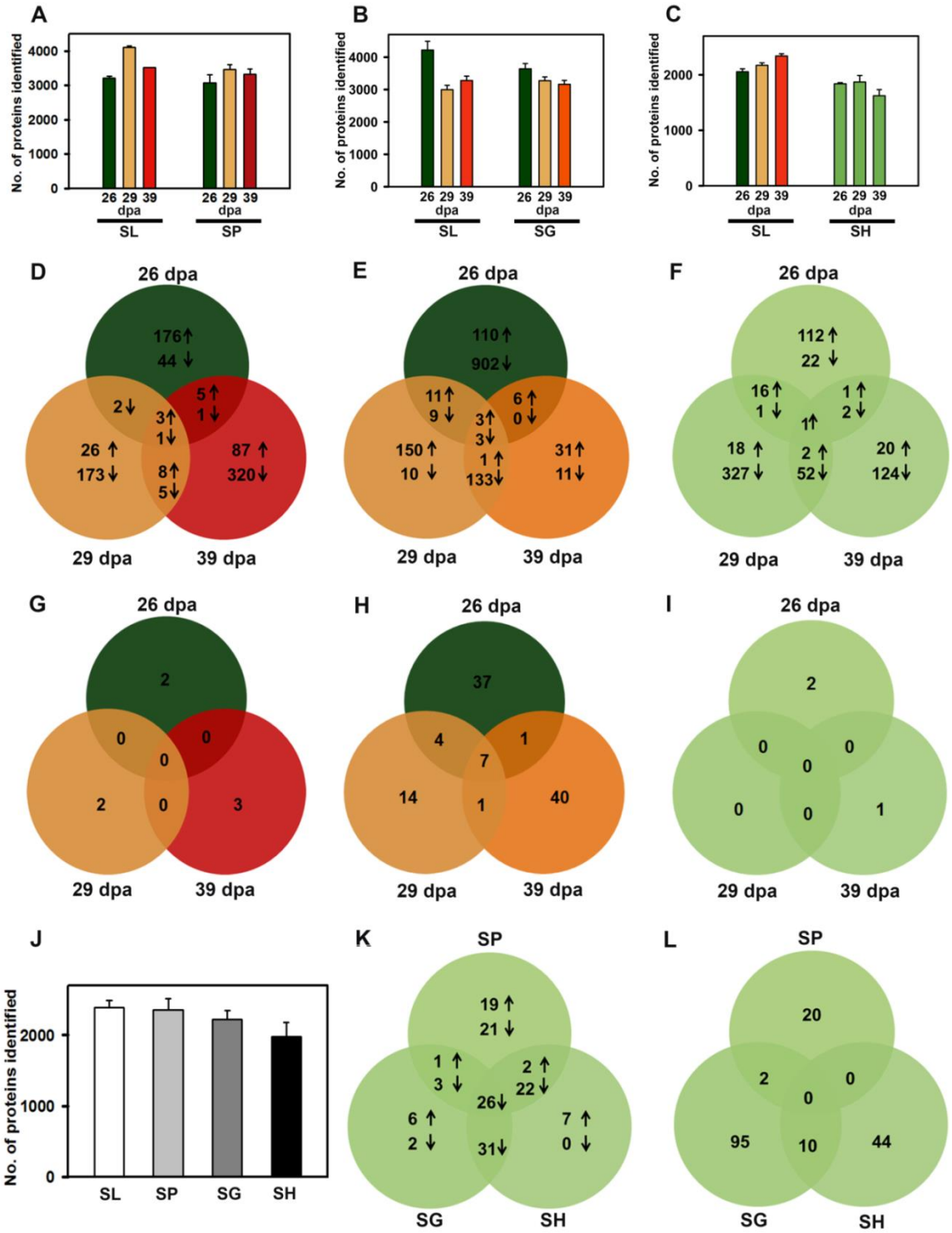


Figure 5.9. Proteome analyses from the fruits and leaves of tomato and wild species. The proteins were isolated from fruits and leaves [n ≥ 3 ± SE; Upregulation (↑), downregulation (↓)]. **A-C**, Number of proteins identified in fruits. **A**, SP and SL; **B**, SG and SL; **C**, SH and SL. **D-F**, Differentially expressed proteins in fruits. **D**, SP; **E**, SG; **F**, SH. **G-I**, Proteins identified only in wild species fruits. **G**, SP; **H**, SG; **I**, SH. **J**, Leaf proteome profiles; **K**, Differentially expressed proteins in leaves; **L**, Proteins identified only in leaves of wild species.

expressed proteins in fruits of wild relatives (SP-851, SG-1380, SH-698) (Fig. 5.9D-F). Comparing with SL, few proteins were detected only in the wild relatives (SP-7, SG-104, SH-3) at different stages (Fig. 5.9G-I, Table 5.7). In SL, no peptide matches corresponding to these proteins were found at any stage and most of these proteins constituted different isoforms of existing proteins (Tables 5.7 and 5.8).

The proteome profiling of the leaf detected around 2100 proteins in all four species (Fig. 5.9J). Compared to the fruits, only few were differentially regulated between wild species and SL. Majority of the proteins were down-regulated and only few were up-regulated in the wild species (SP-94, SG-69, SH-88) (Fig. 5.9K, Table 5.9). Similar to fruit, in leaf few proteins were detected only in wild species (SP-22, SG-107 SH-54; Fig. 5.9L, Table 5.10).

5.3.9 Influence of databases on proteome analyses

When we started this study, only the SL and SP genomes were sequenced, and their corresponding protein databases were available. Consequently, the mass spectra obtained from SG and SH proteomes were searched against SL databases (Fig. 5.9). Though the genome sequences of SG and SH became available in 2014, the annotation of genomes is not yet complete, and the protein databases are still not available. However, Koenig et al., 2013 acquired RNA-Seq data from the leaves of few wild species of tomato clade, and we obtained SH protein fasta file from them. We searched the mass spectra from SH samples against this database. Though using SH database we observed a slight reduction in the total proteins identified, the number of differentially expressed proteins increased from 501 (with SL database, Fig. 5.10) to 698 (Fig. 5.9, Table 5.7). As RNA-Seq data for SG was not available, the SG mass spectra were searched against SP database as SG is phylogenetically closer to SP than SL (Aflitos et al., 2014). Similar to SH, a slight decrease in total protein number was observed in SG when the mass spectra were searched against SP database, but the differentially expressed proteins increased from 1183 (SL database) to 1440 (SP database, Fig. 5.9, Table 5.7, Fig. 5.10). Moreover, the number of proteins present only in SG increased to 104 (Fig. 5.9H, Table 5.7) from 23 (SL database, Fig. 5.10E). Also, the number of proteins present only in SH with no corresponding matched peptides in SL reduced to 3 (SH database, Fig. 5.9I, Table 5.8) from 13 (SL database, Fig. 5.10F). Henceforth, only the data obtained for SH with SH database and SG with SP database (Fig. 5.9, Table 5.7) are considered.

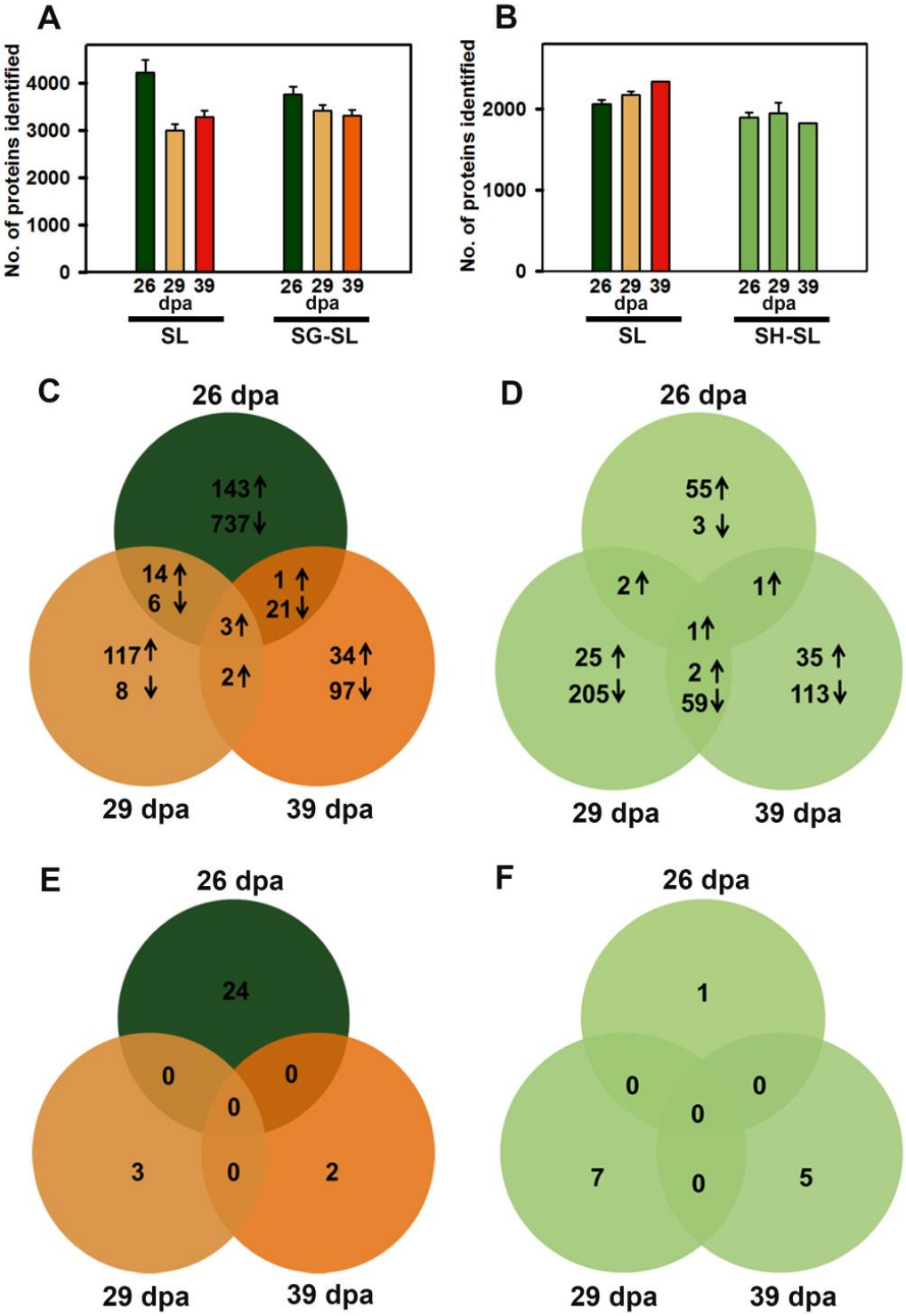


Figure 5.10. Influence of database on protein number A, B-no. of proteins identified; C, D-differentially regulated proteins; E, F-proteins only identified in SG and SH respectively when SG and SH were searched against SL database.

5.3.10 Functional classification of differentially expressed proteins in fruits and leaves of wild species

The functional classification of differentially expressed proteins using Mapman (Usadel et al., 2009) revealed functional classes that were up-regulated (SP-41, SG-42, SH-41) and down-regulated (SP-42, SG-44, SH-41) (Fig. 5.11, Table 5.7). The major up-regulated class varied in all wild relatives: in SP, it was development and storage (16.7%); in SG, it was miscellaneous (7.6%) followed by protein degradation (7.3%); whereas in SH, it was protein synthesis (9.3%). Consistent with chlorophyll retention in SH fruits, the functional classes PS light reaction and Calvin cycle were highly up-regulated (9.2%) in SH, whereas, these were up-regulated by 6.1% in SG and 5.8% in SP (Fig. 5.11). The functional class protein degradation in SP (6.2%) and SG (7.3%) was strongly up-regulated, conversely, SH showed up-regulation of protein synthesis (9.3%). While protein degradation in SP and SG was strongly up-regulated, SH showed up-regulation of protein synthesis highlighting that SH fruit development follows a different trajectory than SG and SP. Similarly, among the down-regulated proteins, variation was observed among the wild relatives. In SP, the functional class abiotic stress (13.8%) was the major down-regulated class; in SG, it was protein synthesis (15.2%), while it was protein degradation (9.9%) in SH.

The functional classification of differentially expressed proteins in leaf revealed functional classes that were up-regulated (SP-06, SG-13, SH-08) and down-regulated (SP-23, SG-28, SH-25) (Fig. 5.12, Table 5.7). Abiotic stress (33.3%) was highly up-regulated in SP whereas protein synthesis (19%) and protein folding (22.2%) were major classes that were up-regulated in SG and SH respectively. In case of down-regulated proteins, PS light reaction (22.3%) and PS Calvin cycle (22.3%) were strongly down-regulated in SP; PS Calvin cycle (14.8%) in SG and protein synthesis (19.7%) in SH were major down-regulated classes.

5.3.11 Hierarchical clustering of differentially expressed proteins in fruit

Hierarchical clustering of differentially expressed proteins as per the functional classification in all the genotypes revealed four clusters (Fig. 5.13). Cluster I (C1 metabolism, Tetrapyrrole synthesis, oxidative pentose phosphate pathway, protein assembly and cofactor ligation, fermentation, PS light reaction, redox) showed a high percentage of proteins at 26 dpa, followed by a decline at 29 dpa and 39 dpa. Cluster II

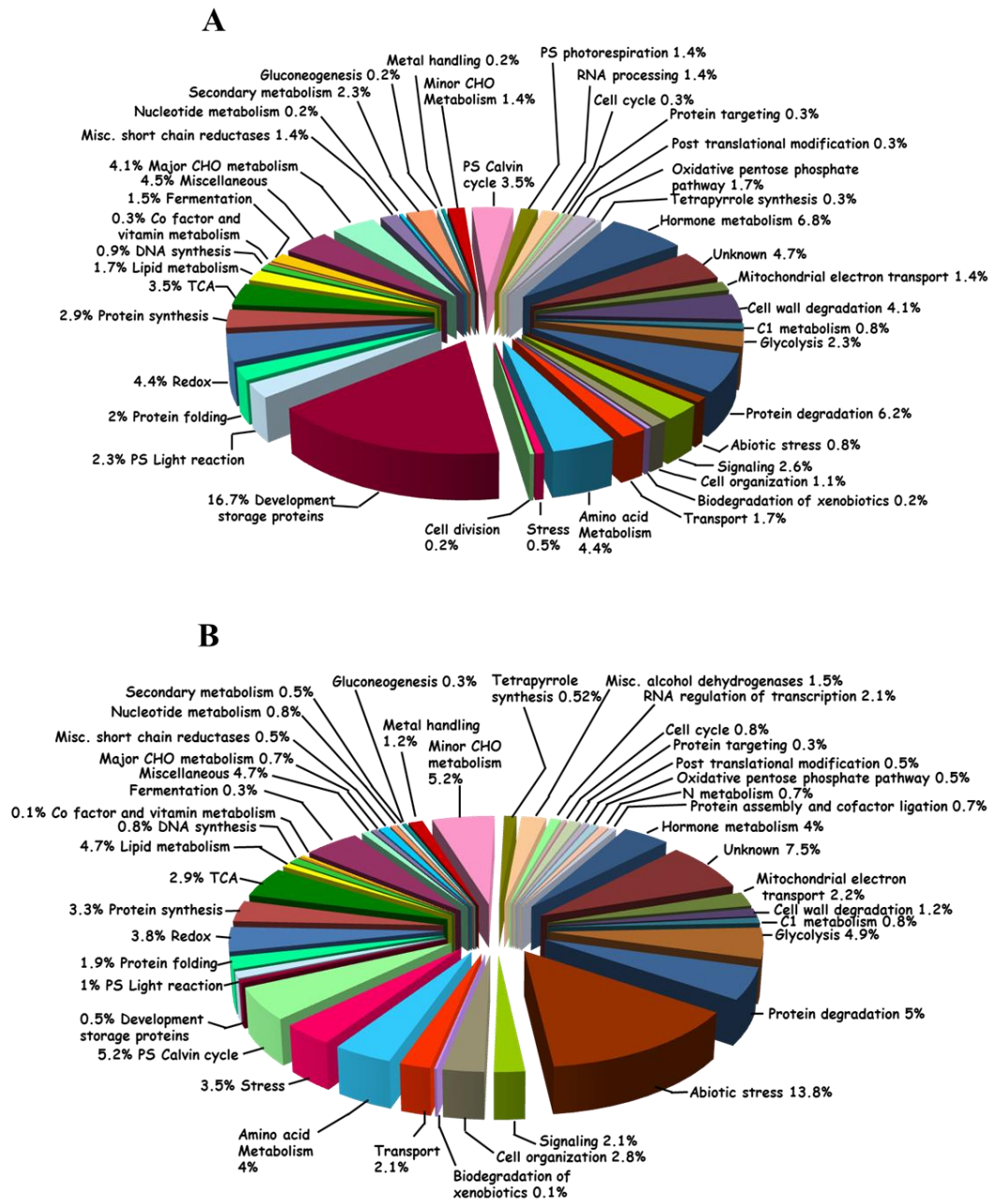

A
Metal handling 0.2%
PS photorespiration 1.4%
Gluconeogenesis 0.2%
RNA processing 1.4%
Minor CHO Metabolism 1.4%
Secondary metabolism 2.3%
Cell cycle 0.3%
Nucleotide metabolism 0.2%
Protein targeting 0.3%
Misc. short chain reductases 1.4%
Post translational modification 0.3%
4.1% Major CHO metabolism
4.5% Miscellaneous
PS Calvin cycle 3.5%
Oxidative pentose phosphate pathway 1.7%
1.5% Fermentation
Tetrapyrrole synthesis 0.3%
0.3% Co factor and vitamin metabolism
Hormone metabolism 6.8%
0.9% DNA synthesis
Unknown 4.7%
1.7% Lipid metabolism
Mitochondrial electron transport 1.4%
3.5% TCA
Cell wall degradation 4.1%
2.9% Protein synthesis
C1 metabolism 0.8%
Glycolysis 2.3%
4.4% Redox
Protein degradation 6.2%
2% Protein folding
Abiotic stress 0.8%
2.3% PS Light reaction
Signaling 2.6%
Cell organization 1.1%
Biodegradation of xenobiotics 0.2%
16.7% Development storage proteins
Transport 1.7%
Cell division 0.2%
Stress 0.5%
Amino acid Metabolism 4.4%
B
Secondary metabolism 0.5%
Gluconeogenesis 0.3%
Tetrapyrrole synthesis 0.52%
Misc. alcohol dehydrogenases 1.5%
RNA regulation of transcription 2.1%
Nucleotide metabolism 0.8%
Cell cycle 0.8%
Metal handling 1.2%
Minor CHO metabolism 5.2%
Protein targeting 0.3%
Misc. short chain reductases 0.5%
Post translational modification 0.5%
Major CHO metabolism 0.7%
Oxidative pentose phosphate pathway 0.5%
Miscellaneous 4.7%
N metabolism 0.7%
Fermentation 0.3%
Protein assembly and cofactor ligation 0.7%
0.1% Co factor and vitamin metabolism
Hormone metabolism 4%
0.8% DNA synthesis
Unknown 7.5%
4.7% Lipid metabolism
Mitochondrial electron transport 2.2%
2.9% TCA
Cell wall degradation 1.2%
3.3% Protein synthesis
C1 metabolism 0.8%
Glycolysis 4.9%
3.8% Redox
1.9% Protein folding
Protein degradation 5%
1% PS Light reaction
0.5% Development storage proteins
5.2% PS Calvin cycle
Abiotic stress 13.8%
3.5% Stress
Signaling 2.1%
Amino acid Metabolism 4%
Transport 2.1%
Cell organization 2.8%
Biodegradation of xenobiotics 0.1%

Figure 5.11

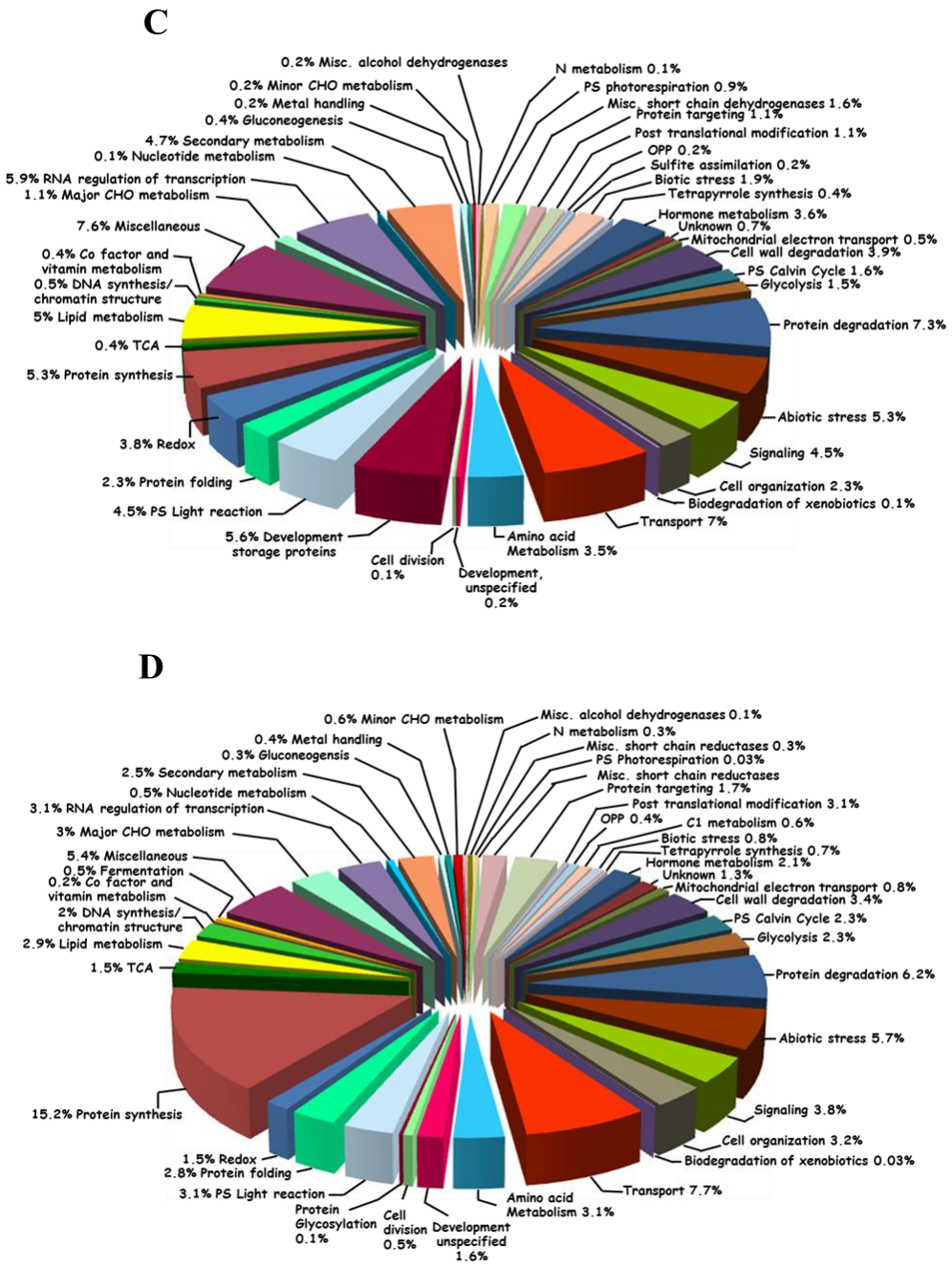

C
0.2% Misc. alcohol dehydrogenases
N metabolism 0.1%
0.2% Minor CHO metabolism
PS photorespiration 0.9%
0.2% Metal handling
Misc. short chain dehydrogenases 1.6%
0.4% Gluconeogenesis
Protein targeting 1.1%
4.7% Secondary metabolism
Post translational modification 1.1%
0.1% Nucleotide metabolism
OPP 0.2%
5.9% RNA regulation of transcription
Sulfite assimilation 0.2%
1.1% Major CHO metabolism
Biotic stress 1.9%
Tetrapyrrole synthesis 0.4%
7.6% Miscellaneous
Hormone metabolism 3.6%
Unknown 0.7%
Mitochondrial electron transport 0.5%
0.4% Co factor and vitamin metabolism
Cell wall degradation 3.9%
0.5% DNA synthesis/ chromatin structure
PS Calvin Cycle 1.6%
Glycolysis 1.5%
5% Lipid metabolism
Protein degradation 7.3%
0.4% TCA
5.3% Protein synthesis
Abiotic stress 5.3%
3.8% Redox
Signaling 4.5%
2.3% Protein folding
Cell organization 2.3%
4.5% PS Light reaction
Biodegradation of xenobiotics 0.1%
Transport 7%
5.6% Development storage proteins
Amino acid Metabolism 3.5%
Cell division 0.1%
Development, unspecified 0.2%
D
0.6% Minor CHO metabolism
Misc. alcohol dehydrogenases 0.1%
0.4% Metal handling
N metabolism 0.3%
0.3% Gluconeogensis
Misc. short chain reductases 0.3%
2.5% Secondary metabolism
PS Photorespiration 0.03%
0.5% Nucleotide metabolism
Misc. short chain reductases
3.1% RNA regulation of transcription
Protein targeting 1.7%
Post translational modification 3.1%
3% Major CHO metabolism
OPP 0.4%
C1 metabolism 0.6%
5.4% Miscellaneous
Biotic stress 0.8%
0.5% Fermentation
Tetrapyrrole synthesis 0.7%
0.2% Co factor and vitamin metabolism
Hormone metabolism 2.1%
Unknown 1.3%
2% DNA synthesis/ chromatin structure
Mitochondrial electron transport 0.8%
Cell wall degradation 3.4%
2.9% Lipid metabolism
PS Calvin Cycle 2.3%
Glycolysis 2.3%
1.5% TCA
Protein degradation 6.2%
Abiotic stress 5.7%
15.2% Protein synthesis
Signaling 3.8%
Cell organization 3.2%
1.5% Redox
Biodegradation of xenobiotics 0.03%
2.8% Protein folding
Transport 7.7%
3.1% PS Light reaction
Amino acid Metabolism 3.1%
Protein Glycosylation 0.1%
Cell division 0.5%
Development unspecified 1.6%

Figure 5.11

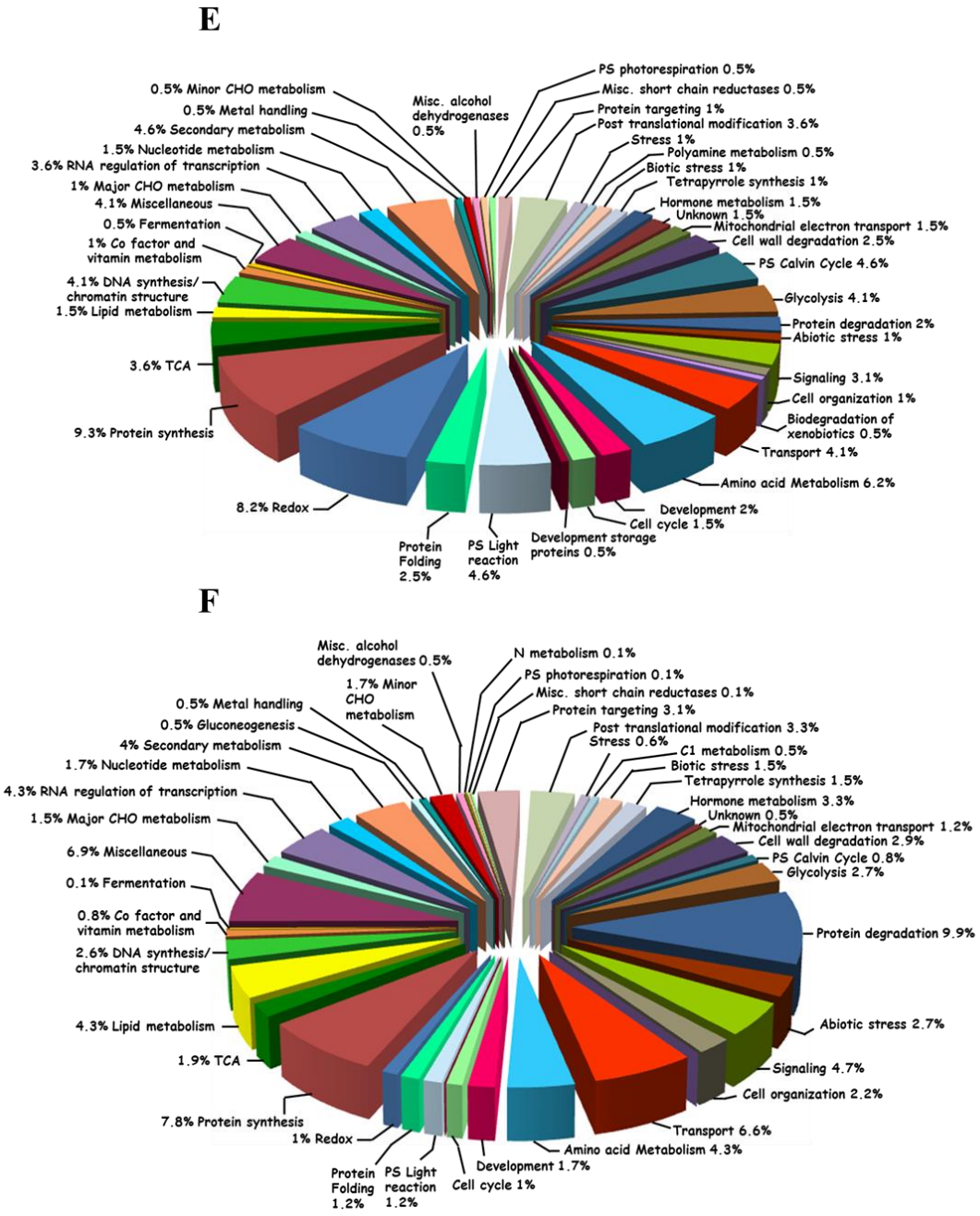


Figure 5.11. Functional classification of differentially expressed proteins in the fruits of wild species. A, SP-SL up-regulated proteins B, SP-SL down-regulated proteins C, SG-SL up-regulated proteins D, SG-SL down-regulated proteins E, SH-SL up-regulated proteins F, SH-SL down-regulated proteins

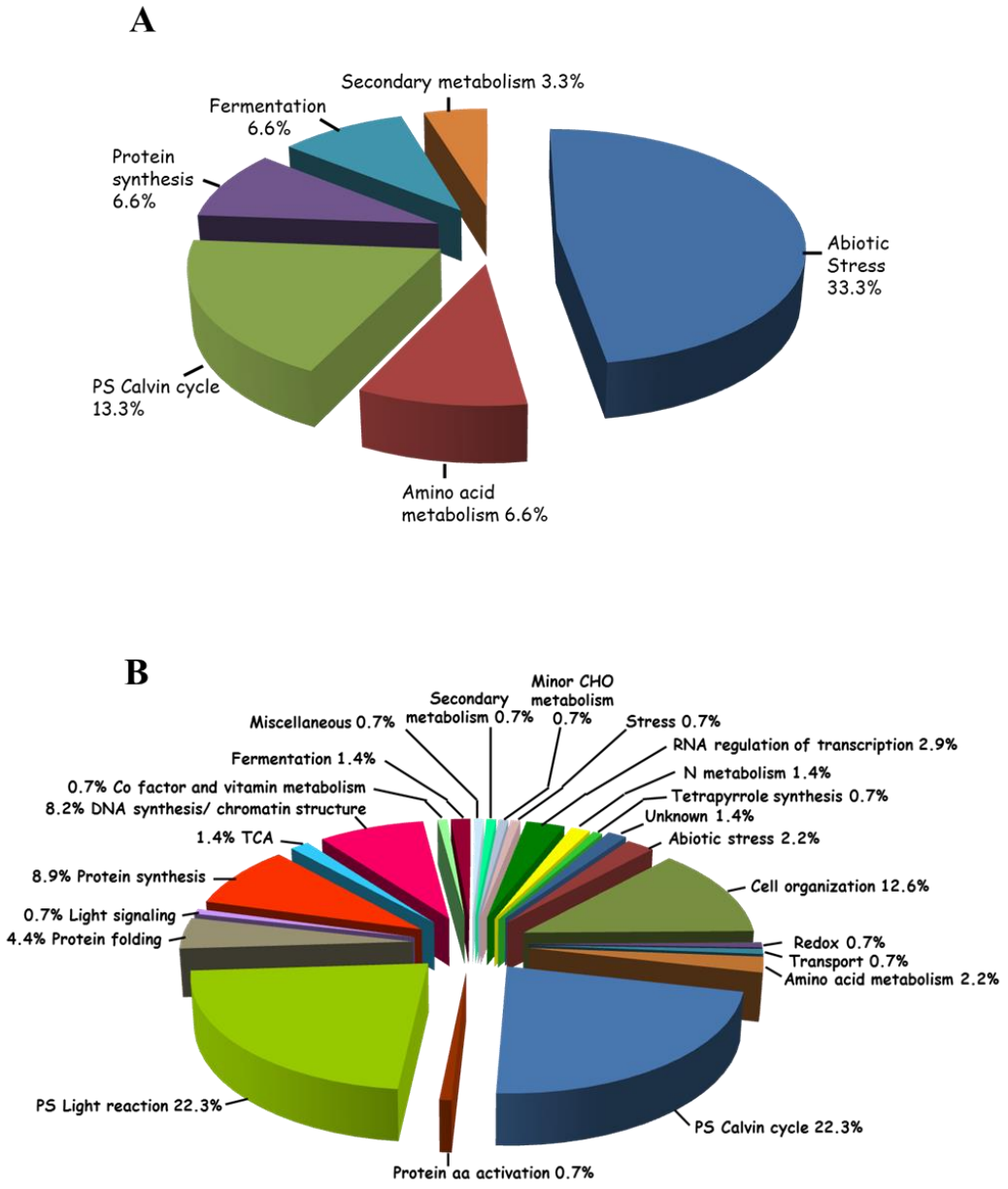

A
Secondary metabolism 3.3%
Fermentation 6.6%
Protein synthesis 6.6%
Abiotic Stress 33.3%
PS Calvin cycle 13.3%
Amino acid metabolism 6.6%
B
Minor CHO metabolism 0.7%
Secondary metabolism 0.7%
Miscellaneous 0.7%
Stress 0.7%
RNA regulation of transcription 2.9%
Fermentation 1.4%
N metabolism 1.4%
0.7% Co factor and vitamin metabolism
Tetrapyrrole synthesis 0.7%
8.2% DNA synthesis/ chromatin structure
Unknown 1.4%
1.4% TCA
Abiotic stress 2.2%
8.9% Protein synthesis
Cell organization 12.6%
0.7% Light signaling
Redox 0.7%
4.4% Protein folding
Transport 0.7%
Amino acid metabolism 2.2%
PS Light reaction 22.3%
PS Calvin cycle 22.3%
Protein aa activation 0.7%

Figure 5.12

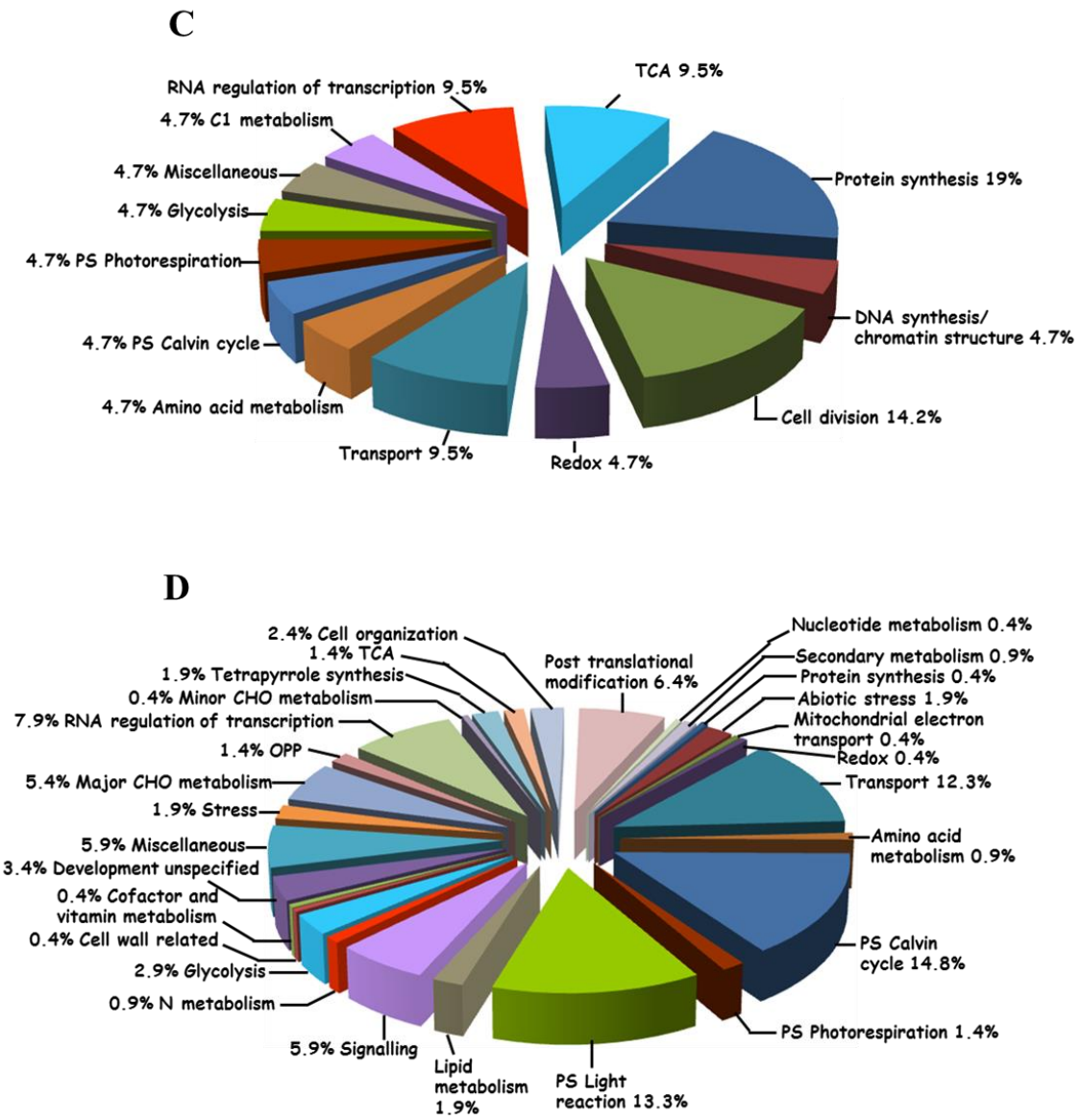

C
TCA 9.5%
RNA regulation of transcription 9.5%
4.7% C1 metabolism
4.7% Miscellaneous
4.7% Glycolysis
4.7% PS Photorespiration
4.7% PS Calvin cycle
4.7% Amino acid metabolism
Transport 9.5%
Redox 4.7%
Protein synthesis 19%
DNA synthesis/ chromatin structure 4.7%
Cell division 14.2%
D
2.4% Cell organization
1.4% TCA
1.9% Tetrapyrrole synthesis
0.4% Minor CHO metabolism
7.9% RNA regulation of transcription
1.4% OPP
5.4% Major CHO metabolism
1.9% Stress
5.9% Miscellaneous
3.4% Development unspecified
0.4% Cofactor and vitamin metabolism
0.4% Cell wall related
2.9% Glycolysis
0.9% N metabolism
5.9% Signalling
Lipid metabolism 1.9%
PS Light reaction 13.3%
Post translational modification 6.4%
Nucleotide metabolism 0.4%
Secondary metabolism 0.9%
Protein synthesis 0.4%
Abiotic stress 1.9%
Mitochondrial electron transport 0.4%
Redox 0.4%
Transport 12.3%
Amino acid metabolism 0.9%
PS Calvin cycle 14.8%
PS Photorespiration 1.4%

Figure 5.12

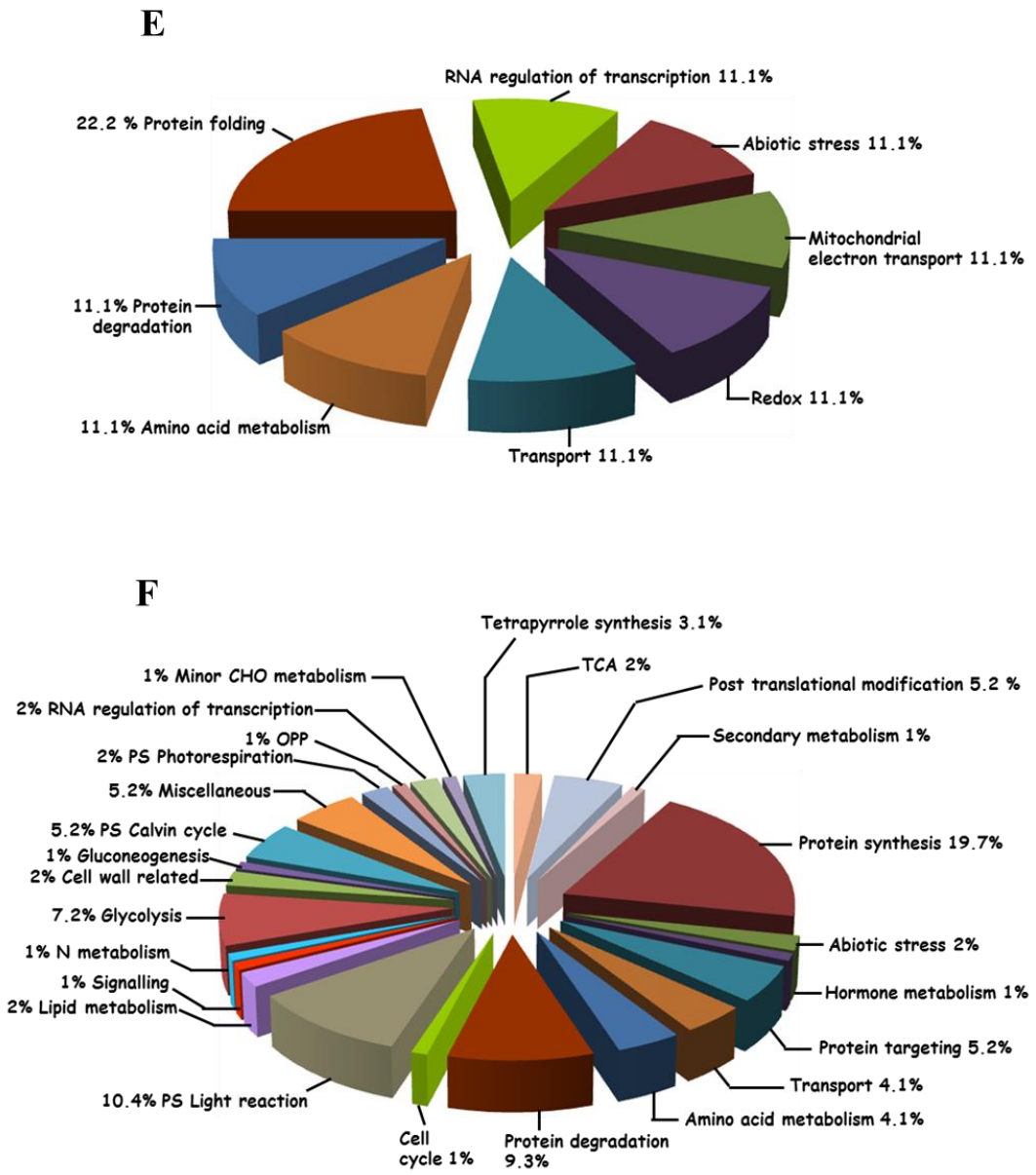


Figure 5.12. Functional classification of differentially expressed proteins in the leaves of wild species. A, SP-SL up-regulated proteins B, SP-SL down-regulated proteins C, SG-SL up-regulated proteins D, SG-SL down-regulated proteins E, SH-SL up-regulated proteins F, SH-SL down-regulated proteins

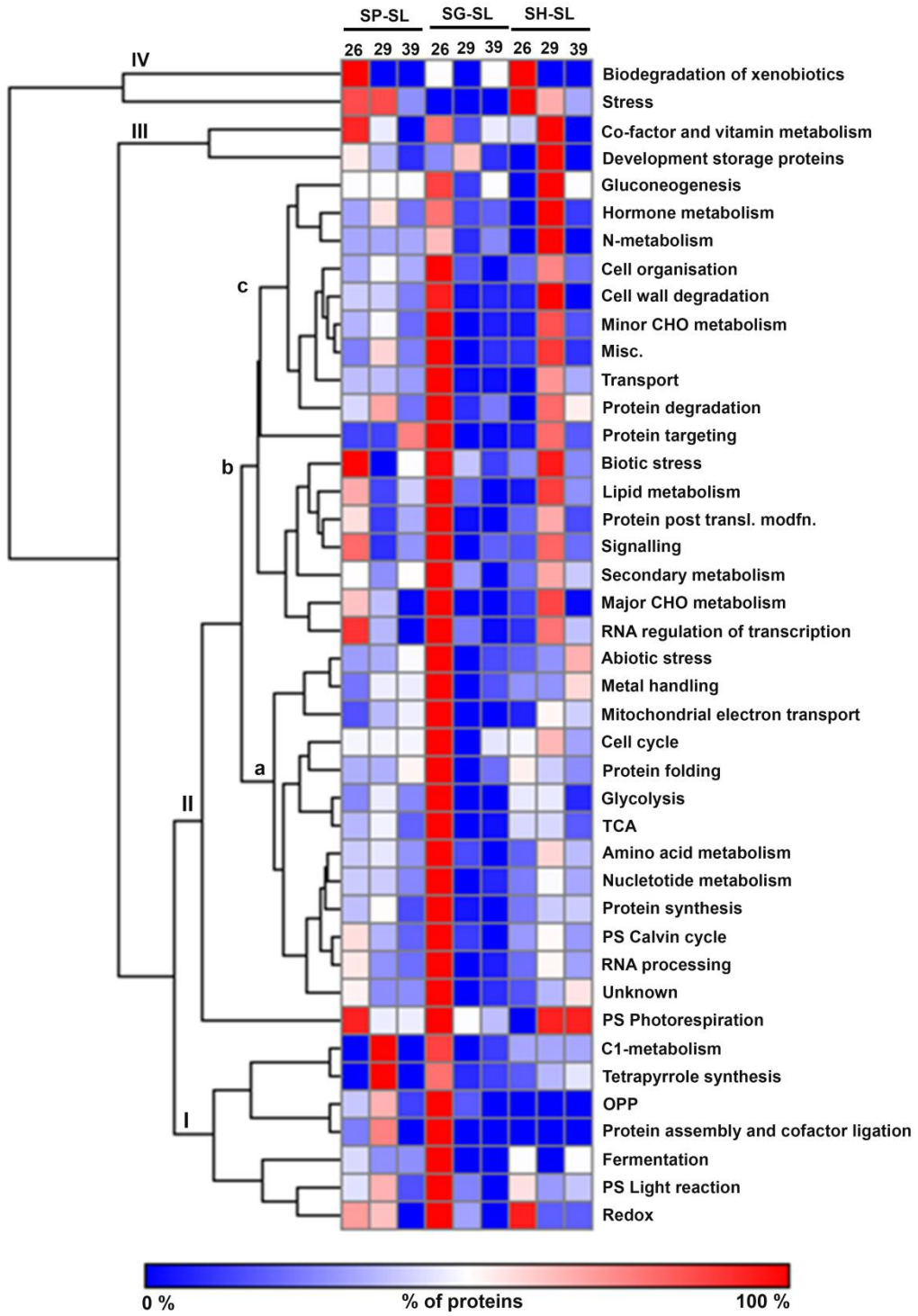


Figure 5.13. Hierarchical clustering of differentially expressed proteins. The differentially expressed proteins in all genotypes at 26, 29 and 39 dpa were hierarchically clustered according to their functional classes. Few of the functional classes that lack a logical pattern of abundance, and unassigned classes were removed. The horizontal scale at the bottom of the heat map represents relative proportion of proteins (Red-high; Blue-low).

was subdivided into 3 subclusters, of which subcluster IIa (abiotic stress, metal handling, electron transport, cell cycle, protein folding, glycolysis, TCA cycle, amino acid metabolism, nucleotide metabolism, protein synthesis, PS Calvin cycle, RNA processing, unknown, PS photorespiration) showed high proportion of proteins at 26 dpa followed by a moderate increase in the protein proportion at 29 and 39 dpa. Subcluster IIb (protein targeting, biotic stress, lipid, secondary and major CHO metabolism, protein PTM, signalling, RNA regulation of transcription) showed large percent of proteins at 26 and 29 dpa with moderate increase at 39 dpa, while subcluster IIc (gluconeogenesis, hormone, N and minor CHO metabolism, cell organisation, cell wall/protein degradation, miscellaneous) showed high protein percentage at 26 and 29 dpa followed by reduction at 39 dpa. In cluster III (co-factor and vitamin metabolism, development storage), protein proportion was high at 29 dpa with moderate increase at 26 dpa followed by reduction at 39 dpa. In cluster IV (xenobiotic biodegradation, stress), protein proportion was in the increasing order of 26 dpa>29 dpa>39 dpa

5.3.12 Protein functional classes involved in chromoplast formation

During chromoplast formation, the chlorophyll is degraded and the plastid ultrastructure is modified to accommodate the high levels of carotenoids formed during ripening. Reportedly, membranous structures and plastoglobules sequester and store the carotenoids. The sequestration is facilitated by up-regulation of carotenoid sequestration proteins like CHRC (Kilambi et al., 2013) and plastid lipid associated protein 3 (PAP3, Solyc08g076480.2.1) (also called plastoglobulin 1 based on high sequence similarity; Nogueira et al., 2013; Kessler et al., 1999). The transition to chromoplast involves a wide range of alterations in the proteome as reported by Barsan et al. (2012). Among differentially expressed proteins, proteins involved in chromoplast formation (Barsan et al., 2012) were classified based on their abundance patterns into seven categories as-stable, continuous increase, early increase, late increase, continuous decrease, early decrease and late decrease (Fig. 5.14). Overall, a majority of the proteins decreased in abundance across all the genotypes (SP-SL: 0-continuous+83-early+42-late=125; SG-SL: 1-continuous+ 256-eraly + 40-late=297 and SH-SL: 0-continuous + 114-early + 43-late-157). Likewise, the proteins which increased in abundance during chromoplast formation constituted second pattern (SP-SL: 0-continuous + 3-early + 20-late = 23; SG-SL: 0-continuous + 67-early + 20-late =87 and SH-SL: 0-continuous + 17-early + 12-late =29). Interestingly, in all wild relatives 26-29 dpa transition led to an overall decrease in protein

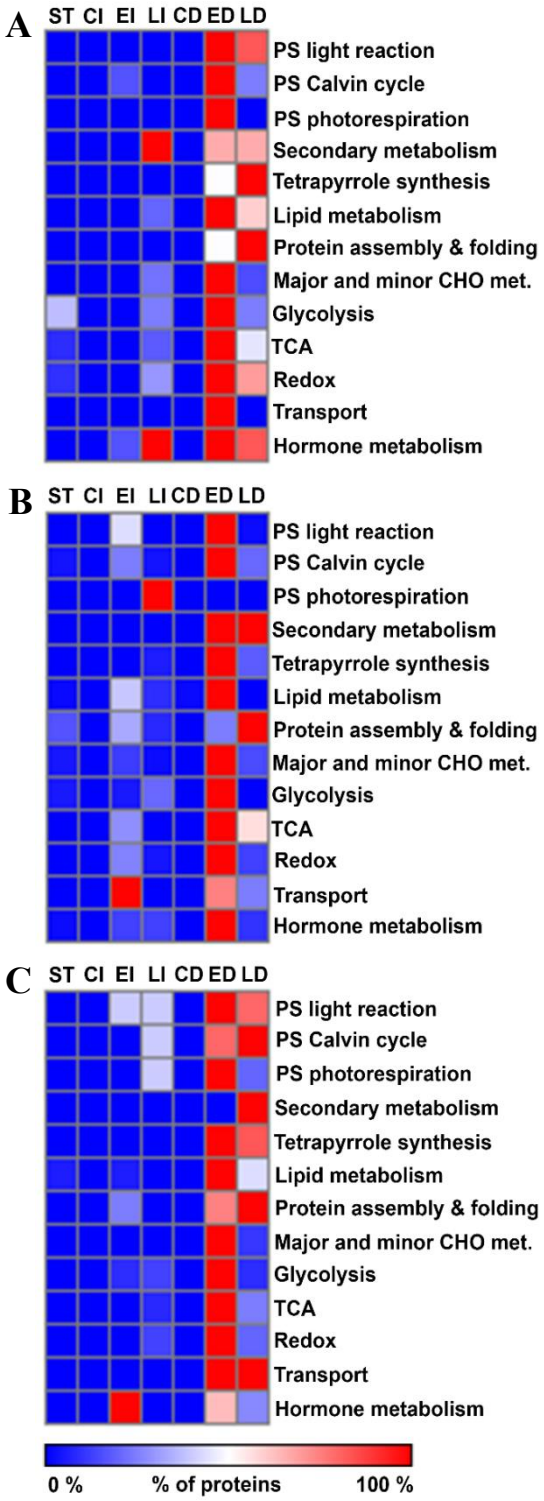


Figure 5.14. Hierarchical clustering of proteins involved in chromoplast transformation. Proteins belonging to the functional classes with a presumed role in chromoplast formation from SP-SL, SG-SL and SH-SL were differentiated based on their abundance pattern as-stable (ST), continuous increase (CI), early increase (EI), late increase (LI), continuous decrease (CD), early decrease (ED), late decrease (LD). The horizontal scale at the bottom of the heat map represents relative proportion of proteins (Red-high; Blue-low).

abundance (SP-SL, 54%; SG-SL, 65%; SH-SL, 61%) (Fig. 5.14). On the other hand, 29-39 dpa transition showed distinct variation in protein abundances (SP-SL, 27% late decrease; SG-SL, 17% early increase; SH-SL, 23% late increase) (Fig. 5.14).

The nature of shifts in proteome complement during tomato chromoplast formation was extensively examined by Barsan et al. (2012). Analogously, the shifts in the proteome profiles of different wild relatives across examined stages were compared to decipher commonality and differences between the species. Above comparison revealed that while a majority of the proteins involved in chromoplast formation behaved similarly to tomato, several species-specific differences were also observed (Table 5.7). For SP-SL, SG-SL and SH-SL, proteins belonging to photosynthesis (SP-100%, SG-70%, SH-69%), Calvin cycle (SP-88%, SG-78%, SH-81%), photorespiration (SP-100%, SH-75%, SG-0), lipid metabolism (SP-88.8%, SG-68%, SH-92%), protein assembly and folding (SP-100%, SG-68%, SH-87.5%), major and minor CHO metabolism (SP, SG-83%, SH-100%), Tetrapyrrole biosynthesis (SP-100%, SG-95%, SH-100%), transport (SP-100%, SG-50%, SH-100%) functional categories decreased in abundance analogous to Barsan et al., 2012.

However, the functional categories such as glycolysis (SP-66.6%, SG, SH-80%), redox (SP-81%, SG-79%, SH-90%), TCA cycle (SP, SG-84%, SH-93%) and hormone metabolism (SP-61%, SG-79%, SH-47%) decreased in abundance (Table 5.7) contrary to that reported in Barsan et al., 2012. 20% of the proteins under glycolysis category in SP-SL remained stable, while 9% proteins in protein assembly and folding were stable in SG-SL, unlike other wild species. 52% of proteins under hormone metabolism increased in abundance in SH. While above comparison showed overlaps in proteome shifts, the observed differences in relative decrease and/or increase in functional classes may contribute to species-specific differences in the chromoplast formation. Moreover, subtle differences within protein complement of a functional class may further contribute to species-specific differences.

5.3.13 SH fruits retain Photosystem II activity

During the transition from 26 to 39 dpa, chlorophyll levels and Chl/Car ratio declined in the fruits of SL, SP and SG while in SH fruits, both were sustained at the same level (Table 5.4). The retention of high Chl/Car ratio in SH fruits indicated that these fruits may have photosynthetic activity unlike red/orange fruited species. The best

indicator of photosynthesis is the light-mediated evolution of oxygen by the activity of photosystem II (PSII). While fruits of all genotypes showed high PSII activity at 26 dpa, it is massively declined in red/orange fruited species (SL-11%, SP-1.1%, SG-0.5%) at 39 dpa (Fig. 15A). Though PSII activity declined at 39 dpa in SH fruits, they still retained >50% of PSII activity.

5.3.14 Chlorophyll destabilization is absent in SH fruits

The retention of green colour in fruit suggested that the process leading to chlorophyll destabilization is absent in SH. This is corroborated by the persistence of one of the isoforms of chlorophyll a/b binding protein (CAB, Solyc09g014520.2.1; 3 fold) and oxygen evolving enhancer protein (OEE, Solyc07g044860.2.1; 8.6 fold), Rubisco activase 1 (Solyc10g086580.1.1; 4 fold) and fructose bisphosphate aldolase (FBP aldolase, Solyc02g084440.2.1; 3.5 fold) in SH fruits at 39 dpa (Table 5.7). Consistent with acquisition of orange/red coloration, CAB and Rubisco activase 1 declined in SP and SG and OEE2 and FBP aldolase levels in SG were similar to SL. In SP, OEE2 and FBP aldolase declined by 4.5 fold and 16 fold respectively compared to SL.

5.3.15 PAO/phyllobilin pathway is compromised in SH fruits

In higher plants, chlorophyll degradation is mediated by PAO/phyllobilin pathway (Christ and Hortensteiner, 2014). Out of 8 proteins that are part of PAO pathway, pheophorbide a oxygenase (PAO) and red chlorophyll catabolite reductase (RCCR) were detected in SP and SG but not in SH fruits. The expression of *pao* and *rccr* genes in SH fruits at 39 dpa was also very low compared to SL (Fig. 5.15B-C). The low levels of PAO and RCCR in SH fruit may have a relation to the retention of chlorophylls. In conformity with low levels of PAO and RCCR proteins, a coupled assay showed lower activity of PAO/RCCR in SH than SL at 39 dpa. The level of pheophorbide a was 10.5 fold higher in SH fruits at 39 dpa than SL, 1.5 fold higher in SP and almost same as SL in SG fruits (Fig. 5.15D). The high level of pheophorbide a indicated that the proteins contributing to its catabolism may not be functional in SH fruits. Out of eleven primary fluorescent catabolites (pFCCs; Fig. 5.15E), three showed absorbance at both 320 nm and 360 nm, whereas, eight showed absorbance at only 320 nm (Fig. 5.16). Interestingly, the mean peak areas (fluorescence emission) of primary fluorescent catabolites (pFCCs) were much higher in SL (2-6.7 fold) than in SH fruits (Fig. 5.15E; Fig. 5.16). The higher levels of

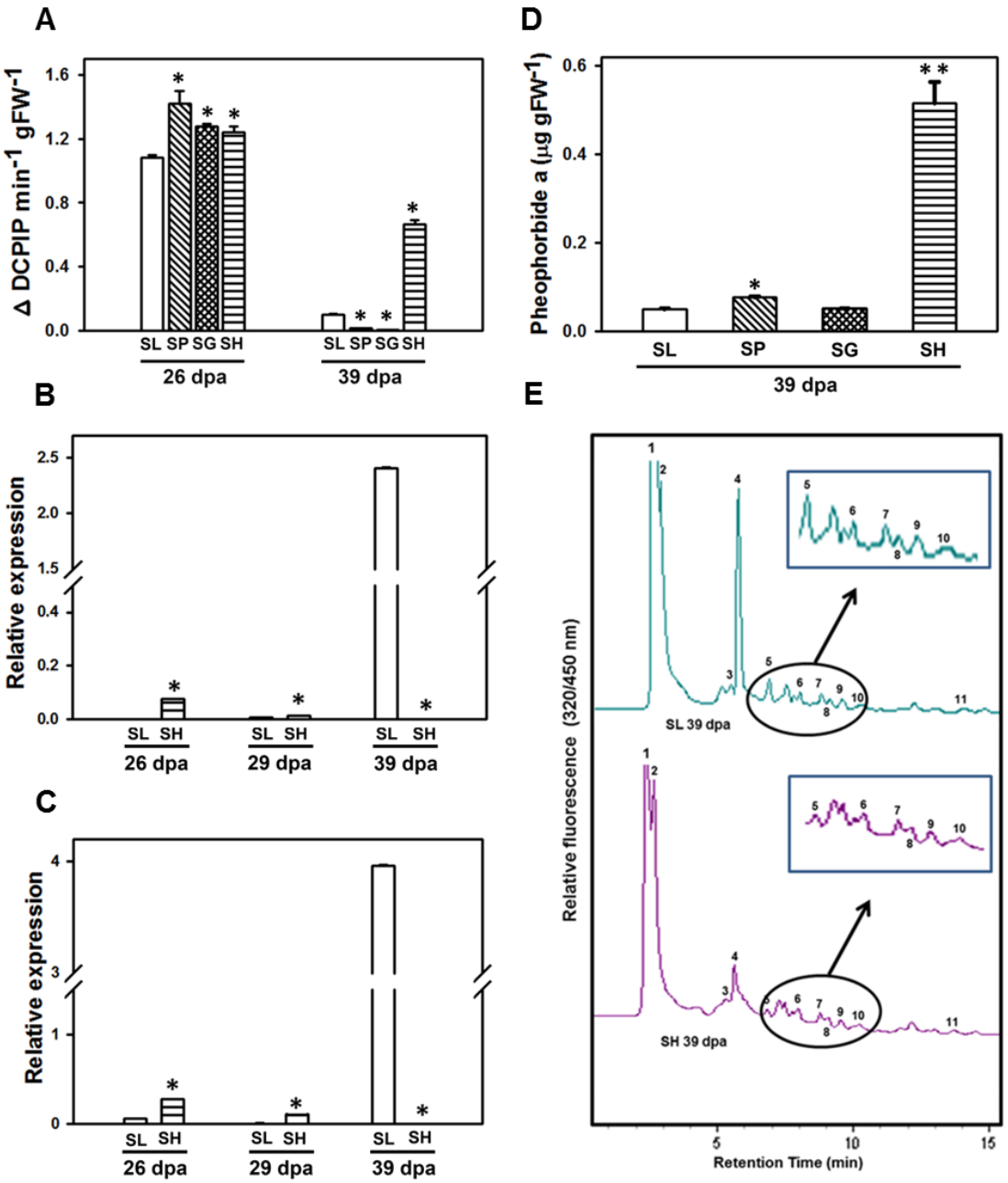


Figure 5.15. Photosynthesis and chlorophyll degradation. **A,** Photosystem II activity in 26 and 39 dpa fruits of tomato and wild species. Relative transcript levels of *pao* **B** and *rccr* C**.** Relative transcript expression levels were obtained after normalization with *β-actin* and *ubiquitin*. D**,** Pheophorbide a levels in 39 dpa fruits of tomato and wild species. **E,** HPLC traces of PAO/RCCR assays using 39 dpa fruit extracts of SL and SH. The inset shows the enlarged view of the peaks. Data are means ± SE (n = 3), * = P ≤ 0.05, ** = P ≤ 0.01.

A

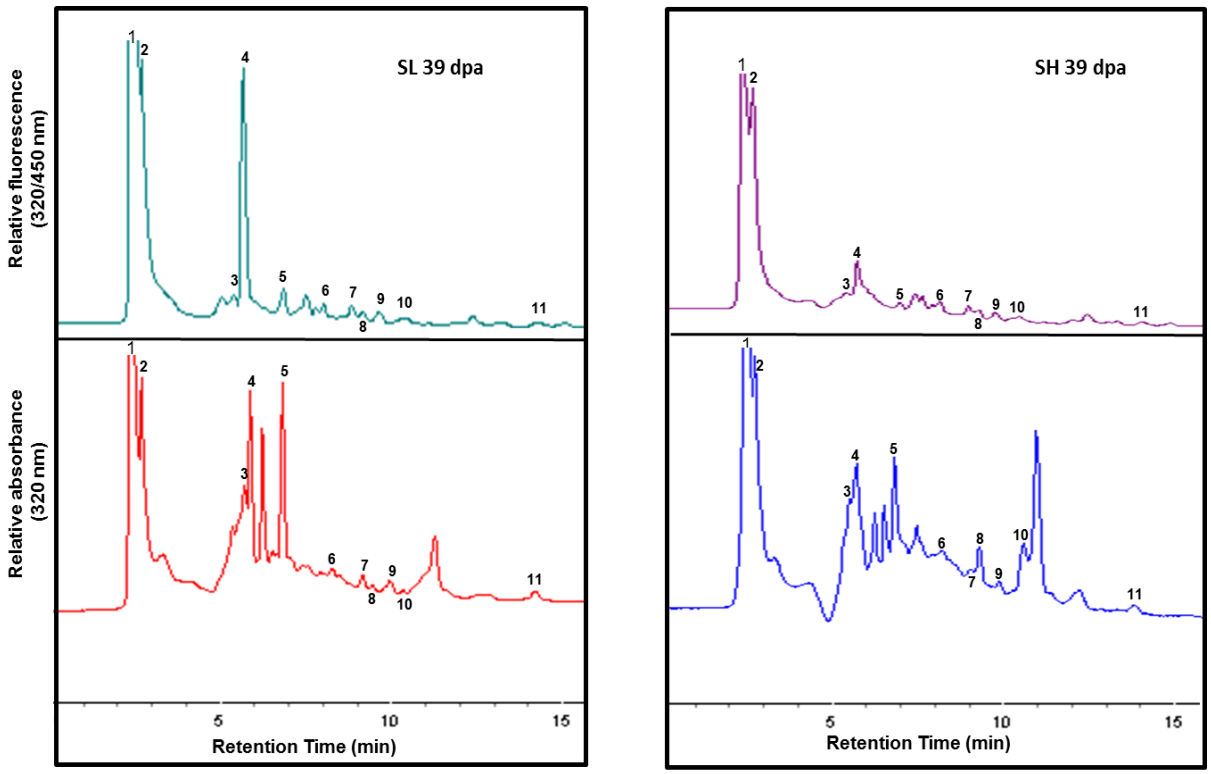

SL 39 dpa
SH 39 dpa
Relative fluorescence (320/450 nm)
Relative absorbance (320 nm)
Retention Time (min)
Retention Time (min)

Figure 5.16

B

Peak No.	Mean Peak area in SL± S.E. (Fluorescence at 320/450 nm)	Mean Peak area in SH± S.E. (Fluorescence at 320/450 nm)	Ratio (SL/SH)	p value	Mean Peak area in SL		Mean Peak area in SH	
					$A_{320\ nm}$	$A_{360\ nm}$	$A_{320\ nm}$	$A_{360\ nm}$
1	8667988.67± 2167647	1299059.66± 187294	6.67	p<0.027	371195.67± 32514	24000± 22345	148478.27± 13005	96700
2	4527947.67± 105534	2069653.33± 373448	2.19	p<0.03	163954.67± 21774	51200± 3456	117110.48± 15553	40000
3	506793.33± 84606	230826.66± 10629	2.20	p<0.03	89920± 1483	123500± 43542	32114.29± 530	45600
4	2271667.67± 257265	461659.33± 47956	4.92	p<0.002	83113.33± 1288	NA	15983.33± 248	NA
5	429221.67± 38624	76461± 2549	5.61	p<0.0008	153863± 19106	NA	28493.15± 3538	NA
6	305893± 25179	85974± 4899	3.56	p<0.001	28661.67± 726	NA	8685.35± 220	NA
7	384425.33± 25827	100407.33± 2418	3.83	p<0.0003	23607± 1097	NA	6053± 281	NA
8	226343± 18026	81262.33± 7793	2.79	p<0.001	15786± 1527	NA	6071.54± 587	NA
9	191336 ± 10048	55701.66± 2362	3.44	p<0.0001	25416.33± 1742	NA	7060± 484	NA
10	191292.66 ± 14444	44768.33± 741	4.28	p<0.0005	9642.33± 321	NA	2351.79± 78	NA
11	106210± 14444	23595± 1161	4.50	p<0.00004	16487.33± 2031	NA	4021.30± 496	NA

Figure 5.16. Absorbance, fluorescence spectra and peak areas obtained after PAO/RCCR assay of 39 dpa fruit extracts of SL and SH.

pFCCs in SL fruits indicated high PAO/RCCR activity and also corroborated with low pheophorbide a level.

5.3.16 Targeted peptide monitoring (TPM) of carotenogenic proteins in fruit

In higher plants, the enzymes of carotenoid pathway are present at very low levels and highly labile to purify (Hirschberg 2001). Examination of proteome profiles in this study detected about 20 proteins related to carotenogenesis, sequestration and cleavage. At the same time, we could not detect cytochrome P450 carotenoid β-carotene hydroxylases, CYP97A11 and CYP97A29. This may be due to their low abundance, as even in purified tomato chromoplasts, these proteins were not detected (Barsan et al., 2012; Wang et al., 2013). From the overall differentially expressed proteins, few proteins related to carotenoid metabolism and accumulation showed both up-regulation (SP-CHRC-9.17 fold, carotenoid cleavage dioxygenase 1B [CCD1B]-6.21 fold; SG-isopentenyl diphosphate isomerase 5G [IDI5G]-13.5 fold) and downregulation (SH-gerenylgeranyl diphosphate synthase 9G [GGPPS9G]-25 fold, carotenoid isomerase [CRTISO]-76.9 fold, LCYB1-66.6 fold) (Table 5.7).

To establish a linkage between carotenoids and expression profiles of carotenogenic genes with the encoded proteins, a targeted proteomic approach was used (Hewel et al., 2012). This approach is akin to western blotting and called “mass western” method (Lehmann et al., 2008; Aebersold et al., 2013; Taylor et al., 2014). TPM is superior to western blots as it can quantify very low abundance proteins and their isoforms. In consonance with high carotenoid levels at 39 dpa, maximum number of proteins mediating carotenoid accumulation was detected at 39 dpa compared to 26 or 29 dpa. Accordingly, 39 dpa was selected as the time point for TPM. Remarkably, the abundance of most proteins did not vary albeit with few exceptions.

In SP, TPM revealed up-regulation of ZDS and CHRC consistent with high levels of lycopene in above species (Fig. 5.17), while DXR showed down-regulation. Comparison of proteins-transcripts levels showed significant correlation ($r \geq 0.8$) only for ZISO and PAP3 (Table 5.5). As fruits of SG prominently accumulate high β-carotene, CYCB was detected only in this species. In SG too, only few proteins showed down-regulation (PSY1) and up-regulation (CCD1B, PAP3 and CHRC). Both positive (DXS, PAP3, CHRC) and negative (CYCB) correlations were found between proteins-transcripts levels (Table 5.5).

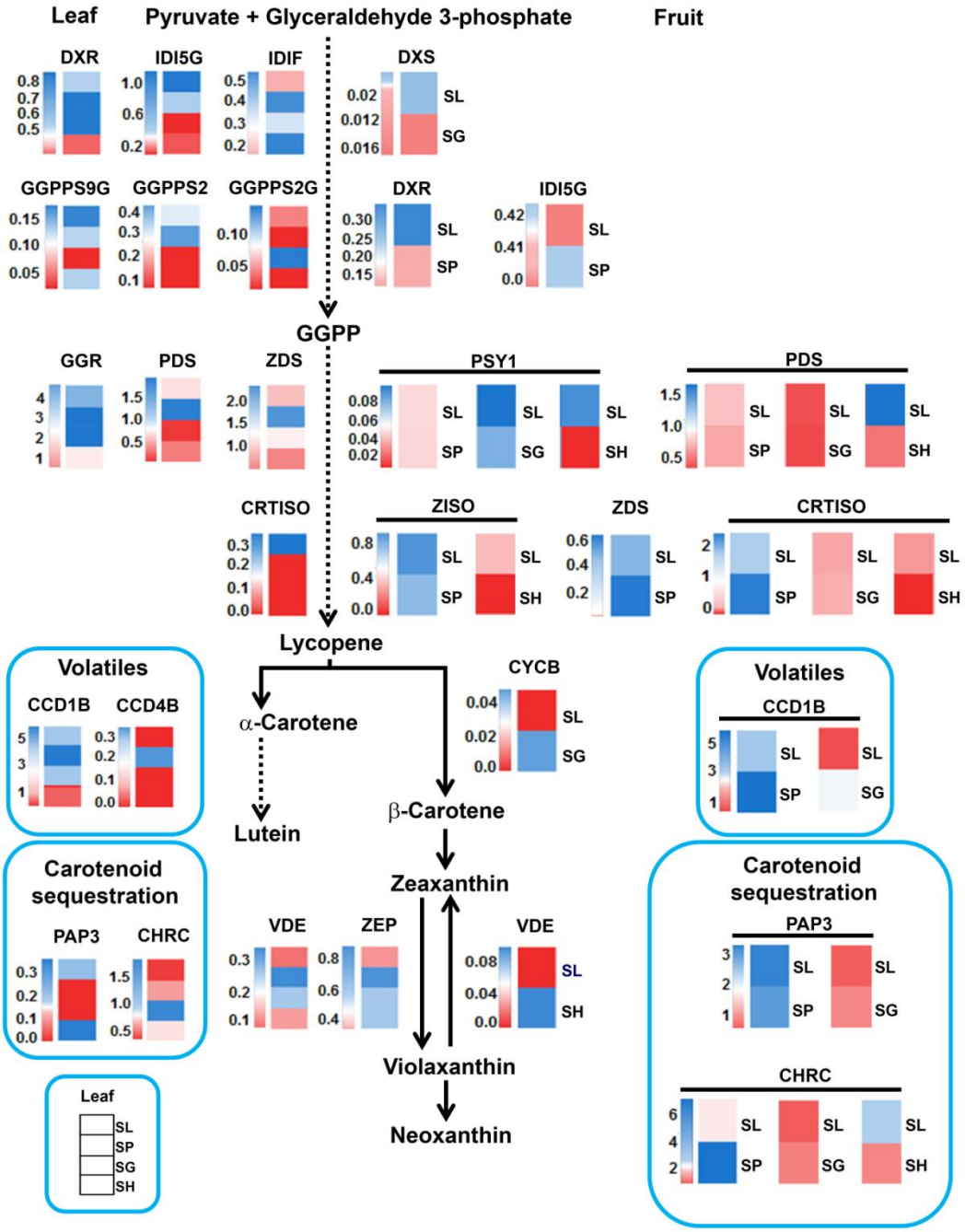


Figure 5.17. Relative abundances of proteins mediating carotenoid biosynthesis, sequestration and volatile formation in 39 dpa fruits and leaves of wild species. Targeted peptide monitoring was employed to quantify the protein abundances relative to internal control proteins. Data are means ± SE (n = 3). The relative abundances of proteins involved in carotenoid biosynthesis are represented at respective locations on the pathway. The proteins mediating carotenoid sequestration and cleavage for volatile formation are enclosed in a rectangle. Dotted arrows indicate multiple steps in the pathway. The vertical scale on left of heat map represents a relative range of protein levels (Red-low; Blue-high).

The detection of relatively few proteins in SH-SL is likely related to low protein abundance due to modified protocol. Interestingly, proteins contributing to lycopene pathway (PSY1, ZISO) were detected only in SL except PDS, whereas VDE was detected only in SH. Compared to SL, PDS (5 fold) and CHRC (2.7) fold were down-regulated in SH. In contrast to SG and SP, reduction in the abundance of CHRC in SH is likely related to the absence of lycopene and low levels of β-carotene. Comparison of proteins-transcripts levels showed no significant correlations in SH (Table 5.5). In TPM analysis, though we observed either single or multiple peptides for other carotenogenic proteins, these were not consistently present in all biological replicates. The stringent conditions used for TPM (see methods for more details) precluded their quantification.

5.3.17 TPM of carotenogenic proteins in leaf

The number of proteotypic peptides (for 22 proteins) chosen for TPM in leaf for each genotype were-121 for SH-SL, 119 for SP-SL and 124 for SG-SL comparisons (Table 5.2). Consistent with high carotenoids in SP leaf, most carotenoid biosynthesis proteins were up-regulated, except GGPPS2G and CRTISO (Fig. 5.17). Comparison of proteins-transcripts levels revealed either negative or no correlation in SP, except ZEP and VDE with positive correlation (Table 5.5). Similar to SP, in SG too, most carotenoid biosynthesis proteins were up-regulated except IDI5G, GGPPS9G, GGPPS2, PDS and CRTISO which were down-regulated. Majority of protein-transcript pairs showed no correlation barring three positive and two negative correlations. In contrast to SP and SG, in SH, carotenoid biosynthesis proteins were both up-regulated (5) and down-regulated (8). Unlike SP and SG, majority of protein-transcript pairs showed positive correlation in SH (Table 5.5).

5.4 Discussion

In the tomato clade, green fruited species are more primitive than orange and red fruited relatives, though they all share the same gene repertories for carotenogenesis (Aflitos et al., 2014; Bolger et al., 2014). Little information is available concerning modulation of carotenogenesis during transition from green to orange and to red coloured fruits. In this study, we used a multipronged approach incorporating information from gene expression, proteome characterization and carotenoid analysis with an aim to reveal the key steps influencing fruit colour transition.

5.4.1 Ethylene biosynthesis is attenuated during green to red fruit transition

Both tomato and pepper have the same complement of carotenoid and ethylene biosynthesis genes, however, ethylene-mediated carotenogenesis and ripening is observed only in tomato (Kim et al., 2014). Higher ethylene emission from SH fruits at 26 and 29 dpa seemingly results from up-regulation of *aco1* and *aco3* genes. The high expression of *aco1* is in conformity with Dal Cin et al. (2009), that QTL 12A regulating high ethylene emission from fruits co-segregate with *aco1* in introgression lines of SH. In wild relatives, regulation of carotenogenesis is not linked to ethylene triggered ripening. Though SH fruits emit high level of ethylene, they do not exhibit fruit softening or coloration. Seemingly in the tomato clade, high ethylene emission appeared earlier than the climacteric rise of ethylene preceding ripening. Considering that all wild relatives emit higher ethylene than SL, the transition of green fruited species to red fruited SL appears to be accompanied by attenuation of ethylene biosynthesis.

5.4.2 Green to red fruit transition involved shift towards β-branch of carotenogenesis

The variation in fruit coloration in tomato clade signifies that the carotenoid biosynthesis in each species is uniquely regulated leading to preferential accumulation of a specific carotenoid. Characteristic accumulation of β-carotene in SG, high lycopene in SP and no preferential accumulation of β-carotene and lycopene in SH support this contention. Genome sequences of tomato clade indicated that the red fruited species SP and SL are closely related followed by orange fruited SG and green fruited SH (Aflitos et al., 2014). Seemingly, fruit coloration followed two transitions; first was high β-carotene accumulation in SG, whereas the second was high lycopene accumulation in SP, marking a progression from green to orange to red fruit coloration. The higher lycopene levels in SP than SL probably resulted in attenuation of β-carotene biosynthesis.

The high β-carotene level in SG marks a shift towards increase in the β-carotene branch and attenuation of the α-carotene branch. Similarly, red fruited species also favoured the β-branch, though lycopene is the major carotenoid. This shift is missing in SH fruits as these two branches contribute almost equally. Evidently the transition from green to orange/red fruits specifically enhanced the β-carotene pathway, which is also consistent with the enlisting of a lycopene-β-cyclase (CYCB) regulating fruit specific carotenogenesis (Mohan et al., 2016). Since β-branch also contributes to most fruit volatiles, this branch may have been favoured to aid seed dispersal (Rodriguez et al., 2013).

Similar to other green fruited species like *S. pennellii* (Bolger et al., 2014), the chloroplast to chromoplast transformation is presumably absent in SH. Ostensibly, SH fruits appear to be at the crossroads of leaf and fruit-specific carotenogenesis. The persistence of neoxanthin, a leaf specific carotenoid in SH fruits indicates sustenance of leaf pathway, whereas disappearance of antheraxanthin, similar to other species, indicates a partial operation of fruit-like pathway. Unlike SP and SG fruits, accumulation of phytoene and phytofluene at 39 dpa (Nogueira et al., 2013) was absent in SH, implying deceleration of carotenoid biosynthesis. Since the above accumulation is specifically observed only in ripe fruits, presumably this distinguishes fruit carotenogenesis from leaf. From foregoing, it is evident that SH fruits lack up-regulation of β-carotene biosynthesis and chromoplast formation.

5.4.3 Expression of genes influencing fruit carotenogenesis is not compromised in SH

The studies on the MEP pathway revealed that the manipulation of *dxs* can affect the downstream isoprenoid metabolism along with carotenoid accumulation in tomato fruits (Lois et al., 2000, Enfissi et al., 2005). Among the genes regulating MEP pathway, the expression of *dxs* seems to be critical for regulating GGPP, aprimary precursor for carotenoid pathway (Ruiz-Sola and Rodriguez-Concepcion, 2012). Considering that all the three wild relatives exhibited higher *dxs* expression than SL, *dxs* expression does not appear to be a limiting factor for carotenoid formation in SH. During tomato fruit ripening, *dxs1* expression shows strong correlation with tocopherol-core biosynthesis pathway genes (Quadrana et al., 2013). Likewise, *dxs* expression positively correlated with the most abundant carotenoid in fruits of wild relatives. The regulation of *dxs* expression seems to be pivotal for fruit specific carotenoid accumulation (Lee et al., 2012). This association appears to be more fruit specific, as in the leaf, the most abundant carotenoid, lutein shows stronger positive correlation with *psy2* than *dxs* in SP and SG.

The lack of fruit coloration in SH could be due to non-functional *psy1* gene and/or its expression. It has been suggested that down-regulation of *psy1* is likely responsible for the green and yellow fruit colours in tomato clade (Melendez-Martinez et al., 2010; Bolger et al., 2014). In SH, *psy1* expression was relatively high in SH compared to SL. However, 39 dpa SH fruits do not accumulate phytoene and phytofluene similar to SP and SG fruits. In tomato, in addition to fruit, *psy1* also regulated coloration of flowers (Fraser et al., 1999). Given that SH and SL flowers are similarly coloured, we can assume that *psy1* functions normally at least during SH flower coloration.

In tomato *Beta* mutant, insertions in *cycb* promoter enhances its expression stimulating β-carotene accumulation (Ronen et al., 2000), yet high *cycb* expression in SH fruit does not increase β-carotene levels. Likewise, *S. pennelli* also shows mismatch between *cycb* expression and carotenoid accumulation (Bolger et al., 2014). Conversely higher β-carotene accumulation in SG related to high *cycb* expression. Considering that *psy1* and *cycb* are two regulatory steps in SL coloration, it appears that carotenogenesis in SH is probably not compromised by lower gene expression at these two steps.

5.4.4 Lack of fruit coloration in SH is not related to expression of ripening regulators

In tomato, key transcription factors regulating ripening show stronger correlations with increase in primary metabolites (Osorio et al., 2011); however, such correlations were amiss with lycopene and β-carotene in fruits of wild relatives. Among transcription factors examined, only few strongly correlated ($r \geq 0.98$) with the accumulation of lycopene and β-carotene (Table 5.5). Interestingly, the accumulation of β-carotene in all wild relatives positively correlated with *aprr2* expression, whereas *erf6* positively correlated with lycopene in SG and SP. The correlation of *aprr2* is consistent with its predicted role to control pigment accumulation in tomato and pepper fruits (Pan et al., 2013). Given that SH lacks substantial β-carotene accumulation like SG, the recruitment of *aprr2* as a regulator seems to precede preferential accumulation of β-carotene in fruits. Observed positive correlation between *erf6* and lycopene is opposite to tomato whereas *erf6* expression negatively correlated with lycopene (Lee et al., 2012). Interestingly, *tagl1* and *cnr* correlated in an opposing fashion with lycopene and β-carotene in SG and SH respectively. Among all species, SH showed stringent correlation ($r \geq 0.98$) of β-carotene with several transcription factors with both positive (*aprr2*, *tagl1*, *ful1*,*ap2a*) and negative (*glk2*, *cnr*) correlations.

5.4.5 Chloroplast to chromoplast transformation is absent in SH fruits

The inability to make carotenoids in SH may stem from the absence of chloroplast to chromoplast transformation. Consistent with this, SH fruits retain thylakoid grana, have few plastoglobules and lack undulating membranes enriched with lycopene crystalloids. The persistence of thylakoid specific proteins such as CAB and OEE corroborate that the pathway regulating chromoplast formation is non-functional in SH fruits (Egea et al., 2011). The persistence may be related to the higher expression of *glk2* in SH fruits

(Bolger et al., 2014) which is consistent with its role in chloroplast development (Powell et al., 2012). Ripe fruits of tomato *gf* mutant, with a lesion in the *stay green* (*sgr*) gene, show similar retention of thylakoids but are brown in colour (Cheung et al., 1993; Barry et al., 2008). Similar to SH fruits, *gf* fruits also exhibit impaired degradation of chlorophyll and retain photosynthetic proteins in ripe fruits (Cheung et al., 1993, Akhtar et al., 1999). Conversely, *gf* fruits exhibit the carotenoid containing membranes with more plastoglobules. Evidently, lesion in *sgr* gene only partially affected chloroplast to chromoplast transformation. Currently, little is known about chromoplast transformation except cauliflower (Lu et al., 2006) and melon (Tzuri et al., 2015) where *Or* gene triggers chromoplast formation. The *Or* gene expression showed species-specific correlations with different carotenoids (Table 5.5). Though OR protein was not detected in this study, Barsan et al. (2012) reported a high level of OR protein in tomato chromoplasts at breaker stage. However, it remains to be determined, whether above correlations have any functional relevance for chromoplast differentiation in tomato clade.

5.4.6 Proteome complement related to photosynthesis is retained in SH fruits

Since 39 dpa SH fruits retain chloroplasts and show normal Hill reaction, it was examined whether the proteome complement of SH fruits differs from SP and SG (Table 5.7). Consistent with higher PSII activity in SH fruits, the chloroplast-specific proteins such as CAB, OEE2, Rubisco activase 1 and FBP aldolase were abundant in SH, in contrast to the decline in SP/SG. It is reported that higher levels of Rubisco activase 1 help in the maintenance of Rubisco activity (Portis et al., 1986). Similarly, increase in the level of a plastidial isoform of FBP aldolase (Solyc02g084440.2.1) in SH may be related to carbon fixation in SH. Above retention of light reaction and Calvin cycle proteins in SH is analogous to green-fruited *S. pennellii* where photosynthesis remains active for a long time in mature fruits (Bolger et al., 2014).

A broader comparison of the different functional classes at 39 dpa revealed up-regulation of proteins belonging to PS Calvin cycle (8.6%) and light reaction (8.6%) in SH (Table 5.11). In contrast, no up-regulation of above functional classes was observed in SP and only a minor up-regulation (1.3%) was observed in SG. The persistence of above functional classes of proteins in SH is also consistent with the observed higher expression of photosynthesis related genes in *S. pennellii* fruits (Bolger et al., 2014).

In concert with persistence of PSII function, the SH fruits retain chlorophyll unlike SG and SP. In tomato, fruit ripening correlated with the disappearance of chlorophyll and the up-regulation of genes mediating PAO/phyllobillin pathway (Guyer et al., 2014). The PAO and RCCR proteins involved in chlorophyll catabolism, though present in ripened fruits of SG and SP were not detected in SH. This was also substantiated by lower activity and gene expression of PAO/RCCR and retention of pheophorbide a in SH fruits. Rather SH fruits accumulate ten-fold higher pheophorbide a than SP/SG. Consistent with this, coupled assay of PAO/RCCR indicated that its activity in SH fruits was much lower than SL. Akin to SH, an Arabidopsis mutant defective in PAO activity shows accumulation of pheophorbide a (Pruzinska et al., 2005).

During chromoplast formation, the disassembly of thylakoids is reportedly associated with a decrease in the levels of FtsH (ATP-dependent filamentation temperature sensitive metalloprotease class) isoforms (Barsan et al., 2012). The isoforms of the above protein participate in the biogenesis, maturation of the plastids and the repair and degradation of PSII (Kato et al., 2012; Liu et al., 2010a). Consistent with this the abundance of FtsH2 and FtsH5 decreased from 26 to 39 dpa in SP and SG fruits, FtsH2 decreased similar to SP/SG, whereas the level of FtsH5 remained stable at 39 dpa in SH (Table 5.7). Since thylakoid loss takes place only when levels of both FtsH2 and FtsH5 drop below a threshold (Kato et al., 2012), it is likely that retention of FtsH5 protein subdues this response in SH fruits. Notwithstanding the overlaps in proteome changes among the wild species, it appears that species-specific subtle shifts in proteome ring about the metabolic shifts related to chromoplast formation.

5.4.7 Lipoxygenase and myosin isoforms are abundant in SH fruits

In tomato fruits post-mature green stage, the carotenoid accumulation and ripening are influenced by jasmonic acid (JA) which regulate this process independently of ethylene (Liu et al., 2015). The proteome profiling of wild relatives fruits showed wide ranging differential regulation of ten isoforms of lipoxygenase. Considering that lipoxygenases play a role in the formation of JA and several volatiles, their activity may influence the ripening process including carotenogenesis. A role for the generation of C5 and C6 volatiles has been shown for TomloxC in tomato fruits as its level (both gene and protein) increases commensurate with ripening (Shen et al., 2014; Chen et al., 2004; Barsan et al., 2012). However, TomloxC (Solyc01g006540.2.1) decreased in abundance at 39 dpa in all the wild species, thus it may not contribute to volatile production in fruits.

Importantly, a very specific increase in four lipoxygenase isoforms (Solyc01g099180.2.1, Solyc01g099190.2.1-TomloxB, Solyc01g099200.2.1, and Solyc01g099210.2.1) was observed in 29 dpa SH fruits, which may have a relation to the distinct profile of volatiles emitted from SH fruits (Mathieu et al., 2009). Among the wild relatives, SH fruits showed most persistent JA levels, though the magnitude declined from 26 to 39 dpa (Fig. 5.18). Though SP (29 dpa), SL and SG (26 dpa) showed high levels of JA, it was below the detection limits at later stages. Apparently, SH fruits though have persistent JA level even at 39 dpa, it does not seem to be related to carotenogenesis in this species as reported in tomato (Liu et al., 2012).

SH fruits have dense trichomes that contribute to the pubescent fruits (Peralta et al., 2008). It is reported that mutations in myosin XI affect the growth of several types of surface cells such as root hairs and leaf pavement cells and contribute to the expansion of trichomes and elongation of stigmatic papillae (Ojangu et al., 2012). Commensurate with a higher density of trichomes on SH fruits, the fruit proteome also shows the abundance of myosin XI isoforms at 29 dpa (Solyc06g008090.2.1-myosin XI-2, Solyc06g083960.1.1-myosin XI-K, Solyc07g041150.2.1-myosin XI-1; Table 5.7) suggesting their role in trichome formation. Barring SG that showed one of the myosin isoforms (Solyc01g081540.2.1-myosin XI-F), myosin isoforms were not detected in other wild species.

5.4.8 PSY1 abundance in SH fruits is below the detection limits

A major drawback in understanding carotenogenesis in tomato fruits is the limited information about the carotenogenic proteins due to their very low abundance. Our earlier proteomic study, employing 2D gels (Kilambi et al., 2013) did not detect proteins related to carotenoid biosynthesis. Only shotgun proteomics of enriched chromoplasts detected some of these proteins (Barsan et al., 2012; Wang et al., 2013). The usage of TPM enabled detection and quantification of a number of carotenogenic proteins in tomato and its wild relatives without enrichment of chromoplasts. Similarly in Norway spruce bark, selected reaction monitoring detected very low abundant proteins including DXS (Zulak et al., 2009). Though TPM detected several carotenogenic proteins, yet few proteins could not be detected, due to their extremely low abundance.

Consistent with overall high expression of carotenogenic genes, TPM detected more proteins in leaf than in fruits. The preponderance of the MEP pathway proteins in the leaf

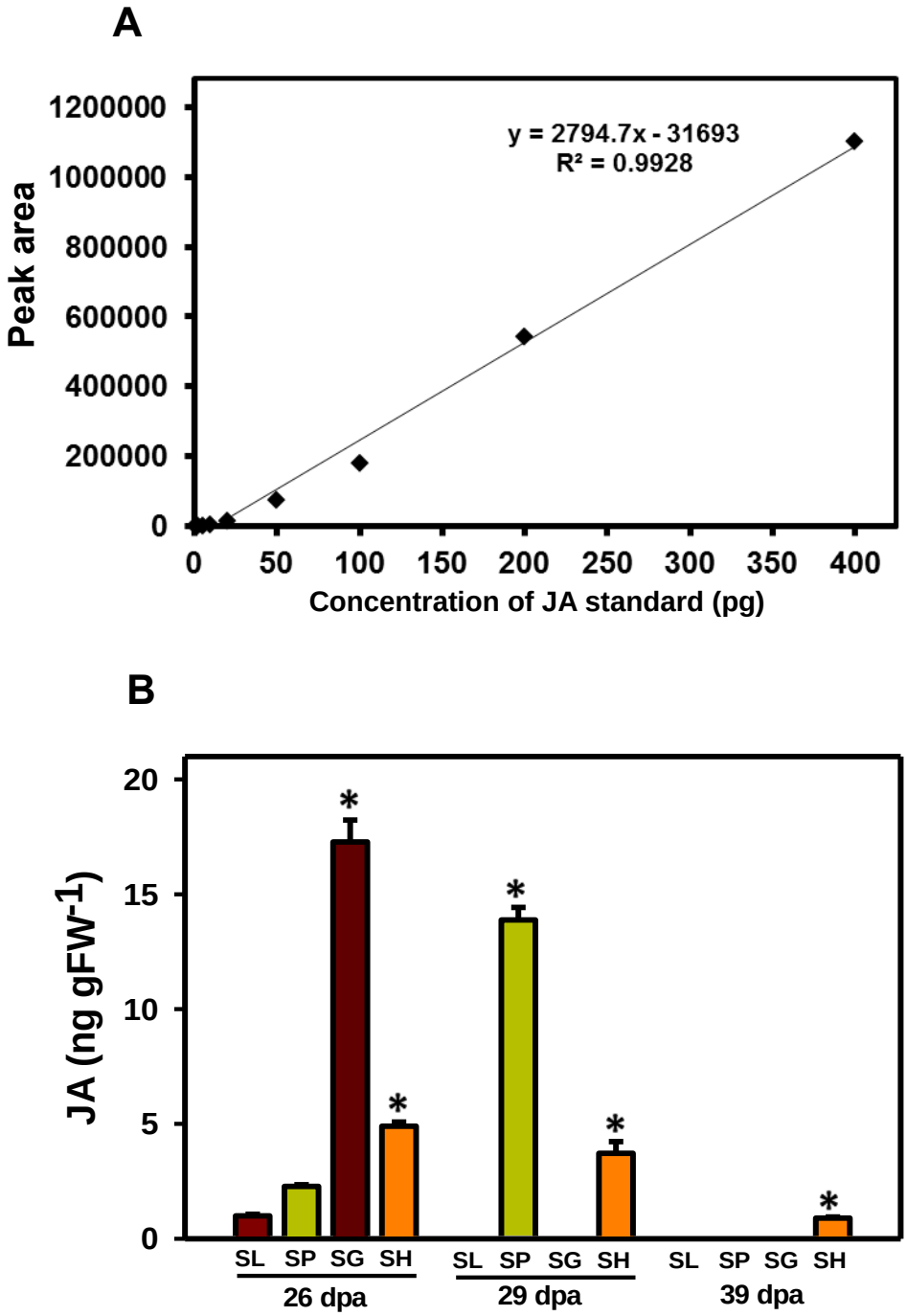


Figure 5.18. Estimation of jasmonate levels in the fruits. Jasmonate was extracted from the fruits at different stages and analysed as described in methods. A, Calibration curve for jasmonate standard. B, Jasmonate levels in the fruit samples were estimated using the calibration curve. Data are means ± SE (n = 3), * = P ≤ 0.05.

reflects its relative importance as it contributes to several isoprenoid derived metabolites, while in the ripening fruit; its products are mostly funnelled into carotenogenesis. Of interest was different isoforms of IDI and GGPPS could be distinguished by TPM in leaf. Probably different isoforms of GGPPS are involved in the formation of specific isoprenoid groups (Rodriguez-Concepcion, 2010; Vallabhaneni and Wurtzel, 2009). Likewise, different IDI isoforms are targeted to different subcellular locations in cells and presumably regulate isoprenoid synthesis in respective compartments (Moise et al., 2013).

In tomato, the formation of phytoene from GGPP is distinctly mediated by a fruit specific PSY1 (Fray and Grierson 1993) and leaf specific PSY2 (Fraser et al., 1999), with no overlap in their functions. Notwithstanding this, in leaf both PSY1 and PSY2 were below the limits of detection. Consistent with enhanced carotenoid levels PSY1 was detected in SP and SG but not in SH fruits. The absence of PSY1 in SH fruits may be related to the lack of preferential lycopene/β-carotene accumulation. As proteins contributing to a metabolic pathway tend to be co-ordinately regulated, it is possible that their abundances may be similarly determined. Accordingly, abundance of proteins contributing to lycopene formation was higher in SL and SP fruits. The abundance of VDE in SH likely reflects operation of leaf specific pathway in fruits. Similarly, increased abundance of CYCB may be related to high β-carotene level in SG fruits. The carotenoid cleavage proteins CCD1B and CCD4B were most abundant in leaf in accordance with their multifarious roles including leaf development (Avendano-Vazquez et al., 2014) and volatile emission (Rambla et al., 2014). Consistent with the fact that aroma volatiles are largely emitted from ripened fruits, CCD1B was detected in SG and SP, but not in SH fruits. However, the *ccd* expression was 9 times higher in *S. pennelli* than SL (Bolger et al., 2014) suggesting a posttranscriptional regulation of this gene in SH fruits.

Accumulation of carotenoids also depends on sequestration, as *high pigment* mutant fruits that are enriched in carotenoids also show increase in CHRC and PAP3 levels (Kilambi et al., 2013; Nogueira et al., 2013). Consistent with high carotenoid levels, the abundance of CHRC was high in SP fruits. On the contrary, the CHRC levels were diminished in SH fruits, as it accumulates little carotenoids. In addition to CHRC, PAP3 was below the detection limits in SH. In addition to CHRC, PAP3 was below the detection limits in SH. Lower levels of these proteins entail that the carotenoid sequestration may be compromised in SH fruits.

The linear correlations noticed between the abundant carotenoids and transcript levels of rate limiting steps in fruits were largely amiss between transcripts and respective proteins. Among the proteins detected in TPM, correlations between protein-transcript pairs were found only for a few proteins in SG and SP and none in SH. Considering that only one correlation was shared between SG and SP, it can be suggested that carotenogenic proteins are regulated posttranscriptionally in a species-specific fashion. Above lack of correlation corroborates the prevailing view that while regulation of abundances of mRNA is more flexible, the protein abundances of mRNA is more flexible, the protein abundances are stringently regulated (Vogel and Marcotte, 2012).

5.4.9 Integrated transcript-protein-metabolite analysis indicate diversity in carotenogenesis regulation in wild relatives

In metabolic pathways, the levels of metabolites are largely governed by feedforward and feedback loops. Given the diversity in preferentially accumulated carotenoids such as high lycopene in SP, β-carotene in SG and no such accumulation in SH fruits, we propose a model depicting interactions underlying carotenogenesis in the wild species (Fig. 5.19). These interactions were derived by correlating (r value ≥ 0.95) the levels of carotenoid intermediates, carotenogenic genes and proteins at 39 dpa in the wild species with tomato as a reference.

One basic question examined in this study was whether green fruited SH employs the leaf pathway in the fruits. Correlation analysis discounted this possibility as our model lacked any overlap in SH fruits and leaves. This absence of commonality is indicative of organ-specific regulation of carotenogenesis in SH. Overall comparison of correlation data across wild relatives further reveals that both the leaf and the fruit carotenogenesis is diversely regulated in species-centric fashion. Considering that carotenogenesis uses similar set of substrates and catalyzing enzymes, the observed diversity reveals that the regulatory circuits governing carotenogenesis are extensively rewired in a species-specific fashion. For example, in the leaf, lutein stimulated different metabolites in β-branch in reciprocal fashion in different species (Fig. 5.19A). At the same time, it reciprocally inhibited violaxanthin levels in SP leaf. The above interactions are also consistent with lutein being the most predominant metabolite in the leaf of all species. Unlike leaf, the carotenoid level in the fruits is regulated in multifarious fashion in orange/red fruited species (Fig. 5.19B). The complexity of these interactions increased from green fruited SH to orange fruited SG. From only one interaction in SH and three in

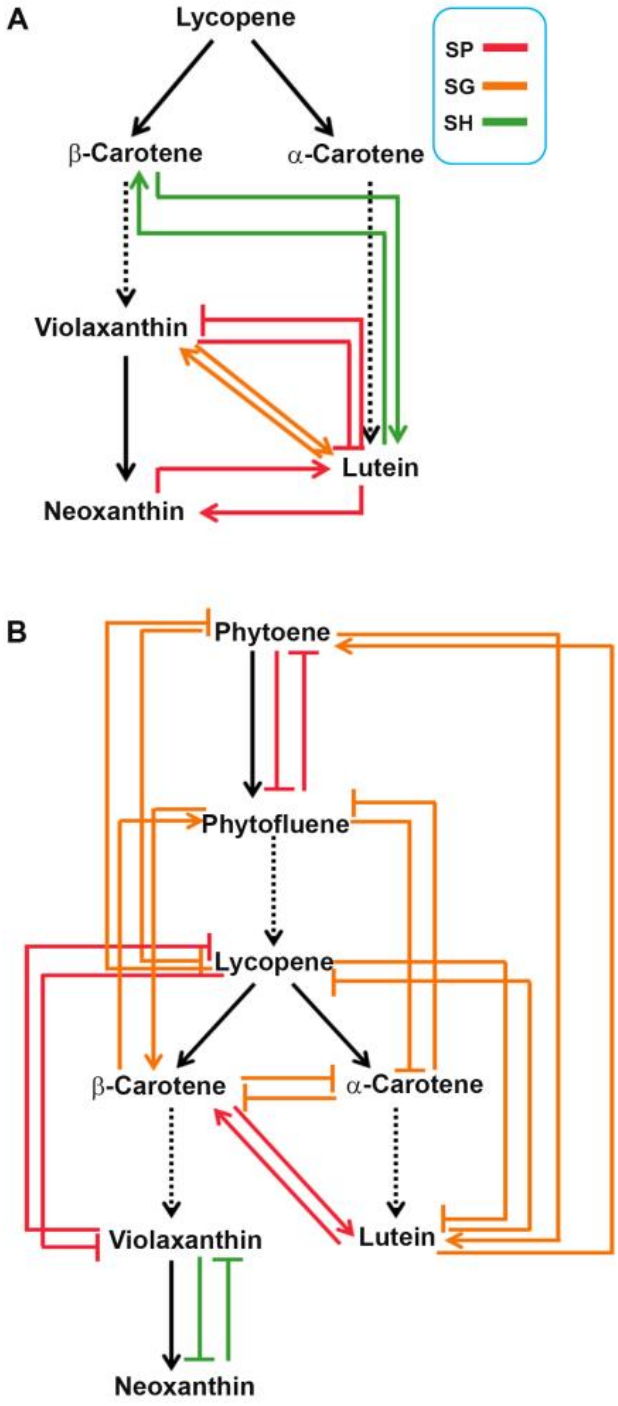


Figure 5.19. Regulation of carotenoid biosynthesis by the products/intermediates of the pathway. Carotenoid interactions in wild species in comparison to tomato are shown in A, leaf and B, fruit. Dotted arrows indicate multiple steps in the pathway. Only carotenoid interactions with $r \geq 0.95$ are mapped on the biosynthetic pathway. Most interactions are reciprocal. The positive and the negative interactions are represented by regular and blunted arrows respectively. The interactions specific to a species are depicted as colored lines; red (SP), orange (SG), green (SH). The correlation coefficient values are given in Table 5.5.

SP, the orange fruited SG had six interactions between metabolites. Amazingly, all these interactions were species-specific and no overlaps were detected between two species or with leaf. From the foregoing, it is evident that carotenogenesis is multifariously modulated in species-centric fashion resulting in preferential accumulation of specific carotenoids.

Though not completely comprehensive, this study indicates that coupling of metabolite variations with those in transcriptome and proteome help to distinguish the transitions during transformation of green to orange/red fruited species. The species-centric regulation of carotenoids highlights that despite the commonality between biochemical steps of carotenogenesis, the overall pathway appears to be uniquely regulated in each species. In the future, more refined systems biology approaches including metabolic flux analysis may unravel the regulatory circuits governing carotenogenesis in more detail.

Chapter 6

To examine the influence of *phototropin1* on tomato fruit quality and shelf life

6.1 Introduction

Tomato fruit ripening is a complex process which is regulated by genetic (transcription factors, signal transducers), hormonal (ethylene, auxin, ABA, JA and brassinosteroids) and environmental (light, temperature) factors (Carrari and Fernie 2006; Seymour et al., 2008; Bouzayen et al., 2010; Opara et al., 2012; Yuan et al., 2015). Ripening causes changes in physiological and biochemical properties of fruits including softening of tissues, pigment synthesis and other primary and secondary metabolic changes that contribute to the color, aroma and flavor, etc. (White, 2002; Pirrello et al., 2009; Seymour et al., 2013).

The most interesting aspect of tomato fruit ripening is the pigment biosynthesis and accumulation which is regulated mainly by ethylene and light (Piringer and Heinge, 1954; Alba et al., 2000; Liu et al., 2004; Liu et al., 2015). Light is not only a source of energy for plants but also acts as an environmental signal (Kimura and Kagawa, 2006). To perceive the quantity, quality and directionality of light, plants utilize photoreceptors. Four main classes of photoreceptors are known in higher plants, viz; phytochromes (Chen and Chory 2011), cryptochromes (Chaves et al., 2011), phototropins (Christie 2007) and UVR8 (Rizzini et al., 2011; Jenkins 2014). Other classes of photoreceptors also exist like Zeitlupe (ZTL), Lov Kelch Protein2 (LKP2) and Flavin binding, Kelch repeat, F-Box1 (FKF1) proteins (Suetsugu and Wada 2013). Of these, fruit localized phytochromes have been shown to regulate the extent of lycopene accumulation and therefore color development in tomato, independent of ethylene (Alba et al., 2000). Phytochromes, either singly or in combination, act as time keeper by modulating duration of different phases of tomato fruit development and ripening (Gupta et al., 2014). In another study, overexpression of *cry2* in tomato fruit resulted in enhanced lycopene and flavonoid composition suggesting the role of this photoreceptor in pigment biosynthesis and /or accumulation (Giliberto et al., 2005). In addition, the fruit specific suppression of *det1* and *Lecop1like* genes in tomato suggests that manipulation of light signal transduction machinery can lead to enhanced carotenoid levels (Liu et al., 2004; Davuluri et al., 2005). Similarly, fruit specific down-regulation of *cul4* and *ddb1* by RNAi resulted in increased pigmentation in the fruits (Wang et al., 2008). The disruption of function of these light signaling components resulted in increased number of plastids thereby increasing the storage space for carotenoids and other pigments in plastoglobules, where the sequestration and storage of carotenoids occurs. Recently, it was shown that the increased

level of CHRC, a plastoglobular protein may be responsible for enhanced carotenoid content in the *hp1* fruits, most probably by increasing the sequestration of carotenoids (Kilambi et al., 2013).

Phototropins are a special class of blue light receptor kinases in plants that mediate root and hypocotyl phototropism (Sakai et al., 2001), chloroplast movement (Kagawa et al., 2001), stomatal opening (Kinoshita et al., 2001) and leaf expansion (Tokutomi et al., 2008). These are plasma membrane associated serine/threonine kinases containing two LOV (light-oxygen-voltage) domains in the N-terminal end and a kinase domain in the C-terminal end (Briggs et al., 2001; Briggs and Christie, 2002; Christie et al., 2012). Phototropin family of photoreceptors is ubiquitous throughout plant kingdom. Two members exist in the phototropin family, PHOT1 and PHOT2 and they have different photosensitivities as determined by their N-terminal domains. PHOT1 mediates low fluence blue light responses (<0.1-1$\mu molm^{-2}s^{-1}$) whereas PHOT2 mediates high fluence blue light responses (≥ 1$\mu molm^{-2}s^{-1}$; Sakai et al., 2001; Higa et al., 2014). On exposure to light, phototropins undergo blue light induced autophosphorylation which is the first step in phototropic signal transduction pathway (Inoue et al., 2008a; Inoue et al., 2011; Boex-Fontvieille et al., 2014; Deng et al., 2014). Until now, three phosphorylation targets for PHOT1 were identified including Blue Light Signaling1 (BLUS1; Takemiya et al., 2013a), ATP-binding cassette B19 (ABCB19; Christie et al., 2011) and Phytochrome Kinase Substrate 4 (PKS4; Demarsy et al., 2012; Kami et al., 2014). In Arabidopsis, along with autophosphorylation, PHOT1 undergoes ubiquitination which requires Non-Phototropic Hypocotyl 3 (NPH3; Roberts et al., 2011; Wan et al., 2012). The role of NPH3 and other related proteins such as Root Phototropism Protein 2 (RPT2; Sakai and Haga 2012) remain to be further elucidated in order to understand their involvement in phototropic signaling.

Nps1 (*Non-phototropic seedling1*) is a dominant mutant of tomato isolated from EMS mutagenized population in a screen for mutants defective in blue light perception. It exhibits a transition from G to A in the *phot1* gene at 3884 bp position close to the LOV2 domain, leading to substitution of Arg495 to His. Recently, it was shown that this mutation in the hinge region of tomato PHOT1 affects protein function by regulating protein degradation (Sharma et al., 2014). Characteristics of the mutant include loss of both low and high blue light phototropic responses, no chloroplast accumulation under low intensity but avoidance under high light intensity, inability of stomata to respond to

blue light, inhibition of opening of cotyledons, etc. The enhancement of lycopene and shelf life in the fruits of this mutant (Sharma S, Ph.D. thesis, 2011) suggests the role of phototropic blue light receptors in regulating fruit pigmentation and postharvest shelf life. In this study, we made an attempt to understand the role of *phototropin1* in mediating fruit coloration and shelf life using proteomic and transcript profiling. In addition, we also introgressed the *Nps1* into local cultivar.

6.2 Materials and methods

6.2.1 Light sources used for screening seedlings of wildtype and mutant seedlings

Blue and green LEDs were obtained from Quality Electronics, Hyderabad, India. The spectral emissions of blue (465 nm) and green (520 nm) were measured with spectroradiometer (International Light Technologies). The blue light used for screening the seedlings was adjusted to required intensity after measuring with a light meter connected to a Quantum sensor (Skye Instruments, UK).

6.2.2 Plant material and growth conditions

Seeds of *Solanum lycopersicum* cv. Ailsa Craig (LA2838; AC from Tomato Genetics Resource Centre, University of California, Davis), *Solanum lycopersicum* cv. Arka Vikas (from IIHR, India); AV) and non-phototropic seedling mutant *Nps1* (Sharma et al., 2014) were used in this study. Seeds of AC, AV, *Nps1* and F_1 and F_2 from AC x *Nps1*, AV x *Nps1* crosses were surface sterilized with 20% (v/v) sodium hypochlorite solution, washed thoroughly and germinated on wet germination papers in a germination box. They were kept in dark for three days and allowed to germinate at 22±5°C. Seedlings of the mutant were exposed to unilateral blue light (0.5 $\mu molm^{-2}s^{-1}$) for 10-12 hours to check for phototropism. Green safe light was used for arranging the seedlings in the dark room. The seedlings were then kept under white light for one more week after which the seedlings were transferred to pots in the green house and grown at 25±5°C during the day and ambient temperatures at night. The seedlings from subsequent generations (F_1 and F_2) from both AV and AC crosses were screened similarly and the plants with desirable characteristics (high lycopene and/or high shelf life) were taken forward to next generations.

For detailed study on fruit ripening, plants of both AC and *Nps1* were grown in three randomized blocks (each block constitutes one biological replicate), with each block consisting of three rows, with five plants each for AC and *Nps1* per row (Fig. 6.1). The

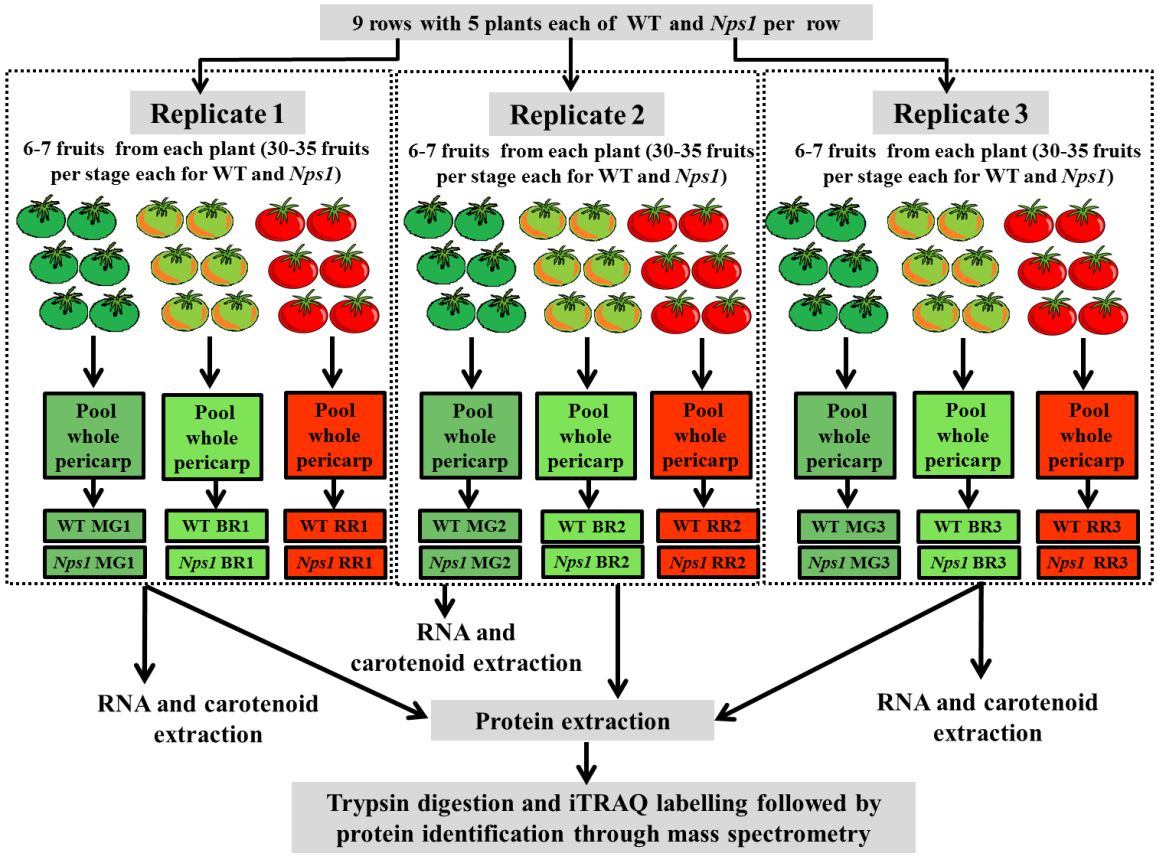


Figure 6.1. Randomized block experimental design describing the growth of plant material, collection of fruits at three ripening stages in three biological replicates for protein, RNA and carotenoid analyses.

flowers were tagged at the time of anthesis for chronological monitoring of fruit developmental stages. To minimize variation, fruits developed only on the first and second truss were used for all experiments. From each block (biological replicate), 30 to 35 fruits per ripening stage per genotype were harvested, seeds were removed, cut into four halves, pooled separately at every ripening stage for both the AC and *Nps1*, flash frozen in liquid nitrogen and stored at -80°C until use.

6.2.3 Determination of ethylene evolution

To measure ethylene evolution after harvesting, fruits were enclosed in air tight boxes (250 ml). After 4 h, 1 ml of head-space gas was removed from the boxes and injected into a Porapak T column connected to a gas chromatograph (GC-17A; Shimadzu) as described in chapter 3. For every sample, ethylene in the head-space was measured at least three times using a minimum of three biological replicates at each ripening stage.

6.2.4 Estimation of carotenoids

Carotenoid extraction was performed from the parents AC and *Nps1* fruits at three ripening stages, (MG, BR and RR) and from AV, and F_1 and F_2 fruits at RR stage using Accela UHPLC coupled to a PDA detector using the protocol described in chapter 4, and Gupta et al., 2014.

6.2.5 Study of fruit pigmentation and senescence under natural conditions

Off-vine senescence study

Fruits of AC and *Nps1* were harvested at red ripe stage and incubated for off-vine senescence study at 16°C and 25°C under natural day/night conditions. The RR fruits of F_1 and F_2 were also examined for off-vine senescence at 25°C.The fruits were photographed for every two days and the pictures were shown (in figures) only for the days where obvious differences in pigmentation and initiation of senescence were observed.

On-vine senescence study

Fruits of AC, *Nps1* were continuously monitored from red ripe stage till onset of senescence and thereafter until complete fall-off of the fruits from the plant. The time taken for the onset of senescence for the wildtype and mutant were compared.

6.2.6 RNA isolation and quantitative real time PCR

RNA isolation and quantitative real time PCR from the fruits of AC and *Nps1* fruits (each with three biological replicates) at different ripening stages- (MG, BR and RR) was carried out using the protocol described in chapter 3 (for primer details, see Annexure 1).

6.2.7 Label-based proteome profiling in *Nps1* using iTRAQ

Proteins were extracted using the protocol described in chapter 3. Protein solutions (100 µg each from AC and *Nps1* at MG, BR and RR stages) were diluted in TNE (50 mM Tris pH 8.0, 100 mM NaCl, 1 mM EDTA) buffer. Rapigest SF reagent (Waters) was added to a final concentration of 0.1% [v/v] and samples were boiled for 5 min. TCEP (Tris (2-carboxyethyl) phosphine) was added to 1 mM and the samples were incubated at 37°C for 30 min. The samples were carboxymethylated with 0.5 mg/ml of iodoacetamide for 30 min at 37°C followed by neutralization with 2 mM TCEP. Proteins samples prepared as above were digested with trypsin (trypsin:protein ratio-1:50) overnight at 37°C. RapiGest was removed by treating the samples with 250 mM HCl at 37°C for 1 h followed by centrifugation at 14000 rpm for 30 min at 4°C. The soluble fraction was then added to a new tube and the peptides were extracted and desalted using Aspire RP30 desalting columns (Thermo Scientific).

The trypsinized samples (4 samples) were labeled with isobaric tags (iTRAQ, ABSCIEX, Ross et al., 2004), where each sample was labeled with a specific tag to its peptides. Each set of experiments were then pooled and fractionated using high pH reverse phase chromatography [HPRP-Xterra C18 reverse phase, 4.6 mm x 10 mm, 5 µ particle size (Waters)]. The chromatography conditions are as follows: the column was heated to 37°C and a linear gradient from 5-35% B (Buffer A-20 mM ammonium formate pH 10 aqueous, buffer B-20 mM ammonium formate pH 10 in 80% ACN:water) was applied for 80 min at 0.5 ml/min flow rate. A total of 30 fractions of 0.5 ml volume were collected for LC MS/MS analysis. Each of these fractions were analyzed by high pressure liquid chromatography (HPLC) coupled with tandem mass spectroscopy (LC-MS/MS) using nano-spray ionization. The nanospray ionization experiments were performed using a TripleTof 5600 hybrid mass spectrometer (ABSCIEX) interfaced with nano scale reversed-phase HPLC (Tempo) using a 10 cm-180 µ ID glass capillary packed with 5 µm C18 Zorbax beads (Agilent Technologies). Peptides were eluted from the C18 column into the mass spectrometer using a linear gradient (5-30%) of ACN at a flow rate of 550 µl/min for 100 min. The buffers used to create ACN gradient were Buffer A (98% water, 2% ACN, 0.2% formic acid and 0.005% TFA) and buffer B (100% ACN, 0.2% formic

acid and 0.005% TFA). MS/MS data were acquired in a data dependent manner in which the MS1 data was acquired for 250 ms at m/z of 400 to 1250 Da and the MS/MS data was acquired from m/z of 50 to 2000 Da. For independent data acquisition (IDA) parameters include MS1-TOF 250 ms, followed by 50 MS2 events of 25 ms each. The IDA criteria, over 200 counts threshold, charge state +2 to +4 with 4 sec exclusion. Proteins were extracted at UOH and iTRAQ was outsourced to Biomolecular and Proteomics Mass Spectrometry facility, University of California and the data was analyzed at UOH.

6.2.8 Data analysis

The acquired MS/MS data were uploaded on the Protein Pilot 4.0 (ABSCIEX) software and searched against iTAG release 2.3 predicted proteins; www.solgenomics.net). Searches were performed using the following parameters: trypsin as proteolytic enzyme, maximum two missed cleavages, carbamidomethylation of cysteine as a fixed modification, oxidation of methionine as a variable modification. After correcting the search results for labeling bias and background signals, the proteins were normalized and then quantified. False discovery rate (FDR) was calculated using automated decoy database search strategy through PSPEP (Proteomics System Performance Evaluation Pipeline) in Protein Pilot software. Proteins with minimum two unique peptides with confidence more than 95% and unused protscore value more than 1.3 were considered for further analysis. The overall p values were determined by student's t-test and Benjamini-Hochberg multiple hypothesis correction was used to determine the corrected q values (FDR). Proteins with minimum two fold (up or down-regulation), p value≤0.05, q value≤ 0.01 were considered to be differentially expressed. The differentially expressed proteins were classified using FunCat scheme (version 2.0) into various functional categories (Ruepp et al., 2006).

6.2.9 Endo-β-mannosidase assay of tomato fruits

Endo-β-mannosidase assay was performed based on the protocol described by Bourgault and Bewley, 2002. Briefly, 20 ml of locust bean gum substrate in McIlvaine buffer (0.1 M citric acid and 0.2 M sodium hydrogen phosphate, pH 5.0) was combined with 0.24 g agarose and the mixture was boiled, cooled, 500 µg/ml of gelatin was added and poured into plates. After the gels were solidified, holes were punched in the gels and sample was loaded into the wells. The plates were incubated for 24 h at 32°C and then stained with Congo red for visualization of clearance zones. Endo-β-mannosidase was

extracted from tomato fruits using the protocol described in Bourgault and Bewley, 2002. About 1 g of tomato fruit tissue was ground in an ice cold mortar in acid washed sea sand with 1.5 ml of 0.1M HEPES KOH (pH 8.0) containing 50 mM DTT, 1% protease inhibitor cocktail. The extract was centrifuged at 21,000 *g* for 10 min at 4°C and the supernatant was adjusted to a final volume of 1.5 ml. Protein concentration of the supernatant was estimated using amido black and used for enzyme assays.

6.2.10 Crossing of WT and *Nps1* plants

Crosses were made between wildtype (AC and AV) and *Nps1* plants and F_1 plants were generated. These F_1 were selfed to generate F_2. The fruits of F_1 and F_2 were examined for their fruit lycopene content and off-vine senescence.

6.2.11 Confirmation of F_1 and F_2 lines of AC♀x*Nps1*♂ and AV♀x*Nps1*♂ crosses

DNA was extracted from the leaves of F_1 and F_2 of AC♀x*Nps1*♂ and AV♀x*Nps1*♂ cross using the protocol as previously described (Sreelakshmi et al., 2010). The extracted DNA was quantified using nanodrop (ND-1000 spectrophotometer) and also on agarose gel. The DNA isolated was used to set up the PCR reaction (20 µL) with the following components,: 25 ng of DNA (5 ng/µL), 2 µL of 10X PCR buffer (10 mM Tris, 1.5 mM $MgCl_2$, 5 mM KCl, 0.1% (w/v) gelatin, 0.005% (v/v) Np-40, pH 8.8, 0.005% (v/v) Tween-20), 1.6 µL of 2.5 mM dNTPs, 1 µL of 4 pmol primers (*phot1* forward and reverse) and 0.18 µL Taq polymerase (in-house isolated). The PCR cycling conditions were: 94°C (initial denaturation) for 4 min, (94°C for 20 sec, annealing at 58°C for 30 sec, 72°C for 30 sec- 35 cycles) and final elongation at 72°C for 10 min. A heteroduplex was generated by mixing equal volumes (1:1) of wildtype and mutant PCR products using the PCR program: 98°C for 8 min; 80°C for 20 sec; 60 cycles of 80°C for 7 sec, -0.3°/cycle. The heteroduplex formed was digested with CEL I enzyme as per the protocol described by Sharma et al., 2011. CEL I reaction for mismatch cleavage contains the following components in a reaction volume of 45 µL: 20 µL of PCR product, 4.5 µL of 10X CEL I digestion buffer (10 mM HEPES buffer pH 7.0, 10 mM $MgCl_2$, 10 µg/ml BSA and 0.002% (v/v) Triton X100) and 0.5 µL of CEL I enzyme (in-house isolated). The reaction was carried out at 45°C for 15 min and the digestion was terminated by adding 2 µL of 75 mM EDTA, pH 8.0. The digested products along with AC or AV as a positive control and undigested samples were loaded onto 1.2% agarose gel and run at 50 V for 3 h to visualize the digested products. The gels were scanned using gel

documentation system (Syngene, Genesys software 1.5.4) and positive lines were identified.

6.2.12 MutMap analysis

The DNA was isolated from two lines that showed long shelf life in F_2, F_2 24 and F_2 36 (mutant-like bulk; F_2) and unmutagenized AC (WT bulk) and DNA was also isolated from 13 lines that showed long shelf life in F3 (mutant-like bulk; F_3) and 15 lines that segregated as WT (WT-like bulk; F_3) using DNeasy Plant Mini Kit (Qiagen) and quantified using Qubit 3 fluorometer (Thermo Fisher Scientific). A shotgun paired end indexed library was prepared (with 2 µg of DNA) using Illumina Truseq Nano DNA library prep kit according to manufacturer's recommendations. This library was denatured, diluted to 18 pM, loaded into a Miseq v3 reagent kit (600 cycles PE, Illumina) and sequenced using Illumina MiSeq Desktop Sequencer. This experiment was done in collaboration with Dr. Brad Till, Plant Breeding and Genetics laboratory, FAO/IAEA Agriculture and Biotechnology Laboratories, Seibersdorf, Austria. The FASTQ sequence read files were generated after demultiplexing the reads with the MiSeq Reporter software. The reads were then aligned to reference sequences of Heinz 1706 using BWA (Burrows-Wheeler Aligner, v0.7.15) using -q20. The sequence alignments generated in SAM format were converted into BAM format using SAM tools (v1.3.1). The BAM files were sorted using picard tools (v1.119). Variant calling was performed on BAM files using GATK's Haplotype Caller (v3.7). The generated vcf files were analyzed and annotated with the help of SIFT 4G (SIFT Annotator v2.4; Vaser et al., 2016) for variant analysis that includes SNP determination and SNP index calculation. In case of F_2, we have considered the SNPs that are identified only in the mutant (SNP index=0.9-1) as we have used unmutagenized AC as WT whereas in F_3, we have considered the common SNPs present in both mutant (SNP index=0.9-1) and segregated WT (SNP index >0 to <0.5). All the NGS data analysis was done by Mr. Prateek Gupta at RTGR, Hyderabad.

6.2.13 Statistical Analysis

Unless otherwise mentioned a minimum of three biological replicates were used for every experiment. Student's t-tests were performed to determine significant differences using Sigmaplot (version 11.0).

6.3 Results

6.3.1 *Nps1* seedlings lack phototropism under unilateral blue light

The seedlings of *Nps1* do not show phototropic bending under low fluence unilateral blue light (Fig. 6.2A; Sharma et al., 2014). After screening under blue light, *Nps1* and AC seedlings were transferred to green house and grown under the conditions as described in the methods. Thereafter the fruit development was monitored in these plants.

6.3.2 Fruit development in the AC and *Nps1*

Tomato is an excellent model for studying fleshy fruit ripening due to the dramatic changes observed in the fruit color during the ripening process. The fruits of *Nps1* exhibited intense red color at red ripe (RR) stage (Fig. 6.2B). When fruit development and ripening were monitored in *Nps1* and AC, a delayed onset of ripening was observed in *Nps1*. Fruits of *Nps1* required nine days longer to reach mature green (MG) stage (43 dpa) when compared to AC (34 dpa) (Fig. 6.2C). Thereafter the mutant followed similar ripening pattern and time interval to AC to attain breaker (BR, AC: 37 dpa; *Nps1*: 46 dpa) and RR (AC: 45 dpa; *Nps1*: 54 dpa) stages.

6.3.3 *Nps1* fruits emit less ethylene

As tomato is a climacteric fruit, its ripening is preceded by increased production of ethylene at all ripening stages. Consistent with this, AC fruits emitted high levels of ethylene, while fruits of *Nps1* emitted less ethylene at the same stages. The amount of ethylene released was higher in fruits of both AC and *Nps1* at breaker stage with the latter emitting lower ethylene levels compared to AC (Fig. 6.2D). This low ethylene emission could be the underlying factor for the slow ripening of the *Nps1* fruits compared to AC.

6.3.4 *Nps1* fruits accumulate high levels of lycopene and β-carotene at red ripe stage

Nps1 fruits exhibit intense red color and when the carotenoid content was measured in AC and *Nps1* across the three ripening stages (Fig. 6.3), a total of ten carotenoids were detected. The precursors of lycopene synthesis, such as phytoene (3.6 fold), phytofluene (5.2 fold) and ζ-carotene, were detected only in RR stage and the levels were higher in *Nps1* compared to AC. The amount of lycopene was 3.1 fold higher in *Nps1* fruits compared to AC at RR stage but the levels were not significantly different from AC at MG and BR stages (Fig. 6.3). The levels of β-carotene were high in MG (2.4 fold), BR (1.5 fold) and RR (1.3 fold) stages in the mutant compared to AC. β-cryptoxanthin, a xanthophyll derived from β-carotene decreased by 1.3 fold at BR stage, increased by 1.8 fold at RR stage whereas it was not detected in MG stage in *Nps1*. In *Nps1* fruits, the

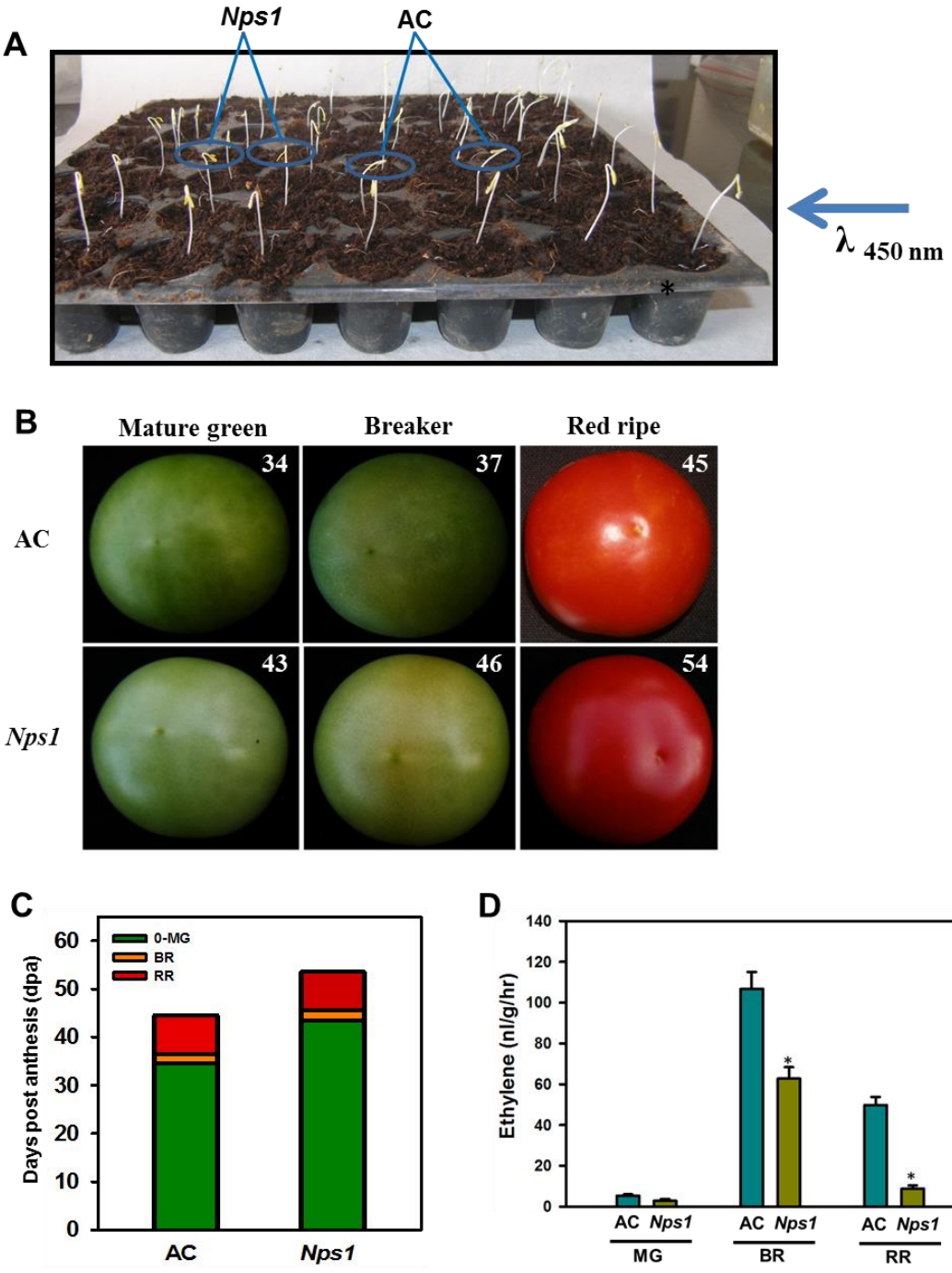


Figure 6.2. Effect of *Nps1* mutation on phototropism, fruit development and ripening. A, Phenotype of and AC and *Nps1* seedlings. Arrow indicates the direction of unilateral blue light. B, Fruit pigmentation in AC and *Nps1* fruits at MG, BR and RR stages. The post-anthesis age of fruit is indicated in days top right corner of photos. C, Chronological development of fruit in AC and *Nps1*. *Nps1* fruits show delay in attaining breaker stage and there by subsequent red ripe stage when compared to AC. Each histogram is the representation of the mean of 15-20 fruits from 30 different plants. MG-mature green, BR-breaker, RR-red ripe. D, Ethylene evolution measured from AC and *Nps1* fruits at different ripening stages (Data are means of $n = 3 \pm$ SE, * = P value ≤ 0.05).

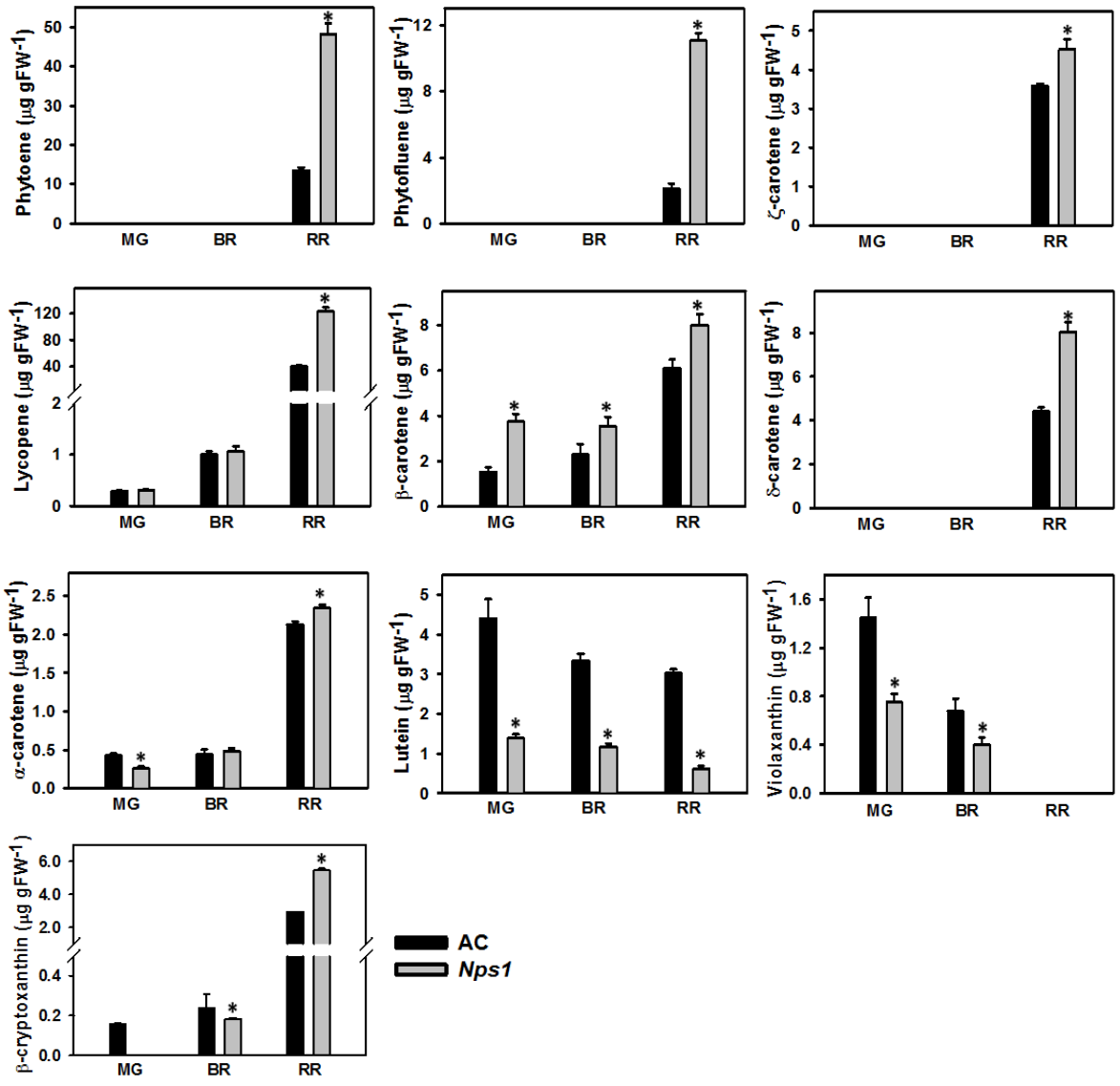


Figure 6.3. Carotenoid profiling in AC and *Nps1* fruits at MG, BR and RR stages. Data are means of $n = 3 \pm$ SE, * = P value ≤ 0.05.

levels of violaxanthin were lower (2 fold) in MG stage and BR stages (1.6 fold) than AC and not detected at RR stage. The level of δ-carotene, a precursor for lutein, was 1.8 fold high in *Nps1* and detected only in RR stage. In the αβ branch, the level of α-carotene decreased by 1.6 fold at MG stage and was 1.2 fold high at RR stage, but present in similar levels at MG stage in *Nps1* compared to AC. The amount of lutein was low at MG (3.2 fold), BR (2.8 fold) and RR (5 fold) stages in *Nps1* fruits compared to AC fruits at the corresponding stages.

6.3.5 Off-vine fruit pigmentation and senescence in *Nps1* under natural light conditions

Previous study on *Nps1* indicated the long postharvest shelf life of its fruits (Sharma S, Ph.D. thesis, 2011). It was of interest to examine the effect of postharvest storage conditions on the shelf life of *Nps1* fruits. Fruits of AC and *Nps1* at red ripe stage were incubated at two temperatures, 16°C and 25°C under natural light conditions to observe off-vine ripening and shelf life. At 16°C, fruits of AC started senescence (wrinkling) on fourth day while fruits of *Nps1* started wrinkling on 10^{th} day, approximately six days later than AC fruits (Fig. 6.4) suggesting late senescence in the mutant fruits. The senescence was further delayed when the fruits were incubated at an optimum temperature of 25°C, where AC fruits started wrinkling on 11^{th} day while the fruits of the mutant started senescence on 24^{th} day (Fig. 6.5A). When the weight of the fruits was measured at two day intervals, *Nps1* fruits lost water slowly compared to AC and also showed lower weight loss than AC (Fig. 6.5B). Based on these results, it can be concluded that the fruits of *Nps1* exhibit longer shelf life than WT. Under these conditions, the time taken for complete spoilage of AC fruit was 25 days (at 16°C) and 36 days (at 25°C), while *Nps1* fruits showed minimum wrinkles even after 72 days (at 25°C).

6.3.6 On-vine fruit senescence studies in *Nps1*

As *Nps1* fruits exhibit prolonged postharvest shelf life, we also checked the on-vine shelf life of these fruits. The fruits of AC and *Nps1* were monitored on-vine for the initiation of senescence. The fruits of AC started senescence on fourth day after RR, whereas *Nps1* fruits started on tenth day (Fig. 6.6). These results suggest that the fruits of *Nps1* stay on-vine relatively fresh for longer period than AC fruits and thus they can be harvested later.

6.3.7 Quantitative RT-PCR for gene expression analysis

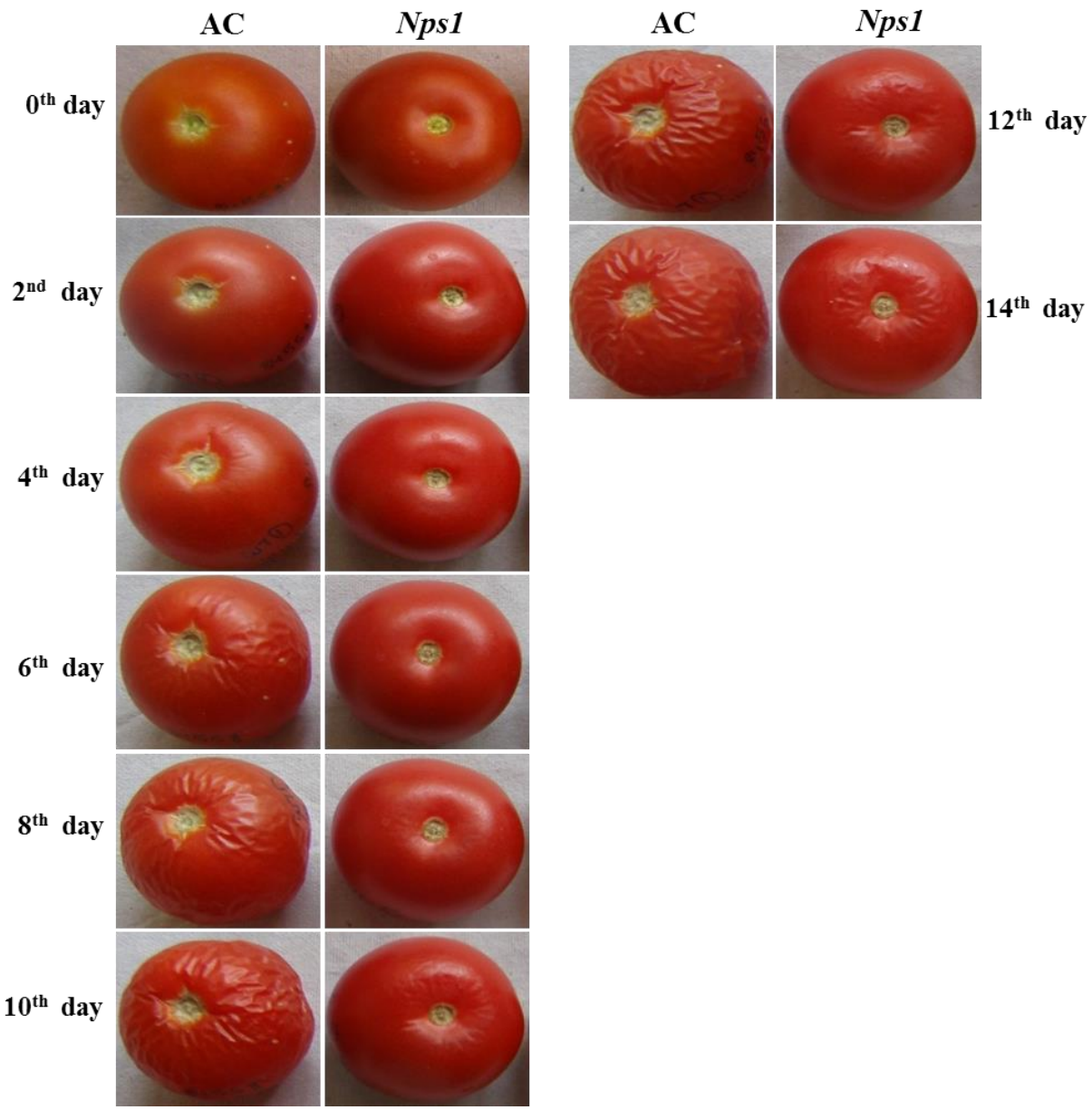


Figure 6.4. Off-vine senescence study of tomato fruits harvested at RR stage and kept under natural light conditions at 16°C (number of replicates, $n \geq 5$). The fruits were photographed on different days indicated left to the photo panels.

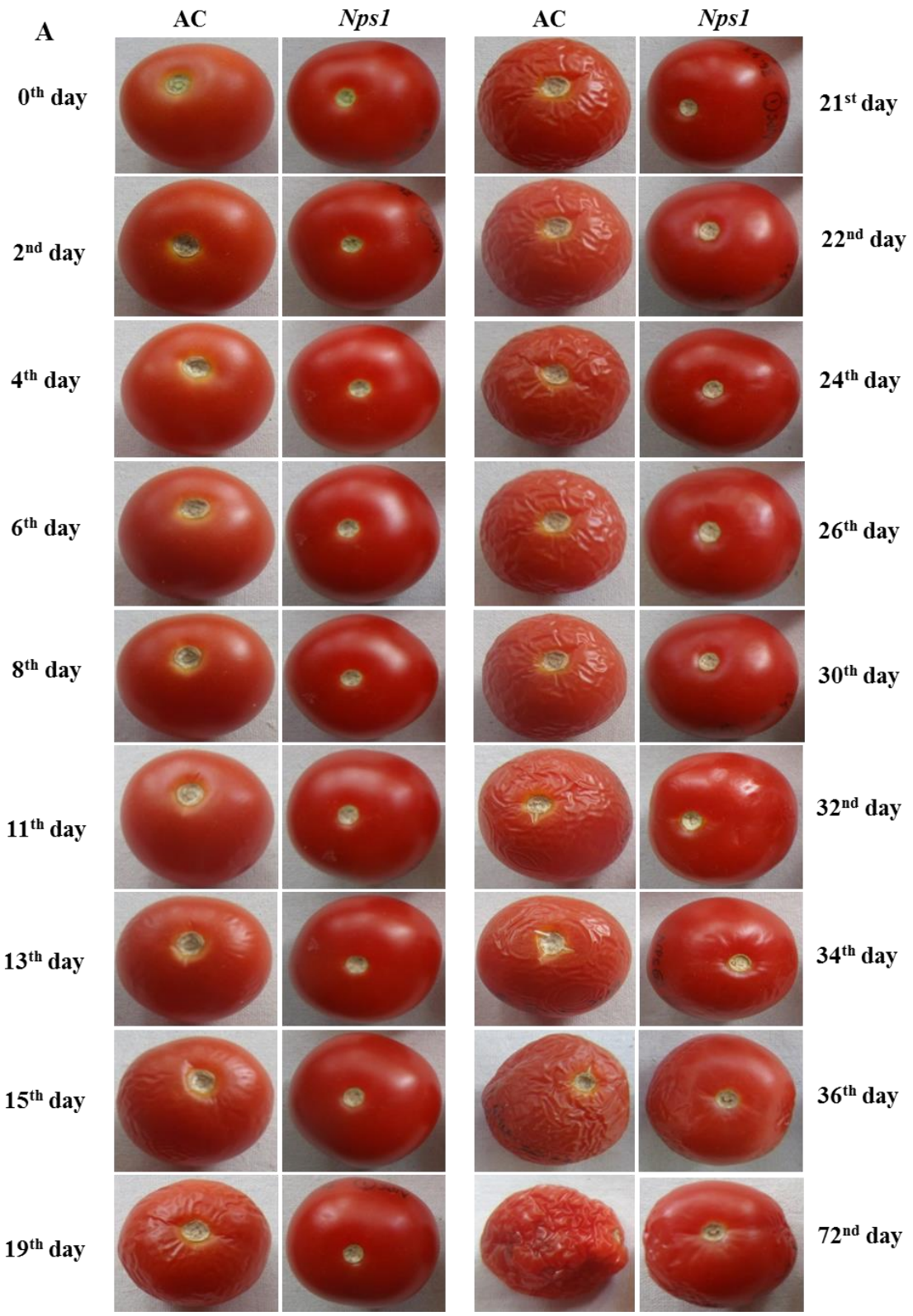


Figure 6.5. A, Off-vine senescence study of tomato fruits harvested at RR stage and incubated under natural light conditions at 25°C (number of replicates, $n \geq 5$). The fruits were photographed on different days indicated left to the photo panels.

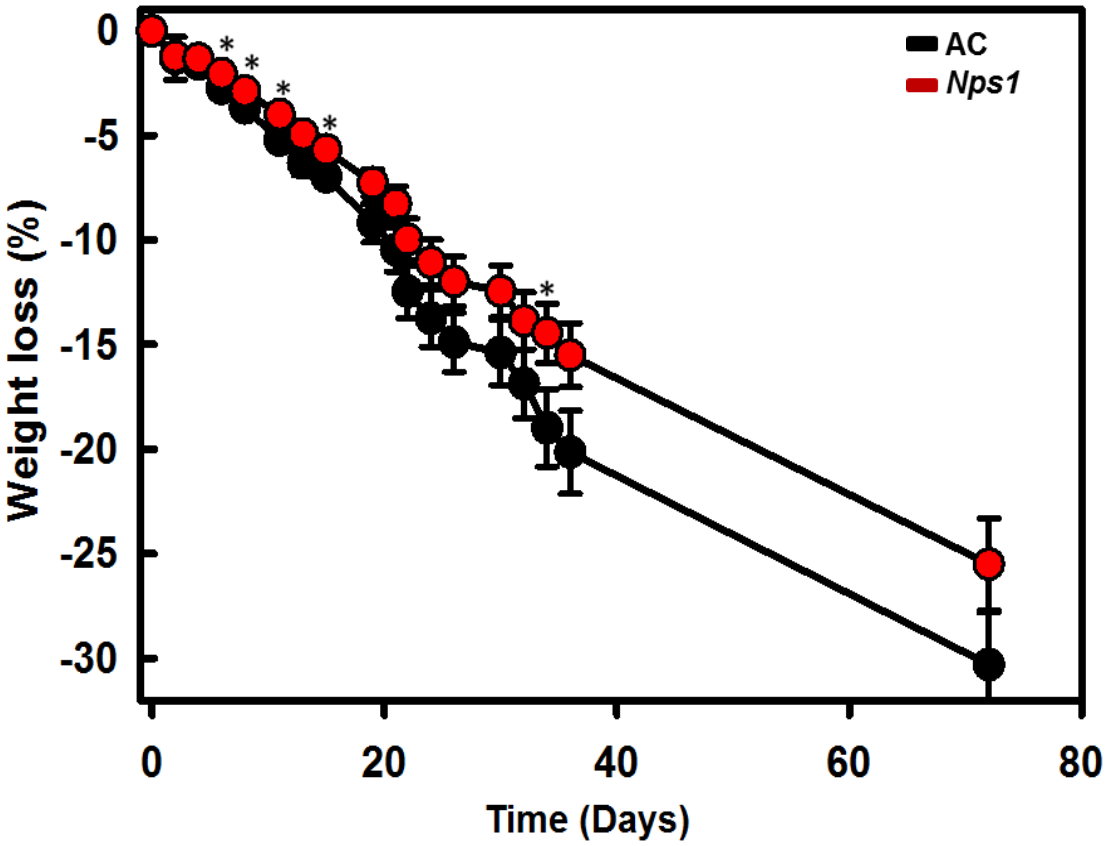


Figure 6.5. B, Post-harvest weight loss in AC and *Nps1* fruits incubated under natural light conditions at 25°C. Data are means of $n \geq 5 \pm$ SE, * = P value ≤ 0.1.

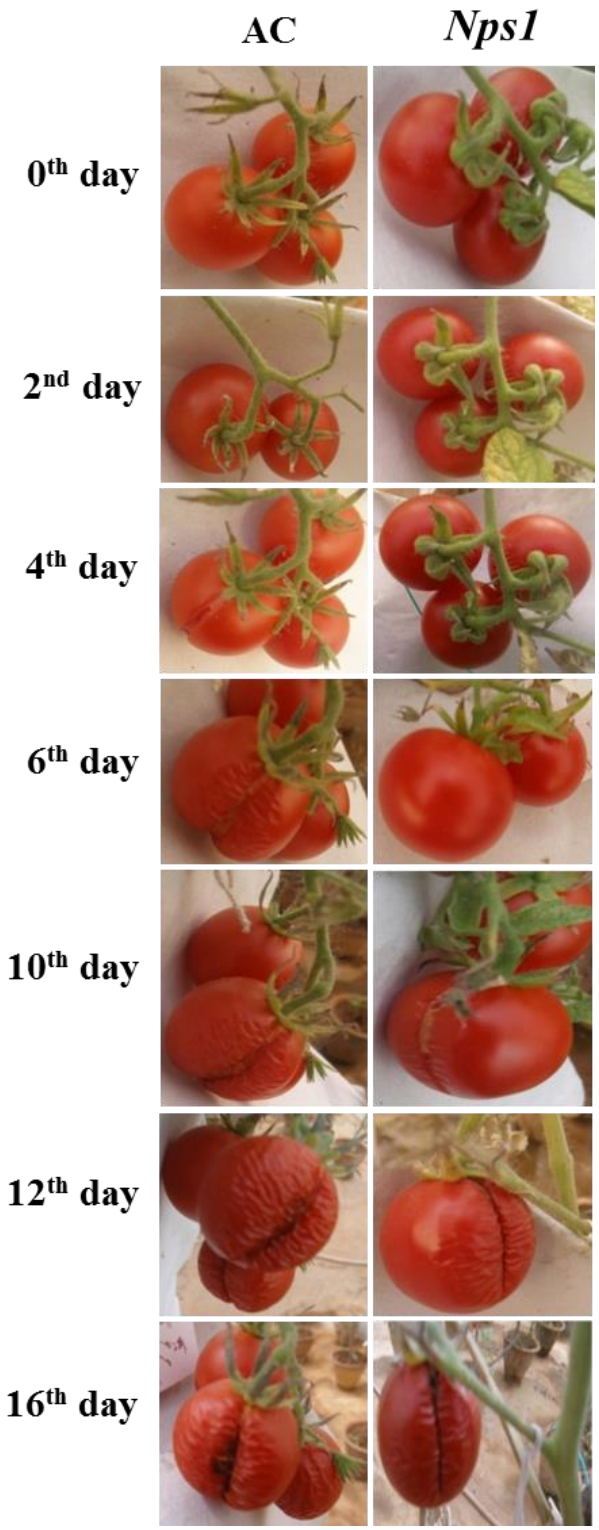


Figure 6.6. On-vine senescence study of RR tomato fruits from AC and *Nps1*. The post-RR stage of fruits in days is indicated at the left side of the photo panels (number of replicates, $n \geq 3$).

Since *Nps1* fruits are rich in lycopene levels, it was of interest to examine the expression of genes in the carotenoid biosynthesis pathway to evaluate the effect of *phot1* mutation on this pathway. The expression profiles of 22 genes involved in carotenoid biosynthesis and degradation were obtained through quantitative real time PCR analysis as shown in Figure 6.7. On the whole, the expression levels of majority of the genes were higher in AC at all ripening stages in comparison with *Nps1*.

When the transcript profiles were examined, it is observed that the transcripts of genes responsible for phytoene formation and desaturation did not show any up-regulation during ripening in the mutant compared to AC. At mature green stage, the expression levels of *ggpps2, psy2, lcyb1* and *nced1* were similar to AC whereas the expression of *dxs, hdr, idi, psy1, zis, crtiso, zds, lcyb2, cycb, lcye* and *crtrb2* were down-regulated. *dxr, pds, zep* and *chrc* were up-regulated in the mutant at mature green stage.

In *Nps1*, *ggpps2* and *ziso* were the most abundant transcripts at BR stage. The expression of *ziso* was 2.6 fold higher in the mutant compared to AC. With the exception of *ggpps2* and *ziso*, all other genes were down-regulated in the mutant when compared to AC at BR stage.

At RR stage, majority of the genes were down-regulated in *Nps1* which include *dxs, dxr, hdr, idi, ggpps2, psy1, psy2, ziso, crtiso, lcyb1, lcyb2, lcye, zep,* and *crtrb2* except *nced1* where expression was similar in both AC and *Nps1*. The expression levels of *pds* (3 fold), *zds,* ($2x10^3$ fold), *cycb* (10 fold) and *chrc* (10 fold) were higher in *Nps1* than AC at RR stage.

Since *Nps1* harbors mutation in *phot1*, we also examined the transcript levels of *phototropin* genes. The transcript levels of *phot1* and *phot2* were higher in the mutant at MG stage than AC and decreased at RR stage. The transcripts of *phot1* and *phot2* were less abundant in all stages. *phot2* levels were very less in the mutant than AC: 300 fold less at BR stage and 14 fold less at RR stage. The expression levels of *phot1*were higher in the mutant (400 fold) at MG stage and decreased during ripening with 5 fold less expression than AC at RR stage (Fig. 6.7). Even though *Nps1* shows *phot1* transcript, the protein is not functional since the phototropism is absent in the mutant under blue light (Sharma et al., 2014).

6.3.8 Proteomic analysis using iTRAQ

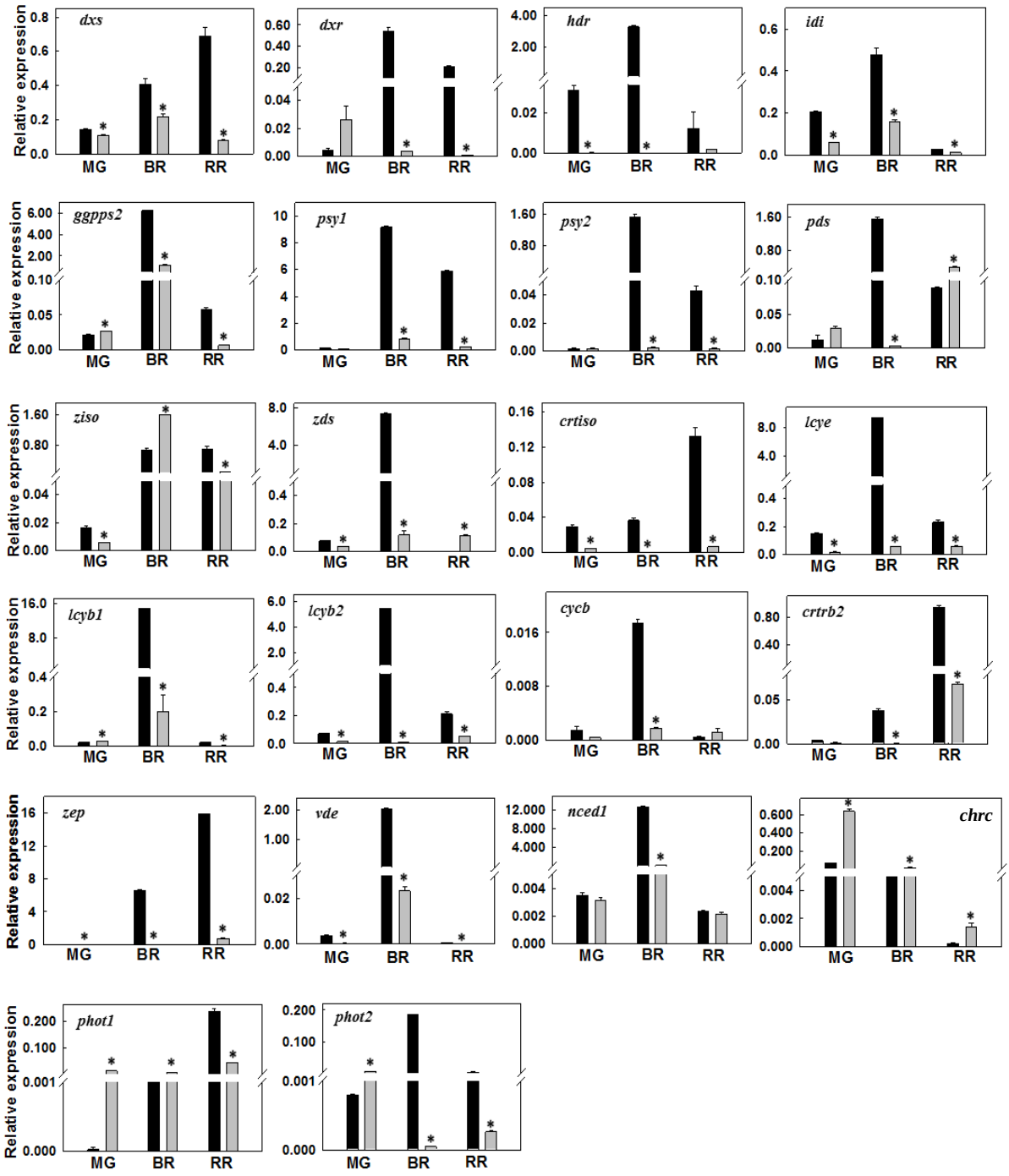


Figure 6.7. The expression profiles of genes involved in carotenoid biosynthesis pathway including their precursors and also for *phototropin1*, *phototropin2* genes were obtained by quantitative real time PCR. The transcript levels were normalized with two internal controls, *β-actin* and *ubiquitin*. Data are means ± SE (n = 3), * = P value ≤ 0.05.

To identify the proteins responsible for high carotenoid content and increased shelf life, an iTRAQ analysis was performed at three ripening stages in both *Nps1* and AC. A total of 2,952 proteins in AC and 2698 proteins in *Nps1* were detected after iTRAQ of which only around 1056 proteins in AC and 953 proteins in *Nps1* showed minimum of two peptide matches and unused prot score >1.3. 138 proteins ($p \leq 0.05$) showed differential expression in AC and 134 proteins ($p \leq 0.05$) in the mutant in any of the stages (BR, RR) throughout the development (Fig. 6.8A; Table 6.1). From these, 96 proteins were common in their identity between AC and the mutant whereas 42 proteins in AC and 38 proteins in *Nps1* were distinct (Fig. 6.8B). When individual stages were compared, in BR stage, 41 proteins were common between AC and the mutant, while 16 proteins in AC and 18 proteins in *Nps1* were differentially expressed (Fig. 6.8C). Similarly, in RR stage, 55 proteins were common between both genotypes and 26 proteins in AC and 20 proteins in *Nps1* were distinct (Fig. 6.8C).

The differentially expressed proteins were classified according to the FunCat scheme (Ruepp et al., 2006). All the proteins were categorized into 13 functional categories (Fig. 6.9). The functional category, C-compound and carbohydrate metabolism (42%) constituted the major category, followed by stress response (14%).

6.3.9 The abundance of cell wall associated proteins increased at RR stage in *Nps1* mutant

As *Nps1* fruits have long shelf life and accumulate more carotenoids, it was interesting to examine the proteins related to the above traits in the differentially expressed proteome data. Proteins related to carotenoid metabolism were not differentially expressed. However, few cell wall related proteins were differentially expressed which may affect fruit shelf life. Mannan-endo-1,4-β-mannosidase (β-MAN), α-mannosidase (α-MAN), polygalacturonase2A (PG2A) and pectinmethylesterase (PME) were the four proteins identified from cell wall modification/ripening related category. The reduced abundance and activity of the above cell wall metabolism related transcripts and enzymes except PME were directly correlated to enhanced shelf life in tomato fruits (Wang et al., 2009; Meli et al., 2010; Fischer and Bennett, 1991; Sitrit and Bennett, 1998; Gaffe et al., 1994; Phan et al., 2007). Of these, the protein abundances of α-MAN in both AC and *Nps1* at BR and RR were similar. The protein abundances of β-MAN were higher by 218 fold, PG2A-91 fold and PE-1.8 fold at RR stage compared to MG stage in *Nps1* mutant (Fig. 6.10). The protein abundances of β-MAN increased by 10 fold at BR stage

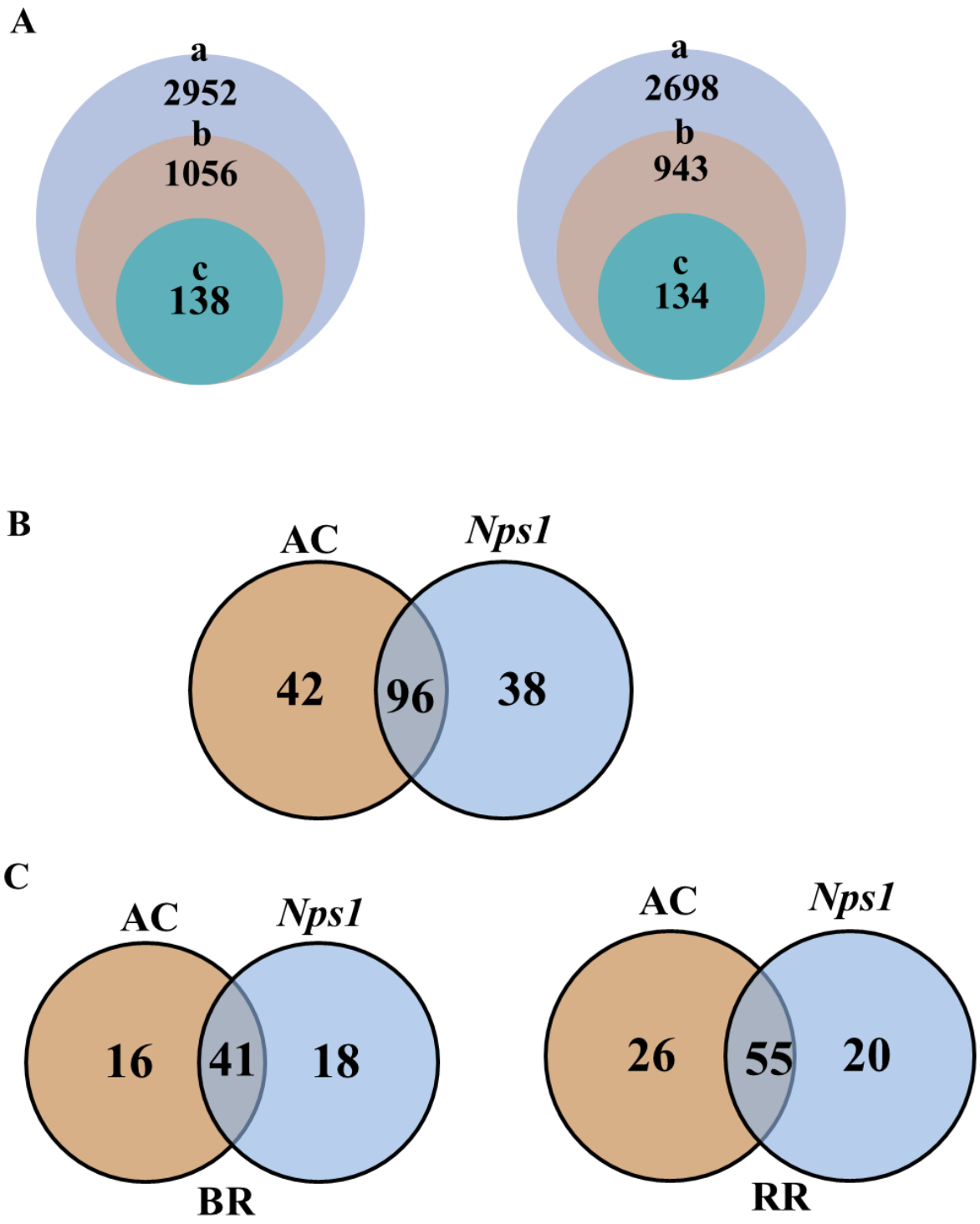


Figure 6.8. Number of proteins that are differentially expressed proteins across developmental stages in AC and *Nps1* obtained by iTRAQ analysis.
A, a. Total number of proteins identified in iTRAQ experiment b. Proteins after filtration, based on minimum peptide matches=2, unused protscore ≥1.3 c. Number of proteins that changed significantly across development in WT and in the mutant
B, Total number of differentially expressed proteins in WT and *Nps1*
C, Total number of differentially expressed proteins in WT and *Nps1* in BR and RR stages when compared to MG stage.

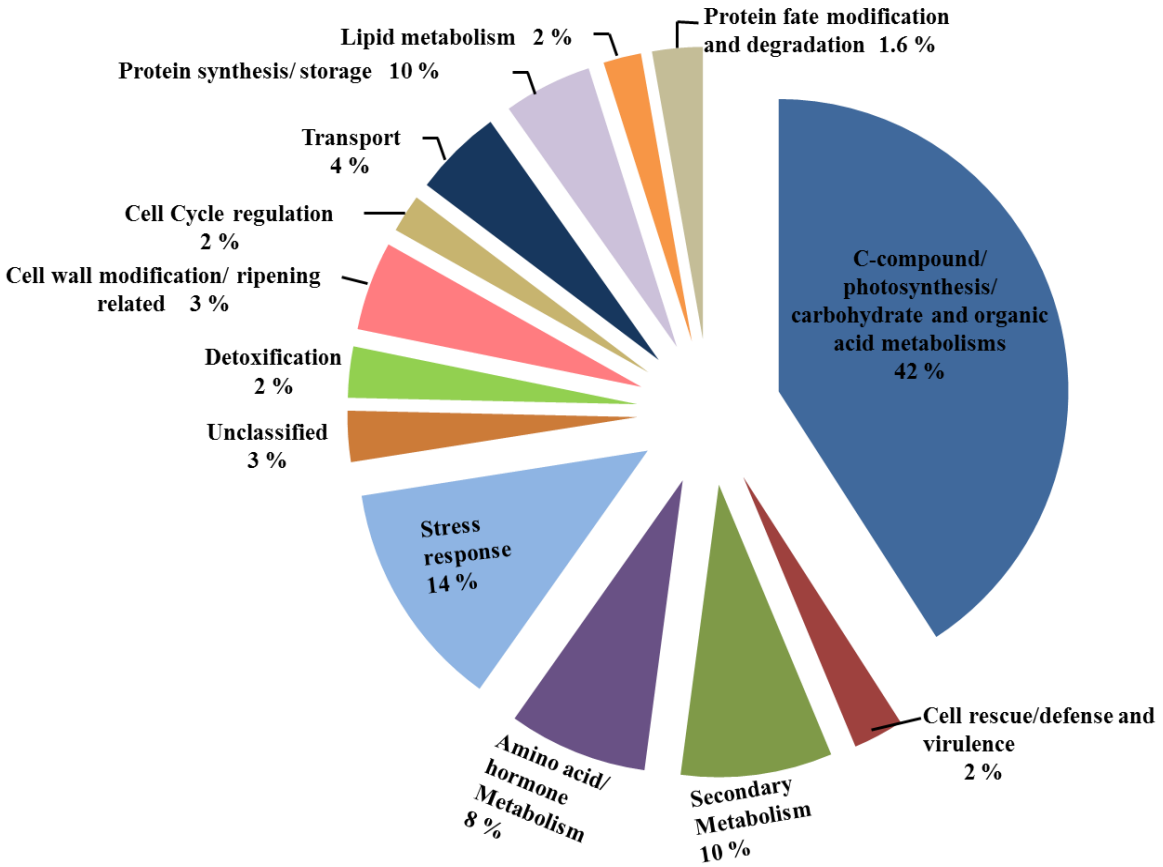


Figure 6.9. Functional classification of differentially expressed proteins in *Nps1* compared to AC according to FunCat scheme.

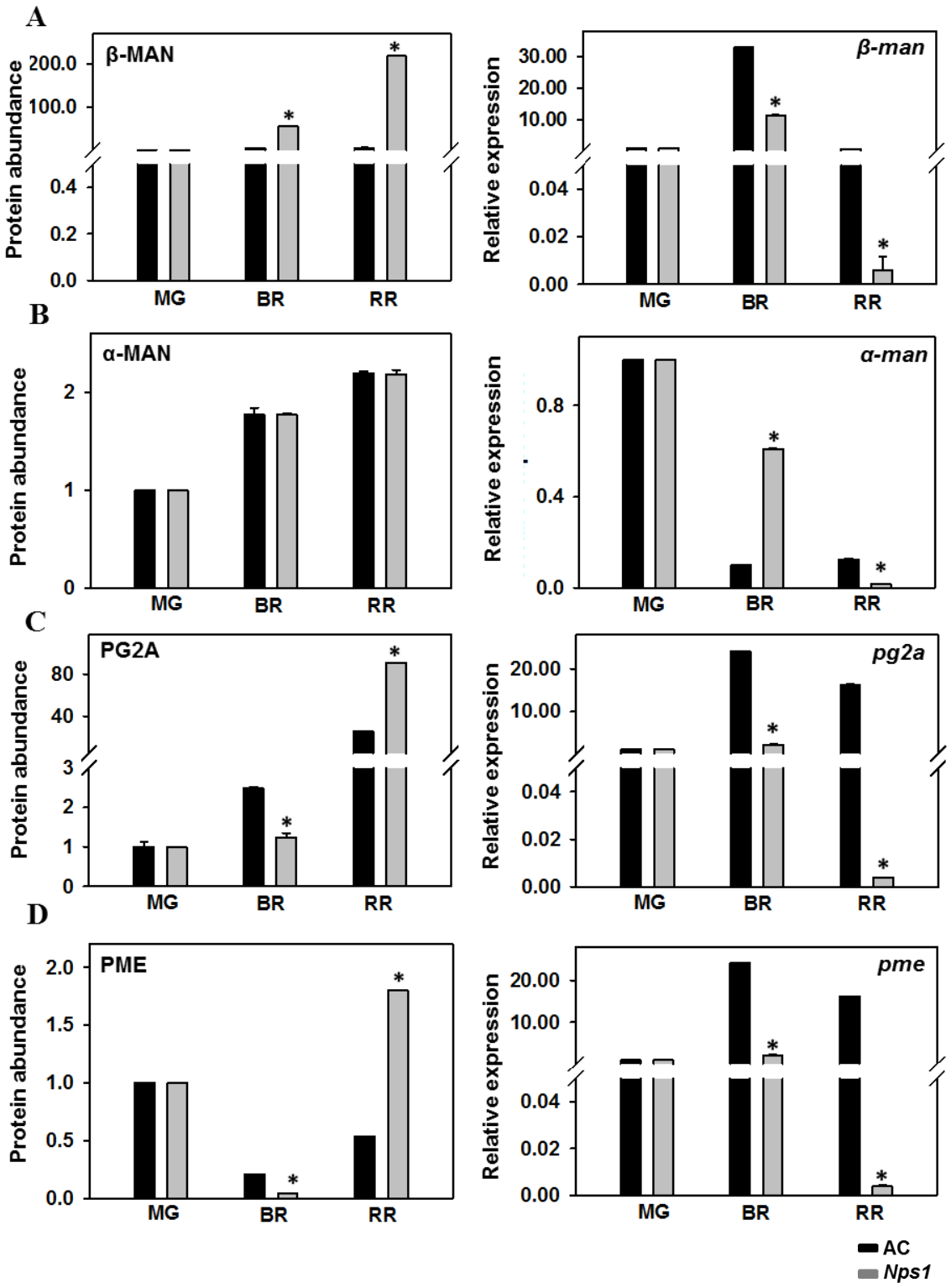


Figure 6.10. Protein and transcript profiles of cell wall modifying enzymes identified by iTRAQ analysis in *Nps1* mutant. A, Mannan endo 1,4 β-mannosidase (β-MAN) B, α-mannosidase (α-MAN) C, Polygalacturonase2A (PG2A) D, Pectinmethylesterase (PME). Data are means of $n = 3 \pm$ SE, * = P value ≤ 0.05.

and 35 fold at RR stage compared to AC while the abundances of α-MAN were similar to AC at both stages. In case of PG2A and PME, the protein abundances at BR stage decreased by 2 fold and 5 fold but increased to 3.6 fold and 3.4 fold respectively at RR stage compared to AC. The transcript levels of the above four genes were low in *Nps1* at RR stage suggesting posttranscriptional regulation of these genes in *Nps1* (Fig. 6.10). The increased accumulation of these cell wall related enzymes at RR stage in the *Nps1* mutant might be related to the enhanced shelf life.

6.3.10 Endo-β-mannosidase assay of *Nps1* fruits

Among the cell wall related proteins, the abundance of β-MAN was very high in *Nps1* than AC. Mannan endo 1, 4 β-mannosidase (β-MAN; endo-β-mannosidase**)** is a cell wall metabolism related enzyme, that cleaves endo 1,4 β-linkages in mannans, glucomannans and galactomannans (Wang et al, 2009). In our study we observed that the protein abundance of *β-man* increased during ripening, but the increase in the mutant was much higher than AC (Fig. 6.10A). In view of its importance in regulating cell wall metabolism, we also examined its enzyme activity in both AC and *Nps1*, to see whether any correlation exists between the abundance of β-MAN and shelf life of *Nps1*. The activity of β-MAN was not observed at MG stage in either AC or in *Nps1*. *Nps1* showed higher activity than AC at BR and RR stages when similar concentrations of protein were loaded into the gel. Based on this observation, a dose response enzyme assay was performed with increasing concentrations of protein from AC and decreasing concentrations of protein from *Nps1*. At BR stage, the clearance zone for 600 µg of protein concentration in AC was almost similar to 160 µg of protein concentration in *Nps1*; suggesting that the activity was 3.75 fold higher in the mutant (Fig. 6.11A). When the clearance zones at RR stage were examined, it was found that in AC at 32 µg protein concentration, the activity was equal to 62 ng protein in *Nps1* indicating the activity of β-MAN is 516 fold higher in *Nps1* than AC (Fig. 6.11B, C). Our results indicate that *Nps1* has high β-MAN enzyme activity than AC at both BR and RR stages.

6.3.11 Introgression of fruit carotenoid content and shelf life characteristics of *Nps1* into local cultivar, AV

In view of the importance of carotenoid rich foods in human health and the commercial value of enhanced postharvest shelf life of fruits, introgression of these traits into local cultivars is beneficial. To increase the commercial and nutritional value of local

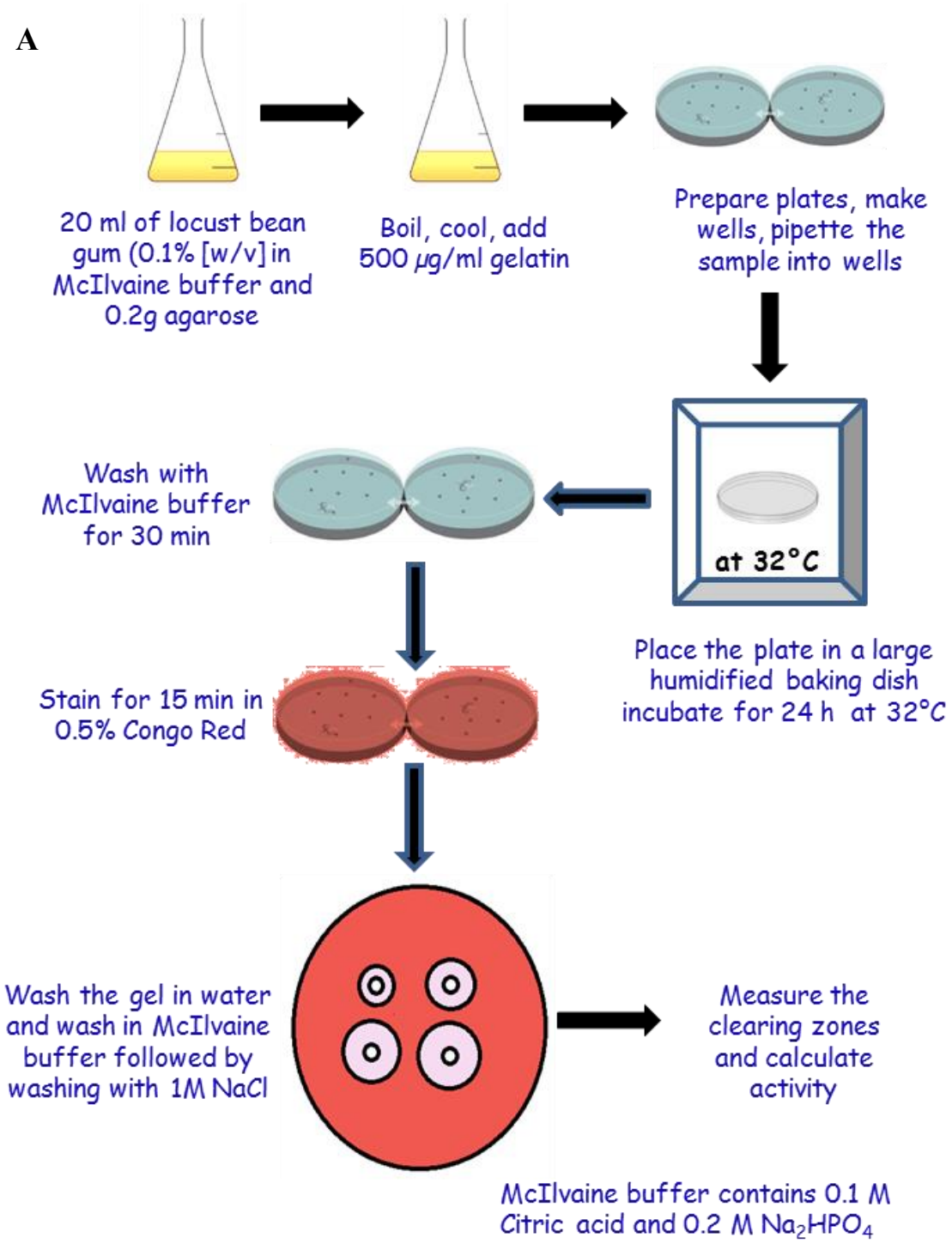


Figure 6.11. Endo-β-mannosidase (β-MAN) activity of fruit samples from AC and *Nps1* loaded onto locust bean gum (LBG) substrate gels. A, Gel diffusion assay protocol for measuring β-MAN activity in AC and *Nps1* fruits.

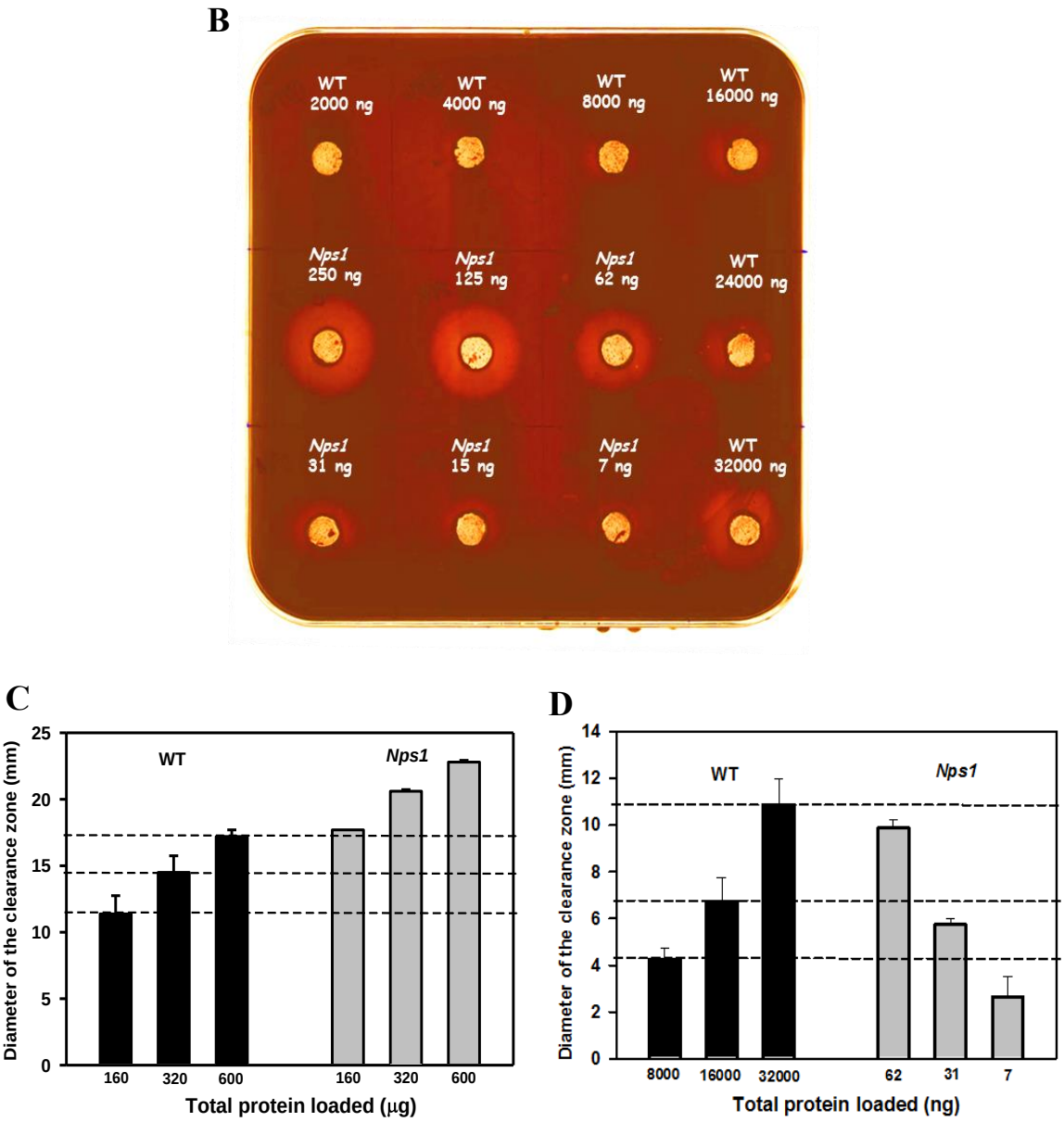


Figure 6.11. B, An assay gel with enzyme extract from AC and *Nps1* was loaded into LBG gels and clearance zones were visualized after staining with Congo Red. Activity of β-MAN in terms of clearance zone plotted against total protein loaded for assaying enzyme activity at C, BR stage and D, RR stage.

cultivar, Arka Vikas, AV, crosses were made between *Nps1* and AV and the generated F_1 and F_2 lines were screened for the above traits. In addition to introgression into AV, the F_1 and F_2 lines were also generated for original mutant background, AC after crossing *Nps1* and AC. The corresponding F_1 and F_2 lines were also screened for their carotenoid content and shelf life.

6.3.12 Confirmation of F_1 lines of AC♀x*Nps1*♂ and AV♀x*Nps1*♂ crosses

As *Nps1* lacks phototropism in response to blue light, this can be used to screen the population obtained from F_1 and F_2 crosses between *Nps1* and AC, AV. During blue light screening, all the F_1 seedlings (both AC♀x*Nps1*♂ and AV♀x*Nps1*♂ crosses) showed partial bending indicating that one copy of the PHOT1 protein is not enough to carry out the gene function (Fig. 6.12A, 6.13A). In addition to phenotype screening, i.e. phototropism, F_1 lines from AV♀x*Nps1*♂ and AC♀x*Nps1*♂ cross were screened genotypically for the presence of mutation in *phot1*. Since F_1 is heterozygous, it can be expected that they carry mutation in *phot1* which was transferred from *Nps1*. The extracted DNA from F_1 seedlings was amplified using *phot1* primers, PCR product was digested with CEL I and the product was run on 1.2 % agarose gel. As expected, all the F_1 lines consisted of the mutation. This was verified by the presence of two digested products (700 bp and 200 bp) on the gel as CEL I cleaves at the site of mismatch in *phot1* gene (Fig. 6.12B, 6.13B).

6.3.13 Confirmation of F_2 lines

The F_2 lines from both AC and AV crosses segregated for their phototropic trait under unilateral blue light. In case of AC♀x*Nps1* cross, out of 162 F_2 seedlings screened, 124 were non-phototropic (111 showed non-bending phenotype and 13 showed partial bending) and 38 were phototropic (Fig. 6.14A); also segregating in Mendelian ratio of 3:1 (non-phototropic:phototropic) ($\chi^2(1, N=162)=0.206$, $p<0.05$). Similarly, in AV♀x*Nps1*♂ cross, out of 182 F_2 seedlings screened under blue light, 136 seedlings were non-phototropic (121 were non-bending and 15 showed partial bending) and 46 seedlings were phototropic (Fig. 6.15A) segregating in 3:1 (non-phototropic:phototropic) Mendelian monogenic phenotypic ratio ($\chi^2(1, N=182)=0.007$, $p<0.05$).

F_2 lines from AV♀x*Nps1*♂ and AC♀x*Nps1*♂ cross were also screened for the presence of mutation in *phot1*. Genotypic segregation in the F_2 population was analyzed after screening all the plants for the presence or absence of mutation in *phot1*. The

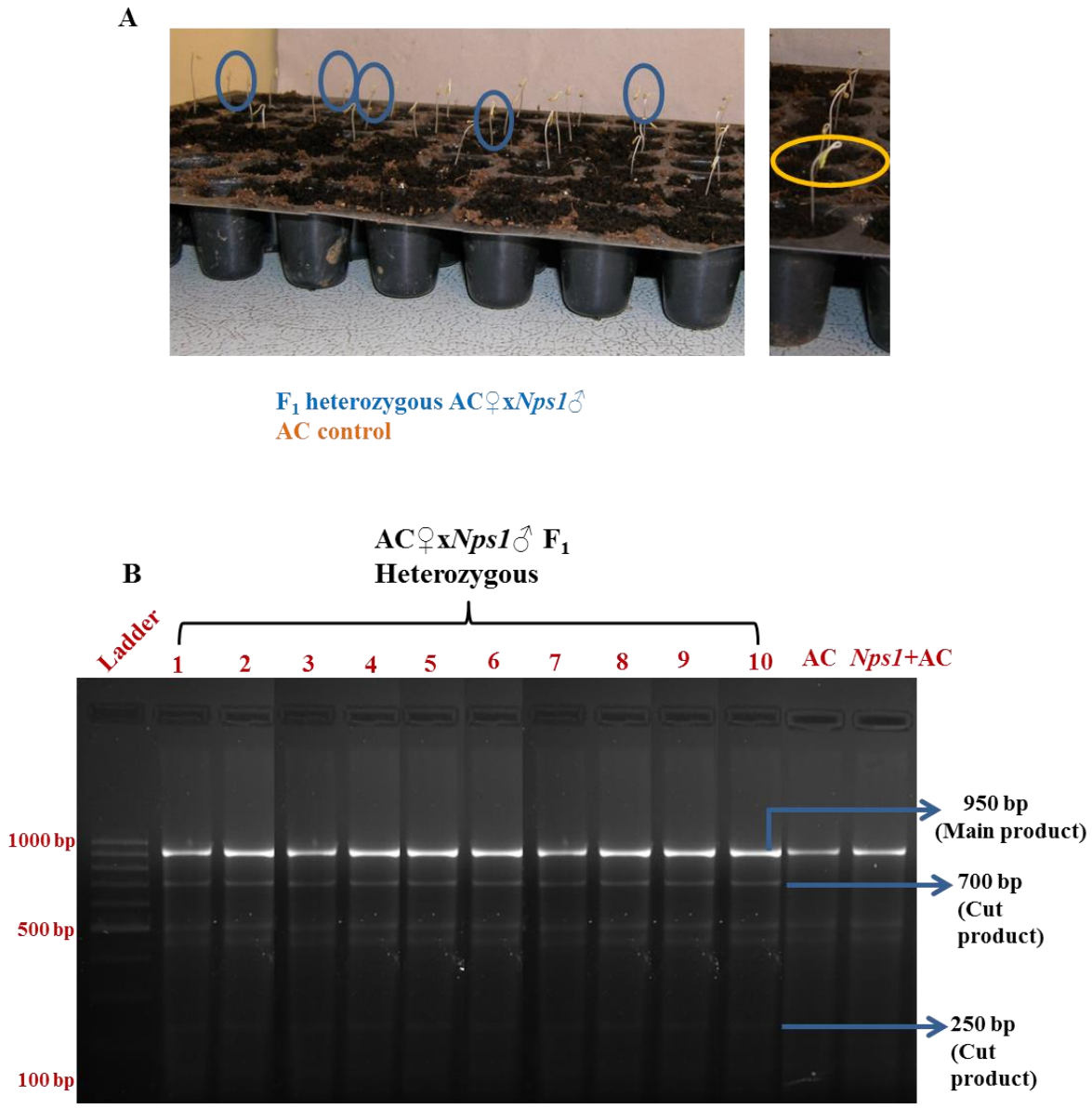


Figure 6.12. A, Blue light screening of F_1 plants obtained from AC♀x*Nps1*♂ cross B, Confirmation of F_1 through CEL-1 digestion. Lanes 1, 3, 5, 7 and 9 are loaded with homoduplex of *Nps1*; and 2, 4, 6, 8 and 10 are loaded with heteroduplex (*Nps1*+AC).

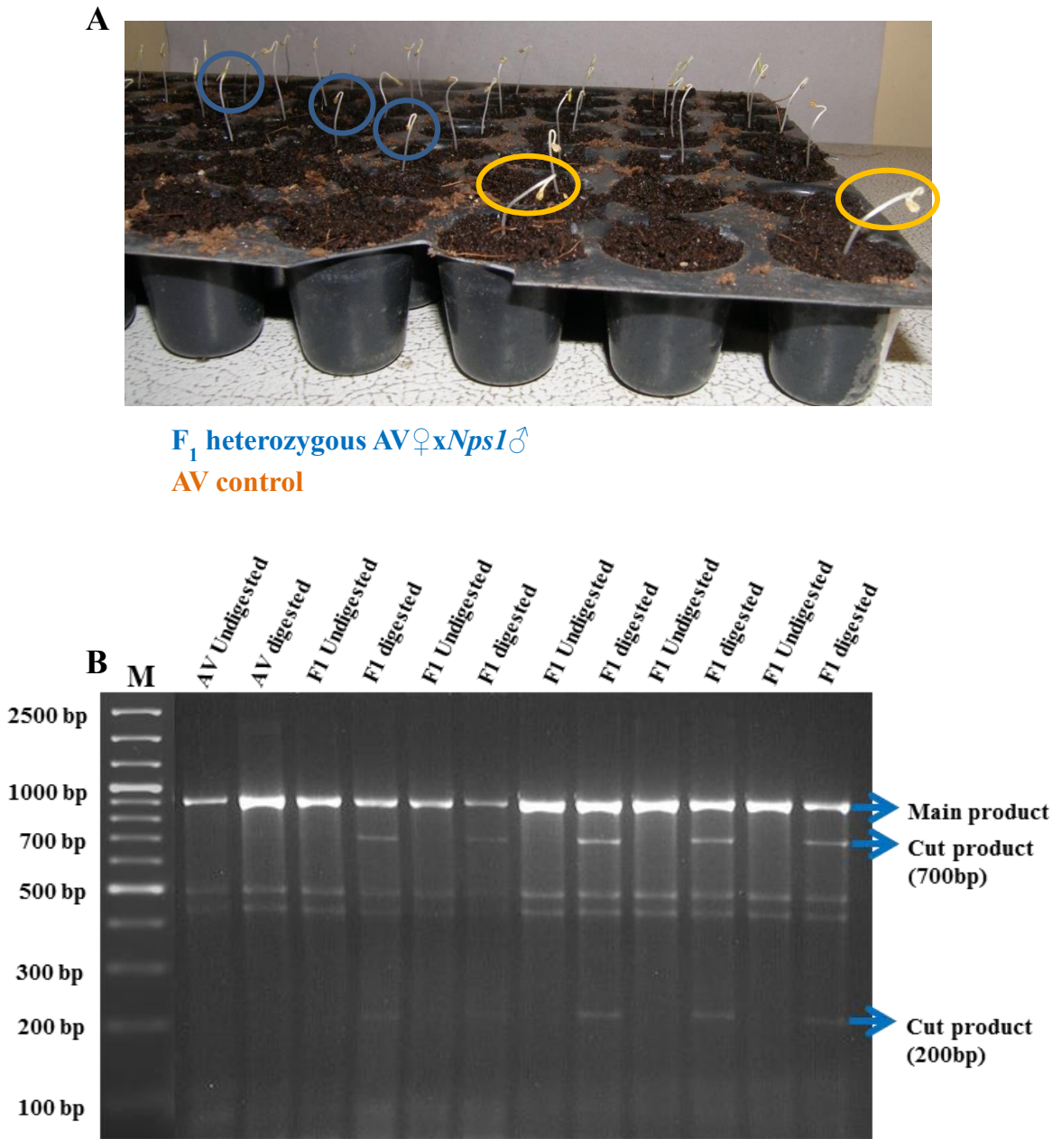


Figure 6.13. A, Blue light screening of F_1 plants obtained from AV♀x*Nps1*♂ cross B, Confirmation of F_1 using CEL-1 digestion, F_1 DNA was digested or undigested with CEL-1 and loaded on gel to visualize the cut products.

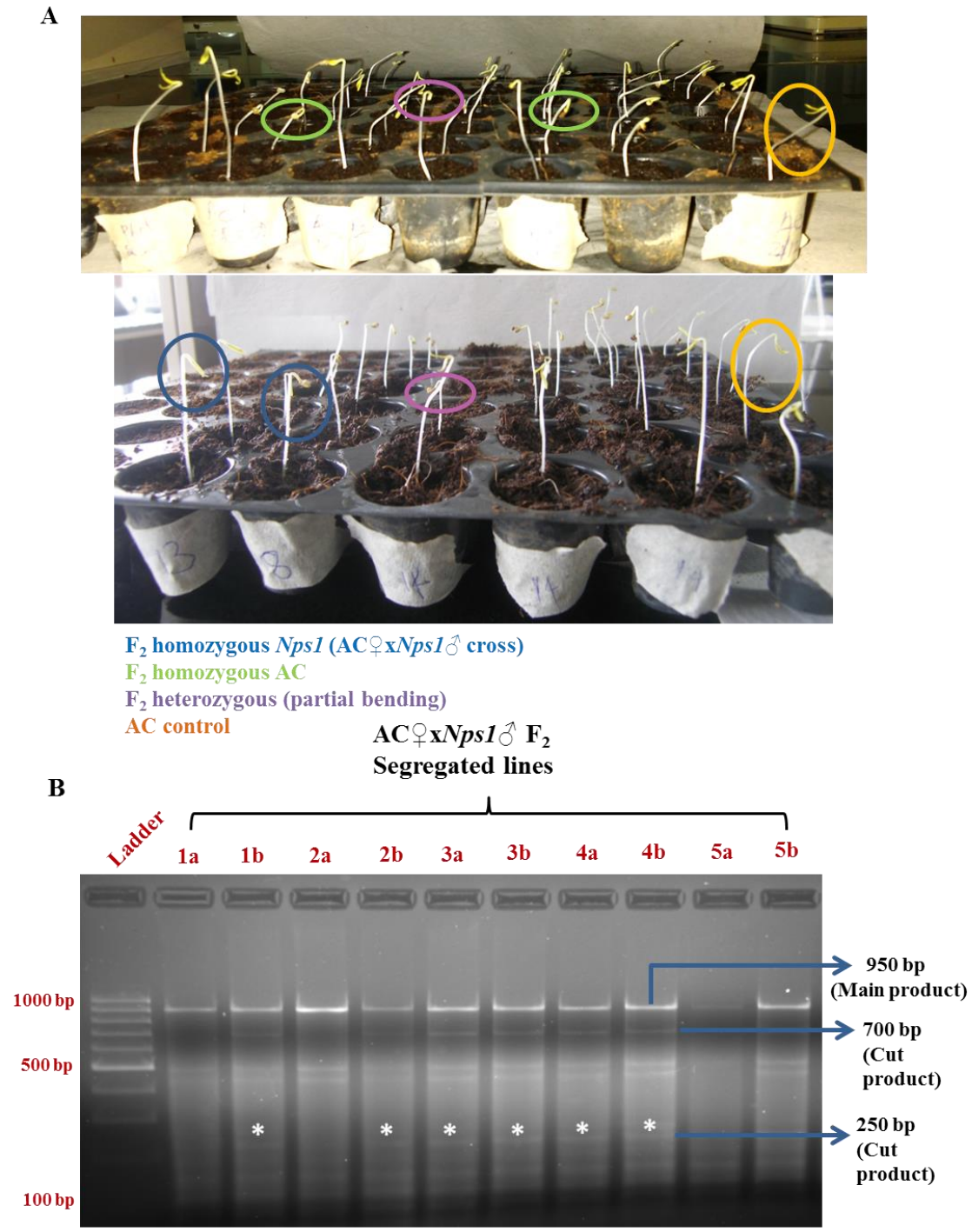


Figure 6.14. A, Blue light screening of F_2 segregated population. B, Cel-1 assay to identify and confirm segregation in F_2 population obtained from AC♀x*Nps1*♂ cross. DNA from F_2 lines was digested either in homoduplex or heteroduplex (mixed with AC DNA) and digested with Cel-I. The digested products were loaded on gel along with undigested controls, run on 1.2% agarose gel and cut products were analyzed. Lanes 1a, 2a, 3a, 4a and 5a are loaded with homoduplex *Nps1*; and lanes 1b, 2b, 3b, 4b and 5b are loaded with heteroduplex *Nps1* (*Nps1*+AC). Note that F_2 lines 1, 2 and 5 are homozygous *Nps1* and lines 3 and 4 are heterozygous *Nps1*. * indicates digested products obtained after Cel-I digestion.

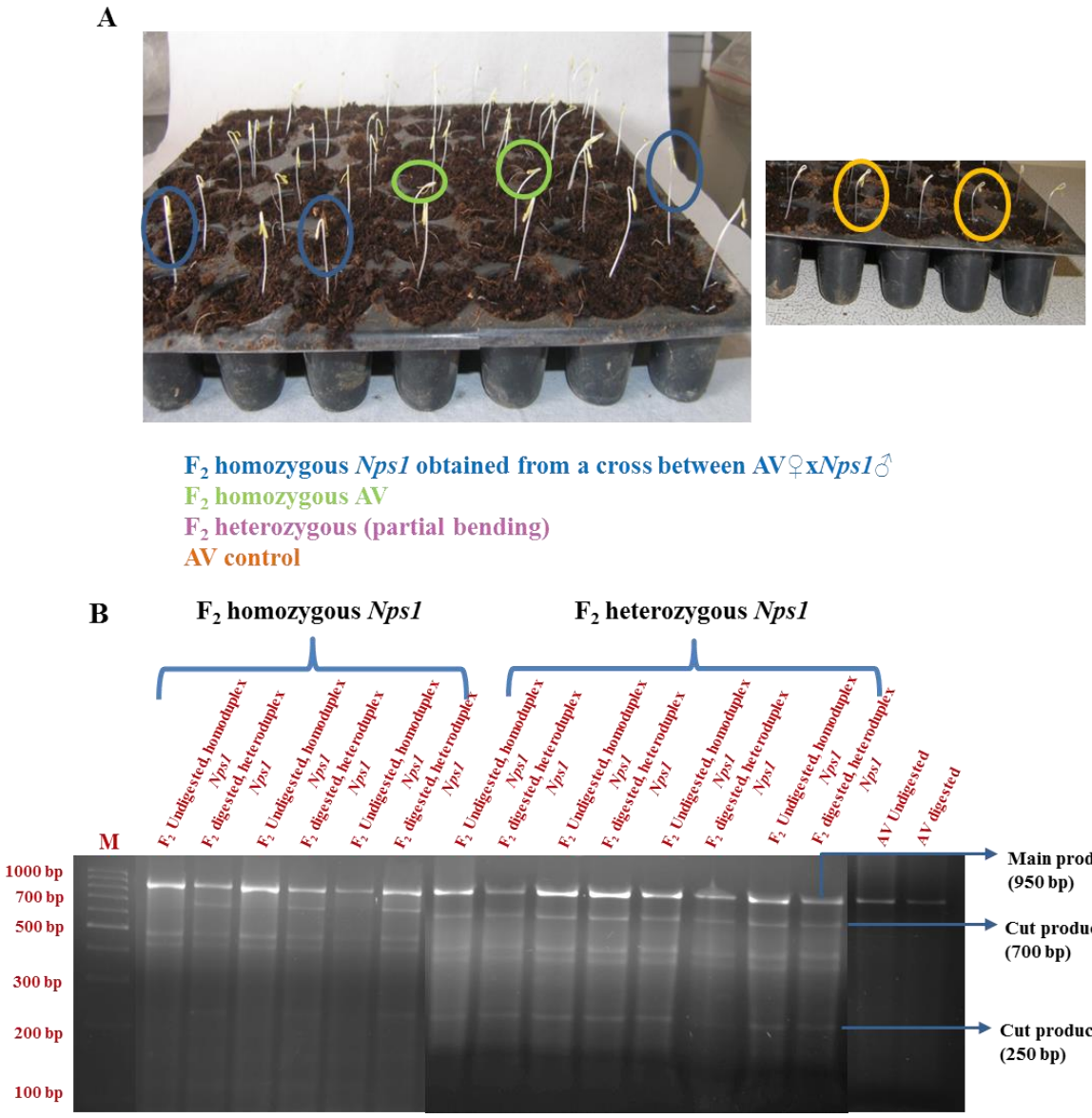


Figure 6.15. A, Blue light screening of F_2 plants. F_2 plants from AV♀x*Nps1*♂ cross were screened for their phototropism along with AV as control. AV shows phototropic bending under unilateral blue light. B, Cel-I assay to identify and confirm segregation in F_2 population obtained from AV♀x*Nps1*♂. DNA from F_2 lines were amplified with *phot1* primers and digested with Cel-I either in homoduplex or heteroduplex (mixed with AV) condition. The digested products were loaded on gel along with undigested controls, run on 1.2% agarose gel and digested products were analyzed.

extracted DNA was amplified with *phot1* primers and the PCR product was digested with CEL I and run on 1.2% agarose gel. Based on the presence of *phot1* mutation as indicated by the presence of digested products on the gel, in AC♀X*Nps1*♂ cross, 52% of the F_2 population was heterozygous for the *phot1* mutation, 26% was homozygous for the mutation whereas 22% of the plants did not contain mutation and segregated as wildtype (Fig. 6.14B). In AC♀x*Nps1*♂ cross, both the phenotype and genotype segregated in 1:2:1 (homozygous mutant: heterozygous: homozygous wildtype) Mendelian ratio.

In AV♀x*Nps1*♂ cross, 43.7% of the F_2 population mutation was homozygous for the *phot1* mutation and 28.7% of the plants possessed *phot1* mutation in heterozygous condition (Fig. 6.15B). In 27.5% of the plants, which are the segregated WT, did not have mutation in *phot1*. However, in AV♀x*Nps1*♂ F_2 segregated population, unlike the phenotypic segregation, genotypic segregation did not follow the Mendelian ratio. This may be due to incomplete introgression of *phot1* mutation into AV.

6.3.14 F_1 and F_2 homozygous *Nps1* fruits accumulate carotenoids and carotenoid precursors

Consistent with the dominant nature of *Nps1* mutant (Sharma et al., 2014), the F_1 fruits exhibited high carotenoid content like parent. The carotenoid levels were also enhanced in F_2 homozygous fruits. The carotenoid content in F_1 and F_2 fruits at RR stage was measured and compared with AC and *Nps1*. A total of ten carotenoids were detected in AC, *Nps1*, F_1 and F_2 (Fig. 6.16). The amounts of carotenoid precursors upstream of lycopene were higher in *Nps1*, F_1 and F_2 fruits than in AC fruits. Phytoene was 3.6 fold high in *Nps1*; 4.9 fold high in F_1; 2.9 fold high in F_2 and phytofluene was 5.2 fold high in *Nps1*; 7.9 fold high in F_1; 3.2 fold high in F_2 fruits compared to AC fruits. Phytofluene gets converted to ζ-carotene through the action of (phytoene desaturase) PDS. ζ-carotene was 1.3 fold high in *Nps1*; 2.5 fold high in F_1; 2 fold high in F_2 fruits. Neurosporene was present only in F_1 and F_2 and not detected in AC and *Nps1*. Lycopene, the major carotenoid in tomato fruits, increased in F_1 and F_2 fruits, it was 3.1 fold high in *Nps1*, 3.4 fold high in F_1; 3.2 fold high in F_2. β-carotene, the cyclization product of lycopene and precursor for vitamin A was 1.3 fold high in *Nps1*; 1.3 fold high in F_1; 1.9 fold high in F_2. β-cryptoxanthin, an oxygenated degradation product of β-carotene was 1.9 fold high in *Nps1*; 2.2 fold high in F_2 but decreased by 1.3 fold in F_1. The levels of δ-carotene, a precursor for lutein, was 1.8 fold high in *Nps1*; 1.7 fold high in F_1 but present in similar levels in F_2 compared to AC. While the level of α-carotene was not significantly different

in *Nps1* and F_2 than AC, it was 2 fold high in F_1. However, the amount of lutein was drastically low in F_1 (24 fold), F_2 (3.7 fold) and in *Nps1* (4.9 fold) compared to AC.

The carotenoid content in F_1 and F_2 homozygous *Nps1* fruits at RR stage was measured and compared with AV and *Nps1*. A total of ten carotenoids were detected among which eight were detected in AV, *Nps1*, F_1 and F_2 (Fig. 6.17). The levels of precursors of the carotenoids, phytoene and phytofluene increased in both F_1 and F_2 than parents. Phytoene was 4 fold high in F_1; 1.8 fold high in F_2; 3.4 fold high in *Nps1* and phytofluene was 3 fold high in F_1; 2.3 fold high in *Nps1* but 2.3 fold low in F_2 compared to AV. ζ-carotene, produced through the activity of PDS was high in F_1 (1.4 fold); decreased by 1.3 fold in F_2; but no significant difference was found in case of *Nps1*. Neurosporene was present only in F_1 and F_2 but not detected in AV and *Nps1*. Lycopene, the major pigment in tomato fruits, was enhanced by 4 fold in F_1; 3.8 fold in F_2 and 3.2 fold in *Nps1*. β-carotene, which is a direct precursor of vitamin A was not significantly high in F_1 whereas it was increased by 2.5 fold in *Nps1* and 3.7 fold in F_2. β-cryptoxanthin, a xanthophyll produced by oxygenation of β-carotene catalyzed by lycopene-β-cyclase was 1.6 fold high in *Nps1* but present in almost similar concentrations in F_1 and not detected in F_2. In αβ branch, δ-carotene was not detected in AV and it was present at significantly high levels in F_2 than *Nps1* and F_1. Despite no significant differences in α-carotene, lutein which is the end product of this branch was 2.7 fold high in *Nps1*; 9.7 fold high in F_2 and F_1 has similar concentration of the lutein as in AV.

6.3.15 Off-vine fruit senescence study in F_1 and F_2 RR fruits obtained from AC♀x*Nps1*♂ cross

The RR fruits of F_1 were incubated at 25°C under natural conditions and continuously monitored for appearance of wrinkles which are the symptoms for the onset of senescence. Under these conditions, F_1 fruits showed less shelf life compared to *Nps1*. While the F_1 fruits started wrinkling on 10^{th} day (Fig. 6.18), the fruits of AC started senescence on 7^{th} day and *Nps1* did not show any signs of senescence during this period. On 14^{th} day, both AC and F_1 fruits showed complete wrinkling all over the fruit surface whereas *Nps1* fruits were still fresh. These results indicate that F_1 fruit has no shelf life compared to its parent, *Nps1* fruit.

In a similar way, RR fruits of F_2 homozygous *Nps1*, F_2 heterozygous *Nps1* and F_2 homozygous segregated wildtype (AC) were incubated at 25°C under natural light

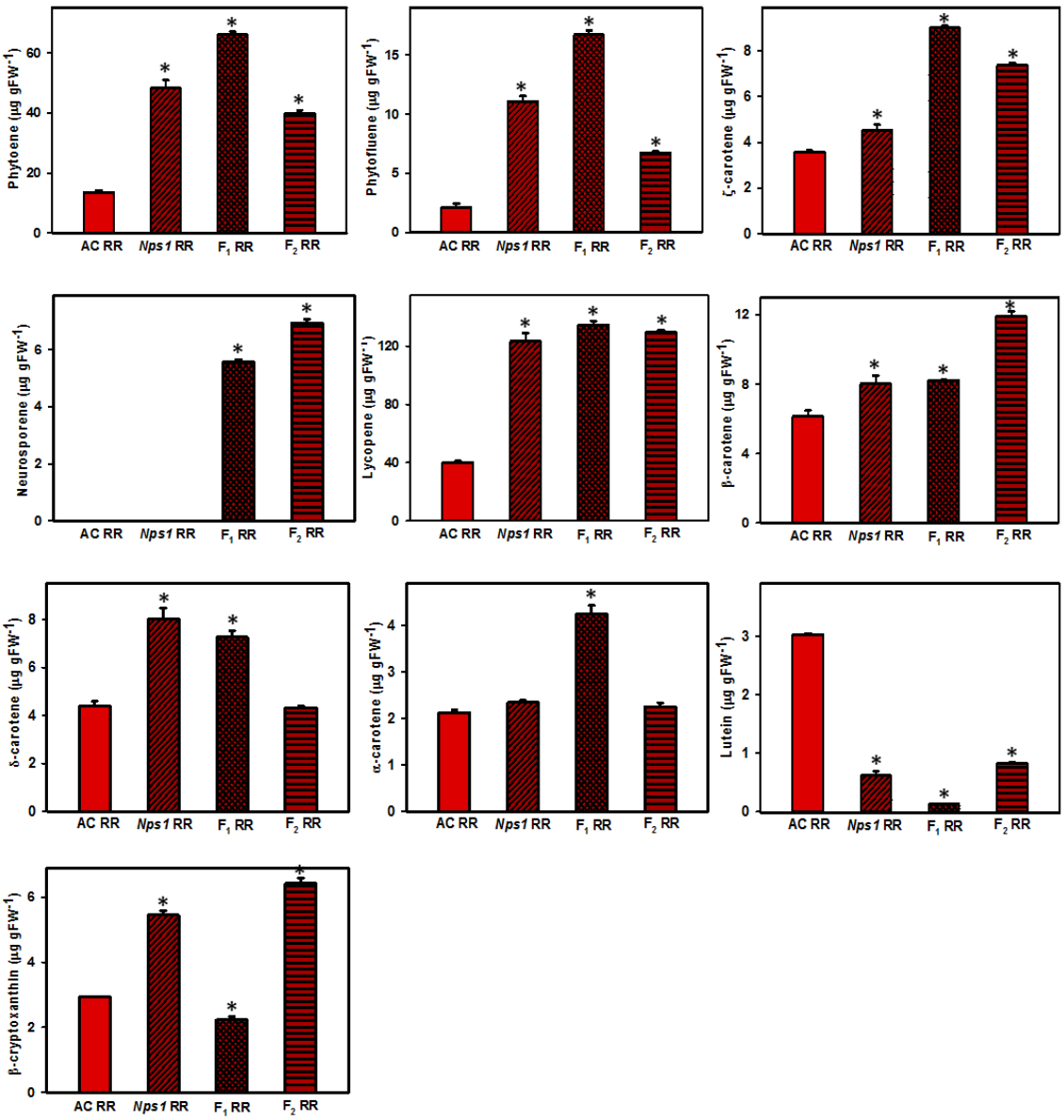


Figure 6.16. Carotenoid profiling in AC, *Nps1*, F_1 (AC♀x*Nps1*♂) and F_2 homozygous *Nps1* fruits at RR stage. Data are means ± SE ($n \geq 3$),* = P value ≤ 0.05.

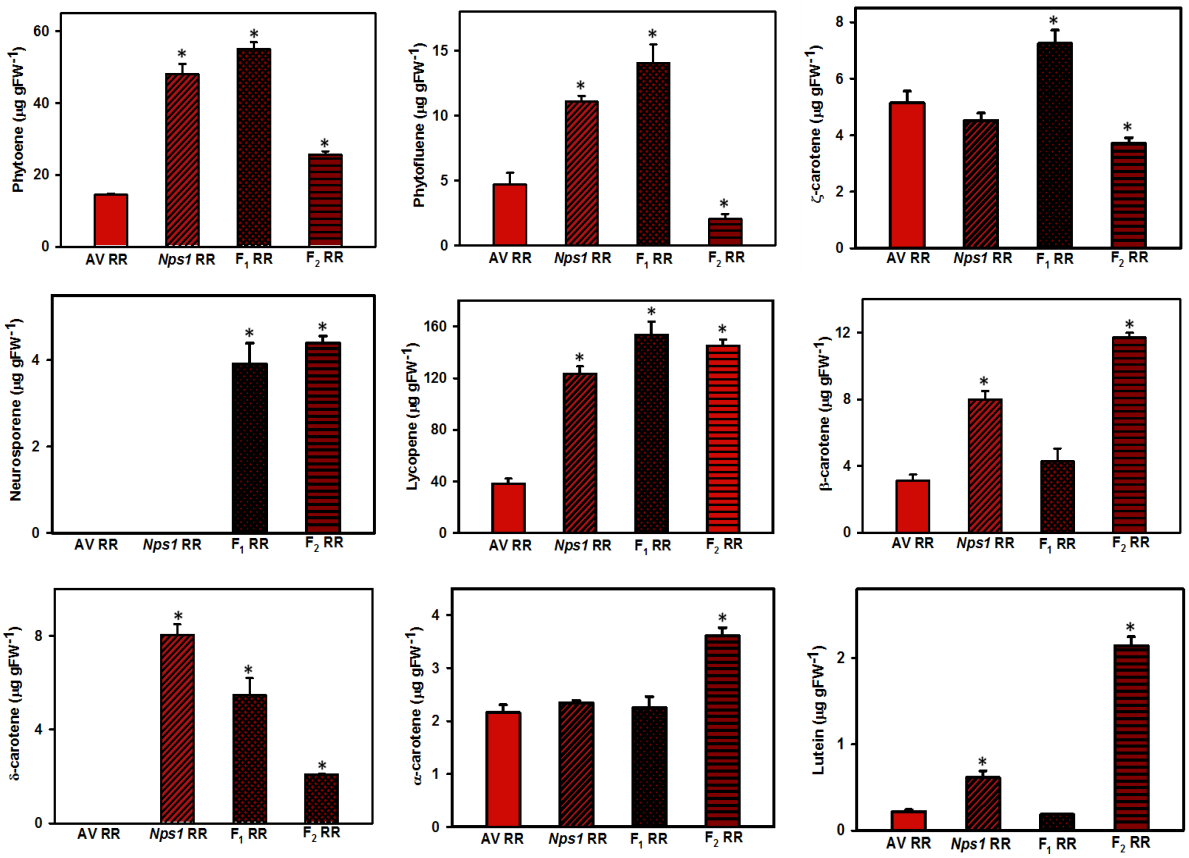


Figure 6.17. Carotenoid profiling in AV, *Nps1*, F_1 (AV♀x*Nps1*♂ cross) and F_2 homozygous *Nps1* fruits at RR stage. Data are means ± SE ($n \geq 3$), * = P value ≤ 0.05.

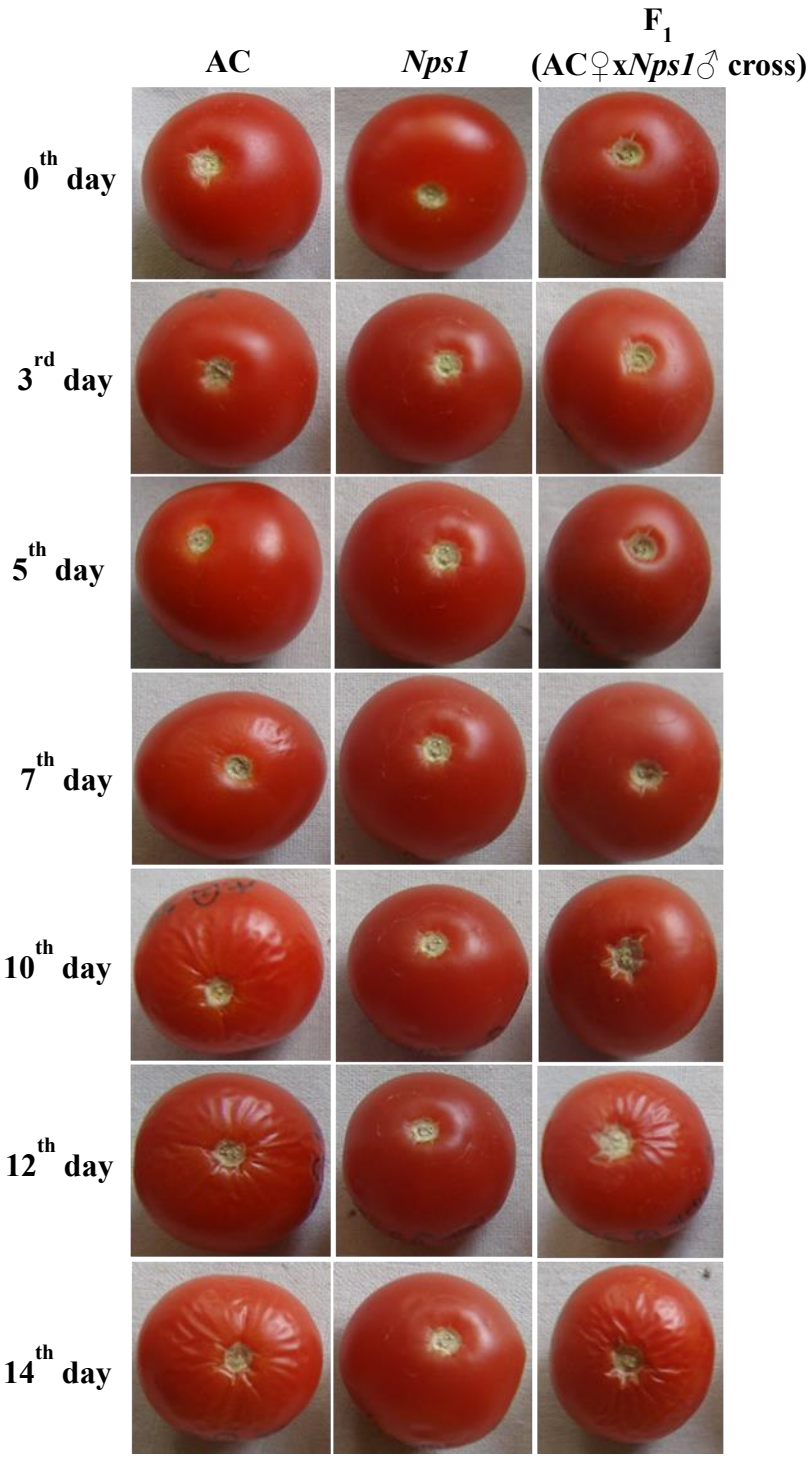


Figure 6.18. Off-vine senescence study in F_1 fruits (obtained from AC♀x*Nps1*♂ cross) harvested at RR stage and incubated at 25°C under natural light conditions (number of replicates, $n \geq 5$). The fruits were photographed on different days indicated left to the photo panels.

conditions to observe off-vine/post-harvest shelf life. While the F_2 homozygous *Nps1* fruits started wrinkling on 6th day, the fruits of AC started senescence on 4th day (Fig. 6.19) and *Nps1* did not show any signs of senescence during this period. On 12th day, F_2 homozygous fruits showed complete wrinkling whereas AC showed complete wrinkling on 10th day. The fruits of segregated wildtype started senescence on 2nd day and they were completely spoiled by 4th day. However, the fruits of heterozygous *Nps1* lines showed interesting phenotypes. All the heterozygous lines except two plants showed off-vine senescence ranging from two to ten days. The RR fruits of these two lines showed postharvest shelf life of 24 (F_2 24) and 36 days (F_2 36) respectively (Fig. 6.20). In RR fruits of F_2 24, the senescence started on 25th day and fruit was completely spoiled on 34th day whereas in RR fruits of F_2 36, the senescence started on 37th day and the fruit was completely spoiled on 40th day (Fig. 6.20).

6.3.16 Off-vine senescence study in RR fruits of F_1 and F_2 obtained from AV♀x*Nps1*♂ cross

Fruits of AV, *Nps1*, F_1, F_2 homozygous *Nps1*, F_2 heterozygous *Nps1* and F_2 segregated WT at red ripe stage were incubated at 25°C under natural light conditions to observe off-vine shelf life. Under these conditions, the senescence was faster in F_1 compared to AV, *Nps1* and F_2 fruits. While the F_1 fruits started wrinkling on 6th day, the fruits of F_2 homozygous *Nps1* started wrinkling on 12th day; F_2 heterozygous *Nps1* fruits on 15th day and the fruits of AV started senescence on 8th day (Fig. 6.21, 6.22) and *Nps1* did not show any signs of senescence during this period. The fruits of segregated homozygous AV started wrinkling on 8th day same as AV. By 15th day, AV, F_1 and F_2 fruits showed complete wrinkling all over the fruit surface whereas *Nps1* fruits were still fresh. F_2 heterozygous *Nps1* fruits spoiled completely on 18th day whereas F_2 homozygous WT completely senesced by 15th day similar to AV. Based on these results it appears that F_1 fruit has no shelf life compared to its parent, *Nps1*. The RR fruits of F_2 homozygous *Nps1* and F_2 heterozygous *Nps1* have intermediary shelf life less than that of its parent, *Nps1* fruits.

6.3.18 "MutMap" or "mapping by sequencing" approach for identification of the candidate gene responsible for long shelf life of *Nps1* fruits

With the advent of NGS technologies for sequencing of whole genomes and the decreasing costs for whole genome sequencing, it is becoming increasing popular to

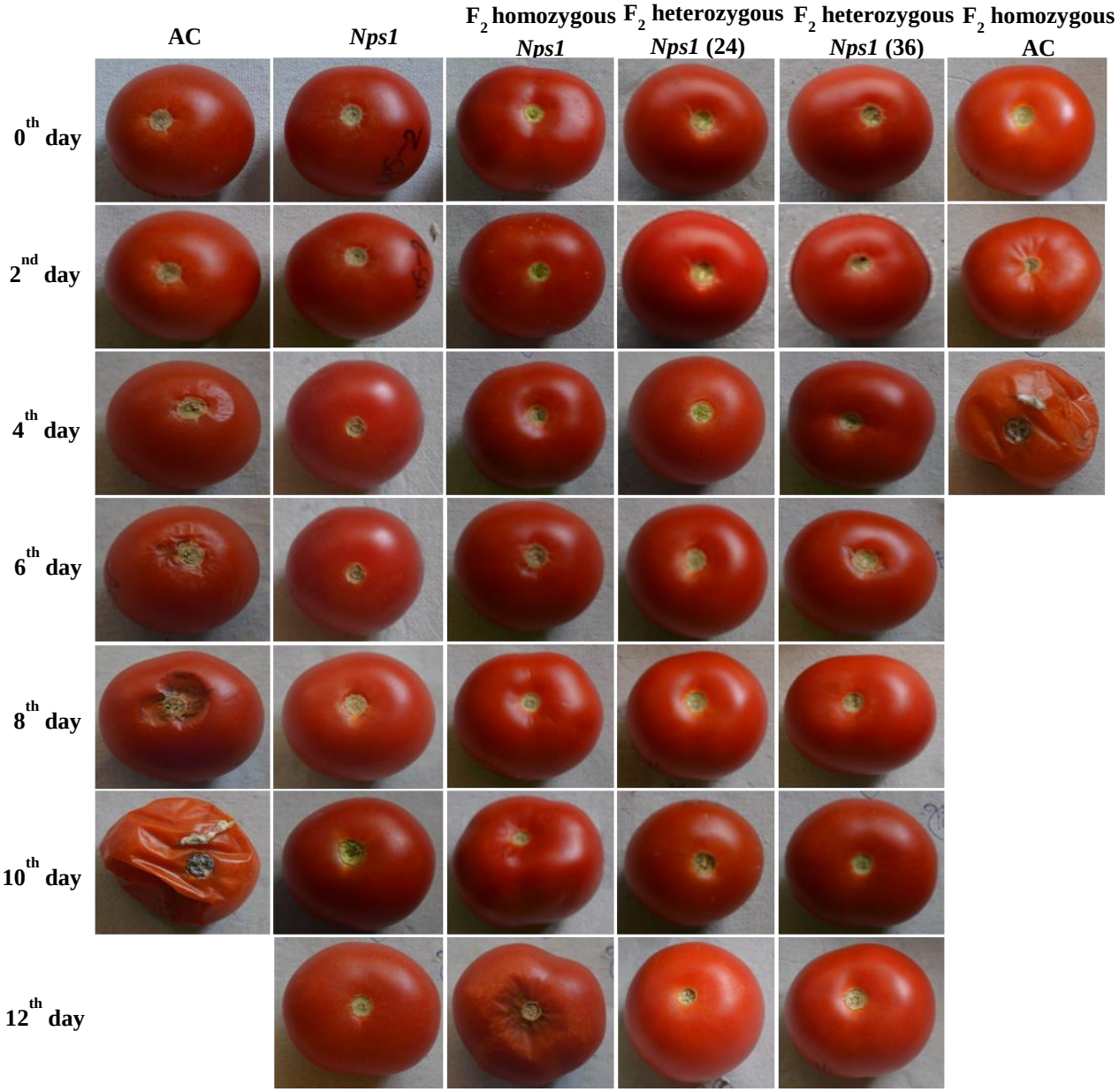


Figure 6.19. Off-vine senescence study in F_2 fruits (obtained from AC♀x*Nps1*♂ cross) harvested at RR stage and incubated at 25°C under natural light conditions (number of replicates, $n \geq 5$). F_2 24- high shelf life line with RR fruit started senescence on 25th day; F_2 36- high shelf life line with RR fruit started senescence on 37th day. The fruits were photographed on different days indicated left to the photo panels.

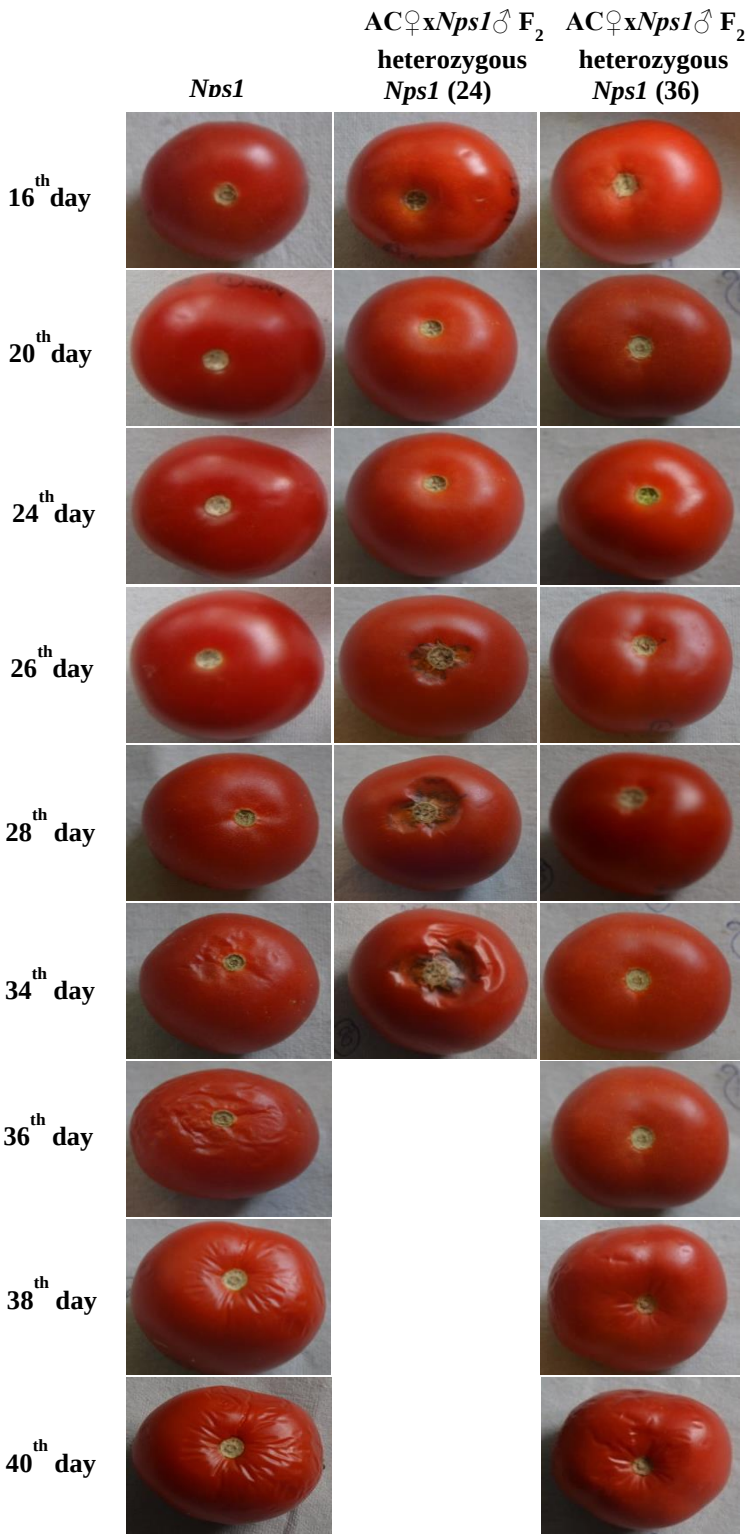


Figure 6.20. Off-vine senescence study in F_2 fruits (obtained from AC♀x*Nps1*♂ cross) harvested at RR stage and incubated at 25°C under natural light conditions (number of replicates, $n \geq 5$). Two F_2 lines with high shelf life (24 days and 36 days) were identified from segregating population. The fruits were photographed on different days indicated left to the photo panels.

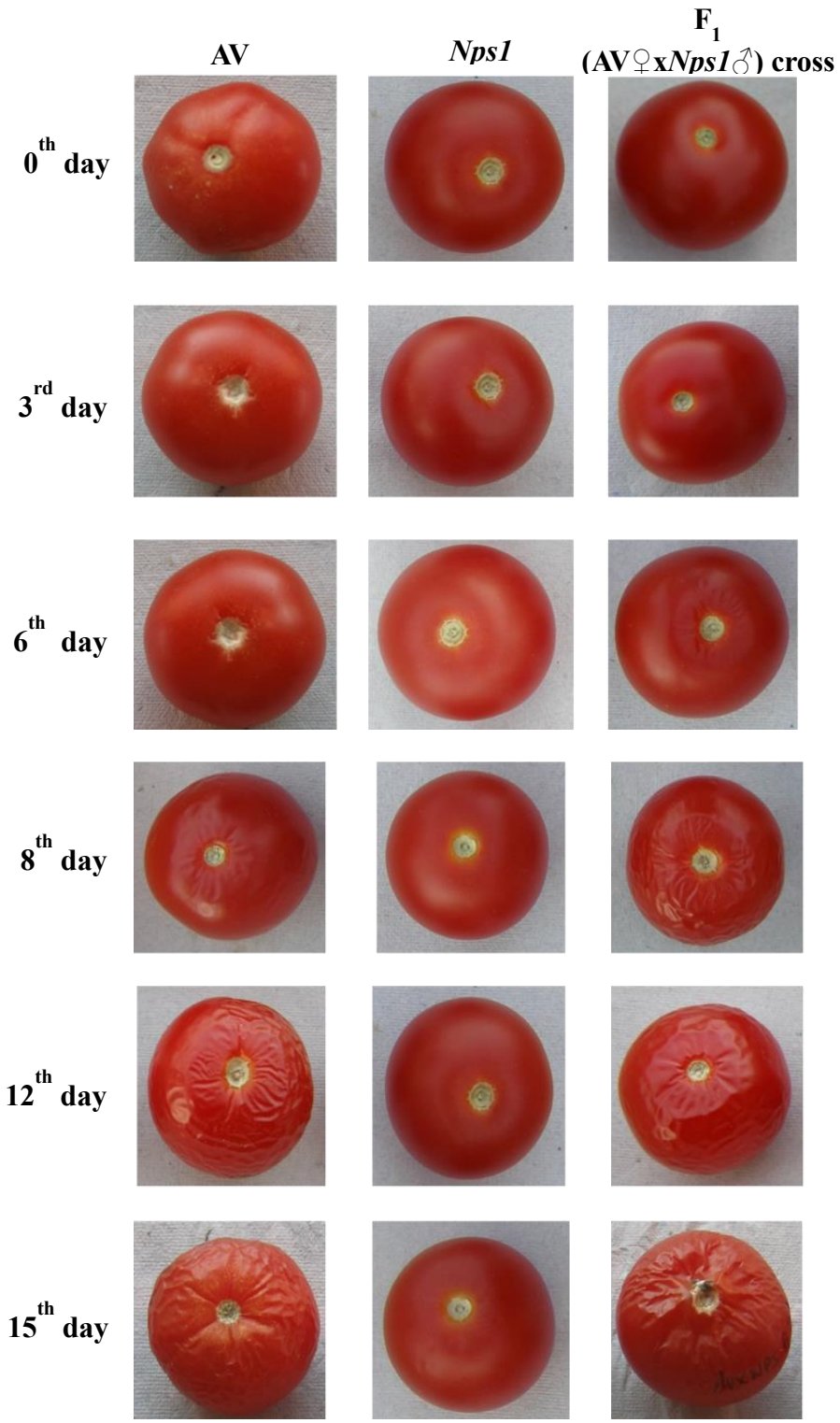


Figure 6.21. Off-vine senescence study in F_1 fruits (AV♀x*Nps1*♂ cross) harvested at RR stage and incubated at 25°C under natural light conditions (number of replicates, $n \geq 5$). The fruits were photographed on different days indicated left to the photo panels.

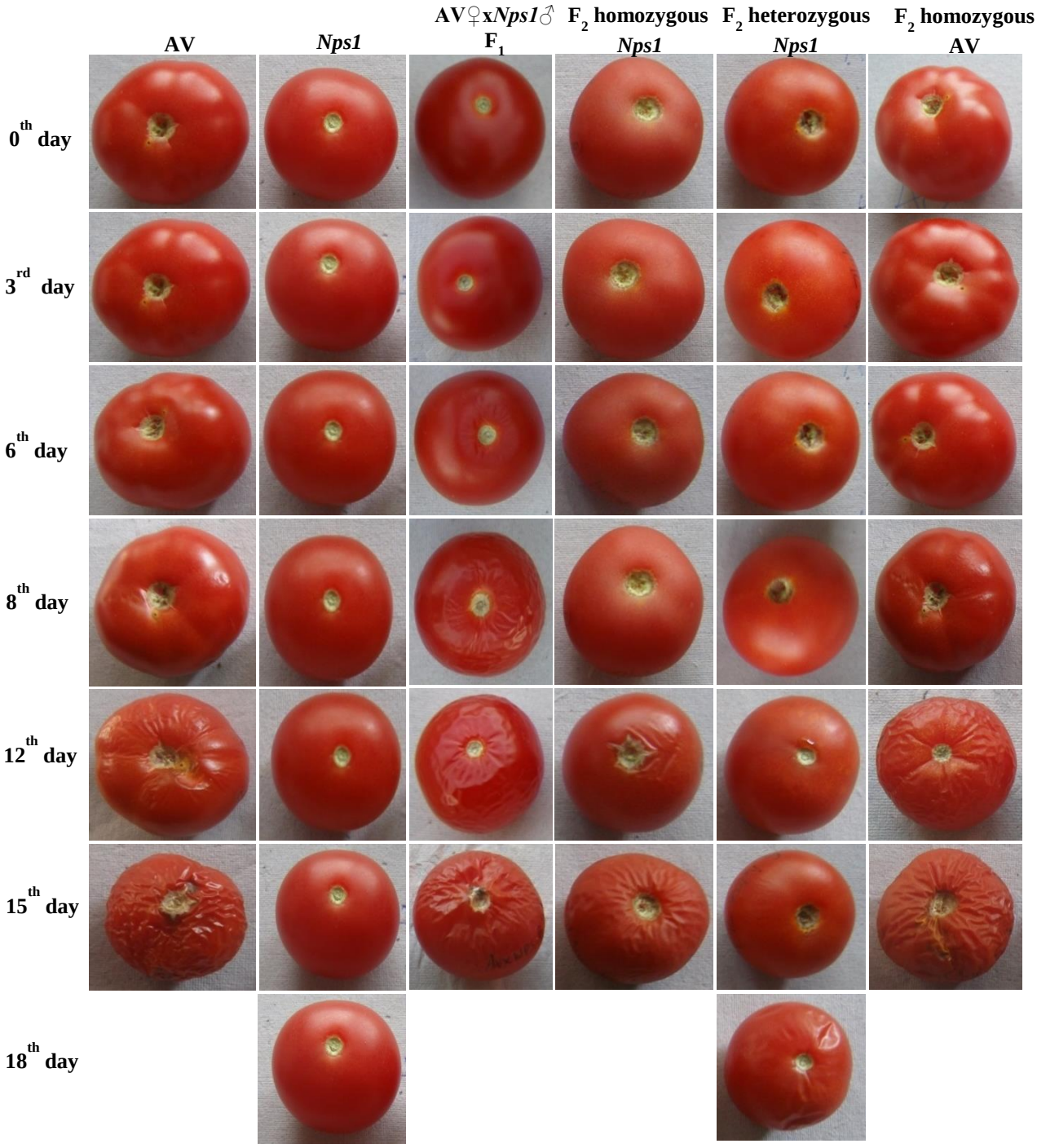


Figure 6.22. Off-vine senescence study in F_2 fruits (obtained from AV♀x*Nps1*♂ cross) harvested at RR stage and incubated at 25°C under natural light conditions (number of replicates, $n \geq 5$). The fruits were photographed on different days indicated left to the photo panels.

apply NGS for identifying candidate genes in several mutagenized populations. Such an approach called, "MutMap" or "mapping by sequencing" has already been applied to crop plants like rice (Abe et al., 2012), barley (Mascher et al., 2014) and tomato (Garcia et al., 2016) for identification of candidate genes responsible for a mutant phenotype. Since introgression of *Nps1* into AV and AC cultivars revealed that the *phot1* mutation is not linked to the enhanced shelf life in *Nps1* fruits, it was of interest to identify the candidate gene responsible for this trait.

As the genetic background of *Nps1* mutation is Ailsa Craig, we considered the F_2 population obtained from AC♀x*Nps1*♂ cross. Based on the phenotypic and genotypic (*phot1* mutation) segregation of postharvest shelf life of AC♀x*Nps1*♂ F_2 population, we identified two heterozygous lines, F_2 24 and F_2 36 with enhanced shelf life of 24 and 36 days respectively. DNA from these two lines was pooled and along with the DNA from unmutagenized AC, NGS was performed on MiSeq as described in methods. Analysis of data obtained from this experiment revealed 1233 SNPs (only in CDS after filtration; Table 6.2). As the number of SNPs is large, it was not possible to narrow down to few probable candidates. Taking this into consideration, we decided to examine the fruit shelf life of the progeny obtained from F_2 24 and $F_2$36 plants. This analysis revealed the further segregation of shelf life in F_3. In F_3, around 13 lines showed long shelf life (20-22 days) than the segregated AC (15 lines; 2-5 days shelf life). Using the DNA from these lines, we made two bulks-segregated WT-like bulk and mutant-like bulk and again sent samples for NGS. The data were analyzed as described in methods and Fig. 6.23, 6.24 assuming that the shelf life locus is recessive with allele frequency/SNP index of 0.9-1 (in AC, the frequency of this allele is between 0-0.5) and this revealed 52 SNPs (nonsynonymous changes; Table 6.3) in CDS). Currently, we are analyzing the data to identify few probable candidates and we shall validate their function using functional genomics approaches.

6.4 Discussion

The directional movements of plants in response to light quality and quantity are one of the most important processes for the optimal growth of plants under changing environment. This directional movement of plants is mediated by blue/UV-A region of the light spectrum, which is perceived by three classes of UV-A/blue light specific receptors; cryptochromes, phototropins and FKF1/Zeitlupe proteins (Christie et al., 2015). Of these photoreceptors, phototropins mediate phototropism, accumulation and avoidance

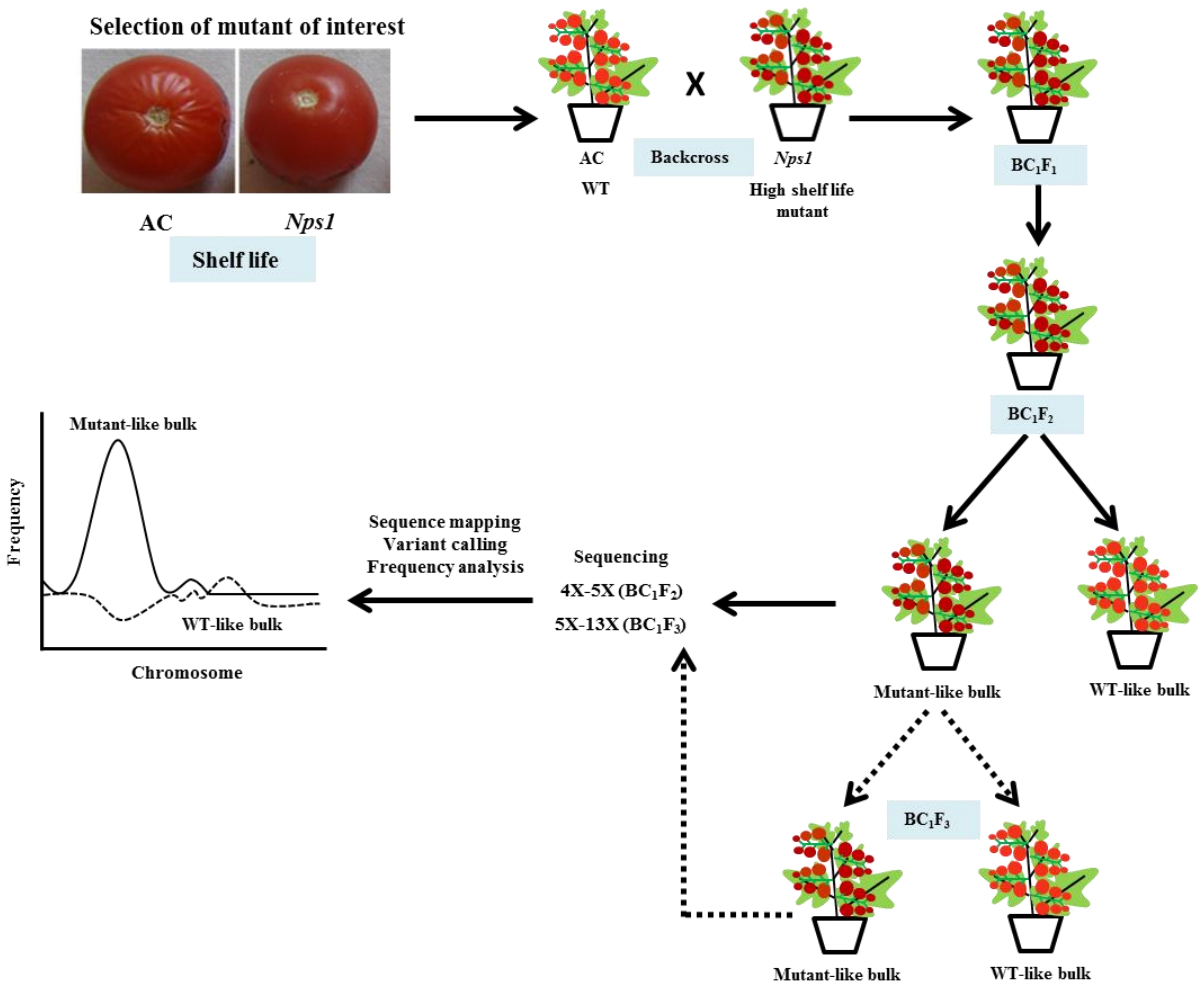


Figure 6.23. An overview of "MutMap" or "mapping by sequencing" approach used to identify the mutation responsible for high shelf life trait in *Nps1* (Adapted from Garcia et al., 2016). Bold arrows indicate the traditional Mutmap approach used in BC_1F_2 and dotted arrows indicate the second attempt made in this study using BC_2F_3.

A

		Shelf life phenotype
WT-1	Unmutagenized AC WT bulk	4 days
WT-2		4 days
WT-3		4 days
WT-4		4 days
F_2-MUT-1	Mutant-like bulk	24 days
F_2-MUT-2		36 days

B

F_3 lines		Shelf life phenotype
WT-1	WT-like bulk	4 days
WT-2		5 days
WT-3		2 days
WT-4		5 days
WT-5		4 days
WT-6		4 days
WT-7		2 days
WT-8		5 days
WT-9		2 days
WT-10		5 days
WT-11		2 days
WT-12		4 days
WT-13		3 days
WT-14		2 days
WT-15		4 days

F_3 lines		Shelf life phenotype
MUT-1	Mutant-like bulk	20 days
MUT-2		22 days
MUT-3		22 days
MUT-4		22 days
MUT-5		20 days
MUT-6		20 days
MUT-7		22 days
MUT-8		22 days
MUT-9		22 days
MUT-10		22 days
MUT-11		22 days
MUT-12		22 days
MUT-13		20 days

Figure 6.24. Post-harvest **s**helf life of long shelf life lines identified from F_2 and F_3 progeny (AC♀ and *Nps1*♂ cross). For NGS experiment, in F_2 (A), two long shelf life lines were pooled as mutant-like bulk and in F_3 (B), the lines with long shelf life (20-22 days) were pooled as mutant-like bulk and the lines with 2-5 days shelf life were pooled as WT-like bulk. In case of F_2 analysis, unmutagenized AC was used as WT.

movements of chloroplasts, stomatal opening, leaf expansion, leaf movements etc. (Christie, 2007). Most of the work on photoperception to signal transduction was carried out mostly in Arabidopsis due to the availability of mutants (Gyula et al., 2003). In tomato, using phototropism as a screen, a *Nonphototropic seedling1* mutant was isolated from an EMS-mutagenized population which was later shown to be deficient in *phot1* function (Sharma et al., 2014). In addition to the effects on phototropism, stomatal opening, chloroplast movement, leaf expansion, preliminary work on this mutant suggested that *phot1* mutation may also affect fruit carotenoid content and shelf life (Sharma S, Ph.D. thesis, 2011). In this study, a detailed molecular analysis was carried out on the influence of *phototropin1* on fruit pigmentation and shelf life.

6.4.1 Fruit development is delayed in *Nps1*

Tomato fruit ripening is accompanied by dramatic color changes that occur at specific developmental phases. For example, the fruits are green at MG, red color breaks at BR stage where less than 10% of the fruit surface is red, followed by RR stage, where 100% of the fruit surface turns red. Chronological monitoring of fruit development showed that *Nps1* attained MG stage nearly nine days later than AC. Thereafter, *Nps1* required nearly same time as AC to reach subsequent stages like BR and RR. However, due to the initial lag period in attaining MG stage, the overall fruit development was delayed in *Nps1*. Our data indicates a role for *phototropin1* in the regulation of fruit development. A similar role was also attributed to phytochromes (except *phyB1*) in prolonging the duration to attain MG stage (Gupta et al., 2014), suggesting that different photoreceptors may regulate fruit development through common pathways.

Ethylene is an important regulator of fruit ripening in climacteric fruits like tomato. It also regulates *phytoene synthase* expression in fruits (Bird et al., 1999). Mutants impaired in ethylene perception (*Nr*, Yen et al., 1995) accumulate very little carotenoids. Considering that fruit development is delayed in *Nps1* fruits, it can be presumed that this could be due to impaired ethylene production. Measurement of ethylene emission in *Nps1* fruits reveal low levels in the mutant. However, this does not delay the transition of fruit development from MG-BR and BR-RR stages in *Nps1*. Such an observation was also made in *hp1*, a light signaling mutant (Kilambi et al., 2013), where, low ethylene levels do not delay the fruit development and impair carotenoid content. On the contrary, both *hp1* and *Nps1* fruits accumulate high levels of carotenoids, suggesting that light acting via photoreceptors like phytochromes and phototropins

modulates carotenoid content independently of ethylene (Alba et al., 2000; Kilambi et al., 2013; Gupta et al., 2014).

6.4.2 Carotenoid biosynthesis is regulated posttranscriptionally in *Nps1*

Tomato fruit ripening is accompanied by chloroplast to chromoplast conversion which involves the degradation of chlorophyll and accumulation of carotenoids. Generally, during ripening, induction of *psy1* and suppression of *cycb* expression occurs, leading to high lycopene content and low β-carotene levels in the ripe fruits (Giuliano et al., 1993; Bramley 2002). As *Nps1* fruits at RR stage are deep red in color and accumulate high carotenoid levels, it is reasonable to expect that the carotenoid biosynthesis is up-regulated in the mutant fruits. However, consistent with the low ethylene levels in *Nps1*, the expression of *psy1*, the rate limiting enzyme did not show any increase in expression at RR stage inspite of high lycopene levels in the mutant. Such a lack of correlation between *psy1* transcript levels and lycopene content was also described earlier in *hp1* mutant and *det1* RNAi lines (Kilambi et al., 2013; Enfissi et al., 2010), signifying the posttranscriptional regulation of *psy1* in tomato fruits. As the β-carotene levels are slightly higher in the *Nps1* fruits than AC, this could be correlated to the enhanced *cycb* expression in the mutant fruits. In addition, the expression of *chrc* also increased in the mutant, leading to enhanced sequestration of carotenoids.

However, protein profiling using iTRAQ did not reveal any carotenoid biosynthesis enzymes to be differentially expressed in the mutant. This could be due to their low abundance and posttranscriptional, posttranslational regulation. Our data is corroborated by recent studies which indicate that carotenoid biosynthesis enzymes are enriched in chromoplasts (Barsan et al., 2012; Wang et al., 2013). In tomato, though few of the pathway enzymes could be seen in shotgun proteomics analysis, the key rate limiting enzyme of the carotenoid biosynthesis, PSY1 and CYCB were below the detection limits (Kilambi et al., 2016). The absence of correlation between transcript, protein and carotenoid levels suggest that the carotenoid metabolism is regulated posttranscriptionally in the *Nps1* fruits.

6.4.3 Concerted up-regulation of cell wall associated proteins may contribute to the long shelf life of *Nps1* fruits

The softening of ripe tomato fruits occurs due to the changes in the cell wall composition and structure (Brummel 2006; Brummel and Harpster, 2001). The cell wall

disassembly during fruit softening is associated with the expression of a number of cell wall modifying genes and corresponding enzymes. Consistent with this, iTRAQ analysis revealed the increased abundance of three cell wall associated proteins β-MAN, PG2A and PME in *Nps1*, while α-MAN levels were similar in *Nps1* and AC fruits. Analysis of the corresponding transcript levels revealed the posttranscriptional regulation of *β-man*, *pg2a*, *pme* and *α-man* (Brummel and Harpster 2001). In addition to the high protein abundance, β-MAN enzyme was also hyperactive (by 518 fold) in RR fruits of *Nps1* than AC, suggesting that it can affect the shelf life. Our results are contradictory to the available literature on these four proteins. When *pg2a* and *α-man* expression was suppressed, an increase in shelf life of tomato fruits could be observed (Langley et al., 1994; Sheehy et al., 1988; Meli et al., 2010), whereas suppression of *pme* (Tieman and Handa 1994) did not affect the fruit shelf life. When *β-man* was suppressed, firmness of the fruits increased compared to control fruits (Wang et al., 2009). In the *β-man* suppressed lines, no correlation was observed between β-MAN activity and firmness of the fruits. In addition to the hydrolytic activity, β-MAN can also act as a mannan transglycosylase. Due to this function, it can transfer mannans to the cell wall leading to its thickness and in turn may also contribute to fruit shelf life. This mannan transglycosylase activity may partially explain the lack of the consistency between firmness and enhanced hydrolytic activity of β-MAN as the hydrolytic activity is most commonly assayed (Wang et al., 2009). It is plausible that the mannan transglycosylase activity of β-MAN may be higher than the hydrolase activity in *Nps1* fruits, there by contributing to its long shelf life. It remains to be examined whether the glycoprotein and cell wall composition is altered in the *Nps1* fruits compared to AC.

Based on the above observations, it appears that a concerted up-regulation of three different cell wall associated proteins may somehow contribute to the rigidity of the cell wall and enhanced shelf life of *Nps1* fruits. It is also possible that *Nps1* may have another lesion in a regulatory/key gene that can alter the cell wall composition. Additional work is needed to understand the above possibilities in greater detail.

6.4.4 *phot1* mutation is linked to carotenoid content but not shelf life

In tomato, influence of photoreceptors on carotenoid levels is being studied. Overexpression of *cry2* led to increased flavonoid and carotenoid content in tomato fruits (Giliberto et al., 2005). Activation of fruit localized phytochromes increased the carotenoid content (Alba et al., 2000). Recently, Gupta et al (2014) showed that

phytochromes regulate carotenoid levels and in addition, they also act as time keeper regulating the duration of different phases during ripening. Consistent with this, our study as well as a previous study (Sharma S, Ph.D. thesis, 2011) revealed the role of *phototropin1* in regulating carotenoid content.

Since *Nps1* fruits exhibit high carotenoid levels and long shelf life, introgression of *Nps1* into local cultivar, AV (and original genetic background, AC) was carried out. Analysis of F_1 and F_2 lines at both phenotype and genotype levels revealed that the high carotenoid content trait could be successfully introgressed into AV (and also in AC background) but not the shelf life trait suggesting that the *phot1* mutation is strongly linked to carotenoid content. It is possible that a locus different than *phot1* may affect the shelf life trait in *Nps1*.

6.4.5 Quest for the gene linked to shelf life trait of *Nps1* fruits

Tomato has a large number of monogenic mutant collections (TGRC-www.tgrc.ucdavis.edu) and TILLING resources, where in mutagenized populations are available in various tomato cultivars (Menda et al., 2004; Saito et al., 2011; Carvalho et al., 2011; Monteiro et al., 2012). As the tomato genome sequence became available (The Tomato genome consortium 2012), efforts are being made towards functional genomics studies so that gene functions can be elucidated and superior tomato cultivars can be developed. However, the identification of a causal gene underlying a mutant phenotype is a long drawn process and often fraught with difficulties. Alternatively, due to the advances made in NGS technologies, whole genome sequencing can be used to identify the gene underlying the phenotype of interest in a fraction of time and cost. “Mapping by sequencing” or “MutMap” is one such approach in which whole genome sequencing has been successfully applied to identify the causal genes in several mutants of interest in crop plants like rice (Abe et al., 2012), barley (Mascher et al., 2014), tomato (Garcia et al., 2016), etc.

In this study, we made an attempt to identify the gene responsible for the shelf life of *Nps1* fruits using “MutMap” or “mapping by sequencing” approach. Initially, NGS using DNA from unmutagenized AC (WT bulk; original genetic background of *Nps1*) and pooled DNA from two lines which showed long shelf life revealed a large number of SNPs. This could be due to two reasons: first, we had only two lines in F_2 that had long shelf life. Second, *Nps1* was isolated from EMS mutagenized population, whereas we

used unmutagenized AC as WT control for NGS, leading to a number of background mutations appearing in the data. As it was not possible to narrow down to few probable candidates, we proceeded to second round of NGS using the F_3 population of the above long shelf life lines. In F_3, around 13 lines showed long shelf life (20-22 days) while rest 15 lines were like AC (2-5 days shelf life). NGS of these two bulks (WT-like bulk and mutant-like bulk) revealed 52 SNPs (only in CDS after filtration, assuming that the shelf life locus is recessive with a SNP index/allele frequency of 0.9-1). Currently, we are analyzing the data to delineate a few probable candidate genes. Once we identify the candidate genes, we shall validate further using functional genomics approaches.

Unlike the recent report on mapping by sequencing in tomato (Garcia et al., 2016), we could not narrow down to probable candidate gene in our study due to few limitations. Our analysis is not robust as the number of individuals in each bulk used for NGS was less (13-15 lines/bulk) and the sequence coverage obtained in our experiment was not great (Fig. 6.25) while Garcia et al. (2016) used about 150 individuals in each bulk and their sequence coverage was around 40x. As a result, we may have missed several SNPs. Nevertheless, this was a pilot experiment and in the future, we plan to increase the population size and perform NGS with a deeper coverage to identify the candidate gene responsible for the shelf life of *Nps1* fruits.

	WT	**Mutant**
Scored phenotype	No shelf life	Long shelf life
Tomato reference genome	Heinz 1706 (SL2.40)	Heinz 1706 (SL2.40)
NGS first round (BC_1F_2 analysis)		
No. of plants per bulk	4	2
No. of paired reads	11583289	21718193
% mapped reads	94.60%	98.60%
Coverage	4.3x	8.1x
NGS second round (BC_1F_3 analysis)		
No. of plants per bulk	15	13
No. of paired reads	38207922	17248046
% mapped reads	99.42%	99.24%
Coverage	13x	5.9x

Figure 6.25. Illumina sequencing of BC_1F_2 and BC_1F_3 bulk individuals exhibiting prolonged postharvest shelf life or without any postharvest shelf life.

Chapter 7

Summary

7.1 Introduction

Tomato fruit ripening is a complex developmental process that enhances palatable qualities of fruit by modifying texture, flavor, color and taste (Seymour et al., 2013; Gillaspy 1993). Carotenoids, the red, orange and yellow colored pigments, are accumulated during ripening in tomato fruits. Carotenoids are sources of vitamin A and antioxidant compounds in the diet and help combating cancer, cardio-vascular diseases and age-related eye diseases in humans (Fraser and Bramley 2004; Fiedor and Burda 2014). In plants, carotenoid biosynthesis occurs in the plastids using precursors derived from non-mevalonate pathway or methylerythritol 4-phosphate pathway (Eisenreich et al., 2001; Milborrow and Lee 1998). A multitude of factors regulates carotenoid metabolism such as light, temperature, transcription factors, ethylene, auxin, jasmonate, brassinosteroids, ABA, heat shock and epigenetic factors (Yuan et al., 2015; Liu et al., 2015). Among these, the light regulates carotenoid metabolism (Bramley 2002; Romer and Fraser 2005), throughout the visible spectrum, using multiple photoreceptors sensing quality, quantity and directionality of light (Christie et al., 2015). Of these, till date only phytochromes and cryptochromes have been shown to influence tomato fruit carotenoid accumulation (Alba et al., 2000; Giliberto et al., 2005). The role of other photoreceptors, such as blue light photoreceptor- phototropin and UV-B photoreceptor- UVR8, in regulation of carotenoid metabolism in tomato is not known.

Apart from photoreceptors, high pigment mutations *hp1* and *hp2*, located in the light signaling pathway genes including *ddb1* (*hp1*; Lieberman et al., 2004; Liu et al., 2004), *det1* (*hp2*; Mustilli et al., 1999) increase the carotenoid content. The RNAi mediated repression of *cop1like* increase the carotenoid content, whereas silencing of *Lehy5* decreases carotenoid levels in tomato fruits (Davuluri et al., 2004; Liu et al., 2004; Davuluri et al., 2005). In addition to *hp1* and *hp2*, tomato has two other high pigment mutants, *hp3* with mutation in *zep* (*zeaxanthin epoxidase*) and *Ip* (*Intense pigment*; Galpaz et al., 2008; Lavi et al., 2009). The enhanced level of carotenoids in three high pigment mutants, *hp1*, *hp2* and *hp3* is associated with increase in plastid (both chloroplast and chromoplast) number and size that enables the accumulation and storage of the high levels of carotenoids in these mutants (Kolotilin et al., 2007; Galpaz et al., 2008; Azari et al., 2010; Enfissi et al., 2010).

In addition to biosynthesis, the efficient sequestration of carotenoids in chromoplasts is also important for high carotenoids accumulation. In cauliflower, *Or* gene

stimulates chromoplasts biogenesis, which creates a metabolic sink for carotenoids storage (Lu et al., 2006; Tzuri et al., 2015; Lopez et al., 2008). In *Arabidopsis*, OR proteins influence carotenoid biosynthesis through posttranscriptional regulation of *psy1* (Zhou et al., 2015). Carotenoid sequestration by plastoglobules is also crucial for enhanced carotenoid accumulation. The plastoglobular proteins such as CHRC and fibrillin reportedly sequester carotenoids and also influences chromoplast differentiation and carotenoid metabolism (Leitner-Dagan et al., 2006; Simkin et al., 2007).

Unlike red colored tomato, most of its closest relatives are green fruited in the nature, with few displaying red and orange colors (Bauchet and Causse 2012). The diversity of coloration in fruits of wild relatives of tomato is attributed to accumulation of distinct carotenoids in a species-specific fashion. It is proposed that the green color of fruits results from down-regulation of *psy1*, encoding the first enzyme of fruit specific carotenoid biogenesis (Melendez-Martinez et al., 2010; Bolger et al., 2014). Though the wild relatives are green-fruited (Ronen et al., 2000; Isaacson et al., 2002), several QTLs have been identified from the wild species that enhances lycopene and β-carotene content in the fruits (Chen et al., 1999; Fulton et al., 2000; Frary et al., 2004; Rousseaux et al., 2005). However, the information regulating carotenogenesis is fragmentary; the molecular mechanisms involved in regulation of fruit color in tomato and its wild species are yet to be fully deciphered.

A combination of "omics" technologies such as phenomics, genomics, proteomics and metabolomics can substantially aid to understand the molecular events that trigger carotenoid biosynthesis and degradation (Ricroch et al., 2011; Pirrello et al., 2009). The correlation of transcript profiles with metabolite abundances and comparison of transcript, protein and metabolite data have helped deciphering the networks regulating fruit ripening (Rohrmann et al., 2011; Lee et al., 2012; Osorio et al., 2011). Similarly, proteomic profiling has been used to identify the proteins involved in fruit development, chromoplast biogenesis and chloroplast to chromoplast development in tomato (Faurobert et al., 2007; Xu et al., 2013; Barsan et al., 2012; Wang et al., 2013).

Though it is known that the carotenoid metabolism in tomato is influenced by various factors, including light and other developmental regulators, yet limited information exists about the specific mechanisms underlying these regulations. In this study, we examined a *high pigment* mutant (*hp1*), three wild species of tomato and a high carotenoid accumulating *phototropin1* mutant (*Nps1*), with emphasis on proteomic

analysis, to uncover the diversity in the regulation of fruit coloration. To unravel the regulation of carotenoid metabolism, the following objectives were defined:

1. To decipher the molecular basis of enhanced carotenoid accumulation in *hp1* mutant of tomato.

2. To understand the molecular basis for diversity in fruit coloration in the tomato clade.

3. To examine the influence of *phototropin1* on tomato fruit quality and shelf life.

7.2 Results

7.2.1 To decipher the molecular basis of enhanced carotenoid accumulation in *hp1* mutant of tomato

In tomato, the high pigmentation of fruits is reportedly regulated by a diverse set of genes encoded by distinct genetic loci: *hp1*, *hp2*, *hp3* and *Ip* (Azari et al., 2010). At the red-ripe (RR) stage, fruits of these mutants possess elevated levels of lycopene and β-carotene, signifying commonality in the up-regulation of carotenoids. Proteome profiling at three ripening stages- mature green (MG), breaker (BR) in *hp1* and its wild-type Alisa Craig (AC) identified 72 differentially abundant proteins. In the proteome data, we specifically examined for the presence of specific enzymes or proteins that may have assisted carotenoid accumulation by regulating biosynthesis, sequestration or degradation. One protein that showed an interesting expression pattern is chromoplast-specific carotenoid associated protein (CHRC). The CHRC protein gradually declined in abundance with the progression of ripening in the wild-type. Contrastingly, in *hp1*, the CHRC protein showed an opposite pattern; its level progressively increased, attaining a peak at RR. Consistent with the increased protein levels, the transcript levels of *chrc* were also high in red ripe fruits of *hp1* compared to WT. Western blotting using CHRC polyclonal antibody from bell pepper (*Capsicum annuum*) revealed a 2 fold increase in the abundance of CHRC protein in the red ripe stage of *hp1* fruits compared with the WT. In this study, we also demonstrated the presence of CHRC in purified plastoglobules. A substantial enrichment of the CHRC protein in the plastoglobules compared to chromoplast membrane fraction is also in conformity with an earlier transmission electron microscopy observation that the plastoglobules are associated with chromoplast membranes in the ripe fruits (Harris and Spurr, 1969). It is assumed that CHRC plays a role in carotenoid storage, and its presence in the chromoplast proteome of tomato, bell

pepper and *Citrus* spp. (Siddique et al., 2006; Barsan et al., 2010; Zeng et al., 2011) is also consistent with this role.

Though *hp1* accumulates more carotenoids, the transcript profiling of carotenoid pathway genes revealed overall up-regulation of the pathway in the WT rather than in *hp1*, except the desaturation steps catalyzed by *pds* and *zds*. Our study showed a lack of correlation between transcript and metabolite profiles leading to lycopene formation. Evidently, the negative correlation between carotenoid pathway transcripts and carotenoids indicates the importance of posttranscriptional regulation in elevating carotenoid levels in *hp1* fruits. On the whole, our results highlight the need for a comprehensive systems approach, including posttranslational regulation, feedback regulation, and metabolite turnover and portioning between different organelles and/ or locations in the cell, to uncover the linkage between metabolic networks regulating fruit ripening (Fernie and Stitt, 2012). The up-regulation of CHRC in the fruits of *hp1* mutant suggests an interrelationship between carotenoid accumulation and CHRC levels. It is likely that higher CHRC levels function to abet the storage of carotenoids and protect them from degradation in *hp1* mutant. However, it remains to be determined whether the up-regulation of CHRC by genetic or transgenic means would improve the storage capacity of carotenoids in tomato fruits. In summary, this study revealed that CHRC likely regulates carotenoid sequestration and storage, which seems to be important for the enhanced accumulation of carotenoids in *high pigment1* tomato fruits.

7.2.2 To understand the molecular basis for diversity in fruit coloration in the tomato clade

Fruits of tomato wild species exhibit diverse colors ranging from green, orange and red, however, the mechanisms underlying acquisition of fruit coloration are largely unknown. In the tomato clade, green fruited species are more primitive than orange and red fruited relatives, though they all share the same gene repertories for carotenogenesis (Aflitos et al., 2014; Bolger et al., 2014). In this study, we used a proteomic approach combined with carotenoid profiling and carotenogenic gene expression to understand the mechanisms governing inter-species diversity in fruit coloration from green-fruited *Solanum habrochaites* (SH), orange-fruited *S. galapagense*, and red-fruited *S. pimpinellifolium* with *S. lycopersicum*, cv. Ailsa Craig (SL, tomato).

Prior to initiating this study, we also optimized a shotgun proteomics method for proteome profiling in the tomato fruits (Kilambi et al., 2016; Chapter 4 in this thesis). We used this optimized GeLCMS method for proteome profiling of fruits and leaves in the tomato clade.

In orange/red -fruited species, increase in carotenoid levels (26→39 dpa; MG to RR), was associated with decline in chlorophylls. However, SH fruits retained similar level of carotenoids and chlorophylls. In leaf only four carotenoids accumulated viz. β-carotene, violaxanthin, neoxanthin and lutein and all four were also present in fruits at 26 dpa. The transition from green to orange/red fruits specifically enhanced the β-carotene pathway, which is also consistent with the enlisting of a lycopene-β-cyclase (CYCB) regulating fruit specific carotenogenesis (Mohan et al., 2016). The persistence of neoxanthin, a leaf specific carotenoid in SH fruits indicates sustenance of leaf pathway, whereas disappearance of antheraxanthin, similar to other species, indicates a partial operation of fruit-like pathway. Ostensibly, SH fruits appear to be at the crossroads of leaf and fruit-specific carotenogenesis. It is also evident that SH fruits lack up-regulation of β-carotene biosynthesis and chromoplast formation. As ethylene is an important regulator of fruit ripening and associated coloration, measurement of ethylene emission revealed that all wild relatives emit higher ethylene than SL. It appears that the transition of green fruited species to red fruited SL is accompanied by attenuation of ethylene biosynthesis. Though SH fruits emit high level of ethylene, they do not exhibit fruit softening or coloration.

Gene expression profiling in wild species was performed to identify the regulation of fruit color at transcript level. The regulation of *dxs* expression seems to be pivotal for fruit specific carotenoid accumulation (Lee et al., 2012). Considering that all the three wild relatives exhibited higher *dxs* expression than SL, *dxs* expression does not appear to be a limiting factor for carotenoid formation in SH. Previous studies suggested that down-regulation of *psy1* is likely responsible for the green and yellow fruit colors in tomato clade (Melendez-Martinez et al., 2010; Bolger et al., 2014). In tomato PSY1 and PSY2 reportedly contribute to fruit and leaf-specific carotenoid formation respectively. Consistent with this, *psy1* expression in orange/red fruits was much higher than *psy2* with high levels in SP and SG at 39 dpa. Conversely in leaf, *psy2* showed higher expression than *psy1*. Though SH is green fruited, yet showed high level of *psy1* compared to *psy2* (66, 158, 860 folds high 26→39 dpa respectively), however, *psy1* level declined after 26

dpa in SH compared to other species. Out of three lycopene β-cyclases (*lycb1*, *lcyb2*, *cycb*) in tomato, only *cycb* drives the β-carotene formation in fruits. Consistent with this, *cycb* expression in fruits was higher than *lycb1* and *lcyb2*; its expression declined in wild species while it increased in SL (26→39 dpa). Though SH formed little β-carotene, it had higher *cycb* expression than orange/red fruited species. Considering that *psy1* and *cycb* are two regulatory steps in SL coloration, it appears that carotenogenesis in SH is probably not compromised by lower gene expression at these two steps. The expression level of carotenogenic transcripts in leaf was higher than fruits and in general, wild species showed higher expression levels than SL. Intriguingly *cycb* expression in leaf was higher than the fruit. Majority of genes contributing to α-/β-carotene pathway were up-regulated in wild species compared to SL.

Using shotgun proteomics approach, we detected a much wider spectrum of proteins than a previous report in tomato (Barsan et al., 2012) in both fruits and leaves. Comparison with SL revealed large number of differentially expressed proteins in fruits of wild relatives (SP-851, SG-1183, SH-501). Compared to the fruits, only few proteins were differentially regulated between wild species and SL. Majority of the proteins was down-regulated and only few were up-regulated in the wild species (SP-94, SG-83; SH-70). Consistent with chlorophyll retention in SH fruit, PS-light reaction class was highly up-regulated in SH. In addition, SH fruits at 39 dpa showed higher PSII activity. The chloroplast-specific proteins such as CAB, OEE2, Rubisco activase 1 and FBP aldolase were abundant in SH, in contrast to the decline in SP/SG. The persistence of proteins from PS Calvin cycle and light reaction in SH is also consistent with the observed higher expression of photosynthesis related genes in *S. pennellii* fruits (Bolger et al., 2014). The PAO and RCCR proteins involved in chlorophyll catabolism, though present in ripened fruits of SG and SP were not detected in SH. This was also substantiated by lower activity and gene expression of PAO/RCCR and retention of pheophorbide a in SH fruits. Akin to SH, an Arabidopsis mutant defective in PAO activity shows accumulation of pheophorbide a (Pruzinska et al., 2005). The inability to make carotenoids in SH may stem from the absence of chloroplast to chromoplast transformation. Consistent with this, SH fruits retain thylakoid grana, have few plastoglobules and lack undulating membranes enriched with lycopene crystalloids.

A major drawback in understanding carotenogenesis in tomato fruits is the limited information about the carotenogenic proteins due to their very low abundance. Only

shotgun proteomics of enriched chromoplasts detected some of these proteins (Barsan et al., 2012; Wang et al., 2013). The usage of Targeted Peptide Monitoring (TPM) in this study enabled detection and quantification of a number of carotenogenic proteins in tomato and its wild relatives without enrichment of chromoplasts. Consistent with overall high expression of carotenogenic genes, TPM detected more proteins in leaf than in fruits. The different isoforms of IDI and GGPPS could be distinguished by TPM in leaf. Also, in leaf, both PSY1 and PSY2 were below the limits of detection. Consistent with enhanced carotenoid levels, PSY1 was detected in SP and SG but not in SH fruits. The absence of PSY1 in SH fruits may be related to the lack of preferential lycopene/β-carotene accumulation. The abundance of VDE in SH likely reflects operation of leaf specific pathway in fruits. Similarly, increased abundance of CYCB may be related to high β-carotene level in SG fruits. Accumulation of carotenoids also depends on sequestration, as *high pigment* mutant fruits that are enriched in carotenoids also show increase in CHRC and PAP3 levels (Kilambi et al., 2013; Nogueira et al., 2013). Consistent with high carotenoid levels, the abundance of CHRC was high in SP fruits. On the contrary, the CHRC levels were diminished in SH fruits, as it accumulates little carotenoids. Above lack of correlation corroborates the prevailing view that while regulation of abundances of mRNA is more flexible, the protein abundances are stringently regulated (Vogel and Marcotte, 2012).

To decipher carotenogenesis regulation, we integrated the carotenoids, carotenogenic proteins, and carotenogenic transcript data in fruits at 39 dpa and leaf in the wild species and this revealed interesting observations. Unlike leaf, the carotenoid level in the fruits is regulated in multifarious fashion in orange/red fruited species. The complexity of these interactions increased from green fruited SH to orange fruited SG. Interestingly, all these interactions were species-specific and no overlaps were detected between two species or with leaf. In the future, more refined systems biology approaches including metabolic flux analysis may unravel the regulatory circuits governing carotenogenesis in more detail.

7.2.3 To examine the influence of *phototropin1* on tomato fruit quality and shelf life

Light dependent regulation of carotenogenesis is well known in tomato (Bramley 2002; Romer and Fraser 2005). In plants, photoreceptors modulate developmental processes, with respect to its ambient light environment, by detecting different regions of visible spectrum (Christie et al., 2015). Till date, only phytochromes and cryptochromes

have been reported to influence carotenoid accumulation in tomato (Alba et al., 2000; Giliberto et al., 2005). The information on other photoreceptors like phototropins and UVR8 on tomato pigmentation is probably lacking due to paucity of mutants. In this study we used a dominant *phototropin1* mutant- *Nps1* which lacks phototropism in tomato (Sharma et al., 2014). The *Nps1* fruits also exhibit high carotenoid content and enhanced shelf life (Sharma S Ph.D. thesis, 2011). In this study, a detailed molecular analysis was carried out to determine the influence of *phototropin1* on fruit pigmentation and shelf life using *Nps1* and its WT, AC.

Tomato fruit ripening is accompanied by dramatic color changes that occur at specific developmental phases. Consistent with this, AC fruits followed normal development and ripening while *Nps1* fruits required 9 days longer than AC to reach the MG stage, and thereafter the duration of fruit ripening in the *Nps1* mutant was similar to AC. However, due to the prolonged growth period to attain the MG stage, the overall fruit development was delayed in *Nps1*. Our data indicates a role for *phototropin1* in the regulation of the fruit growth, similar that observed for phytochromes (except *phyB1*), where too, duration to attain MG stage is prolonged (Gupta et al., 2014). It appears that different photoreceptors converge at common pathways to regulate fruit development.

The measurement of ethylene emission in *Nps1* fruits revealed low levels in the mutant. However, lower ethylene emission did not affect the transition of fruit development from MG-BR and BR-RR stages in *Nps1*. The fruits of *Nps1* at red ripe stage accumulate high levels of lycopene along with phytoene, phytofluene and ζ-carotene as indicated by the intense red color of the *Nps1* fruits. The accumulation of high levels of carotenoids is akin to *hp1*, a light signaling mutant (Kilambi et al., 2013), where too, low ethylene emission does not affect fruit development and impair carotenoid content. Considering that both *hp1* and *Nps1* fruits accumulate high levels of carotenoids, it appears that light acting via photoreceptors like phytochromes and phototropins modulates carotenoid content independently of ethylene (Alba et al., 2000; Kilambi et al., 2013; Gupta et al., 2014).

Generally, during ripening, induction of *psy1* and suppression of *cycb* expression occurs, leading to high lycopene content and low β-carotene levels in the ripe fruits (Giuliano et al., 1993; Bramley 2002). As *Nps1* fruits accumulate high carotenoid levels, it is reasonable to expect that the carotenoid biosynthesis is up-regulated in the mutant fruits. However, consistent with the low ethylene levels in *Nps1*, the expression of *psy1*,

the rate limiting enzyme did not show any increase in expression at RR stage in spite of high lycopene levels in the mutant. Such a lack of correlation between *psy1* transcript levels and lycopene content was also described earlier in *hp1* mutant and *det1* RNAi lines (Kilambi et al., 2013; Enfissi et al., 2010), signifying the posttranscriptional regulation of *psy1* in tomato fruits. As the β-carotene levels are slightly higher in the *Nps1* fruits than AC, this could be correlated to the enhanced *cycb* expression in the mutant fruits. In addition, the expression of *chrc* also increased in the mutant, leading to enhanced sequestration of carotenoids.

In addition to high carotenoid content, *Nps1* fruits exhibit prolonged shelf life (Sharma S, Ph.D. thesis, 2011). To examine the effect of postharvest storage conditions on the shelf life, fruits of AC and *Nps1* at red ripe stage were incubated at two temperatures, 16°C and 25°C under natural light conditions to observe shelf life. Under these conditions, the time taken for complete spoilage of AC fruit was 25 days (at 16°C) and 36 days (at 25°C), while *Nps1* fruits showed minimum wrinkles even after 40 days (at 16°C), and 72 days (at 25°C), suggesting that senescence is delayed in the mutant fruits. Moreover, the fruits of *Nps1* stayed on-vine relatively fresh for longer period than AC fruits and thus they can be harvested later.

As *Nps1* fruits have long shelf life and accumulate more carotenoids, proteome profiling by iTRAQ was carried out. Of interest was to examine the proteins related to the above traits in the differentially expressed proteome data, however, we did not detect any proteins related to carotenoid metabolism to be differentially expressed and this could be due to their low abundance. When a tomato fruit ripens, softening occurs due to the changes in the cell wall composition and structure (Brummell 2006; Brummel and Harpster, 2001) and is associated with the expression of a number of cell wall modifying genes and corresponding enzymes. Consistent with this, iTRAQ analysis revealed the increased abundance of three cell wall associated proteins β-MAN, PG2A and PME in *Nps1*, while α-MAN levels were similar in *Nps1* and AC fruits. Analysis of the corresponding transcript levels revealed the posttranscriptional regulation of *β-man, pg2a, pme* and *α-man* (Brummell and Harpster 2001). In addition to the high protein abundance (200 fold), β-MAN enzyme was also hyperactive (by 518 fold) in RR fruits of *Nps1* than AC, suggesting that it can affect the shelf life.

Our results are contradictory to the available literature on the above four proteins. When *pg2a* and *α-man* expression was suppressed, an increase in shelf life of tomato

fruits could be observed (Langley et al., 1994; Sheehy et al., 1988; Meli et al., 2010), whereas suppression of *pme* (Tieman and Handa 1994) did not affect the fruit shelf life. When *β-man* was suppressed, firmness of the fruits increased compared to control fruits (Wang et al., 2009). In the *β-man* suppressed lines, no correlation was observed between β-MAN activity and firmness of the fruits. In addition to the hydrolytic activity, β-MAN can also act as a mannan transglycosylase. Due to this function, it can transfer mannans to the cell wall leading to its thickness and in turn may also contribute to fruit shelf life. It is plausible that the mannan transglycosylase activity of β-MAN may be higher than the hydrolase activity in *Nps1* fruits, there by contributing to its long shelf life. Based on the above observations, it appears that a concerted up-regulation of three different cell wall associated proteins may somehow contribute to the rigidity of the cell wall and enhanced shelf life of *Nps1* fruits. It is also possible that *Nps1* may have another lesion in a regulatory/key gene that can alter the cell wall composition. Additional work is needed to understand the above possibilities in greater detail.

Since *Nps1* fruits exhibit high carotenoid levels and long shelf life, introgression of *Nps1* into local cultivar, AV (and original genetic background, AC) was carried out. Analysis of F_1 and F_2 lines at both phenotype and genotype levels revealed that the high carotenoid content trait could be successfully introgressed into AV (and also in AC background) but not the shelf life trait suggesting that the *phot1* mutation is strongly linked to carotenoid content. It appears that a locus different than *phot1* affects the shelf life trait in *Nps1*.

As *phot1* is not linked to fruit shelf life, we also made an attempt to identify the gene responsible for the shelf life of *Nps1* fruits using "MutMap" or "mapping by sequencing" approach. Initially, NGS using DNA from unmutagenized AC (WT bulk; original genetic background of *Nps1*) and pooled DNA from two lines which showed long shelf life revealed a large number of SNPs. As it was not possible to narrow down to few probable candidates, we proceeded to second round of NGS using the F_3 population of the above long shelf life lines. In F_3, around 13 lines showed long shelf life (20-22 days) while rest 15 lines were like AC (2-5 days shelf life). NGS of these two bulks (WT-like bulk and mutant-like bulk) revealed 52 SNPs (only in CDS after filtration, assuming that the shelf life locus is recessive with a SNP index/allele frequency of 0.9-1). Currently, we are analyzing the data to delineate a few probable candidate genes. Once we identify the candidate genes, we shall validate them further using functional genomics

approaches. Nevertheless, this was a pilot experiment and in the future, we plan to increase the population size and perform NGS with a deeper coverage to identify the candidate gene responsible for the shelf life of *Nps1* fruits.

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Annexures

Annexure 1

Primers used for quantitative real time PCR analysis in this study

Gene	Forward primer (5′ to 3′)	Reverse primer (5′ to 3′)	Product size (bp)
dxs	AAATGGGATCGGTGTAGAGC	TGCTGAGCCATATCCCAATA	115
dxr	AGCAGGGTGTGATTGAGGTT	GTCTTTTCCTGCTTCGATGG	113
hdr	TACGGGATGCCTAAGGCTAA	TTCACCACATGCTTTTCTCG	112
idi5g	CCAGACGAAGTTGCTGACAT	TCCCACCATTTGAACAAGAA	143
idif	GCCTTTACTCTCCAGGAATCAG	ATTCCCCATTCACATCATAAGG	118
idi4g	GAGAGGAATTGATGGGAACAAG	GAAGTTATAGGGGAGGCGATG	93
ggpps2	ATCAATGGAGCAGCTTTGTG	GCGGTTGATAAAACGACGTA	128
ggpps2g	AATTTGCAAGATGTATTGGTTTG	AAGTCCTTCCCAGCTGTTTTC	100
ggpps9g	AAAGAAAACTTGGCCGTTATTG	TCTAGGCAATGAAACCAAACTG	100
ggr	TTACTGGCCAACATACAAGGTG	ACATACTCATCAGCGCACATCT	102
psy1	TGAATTAGCACAGGCAGGTC	TCAATTCTGTCACGCCTTTC	140
psy2	AATTCCGAGGTCTCATACGG	CCTTTCCACATCGAATTCCT	110
pds	TATCATCAACGTTCCGTGCT	TATCGGTTTGTGACCAGCAT	122
ziso	AGAGCGTGCTTTTCGTGTATTG	ATTGCCATAACTGCACTCCATC	107
zds	TCCAAAAGGGCTATTTCCAC	TTGATCCAAGAGCTCCACAG	115
crtiso	GAGATCGCCAAATCCTTAGC	CAGAAAGCTTCACTCCCACA	118
lcyb1	CGATGCAACTGGCTTCTCTA	AATGAGAATCTCGCCAATCC	149
lcyb2	ATTTGTGGCCCATAGAAAGG	TGACAAGAAACCATGCCAAT	146
cycb	TCTTCTCAAGCCTTTTCCATC	TGGTGGGACTTAGAAAAGAAGG	92
lcye	TTAGTCGCCATTTTCTGCAC	TCACCCTCGCACTCTACAAG	130
crtrb1	CAAACGCTGTTCCAGCAATA	TCTTGTGAACCAAACCATCG	141
crtrb2	CGCCATAACAAATGCTGTTC	ATGAACCAGTCCATCGTGAA	148
zep	GGTCGTGTTACATTGCTTGG	TGCATGCTTTTTCAAGTTCC	118
vde	GTGCAGCTAATGTTGCCTGT	GGGAGACTGCACACTCATTG	126

nxs	GATGAGCTTGTGGTGATTGC	ACAACCTTCCGTCCATGAAG	113
cyp97a29	GTGCCATTGTACCAGCATTG	TGCAGCAACATCAAGCTTTT	101
cyp97c11	TGCTGAGAGAATGGTGGAGA	GTGCAAGGCCAATAACATCA	107
ccd1b	AGCTAGGAAAATCAAAGGAATAGATGG	TTCAGAAAGAGTGACGTGTTGATC	107
pap3	AAGAAGTGTGCTGAAATAAAATGTG	AAGCTGAAATTACAGATGATTGACC	104
chrc	ACCAATAGGGGTTTGAGTGC	GCCGTTGAGAAGAGTCAAGG	120
nor	GGCAATATTCGGAGAGCAAG	TTCCGGTAGCCTTCCAATAA	113
rin	ATGGCATTGTGGTGAGCAAAG	GTTGATGGTGCTGCATTTTCG	147
cnr	AAATTTGGGCTGAAGAAGCA	AATCCGGGAATTGACAGAAG	115
tagl1	CAGCCAAATTACGAAGATGC	CAAGCTGGAGAGGAGTTTGG	109
Or	GGAGTTGCAGGAAATTCGAG	ATCCCAAGCTCAGCACTCTT	104
erf6	TCCCTACTACCCCATGGAAA	GATCAGATGGCTCCAATTCC	101
ful1	TTGGGGAAGCATACCAGAGT	ATGACGAAGCATCCATTGTG	119
ful2	AGAAAGAGATGGCCCAACAG	TTGGGTATGCTTCCCCTATG	117
aprr2	CTAATCATGTTGCCCCAGGT	GTCTCTGCAGGTTTCCATCC	118
glk2	GGCACTCCTTGTTTTTCTGC	GCAAATCAGAGGCAACTGTG	118
hb1	TTCTATTTAATCTGAAAACGGGAAA	ACAGTAATCTAGCAGGAGTTTCCAA	101
ap2a	AATGGATTAGTGGGGAACAAAA	CTCCGGTAAAAGGTAACACCAC	113
pif1	CCAATTACAGGGCAGGAATC	GGTGCTGCCGTTTACTGTACTA	118
rap2.2	CGTGATCCAAGGAAAGGTATTC	TTAGCTTTCTTGCCTCTGATCC	110
acs2	AAGCTTAACGTCTCGCCTGGAT	AGCGCAATATCAACCGTTCCAT	101
acs4	TATTGAAAGCGCGAAAAGGT	CGCAAATCCATCCAACAATA	117
aco1	AAGAGGCAGAGGAAAGTACACA	GGATCACTTTCCATTGCCTTCA	130
aco3	GTTCTTGGAAGTTATACAAACGTAGC	ACACAACAATCACACACACATACAC	80
pao	CATCTCAAGGACCTGAAGCTAA	TCATCAGGCCAAACAAAGAGTA	102
rccr	GGCTGTTCCACTCTCCTCTG	GAGCAACAGAAGCGTTTTCC	105
phot1	CAAAAGTTGTTCAGCCAAAGC	CCAGTGGTTTAATTGGCTTGA	120

phot2	TTGGTGGGCTTTAGGAATCTT	ACCGGAATGCTACTAGGGAAA	119
β-mann	TCAGGGATTGGATTTTGTGA	TCTTTGCACTGCCCATTCTA	124
α-mann	ATGGCCAATTGGAGCTAATG	TGCATTTTCCAAGAGCACAG	102
pg-β subunit	GGTTCTCCCCGTGACAATAA	GCCGCGTAATTTGTGAATTT	122
pme	CTTGGTAGGCCATGGAAAAA	AAAATCTCCGTGCCACTCA	102
β-actin	TGTCCCTATTTACGAGGGTTATGC	CAGTTAAATCACGACCAGCAAGAT	108
ubiquitin3	GCCGACTACAACATCCAGAAGG	TGCAACACAGCGAGCTTAACC	110

dxs, deoxy-xylulose 5-phosphate synthase; *dxr*, deoxy-xylulose 5-phosphate reductase; *hdr*, 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; *idi*, isopentenyl diphosphate synthase (isoforms *f* and *5g*); *ggpps*, geranyl geranyl diphosphate synthase (isoforms *2*, *2g* and *9g*); *ggr*, geranyl geranyl reductase; *psy1*, phytoene synthase 1; *psy2*, phytoene synthase 2; *pds*, phytoene desaturase; *ziso*, ζ-carotene isomerase; *crtiso*, carotenoid isomerase; *zds*, ζ-carotene desaturase; *lcyb1*, lycopene β-cyclase1; *lcyb2*, lycopene β-cyclase2; *cycb*, chromoplast specific lycopene β-cyclase; *lcye*, lycopene ε-cyclase; *crtrb1*, β-carotene hydroxylase 1, *crtrb2*, β-carotene hydroxylase 2; *zep*, zeaxanthin epoxidase; *vde*, violoxanthin deepoxidase; *nxs*, neoxanthin synthase; *cyp97a29*, cytochrome P450 carotenoid β-hydroxylase A29; *cyp97c11*, cytochrome P450 carotenoid ε-hydroxylase C11; *ccd1b*, carotenoid cleavage dioxygenase1b; *pap3*, plastid lipid associated protein 3; *chrc*, chromoplast specific carotenoid associated protein; *nor,* Nonripening*; rin,* ripening inhibitor; *cnr,* Colorless nonripening; *tagl1,* tomato agamous-like 1; *Or,* DnaJ Cys-rich zinc finger domain-containing protein; *erf6,* ethylene response factor 6; *ful1,* fruitful 1; *ful2,* fruitful 2; *aprr2,* Arabidopsis pseudo response regulator 2-like; *glk2,* golden 2-like; *hb1,* HD-Zip homeobox protein1; *ap2a,* apetala 2a; *pif1,* phytochrome interacting factor 1; *rap2.2,* related to *ap*2.2; *acs,* 1-aminocyclopropane-1-carboxylate synthase (isoforms *2* and *4*); *aco,* 1-aminocyclopropane-1-carboxylic acid oxidase (isoforms *1* and *3*); *pao*, pheophorbide *a* oxygenase; *rccr*- red chlorophyll catabolite reductase; *phot1*, phototropin 1; *phot2*, phototropin 2; *β-mann,* β-mannosidase; *α-mann,* α-mannosidase; *pg-βsubunit,* polygalacturonase-β subunit*; pme*, pectin methyl esterase*; β-actin; ubiquitin3.*

Table 3.1. Identification of differentially expressed proteins in both WT and *hp1* fruits by MALDI-TOF-TOF analysis

Spot no.[a]	Accession no.[b]	Protein	Species	Theo.M_r (kD)/ pI[c]	Exp.M_r (kD)/ pI[d]	NP[e]	SC[f] (%)	Mean Spot volume (%)					
								WT			*hp1*		
								MG	BR	RR	MG	BR	RR
1	gi|114421	ATP synthase sub unit β	*Nicotiana plumbaginifolia*	59.9/5.95	58.0/5.2	2	4	0.108	0.172	0.101	0.241	0.120	0.067
2	AT4G338970.1	Fructose bisphosphate aldolase 2	*Arabidopsis thaliana*	23.0/5.24	45.0/6.7	2	12	1.162	0.583	0.648	1.048	0.590	0.503
3	N.D[h]	Predicted protein	-	42.0/9.36	40.0/6.7	1	6	0.739	0.086	0.113	0.543	0.199	0.220
4	gi|255555933	Phospho ribulose kinase, putative	*Ricinus communis*	45.2/5.83	45.0/5.4	2	9	0.651	0.331	1.034	0.531	0.394	0.715
5	gi|399024	Fructose bisphosphate aldolase 1	*Pisum sativum*	38.7/5.83	39.0/6.3	2	9	0.188	0.015	0.062	0.154	0.070	0.00[i]
6	gi|809113	33KDa protein of oxygen evolving complex	*Solanum tuberosum*	35.4/5.87	35.0/5.4	2	7	0.765	0.455	0.061	0.678	0.537	0.074
7	gi|6066418	Ascorbate peroxidase	*Solanum lycopersicum*	27.8/5.73	30.0/6.0	2	12	0.393	0.363	0.113	0.344	0.164	0.121
8	gi|38112662	Triose phosphate isomerase, cytosolic	*Solanum chacoense*	27.2/5.73	29.0/6.7	13	65	0.473	0.350	0.240	0.426	0.227	0.202
9	CB1A_ARATH	Chlorophyll a/b binding protein 2	A. *thaliana*	28.2/5.29	25.0/5.5	2	6	0.305	0.077	0.123	0.146	0.091	0.081
10	N.D[h]	-	-	-	-	-	-	0.203	0.226	0.152	0.191	0.191	0.128
11	gi|399213	ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B	S. *lycopersicum*	102.4/5.86	100.0/5.8	3	5	0.163	0.115	0.157	0.236	0.117	0.128
12	RBL_SOLLC	Rubisco large chain	S. *lycopersicum*	53.4/6.55	72.0/6.8	2	5	0.793	0.230	0.152	0.329	0.194	0.181
13	gi|3913651	Ferredoxin-NADP reductase,leaf type isozyme, chloroplastic	*Nicotiana tobacum*	40.7/8.37	43.0/6.3	2	11	0.175	0.076	0.071	0.220	0.153	0.065
14	N.D.[h]	Fd-NADP Reductase/ protein stabilizing Mn	N. *tobacum*	40.7/8.37	35.0/5.0	1	5	0.155	0.166	0.124	0.098	0.196	0.118

Spot no.[a]	Accession no.[b]	Protein	Species	Theo.M_r (kD)/ pI[c]	Exp.M_r (kD)/ pI[d]	NP[e]	SC[f] (%)	Mean Spot volume (%)					
								WT			*hp1*		
								MG	BR	RR	MG	BR	RR
		complex											
15	N.D.[h]	-		-	-	-	-	0.226	0.121	0.148	0.247	0.114	0.107
16	gi|3219762	Full Actin 54	N. *tobacum*	37.5/5.66	53.0/5.6	2	12	0.206	0.145	0.010	0.229	0.149	0.149
17	gi|21599	UTP-glucose-1-phosphate uridylytransferase	S. *tuberosum*	52.0/5.39	62.0/6.2	3	12	0.428	0.491	0.147	0.425	0.247	0.161
18	METK1_SOLLC	S-Adenosyl Methionine Synthase1	S. *lycopersicum*	43.7/5.52	52.0/6.2	2	7	0.370	0.248	0.210	0.324	0.185	0.187
19	gi|82400156	Phospho glycerate kinase precursor	S. *tuberosum*	50.6/7.68	50.0/5.8	3	9	0.238	0.072	0.055	0.291	0.129	0.063
20	AT4G17190.1	Farnesyl diphosphate synthase 2	A. *thaliana*	41.4/5.33	39.0/6.7	1	3	0.227	0.166	0.084	0.241	0.162	0.093
21	gi_132095	Rubisco smaller sub unit	S. *lycopersicum*	20.4/6.59	13.0/5.4	3	17	0.862	0.431	0.152	0.742	0.546	0.369
22	gi_131921	Rubisco larger subunit	S. *lycopersicum*	51.9/6.09	53.0/6.98	2	5	1.746	0.580	0.825	3.688	1.236	1.575
23	gi_3913651	Ferredoxin NADP reductase	N. *tobacum*	40.7/8.37	40.0/6.5	2	11	0.338	0.113	0.058	0.291	0.129	0.063
24	gi_169039	Aldolase	P. *sativum*	37.9/5.47	42.0/5.6	6	26	0.153	0.051	0.080	0.103	0.119	0.059
25	gi_238563983	Chloroplast sedoheptulose 1-7 biphosphatase	*Achillea asiatica*	43.0/6.07	44.0/5.8	3	9	0.310	0.173	0.139	0.192	0.210	0.078
26	gi_131386	Chloroplast oxygen evolving enhancer protein-1	*Spinacia oleracea*	50.8/5.58	37.0/5.5	2	11	0.371	0.171	0.020	0.367	0.334	0.063
27	gi_11134054	Chloroplast oxygen evolving enhancer protein-1	S. *lycopersicum*	35.3/5.89	37.0/5.4	2	13	0.219	0.155	0.037	0.182	0.237	0.065
28	gi_170402	Chlorophyll a-b binding protein	S. *lycopersicum*	28.2/5.15	36.0/5.2	3	15	0.236	0.011	0.036	0.115	0.06	0.052
29	gi_132095	Rubisco smaller subunit 2A	S. *lycopersicum*	20.4/6.59	13.0/5.5	2	13	0.318	0.093	0.059	0.324	0.237	0.122

Spot no.[a]	Accession no.[b]	Protein	Species	Theo.M_r (kD)/ pI[c]	Exp.M_r (kD)/ pI[d]	NP[e]	SC[f] (%)	Mean Spot volume (%)					
								WT			*hp1*		
								MG	BR	RR	MG	BR	RR
30	gi_132079	Rubisco smaller subunit 1	S. *lycopersicum*	20.5/7.57	13.0/5.3	2	11	0.425	0.148	0.044	0.238	0.113	0.109
31	gi_21780187	Chloroplast chaperonin 10-like protein	S. *lycopersicum*	26.7/7.77	29.0/6.6	1	8	0.114	0.151	0.138	0.192	0.112	0.227
32	gi_2150027	NADP Malic enzyme	S. *lycopersicum*	70.5/5.93	75.0/6.0	13	27	0.105	0.059	0.052	0.110	0.061	0.098
33	gi_40457328	Glutamine synthase	*Nicotiana attenuata*	47.7/6.73	52.0/5.2	2	9	0.175	0.065	0.065	0.129	0.099	0.048
34	N.D.[h]	Hypothetical protein		16.4/9.22	17.7/5.3	1	5	0.216	0.148	0.043	0.129	0.096	0.045
35	SUT33_ARATH	Probable sulphate transporter 3.3	A. *thaliana*	69.3/5.9	43.0/6.0/	1	4	0.287	0.172	0.202	0.182	0.228	0.258
36	gi_10720247	Rubisco activase	*Solanum pennellii*	50.8/8.61	52.0/5.6	2	9	0.144	0.053	0.00[h]	0.085	0.039	0.00[i]
37	N.D.[h]	Rieske Fe/S protein of cytochrome b6/f complex		24.5/7.59	22.0/5.5	1	5	0.191	0236.	0.021	0.219	0.185	0.166
38	RBL_A98CESA	Ribulose bisphosphate carboxylase large chain	*Acer saccharum*	52.0/6.19	100.0/6.3	1	2	0.197	0.113	0.065	0.239	0.055	0.060
39	gi1762130	Chaperonin 60 β-subunit	S. *tuberosum*	63.2/5.72	94.0/5.3	2	4	0.256	0.268	0.479	0.282	0.292	0.434
40	gi6688527	ATP Synthase β subunit	S. *lycopersicum*	53.4/5.15	65.0/5.4	5	17	0.657	0.427	0.227	0.802	0.673	0.313
41	gi1196440	ACC Oxidase homologue (E8)	S. *lycopersicum*	41.5/5.61	52.0/5.8	4	13	0.174	0.634	1.973	0.053	0.403	2.383
42	gi|10798652	Malate dehydrogenase	*Solanum chilense*	36.0/5.91	51.0/6.0	3	6	0.479	0.473	0.267	0.472	0.213	0.207
43	gi283049930	Chloroplast manganese stabilizing protein	*Capsicum annum*	30.2/8.15	37.0/5.3	6	24	0.824	0.366	0.040	0.102	0.223	0.807

Spot no.[a]	Accession no.[b]	Protein	Species	Theo.M_r (kD)/ pI[c]	Exp.M_r (kD)/ pI[d]	NP[e]	SC[f] (%)	Mean Spot volume (%)					
								WT			*hp1*		
								MG	BR	RR	MG	BR	RR
44	N.D.[h]	-	-	-	-	-	-	0.260	0.291	0.125	0.316	0.232	0.111
45	gi266856	Oxygen-evolving enhancer protein 2, chloroplastic	S. *lycopersicum*	27.9/8.26	24.7/5.3	4	21	0.715	0.321	0.061	0.635	0.586	0.079
46	gi469070	RNA-binding glycine-rich protein-1a	*Nicotiana sylvestris*	15.6/5.58	18.0/5.4	2	19	0.159	0.281	0.235	0.224	0.197	0.394
47	N.D.[h]	Actin-depolymerizing factor 6		16.8/5.8	20.0/5.6	1	-	2.433	2.306	0.963	2.042	1.636	1.038
48	N.D.[h]	Bifunctional nitrilase/ nitrile hydratase		18.9/5.8	17.0/5.9	1	-	0.301	0.317	0.122	0.175	0.141	0.088
49	gi134612	Superoxide dismutase [Cu-Zn] 1	S. *lycopersicum*	15.4/5.83	17.0/5.7	2	8	0.255	0.630	0.662	0.384	0.312	0.768
50	gi4836469	17.7kD class I small heat shock protein	S. *lycopersicum*	17.7/5.4	52.0/5.3	4	-	0.096	0.049	0.238	0.247	0.104	0.00[i]
51	N.D.[h]	Ubiquitin carboxyl-terminal hydrolase 5		104.8/5.52	12.0/6.7	1	2	0.203	0.088	0.052	0.248	0.046	0.016
52	S47974	Nucleoside diphosphate kinase	S. *lycopersicum*	15.4/7.04	17.0/6.08	2	17	0.265	0.324	0.229	0.393	0.192	0.155
53	gi|124701	Acid β-fructofurnanosidase	S. *lycopersicum*	70.3/5.54	33.0/5.4	4	8	0.033	0.115	0.979	0.050	0.066	0.457
54	N.D.[h]	-		-	-	-	-	0.128	0.119	0.343	0.289	0.177	0.445
55	gi|26454609	14-3-3 protein 7	S. *lycopersicum*	28.9/4.96	31.0/5.0	2	15	0.145	0.190	0.387	0.184	0.162	0.355
56	gi|1709692	Peptide methionine sulfoxide reductase	S. *lycopersicum*	22.2/6.1	23.0/6.4	3	20	0.004	0.151	0.277	0.020	0.109	0.345
57	N.D.[h]	-		-	-	-	-	$2x10^{-3}$	0.190	0.415	0.007	0.017	0.374
58	Q38JD4_LYCES	Temperature induced lipocalin	S. *lycopersicum*	21.5/6.16	22.0/6.4	2	9	0.199	0.119	0.377	0.010	0.196	0.403
59	N.D.[h]	Hypothetical protein		-	22.0/6.8	1	-	0.002	0.143	0.126	0.003	0.202	0.163
60	gi|232273	17.8kDa class I heat shock protein	S. *lycopersicum*	17.7/5.84	22.0/6.0	2	23	0.00[g]	0.00[j]	0.330	0.00[g]	0.00[j]	0.069
61	gi|75279027	17.6kDa class I heat	*Solanum*	17.5/5.22	24.0/5.8	2	23	0.241	0.432	1.237	0.300	0308.	1.060

Spot no.[a]	Accession no.[b]	Protein	Species	Theo.M_r (kD)/ pI[c]	Exp.M_r (kD)/ pI[d]	NP[e]	SC[f] (%)	Mean Spot volume (%)					
								WT			*hp1*		
								MG	BR	RR	MG	BR	RR
		shock protein	*peruvianum*										
62	HSP11_SOLLC	17.8kDa class I heat shock protein	S. *lycopersicum*	17.7/5.84	21.0/5.6	2	23	0.625	1.247	1.745	0.825	0.773	1.77
63	Q6X1D0_LYCES	Iron superoxide dismutase	S. *lycopersicum*	27.9/6.53	22.0/6.0	2	8	0.092	0.071	0.073	0.094	0.062	0.098
64	GSTXC_TOBAC	Glutathione S-transferase	N. *tobacum*	25.9/5.9	21.0/5.7	2	5	0.093	0.17	0.302	0.086	0.041	0.299
65	EM_EST:DV103918	Heat-shock up-regulated genes cDNA clone	S. *lycopersicum*	25.8/8.94	26.0/5.5	1	6	0.089	0.104	0.093	0.099	0.074	0.290
66	CHRC_CUCSA	Chromoplast-specific carotenoid-associated protein	*Cucumis sativus*	35.6/4.32	35.0/4.8	2	16	0.351	0.174	0.148	0.083	0.138	0.350
67	Q9ZTV1_CANLI	Charperonion groEL	*Canavalia lineata*	61.4/4.77	62.5/5.0	2	5	0.296	0.326	0.387	0.304	0.312	0.501
68	HSP7S_PEA	Heat shock protein Hsp70	P. *sativum*	75.5/5.19	75.0/5.1	4	1	0.162	0.306	0.767	0.197	0.246	0.867
69	ADH_FRAAN	Alcohol dehydrogenase	*FragariaX ananassa*	42.7/6.61	25.0/5.4	2	8	0.05	0.076	0.634	0.023	0.085	0.079
70	N.D.[h]	-		-	-	-	-	0.199	0.309	0.147	0.157	0.130	0.154
71	N.D.[h]	-		-	-	-	-	0.209	0.286	0.553	0.207	0.249	0.782
72	N.D.[h]	Small heat shock protein	S. *lycopersicum*	-	22.0/6.3	1	-	0.014	0.298	0.326	0.058	0.075	0.241

[a]Spot number corresponding to spots in Figure 4.

[b]Accession number from different databases searched for a matched protein.

[c]Theoretical molecular mass and isoelectric point based on amino acid sequence.

[d]Experimental molecular mass and isoelectric point estimated from the 2D gels.

[e]Number of unique peptides identified for a given protein.

[f]Amino acid sequence coverage for the identified proteins.

[g]Expression of this protein was not detected in mature green fruits of wild type and *hp1*.

[h]Expression of this protein was not detected in wild type at this ripening stage.

[i] Expression of this protein was not detected in red ripe fruits of wild type and *hp1*.

[j] Expression of this protein was not detected in breaker fruits of wild type and *hp1*.

[h]Not Determined (N.D.) –proteins which were below the Mascot significance threshold and hence not identified.

Table 3.2. The differentially expressed proteins (Table 3.1) identified in this study were compared with other studies (Rocco et al., 2006; Faurobert et al., 2007; Qin et al., 2012) to identify similarities and differences in the proteome complement. The table lists the proteins that are specifically identified in the current study.

Spot number	Name of the protein
4	Phospho ribulose kinase, putative
6	33KDa protein of Oxygen evolving complex
11	ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B
13	Ferredoxin-NADP reductase,leaf type isozyme, chloroplastic
16	Full Actin 54
23	Ferredoxin NADP reductase
25	Chloroplast sedoheptulose 1-7 biphosphatase
32	NADP Malic enzyme
33	Glutamine synthase
43	Chloroplast manganese stabilizing protein
44	RNA-binding glycine-rich protein-1a
52	Nucleoside diphosphate kinase
63	Iron superoxide dismutase
66	Chromoplast-specific carotenoid-associated protein

Table 4.1. Details of gradient used for different fractionation techniques

Fractionation technique	Run time	Gradient employed
In-gel (GeLCMS)	118 min	5%-30% B (0-100 min), 30%-95% B (101-103 min), 95% B hold (104-106 min), 95%-5% B (107-113 min), 5% B hold (114-118 min)
SAX	100 min	8%-45% B (0-82 min), 45%-95% B (83-85 min), 95% B hold (86-88 min), 95%-5% B (89-95 min), 5% B hold (96-100 min)
FASP-SAX	95 min	5%-8% B (0-10 min), 8%-18% B (11-25 min), 18%-25% B (26-40 min), 25-32% B (41-55 min), 32%-40% B (56-65 min), 40%-52% B (66-70 min), 52%-95% B (71-78 min), 95% B hold (79-85 min), 95%-5% B (86-88 min), 5% B hold (89-95 min)
PEP-IEF, FASP-PEP-IEF	60 min	5%-30% B (0 -48 min), 30%-95% B (49-53 min), 95% B hold (54-56 min), 95%-5% B (57-58 min), 5% B hold (59-60 min)
In-solution	150 min	5%-30% B (0-128 min),30%-95% B (129-131 min), 95% B hold (132-138 min), 95%-5% B (139-145 min), 5% B hold (146-150 min)

Table 4.2. Effect of solubilizing agents on protein identification

Protocol	Protein extraction method	Buffers used for solubilization of pellet	Number of proteins identified
In-solution	Phenol extraction and precipitation with ice cold ammonium acetate in methanol	2D lysis buffer (urea 7 M, thio urea 2 M, CHAPS 4% (w/v))	09
In-solution	Phenol extraction and precipitation with ice cold ammonium acetate in methanol	SDS buffer[a] (0.5 M Tris-Hcl pH 6.8, 50% (v/v) glycerol, 10% (w/v) SDS, 0.2 M DTT)	08
In-solution	Phenol extraction and precipitation with ice cold ammonium acetate in methanol	2D lysis buffer+ SDS buffer[a] (urea 7 M, thio urea 2 M, CHAPS 4% (w/v), 0.5 M Tris-Hcl pH 6.8, 50% (v/v) glycerol, 10% (w/v) SDS, 0.2 M DTT)	10
In-solution	TCA extraction and precipitation with 80 % acetone (chilled)	2D Lysis buffer (urea 7 M, thio urea 2 M, CHAPS 4% (w/v))	0
In-solution without precipitation	Boiling in SDS buffer[c]	50 mM ammonium bicarbonate	0
In-solution with Guanidium Hydrochloride	Phenol extraction and precipitation with ice cold ammonium acetate in methanol	50 mM ammonium bicarbonate, 6 M Guanidium Hydrochloride	233
In-solution with Invitrosol	Boiling with SDS buffer[a] and precipitated with 80% acetone (chilled)	50 mM ammonium bicarbonate, Invitrosol	888
In-solution without Invitrosol	Boiling with SDS buffer[a] and precipitated with 80% acetone (chilled)	50 mM ammonium bicarbonate	814
In-solution with Rapigest	Boiling with SDS buffer[a] and precipitated with 80% acetone (chilled)	50 mM ammonium bicarbonate, Rapigest	402
In-solution without Rapigest	Boiling with SDS buffer[a] and precipitated with 80% acetone (chilled)	50 mM ammonium bicarbonate	720
In-solution with urea	Boiling with SDS buffer[b] and precipitated with 80% acetone (chilled)	8 M Urea	610

Table 4.3. Differentially expressed proteins identified in AV in comparison to AC using nanoLC-MS/MS.

Label free quantitation was employed by counting the number of spectra and normalizing the total spectra through NSAF using Scaffold software to identify the differentially expressed proteins in AV compared to AC. Stringent selection criteria were imposed to identify these proteins (p value≤0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR= 0.1%).

Proteins up-regulated in AV in comparison with AC

Accession.Number	DESCRIPTION	Molecula	Fold.Cha	AC.1.1	AC.2.1	AC.3.1	AV.1.1	AV.2.1	AV.3.1	P value	AC.1.1	AC.2.1	AC.3.1	AV.1.1	AV.2.1	AV.3.1	MAPMAN CLASS	MAPMAN DESCRIPTION
Solyc04g074510.2.1	functional description:14-3-3 protein beta/alpha-B (AHRD V1 -- 1	30 kDa	2.2	0.00992	0.0277	0.00313	0.0376	0.01387	0.03878	0.04	2	5	1	4	3	6	signalling 14-3-3 proteins	14-3-3 protein beta/alpha-B
Solyc04g074230.2.1	functional description:14-3-3 protein sigma gamma zeta beta/alpha	31 kDa	3.7	0.00941	0	0.00288	0.00636	0.01838	0.02075	0.00012	2	0	1	1	3	3	signalling 14-3-3 proteins	14-3-3 protein sigma gamma zeta beta/alpha
Solyc07g049530.2.1	functional description:1-aminocyclopropane-1-carboxylate oxidas	36 kDa	5.2	0	0.00465	0.00487	0.03224	0	0.01752	0.025	0	2	2	5	0	2	hormone metabolism ethylene syr	1-aminocyclopropane-1-carboxylate oxidase
Solyc07g044840.2.1	functional description:2 3-bisphosphoglycerate-independent phosp	61 kDa	2.6	0.01201	0.00133	0.01369	0.01646	0.02153	0.03357	0.0014	5	1	7	6	7	12	glycolysis cytosolic branch phospl	2 3-bisphosphoglycerate-independent phosphoglycerate mutase
Solyc01g099760.2.1	functional description:26S protease regulatory subunit 6A homolo	47 kDa	2.4	0.01322	0.0158	0.02814	0.03262	0.07502	0.02958	0.0007	4	6	9	10	14	9	stress abiotic heat	26S protease regulatory subunit 6A homolog
Solyc01g104920.2.1	functional description:26S protease regulatory subunit 8 homolog (	76 kDa	2.7	0.00426	0.00094	0.00145	0.0037	0.00762	0.00679	0.027	2	1	1	2	2	2	protein degradation AAA type	26S protease regulatory subunit 8 homolog
Solyc02g083710.2.1	functional description:26S proteasome non-ATPase regulatory sub	43 kDa	4.6	0	0.00368	0.00633	0.00571	0.02444	0.01552	0.0049	0	2	2	2	7	4	protein degradation ubiquitin E2	26S proteasome non-ATPase regulatory subunit 4
Solyc07g009140.2.1	functional description:26S proteasome non-ATPase regulatory sub	44 kDa	2.9	0.0058	0.00192	0.00441	0.00596	0.01984	0.00972	0.037	2	1	2	1	4	2	hormone metabolism brassinoster	26S proteasome non-ATPase regulatory subunit 6
Solyc08g082700.2.1	functional description:26S proteasome non-ATPase regulatory sub	31 kDa	11	0.00313	0.00274	0	0.01268	0.01374	0.03617	0.001	1	1	0	2	2	4	protein degradation ubiquitin prot	26S proteasome non-ATPase regulatory subunit 8
Solyc07g053650.2.1	functional description:26S proteasome regulatory subunit (AHRD	90 kDa	2.5	0.00485	0.00088	0.00117	0.00262	0.01489	0	0.028	3	1	1	2	11	0	stress biotic heat shock proteins	26S proteasome regulatory subunit
Solyc01g008370.2.1	functional description:26S proteasome regulatory subunit (AHRD	35 kDa	2.7	0.02287	0.00798	0	0.01625	0.03197	0.03353	0.039	5	2	0	2	6	7	protein degradation ubiquitin prot	26S proteasome regulatory subunit
Solyc02g062460.2.1	functional description:2-oxoglutarate-dependent dioxygenase (AH	37 kDa	3.9	0.0156	0.00456	0.00239	0.02637	0.05332	0.0086	0.011	4	2	1	4	7	1	hormone metabolism ethylene syr	2-oxoglutarate-dependent dioxygenase
Solyc01g068530.2.1	functional description:30S ribosomal protein S9 (AHRD V1 - C5J)	17 kDa	4.1	0.00746	0.01485	0	0.046	0.02918	0.01668	0.018	1	3	0	4	2	1	protein synthesis ribosome biogen	30S ribosomal protein S9
Solyc08g076450.2.1	functional description:3-beta hydroxysteroid dehydrogenase/isome	33 kDa	3.6	0.01355	0.00476	0.00498	0.03298	0.02381	0.02688	0.0083	3	2	2	4	4	3	RNA regulation of transcription u	3-beta hydroxysteroid dehydrogenase/isomerase family protein
Solyc09g091470.2.1	functional description:3-ketoacyl CoA thiolase 2 (AHRD V1 C8Y	49 kDa	3.3	0.00634	0.01263	0.00864	0.04679	0.02267	0.02222	0.00041	2	6	4	9	5	6	amino acid metabolism degradatic	3-ketoacyl CoA thiolase 2
Solyc03g097470.2.1	functional description:3-oxoacyl- (AHRD V1 - D5A3B9 SPIPL):	46 kDa	9.5	0.00206	0.00383	0	0.01169	0.01725	0.02679	0.00014	1	2	0	4	4	6	lipid metabolism FA synthesis anc	3-oxoacyl-
Solyc01g091190.2.1	functional description:3-phosphoshikimate 1-carboxyvinyltransfer	56 kDa	4.6	0.00645	0	0.00164	0.00221	0.02525	0.00962	0.0012	2	0	1	1	8	4	amino acid metabolism synthesis	3-phosphoshikimate 1-carboxyvinyltransferase
Solyc03g097900.2.1	functional description:40S ribosomal protein S1 (AHRD V1 - RS3/	30 kDa	4.8	0.01358	0.01264	0	0.02895	0.06645	0.03097	0.00051	4	3	0	5	10	6	protein synthesis ribosome biogen	40S ribosomal protein S1
Solyc12g096300.1.1	functional description:40S ribosomal protein S6 (AHRD V1 - B6T	28 kDa	3.6	0.01068	0.02981	0	0.03035	0.06965	0.04638	0.0022	2	8	0	4	8	8	protein synthesis ribosome biogen	40S ribosomal protein S6
Solyc12g096150.1.1	functional description:60S ribosomal protein L13 (AHRD V1 - Q3	24 kDa	3	0.0129	0.02402	0	0.04891	0.01804	0.04485	0.031	3	5	0	5	2	5	protein synthesis ribosomal protei	60S ribosomal protein L13
Solyc09g007250.2.1	functional description:60S ribosomal protein L4/L1 (AHRD V1 - I	45 kDa	2.1	0.01928	0.01097	0.02094	0.02832	0.03773	0.04314	0.0078	7	4	10	8	10	11	protein synthesis ribosome biogen	60S ribosomal protein L4/L1
Solyc10g086010.1.1	functional description:60S ribosomal protein L4/L1 (AHRD V1 - I	48 kDa	2.9	0.00514	0	0.00586	0.01586	0.01006	0.00575	0.016	2	0	3	4	4	2	protein synthesis ribosomal protei	60S ribosomal protein L4/L1
Solyc04g005160.1.1	functional description:6-phosphogluconate dehydrogenase decarb	52 kDa	2.9	0.00237	0.0063	0.01083	0.01221	0.02091	0.02391	0.0091	1	4	5	5	7	6	OPP oxidative PP 6-phosphogluc	6-phosphogluconate dehydrogenase decarboxylating
Solyc05g010260.2.1	functional description:6-phosphogluconate dehydrogenase decarb	30 kDa	4.4	0	0.00274	0.00314	0.00424	0.01211	0.00923	0.024	0	1	1	1	2	1	OPP oxidative PP 6-phosphogluc	6-phosphogluconate dehydrogenase decarboxylating
Solyc01g008330.2.1	functional description:Acetyl-CoA carboxylase biotin carboxylase	59 kDa	3.7	0.00417	0.00139	0.0111	0.01073	0.0245	0.02568	0.00051	1	1	6	4	10	7	lipid metabolism FA synthesis anc	Acetyl-CoA carboxylase biotin carboxylase
Solyc01g007340.2.1	functional description:Acetyl-coenzyme A carboxylase carboxyl tı	58 kDa	3.7	0	0.00386	0.00396	0.00505	0.01455	0.00926	0.021	0	3	2	1	6	4	cell wall modification	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
Solyc08g076990.2.1	functional description:Acetylornithine deacetylase (AHRD V1 - B	48 kDa	2.9	0.00511	0.00508	0.00388	0.00788	0.02498	0.00857	0.027	2	3	2	3	7	3	protein degradation	Acetylornithine deacetylase
Solyc08g075210.1.1	functional description:Acyltransferase-like protein (AHRD V1 -- (	47 kDa	4.2	0.00528	0.00525	0.00201	0.00814	0.02065	0.02361	0.0023	2	2	1	3	6	5	secondary metabolism phenylpror	Acyltransferase-like protein
Solyc09g092380.2.1	functional description:Adenosylhomocysteinase (AHRD V1 Q2X	53 kDa	2.2	0.04019	0.02891	0.00519	0.04934	0.0613	0.05476	0.0056	12	8	3	12	13	12	amino acid metabolism degradatic	Adenosylhomocysteinase
Solyc10g051340.1.1	functional description:Adenylyl cyclase-associated protein (AHRD	51 kDa	3.5	0.00237	0.00158	0.00542	0.00488	0.01162	0.01594	0.023	1	1	3	1	4	6	RNA regulation of transcription A	Adenylyl cyclase-associated protein
Solyc06g063090.2.1	functional description:Alanine aminotransferase (AHRD V1 O6V	59 kDa	3.1	0	0.00274	0.00628	0.00849	0.00808	0.01154	0.042	0	2	3	4	4	4	amino acid metabolism synthesis	Alanine aminotransferase
Solyc04g054310.2.1	functional description:Alanine-glyoxylate aminotransferase (AHR	52 kDa	2.2	0.01182	0.00942	0.02517	0.02188	0.05321	0.0291	0.0032	5	5	10	9	18	10	amino acid metabolism synthesis	Alanine-glyoxylate aminotransferase
Solyc02g085730.2.1	functional description:Allene oxide cyclase (AHRD V1 O9LEG5	27 kDa	9.7	0.00342	0	0.00314	0.02081	0.02004	0.02262	0.0021	1	0	1	2	2	2	stress abiotic drought/salt	Allene oxide cyclase
Solyc04g005340.2.1	functional description:Alpha-1 4-glucan protein synthase (AHRD	41 kDa	5.8	0.00234	0	0.00215	0.00474	0.0137	0.00773	0.033	1	0	1	1	4	2	cell wall cell wall proteins RGP	Alpha-1 4-glucan protein synthase
Solyc01g104170.2.1	functional description:Ankyrin repeat domain-containing protein 2	37 kDa	8.1	0	0.00709	0.0024	0.02887	0.0284	0.01985	0.00015	0	2	1	6	7	5	RNA regulation of transcription A	Ankyrin repeat domain-containing protein 2
Solyc04g073990.2.1	functional description:Annexin (AHRD V1 - O42657 CAPAN): c	36 kDa	2.2	0.04797	0.04203	0	0.08022	0.06312	0.05884	0.013	12	12	0	14	10	10	cell organisation	Annexin
Solyc01g007380.1.1	functional description:Apocytochrome f (AHRD V1 - D3WBH0 (	35 kDa	3.8	0.00277	0.01804	0	0.00787	0.03871	0.03248	0.0078	1	5	0	2	9	6	PS lightreaction cytochrome b6/f	Apocytochrome f
Solyc02g069260.2.1	functional description:ARGONAUTE 1 (AHRD V1 - D6RUV9 T(	116 kDa	9.5	0	0.00063	0.00096	0.00123	0.01113	0.0027	0.00069	0	1	1	1	10	3	DNA repair	ARGONAUTE 1
Solyc09g007270.2.1	functional description:Ascorbate peroxidase (AHRD V1 B9VRH6	28 kDa	2.1	0.12353	0.03223	0.10436	0.23022	0.14669	0.1766	0.00081	15	7	12	16	16	13	redox ascorbate and glutathione a	Ascorbate peroxidase
Solyc05g056250.2.1	functional description:Asparaginyl-tRNA synthetase (AHRD V1 (	61 kDa	2.4	0.00542	0.0024	0.00554	0.01412	0.00969	0.00863	0.031	2	2	3	5	5	5	protein aa activation aspartate-tRl	Asparaginyl-tRNA synthetase
Solyc08g041870.2.1	functional description:Aspartate aminotransferase (AHRD V1 O2	51 kDa	2.4	0	0.00848	0.01305	0.01662	0.01597	0.0183	0.038	0	4	6	4	5	6	mitochondrial electron transport /	Aspartate aminotransferase
Solyc01g096450.2.1	functional description:Aspartic proteinase nepenthesin-1 (AHRD	48 kDa	2.3	0.00333	0.01179	0.02041	0.02022	0.03331	0.02757	0.0089	1	6	8	6	7	7	RNA regulation of transcription p	Aspartic proteinase nepenthesin-1
Solyc03g111180.2.1	functional description:Aspartyl aminopeptidase-like protein (AHR	53 kDa	2.1	0.00928	0.00308	0.01764	0.01193	0.0227	0.02855	0.028	4	2	7	5	7	5	protein degradation aspartate prot	Aspartyl aminopeptidase-like protein
Solyc01g059880.2.1	functional description:ATP citrate lyase a-subunit (AHRD V1 O9	66 kDa	2.3	0.00242	0.00537	0.00826	0.00632	0.0156	0.01545	0.024	1	4	5	3	7	8	protein degradation ubiquitin E3 I	ATP citrate lyase a-subunit
Solyc03g052980.2.1	functional description:ATP dependent RNA helicase (AHRD V1	66 kDa	2.4	0.00326	0.00356	0.00315	0.00352	0.01636	0.00431	0.048	2	3	2	2	7	2	RNA processing RNA helicase	ATP dependent RNA helicase
Solyc01g007320.2.1	functional description:ATP synthase subunit beta chloroplastic (A	66 kDa	3.3	0.00436	0.00271	0.00689	0.03102	0.00407	0.01138	0.011	3	2	3	10	2	4	PS lightreaction ATP synthase bet	ATP synthase subunit beta chloroplastic
Solyc12g042060.1.1	functional description:ATP-dependent clp protease ATP-binding s	102 kDa	5.1	0.00242	0	0.00092	0.00374	0.00237	0.01085	0.0044	2	0	1	3	2	7	protein degradation serine proteas	ATP-dependent clp protease ATP-binding subunit
Solyc04g016470.2.1	functional description:Beta-1 3-glucanase (AHRD V1 - B2ZP01 V	38 kDa	2.2	0.02825	0.04542	0	0.04381	0.08618	0.03013	0.03	10	14	0	8	10	6	misc beta 1 3 glucan hydrolases g	Beta-1 3-glucanase
Solyc12g008840.1.1	functional description:Beta-galactosidase (AHRD V1 - O81100 S(	80 kDa	3.4	0.00204	0	0.00278	0.00177	0.00437	0.01038	0.012	1	0	2	1	2	6	development late embryogenesis a	Beta-galactosidase
Solyc11g008810.1.1	functional description:Beta-hexosaminidase b (AHRD V1 Q17BL	56 kDa	4.6	0.00297	0	0.00202	0.00258	0.01485	0.00567	0.0078	1	0	1	1	6	2	protein glycosylation alpha-1 6-m	Beta-hexosaminidase b
Solyc03g113800.2.1	functional description:Betaine aldehyde dehydrogenase (AHRD V	56 kDa	2.8	0.01329	0.00441	0.00842	0.0296	0.01734	0.02725	0.0011	6	3	4	10	7	8	fermentation aldehyde dehydroge	Betaine aldehyde dehydrogenase
Solyc01g099090.2.1	functional description:Beta-mannosidase (AHRD V1 - D7IJR3 9E	111 kDa	6.8	0.00115	0	0.00088	0.00119	0.01129	0.00129	0.0027	1	0	1	1	9	1	cell wall degradation mannan-xylo	Beta-mannosidase
Solyc05g007060.2.1	functional description:Bifunctional N-succinyldiaminopimelate-am	37 kDa	7.1	0.00271	0.00252	0	0.00385	0.02273	0.0106	0.015	1	1	0	1	5	2	misc nitrilases nitrile lyases berb	Bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transamina
Solyc08g074290.2.1	functional description:BRI1-KD interacting protein 129 (Fragment	51 kDa	2.1	0.00754	0.00834	0.01911	0.00775	0.03689	0.02812	0.031	2	4	9	2	11	7	DNA repair	BRI1-KD interacting protein 129 (Fragment)
Solyc05g056230.2.1	functional description:Calreticulin 2 calcium-binding protein (AHF	51 kDa	2.4	0.01033	0.01029	0.00785	0.01328	0.02275	0.03179	0.018	3	6	3	5	7	10	signalling calcium	Calreticulin 2 calcium-binding protein
Solyc07g041900.2.1	functional description:Cathepsin L-like cysteine proteinase (AHRI	39 kDa	3.2	0.0211	0.02058	0.01293	0.05231	0.05838	0.06201	0.00021	5	4	4	7	7	6	protein degradation cysteine prote	Cathepsin L-like cysteine proteinase
Solyc01g088400.2.1	functional description:CER1 (AHRD V1 -- B6TFH3 MAIZE): co	73 kDa	5.4	0.00477	0.00231	0	0.0103	0.00709	0.02098	0.00026	3	2	0	5	4	7	hormone metabolism brassinoster	CER1
Solyc01g103450.2.1	functional description:Chaperone DnaK (AHRD V1 - O1SKX2 M	75 kDa	4	0.00477	0.00211	0.00242	0.00654	0.00778	0.02314	0.0028	3	2	2	4	4	8	stress abiotic heat	Chaperone DnaK
Solyc04g081570.2.1	functional description:Chaperone protein htpG (AHRD V1 -- HTP	93 kDa	2.3	0.01106	0.00716	0.00713	0.00929	0.02878	0.01947	0.0014	7	7	5	6	18	11	stress abiotic heat	Chaperone protein htpG
Solyc11g069790.1.1	functional description:chaperonin (AHRD V1 - B2IXD2 NOSP7):	62 kDa	6.6	0.00151	0.0014	0.00143	0.00857	0.00632	0.01375	0.0045	1	1	1	4	2	5	PS calvin cycle rubisco interactin	chaperonin
Solyc04g082780.2.1	functional description:Cinnamoyl CoA reductase-like 1 (AHRD V	36 kDa	5.7	0.00552	0.00771	0	0.02354	0.02316	0.02878	0.0013	1	3	0	5	5	7	secondary metabolism flavonoids	Cinnamoyl CoA reductase-like 1
Solyc02g069800.1.1	functional description:CXE carboxylesterase (AHRD V1 -- O0ZPI	37 kDa	3.8	0.01851	0.00985	0	0.0188	0.05547	0.03447	0.0012	5	3	0	4	11	7	biodegradation of xenobiotics	CXE carboxylesterase
Solyc09g082060.2.1	functional description:Cysteine synthase (AHRD V1 Q3LAG5 T(	34 kDa	2.7	0.01363	0.01523	0	0.01163	0.03812	0.02843	0.039	4	6	0	3	6	6	amino acid metabolism synthesis	Cysteine synthase
Solyc09g066150.1.1	functional_description:Cytochrome P450	58 kDa	2.3	0.01762	0.0156	0.02002	0.0255	0.05879	0.03556	0.00031	6	11	8	7	17	12	protein targeting secretory pathwa	Cytochrome P450
Solyc03g096990.2.1	functional description:Cytochrome P450 89A2 (AHRD V1 - C89A	63 kDa	2.7	0.0027	0.0012	0.00368	0	0.01351	0.00688	0.043	1	1	2	0	4	2	misc cytochrome P450	Cytochrome P450 89A2
Solyc01g091690.2.1	functional description:Dehydration-responsive family protein (AH	72 kDa	3	0.00232	0.00205	0.00158	0.00402	0.00497	0.00886	0.043	1	2	1	2	2	5	stress abiotic drought/salt	Dehydration-responsive family protein
Solyc08g069030.2.1	functional description:Delta-aminolevulinic acid dehydratase (AH	47 kDa	4.4	0	0.00345	0.00395	0.00535	0.01527	0.01164	0.018	0	1	2	2	4	3	tetrapyrrole synthesis ALA dehyd	Delta-aminolevulinic acid dehydratase
Solyc11g007720.1.1	functional description:Dihydrolipoyllysine-residue acetyltransfera	69 kDa	2.4	0.0031	0.00339	0.0045	0.00335	0.01728	0.00614	0.033	2	2	2	2	7	2	TCA / organic transformation TC.	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase (
Solyc02g081160.2.1	functional description:Diphosphate-fructose-6-phosphate 1-phosph	62 kDa	5.4	0.00197	0.0013	0.00598	0.00606	0.01539	0.02859	0.00015	1	1	3	2	5	9	glycolysis plastid branch pyropho	Diphosphate-fructose-6-phosphate 1-phosphotransferase
Solyc11g006460.1.1	functional description:DNAJ chaperone (AHRD V1 - B0W7V8 C	47 kDa	3.6	0	0.00177	0.00812	0.00274	0.02089	0.01194	0.023	0	1	2	1	5	3	stress abiotic heat	DNAJ chaperone
Solyc01g088510.2.1	functional description:Dynamin like protein (AHRD V1 - D3BTL7	58 kDa	2.7	0.00195	0.00426	0.00377	0.00211	0.01739	0.00772	0.045	1	3	2	1	5	2	protein degradation ubiquitin E3 I	Dynamin like protein
Solyc11g072190.1.1	functional description:Elongation factor beta-1 (AHRD V1 - A2YI	25 kDa	4.5	0.01471	0.01291	0.00338	0.0522	0.0377	0.04862	0.001	3	4	1	5	5	6	redox thioredoxin	Elongation factor beta-1
Solyc02g082920.2.1	functional description:Endochitinase (Chitinase) (AHRD V1 Q43	28 kDa	4.7	0.0066	0.00579	0	0.01338	0.03382	0.01091	0.014	1	1	0	2	3	2	stress biotic PR-proteins PR3/4/8/	Endochitinase (Chitinase)
Solyc09g009020.2.1	functional description:Enolase (AHRD V1 - C5J0G6 TOBAC): cc	48 kDa	2.8	0.01796	0.00557	0.00378	0.0312	0.01395	0.03121	0.013	6	3	2	8	3	8	glycolysis cytosolic branch enolas	Enolase
Solyc05g054350.2.1	functional description:Epoxide hydrolase (AHRD V1 O41414 SC	36 kDa	4.7	0.01104	0.00514	0	0.03139	0.01544	0.02878	0.003	4	2	0	4	3	5	misc misc2	Epoxide hydrolase
Solyc05g055210.1.1	functional description:Eukaryotic peptide chain release factor subı	49 kDa	3.7	0.00256	0.0017	0.00778	0.01053	0.02003	0.01432	0.0063	1	1	3	3	8	4	protein synthesis release	Eukaryotic peptide chain release factor subunit 1-3-like
Solyc01g087120.2.1	functional description:F1-ATP synthase delta subunit (AHRD V1 -	26 kDa	2.7	0.00698	0.02146	0.02247	0.0425	0.02557	0.06927	0.024	2	6	6	4	4	4	mitochondrial electron transport /	F1-ATP synthase delta subunit
Solyc12g099440.1.1	functional description:Fatty acid oxidation complex subunit alpha	79 kDa	2.9	0.00406	0.0018	0.00415	0.0088	0.0116	0.00905	0.0055	2	2	2	4	5	6	lipid metabolism lipid degradation	Fatty acid oxidation complex subunit alpha
Solyc05g052470.2.1	functional description:Ferritin (AHRD V1 - A7UGG8 SOLTU): c	29 kDa	4.1	0.00647	0.00568	0.0119	0.03281	0.02843	0.03743	0.00069	1	2	4	4	3	6	metal handling binding chelation	Ferritin
Solyc06g050980.2.1	functional description:Ferritin (AHRD V1 - O308A9 SOLTU): co	28 kDa	3.5	0.00333	0.02043	0.01223	0.03372	0.05357	0.03848	0.0039	1	6	4	4	8	5	metal handling binding chelation	Ferritin
Solyc01g006280.2.1	functional description:Formate-tetrahydrofolate ligase (AHRD V1	67 kDa	2.3	0.00465	0.00618	0.00634	0.01413	0.0133	0.01185	0.027	2	5	3	7	6	5	RNA regulation of transcription c	Formate-tetrahydrofolate ligase
Solyc02g091490.2.1	functional description:Fructokinase 3 (AHRD V1 - O6VWJ5 SOL	42 kDa	3.9	0.01367	0.00636	0	0.02914	0.01911	0.02969	0.00017	5	3	0	7	4	7	minor CHO metabolism others	Fructokinase 3
Solyc12g056530.1.1	functional description:Fructose-1 6-bisphosphatase class 1 (AHRL	37 kDa	4	0.02606	0.00243	0	0.01482	0.06094	0.03736	0.00048	7	1	0	4	10	8	stress biotic receptors	Fructose-1 6-bisphosphatase class 1
Solyc02g084440.2.1	functional description:Fructose-bisphosphate aldolase (AHRD V1	42 kDa	3.2	0.02486	0.01473	0	0.02249	0.06004	0.04419	0.00088	7	6	0	7	11	8	PS calvin cycle aldolase	Fructose-bisphosphate aldolase
Solyc05g008600.2.1	functional description:Fructose-bisphosphate aldolase (AHRD V1	43 kDa	4	0.01794	0.00418	0	0.01275	0.03763	0.03801	0.0012	4	2	0	4	7	6	PS calvin cycle aldolase	Fructose-bisphosphate aldolase
Solyc00g011890.2.1	functional description:Galactokinase like protein (AHRD V1 O23	114 kDa	3.3	0.00285	0	0.00194	0.00371	0.00407	0.00816	0.0036	2	0	2	3	3	7	minor CHO metabolism galactose	Galactokinase like protein
Solyc01g099040.2.1	functional description:GDSL esterase/lipase At5g03980 (AHRD V	43 kDa	3.2	0.01177	0.00586	0.00895	0.0121	0.04607	0.02634	0.001	4	3	4	4	15	8	misc GDSL-motif lipase	GDSL esterase/lipase At5g03980
Solyc12g014380.1.1	functional_description:Glucose-6-phosphate isomerase 1	63 kDa	6.9	0.00197	0.00131	0.0015	0.00202	0.01541	0.01542	0.00072	1	1	1	1	7	6	glycolysis plastid branch glucose-	Glucose-6-phosphate isomerase 1
Solyc08g005630.2.1	functional description:Glucose-methanol-choline oxidoreductase (	86 kDa	6.2	0.00145	0	0.0011	0.00297	0.00141	0.01132	0.0096	1	0	1	2	1	6	not assigned no ontology	Glucose-methanol-choline oxidoreductase
Solyc03g114710.2.1	functional description:Glucosyltransferase (AHRD V1 B5MGN9	50 kDa	6.2	0.00249	0.00165	0	0.00256	0.01462	0.00836	0.0096	1	1	0	1	3	3	misc UDP glucosyl and glucorony	Glucosyltransferase
Solyc01g102410.2.1	functional description:Glutaminyl-tRNA synthetase (AHRD V1 - (	84 kDa	2.5	0.00199	0.00617	0.00543	0.00865	0.01567	0.01016	0.019	1	6	3	3	7	6	protein aa activation glutamate-tR	Glutaminyl-tRNA synthetase
Solyc12g011310.1.1	functional description:Glutathione S-transferase (AHRD V1 - Q0P	26 kDa	3.8	0.02668	0.00334	0.00701	0.00773	0.05024	0.0819	0.0012	4	1	2	1	7	6	misc glutathione S transferases	Glutathione S-transferase
Solyc04g009030.2.1	functional description:Glyceraldehyde-3-phosphate dehydrogenas	43 kDa	3.8	0.01554	0.00413	0	0.00947	0.02794	0.03763	0.0027	5	2	0	3	5	8	PS calvin cycle GAP	Glyceraldehyde-3-phosphate dehydrogenase
Solyc06g071920.2.1	functional description:Glyceraldehyde-3-phosphate dehydrogenas	37 kDa	2.2	0.0815	0.01468	0.00498	0.07101	0.09925	0.04797	0.00014	16	5	2	11	9	8	glycolysis cytosolic branch glycer	Glyceraldehyde-3-phosphate dehydrogenase
Solyc03g118170.2.1	functional description:Glycyl-tRNA synthetase (AHRD V1 D7KE	70 kDa	2.2	0.00482	0.00351	0.00311	0	0.01254	0.01273	0.00049	3	3	2	0	6	4	protein aa activation glycine-tRN.	Glycyl-tRNA synthetase
Solyc08g078510.2.1	functional description:GRAM-containing/ABA-responsive protein	31 kDa	3.1	0.02223	0.0473	0.00301	0.05417	0.11544	0.05795	0.00035	4	9	1	8	13	10	hormone metabolism abscisic acic	GRAM-containing/ABA-responsive protein (Fragment)
Solyc09g090330.2.1	functional description:Harpin binding protein 1 (AHRD V1 -- Q5C	30 kDa	2.6	0.01512	0.01327	0.01112	0.03067	0.02658	0.04499	0.035	3	3	3	3	4	5	cell organisation	Harpin binding protein 1
Solyc12g043120.1.1	functional description:Heat shock protein 4 (AHRD V1 - B6U237	93 kDa	3.1	0.00708	0	0.00342	0.00892	0.00921	0.01402	0.0013	6	0	3	7	6	6	major CHO metabolism degradati	Heat shock protein 4
Solyc07g061790.2.1	functional description:Heme-binding protein 2 (AHRD V1 B6T0C	26 kDa	4.3	0.00729	0.0128	0.01675	0.04435	0.04804	0.06627	0.00046	2	3	3	2	5	5	protein degradation ubiquitin ubiq	Heme-binding protein 2
Solyc01g102800.2.1	functional description:Histidyl-tRNA synthetase (AHRD V1 -- O5	96 kDa	5.2	0	0.00074	0.00114	0.00145	0.00719	0.00107	0.042	0	1	1	1	6	1	protein aa activation histidine-tRN	Histidyl-tRNA synthetase
Solyc11g065490.1.1	- functional description:Homology to unknown gene (Fragment) (/	44 kDa	3.5	0	0.00316	0.00487	0.0093	0.0051	0.01365	0.043	0	2	1	2	2	3	DNA synthesis/chromatin structu	Homology to unknown gene (Fragment)
Solyc06g073060.2.1	functional description:Iaa-amino acid hydrolase 6 (AHRD V1 A9I	47 kDa	3	0.0026	0.00518	0.00395	0.01337	0.01272	0.00873	0.042	1	2	2	5	4	2	hormone metabolism auxin synthe	Iaa-amino acid hydrolase 6
Solyc01g060470.2.1	functional description:Importin alpha-1b subunit (AHRD V1 - B6T	59 kDa	2.1	0.02743	0.01261	0.03048	0.03688	0.04749	0.06138	0.00081	8	8	15	11	11	12	PS calvin cycle rubisco interactin	Importin alpha-1b subunit
Solyc08g041890.2.1	functional description:Importin alpha-1b subunit (AHRD V1 - B6T	64 kDa	3.4	0.00194	0.00129	0.00147	0.00399	0.00569	0.00651	0.0083	1	1	1	2	3	3	PS calvin cycle rubisco interactin	Importin alpha-1b subunit
Solyc01g104070.2.1	functional description:Importin beta (AHRD V1 -- D2VK12 NAE	115 kDa	2.3	0.00281	0.00311	0.00766	0.00488	0.01507	0.01164	0.0044	2	4	7	3	13	7	protein targeting nucleus	Importin beta
Solyc02g081400.2.1	functional description:Intracellular protease PfpI family protein ex	42 kDa	5	0.00685	0.00425	0	0.01623	0.01277	0.02679	0.0035	2	2	0	4	3	7	development unspecified	Intracellular protease PfpI family protein expressed
Solyc01g005560.2.1	functional description:Isocitrate dehydrogenase (AHRD V1 - D2D	47 kDa	3.1	0.00355	0.00629	0.00968	0.03393	0.01016	0.01585	0.0084	1	4	4	10	4	5	RNA transcription	Isocitrate dehydrogenase
Solyc11g012140.1.1	functional description:Isoleucyl-tRNA synthetase (AHRD V1 - Q6	135 kDa	2.1	0.00374	0.00055	0.0034	0.00108	0.00981	0.00556	0.016	3	1	4	1	8	6	protein aa activation isoleucine-tF	Isoleucyl-tRNA synthetase
Solyc08g075390.2.1	functional description:Isopentenyl-diphosphate delta-isomerase fa	89 kDa	2.8	0.00127	0.00278	0.00246	0	0.01137	0.00673	0.045	1	3	2	0	6	3	nucleotide metabolism salvage NU	Isopentenyl-diphosphate delta-isomerase family protein
Solyc05g024410.2.1	functional description:Kelch-like protein 9 (AHRD V1 - KLHL9 I	36 kDa	3.3	0.00544	0.02024	0	0.01159	0.038	0.03542	0.011	2	6	0	3	8	7	secondary metabolism sulfur-cont	Kelch-like protein 9
Solyc07g053280.2.1	functional description:Ketol-acid reductoisomerase (AHRD V1 - I	64 kDa	3.2	0.00377	0.005	0.01575	0.00968	0.03869	0.02949	0.0002	2	4	7	5	12	10	amino acid metabolism synthesis l	Ketol-acid reductoisomerase
Solyc05g013070.2.1	functional description:Kinase family protein (AHRD V1 D7KBF8	49 kDa	6.5	0.00257	0	0.00195	0.00264	0.01255	0.01435	0.0051	1	0	1	1	3	4	protein postranslational modificat	Kinase family protein
Solyc01g099160.2.1	functional description:Lipoxygenase (AHRD V1 Q9FT17 SOLLC	98 kDa	2.3	0.00694	0.00169	0.00672	0.00375	0.02582	0.00611	0.0018	6	2	5	3	15	4	hormone metabolism jasmonate sy	Lipoxygenase
Solyc09g011880.2.1	functional description:LOC556397 protein (Fragment) (AHRD V1	48 kDa	3.9	0	0.00606	0.00233	0.00891	0.01467	0.00872	0.034	0	2	1	2	5	3	stress abiotic heat	LOC556397 protein (Fragment)
Solyc03g025720.2.1	functional description:Long-chain-fatty-acid--CoA ligase (AHRD	56 kDa	4.1	0.00214	0	0.00325	0.0066	0.00837	0.00718	0.024	1	0	2	3	3	2	cell organisation	Long-chain-fatty-acid--CoA ligase
Solyc04g015750.2.1	functional description:Magnesium chelatase H subunit (AHRD V1	154 kDa	6.5	0.00107	0	0.00073	0	0.00763	0.00408	0.00037	1	0	1	0	8	6	tetrapyrrole synthesis magnesium	Magnesium chelatase H subunit
Solyc01g008710.2.1	functional description:Mannan endo-1 4-beta-mannosidase (AHRI	45 kDa	3	0.0075	0.01093	0.00726	0.03242	0.01116	0.03302	0.0021	3	5	3	9	3	7	cell wall degradation mannan-xylo	Mannan endo-1 4-beta-mannosidase
Solyc02g078990.2.1	functional description:Mercaptopyruvate sulfurtransferase-like prc	35 kDa	2.6	0.00836	0.01037	0	0.00396	0.02727	0.01816	0.012	2	2	0	1	6	4	amino acid metabolism degradatic	Mercaptopyruvate sulfurtransferase-like protein
Solyc02g065280.2.1	functional description:Methyl jasmonate esterase (AHRD V1 - Q5	30 kDa	7.4	0.00315	0.00276	0.00579	0.03194	0.01845	0.03644	0.0004	1	1	2	3	2	4	misc nitrilases nitrile lyases berb	Methyl jasmonate esterase
Solyc01g106080.2.1	functional description:Methylmalonate-semialdehyde dehydrogena	58 kDa	2.6	0.00417	0.00138	0.00633	0.00857	0.01019	0.01165	0.047	2	1	3	4	3	4	secondary metabolism N misc bet	Methylmalonate-semialdehyde dehydrogenase
Solyc11g062190.1.1	functional description:Mitochondrial ADP/ATP carrier proteins (A	42 kDa	2.3	0.05321	0.03446	0	0.04275	0.10674	0.05126	0.0048	14	13	0	10	16	9	transport metabolite transporters a	Mitochondrial ADP/ATP carrier proteins
Solyc02g094470.2.1	functional description:Mitochondrial phosphate carrier protein (AI	38 kDa	3.2	0.00836	0.00609	0.00809	0.01204	0.02797	0.03312	0.0022	3	2	3	4	7	7	transport metabolite transporters a	Mitochondrial phosphate carrier protein
Solyc12g008630.1.1	functional description:Mitochondrial processing peptidase alpha su	55 kDa	2.3	0.01553	0.00736	0.01518	0.0365	0.0304	0.01986	0.0034	4	5	6	11	9	6	protein targeting mitochondria	Mitochondrial processing peptidase alpha subunit
Solyc02g088700.2.1	functional description:Mitochondrial processing peptidase beta sul	59 kDa	3.1	0.00631	0.00279	0.00639	0.00432	0.02468	0.01882	0.0044	3	2	4	2	9	6	protein targeting mitochondria	Mitochondrial processing peptidase beta subunit
Solyc01g098920.2.1	functional description:Mitochondrial Rho GTPase 1 (AHRD V1 E	71 kDa	3.8	0	0.00506	0.00312	0.00595	0.01634	0.00874	0.0086	0	5	2	3	9	6	signalling G-proteins	Mitochondrial Rho GTPase 1
Solyc08g014420.2.1	functional description:Mitogen-activated protein kinase 2 (AHRD	45 kDa	5.8	0	0.00188	0.00216	0.00292	0.01111	0.00953	0.032	0	1	1	1	4	3	protein postranslational modificat	Mitogen-activated protein kinase 2
Solyc09g009390.2.1	functional description:Monodehydroascorbate reductase (NADH)-	47 kDa	2.7	0.03274	0.00381	0	0.04363	0.01717	0.03734	0.0075	11	1	0	13	5	10	redox ascorbate and glutathione a	Monodehydroascorbate reductase (NADH)-like protein
Solyc01g080640.2.1	functional description:Multidrug resistance protein ABC transport	169 kDa	3.7	0.00098	0.00174	0.00067	0.00513	0.00493	0.00251	0.011	1	4	1	4	5	2	transport ABC transporters and m	Multidrug resistance protein ABC transporter family
Solyc02g070770.2.1	functional description:NAD-dependent epimerase/dehydratase (AI	32 kDa	5.6	0.00607	0.00565	0	0.00431	0.03394	0.02768	0.004	2	1	0	1	5	5	signalling light	NAD-dependent epimerase/dehydratase
Solyc01g097340.2.1	functional description:NAD-dependent epimerase/dehydratase fan	42 kDa	3	0.00297	0.00197	0.00452	0	0.01164	0.01664	0.015	1	1	2	0	2	3	redox ascorbate and glutathione a	NAD-dependent epimerase/dehydratase family protein-like protein
Solyc10g051350.1.1	functional description:NADH-quinone oxidoreductase subunit I (A	26 kDa	6.9	0.00365	0	0.0067	0.00739	0.02135	0.04217	0.0031	1	0	2	1	4	6	mitochondrial electron transport /	NADH-quinone oxidoreductase subunit I
Solyc12g044600.2.1	functional description:NADP-dependent malic enzyme chloroplast	70 kDa	4.7	0.0035	0	0.00133	0.0018	0.00513	0.01564	0.0011	2	0	1	1	3	5	TCA / organic transformation oth	NADP-dependent malic enzyme chloroplastic
Solyc03g120350.2.1	functional description:N-alpha-acetyltransferase 16 NatA auxiliary	103 kDa	3.1	0.00164	0	0.00112	0	0.00235	0.00628	0.042	1	0	1	0	2	6	misc acyl transferases	N-alpha-acetyltransferase 16 NatA auxiliary subunit
Solyc10g081030.1.1	functional description:Nascent polypeptide-associated complex alı	22 kDa	3.5	0.02517	0.01841	0.02699	0.09357	0.06757	0.0832	0.00055	5	4	6	7	9	8	cell unspecified	Nascent polypeptide-associated complex alpha subunit-like protein
Solyc03g006140.2.1	functional description:Neutral ceramidase (AHRD V1 A9YFM2	84 kDa	4.4	0	0.00194	0.00111	0.00151	0.00716	0.00491	0.042	0	2	1	1	4	2	lipid metabolism exotics (steroids	Neutral ceramidase
Solyc08g062190.2.1	functional description:Nitrilase 2 (AHRD V1 - D3BLP1 POLPA):	41 kDa	6.2	0.00478	0.00889	0	0.01358	0.03673	0.03424	0.00014	2	3	0	3	7	7	misc nitrilases nitrile lyases berb	Nitrilase 2
Solyc06g071000.2.1	functional description:N-succinylglutamate 5-semialdehyde dehyd	62 kDa	2.4	0.00808	0.00268	0.01074	0.01245	0.02568	0.01355	0.011	4	2	7	5	10	6	amino acid metabolism degradatic	N-succinylglutamate 5-semialdehyde dehydrogenase
Solyc05g008830.2.1	functional description:Octicosapeptide/Phox/Bem1p domain-conta	70 kDa	3.4	0.00155	0.00226	0.0015	0.00168	0.01211	0.0041	0.036	1	2	1	1	5	2	protein postranslational modificat	Octicosapeptide/Phox/Bem1p domain-containing protein
Solyc01g106320.2.1	functional description:Octicosapeptide/Phox/Bem1p domain-conta	54 kDa	3.8	0.00227	0	0.00345	0.00233	0.00666	0.01269	0.042	1	0	2	1	3	4	development multitarget target of	Octicosapeptide/Phox/Bem1p domain-containing protein
Solyc04g076820.1.1	functional description:Octicosapeptide/Phox/Bem1p domain-conta	52 kDa	9.4	0.00236	0	0.00179	0.00243	0.02078	0.01584	0.0002	1	0	1	1	6	3	RNA regulation of transcription g	Octicosapeptide/Phox/Bem1p domain-containing protein
Solyc02g091580.2.1	functional description:Oligopeptidase A (AHRD V1 - Q9LSL3 AI	91 kDa	2.1	0.00371	0.0036	0.00598	0.00267	0.0193	0.00653	0.027	3	4	5	2	11	4	hormone metabolism brassinoster	Oligopeptidase A
Solyc08g080640.1.1	functional description:Osmotin-like protein (Fragment) (AHRD V1	27 kDa	2.2	0.01014	0.03559	0.04039	0.09595	0.07424	0.02234	0.037	2	7	6	7	10	3	stress abiotic	Osmotin-like protein (Fragment)
Solyc08g080650.1.1	functional description:Osmotin-like protein (Fragment) (AHRD V1	27 kDa	8.2	0	0.00298	0.00624	0.03441	0.02982	0.01122	0.0036	0	1	1	2	3	2	stress abiotic	Osmotin-like protein (Fragment)
Solyc02g065400.2.1	functional description:Oxygen-evolving enhancer protein 1 of pho	35 kDa	3.2	0.00808	0.02256	0.00255	0.01531	0.02636	0.06318	0.0057	3	6	1	3	4	11	PS lightreaction photosystem II P:	Oxygen-evolving enhancer protein 1 of photosystem II
Solyc00g174340.1.1	functional description:Pathogenesis-related protein 1b (AHRD V1	18 kDa	5.7	0	0.00411	0.00632	0.00805	0.03977	0.01182	0.024	0	1	1	1	5	2	stress biotic PR-proteins PR1 (ant	Pathogenesis-related protein 1b
Solyc03g111690.2.1	functional description:Pectate lyase (AHRD V1 Q2Z1Y4 PRUM	44 kDa	5.5	0.00207	0.00364	0	0.0084	0.0091	0.01369	0.022	1	1	0	2	3	3	cell wall degradation pectate lyase	Pectate lyase
Solyc06g009190.2.1	functional description:Pectinesterase (AHRD V1 - B9SAU4 RICC	63 kDa	3.5	0.00523	0.00463	0.00713	0.01135	0.02429	0.02332	0.00019	2	3	4	5	8	8	misc invertase/pectin methylester:	Pectinesterase
Solyc02g087190.1.1	functional description:Peroxidase 65 (AHRD V1 B6TYF5 MAIZ	36 kDa	3.7	0.0054	0.01006	0.00256	0.02688	0.01888	0.02113	0.015	2	3	1	4	4	5	misc peroxidases	Peroxidase 65
Solyc09g064940.2.1	functional description:Phenazine biosynthesis protein PhzF family	32 kDa	7.4	0.00286	0.00251	0.00263	0.02319	0.01256	0.02363	0.0031	1	1	1	3	2	3	not assigned no ontology	Phenazine biosynthesis protein PhzF family
Solyc07g055060.2.1	functional description:Phosphoenolpyruvate carboxylase 1 (AHRI	110 kDa	3.4	0.00828	0.00075	0.003	0.00112	0.01501	0.0246	0.0031	7	1	3	1	10	12	glycolysis cytosolic branch phospl	Phosphoenolpyruvate carboxylase 1
Solyc08g066800.2.1	functional description:Phospholipase D (AHRD V1 Q9FR61 SOI	92 kDa	4.2	0.00371	0	0.0012	0.00134	0.01103	0.00816	0.0038	3	0	1	1	7	4	RNA regulation of transcription T	Phospholipase D
Solyc03g123760.2.1	functional_description:Phytoene desaturase	65 kDa	2.1	0.00253	0.00336	0.00172	0.0022	0.00904	0.00483	0.024	1	3	1	1	4	2	cell wall precursor synthesis UXS	Phytoene desaturase
Solyc04g007560.2.1	functional description:pH-response regulator protein palA/RIM20	102 kDa	3.8	0	0.00072	0.00332	0.00282	0.01045	0.00207	0.017	0	1	3	2	6	2	RNA transcription	pH-response regulator protein palA/RIM20
Solyc08g076480.2.1	functional description:Plastid lipid-associated protein 3 chloroplast	37 kDa	4.9	0.01803	0.0048	0	0.00732	0.04682	0.05707	0.0001	4	2	0	2	7	8	cell organisation	Plastid lipid-associated protein 3 chloroplastic
Solyc07g065090.1.1	functional description:Polygalacturonase inhibitor protein (AHRD	36 kDa	3.1	0.0061	0.00667	0.00295	0.02308	0.01701	0.00806	0.017	2	3	1	6	3	2	signalling receptor kinases leucine	Polygalacturonase inhibitor protein
Solyc01g108600.2.1	functional description:Presequence protease mitochondrial (AHRI	121 kDa	2.1	0.00275	0.00304	0.0075	0.00716	0.01475	0.00613	0.018	2	5	8	6	12	6	protein degradation metalloprotea	Presequence protease mitochondrial

Solyc10g008140.2.1	functional_description:Prohibitin 1-like protein (AHRD V1 - Q9AX	32 kDa	2.8	0.02146	0.02854	0	0.03487	0.06001	0.04396	0.0094	6	9	0	8	8	7	cell cycle	Prohibitin 1-like protein
Solyc12g009140.1.1	functional_description:Proteasome subunit alpha type (AHRD V1 -	27 kDa	2.3	0.01441	0.05364	0	0.05632	0.04532	0.05633	0.04	3	11	0	8	7	9	protein degradation ubiquitin prot	Proteasome subunit alpha type
Solyc01g111450.2.1	functional_description:Proteasome subunit alpha type (AHRD V1 -	27 kDa	4.3	0.01006	0.00294	0	0.0136	0.01964	0.02216	0.025	2	1	0	1	3	3	protein postranslational modificat	Proteasome subunit alpha type
Solyc02g081700.1.1	functional_description:Proteasome subunit alpha type (AHRD V1 -	27 kDa	7.1	0.00337	0.00591	0	0.03413	0.01479	0.01669	0.0061	1	2	0	3	2	2	secondary metabolism flavonoids	Proteasome subunit alpha type
Solyc10g008010.2.1	functional_description:Proteasome subunit alpha type (AHRD V1 -	26 kDa	3.7	0	0.02686	0.00302	0.06474	0.0366	0.00997	0.0019	0	1	1	1	7	3	protein degradation ubiquitin prot	Proteasome subunit alpha type
Solyc07g016200.2.1	functional_description:Proteasome subunit beta type (AHRD V1 -	25 kDa	3.2	0.00354	0.00621	0.01951	0.02152	0.03108	0.04092	0.022	1	1	5	2	5	5	protein degradation ubiquitin prot	Proteasome subunit beta type
Solyc05g056400.2.1	functional_description:Protein disulfide isomerase (AHRD V1 O6I	59 kDa	2.9	0.00634	0.0014	0.00161	0.00869	0.00207	0.01656	0.0011	2	1	1	4	1	4	redox thioredoxin	Protein disulfide isomerase
Solyc06g060290.2.1	functional_description:Protein disulfide isomerase (AHRD V1 B1(	49 kDa	2.2	0.01277	0.01017	0.01747	0.021	0.03498	0.03142	0.00076	5	5	8	6	12	10	misc short chain dehydrogenase/r	Protein disulfide isomerase
Solyc04g049450.2.1	functional_description:Protein disulfide isomerase L-2 (AHRD V1	63 kDa	3.5	0.00354	0.00129	0.00686	0.00191	0.01779	0.02106	0.0026	2	1	4	1	9	8	redox thioredoxin	Protein disulfide isomerase L-2
Solyc11g069400.1.1	functional_description:Protein disulfide isomerase L-2 (AHRD V1	65 kDa	7.5	0	0.00125	0.00333	0	0.01151	0.02271	0.00039	0	1	2	0	2	8	redox thioredoxin	Protein disulfide isomerase L-2
Solyc10g081240.1.1	functional_description:Protein grpE (AHRD V1 -- B0CAY8 ACAI	42 kDa	3.8	0.00933	0.00434	0	0.01657	0.02282	0.01216	0.019	2	2	0	4	6	3	transport amino acids	Protein grpE
Solyc01g095900.2.1	functional_description:Protein TIF31 homolog (AHRD V1 TIF31	209 kDa	6	0	0.00034	0.00053	0	0.00278	0.00248	0.014	0	1	1	0	4	4	protein degradation cysteine prote	Protein TIF31 homolog
Solyc02g082220.2.1	functional_description:Protein transport protein SEC24 (AHRD V1	114 kDa	2.1	0.00573	0.00063	0.00195	0.00249	0.00921	0.00547	0.021	3	1	2	2	7	5	RNA regulation of transcription u	Protein transport protein SEC24
Solyc02g087300.1.1	functional_description:Protein transport SEC13-like protein (AHRI	32 kDa	4.4	0.00293	0.00819	0	0.02085	0.01231	0.0153	0.029	1	3	0	4	2	2	protein targeting secretory pathwa	Protein transport SEC13-like protein
Solyc08g016750.2.1	functional_description:Pyruvate dehydrogenase E1 component sub	44 kDa	7.1	0.00217	0.00202	0	0.00926	0.00911	0.01132	0.015	1	1	0	2	2	2	TCA / organic transformation TC.	Pyruvate dehydrogenase E1 component subunit beta
Solyc04g008740.2.1	functional_description:Pyruvate kinase (AHRD V1 Q3S1N4 SOL	55 kDa	2.1	0.01535	0.00291	0.01	0.00676	0.03433	0.01963	0.013	6	2	5	3	11	6	glycolysis cytosolic branch pyruv	Pyruvate kinase
Solyc10g083720.1.1	functional_description:Pyruvate kinase (AHRD V1 - Q94KE3 AR	57 kDa	3.1	0.00849	0	0.00484	0.00218	0.02907	0.0095	0.0048	4	0	3	1	9	4	lipid metabolism FA synthesis and	Pyruvate kinase
Solyc01g080460.2.1	functional_description:Pyruvate phosphate dikinase (AHRD V1 - (	106 kDa	6.2	0.00116	0.00077	0.00088	0.00357	0.00227	0.01167	0.0024	1	1	1	2	2	7	gluconeogenesis / glyoxylate cycl	Pyruvate phosphate dikinase
Solyc12g017570.1.1	functional_description:Rab GDP dissociation inhibitor (AHRD V1	50 kDa	4.3	0.00504	0	0.00575	0.00518	0.02465	0.01691	0.0017	1	0	3	2	9	5	signalling G-proteins	Rab GDP dissociation inhibitor
Solyc06g082120.2.1	functional_description:Ran GTPase binding protein (AHRD V1 C	24 kDa	4.1	0.00791	0.00694	0.00727	0.01605	0.02897	0.04577	0.011	2	2	2	2	4	6	signalling G-proteins	Ran GTPase binding protein
Solyc02g093530.2.1	functional_description:Ras-related protein Rab-2-A (AHRD V1 - E	23 kDa	5	0	0.00694	0.00364	0.01605	0.01738	0.01962	0.0083	0	1	1	2	2	3	signalling G-proteins	Ras-related protein Rab-2-A
Solyc02g091840.2.1	functional_description:Receptor like kinase RLK	111 kDa	7.1	0	0.00129	0.00099	0.00126	0.00934	0.00555	0.0013	0	1	1	1	6	4	development unspecified	Receptor like kinase RLK
Solyc03g025850.2.1	functional_description:Remorin 1 (AHRD V1 - O9XEX8 SOLLC)	22 kDa	3.1	0.01349	0.04187	0	0.01279	0.06917	0.08793	0.0083	2	6	0	2	7	9	RNA regulation of transcription p	Remorin 1
Solyc10g007760.2.1	functional_description:Ribose-phosphate pyrophosphokinase 4 (AI	36 kDa	3.2	0.01651	0.00256	0	0.01173	0.03078	0.01793	0.034	5	1	0	2	6	4	cell division	Ribose-phosphate pyrophosphokinase 4
Solyc06g073310.2.1	functional_description:Ribosomal L9-like protein (AHRD V1 - B3	22 kDa	2.6	0.04733	0.00755	0.01187	0.0349	0.06931	0.07112	0.011	8	2	3	4	6	8	protein synthesis ribosome biogen	Ribosomal L9-like protein
Solyc07g041310.2.1	functional_description:Ribosomal protein (AHRD V1 - B3TLR8 E	27 kDa	3.9	0.02595	0.0138	0	0.04743	0.06738	0.03866	0.0012	3	3	0	7	8	5	protein synthesis ribosome biogen	Ribosomal protein
Solyc03g044000.1.1	functional_description:Ribosomal protein L26 (AHRD V1 - A8HM	17 kDa	4.3	0	0.01004	0.02102	0.03478	0.03349	0.06615	0.011	0	2	4	2	3	5	protein synthesis ribosome biogen	Ribosomal protein L26
Solyc01g104590.2.1	functional_description:Ribosomal protein L3 (AHRD V1 - O6SKP	44 kDa	5.5	0.00256	0.00187	0.00248	0.01663	0.01144	0.01016	0.0027	1	1	1	5	4	3	protein synthesis ribosome biogen	Ribosomal protein L3
Solyc06g064470.2.1	functional_description:Ribosomal protein L7a (AHRD V1 - A8J56	29 kDa	2.9	0.00687	0.02238	0	0.01953	0.03361	0.03133	0.044	1	4	0	2	5	4	protein synthesis ribosome biogen	Ribosomal protein L7a
Solyc10g078620.1.1	functional_description:Ribosomal protein S5 (AHRD V1 - A8J2I5	24 kDa	3.1	0.02718	0.02726	0.02498	0.07873	0.04549	0.12192	0.001	5	4	4	7	5	8	protein synthesis ribosomal protei	Ribosomal protein S5
Solyc01g007330.2.1	functional_description:Ribulose bisphosphate carboxylase large ch	53 kDa	4	0.00557	0.00346	0.00352	0.01056	0.01039	0.02905	0.0062	2	2	2	4	3	8	PS calvin cycle rubisco large subu	Ribulose bisphosphate carboxylase large chain
Solyc03g097110.2.1	functional_description:RNA recognition motif-containing protein (	30 kDa	3.5	0.00319	0.02077	0.00302	0.02265	0.03119	0.04154	0.0095	1	7	1	4	5	6	protein synthesis ribosome biogen	RNA recognition motif-containing protein
Solyc07g006570.2.1	functional_description:S8-RNase (Fragment) (AHRD V1 -- Q5XPJ	27 kDa	4.9	0	0.00306	0.007	0.02839	0	0.0206	0.024	0	1	1	4	0	3	secondary metabolism N misc alk	S8-RNase (Fragment)
Solyc01g101060.2.1	functional_description:S-adenosylmethionine synthase (AHRD V1	43 kDa	3.7	0	0.00166	0.00767	0.00977	0.01073	0.01434	0.017	0	1	3	3	4	6	metal handling binding chelation	S-adenosylmethionine synthase
Solyc12g017830.1.1	functional_description:Sec7 guanine nucleotide exchange factor (A	196 kDa	5.5	0	0.00037	0.00057	0	0.00357	0.00159	0.024	0	1	1	0	5	3	signalling G-proteins	Sec7 guanine nucleotide exchange factor
Solyc04g076790.2.1	functional_description:Serine hydroxymethyltransferase (AHRD V	57 kDa	2.1	0.01298	0.00431	0.0148	0.02224	0.01693	0.02904	0.016	6	3	7	8	7	9	amino acid metabolism synthesis	Serine hydroxymethyltransferase
Solyc07g062970.2.1	functional_description:Serine/threonine phosphatase family protein	31 kDa	2.1	0.04713	0.06142	0.00893	0.08039	0.08786	0.07781	0.021	11	13	3	13	10	11	RNA regulation of transcription s	Serine/threonine phosphatase family protein
Solyc05g055060.2.1	functional_description:Serine/threonine-protein phosphatase (AHR	37 kDa	5.7	0.00273	0.00254	0	0.00388	0.01525	0.01066	0.045	1	1	0	1	2	2	DNA synthesis/chromatin structu	Serine/threonine-protein phosphatase
Solyc04g016360.2.1	functional_description:S-formylglutathione hydrolase (AHRD V1	32 kDa	3	0.01872	0.03195	0	0.03548	0.05234	0.06506	0.0033	4	8	0	7	7	7	C1-metabolism	S-formylglutathione hydrolase
Solyc01g067750.2.1	functional_description:Shikimate dehydrogenase (AHRD V1 - B6T	59 kDa	3.5	0.00205	0.00136	0.00468	0.00633	0.00803	0.01378	0.023	1	1	3	3	4	5	amino acid metabolism synthesis	Shikimate dehydrogenase
Solyc07g047800.2.1	functional_description:Short-chain dehydrogenase/reductase famil	30 kDa	2.1	0.015	0.01366	0.00726	0.04052	0.0251	0.00991	0.039	3	3	2	7	5	2	misc short chain dehydrogenase/r	Short-chain dehydrogenase/reductase family protein
Solyc11g062270.1.1	functional_description:Signal recognition particle protein (SRP72)	72 kDa	3.6	0	0.00438	0.00436	0.00487	0.01508	0.0119	0.0044	0	4	3	3	7	6	protein targeting secretory pathwa	Signal recognition particle protein (SRP72)
Solyc01g010750.2.1	functional_description:Stress responsive protein (AHRD V1 B6ST	38 kDa	5.3	0.00542	0.00252	0.00257	0.02311	0.01894	0.01413	0.0067	1	1	1	4	5	4	protein synthesis ribosome biogen	Stress responsive protein
Solyc01g087850.2.1	functional_description:Subtilisin-like protease (AHRD V1 -- O827	82 kDa	3.9	0.00387	0.00172	0	0.00841	0.00831	0.00494	0.0061	1	2	0	4	6	4	protein degradation subtilases	Subtilisin-like protease
Solyc02g092670.1.1	functional_description:Subtilisin-like protease (AHRD V1 - A9XG	80 kDa	2.1	0.00196	0.00693	0.01066	0.01188	0.01677	0.01246	0.029	1	8	6	6	10	9	signalling calcium	Subtilisin-like protease
Solyc08g079870.1.1	functional_description:Subtilisin-like protease (AHRD V1 -- O9LW	79 kDa	2.7	0.00198	0.0035	0.00539	0.00172	0.02405	0.00378	0.013	1	4	4	1	11	3	protein degradation subtilases	Subtilisin-like protease
Solyc02g085350.2.1	functional_description:Succinate dehydrogenase flavoprotein subu	69 kDa	2.4	0.00533	0.00236	0.00811	0.01097	0.01566	0.01194	0.02	2	2	6	6	6	5	signalling calcium	Succinate dehydrogenase flavoprotein subunit
Solyc02g093680.2.1	functional_description:Succinate dehydrogenase iron-sulfur protein	31 kDa	3.9	0.00647	0.01505	0	0.04137	0.01356	0.0295	0.0097	2	3	0	6	3	5	DNA synthesis/chromatin structu	Succinate dehydrogenase iron-sulfur protein
Solyc09g090700.1.1	functional_description:Succinate semialdehyde dehydrogenase (AH	56 kDa	3.1	0.00643	0.00142	0.00326	0.01322	0.00629	0.01438	0.017	3	1	2	6	2	5	TCA / organic transformation oth	Succinate semialdehyde dehydrogenase
Solyc09g082860.2.1	functional_description:Sulfate adenylyltransferase (AHRD V1 Q4	52 kDa	3.4	0	0.0032	0.00733	0.00248	0.03066	0.0027	0.017	0	2	2	1	10	1	S-assimilation APS	Sulfate adenylyltransferase
Solyc11g065620.1.1	functional_description:Sulfite reductase (AHRD V1 O82802 TOB	78 kDa	2.3	0.00433	0.00421	0.00698	0.00468	0.02093	0.00953	0.018	2	3	4	3	7	5	S-assimilation sulfite redox	Sulfite reductase
Solyc03g121040.2.1	functional_description:Taurine catabolism dioxygenase TauD/TfdA	36 kDa	3.9	0.01097	0.01021	0	0.0273	0.03452	0.02145	0.0051	3	3	0	5	4	4	signalling receptor kinases lysine	Taurine catabolism dioxygenase TauD/TfdA family
Solyc03g118910.1.1	functional_description:T-complex protein 1 subunit delta (AHRD V	58 kDa	4.1	0.00274	0.00242	0.00559	0.01425	0.01564	0.01394	0.00096	1	1	3	5	6	4	protein folding	T-complex protein 1 subunit delta
Solyc05g056310.2.1	functional_description:T-complex protein 1 subunit gamma (AHRI	61 kDa	3.1	0.00602	0	0.00305	0.00413	0.00786	0.01572	0.023	3	0	2	2	3	6	protein folding	T-complex protein 1 subunit gamma
Solyc07g006180.2.1	functional_description:Tetratricopeptide repeat protein 4 homolog	29 kDa	5.4	0.00339	0.00948	0	0.02413	0.01899	0.02655	0.0067	1	3	0	4	4	6	not assigned no ontology pentatric	Tetratricopeptide repeat protein 4 homolog
Solyc02g082250.2.1	functional_description:Thioredoxin reductase (AHRD V1 B9SRA	39 kDa	6.1	0.00483	0.00225	0	0.01716	0.01688	0.00944	0.0077	2	1	0	4	4	2	redox thioredoxin	Thioredoxin reductase
Solyc08g074550.2.1	functional_description:Threonyl-tRNA synthetase (AHRD V1 - O1	78 kDa	5.3	0.00148	0	0.00143	0.00159	0.00988	0.0039	0.012	1	0	1	1	6	2	protein aa activation threonine-tR	Threonyl-tRNA synthetase
Solyc10g018300.1.1	functional_description:Transketolase 1 (AHRD V1 O78327 CAP	80 kDa	2.2	0.00597	0.00529	0.00542	0.00518	0.01707	0.01521	0.01	3	5	4	2	8	7	PS calvin cycle transketolase	Transketolase 1
Solyc00g007270.2.1	functional_description:Translation initiation factor (AHRD V1 - A	26 kDa	7.6	0	0.00299	0.00626	0.02073	0.00998	0.03942	0.0031	0	1	2	3	1	4	cell organisation	Translation initiation factor
Solyc06g084210.2.1	functional_description:Transport protein SEC24 (AHRD V1 - C1H	115 kDa	2.6	0.00138	0.00122	0.0047	0.00359	0.00887	0.00615	0.016	1	2	4	3	6	5	misc UDP glucosyl and glucorony	Transport protein SEC24
Solyc04g011510.2.1	functional_description:Triosephosphate isomerase (AHRD V1 O3	28 kDa	3.2	0.01156	0.00561	0.00745	0.04994	0.00859	0.02035	0.0044	3	2	2	8	2	4	PS calvin cycle TPI	Triosephosphate isomerase
Solyc03g025630.2.1	functional_description:Tripeptidyl-peptidase 2 (AHRD V1 - TPP2	25 kDa	5.9	0	0.00305	0.0047	0.01196	0.02463	0.00878	0.024	0	1	1	1	3	1	protein degradation serine proteas	Tripeptidyl-peptidase 2
Solyc12g096190.1.1	functional_description:Tryptophan synthase beta chain (AHRD V1	54 kDa	6.6	0.00227	0.00302	0.00173	0.01169	0.02224	0.01272	0.00019	1	2	1	4	5	3	stress abiotic	Tryptophan synthase beta chain
Solyc12g044740.1.1	functional_description:Ubiquitin carboxyl-terminal hydrolase (AHI	54 kDa	4.5	0.00232	0.00154	0.00528	0.00476	0.01812	0.01813	0.0029	1	1	3	2	7	7	protein degradation ubiquitin ubiq	Ubiquitin carboxyl-terminal hydrolase
Solyc06g007320.2.1	functional_description:Ubiquitin-activating enzyme E1 (AHRD V1	114 kDa	2.8	0.00294	0	0.00095	0.00846	0	0.00259	0.036	2	0	1	8	0	2	protein degradation ubiquitin E1	Ubiquitin-activating enzyme E1
Solyc02g067080.2.1	functional_description:UDP-D-glucose dehydrogenase (AHRD V1	57 kDa	3.8	0	0.00256	0.00395	0.00754	0.00828	0.00923	0.027	0	2	2	3	3	4	cell wall precursor synthesis UGD	UDP-D-glucose dehydrogenase
Solyc02g070020.1.1	functional_description:UDP-glucosyltransferase (AHRD V1 - O8L	54 kDa	2.7	0.00616	0.0109	0.00629	0.02138	0.0242	0.01765	0.0071	2	7	2	6	7	6	cell wall pectinesterases PME	UDP-glucosyltransferase
Solyc10g085230.1.1	functional_description:UDP-glucosyltransferase (AHRD V1 C0LN	54 kDa	3.2	0.00471	0.00313	0.00716	0.00484	0.01152	0.03161	0.0093	1	2	2	2	2	7	hormone metabolism cytokinin sy	UDP-glucosyltransferase
Solyc10g085880.1.1	functional_description:UDP-glucosyltransferase family 1 protein (/	40 kDa	4.6	0.00773	0.00959	0	0.02197	0.01801	0.04028	0.0016	3	4	0	6	4	8	hormone metabolism cytokinin sy	UDP-glucosyltransferase family 1 protein
Solyc01g073640.2.1	functional_description:Uncharacterized oxidoreductase Mb1385 (/	27 kDa	4	0.02578	0.00566	0	0.02614	0.00472	0.09588	0.0012	4	2	0	3	1	5	misc short chain dehydrogenase/r	Uncharacterized oxidoreductase Mb1385
Solyc03g006680.2.1	functional_description:Universal stress protein (AHRD V1 -- D6BI	27 kDa	2.6	0.01081	0.04359	0	0.0512	0.04532	0.04694	0.023	2	11	0	8	6	8	stress abiotic unspecified	Universal stress protein
Solyc02g078540.2.1	functional_description:Unknown Protein (AHRD V1): contains Int	36 kDa	2.8	0.0068	0.00677	0.01034	0.00699	0.02661	0.03423	0.017	2	3	4	1	5	6	not assigned unknown	Unknown Protein
Solyc09g011300.2.1	functional_description:Uracil phosphoribosyltransferase (AHRD V	31 kDa	4.2	0.00292	0.00768	0.01073	0.03551	0.02137	0.03377	0.0046	1	2	3	5	4	5	nucleotide metabolism salvage ph	Uracil phosphoribosyltransferase
Solyc01g110120.2.1	functional_description:V-type proton ATPase subunit a (AHRD V1	93 kDa	4.4	0.00365	0	0.00118	0.00131	0.00543	0.01446	0.0038	2	0	1	1	3	8	cell wall precursor synthesis UXS	V-type proton ATPase subunit a
Solyc11g065920.1.1	functional_description:Xanthine dehydrogenase/oxidase (AHRD V	151 kDa	2.2	0.00324	0.00191	0.00221	0.00375	0.00849	0.00413	0.022	2	4	3	4	9	5	hormone metabolism abscisic acid	Xanthine dehydrogenase/oxidase
Solyc01g099630.2.1	functional_description:Xyloglucan endotransglucosylase/hydrolase	34 kDa	7.3	0	0.00221	0.00679	0.0173	0.00712	0.04126	0.00022	0	1	2	4	1	9	cell wall modification	Xyloglucan endotransglucosylase/hydrolase 5
Solyc07g006650.2.1	functional_description:Xylose isomerase (AHRD V1 - B9T2E0 RI	45 kDa	2.2	0.03372	0.02611	0.04059	0.03756	0.10723	0.07859	0.00011	9	11	14	10	28	19	minor CHO metabolism others xy	Xylose isomerase
Solyc02g078940.2.1	functional_description:Zinc-binding dehydrogenase superfamily (O	35 kDa	3.7	0.02454	0.00254	0	0.01163	0.05336	0.03553	0.0022	7	1	0	3	8	5	secondary metabolism phenylprop	Zinc-binding dehydrogenase superfamily (Quinone oxidoreductase NADPH dependen
Solyc12g098710.1.1	functional_description:15-cis-zeta-carotene isomerase	42 kDa	10	0	0.00219	0.00272	0.00694	0.01143	0.01018	0.0041	0	0	1	2	2	2	transport unspecified cations	15-cis-zeta-carotene isomerase

Total proteins=235

Proteins down-regulated in AV in comparison with AC

Accession.Number	DESCRIPTION	Molecula	Fold.Cha	AC.1.1	AC.2.1	AC.3.1	AV.1.1	AV.2.1	AV.3.1	P Value	AC.1.1	AC.2.1	AC.3.1	AV.1.1	AV.2.1	AV.3.1	MAPMA	MAPMAN DESCRIPTION
Solyc11g010470.1.1	functional description:14-3-3 protein beta/alpha (AHRD V1 -- 1433B	28 kDa	0.4	0.01348	0.01789	0.02049	0.01385	0.00439	0.00502	0.019	3	5	3	3	1	1	metal han	14-3-3 protein beta/alpha
Solyc04g007980.2.1	functional description:1-aminocyclopropane-1-carboxylate oxidase (AI	41 kDa	0.4	0.00306	0.01826	0.0302	0.01571	0	0.00342	0.0043	1	6	10	5	0	1	hormone r	1-aminocyclopropane-1-carboxylate oxidase
Solyc06g083620.2.1	functional description:26S protease regulatory subunit 4 (AHRD V1 - I	49 kDa	0.3	0.00225	0.01309	0.00652	0	0.00251	0.00297	0.02	1	7	3	0	1	1	protein de	26S protease regulatory subunit 4
Solyc05g013030.1.1	functional description:26S proteasome regulatory subunit (AHRD V1 -	47 kDa	0.3	0.00697	0.00772	0.0095	0.00605	0	0.00222	0.039	2	4	4	2	0	1	protein de	26S proteasome regulatory subunit
Solyc02g070570.2.1	functional description:30S ribosomal protein S11 (AHRD V1 - RS11 (	16 kDa	0.3	0.03544	0.03849	0.07272	0.03359	0	0.0077	0.00018	5	6	11	3	0	1	protein sy	30S ribosomal protein S11
Solyc05g009030.2.1	functional description:3-isopropylmalate dehydrogenase (AHRD V1 B	43 kDa	0.3	0.01377	0.01646	0.01885	0.01416	0.0027	0	0.0043	4	6	6	5	1	0	secondary	3-isopropylmalate dehydrogenase
Solyc07g062610.2.1	functional description:4-methyl-5(B-hydroxyethyl)-thiazole monophos	42 kDa	0.3	0.00286	0.00759	0.01305	0.00294	0	0.0032	0.023	1	3	5	1	0	1	Co-factor	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis enzyme ThiJ
Solyc01g099830.2.1	functional description:60S ribosomal protein L22-2 (AHRD V1 - D7L	14 kDa	0.4	0.11352	0.0879	0.08594	0.04063	0.0489	0.02208	0.00011	5	6	6	2	3	1	protein sy	60S ribosomal protein L22-2
Solyc01g108560.2.1	functional description:Acetyl esterase (AHRD V1 AES SHIFL); conta	34 kDa	0.4	0.05945	0.02466	0.0452	0.03438	0.01091	0.00831	0.00097	7	7	9	5	1	1	biodegrad	Acetyl esterase
Solyc04g077970.2.1	functional description:Adenine phosphoribosyltransferase-like (AHRD	29 kDa	0.4	0.02523	0.01675	0.00959	0.00865	0.00823	0.0047	0.046	6	4	2	2	1	1	nucleotide	Adenine phosphoribosyltransferase-like
Solyc11g072410.1.1	functional description:Adenylate kinase isoenzyme 6 (AHRD V1 -- B5	20 kDa	0.3	0.00943	0.02483	0.01734	0.00956	0	0.00779	0.029	1	3	3	1	0	1	RNA regu	Adenylate kinase isoenzyme 6
Solyc05g005190.2.1	functional description:ADP-ribosylation factor (AHRD V1 - Q76ME3	21 kDa	0.2	0.02444	0.02525	0.01665	0.00707	0.00582	0	0.0056	2	6	3	1	1	0	protein ta	ADP-ribosylation factor
Solyc08g005770.2.1	functional description:Alcohol acetyltransferase (AHRD V1 - B1A9J8	50 kDa	0.2	0.0538	0.01428	0.0016	0	0.01297	0.00133	0.0094	12	2	1	0	6	1	major CH	Alcohol acetyltransferase
Solyc09g082720.2.1	functional description:Aldo/keto reductase family protein (AHRD V1	38 kDa	0.3	0.01709	0.01514	0.00582	0.00371	0.00306	0.00545	0.023	4	6	2	1	1	2	transport	Aldo/keto reductase family protein
Solyc11g067160.1.1	functional description:Aldo/keto reductase family protein (AHRD V1 -	44 kDa	0.3	0.00281	0.01679	0.01495	0.00578	0.0055	0	0.0098	1	6	6	2	2	0	minor CH	Aldo/keto reductase family protein
Solyc01g008070.2.1	functional description:Alpha/beta superfamily hydrolase (AHRD V1 D	48 kDa	0.4	0	0.01547	0.0059	0.00266	0.00253	0.0029	0.036	0	8	3	1	1	1	not assign	Alpha/beta superfamily hydrolase
Solyc06g050770.2.1	functional description:Alpha-soluble NSF attachment protein (AHRD V	33 kDa	0.3	0.01548	0.01028	0.00588	0.00398	0	0.00433	0.036	4	3	2	1	0	1	protein ta	Alpha-soluble NSF attachment protein
Solyc05g052260.2.1	functional description:Appr-1-p processing domain protein (AHRD V1	21 kDa	0.3	0.02769	0.01718	0.03496	0.01312	0.00645	0.00601	0.0033	4	3	5	1	1	1	DNA synt	Appr-1-p processing domain protein
Solyc12g056830.1.1	functional description:ATP synthase delta subunit (AHRD V1 - Q7XY	27 kDa	0.3	0.01063	0.0099	0.03021	0.00504	0.00496	0.00462	0.0054	2	2	5	1	1	1	PS lightre	ATP synthase delta subunit
Solyc11g039980.1.1	functional description:ATP synthase subunit alpha (AHRD V1 - Q5M9	18 kDa	0.4	0.0464	0.08451	0.06733	0.0188	0.03882	0.03064	0.0026	7	7	8	2	4	4	RNA proc	ATP synthase subunit alpha
Solyc11g069270.1.1	functional description:Beta-galactosidase (AHRD V1 - Q9LLT0 SOLI	93 kDa	0.3	0.00131	0.00523	0.00299	0.00135	0.00128	0	0.036	1	4	3	1	1	0	RNA regu	Beta-galactosidase
Solyc03g118040.2.1	functional description:Calcium-binding protein Calnexin (AHRD V1 -	61 kDa	0.4	0.00208	0.00276	0.01897	0.00214	0.00407	0.00233	0.023	1	2	10	1	1	1	signalling	Calcium-binding protein Calnexin
Solyc01g087260.2.1	functional_description:Carotenoid cleavage dioxygenase 1B	61 kDa	0.4	0.00271	0.00599	0.00737	0.00235	0.00193	0.00172	0.023	1	5	4	1	1	1	secondary	Carotenoid cleavage dioxygenase 1B
Solyc02g069100.2.1	functional description:Cathepsin B (AHRD V1 - Q1HER6 NICBE); c	39 kDa	0.3	0.01264	0.01049	0.00721	0.0065	0.00309	0	0.036	4	4	2	2	1	0	protein de	Cathepsin B
Solyc12g042830.1.1	functional description:class I heat shock protein (AHRD V1 -- Q69BI7	9 kDa	0.3	0.06729	0.02088	0.03187	0.01594	0	0.01462	0.015	4	1	1	1	0	1	RNA proc	class I heat shock protein
Solyc04g014480.2.1	functional description:class I heat shock protein 3 (AHRD V1 - B6TQI	16 kDa	0.3	0.01822	0.0653	0.08806	0	0.00791	0.04446	0.011	2	3	11	0	2	6	stress abi	class I heat shock protein 3
Solyc09g015020.1.1	functional description:class I heat shock protein 3 (AHRD V1 - B6TDI	18 kDa	0.2	0.13725	0.08198	0.03224	0	0.00745	0.04186	0.019	6	1	5	0	2	7	hormone r	class I heat shock protein 3
Solyc11g020330.1.1	functional description:class IV heat shock protein (AHRD V1 - B6TXI	21 kDa	0.2	0.06258	0.04983	0.04854	0	0.00302	0.02159	0.00016	6	2	8	0	1	5	stress abi	class IV heat shock protein
Solyc10g005110.2.1	functional description:Coproporphyrinogen III oxidase aerobic (AHRD	45 kDa	0.3	0.00561	0.01861	0.02557	0.00576	0.00823	0.00314	0.0028	2	8	9	2	3	1	hormone r	Coproporphyrinogen III oxidase aerobic
Solyc09g005700.2.1	functional description:Diaminopimelate epimerase family protein (AHF	39 kDa	0.2	0.00616	0.01432	0.00703	0.00317	0	0.00345	0.014	2	7	3	1	0	1	amino aci	Diaminopimelate epimerase family protein
Solyc07g006790.2.1	functional description:Dihydrolipoyllysine-residue acetyltransferase co	60 kDa	0.3	0.01083	0.01577	0.01222	0.00195	0.00604	0.00238	0.0015	5	9	7	1	2	1	TCA / org	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase co
Solyc08g080680.2.1	functional description:Elicitor-responsive protein 3 (AHRD V1 -- B6U	16 kDa	0.3	0.02733	0	0.03425	0	0.00395	0.01212	0.033	3	0	5	0	1	2	not assign	Elicitor-responsive protein 3
Solyc12g010060.1.1	functional description:Eukaryotic translation initiation factor 5A (AHR	18 kDa	0.3	0.02215	0.02577	0.05769	0.01574	0	0.01444	0.0012	3	4	8	2	0	2	misc nitril	Eukaryotic translation initiation factor 5A
Solyc07g065540.1.1	functional description:Fasciclin-like arabinogalactan protein 10 (AHRI	44 kDa	0.4	0.01078	0.00602	0.01429	0.00613	0.00301	0.00281	0.013	4	3	5	2	1	1	cell wall c	Fasciclin-like arabinogalactan protein 10
Solyc05g053620.2.1	functional description:F-box protein PP2-B1 (AHRD V1 -- PP2B1 AF	19 kDa	0.2	0.04047	0.03996	0.0279	0.01026	0.00741	0	0.00022	5	5	5	1	1	0	cell organ	F-box protein PP2-B1
Solyc09g057670.2.1	functional description:FK506-binding protein 2 (EC 5.2.1.8)(Peptidyl-	16 kDa	0.3	0.05042	0.03441	0.0412	0.01136	0.02461	0	0.0017	5	6	6	1	3	0	protein fo	FK506-binding protein 2 (EC 5.2.1.8)(Peptidyl-prolyl cis-trans isomerase)(PPIase)(Ro
Solyc08g006720.2.1	functional description:Glutathione peroxidase (AHRD V1 - D6BR59	26 kDa	0.2	0.00372	0.01386	0.04231	0.00529	0	0.00485	0.00057	1	4	9	1	0	1	redox asc	Glutathione peroxidase
Solyc12g056230.1.1	functional description:Glutathione peroxidase (AHRD V1 - B9GKI5 P	19 kDa	0.4	0.03437	0.03016	0.05868	0.01992	0.00719	0.02435	0.0035	5	5	8	2	1	2	redox asc	Glutathione peroxidase
Solyc04g082630.2.1	functional description:Glyceraldehyde-3-phosphate dehydrogenase B (	51 kDa	0.3	0.00705	0.02339	0.02144	0	0.0069	0.00789	0.00026	2	10	9	0	3	3	protein pc	Glyceraldehyde-3-phosphate dehydrogenase B
Solyc02g068740.2.1	functional description:Glycine cleavage system H protein 1 (AHRD V1	17 kDa	0.4	0.02168	0.02854	0.01993	0.01099	0.01588	0	0.033	3	4	3	1	2	0	PS photor	Glycine cleavage system H protein 1
Solyc06g069010.2.1	functional description:Guanine nucleotide-binding protein beta subunit	36 kDa	0.4	0.00686	0.00683	0.01043	0	0.00671	0.00384	0.0026	2	3	3	0	1	1	RNA regu	Guanine nucleotide-binding protein beta subunit-like protein
Solyc06g036290.2.1	functional description:Heat shock protein 90 (Fragment) (AHRD V1 --	70 kDa	0.2	0.00876	0.01223	0.00415	0	0.00204	0.00381	0.0012	5	7	3	0	1	1	stress abi	Heat shock protein 90 (Fragment)
Solyc02g065240.2.1	functional description:Hydrolase alpha/beta fold family protein (AHRD	30 kDa	0.3	0.02792	0.03214	0.02664	0.01454	0.00399	0.00356	0.00035	4	10	7	3	1	1	hormone r	Hydrolase alpha/beta fold family protein
Solyc01g088590.2.1	functional description:Invertase inhibitor (AHRD V1 - A7IZL0 COFC	21 kDa	0.3	0.00476	0.0133	0.02707	0.00677	0.00666	0	0.025	1	3	4	1	1	0	misc inver	Invertase inhibitor
Solyc03g098740.1.1	functional description:Kunitz trypsin inhibitor (AHRD V1 B8Y888 T	22 kDa	0.3	0.0089	0.02072	0.01265	0	0.00623	0.0058	0.025	1	3	2	0	1	1	stress biot	Kunitz trypsin inhibitor
Solyc11g069040.2.1	functional description:Lactoylglutathione lyase (AHRD V1 B5XCC9	21 kDa	0.2	0.03831	0.03121	0.04082	0.01362	0	0.01248	0.00016	5	5	7	2	0	2	amino aci	Lactoylglutathione lyase
Solyc03g115990.1.1	functional description:Malate dehydrogenase (AHRD V1 O48906 MI	43 kDa	0.3	0.01431	0.01268	0.00488	0.00621	0	0.00456	0.023	3	6	2	2	0	2	TCA / org	Malate dehydrogenase
Solyc09g098150.2.1	functional description:Metacaspase 7 (AHRD V1 - D7KWG9 ARALY	46 kDa	0.3	0.00852	0.02181	0.0121	0.00908	0	0.00278	0.00076	4	9	5	3	0	1	protein de	Metacaspase 7
Solyc01g005620.2.1	functional description:Mitochondrial 2-oxoglutarate/malate carrier prot	32 kDa	0.4	0.0113	0.01	0.0229	0.00387	0.00737	0.00843	0.046	3	4	5	1	2	2	transport	Mitochondrial 2-oxoglutarate/malate carrier protein
Solyc08g082010.2.1	functional description:Myosin heavy chain-like protein (AHRD V1 -- (	153 kDa	0.4	0.0066	0.00195	0.00824	0	0.00314	0.0028	0.02	6	4	9	0	4	4	cell organ	Myosin heavy chain-like protein
Solyc01g110450.2.1	functional description:NADP dependent sorbitol 6-phosphate dehydro	35 kDa	0.4	0.02863	0.0169	0.01301	0.00828	0.00341	0.00912	0.018	6	7	4	2	1	2	minor CH	NADP dependent sorbitol 6-phosphate dehydrogenase (Fragment)
Solyc03g097700.2.1	functional description:O-methyltransferase (AHRD V1 - A5HJZ9 VIT	39 kDa	0.4	0.00317	0.01893	0.01686	0.00326	0	0.01063	0.0098	1	6	4	1	0	3	secondary	O-methyltransferase
Solyc08g067030.2.1	functional description:Os01g0611000 protein (Fragment) (AHRD V1 -	41 kDa	0.4	0.02713	0.01201	0.00917	0.0031	0.0118	0.00337	0.02	7	5	3	1	4	1	not assign	Os01g0611000 protein (Fragment)
Solyc07g005210.2.1	functional description:Outer membrane lipoprotein blc (AHRD V1 -- D	21 kDa	0.2	0.02256	0.08315	0.05392	0	0.01322	0.01492	0.033	3	8	6	0	1	1	transport	Outer membrane lipoprotein blc
Solyc08g078250.2.1	functional description:Palmitoyl-protein thioesterase 1 (AHRD V1 B4	40 kDa	0.3	0.01566	0.01872	0.01905	0.00644	0.00613	0.0035	0.0028	5	7	6	2	1	1	protein aa	Palmitoyl-protein thioesterase 1
Solyc07g064180.2.1	functional description:Pectinesterase (AHRD V1 - B9RXQ4 RICCO);	61 kDa	0.3	0.00268	0.00831	0.00731	0.00233	0	0.00342	0.041	1	6	3	1	0	2	protein pc	Pectinesterase
Solyc01g006900.2.1	functional description:Phosphatidylglycerol/phosphatidylinositol trans	18 kDa	0.3	0.0613	0.03112	0.06861	0.04753	0	0.00726	0.00019	3	4	8	4	0	1	amino aci	Phosphatidylglycerol/phosphatidylinositol transfer protein
Solyc08g076220.2.1	functional description:Phosphoribulokinase/uridine kinase (AHRD V1	44 kDa	0.1	0.0028	0.02042	0.01913	0.00287	0	0.00313	0.00014	1	10	7	1	0	1	PS calvin	Phosphoribulokinase/uridine kinase
Solyc02g014150.2.1	functional description:Photosystem II stability/assembly factor Ycf48-l	41 kDa	0.3	0.00297	0.01378	0.01353	0.00305	0.0029	0.00332	0.015	1	6	4	1	1	1	PS lightre	Photosystem II stability/assembly factor Ycf48-like protein
Solyc02g081170.2.1	functional description:Plastid-lipid-associated protein chloroplastic (A	36 kDa	0.3	0.0153	0.03344	0.0148	0.01323	0.00341	0.00404	0.0037	4	9	4	3	1	1	cell organ	Plastid-lipid-associated protein chloroplastic
Solyc02g067460.2.1	functional description:Porin/voltage-dependent anion-selective channel	30 kDa	0.4	0.04458	0.03228	0.02465	0.02916	0.00396	0.00453	0.0018	6	9	5	4	1	1	transport	Porin/voltage-dependent anion-selective channel protein
Solyc07g066470.2.1	functional description:Porphobilinogen deaminase (AHRD V1 - B6TV	39 kDa	0.2	0.00919	0.0122	0.0233	0	0.006	0.00343	0.0015	3	4	7	0	2	1	hormone r	Porphobilinogen deaminase
Solyc11g069150.1.1	eviden functional description:Proteasome subunit beta type (AHRD V1	28 kDa	0.4	0.02283	0.02121	0.01041	0.00939	0.00893	0.00511	0.046	4	4	3	2	1	1	protein de	Proteasome subunit beta type
Solyc09g082320.2.1	functional description:Proteasome subunit beta type (AHRD V1 - B9R	23 kDa	0.2	0.01737	0.03639	0.02468	0.01235	0.00607	0	0.00069	3	7	4	2	1	0	protein de	Proteasome subunit beta type
Solyc01g079820.2.1	functional description:Redoxin domain protein (AHRD V1 -- A1WHD	21 kDa	0.3	0.01399	0.01736	0.03092	0.00663	0	0.01216	0.0089	3	2	4	1	0	1	redox per	Redoxin domain protein
Solyc02g079100.2.1	functional description:Riboflavin kinase (AHRD V1 - A8IM09 CHLR	42 kDa	0.2	0	0.01157	0.01546	0	0.00284	0.00325	0.0086	0	6	7	0	1	1	Co-factor	Riboflavin kinase
Solyc11g042610.1.1	functional description:Ribosomal protein S5 (AHRD V1 - A8J2I5 CH	24 kDa	0.4	0.0265	0.04222	0.02418	0.0327	0.00519	0	0.009	4	8	4	2	1	0	protein sy	Ribosomal protein S5
Solyc02g063150.2.1	functional description:Ribulose bisphosphate carboxylase small chain (	20 kDa	0.4	0.00979	0.01823	0.0649	0.02783	0	0.00638	0.0032	2	3	11	4	0	1	PS calvin	Ribulose bisphosphate carboxylase small chain
Solyc02g066930.2.1	functional description:RNA-binding protein (AHRD V1 -- Q941H9 T(	22 kDa	0.3	0.02051	0.04582	0	0.01166	0.00574	0	0.002	3	7	0	1	1	0	RNA RN	RNA-binding protein
Solyc06g065470.2.1	functional description:RNA-binding protein 8A (AHRD V1 -- B6TR37	22 kDa	0.4	0.01363	0.01692	0.01721	0.00646	0.00635	0.00592	0.037	2	3	3	1	1	1	RNA RN	RNA-binding protein 8A
Solyc10g085040.1.1	functional description:Soul heme-binding family protein (AHRD V1 - I	22 kDa	0.3	0.01781	0.01243	0.01265	0.00633	0.00623	0	0.025	4	3	2	1	1	0	redox hen	Soul heme-binding family protein
Solyc06g060260.2.1	functional_description:Stromal ascorbate peroxidase 7	38 kDa	0.3	0.01945	0.01506	0.00986	0.01	0.00317	0	0.0098	5	5	4	2	1	0	redox asc	Stromal ascorbate peroxidase 7
Solyc01g112280.2.1	functional description:Succinyl-diaminopimelate desuccinylase (AHRI	50 kDa	0.2	0.00223	0.00973	0.00862	0.00241	0.00248	0	0.032	1	4	3	1	1	0	protein de	Succinyl-diaminopimelate desuccinylase
Solyc01g100760.2.1	functional description:Susceptibility homeodomain transcription factor	19 kDa	0.4	0.01621	0.03018	0.04605	0.03072	0	0.00704	0.0079	3	4	4	3	0	1	not assign	Susceptibility homeodomain transcription factor (Fragment)
Solyc07g049450.2.1	functional description:Thioredoxin/protein disulfide isomerase (AHRD	47 kDa	0.2	0.00231	0.01009	0.0134	0.0025	0	0.00305	0.013	1	5	5	1	0	1	redox thic	Thioredoxin/protein disulfide isomerase
Solyc08g065640.2.1	functional description:Thioredoxin-like protein (AHRD V1 -- Q2UPJ7	23 kDa	0.4	0.03475	0.02426	0.03291	0.03087	0	0.00566	0.003	5	5	4	3	0	1	not assign	Thioredoxin-like protein
Solyc00g006800.2.1	functional description:Transaldolase (AHRD V1 - Q9FVH1 SOLLC);	48 kDa	0.4	0.02362	0.01942	0.02759	0.00586	0.01206	0.0129	0.0069	5	10	8	2	5	6	lipid meta	Transaldolase
Solyc01g111120.2.1	functional description:Triosephosphate isomerase (AHRD V1 D6N3G	35 kDa	0.3	0.01372	0.01366	0.01304	0.00705	0	0.00384	0.006	4	5	2	2	0	1	PS calvin	Triosephosphate isomerase
Solyc01g056940.2.1	functional description:Ubiquitin (AHRD V1 - D3PHG3 9MAXI); cont	18 kDa	0.4	0.00847	0	0.11823	0	0.01838	0.03005	0.0018	1	0	9	0	3	6	protein de	Ubiquitin
Solyc01g007860.2.1	functional description:Ubiquitin-conjugating enzyme family protein-lik	17 kDa	0.2	0.01821	0.0113	0.04023	0.00863	0	0.00791	0.0087	2	1	4	1	0	1	protein de	Ubiquitin-conjugating enzyme family protein-like

Total proteins=80

Table 4.4. Proteins identified only in AC and in AV.

Label free quantitation was employed by counting the number of spectra and normalizing the total spectra through NSAF using Scaffold software to identify the proteins present only in AC or AV. Stringent selection criteria were imposed to identify these proteins (p value≤0.05, minimum 2 peptides for identification, FDR= 0.1%).

Proteins present only in AC

Accession.Number	DESCRIPTION	Molecula	Fold.Cha	AC.1.1	AC.2.1	AC.3.1	AV.1.1	AV.2.1	AV.3.1	P Value	AC.1.1	AC.2.1	AC.3.1	AV.1.1	AV.2.1	AV.3.1	MAPMAN CLASS	MAPMAN DESCRIPTION
Solyc07g049530.2.1	functional description:1-aminocyclopropane-1-carboxylate oxidase	36 kDa	0	0	0.04008	0.00901	0	0	0	0.0013	0	3	4	0	0	0	hormone metabolism ethylene synthesis-degradation 1-	1-aminocyclopropane-1-carboxylate oxidase
Solyc02g085040.2.1	functional description:2345-tetrahydropyridine-26-dicarboxylate N-	29 kDa	0	0.00414	0.011	0.0063	0	0	0	0.013	1	3	2	0	0	0	mitochondrial electron transport / ATP synthesis NAD	2 3 4 5-tetrahydropyridine-2 6-dicarboxylate N-acetyltransferase
Solyc01g007580.2.1	functional description:30S ribosomal protein S8 (AHRD V1 - D4PB	16 kDa	0	0.00623	0.0164	0.01145	0	0	0	0.038	1	3	2	0	0	0	protein synthesis ribosomal protein prokaryotic chlorop	30S ribosomal protein S8
Solyc12g042650.1.1	functional description:40S ribosomal protein S12 (AHRD V1 - O8H	15 kDa	0	0.00628	0	0.02381	0	0	0	0.036	1	0	3	0	0	0	protein synthesis ribosome biogenesis	40S ribosomal protein S12
Solyc03g115360.2.1	functional description:40S ribosomal protein S19-like (AHRD V1 -	16 kDa	0	0	0.02739	0.01405	0	0	0	0.0053	0	5	2	0	0	0	protein synthesis ribosome biogenesis	40S ribosomal protein S19-like
Solyc12g039120.1.1	functional description:40S ribosomal protein S19-like (AHRD V1 -	16 kDa	0	0.01167	0.02049	0.0161	0	0	0	0.0025	2	3	3	0	0	0	protein synthesis ribosomal protein eukaryotic 40S sub	40S ribosomal protein S19-like
Solyc06g069090.2.1	functional description:40S ribosomal protein S7-like protein (AHRD	22 kDa	0	0	0.01367	0.00526	0	0	0	0.038	0	3	1	0	0	0	protein synthesis ribosomal protein eukaryotic 40S sub	40S ribosomal protein S7-like protein
Solyc01g007600.2.1	functional description:50S ribosomal protein L16 chloroplastic (AH	13 kDa	0	0	0.02483	0.01301	0	0	0	0.038	0	3	1	0	0	0	protein synthesis ribosomal protein prokaryotic chlorop	50S ribosomal protein L16 chloroplastic
Solyc07g009330.2.1	functional description:60S acidic ribosomal protein P3 (AHRD V1 -	12 kDa	0	0.03507	0.00616	0	0	0	0	0.038	2	1	0	0	0	0	protein synthesis ribosomal protein eukaryotic 60S sub	60S acidic ribosomal protein P3
Solyc12g008720.1.1	functional description:60S ribosomal protein L31 (AHRD V1 - B6V	14 kDa	0	0.00696	0.03052	0.01279	0	0	0	0.013	1	5	2	0	0	0	protein synthesis ribosome biogenesis	60S ribosomal protein L31
Solyc05g007560.2.1	functional description:60S ribosomal protein L34 (AHRD V1 - B6U	14 kDa	0	0.01477	0.00687	0.01399	0	0	0	0.036	1	1	2	0	0	0	protein synthesis ribosome biogenesis	60S ribosomal protein L34
Solyc06g036050.2.1	functional description:60S ribosomal protein L36 (AHRD V1 - B9I	16 kDa	0	0.02568	0.01195	0.01824	0	0	0	0.0025	2	2	3	0	0	0	protein synthesis ribosomal protein eukaryotic 60S sub	60S ribosomal protein L36
Solyc08g082180.2.1	functional description:Abscisic acid receptor PYL9 (AHRD V1 -- P	22 kDa	0	0.00938	0.01309	0.01332	0	0	0	0.0049	1	2	2	0	0	0	stress abiotic unspecified	Abscisic acid receptor PYL9
Solyc04g015830.2.1	functional description:Actin-binding protein gelsolin (AHRD V1 - D	104 kDa	0	0.00236	0	0.00359	0	0	0	0.025	2	0	3	0	0	0	cell organisation	Actin-binding protein gelsolin
Solyc09g082730.2.1	functional description:Aldo/keto reductase family protein (AHRD V	38 kDa	0	0.00426	0.00377	0	0	0	0	0.038	1	2	0	0	0	0	hormone metabolism auxin induced-regulated-responsi	Aldo/keto reductase family protein
Solyc04g007160.1.1	functional description:Alpha-glucosidase (AHRD V1 - Q9LEC9 SC	30 kDa	0	0.00548	0.00728	0.00374	0	0	0	0.039	1	2	1	0	0	0	misc gluco- galacto- and mannosidases alpha-galactosi	Alpha-glucosidase
Solyc12g010180.1.1	functional description:Anthranilate synthase (AHRD V1 - A1KAT4	31 kDa	0	0	0.01166	0.00297	0	0	0	0.036	0	3	1	0	0	0	amino acid metabolism synthesis aromatic aa tryptopha	Anthranilate synthase
Solyc01g079880.2.1	functional description:Asparagine synthetase (AHRD V1 O9ZST6	25 kDa	0	0.01896	0.01887	0.00721	0	0	0	0.00061	4	5	2	0	0	0	mitochondrial electron transport / ATP synthesis electr	Asparagine synthetase
Solyc06g066000.1.1	functional description:ATP synthase subunit b&apos (AHRD V1 - I	24 kDa	0	0.01872	0.01314	0.00344	0	0	0	0.0043	4	4	1	0	0	0	stress biotic receptors	ATP synthase subunit b'
Solyc02g081550.2.1	functional description:ATP-dependent Zn protease cell division pro	73 kDa	0	0.00148	0.00324	0.00287	0	0	0	0.031	1	3	2	0	0	0	protein degradation metalloprotease	ATP-dependent Zn protease cell division protein FtsH homolog
Solyc05g054710.2.1	functional description:Beta-hexosaminidase b (AHRD V1 Q17BL1	63 kDa	0	0.00181	0.00263	0.00874	0	0	0	0.0096	1	2	4	0	0	0	protein glycosylation alpha-1 6-mannosyl-glycoprotein	Beta-hexosaminidase b
Solyc03g083520.2.1	functional description:Calmodulin (AHRD V1 - B6T4U8 MAIZE):	17 kDa	0	0.03339	0.00488	0	0	0	0	0.022	5	1	0	0	0	0	signalling calcium	Calmodulin
Solyc01g100380.2.1	functional description:Calreticulin 2 calcium-binding protein (AHRI	48 kDa	0	0.00425	0.00198	0.00402	0	0	0	0.036	2	1	2	0	0	0	signalling calcium	Calreticulin 2 calcium-binding protein
Solyc01g079860.2.1	functional description:Carbohydrate kinase YjeF related protein (A	34 kDa	0	0	0.00461	0.00792	0	0	0	0.046	0	2	3	0	0	0	minor CHO metabolism others	Carbohydrate kinase YjeF related protein
Solyc02g067750.2.1	functional description:Carbonic anhydrase (AHRD V1 - B1VK36 S	29 kDa	0	0.00782	0.0114	0.00378	0	0	0	0.017	2	3	1	0	0	0	secondary metabolism unspecified	Carbonic anhydrase
Solyc03g019720.2.1	functional description:Carnitine operon protein caiE (AHRD V1 D.	28 kDa	0	0.00352	0.01964	0	0	0	0	0.0096	1	5	0	0	0	0	transport NDP-sugars at the ER	Carnitine operon protein caiE
Solyc11g071830.1.1	functional description:Chaperone protein dnaj (AHRD V1 - O17AX	47 kDa	0	0.00716	0.00522	0.00693	0	0	0	0.0054	3	2	2	0	0	0	stress abiotic heat	Chaperone protein dnaj
Solyc06g076520.1.1	functional description:class I heat shock protein (AHRD V1 - O69E	18 kDa	0	0.01296	0.0236	0.00627	0	0	0	0.0096	2	4	1	0	0	0	hormone metabolism auxin induced-regulated-responsi	class I heat shock protein
Solyc01g102960.2.1	functional description:class IV heat shock protein (AHRD V1 - B6T	22 kDa	0	0.0156	0.01727	0.00532	0	0	0	0.0053	2	4	1	0	0	0	stress abiotic heat	class IV heat shock protein
Solyc05g055310.2.1	functional description:Copper chaperone (AHRD V1 Q84KJ2 SOI	9 kDa	0	0.07213	0.01809	0	0	0	0	0.0075	6	2	0	0	0	0	RNA regulation of transcription unclassified	Copper chaperone
Solyc01g068620.2.1	functional description:Cyclase/dehydrase (AHRD V1 -- D7E269 N	33 kDa	0	0.00917	0	0.00579	0	0	0	0.036	2	0	2	0	0	0	not assigned unknown	Cyclase/dehydrase
Solyc01g103220.2.1	functional description:Cytochrome c (AHRD V1 - B6SKR4 MAIZ	12 kDa	0	0.00791	0.01473	0.01498	0	0	0	0.036	1	1	2	0	0	0	mitochondrial electron transport / ATP synthesis cytoc	Cytochrome c
Solyc06g005260.2.1	functional description:Cytoplasmic glutaredoxin thioltransferase glu	11 kDa	0	0.02319	0.01357	0.0071	0	0	0	0.038	2	2	1	0	0	0	redox glutaredoxins	Cytoplasmic glutaredoxin thioltransferase glutathione-dependent disulfide oxidoreductase
Solyc07g066650.2.1	functional description:DCN1-like protein 2 (AHRD V1 - B6TM27	30 kDa	0	0	0.00563	0.01181	0	0	0	0.038	0	2	3	0	0	0	protein synthesis ribosome biogenesis	DCN1-like protein 2
Solyc07g039450.2.1	functional description:Density-regulated protein (AHRD V1 - B6SC	21 kDa	0	0	0.00882	0.01346	0	0	0	0.036	0	2	3	0	0	0	cell vesicle transport	Density-regulated protein
Solyc09g064720.2.1	functional description:Dienelactone hydrolase family protein (AHR	26 kDa	0	0.00468	0.02796	0	0	0	0	0.0021	1	7	0	0	0	0	misc misc2	Dienelactone hydrolase family protein
Solyc10g079830.1.1	functional description:Dihydroneopterin aldolase (AHRD V1 O6TI	15 kDa	0	0.01363	0	0.01936	0	0	0	0.036	2	0	3	0	0	0	major CHO metabolism degradation starch transporter	Dihydroneopterin aldolase
Solyc02g071150.2.1	functional description:DNA-binding protein (AHRD V1 B7R4T4 S	15 kDa	0	0.02608	0.00572	0.01199	0	0	0	0.022	3	1	2	0	0	0	redox ascorbate and glutathione	DNA-binding protein
Solyc05g007100.2.1	functional description:DNA-binding protein p24 (AHRD V1 - Q9LI	30 kDa	0	0.00331	0.00616	0.00626	0	0	0	0.036	1	2	1	0	0	0	DNA unspecified	DNA-binding protein p24
Solyc04g009770.2.1	functional description:DNAJ chaperone (AHRD V1 - Q1HR50 AE	47 kDa	0	0	0.00469	0.00481	0	0	0	0.043	0	3	2	0	0	0	stress abiotic heat	DNAJ chaperone
Solyc11g070050.1.1	- functional description:DUF866 domain protein (AHRD V1 -- A1C	19 kDa	0	0.02135	0.00994	0.02022	0	0	0	0.0013	2	2	2	0	0	0	redox ascorbate and glutathione	DUF866 domain protein
Solyc04g011540.2.1	functional description:Elicitor-responsive protein 1 (AHRD V1 -- B	18 kDa	0	0.00557	0.00519	0.01583	0	0	0	0.036	1	1	3	0	0	0	not assigned no ontology C2 domain-containing protein	Elicitor-responsive protein 1
Solyc03g116590.2.1	functional description:Embryo-specific 3 (AHRD V1 - Q2HUA9 M	22 kDa	0	0	0.01619	0.01091	0	0	0	0.036	0	1	3	0	0	0	development unspecified	Embryo-specific 3
Solyc10g006290.2.1	functional description:Endoribonuclease L-PSP family protein (AH	20 kDa	0	0.01339	0.01959	0.01641	0	0	0	0.0015	3	4	4	0	0	0	RNA processing ribonucleases	Endoribonuclease L-PSP family protein
Solyc05g018410.1.1	functional description:Enoyl-CoA hydratase (AHRD V1 A3WX21	33 kDa	0	0	0.0099	0.00283	0	0	0	0.046	0	4	1	0	0	0	amino acid metabolism degradation aspartate family ly	Enoyl-CoA hydratase
Solyc02g079060.2.1	functional description:Eukaryotic translation initiation factor 3 subu	25 kDa	0	0.01008	0.01003	0.00383	0	0	0	0.025	2	3	1	0	0	0	RNA regulation of transcription unclassified	Eukaryotic translation initiation factor 3 subunit J
Solyc09g090580.2.1	functional description:Eukaryotic translation initiation factor 4E-2 (	23 kDa	0	0.00443	0.0165	0.0042	0	0	0	0.019	1	3	1	0	0	0	protein synthesis initiation	Eukaryotic translation initiation factor 4E-2
Solyc07g005560.2.1	functional description:Eukaryotic translation initiation factor 5A (A	18 kDa	0	0.00554	0.00515	0.01573	0	0	0	0.0024	1	1	3	0	0	0	protein synthesis initiation	Eukaryotic translation initiation factor 5A
Solyc03g043750.2.1	functional description:FAD-dependent pyridine nucleotide-disulphi	60 kDa	0	0.00183	0.00534	0.00355	0	0	0	0.017	1	4	2	0	0	0	mitochondrial electron transport / ATP synthesis NAD	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
Solyc11g007120.1.1	functional description:Fe/S biogenesis protein nfuA (AHRD V1 NF	30 kDa	0	0.00319	0	0.02415	0	0	0	0.0025	1	0	5	0	0	0	protein assembly and cofactor ligation	Fe/S biogenesis protein nfuA
Solyc01g097800.2.1	functional description:Galactose-6-phosphate isomerase subunit lac	34 kDa	0	0.01434	0.00714	0.00273	0	0	0	0.0072	3	3	1	0	0	0	DNA repair	Galactose-6-phosphate isomerase subunit lacB
Solyc09g005620.2.1	functional description:Glutaredoxin (AHRD V1 -- D7G070 ECTSI	32 kDa	0	0.0091	0.0226	0.00575	0	0	0	0.00018	3	6	2	0	0	0	transport calcium	Glutaredoxin
Solyc06g073460.2.1	functional description:Glutathione peroxidase (AHRD V1 - Q7XZS	19 kDa	0	0	0.00988	0.01507	0	0	0	0.019	0	2	2	0	0	0	redox ascorbate and glutathione glutathione	Glutathione peroxidase
Solyc10g084400.1.1	functional description:Glutathione S-transferase (AHRD V1 - Q76K	27 kDa	0	0.00952	0.02843	0.01085	0	0	0	0.00018	2	7	3	0	0	0	transport amino acids	Glutathione S-transferase
Solyc02g087250.2.1	functional description:Group II intron splicing factor CRS1-like (AI	141 kDa	0	0.00199	0.00232	0.00183	0	0	0	0.0043	3	3	2	0	0	0	misc myrosinases-lectin-jacalin	Group II intron splicing factor CRS1-like
Solyc02g081830.2.1	functional description:HAD-superfamily hydrolase (AHRD V1 - D5	29 kDa	0	0.00692	0.01289	0	0	0	0	0.019	2	4	0	0	0	0	development unspecified	HAD-superfamily hydrolase
Solyc06g084090.2.1	functional description:Histone H2A (AHRD V1 -- C5XX54 SORB	22 kDa	0	0.00873	0.00813	0.00827	0	0	0	0.00035	2	2	1	0	0	0	lipid metabolism FA synthesis and FA elongation beta l	Histone H2A
Solyc09g082710.2.1	functional description:Histone H2A (AHRD V1 - B9MZP0 POPTR	15 kDa	0	0.00624	0.00581	0.02955	0	0	0	0.00018	1	1	4	0	0	0	DNA synthesis/chromatin structure histone	Histone H2A
Solyc00g009060.2.1	functional description:Hypoxanthine phosphoribosyltransferase (AI	22 kDa	0	0.0089	0.02901	0.01687	0	0	0	0.00018	1	6	3	0	0	0	lipid metabolism phospholipid synthesis	Hypoxanthine phosphoribosyltransferase
Solyc12g010840.1.1	functional description:Ketol-acid reductoisomerase (AHRD V1 - D7	64 kDa	0	0.00169	0.00123	0.00327	0	0	0	0.0011	1	1	2	0	0	0	amino acid metabolism synthesis branched chain group	Ketol-acid reductoisomerase
Solyc02g076820.2.1	functional description:Light-dependent short hypocotyls 1 (AHRD	21 kDa	0	0	0.01718	0.02185	0	0	0	0.0025	0	4	3	0	0	0	signalling light	Light-dependent short hypocotyls 1
Solyc08g014000.2.1	functional description:Lipoxygenase (AHRD V1 O43190 SOLTU)	97 kDa	0	0.01075	0.00734	0.00082	0	0	0	0.00024	6	2	1	0	0	0	hormone metabolism jasmonate synthesis-degradation	Lipoxygenase
Solyc04g054990.2.1	functional description:Lipoxygenase homology domain-containing p	24 kDa	0	0.00414	0.00385	0.01568	0	0	0	0.019	1	1	3	0	0	0	not assigned no ontology	Lipoxygenase homology domain-containing protein 1
Solyc00g060810.2.1	functional description:Major latex-like protein (AHRD V1 -- B5TH	17 kDa	0	0.0101	0.03577	0.02753	0	0	0	0.0002	1	5	3	0	0	0	stress abiotic unspecified	Major latex-like protein
Solyc08g029160.1.1	functional description:Membrane-associated progesterone receptor	11 kDa	0	0.04174	0.00733	0	0	0	0	0.038	3	1	0	0	0	0	RNA transcription	Membrane-associated progesterone receptor component 2
Solyc08g015960.2.1	functional description:Methionyl-tRNA synthetase (AHRD V1 -- B	31 kDa	0	0.00309	0.01437	0.00292	0	0	0	0.0096	1	3	1	0	0	0	RNA RNA binding	Methionyl-tRNA synthetase
Solyc04g078380.1.1	functional description:MFP1 attachment factor 1 (AHRD V1 -- O9I	16 kDa	0	0.01166	0	0.02208	0	0	0	0.019	2	0	3	0	0	0	cell organisation	MFP1 attachment factor 1
Solyc11g072450.1.1	functional description:Mitochondrial F0 ATP synthase D chain (AH	20 kDa	0	0.0211	0.00982	0.01998	0	0	0	0.0013	3	2	4	0	0	0	protein degradation ubiquitin E3 RING	Mitochondrial F0 ATP synthase D chain
Solyc10g078690.1.1	functional description:Mitochondrial protein translocase family (Fra	22 kDa	0	0.01278	0.00397	0.01614	0	0	0	0.0049	3	1	4	0	0	0	RNA regulation of transcription unclassified	Mitochondrial protein translocase family (Fragment)
Solyc01g104740.2.1	functional description:Multiprotein bridging factor 1 (AHRD V1 - C	16 kDa	0	0.0343	0.0301	0.01051	0	0	0	0.00049	4	4	1	0	0	0	hormone metabolism ethylene induced-regulated-respo	Multiprotein bridging factor 1
Solyc08g006510.2.1	functional description:NAD dependent epimerase/dehydratase fami	31 kDa	0	0.01776	0.0026	0	0	0	0	0.022	4	1	0	0	0	0	not assigned unknown	NAD dependent epimerase/dehydratase family protein
Solyc10g081440.1.1	functional description:NADH cytochrome b5 reductase (AHRD V1	31 kDa	0	0.00637	0.0089	0	0	0	0	0.036	2	3	0	0	0	0	PS lightreaction photosystem II PSII polypeptide subur	NADH cytochrome b5 reductase
Solyc03g007660.2.1	functional description:NADH dehydrogenase (AHRD V1 - D3BQF	20 kDa	0	0.00509	0.00474	0.02411	0	0	0	0.0096	1	1	5	0	0	0	mitochondrial electron transport / ATP synthesis NAD	NADH dehydrogenase
Solyc02g072160.2.1	functional description:NADH ubiquinone oxidoreductase complex I	63 kDa	0	0.00346	0.00378	0.00167	0	0	0	0.031	2	2	1	0	0	0	signalling light	NADH ubiquinone oxidoreductase complex I intermediate-associated protein 30
Solyc07g009160.2.1	functional description:Neighbor of COX4 (AHRD V1 - D3PHS4 9I	23 kDa	0	0.00434	0.00809	0.01645	0	0	0	0.0096	1	2	4	0	0	0	RNA regulation of transcription MADS box transcripti	Neighbor of COX4
Solyc03g083390.2.1	functional description:Nuclear movement protein nudc (AHRD V1	34 kDa	0	0.0037	0.01721	0.01408	0	0	0	0.00033	1	7	4	0	0	0	cell organisation	Nuclear movement protein nudc
Solyc02g068150.2.1	functional description:Nuclear transport factor 2 (AHRD V1 - B3TI	14 kDa	0	0.01441	0.00671	0.04093	0	0	0	0.0025	2	1	3	0	0	0	protein targeting nucleus	Nuclear transport factor 2
Solyc11g068830.1.1	functional description:Orotidine 5&apos-phosphate decarboxylase (	52 kDa	0	0	0.00762	0.00202	0	0	0	0.031	0	4	1	0	0	0	protein targeting mitochondria	Orotidine 5'-phosphate decarboxylase (Orotate phosphoribosyltransferase)
Solyc01g080410.2.1	functional description:Peptide methionine sulfoxide reductase msrE	15 kDa	0	0	0.00611	0.02486	0	0	0	0.036	0	1	4	0	0	0	lipid metabolism FA synthesis and FA elongation pyru	Peptide methionine sulfoxide reductase msrB
Solyc07g062060.2.1	functional description:Peptide methionine sulfoxide reductase msrE	16 kDa	0	0.01796	0.00557	0.01701	0	0	0	0.0096	3	1	3	0	0	0	protein aa activation	Peptide methionine sulfoxide reductase msrB
Solyc01g009990.2.1	functional description:Peptidyl-prolyl cis-trans isomerase (AHRD V	27 kDa	0	0.01189	0.00526	0.0081	0	0	0	0.02	2	2	2	0	0	0	cell cycle peptidylprolyl isomerase	Peptidyl-prolyl cis-trans isomerase
Solyc01g096520.2.1	functional description:Peptidyl-prolyl cis-trans isomerase (AHRD V	21 kDa	0	0.00466	0	0.01767	0	0	0	0.036	1	0	3	0	0	0	cell cycle peptidylprolyl isomerase	Peptidyl-prolyl cis-trans isomerase
Solyc11g008990.1.1	functional description:Phage shock protein A PspA (AHRD V1 - B7	36 kDa	0	0.00678	0.01125	0.00258	0	0	0	0.0072	2	4	1	0	0	0	cell wall precursor synthesis UXS	Phage shock protein A PspA
Solyc04g058090.2.1	functional description:Phosphoribosylformylglycinamidine cyclo-lig	43 kDa	0	0.00554	0.00551	0.0021	0	0	0	0.025	2	2	1	0	0	0	nucleotide metabolism synthesis purine AIR synthase	Phosphoribosylformylglycinamidine cyclo-ligase
Solyc03g114930.2.1	functional description:Photosystem II oxygen evolving complex pro	28 kDa	0	0.0072	0	0.01023	0	0	0	0.036	2	0	2	0	0	0	PS lightreaction photosystem II PSII polypeptide subur	Photosystem II oxygen evolving complex protein PsbP
Solyc04g082010.1.1	functional description:Plastocyanin (AHRD V1 - O0W9E5 SOLCC	17 kDa	0	0.01964	0.00862	0.00903	0	0	0	0.013	2	1	1	0	0	0	lipid metabolism lipid degradation lysophospholipases	Plastocyanin
Solyc06g076890.1.1	functional description:Pleckstrin homology domain-containing prot	17 kDa	0	0.01846	0.00573	0.01748	0	0	0	0.0096	2	1	2	0	0	0	signalling phosphinositides	Pleckstrin homology domain-containing protein 1
Solyc01g096430.2.1	functional description:Predicted NADPH-dependent FMN reductas	21 kDa	0	0.00457	0.01275	0.00865	0	0	0	0.019	1	2	2	0	0	0	not assigned no ontology	Predicted NADPH-dependent FMN reductase
Solyc02g080940.2.1	functional description:Proline synthetase co-transcribed bacterial h	26 kDa	0	0.01094	0.00679	0	0	0	0	0.036	2	2	0	0	0	0	DNA synthesis/chromatin structure	Proline synthetase co-transcribed bacterial homolog protein
Solyc03g120720.2.1	functional description:Protein disulfide isomerase L-3b (AHRD V1	61 kDa	0	0.00556	0.00946	0.00538	0	0	0	0.00053	3	5	3	0	0	0	redox thioredoxin	Protein disulfide isomerase L-3b
Solyc07g054210.2.1	functional description:Protochlorophyllide reductase like protein (A	43 kDa	0	0.0028	0.0093	0.00213	0	0	0	0.013	1	4	1	0	0	0	tetrapyrrole synthesis protochlorophyllide reductase	Protochlorophyllide reductase like protein
Solyc05g053940.2.1	functional description:Ras-related protein Rab-1A (AHRD V1 - B6	22 kDa	0	0.00411	0.01443	0.01134	0	0	0	0.0024	1	3	1	0	0	0	signalling G-proteins	Ras-related protein Rab-1A
Solyc07g055290.2.1	functional description:Ras-related protein Rab-25 (AHRD V1 - RA	24 kDa	0	0.00406	0.0227	0.00385	0	0	0	0.0049	1	5	1	0	0	0	signalling G-proteins	Ras-related protein Rab-25
Solyc11g008430.1.1	functional description:Ras-related protein Rab-5C (AHRD V1 - C1I	22 kDa	0	0	0.00412	0.01678	0	0	0	0.036	0	1	3	0	0	0	signalling G-proteins	Ras-related protein Rab-5C
Solyc09g007850.2.1	functional description:RNA-binding protein (AHRD V1 - C6F119 :	31 kDa	0	0.00917	0.00853	0.02026	0	0	0	0.00018	3	2	6	0	0	0	RNA RNA binding	RNA-binding protein
Solyc10g081180.1.1	functional description:RNA-binding protein (AHRD V1 O941H8 S	22 kDa	0	0.00403	0.02249	0	0	0	0	0.0096	1	4	0	0	0	0	RNA RNA binding	RNA-binding protein
Solyc01g097910.2.1	functional description:Rubredoxin family protein (AHRD V1 -- D7I	23 kDa	0	0.0086	0.004	0.00815	0	0	0	0.036	2	1	2	0	0	0	protein assembly and cofactor ligation	Rubredoxin family protein
Solyc10g005100.2.1	functional description:Salt stress root protein RS1 (AHRD V1 -- SR	22 kDa	0	0.01467	0.00974	0.01	0	0	0	0.01	2	2	1	0	0	0	signalling phosphinositides	Salt stress root protein RS1
Solyc12g099820.1.1	functional description:Signal recognition particle protein (AHRD V	12 kDa	0	0.03242	0.00711	0.00745	0	0	0	0.038	3	1	1	0	0	0	protein targeting secretory pathway ER	Signal recognition particle protein
Solyc11g040110.1.1	functional description:SnRK1-interacting protein 1 (AHRD V1 - B6	23 kDa	0	0.00412	0.01151	0.01171	0	0	0	0.0096	1	3	2	0	0	0	RNA regulation of transcription chromatin remodeling	SnRK1-interacting protein 1
Solyc07g061990.2.1	functional description:Solanesyl diphosphate synthase (AHRD V1 -	44 kDa	0	0	0.00373	0.00641	0	0	0	0.046	0	2	3	0	0	0	secondary metabolism isoprenoids non-mevalonate pat	Solanesyl diphosphate synthase
Solyc06g053480.2.1	functional description:Stearoyl-acyl carrier protein desaturase (AHI	45 kDa	0	0.00563	0.00935	0.00428	0	0	0	0.0039	2	5	2	0	0	0	protein synthesis ribosome biogenesis	Stearoyl-acyl carrier protein desaturase
Solyc06g062950.1.1	functional description:Subtilisin-like protease (AHRD V1 -- A9XG4	83 kDa	0	0.00323	0.00283	0.00198	0	0	0	0.013	3	2	1	0	0	0	signalling calcium	Subtilisin-like protease
Solyc11g066390.1.1	functional description:Superoxide dismutase (AHRD V1 - O7XAV2	22 kDa	0	0.00408	0.0038	0.03094	0	0	0	0.0013	1	1	7	0	0	0	protein synthesis ribosome biogenesis	Superoxide dismutase
Solyc07g005200.2.1	functional description:Synaptobrevin homolog YKT6 (AHRD V1 --	23 kDa	0	0.00445	0.00829	0.00843	0	0	0	0.036	1	2	2	0	0	0	cell vesicle transport	Synaptobrevin homolog YKT6
Solyc01g008160.2.1	functional description:Tetratricopeptide repeat-containing protein (	36 kDa	0	0.00554	0.00258	0.00524	0	0	0	0.036	2	1	2	0	0	0	DNA synthesis/chromatin structure retrotransposon/tra	Tetratricopeptide repeat-containing protein
Solyc10g037980.1.1	functional description:Thioredoxin domain-containing protein 17 (A	15 kDa	0	0.01897	0.01665	0	0	0	0	0.038	3	3	0	0	0	0	not assigned no ontology	Thioredoxin domain-containing protein 17
Solyc12g009600.1.1	functional description:Thylakoid lumenal protein (AHRD V1 - B6S	23 kDa	0	0.0159	0.01047	0	0	0	0	0.022	4	3	0	0	0	0	not assigned no ontology	Thylakoid lumenal protein
Solyc01g096530.2.1	functional description:Trafficking protein particle complex subunit	21 kDa	0	0.00898	0.02757	0.01238	0	0	0	0.0015	2	6	2	0	0	0	transport misc	Trafficking protein particle complex subunit 3
Solyc02g094440.2.1	functional description:Translocon-associated protein subunit beta (	21 kDa	0	0	0.0136	0.00523	0	0	0	0.038	0	3	1	0	0	0	not assigned no ontology	Translocon-associated protein subunit beta
Solyc06g005490.2.1	functional description:Triosephosphate isomerase (AHRD V1 O3H	28 kDa	0	0.0087	0.00578	0.00331	0	0	0	0.00061	2	2	1	0	0	0	PS calvin cycle TPI	Triosephosphate isomerase
Solyc01g068400.2.1	functional description:Tubulin-specific chaperone A (AHRD V1 C	9 kDa	0	0.02197	0.03855	0	0	0	0	0.038	2	3	0	0	0	0	protein folding	Tubulin-specific chaperone A
Solyc10g012240.2.1	functional description:Ubiquitin-conjugating enzyme (AHRD V1 - I	21 kDa	0	0	0.02402	0.00839	0	0	0	0.013	0	3	2	0	0	0	protein degradation ubiquitin E2	Ubiquitin-conjugating enzyme
Solyc05g054540.2.1	functional description:Ubiquitin-conjugating enzyme 13 E2 (AHRD	19 kDa	0	0.00982	0.01293	0.01354	0	0	0	0.013	2	3	2	0	0	0	protein degradation ubiquitin E2	Ubiquitin-conjugating enzyme 13 E2
Solyc01g059930.2.1	functional description:Universal stress protein (AHRD V1 - D6BRI	18 kDa	0	0.00544	0.01012	0.02059	0	0	0	0.0096	1	2	4	0	0	0	misc myrosinases-lectin-jacalin	Universal stress protein
Solyc06g084540.2.1	functional description:Universal stress protein (AHRD V1 - B4UW	17 kDa	0	0.01693	0	0.03207	0	0	0	0.0025	3	0	4	0	0	0	hormone metabolism ethylene induced-regulated-respo	Universal stress protein
Solyc09g011660.2.1	functional description:Universal stress protein 1 (AHRD V1 - B0YC	19 kDa	0	0.00509	0.0268	0.01404	0	0	0	0.0043	1	4	3	0	0	0	development unspecified	Universal stress protein 1
Solyc09g011670.2.1	functional description:Universal stress protein family protein (AHR	19 kDa	0	0.01018	0.0134	0.00936	0	0	0	0.022	2	3	1	0	0	0	RNA regulation of transcription putative transcription r	Universal stress protein family protein
Solyc06g073900.2.1	functional_description:Unknown Protein (AHRD V1)	17 kDa	0	0.00599	0.00557	0.02268	0	0	0	0.019	1	1	3	0	0	0	transport peptides and oligopeptides	Unknown Protein
Solyc04g082640.2.1	functional_description:Unknown Protein (AHRD V1)	18 kDa	0	0.00494	0.013	0.01362	0	0	0	0.022	1	3	2	0	0	0	misc calcineurin-like phosphoesterase family protein	Unknown Protein
Solyc10g007320.2.1	functional description:Uroporphyrinogen decarboxylase (AHRD V1	46 kDa	0	0	0.00354	0.00607	0	0	0	0.046	0	2	2	0	0	0	signalling G-proteins	Uroporphyrinogen decarboxylase
Solyc12g098150.1.1	functional description:Voltage-gated potassium channel beta subuni	37 kDa	0	0.00339	0.00675	0.00515	0	0	0	0.025	1	3	2	0	0	0	transport potassium	Voltage-gated potassium channel beta subunit
Solyc04g049330.2.1	functional description:V-type proton ATPase subunit G 1 (AHRD V	13 kDa	0	0.08272	0.0066	0	0	0	0	0.0015	9	1	0	0	0	0	transport p- and v-ATPases H+-transporting two-secto	V-type proton ATPase subunit G 1

Total proteins=123

Proteins present only in AV

Accession.Number	DESCRIPTION	Molecula	Fold.Cha	AC.1.1	AC.2.1	AC.3.1	AV.1.1	AV.2.1	AV.3.1	P Value	AC.1.1	AC.2.1	AC.3.1	AV.1.1	AV.2.1	AV.3.1	MAPMAN CLASS	MAPMAN DESCRIPTION
Solyc12g010860.1.1	functional description:14-3-3 protein beta/alpha (AHRD	29 kDa	Inf	0	0	0	0.01297	0.00937	0.01057	0.0055	0	0	0	2	1	2	signalling 14-3-3 proteins	14-3-3 protein beta/alpha
Solyc03g095900.2.1	functional description:1-aminocyclopropane-1-carboxyla	42 kDa	Inf	0	0	0	0.01697	0.00668	0.01556	0.00017	0	0	0	5	2	3	secondary metabolism sulfur-co	1-aminocyclopropane-1-carboxylate oxidase-like protein
Solyc03g114340.2.1	functional description:1-deoxy-D-xylulose-5-phosphate r	51 kDa	Inf	0	0	0	0.00242	0.00921	0.00263	0.0095	0	0	0	1	4	1	protein postranslational modifica	1-deoxy-D-xylulose-5-phosphate reductoisomerase
Solyc02g062600.2.1	functional description:2345-tetrahydropyridine-26-dicarb	29 kDa	Inf	0	0	0	0	0.01368	0.01544	0.0055	0	0	0	0	2	3	redox ascorbate and glutathione	2 3 4 5-tetrahydropyridine-2 6-dicarboxylate N-acetyltransferase
Solyc11g069720.1.1	functional description:26S protease regulatory subunit 6E	90 kDa	Inf	0	0	0	0.00429	0	0.00622	0.0044	0	0	0	3	0	4	cell division	26S protease regulatory subunit 6B homolog
Solyc05g053140.2.1	functional description:26S proteasome non-ATPase regul	44 kDa	Inf	0	0	0	0.00663	0.00546	0.00487	0.012	0	0	0	2	2	2	protein degradation ubiquitin pro	26S proteasome non-ATPase regulatory subunit 13
Solyc02g068310.2.1	functional description:2-oxoglutarate-dependent dioxyge	34 kDa	Inf	0	0	0	0	0.007	0.01248	0.012	0	0	0	0	2	2	hormone metabolism ethylene s	2-oxoglutarate-dependent dioxygenase
Solyc03g119360.2.1	functional description:40S ribosomal protein S7-like prot	22 kDa	Inf	0	0	0	0	0.02702	0.00307	0.0033	0	0	0	0	7	1	protein synthesis ribosomal prot	40S ribosomal protein S7-like protein
Solyc03g117870.2.1	functional description:4-coumarate CoA ligase (AHRD V	60 kDa	Inf	0	0	0	0.00396	0.00408	0.00483	0.0073	0	0	0	2	2	2	secondary metabolism phenylpr	4-coumarate CoA ligase
Solyc01g009010.2.1	functional description:4-diphosphocytidyl-2-C-methyl-D-	44 kDa	Inf	0	0	0	0.0063	0.00619	0.00577	0.013	0	0	0	2	2	2	secondary metabolism isoprenoi	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
Solyc01g087730.2.1	functional description:50S ribosomal protein L1 (AHRD	37 kDa	Inf	0	0	0	0	0.00733	0.01025	0.027	0	0	0	0	2	3	protein synthesis ribosomal prot	50S ribosomal protein L1
Solyc09g007560.2.1	functional description:50S ribosomal protein L5 (AHRD	29 kDa	Inf	0	0	0	0	0.00923	0.01041	0.031	0	0	0	0	2	2	protein synthesis ribosomal prot	50S ribosomal protein L5
Solyc10g078960.1.1	functional description:60S ribosomal protein L21-like pro	19 kDa	Inf	0	0	0	0	0.01398	0.01072	0.018	0	0	0	0	2	3	protein synthesis ribosome bioge	60S ribosomal protein L21-like protein
Solyc07g043360.1.1	functional description:60S ribosomal protein L27 (AHRD	16 kDa	Inf	0	0	0	0	0.00425	0.01736	0.018	0	0	0	0	1	2	signalling phosphinositides	60S ribosomal protein L27
Solyc09g020130.2.1	functional description:60S ribosomal protein L5-1 (AHRI	35 kDa	Inf	0	0	0	0	0.00812	0.00917	0.031	0	0	0	0	2	2	protein synthesis ribosome bioge	60S ribosomal protein L5-1
Solyc12g096220.1.1	functional description:60S ribosomal protein L7 (AHRD	82 kDa	Inf	0	0	0	0	0.00866	0.00322	0.00019	0	0	0	0	6	3	signalling G-proteins	60S ribosomal protein L7
Solyc03g095620.2.1	functional description:ABC-1 domain protein (AHRD V1	60 kDa	Inf	0	0	0	0	0.0163	0.00233	0.00093	0	0	0	0	5	1	transport ABC transporters and	ABC-1 domain protein
Solyc07g045350.2.1	functional description:Acetyl-CoA C-acetyltransferase pr	41 kDa	Inf	0	0	0	0.00312	0.0092	0.00572	0.0063	0	0	0	1	3	1	amino acid metabolism degradat	Acetyl-CoA C-acetyltransferase protein
Solyc08g080370.2.1	functional description:Acetylornithine aminotransferase (	49 kDa	Inf	0	0	0	0.00274	0.00808	0.00753	0.0063	0	0	0	1	3	2	amino acid metabolism synthesi	Acetylornithine aminotransferase
Solyc03g082910.2.1	functional description:Acyl-CoA-binding domain-contain	38 kDa	Inf	0	0	0	0	0.00633	0.00723	0.045	0	0	0	0	2	2	lipid metabolism FA synthesis an	Acyl-CoA-binding domain-containing protein 6
Solyc07g053310.2.1	functional description:Adaptin ear-binding coat-associate	32 kDa	Inf	0	0	0	0.0089	0.01313	0.01632	0.0015	0	0	0	2	2	4	signalling MAP kinases	Adaptin ear-binding coat-associated protein 1
Solyc08g077300.2.1	functional description:Adenylate kinase (AHRD V1 B6T	24 kDa	Inf	0	0	0	0	0.01593	0.00543	0.01	0	0	0	0	3	1	nucleotide metabolism phosphot	Adenylate kinase
Solyc08g076920.2.1	functional description:ADP-ribosylation factor GTPase-a	44 kDa	Inf	0	0	0	0.00558	0.00797	0.00911	0.002	0	0	0	2	2	3	signalling G-proteins	ADP-ribosylation factor GTPase-activating protein 3
Solyc12g038970.1.1	functional description:Agmatine deiminase (AHRD V1 I	42 kDa	Inf	0	0	0	0.00672	0.01321	0.00616	0.0031	0	0	0	2	2	1	RNA regulation of transcription	Agmatine deiminase
Solyc03g019790.2.1	functional description:Alpha-galactosidase (AHRD V1 C	45 kDa	Inf	0	0	0	0.00414	0.01494	0.00675	0.00096	0	0	0	1	4	1	minor CHO metabolism galactos	Alpha-galactosidase
Solyc04g008730.2.1	functional description:Alpha-galactosidase 1 (AHRD V1	47 kDa	Inf	0	0	0	0	0.00593	0.00553	0.0031	0	0	0	0	2	2	minor CHO metabolism galactos	Alpha-galactosidase 1
Solyc12g013700.1.1	functional description:Aluminum-induced protein-like pro	28 kDa	Inf	0	0	0	0.01333	0	0.02173	0.0055	0	0	0	2	0	3	hormone metabolism auxin indu	Aluminum-induced protein-like protein
Solyc10g074580.1.1	functional description:Aminoacylase ACY1 and related n	42 kDa	Inf	0	0	0	0	0.01301	0.00606	0.013	0	0	0	0	4	2	signalling calcium	Aminoacylase ACY1 and related metalloexopeptidases (ISS)
Solyc12g006450.1.1	functional description:Aminotransferase-like protein (AH	57 kDa	Inf	0	0	0	0	0.00636	0.00242	0.0044	0	0	0	0	3	1	amino acid metabolism synthesi	Aminotransferase-like protein
Solyc05g009920.2.1	functional description:Anion-transporting ATPase (AHRI	51 kDa	Inf	0	0	0	0	0.00806	0.00501	0.027	0	0	0	0	3	2	not assigned no ontology hydrox	Anion-transporting ATPase
Solyc01g097540.2.1	functional description:Annexin 3 (AHRD V1 - A9X4R3	36 kDa	Inf	0	0	0	0.00396	0.01169	0.00726	0.013	0	0	0	1	3	2	misc oxidases - copper flavone	Annexin 3
Solyc06g006100.2.1	functional description:Anthranilate synthase component I	66 kDa	Inf	0	0	0	0	0.00746	0.00853	0.002	0	0	0	0	4	4	RNA regulation of transcription	Anthranilate synthase component I family protein expressed
Solyc10g008800.2.1	functional description:Apoptosis inhibitor 5 (AHRD V1 -	62 kDa	Inf	0	0	0	0	0.01378	0.0045	0.00093	0	0	0	0	3	2	development unspecified	Apoptosis inhibitor 5
Solyc12g008570.1.1	functional description:Arginyl-tRNA synthetase (AHRD	73 kDa	Inf	0	0	0	0.00177	0.00337	0.00193	0.045	0	0	0	1	2	1	protein aa activation arginine-tR	Arginyl-tRNA synthetase
Solyc01g111510.2.1	functional description:Ascorbate peroxidase (AHRD V1	32 kDa	Inf	0	0	0	0.0059	0.00426	0.01442	0.0004	0	0	0	1	1	2	RNA regulation of transcription	Ascorbate peroxidase
Solyc04g054710.2.1	functional description:Aspartate aminotransferase (AHRI	51 kDa	Inf	0	0	0	0	0.01368	0.00521	0.002	0	0	0	0	5	1	amino acid metabolism synthesi	Aspartate aminotransferase
Solyc08g068330.2.1	functional description:Aspartate aminotransferase (AHRI	50 kDa	Inf	0	0	0	0	0.00274	0.00766	0.013	0	0	0	0	1	2	cell wall precursor synthesis UX	Aspartate aminotransferase
Solyc01g096040.2.1	functional description:Aspartic proteinase nepenthesin I (	51 kDa	Inf	0	0	0	0.00352	0.00508	0.01147	0.0023	0	0	0	1	2	3	RNA regulation of transcription	Aspartic proteinase nepenthesin I
Solyc06g074000.1.1	functional description:Aspartic proteinase nepenthesin-2	50 kDa	Inf	0	0	0	0.00468	0.00724	0	0.017	0	0	0	2	3	0	protein degradation aspartate pr	Aspartic proteinase nepenthesin-2
Solyc02g080540.1.1	functional description:ATP synthase gamma chain (AHR	41 kDa	Inf	0	0	0	0.00449	0.00649	0.00732	0.013	0	0	0	1	2	2	PS lightreaction ATP synthase g	ATP synthase gamma chain
Solyc03g120980.2.1	functional description:ATP-binding cassette transporter (	170 kDa	Inf	0	0	0	0	0.00211	0.00125	0.026	0	0	0	0	2	2	transport ABC transporters and	ATP-binding cassette transporter
Solyc07g044760.2.1	functional description:ATP-dependent RNA helicase (AH	67 kDa	Inf	0	0	0	0.00365	0.00521	0.00596	0.002	0	0	0	2	2	1	protein synthesis initiation	ATP-dependent RNA helicase
Solyc11g033280.1.1	functional description:ATP-dependent RNA helicase FAI	44 kDa	Inf	0	0	0	0.00294	0.01679	0.0096	0.00075	0	0	0	1	4	3	protein synthesis initiation	ATP-dependent RNA helicase FAL1
Solyc07g055320.2.1	functional description:ATP-dependent Zn protease cell di	74 kDa	Inf	0	0	0	0	0.00316	0.00722	0.0095	0	0	0	0	2	4	protein degradation metalloprote	ATP-dependent Zn protease cell division protein FtsH homolog
Solyc07g065010.2.1	functional description:Bactericidal permeability-increasin	54 kDa	Inf	0	0	0	0	0.00249	0.01126	0.013	0	0	0	0	1	4	not assigned no ontology	Bactericidal permeability-increasing protein
Solyc06g073740.2.1	functional description:Beta-D-glucosidase (AHRD V1 Q	68 kDa	Inf	0	0	0	0.00173	0.00535	0.00422	0.0032	0	0	0	1	2	2	cell wall degradation cellulases a	Beta-D-glucosidase
Solyc11g018500.1.1	functional description:Beta-galactosidase (AHRD V1 - B	78 kDa	Inf	0	0	0	0.00155	0.0032	0.0019	0.038	0	0	0	1	2	1	nucleotide metabolism synthesis	Beta-galactosidase
Solyc03g119080.2.1	functional description:Beta-glucosidase (AHRD V1 D7L	59 kDa	Inf	0	0	0	0	0.01205	0.00674	0.0031	0	0	0	0	4	3	misc gluco- galacto- and manno	Beta-glucosidase
Solyc11g008720.1.1	functional description:Beta-glucosidase G4 (AHRD V1 -	58 kDa	Inf	0	0	0	0	0.01325	0.00784	0.00062	0	0	0	0	5	3	misc gluco- galacto- and manno	Beta-glucosidase G4
Solyc01g081610.2.1	functional description:Beta-hexosaminidase 1 (AHRD V	64 kDa	Inf	0	0	0	0.002	0.0019	0.00653	0.021	0	0	0	1	1	2	protein glycosylation alpha-1 3-i	Beta-hexosaminidase 1
Solyc01g098700.2.1	functional description:Branched-chain amino acid aminot	58 kDa	Inf	0	0	0	0.00221	0.00421	0.00722	0.0095	0	0	0	1	2	2	misc aminotransferases aminotra	Branched-chain amino acid aminotransferase-like protein
Solyc01g094220.2.1	functional description:Carbonyl reductase 3 (AHRD V1	33 kDa	Inf	0	0	0	0.01129	0.00407	0.0092	0.013	0	0	0	2	1	2	protein degradation ubiquitin E3	Carbonyl reductase 3
Solyc12g088670.1.1	functional description:Cathepsin B-like cysteine proteinas	51 kDa	Inf	0	0	0	0	0.00984	0.00252	0.0033	0	0	0	0	4	1	transport major intrinsic proteins	Cathepsin B-like cysteine proteinase
Solyc03g121640.2.1	functional description:chaperonin (AHRD V1 - D3NRF5	61 kDa	Inf	0	0	0	0.00201	0.00573	0	0.045	0	0	0	1	2	0	protein folding	chaperonin
Solyc05g053470.2.1	functional description:chaperonin (AHRD V1 - D2LE93	61 kDa	Inf	0	0	0	0.0022	0	0.00806	0.027	0	0	0	1	0	4	protein folding	chaperonin
Solyc09g091180.2.1	functional description:chaperonin (AHRD V1 - Q6N0B9	62 kDa	Inf	0	0	0	0.00218	0	0.00399	0.027	0	0	0	1	0	2	stress abiotic heat	chaperonin
Solyc10g055800.1.1	functional description:Chitinase (AHRD V1 - B9VRK7 (	35 kDa	Inf	0	0	0	0.00515	0.01115	0	0.031	0	0	0	1	3	0	stress biotic PR-proteins PR3/4/	Chitinase
Solyc07g005100.2.1	functional description:Chitinase-like protein (AHRD V1 -	42 kDa	Inf	0	0	0	0	0.02636	0.00614	0.00072	0	0	0	0	6	2	stress biotic PR-proteins PR3/4/	Chitinase-like protein
Solyc01g008550.2.1	functional description:Cinnamoyl CoA reductase-like pro	35 kDa	Inf	0	0	0	0	0.03097	0.00722	0.00072	0	0	0	0	5	2	secondary metabolism flavonoid	Cinnamoyl CoA reductase-like protein
Solyc01g073740.2.1	functional description:Citrate synthase (AHRD V1 - O24	53 kDa	Inf	0	0	0	0.00797	0.01568	0.00731	0.00017	0	0	0	2	4	2	TCA / organic transformation T(	Citrate synthase
Solyc06g082560.1.1	functional description:ClpB chaperone (AHRD V1 - D6(	95 kDa	Inf	0	0	0	0.00147	0.0029	0.00406	0.013	0	0	0	1	1	2	stress abiotic heat	ClpB chaperone
Solyc10g081920.1.1	functional description:Coatomer subunit beta-1 (AHRD \	102 kDa	Inf	0	0	0	0	0.00366	0.00434	0.0073	0	0	0	0	3	3	cell vesicle transport	Coatomer subunit beta-1
Solyc10g012370.2.1	functional description:Cysteine synthase (AHRD V1 Q7	38 kDa	Inf	0	0	0	0.00718	0.00706	0.01316	0.0031	0	0	0	2	2	3	RNA transcription	Cysteine synthase
Solyc04g071140.2.1	functional description:Decarboxylase family protein (AH	54 kDa	Inf	0	0	0	0.00716	0	0.00519	0.021	0	0	0	2	0	1	misc cytochrome P450	Decarboxylase family protein
Solyc05g056580.2.1	functional description:Dehydration-responsive family pro	91 kDa	Inf	0	0	0	0	0.00389	0.00231	0.026	0	0	0	0	2	1	stress abiotic drought/salt	Dehydration-responsive family protein
Solyc01g109850.2.1	functional description:Diaminopimelate decarboxylase (A	53 kDa	Inf	0	0	0	0.00525	0.00516	0.00722	0.0063	0	0	0	2	2	3	stress biotic receptors	Diaminopimelate decarboxylase
Solyc01g066520.2.1	functional description:Dihydrolipoyllysine-residue acetylt	55 kDa	Inf	0	0	0	0	0.0065	0.01487	0.00093	0	0	0	0	3	5	amino acid metabolism degradat	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex
Solyc02g078260.2.1	functional description:DNA-directed RNA polymerase (A	135 kDa	Inf	0	0	0	0	0.00354	0.00079	0.026	0	0	0	0	4	1	RNA transcription	DNA-directed RNA polymerase
Solyc01g109410.2.1	functional description:Dolichyl-diphosphooligosaccharide	48 kDa	Inf	0	0	0	0	0.01009	0.00288	0.021	0	0	0	0	3	1	protein glycosylation	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit
Solyc11g007830.1.1	functional description:Dual-specificity protein-like phosp	42 kDa	Inf	0	0	0	0	0.01339	0.00624	0.013	0	0	0	0	3	2	protein postranslational modifica	Dual-specificity protein-like phosphatase 3
Solyc06g011280.2.1	functional description:Elongation factor 1-gamma (AHRI	47 kDa	Inf	0	0	0	0	0.02368	0.00334	0.0004	0	0	0	0	7	1	protein synthesis elongation	Elongation factor 1-gamma
Solyc07g007210.2.1	functional description:Elongation factor like protein (AHI	103 kDa	Inf	0	0	0	0	0.00342	0.00203	0.026	0	0	0	0	3	2	protein synthesis elongation	Elongation factor like protein
Solyc09g073000.2.1	functional description:Elongation factor Tu (AHRD V1 I	49 kDa	Inf	0	0	0	0.00479	0.00247	0.00293	0.0077	0	0	0	2	1	1	redox ascorbate and glutathione	Elongation factor Tu
Solyc06g071790.2.1	functional description:Elongation factor Tu (AHRD V1 I	49 kDa	Inf	0	0	0	0	0.00815	0.00307	0.031	0	0	0	0	3	1	protein synthesis elongation	Elongation factor Tu
Solyc09g010210.2.1	functional description:Endoglucanase 1 (AHRD V1 - B6	54 kDa	Inf	0	0	0	0.00262	0.01078	0.00576	0.0014	0	0	0	1	4	2	DNA synthesis/chromatin struct	Endoglucanase 1
Solyc01g080930.2.1	functional description:Enoyl-CoA-hydratase (AHRD V1	43 kDa	Inf	0	0	0	0.00668	0.00275	0.00491	0.026	0	0	0	2	1	2	amino acid metabolism degradat	Enoyl-CoA-hydratase
Solyc01g090700.2.1	functional description:Enoyl-CoA-hydratase (AHRD V1	45 kDa	Inf	0	0	0	0.00624	0.00307	0.00572	0.027	0	0	0	2	1	2	amino acid metabolism degradat	Enoyl-CoA-hydratase
Solyc06g082580.2.1	functional description:Eukaryotic translation initiation fac	34 kDa	Inf	0	0	0	0	0.01227	0.01143	0.013	0	0	0	0	2	3	protein synthesis initiation	Eukaryotic translation initiation factor 2 beta subunit-like
Solyc03g120010.2.1	functional description:Eukaryotic translation initiation fac	39 kDa	Inf	0	0	0	0.00354	0.02088	0.00973	0.00072	0	0	0	1	5	2	protein postranslational modifica	Eukaryotic translation initiation factor 3 subunit 2
Solyc01g112000.2.1	functional description:Expansin-like protein (AHRD V1 -	28 kDa	Inf	0	0	0	0	0.01874	0.01057	0.0055	0	0	0	0	3	2	cell wall modification	Expansin-like protein
Solyc10g005960.1.1	functional description:Fasciclin-like arabinogalactan prot	44 kDa	Inf	0	0	0	0.00831	0	0.00301	0.045	0	0	0	3	0	1	cell wall cell wall proteins AGPs	Fasciclin-like arabinogalactan protein 10
Solyc07g021540.2.1	functional description:FIP1 (AHRD V1 -- B6TPG9 MAI	29 kDa	Inf	0	0	0	0.00646	0.00467	0.0158	0.013	0	0	0	1	1	2	hormone metabolism abscisic ac	FIP1
Solyc06g073190.2.1	functional description:Fructokinase-like (AHRD V1 - Q3	35 kDa	Inf	0	0	0	0	0.00699	0.00357	0.033	0	0	0	0	2	1	major CHO metabolism degrada	Fructokinase-like
Solyc06g007340.2.1	functional description:Gamma-interferon-inducible lysoso	29 kDa	Inf	0	0	0	0	0.01129	0.00692	0.01	0	0	0	0	4	3	RNA regulation of transcription	Gamma-interferon-inducible lysosomal thiol reductase
Solyc09g082990.2.1	functional description:GDP-D-mannose-3AC 5AC -epim	43 kDa	Inf	0	0	0	0.0034	0	0.005	0.0014	0	0	0	1	0	2	cell wall precursor synthesis UX	GDP-D-mannose-3' 5'-epimerase 2
Solyc12g017460.1.1	functional description:GDSL esterase/lipase At1g28590 (	41 kDa	Inf	0	0	0	0.00347	0.00286	0.01273	0.0059	0	0	0	1	1	5	lipid metabolism lipid degradatic	GDSL esterase/lipase At1g28590
Solyc05g013690.2.1	functional description:GDSL esterase/lipase At3g26430 (	43 kDa	Inf	0	0	0	0	0.00642	0.00898	0.027	0	0	0	0	2	2	misc GDSL-motif lipase	GDSL esterase/lipase At3g26430
Solyc03g111550.2.1	functional description:GDSL esterase/lipase At3g48460 (	37 kDa	Inf	0	0	0	0.00697	0.00332	0.00758	0.021	0	0	0	2	1	1	misc GDSL-motif lipase	GDSL esterase/lipase At3g48460
Solyc07g042910.2.1	functional description:Genomic DNA chromosome 5 TA(	124 kDa	Inf	0	0	0	0	0.00194	0.00347	0.012	0	0	0	0	1	3	RNA regulation of transcription	Genomic DNA chromosome 5 TAC clone K21L19
Solyc07g005330.2.1	functional description:Glucan endo-1 3-beta-glucosidase	51 kDa	Inf	0	0	0	0.00705	0	0.00287	0.038	0	0	0	3	0	1	misc beta 1 3 glucan hydrolases	Glucan endo-1 3-beta-glucosidase
Solyc05g025500.2.1	functional description:Glucan endo-1 3-beta-glucosidase	53 kDa	Inf	0	0	0	0	0.00681	0.00779	0.0095	0	0	0	0	3	3	misc beta 1 3 glucan hydrolases	Glucan endo-1 3-beta-glucosidase 6
Solyc08g074390.2.1	functional description:Glucan endo-1 3-beta-glucosidase	53 kDa	Inf	0	0	0	0	0.00895	0.00256	0.021	0	0	0	0	4	1	misc gluco- galacto- and manno	Glucan endo-1 3-beta-glucosidase 6
Solyc03g063560.2.1	functional description:Glutamate synthase (Ferredoxin) (.	177 kDa	Inf	0	0	0	0.00066	0	0.00406	0.0073	0	0	0	1	0	5	N-metabolism ammonia metabo	Glutamate synthase (Ferredoxin)
Solyc04g009200.2.1	functional description:Glutamate-1-semialdehyde-2 1-am	52 kDa	Inf	0	0	0	0	0.01028	0.00958	0.0031	0	0	0	0	4	3	misc oxidases - copper flavone	Glutamate-1-semialdehyde-2 1-aminomutase
Solyc08g081010.2.1	functional description:Glutamate-cysteine ligase (AHRD	59 kDa	Inf	0	0	0	0.00241	0.00474	0.01104	0.0031	0	0	0	1	2	3	redox ascorbate and glutathione	Glutamate-cysteine ligase
Solyc11g069290.1.1	functional description:Glutamine amidotransferase subun	27 kDa	Inf	0	0	0	0.00674	0.01948	0	0.013	0	0	0	1	3	0	tetrapyrrole synthesis GSA	Glutamine amidotransferase subunit pdxT
Solyc01g081310.2.1	functional description:Glutathione-S-transferase (AHRD	26 kDa	Inf	0	0	0	0	0.0163	0.0184	0.0055	0	0	0	0	2	2	development unspecified	Glutathione-S-transferase
Solyc03g120430.2.1	functional description:Glycerate kinase (AHRD V1 C1D	51 kDa	Inf	0	0	0	0	0.00548	0.00766	0.027	0	0	0	0	2	3	PS photorespiration glycerate ki	Glycerate kinase
Solyc07g065520.2.1	functional description:Glycine-rich RNA-binding protein	81 kDa	Inf	0	0	0	0.00143	0.00592	0	0.017	0	0	0	1	3	0	RNA RNA binding	Glycine-rich RNA-binding protein
Solyc07g066430.2.1	functional description:GTP-binding protein (AHRD V1 I	46 kDa	Inf	0	0	0	0.00895	0.00294	0.00547	0.013	0	0	0	2	1	2	signalling G-proteins	GTP-binding protein
Solyc09g090660.2.1	functional description:Guanine nucleotide-binding protein	56 kDa	Inf	0	0	0	0	0.0063	0.0024	0.045	0	0	0	0	3	1	RNA processing splicing	Guanine nucleotide-binding protein subunit beta-like protein
Solyc07g043560.2.1	functional description:Heat shock protein 4 (AHRD V1 -	99 kDa	Inf	0	0	0	0.00144	0.00355	0.00317	0.0059	0	0	0	1	3	3	stress abiotic heat	Heat shock protein 4
Solyc03g032070.2.1	functional description:Holliday junction ATP-dependent I	52 kDa	Inf	0	0	0	0.00245	0.00467	0.00267	0.045	0	0	0	1	2	1	RNA regulation of transcription	Holliday junction ATP-dependent DNA helicase ruvB
Solyc01g098110.2.1	functional description:Hydrolase alpha/beta fold family p	76 kDa	Inf	0	0	0	0	0.00985	0.00389	0.0014	0	0	0	0	5	2	misc acyl transferases	Hydrolase alpha/beta fold family protein
Solyc12g011430.1.1	functional description:Hydroxyacylglutathione hydrolase	31 kDa	Inf	0	0	0	0.00596	0.00861	0.01457	0.0055	0	0	0	1	1	3	cell wall precursor synthesis UX	Hydroxyacylglutathione hydrolase
Solyc07g005760.2.1	functional description:Hydroxycinnamoyl CoA shikimate	48 kDa	Inf	0	0	0	0	0.00245	0.00874	0.026	0	0	0	0	1	4	secondary metabolism phenylpr	Hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase
Solyc07g006560.2.1	functional description:Hypersensitive response assisting p	17 kDa	Inf	0	0	0	0	0.04233	0.00787	0.0006	0	0	0	0	7	2	RNA processing ribonucleases	Hypersensitive response assisting protein
Solyc01g106430.2.1	functional description:Inorganic pyrophosphatase family	32 kDa	Inf	0	0	0	0.00584	0.00422	0.01903	0.0055	0	0	0	1	1	3	RNA regulation of transcription	Inorganic pyrophosphatase family protein
Solyc06g051720.2.1	functional description:Isoamyl acetate-hydrolyzing estera	29 kDa	Inf	0	0	0	0	0.01433	0.03773	0.00017	0	0	0	0	2	4	misc GDSL-motif lipase	Isoamyl acetate-hydrolyzing esterase
Solyc01g007920.2.1	functional description:Isochorismatase family protein (AI	23 kDa	Inf	0	0	0	0.0166	0	0.02029	0.013	0	0	0	1	0	2	protein synthesis ribosome bioge	Isochorismatase family protein
Solyc05g056270.2.1	functional description:Isocitrate lyase (AHRD V1 -- Q2T	55 kDa	Inf	0	0	0	0.00249	0.00491	0.00457	0.027	0	0	0	1	2	2	gluconeogenesis / glyoxylate cyc	Isocitrate lyase
Solyc01g107700.2.1	functional description:Kynurenine formamidase (AHRD	30 kDa	Inf	0	0	0	0.00933	0.01835	0.00428	0.0063	0	0	0	2	3	1	mitochondrial electron transport	Kynurenine formamidase
Solyc07g052240.2.1	functional description:Laccase-22 (AHRD V1 -- LAC22	61 kDa	Inf	0	0	0	0.00397	0.0041	0.00485	0.0073	0	0	0	2	1	2	RNA regulation of transcription	Laccase-22
Solyc08g079090.2.1	functional description:Laccase-22 (AHRD V1 -- LAC22	66 kDa	Inf	0	0	0	0	0.00567	0.00671	0.0073	0	0	0	0	3	2	cell wall pectinesterases misc	Laccase-22
Solyc12g007310.1.1	functional description:Lactoylglutathione lyase (AHRD V	40 kDa	Inf	0	0	0	0	0.00318	0.00649	0.033	0	0	0	0	1	3	biodegradation of xenobiotics la	Lactoylglutathione lyase
Solyc01g095150.2.1	functional description:Late embryogenesis abundant prot	19 kDa	Inf	0	0	0	0	0.01318	0.04041	0.00011	0	0	0	0	3	7	development late embryogenesis	Late embryogenesis abundant protein (Fragment)
Solyc11g005150.1.1	functional description:Leucine-rich repeat family protein	67 kDa	Inf	0	0	0	0	0.01801	0.0056	0.00017	0	0	0	0	4	2	cell wall cell wall proteins LRR	Leucine-rich repeat family protein
Solyc01g006540.2.1	functional description:Lipoxygenase (AHRD V1 Q9657:	102 kDa	Inf	0	0	0	0.01698	0.0032	0	0.033	0	0	0	1	4	0	hormone metabolism jasmonate	Lipoxygenase
Solyc06g073280.2.1	functional description:LL-diaminopimelate aminotransfer	50 kDa	Inf	0	0	0	0.00734	0.0053	0.00898	0.0023	0	0	0	1	2	2	amino acid metabolism synthesi	LL-diaminopimelate aminotransferase
Solyc01g107670.2.1	functional description:LRR receptor-like serine/threonine	42 kDa	Inf	0	0	0	0	0.00973	0.02116	0.00072	0	0	0	0	2	3	signalling receptor kinases leuci	LRR receptor-like serine/threonine-protein kinase RLP
Solyc10g050110.1.1	functional description:LRR receptor-like serine/threonine	49 kDa	Inf	0	0	0	0.00285	0.01401	0.00261	0.0063	0	0	0	1	4	1	cell wall cell wall proteins LRR	LRR receptor-like serine/threonine-protein kinase RLP
Solyc01g006980.2.1	functional description:Malonyl CoA-acyl carrier protein t	38 kDa	Inf	0	0	0	0.01403	0.0069	0.00965	0.0015	0	0	0	3	2	2	lipid metabolism FA synthesis an	Malonyl CoA-acyl carrier protein transacylase containing protein expressed
Solyc01g108030.2.1	functional description:Methylcrotonoyl-CoA carboxylase	62 kDa	Inf	0	0	0	0	0.00586	0.00231	0.038	0	0	0	0	3	1	amino acid metabolism degradat	Methylcrotonoyl-CoA carboxylase beta subunit
Solyc01g107550.2.1	functional description:Methylthioribose kinase (AHRD V	48 kDa	Inf	0	0	0	0	0.00885	0.0055	0.027	0	0	0	0	2	1	DNA unspecified	Methylthioribose kinase
Solyc00g009020.2.1	functional description:Mitochondrial ATP synthase (AHF	28 kDa	Inf	0	0	0	0	0.01422	0.00726	0.0059	0	0	0	0	4	2	mitochondrial electron transport	Mitochondrial ATP synthase
Solyc09g011920.2.1	functional description:Mitochondrial uncoupling protein (	32 kDa	Inf	0	0	0	0.00553	0.00799	0.00902	0.013	0	0	0	1	2	2	mitochondrial electron transport	Mitochondrial uncoupling protein
Solyc09g065830.2.1	functional description:NADH ubiquinone oxidoreductase	28 kDa	Inf	0	0	0	0.00494	0.01457	0.00906	0.013	0	0	0	1	3	1	mitochondrial electron transport	NADH ubiquinone oxidoreductase subunit
Solyc11g070030.1.1	functional description:NADH-quinone oxidoreductase su	24 kDa	Inf	0	0	0	0	0.00807	0.00825	0.033	0	0	0	0	3	2	PS lightreaction NADH DH	NADH-quinone oxidoreductase subunit B
Solyc10g047630.1.1	functional description:Nitrilase/cyanide hydratase and ap	46 kDa	Inf	0	0	0	0	0.00302	0.01408	0.013	0	0	0	0	1	4	nucleotide metabolism degradati	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase
Solyc12g026430.1.1	functional description:Nucleobase ascorbate transporter (	58 kDa	Inf	0	0	0	0.00241	0.00594	0.0053	0.0059	0	0	0	1	1	3	transport misc	Nucleobase ascorbate transporter
Solyc02g050240.2.1	functional description:Oligopeptidase (Protease II) (AHR	43 kDa	Inf	0	0	0	0	0.00874	0.00345	0.038	0	0	0	0	2	1	protein degradation serine prote:	Oligopeptidase (Protease II)
Solyc03g098600.2.1	functional description:Oligosaccharyl transferase STT3 su	82 kDa	Inf	0	0	0	0.00177	0.00291	0.00259	0.026	0	0	0	1	1	2	stress abiotic drought/salt	Oligosaccharyl transferase STT3 subunit
Solyc04g080610.2.1	functional description:Ornithine carbamoyltransferase (A	41 kDa	Inf	0	0	0	0.00674	0.01656	0.01544	0.00017	0	0	0	2	3	3	protein postranslational modifica	Ornithine carbamoyltransferase
Solyc04g015620.2.1	functional description:Os01g0611000 protein (Fragment)	40 kDa	Inf	0	0	0	0	0.00887	0.00338	0.045	0	0	0	0	2	1	RNA regulation of transcription	Os01g0611000 protein (Fragment)
Solyc01g087540.2.1	functional description:Os01g0611000 protein (Fragment)	40 kDa	Inf	0	0	0	0.00343	0.00675	0.01259	0.0063	0	0	0	1	2	4	protein degradation ubiquitin E2	Os01g0611000 protein (Fragment)
Solyc04g074410.1.1	functional description:Os06g0220000 protein (Fragment)	33 kDa	Inf	0	0	0	0	0.01588	0.0111	0.0063	0	0	0	0	3	3	protein targeting chloroplast	Os06g0220000 protein (Fragment)
Solyc04g053080.2.1	functional description:OTU domain-containing protein 6E	34 kDa	Inf	0	0	0	0.00815	0.00401	0.00747	0.027	0	0	0	2	1	2	protein degradation cysteine pro	OTU domain-containing protein 6B
Solyc04g072240.2.1	functional description:Oxidoreductase family protein (AF	40 kDa	Inf	0	0	0	0.00349	0.00686	0.0064	0.027	0	0	0	1	1	2	not assigned no ontology	Oxidoreductase family protein
Solyc10g074590.1.1	functional description:Pantothenate kinase 4 (AHRD V1	41 kDa	Inf	0	0	0	0.00686	0.00675	0.00315	0.027	0	0	0	2	1	1	Co-factor and vitamine metaboli	Pantothenate kinase 4
Solyc06g069030.2.1	functional description:PAP fibrillin domain containing pro	28 kDa	Inf	0	0	0	0	0.00986	0.01113	0.031	0	0	0	0	2	1	not assigned unknown	PAP fibrillin domain containing protein expressed
Solyc02g065470.1.1	functional description:Pathogenesis-related protein (AHR	20 kDa	Inf	0	0	0	0	0.01911	0.01628	0.0019	0	0	0	0	4	4	stress biotic	Pathogenesis-related protein
Solyc06g071840.1.1	functional description:Pectate lyase (AHRD V1 Q2Z1Y	40 kDa	Inf	0	0	0	0	0.0069	0.00965	0.013	0	0	0	0	1	2	cell wall degradation pectate lya	Pectate lyase
Solyc01g079450.2.1	functional description:Peptidase S9 prolyl oligopeptidase	109 kDa	Inf	0	0	0	0	0.00341	0.00269	0.017	0	0	0	0	2	2	not assigned unknown	Peptidase S9 prolyl oligopeptidase active site domain protein
Solyc03g093690.2.1	functional description:Peptide methionine sulfoxide reduc	29 kDa	Inf	0	0	0	0	0.01115	0.00456	0.0011	0	0	0	0	3	1	protein postranslational modifica	Peptide methionine sulfoxide reductase msrA
Solyc02g079500.2.1	functional description:Peroxidase (AHRD V1 Q50LG4	39 kDa	Inf	0	0	0	0.01395	0.00672	0.00379	0.0055	0	0	0	2	2	1	misc peroxidases	Peroxidase
Solyc04g071890.2.1	functional description:Peroxidase 4 (AHRD V1 B7UCP	38 kDa	Inf	0	0	0	0.0062	0.00959	0.00379	0.0073	0	0	0	2	3	1	misc peroxidases	Peroxidase 4
Solyc06g069180.2.1	functional description:Phosphatase 2A regulatory A subu	65 kDa	Inf	0	0	0	0	0.00188	0.00646	0.0044	0	0	0	0	1	3	protein postranslational modifica	Phosphatase 2A regulatory A subunit
Solyc06g075540.2.1	functional description:Phosphatidyl synthase (AHRD V1	42 kDa	Inf	0	0	0	0.0033	0.01297	0.01209	0.0015	0	0	0	1	2	2	not assigned no ontology	Phosphatidyl synthase
Solyc01g111250.2.1	functional description:Phosphatidylinositol-specific phosp	37 kDa	Inf	0	0	0	0.00402	0	0.01182	0.026	0	0	0	1	0	4	lipid metabolism lipid degradatic	Phosphatidylinositol-specific phospholipase c
Solyc04g076880.2.1	functional description:Phosphoenolpyruvate carboxykina	73 kDa	Inf	0	0	0	0.00174	0.00331	0.00945	0.002	0	0	0	1	2	5	lipid metabolism lipid transfer pr	Phosphoenolpyruvate carboxykinase
Solyc05g048760.2.1	functional_description:Phosphomannomutase 2	29 kDa	Inf	0	0	0	0.00672	0.00485	0.01643	0.013	0	0	0	1	1	3	cell wall precursor synthesis pho	Phosphomannomutase 2
Solyc11g022460.1.1	functional description:Phosphoribosylanthranilate transfe	84 kDa	Inf	0	0	0	0	0.00713	0.00127	0.012	0	0	0	0	5	1	protein postranslational modifica	Phosphoribosylanthranilate transferase like protein
Solyc10g080420.1.1	functional description:Phosphoribosyltransferase (Fragm	63 kDa	Inf	0	0	0	0	0.00776	0.00865	0.0014	0	0	0	0	4	3	amino acid metabolism synthesi	Phosphoribosyltransferase (Fragment)
Solyc08g074630.1.1	functional description:Polyphenol oxidase (AHRD V1 - (	66 kDa	Inf	0	0	0	0.00196	0	0.00639	0.045	0	0	0	1	0	3	secondary metabolism simple ph	Polyphenol oxidase
Solyc06g007620.2.1	functional description:POT family domain containing pro	20 kDa	Inf	0	0	0	0	0.00641	0.0131	0.033	0	0	0	0	2	3	not assigned unknown	POT family domain containing protein expressed
Solyc02g091410.2.1	functional description:Pro-apoptotic serine protease nma	122 kDa	Inf	0	0	0	0.00115	0.0038	0.00254	0.0028	0	0	0	1	4	3	protein degradation serine prote:	Pro-apoptotic serine protease nma111-like protein
Solyc10g049620.1.1	functional description:Progesterone 5-beta-reductase (AI	44 kDa	Inf	0	0	0	0	0.00958	0.01786	0.0015	0	0	0	0	3	5	development unspecified	Progesterone 5-beta-reductase
Solyc01g096870.2.1	functional description:Prolyl-tRNA synthetase (AHRD V	61 kDa	Inf	0	0	0	0.0021	0.008	0.00686	0.002	0	0	0	1	2	2	stress abiotic drought/salt	Prolyl-tRNA synthetase
Solyc08g005970.2.1	functional description:Protein arginine N-methyltransfera	74 kDa	Inf	0	0	0	0	0.00483	0.00287	0.026	0	0	0	0	2	2	C1-metabolism	Protein arginine N-methyltransferase
Solyc01g006490.2.1	functional description:Protein YdiU (AHRD V1 - B5N5F	64 kDa	Inf	0	0	0	0	0.00381	0.00436	0.045	0	0	0	0	2	2	protein synthesis ribosome bioge	Protein YdiU
Solyc02g091340.2.1	functional description:Pyridoxal kinase (AHRD V1 Q4J	34 kDa	Inf	0	0	0	0	0.01203	0.00747	0.027	0	0	0	0	3	1	minor CHO metabolism others	Pyridoxal kinase
Solyc02g068640.2.1	functional description:Pyrroline-5-carboxylate reductase	29 kDa	Inf	0	0	0	0	0.00886	0.02499	0.0023	0	0	0	0	2	5	amino acid metabolism synthesi	Pyrroline-5-carboxylate reductase
Solyc02g077240.2.1	functional description:Pyruvate decarboxylase (AHRD V	63 kDa	Inf	0	0	0	0	0.00746	0.00213	0.00093	0	0	0	0	4	1	fermentation PDC	Pyruvate decarboxylase
Solyc04g005080.2.1	functional description:Pyruvate dehydrogenase E1 compo	43 kDa	Inf	0	0	0	0.00322	0.0095	0.00591	0.0063	0	0	0	1	2	2	TCA / organic transformation T(	Pyruvate dehydrogenase E1 component alpha subunit
Solyc05g006520.2.1	functional description:Pyruvate dehydrogenase E1 compo	43 kDa	Inf	0	0	0	0.00322	0.01267	0.00591	0.0063	0	0	0	1	4	2	TCA / organic transformation T(	Pyruvate dehydrogenase E1 component alpha subunit
Solyc08g077180.2.1	functional description:Pyruvate kinase (AHRD V1 Q53\	64 kDa	Inf	0	0	0	0.00198	0.00189	0.00431	0.045	0	0	0	1	1	2	lipid metabolism FA synthesis an	Pyruvate kinase
Solyc08g015860.2.1	functional description:Rab GDP dissociation inhibitor (AI	50 kDa	Inf	0	0	0	0	0.00493	0.00282	0.00093	0	0	0	0	2	1	signalling G-proteins	Rab GDP dissociation inhibitor
Solyc01g079680.2.1	functional description:Ran GTPase activating protein (Fra	60 kDa	Inf	0	0	0	0.00209	0.00597	0	0.045	0	0	0	1	3	0	signalling G-proteins	Ran GTPase activating protein (Fragment)
Solyc09g065190.1.1	functional description:Ran GTPase-activating protein 1 (/	58 kDa	Inf	0	0	0	0	0.0041	0.00234	0.045	0	0	0	0	2	1	signalling G-proteins	Ran GTPase-activating protein 1
Solyc03g006580.2.1	functional description:Ran-binding proteins 9/10 homolog	27 kDa	Inf	0	0	0	0.01399	0.0101	0	0.031	0	0	0	2	1	0	not assigned no ontology	Ran-binding proteins 9/10 homolog
Solyc09g059310.2.1	functional description:Ras GTPase-activating protein-binc	51 kDa	Inf	0	0	0	0	0.0047	0.00556	0.0073	0	0	0	0	2	2	protein targeting nucleus	Ras GTPase-activating protein-binding protein 2
Solyc11g064890.1.1	functional description:Receptor-like kinase (AHRD V1 -	55 kDa	Inf	0	0	0	0	0.00433	0.00772	0.012	0	0	0	0	1	4	protein postranslational modifica	Receptor-like kinase
Solyc12g098820.1.1	functional description:Receptor-like kinase (AHRD V1 -	40 kDa	Inf	0	0	0	0	0.01027	0.00319	0.00072	0	0	0	0	2	1	protein postranslational modifica	Receptor-like kinase
Solyc12g098980.1.1	functional description:Receptor-like kinase (AHRD V1 -	39 kDa	Inf	0	0	0	0	0.007	0.01957	0.0031	0	0	0	0	1	5	protein postranslational modifica	Receptor-like kinase
Solyc05g018620.2.1	functional description:Regulator of chromosome condens	34 kDa	Inf	0	0	0	0	0.00356	0.01223	0.045	0	0	0	0	1	3	cell division	Regulator of chromosome condensation (RCC1)-like protein
Solyc06g035920.2.1	functional description:Remorin 1 (AHRD V1 - Q9XEX8	21 kDa	Inf	0	0	0	0	0.02643	0.03729	0.0004	0	0	0	0	4	4	RNA regulation of transcription	Remorin 1
Solyc01g095200.2.1	functional description:Reticulon family protein (AHRD V	30 kDa	Inf	0	0	0	0.00958	0.01884	0.01317	0.0015	0	0	0	2	4	3	protein targeting secretory pathw	Reticulon family protein
Solyc10g009570.2.1	functional description:Rhodanese-related sulfurtransferas	57 kDa	Inf	0	0	0	0	0.0047	0.00657	0.027	0	0	0	0	2	2	misc rhodanese	Rhodanese-related sulfurtransferase
Solyc12g018990.1.1	functional description:Ribonucleoside hydrolase 1 (AHRI	34 kDa	Inf	0	0	0	0.00392	0.00772	0.01799	0.0031	0	0	0	1	2	4	nucleotide metabolism degradati	Ribonucleoside hydrolase 1
Solyc02g092430.1.1	functional description:Ribosomal protein L26 (AHRD V1	17 kDa	Inf	0	0	0	0	0.01675	0.0189	0.0025	0	0	0	0	2	2	protein synthesis ribosomal prot	Ribosomal protein L26
Solyc11g005170.1.1	functional description:RNA splicing factor (AHRD V1 --	66 kDa	Inf	0	0	0	0	0.00386	0.00457	0.038	0	0	0	0	2	2	RNA RNA binding	RNA splicing factor
Solyc11g065240.1.1	functional description:Saccharopine dehydrogenase famil	47 kDa	Inf	0	0	0	0	0.00509	0.00873	0.021	0	0	0	0	2	3	protein degradation ubiquitin E3	Saccharopine dehydrogenase family protein expressed

Solyc04g077670.2.1	functional	description:Serine carboxypeptidase 1 (AHRD	55 kDa	Inf	0	0	0	0	0.0051	0.01188	0.0063	0	0	0	0	2	3	protein degradation serine prote	Serine carboxypeptidase 1
Solyc06g073960.2.1	functional	description:Serine/threonine-protein phosphati	106 kDa	Inf	0	0	0	0.00129	0.00317	0.00283	0.0059	0	0	0	1	3	2	DNA synthesis/chromatin struct	Serine/threonine-protein phosphatase
Solyc12g038370.1.1	functional	description:Single-stranded DNA-binding prot	25 kDa	Inf	0	0	0	0.01478	0	0.01807	0.013	0	0	0	2	0	2	RNA regulation of transcription	Single-stranded DNA-binding protein
Solyc09g020110.2.1	functional	description:S-like RNase (Fragment) (AHRD '	29 kDa	Inf	0	0	0	0.00651	0.0047	0.03184	0.00096	0	0	0	1	1	4	stress abiotic heat	S-like RNase (Fragment)
Solyc04g079270.2.1	functional	description:Sortina and assembly machinery c	58 kDa	Inf	0	0	0	0	0.00418	0.00478	0.045	0	0	0	0	2	2	not assigned no ontology	Sorting and assembly machinery component 50 homolog
Solyc03g113220.2.1	functional	description:SPFH domain/band 7 family protei	31 kDa	Inf	0	0	0	0	0.02173	0.00405	0.013	0	0	0	0	5	1	protein degradation serine prote	SPFH domain/band 7 family protein
Solyc02g077920.2.1	functional	description:Squamosa promoter binding-like pi	16 kDa	Inf	0	0	0	0	0.01265	0.01724	0.018	0	0	0	0	3	3	development squamosa promote	Squamosa promoter binding-like protein
Solyc04g071540.2.1	functional	description:Sterol 3-beta-glucosyltransferase (	71 kDa	Inf	0	0	0	0	0.00346	0.0041	0.038	0	0	0	0	1	2	lipid metabolism exotics (steroid	Sterol 3-beta-glucosyltransferase
Solyc06g048410.2.1	functional	description:Superoxide dismutase (AHRD V1	28 kDa	Inf	0	0	0	0	0.01151	0.01177	0.0033	0	0	0	0	4	4	mitochondrial electron transport	Superoxide dismutase
Solyc06g049080.2.1	functional	description:Superoxide dismutase (AHRD V1	25 kDa	Inf	0	0	0	0	0.01509	0.00514	0.01	0	0	0	0	4	1	redox dismutases and catalases	Superoxide dismutase
Solyc02g070500.1.1	functional	description:Susceptibility homeodomain transc	17 kDa	Inf	0	0	0	0	0.0117	0.03986	0.0006	0	0	0	0	2	4	secondary metabolism isoprenoi	Susceptibility homeodomain transcription factor (Fragment)
Solyc05g013990.2.1	functional	description:T-complex protein 1 subunit epsilo	59 kDa	Inf	0	0	0	0	0.00409	0.00702	0.021	0	0	0	0	2	2	protein folding	T-complex protein 1 subunit epsilon
Solyc11g066130.1.1	functional	description:Thaumatin-like protein (AHRD V1	27 kDa	Inf	0	0	0	0	0.01365	0.00233	0.018	0	0	0	0	4	1	stress biotic	Thaumatin-like protein
Solyc03g118550.2.1	functional	description:Thioredoxin h2 (AHRD V1 -- A1E	43 kDa	Inf	0	0	0	0.00298	0.0085	0	0.045	0	0	0	1	2	0	redox thioredoxin	Thioredoxin h2
Solyc04g079000.2.1	functional	description:Tic22 (AHRD V1 - Q9ZST9_PEA	32 kDa	Inf	0	0	0	0.01156	0.00834	0.00471	0.013	0	0	0	2	1	1	protein targeting chloroplast	Tic22
Solyc09g090930.2.1	functional	description:TPR domain protein (AHRD V1 I	45 kDa	Inf	0	0	0	0.00289	0.0055	0.00943	0.0095	0	0	0	1	1	3	not assigned unknown	TPR domain protein
Solyc06g065840.2.1	functional	description:Trafficking protein particle comple	130 kDa	Inf	0	0	0	0	0.00356	0.00079	0.026	0	0	0	0	4	1	not assigned no ontology	Trafficking protein particle complex subunit 9
Solyc08g079070.2.1	functional	description:Transaldolase (AHRD V1 D6N3C	44 kDa	Inf	0	0	0	0	0.00936	0.01745	0.0015	0	0	0	0	3	5	OPP non-reductive PP transalde	Transaldolase
Solyc07g007030.1.1	functional	description:Transmembrane 9 superfamily pro	75 kDa	Inf	0	0	0	0	0.00802	0.00286	0.0059	0	0	0	0	5	2	DNA unspecified	Transmembrane 9 superfamily protein member 2
Solyc06g062590.2.1	functional	description:Transmembrane 9 superfamily pro	73 kDa	Inf	0	0	0	0	0.0033	0.00441	0.026	0	0	0	0	2	2	DNA unspecified	Transmembrane 9 superfamily protein member 4
Solyc05g026540.2.1	functional	description:Transmembrane protein 214 (AHR	64 kDa	Inf	0	0	0	0.0022	0.00904	0.00483	0.0014	0	0	0	1	4	2	not assigned unknown	Transmembrane protein 214
Solyc06g083630.2.1	functional	description:Transport protein YIF1 (AHRD V	33 kDa	Inf	0	0	0	0	0.01079	0.00962	0.012	0	0	0	0	2	1	RNA regulation of transcription	Transport protein YIF1
Solyc04g016220.2.1	functional	description:UDP-glucose glucosyltransferase (	25 kDa	Inf	0	0	0	0	0.00486	0.01668	0.045	0	0	0	0	1	2	misc UDP glucosyl and glucoron	UDP-glucose glucosyltransferase
Solyc08g006330.2.1	functional	description:UDP-glucose salicylic acid glucosy	52 kDa	Inf	0	0	0	0	0.00925	0.00824	0.0028	0	0	0	0	2	2	DNA synthesis/chromatin struct	UDP-glucose salicylic acid glucosyltransferase
Solyc01g109710.2.1	functional	description:Universal stress protein (AHRD V1	19 kDa	Inf	0	0	0	0	0.00972	0.01655	0.01	0	0	0	0	2	3	stress abiotic unspecified	Universal stress protein
Solyc03g117280.2.1	functional	description:Unknown Protein (AHRD V1)	59 kDa	Inf	0	0	0	0	0.0118	0.00351	0.0028	0	0	0	0	6	2	DNA synthesis/chromatin struct	Unknown Protein
Solyc12g099400.1.1	functional	description:Unknown Protein (AHRD V1)	35 kDa	Inf	0	0	0	0	0.01187	0.00447	0.031	0	0	0	0	2	1	not assigned unknown	Unknown Protein
Solyc07g064690.1.1	functional	description:Unknown Protein (AHRD V1): coi	14 kDa	Inf	0	0	0	0	0.00444	0.02726	0.018	0	0	0	0	1	4	not assigned unknown	Unknown Protein
Solyc03g117890.2.1	functional	description:Unknown protein DS12 from 2D-P	31 kDa	Inf	0	0	0	0.0059	0.01278	0.00481	0.013	0	0	0	1	2	1	RNA regulation of transcription	Unknown protein DS12 from 2D-PAGE of leaf chloroplastic
Solyc06g048730.2.1	functional	description:Uroporphyrinogen decarboxylase (	43 kDa	Inf	0	0	0	0	0.00958	0.01191	0.0063	0	0	0	0	3	3	RNA regulation of transcription	Uroporphyrinogen decarboxylase
Solyc04g050240.2.1	functional	description:Vacuolar protein sorting-associates	35 kDa	Inf	0	0	0	0	0.01235	0.01151	0.013	0	0	0	0	3	2	protein targeting secretory paths	Vacuolar protein sorting-associated protein 26-like protein
Solyc03g115760.2.1	functional	description:Vesicle transport v-SNARE 11-like	25 kDa	Inf	0	0	0	0.00766	0	0.02497	0.013	0	0	0	1	0	3	cell vesicle transport	Vesicle transport v-SNARE 11-like
Solyc01g097810.2.1	functional	description:Zeta-carotene desaturase	65 kDa	Inf	0	0	0	0	0.01117	0.00638	0.00093	0	0	0	0	5	3	secondary metabolism isoprenoi	Zeta-carotene desaturase

Total proteins=215

Table 5.1. Peptides used for targeted proteomic monitoring of carotenogenic proteins in 39 dpa fruits of tomato and wild species.

A list of proteotypic peptides with precursor m/z values and expected retention times for the carotenogenic proteins obtained from initial proteome profiling experiments from 39 dpa fruits of wild species and tomato is given here. These peptides are used in inclusion list for TPM.

List of peptides chosen for TPM in SP-SL fruit

Protein	m/z	Rt window		CE%	Peptide sequence
1-deoxy-D-xylulose-5-phosphate synthase 1	515.287	18.5	34.5	35	GLQVTVADAR
(Solyc01g067890.2.1)	465.273	33.76	49.76	35	TTGPVLIHVVTEK
	569.818	77.39	103.39	35	ILWDVGHQSYPHKILTGRR
	513.308	24.15	40.15	35	GIPLEVGKGR
	519.268	15	31	35	QTDGLAGFTK
1-deoxy-D-xylulose-5-phosphate synthase	710.065	88.78	104.78	35	GLLLSSIRDPNPVVFFEPK
(Solyc01g028900.2.1)	408.249	43.88	57.88	35	VVIPRSPQQAK
	572.644	48.35	64.35	35	TLIPWDKETVEASVK
1-deoxy-D-xylulose 5-phosphate reductoisomerase	499.78	71.8	87.8	35	ISYLDIFK
(Solyc03g114340.2.1)	553.32	36.17	52.17	35	IILTASGGAFR
	532.293	41.42	57.42	35	AVELFISER
	553.317	57.23	73.23	35	GDAGSVFVLIK
Farnesyltransferase/type I geranylgeranyltransferase	717.882	42.88	58.88	35	ELEVNYTVQAIR
(Solyc06g073390.2.1)	545.956	44.25	60.25	35	LGADAVTNELEFTKK
	879.9707	79.08	94.08	35	SMVRVQLLQSQNAER
	646.3384	81.64	97.64	35	NYQIWHHRRWLAEK
Geranylgeranyl pyrophosphate synthase 2	513.83	52.4	68.4	35	ILVAVAELAK
(Solyc04g079960.1.1)	736.417	99.21	115.21	35	AAPLIALADYIANR
	572.792	6.14	22.14		QQLAAFDSHK
Geranylgeranyl pyrophosphate synthase	599.64	93.13	110.13	35	AAPLFALANYIAYREN
(Solyc02g085700.1.1)	611.808	8.7	24.7	35	SREFAEELNK
	509.282	3.93	19.93	35	TAGKDLVADK
Geranylgeranyl pyrophosphate synthase	501.279	30.6	46.6	35	VVDDILEAK
(Solyc09g008920.2.1)	572.797	39	55	35	SYVSVYGIEK
	528.27	79.56	95.56	35	TYWTTLISDINQK
Isopentenyl-diphosphate delta-isomerase family pro	407.23	46.9	62.9	35	FLMDKDLLPK
(Solyc08g075390.2.1)	557.325	72.64	88.64	35	ADIVGLWALR
	645.358	52.42	68.42	35	LFGDQLQVLEK
	666.881	48.99	64.99	35	VIQLLYNAGDVK
	729.374	69.1	85.1	35	GQALQFNYLFEK
	752.367	70.33	86.33	35	DSLQQDKQEEAMGFFNVIR
	779.39	34.8	50.8	35	GPQTVAFNLPNDER
Isopentenyl-diphosphate delta-isomerase type I (Sol	531.8	38.25	54.25	35	YELLLQQR
(Solyc04g056390.2.1)	580.31	72.15	88.15	35	AFSVFIFNSK
	737.873	36.75	52.75	35	ESELIEENSLGVR
	840.792	90.88	106.88	35	KLLDELGIPGEDVPVDQFIPLGR
	547.817	64.68	80.68	35	LVVDNFLFK
Isopentenyl-diphosphate delta-isomerase type I	729.875	41.75	57.75	35	ESELIEENALGVR
(Solyc05g055670.2.1)	841.454	83.57	99.57	35	KLLDELGIPAEDVPVDQFTPLGR
	370.868	23.25	35.25	35	IESENLLHR
Phytoene synthase 1	493.62	76.53	92.53	35	FPVWASLVLYRK
(Solyc03g031860.2.1)	675.882	91.81	107.81	35	FPVWASLVLYR
	803.06	76.33	92.33	35	VYLPQDELAQAGLSDEDIFAGR
	947.492	85.71	101.71	35	STNELEVKPDIPIPGNLGLLSEAYDR
	1259.19	100.4	116.4	35	ATTESVYNAALALGIANQLTNILR
Phytoene desaturase	556.315	28.14	44.14	35	YLADAGHKPILLEAR
(Solyc03g123760.2.1)	631.324	63.44	79.44	35	QGVPDRVTDEVFIAMSK
	663.345	41.18	57.18	35	YLASMEGAVLSGK
	780.883	57.54	73.54	35	SPIEGFYLAGDYTK
	802.138	70.13	86.13	35	ASPRPTKPLEIVIAGAGLGGLSTAK
	882.438	54.12	70.12	35	ELATLFPDEISADQSK
15-cis-zeta-carotene isomerase	395.2	6.4	22.4	35	DKGEELIGER
(Solyc12g098710.1.1)	521.266	23.2	38.2	35	YGEAFEVVK
	687.395	91.34	107.34	35	TSIIPFAAILDGR
Zeta-carotene desaturase	605.37	50.37	66.37	35	NAVALALSPVVR
(Solyc01g097810.2.1)	640.408	62.8	74.8	35	LVGVPVVTVQLR
	698.383	47.46	63.46	35	ALVDPDGALQQIR
	787.397	65	81	35	TPVENFFLAGSYTK
	811.895	72.15	88.15	35	YNGWVTELQDLER
	843.9	88.07	104.07	35	DLDNVSFSEWFLSK
Carotenoid isomerase, chloroplastic	429.57	53.51	69.51	35	APSFLSIHMGVK
(Solyc10g081650.1.1)	458.566	18.72	34.72	35	GLDDHGSQILYR
	475.255	20.09	36.09	35	VAADLGFEK
	507.058	86.88	102.88	35	IHREYDDFIEELVSKFPHEK
	532.007	96.12	112.12	35	EYDDFIEELVSKFPHEK
	631.649	70.51	86.51	35	IHREYDDFIEELVSK
	632.596	71.54	87.54	35	KLEVIPDPTTVHFHLPNDLSVR
	639.357	61.94	73.94	35	IFNSLNSLELK
	716.351	37.8	53.8	35	YVIPGGSSGFYER
	743.85	80.21	96.21	35	EYDDFIEELVSK
	857.951	42.25	58.25	35	HFGGINYPVGGVGEIAK
Carotenoid cleavage dioxygenase 1A	665.356	30.6	46.6	35	YVYGTTLNSIAK
(Solyc01g087250.2.1)	735.896	44.14	60.14	35	TMSAEPVAVVELPK
	628.867	82.28	98.28	35	AIDLLEWGIVK
	665.356	29.6	45.6	35	YVYGTTLNSIAK
Carotenoid cleavage dioxygenase 1B	415.204	14.5	30.5	35	FDLHAEPETGK
(Solyc01g087260.2.1)	418.555	18.08	34.08	35	LKQEEFFGGAK
	552.789	26.3	42.3	35	LSEAAVDFPR
	561.8	42.85	58.85	35	FGSEAIFVPR
	585.298	28.85	44.85	35	QLAYSFDPTK
	627.82	78.14	94.14	35	RVPFGFHAFFVTEEQIQEQAK
	642.686	68.25	84.25	35	TKLEVGGNVPGIFDLGPGR
	672.37	90.32	106.32	35	AIDWVEWAIIK
	695.358	22.57	38.57	35	LQNPDLDAIKGTEKEEQR
	976.547	92.61	108.61	35	YVYGTILNNVAQITGVVK
plastid lipid associated protein 3	454.269	54.28	70.28	35	ISRGDGGLFVLVK
(Solyc08g076480.2.1)	502.793	58.92	74.92	35	GDGGLFVLVK
	558.963	69.45	85.45	35	SNINLPETVDLFGQK
	684.812	54.75	70.75	35	MVEFVDEWGEK
	740.748	98.74	114.74	35	ISLSPVQQSLGPLENAVAGIAR
	797.378	53.65	69.65	35	MVEFVDEWGEKSEPEPGPVTK
Plastid-lipid-associated protein, chloroplastic	487.951	50.75	66.75	35	ISRGDAGSVFVLIK
(Solyc02g081170.2.1)	636.303	22.6	38.6	35	QLADSFYGTNR
	736.915	86.52	102.53	35	AEIVELITQLESK
	738.897	46.78	62.78	35	GLITSVQDTASSVAK
	844.79	58.58	74.58	35	ISPGGVAVVDEEPPKEPSEIELLK
	887.483	50.42	67.42	35	ISPGGVAVVDEEPPKEPSEIELLKK

List of peptides chosen for TPM in SG-SL fruit

Protein	m/z	Rt window		CE%	Peptide sequence
1-deoxy-D-xylulose-5-phosphate synthase 1	499.52121	43.92	59.92	35	AYDQVVHDVDLQKLPVR
(Solyc01g067890.2.1)	569.81787	75.39	101.39	35	ILWDVGHQSYPHKILTGRR
	513.3075	22.15	38.15	35	GIPLEVGKGR
	465.27316	35.33	51.33	35	TTGPVLIHVVTEK
	515.28699	16.38	32.38	35	GLQVTVADAR
1-deoxy-D-xylulose-5-phosphate synthase	710.06525	87.29	103.29	35	GLLLSSIRDPNPVVFFEPK
(Solyc01g028900.2.1)	408.24899	42.88	56.88	35	VVIPRSPQQAK
	572.64398	47.35	63.35	35	TLIPWDKETVEASVK
1-deoxy-D-xylulose 5-phosphate reductoisomerase	532.29285	41.42	57.42	35	AVELFISER
(Solyc03g114340.2.1)	553.31726	57.23	73.23	35	GDAGSVFVLIK
	554.98	68.56	84.56	35	ETLIAGGPFVLPLAHK
	652.31854	38	54	35	APDNVKYPSMDLAYSAGR
Farnesyltransferase/type I geranylgeranyltransferas	545.95587	43.25	59.25	35	LGADAVTNELEFTKK
(Solyc06g073390.2.1)	879.9707	78.08	93.08	35	SMVRVQLLQSQNAER
	646.33844	80.64	96.64	35	NYQIWHHRRWLAEK
	717.88165	41.07	57.07	35	ELEVNYTVQAIR
Geranylgeranyl pyrophosphate synthase 2	491.28	97.21	113.21	35	AAPLIALADYIANR
(Solyc04g079960.1.1)	513.83002	49.63	65.63	35	ILVAVAELAK
	572.79248	5.14	21.14	35	QQLAAFDSHK
Geranylgeranyl pyrophosphate synthase	599.64	93.13	110.13	35	AAPLFALANYIAYREN
(Solyc02g085700.1.1)	611.8075	7.7	23.7	35	SREFAEELNK
	509.28195	2.93	18.93	35	TAGKDLVADK
Geranylgeranyl pyrophosphate synthase	501.27917	25.54	41.54	35	VVDDILEAK
(Solyc09g008920.2.1)	528.27	79.56	95.56	35	TYWTTLISDINQK
	572.79742	30	46	35	SYVSVYGIEK
Isopentenyl-diphosphate delta-isomerase family pr	407.23001	49.41	65.41	35	FLMDKDLLPK
(Solyc08g075390.2.1)	557.32544	71.94	87.94	35	ADIVGLWALR
	607.308	68.34	84.34	35	FGLEEAHGKGQALQFNYLFEK
	645.35797	55.06	71.06	35	LFGDQLQVLEK
	666.88074	48.21	64.21	35	VIQLLYNAGDVK
	678.37463	46.38	62.38	35	ELQEELGVTLPK
	729.37366	67	83	35	GQALQFNYLFEK
	752.367	68.22	84.22	35	DSLQQDKQEEAMGFFNVIR
	779.39001	36.76	52.76	35	GPQTVAFNLPNDER
Isopentenyl-diphosphate delta-isomerase type I	531.79999	35.45	51.45	35	YELLLQQR
(Solyc04g056390.2.1)	547.81677	66.88	82.88	35	LVVDNFLFK
	580.31	72.92	88.93	35	AFSVFIFNSK
	737.87305	34.11	50.11	35	ESELIEENSLGVR
	840.79248	90.8	106.8	35	KLLDELGIPGEDVPVDQFIPLGR
Isopentenyl-diphosphate delta-isomerase type I	729.87512	40.39	55.39	35	ESELIEENALGVR
(Solyc05g055670.2.1)	841.454	81.96	97.96	35	KLLDELGIPAEDVPVDQFTPLGR
	370.86823	23.25	35.25	35	IESENLLHR
Phytoene synthase 1	493.62	78.36	94.36	35	FPVWASLVLYRK
(Solyc03g031860.2.1)	675.88214	91.76	107.76	35	FPVWASLVLYR
	803.06012	79.24	91.24	35	VYLPQDELAQAGLSDEDIFAGR
	947.492	78.19	106.19	35	STNELEVKPDIPIPGNLGLLSEAYDR
	1204.0918	75.83	88.83	35	VYLPQDELAQAGLSDEDIFAGR
	1259.187	98.55	114.55	35	ATTESVYNAALALGIANQLTNILR
Phytoene desaturase	417.48843	27.26	45.26	35	YLADAGHKPILLEAR
(Solyc03g123760.2.1)	588.66998	88.5	104.5	35	LVGVPVINVHIWFDR
	601.85144	66.99	82.99	35	ASPRPTKPLEIVIAGAGLGGLSTAK
	620.3197	44.51	60.51	35	VTDEVFIAMSK
	631.32397	61.27	77.27	35	QGVPDRVTDEVFIAMSK
	663.3446	41.93	57.93	35	YLASMEGAVLSGK
	780.88342	56.44	72.44	35	SPIEGFYLAGDYTK
	882.438	51.14	68.14	35	ELATLFPDEISADQSK
15-cis-zeta-carotene isomerase	395.2	4.42	20.42	35	DKGEELIGER
(Solyc12g098710.1.1)	521.26593	22.71	38.71	35	YGEAFEVVK
	687.39453	90.05	106.05	35	TSIIPFAAILDGR
Zeta-carotene desaturase	553.9444	72.01	88.01	35	WRELEFFDNIYK
(Solyc01g097810.2.1)	605.37	46.44	62.44	35	NAVALALSPVVR
	640.40778	54.99	70.99	35	LVGVPVVTVQLR
	698.38257	42.41	58.41	35	ALVDPDGALQQIR
	708.72156	79.61	95.61	35	FPVGAPLHGINAFLSTNQLK
	787.39722	60.16	76.16	35	TPVENFFLAGSYTK
	843.90002	86.65	102.65	35	DLDNVSFSEWFLSK
Carotenoid isomerase, chloroplastic	429.57001	52.71	68.71	35	APSFLSIHMGVK
(Solyc10g081650.1.1)	507.05792	85.08	101.08	35	IHREYDDFIEELVSKFPHEK
	573.29999	98.91	115.91	35	SLEEPIYLFGQFFK
	623.33966	32.08	48.08	35	ANVTSIILDNGK
	631.64856	65.51	85.51	35	IHREYDDFIEELVSK
	632.596	69.09	85.09	35	KLEVIPDPTTVHFHLPNDLSVR
	639.35699	47.85	63.85	35	IFNSLNSLELK
	716.35059	37.99	52.99	35	YVIPGGSSGFYER
	743.84998	76.82	92.82	35	EYDDFIEELVSK
	755.94147	92.78	108.78	35	GNLNLITQALAAVGR
	857.95068	40.09	56.09	35	HFGGINYPVGGVGEIAK
Chromoplast specific lycopene beta cyclase	521.81158	69.05	88.05	35	LIGNLAIESL
(Solyc06g074240.1.1)	655.07532	57.51	76.51	35	NHGYQIAHGVLVEVDNHPFDLDK
	799.46002	71.57	91.57	35	AQFDVIIIGAGPAGLR
Carotenoid cleavage dioxygenase 1A	627.33002	13.94	29.94	35	LKQEEFFGGAK
(Solyc01g087250.2.1)	628.86676	81.28	97.28	35	AIDLLEWGIVK
	665.356	28.6	44.6	35	YVYGTTLNSIAK
	735.89557	42.14	58.14	35	TMSAEPVAVVELPK
Carotenoid cleavage dioxygenase 1B	418.55499	20.03	36.03	35	LKQEEFFGGAK
(Solyc01g087260.2.1)	561.80005	43.79	59.79	35	FGSEAIFVPR
	607.67578	24.36	40.36	35	IEGVVVVDPKPQNGVAAK
	622.29999	8.05	24.05	35	FDLHAEPETGK
	627.82	75.62	91.62	35	RVPFGFHAFFVTEEQIQEQAK
	642.6864	66.99	82.99	35	TKLEVGGNVPGIFDLGPGR
	672.3703	89.03	105.03	35	AIDWVEWAIIK
	695.35773	16.57	32.57	35	LQNPDLDAIKGTEKEEQR
	699.01935	61.78	77.78	35	ILEDGDLQTLGMLDYDKR
	735.89844	46.07	62.07	35	TMSAEPVAVVELPK
	820.40002	75.56	91.56	35	FAPVAGYHWFDGDGMIHGLQIK
	848.95483	69.98	85.98	35	LEVGGNVPGIFDLGPGR
	976.547	90.59	106.59	35	YVYGTILNNVAQITGVVK
Plastid lipid associated protein 3	386.87643	16.87	32.87	35	EGNFKPPEIK
(Solyc08g076480.2.1)	454.2691	52.28	68.28	35	ISRGDGGLFVLVK
	476.51285	47.31	63.31	35	IQVEFKEGNFKPPEIK
	502.79291	57.24	73.24	35	GDGGLFVLVK
	544.3255	47.42	63.42	35	TISGQPPLKIPIPGGR
	684.81189	53.63	69.63	35	MVEFVDEWGEK
	740.74792	97.58	113.58	35	ISLSPVQQSLGPLENAVAGIAR
	797.37799	53.29	69.29	35	MVEFVDEWGEKSEPEPGPVTK
	837.93726	68.25	84.25	35	SNINLPETVDLFGQK
Plastid-lipid-associated protein, chloroplastic	392.7561	28.15	44.15	35	GNLLLVR
(Solyc02g081170.2.1)	420.74554	13.85	29.85	35	EGSPLLKP
	487.9512	53.02	69.02	35	ISRGDAGSVFVLIK
	553.32001	35.01	51.01	35	IILTASGGAFR
	636.30328	20.24	37.24	35	QLADSFYGTNR
	738.89728	44.89	60.89	35	GLITSVQDTASSVAK
	759.75	96.76	112.76	35	IDLSPFKGLITSVQDTASSVAK
	787.75	96.57	112.57	35	GLSASSETRAEIVELITQLESK
	844.78998	55.92	71.92	35	ISPGGVAVVDEEPPKEPSEIELLK
	887.48285	49.15	65.15	35	ISPGGVAVVDEEPPKEPSEIELLKK

List of peptides chosen for TPM in SH-SL fruit

Protein	m/z	Rt window		CE%	Peptide sequence
1-deoxy-D-xylulose-5-phosphate synthase	710.065	17.96	31.96	35	GLLLSSIRDPNPVVFFEPK
(Solyc01g028900.2.1)	408.249	5.75	19.75	35	VVIPRSPQQAK
	572.644	7.35	21.35	35	TLIPWDKETVEASVK
1-deoxy-D-xylulose 5-phosphate reductoisomerase	499.78	12.95	26.95	35	ISYLDIFK
(Solyc03g114340.2.1)	553.32	4.04	18.04	35	IILTASGGAFR
	885.01	13.85	27.85	35	VVALAAGSNVTLLADQVK
	532.293	5.35	19.35	35	AVELFISER
Farnesyltransferase/type I geranylgeranyltransferas	561.66	16.21	32.21	35	VVLEALGVDLREELK
(Solyc06g073390.2.1)	646.338	20.32	34.32	35	NYQIWHHRRWLAEK
	717.882	11.07	25.07	35	ELEVNYTVQAIR
Geranylgeranyl pyrophosphate synthase 2	491.28	21.14	35.14	35	AAPLIALADYIANR
(Solyc04g079960.1.1)	513.83	6.25	23.25	35	ILVAVAELAK
	572.792	1.54	15.54	35	QQLAAFDSHK
Geranylgeranyl pyrophosphate synthase	777.427	23.18	37.18	35	AAPLFALANYIAYR
(Solyc02g085700.1.1)	808.77	24.36	38.36	35	TAALLEGSVVLGAILGGAPDEDVEK
	898.972	21.5	35.5	35	AAPLFALANYIAYREN
Geranylgeranyl pyrophosphate synthase	830.907	19.88	33.88	35	VMPLYSFLDYAADR
(Solyc09g008920.2.1)	791.909	16.63	30.63	35	TYWTTLISDINQK
	572.798	5.05	19.05	35	SYVSVYGIEK
	517.78	7.39	21.39	35	KTENKTEGK
Isopentenyl-diphosphate delta-isomerase family pro	542.618	6.71	22.41	35	LELQELHSSLEEAK
(Solyc08g075390.2.1)	557.325	14.24	33.24	35	ADIVGLWALR
	666.881	8.51	30.51	35	VIQLLYNAGDVK
	678.375	6.45	21.45	35	ELQEELGVTLPK
	710.38	7.21	21.21	35	NLPLDDIYKSENVTAAPIR
	729.374	13.43	27.43	35	GQALQFNYLFEK
	779.39	6.19	21.19	35	GPQTVAFNLPNDER
Isopentenyl-diphosphate delta-isomerase type I	365.536	5.34	19.34	35	IEAENLLHR
(Solyc04g056390.2.1)	531.8	8.74	22.74	35	YELLLQQR
	547.817	15.15	31.15	35	LVVDNFLFK
	572.797	6.05	18.05	35	SYVSVYGIEK
	580.31	72.92	88.93	35	AFSVFIFNSK
	601.982	12.85	26.85	35	KADAGEEGLKLSPWFR
	737.873	7.71	21.71	35	ESELIEENSLGVR
	840.792	19.82	33.82	35	KLLDELGIPGEDVPVDQFIPLGR
Isopentenyl-diphosphate delta-isomerase type I	666.835	8.49	21.49	35	DVNVHPNPDEVADIKYVNQEQLK
(Solyc05g055670.2.1)	729.875	8.09	24.09	35	ESELIEENALGVR
	831.41	5.69	19.69	35	DVNVHPNPDEVADIK
	370.868	2.32	16.32	35	IESENLLHR
	888.779	8.46	22.46	35	DVNVHPNPDEVADIKYVNQEQLK
Phytoene synthase 1	493.62	16.87	30.87	35	FPVWASLVLYRK
(Solyc03g031860.2.1)	536.84	14.26	28.26	35	LIALPIAYAK
	675.883	21.35	27.35	35	FPVWASLVLYR
	675.882	20	34	35	FPVWASLVLYR
	899.927	7.51	21.51	35	ILDEIEANDYNNFTK
	947.492	18.17	32.17	35	STNELEVKPDIPIPGNLGLLSEAYDR
	1204.09	16.96	30.96	35	VYLPQDELAQAGLSDEDIFAGR
	1259.19	26.54	41.54	35	ATTESVYNAALALGIANQLTNILR
Phytoene desaturase	473.778	17.8	31.8	35	LVGVPVINVHIWFDRK
(Solyc03g123760.2.1)	507.25	10.56	24.56	35	LLLPEDWK
	601.851	14.01	29.01	35	ASPRPTKPLEIVIAGAGLGGLSTAK
	631.324	13.59	28.59	35	QGVPDRVTDEVFIAMSK
	640.35	14.66	29.66	35	LLLPEDWKEIPYFQK
	780.883	13.04	28.04	35	SPIEGFYLAGDYTK
	802.134	14.68	28.68	35	ASPRPTKPLEIVIAGAGLGGLSTAK
	882.438	12.09	27.09	35	ELATLFPDEISADQSK
	1015.07	30.8	44.8	35	FDFSEALPAPLNGILAILK
15-cis-zeta-carotene isomerase	687.395	21.09	35.09	35	TSIIPFAAILDGR
(Solyc12g098710.1.1)	395.2	1.85	15.85	35	DKGEELIGER
	521.266	2.75	16.75	35	YGEAFEVVK
Zeta-carotene desaturase	553.944	13.01	27.01	35	WRELEFFDNIYK
(Solyc01g097810.2.1)	605.37	6.44	20.44	35	NAVALALSPVVR
	640.408	8.99	22.99	35	LVGVPVVTVQLR
	698.383	42.41	58.41	35	ALVDPDGALQQIR
Carotenoid isomerase, chloroplastic	632.596	14.57	27.57	35	KLEVIPDPTTVHFHLPNDLSVR
(Solyc10g081650.1.1)	716.351	5.94	19.94	35	YVIPGGSSGFYER
	755.941	19.62	33.62	35	GNLNLITQALAAVGR
	794.97	25.49	39.49	35	LLFEVAPLGFLIEK
	859.446	25.63	39.63	35	SLEEPIYLFGQFFK
Violaxanthin de-epoxidase	643.01	13.32	27.32	35	KSDVGDFPVPDPSVLVQK
(Solyc04g050930.2.1)	646.371	17.05	32.05	35	SSVLPETIIPELQIAAQK
	710.839	6.85	20.85	35	ELQQDEENFIR
	837.383	10.87	24.87	35	NDAWDGYGGSVLYTR
	908.977	18.42	32.42	35	TIIKEVEEIEEEVEK
	969.051	18.25	32.25	35	SSVLPETIIPELQIAAQK
Carotenoid cleavage dioxygenase 1A	628.867	19.42	35.42	35	AIDLLEWGIVK
(Solyc01g087250.2.1)	418.557	3.36	17.36	35	LKQEEFFGGAK
	735.896	5.25	20.25	35	TMSAEPVAVVELPK
Carotenoid cleavage dioxygenase 1B	561.8	9.54	25.54	35	FGSEAIFVPR
(Solyc01g087260.2.1)	607.676	3.59	20.59	35	IEGVVVVDPKPQNGVAAK
	642.686	13.87	28.87	35	TKLEVGGNVPGIFDLGPGR
	672.37	17.16	35.16	35	AIDWVEWAIIK
	848.955	16.51	30.51	35	LEVGGNVPGIFDLGPGR
	976.547	21.33	35.33	35	YVYGTILNNVAQITGVVK
plastid lipid associated protein 3	454.269	12.2	26.2	35	ISRGDGGLFVLVK
(Solyc08g076480.2.1)	502.793	13.85	27.85	35	GDGGLFVLVK
	740.748	21.44	37.44	35	ISLSPVQQSLGPLENAVAGIAR
	797.378	11.22	25.22	35	MVEFVDEWGEKSEPEPGPVTK
	815.986	10.75	24.75	35	TISGQPPLKIPIPGGR
	1110.62	21.75	35.75	35	ISLSPVQQSLGPLENAVAGIAR
Plastid-lipid-associated protein, chloroplastic	487.951	12.97	26.97	35	ISRGDAGSVFVLIK
(Solyc02g081170.2.1)	491.613	18.51	33.51	35	AEIVELITQLESK
	636.303	4.5	21.5	35	QLADSFYGTNR
	736.914	19.96	33.96	35	AEIVELITQLESK
	738.897	9.99	23.99	35	GLITSVQDTASSVAK
	787.75	21	36	35	GLSASSETRAEIVELITQLESK

Table 5.2 Peptides used for TPM of carotenogenic proteins in the leaves.

A list of proteotypic peptides with precursor m/z values and expected retention times for the carotenogenic proteins obtained from initial proteome profiling experiments from leaves of wild species and tomato is given here. These peptides are used in inclusion list for TPM.

List of peptides chosen for TPM in SP-SL leaf

Protein	m/z	Rt window		CE%	Peptide sequence
1-deoxy-D-xylulose-5-phosphate reductoisomerase	499.779	68.79	80.79	35	ISYLDIFK
(Solyc03g114340.2.1)	532.293	43.1	57.1	35	AVELFISER
	553.322	35.95	49.95	35	IILTASGGAFR
	554.992	72.64	84.64	35	ETLIAGGPFVLPLAHK
	665.806	38.15	50.15	35	YPSMDLAYSAGR
	670.592	85.28	97.28	35	HREELVSSPSLEEIIHYDLWAR
	885.012	61.35	73.35	35	VVALAAGSNVTLLADQVK
Farnesyltransferase/type I geranylgeranyltransferase a	518.767	20.5	34.5	35	IGTDIQDFK
(Solyc06g073390.2.1)	717.883	49.08	61.08	35	ELEVNYTVQAIR
	545.956	52.25	62.25	35	LGADAVTNELEFTKK
Geranylgeranyl pyrophosphate synthase 2	491.282	97.23	111.23	35	AAPLIALADYIANR
(Solyc04g079960.1.1)	736.416	98.73	110.73	35	AAPLIALADYIANR
	513.83	52.4	68.4	35	ILVAVAELAK
	572.792	6.14	22.14	35	QQLAAFDSHK
Geranylgeranyl pyrophosphate synthase	567.793	22.44	34.44	35	AQLVGFDQEK
(Solyc02g085700.1.1)	599.649	92.41	104.41	35	AAPLFALANYIAYREN
	777.425	97.01	109.01	35	AAPLFALANYIAYR
	898.972	93.97	105.97	35	AAPLFALANYIAYREN
	402.228	23.36	35.36	35	TAGKDLVADKVTYPK
	391.889	24.36	36.36	35	HLEFIHLHK
Geranylgeranyl pyrophosphate synthase	501.281	27.81	39.81	35	VVDDILEAK
(Solyc09g008920.2.1)	528.277	85.83	97.83	35	TYWTTLISDINQK
	572.797	32.77	44.77	35	SYVSVYGIEK
	791.909	79.23	91.23	35	TYWTTLISDINQK
	830.907	91.22	104.22	35	VMPLYSFLDYAADR
Geranylgeranyl reductase	489.765	36.41	48.41	35	EVLDAYLR
(Solyc03g115980.1.1)	567.811	59.24	71.24	35	GGIETFLIER
	571.849	50.92	62.92	35	LAVNTIGSLVR
	614.63	33.97	45.97	35	APNSPYVLHYTSYDSK
	632.35	37.09	49.09	35	VALVGDAAGYVTK
	744.912	76.28	88.28	35	AAEAGASVLNGLFLR
	759.438	102.25	114.25	35	VAPGNPIEDLKLAVNTIGSLVR
	767.917	1.18	13.18	35	VEAHPIPEHPRPR
	805.447	35.39	47.39	35	VAVIGGGPAGGAAAETLAK
	921.437	34.02	44.02	35	APNSPYVLHYTSYDSK
	923.935	55.98	67.98	35	SINAGDYEYAIAFQER
Isopentenyl-diphosphate delta-isomerase family prote	489.765	30.06	42.06	35	EVLDAYLR
(Solyc08g075390.2.1)	557.325	73.07	86.07	35	ADIVGLWALR
	645.357	56.42	68.42	35	LFGDQLQVLEK
	666.879	49.28	61.28	35	VIQLLYNAGDVK
	752.366	71	85	35	DSLQQDKQEEAMGFFNVIR
Isopentenyl-diphosphate delta-isomerase type I	531.799	37.88	47.88	35	YELLLQQR
(Solyc04g056390.2.1)	547.816	69.04	81.04	35	LVVDNFLFK
	559.286	67.66	81.66	35	ADAGEEGLKLSPWFR
	580.13	73.02	86.02	35	AFSVFIFNSK
	591.542	94.56	106.56	35	APSDGKWGEHELDYLLFMVR
	601.982	63.99	75.99	35	KADAGEEGLKLSPWFR
	737.87	35.76	49.76	35	ESELIEENSLGVR
	798.095	96.17	108.17	35	LLDELGIPGEDVPVDQFIPLGR
	840.795	92.43	104.43	35	KLLDELGIPGEDVPVDQFIPLGR
Isopentenyl-diphosphate delta-isomerase type I	370.868	23.25	35.25	35	IESENLLHR
(Solyc05g055670.2.1)	841.454	84.06	96.06	35	KLLDELGIPAEDVPVDQFTPLGR
	729.874	42.8	54.8	35	ESELIEENALGVR
Phytoene synthase 2 (Solyc02g081330.2.1)	769.381	27.99	39.99	35	QGWNFGFLNADLR
	877.415	51.58	63.58	35	DMVEGMRMDLWKSR
Phytoene desaturase	556.341	53.8	65.8	35	YLADAGHKPILLEAR
(Solyc03g123760.2.1)	620.317	45.74	57.74	35	VTDEVFIAMSK
	663.345	42.35	54.35	35	YLASMEGAVLSGK
	780.884	56.25	69.25	35	SPIEGFYLAGDYTK
	802.134	68.45	80.45	35	ASPRPTKPLEIVIAGAGLGGLSTAK
	882.437	55.31	67.31	35	ELATLFPDEISADQSK
	1015.97	101.56	113.56	35	FDFSEALPAPLNGILAILK
15-cis-zeta-carotene isomerase	687.39	89.22	101.22	35	TSIPFAAILDGR
(Solyc12g098710.1.1)	395.2	6.4	22.4	35	DKGEELIGER
	521.266	23.2	38.2	35	YGEAFEVVK
Zeta-carotene desaturase	587.82	31.11	43.11	35	ITAAELNDISK
(Solyc01g097810.2.1)	605.367	49.15	61.15	35	NAVALALSPVVR
	640.407	61.53	73.53	35	LVGVPVVTVQLR
	708.725	79.97	91.97	35	FPVGAPLHGINAFLSTNQLK
	787.395	63.04	75.05	35	TPVENFFLAGSYTK
	811.895	72.57	84.57	35	YNGWVTELQDLER
	843.903	86.62	98.62	35	DLDNVSFSEWFLSK
Carotenoid isomerase, chloroplastic	632.596	70.81	82.81	35	KLEVIPDPTTVHFHLPNDLSVR
(Solyc10g081650.1.1)	859.445	102.13	114.13	35	SLEEPIYLFGQFFK
	475.255	20.09	36.09	35	VAADLGFEK
Carotenoid isomerase-like	603.677	81.03	93.03	35	ISLKSHVENIVVEKGR
(Solyc05g010180.2.1)	629.313	54.74	67.74	35	YGQDVLVLESHDVAGGAAHSFDVK
	656.583	65.71	77.71	35	HVLHAYTPGTEPFEIWEGLDRR
	823.075	73.65	85.65	35	HVLHAYTPGTEPFEIWEGLDR
Lycopene epsilon cyclase (Solyc12g008980.1.1)	937.133	66.08	78.08	35	IKEIYEEEWSYIPVGGSLPNTEQK
Zeaxanthin epoxidase, chloroplastic	493.236	38.95	50.95	35	FHPSDVIEFGSDK
(Solyc02g090890.2.1)	537.309	52.19	68.19	35	MTLQQILAR
	667.361	53.34	67.34	35	FTGDLLVGADGIR
	759.394	61.72	73.72	35	SAESGSPVDIISSLR
	1333.71	54.22	66.22	35	FTGDLLVGADGIR
Violaxanthin de-epoxidase	500.8	48.87	62.87	35	LFGNALPIR
(Solyc04g050930.2.1)	584.294	46.21	58.21	35	IGTPDGGFFTR
	606.318	80.46	92.46	35	TIIKEVEEIEEEVEK
	681.32	21.82	33.82	35	EVEEIEEEVEK
	682.041	96.11	108.11	35	TIIKEVEEIEEEVEKVK
	714.688	79.83	91.83	35	LFEGFKELQQDEENFIR
	876.412	55.3	79.3	35	VENSPDDYIFVYYK
	969.051	82.59	94.59	35	SSVLPETIIPELQIAAQK
Carotenoid cleavage dioxygenase 1B	415.203	14.42	26.42	35	FDLHAEPETGK
(Solyc01g087260.2.1)	418.555	26.62	38.62	35	LKQEEFFGGAK
	521.769	31.54	43.54	35	LQNPDLDAIKGTEKEEQR
	527.97	29.33	41.33	35	LLALHEGDKPYVVK
	552.787	33.84	45.84	35	LSEAAVDFPR
	561.799	41.21	53.21	35	FGSEAIFVPR
	642.686	67.73	79.73	35	TKLEVGGNVPGIFDLGPGR
	976.545	91.13	103.13	35	YVYGTILNNVAQITGVVK
Carotenoid cleavage dioxygenase 4B	500.773	11.3	23.3	35	IEERPQTTTTITKPQEK
(Solyc08g075490.2.1)	727.329	39.55	51.55	35	NPSIDEDDGYVVSYVHNEK
	735.894	89.85	101.85	35	YGPIPPFITYFR
Plastid lipid associated protein 3	454.27	55.07	67.07	35	ISRGDGGLFVLVK
(Solyc08g076480.2.1)	502.791	58.42	70.42	35	GDGGLFVLVK
	544.326	49.01	63.01	35	TISGQPPLKIPIPGGR
	558.962	69.95	81.95	35	SNINLPETVDLFGQK
	574.947	72.77	84.77	35	SWLLTTVLDKDMR
	635.015	48.87	60.87	35	IQVEFKEGNFKPPEIK
	740.75	98.9	110.9	35	ISLSPVQQSLGPLENAVAGIAR
	797.38	50.56	62.56	35	MVEFVDEWGEKSEPEPGPVTK
Plastid-lipid-associated protein, chloroplastic (CHRC	478.774	11.07	24.07	35	SISSQPPIK
(Solyc02g081170.2.1)	487.954	56.88	67.88	35	ISRGDAGSVFVLIK
	636.304	22.08	36.08	35	QLADSFYGTNR
	738.898	46.82	58.82	35	GLITSVQDTASSVAK
	825.447	57.32	69.32	35	NPNPAPTEALTLLNGK
	844.785	57.91	71.91	35	ISPGGVAVVDEEPPKEPSEIELLK
	887.484	52.52	64.52	35	ISPGGVAVVDEEPPKEPSEIELLKK

List of peptides chosen for TPM in SG-SL leaf

Protein	m/z	Rt window		CE %	Peptide sequence
1-deoxy-D-xylulose-5-phosphate reductoisomerase	499.779	62.72	74.72	35	ISYLDIFK
(Solyc03g114340.2.1)	532.293	44.63	56.63	35	AVELFISER
	553.322	37.09	49.09	35	IILTASGGAFR
	554.992	72.64	84.64	35	ETLIAGGPFVLPLAHK
	665.806	38.15	50.15	35	YPSMDLAYSAGR
	670.592	84.34	96.34	35	HREELVSSPSLEEIIHYDLWAR
	703.85	33.43	45.43	35	AGGTMTGVLSAANEK
	885.012	60.98	72.98	35	VVALAAGSNVTLLADQVK
Farnesyltransferase/type I geranylgeranyltransferase alpha subunit	518.767	27.5	39.5	35	IGTDIQDFK
(Solyc06g073390.2.1)	717.883	44.08	56.08	35	ELEVNYTVQAIR
	545.956	50.25	63.25	35	LGADAVTNELEFTKK
Geranylgeranyl pyrophosphate synthase 2	491.282	92.15	114.15	35	AAPLIALADYIANR
(Solyc04g079960.1.1)	736.416	99.65	111.65	35	AAPLIALADYIANR
	513.83	52.4	68.4	35	ILVAVAELAK
	572.792	6.14	22.14	35	QQLAAFDSHK
Geranylgeranyl pyrophosphate synthase	567.793	23.78	35.78	35	AQLVGFDQEK
(Solyc02g085700.1.1)	599.649	92.41	104.41	35	AAPLFALANYIAYREN
	777.425	97.22	109.22	35	AAPLFALANYIAYR
	898.972	94.52	105.52	35	AAPLFALANYIAYREN
	402.228	23.36	35.36	35	TAGKDLVADKVTYPK
	391.889	24.36	36.36	35	HLEFIHLHK
Geranylgeranyl pyrophosphate synthase	501.281	28.58	40.58	35	VVDDILEAK
(Solyc09g008920.2.1)	528.277	85.83	97.83	35	TYWTTLISDINQK
	572.797	37.12	49.12	35	SYVSVYGIEK
	791.909	81.2	93.2	35	TYWTTLISDINQK
	830.907	92.38	104.38	35	VMPLYSFLDYAADR
Geranylgeranyl reductase	489.765	41.03	53.03	35	EVLDAYLR
(Solyc03g115980.1.1)	567.811	60.27	72.27	35	GGIETFLIER
	571.849	49.55	62.55	35	LAVNTIGSLVR
	614.63	34.64	46.64	35	APNSPYVLHYTSYDSK
	632.35	37.09	49.09	35	VALVGDAAGYVTK
	744.912	76.13	88.13	35	AAEAGASVLNGLFLR
	759.438	102.25	114.25	35	VAPGNPIEDLKLAVNTIGSLVR
	767.917	1.48	13.48	35	VEAHPIPEHPRPR
	805.447	35.62	47.62	35	VAVIGGGPAGGAAAETLAK
	921.437	30.63	42.63	35	APNSPYVLHYTSYDSK
	923.935	56.49	68.49	35	SINAGDYEYAIAFQER
Isopentenyl-diphosphate delta-isomerase family protein	489.765	31.06	44.06	35	EVLDAYLR
(Solyc08g075390.2.1)	557.325	73.13	85.13	35	ADIVGLWALR
	645.357	56.73	68.73	35	LFGDQLQVLEK
	666.879	49.28	61.28	35	VIQLLYNAGDVK
	752.366	72	84	35	DSLQQDKQEEAMGFFNVIR
Isopentenyl-diphosphate delta-isomerase type I	365.536	29.5	41.5	35	IEAENLLHR
(Solyc04g056390.2.1)	531.799	36.15	48.15	35	YELLLQQR
	547.816	71.61	84.61	35	LVVDNFLFK
	559.286	67.66	79.66	35	ADAGEEGLKLSPWFR
	580.13	74.1	88.1	35	AFSVFIFNSK
	591.542	94.99	106.99	35	APSDGKWGEHELDYLLFMVR
	601.982	63.55	75.55	35	KADAGEEGLKLSPWFR
	737.87	36.95	54.95	35	ESELIEENSLGVR
	798.095	96.14	108.14	35	LLDELGIPGEDVPVDQFIPLGR
	840.795	90.59	102.59	35	KLLDELGIPGEDVPVDQFIPLGR
Isopentenyl-diphosphate delta-isomerase type I	370.868	23.25	35.25	35	IESENLLHR
(Solyc05g055670.2.1)	729.874	42.8	54.8	35	ESELIEENALGVR
	841.454	84.09	96.09	35	KLLDELGIPAEDVPVDQFTPLGR
Phytoene synthase 2 (Solyc02g081330.2.1)	769.381	27.99	39.99	35	QGWNFGFLNADLR
	877.415	47.58	59.58	35	DMVEGMRMDLWKSR
Phytoene desaturase	556.341	22.35	34.35	35	YLADAGHKPILLEAR
(Solyc03g123760.2.1)	620.317	46.38	58.38	35	VTDEVFIAMSK
	663.345	46.52	58.52	35	YLASMEGAVLSGK
	780.884	57.71	69.71	35	SPIEGFYLAGDYTK
	802.134	65.7	77.7	35	ASPRPTKPLEIVIAGAGLGGLSTAK
	882.437	50.63	62.63	35	ELATLFPDEISADQSK
	1015.97	101.56	113.56	35	FDFSEALPAPLNGILAILK
15-cis-zeta-carotene isomerase	687.39	91.5	103.5	35	TSIIPFAAILDGR
(Solyc12g098710.1.1)	395.2	6.4	22.4	35	DKGEELIGER
	521.266	23.2	38.2	35	YGEAFEVVK
Zeta-carotene desaturase	587.82	24.81	36.81	35	ITAAELNDISK
(Solyc01g097810.2.1)	605.367	48.85	60.85	35	NAVALALSPVVR
	640.407	59.91	71.91	35	LVGVPVVTVQLR
	708.725	79.97	92.97	35	FPVGAPLHGINAFLSTNQLK
	821.873	44.34	56.34	35	QDYIDSMEGATLSGR
	843.903	87.26	99.26	35	DLDNVSFSEWFLSK
	787.395	63.92	75.92	35	TPVENFFLAGSYTK
	811.895	74.12	86.12	35	YNGWVTELQDLER
Carotenoid isomerase, chloroplastic	632.596	65.41	78.41	35	KLEVIPDPTTVHFHLPNDLSVR
(Solyc10g081650.1.1)	859.445	100.28	112.28	35	SLEEPIYLFGQFFK
	475.255	20.09	36.09	35	VAADLGFEK
Carotenoid isomerase-like	603.677	81.03	93.03	35	ISLKSHVENIVVEKGR
(Solyc05g010180.2.1)	629.313	61.74	73.74	35	YGQDVLVLESHDVAGGAAHSFDVK
	656.583	62.71	84.71	35	HVLHAYTPGTEPFEIWEGLDRR
	823.075	74.51	86.51	35	HVLHAYTPGTEPFEIWEGLDR
Lycopene epsilon cyclase (Solyc12g008980.1.1)	937.133	66.08	78.08	35	IKEIYEEEWSYIPVGGSLPNTEQK
Zeaxanthin epoxidase, chloroplastic	493.236	43.95	57.95	35	FHPSDVIEFGSDK
(Solyc02g090890.2.1)	537.309	52.93	64.93	35	MTLQQILAR
	541.287	65.1	79.1	35	GFDVLVFER
	667.361	54.78	67.78	35	FTGDLLVGADGIR
	759.394	63.55	74.44	35	SAESGSPVDIISSLR
	1333.71	54.22	66.22	35	FTGDLLVGADGIR
Violaxanthin de-epoxidase	500.8	48.87	60.87	35	LFGNALPIR
(Solyc04g050930.2.1)	584.294	46.21	58.21	35	IGTPDGGFFTR
	606.318	83.48	95.48	35	TIIKEVEEIEEEVEK
	681.32	25.69	37.69	35	EVEEIEEEVEK
	682.041	96.11	108.11	35	TIIKEVEEIEEEVEKVK
	714.688	79.75	91.75	35	LFEGFKELQQDEENFIR
	876.412	55.3	79.3	35	VENSPDDYIFVYYK
	969.051	80.91	92.91	35	SSVLPETIIPELQIAAQK
Carotenoid cleavage dioxygenase 1B	415.203	22.42	34.42	35	FDLHAEPETGK
(Solyc01g087260.2.1)	418.555	26.62	38.62	35	LKQEEFFGGAK
	521.769	31.54	43.54	35	LQNPDLDAIKGTEKEEQR
	527.97	29.33	41.33	35	LLALHEGDKPYVVK
	552.787	33.84	45.84	35	LSEAAVDFPR
	561.799	45.28	57.28	35	FGSEAIFVPR
	642.686	67.49	79.49	35	TKLEVGGNVPGIFDLGPGR
	976.545	92.13	104.92	35	YVYGTILNNVAQITGVVK
Carotenoid cleavage dioxygenase 4B	500.773	11.3	23.3	35	IEERPQTTTTITKPQEK
(Solyc08g075490.2.1)	727.329	41.12	53.12	35	NPSIDEDDGYVVSYVHNEK
	735.894	83.38	95.38	35	YGPIPPFITYFR
Plastid lipid associated protein 3	454.27	54.05	66.05	35	ISRGDGGLFVLVK
(Solyc08g076480.2.1)	502.791	58.74	70.74	35	GDGGLFVLVK
	544.326	51.55	63.55	35	TISGQPPLKIPIPGGR
	558.962	74.95	86.95	35	SNINLPETVDLFGQK
	574.947	72.77	86.77	35	SWLLTTYLDKDMR
	635.015	49.67	61.67	35	IQVEFKEGNFKPPEIK
	740.75	98.23	110.26	35	ISLSPVQQSLGPLENAVAGIAR
	797.38	50.56	62.56	35	MVEFVDEWGEKSEPEPGPVTK
	837.937	69.74	81.74	35	SNINLPETVDLFGQK
Plastid-lipid-associated protein, chloroplastic(CHRC)	478.774	11.07	22.07	35	SISSQPPIK
(Solyc02g081170.2.1)	487.954	56.02	68.02	35	ISRGDAGSVFVLIK
	636.304	24.63	36.63	35	QLADSFYGTNR
	738.898	48.09	60.09	35	GLITSVQDTASSVAK
	825.447	57.5	69.5	35	NPNPAPTEALTLLNGK
	844.785	57.88	69.99	35	ISPGGVAVVDEEPPKEPSEIELLK
	887.484	51.72	62.72	35	ISPGGVAVVDEEPPKEPSEIELLKK

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Protein	m/z	Rt window		CE %	Peptide sequence
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(Solyc03g114340.2.1)	532.293	45.06	58.06	35	AVELFISER
	553.322	38.13	50.13	35	IILTASGGAFR
	554.992	72.64	84.64	35	ETLIAGGPFVLPLAHK
	665.806	37.68	49.68	35	YPSMDLAYSAGR
	670.592	85.1	97.1	35	HREELVSSPSLEEIIHYDLWAR
	885.012	61.79	73.79	35	VVALAAGSNVTLLADQVK
Farnesyltransferase/type I geranylgeranyltransferase alpha subunit	518.767	27.5	39.5	35	IGTDIQDFK
(Solyc06g073390.2.1)	717.883	49.08	61.08	35	ELEVNYTVQAIR
	545.956	55.25	68.25	35	LGADAVTNELEFTKK
Geranylgeranyl pyrophosphate synthase 2	491.282	98.15	110.15	35	AAPLIALADYIANR
(Solyc04g079960.1.1)	736.416	99.65	111.65	35	AAPLIALADYIANR
	513.83	52.4	68.4	35	ILVAVAELAK
	572.792	6.14	22.14	35	QQLAAFDSHK
Geranylgeranyl pyrophosphate synthase	567.793	24.21	36.21	35	AQLVGFDQEK
(Solyc02g085700.1.1)	599.649	92.41	104.41	35	AAPLFALANYIAYREN
	777.425	98.49	110.49	35	AAPLFALANYIAYR
	898.972	95.77	107.77	35	AAPLFALANYIAYREN
	402.228	23.36	35.36	35	TAGKDLVADKVTYPK
	391.889	24.36	36.36	35	HLEFIHLHK
Geranylgeranyl pyrophosphate synthase	501.281	24.53	36.53	35	VVDDILEAK
(Solyc09g008920.2.1)	528.277	80.79	94.79	35	TYWTTLISDINQK
	572.797	37.12	49.12	35	SYVSVYGIEK
	791.909	81.23	93.23	35	TYWTTLISDINQK
	830.907	93.22	105.22	35	VMPLYSFLDYAADR
Geranylgeranyl reductase	489.765	41.03	53.03	35	EVLDAYLR
(Solyc03g115980.1.1)	567.811	59.24	71.24	35	GGIETFLIER
	571.849	51.44	63.44	35	LAVNTIGSLVR
	614.63	34.61	46.61	35	APNSPYVLHYTSYDSK
	632.35	38.96	50.96	35	VALVGDAAGYVTK
	744.912	77.3	89.3	35	AAEAGASVLNGLFLR
	759.438	102.25	114.25	35	VAPGNPIEDLKLAVNTIGSLVR
	767.917	1.48	13.48	35	VEAHPIPEHPRPR
	805.447	37.72	47.72	35	VAVIGGGPAGGAAAETLAK
	921.437	35.35	47.35	35	APNSPYVLHYTSYDSK
	923.935	57.02	69.02	35	SINAGDYEYAIAFQER
Isopentenyl-diphosphate delta-isomerase family protein	489.765	31.02	43.01	35	EVLDAYLR
(Solyc08g075390.2.1)	557.325	73.74	85.74	35	ADIVGLWALR
	645.357	57.11	69.11	35	LFGDQLQVLEK
	666.879	49.88	61.88	35	VIQLLYNAGDVK
	752.366	72	84	35	DSLQQDKQEEAMGFFNVIR
Isopentenyl-diphosphate delta-isomerase type I	531.799	36.07	48.07	35	YELLLQQR
Solyc04g056390.2.1	547.816	70.88	82.88	35	LVVDNFLFK
	559.286	67.11	79.11	35	ADAGEEGLKLSPWFR
	580.13	73.04	85.04	35	AFSVFIFNSK
	591.542	93.12	105.12	35	APSDGKWGEHELDYLLFMVR
	601.982	58.09	70.09	35	KADAGEEGLKLSPWFR
	737.87	37.4	49.4	35	ESELIEENSLGVR
	798.095	86.14	98.14	35	LLDELGIPGEDVPVDQFIPLGR
	840.795	92.77	104.77	35	KLLDELGIPGEDVPVDQFIPLGR
Isopentenyl-diphosphate delta-isomerase type I	370.868	23.34	35.34	35	IESENLLHR
(Solyc05g055670.2.1)	841.454	85.92	97.92	35	KLLDELGIPAEDVPVDQFTPLGR
	729.874	42.8	54.8	35	ESELIEENALGVR
Phytoene synthase 2 (Solyc02g081330.2.1)	769.381	27.99	39.99	35	QGWNFGFLNADLR
	877.415	51.59	63.58	35	DMVEGMRMDLWKSR
Phytoene desaturase	556.341	33.66	45.66	35	YLADAGHKPILLEAR
(Solyc03g123760.2.1)	620.317	47.43	59.43	35	VTDEVFIAMSK
	663.345	43.46	55.46	35	YLASMEGAVLSGK
	780.884	58.25	70.25	35	SPIEGFYLAGDYTK
	802.134	65.7	77.7	35	ASPRPTKPLEIVIAGAGLGGLSTAK
	882.437	61.63	73.63	35	ELATLFPDEISADQSK
	1015.97	101.56	113.56	35	FDFSEALPAPLNGILAILK
15-cis-zeta-carotene isomerase	687.39	89.13	101.13	35	TSIIPFAAILDGR
(Solyc12g098710.1.1)	395.2	6.4	22.4	35	DKGEELIGER
	521.266	23.2	38.2	35	YGEAFEVVK
Zeta-carotene desaturase	587.82	28.43	40.43	35	ITAAELNDISK
(Solyc01g097810.2.1)	605.367	48.85	60.85	35	NAVALALSPVVR
	640.407	59.96	71.96	35	LVGVPVVTVQLR
	708.725	78.57	90.57	35	FPVGAPLHGINAFLSTNQLK
	787.395	64.79	76.79	35	TPVENFFLAGSYTK
	811.895	74.24	86.27	35	YNGWVTELQDLER
	821.873	46.27	57.27	35	QDYIDSMEGATLSGR
	843.903	87.51	99.51	35	DLDNVSFSEWFLSK
Carotenoid isomerase, chloroplastic	632.596	70.71	82.71	35	KLEVIPDPTTVHFHLPNDLSVR
(Solyc10g081650.1.1)	859.445	102.13	114.13	35	SLEEPIYLFGQFFK
	475.255	20.09	36.09	35	VAADLGFEK
Carotenoid isomerase-like	603.677	81.03	93.03	35	ISLKSHVENIVVEKGR
(Solyc05g010180.2.1)	629.313	61.74	74.74	35	YGQDVLVLESHDVAGGAAHSFDVK
	656.583	71.71	84.71	35	HVLHAYTPGTEPFEIWEGLDRR
	823.075	74.51	86.51	35	HVLHAYTPGTEPFEIWEGLDR
Lycopene epsilon cyclase (Solyc12g008980.1.1)	937.133	66.08	80.08	35	IKEIYEEEWSYIPVGGSLPNTEQK
Zeaxanthin epoxidase, chloroplastic	493.236	38.95	50.95	35	FHPSDVIEFGSDK
(Solyc02g090890.2.1)	537.309	58.53	70.53	35	MTLQQILAR
	541.287	58.1	70.1	35	GFDVLVFER
	667.361	55.16	67.16	35	FTGDLLVGADGIR
	759.394	63.34	75.34	35	SAESGSPVDIISSLR
	1333.71	54.22	66.22	35	FTGDLLVGADGIR
Violaxanthin de-epoxidase	500.8	49.87	59.87	35	LFGNALPIR
(Solyc04g050930.2.1)	584.294	46.21	58.21	35	IGTPDGGFFTR
	606.318	80.86	92.86	35	TIIKEVEEIEEEVEK
	681.32	26.37	38.37	35	EVEEIEEEVEK
	682.041	96.11	108.11	35	TIIKEVEEIEEEVEKVK
	714.688	81.9	95.9	35	LFEGFKELQQDEENFIR
	876.412	63.2	75.2	35	VENSPDDYIFVYYK
	969.051	83.19	95.19	35	SSVLPETIIPELQIAAQK
Carotenoid cleavage dioxygenase 1B	415.203	22.42	34.42	35	FDLHAEPETGK
(Solyc01g087260.2.1)	418.555	26.62	38.62	35	LKQEEFFGGAK
	521.769	30.54	44.54	35	LQNPDLDAIKGTEKEEQR
	527.97	29.33	41.33	35	LLALHEGDKPYVVK
	552.787	33.84	45.84	35	LSEAAVDFPR
	561.799	46.36	57.36	35	FGSEAIFVPR
	642.686	68.02	80.02	35	TKLEVGGNVPGIFDLGPGR
	976.545	91.5	103.5	35	YVYGTILNNVAQITGVVK
Carotenoid cleavage dioxygenase 4B	500.773	11.3	23.3	35	IEERPQTTTTITKPQEK
(Solyc08g075490.2.1)	727.329	46.55	58.55	35	NPSIDEDDGYVVSYVHNEK
	735.894	94.85	106.85	35	YGPIPPFITYFR
Plastid lipid associated protein 3	454.27	55.43	67.43	35	ISRGDGGLFVLVK
(Solyc08g076480.2.1)	502.791	59.2	71.2	35	GDGGLFVLVK
	544.326	51.55	63.55	35	TISGQPPLKIPIPGGR
	558.962	74.95	86.95	35	SNINLPETVDLFGQK
	574.947	73.77	83.88	35	SWLLTTYLDKDMR
	635.015	49.89	61.89	35	IQVEFKEGNFKPPEIK
	740.75	96.52	111.52	35	ISLSPVQQSLGPLENAVAGIAR
	797.38	50	62	35	MVEFVDEWGEKSEPEPGPVTK
Plastid-lipid-associated protein, chloroplastic	478.774	7.56	19.56	35	SISSQPPIK
(Solyc02g081170.2.1)	487.954	57.51	69.51	35	ISRGDAGSVFVLIK
	636.304	24.74	36.74	35	QLADSFYGTNR
	738.898	48.06	60.06	35	GLITSVQDTASSVAK
	825.447	57.22	69.22	35	NPNPAPTEALTLLNGK
	844.785	59.88	71.88	35	ISPGGVAVVDEEPPKEPSEIELLK
	887.484	51.52	63.52	35	ISPGGVAVVDEEPPKEPSEIELLKK

Table 5.3 Internal control proteins and peptides used for targeted proteome monitoring.

Few housekeeping proteins with uniform abundance across wild species and tomato were selected as internal controls and given here. Their abundances were used for quantification of carotenogenic proteins as described in methods.

Internal reference protein	***S.pimpinellifolium***		***S.galapagense***		***S.habrochaites***	
	Fruit	Leaf	Fruit	Leaf	Fruit	Leaf
Fructose-1 6-bisphosphatase class 1 (Solyc5g052600.2.1)	✓	✓	-	✓	✓	✓
Harpin binding protein 1 (Solyc9g090330.2.1)	-	✓	-	-	✓	-
Dihydrolipoyl dehydrogenase (Solyc5g053300.2.1)	✓	-	✓	✓	✓	✓
Peptidyl-prolyl cis-trans isomerase (Solyc1g111170.2.1)	✓	✓	✓	✓	✓	✓
Calcium-binding protein Calnexin (Solyc3g118040.2.1)	✓	✓	✓	✓	-	✓

List of internal reference peptides used in TPM of carotenoid pathway proteins in SP, SG and SH (fruit)

Internal reference protein for SP-SL	m/z	RT window		CE%	Peptide sequence
Peptidyl-prolyl cis-trans isomerase	380.85999	10.91	26.91	35	FNDENFVKK
	506.74045	19.04	35.04	35	FNDENFVK
	595.66296	54.28	70.28	35	HVVFGQVVEGMDVIKK
Calcium-binding protein Calnexin	389.88754	46.81	62.81	35	VAGIPFLGEHK
	473.19312	18.55	34.55	35	YLRPQEAGWTAK
	516.91174	26.29	42.29	35	SEGHDDYGLLVSEK
	575.95502	50.27	66.27	35	WIVSEKEDYSGVWK
	741.81226	52.17	68.17	35	FYESFDEAFDGR
	909.40717	69.04	85.04	35	GFDNESPYTIMFGPDK
Dihydrolipoyl dehydrogenase	412.56793	36.56	53.56	35	VGKFPFLANSR
	565.8241	23.41	39.41	35	NIIIATGSDVK
	567.31372	43.83	59.83	35	VPFTSGLGLDK
	602.82014	16.95	32.95	35	VVSVDTVGDSVK
	693.35901	56.7	72.7	35	FLSPSEVSVDTVEGGNTIVK
	750.43976	52.55	68.55	35	IVSSTGALALTEIPK
	785.08423	79.27	95.27	35	FASNVPGVYAIGDVIPGPMLAHK
Fructose-1 6-bisphosphatase class 1	594.78137	18.91	34.91	35	FEETLYGSSR
	618.33746	33.15	49.15	35	GIFTNVTSPTAK
	673.85046	56.13	72.13	35	EQVAAAMGIFGPR
	794.96997	101.3	117.3	35	LLFEVAPLGFLIEK
Harpin binding protein 1	692.92078	81.01	97.01	35	LLPITLGQVFQR
	509.75433	16.1	32.1	35	GLAASEDDLK
	811.45001	53.8	69.8	35	TTGNLSQLPPLEVPR

Internal reference protein for SG-SL	m/z	RT window		CE%	Peptide sequence
Peptidyl-prolyl cis-trans isomerase	380.85999	17.24	33.24	35	FNDENFVKK
	675.85321	54.97	70.97	35	VVMELFADTTPK
	710.88226	67.56	83.56	35	VFFDLTIGGAPAGR
	828.94	61.9	77.9	35	HVVFGQVVEGMDVIK
Calcium-binding protein Calnexin	473.91794	17.64	33.64	35	YLRPQEAGWTAK
	575.95447	48.62	64.62	35	WIVSEKEDYSGVWK
	639.83771	32.86	48.86	35	DGTVVLQYEVR
	909.40222	67.75	83.75	35	GFDNESPYTIMFGPDK
Dihydrolipoyl dehydrogenase	412.57001	41.18	57.18	35	VGKFPFLANSR
	515.77441	14.93	30.93	35	AIDDAEGIVK
	565.82629	21.3	37.3	35	NIIIATGSDVK
	860.11078	90.5	106.5	35	LGSEVTVVEFASDIVPTMDGEVRK
	1039.5354	54.19	70.19	35	FLSPSEVSVDTVEGGNTIVK
Fructose-1 6-bisphosphatase class 1	794.96997	98.38	114.38	35	LLFEVAPLGFLIEK
	594.78137	16.91	32.91	35	FEETLYGSSR
	618.33746	31.15	47.15	35	GIFTNVTSPTAK
	673.85046	54.13	70.13	35	EQVAAAMGIFGPR
Harpin binding protein 1	580.31323	7.97	23.97	35	EAEAELIGSLK
	811.44635	51.8	67.8	35	TTGNLSQLPPLEVPR
	509.75433	14.1	30.1	35	GLAASEDDLK

Internal reference protein for SH-SL	m/z	RT window		CE%	Peptide sequence
Peptidyl-prolyl cis-trans isomerase	380.85999	3.37	17.37	35	FNDENFVKK
	710.88226	16.52	31.52	35	VFFDLTIGGAPAGR
	675.85321	11.2	29.2	35	VVMELFADTTPK
	828.94	13.25	27.25	35	HVVFGQVVEGMDVIK
Calcium-binding protein Calnexin	505.79892	17.24	31.24	35	LVFDLLYK
	575.95447	8.37	27.37	35	WIVSEKEDYSGVWK
	617.97589	1.23	17.23	35	QKAEEEAESGGLKGYQK
Dihydrolipoyl dehydrogenase	412.57001	10.19	24.19	35	VGKFPFLANSR
	476.25391	11.4	25.4	35	FPFLANSR
	565.82629	4.79	19.79	35	NIIIATGSDVK
	750.43976	11.64	26.64	35	IVSSTGALALTEIPK
	833.11005	18.79	32.79	35	LTLEPAAGGEQTTLEADVVLVSAGR
Fructose-1 6-bisphosphatase class 1	594.7793	3.56	17.56	35	FEETLYGSSR
	618.33508	6.99	22.99	35	GIFTNVTSPTAK
	673.84778	13.9	25.9		EQVAAAMGIFGPR
	794.96997	25.49	39.49	35	LLFEVAPLGFLIEK
	605.30634	13.9	27.9	35	NEIIRFEETLYGSSR
Harpin binding protein 1	692.91846	17.44	34.44	35	LLPITLGQVFQR
	976.79059	11.88	27.88	35	IPDQFRPPSNTGSGEFEVTYIDSDTR
	580.31323	9.28	34.13	35	EAEAELIGSLK
	811.44635	11.85	26.85	35	TTGNLSQLPPLEVPR

Note : RT values for SH-SL vary when compared to SG-SL and SP-SL owing to shorter run time (see methods for more details).

List of internal reference peptides used in TPM of carotenoid pathway proteins in SP, SG and SH (leaf)

Internal reference protein	m/z	Rt window		CE%	Peptide sequence
Peptidyl-prolyl cis-trans isomerase	380.8616	18.26	30.26	35	FNDENFVKK
	474.2595	71.4	84.4	35	VFFDLTIGGAPAGR
	506.7405	22.19	34.19	35	FNDENFVK
	570.788	13.81	25.81	35	FNDENFVKK
	595.663	54.67	66.67	35	HVVFGQVVEGMDVIKK
	675.8515	56.83	68.83	35	VVMELFADTTPK
	710.8816	69.67	82.67	35	VFFDLTIGGAPAGR
	828.9431	62.95	74.95	35	HVVFGQVVEGMDVIK
Calcium-binding protein Calnexin	389.8875	51.87	63.87	35	VAGIPFLGEHK
	505.7997	71.01	83.01	35	LVFDLLYK
	551.6235	31.32	43.32	35	GKWHAPLIDNPNYK
	575.955	41.82	66.82	35	WIVSEKEDYSGVWK
	617.9742	2.71	15.71	35	QKAEEEAESGGLKGYQK
	741.8123	53.45	65.45	35	FYESFDEAFDGR
	909.4072	69.37	81.37	35	GFDNESPYTIMFGPDK
Dihydrolipoyl dehydrogenase	412.5679	42.52	54.52	35	VGKFPFLANSR
	476.2539	43.84	55.84	35	FPFLANSR
	515.7722	18.41	31.41	35	AIDDAEGIVK
	543.3256	39.03	51.03	35	IVSSTGALALTEIPKK
	565.8241	25.02	37.02	35	NIIIATGSDVK
	693.359	61.37	73.37	35	FLSPSEVSVDTVEGGNTIVK
	739.3435	32.13	38.13	35	EAAMATYDKPIHM
	750.4398	53.6	65.6	35	IVSSTGALALTEIPK
	833.1101	80.87	92.87	35	LTLEPAAGGEQTTLEADVVLVSAGR
	860.1063	91.02	103.02	35	LGSEVTVVEFASDIVPTMDGEVRK
Fructose-1 6-bisphosphatase class 1	477.2934	15.27	27.27	35	LKAGAPVGAAV
	530.316	100.36	112.36	35	LLFEVAPLGFLIEK
	594.7793	20.99	32.99	35	FEETLYGSSR
	618.3351	34.49	46.49	35	GIFTNVTSPTAK
	673.8478	55.49	67.49	35	EQVAAAMGIFGPR
	794.9705	101.05	113.05	35	LLFEVAPLGFLIEK
	816.775	70.35	82.35	35	QSVLDKVIVNLDDRTQVAYGSK
	817.433	56.75	68.75	35	YTGGMVPDVNQIIVK
	907.4569	62.06	74.06	35	NEIIRFEETLYGSSR
Harpin binding protein 1	509.7543	17.1	29.1	35	GLAASEDDLK
	515.3043	30.21	42.21	35	LLSAVSGLNR
	573.8042	7.54	19.54	35	GLAASEDDLKK
	692.9185	80.12	92.12	35	LLPITLGQVFQR
	976.7906	58.37	70.37	35	IPDQFRPPSNTGSGEFEVTYIDSDTR
	626.8433	78.5	91.5	35	TLGGSRPGPPTGR

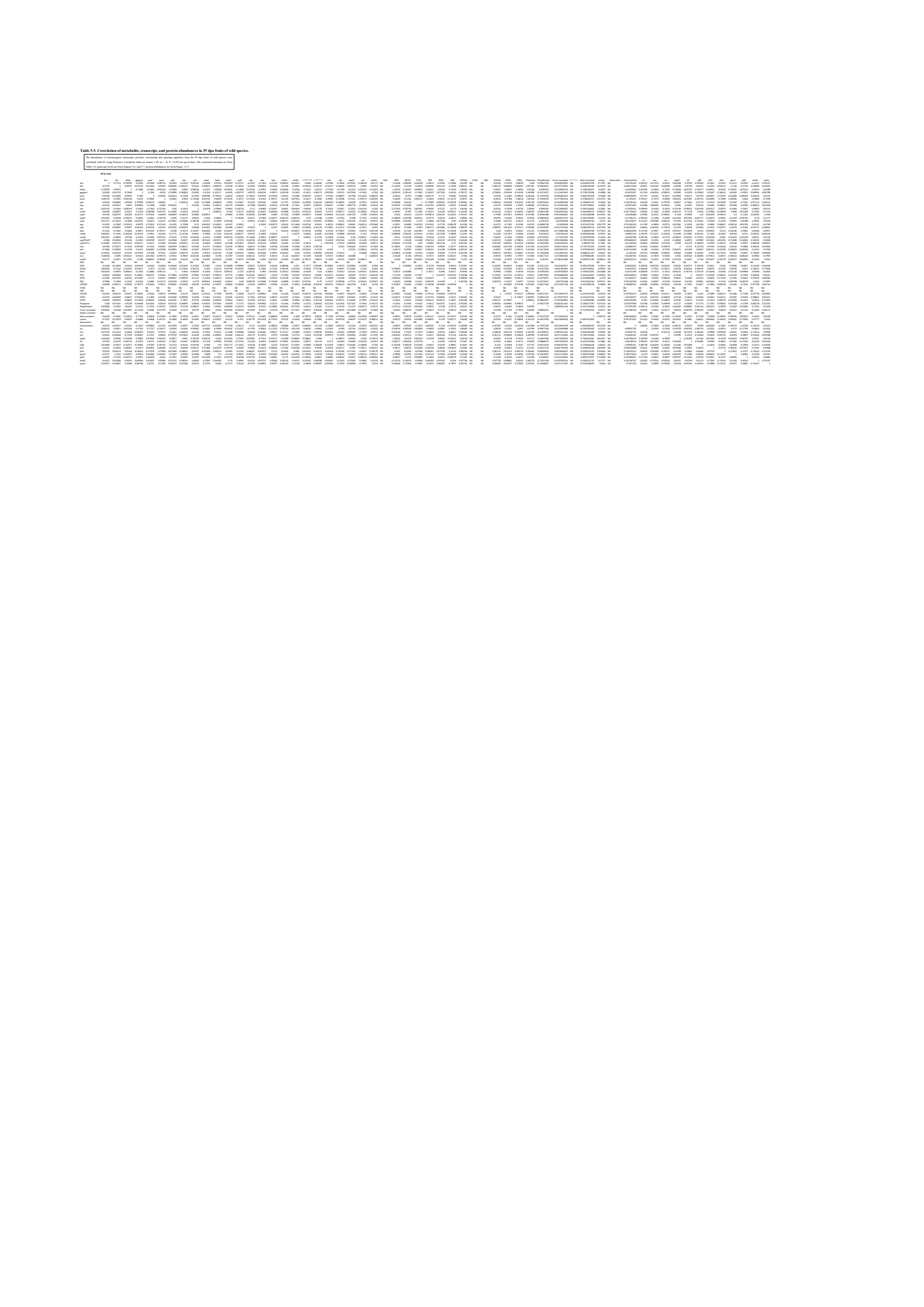
Note : Rt values are constant for SP-SL,SG-SL and SH-SL owing to the same run time (118minutes)

SP - Solanum pimpinellifolium
SG - Solanum galapagense
SH - Solanum habrochaites
SL - Solanum lycopersicum

Table 5.5. Correlation of metabolite, transcript, and protein abundances in 39 dpa fruits of wild species.

The abundances of carotenogenic transcripts, proteins, carotenoids and ripening regulators from the 39 dpa fruits of wild species were correlated with SI, using Pearson's correlation (data are means ± SE (n = 3), P ≤ 0.05) are given here. The carotenoid amounts are from Table 5.4, transcript levels are from Figures 5.6 and 5.7, protein abundances are from Figure 5.17.

SP-SL fruit



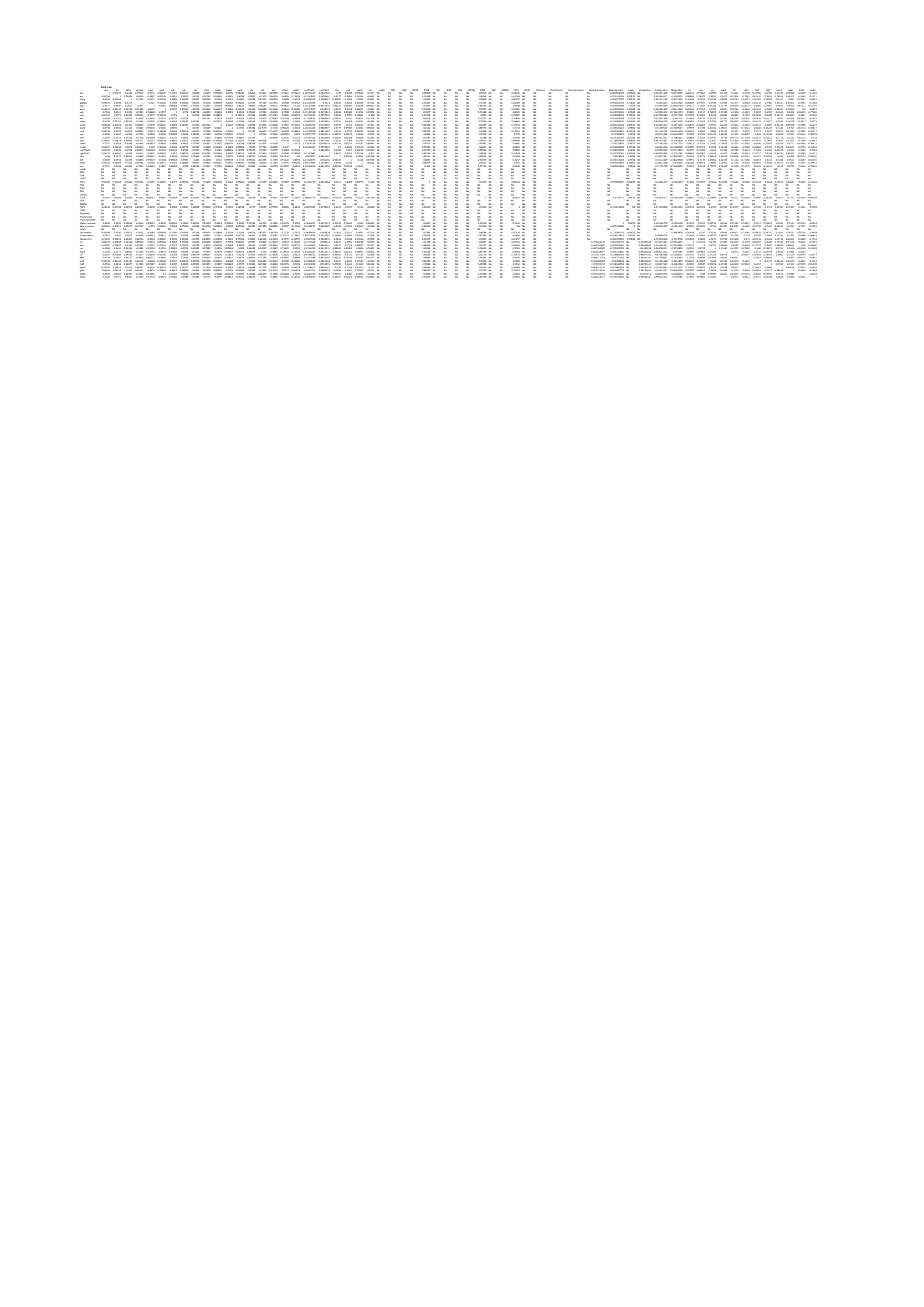


Table 5.5. Correlation of metabolite, transcript, and protein abundances in leaves.

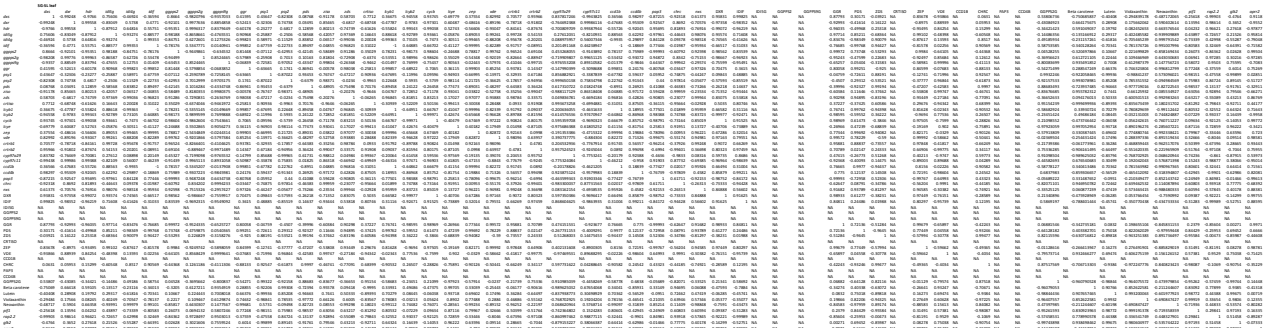
The abundances of carotenogenic transcripts, proteins, carotenoids and ripening regulators from the leaves of 15-day-old seedlings were correlated with SL using Pearson's correlation (n ≥ 3 ± SE; P ≤ 0.05) and given here. The carotenoid amounts are from Table 5.4; transcript levels are from Figures 5.6 and 5.7; protein abundances are from Figure 5.17.

SP-SL leaf

	dxs	*dxr*	*hdr*	*idi5g*	*idi4g*	*idif*	*ggpps2*	*ggpps2g*	*ggpps9g*	*ggr*	*psy1*	*psy2*	*pds*	*ziso*	*zds*	*crtiso*	*lcyb1*	*lcyb2*	*cycb*	*lcye*
dxs	1	-0.996	-0.04229	0.997367	0.259106	0.939595	0.935295	0.346852	-0.7102	-0.89444	0.793131	0.077204	-0.46719	-0.2591	0.000885	-0.06345	0.555211	-0.99998	0.581476	-0.5073
dxr	-0.996	1	0.131357	-0.9869	-0.17181	-0.96641	-0.96316	-0.42923	0.770235	0.850921	-0.73557	0.01215	0.544287	0.344326	-0.09019	0.15233	-0.62727	0.995455	-0.50649	0.428304
hdr	-0.04229	0.131357	1	0.030278	0.954026	-0.38172	-0.39311	-0.95175	0.73341	-0.40897	0.574961	0.992858	0.903126	0.975945	-0.99914	0.999776	-0.85445	0.036353	0.788243	-0.83954
idi5g	0.997367	-0.9869	0.030278	1	0.328472	0.912296	0.907168	0.277916	-0.65727	-0.92451	0.835214	0.149309	-0.40183	-0.18837	-0.07164	0.009094	0.49343	-0.99778	0.638948	-0.56846
idi4g	0.259106	-0.17181	0.954026	0.328472	1	-0.08714	-0.09944	-0.81602	0.495943	-0.66368	0.793756	0.98297	0.732911	0.865732	-0.96562	0.947462	-0.65945	-0.26484	0.936444	-0.96378
idif	0.939595	-0.96641	-0.38172	0.912296	-0.08714	1	0.999924	0.64694	-0.90827	-0.68734	0.536751	-0.26873	-0.74161	-0.57405	0.343121	-0.40122	0.806359	-0.93754	0.267878	-0.18168
ggpps2	0.935295	-0.96316	-0.39311	0.907168	-0.09944	0.999924	1	0.65631	-0.91337	-0.67831	0.526288	-0.2806	-0.74984	-0.58412	0.354697	-0.4125	0.813602	-0.93317	0.255957	-0.16952
ggpps2g	0.346852	-0.42923	-0.95175	0.277916	-0.81602	0.64694	0.65631	1	-0.90663	0.109198	-0.29614	-0.90834	-0.99131	-0.99576	0.938227	-0.95804	0.972653	-0.34127	-0.56137	0.632315
ggpps9g	-0.7102	0.770235	0.73341	-0.65727	0.495943	-0.90827	-0.91337	-0.90663	1	0.320398	-0.13451	0.647072	0.954245	0.863973	-0.70463	0.747647	-0.97984	0.706	0.159789	-0.24641
ggr	-0.89444	0.850921	-0.40897	-0.92451	-0.66368	-0.68734	-0.67831	0.109198	0.320398	1	-0.98177	-0.51492	0.022477	-0.20018	0.446405	-0.38954	-0.12466	0.897078	-0.88392	0.839126
psy1	0.793131	-0.73557	0.574961	0.835214	0.793756	0.536751	0.526288	-0.29614	-0.13451	-0.98177	1	0.668465	0.167955	0.382752	-0.60835	0.557498	-0.0662	-0.79674	0.956688	-0.92722
psy2	0.077204	0.01215	0.992858	0.149309	0.98297	-0.26873	-0.2806	-0.90834	0.647072	-0.51492	0.668465	1	0.84545	0.942965	-0.99695	0.990108	-0.78636	-0.08313	0.856028	-0.89836
pds	-0.46719	0.544287	0.903126	-0.40183	0.732911	-0.74161	-0.74984	-0.99131	0.954245	0.022477	0.167955	0.84545	1	0.975013	-0.88457	0.91202	-0.99475	0.461924	0.44766	-0.52494
ziso	-0.2591	0.344326	0.975945	-0.18837	0.865732	-0.57405	-0.58412	-0.99576	0.863973	-0.20018	0.382752	0.942965	0.975013	1	-0.96608	0.980345	-0.94716	0.253353	0.635121	-0.7009
zds	0.000885	-0.09019	-0.99914	-0.07164	-0.96562	0.343121	0.354697	0.938227	-0.70463	0.446405	-0.60835	-0.99695	-0.88457	-0.96608	1	-0.99804	0.832201	0.005059	-0.81305	0.861322
crtiso	-0.06345	0.15233	0.999776	0.009094	0.947462	-0.40122	-0.4125	-0.95804	0.747647	-0.38954	0.557498	0.990108	0.91202	0.980345	-0.99804	1	-0.86526	0.057518	0.775029	-0.82785
lcyb1	0.555211	-0.62727	-0.85445	0.49343	-0.65945	0.806359	0.813602	0.972653	-0.97984	-0.12466	-0.0662	-0.78636	-0.99475	-0.94716	0.832201	-0.86526	1	-0.55026	-0.35381	0.435086
lcyb2	-0.99998	0.995455	0.036353	-0.99778	-0.26484	-0.93754	-0.93317	-0.34127	0.706	0.897078	-0.79674	-0.08313	0.461924	0.253353	0.005059	0.057518	-0.55026	1	-0.5863	0.512412
cycb	0.581476	-0.50649	0.788243	0.638948	0.936444	0.267878	0.255957	-0.56137	0.159789	-0.88392	0.956688	0.856028	0.44766	0.635121	-0.81305	0.775029	-0.35381	-0.5863	1	-0.99609
lcye	-0.5073	0.428304	-0.83954	-0.56846	-0.96378	-0.18168	-0.16952	0.632315	-0.24641	0.839126	-0.92722	-0.89836	-0.52494	-0.7009	0.861322	-0.82785	0.435086	0.512412	-0.99609	1
zep	0.95954	-0.98085	-0.3219	0.936592	-0.02333	0.997958	0.997093	0.596911	-0.87969	-0.73233	0.58955	-0.20665	-0.69724	-0.52057	0.282422	-0.34189	0.766934	-0.95785	0.328872	-0.24412
vde	0.635119	-0.70157	-0.79858	0.577427	-0.58147	0.861144	0.867357	0.944755	-0.99484	-0.22265	0.033294	-0.72108	-0.97966	-0.9106	0.772976	-0.81116	0.995049	-0.63052	-0.2591	0.34345
crtrb1	0.867784	-0.9087	-0.5332	0.829458	-0.25512	0.985463	0.987486	0.767084	-0.96615	-0.55395	0.385604	-0.42846	-0.84479	-0.70481	0.49771	-0.551	0.895114	-0.86481	0.100302	-0.01197
crtrb2	0.887224	-0.92488	-0.49845	0.851428	-0.2157	0.991542	0.99307	0.740435	-0.95489	-0.58725	0.422705	-0.39147	-0.8224	-0.67546	0.462125	-0.51671	0.876297	-0.88447	0.14057	-0.05252
cyp97a29	0.677045	-0.60861	0.706648	0.728637	0.886235	0.384244	0.372811	-0.45542	0.037269	-0.93468	0.985211	0.786015	0.33438	0.535387	-0.73534	0.691498	-0.23619	-0.68141	0.992421	-0.97768
cyp97c11	-0.96603	0.985253	0.299038	-0.94475	-0.00072	-0.99613	-0.99497	-0.57744	0.867998	0.748494	-0.60881	0.18306	0.679798	0.499886	-0.25927	0.319188	-0.75128	0.964481	-0.35149	0.267375
ccd1b	-0.11807	0.206287	0.99711	-0.04574	0.9285	-0.45083	-0.46182	-0.97231	0.782932	-0.33846	0.511144	0.980926	0.933135	0.989687	-0.99311	0.998496	-0.89145	0.112166	0.739217	-0.79585
ccd4b	0.999796	-0.99399	-0.02209	0.998629	0.27858	0.932483	0.92795	0.32782	-0.69582	-0.90329	0.805282	0.097344	-0.44922	-0.23952	-0.01933	-0.04326	0.538283	-0.9999	0.597804	-0.52462
pap3	-0.97062	0.988234	0.281436	-0.95062	-0.01911	-0.99435	-0.99296	-0.56233	0.858718	0.760565	-0.6233	0.164946	0.666193	0.483871	-0.24146	0.301703	-0.73901	0.969177	-0.36865	0.285053
chrc	-0.97569	0.952223	-0.17768	-0.98902	-0.46446	-0.84175	-0.83501	-0.13289	0.53866	0.970693	-0.90732	-0.29381	0.262079	0.041145	0.218276	-0.15679	-0.35946	0.976979	-0.74563	0.683815
nxs	0.964331	-0.98412	-0.30525	0.942594	-0.0058	0.996684	0.995603	0.582748	-0.87121	-0.74416	0.603625	-0.18946	-0.68456	-0.50552	0.265554	-0.32535	0.755561	-0.96274	0.345385	-0.26109
DXR	0.15102	-0.2387	-0.99403	0.078929	-0.91564	0.480261	0.491058	0.979544	-0.80318	0.306991	-0.48229	-0.97392	-0.94457	-0.9939	0.988664	-0.99612	0.906018	-0.14514	-0.71642	0.775275
IDIF	-0.90763	0.866515	-0.381	-0.93569	-0.6406	-0.70912	-0.70036	0.078893	0.349081	0.999537	-0.97553	-0.48859	0.052896	-0.17026	0.418963	-0.36133	-0.1548	0.910112	-0.86927	0.822182
IDI5G	-0.58893	0.514395	-0.78255	-0.64599	-0.93318	-0.27672	-0.26483	0.553741	-0.15071	0.888177	-0.95932	-0.85124	-0.43942	-0.62799	0.807663	-0.76919	0.345194	0.593724	-0.99996	0.995232
GGPPS2	0.212075	-0.29851	-0.98535	0.140641	-0.88893	0.533768	0.544172	0.990144	-0.8386	0.247338	-0.42699	-0.95796	-0.96313	-0.99883	0.977441	-0.98874	0.930537	-0.20626	-0.67174	0.734583
GGPPS9G	0.283527	-0.36804	-0.9701	0.213232	-0.85275	0.594643	0.604529	0.997774	-0.87647	0.175249	-0.35918	-0.93421	-0.98034	-0.99968	0.959215	-0.97502	0.954997	-0.27782	-0.61531	0.682575
GGR	-0.20682	0.11861	-0.96876	-0.27723	-0.99855	0.140564	0.152782	0.845906	-0.5419	0.622514	-0.75992	-0.99143	-0.76842	-0.89138	0.978196	-0.96329	0.6989	0.21263	-0.91623	0.948057
PDS	0.950766	-0.97465	-0.34984	0.925787	-0.05297	0.999413	0.998914	0.620445	-0.89341	-0.71181	0.565333	-0.23558	-0.7182	-0.54567	0.31075	-0.36961	0.78563	-0.94891	0.300717	-0.21525
ZDS	-0.5822	0.652487	0.836942	-0.5217	0.634428	-0.82533	-0.83224	-0.96451	0.985863	0.157147	0.033426	0.765672	0.990858	0.936129	-0.81356	0.84835	-0.99946	0.577355	0.322931	-0.40531
CRTISO	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZEP	0.981741	-0.96083	0.148532	0.992951	0.438103	0.857327	0.850903	0.162105	-0.56331	-0.96317	0.894505	0.26545	-0.29047	-0.07064	-0.18935	0.127547	0.386863	-0.98285	0.725617	-0.66196
VDE	0.88042	-0.91925	-0.51101	0.84371	-0.22988	0.98955	0.991255	0.750133	-0.95911	-0.57542	0.40948	-0.40481	-0.83059	-0.68612	0.474975	-0.5291	0.883212	-0.87759	0.126155	-0.03799
CCD1B	0.557853	-0.62975	-0.85279	0.496193	-0.65705	0.808235	0.815447	0.971909	-0.98047	-0.12782	-0.06302	-0.78439	-0.99442	-0.94614	0.830433	-0.86366	0.999995	-0.55291	-0.35083	0.432221
CHRC	-0.68808	0.750137	0.754088	-0.63364	0.522569	-0.89489	-0.90034	-0.91925	0.999521	0.290939	-0.10379	0.670348	0.963039	0.879137	-0.72625	0.767834	-0.98555	0.683753	0.19025	-0.27627
PAP3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCD4B	0.408734	-0.48861	-0.92912	0.341467	-0.77558	0.696435	0.705246	0.997766	-0.93279	0.04255	-0.23167	-0.87837	-0.99789	-0.98739	0.913015	-0.93675	0.985996	-0.4033	-0.50483	0.579149
GGPPS2G	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Beta carotene	-0.96828	0.986725	0.290608	-0.9476	-0.00954	-0.99532	-0.99405	-0.57022	0.863584	0.754316	-0.61578	0.174379	0.673301	0.492226	-0.25074	0.310815	-0.74543	0.966774	-0.35974	0.275865
Lutein	-0.11137	0.199677	0.9976	-0.039	0.930985	-0.4448	-0.45583	-0.97071	0.778715	-0.34481	0.516935	0.982216	0.930687	0.988697	-0.99388	0.998843	-0.88837	0.105456	0.743747	-0.79991
Violaxanthin	-0.09434	0.005053	-0.99066	-0.1663	-0.98599	0.252118	0.264052	0.901013	-0.63386	0.529587	-0.68116	-0.99985	-0.83614	-0.9371	0.995456	-0.98755	0.775619	0.10026	-0.86479	0.905787
Neoxanthin	-0.28785	0.37223	0.968993	-0.21763	0.850387	-0.59826	-0.60811	-0.99806	0.878636	-0.17081	0.354972	0.932595	0.981216	0.999553	-0.95793	0.974011	-0.95632	0.28215	0.611754	-0.67927
pif1	-0.91401	0.874123	-0.36667	-0.94102	-0.62867	-0.71993	-0.71131	0.063483	0.363516	0.998947	-0.97202	-0.47505	0.068316	-0.15502	0.404885	-0.34688	-0.17005	0.916404	-0.86153	0.81329
rap2.2	-0.93407	0.962233	0.396263	-0.90572	0.102858	-0.99988	-0.99999	-0.6589	0.914761	0.675785	-0.52337	0.283898	0.752102	0.586902	-0.3579	0.415627	-0.81559	0.931935	-0.25264	0.166135
glk2	0.87787	-0.91713	-0.5156	0.840826	-0.23508	0.988764	0.990535	0.75366	-0.96061	-0.57104	0.404593	-0.40969	-0.83355	-0.69	0.479676	-0.53364	0.885708	-0.87501	0.120846	-0.03264
aprr2	-0.92522	0.887632	-0.33997	-0.9503	-0.60621	-0.73945	-0.73108	0.034969	0.389962	0.997231	-0.96492	-0.44974	0.096768	-0.12676	0.378618	-0.31997	-0.19811	0.927457	-0.84669	0.796349

	zep	*vde*	*crtrb1*	*crtrb2*	*cyp97a29*	*cyp97c11*	*ccd1b*	*ccd4b*	*pap3*	*chrc*	*nxs*	DXR	IDIF	IDI5G	GGPPS2	GGPPS9G	GGR	PDS	ZDS	CRTISO
dxs	0.95954	0.635119	0.867784	0.887224	0.677045	-0.96603	-0.11807	0.999796	-0.97062	-0.97569	0.964331	0.15102	-0.90763	-0.58893	0.212075	0.283527	-0.20682	0.950766	-0.5822	NA
dxr	-0.98085	-0.70157	-0.9087	-0.92488	-0.60861	0.985253	0.206287	-0.99399	0.988234	0.952223	-0.98412	-0.2387	0.866515	0.514395	-0.29851	-0.368041	0.11861	-0.97465	0.652487	NA
hdr	-0.3219	-0.79858	-0.5332	-0.49845	0.706648	0.299038	0.99711	-0.02209	0.281436	-0.17768	-0.30525	-0.99403	-0.381	-0.78255	-0.98535	-0.970098	-0.96876	-0.34984	0.836942	NA
idi5g	0.936592	0.577427	0.829458	0.851428	0.728637	-0.94475	-0.04574	0.998629	-0.95062	-0.98902	0.942594	0.078929	-0.93569	-0.64599	0.140641	0.2132316	-0.27723	0.925787	-0.5217	NA
idi4g	-0.02333	-0.58147	-0.25512	-0.2157	0.886235	-0.00072	0.9285	0.27858	-0.01911	-0.46446	-0.0058	-0.91564	-0.6406	-0.93318	-0.88893	-0.852751	-0.99855	-0.05297	0.634428	NA
idif	0.997958	0.861144	0.985463	0.991542	0.384244	-0.99613	-0.45083	0.932483	-0.99435	-0.84175	0.996684	0.480261	-0.70912	-0.27672	0.533768	0.5946435	0.140564	0.999413	-0.82533	NA
ggpps2	0.997093	0.867357	0.987486	0.99307	0.372811	-0.99497	-0.46182	0.92795	-0.99296	-0.83501	0.995603	0.491058	-0.70036	-0.26483	0.544172	0.604529	0.152782	0.998914	-0.83224	NA
ggpps2g	0.596911	0.944755	0.767084	0.740435	-0.45542	-0.57744	-0.97231	0.32782	-0.56233	-0.13289	0.582748	0.979544	0.078893	0.553741	0.990144	0.9977735	0.845906	0.620445	-0.96451	NA
ggpps9g	-0.87969	-0.99484	-0.96615	-0.95489	0.037269	0.867998	0.782932	-0.69582	0.858718	0.53866	-0.87121	-0.80318	0.349081	-0.15071	-0.8386	-0.876474	-0.5419	-0.89341	0.985863	NA
ggr	-0.73233	-0.22265	-0.55395	-0.58725	-0.93468	0.748494	-0.33846	-0.90329	0.760565	0.970693	-0.74416	0.306991	0.999537	0.888177	0.247338	0.1752495	0.622514	-0.71181	0.157147	NA
psy1	0.58955	0.033294	0.385604	0.422705	0.985211	-0.60881	0.511144	0.805282	-0.6233	-0.90732	0.603625	-0.48229	-0.97553	-0.95932	-0.42699	-0.359184	-0.75992	0.565333	0.033426	NA
psy2	-0.20665	-0.72108	-0.42846	-0.39147	0.786015	0.18306	0.980926	0.097344	0.164946	-0.29381	-0.18946	-0.97392	-0.48859	-0.85124	-0.95796	-0.934213	-0.99143	-0.23558	0.765672	NA
pds	-0.69724	-0.97966	-0.84479	-0.8224	0.33438	0.679798	0.933135	-0.44922	0.666193	0.262079	-0.68456	-0.94457	0.052896	-0.43942	-0.96313	-0.980336	-0.76842	-0.7182	0.990858	NA
ziso	-0.52057	-0.9106	-0.70481	-0.67546	0.535387	0.499886	0.989687	-0.23952	0.483871	0.041145	-0.50552	-0.9939	-0.17026	-0.62799	-0.99883	-0.999678	-0.89138	-0.54567	0.936129	NA
zds	0.282422	0.772976	0.49771	0.462125	-0.73534	-0.25927	-0.99311	-0.01933	-0.24146	0.218276	0.265554	0.988664	0.418963	0.807663	0.977441	0.9592149	0.978196	0.31075	-0.81356	NA
crtiso	-0.34189	-0.81116	-0.551	-0.51671	0.691498	0.319188	0.998496	-0.04326	0.301703	-0.15679	-0.32535	-0.99612	-0.36133	-0.76919	-0.98874	-0.975022	-0.96329	-0.36961	0.84835	NA
lcyb1	0.766934	0.995049	0.895114	0.876297	-0.23619	-0.75128	-0.89145	0.538283	-0.73901	-0.35946	0.755561	0.906018	-0.1548	0.345194	0.930537	0.9549969	0.6989	0.78563	-0.99946	NA
lcyb2	-0.95785	-0.63052	-0.86481	-0.88447	-0.68141	0.964481	0.112166	-0.9999	0.969177	0.976979	-0.96274	-0.14514	0.910112	0.593724	-0.20626	-0.277821	0.21263	-0.94891	0.577355	NA
cycb	0.328872	-0.2591	0.100302	0.14057	0.992421	-0.35149	0.739217	0.597804	-0.36865	-0.74563	0.345385	-0.71642	-0.86927	-0.99996	-0.67174	-0.615314	-0.91623	0.300717	0.322931	NA
lcye	-0.24412	0.34345	-0.01197	-0.05252	-0.97768	0.267375	-0.79585	-0.52462	0.285053	0.683815	-0.26109	0.775275	0.822182	0.995232	0.734583	0.682575	0.948057	-0.21525	-0.40531	NA
zep	1	0.826913	0.972598	0.981227	0.442432	-0.99971	-0.3929	0.953652	-0.9991	-0.87451	0.999846	0.423252	-0.75271	-0.33754	0.478662	0.5420732	0.077034	0.99956	-0.78757	NA
vde	0.826913	1	0.934991	0.919838	-0.13845	-0.81315	-0.842	0.619374	-0.8023	-0.45042	0.816923	0.859471	-0.25222	0.250213	0.889537	0.920791	0.62436	0.843228	-0.99777	NA
crtrb1	0.972598	0.934991	1	0.999177	0.22181	-0.96673	-0.59593	0.85756	-0.96186	-0.73779	0.968371	0.622295	-0.57903	-0.10944	0.669673	0.7225894	0.306724	0.979066	-0.90926	NA
crtrb2	0.981227	0.919838	0.999177	1	0.261172	-0.9763	-0.56287	0.877715	-0.97216	-0.76456	0.977694	0.590037	-0.61162	-0.14966	0.639004	0.6939603	0.267872	0.986515	-0.89163	NA
cyp97a29	0.442432	-0.13845	0.22181	0.261172	1	-0.46387	0.650854	0.691785	-0.48009	-0.82186	0.458092	-0.62525	-0.92343	-0.99351	-0.57562	-0.513781	-0.86005	0.415638	0.204179	NA
cyp97c11	-0.99971	-0.81315	-0.96673	-0.9763	-0.46387	1	0.370665	-0.96061	0.999831	0.885926	-0.99998	-0.40134	0.768331	0.360082	-0.45741	-0.521705	-0.05303	-0.99856	0.772525	NA
ccd1b	-0.3929	-0.842	-0.59593	-0.56287	0.650854	0.370665	1	-0.09797	0.35352	-0.10241	-0.37671	-0.99945	-0.30967	-0.733	-0.99546	-0.985733	-0.94712	-0.42	0.8761	NA
ccd4b	0.953652	0.619374	0.85756	0.877715	0.691785	-0.96061	-0.09797	1	-0.96556	-0.97992	0.958782	0.131004	-0.91593	-0.60515	0.192275	0.2640821	-0.22656	0.944307	-0.56564	NA
pap3	-0.9991	-0.8023	-0.96186	-0.97216	-0.48009	0.999831	0.35352	-0.96556	1	0.894307	-0.99969	-0.38442	0.779974	0.37718	-0.44097	-0.505925	-0.03466	-0.9974	0.760715	NA
chrc	-0.87451	-0.45042	-0.73779	-0.76456	-0.82186	0.885926	-0.10241	-0.97992	0.894307	1	-0.88289	0.069277	0.977558	0.75172	0.007235	-0.066489	0.416192	-0.85974	0.389877	NA
nxs	0.999846	0.816923	0.968371	0.977694	0.458092	-0.99998	-0.37671	0.958782	-0.99969	-0.88289	1	0.407297	-0.76415	-0.354	0.463189	0.5272516	0.059536	0.998886	-0.77665	NA
DXR	0.423252	0.859471	0.622295	0.590037	-0.62525	-0.40134	-0.99945	0.131004	-0.38442	0.069277	0.407297	1	0.277881	0.709975	0.998073	0.9907838	0.935925	0.449939	-0.89164	NA
IDIF	-0.75271	-0.25222	-0.57903	-0.61162	-0.92343	0.768331	-0.30967	-0.91593	0.779974	0.977558	-0.76415	0.277881	1	0.87378	0.217732	0.1452027	0.598405	-0.73286	0.187133	NA
IDI5G	-0.33754	0.250213	-0.10944	-0.14966	-0.99351	0.360082	-0.733	-0.60515	0.37718	0.75172	-0.354	0.709975	0.87378	1	0.664904	0.6080425	0.912512	-0.30947	-0.31422	NA
GGPPS2	0.478662	0.889537	0.669673	0.639004	-0.57562	-0.45741	-0.99546	0.192275	-0.44097	0.007235	0.463189	0.998073	0.217732	0.664904	1	0.9972801	0.912264	0.504493	-0.91802	NA
GGPPS9G	0.542073	0.920791	0.722589	0.69396	-0.51378	-0.52171	-0.98573	0.264082	-0.50592	-0.06649	0.527252	0.990784	0.145203	0.608042	0.99728	1	0.879593	0.566759	-0.94475	NA
GGR	0.077034	0.62436	0.306724	0.267872	-0.86005	-0.05303	-0.94712	-0.22656	-0.03466	0.416192	0.059536	0.935925	0.598405	0.912512	0.912264	0.8795925	1	0.106573	-0.67506	NA
PDS	0.99956	0.843228	0.979066	0.986515	0.415638	-0.99856	-0.42	0.944307	-0.9974	-0.85974	0.998886	0.449939	-0.73286	-0.30947	0.504493	0.566759	0.106573	1	-0.80551	NA
ZDS	-0.78757	-0.99777	-0.90926	-0.89163	0.204179	0.772525	0.8761	-0.56564	0.760715	0.389877	-0.77665	-0.89164	0.187133	-0.31422	-0.91802	-0.944752	-0.67506	-0.80551	1	NA
CRTISO	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZEP	0.888458	0.476591	0.757409	0.783266	0.804676	-0.89924	0.072978	0.985386	-0.90713	-0.99956	0.896371	-0.03978	-0.97091	-0.73191	0.022306	0.0959325	-0.38915	0.874454	-0.41691	NA
VDE	0.978318	0.925447	0.999661	0.999894	0.247104	-0.97305	-0.57483	0.870653	-0.96865	-0.7551	0.974535	0.601718	-0.60005	-0.13527	0.650124	0.7043591	0.281857	0.984031	-0.89812	NA
CCD1B	0.76897	0.99536	0.896527	0.877825	-0.2331	-0.75337	-0.89	0.54096	-0.74115	-0.36242	0.75764	0.904668	-0.15794	0.342208	0.929368	0.954049	0.696622	0.787593	-0.99956	NA
CHRC	-0.86456	-0.9975	-0.9577	-0.94524	0.068165	0.852221	0.801803	-0.67327	0.842454	0.512338	-0.85561	-0.82123	0.319925	-0.18122	-0.85505	-0.890948	-0.56764	-0.87908	0.990574	NA
PAP3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCD4B	0.649174	0.964541	0.808228	0.783682	-0.39493	-0.63069	-0.95453	0.390199	-0.61631	-0.1988	0.635734	0.963913	0.012121	0.496877	0.978576	0.9910893	0.808388	0.671449	-0.97999	NA
GGPPS2G	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Beta carotene	-0.99946	-0.80798	-0.96443	-0.97436	-0.47167	0.999961	0.362457	-0.96303	0.999954	0.889983	-0.99988	-0.39324	0.773948	0.368298	-0.44954	-0.514158	-0.04422	-0.99804	0.766894	NA
Lutein	-0.38668	-0.83834	-0.59049	-0.55728	0.655964	0.364388	0.999977	-0.09125	0.347197	-0.10912	-0.37045	-0.9992	-0.31608	-0.73757	-0.99479	-0.984574	-0.94926	-0.41386	0.872826	NA
Violaxanthin	0.18979	0.70905	0.412855	0.375578	-0.79653	-0.16612	-0.97744	-0.11445	-0.14795	0.310212	0.172541	0.969874	0.503523	0.860141	0.952887	0.9279381	0.993528	0.218827	-0.75449	NA
Neoxanthin	-0.54586	-0.92254	-0.7257	-0.6972	0.509907	0.525547	0.984964	-0.26843	0.509809	0.070987	-0.53108	-0.99016	-0.14074	-0.60446	-0.99694	-0.99999	-0.87744	-0.57047	0.94622	NA
pif1	-0.7628	-0.26714	-0.59156	-0.62377	-0.91739	0.778128	-0.29494	-0.92202	0.789549	0.980696	-0.77402	0.263008	0.999881	0.866163	0.202628	0.1299006	0.585957	-0.74328	0.202286	NA
rap2.2	-0.99683	-0.86906	-0.98802	-0.99347	-0.36962	0.994622	0.464867	-0.92666	0.992549	0.833121	-0.99528	-0.49405	0.697907	0.26152	-0.54705	-0.60726	-0.15617	-0.99875	0.834138	NA
glk2	0.977196	0.92746	0.999786	0.999802	0.241917	-0.97181	-0.5792	0.868009	-0.96731	-0.75159	0.973322	0.605982	-0.59576	-0.12997	0.65418	0.7081466	0.286986	0.983064	-0.90046	NA
aprr2	-0.78094	-0.29454	-0.61433	-0.64582	-0.90566	0.795741	-0.26754	-0.9327	0.806746	0.985878	-0.79178	0.23536	0.999032	0.851543	0.174591	0.1015431	0.562585	-0.76207	0.23016	NA

	ZEP	VDE	CCD1B	CHRC	PAP3	CCD4B	GGPPS2G	Beta carotene	Lutein	Violaxanthin	Neoxanthin	*pif1*	*rap2.2*	*glk2*	*aprr2*
dxs	0.981741	0.88042	0.557853	-0.68808	NA	0.408734	NA	-0.968276897	-0.11137	-0.094343461	-0.287848357	-0.91401	-0.93407	0.87787	-0.92522
dxr	-0.96083	-0.91925	-0.62975	0.750137	NA	-0.48861	NA	0.986724614	0.199677	0.005052852	0.372229933	0.874123	0.962233	-0.91713	0.887632
hdr	0.148532	-0.51101	-0.85279	0.754088	NA	-0.92912	NA	0.290608059	0.9976	-0.990658792	0.968993255	-0.36667	0.396263	-0.5156	-0.33997
idi5g	0.992951	0.84371	0.496193	-0.63364	NA	0.341467	NA	-0.947604536	-0.039	-0.166296446	-0.21763497	-0.94102	-0.90572	0.840826	-0.9503
idi4g	0.438103	-0.22988	-0.65705	0.522569	NA	-0.77558	NA	-0.009540809	0.930985	-0.985985804	0.850386825	-0.62867	0.102858	-0.23508	-0.60621
idif	0.857327	0.98955	0.808235	-0.89489	NA	0.696435	NA	-0.995318917	-0.4448	0.252117747	-0.598262819	-0.71993	-0.99988	0.988764	-0.73945
ggpps2	0.850903	0.991255	0.815447	-0.90034	NA	0.705246	NA	-0.994049225	-0.45583	0.264051512	-0.608114843	-0.71131	-0.99999	0.990535	-0.73108
ggpps2g	0.162105	0.750133	0.971909	-0.91925	NA	0.997766	NA	-0.570216057	-0.97071	0.901013171	-0.99806412	0.063483	-0.6589	0.75366	0.034969
ggpps9g	-0.56331	-0.95911	-0.98047	0.999521	NA	-0.93279	NA	0.863583572	0.778715	-0.633860213	0.87863564	0.363516	0.914761	-0.96061	0.389962
ggr	-0.96317	-0.57542	-0.12782	0.290939	NA	0.04255	NA	0.754315654	-0.34481	0.529586672	-0.170808236	0.998947	0.675785	-0.57104	0.997231
psy1	0.894505	0.40948	-0.06302	-0.10379	NA	-0.23167	NA	-0.615781382	0.516935	-0.681160846	0.354971621	-0.97202	-0.52337	0.404593	-0.96492
psy2	0.26545	-0.40481	-0.78439	0.670348	NA	-0.87837	NA	0.174379392	0.982216	-0.999852024	0.932594737	-0.47505	0.283898	-0.40969	-0.44974
pds	-0.29047	-0.83059	-0.99442	0.963039	NA	-0.99789	NA	0.673300933	0.930687	-0.836137915	0.981216074	0.068316	0.752102	-0.83355	0.096768
ziso	-0.07064	-0.68612	-0.94614	0.879137	NA	-0.98739	NA	0.492226151	0.988697	-0.937098456	0.999553327	-0.15502	0.586902	-0.69	-0.12676
zds	-0.18935	0.474975	0.830433	-0.72625	NA	0.913015	NA	-0.250736844	-0.99388	0.995455791	-0.957930474	0.404885	-0.3579	0.479676	0.378618
crtiso	0.127547	-0.5291	-0.86366	0.767834	NA	-0.93675	NA	0.31081501	0.998843	-0.987547346	0.974010678	-0.34688	0.415627	-0.53364	-0.31997
lcyb1	0.386863	0.883212	0.999995	-0.98555	NA	0.985996	NA	-0.745425549	-0.88837	0.775619093	-0.956324719	-0.17005	-0.81559	0.885708	-0.19811
lcyb2	-0.98285	-0.87759	-0.55291	0.683753	NA	-0.4033	NA	0.966774292	0.105456	0.100260117	0.282150041	0.916404	0.931935	-0.87501	0.927457
cycb	0.725617	0.126155	-0.35083	0.19025	NA	-0.50483	NA	-0.359736491	0.743747	-0.864793441	0.611753629	-0.86153	-0.25264	0.120846	-0.84669
lcye	-0.66196	-0.03799	0.432221	-0.27627	NA	0.579149	NA	0.275865398	-0.79991	0.905787445	-0.679272645	0.81329	0.166135	-0.03264	0.796349
zep	0.888458	0.978318	0.76897	-0.86456	NA	0.649174	NA	-0.999459629	-0.38668	0.189789889	-0.545856888	-0.7628	-0.99683	0.977196	-0.78094
vde	0.476591	0.925447	0.99536	-0.9975	NA	0.964541	NA	-0.807981826	-0.83834	0.709049621	-0.922540512	-0.26714	-0.86906	0.92746	-0.29454
crtrb1	0.757409	0.999661	0.896527	-0.9577	NA	0.808228	NA	-0.964430814	-0.59049	0.412855267	-0.725699176	-0.59156	-0.98802	0.999786	-0.61433
crtrb2	0.783266	0.999894	0.877825	-0.94524	NA	0.783682	NA	-0.974357473	-0.55728	0.375578392	-0.697199921	-0.62377	-0.99347	0.999802	-0.64582
cyp97a29	0.804676	0.247104	-0.2331	0.068165	NA	-0.39493	NA	-0.47167074	0.655964	-0.796533491	0.509906791	-0.91739	-0.36962	0.241917	-0.90566
cyp97c11	-0.89924	-0.97305	-0.75337	0.852221	NA	-0.63069	NA	0.999961084	0.364388	-0.166120546	0.525546679	0.778128	0.994622	-0.97181	0.795741
ccd1b	0.072978	-0.57483	-0.89	0.801803	NA	-0.95453	NA	0.362457349	0.999977	-0.977436808	0.984963773	-0.29494	0.464867	-0.5792	-0.26754
ccd4b	0.985386	0.870653	0.54096	-0.67327	NA	0.390199	NA	-0.963027276	-0.09125	-0.114450645	-0.268428538	-0.92202	-0.92666	0.868009	-0.9327
pap3	-0.90713	-0.96865	-0.74115	0.842454	NA	-0.61631	NA	0.999954186	0.347197	-0.147954535	0.509809248	0.789549	0.992549	-0.96731	0.806746
chrc	-0.99956	-0.7551	-0.36242	0.512338	NA	-0.1988	NA	0.88998299	-0.10912	0.310212409	0.070987111	0.980696	0.833121	-0.75159	0.985878
nxs	0.896371	0.974535	0.75764	-0.85561	NA	0.635734	NA	-0.999882396	-0.37045	0.172540901	-0.531077745	-0.77402	-0.99528	0.973322	-0.79178
DXR	-0.03978	0.601718	0.904668	-0.82123	NA	0.963913	NA	-0.39324284	-0.9992	0.969873841	-0.990162984	0.263008	-0.49405	0.605982	0.23536
IDIF	-0.97091	-0.60005	-0.15794	0.319925	NA	0.012121	NA	0.773948193	-0.31608	0.503523259	-0.140739752	0.999881	0.697907	-0.59576	0.999032
IDI5G	-0.73191	-0.13527	0.342208	-0.18122	NA	0.496877	NA	0.368298021	-0.73757	0.860141295	-0.604456385	0.866163	0.26152	-0.12997	0.851543
GGPPS2	0.022306	0.650124	0.929368	-0.85505	NA	0.978576	NA	-0.449543133	-0.99479	0.952886651	-0.996937567	0.202628	-0.54705	0.65418	0.174591
GGPPS9G	0.095933	0.704359	0.954049	-0.89095	NA	0.991089	NA	-0.514158362	-0.98457	0.927938057	-0.999989833	0.129901	-0.60726	0.708147	0.101543
GGR	-0.38915	0.281857	0.696622	-0.56764	NA	0.808388	NA	-0.044220322	-0.94926	0.993527533	-0.877438416	0.585957	-0.15617	0.286986	0.562585
PDS	0.874454	0.984031	0.787593	-0.87908	NA	0.671449	NA	-0.998044973	-0.41386	0.218827438	-0.570468317	-0.74328	-0.99875	0.983064	-0.76207
ZDS	-0.41691	-0.89812	-0.99956	0.990574	NA	-0.97999	NA	0.766893508	0.872826	-0.754493316	0.946220019	0.202286	0.834138	-0.90046	0.23016
CRTISO	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZEP	1	0.774141	0.389793	-0.53748	NA	0.227662	NA	-0.903063955	0.079708	-0.281995886	-0.100419986	-0.97449	-0.84909	0.770743	-0.9805
VDE	0.774141	1	0.884698	-0.94989	NA	0.792633	NA	-0.970981814	-0.56929	0.389018375	-0.70755279	-0.61233	-0.9917	0.999986	-0.63465
CCD1B	0.389793	0.884698	1	-0.98608	NA	0.985461	NA	-0.747541218	-0.8869	0.773608251	-0.955390489	-0.17318	-0.81743	0.88718	-0.20122
CHRC	-0.53748	-0.94989	-0.98608	1	NA	-0.9435	NA	0.847572336	0.797751	-0.657483901	0.892986635	0.334523	0.901825	-0.95155	0.361288
PAP3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCD4B	0.227662	0.792633	0.985461	-0.9435	NA	1	NA	-0.623821028	-0.9525	0.870021625	-0.991679859	-0.00333	-0.70768	0.795884	-0.03187
GGPPS2G	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Beta carotene	-0.90306	-0.97098	-0.74754	0.847572	NA	-0.62382	NA	1	0.356158	-0.157414544	0.51802068	0.783639	0.993669	-0.96969	0.801053
Lutein	0.079708	-0.56929	-0.8869	0.797751	NA	-0.9525	NA	0.35615794	1	-0.978840363	0.983775168	-0.30138	0.45888	-0.57368	-0.27404
Violaxanthin	-0.282	0.389018	0.773608	-0.65748	NA	0.870022	NA	-0.157414544	-0.97884	1	-0.926247877	0.490116	-0.26736	0.393941	0.465034
Neoxanthin	-0.10042	-0.70755	-0.95539	0.892987	NA	-0.99168	NA	0.51802068	0.983775	-0.926247877	1	-0.12543	0.610836	-0.71132	-0.09706
pif1	-0.97449	-0.61233	-0.17318	0.334523	NA	-0.00333	NA	0.78363856	-0.30138	0.490115977	-0.125428252	1	0.708888	-0.60809	0.999592
rap2.2	-0.84909	-0.9917	-0.81743	0.901825	NA	-0.70768	NA	0.993669413	0.45888	-0.267361047	0.610836489	0.708888	1	-0.991	0.728733
glk2	0.770743	0.999986	0.88718	-0.95155	NA	0.795884	NA	-0.96968846	-0.57368	0.39394134	-0.711323261	-0.60809	-0.991	1	-0.63051
aprr2	-0.9805	-0.63465	-0.20122	0.361288	NA	-0.03187	NA	0.801052728	-0.27404	0.465033541	-0.097056151	0.999592	0.728733	-0.63051	1



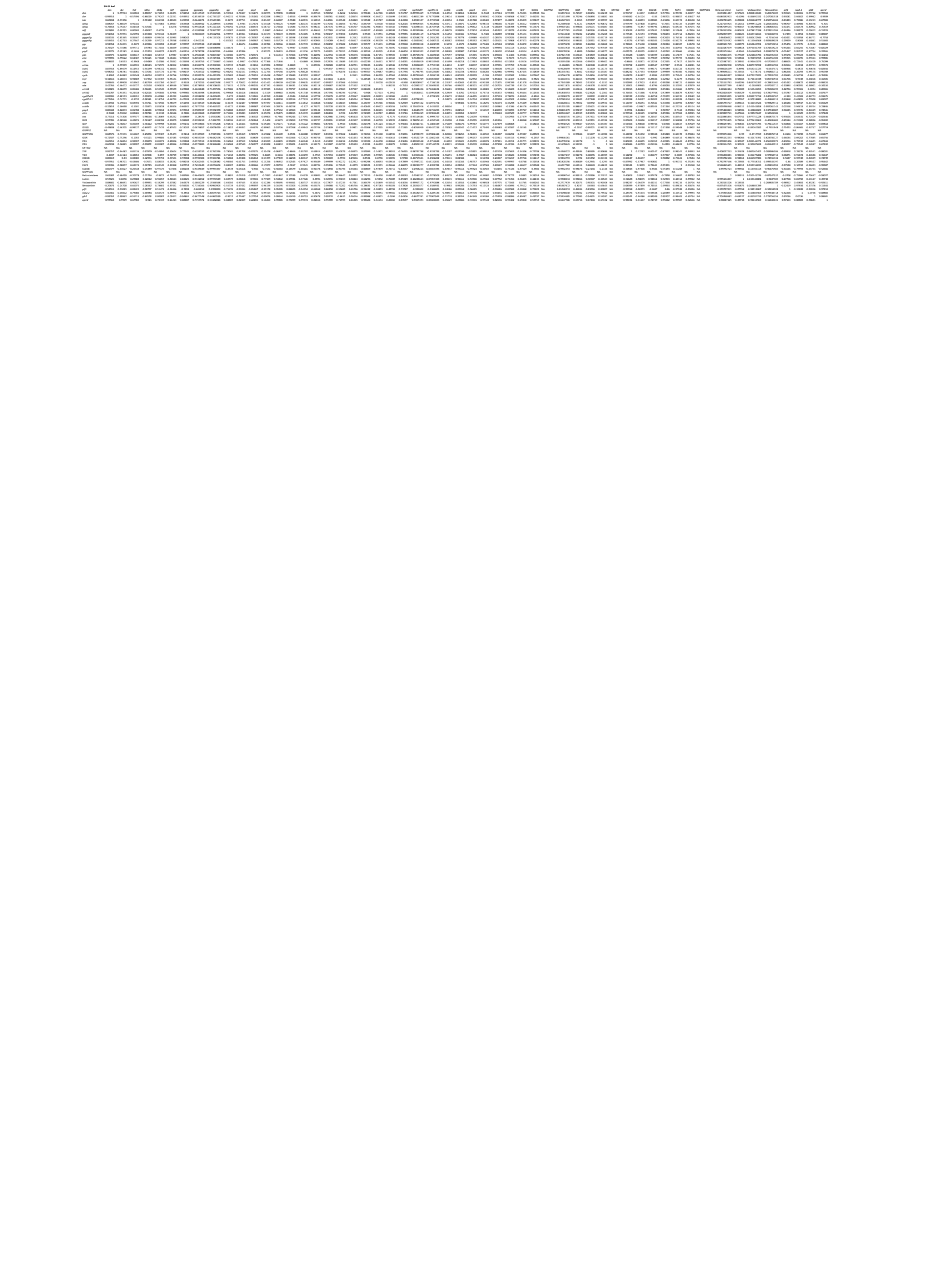


Table 5.6. Patterns of gene expression for carotenoid pathway transcripts in fruits of wild species.

Comparison of abundances of carotenogenic transcripts from 26, 29 and 39 dpa fruits of wild species and tomato (data are means ± SE (n = 3), $P \leq 0.05$) . The transcript levels are from Figure 5.6.

Table 5.7. Differentially expressed proteins identified in the fruits of wild species at different developmental stages using nanoLC-MS-MS.

Label-free quantitation was employed by matching retention times of the peaks and measuring area under the matched peaks using Sieve 2.1 software (Thermo Scientific) to identify the differentially expressed proteins in SP-SL, SG-SL, SH-SL pairs. Stringent selection criteria were imposed to identify these proteins (p value≤0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR=1%).

List of upregulated proteins in SP-SL

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO (SP/SL)	STD.DEV	P.VALUE	FOLD CHANGE (SP/SL)	P.MANCLASS
Sopim07g064170	Pectinesterase	5	2.50228306	0.784584721	1.74704E-05	2.50228306	cell wall
Solyc09g025210.2.1	Legumin 11S_globulin	4	5.321790659	2.409426112	9.9E-20	5.321790659	development storage proteins
Sopim09g025210	Legumin 11S_globulin	4	5.321790659	2.409426112	9.9E-20	5.321790659	development storage proteins
Solyc09g072560.2.1	Legumin 11S_globulin	2	7.643570817	3.919540151	2.79976E-10	7.643570817	development storage proteins
Sopim09g072560	Legumin 11S_globulin	2	7.643570817	3.919540151	2.79976E-10	7.643570817	development storage proteins
Sopim08g014000	Lipoxygenase	2	9.347445544	10.138859	0.00014757	9.347445544	hormone metabolism jasmonate
Sopim03g005580	Legumin 11S_globulin	2	10.24002128	8.349172057	6.89869E-06	10.24002128	development storage proteins
Sopim09g082340	Vicilin_like protein	12	35.83124346	10.12858165	9.9E-20	35.83124346	development storage proteins
Sopim07g044840	2 3_bisphosphoglycerate_independent phosphoglycerate mutase	10	4.284041612	1.2067872	9.9E-20	4.284041612	unknown
Sopim01g007320	ATP synthase subunit beta chloroplastic	10	7.670543083	1.584801056	9.9E-20	7.670543083	mitochondrial electron transport
Sopim06g005970	Beta_D_glucosidase	10	3.008550051	1.062888711	1.48306E-09	3.008550051	cell wall
Sopim01g007330	Ribulose bisphosphate carboxylase large chain	10	4.66657038	0.677794042	9.9E-20	4.66657038	PS Calvin cycle
Sopim10g085550	Enolase	9	4.313493467	0.995411393	9.9E-20	4.313493467	glycolysis
Sopim11g066100	heat shock protein	8	2.971498541	0.842317551	9.9E-20	2.971498541	abiotic stress heat
Sopim09g009020	Enolase	8	2.734156889	0.540234568	9.9E-20	2.734156889	glycolysis
Sopim03g118040	Calcium_binding protein Calnexin	7	4.812434198	1.093185741	9.9E-20	4.812434198	signaling calcium
Sopim09g009260	Fructose_bisphosphate aldolase	7	3.479084171	0.724523559	1.52101E-14	3.479084171	PS Calvin cycle
Sopim10g080940	Tubulin beta chain	7	4.76297149	2.056930407	4.73673E-06	4.76297149	cell organisation
Sopim12g010040	Leucyl aminopeptidase	7	3.795351344	0.711996763	9.9E-20	3.795351344	protein degradation
Sopim11g008870	Methylenetetrahydrofolate reductase	7	3.025005335	0.975861552	2.38698E-10	3.025005335	c1 metabolism
Sopim00g006800	Transaldolase	7	4.298358535	1.183952909	9.10383E-15	4.298358535	oxidative pentose phosphate pathway
Sopim10g055670	V_type ATP synthase beta chain	6	4.743295053	1.139651563	9.9E-20	4.743295053	mitochondrial electron transport
Sopim10g081510	5_methyltetrahydropteroyltriglutamate__homocysteine methyltransferase	6	5.055925543	2.020445184	9.9E-20	5.055925543	amino acid metabolism
Sopim12g010020	Leucyl aminopeptidase	6	104.1665616	59.31981861	1.16886E-08	104.1665616	protein degradation
Sopim09g025210	Legumin 11S_globulin	6	28.52092199	13.72092293	4.46952E-09	28.52092199	development storage proteins
Sopim04g050930	Phosphoglucomutase/phosphomannomutase family protein	6	4.505135779	1.870339716	1.43952E-07	4.505135779	glycolysis
Sopim10g083570	Fructose_bisphosphate aldolase	6	3.428036462	1.00949084	5.4734E-14	3.428036462	PS Calvin cycle
Sopim04g043540	Phosphoglucomutase	6	3.023743664	0.705418383	9.9E-20	3.023743664	unknown
Sopim02g091560	Serine hydroxymethyltransferase	5	4.234006077	1.556447416	2.42662E-06	4.234006077	PS Photorespiration
Sopim12g098490	Serine hydroxymethyltransferase	5	4.34522565	1.473775046	9.9E-20	4.34522565	c1 metabolism
Sopim12g099930	Serine_glyoxylate aminotransferase	5	7.861813776	2.992565481	4.21885E-15	7.861813776	PS Photorespiration
Sopim01g108450	Serine carboxypeptidase 1	5	2.294171018	1.297478191	5.93969E-14	2.294171018	protein degradation
Sopim03g114500	Enolase	5	4.594063939	1.458844081	5.54001E-14	4.594063939	glycolysis
Sopim12g099440	Fatty acid oxidation complex subunit alpha	5	4.75791328	2.136733046	2.46111E-07	4.75791328	lipid metabolism
Sopim11g069000	T_complex protein 1 subunit beta	5	3.640769737	1.367993346	3.62656E-07	3.640769737	protein folding
Sopim05g008460	ATP synthase subunit beta	5	3.622138982	1.174364772	9.9E-20	3.622138982	mitochondrial electron transport
Sopim02g087240	NADH_quinone oxidoreductase F subunit family protein	4	4.324843029	1.914775333	1.07205E-06	4.324843029	mitochondrial electron transport
Sopim09g092390	Adenosylhomocysteinase	4	3.450408156	0.73408149	9.9E-20	3.450408156	unknown
Sopim01g058390	Galactokinase	4	4.10410754	1.265127043	9.9E-20	4.10410754	cell wall
Sopim06g005940	Protein disulfide isomerase	4	4.765269565	2.832632418	0.000248642	4.765269565	amino acid metabolism
Sopim01g007500	Photosystem II CP47 chlorophyll apoprotein	4	3.961580566	1.071476366	2.33147E-15	3.961580566	PS Light reaction
Sopim08g014000	Lipoxygenase	4	17.31283138	10.1962995	1.01164E-07	17.31283138	hormone metabolism jasmonate
Sopim03g118910	T_complex protein 1 subunit delta	4	3.65143651	1.241748878	2.09832E-14	3.65143651	protein folding
Sopim09g072560	Legumin 11S_globulin	4	4.830505746	2.017130323	4.32987E-15	4.830505746	development storage proteins
Sopim04g082460	Catalase	4	24.55266097	8.359273464	9.9E-20	24.55266097	redox
Sopim06g083620	26S protease regulatory subunit 4	4	3.300677635	1.216957583	5.11007E-07	3.300677635	protein degradation
Sopim03g113800	Betaine aldehyde dehydrogenase	4	3.553101321	0.900614173	9.9E-20	3.553101321	fermentation
Sopim07g064170	Pectinesterase	4	4.10410754	1.265127043	9.9E-20	4.10410754	cell wall
Sopim01g005000	Glutamate decarboxylase	4	4.765269565	2.832632418	0.000248642	4.765269565	amino acid metabolism
Sopim09g065190	Ran GTPase_activating protein 1	4	3.638911577	1.931908503	0.000355149	3.638911577	signaling G proteins
Sopim07g062530	Phosphoenolpyruvate carboxylase 2	3	3.115527941	1.559968416	0.003555731	3.115527941	unknown
Sopim08g016170	3_oxoacyl_[Acyl carrier protein] synthase II	3	6.777179638	2.956368568	0.004931247	6.777179638	lipid metabolism
Sopim01g110450	NADP dependent sorbitol 6_phosphate dehydrogenase	3	4.5824	1.310025246	0.001776061	4.5824	minor CHO metabolism
Sopim03g114150	Aldehyde dehydrogenase	3	4.612598836	2.472277133	6.95891E-05	4.612598836	fermentation
Sopim03g025320	Hydroxycinnamoyl transferase	3	4.673237871	2.677342907	3.58291E-05	4.673237871	secondary metabolism
Sopim08g018530	Reductase	3	3.142900396	1.690245373	7.73435E-06	3.142900396	redox
Sopim01g005560	Isocitrate dehydrogenase	3	7.129204131	3.176595719	2.36166E-11	7.129204131	TCA
Sopim01g087260	Carotenoid cleavage dioxygenase 1B	3	6.210003236	2.799238098	2.11069E-10	6.210003236	hormone metabolism abscisic acid
Sopim10g079500	Inosine_5_apos_monophosphate dehydrogenase	3	3.33984798	1.145709101	0.000261952	3.33984798	nucleotide metabolism
Sopim07g055320	ATP_dependent Zn protease cell division protein FtsH homolog	3	4.145669527	2.470892067	0.000139695	4.145669527	protein degradation
Sopim05g053810	Serine hydroxymethyltransferase	3	5.444755027	3.352416254	3.09848E-05	5.444755027	c1 metabolism
Sopim11g066250	Serine carboxypeptidase	3	8.521350262	7.869981824	0.000301399	8.521350262	protein degradation serine protease
Sopim05g050970	Transketolase 1	3	3.062377097	1.470018485	3.21301E-08	3.062377097	PS calvin cycle transketolase
Sopim09g090150	Legumin 11S_globulin	3	28.30298264	14.3064917	1.54675E-05	28.30298264	development storage proteins
Sopim02g067080	UDP_D_glucose dehydrogenase	3	4.544329271	1.574726693	4.49632E-10	4.544329271	cell wall precursor synthesis.UGD
Sopim06g060290	Protein disulfide isomerase	3	7.60596207	4.964025896	1.70742E-05	7.60596207	redox thioredoxin
Sopim05g056110	T_complex protein 1 subunit gamma	3	3.005272849	1.554611001	6.95663E-06	3.005272849	protein folding
Sopim01g067750	Shikimate dehydrogenase	3	5.032230607	2.778638342	6.25572E-06	5.032230607	amino acid metabolism.synthesis.aromatic aa.chorismate dehydroquinate/shikimate dehydrogenase
Sopim11g008280	Serine carboxypeptidase	3	16.97312218	9.443282949	9.15887E-06	16.97312218	protein degradation.serine protease
Sopim07g006570	SI_RNase	3	29.92618791	6.285419832	4.26897E-07	29.92618791	RNA processing.ribonucleases
Sopim03g112070	Phosphoglycerate dehydrogenase	3	3.51033707	2.010823269	1.30376E-06	3.51033707	amino acid metabolism.synthesis.serine-alycine-cysteine group.serine phosphoglycerate dehydrogenase
Sopim06g076640	Tubulin beta chain	3	4.366702766	2.057720587	7.48446E-12	4.366702766	cell.organisation
Sopim11g069270	Beta_galactosidase	3	6.682599252	2.79442626	4.39294E-07	6.682599252	misc gluco-, galacto- and mannosidases.beta-galactosidase
Sopim02g082760	Catalase	3	4.366730935	4.868986831	2.26467E-05	4.366730935	redox.dismutases and catalases
Sopim12g017570	Rab GDP dissociation inhibitor	3	3.343702409	1.156995841	3.33067E-16	3.343702409	signalling.G-proteins
Sopim02g036350	1_aminocyclopropane_1_carboxylate oxidase	3	9.360008243	8.560938297	0.000102661	9.360008243	hormone metabolism.ethylene.synthesis-degradation
Sopim12g010030	Leucyl aminopeptidase	3	42.66260755	25.91052996	0.000347263	42.66260755	protein degradation
Sopim01g094200	NAD_dependent malic enzyme 2	3	3.53636976	1.699229148	1.11022E-16	3.53636976	TCA / org. transformation.other organic acid transformaitons.malic
Sopim01g106080	Methylmalonate_semialdehyde dehydrogenase	3	6.111391464	2.197184529	0.003729051	6.111391464	amino acid metabolism.degradation.branched-chain group valine
Sopim12g055800	V_type ATP synthase alpha chain	3	3.420113436	2.02999946	1.73717E-11	3.420113436	transport.p- and v-ATPases.H+-transporting two-sector ATPase
Sopim08g075210	Acyltransferase_like protein	3	16.18140206	8.192362818	1.01217E-05	16.18140206	secondary metabolism.phenylpropanoids
Sopim08g006890	Tubulin alpha_3 chain	3	4.139159417	1.098979141	9.9E-20	4.139159417	cell.organisation
Sopim11g005640	Ubiquitin	3	4.96562129	1.887082282	5.2375E-11	4.96562129	protein degradation.ubiquitin.ubiquitin
Sopim03g122310	Aldehyde dehydrogenase 7b	2	2.893362786	1.393817251	1.32073E-08	2.893362786	TCA / org. transformation.other organic acid transformaitons.misc
Sopim06g063370	Chlorophyll a_b binding protein 1A_ chloroplastic	2	13.74161408	5.467633303	0.000909333	13.74161408	PS.lightreaction photosystem II.LHC-II
Sopim05g009190	Cysteinyl tRNA synthetase	2	5.217481938	3.493738856	0.0011367	5.217481938	protein aa activation cysteine-tRNA ligase
Sopim03g112910	Pantothenate kinase	2	4.602176393	3.188804292	0.007898019	4.602176393	Co-factor and vitamine metabolism.pantothenate.pantothenate kinase (PANK)
Sopim01g111440	Senescence_associated protein 12	2	2.846581825	2.005183898	0.015248131	2.846581825	development unspecified
Sopim12g095760	Diphosphate__fructose_6_phosphate 1_phosphotransferase	2	5.194906176	2.76426201	6.35467E-09	5.194906176	not assigned.unknown
Sopim12g094640	Glyceraldehyde_3_phosphate dehydrogenase B	2	7.553741335	7.55903	0.013351764	7.553741335	PS.calvin cycle GAP
Sopim04g063280	Vacuolar protein sorting_associated protein 27	2	3.946030881	2.893253757	4.67187E-05	3.946030881	cell.vesicle transport
Sopim09g091180	chaperonin	2	3.530603661	2.157265138	3.69511E-06	3.530603661	protein.folding
Sopim01g111630	Glycolate/hydroxypyruvate reductase B	2	3.462289823	1.97317205	0.001963019	3.462289823	PS.photorespiration.hydroxypyruvate reductase
Sopim11g066720	Bifunctional polymyxin resistance arnA protein	2	3.171972366	2.574442753	0.000230035	3.171972366	cell wall.precursor synthesis.AXS
Sopim01g009990	Peptidyl_prolyl cis_trans isomerase	2	7.150649027	3.560611697	9.92662E-09	7.150649027	cell.cycle.peptidylprolyl isomerase
Sopim09g090700	Succinate semialdehyde dehydrogenase	2	2.765006726	1.505819746	0.000442021	2.765006726	TCA / org. transformation.other organic acid transformaitons.misc
Sopim11g065670	Ribosomal protein L12	2	7.647910717	6.546793741	0.009123812	7.647910717	protein.synthesis.ribosomal protein.eukaryotic 60S subunit.L12
Sopim11g007990	Malate dehydrogenase	2	4.427878613	4.451630877	0.004974057	4.427878613	TCA / org. transformation.other organic acid transformaitons.cyt MDH
Sopim09g083410	Amidase hydantoinase/carbamoylase family protein expressed	2	3.803402486	2.220056664	1.58677E-06	3.803402486	protein.degradation
Sopim04g053120	4_alpha_glucanotransferase	2	6.763076279	4.659237283	0.004919257	6.763076279	maior CHO metabolism.degradation.starch.D enzyme
Sopim09g091840	Glutathione_disulfide reductase	2	4.033816107	2.250174104	1.27763E-07	4.033816107	redox.ascorbate and glutathione.glutathione
Sopim07g064810	Imidazole glycerol phosphate synthase subunit hisF	2	4.476278539	2.011232887	0.003553292	4.476278539	amino acid metabolism.synthesis.histidine.N-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide
Sopim01g088080	T_complex protein theta subunit	2	3.463845147	1.872003189	5.49824E-05	3.463845147	protein.folding
Sopim12g008510	Hexokinase	2	6.125648298	3.632887022	1.6704E-05	6.125648298	major CHO metabolism.degradation.sucrose.hexokinase
Sopim12g009410	Pyruvate dehydrogenase E1 component alpha subunit	2	2.694861737	1.572541095	0.002154055	2.694861737	TCA / org. transformation.TCA.pyruvate DH.E1
Sopim07g062650	Malate dehydrogenase	2	2.625804777	1.74623285	0.001295196	2.625804777	TCA / org. transformation. TCA.malate DH
Sopim01g110360	Fructose_bisphosphate aldolase	2	4.706784373	3.207610784	0.007023894	4.706784373	PS.calvin cycle aldolase
Sopim10g051340	Adenylyl cyclase_associated protein	2	2.623245679	1.522457314	8.38467E-05	2.623245679	DNA.unspecified
Sopim07g056540	L_lactate dehydrogenase	2	7.149441736	4.701720526	2.26485E-06	7.149441736	PS.photorespiration.glycolate oxydase
Sopim01g110360	Fructose_bisphosphate aldolase	2	4.706784373	3.207610784	0.007023894	4.706784373	PS.calvin cycle aldolase
Sopim03g005780	Chlorophyll a_b binding protein 3C_like	2	4.669417132	4.250687214	0.00093012	4.669417132	PS.lightreaction photosystem II.LHC-II
Sopim08g067320	Chlorophyll a_b binding protein	2	4.669417132	4.250687214	0.00093012	4.669417132	PS.lightreaction photosystem II.LHC-II
Sopim01g007530	Cytochrome b6	2	6.270972844	4.345036645	2.21155E-07	6.270972844	PS.lightreaction.cytochrome b6/f.cytochrome b6 (CYB6)
Sopim04g008740	Pyruvate kinase	2	3.344867958	1.506562408	5.01814E-06	3.344867958	glycolysis.plastid branch.pyruvate kinase (PK), lipid metabolism.FA synthesis and FA elongation.pyruvate kinase
Sopim10g085790	Atp_dependent RNA helicase	2	3.535208681	2.715216552	0.000165958	3.535208681	RNA processing.RNA helicase, DNA.synthesis/chromatin structure
Sopim05g010260	6_phosphogluconate dehydrogenase decarboxylating	2	5.822342337	3.940219113	0.00859185	5.822342337	OPP.oxidative PP 6-phosphogluconate dehydrogenase
Sopim11g039830	Glycyl_tRNA synthetase	2	5.12543825	2.494046231	0.004873332	5.12543825	protein aa activation.glycine-tRNA ligase
Sopim01g109410	Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit	2	4.800449378	2.891246952	3.81809E-07	4.800449378	protein.glycosylation
Sopim03g065340	Phosphoryl ase	2	5.577178337	3.523833734	0.00216482	5.577178337	major CHO metabolism.degradation.starch.starch phosphorylase
Sopim03g113790	Mannose_1_phosphate guanyltransferase	2	3.519826817	2.063064152	0.000505949	3.519826817	cell wall.precursor synthesis
Sopim03g121270	IAA_amino acid hydrolase	2	3.263489505	2.663421372	0.001759234	3.263489505	hormone metabolism.auxin.synthesis-degradation
Sopim10g018300	Transketolase 1	2	3.582418219	2.849490992	0.012267039	3.582418219	PS.calvin cycle transketolase
Sopim01g090750	T_complex protein 1 subunit alpha	2	2.307777517	1.20307245	1.9085E-05	2.307777517	protein.folding
Sopim04g054740	Inositol_3_phosphate synthase	2	21.75938752	11.15727118	0.003206508	21.75938752	minor CHO metabolism.myo-inositol.InsP Synthases
Sopim02g069460	Photosystem I reaction center subunit III	2	4.355801642	1.89975629	1.27084E-08	4.355801642	PS.lightreaction photosystem I.PSI polypeptide subunits
Sopim03g111730	Cathepsin B_like cysteine proteinase	2	40.46617405	22.5021449	3.70348E-10	40.46617405	protein.degradation.cysteine protease
Sopim03g121070	Hexokinase	2	3.13234973	1.77012571	2.33809E-06	3.13234973	major CHO metabolism.degradation.sucrose.hexokinase
Sopim06g063240	Os03g0169000 protein (Fragment)	2	2.612627956	1.415361533	0.009674688	2.612627956	hormone metabolism.auxin.induced-regulated-responsive-activated
Sopim02g063150	Ribulose bisphosphate carboxylase small chain	2	8.101970565	7.750914208	1.42908E-05	8.101970565	PS.calvin cycle rubisco small subunit
Sopim09g007250	60S ribosomal protein L4/L1	2	4.133036727	1.182781535	9.9E-20	4.133036727	protein.synthesis.ribosomal protein.eukaryotic 60S subunit.L4/L1
Sopim12g056120	6_phosphogluconate dehydrogenase decarboxylating	2	5.736338291	3.048073676	0.000562917	5.736338291	OPP.oxidative PP 6-phosphogluconate dehydrogenase
Sopim02g093830	Glucose_6_phosphate 1_dehydrogenase	2	3.400475936	2.151532763	2.62194E-05	3.400475936	OPP.oxidative PP G6PD
Sopim12g044740	Ubiquitin carboxyl_terminal hydrolase	2	6.166604842	3.138536701	8.74975E-06	6.166604842	protein.degradation.ubiquitin.ubiquitin protease
Sopim04g008730	Alpha_galactosidase 1	2	7.98405987	8.056080451	0.004743098	7.98405987	minor CHO metabolism.galactose alpha-galactosidases
Sopim11g069720	26S protease regulatory subunit 6B homolog	2	3.157461054	1.667103404	7.95253E-13	3.157461054	protein.degradation.AAA type, protein degradation.ubiquitin.proteasom, cell.division
Sopim09g009530	Hydrolase alpha/beta fold family protein	2	13.27488879	8.702998516	1.6106E-06	13.27488879	not assigned.unknown
Sopim06g064650	11_beta_hydroxysteroid dehydrogenase_like	2	81.19123739	85.25447285	0.009956089	81.19123739	misc.short chain dehydrogenase/reductase (SDR)
Sopim08g079260	Serine/threonine_protein phosphatase	2	3.526457382	1.290801147	4.40886E-05	3.526457382	redox.thioredoxin
Sopim07g065090	Polygalacturonase inhibitor protein	2	13.99365342	5.215062283	9.9E-20	13.99365342	signalling.receptor kinases.leucine rich repeat XI
Sopim03g034220	Ribulose bisphosphate carboxylase small chain	2	6.108677396	5.650391528	1.14156E-05	6.108677396	PS.calvin cycle rubisco small subunit
Sopim07g064190	Pectinesterase	2	3.685454893	1.414705416	4.62037E-05	3.685454893	cell wall.pectin*esterases.PME
Sopim12g011000	Citrate synthase	2	9.166105542	5.221471894	8.35192E-05	9.166105542	gluconeogenesis' glyoxylate cycle.citrate synthase
Sopim04g081400	Hexokinase 1	2	6.47693283	4.033232399	0.002363974	6.47693283	major CHO metabolism.degradation.sucrose.hexokinase
Sopim05g009530	Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex	2	6.461507513	3.141079816	2.32181E-11	6.461507513	TCA / org. transformation.TCA.pyruvate DH.E2
Sopim11g056680	LRR receptor_like serine/threonine_protein kinase	2	3.853096031	1.582579303	0.00023421	3.853096031	signalling.receptor kinases.leucine rich repeat XI
Sopim12g099260	ATP citrate lyase a_subunit	2	8.765092124	5.539804007	0.000165777	8.765092124	TCA / org. transformation.other organic acid transformaitons.atp-citrate lyase
Sopim02g078360	Thioredoxin family protein	2	8.948759879	2.795295453	0.001130167	8.948759879	redox.thioredoxin
Sopim09g065470	Vicilin (Fragment)	2	48.75390342	32.90157116	9.12166E-07	48.75390342	development storage proteins
Sopim12g096000	ATP_dependent RNA helicase eIF4A	2	3.688269974	2.226754	1.81302E-11	3.688269974	RNA.processing.RNA helicase, DNA.synthesis/chromatin structure
Sopim08g082820	Heat shock protein	2	5.046185191	4.21606163	0.002362331	5.046185191	stress.abiotic heat
Sopim04g005160	6_phosphogluconate dehydrogenase decarboxylating	2	4.771463278	4.350326283	0.001670622	4.771463278	OPP.oxidative PP 6-phosphogluconate dehydrogenase
Sopim01g100360	Dihydrolipoyl dehydrogenase	2	7.015870598	2.571533619	9.95488E-12	7.015870598	lipid metabolism.FA synthesis and FA elongation.pyruvate DH, redox.ascorbate and glutathione.glutathione
Sopim02g088690	UDP_glucose 6_dehydrogenase	2	3.979633412	1.789579682	1.87475E-08	3.979633412	cell wall.precursor synthesis.UGD
Sopim03g119080	Beta_glucosidase	2	9.753243295	8.984829551	0.001591736	9.753243295	misc gluco-, galacto- and mannosidases
Sopim01g079090	Protoporphyrinogen oxidase	2	3.32298526	1.461849507	3.45205E-05	3.32298526	tetrapyrrole synthesis.protoporphyrin IX oxidase
Sopim07g062130	Dtdp_glucose 4 6_dehydratase	2	4.656174882	2.574792646	0.004084165	4.656174882	cell wall.precursor synthesis.UDP-glucose 4,6-dehydratase
Sopim09g008670	Threonine ammonia_lyase biosynthetic	2	7.620412166	6.607545274	0.000237077	7.620412166	amino acid metabolism.degradation.aspartate family.threonine
Sopim07g066610	Phosphoglycerate kinase	2	3.582710002	1.475416985	3.77635E-11	3.582710002	PS.calvin cycle.phosphoglycerate kinase
Sopim11g069430	Aquaporin 1	2	5.720691626	2.768791014	0.000288206	5.720691626	transport.Major Intrinsic Proteins.PIP
Sopim12g096220	60S ribosomal protein L7	5	4.955738398	2.507045203	5.45667E-07	4.955738398	signalling.G-proteins

Sopim09g025210	Legumin 11S_globulin	5	81.06218278	34.23499311	9.9E-20	81.06218278	development.storage proteins
Sopim09g072560	Legumin 11S_globulin	4	9.831896551	5.098000888	2.12719E-13	9.831896551	development.storage proteins
Sopim05g041910	Membrane protein	3	3.48077309	1.723286038	0.000724148	3.48077309	hormone metabolism.auxin.induced-regulated-responsive-activated
Sopim07g008370	60S ribosomal protein L7	3	4.955738398	3.23658144	6.12705E-05	4.955738398	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L7
Sopim09g090150	Legumin 11S_globulin	2	202.0429052	244.153671	3.55428E-10	202.0429052	development.storage proteins
Sopim03g005580	Legumin 11S_globulin	2	7.318241495	13.32268449	0.003588108	7.318241495	development.storage proteins
Sopim09g082340	Vicilin_like protein	11	12.65137504	10.90655436	9.9E-20	12.65137504	development.storage proteins
Sopim08g007620	Subtilisin_like protease	2	2.753112801	2.167573005	0.001927192	2.753112801	protein.degradation.subtilases
Sopim01g006540	Lipoxygenase	2	4.157298567	4.131525261	2.56261E-06	4.157298567	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Sopim09g025210	Legumin 11S_globulin	27	5.500425807	2.758397246	9.9E-20	5.500425807	development.storage proteins
Sopim09g090150	Legumin 11S_globulin	8	82.6069646	20.48787954	9.9E-20	82.6069646	development.storage proteins
Sopim03g005580	Legumin 11S_globulin	7	1513.742671	2120.448177	9.9E-20	1513.742671	development.storage proteins
Sopim09g082340	Vicilin_like protein	5	7.01276248	5.692187031	9.9E-20	7.01276248	development.storage proteins
Sopim01g098850	Short_chain dehydrogenase/reductase family protein	3	5.849076428	3.000058807	9.9E-20	5.849076428	misc.short chain dehydrogenase/reductase (SDR)
Sopim01g065490	Aldo/keto reductase	3	8.19232186	4.822511927	3.18653E-10	8.19232186	hormone metabolism.auxin.induced-regulated-responsive-activated
Sopim11g066130	Thaumatin_like protein	2	10.40263453	15.76734627	0.01594545	10.40263453	stress.biotic
Sopim09g072560	Legumin 11S_globulin	38	8.323596149	3.549591362	9.9E-20	8.323596149	development.storage proteins
Sopim09g025210	Legumin 11S_globulin	29	9.86241371	7.941229389	9.9E-20	9.86241371	development.storage proteins
Sopim03g005580	Legumin 11S_globulin	17	55.11944106	78.61489956	9.9E-20	55.11944106	development.storage proteins
Sopim03g083910	Acid beta_fructofuranosidase	6	7.324459102	3.468358726	9.9E-20	7.324459102	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Sopim09g072900	Dienelactone hydrolase family protein	4	14.00486233	20.97979952	9.9E-20	14.00486233	misc.misc2
Sopim02g080880	Aspartic proteinase	4	164.9848045	203.9030197	4.30989E-13	164.9848045	protein.degradation.aspartate protease
Sopim05g054760	Dehydroascorbate reductase (Fragment)	4	27.32247835	36.63517387	9.9E-20	27.32247835	redox.ascorbate and glutathione.ascorbate
Sopim07g041490	Stress responsive alpha_beta barrel domain protein	4	67.88120324	69.16699894	1.62093E-13	67.88120324	not assigned.unknown
Sopim01g097460	Ribose_5_phosphate isomerase	3	5.224460835	4.003410643	5.59847E-08	5.224460835	OPP.non-reductive PP.ribose 5-phosphate isomerase
Sopim07g009380	Xyloglucan endotransglucosylase/hydrolase 2	3	9.765219934	9.102343912	3.34558E-11	9.765219934	cell wall.modification
Sopim03g034220	Ribulose bisphosphate carboxylase small chain	3	14.72565296	12.00674756	9.9E-20	14.72565296	PS.calvin cycle.rubisco small subunit
Sopim02g063070	14_3_3 protein beta/alpha_1	3	13.79139172	18.55480305	3.9091E-13	13.79139172	signalling.14-3-3 proteins
Sopim11g069270	Beta_galactosidase	3	3.538526844	4.142898572	2.77417E-10	3.538526844	misc.gluco-, galacto- and mannosidases.beta-galactosidase
Sopim12g006140	Chlorophyll a_b binding protein 37_ chloroplastic	2	154.5831809	45.20487159	1.5099E-14	154.5831809	PS.lightreaction.photosystem II.LHC-II
Sopim06g050980	Ferritin	2	4.043592902	6.076481323	5.21288E-06	4.043592902	metal handling.binding, chelation and storage
Sopim06g073300	60S ribosomal protein L27	2	13.32290768	14.49320898	3.5459E-08	13.32290768	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L27
Sopim02g084440	Fructose_bisphosphate aldolase	2	46.4234859	46.77935169	3.59712E-14	46.4234859	PS.calvin cycle.aldolase
Sopim04g081970	Thioredoxin	2	13.91191167	13.25772716	2.19434E-07	13.91191167	redox.thioredoxin
Sopim09g090980	Major allergen Mal d 1	2	8.849743905	5.247083324	5.43027E-10	8.849743905	RNA.processing.ribonucleases
Sopim12g096930	Caleosin	2	60.00875292	68.80716884	8.30469E-12	60.00875292	development.unspecified
Sopim10g008010	Proteasome subunit alpha type	2	7.317167763	6.198724123	1.31806E-12	7.317167763	protein.degradation.ubiquitin.proteasom
Sopim09g072560	Legumin 11S_globulin	24	12.39343564	13.2152452	9.9E-20	12.39343564	development.storage proteins
Sopim09g025210	Legumin 11S_globulin	10	22.92220759	31.80061644	9.9E-20	22.92220759	development.storage proteins
Sopim03g005580	Legumin 11S_globulin	9	65.24662151	81.65156256	9.9E-20	65.24662151	development.storage proteins
Sopim07g044860	Oxygen_evolving enhancer protein 2_ chloroplastic	3	3.579574929	1.987840904	9.9E-20	3.579574929	PS.lightreaction.photosystem II.PSII polypeptide subunits
Sopim01g006900	Phosphatidylglycerol/phosphatidylinositol transfer protein	2	3.236585675	2.140049378	9.52009E-07	3.236585675	not assigned.unknown
Sopim09g025210	Legumin 11S_globulin	7	5.892931188	5.671308671	9.9E-20	5.892931188	development.storage proteins
Sopim04g007770	Major latex_like protein	2	5.528898002	8.454097472	3.03437E-11	5.528898002	not assigned.unknown
Sopim03g083910	Acid beta_fructofuranosidase	10	5.283271571	0.693927296	9.9E-20	5.283271571	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Solyc03g083910.2.1	Acid beta_fructofuranosidase	5	5.944118738	0.837447513	9.9E-20	5.944118738	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Sopim09g025210	Legumin 11S_globulin	4	7.631859441	4.486130882	3.8301E-11	7.631859441	development.storage proteins
Sopim12g013690	Monooxygenase FAD_binding protein	3	3.352310392	0.776900555	8.28846E-10	3.352310392	misc.oxidases - copper, flavone etc.
Sopim09g072560	Legumin 11S_globulin	3	5.053522095	2.950273181	5.87308E-13	5.053522095	development.storage proteins
Sopim03g005580	Legumin 11S_globulin	3	9.4813748	3.949340503	6.06617E-09	9.4813748	development.storage proteins
Sopim09g082340	Vicilin_like protein	3	27.1761561	11.48492177	4.6152E-13	27.1761561	development.storage proteins
Sopim06g073740	Beta_D_glucosidase	3	2.069062634	0.790124956	9.9E-20	2.069062634	cell wall.degradation.cellulases and beta -1,4-glucanases
Sopim01g099190	Lipoxygenase	3	9.341564342	9.155426294	9.9E-20	9.341564342	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Sopim01g096450	Aspartic proteinase nepenthesin_1	2	8.459850536	9.866911172	0.007561492	8.459850536	RNA.regulation of transcription.unclassified
Sopim01g098850	Short_chain dehydrogenase/reductase family protein	2	5.557281003	4.10366326	6.18825E-05	5.557281003	misc.short chain dehydrogenase/reductase (SDR)
Sopim08g013860	NAD_dependent malic enzyme 2	2	3.453164669	3.447285335	1.38367E-09	3.453164669	TCA / org. transformation.other organic acid transformaitons.malic
Sopim10g076510	Pyruvate decarboxylase	2	13.09225672	18.48505743	3.88354E-08	13.09225672	fermentation.PDC
Sopim03g097700	O_methyltransferase	2	5.532812495	1.217749133	9.9E-20	5.532812495	secondary metabolism.phenylpropanoids
Sopim08g006770	Anthocyanidin synthase	2	13.7967221	4.692886135	4.79081E-06	13.7967221	hormone metabolism.ethylene.synthesis-degradation
Sopim03g083910	Acid beta_fructofuranosidase	14	5.627020087	0.366745506	9.9E-20	5.627020087	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Sopim09g082340	Vicilin_like protein	11	17.06641682	5.533543654	9.9E-20	17.06641682	development.storage proteins
Sopim09g072560	Legumin 11S_globulin	7	176.9490558	318.3734605	9.9E-20	176.9490558	development.storage proteins
Sopim10g076510	Pyruvate decarboxylase	6	6.057272353	2.692021805	7.46603E-12	6.057272353	fermentation.PDC
Sopim02g082760	Catalase	6	3.671048742	1.035718233	8.88678E-12	3.671048742	redox.dismutases and catalases
Solyc03g083910.2.1	Acid beta_fructofuranosidase	4	5.555138911	0.382914853	9.9E-20	5.555138911	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Sopim08g075210	Acyltransferase_like protein	4	4.090075804	0.92513968	5.17364E-14	4.090075804	secondary metabolism.phenylpropanoids
Sopim08g006770	_Anthocyanidin synthase	4	9.271557197	4.482255576	1.79994E-06	9.271557197	hormone metabolism.ethylene.synthesis-degradation
Sopim01g005560	Isocitrate dehydrogenase	4	3.365561973	1.073401644	1.77636E-15	3.365561973	TCA / org. transformation.TCA.IDH
Sopim02g079170	NADH dehydrogenase like protein	3	2.577000584	0.947669515	0.000818709	2.577000584	mitochondrial electron transport / ATP synthesis.NADH-DH.type II.external
Sopim01g111970	Laccase 1a	3	2.931073355	1.480333149	2.78179E-08	2.931073355	misc.oxidases - copper, flavone etc.
Sopim04g015200	6_phosphofructokinase 2	3	4.047680544	2.212974667	9.9E-20	4.047680544	glycolysis.plastid branch.phosphofructokinase (PFK)
Sopim01g098850	Short_chain dehydrogenase/reductase family protein	3	10.9694745	11.72621427	9.9E-20	10.9694745	misc.short chain dehydrogenase/reductase (SDR)
Sopim09g066150	Cytochrome P450	3	2.885667476	0.601094422	9.9E-20	2.885667476	misc.cytochrome P450
Sopim10g085880	UDP_glucosyltransferase family 1 protein	3	3.180538756	1.297325307	8.4404E-11	3.180538756	misc.UDP glucosyl and glucoronyl transferases
Sopim09g008770	Group 3 late embryogenesis abundant protein	3	84.24238034	167.2906587	1.11022E-16	84.24238034	development.late embryogenesis abundant
Sopim06g073740	Beta_D_glucosidase	3	5.652084773	2.841566479	2.22045E-16	5.652084773	cell wall.degradation.cellulases and beta -1,4-glucanases
Sopim01g099190	Lipoxygenase	3	55.48009521	77.96839331	9.9E-20	55.48009521	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Sopim03g097700	O_methyltransferase	3	11.78543617	1.886950233	9.9E-20	11.78543617	secondary metabolism.phenylpropanoids
Sopim01g104850	Serine carboxypeptidase F13S12.6	3	3.267167195	1.239280475	0.005178784	3.267167195	protein.degradation.serine protease
Sopim09g065470	Vicilin (Fragment)	3	21.39062455	4.562614725	9.9E-20	21.39062455	development.storage proteins
Solyc03g097700.2.1	O_methyltransferase	2	11.78540057	1.886950233	9.9E-20	11.78540057	secondary metabolism.phenylpropanoids
Sopim01g096450	Aspartic proteinase nepenthesin_1	2	3.795309609	1.162683026	8.68194E-14	3.795309609	RNA.regulation of transcription.unclassified
Sopim07g006790	Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex	2	4.017734743	1.94516025	6.98468E-05	4.017734743	TCA / org. transformation.TCA.pyruvate DH.E2
Sopim08g066240	Decarboxylase family protein	2	6.117501566	3.140112485	7.20001E-07	6.117501566	amino acid metabolism.degradation.histidine
Sopim04g015620	Os01g0611000 protein (Fragment)	2	34.18605765	36.29677069	1.0979E-09	34.18605765	not assigned.unknown
Sopim08g074620	Polyphenol oxidase	2	16.44092064	13.68895172	0.005310289	16.44092064	not assigned.unknown
Sopim08g081530	Reductase	2	5.944883612	3.454341981	9.9E-20	5.944883612	redox.ascorbate and glutathione.ascorbate
Sopim12g055800	V_type ATP synthase alpha chain	2	2.548973347	1.8872843	2.67439E-10	2.548973347	transport.p- and v-ATPases.H+-transporting two-sector ATPase
Sopim09g025210	Legumin 11S_globulin	2	4.724034917	3.166660289	0.000116813	4.724034917	development.storage proteins
Sopim01g088400	CER1	2	34.14534418	29.62444312	1.40835E-07	34.14534418	secondary metabolism.wax
Sopim03g111010	Glyceraldehyde_3_phosphate dehydrogenase	2	10.40613066	5.019839655	3.28864E-06	10.40613066	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Sopim01g006290	Peroxidase	2	2.926811039	1.036025147	4.79761E-06	2.926811039	misc.peroxidases
Sopim03g005580	Legumin 11S_globulin	2	23.78244802	9.026833213	6.9974E-12	23.78244802	development.storage proteins
Sopim09g025210	Legumin 11S_globulin	23	4.799228629	1.41162602	9.9E-20	4.799228629	development.storage proteins
Sopim09g072560	Legumin 11S_globulin	12	5.433771819	1.955815227	9.9E-20	5.433771819	development.storage proteins
Sopim09g082340	Vicilin_like protein (Fragment)	12	12.72775628	6.315392212	9.9E-20	12.72775628	development.storage proteins
Sopim03g097700	O_methyltransferase	8	13.37075693	2.798186409	9.9E-20	13.37075693	secondary metabolism.phenylpropanoids
Sopim03g083910	Acid beta_fructofuranosidase	6	5.231461928	0.668872697	9.9E-20	5.231461928	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Sopim04g012110	Receptor like kinase_ RLK_	5	2.463077788	0.547117526	3.15515E-05	2.463077788	signalling.receptor kinases.leucine rich repeat XI
Sopim03g005580	Legumin 11S_globulin	5	36.26649345	19.44579109	9.9E-20	36.26649345	development.storage proteins
Sopim01g098850	Short_chain dehydrogenase/reductase family protein	5	13.63445169	2.823169788	9.9E-20	13.63445169	misc.short chain dehydrogenase/reductase (SDR)
Sopim03g005020	Lipase	5	5.093808779	2.6208271	2.58016E-13	5.093808779	lipid metabolism.lipid degradation.lipases.triacylglycerol lipase
Sopim09g090150	Legumin 11S_globulin	5	12.91338721	11.03119892	9.9E-20	12.91338721	development.storage proteins
Sopim02g062460	2_oxoglutarate_dependent dioxygenase	4	4.982348768	1.566661837	6.65024E-14	4.982348768	hormone metabolism.ethylene.synthesis-degradation, hormone metabolism.gibberelin.synthesis-degradation
Solyc02g062460.2.1	2_oxoglutarate_dependent dioxygenase	3	4.579534054	1.645028854	2.34182E-11	4.579534054	hormone metabolism.gibberelin.synthesis-degradation, hormone metabolism.ethylene.synthesis-degradation
Sopim09g066150	Cytochrome P450_	3	3.391233062	1.328961059	1.09213E-12	3.391233062	misc.cytochrome P450
Sopim06g048530	Hydroxyacylglutathione hydrolase	3	5.047698453	4.791566979	9.11493E-14	5.047698453	Biodegradation of Xenobiotics.hydroxyacylglutathione hydrolase
Sopim07g064180	Pectinesterase	3	3.369742211	2.699131703	4.44089E-16	3.369742211	cell wall.pectin*esterases.PME
Sopim07g064190	Pectinesterase	3	99999.9	57734.96918	6.3205E-13	99999.9	cell wall.pectin*esterases.PME
Sopim09g065470	Vicilin (Fragment)	3	85.74395153	26.26510367	9.9E-20	85.74395153	development.storage proteins
Solyc09g082720.2.1	Aldo/keto reductase family protein	2	2.122496337	0.9075683	0.000845394	2.122496337	hormone metabolism.auxin.induced-regulated-responsive-activated
Solyc09g089580.2.1	1_aminocyclopropane_1_carboxylate oxidase_like protein	2	2.269448831	0.743396191	9.9E-20	2.269448831	hormone metabolism.ethylene.synthesis-degradation
Sopim09g089580	1_aminocyclopropane_1_carboxylate oxidase_like protein	2	2.269448831	0.743396191	9.9E-20	2.269448831	hormone metabolism.ethylene.synthesis-degradation
Solyc09g066150.1.1	Cytochrome P450	2	3.338823614	1.33110164	1.72913E-10	3.338823614	misc.cytochrome P450
Sopim02g093290	Nicotinate phosphoribosyltransferase_like protein	2	3.575738377	0.822381473	0.000563986	3.575738377	not assigned.unknown
Sopim10g076510	Pyruvate decarboxylase	2	3.419064218	1.04774004	2.8814E-05	3.419064218	fermentation.PDC
Sopim09g082720	Aldo/keto reductase family protein	2	2.132218673	0.784067304	0.000318325	2.132218673	hormone metabolism.auxin.induced-regulated-responsive-activated
Sopim08g066240	Decarboxylase family protein	2	3.273748092	1.670849957	1.2572E-10	3.273748092	amino acid metabolism.degradation.histidine
Sopim04g015620	Os01g0611000 protein (Fragment)	2	36.79876224	57.95673295	4.09758E-09	36.79876224	not assigned.unknown
Sopim03g019790	Alpha_galactosidase	2	3.488636039	2.930974412	1.60043E-07	3.488636039	minor CHO metabolism.galactose.alpha-galactosidases
Sopim08g006770	Anthocyanidin synthase (Fragment)	2	18.94617974	14.30767323	9.9E-20	18.94617974	hormone metabolism.ethylene.synthesis-degradation
Sopim07g056430	Glutathione S_transferase_like protein	2	8.880654037	4.333740102	5.10477E-07	8.880654037	misc.glutathione S transferases
Sopim05g054760	Dehydroascorbate reductase (Fragment)	2	4.00554342	3.810530597	2.72597E-06	4.00554342	redox.ascorbate and glutathione.ascorbate
Sopim06g068060	Sister chromatid cohesion protein PDS5 homolog B	2	18.7908557	14.28025071	0.000198259	18.7908557	not assigned.unknown
Sopim02g065260	Alpha_hydroxynitrile lyase	2	9.067915203	6.583049664	2.51514E-06	9.067915203	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases
Sopim09g072560	Legumin 11S_globulin	28	9.0795225	1.264081204	9.9E-20	9.0795225	development.storage proteins
Sopim03g005580	Legumin 11S_globulin	8	12.68765848	4.876882016	9.9E-20	12.68765848	development.storage proteins
Sopim09g025210	Legumin 11S_globulin	6	484.7195665	346.1009065	9.9E-20	484.7195665	development.storage proteins
Sopim05g054760	Dehydroascorbate reductase (Fragment)	3	290.5925306	332.4739285	8.54173E-10	290.5925306	redox.ascorbate and glutathione.ascorbate
Sopim09g082340	Vicilin_like protein (Fragment)	3	17.93192855	30.35790064	3.08642E-14	17.93192855	development.storage proteins
Sopim09g090150	Legumin 11S_globulin	3	323.3095288	596.6674875	9.9E-20	323.3095288	development.storage proteins
Solyc02g070640.2.1	60S ribosomal protein L18a	2	2.840863488	1.940993334	0.00896529	2.840863488	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L18A
Sopim09g065470	Vicilin (Fragment)	2	9.865725419	6.724430731	4.07628E-09	9.865725419	development.storage proteins
Sopim07g064600	Endoribonuclease L_PSP family protein	2	5.413419259	4.264496892	9.20924E-08	5.413419259	RNA.processing.ribonucleases
Sopim02g065270	Esterase PIR7B	2	21.66132114	9.633727617	9.9E-20	21.66132114	not assigned.unknown
Solyc02g081170.2.1	Plastid_lipid_associated protein_ chloroplastic	2	9.172378117	0.124698856	0.007037033	9.172378117	cell organisation
Sopim09g025210	Legumin 11S_globulin	10	2.954569701	2.844331886	9.9E-20	2.954569701	development.storage proteins
Sopim03g005580	Legumin 11S_globulin	9	7.382082387	5.223039695	9.9E-20	7.382082387	development.storage proteins
Sopim03g083910	Acid beta_fructofuranosidase	4	6.572780853	0.622369188	9.9E-20	6.572780853	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Sopim06g076540	class I heat shock protein	3	4.773049786	1.363577611	9.9E-20	4.773049786	stress.abiotic.heat
Sopim09g090150	Legumin 11S_globulin	3	101.6556401	106.4912057	9.9E-20	101.6556401	development.storage proteins
Solyc03g083910.2.1	Acid beta_fructofuranosidase	2	6.589136449	0.626588562	9.9E-20	6.589136449	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Solyc06g076540.1.1	class I heat shock protein	2	4.82709336	1.473939781	9.9E-20	4.82709336	stress.abiotic.heat
Sopim03g112360	60S ribosomal protein L27A	2	19.59412934	29.92830334	7.46833E-10	19.59412934	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L27A
Sopim03g005580	Legumin 11S_globulin	4	8.224331721	10.66065731	9.9E-20	8.224331721	development.storage proteins
Sopim09g082340	Vicilin_like protein (Fragment)	2	19.04337236	14.67820817	6.74963E-05	19.04337236	development.storage proteins
Solyc05g014790.1.1	Lipoxygenase	2	3.4567	0.622369188	9.9E-20	3.4567	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Solyc01g009680.1.1	Lipoxygenase	2	4.2578	1.363577611	9.9E-20	4.2578	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase

Table 5.7. Differentially expressed proteins identified in the fruits of wild species at different developmental stages using nanoLC-MS-MS.

Label-free quantitation was employed by matching retention times of the peaks and measuring area under the matched peaks using Sieve 2.1 software (Thermo Scientific) to identify the differentially expressed proteins in SP-SL, SG-SL, SH-SL pairs. Stringent selection criteria were imposed to identify these proteins (p value≤0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR=1%).

List of downregulated proteins in SP-SL

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO (SP/SL)	STD.DEV	PVALUE	FOLD CHANGE (SP/SL)	MAPMANCLASS
Sopim06g076560	class I heat shock protein	2	0.168302491	0.110493529	0.000268042	5.941682708	stress.abiotic.heat
Sopim01g044360	Importin beta_3	2	0.244105672	0.072551585	0.002066627	4.096586492	protein.targeting.nucleus
Sopim09g009260	Fructose_bisphosphate aldolase	2	0.318767296	0.099886088	2.55684E-13	3.137084682	PS.calvin cycle.aldolase
Sopim08g062450	class II heat shock protein	2	0.135281965	0.052015234	5.22276E-05	7.391968331	stress.abiotic.heat
Sopim06g036290	Heat shock protein 90 (Fragment)	2	0.060961422	0.059063789	0.003328679	16.40381687	stress.abiotic.heat
Sopim12g015880	Heat shock protein 90	2	0.200316814	0.086308714	0.00067285	4.992092179	stress.abiotic.heat
Sopim09g011080	Ribulose_1 5_bisphosphate carboxylase/oxygenase activase 1	3	0.075012826	0.063556322	1.44139E-06	13.33105358	PS.calvin cycle.rubisco interacting
Sopim02g078540	Unknown Protein	2	0.079741976	0.069109204	2.57087E-06	12.54044672	not assigned.unknown
Sopim11g005330	Actin	2	0.141413693	0.112490928	9.9E-20	7.071450995	cell.organisation
Sopim08g076980	Acetylornithine deacetylase or succinyl_diaminopimelate desuccinylase	2	0.08850574	0.059527377	4.4167E-10	11.29870215	protein.degradation
Sopim04g073990	Annexin	4	0.309161222	0.098846712	9.9E-20	3.234558314	cell.organisation
Sopim08g078250	Palmitoyl_protein thioesterase 1	3	0.226358994	0.139634707	8.51311E-09	4.417761275	protein.postranslational modification
Sopim05g054350	Epoxide hydrolase	2	0.280514453	0.238380199	2.63236E-06	3.564878699	misc.misc2
Sopim09g082060	Cysteine synthase	2	0.207016881	0.154548336	5.49577E-07	4.830523939	amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL
Sopim09g064940	Phenazine biosynthesis protein PhzF family	2	0.253468283	0.213653973	3.09473E-09	3.945266795	not assigned.unknown
Sopim12g099430	Epoxide hydrolase 1	2	0.281662336	0.16483306	1.90471E-09	3.55035045	misc.misc2
Sopim00g006800	Transaldolase	2	0.216331868	0.254694838	0.014628032	4.622527452	OPP.non-reductive PP.transaldolase
Sopim12g011310	Glutathione S_transferase	2	0.023885618	0.039123886	0.000352555	41.8661978	misc.glutathione S transferases
Solyc11g005640.1.1	Ubiquitin	2	0.048466256	0.041255238	0.010640103	20.63291207	protein.degradation.ubiquitin.ubiquitin
Solyc11g066100.1.1	heat shock protein	6	0.13994609	0.048153332	1.00364E-13	7.145608727	stress.abiotic.heat
Solyc02g087770.2.1	Aldose_1_epimerase_like protein	5	0.068285293	0.044795288	0.000136531	14.64444172	minor CHO metabolism.others
Solyc07g063040.2.1	Enolase_phosphatase E_1	4	0.085406347	0.056268042	0.000167322	11.70873162	minor CHO metabolism.others
Solyc08g062920.2.1	:Elongation factor EF_2	4	0.10111401	0.047229834	7.19425E-14	9.889826339	protein.synthesis.elongation
Solyc05g008460.2.1	ATP synthase subunit beta	4	0.271623863	0.073385538	9.9E-20	3.681561662	mitochondrial electron transport / ATP synthesis.F1-ATPase
Sopim05g008460	ATP synthase subunit beta	3	0.273188214	0.072704566	9.9E-20	3.660480027	mitochondrial electron transport / ATP synthesis.F1-ATPase
Solyc11g011960.1.1	UTP_glucose 1 phosphate uridylyltransferase	3	0.295754076	0.098421445	4.34618E-11	3.381187546	glycolysis.unclear/dually targeted.UGPase
Sopim11g011960	UTP_glucose 1 phosphate uridylyltransferase	3	0.316251918	0.110696246	4.18302E-10	3.162036163	glycolysis.unclear/dually targeted.UGPase
Solyc01g098880.2.1	Seryl_tRNA synthetase	3	0.365137918	0.153422129	0.000142182	2.738691194	protein.aa activation.serine-tRNA ligase
Solyc12g094620.1.1	Catalase	3	0.073346158	0.048439388	0.002095943	13.63397929	redox.dismutases and catalases
Solyc12g015880.1.1	Heat shock protein 90	3	0.308580057	0.113565271	4.87408E-06	3.240650124	stress.abiotic.heat
Solyc03g123830.2.1	Phosphoglycerate dehydrogenase	3	0.115440139	0.024522333	9.9E-20	8.662498209	amino acid metabolism.synthesis.serine-glycine-cysteine
Sopim11g066100	heat shock protein	2	0.264110872	0.113407439	8.82694E-12	3.786288664	stress.abiotic.heat
Sopim05g050120	Malic enzyme _	2	0.211440613	0.037448698	1.33227E-14	4.729460367	TCA / org. transformation.other organic acid transformaitons.malic
Solyc04g007770.2.1	Major latex_like protein	2	0.216551855	0.200913246	2.96013E-07	4.6178316	not assigned.unknown
Sopim04g007770	Major latex_like protein	2	0.216551855	0.200913246	2.96013E-07	4.6178316	not assigned.unknown
Solyc10g085550.1.1	Enolase	2	0.369467154	0.196106061	0.000291643	2.706600545	glycolysis.cytosolic branch.enolase
Sopim10g085550	Enolase	2	0.337735546	0.147494411	8.71464E-05	2.960896514	glycolysis.cytosolic branch.enolase
Sopim02g085350	Succinate dehydrogenase flavoprotein subunit	2	0.321901001	0.156363563	6.91887E-05	3.106545168	TCA / org. transformation.TCA.succinate dehydrogenase
Sopim03g123830	Phosphoglycerate dehydrogenase	2	0.114736613	0.024673893	9.9E-20	8.715613706	amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase
Sopim12g005860	3_isopropylmalate dehydratase large subunit	2	0.273007505	0.182281236	0.00187457	3.662902971	TCA / org. transformation.TCA.aconitase
Sopim01g007320	ATP synthase subunit beta chloroplastic	2	0.249650939	0.111824024	0.000520225	4.005592778	mitochondrial electron transport / ATP synthesis.F1-ATPase
Solyc06g009960.1.1	Elongation factor 1_alpha	2	0.133957161	0.021535345	1.11022E-16	7.465073092	protein.synthesis.elongation
Solyc09g009020.2.1	Enolase	2	0.343232572	0.199431355	4.4598E-09	2.913476409	glycolysis.cytosolic branch.enolase
Solyc02g085350.2.1	fSuccinate dehydrogenase flavoprotein subunit	2	0.2426459	0.159338125	1.97052E-05	4.121231809	TCA / org. transformation.TCA.succinate dehydrogenase
Solyc01g028810.2.1	chaperonin	2	0.08379502	0.020138949	6.39274E-07	11.9338834	protein.folding
Solyc02g088610.2.1	ATP_dependent chaperone ClpB	2	0.152335656	0.123689555	0.002874	6.564451336	stress.abiotic.heat
Solyc12g005860.1.1	3_isopropylmalate dehydratase large subunit	2	0.243789518	0.163709393	0.000513388	4.101899074	TCA / org. transformation.TCA.aconitase
Solyc10g079860.1.1	Beta_1 3_glucanase	2	0.116799845	0.08889965	0.002086053	8.561655166	misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase
Solyc01g007330.2.1	Ribulose bisphosphate carboxylase large chain	2	0.346680183	0.13673553	2.77159E-08	2.884502923	PS.calvin cycle.rubisco large subunit
Solyc05g056310.2.1	T_complex protein 1 subunit gamma	2	0.178271879	0.139011378	6.92614E-05	5.609409671	protein.folding
Solyc05g050120.2.1	Malic enzyme	2	0.167025332	0.053942616	2.60125E-13	5.987115769	TCA / org. transformation.other organic acid transformaitons.malic
Solyc06g036290.2.1	Heat shock protein 90	2	0.245368218	0.209168738	0.001723238	4.07550745	stress.abiotic.heat
Solyc11g069000.1.1	T_complex protein 1 subunit beta	2	0.12724971	0.032684247	5.36288E-10	7.858564077	protein.folding
Solyc02g062500.2.1	2_oxoglutarate_dependent dioxygenase	2	0.005003539	0.005088401	9.79523E-06	199.8585544	hormone metabolism.gibberelin.synthesis-degradation
Solyc11g069790.1.1	chaperonin	2	0.207716677	0.137268143	1.83232E-05	4.814249932	protein.folding
Solyc02g062500.2.1	2_oxoglutarate_dependent dioxygenase	15	0.002148825	0.000865885	1.55431E-15	465.3705745	hormone metabolism.gibberelin.synthesis-degradation
Solyc11g011380.1.1	Glutamine synthetase	8	0.120466859	0.027867913	9.9E-20	8.301038244	N-metabolism.ammonia metabolism.glutamine synthase
Sopim09g009260	Fructose_bisphosphate aldolase	7	0.283168797	0.083426429	2.62729E-11	3.531462542	PS.calvin cycle.aldolase
Solyc01g112280.2.1	Succinyl_diaminopimelate desuccinylase	6	0.075276045	0.029653365	0.000251339	13.28443862	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases,
Sopim10g083570	Fructose_bisphosphate aldolase	6	0.239528309	0.054035759	9.9E-20	4.174871865	PS.calvin cycle.aldolase
Solyc01g110450.2.1	NADP dependent sorbitol 6_phosphate dehydrogenase	5	0.150802894	0.044058465	1.11022E-16	6.631172459	minor CHO metabolism.others
Solyc06g009960.1.1	Elongation factor 1_alpha	5	0.163615955	0.031014825	9.9E-20	6.111873375	protein.synthesis.elongation
Solyc11g005330.1.1	Actin	5	0.069014632	0.01323074	9.9E-20	14.48968105	cell.organisation
Sopim12g099430	Epoxide hydrolase 1	5	0.157697601	0.089959569	1.67556E-05	6.341250562	misc.misc2
Solyc03g118040.2.1	Calcium_binding protein Calnexin	4	0.232737383	0.090790543	8.95002E-07	4.296688338	signalling.calcium
Solyc06g059740.2.1	Alcohol dehydrogenase 2	4	0.211811843	0.047292829	9.9E-20	4.721171327	misc.alcohol dehydrogenases
Solyc05g054350.2.1	Epoxide hydrolase	4	0.004592914	0.004969904	4.32987E-15	217.7266917	misc.misc2
Sopim12g040510	Guanine nucleotide_binding protein beta subunit_like protein	4	0.330849565	0.077499138	3.63882E-10	3.022521735	signalling.G-proteins
Sopim11g011380	Glutamine synthetase	4	0.142527311	0.076960284	9.9E-20	7.016199141	N-metabolism.ammonia metabolism.glutamine synthase
Solyc10g078930.1.1	Activator of heat shock protein ATPase homolog 1	3	0.230457075	0.154473733	0.001928717	4.339202863	not assigned.unknown
Sopim11g069700	Elongation factor 1_alpha	3	0.126737994	0.037859318	1.95399E-14	7.890293739	protein.synthesis.elongation
Solyc03g025270.2.1	rRNA 2_apos_O_methyltransferase fibrillarin	3	0.109142962	0.04493777	9.67011E-08	9.162294864	RNA.processing
Sopim01g110450	NADP dependent sorbitol 6_phosphate dehydrogenase	3	0.181840876	0.087332804	1.9984E-15	5.499313599	minor CHO metabolism.others
Sopim09g025210	Legumin 11S_globulin	3	0.188478817	0.154199436	0.000167101	5.305636023	development.storage proteins
Solyc10g085830.1.1	O_methyltransferase 1	3	0.001224634	0.002010991	4.46097E-05	816.5707333	misc.O-methyl transferases
Solyc07g062650.2.1	Malate dehydrogenase	3	0.319733551	0.095937474	1.11022E-16	3.127604208	TCA / org. transformation.TCA.malate DH
Sopim07g062650	Malate dehydrogenase	3	0.319733551	0.095937474	1.11022E-16	3.127604208	TCA / org. transformation.TCA.malate DH
Solyc03g097790.2.1	V_type proton ATPase subunit C	3	0.241843102	0.104150223	4.57951E-08	4.134912231	transport.p- and v-ATPases
Sopim05g014470	Glyceraldehyde 3_phosphate dehydrogenase	3	0.308352524	0.064523283	9.9E-20	3.243041395	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc12g040510.1.1	Guanine nucleotide_binding protein beta subunit_like protein	3	0.324553862	0.121297863	1.33861E-08	3.081152679	signalling.G-proteins
Solyc08g014340.2.1	Cysteine synthase	3	0.299170831	0.115744321	6.4345E-08	3.342571861	amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL
Sopim08g014340	Cysteine synthase	3	0.299170831	0.115744321	6.4345E-08	3.342571861	amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL
Solyc04g016360.2.1	S_formylglutathione hydrolase	3	0.31759581	0.103458208	2.14488E-07	3.148656151	not assigned.unknown
Solyc10g083570.1.1	Fructose_bisphosphate aldolase	3	0.21664759	0.060767016	9.9E-20	4.615791015	PS.calvin cycle.aldolase
Solyc12g099430.1.1	Epoxide hydrolase 1	3	0.1383936	0.075070745	1.16197E-07	7.225767652	misc.misc2
Solyc09g011080.2.1	Ribulose_1 5_bisphosphate carboxylase/oxygenase activase 1	3	0.244279036	0.177713048	0.000235173	4.093679172	PS.calvin cycle.rubisco interacting
Solyc02g081400.2.1	Intracellular protease PfpI family protein expressed	3	0.324455899	0.12578215	4.42789E-11	3.082082963	not assigned.unknown
Sopim02g081400	Intracellular protease PfpI family protein expressed	3	0.324455899	0.12578215	4.42789E-11	3.082082963	not assigned.unknown
Solyc04g016470.2.1	Beta_1 3_glucanase	3	0.137825268	0.046447022	2.17412E-10	7.255563606	misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase
Solyc11g069790.1.1	chaperonin	3	0.212953214	0.111820008	3.7721E-08	4.695867146	protein.folding
Solyc02g083860.2.1	:Flavanone 3_hydroxylase	3	0.301627752	0.104045647	0.000206032	3.315344798	hormone metabolism.ethylene.synthesis-degradation
Solyc09g009020.2.1	Enolase	3	0.220300489	0.070620068	3.46333E-09	4.539254568	glycolysis.cytosolic branch.enolase
Solyc04g011400.2.1	UDP_glucose 4_epimerase	3	0.207916005	0.097013997	0.000154209	4.809634539	cell wall.precursor synthesis.UXS
Solyc07g066610.2.1	Phosphoglycerate kinase	3	0.31475634	0.118610589	8.58527E-06	3.177060706	PS.calvin cycle.phosphoglycerate kinase
Solyc09g009260.2.1	Fructose_bisphosphate aldolase	3	0.290664204	0.080975884	1.46549E-14	3.44039612	PS.calvin cycle.aldolase
Solyc07g066600.2.1	Phosphoglycerate kinase	3	0.249936686	0.105947815	7.97974E-09	4.001013275	PS.calvin cycle.phosphoglycerate kinase
Sopim07g066600	Phosphoglycerate kinase	3	0.249936686	0.105947815	7.97974E-09	4.001013275	PS.calvin cycle.phosphoglycerate kinase
Solyc12g096000.1.1	ATP_dependent RNA helicase eIF4A	3	0.21011788	0.074436861	1.11022E-16	4.759233254	RNA.processing.RNA helicase
Solyc05g014470.2.1	Glyceraldehyde 3_phosphate dehydrogenase	3	0.308352524	0.064523283	9.9E-20	3.243041395	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Sopim06g069010	Guanine nucleotide_binding protein beta subunit_like protein	2	0.440395755	0.141467828	1.80703E-05	2.270684923	signalling.G-proteins
Sopim05g008460	ATP synthase subunit beta	2	0.21609178	0.157840721	0.000202447	4.627663298	mitochondrial electron transport / ATP synthesis.F1-ATPase
Sopim03g118040	Calcium_binding protein Calnexin	2	0.195800928	0.143948338	5.93943E-05	5.107228101	signalling.calcium
Solyc06g036290.2.1	Heat shock protein 90	2	0.18771599	0.094464064	1.4964E-07	5.32719668	stress.abiotic.heat
Sopim10g055670	V_type ATP synthase beta chain	2	0.33940342	0.178463455	2.97679E-09	2.946346268	mitochondrial electron transport / ATP synthesis.F1-ATPase, transport.p- and v-ATPases.H+-transporting two-sector ATPase
Solyc02g014150.2.1	Photosystem II stability/assembly factor Ycf48_like protein	2	0.222065988	0.095672557	1.95044E-07	4.503165966	protein.assembly and cofactor ligation
Sopim02g014150	Photosystem II stability/assembly factor Ycf48_like protein	2	0.222065988	0.095672557	1.95044E-07	4.503165966	protein.assembly and cofactor ligation
Solyc09g082720.2.1	Aldo/keto reductase family protein	2	0.193106193	0.087413532	8.70223E-06	5.178497814	hormone metabolism.auxin.induced-regulated-responsive-activated
Sopim12g010040	Leucyl aminopeptidase	2	0.248450922	0.157247574	0.000334286	4.024939786	protein.degradation
Sopim09g082990	GDP_D_mannose_3AC_5AC _epimerase 2	2	0.297149653	0.129840304	2.47607E-07	3.365307646	cell wall.precursor synthesis.UXS
Solyc09g082060.2.1	Cysteine synthase	2	0.181119694	0.125136602	2.89004E-08	5.521210752	amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL
Solyc10g055670.1.1	V_type ATP synthase beta chain	2	0.255909884	0.132498453	2.59758E-08	3.907625543	mitochondrial electron transport / ATP synthesis.F1-ATPase
Solyc08g041870.2.1	Aspartate aminotransferase	2	0.336011833	0.166248328	2.34122E-06	2.976085671	amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase
Solyc04g072240.2.1	Oxidoreductase family protein	2	0.038798197	0.029331664	0.000405988	25.77439377	not assigned.unknown
Solyc10g081440.1.1	NADH cytochrome b5 reductase	2	0.012859995	0.018816591	0.000917209	77.76052511	N-metabolism.nitrate metabolism.NR
Solyc04g009030.2.1	Glyceraldehyde_3_phosphate dehydrogenase	2	0.183812514	0.080341504	2.70211E-06	5.440326012	PS.calvin cycle.GAP
Solyc05g056540.2.1	Alcohol dehydrogenase_like protein	2	0.249577638	0.131229359	0.002086293	4.006769223	fermentation.ADH
Solyc04g009200.2.1	Glutamate_1_semialdehyde_2 1_aminomutase	2	0.222863255	0.137765787	0.000452321	4.487056431	tetrapyrrole synthesis.GSA
Sopim07g055210	Aspartate aminotransferase	2	0.300447702	0.138056393	0.002207478	3.328366282	amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase
Sopim11g062190	Mitochondrial ADP/ATP carrier proteins	2	0.211532957	0.038851134	2.54241E-14	4.727395751	major CHO metabolism.synthesis.starch.transporter
Solyc06g076640.2.1	Tubulin beta chain	2	0.255083276	0.108200265	1.1518E-06	3.920288363	cell.organisation
Sopim12g089310	Tubulin beta_1 chain	2	0.255083276	0.108200265	1.1518E-06	3.920288363	cell.organisation
Sopim04g073990	Annexin	2	0.068372547	0.035015744	4.71081E-08	14.62575327	cell.organisation
Sopim12g096000	ATP_dependent RNA helicase eIF4A	2	0.231121895	0.081004089	6.66134E-16	4.326721186	RNA.processing.RNA helicase
Solyc03g121270.2.1	IAA_amino acid hydrolase	2	0.16062481	0.142861353	0.000136738	6.225688289	hormone metabolism.auxin.synthesis-degradation
Solyc03g115110.2.1	ATP synthase gamma chain	2	0.236906001	0.133154904	1.88381E-06	4.221083457	mitochondrial electron transport / ATP synthesis.F1-ATPase
Sopim03g115110	ATP synthase gamma chain	2	0.236906001	0.133154904	1.88381E-06	4.221083457	mitochondrial electron transport / ATP synthesis.F1-ATPase
Solyc11g018550.2.1	Thylakoid_bound ascorbate peroxidase 6	2	0.219342413	0.179648738	3.8028E-05	4.559081779	redox.ascorbate and glutathione.ascorbate
Solyc06g071920.2.1	Glyceraldehyde_3_phosphate dehydrogenase	2	0.244337678	0.074770543	5.55112E-16	4.092696659	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc08g061850.2.1	Ribosomal protein	2	0.322454834	0.228483627	0.000215026	3.101209518	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S3
Sopim08g062660	Ran GTPase binding protein	2	0.354896372	0.085964612	1.8178E-07	2.817723933	signalling.G-proteins
Solyc01g094220.2.1	Carbonyl reductase 3	2	0.221727733	0.177209758	0.014810776	4.510035734	misc.short chain dehydrogenase/reductase (SDR)
Sopim11g005330	Actin	2	0.066647634	0.01332739	9.9E-20	15.00428363	cell.organisation
Sopim05g054350	Epoxide hydrolase	2	0.164544897	0.067534635	1.4555E-13	6.077368663	misc.misc2
Sopim11g013440	Eukaryotic translation initiation factor 3 subunit 5_	2	0.324626106	0.100355691	4.42487E-07	3.080466979	protein.degradation.ubiquitin.proteasom
Solyc10g006980.2.1	3_deoxy_manno_octulosonate cytidylyltransferase	2	0.400660062	0.256367679	0.006185007	2.495881409	cell wall.precursor synthesis.KDO pathway.CMP-KDO Synthetase
Solyc01g058390.2.1	Galactokinase	2	0.212288198	0.068235389	4.50819E-06	4.710577452	minor CHO metabolism.galactose.galactokinases
Solyc10g085550.1.1	Enolase	2	0.178865224	0.099691619	4.11425E-08	5.590801718	glycolysis.cytosolic branch.enolase
Sopim06g005490	Triosephosphate isomerase	2	0.289668122	0.2145789	0.000448674	3.452226613	PS.calvin cycle.TPI, glycolysis.cytosolic branch.triosephosphate isomerase (TPI)
Solyc07g051850.2.1	Aspartic proteinase	2	0.297410138	0.07690287	9.9E-20	3.362360163	protein.degradation.aspartate protease
Sopim05g023800	GTP_binding nuclear protein Ran_A1	2	0.192295315	0.045389374	8.86938E-06	5.200334709	signalling.G-proteins
Solyc05g053810.2.1	Serine hydroxymethyltransferase	2	0.151132788	0.106733998	0.000507858	6.616697882	C1-metabolism.glycine hydroxymethyltransferase
Solyc05g018590.2.1	26S protease regulatory subunit 8 homolog A	2	0.227339112	0.169066119	0.003693739	4.398715175	protein.degradation.ubiquitin.proteasom
Solyc02g067180.2.1	Cystathionine gamma synthase	2	0.076639828	0.041900011	0.000669527	13.04804603	amino acid metabolism.synthesis.aspartate family.methionine.cystathionine gamma-synthase
Solyc02g084440.2.1	Fructose_bisphosphate aldolase	2	0.098364067	0.095902196	3.362E-10	10.16631408	PS.calvin cycle.aldolase
Solyc03g083910.2.1	Acid beta_fructofuranosidase	2	0.163450541	0.118916016	2.56336E-06	6.118058667	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Solyc11g062190.1.1	Mitochondrial ADP/ATP carrier proteins	2	0.211532957	0.038851134	2.54241E-14	4.727395751	major CHO metabolism.synthesis.starch.transporter
Solyc05g008460.2.1	ATP synthase subunit beta	2	0.3026632	0.222658466	0.01015747	3.304002603	mitochondrial electron transport / ATP synthesis.F1-ATPase
Solyc06g068860.2.1	Alpha_mannosidase	2	0.376636344	0.20463728	0.005407185	2.655081	misc.gluco-, galacto- and mannosidases.alpha-mannosidase
Sopim07g066610	Phosphoglycerate kinase	2	0.233628929	0.136859192	6.3364E-05	4.280291854	PS.calvin cycle.phosphoglycerate kinase
Sopim02g084440	Fructose_bisphosphate aldolase	2	0.260658876	0.149082318	0.002811634	3.836431797	PS.calvin cycle.aldolase
Sopim01g007320	ATP synthase subunit beta chloroplastic	2	0.309262385	0.206923628	0.010486118	3.233500255	mitochondrial electron transport / ATP synthesis.F1-ATPase
Sopim09g082730	Aldo/keto reductase family protein	2	0.182536361	0.082960188	1.6768E-05	5.478360541	hormone metabolism.auxin.induced-regulated-responsive-activated
Solyc12g096220.1.1	60S ribosomal protein L7	6	0.000251082	0.000113412	9.9E-20	3982.759721	signalling.G-proteins
Solyc10g084400.1.1	Glutathione S_transferase	4	0.015411173	0.006563579	9.9E-20	64.88798619	misc.glutathione S transferases
Solyc05g005490.2.1	Carbonic anhydrase	3	0.24843345	0.135937831	9.9E-20	4.025222852	TCA / org. transformation.carbonic anhydrases
Sopim05g005490	Carbonic anhydrase	3	0.24843345	0.135937831	9.9E-20	4.025222852	TCA / org. transformation.carbonic anhydrases
Solyc06g076560.1.1	class I heat shock protein	2	0.016643141	0.007774331	9.9E-20	60.08481235	stress.abiotic.heat
Solyc04g011510.2.1	Triosephosphate isomerase	2	0.352001969	0.189826087	0.002345402	2.840893203	PS.calvin cycle.TPI, glycolysis.cytosolic branch.triosephosphate isomerase (TPI)
Solyc01g099900.2.1	Ribosomal protein L18	2	0.151726672	0.124326281	2.96876E-05	6.590799026	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L18

Solyc03g083910.2.1	Acid beta_fructofuranosidase	2	0.22183573	0.181161137	0.000213873	4.507840101	major CHO metabolism.degradation.sucrose.invertases.vacuolar
Solyc09g010930.2.1	NAD_dependent epimerase/dehydratase	2	0.039570985	0.051508408	5.81996E-07	25.27104168	protein.degradation
Solyc09g007270.2.1	Ascorbate peroxidase	2	0.174770657	0.145416427	9.9E-20	5.721784289	redox.ascorbate and glutathione.ascorbate
Sopim09g007270	Ascorbate peroxidase	2	0.174770657	0.145416427	9.9E-20	5.721784289	redox.ascorbate and glutathione.ascorbate
Solyc05g050800.2.1	Phosphoglycerate mutase family protein	2	0.091722787	0.073824628	7.99751E-07	10.90241625	not assigned.unknown
Sopim06g060340	Chloroplast photosystem II_associated protein	2	0.361682297	0.104954498	9.9E-20	2.764857468	PS.lightreaction.photosystem II.PSII polypeptide subunits
Sopim10g084400	Glutathione S_transferase	2	0.091749827	0.03990399	1.39831E-10	10.89920312	misc.glutathione S transferases
Solyc06g005360.2.1	Actin depolymerizing factor 3	2	0.293805063	0.147758499	1.17432E-09	3.403617317	cell.organisation
Sopim06g005360	Actin depolymerizing factor 3	2	0.293805063	0.147758499	1.17432E-09	3.403617317	cell.organisation
Solyc05g005690.1.1	30S ribosomal protein S9	2	0.265961913	0.161263097	1.68491E-05	3.759936867	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S16
Solyc06g005160.2.1	Ascorbate peroxidase	2	0.189989378	0.142790191	0.000393155	5.263452151	redox.ascorbate and glutathione.ascorbate
Solyc06g060340.2.1	Chloroplast photosystem II_associated protein	2	0.361682297	0.104954498	9.9E-20	2.764857468	PS.lightreaction.photosystem II.PSII polypeptide subunits
Solyc06g076560.1.1	class I heat shock protein	8	0.079208323	0.020424235	9.9E-20	12.62493589	stress.abiotic.heat
Sopim06g076560	class I heat shock protein	7	0.084308037	0.021999293	9.9E-20	11.86126541	stress.abiotic.heat
Solyc06g076520.1.1	class I heat shock protein	3	0.29452652	0.088735995	9.9E-20	3.395279985	stress.abiotic.heat
Sopim06g076520	class I heat shock protein	3	0.29452652	0.088735995	9.9E-20	3.395279985	stress.abiotic.heat
Solyc11g040110.1.1	SnRK1_interacting protein 1	3	0.196844846	0.17791456	0.000585256	5.080143166	not assigned.unknown
Solyc06g076570.1.1	class I heat shock protein	3	0.093984656	0.096932718	0.000761392	10.64003471	stress.abiotic.heat
Solyc01g102960.2.1	class IV heat shock protein	2	0.129674489	0.094240349	1.01108E-10	7.711617031	stress.abiotic.heat
Sopim03g096850	Genomic DNA chromosome 5 P1 clone MKP11	2	0.172756601	0.083693157	1.10496E-09	5.788490828	protein.assembly and cofactor ligation
Solyc12g027720.1.1	ATP synthase subunit b_ chloroplastic	2	0.246615497	0.191036697	0.000187793	4.054895221	not assigned.unknown
Solyc09g015020.1.1	class I heat shock protein 3	2	0.214244129	0.157127924	9.9E-20	4.667572468	stress.abiotic.heat
Sopim09g015020	class I heat shock protein 3	2	0.214244129	0.157127924	9.9E-20	4.667572468	stress.abiotic.heat
Sopim07g062060	Peptide methionine sulfoxide reductase msrB	2	0.236469437	0.153563118	0.000476123	4.228876307	RNA.regulation of transcription.putative transcription regulator
Solyc07g062060.2.1	Peptide methionine sulfoxide reductase msrB	2	0.236469437	0.153563118	0.000476123	4.228876307	RNA.regulation of transcription.putative transcription regulator
Solyc11g005330.1.1	Actin	2	0.212839251	0.229584625	3.70176E-05	4.698381494	cell.organisation
Solyc09g008650.2.1	Peptidyl_prolyl cis_trans isomerase	2	0.014431147	0.010534855	1.42992E-05	69.29456356	protein.folding
Sopim01g099780	Translationally_controlled tumor protein homolog	2	0.244858885	0.181552554	7.8004E-11	4.083984941	not assigned.unknown
Solyc01g099780.2.1	Translationally_controlled tumor protein homolog	2	0.244858885	0.181552554	7.8004E-11	4.083984941	not assigned.unknown
Solyc08g082570.2.1	CccP Conserved Cys_containing protein (IC)	2	0.009303112	0.013757688	0.000441401	107.4909146	not assigned.unknown
Solyc01g096590.2.1	30S ribosomal protein S10	2	0.219393272	0.187521988	6.32294E-05	4.558024924	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S20
Sopim01g096590	30S ribosomal protein S10	2	0.219393272	0.187521988	6.32294E-05	4.558024924	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S20
Solyc12g005630.1.1	Cytochrome b6_f complex iron_sulfur subunit	2	0.237641134	0.229972441	7.86074E-08	4.208025701	PS.lightreaction.cytochrome b6/f.iron sulfur subunit
Solyc11g020330.1.1	class IV heat shock protein	2	0.200091525	0.154564377	2.52377E-08	4.99771292	stress.abiotic.heat
Solyc08g077710.2.1	60S ribosomal protein L37a	2	0.172762798	0.142142606	4.44089E-16	5.788283177	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L37A
Sopim08g077710	60S ribosomal protein L37a	2	0.172762798	0.142142606	4.44089E-16	5.788283177	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L37A
Solyc03g096850.2.1	Genomic DNA chromosome 5 P1 clone MKP11	2	0.172756601	0.083693157	1.10496E-09	5.788490828	protein.assembly and cofactor ligation
Solyc04g081330.2.1	Chromosome 11 contig 1 DNA sequence.	2	0.030740715	0.029751803	4.40248E-12	32.5301481	not assigned.unknown
Solyc12g005860.1.1	3_isopropylmalate dehydratase large subunit	12	0.052534854	0.008146345	9.9E-20	19.03498198	TCA / org. transformation.TCA.aconitase
Solyc08g014000.2.1	Lipoxygenase	9	0.097746363	0.023141017	9.9E-20	10.23055965	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Solyc08g062920.2.1	Elongation factor EF_2	7	0.280532605	0.081823523	1.50546E-13	3.564648043	protein.synthesis.elongation
Solyc06g059740.2.1	Alcohol dehydrogenase 2	6	0.27552311	0.051826478	9.9E-20	3.629459609	misc.alcohol dehydrogenases
Solyc06g036290.2.1	Heat shock protein 90	6	0.194531607	0.028857763	9.9E-20	5.140552805	stress.abiotic.heat
Solyc07g062530.2.1	Phosphoenolpyruvate carboxylase 2	6	0.145818902	0.035505128	9.9E-20	6.857821489	not assigned.unknown
Solyc06g009960.1.1	Elongation factor 1_alpha	5	0.437776272	0.072092466	4.79616E-14	2.284271817	protein.synthesis.elongation
Solyc00g060810.2.1	Major latex_like protein	5	0.129259813	0.057694963	9.9E-20	7.736356529	stress.abiotic.unspecified
Sopim07g066600	Phosphoglycerate kinase	5	0.110259495	0.036450844	2.04281E-14	9.069513657	PS.calvin cycle.phosphoglycerate kinase
Sopim10g081510	5_methyltetrahydropteroyltriglutamate__homocysteine methyltransferase	5	0.309648398	0.062503896	9.9E-20	3.229469314	amino acid metabolism.synthesis.aspartate family.methionine
Solyc07g051850.2.1	Aspartic proteinase	4	0.184917634	0.061986076	9.9E-20	5.407813085	protein.degradation.aspartate protease
Solyc07g052350.2.1	3_isopropylmalate dehydratase large subunit	4	0.135248689	0.047783546	2.36427E-10	7.393787028	TCA / org. transformation.TCA.aconitase
Solyc10g007290.2.1	Phosphoenolpyruvate carboxylase	4	0.235815047	0.060850536	2.05391E-14	4.240611502	not assigned.unknown
Solyc05g050120.2.1	Malic enzyme	4	0.320674325	0.108914043	2.70561E-13	3.118428645	TCA / org. transformation.other organic acid transformaitons.malic
Solyc11g069790.1.1	chaperonin	4	0.165520393	0.071214812	8.29706E-07	6.041551636	protein.folding
Solyc01g099190.2.1	Lipoxygenase	4	0.110729054	0.045938505	9.9E-20	9.031053402	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Sopim06g036290	Heat shock protein 90	4	0.187553183	0.029764788	9.9E-20	5.331820996	stress.abiotic.heat
Sopim01g099190	Lipoxygenase	4	0.110729054	0.045938505	9.9E-20	9.031053402	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Sopim12g005860	3_isopropylmalate dehydratase large subunit	4	0.089414783	0.023244024	9.9E-20	11.18383294	TCA / org. transformation.TCA.aconitase
Sopim08g014000	Lipoxygenase	4	0.095487045	0.028054387	9.9E-20	10.47262483	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Solyc11g012160.1.1	Fumarylacetoacetase	3	0.278707922	0.165092101	0.00160832	3.587985557	amino acid metabolism.degradation.aromatic aa.tyrosine
Solyc10g081440.1.1	NADH cytochrome b5 reductase	3	0.137200405	0.051478094	1.21818E-05	7.288608198	N-metabolism.nitrate metabolism.NR
Solyc10g085830.1.1	O_methyltransferase 1	3	0.053741164	0.032048219	8.64965E-11	18.60771019	misc.O-methyl transferases
Sopim08g081250	Aminopeptidase N	3	0.429539518	0.096116072	1.07131E-05	2.328074501	protein.degradation
Solyc07g066600.2.1	Phosphoglycerate kinase	3	0.336347896	0.078152385	6.9611E-14	2.973112104	PS.calvin cycle.phosphoglycerate kinase
Solyc06g065520.2.1	T_complex protein eta subunit	3	0.224082146	0.116924583	8.23963E-06	4.462649163	protein.folding
Solyc10g081510.1.1	5_methyltetrahydropteroyltriglutamate__homocysteine methyltransferase	3	0.295694653	0.072776161	9.9E-20	3.381867037	amino acid metabolism.synthesis.aspartate family.methionine
Solyc08g081250.2.1	Aminopeptidase N	3	0.117677703	0.057995244	2.48999E-06	8.497786518	protein.degradation
Solyc01g008710.2.1	Mannan endo_1 4_beta_mannosidase	3	0.007780955	0.006498005	1.40488E-06	128.5189262	cell wall.degradation.mannan-xylose-arabinose-fucose
Solyc09g092390.2.1	Adenosylhomocysteinase	3	0.289736218	0.087437286	2.70894E-14	3.45141525	not assigned.unknown
Solyc01g080460.2.1	Pyruvate phosphate dikinase	3	0.212498652	0.115195401	1.33148E-08	4.705912197	gluconeogenese/ glyoxylate cycle.pyruvate dikinase
Solyc02g085350.2.1	Succinate dehydrogenase flavoprotein subunit	3	0.135543926	0.063509536	5.6026E-05	7.377682113	TCA / org. transformation.TCA.succinate dehydrogenase
Sopim07g051850	Aspartic proteinase	3	0.197556031	0.09068989	9.4369E-15	5.061855073	protein.degradation.aspartate protease
Sopim11g069700	Elongation factor 1_alpha	3	0.467164519	0.091002359	3.05046E-08	2.140573522	protein.synthesis.elongation
Solyc08g005630.2.1	Glucose_methanol_choline oxidoreductase	2	0.037342545	0.025906681	0.000487494	26.77910647	not assigned.unknown
Solyc11g066100.1.1	heat shock protein	2	0.184776105	0.090657603	4.26499E-07	5.411955183	stress.abiotic.heat
Solyc12g010950.1.1	Alcohol dehydrogenase zinc_containing	2	0.215289914	0.108224098	0.01542488	4.644899446	misc.oxidases - copper, flavone etc.
Solyc06g083190.2.1	Peptidyl_prolyl cis_trans isomerase	2	0.164771349	0.084620151	8.5892E-07	6.069016299	cell.cycle.peptidylprolyl isomerase
Sopim10g007290	Phosphoenolpyruvate carboxylase	2	0.258642884	0.067424236	1.33549E-12	3.866334869	not assigned.unknown
Sopim03g115230	ClpB chaperone	2	0.211742681	0.050776265	9.9E-20	4.722713417	stress.abiotic.heat
Solyc07g020860.2.1	Peroxiredoxin	2	0.091596258	0.067250544	1.3867E-05	10.9174766	redox.peroxiredoxin
Solyc03g115230.2.1	ClpB chaperone	2	0.211742681	0.050776265	9.9E-20	4.722713417	stress.abiotic.heat
Sopim01g112280	Succinyl_diaminopimelate desuccinylase	2	0.224856477	0.17432397	0.002196481	4.447281277	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases
Solyc03g123760.2.1	Phytoene desaturase	2	0.103863684	0.14193362	9.68409E-07	9.62800433	secondary metabolism.isoprenoids.carotenoids.phytoene dehydrogenase
Sopim05g050120	Malic enzyme	2	0.323793793	0.151163942	1.78315E-09	3.08838533	TCA / org. transformation.other organic acid transformaitons.malic
Solyc05g005480.2.1	Oxidoreductase zinc_binding dehydrogenase	2	0.17361542	0.110483541	2.95871E-05	5.759857045	misc.oxidases - copper, flavone etc.
Solyc05g053810.2.1	Serine hydroxymethyltransferase	2	0.382606895	0.132313623	0.001013181	2.613648664	C1-metabolism.glycine hydroxymethyltransferase
Solyc09g007540.2.1	Valyl_tRNA synthetase	2	0.359387003	0.185339385	0.010241405	2.782515762	protein.aa activation.valine-tRNA ligase
Solyc03g113800.2.1	Betaine aldehyde dehydrogenase	2	0.253493548	0.140961378	0.006216286	3.944873586	fermentation.aldehyde dehydrogenase
Solyc12g014250.1.1	Phosphoenolpyruvate carboxylase 1	2	0.370993367	0.141564544	0.002581629	2.695465978	not assigned.unknown
Solyc07g053280.2.1	Ketol_acid reductoisomerase	2	0.29623439	0.133575536	0.002830333	3.375705303	amino acid metabolism.synthesis.branched chain group.common
Sopim10g085550	Enolase	2	0.257235741	0.143573408	8.25673E-13	3.887484667	glycolysis.cytosolic branch.enolase
Sopim03g007890	Heat shock protein 90 (Fragment)	2	0.086349775	0.042129579	2.66795E-05	11.5808061	stress.abiotic.heat
Solyc07g064170.2.1	Pectinesterase	2	0.375957092	0.179121299	9.71351E-05	2.659878009	cell wall.pectin*esterases.PME
Solyc10g049620.1.1	Progesterone 5_beta_reductase	2	0.129661639	0.139419386	6.87831E-05	7.712381307	development.unspecified
Solyc07g066610.2.1	Phosphoglycerate kinase	2	0.392162613	0.212846902	0.000836957	2.549962612	PS.calvin cycle.phosphoglycerate kinase
Solyc02g088610.2.1	ATP_dependent chaperone ClpB	2	0.28100958	0.132080851	3.64274E-11	3.558597539	stress.abiotic.heat
Sopim02g088610	ATP_dependent chaperone ClpB	2	0.28100958	0.132080851	3.64274E-11	3.558597539	stress.abiotic.heat
Solyc04g077970.2.1	Adenine phosphoribosyltransferase_like	2	0.242759707	0.233430037	0.000285482	4.119299746	nucleotide metabolism.salvage.phosphoribosyltransferases.aprt
Sopim04g077970	Adenine phosphoribosyltransferase_like	2	0.242759707	0.233430037	0.000285482	4.119299746	nucleotide metabolism.salvage.phosphoribosyltransferases.aprt
Sopim01g007330	Ribulose bisphosphate carboxylase large chain	2	0.396558403	0.221705368	0.000558195	2.521696658	PS.calvin cycle.rubisco large subunit
Solyc09g009020.2.1	Enolase	2	0.290831069	0.139477069	1.57282E-06	3.438422185	glycolysis.cytosolic branch.enolase
Solyc10g085550.1.1	Enolase	2	0.257235741	0.143573408	8.25673E-13	3.887484667	glycolysis.cytosolic branch.enolase
Solyc11g020040.1.1	Chaperone DnaK	2	0.165602341	0.089708922	0.008452127	6.038561979	stress.abiotic.heat
Solyc02g062460.2.1	2_oxoglutarate_dependent dioxygenase	2	0.027433204	0.012181103	0.000846958	36.45217635	hormone metabolism.ethylene.synthesis-degradation
Solyc07g043320.2.1	Unknown Protein	2	0.356303357	0.220730287	0.015384142	2.806597185	cell.organisation
Solyc03g113030.2.1	Aldose 1_epimerase_like protein	2	0.314959561	0.20026008	0.002918678	3.175010777	minor CHO metabolism.others
Sopim07g052350	3_isopropylmalate dehydratase large subunit	2	0.445361467	0.199355391	0.000481746	2.24536713	TCA / org. transformation.TCA.aconitase
Solyc01g007330.2.1	Ribulose bisphosphate carboxylase large chain	2	0.081416958	0.039562821	0.000403798	12.28245348	PS.calvin cycle.rubisco large subunit
Solyc11g051160.1.1	Phosphatidylinositol transfer protein SFH5	2	0.262432998	0.134112466	2.66454E-15	3.810496428	transport.misc
Solyc02g092670.1.1	Subtilisin_like protease	2	0.267579075	0.164280949	0.000825031	3.737213009	protein.degradation.subtilases
Solyc11g005330.1.1	Actin	2	0.240831723	0.153098136	0.010001898	4.152276903	cell.organisation
Solyc06g009050.2.1	Universal stress protein	2	0.004017758	0.003107532	9.44652E-06	248.8950474	stress.abiotic.unspecified
Solyc03g007890.2.1	Heat shock protein 90	2	0.086349775	0.042129579	2.66795E-05	11.5808061	stress.abiotic.heat
Solyc06g068090.2.1	Phospholipase D	2	0.158558308	0.076578027	1.10077E-05	6.306828129	lipid metabolism.lipid degradation.lysophospholipases
Solyc06g051310.2.1	Clathrin heavy chain	2	0.289611633	0.156642514	0.000201983	3.452899977	cell.vesicle transport
Sopim02g063070	14_3_3 protein beta/alpha_1	2	0.395346836	0.106592968	4.0693E-05	2.52942457	signalling.14-3-3 proteins
Sopim05g010670	Chaperone protein htpG	2	0.385826697	0.18064106	4.4578E-10	2.591837238	stress.abiotic.heat
Solyc06g059740.2.1	Alcohol dehydrogenase 2	10	0.363509508	0.039647348	9.9E-20	2.750959678	misc.alcohol dehydrogenases
Solyc02g088610.2.1	ATP_dependent chaperone ClpB	9	0.076876337	0.024197726	9.9E-20	13.00790377	stress.abiotic.heat
Solyc12g094620.1.1	Catalase	8	0.183544679	0.028091555	9.9E-20	5.448264733	redox.dismutases and catalases
Solyc08g079170.2.1	Stress_induced protein sti1_like protein	7	0.29203451	0.047225437	9.9E-20	3.424252837	stress
Solyc02g062500.2.1	2_oxoglutarate_dependent dioxygenase	7	0.011132799	0.004633552	1.53797E-10	89.82466887	hormone metabolism.gibberelin.synthesis-degradation
Solyc07g062530.2.1	Phosphoenolpyruvate carboxylase 2	7	0.203088955	0.06755992	2.78666E-14	4.923950701	not assigned.unknown
Solyc11g011960.1.1	UTP_glucose 1 phosphate uridylyltransferase	6	0.268084214	0.080021574	9.9E-20	3.730171154	glycolysis.unclear/dually targeted.UGPase
Solyc06g036290.2.1	Heat shock protein 90 (Fragment)	6	0.223115935	0.062278174	9.9E-20	4.481974815	stress.abiotic.heat
Solyc06g083190.2.1	Peptidyl_prolyl cis_trans isomerase	6	0.039805743	0.011893448	1.11022E-16	25.12200307	cell.cycle.peptidylprolyl isomerase
Solyc05g053810.2.1	Serine hydroxymethyltransferase	6	0.31926963	0.058940165	4.8241E-09	3.132148833	C1-metabolism.glycine hydroxymethyltransferase
Solyc11g020040.1.1	Chaperone DnaK	6	0.260344329	0.07473221	1.48377E-11	3.841066966	stress.abiotic.heat
Sopim11g011960	UTP_glucose 1 phosphate uridylyltransferase	6	0.261977503	0.081658255	9.9E-20	3.817121656	glycolysis.unclear/dually targeted.UGPase
Solyc04g011440.2.1	heat shock protein	5	0.140949944	0.046134456	2.66271E-06	7.094717265	stress.abiotic.heat
Solyc09g009020.2.1	Enolase	5	0.21841556	0.038330866	9.9E-20	4.57842839	glycolysis.cytosolic branch.enolase
Solyc02g062460.2.1	2_oxoglutarate_dependent dioxygenase	5	0.025576808	0.012816399	5.48103E-07	39.097921	hormone metabolism.ethylene.synthesis-degradation
Solyc10g085550.1.1	Enolase	5	0.400321929	0.070230501	9.9E-20	2.497989562	glycolysis.cytosolic branch.enolase
Solyc01g106210.2.1	Chaperone DnaK	5	0.358211309	0.13526564	8.09218E-05	2.791648324	stress.abiotic.heat
Solyc03g121270.2.1	IAA_amino acid hydrolase	4	0.330936056	0.065232474	9.9E-20	3.021731791	hormone metabolism.auxin.synthesis-degradation
Solyc12g014250.1.1	Phosphoenolpyruvate carboxylase 1	4	0.346178213	0.115250216	2.14484E-12	2.888685542	not assigned.unknown
Sopim09g009020	Enolase	4	0.171897507	0.048167802	9.9E-20	5.817420017	glycolysis.cytosolic branch.enolase
Solyc08g007700.1.1	Subtilisin_like protease	4	0.021717675	0.008600673	1.57953E-08	46.04544561	protein.degradation.subtilases
Solyc08g079870.1.1	Subtilisin_like protease	4	0.004571932	0.004239923	1.23169E-06	218.7259171	protein.degradation.subtilases
Solyc08g079920.1.1	Subtilisin_like protease	4	0.021717675	0.008600673	1.57953E-08	46.04544561	protein.degradation.subtilases
Solyc11g066100.1.1	heat shock protein	4	0.056487896	0.020687173	2.36063E-11	17.70290759	stress.abiotic.heat
Solyc10g085830.1.1	O_methyltransferase 1	4	0.011660984	0.010972867	4.00288E-11	85.7560577	misc.O-methyl transferases
Solyc07g066600.2.1	Phosphoglycerate kinase	4	0.282615284	0.063202668	1.50213E-12	3.538379052	PS.calvin cycle.phosphoglycerate kinase
Solyc12g005860.1.1	3_isopropylmalate dehydratase large subunit	4	0.069038731	0.038811245	3.02965E-11	14.48462309	TCA / org. transformation.TCA.aconitase
Solyc12g096000.1.1	ATP_dependent RNA helicase eIF4A	4	0.250870414	0.050781597	9.9E-20	3.98612169	RNA.processing.RNA helicase, DNA.synthesis/chromatin structure
Sopim02g088610	ATP_dependent chaperone ClpB	4	0.050535868	0.026825871	9.9E-20	19.78792583	stress.abiotic.heat
Solyc08g014000.2.1	Lipoxygenase	3	0.170498119	0.066948848	7.57793E-05	5.865167334	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Solyc11g069800.1.1	cytochrome P450	3	0.080138566	0.048055406	5.80344E-08	12.47838647	hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase
Solyc12g055800.1.1	V_type ATP synthase alpha chain	3	0.242914848	0.136376818	1.88738E-15	4.116668895	transport.p- and v-ATPases.H+-transporting two-sector ATPase
Solyc03g115230.2.1	ClpB chaperone	3	0.088351649	0.050258151	5.17526E-08	11.31840782	stress.abiotic.heat
Solyc01g008710.2.1	Mannan endo_1 4_beta_mannosidase	3	0.023856211	0.015811824	1.29153E-06	41.91780546	cell wall.degradation.mannan-xylose-arabinose-fucose
Sopim06g036290	Heat shock protein 90	3	0.322347786	0.102767977	1.11022E-16	3.102239396	stress.abiotic.heat
Solyc01g006280.2.1	Formate_tetrahydrofolate ligase	3	0.380587587	0.112884638	8.41757E-06	2.627516071	C1-metabolism
Solyc11g069790.1.1	chaperonin	3	0.189053918	0.024587362	1.33604E-12	5.289496294	protein.folding
Solyc01g006540.2.1	Lipoxygenase	3	0.102302962	0.03703062	0.000495411	9.774888022	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Solyc08g005770.2.1	Alcohol acetyltransferase	3	0.184282186	0.081285062	4.44089E-16	5.426460494	secondary metabolism.phenylpropanoids
Sopim08g005770	Alcohol acetyltransferase	3	0.184282186	0.081285062	4.44089E-16	5.426460494	secondary metabolism.phenylpropanoids
Sopim12g014250	Phosphoenolpyruvate carboxylase 1	3	0.290297971	0.145335574	3.39458E-08	3.444736441	not assigned.unknown
Solyc01g080460.2.1	Pyruvate phosphate dikinase	3	0.154829706	0.036532867	2.30305E-07	6.458708887	gluconeogenese/ glyoxylate cycle.pyruvate dikinase
Solyc03g043750.2.1	FAD_dependent pyridine nucleotide_disulphide oxidoreductase	3	0.415876278	0.071198797	2.07733E-09	2.40456129	mitochondrial electron transport / ATP synthesis.NADH-DH.type II.mitochondrial
Solyc01g007320.2.1	ATP synthase subunit beta chloroplastic	3	0.032813501	0.012549119	3.04823E-12	30.47526097	mitochondrial electron transport / ATP synthesis.F1-ATPase
Sopim01g007320	ATP synthase subunit beta chloroplastic	3	0.032813501	0.012549119	3.04823E-12	30.47526097	mitochondrial electron transport / ATP synthesis.F1-ATPase
Sopim12g055800	V_type ATP synthase alpha chain	3	0.322031644	0.108115615	4.66294E-15	3.105284897	transport.p- and v-ATPases.H+-transporting two-sector ATPase
Sopim07g066600	Phosphoglycerate kinase	3	0.283056688	0.064565505	6.13931E-12	3.53286123	PS.calvin cycle.phosphoglycerate kinase
Solyc08g082820.2.1	Heat shock protein	2	0.222915309	0.1378989	3.5698E-09	4.486008636	stress.abiotic.heat
Solyc06g005160.2.1	Ascorbate peroxidase	2	0.126209269	0.154339805	0.004132597	7.923348348	redox.ascorbate and glutathione.ascorbate
Solyc03g007890.2.1	Heat shock protein 90	2	0.010354108	0.018187274	0.00012428	96.58002844	stress.abiotic.heat
Solyc05g050120.2.1	Malic enzyme	2	0.39825823	0.194150741	1.66311E-13	2.510933672	TCA / org. transformation.other organic acid transformaitons.malic
Sopim05g050120	Malic enzyme	2	0.39825823	0.194150741	1.66311E-13	2.510933672	TCA / org. transformation.other organic acid transformaitons.malic
Solyc11g066060.1.1	heat shock protein	2	0.401475459	0.207250899	1.55775E-12	2.490812269	stress.abiotic.heat

Sopim11g066060	heat shock protein	2	0.401475459	0.207250899	1.55775E-12	2.490812269	stress.abiotic.heat
Solyc01g087820.2.1	Subtilisin_like protease	2	0.113559775	0.087004027	8.50309E-05	8.805935032	protein.degradation.subtilases
Solyc11g010630.2.1	Unknown Protein	2	0.499566853	0.187180735	0.005489686	2.001734091	protein.postranslational modification
Solyc04g045340.2.1	Phosphoglucomutase	2	0.387737748	0.267236114	7.97879E-10	2.579062796	not assigned.unknown
Sopim04g045340	Phosphoglucomutase	2	0.387737748	0.267236114	7.97879E-10	2.579062796	not assigned.unknown
Solyc09g057660.2.1	Peptidyl_prolyl cis_trans isomerase	2	0.135850966	0.117355635	0.00065233	7.361007635	cell.cycle.peptidylprolyl isomerase
Sopim07g062530	Phosphoenolpyruvate carboxylase 2	2	0.280576982	0.168647197	4.32816E-09	3.564084243	not assigned.unknown
Solyc10g078930.1.1	Activator of heat shock protein ATPase homolog 1	2	0.194816196	0.143831543	1.11196E-06	5.133043446	not assigned.unknown
Solyc09g009390.2.1	Monodehydroascorbate reductase (NADH)_like protein	2	0.07985118	0.062243298	9.60121E-12	12.52329651	redox.ascorbate and glutathione.ascorbate
Sopim09g009390	Monodehydroascorbate reductase (NADH)_like protein	2	0.07985118	0.062243298	9.60121E-12	12.52329651	redox.ascorbate and glutathione.ascorbate
Solyc02g081550.2.1	ATP_dependent Zn protease cell division protein FtsH homolog	2	0.131776362	0.061582803	0.000799198	7.588614385	protein.degradation.metalloprotease
Solyc04g054310.2.1	Alanine_glyoxylate aminotransferase	2	0.342869695	0.153317838	5.43001E-07	2.91655989	amino acid metabolism.synthesis.central amino acid metabolism.alanine.alanine-
Solyc08g081250.2.1	Aminopeptidase N	2	0.429001697	0.197349848	4.64418E-05	2.330993108	protein.degradation
Sopim08g081250	Aminopeptidase N	2	0.429001697	0.197349848	4.64418E-05	2.330993108	protein.degradation
Solyc10g085790.1.1	Atp_dependent RNA helicase	2	0.369529442	0.21257208	0.000765318	2.706144317	RNA.processing.RNA helicase
Solyc11g012900.1.1	Small glutamine_rich tetratricopeptide repeat_containing protein A	2	0.364555552	0.132620525	7.76735E-05	2.743066166	protein.postranslational modification
Solyc12g056120.1.1	6_phosphogluconate dehydrogenase decarboxylating	2	0.391399389	0.220584942	0.000393504	2.554935007	OPP.oxidative PP.6-phosphogluconate dehydrogenase
Sopim12g056120	6_phosphogluconate dehydrogenase decarboxylating	2	0.391399389	0.220584942	0.000393504	2.554935007	OPP.oxidative PP.6-phosphogluconate dehydrogenase
Sopim03g121270	IAA_amino acid hydrolase	2	0.255940447	0.108488744	8.19345E-14	3.907158921	hormone metabolism.auxin.synthesis-degradation
Sopim12g096000	ATP_dependent RNA helicase eIF4A	2	0.291489522	0.058455238	9.9E-20	3.430655046	RNA.processing.RNA helicase
Sopim12g094620	Catalase	2	0.208728828	0.036990635	9.9E-20	4.79090506	redox.dismutases and catalases
Solyc08g063080.2.1	UDP_sulfoquinovose synthase	2	0.348890188	0.076783575	5.93948E-08	2.866231363	lipid metabolism.glycolipid synthesis.UDP-sulfoquinovose synthase
Solyc08g062450.1.1	class II heat shock protein	2	0.207914047	0.095568949	0.000477782	4.809679848	stress.abiotic.heat
Solyc11g012160.1.1	Fumarylacetoacetase	2	0.4588999	0.198302273	1.61325E-05	2.179124469	amino acid metabolism.degradation.aromatic aa.tyrosine
Solyc02g067750.2.1	Carbonic anhydrase	2	0.027769721	0.016700062	1.64799E-06	36.01044405	TCA / org. transformation.carbonic anhydrases
Solyc04g014600.2.1	Universal stress protein family protein	2	0.175891581	0.182243601	0.012007585	5.68532044	stress.abiotic.cold
Solyc02g067180.2.1	Cystathionine gamma synthase	2	0.301394258	0.145515902	0.000256108	3.317913244	amino acid metabolism.synthesis.aspartate family.methionine.cystathionine gamma-
Solyc01g103450.2.1	Chaperone DnaK	2	0.032170555	0.02341356	2.2113E-10	31.08432553	stress.abiotic.heat
Solyc01g098880.2.1	Seryl_tRNA synthetase	2	0.241172713	0.08437132	7.5273E-09	4.146406072	protein.aa activation.serine-tRNA ligase
Solyc06g009750.2.1	Importin alpha_1b subunit	2	0.091923617	0.023977183	1.0657E-12	10.87859713	protein.targeting.nucleus
Solyc02g081170.2.1	Plastid_lipid_associated protein_ chloroplastic	2	0.109646596	0.124698856	0.007037033	9.120210185	cell.organisation
Solyc06g071000.2.1	N_succinylglutamate 5_semialdehyde dehydrogenase	2	0.273624392	0.184748398	0.000107794	3.654644941	amino acid metabolism.degradation.glutamate family.proline
Sopim06g071000	N_succinylglutamate 5_semialdehyde dehydrogenase	2	0.273624392	0.184748398	0.000107794	3.654644941	amino acid metabolism.degradation.glutamate family.proline
Sopim05g053810	Serine hydroxymethyltransferase	2	0.403560748	0.157103301	2.42131E-06	2.477941684	C1-metabolism.glycine hydroxymethyltransferase
Solyc01g067590.2.1	5_apos_AMP_activated protein kinase gamma_1 subunit	2	0.13537423	0.076516488	4.3912E-05	7.386930311	protein.postranslational modification
Sopim03g095620	ABC_1 domain protein	2	0.374877498	0.087755066	6.27665E-12	2.66753808	transport.ABC transporters and multidrug resistance systems
Solyc12g043120.1.1	Heat shock protein 4	2	0.295875347	0.211339781	0.004362252	3.379801692	stress.abiotic.heat
Solyc03g118040.2.1	Calcium_binding protein Calnexin	2	0.447372826	0.169910198	0.000941451	2.23527211	signalling.calcium
Solyc03g095620.2.1	ABC_1 domain protein	2	0.374877498	0.087755066	6.27665E-12	2.66753808	transport.ABC transporters and multidrug resistance systems
Solyc06g062840.2.1	Threonine synthase	2	0.450958059	0.128321586	0.000461263	2.217501119	amino acid metabolism.synthesis.aspartate family.threonine.threonine synthase
Solyc07g064980.2.1	Vacuolar protein sorting_associated protein VTA1 homolog	2	0.338160971	0.080061222	6.70621E-06	2.957171546	not assigned.unknown
Sopim06g083190	Peptidyl_prolyl cis_trans isomerase	2	0.258750875	0.049776923	2.05427E-08	3.864721232	cell.cycle.peptidylprolyl isomerase
Sopim04g005030	Phosphoglucomutase/phosphomannomutase family protein	2	0.435587341	0.164209431	0.003766333	2.295750831	glycolysis.plastid branch.phosphoglucomutase (PGM)
Sopim04g054310	Alanine_glyoxylate aminotransferase	2	0.342869695	0.153317838	5.43001E-07	2.91655989	amino acid metabolism.synthesis.central amino acid metabolism.alanine.alanine-
Sopim08g063080	UDP_sulfoquinovose synthase	2	0.348890188	0.076783575	5.93948E-08	2.866231363	lipid metabolism.glycolipid synthesis.UDP-sulfoquinovose synthase
Solyc02g067750.2.1	Carbonic anhydrase	5	0.015147886	0.00754444	3.88578E-15	66.01581028	TCA / org. transformation.carbonic anhydrases
Solyc03g118650.2.1	Aldose 1_epimerase_like protein	5	0.020812381	0.015806855	0.000399764	48.04832344	minor CHO metabolism.others
Solyc07g051850.2.1	Aspartic proteinase	4	0.249869137	0.042518722	9.9E-20	4.002094903	protein.degradation.aspartate protease
Solyc10g079860.1.1	Beta_1 3_glucanase	4	0.01194388	0.008553421	5.96726E-09	83.72488847	misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase
Solyc08g062450.1.1	class II heat shock protein	4	0.170538166	0.056459014	1.56768E-11	5.863790058	stress.abiotic.heat
Solyc00g060810.2.1	Major latex_like protein	4	0.18149571	0.011354481	9.9E-20	5.509772104	stress.abiotic.unspecified
Solyc09g010930.2.1	NAD_dependent epimerase/dehydratase	4	0.008456001	0.002515769	1.08025E-13	118.2592135	protein.degradation
Solyc06g048570.2.1	Hydrolase alpha/beta fold family protein expressed	3	0.071744098	0.050174737	0.003286425	13.9384287	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases
Solyc01g080010.2.1	Xylanase inhibitor (Fragment)	3	0.429126098	0.083896817	9.99201E-16	2.330317369	protein.degradation.aspartate protease
Solyc02g081170.2.1	Plastid_lipid_associated protein_ chloroplastic	3	0.118773587	0.048495719	0.000211397	8.419380312	cell.organisation
Solyc04g016470.2.1	Beta_1 3_glucanase	3	0.160848233	0.091405431	3.31373E-09	6.217040639	misc.beta 1,3 glucan hydrolases.glucan endo-1,3-beta-glucosidase
Solyc01g090750.2.1	T_complex protein 1 subunit alpha	2	0.220071702	0.218611916	0.004429119	4.543973587	protein.folding
Solyc09g009260.2.1	Fructose_bisphosphate aldolase	2	0.337495708	0.17022891	0.00112948	2.963000648	PS.calvin cycle.aldolase
Solyc10g083570.1.1	Fructose_bisphosphate aldolase	2	0.356041124	0.259143391	0.006891393	2.808664314	PS.calvin cycle.aldolase
Solyc04g014600.2.1	Universal stress protein family protein	2	0.175090516	0.138860795	1.104E-08	5.71133162	stress.abiotic.cold
Solyc04g073990.2.1	Annexin	2	0.076534992	0.03107555	1.99458E-06	13.06591885	cell.organisation
Sopim04g073990	Annexin	2	0.076534992	0.03107555	1.99458E-06	13.06591885	cell.organisation
Sopim08g062450	class II heat shock protein	2	0.186752929	0.069242739	1.26639E-10	5.354668353	stress.abiotic.heat
Sopim07g051850	Aspartic proteinase	2	0.288417491	0.052062905	9.9E-20	3.467196106	protein.degradation.aspartate protease
Solyc08g078510.2.1	GRAM_containing/ABA_responsive protein	2	0.181351752	0.065141309	0.0011803	5.514145788	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
Solyc03g082420.2.1	Heat shock protein	2	0.193753906	0.111535759	2.13724E-05	5.161186275	stress.abiotic.heat
Solyc10g055810.1.1	Endochitinase (Chitinase)	2	0.223998698	0.106277724	8.53806E-07	4.464311673	stress.biotic
Sopim01g080010	Xylanase inhibitor	2	0.419286772	0.106609484	2.9976E-15	2.385002502	protein.degradation.aspartate protease
Sopim00g060810	Major latex_like protein	2	0.18077138	0.011457181	9.9E-20	5.531849138	stress.abiotic.unspecified
Solyc02g069800.1.1	CXE carboxylesterase	2	0.127129186	0.041626429	0.000570425	7.866014319	Biodegradation of Xenobiotics
Solyc02g082920.2.1	Endochitinase (Chitinase)	2	0.001789096	0.003613151	0.000135699	558.9416007	stress.biotic
Solyc10g078740.1.1	Enoyl reductase	2	0.131671635	0.064216965	3.3738E-06	7.59465014	lipid metabolism.FA synthesis and FA elongation.enoyl ACP reductase
Solyc09g090140.2.1	Malate dehydrogenase	2	0.005468117	0.009576506	0.013718159	182.8783209	TCA / org. transformation.other organic acid transformaitons.cyt MDH
Solyc05g005490.2.1	Carbonic anhydrase	2	0.221804867	0.060739862	9.9E-20	4.508467339	TCA / org. transformation.carbonic anhydrases
Sopim05g005490	Carbonic anhydrase	2	0.221804867	0.060739862	9.9E-20	4.508467339	TCA / org. transformation.carbonic anhydrases
Solyc04g011510.2.1	Triosephosphate isomerase	2	0.274016774	0.127464951	4.17105E-09	3.649411624	PS.calvin cycle.TPI, glycolysis.cytosolic branch.triosephosphate isomerase (TPI)
Solyc05g014470.2.1	Glyceraldehyde 3_phosphate dehydrogenase	2	0.34322754	0.085719382	2.36341E-09	2.913519117	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Sopim03g115990	Malate dehydrogenase	2	0.490946267	0.230426602	0.016505805	2.036882785	TCA / org. transformation.TCA.malate DH
Solyc03g082420.2.1	Heat shock protein	13	0.174024675	0.022731851	9.9E-20	5.746311541	stress.abiotic.heat
Sopim03g082420	Heat shock protein	10	0.173173561	0.021742847	9.9E-20	5.774553546	stress.abiotic.heat
Solyc08g078700.2.1	Heat shock protein 22	7	0.143927526	0.051975348	9.32587E-15	6.947941275	stress.abiotic.heat
Solyc06g007340.2.1	Gamma_interferon_inducible lysosomal thiol reductase	5	0.27515184	0.04688106	9.9E-20	3.63435694	not assigned.unknown
Solyc05g054760.2.1	Dehydroascorbate reductase	5	0.011180214	0.002839621	2.78084E-05	89.44372302	redox.ascorbate and glutathione.ascorbate
Solyc05g014280.2.1	Heat shock protein	5	0.076477619	0.020439181	9.9E-20	13.07572091	stress.abiotic.heat
Solyc07g062970.2.1	Serine/threonine phosphatase family protein	4	0.159634263	0.11072134	1.96488E-07	6.264319349	protein.postranslational modification
Solyc09g082320.2.1	Proteasome subunit beta type	4	0.00545395	0.002823854	5.92304E-13	183.353348	protein.degradation.ubiquitin.proteasom
Solyc02g084440.2.1	Fructose_bisphosphate aldolase	4	0.063949175	0.034239805	8.83507E-11	15.63741822	PS.calvin cycle.aldolase
Solyc06g059740.2.1	Alcohol dehydrogenase 2	4	0.171020949	0.01657164	9.9E-20	5.847236865	misc.alcohol dehydrogenases
Solyc01g007740.2.1	Peroxiredoxin	4	0.118448537	0.035704669	9.9E-20	8.442484993	edox.peroxiredoxin.BAS1
Solyc06g076560.1.1	class I heat shock protein	3	0.145798488	0.061444455	3.33067E-15	6.858781676	stress.abiotic.heat
Solyc08g062820.2.1	Cytokinin riboside 5_apos;_monophosphate phosphoribohydrolase LOG	3	0.225400747	0.078850562	1.35592E-12	4.436542528	amino acid metabolism.degradation.aspartate family.lysine
Sopim09g082320	Proteasome subunit beta type	3	0.326167964	0.105549636	5.54455E-09	3.065905027	protein.degradation.ubiquitin.proteasom
Solyc03g113930.1.1	class IV heat shock protein	3	0.210452773	0.135368383	5.88946E-09	4.751659899	stress.abiotic.heat
Solyc05g008600.2.1	Fructose_bisphosphate aldolase	3	0.17148752	0.083561984	4.34225E-10	5.831328123	PS.calvin cycle.aldolase
Sopim09g009380	Protein kinase_like protein	3	0.207136736	0.120061344	2.96117E-05	4.827728859	protein.postranslational modification
Solyc06g036290.2.1	Heat shock protein 90	3	0.025925521	0.025947803	1.25219E-05	38.57203102	stress.abiotic.heat
Sopim05g014280	Heat shock protein	3	0.124111212	0.036125284	9.9E-20	8.057289795	stress.abiotic.heat
Sopim11g022590	Kunitz trypsin inhibitor 4	3	0.354363924	0.06950665	9.9E-20	2.821957688	not assigned.unknown
Solyc09g011490.2.1	Glutathione S_transferase_like protein	2	0.035843942	0.04213953	0.009155476	27.89871704	misc.glutathione S transferases
Solyc02g065240.2.1	Hydrolase alpha/beta fold family protein	2	0.007599016	0.007398472	1.81158E-06	131.5959782	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases
Solyc10g008010.2.1	Proteasome subunit alpha type	2	0.349305389	0.15821096	1.43776E-06	2.862824427	protein.degradation.ubiquitin.proteasom
Sopim10g008010	Proteasome subunit alpha type	2	0.349305389	0.15821096	1.43776E-06	2.862824427	protein.degradation.ubiquitin.proteasom
Solyc08g016670.2.1	Calcyclin_binding protein	2	0.002310891	0.003982139	6.45615E-06	432.7335737	not assigned.unknown
Solyc07g044860.2.1	Oxygen_evolving enhancer protein 2_ chloroplastic	2	0.218412445	0.130234713	3.57969E-12	4.578493685	PS.lightreaction.photosystem II.PSII polypeptide subunits
Sopim08g062820	Cytokinin riboside 5_apos;_monophosphate phosphoribohydrolase LOG	2	0.210010686	0.09545738	1.07888E-07	4.761662461	amino acid metabolism.degradation.aspartate family.lysine
Solyc02g065280.2.1	Methyl jasmonate esterase	2	0.004814416	0.007635465	0.00022995	207.7095202	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases
Sopim06g007340	Gamma_interferon_inducible lysosomal thiol reductase	2	0.337883774	0.068968039	9.9E-20	2.95959758	not assigned.unknown
Solyc07g061790.2.1	Heme_binding protein 2	2	0.345522436	0.208190875	2.37132E-05	2.894168061	tetrapyrrole synthesis.unspecified
Sopim07g061790	Heme_binding protein 2	2	0.420797828	0.209791393	1.02866E-05	2.376438123	tetrapyrrole synthesis.unspecified
Sopim08g076000	Cc_nbs_lrr_ resistance protein_	2	0.301223073	0.110697026	0.000418327	3.319798816	stress.biotic
Solyc12g094620.1.1	Catalase	2	0.052263509	0.021573484	1.01435E-10	19.13380907	redox.dismutases and catalases
Solyc03g118120.2.1	Transferase transferring glycosyl groups	2	0.052009849	0.048609256	1.03999E-05	19.2271276	not assigned.unknown
Solyc01g103380.2.1	Ras_related protein Rab_25	2	0.45218638	0.071376132	9.9E-20	2.21147749	signalling.G-proteins
Sopim01g103380	Ras_related protein Rab_25	2	0.45218638	0.071376132	9.9E-20	2.21147749	signalling.G-proteins
Solyc09g005620.2.1	Glutaredoxin	2	0.302490246	0.043062757	9.9E-20	3.305891718	transport.calcium
Sopim08g078700	Heat shock protein 22	2	0.205414883	0.110846529	2.45581E-09	4.868196425	stress.abiotic.heat
Solyc06g076570.1.1	class I heat shock protein	2	0.330851847	0.225003401	0.000231385	3.02250088	stress.abiotic.heat
Solyc03g098700.1.1	Cysteine protease inhibitor 8	2	0.140481689	0.04529157	2.11273E-05	7.11836544	not assigned.unknown
Solyc02g067750.2.1	Carbonic anhydrase	2	0.008718031	0.004582178	2.18606E-10	114.7048002	TCA / org. transformation.carbonic anhydrases
Solyc10g084400.1.1	Glutathione S_transferase	2	0.00041999	0.000829877	0.000417157	2381.0108	misc.glutathione S transferases
Solyc11g022590.1.1	Kunitz trypsin inhibitor 4 (Fragment)	2	0.355554267	0.07183428	9.9E-20	2.812510194	not assigned.unknown
Solyc11g012910.1.1	Cation transport regulator protein	2	0.272677244	0.114922805	3.50427E-05	3.667339392	transport.unspecified cations
Solyc08g076450.2.1	3_beta hydroxysteroid dehydrogenase/isomerase family protein	2	0.369365922	0.059657094	9.9E-20	2.707342343	not assigned.unknown
Sopim08g076450	3_beta hydroxysteroid dehydrogenase/isomerase family protein	2	0.369365922	0.059657094	9.9E-20	2.707342343	not assigned.unknown
Solyc08g079020.2.1	Adenine phosphoribosyltransferase_like protein	2	0.121123432	0.025368587	9.9E-20	8.256040801	nucleotide metabolism.salvage.phosphoribosyltransferases.aprt
Sopim08g079020	Adenine phosphoribosyltransferase_like protein	2	0.121123432	0.025368587	9.9E-20	8.256040801	nucleotide metabolism.salvage.phosphoribosyltransferases.aprt
Solyc04g011510.2.1	Triosephosphate isomerase	2	0.087229545	0.060675694	1.51264E-06	11.46400575	PS.calvin cycle.TPI
Solyc09g015020.1.1	class I heat shock protein 3	2	0.085037506	0.035215645	1.66533E-15	11.75951705	stress.abiotic.heat
Solyc12g100160.1.1	50S ribosomal protein L6	2	0.478486351	0.051320814	0.000333392	2.089923772	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L6
Solyc05g014470.2.1	Glyceraldehyde 3_phosphate dehydrogenase	2	0.211999884	0.086985478	4.29262E-06	4.716983723	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc02g088100.2.1	Expansin	2	0.057964092	0.02879425	1.76419E-06	17.25206014	cell wall.modification
Sopim09g005620	Glutaredoxin	2	0.302490246	0.043062757	9.9E-20	3.305891718	transport.calcium
Solyc06g069090.2.1	40S ribosomal protein S7_like protein	2	0.091007204	0.055454124	6.56142E-14	10.9881411	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S7
Solyc05g053470.2.1	chaperonin	2	0.101480744	0.087690526	8.1712E-05	9.854086257	protein.folding
Sopim01g102660	Maleylacetoacetate isomerase / glutathione S_transferase	2	0.347766433	0.133051026	2.20267E-07	2.875493164	misc.glutathione S transferases
Sopim03g025950	Membrane_associated progesterone receptor component 1	2	0.260645002	0.154803238	2.74411E-07	3.836636002	redox.ascorbate and glutathione
Sopim01g099190	Lipoxygenase	2	0.396508521	0.223318563	0.013692341	2.522013897	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Sopim06g076560	class I heat shock protein	2	0.135982846	0.06497027	8.82405E-13	7.353868736	stress.abiotic.heat
Sopim05g014470	Glyceraldehyde 3_phosphate dehydrogenase	2	0.211999884	0.086985478	4.29262E-06	4.716983723	lycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc06g076570.1.1	class I heat shock protein	10	0.340859609	0.023061324	9.9E-20	2.933759158	stress.abiotic.heat
Solyc04g014600.2.1	Universal stress protein family protein	10	0.062471565	0.021470009	9.9E-20	16.00728272	stress.abiotic.cold
Solyc08g062450.1.1	class II heat shock protein	9	0.034602585	0.010709805	9.9E-20	28.8995746	stress.abiotic.heat
Sopim06g076570	class I heat shock protein	9	0.348998327	0.023666881	9.9E-20	2.865343249	stress.abiotic.heat
Solyc09g015000.2.1	class I heat shock protein	7	0.173325178	0.023588437	9.9E-20	5.769502235	stress.abiotic.heat
Solyc11g020330.1.1	class IV heat shock protein	6	0.005944276	0.002300361	9.9E-20	168.229067	stress.abiotic.heat
Solyc01g102960.2.1	class IV heat shock protein	6	0.023255631	0.004053352	9.9E-20	43.00033836	stress.abiotic.heat
Solyc09g015020.1.1	class I heat shock protein 3	6	0.061457824	0.006221741	9.9E-20	16.27132119	stress.abiotic.heat
Sopim04g014600	Universal stress protein family protein	6	0.058718625	0.022118072	9.9E-20	17.03037155	stress.abiotic.cold
Sopim03g113930	class IV heat shock protein	6	0.032607249	0.010766955	9.9E-20	30.668027	stress.abiotic.heat
Sopim01g102960	class IV heat shock protein	5	0.023282736	0.004051571	9.9E-20	42.95027871	stress.abiotic.heat
Solyc05g014280.2.1	Heat shock protein	5	0.037276095	0.021602698	9.9E-20	26.8268444	stress.abiotic.heat
Solyc08g006720.2.1	Glutathione peroxidase	5	0.122207966	0.088943734	3.33067E-15	8.182772608	redox.ascorbate and glutathione.glutathione
Sopim09g015000	class I heat shock protein	5	0.165701169	0.022886069	9.9E-20	6.034960428	stress.abiotic.heat
Sopim08g006720	Glutathione peroxidase	4	0.154077789	0.113889989	7.99361E-15	6.490228121	redox.ascorbate and glutathione.glutathione
Solyc01g100370.2.1	Universal stress protein	4	0.094357698	0.041090603	2.44922E-06	10.59796943	stress.abiotic.unspecified
Solyc03g113930.1.1	class IV heat shock protein	4	0.033438648	0.012176867	9.9E-20	29.90551498	stress.abiotic.heat
Solyc08g062340.2.1	Class II small heat shock protein Le_HSP17.6	4	0.019788805	0.021439097	9.9E-20	50.53362127	stress.abiotic.heat
Sopim11g020330	class IV heat shock protein	4	0.072913481	0.032754125	9.9E-20	13.71488491	stress.abiotic.heat
Solyc09g082650.2.1	Acireductone dioxygenase	3	0.132371824	0.077951906	6.80657E-10	7.554477732	metal handling.regulation
Solyc01g006900.2.1	Phosphatidylglycerol/phosphatidylinositol transfer protein	3	0.086777815	0.093071144	0.000221741	11.52368269	not assigned.unknown
Solyc07g020860.2.1	Peroxiredoxin	3	0.137598303	0.070903001	1.88738E-14	7.267531471	redox.peroxiredoxin
Solyc06g066000.1.1	ATP synthase subunit b	3	0.097244716	0.074340232	9.9E-20	10.28333506	PS.lightreaction.ATP synthase
Sopim05g014280	Heat shock protein	3	0.056799849	0.042349544	9.9E-20	17.60568046	stress.abiotic.heat
Solyc12g056230.1.1	Glutathione peroxidase	3	0.074628623	0.070615663	1.00549E-08	13.3996844	redox.ascorbate and glutathione.glutathione
Solyc00g060810.2.1	Major latex_like protein	3	0.007915622	0.0055069	1.15241E-13	126.3324532	stress.abiotic.unspecified
Solyc06g059740.2.1	Alcohol dehydrogenase 2	3	0.03924209	0.036097371	9.9E-20	25.48284267	misc.alcohol dehydrogenases
Solyc05g014470.2.1	Glyceraldehyde 3_phosphate dehydrogenase	3	0.027338378	0.02827693	0.000154723	36.57861444	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Sopim08g062450	class II heat shock protein	3	0.033666439	0.01182412	9.9E-20	29.70317075	stress.abiotic.heat
Solyc06g076560.1.1	:class I heat shock protein	3	0.029756388	0.003048093	9.9E-20	33.60622907	stress.abiotic.heat

Sopim09g015020	class I heat shock protein 3	3	0.06035365	0.006406222	9.9E-20	16.56900631	stress.abiotic.heat
Sopim06g076560	class I heat shock protein	3	0.029756388	0.003048093	9.9E-20	33.60622907	stress.abiotic.heat
Sopim01g109660	Glycine_rich RNA_binding protein	2	0.277674537	0.146736198	2.92758E-05	3.601338504	RNA.RNA binding
Sopim01g100370	Universal stress protein	2	0.101569123	0.07174907	0.000483416	9.84551184	stress.abiotic.unspecified
Solyc01g097450.2.1	Thioredoxin_like protein 1	2	0.077294652	0.137874147	0.112982349	12.93750568	not assigned.unknown
Solyc04g009690.1.1	Cc_nbs_lrr_ resistance protein	2	0.044549737	0.056853692	0.01298267	22.44682168	stress.biotic
Solyc08g080940.2.1	Glutathione peroxidase	2	0.175209098	0.2183122	0.000226904	5.707466184	redox.ascorbate and glutathione.glutathione
Solyc12g100220.1.1	Short_chain dehydrogenase/reductase SDR	2	0.184303208	0.107738525	5.72602E-05	5.425841532	misc.short chain dehydrogenase/reductase (SDR)
Solyc04g080540.2.1	ST225	2	0.063655509	0.068538685	5.342E-06	15.70955949	not assigned.unknown
Sopim09g082650	Acireductone dioxygenase	2	0.200835695	0.170736224	5.52144E-08	4.979194571	metal handling.regulation
Solyc01g100790.1.1	Pentatricopeptide repeat_containing protein	2	0.140078201	0.203676005	0.008860329	7.138869545	RNA.regulation of transcription.MYB domain transcription factor family
Solyc09g091470.2.1	3_ketoacyl CoA thiolase 2	2	0.137931865	0.187207175	9.01478E-08	7.249956345	amino acid metabolism.degradation.branched-chain group.shared
Solyc12g094620.1.1	Catalase	2	0.008467269	0.006055574	0.000488055	118.1018375	redox.dismutases and catalases
Sopim06g066000	ATP synthase subunit b_apos	2	0.124740384	0.096654442	9.9E-20	8.016650018	PS.lightreaction.ATP synthase
Solyc09g090980.2.1	Major allergen Mal d 1	2	0.138202359	0.078529705	1.61116E-12	7.235766515	RNA.processing.ribonucleases
Solyc01g106620.2.1	Pathogenesis_related protein 1a	2	0.027328855	0.032234299	0.001583072	36.59136101	stress.biotic
Solyc12g014290.1.1	Multiprotein bridging factor 1b	2	0.124734743	0.177359343	0.000527971	8.01701253	hormone metabolism.ethylene.induced-regulated-responsive-activated
Solyc10g085550.1.1	Enolase	2	0.020307446	0.017097052	0.000654038	49.2430217	glycolysis.cytosolic branch.enolase
Solyc07g051850.2.1	Aspartic proteinase	2	0.21642276	0.16883533	1.0803E-07	4.620586111	protein.degradation.aspartate protease
Solyc04g054980.2.1	Lipoxygenase homology domain_containing protein 1	2	0.206537081	0.265391624	3.24452E-05	4.841745576	not assigned.unknown
Solyc04g054990.2.1	Lipoxygenase homology domain_containing protein 1	2	0.060406181	0.088422183	0.010417517	16.55459738	not assigned.unknown
Solyc07g062060.2.1	Peptide methionine sulfoxide reductase msrB	2	0.265312341	0.147102584	3.65816E-05	3.76914243	RNA.regulation of transcription.putative transcription regulator
Solyc01g095150.2.1	Late embryogenesis abundant protein	2	0.053851247	0.07543097	7.95146E-05	18.56967216	development.late embryogenesis abundant
Solyc01g111170.2.1	Peptidyl_prolyl cis_trans isomerase	2	0.160351443	0.16240711	0.001186666	6.236301184	cell.cycle.peptidylprolyl isomerase
Sopim07g020860	Peroxiredoxin	2	0.13044778	0.07211297	1.83187E-14	7.665902767	redox.peroxiredoxin
Solyc04g014480.2.1	class I heat shock protein 3	3	0.080218796	0.061474095	2.14688E-07	12.46590637	stress.abiotic.heat
Solyc09g055420.1.1	Nucleoside diphosphate kinase	2	0.299907564	0.206467051	0.003075449	3.33436072	nucleotide metabolism.phosphotransfer and pyrophosphatases.nucleoside
Solyc01g073640.2.1	Uncharacterized oxidoreductase Mb1385	2	0.050418331	0.035347912	0.000415023	19.83405583	misc.short chain dehydrogenase/reductase (SDR)
Sopim05g014280	Heat shock protein	3	0.124111212	0.036125284	9.9E-20	8.057289795	stress.abiotic.heat
Sopim11g022590	Kunitz trypsin inhibitor 4 (Fragment)	3	0.354363924	0.06950665	9.9E-20	2.821957688	not assigned.unknown
Solyc09g011490.2.1	Glutathione S_transferase_like protein	2	0.035843942	0.04213953	0.009155476	27.89871704	misc.glutathione S transferases
Solyc02g065240.2.1	Hydrolase alpha/beta fold family protein	2	0.007599016	0.007398472	1.81158E-06	131.5959782	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases
Solyc10g008010.2.1	Proteasome subunit alpha type	2	0.349305389	0.15821096	1.43776E-06	2.862824427	protein.degradation.ubiquitin.proteasom
Sopim10g008010	Proteasome subunit alpha type	2	0.349305389	0.15821096	1.43776E-06	2.862824427	protein.degradation.ubiquitin.proteasom
Solyc08g016670.2.1	Calcyclin_binding protein	2	0.002310891	0.003982139	6.45615E-06	432.7335737	not assigned.unknown
Solyc11g069790.1.1	chaperonin	3	0.189053918	0.024587362	1.33604E-12	5.289496294	protein.folding
Solyc01g006540.2.1	Lipoxygenase	3	0.102302962	0.03703062	0.000495411	9.774888022	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
Solyc08g005770.2.1	Alcohol acetyltransferase	3	0.184282186	0.081285062	4.44089E-16	5.426460494	secondary metabolism.phenylpropanoids
Sopim08g005770	Alcohol acetyltransferase	3	0.184282186	0.081285062	4.44089E-16	5.426460494	secondary metabolism.phenylpropanoids
Sopim12g014250	Phosphoenolpyruvate carboxylase 1	3	0.290297971	0.145335574	3.39458E-08	3.444736441	not assigned.unknown
Sopim09g011080	Ribulose_1 5_bisphosphate carboxylase/oxygenase activase 1	3	0.07501282	0.063556322	1.44139E-06	13.33105358	PS.calvin cycle.rubisco interacting
Sopim02g078540	Unknown Protein	2	0.079741976	0.069109204	2.57087E-06	12.54044672	not assigned.unknown
Sopim11g005330	Actin	2	0.141413693	0.112490928	9.9E-20	7.071450995	cell.organisation
Sopim08g076980	Acetylornithine deacetylase or succinyl_diaminopimelate desuccinylase	2	0.08850574	0.059527377	4.4167E-10	11.29870215	protein.degradation
Sopim04g073990	Annexin	4	0.309161222	0.098846712	9.9E-20	3.234558314	cell.organisation
Sopim08g078250	Palmitoyl_protein thioesterase 1	3	0.226358994	0.139634707	8.51311E-09	4.417761275	protein.postranslational modification
Sopim05g054350	Epoxide hydrolase	2	0.280514453	0.238380199	2.63236E-06	3.564878699	misc.misc2
Sopim09g082990	GDP_D_mannose_3AC_5AC _epimerase 2	2	0.297149653	0.129840304	2.47607E-07	3.365307646	cell wall.precursor synthesis.UXS
Solyc09g082060.2.1	Cysteine synthase	2	0.181119694	0.125136602	2.89004E-08	5.521210752	amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL

Table 5.7. Differentially expressed proteins identified in the fruits of wild species at different developmental stages using nanoLC-MS-MS.

Label-free quantitation was employed by matching retention times of the peaks and measuring area under the matched peaks using Sieve 2.1 software (Thermo Scientific) to identify the differentially expressed proteins in SP-SL, SG-SL, SH-SL pairs. Stringent selection criteria were imposed to identify these proteins (p value≤0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR=1%).

List of upregulated proteins in SG-SL

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO (SG/SL)	STD.DEV	PVALUE	FOLD CHANGE (SG/SL)	MAPMANCLASS
Sopim00g187050	Leucyl aminopeptidase	5	44.22114173	20.67758473	2.53E-05	44.22114173	stress abiotic unspecified
Sopim01g006580	2oxoglutaratedependent dioxygenase	3	4.838919805	2.672094902	2.01E-06	4.838919805	hormone metabolism gibberelin synthesisdegradation
Sopim01g006610	2oxoglutaratedependent dioxygenase	3	214.7554687	120.1600261	7.59E-05	214.7554687	hormone metabolism gibberelin synthesisdegradation
Sopim01g006900	Phosphatidylglycerol/phosphatidylinositol transfer protein	3	10.59127911	6.167228093	0.00014287	10.59127911	amino acid metabolism synthesis branched chain group common
Sopim01g006940	PolyU binding splicing factor PUF60	2	9.902622224	8.435175097	1.31E-08	9.902622224	RNA RNA binding
Sopim01g008950	Calmodulin 5/6/7/8like protein	2	12.52057531	13.59615003	0.008376995	12.52057531	signalling calcium
Sopim01g097350	Calcium binding EF hand family protein	2	13.15586453	9.829102425	0.000291187	13.15586453	signalling calcium
Sopim01g101240	Aspartic proteinase	3	12.47648623	6.433291966	3.35E-05	12.47648623	protein degradation aspartate protease
Sopim01g102960	class IV heat shock protein	10	51.38248236	15.48796083	2.32E-13	51.38248236	stress abiotic heat
Sopim01g103480	Coatomer subunit delta	3	5.32059575	2.08380886	0.00068747	5.32059575	cell vesicle transport
Sopim01g106320	Octicosapeptide/Phox/Bem1p domaincontaining protein	5	10.14476067	3.176179056	1.28E-06	10.14476067	DNA synthesis/chromatin structure
Sopim01g107870	PolyA RNA binding protein	2	10.22367993	6.347155989	0.006257276	10.22367993	RNA processing
Sopim02g021220	Subtilisinlike protease	3	2.850307041	1.034172265	0.000221102	2.850307041	signalling calcium
Sopim02g021560	Heterogeneous nuclear ribonucleoprotein A3like protein 2	2	6.628047139	4.673842076	0.010759048	6.628047139	protein postranslational modification
Sopim02g065400	Oxygenevolving enhancer protein 1 of photosystem II	2	3.42301737	2.678838012	0.001064375	3.42301737	PS lightreaction photosystem II PSII polypeptide subunits
Sopim02g070940	Chlorophyll a/b binding protein	3	7.68962533	5.742287172	0.002258607	7.68962533	PS lightreaction photosystem II PSII polypeptide subunits
Sopim02g070980	Chlorophyll a/b binding protein	3	7.68962533	5.742287172	0.002258607	7.68962533	PS lightreaction photosystem II PSII polypeptide subunits
Sopim02g070990	Chlorophyll a/b binding protein	3	7.68962533	5.742287172	0.002258607	7.68962533	PS lightreaction photosystem II PSII polypeptide subunits
Sopim02g071000	Chlorophyll a/b binding protein	3	7.68962533	5.742287172	0.002258607	7.68962533	PS lightreaction photosystem II PSII polypeptide subunits
Sopim07g056540	L_lactate dehydrogenase	3	14.60685724	2.919445915	0.00035348	14.60685724	PS photorespiration glycolate oxydase
Sopim02g067460	Porin/voltagedependent anionselective channel protein	6	4.110167413	1.72921265	4.02E-07	4.110167413	Cofactor and vitamine metabolism folate and vitamine K vitamine K isochorismate synthase
Sopim02g078040	Pistil extensin like protein Fragment	3	20.75350126	10.54076527	5.11E-11	20.75350126	cell wall cell wall proteins proline rich proteins
Sopim02g079750	Flavoprotein wrbA	7	28.97506229	7.071263303	9.90E-20	28.97506229	lipid metabolism exotics steroids squalene etc
Sopim02g080880	Aspartic proteinase	4	3.876253666	2.212978471	1.78E-06	3.876253666	protein degradation aspartate protease
Sopim02g085040	2,3,4,5 tetrahydropyridine 2, 6 dicarboxylate N-acetyltransferase	2	6.628047139	4.673842076	0.010759048	6.628047139	misc UDP glucosyl and glucoronyl transferases
Sopim02g085590	Vicilin Fragment	2	26.11277397	30.76183338	0.00289761	26.11277397	amino acid metabolism synthesis branched chain group common
Sopim02g087190	Peroxidase 65	2	18.05052552	20.660225	0.002494746	18.05052552	misc peroxidases
Sopim03g005580	Legumin 11Sglobulin	4	3.876253666	2.212978471	1.78E-06	3.876253666	development storage proteins
Sopim03g033690	Peroxidase	3	5.897165724	5.642622134	0.001884322	5.897165724	misc peroxidases
Sopim03g058920	Porin/voltage dependent anion selective channel protein	2	4.094154957	3.531779038	0.000664666	4.094154957	transport sugars
Sopim03g082920	Heat shock protein	5	3.712894101	1.32088201	3.59E-07	3.712894101	cell wall hemicellulose synthesis
Sopim03g094010	Glutamate dehydrogenase	2	2.834257784	0.991924736	8.91E-05	2.834257784	DNA unspecified
Sopim03g096040	Mitochondrial peroxiredoxin 1Cys Prx with thioredoxin peroxidase activity	2	100.8681119	99.26551329	0.004083095	100.8681119	redox peroxiredoxin PER1
Sopim03g098050	Calmodulin 3 protein	2	18.3568559	12.73119251	0.002678164	18.3568559	signalling calcium
Sopim03g111730	Cathepsin B like cysteine proteinase	8	4.943842453	2.098480602	5.95E-10	4.943842453	protein degradation cysteine protease
Sopim03g112440	Oleosin	2	6.650432485	7.763333353	0.005530953	6.650432485	RNA regulation of transcription C2H2 zinc finger family
Sopim03g117020	Stromal cell derived factor 2	3	3.300009134	1.97084958	0.000798157	3.300009134	not assigned no ontology
Sopim03g117630	heat shock protein	2	3.140842082	0.988381763	0.007856556	3.140842082	misc cytochrome P450
Sopim04g011440	heat shock protein	2	2.834257784	0.991924736	8.91E-05	2.834257784	cell wall hemicellulose synthesis
Sopim04g014720	60S ribosomal protein L6	3	26.76730053	20.55832887	0.00066161	26.76730053	protein synthesis ribosomal protein eukaryotic 60S subunit L6
Sopim04g015340	Serine carboxypeptidase K10B22	6	24.59966417	6.933015385	9.90E-20	24.59966417	protein degradation serine protease
Sopim04g080880	Cathepsin B like cysteine proteinase	2	6.628047139	4.673842076	0.010759048	6.628047139	protein degradation cysteine protease
Sopim04g080960	Cysteine proteinase cathepsin F	11	58.59102908	15.2186527	9.90E-20	58.59102908	protein degradation cysteine protease
Sopim05g051260	Endo1 4betaxylanase	2	9.902622224	8.435175097	1.31E-08	9.902622224	cell wall degradation mannanxylosearabinosefucose
Sopim05g051660	Gibberellin receptor GID1L2	2	25.20933069	20.11003419	0.004221995	25.20933069	biodegradation of xenobiotics
Sopim05g052690	Eukaryotic translation initiation factor 3 subunit 5	2	49.02305461	55.7018655	0.006223027	49.02305461	protein degradation ubiquitin proteasom
Sopim05g053350	Desiccation related protein PCC1362	4	7.665096878	4.775734571	9.33E-09	7.665096878	signalling receptor kinases misc
Sopim05g054070	60S ribosomal protein L6	3	18.38228151	12.4468577	1.61E-09	18.38228151	protein synthesis ribosomal protein eukaryotic 60S subunit L6
Sopim05g056400	Protein disulfide isomerase	3	14.04159761	6.209111779	5.96E-05	14.04159761	misc short chain dehydrogenase/reductase SDR
Sopim06g005160	Ascorbate peroxidase	2	57.83135177	61.36903054	0.003933407	57.83135177	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Sopim06g005940	Protein disulfide isomerase	2	4.36253881	3.501083207	0.002629751	4.36253881	misc short chain dehydrogenase/reductase SDR
Sopim06g034040	Oleosin	2	5.251929528	4.182936241	0.004312302	5.251929528	lipid metabolism TAG synthesis
Sopim06g052050	Heat shock protein	4	5.237930302	2.305144991	1.02E-05	5.237930302	transport misc
Sopim06g063370	Chlorophyll ab binding protein 1A chloroplastic	3	40.52186401	36.50865646	0.002127315	40.52186401	PS lightreaction photosystem II LHCII
Sopim06g071910	3 oxoacyl reductase	2	5.634044954	6.638789697	0.012424223	5.634044954	lipid metabolism FA synthesis and FA elongation ACP oxoacyl reductase
Sopim06g076540	class I heat shock protein	5	308.0432665	148.0337788	2.87E-10	308.0432665	stress abiotic heat
Sopim06g076570	class I heat shock protein	2	5.907361022	5.29322281	0.013817251	5.907361022	hormone metabolism auxin inducedregulatedresponsiveactivated
Sopim06g076660	Proliferating cell nuclear antigen	3	7.051764372	6.353751405	5.68E-05	7.051764372	RNA regulation of transcription putative transcription regulator
Sopim06g083030	Serine carboxypeptidase 1	3	2.850307041	1.034172265	0.000221102	2.850307041	protein degradation serine protease
Sopim07g005820	heat shock protein	2	2.834257784	0.991924736	8.91E-05	2.834257784	protein folding
Sopim07g005960	Serine carboxypeptidase K10B22	2	13.80663205	11.48173288	0.009623522	13.80663205	cell wall precursor synthesis UXS
Sopim07g009380	Xyloglucan endotransglucosylase/hydrolase 2	2	55.55897783	39.50437775	1.19E-08	55.55897783	cell wall modification
Sopim07g041490	Stress responsive alpha beta barrel domain protein	5	57.92131734	12.82158484	9.90E-20	57.92131734	not assigned no ontology
Sopim07g049450	Thioredoxin/protein disulfide isomerase	3	3.511589054	0.980416101	0.000171983	3.511589054	hormone metabolism brassinosteroid synthesisdegradation BRs DET2
Sopim07g056610	Carboxyl terminal proteinase	3	34.70577267	28.09354654	0.00015285	34.70577267	protein degradation
Sopim07g061800	Heme binding protein 2	2	104.1224368	70.68312262	0.00041963	104.1224368	tetrapyrrole synthesis unspecified
Sopim07g064160	Thiazole biosynthetic enzyme	4	32.44643589	25.8237786	1.34E-06	32.44643589	Cofactor and vitamine metabolism thiamine
Sopim07g065540	Fasciclinlike arabinogalactan protein 10	3	2.25659861	0.86577988	0.000104766	2.25659861	cell wall cell wall proteins AGPs AGP
Sopim07g065900	Fructose bis phosphate aldolase	2	13.98642953	6.216253754	0.010651802	13.98642953	PS calvin cycle aldolase
Sopim07g066580	Mercaptopyruvate sulfurtransferase like protein	3	120.9154109	83.15215961	0.001224227	120.9154109	misc rhodanese
Sopim07g066600	Phosphoglycerate kinase	2	7.049994471	6.916881228	0.001786464	7.049994471	glycolysis cytosolic branch 3phosphoglycerate kinase PGK
Sopim08g007620	Subtilisinlike protease	6	11.7443062	4.67563013	4.37E-08	11.7443062	protein degradation subtilases
Sopim08g065780	Vacuolar processing enzyme	6	4.110167413	1.72921265	4.02E-07	4.110167413	protein targeting secretory pathway vacuole
Sopim08g065790	Vacuolar processing enzyme	2	6.326608741	5.431404375	0.000177831	6.326608741	protein degradation cysteine protease
Sopim08g074620	Polyphenol oxidase	9	9.56024074	2.232257275	7.03E-08	9.56024074	secondary metabolism simple phenols
Sopim08g074630	Polyphenol oxidase	9	9.56024074	2.232257275	7.03E-08	9.56024074	secondary metabolism simple phenols
Sopim08g077840	Cupin 2 conserved barrel domain protein	2	6.11219667	6.185714069	0.000311637	6.11219667	RNA regulation of transcription triplehelix transcription factor family Trihelix
Sopim08g079160	Vacuolar processing enzyme	2	3.440672281	3.37204177	0.003802504	3.440672281	protein targeting secretory pathway vacuole
Sopim08g079880	Subtilisinlike protease	3	74.56964349	36.28616922	1.01E-05	74.56964349	protein degradation subtilases
Sopim08g080490	2S albumin seed storage protein Fragment	3	5.897165724	5.642622134	0.001884322	5.897165724	protein targeting mitochondria
Sopim08g082820	Heat shock protein	5	3.712894101	1.32088201	3.59E-07	3.712894101	protein folding
Sopim09g008670	Threonine ammonia lyase biosynthetic	6	8.818934136	2.091461988	4.86E-07	8.818934136	amino acid metabolism degradation aspartate family threonine
Sopim09g025210	Legumin 11Sglobulin	5	42.01427805	20.79819882	3.38E-05	42.01427805	development storage proteins
Sopim09g065470	Vicilin Fragment	2	2.143120007	0.543500032	0.006137625	2.143120007	misc glutathione S transferases
Sopim09g072560	Legumin 11S globulin	2	68.08390079	42.66978997	0.001122504	68.08390079	development storage proteins
Sopim09g082340	Vicilinlike protein Fragment	10	17.64736893	7.924048618	2.60E-09	17.64736893	development storage proteins
Sopim09g084450	Chymotrypsin inhibitor 2	2	6.628047139	4.673842076	0.010759048	6.628047139	stress biotic PRproteins PR6 proteinase inhibitors
Sopim09g090150	Legumin 11Sglobulin	4	11.83353044	8.810075878	0.000229191	11.83353044	development storage proteins
Sopim09g090990	Major allergen Mal d 1	35	31.66349999	5.733078888	9.90E-20	31.66349999	transport ABC transporters and multidrug resistance systems
Sopim10g005430	Flavoprotein wrbA	3	10.59127911	6.167228093	0.00014287	10.59127911	lipid metabolism exotics steroids squalene etc
Sopim10g007690	Chlorophyll ab binding protein 8	6	2.35909661	0.93309009	9.99E-14	2.35909661	PS lightreaction photosystem I LHCI
Sopim10g077010	Calmodulin 2	2	18.3568559	12.73119251	0.002678164	18.3568559	PS lightreaction photosystem II PSII polypeptide subunits
Sopim10g081170	Calmodulin 2	2	4.965386618	5.034175385	0.001704055	4.965386618	PS lightreaction photosystem II PSII polypeptide subunits
Sopim11g006250	GDSL esterase/lipase At5g33370	26	7.9749005	3.435219567	9.90E-20	7.9749005	misc GDSLmotif lipase
Sopim11g008990	Phage shock protein A PspA	2	6.096559826	6.223470843	0.000494328	6.096559826	cell wall precursor synthesis UXS
Sopim11g012110	60S ribosomal protein L6	3	6.151908607	3.906156246	0.0001012	6.151908607	protein synthesis ribosomal protein eukaryotic 60S subunit L6
Sopim11g013260	Prohibitin	2	12.10158043	11.12227146	0.007546751	12.10158043	mitochondrial electron transport / ATP synthesis NADHDH type I complex I
Sopim11g013440	Eukaryotic translation initiation factor 3 subunit 5	2	70.55503707	83.42100645	0.006036636	70.55503707	protein degradation ubiquitin proteasom
Sopim11g066100	heat shock protein	2	2.834257784	0.991924736	8.91E-05	2.834257784	protein folding
Sopim11g066130	Thaumatinlike protein	3	20.4655429	26.67587183	5.53E-05	20.4655429	stress biotic
Sopim12g005200	Electron transfer flavoprotein alpha subunit	2	26.00369329	22.21398467	0.001237232	26.00369329	mitochondrial electron transport / ATP synthesis electron transfer flavoprotein
Sopim12g010020	Leucyl aminopeptidase	4	4.664950502	2.226263398	3.39E-08	4.664950502	protein degradation
Sopim12g010820	Group 3 late embryogenesis abundant protein	2	36.6521854	31.76813072	0.005474069	36.6521854	development late embryogenesis abundant
Sopim12g010920	Oleosin	4	10.93272065	6.486579576	3.66E-05	10.93272065	lipid metabolism TAG synthesis
Sopim12g017460	GDSL esterase/lipase At1g28590	2	4.107144393	4.249644955	0.001962345	4.107144393	misc GDSLmotif lipase
Sopim12g088720	Polyadenylate binding protein 2	2	2.834257784	0.991924736	8.91E-05	2.834257784	RNA processing
Sopim00g006800	Transaldolase	2	12.98886491	7.073650319	0.001996703	12.98886491	lipid metabolism FA synthesis and FA elongation long chain fatty acid CoA ligase
Sopim01g006540	Lipoxygenase	3	7.118189012	3.511079984	0.000245662	7.118189012	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim01g007320	ATP synthase subunit beta chloroplastic	2	6.108041425	4.122944572	0.007815648	6.108041425	PS lightreaction ATP synthase beta subunit
Sopim01g007740	Peroxiredoxin	3	3.702119292	0.823340318	4.50E-05	3.702119292	redox peroxiredoxin BAS1
Sopim01g008330	AcetylCoA carboxylase biotin carboxylase	2	3.295236189	1.73452799	0.006306768	3.295236189	amino acid metabolism degradation branched chain group leucine
Sopim01g009180	5 methyltetrahydropteroyl triglutamate homocysteine methyltransferase	2	9.658463601	6.364575087	0.009533471	9.658463601	amino acid metabolism synthesis aspartate family methionine methionine synthase
Sopim01g028810	chaperonin	3	7.820238288	2.095669131	0.000769682	7.820238288	protein folding
Sopim01g059880	ATP citrate lyase a subunit	2	3.304190987	0.763752269	0.005853588	3.304190987	TCA / organic transformation other organic acid transformations atpcitrate lyase
Sopim07g047800	Short_chain dehydrogenase/reductase family protein	2	6.0285	0.9884	0.0143	6.0285	misc short chain dehydrogenase/reductase SDR
Sopim09g009390	Monodehydroascorbate reductase	2	18.0157	6.8315	0.0007	18.0157	redox
Sopim01g007320	ATP synthase subunit beta chloroplastic	2	6.1080	4.1229	0.0078	6.1080	Pslight reaction
Solyc01g009180.2.1	5_methyltetrahydropteroyltriglutamate__homocysteine methyltransferase	2	9.6585	6.3646	0.0095	9.6585	amino acid metabolism synthesis aspartate family methionine methionine synthase
Sopim01g009180	5_methyltetrahydropteroyltriglutamate__homocysteine methyltransferase	2	9.6585	6.3646	0.0095	9.6585	amino acid metabolism synthesis aspartate family methionine methionine synthase
Solyc07g055320.2.1	ATP_dependent Zn protease cell division protein FtsH homolog	2	3.8176	1.8736	0.0083	3.8176	cell division proteases
Sopim09g090980	Major allergen Mal d 1	2	27.0488	11.9931	0.0022	27.0488	transport ABC transporters and multidrug resistance systems
Solyc02g088610.2.1	ATP_dependent chaperone ClpB	2	9.4124	4.9201	0.0006	9.4124	stress abiotic heat
Sopim01g087070	Mitochondrial ADP/ATP carrier proteins	2	7.6346	2.1659	0.0087	7.6346	transport metabolite transporters at the envelope membrane
Sopim10g080710	Asparaginyl_tRNA synthetase 2	2	6.8455	5.6786	0.0136	6.8455	amino acid metabolism
Sopim01g111170	Peptidyl prolyl cis trans isomerase	2	10.14296695	4.089061571	0.002762369	10.14296695	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Sopim02g023970	GTPbinding protein	2	8.270059962	2.59703405	0.000728891	8.270059962	signalling Gproteins
Sopim02g063130	UV excision repair protein RAD23	2	4.003469774	2.363275941	0.007361863	4.003469774	protein degradation ubiquitin ubiquitin
Sopim02g063490	Malate dehydrogenase	2	14.09552931	13.39737251	2.34E-05	14.09552931	RNA regulation of transcription ABI3/VP1related B3domaincontaining transcription factor family
Sopim02g070940	Chlorophyll a/b binding protein	3	7.68962533	5.742287172	0.002258607	7.68962533	PS lightreaction photosystem II LHCII
Sopim02g070980	Chlorophyll a/b binding protein	3	7.68962533	5.742287172	0.002258607	7.68962533	PS lightreaction photosystem II LHCII
Sopim02g071000	Chlorophyll a/b binding protein	3	7.68962533	5.742287172	0.002258607	7.68962533	PS lightreaction photosystem II LHCII
Sopim02g079510	Peroxidase	2	4.391890758	1.601764055	0.002545781	4.391890758	misc peroxidases
Sopim02g083860	Flavanone 3 hydroxylase	2	11.64700884	9.753897907	0.003904325	11.64700884	hormone metabolism ethylene synthesisdegradation
Sopim02g088610	ATPdependent chaperone ClpB	2	9.412432139	4.920108439	0.000567585	9.412432139	stress abiotic heat
Sopim02g090030	Oxygen evolving enhancer protein 1 of photosystem II	2	3.140605836	1.12484266	0.01531319	3.140605836	PS lightreaction photosystem II PSII polypeptide subunits
Sopim02g091580	Oligopeptidase A	3	19.31314056	4.257517884	2.50E-06	19.31314056	hormone metabolism brassinosteroid synthesisdegradation sterols SMT1
Sopim02g094120	Sulfite oxidase	2	2.724833745	0.302624815	0.000746506	2.724833745	Nmetabolism nitrate metabolism NR
Sopim03g005760	Chlorophyll ab binding protein 3Clike	2	7.911171094	7.591467165	0.009753886	7.911171094	PS lightreaction photosystem II LHCII
Sopim03g005770	Chlorophyll ab binding protein 3Clike	2	7.911171094	7.591467165	0.009753886	7.911171094	PS lightreaction photosystem II LHCII
Sopim03g005780	Chlorophyll ab binding protein 3Clike	2	7.911171094	7.591467165	0.009753886	7.911171094	PS lightreaction photosystem II PSII polypeptide subunits
Sopim03g025730	Tubulin beta chain	2	4.755615756	0.904746681	0.009175944	4.755615756	secondary metabolism phenylpropanoids
Sopim03g083910	Acid betafructofuranosidase	8	8.665259203	0.670755071	1.43E-14	8.665259203	major CHO metabolism degradation sucrose invertases vacuolar
Sopim03g097700	Omethyltransferase	2	3.321233861	0.363221823	0.014048444	3.321233861	secondary metabolism phenylpropanoids lignin biosynthesis COMT
Sopim03g111010	Glyceraldehyde3phosphate dehydrogenase	2	3.029440659	0.593574999	0.000316457	3.029440659	glycolysis cytosolic branch glyceraldehyde 3phosphate dehydrogenase GAPDH
Sopim03g118040	Calcium binding protein Calnexin	2	4.665344073	2.327173888	0.008637404	4.665344073	signalling calcium
Sopim03g118340	ATP-dependent clp protease ATPbinding subunit	2	8.765193553	0.476670831	3.49E-05	8.765193553	stress abiotic heat
Sopim03g118760	Tubulin beta chain	3	4.77533606	0.901622257	0.002432158	4.77533606	cell organisation
Sopim04g009030	Glyceraldehyde 3 phosphate dehydrogenase	2	4.371977008	2.624663947	0.009333279	4.371977008	PS calvin cycle GAP
Sopim04g011510	Triose phosphate isomerase	2	26.27906351	12.59642249	1.63E-05	26.27906351	glycolysis cytosolic branch triosephosphate isomerase TPI
Sopim04g015560	Beta D glucosidase	2	10.69574018	5.543374581	0.011546006	10.69574018	misc gluco galacto and mannosidases
Sopim04g045340	Phosphoglucomutase	3	4.969730313	1.547425508	0.001300648	4.969730313	glycolysis cytosolic branch phosphoglucomutase PGM
Sopim04g063290	30S ribosomal protein S5	2	5.513805999	3.224071869	0.001911945	5.513805999	protein synthesis ribosomal protein eukaryotic 40S subunit S2
Sopim04g074300	30S ribosomal protein S5	2	17.69393891	9.386849255	0.001076181	17.69393891	protein synthesis ribosome biogenesis
Sopim04g074480	3 deoxy 7 phosphoheptulonate synthase/Phospho 2 dehydro 3 deoxyheptonate aldolas	2	6.965997428	4.173747391	0.003661629	6.965997428	amino acid metabolism synthesis aromatic aa chorismate 3deoxyDarabinoheptulosonate 7phosphate synthase
Sopim04g080850	Thioredoxin	2	55.37589774	9.610960866	0.000234906	55.37589774	DNA synthesis/chromatin structure
Sopim04g081490	Tubulin beta1 chain	2	4.755615756	0.904746681	0.009175944	4.755615756	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Sopim04g082010	Plastocyanin	2	4.182095239	1.744185695	0.005730557	4.182095239	PS lightreaction other electron carrier ox/red plastocyanin
Sopim04g082140	Laccase 22	2	8.886283837	1.379947053	0.015052779	8.886283837	RNA regulation of transcription C2H2 zinc finger family
Sopim04g082250	ATP-dependent zinc metalloprotease FTSH chloroplastic Fragment	2	7.680260549	4.759564101	0.011998827	7.680260549	protein degradation metalloprotease
Sopim04g082880	Diphosphate fructose 6 phosphate 1 phosphotransferase	2	5.675904027	1.988068461	0.00518535	5.675904027	glycolysis cytosolic branch pyrophosphatefructose6P phosphotransferase
Sopim05g050120	Malic enzyme	3	3.667687342	0.912025736	2.75E-05	3.667687342	TCA / organic transformation other organic acid transformations malic
Sopim05g050970	Transketolase 1	2	6.411713472	1.355285077	0.004799973	6.411713472	OPP nonreductive PP transketolase
Sopim05g054760	Dehydro ascorbate reductase Fragment	2	4.160937177	0.473406144	0.000561945	4.160937177	lipid metabolism FA synthesis and FA elongation long chain fatty acid CoA ligase
Sopim05g055760	Isopentenyl diphosphate deltaisomerase	2	13.58837725	9.283833603	0.000524139	13.58837725	RNA regulation of transcription unclassified
Sopim06g005060	Elongation factor 1alpha	2	5.159180809	1.23585361	0.001376042	5.159180809	protein synthesis elongation
Sopim06g005910	Tubulin beta chain	2	4.836515466	3.542514294	0.009008914	4.836515466	secondary metabolism phenylpropanoids
Sopim06g009020	Glutathione S transferase	2	5.618268021	2.218600407	0.002642602	5.618268021	misc glutathione S transferases
Sopim06g009960	Elongation factor 1alpha	2	5.159180809	1.23585361	0.001376042	5.159180809	protein synthesis elongation
Sopim06g011280	Elongation factor 1gamma	3	5.742188845	3.279091064	0.002032012	5.742188845	protein synthesis elongation
Sopim06g035970	Tubulin beta chain	3	5.141748033	3.413609711	0.002644476	5.141748033	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Sopim06g060290	Protein disulfide isomerase	2	2.375923476	0.622124326	0.00667601	2.375923476	redox thioredoxin
Sopim06g063330	Vtype ATP synthase alpha chain	2	6.035243111	2.167452804	0.00115832	6.035243111	PS lightreaction ATP synthase
Sopim06g073740	Beta D glucosidase	2	5.956148765	4.093798316	0.004020369	5.956148765	misc gluco galacto and mannosidases
Sopim06g076640	Tubulin beta chain	2	4.836515466	3.542514294	0.009008914	4.836515466	cell organisation
Sopim07g006560	Hypersensitive response assisting protein	2	7.089278254	7.584885648	0.013685889	7.089278254	RNA processing ribonucleases
Sopim07g006650	Xylose isomerase	2	22.18931823	12.235753	0.00493363	22.18931823	minor CHO metabolism others xylose isomerase
Sopim07g016150	Elongation factor 1beta	2	2.744428597	0.493047431	0.006334669	2.744428597	protein synthesis elongation
Sopim07g041900	Cathepsin L like cysteine proteinase	2	7.815685841	7.544371743	0.015664318	7.815685841	protein degradation cysteine protease
Sopim07g044860	Oxygen evolving enhancer protein 2 chloroplastic	2	3.440569895	0.948054337	0.004312912	3.440569895	transport major intrinsic proteins NIP

Sopim07g047800	Short chain dehydrogenase/reductase family protein	2	6.028538953	0.988363208	0.014308211	6.028538953	misc short chain dehydrogenase/reductase SDR
Sopim07g047850	Chlorophyll ab binding protein 4 chloroplastic	3	8.779338817	7.231430909	0.00161447	8.779338817	PS lightreaction photosystem II LHCII
Sopim07g053280	Ketolacid reductoisomerase	2	3.95441201	2.749813588	0.014440802	3.95441201	amino acid metabolism synthesis branched chain group common ketolacid reductoisomerase
Sopim07g053830	Mitochondrial ADP/ATP carrier protein	3	3.586448914	0.737254365	0.001057907	3.586448914	transport metabolite transporters at the envelope membrane
Sopim07g055320	ATPdependent Zn protease cell division protein FtsH homolog	2	3.817574165	1.873614944	0.008277301	3.817574165	protein degradation metalloprotease
Sopim07g056540	L lactate dehydrogenase	3	14.60685724	2.919445915	0.00035348	14.60685724	PS photorespiration glycolate oxydase
Sopim07g064180	Pectinesterase	2	24.71636749	3.780652364	4.82E-05	24.71636749	cell wall pectinesterases PME
Sopim07g065840	Heat shock protein 90	2	3.32494132	1.156397902	0.00583141	3.32494132	stress abiotic heat
Sopim08g014000	Lipoxygenase	2	5.842646375	2.824764141	0.010565633	5.842646375	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim08g021990	26S protease regulatory subunit 6A homolog	2	6.374331689	4.169597072	0.005060473	6.374331689	protein degradation ubiquitin proteasom
Sopim08g068330	Aspartate aminotransferase	2	4.388127817	1.06180588	0.009143998	4.388127817	transport amino acids
Sopim08g074940	Aspartic proteinase nepenthesin2	2	120.9377332	61.54509086	0.000047898	120.9377332	RNA regulation of transcription AP2/EREBP APETALA2/ethyleneresponsive element binding protein family
Sopim08g080640	Osmotinlike protein Fragment	7	16.29391252	3.402236726	4.00E-09	16.29391252	stress abiotic
Sopim09g009390	Mono dehydroascorbate reductase NADHlike protein	2	18.01571025	6.831487181	0.000650104	18.01571025	redox ascorbate and glutathione ascorbate
Sopim09g011030	Hsp70 nucleotide exchange factor fes1	2	3.909228832	1.576275278	0.003461435	3.909228832	not assigned no ontology armadillo/betacatenin repeat family protein
Sopim09g090980	Major allergen Mal d 1	5	12.86422334	1.8489696	3.35E-08	12.86422334	transport ABC transporters and multidrug resistance systems
Sopim09g091470	3ketoacyl CoA thiolase 2	3	5.824131105	2.134902272	0.000522524	5.824131105	amino acid metabolism degradation branched chain group shared
Sopim09g092380	Adenosyl homocysteinase	2	2.518501354	0.439814489	0.006495934	2.518501354	amino acid metabolism degradation aspartate family methionine
Sopim09g092390	Adenosylhomocysteinase	2	2.518501354	0.439814489	0.006495934	2.518501354	amino acid metabolism degradation aspartate family methionine
Sopim09g098120	DUF1264 domain protein	2	14.1713634	8.737299205	0.015662779	14.1713634	development storage proteins
Sopim10g007600	L lactate dehydrogenase	3	5.686989739	2.685574011	0.000559165	5.686989739	signalling receptor kinases Catharanthus roseuslike RLK1
Sopim10g080710	Asparaginyl tRNA synthetase 2	2	6.845475031	5.678592855	0.013616972	6.845475031	protein an activation asparaginetRNA ligase
Sopim10g080940	Tubulin beta chain	2	4.836515466	3.542514294	0.009008914	4.836515466	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Sopim10g081510	5 methyltetrahydropteroyl triglutamate homocysteine methyltransferase	3	11.22473158	3.477687069	0.00093476	11.22473158	amino acid metabolism synthesis aspartate family methionine methionine synthase
Sopim10g082030	Peroxiredoxin	3	3.830589871	0.538765456	5.23E-06	3.830589871	redox peroxiredoxin BAS1
Sopim10g083570	Fructose bis phosphate aldolase	4	6.067725067	0.462332298	2.46E-08	6.067725067	RNA regulation of transcription AtSR transcription factor family
Sopim10g084350	60S ribosomal protein L4B L1	3	3.611420679	0.196839584	2.18E-07	3.611420679	protein synthesis ribosomal protein eukaryotic 60S subunit L4/L1
Sopim10g085020	Tubulin beta chain	2	4.755615756	0.904746681	0.009175944	4.755615756	cell organisation
Sopim10g086010	60S ribosomal protein L4/L1	2	3.583146598	0.19984098	1.59E-05	3.583146598	protein synthesis ribosomal protein eukaryotic 60S subunit L4/L1
Sopim10g086150	Single stranded DNA binding protein	2	11.83839325	5.076363448	0.003623034	11.83839325	RNA RNA binding
Sopim10g086760	Tubulin beta chain	2	4.755615756	0.904746681	0.009175944	4.755615756	cell organisation
Sopim11g000980	Phospho 2 dehydro 3 deoxyheptonate aldolase 1	2	6.965997428	4.173747391	0.003661629	6.965997428	transport ABC transporters and multidrug resistance systems
Sopim11g010960	Alcohol dehydrogenase	2	9.823556585	6.133820862	0.001750698	9.823556585	transport peptides and oligopeptides
Sopim11g062130	Mitochondrial ADP/ATP carrier protein	3	3.586448914	0.737254365	0.001057907	3.586448914	major CHO metabolism synthesis starch transporter
Sopim11g062190	Mitochondrial ADP/ATP carrier protein	3	3.586448914	0.737254365	0.001057907	3.586448914	major CHO metabolism synthesis starch transporter
Sopim11g069700	Elongation factor 1alpha	2	5.116859689	1.276530153	0.000533545	5.116859689	protein synthesis elongation
Sopim11g069790	chaperonin	2	4.137975396	1.84636996	0.003080239	4.137975396	PS calvin cycle rubisco interacting
Sopim11g072190	Elongation factor beta1	2	9.009188374	2.34362963	0.009781215	9.009188374	redox thioredoxin
Sopim12g006140	Chlorophyll ab binding protein 37	2	9.114611494	9.122591124	0.004254829	9.114611494	PS lightreaction photosystem II LHCII
Sopim12g015880	Heat shock protein 90	2	3.32494132	1.156397902	0.00583141	3.32494132	RNA regulation of transcription MYBrelated transcription factor family
Sopim12g042060	ATPdependent clp protease ATPbinding subunit	3	8.771202455	0.47640889	1.07E-05	8.771202455	stress abiotic heat
Sopim12g055800	Vtype ATP synthase alpha chain	2	2.392715362	0.31932568	0.006876895	2.392715362	PS lightreaction ATP synthase
Sopim12g056250	Glutathione S transferase	2	10.6794915	2.886218468	0.014847924	10.6794915	misc glutathione S transferases
Sopim12g057110	14-3-3 Fragment	2	22.6405927	9.322545543	0.002183146	22.6405927	signalling 1433 proteins
Sopim12g089310	Tubulin beta1 chain	3	4.77533606	0.901622257	0.002432158	4.77533606	secondary metabolism phenylpropanoids
Sopim12g098500	Adenosyl homocysteinase	2	2.518501354	0.439814489	0.006495934	2.518501354	amino acid metabolism degradation aspartate family methionine
Sopim12g099440	Fatty acid oxidation complex subunit alpha	2	8.348932551	3.931028481	0.00084388	8.348932551	lipid metabolism lipid degradation betaoxidation multifunctional
Sopim00g187050	Leucyl aminopeptidase	2	7.887761667	6.585954018	0.007864816	7.887761667	protein degradation
Sopim01g007330	Ribulose bisphosphate carboxylase large chain	2	3.164406233	1.649819673	0.001863312	3.164406233	protein synthesis ribosomal protein prokaryotic chloroplast 30S subunit S15
Sopim01g010760	Porin/voltage dependent anion selective channel protein	2	3.110320399	2.084876253	0.007762058	3.110320399	transport porins
Sopim01g099150	Lipoxygenase	2	2.986903776	1.61305704	0.003048303	2.986903776	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim01g099160	Lipoxygenase	2	2.986903776	1.61305704	0.003048303	2.986903776	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim01g108880	1 aminocyclopropane 1 carboxylate oxidase	3	4.61571989	2.304467608	3.79E-05	4.61571989	hormone metabolism ethylene synthesisdegradation 1aminocyclopropane1carboxylate oxidase
Sopim02g062460	2 oxoglutarate dependent dioxygenase	3	3.25783887	1.168020833	0.000272732	3.25783887	hormone metabolism ethylene synthesisdegradation
Sopim02g063070	14 3 3 protein beta/alpha 1	2	3.76846304	1.617130456	0.000121481	3.76846304	signalling 1433 proteins
Sopim02g082760	Catalase	2	5.35026119	2.113989431	0.000517337	5.35026119	redox dismutases and catalases
Sopim03g006140	Neutral ceramidase	2	9.432782607	4.519733716	0.000785945	9.432782607	protein degradation ubiquitin E3 RING
Sopim03g034180	14 3 3 protein beta/alpha 1	3	3.819887023	1.555597382	2.17E-05	3.819887023	signalling 1433 proteins
Sopim03g097700	O methyltransferase	5	6.148290545	1.976102588	1.56E-09	6.148290545	misc Omethyl transferases
Sopim04g012120	14 3 3 protein beta/alpha 1	2	5.233637563	3.488262698	0.001280963	5.233637563	signalling 1433 proteins
Sopim04g074510	14 3 3 protein beta/alpha B	2	5.233637563	3.488262698	0.001280963	5.233637563	signalling 1433 proteins
Sopim09g090150	Legumin 11S globulin	7	98.48779196	10.13579529	1.96154E-11	98.48779196	development storage proteins
Sopim07g064180	Pectinesterase	3	48.53396972	5.891428559	2.62667E-06	48.53396972	Cell wall
Sopim09g090980	Major allergen Mal d 1	3	5.415143012	2.908287622	0.000216977	5.415143012	cell wall pectinesterases PME
Sopim02g094120	Sulfite oxidase	2	2.724833745	0.302624815	0.000746506	2.724833745	sulfite assimilation
Sopim03g097700	O methyltransferase	2	3.321233861	0.363221823	0.014048444	3.321233861	secondary metabolism
Sopim10g085870	UDP glucosyltransferase family 1 protein	4	2.993254737	1.806602059	7.86E-05	2.993254737	stress abiotic light
Sopim11g006550	Uricase	3	3.529891972	3.09816567	0.000968591	3.529891972	nucleotide metabolism degradation
Sopim11g010200	14 3 3 protein beta/alpha 1	2	5.233637563	3.488262698	0.001280963	5.233637563	signalling 1433 proteins
Solyc12g088670.1.1	Cathepsin B like cysteine proteinase	2	3.872629379	2.161528481	0.001327415	3.872629379	protein degradation cysteine protease
Solyc01g010760.2.1	Porin/voltage dependent anion selective channel protein	2	3.110320399	2.084876253	0.007762058	3.110320399	transport porins
Solyc11g006550.1.1	Uricase	3	3.529891972	3.09816567	0.000968591	3.529891972	nucleotide metabolism degradation
Sopim07g041900	Cathepsin L like cysteine proteinase	5	4.352619635	1.389987631	1.51472E-09	4.352619635	protein degradation cysteine protease
Solyc12g057110.2.1	14 3 3 (Fragment)	4	6.54261611	2.761267613	0.000136202	6.54261611	signalling 1433 proteins
Sopim12g057110	14 3 3 (Fragment)	4	5.148790108	2.749396825	0.000141461	5.148790108	signalling 1433 proteins
Solyc02g062460.2.1	2 oxoglutarate dependent dioxygenase	3	3.25783887	1.168020833	0.000272732	3.25783887	hormone metabolism gibberelin synthesisdegradation
Solyc06g076540.1.1	class I heat shock protein	5	308.0432665	148.0337788	2.87471E-10	308.0432665	stress abiotic heat
Solyc06g076570.1.1	class I heat shock protein	5	64.14245151	12.77515121	5.59405E-06	64.14245151	stress abiotic heat
Sopim07g041490	Stress responsive alpha_beta barrel domain protein	5	57.92131734	12.82158484	9.9E-20	57.92131734	stress biotic
Sopim11g066130	Thaumatin_like protein	3	66.33614975	42.44341568	0.00168229	66.33614975	stress biotic
Sopim08g074630	Polyphenol oxidase	9	9.56024074	2.232257275	7.02949E-08	9.56024074	secondary metabolism simple phenols
Sopim08g007620	Subtilisin_like protease	6	11.7443062	4.67563013	4.36563E-08	11.7443062	protein degradation
Sopim09g008670	Threonine ammonia_lyase biosynthetic	6	8.818934136	2.091461988	4.86186E-07	8.818934136	amino acid metabolism degradation aspartate family threonine
Sopim07g061800	Heme_binding protein 2	2	7.951711694	4.194451759	0.001530687	7.951711694	tetrapyrrole synthesis unspecified
Sopim04g082880	Diphosphate__fructose_6_phosphate 1_phosphotransferase	2	5.675904027	1.988068461	0.00518535	5.675904027	glycolysis cytosolic branch pyrophosphatefructose6P phosphotransferase
Sopim08g074940	Aspartic proteinase nepenthesin_2	2	174.5090924	116.6226778	0.002263967	174.5090924	protein degradation
Sopim03g005760	Chlorophyll a_b binding protein 3C_like	2	7.911171094	7.591467165	0.009753886	7.911171094	PS lightreaction photosystem II LHCII
Sopim03g005770	Chlorophyll a_b binding protein 3C_like	2	7.911171094	7.591467165	0.009753886	7.911171094	PS lightreaction photosystem II LHCII
Sopim03g005780	Chlorophyll a_b binding protein 3C_like	2	7.911171094	7.591467165	0.009753886	7.911171094	PS lightreaction photosystem II LHCII
Solyc11g010200.1.1	14 3 3 protein beta/alpha 1	2	5.233637563	3.488262698	0.001280963	5.233637563	signalling 1433 proteins
Solyc11g010470.1.1	14 3 3 protein beta/alpha	2	3.087243074	1.459612087	0.000521488	3.087243074	signalling 1433 proteins
Sopim04g012120	14 3 3 protein beta/alpha 1	2	5.233637563	3.488262698	0.001280963	5.233637563	signalling 1433 proteins
Sopim04g074510	14 3 3 protein beta/alpha B	2	5.233637563	3.488262698	0.001280963	5.233637563	signalling 1433 proteins
Sopim11g010200	14 3 3 protein beta/alpha 1	2	5.233637563	3.488262698	0.001280963	5.233637563	signalling 1433 proteins
Sopim11g010470	14 3 3 protein beta/alpha	2	3.087243074	1.459612087	0.000521488	3.087243074	signalling 1433 proteins
Solyc10g082030.1.1	Peroxiredoxin	3	3.830589871	0.538765456	5.2343E-06	3.830589871	redox
Sopim09g082340	Vicilin_like protein	3	21.22908657	19.99686634	1.30711E-06	21.22908657	development storage proteins
Sopim09g052210	Legumin 11S_globulin	3	181.4703891	200.5808351	0.000467475	181.4703891	development storage proteins
Sopim03g112440	Oleosin	2	669.7381526	361.3354673	0.007888259	669.7381526	RNA regulation of transcription C2H2 zinc finger family
Sopim03g118040	Calcium_binding protein Calnexin	2	4.665344073	2.327173888	0.008637404	4.665344073	signalling calcium
Solyc11g072190.1.1	Elongation factor beta_1	2	9.009188374	2.343627963	0.009781215	9.009188374	protein synthesis elongation
Sopim11g072190	Elongation factor beta_1	2	9.009188374	2.343627963	0.009781215	9.009188374	protein synthesis elongation
Sopim01g098000	Elongation factor_like protein	2	4.347806483	0.333734895	0.001337791	4.347806483	protein synthesis elongation
Sopim12g055800	V_type ATP synthase alpha chain	2	2.392715362	0.31932568	0.006876895	2.392715362	PS lightreaction ATP synthase
Sopim08g074940	Aspartic proteinase nepenthesin_2	2	120.9377332	61.54509086	0.000047898	120.9377332	protein degradation
Sopim04g082250	ATP_dependent zinc metalloprotease FTSH_ chloroplastic (Fragment)	2	7.680260549	4.759564101	0.011998827	7.680260549	cell division proteases
Sopim07g016150	Elongation factor 1_beta	2	2.744428597	0.493047431	0.006334669	2.744428597	protein synthesis elongation
Sopim02g080880	Aspartic proteinase	2	22.48595894	4.286470665	0.001599118	22.48595894	protein degradation
Sopim09g011030	Hsp70 nucleotide exchange factor fes1	2	3.909228832	1.576275278	0.003461435	3.909228832	abiotic stress heat
Solyc06g005940.2.1	Protein disulfide isomerase	2	2.284100838	0.552536497	0.008843912	2.284100838	misc short chain dehydrogenase/reductase SDR
Sopim06g005940	Protein disulfide isomerase	2	2.284100838	0.552536497	0.008843912	2.284100838	misc short chain dehydrogenase/reductase SDR
Sopim07g064180	Pectinesterase	2	24.71636749	3.780652364	4.82233E-05	24.71636749	cell wall pectinesterases PME
Solyc09g090990.2.1	Major allergen Mal d 1	35	31.66349999	5.733078888	9.9E-20	31.66349999	transport ABC transporters and multidrug resistance systems
Sopim09g090990	Major allergen Mal d 1	33	27.46200428	6.373964524	9.9E-20	27.46200428	transport ABC transporters and multidrug resistance systems
Solyc01g102960.2.1	class IV heat shock protein	16	56.86433258	9.726816627	9.9E-20	56.86433258	abiotic stress.heat
Sopim01g102960	class IV heat shock protein	10	51.38248236	15.48796083	2.31591E-13	51.38248236	abiotic stress.heat
Sopim04g015340	Serine carboxypeptidase K10B2.2	6	24.59966417	6.933015385	9.9E-20	24.59966417	protein degradation
Sopim10g007690	Chlorophyll a_b binding protein 8_ chloroplastic	6	2.35909661	0.93309009	9.99201E-14	2.35909661	PS light reaction
Sopim07g006560	Hypersensitive response assisting protein	2	7.089278254	7.584885648	0.013685889	7.089278254	RNA processing ribonucleases
Sopim09g098120	DUF1264 domain protein	2	17.04173476	16.58638931	0.000340605	17.04173476	protein of unknown function
Sopim02g079510	Peroxidase	2	4.391890758	1.601764055	0.002545781	4.391890758	redox
Sopim01g097240	Pathogenesis_related protein 4B	2	6.417220639	2.960243389	0.010692818	6.417220639	stress biotic
Sopim04g082010	Plastocyanin	2	4.182095239	1.744185695	0.005730557	4.182095239	PS light reaction
Solyc05g050710.2.1	Lecithin cholesterol acyltransferase	2	2.742623597	1.87960459	0.007248508	2.742623597	lipid metabolism
Solyc02g082760.2.1	Catalase	2	5.35026119	2.113989431	0.000517337	5.35026119	redox catalases
Solyc03g006140.2.1	Neutral ceramidase	2	9.432782607	4.519733716	0.000785945	9.432782607	protein degradation
Solyc00g187050.2.1	Leucyl aminopeptidase	2	7.887761667	6.585954018	0.007864816	7.887761667	stress abiotic unspecified
Solyc11g011380.1.1	Glutamine synthetase	2	1143.93295	1647.243756	0.007032115	1143.93295	aminoacid metabolism
Solyc10g007600.2.1	L_lactate dehydrogenase	6	8.223574547	3.008546176	3.92424E-10	8.223574547	PS photorespiration glycolate oxydase
Solyc07g056540.2.1	L_lactate dehydrogenase	5	10.45933339	4.557147086	2.06664E-05	10.45933339	PS photorespiration glycolate oxydase
Sopim07g005960	Serine carboxypeptidase K10B22	2	13.80663205	11.48173288	0.009623522	13.80663205	cell wall precursor synthesis UXS

Table 5.7. Differentially expressed proteins identified in the fruits of wild species at different developmental stages using nanoLC-MS-MS.

Label-free quantitation was employed by matching retention times of the peaks and measuring area under the matched peaks using Sieve 2.1 software (Thermo Scientific) to identify the differentially expressed proteins in SP-SL, SG-SL, SH-SL pairs. Stringent selection criteria were imposed to identify these proteins (p value≤0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR=1%).

List of downregulated proteins in SG-SL

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO (SG/SL)	STD.DEV	PVALUE	FOLD CHANGE (SG/SL)	MAPMANCLASS
Sopim00g009060	Hypoxanthine phosphoribosyltransferase	2	0.09161815	0.11833612	0.001885799	10.91486785	lipid metabolism phospholipid synthesis
Sopim00g014830	NADHquinone oxidoreductase subunit D	2	0.03467832	0.03436348	0.013784601	28.83646036	stress abiotic drought/salt
Sopim00g017210	Actin	4	0.239414718	0.08514229	1.32E-05	4.176852653	cell organisation
Sopim00g042130	ATP synthase subunit alpha	3	0.148109856	0.04045335	4.10E-09	6.751745137	cell cycle
Sopim00g071180	Cysteine proteinase inhibitor	2	0.004794588	0.00691382	0.001104507	208.5684943	protein degradation inhibitors
Sopim00g257110	HATPase	2	0.082188765	0.04448287	0.000295353	12.16711311	tetrapyrrole synthesis ALA dehydratase
Sopim01g005210	Alpha alphatrehalosephosphate synthase UDPforming	2	0.057571171	0.01993746	1.60E-05	17.36980476	minor CHO metabolism trehalose TPS
Sopim01g005620	Mitochondrial 2oxoglutarate/malate carrier protein	4	0.315144808	0.12567987	0.000350116	3.173144455	transport metabolite transporters at the mitochondrial membrane
Sopim01g006280	Formatetetrahydrofolate ligase	7	0.114110674	0.05100479	7.15E-08	8.763422079	RNA regulation of transcription chromatin remodeling factors
Sopim01g007150	Coatomer subunit beta1	10	0.009645061	0.00291338	3.23E-13	103.6800078	cell vesicle transport
Sopim01g007320	ATP synthase subunit beta	2	0.02900185	0.02714775	0.002998042	34.480559	PS lightreaction ATP synthase epsilon chain
Sopim01g007330	Ribulose bisphosphate carboxylase large chain	6	0.071276983	0.04840665	8.33E-07	14.02977452	protein synthesis ribosomal protein prokaryotic chloroplast 30S subunit S15
Sopim01g007380	Apocytochrome f	5	0.071028108	0.02253456	1.27E-06	14.07893337	PS lightreaction cytochrome b6/f apocytochrome f CYF
Sopim01g007500	Photosystem II CP47 chlorophyll apoprotein	2	0.144076535	0.06111209	8.47E-05	6.940755481	PS lightreaction photosystem II PSII polypeptide subunits
Sopim01g007610	30S ribosomal protein S3 chloroplastic	2	0.015365629	0.02096955	0.004854366	65.08031659	protein synthesis ribosomal protein prokaryotic unknown organellar
Sopim01g007670	30S ribosomal protein S7 chloroplastic	5	0.359699979	0.11742979	4.14E-05	2.780094686	protein synthesis ribosomal protein prokaryotic chloroplast 30S subunit S7
Sopim01g008000	ADPribosylation factor	2	0.059663858	0.08020281	8.96E-06	16.7605655	protein postranslational modification
Sopim01g008370	26S proteasome regulatory subunit	2	0.34237867	0.14884216	0.001995309	2.920742697	protein degradation ubiquitin proteasom
Sopim01g008850	CBLinteracting protein kinase 18	2	0.056652284	0.05620757	0.001494835	17.65153899	protein postranslational modification
Sopim01g008960	Argonaute 4like protein	2	0.173517403	0.20726226	0.010410931	5.763110689	development unspecified
Sopim01g009180	5 methyl tetrahydropteroyl triglutamate homocysteine methyltransferase	2	0.100590131	0.10267189	0.001177675	9.941333111	amino acid metabolism synthesis aspartate family methionine methionine synthase
Sopim01g009230	Xanthine dehydrogenase/oxidase	2	0.064702136	0.06359811	0.115388532	15.4554403	misc acid and other phosphatases
Sopim01g009310	Sterol reductase	2	0.069204739	0.03290721	0.000642023	14.44987749	hormone metabolism brassinosteroid synthesisdegradation sterols DWF5
Sopim01g009420	Bifunctional polymyxin resistance arnA protein	2	0.45409295	0.18810373	0.005962099	2.202192304	cell wall precursor synthesis UXS
Sopim01g009990	Peptidyl prolyl cis trans isomerase	2	0.337123832	0.10299067	2.22E-05	2.966269083	cell cycle peptidylprolyl isomerase
Sopim01g010200	LTR Gagpolpolymerase 3	4	0.122266678	0.03127734	0.000129559	8.178843299	not assigned unknown
Sopim01g010540	Ribosomal protein	3	0.039689912	0.01583373	0.00222305	25.19531915	protein synthesis ribosome biogenesis
Sopim01g010870	Dehydration responsive family protein	3	0.038920518	0.03011098	3.07E-05	25.69338877	signalling light
Sopim01g014210	ADP ATP carrier protein-like	2	0.057870237	0.02041649	3.17E-05	17.28003982	major CHO metabolism synthesis starch transporter
Sopim01g028810	chaperonin	16	0.229520285	0.05298055	7.77E-16	4.356913377	PS calvin cycle rubisco interacting
Sopim01g044360	Importin beta3	11	3.76E-05	6.16E-05	1.32E-11	26595.74468	protein targeting nucleus
Sopim01g056940	Ubiquitin	4	0.09121905	0.03297736	1.91E-08	10.96262239	protein degradation ubiquitin ubiquitin
Sopim01g058730	Os03g0310500 protein Fragment	3	0.087126937	0.07018292	0.000104187	11.47750666	development unspecified
Sopim01g059880	ATP citrate lyase asubunit	3	0.33686106	0.16305348	0.001355527	2.968582952	TCA / organic transformation other organic acid transformations atpcitrate lyase
Sopim01g060180	AMPdependent synthetase and ligase	2	0.132387491	0.06902251	0.000585224	7.553583745	gluconeogenesis / glyoxylate cycle
Sopim01g060470	Importin alpha1b subunit	5	0.163470633	0.05666184	1.62E-08	6.117306709	PS calvin cycle rubisco interacting
Sopim01g068530	30S ribosomal protein S9	3	0.087200603	0.02878126	1.47E-06	11.46781061	protein synthesis ribosome biogenesis
Sopim01g074030	Betaglucosidase 01	3	0.016302742	0.00778	1.72E-06	61.33937469	misc gluco galacto and mannosidases
Sopim01g079090	Protoporphyrinogen oxidase	2	0.176770251	0.05764678	0.001656473	5.657060475	tetrapyrrole synthesis protoporphyrin IX oxidase
Sopim01g080460	Pyruvate phosphate dikinase	7	0.005482242	0.0028289	8.14E-06	182.4071247	gluconeogenesis / glyoxylate cycle pyruvate dikinase
Sopim01g080640	Multidrug resistance protein ABC transporter family	2	0.181316008	0.09672002	0.000803512	5.51523283	transport ABC transporters and multidrug resistance systems
Sopim01g081070	Protein transport protein Sec23	2	0.049547698	0.0337258	0.01644867	20.18257236	protein targeting secretory pathway golgi
Sopim01g081540	Myosin XIF	2	0.165164753	0.10386602	0.000537071	6.054560564	cell organisation
Sopim01g086750	Protein TIF31 homolog	6	0.03838449	0.01815195	1.01E-10	26.05218931	protein degradation cysteine protease
Sopim01g087070	Mitochondrial ADP/ATP carrier protein	6	0.014987099	0.00911867	1.63E-06	66.7240538	major CHO metabolism synthesis starch transporter
Sopim01g087260	Carotenoid cleavage dioxygenase 1B	4	0.00197444	0.00081304	8.93E-05	506.4727214	secondary metabolism isoprenoids carotenoids carotenoid cleavage dioxygenase
Sopim01g088020	Protein transport protein sec31	9	0.059932115	0.01899683	1.42E-10	16.68554497	not assigned no ontology
Sopim01g088080	Tcomplex protein theta subunit	3	0.013739689	0.01535995	0.000360196	72.78185118	protein folding
Sopim01g088370	Eukaryotic translation initiation factor 3 subunit B	5	0.10442811	0.06843334	3.06E-05	9.575965705	protein synthesis initiation
Sopim01g088510	Dynamin like protein	3	0.405957231	0.14481899	0.000541321	2.463313678	misc dynamin
Sopim01g088560	Ras related protein Rab6A	3	0.337521092	0.11533271	0.000839638	2.962777805	signalling Gproteins
Sopim01g090750	Tcomplex protein 1 subunit alpha	3	0.013837579	0.01488637	0.000358841	72.26697676	protein folding
Sopim01g090780	Ccr4Not transcription complex subunit	2	0.015885563	0.02423074	0.009136615	62.95023979	RNA regulation of transcription putative transcription regulator
Sopim01g091220	40S ribosomal protein S13	4	0.199211198	0.03809272	4.92E-06	5.019798134	protein synthesis ribosomal protein eukaryotic 40S subunit S13
Sopim01g091460	ARF guaninenucleotide exchange factor 2	4	0.059367215	0.02250663	6.36E-05	16.84431382	signalling Gproteins
Sopim01g091640	Dehydration responsive protein	2	0.050627137	0.08212513	0.015668018	19.75225263	stress abiotic drought/salt
Sopim01g091690	Dehydrationresponsive family protein	2	0.057437865	0.07252587	0.003713909	17.41011787	protein synthesis ribosome biogenesis
Sopim01g094030	Syt1 synaptotagmin Ca2dependent lipid binding protein putative IC	2	0.069898465	0.0563227	0.000816726	14.30646581	signalling calcium
Sopim01g094200	NADdependent malic enzyme 2	7	0.330051581	0.0346757	4.76E-09	3.02982945	major CHO metabolism degradation sucrose hexokinase
Sopim01g094350	ATPdependent RNA Helicase	2	0.178636374	0.1582296	0.000880786	5.597964052	RNA processing RNA helicase
Sopim01g094700	Glycerol 3 phosphate acyltransferase 4	3	0.063195271	0.01882723	3.49E-05	15.82396885	lipid metabolism phospholipid synthesis
Sopim01g095970	Dynamin 2	2	0.273192039	0.13790043	0.001489091	3.660428773	minor CHO metabolism myoinositol polyphosphatases
Sopim01g096060	Nuclear envelope protein that mediates the nuclear export of importin alpha Srp1p	6	0.005007353	0.00387736	1.22E-07	199.7063119	stress biotic
Sopim01g096290	Ubiquitin	4	0.09121905	0.03297736	1.91E-08	10.96262239	protein synthesis ribosomal protein eukaryotic 60S subunit L40
Sopim01g096870	Prolyl tRNA synthetase	3	0.253537411	0.14769094	0.000832202	3.9441911	protein aa activation bifunctional aminoacyltRNA synthetase
Sopim01g097340	NAD dependent epimerase/dehydratase family protein-like protein	3	0.280704115	0.13066941	0.000828339	3.562470041	cell wall precursor synthesis UXS
Sopim01g097760	Ribosomal protein L7a	2	0.223147001	0.17715024	0.001852979	4.481350838	protein synthesis ribosomal protein eukaryotic 60S subunit L7A
Sopim01g097770	Serine/threonine protein kinase	2	0.189170883	0.08438949	0.002453036	5.286225788	signalling light
Sopim01g098640	UPF0603 protein At1g54780 chloroplastic	5	0.047464008	0.03662645	3.09E-05	21.06859581	not assigned no ontology
Sopim01g098700	Branched chain amino acid aminotransferase like protein	3	0.349895249	0.09133045	8.70E-05	2.857998223	misc aminotransferases aminotransferase class IV family protein
Sopim01g098920	Mitochondrial Rho GTPase 1	2	0.079438167	0.06473975	0.01643218	12.58840728	protein degradation ubiquitin E3 SCF FBOX
Sopim01g099150	Lipoxygenase	2	0.091976109	0.05657586	0.000544547	10.87238861	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim01g099160	Lipoxygenase	2	0.094764434	0.08742455	0.012969266	10.55248217	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim01g099180	Lipoxygenase	2	0.096408432	0.07662896	0.000777094	10.37253671	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim01g099190	Lipoxygenase	11	0.080066539	0.02796847	4.55E-09	12.48961192	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim01g099350	AcylCoA binding protein 4	2	0.043355857	0.02134703	0.003962731	23.06493446	lipid metabolism FA synthesis and FA elongation acylCoA binding protein
Sopim01g099670	40S ribosomal protein S10-like	4	0.083829238	0.01985301	4.18E-10	11.92901217	protein synthesis ribosome biogenesis
Sopim01g099770	Translationally controlled tumor protein homolog	2	0.261263872	0.11310504	6.12E-05	3.827547959	development unspecified
Sopim01g099780	Translationally controlled tumor protein homolog	2	0.261263872	0.11310504	6.12E-05	3.827547959	development unspecified
Sopim01g099900	Ribosomal protein L18	4	0.271133096	0.08139651	3.87E-06	3.688225505	protein synthesis ribosomal protein eukaryotic 60S subunit L18
Sopim01g100370	Universal stress protein	2	0.039466506	0.02986201	0.002592975	25.33794099	hormone metabolism ethylene inducedregulatedresponsiveactivated
Sopim01g100380	Calreticulin 2 calcium binding protein	3	0.290258336	0.17386672	0.001554207	3.445206824	signalling calcium
Sopim01g100390	Pyrophosphate energized proton pump	3	0.009161051	0.00795403	0.000549163	109.1577811	transport amino acids
Sopim01g100720	Importin alpha1b subunit	2	0.246909682	0.15086972	0.002242445	4.050063942	PS calvin cycle rubisco interacting
Sopim01g100860	ADPribosylation factor	2	0.059663858	0.08020281	8.96E-06	16.7605655	protein targeting secretory pathway unspecified
Sopim01g100870	ADP ribosylation factor	2	0.059663858	0.08020281	8.96E-06	16.7605655	protein postranslational modification
Sopim01g101060	S-adenosylmethionine synthase	7	0.366194494	0.07628558	9.25E-09	2.730789284	metal handling binding chelation and storage
Sopim01g102310	Unknown Protein	3	0.120942912	0.06261249	0.000136563	8.268363838	development unspecified
Sopim01g102410	Glutaminyl tRNA synthetase	5	0.040572963	0.01231995	5.85E-05	24.64695517	tetrapyrrole synthesis glutRNA synthetase
Sopim01g102510	Genomic DNA chromosome 5 P1 clone MXC17	2	0.056587687	0.05621414	0.009442083	17.6716889	not assigned no ontology
Sopim01g102940	Methionine s-methyltransferase	7	0.068847306	0.02343028	1.90E-08	14.52489659	amino acid metabolism synthesis aspartate family methionine methionine Smethyltransferase
Sopim01g103010	Cullin-associated NEDD8 dissociated protein 2	13	0.027837347	0.00648055	2.04E-13	35.92296349	development unspecified
Sopim01g103450	Chaperone DnaK	2	0.339646757	0.1465837	0.000780963	2.944235384	stress abiotic heat
Sopim01g103480	Coatomer subunit delta	3	0.217372081	0.08048038	7.68E-06	4.600406802	cell vesicle transport
Sopim01g103930	Transmembrane 9 superfamily protein member 3	3	0.03730679	0.02304963	5.97E-05	26.804772	DNA unspecified
Sopim01g104040	UDP-glucose glycoprotein glucosyltransferase	5	0.071505633	0.02531318	0.00019629	13.98491221	protein glycosylation UDPglucose glycoprotein glucosyltransferase
Sopim01g104070	Importin beta	10	0.010901545	0.00456471	1.46E-07	91.73011715	protein targeting nucleus
Sopim01g104170	Ankyrin repeat domain containing protein 2	5	0.135186247	0.05325103	2.06E-08	7.397202172	cell organisation
Sopim01g104590	Ribosomal protein L3	5	0.04897419	0.03817931	0.000172378	20.41891862	protein synthesis ribosome biogenesis
Sopim01g104770	Actin	5	0.250024789	0.07144892	1.86E-06	3.999603415	cell organisation
Sopim01g104920	26S protease regulatory subunit 8 homolog	3	0.288816226	0.14908964	0.001608318	3.462409345	protein degradation AAA type
Sopim01g105030	Chlorophyll ab binding protein chloroplastic	4	0.081308253	0.04782619	0.000162206	12.29887451	PS lightreaction photosystem II LHCII
Sopim01g105050	Chlorophyll ab binding protein chloroplastic	4	0.081308253	0.04782619	0.000162206	12.29887451	PS lightreaction photosystem II LHCII
Sopim01g105540	2-oxoglutarate/malate translocator	2	0.202896372	0.09057568	0.001690105	4.928624352	transport metabolite transporters at the mitochondrial membrane
Sopim01g105980	Unknown Protein	2	0.126484347	0.10280215	0.001489538	7.906116636	not assigned unknown
Sopim01g106090	Photosystem II oxygen evolving complex protein PsbP	2	0.327397249	0.14104818	0.002305906	3.054393411	PS lightreaction photosystem II PSII polypeptide subunits
Sopim01g106320	Octicosapeptide/Phox/Bem1p domain containing protein	2	0.280133627	0.21478449	0.009618308	3.569724958	development multitarget target of rapamycin
Sopim01g106330	Glutamyl tRNA Gln amidotransferase subunit A	3	0.136259727	0.12300665	0.000898847	7.338925609	lipid metabolism FA synthesis and FA elongation pyruvate kinase
Sopim01g106820	Peptidase M50 family	5	0.062627248	0.01948801	7.07E-06	15.9674907	protein degradation metalloprotease
Sopim01g108630	Nitrite reductase	2	0.336479268	0.08623499	0.006604539	2.971951306	Nmetabolism nitrate metabolism nitrite reductase
Sopim01g109350	WD40 repeat containing protein	2	0.016426777	0.02589767	0.001751856	60.87621449	lipid metabolism lipid degradation lysophospholipases
Sopim01g109410	Dolichyl diphospho oligosaccharide protein glycosyltransferase subunit	6	0.087770175	0.0221343	2.02E-06	11.39339189	protein glycosylation
Sopim01g109540	Coatomer subunit gamma	15	0.01087444	0.00322643	3.33E-16	91.95875834	cell vesicle transport
Sopim01g109580	Adenylyl cyclase-associated protein	2	0.211285669	0.1965542	0.008160017	4.732928668	RNA regulation of transcription AtSR transcription factor family
Sopim01g109840	Diaminopimelate decarboxylase 2 chloroplastic	2	0.246022585	0.13590961	0.007094399	4.064667478	not assigned unknown
Sopim01g109850	Diaminopimelate decarboxylase	3	0.33397394	0.09668994	6.54E-06	2.994245599	signalling Gproteins
Sopim01g110120	Vtype proton ATPase subunit a	22	0.027505632	0.00423467	9.90E-20	36.35619062	transport p and vATPases
Sopim01g110360	Fructose bisphosphate aldolase	4	0.395973429	0.07630136	3.44E-06	2.525421977	PS calvin cycle aldolase
Sopim01g111510	Ascorbate peroxidase	2	0.036726495	0.05703673	0.006524245	27.22829935	RNA regulation of transcription AtSR transcription factor family
Sopim01g111520	Synaptotagmin	5	0.038502444	0.01839761	2.31E-06	25.97237723	stress abiotic cold
Sopim01g111710	26S proteasome nonATPase regulatory subunit 3	7	0.02793947	0.00898704	8.40E-07	35.79165961	protein degradation ubiquitin proteasom
Sopim01g111760	Vtype ATP synthase beta chain	5	0.093003938	0.04540764	3.74E-05	10.75223288	mitochondrial electron transport / ATP synthesis F1ATPase
Sopim01g111780	Importin beta2 subunit	8	0.003143637	0.00251975	1.57E-09	318.1028853	protein targeting nucleus
Sopim01g112100	Dimethylaniline monooxygenase 5	5	0.001361154	0.00184662	5.36E-05	734.6707279	misc oxidases copper flavone etc
Sopim02g014150	Photosystem II stability/assembly factor Ycf48like protein	2	0.377865451	0.29054442	0.16324491	2.646444647	protein assembly and cofactor ligation
Sopim02g020980	4 alphaglucanotransferase	9	0.013380367	0.00599398	2.92E-09	74.7363656	major CHO metabolism degradation starch D enzyme
Sopim02g021650	DNA damage binding protein 1	2	0.069795242	0.01549406	0.00116058	14.32762422	protein degradation ubiquitin E3 DCX
Sopim02g030170	FAD linked oxidase domain protein	6	0.066666878	0.01769775	4.22E-07	14.99995245	hormone metabolism brassinosteroid synthesisdegradation sterols DWF1
Sopim02g031910	Serine/threonine protein kinase	3	0.112848557	0.05731704	0.002038286	8.861433647	protein postranslational modification
Sopim02g063090	T complex protein 1 subunit zeta	5	0.281615793	0.05837111	1.01E-06	3.550937216	protein postranslational modification
Sopim02g064670	Ribosomal protein L26like 1	10	0.17286876	0.01821913	8.22E-15	5.784735194	protein synthesis ribosomal protein eukaryotic 60S subunit L26
Sopim02g065300	LeucyltRNA synthetase	11	0.067195883	0.01877465	1.88E-13	14.88186412	protein folding
Sopim02g067030	5 aposAMP-activated protein kinase catalytic subunit alpha2	2	0.162749717	0.15893079	0.002886142	6.144403925	signalling in sugar and nutrient physiology misc
Sopim02g067080	UDP-D-glucose dehydrogenase	2	0.030684676	0.01799009	0.000615318	32.58955708	cell wall precursor synthesis UGD
Sopim02g067690	Glucosyl transferase-like protein	2	0.047699359	0.02583874	0.004748088	20.96464231	misc UDP glucosyl and glucoronyl transferases
Sopim02g069120	Zinc finger protein ZPR1	2	0.37307165	0.11368702	0.001537574	2.680450257	RNA regulation of transcription C2H2 zinc finger family
Sopim02g069140	Leucyl tRNA synthetase	4	0.040417512	0.02722781	0.000570229	24.74175056	protein folding
Sopim02g069450	Photosystem I reaction center subunit III	2	0.217946664	0.09625239	0.003370771	4.588278534	PS lightreaction photosystem I PSI polypeptide subunits
Sopim02g069460	Photosystem I reaction center subunit III	4	0.049636737	0.02423825	4.29E-05	20.14636861	PS lightreaction photosystem I PSI polypeptide subunits
Sopim02g070260	Protein phosphatase 1 regulatory subunit 7	2	0.034187276	0.02346028	0.001741578	29.25064869	development unspecified
Sopim02g070310	Ribosomal protein L32	4	0.330376344	0.09070492	1.56E-06	3.026851099	protein synthesis ribosomal protein eukaryotic 60S subunit L32
Sopim02g070320	40S ribosomal protein S4like protein	6	0.112758283	0.065873	3.17E-06	8.868528089	protein synthesis ribosomal protein eukaryotic 40S subunit S4
Sopim02g070330	40S ribosomal protein S4like protein	6	0.112758283	0.065873	3.17E-06	8.868528089	protein synthesis ribosomal protein eukaryotic 40S subunit S4
Sopim02g070360	40S ribosomal protein S4like protein	6	0.112758283	0.065873	3.17E-06	8.868528089	protein synthesis ribosomal protein eukaryotic 40S subunit S4
Sopim02g070570	30S ribosomal protein S11	5	0.346260428	0.1157347	6.58E-05	2.887999665	protein synthesis ribosomal protein eukaryotic 40S subunit S14
Sopim02g070640	60S ribosomal protein L18a	4	0.096298789	0.03605908	0.007124688	10.38434658	protein synthesis ribosomal protein eukaryotic 60S subunit L18A
Sopim02g070940	Chlorophyll a/b binding protein	3	0.156252539	0.06550899	2.75E-06	6.399896004	PS lightreaction photosystem II LHCII
Sopim02g070980	Chlorophyll a/b binding protein	3	0.156252539	0.06550899	2.75E-06	6.399896004	PS lightreaction photosystem II LHCII
Sopim02g070990	Chlorophyll a/b binding protein	3	0.156252539	0.06550899	2.75E-06	6.399896004	PS lightreaction photosystem II LHCII
Sopim02g071000	Chlorophyll a/b binding protein	3	0.156252539	0.06550899	2.75E-06	6.399896004	PS lightreaction photosystem II LHCII
Sopim02g071330	SH3 domain containing guanine exchange factor	2	0.013104198	0.01364724	0.000640553	76.31142326	transport peptides and oligopeptides
Sopim02g072130	Protein transport protein SEC61 alpha subunit	3	0.087220689	0.03346868	5.00E-07	11.46516969	transport misc
Sopim02g076720	Phosphoribosyl formyl glycinamidine synthase	2	0.069413764	0.1024246	0.009490605	14.40636471	nucleotide metabolism synthesis purine FGAR amidotransferase
Sopim02g078540	Unknown Protein	2	0.000514712	0.00093867	0.001186269	1942.834051	not assigned unknown
Sopim02g078570	Epoxide hydrolase 3	6	0.001040894	0.00109249	1.21E-06	960.7126182	misc GDSLmotif lipase
Sopim02g078900	NADH dehydrogenase	2	0.05621641	0.03540596	0.000922565	17.78840022	mitochondrial electron transport / ATP synthesis NADHDH type II internal matrix
Sopim02g080540	ATP synthase gamma chain	3	0.215700636	0.11880586	0.000757261	4.636054944	PS lightreaction ATP synthase gamma chain
Sopim02g081160	Diphosphate fructose 6 phosphate 1 phosphotransferase	6	0.04115956	0.01297584	6.91E-08	24.29569218	glycolysis plastid branch pyrophosphatefructose6P phosphotransferase
Sopim02g082000	30S ribosomal protein S19	2	0.374358438	0.12253269	0.000310039	2.671236704	protein synthesis ribosome biogenesis
Sopim02g082220	Protein transport protein SEC24	2	0.107820242	0.05209058	0.000612672	9.274696304	protein targeting secretory pathway golgi
Sopim02g082760	Catalase	2	0.270357358	0.1186906	0.000236699	3.698808153	redox dismutases and catalases
Sopim02g083560	Vacuolar protein sorting 35	2	0.024763431	0.01499154	0.00361618	40.38212637	secondary metabolism flavonoids chalcones
Sopim02g084360	Vtype proton ATPase 16 kDa proteolipid subunit c2	2	0.234332388	0.14588747	0.014925101	4.267442536	transport p and vATPases H+transporting twosector ATPase subunit C
Sopim02g084440	Fructose bisphosphate aldolase	2	0.369917146	0.09269461	9.84E-05	2.703308054	lipid metabolism FA synthesis and FA elongation pyruvate kinase
Sopim02g084690	FGGAP repeat containing protein	2	0.000780297	0.00115514	0.007171847	1281.563302	protein degradation ubiquitin E2
Sopim02g085350	Succinate dehydrogenase flavoprotein subunit	2	0.06269737	0.0428838	0.0002836	15.94963234	TCA / organic transformation TCA succinate dehydrogenase
Sopim02g085790	T complex protein 1 subunit zeta	6	0.256082703	0.05446718	1.06E-07	3.90498846	protein folding
Sopim02g086160	D-xylose transporter	2	0.064164003	0.04183402	0.004706747	15.58506255	major CHO metabolism degradation starch transporter
Sopim02g086240	50S ribosomal protein L5	3	0.22291556	0.05229374	3.44E-05	4.486003579	protein synthesis ribosomal protein eukaryotic 60S subunit L16
Sopim02g086460	Unknown Protein	2	0.059561265	0.00927863	3.51E-06	16.78943521	cell organisation
Sopim02g087250	Group II intron splicing factor CRS1like	2	0.008894527	0.00839213	0.003776303	112.4286879	development unspecified
Sopim02g087770	Aldose 1 epimerase-like protein	4	0.228379956	0.05154527	3.47E-07	4.378667977	redox misc
Sopim02g087880	Tubulin alpha7 chain	4	0.083503332	0.02097844	2.22E-07	11.97557003	RNA regulation of transcription bZIP transcription factor family

Sopim02g087930	60S ribosomal protein L34	3	0.339801758	0.08288526	0.000245007	2.942892367	protein synthesis ribosomal protein eukaryotic 60S subunit L34
Sopim02g088100	Expansin	4	0.075381937	0.06057649	8.54E-05	13.26577745	cell wall modification
Sopim02g088610	ATP-dependent chaperone ClpB	2	0.331957066	0.17631189	0.008808975	3.012437759	stress abiotic heat
Sopim02g088700	Mitochondrial processing peptidase beta subunit	5	0.009338835	0.01069125	0.000207823	107.0797375	protein targeting mitochondria
Sopim02g089260	E3 ubiquitin protein ligase UBR4	4	0.049551505	0.02706937	8.92E-06	20.18102175	hormone metabolism auxin signal transduction
Sopim02g089630	Proline dehydrogenase	2	0.038065085	0.03192391	8.18E-05	26.27079383	amino acid metabolism degradation glutamate family proline
Sopim02g090570	Transducin family protein	3	0.044986155	0.02561636	0.000911872	22.22906136	not assigned no ontology
Sopim02g090860	Phenylalanyl tRNA synthetase alpha chain	2	0.248412135	0.22208279	0.008962226	4.025568236	protein aa activation phenylalaninetRNA ligase
Sopim02g091100	Oxalyl CoA decarboxylase	7	0.175710272	0.05202416	1.79E-07	5.69118691	fermentation PDC
Sopim02g091560	Serine hydroxymethyltransferase	9	0.142094702	0.05822443	1.59E-11	7.037560063	amino acid metabolism synthesis serineglycinecysteine group glycine
Sopim02g091840	Receptor like kinase RLK	3	0.28515214	0.18647433	0.003415836	3.506899861	stress biotic PRproteins
Sopim02g091870	Tubulin alpha3 chain	5	0.370039214	0.1206488	0.000176867	2.70241629	cell organisation
Sopim02g092000	Unknown Protein	2	0.050292532	0.04639384	0.008619647	19.88366782	not assigned unknown
Sopim02g092430	Ribosomal protein L26	10	0.199674834	0.02057526	9.90E-20	5.008142388	protein synthesis ribosome biogenesis
Sopim02g093630	Uncharacterized membrane protein At3g27390	3	0.170086986	0.06066916	1.18E-05	5.879344584	not assigned unknown
Sopim02g093830	Glucose 6 phosphate 1 dehydrogenase	9	0.108632157	0.02771252	8.69E-12	9.205377373	OPP oxidative PP glucose6phosphate 1dehydrogenase G6PD
Sopim02g093900	Cytochrome c1	5	0.034112963	0.01523825	9.43E-09	29.31436944	signalling receptor kinases DUF 26
Sopim02g094470	Mitochondrial phosphate carrier protein	2	0.102806832	0.09743494	0.004996132	9.726980012	RNA processing
Sopim03g005600	Dehydration responsive protein-like	2	0.145211313	0.15160908	0.010466274	6.886515791	stress abiotic drought/salt
Sopim03g005760	Chlorophyll ab binding protein 3Clike	6	0.075520394	0.01797925	4.96E-08	13.24145634	PS lightreaction photosystem II LHCII
Sopim03g005770	Chlorophyll ab binding protein 3Clike	5	0.15985697	0.05768993	3.62E-07	6.255592108	PS lightreaction photosystem II LHCII
Sopim03g005780	Chlorophyll ab binding protein 3Clike	4	0.125073963	0.03826967	4.56E-07	7.995269167	PS lightreaction photosystem II PSII polypeptide subunits
Sopim03g007890	Heat shock protein 90 Fragment	3	0.013587134	0.01274072	0.001251159	73.59903862	RNA regulation of transcription MYBrelated transcription factor family
Sopim03g025320	Hydroxycinnamoyl transferase	4	0.304365223	0.11680429	0.000409886	3.285526481	secondary metabolism phenylpropanoids
Sopim03g025630	Tripeptidylpeptidase 2	2	0.042881114	0.04897456	0.010367683	23.32028967	protein degradation serine protease
Sopim03g025730	Tubulin beta chain	14	0.130872223	0.021532	9.90E-20	7.641040834	secondary metabolism phenylpropanoids
Sopim03g033400	Vacuolar protein sorting 35	2	0.024763431	0.01499154	0.00361618	40.38212637	stress biotic signalling
Sopim03g034170	Uncharacterized conserved membrane protein	2	0.373208468	0.1619426	0.002262771	2.679467605	cell cycle
Sopim03g044000	Ribosomal protein L26	10	0.265994783	0.03245568	2.01E-14	3.75947223	protein synthesis ribosomal protein eukaryotic 60S subunit L26
Sopim03g045090	cDNA clone 001043A08 full insert sequence	2	0.13150272	0.05542175	0.001982821	7.604405445	protein degradation subtilases
Sopim03g063560	Glutamate synthase Ferredoxin	35	0.004938647	0.00186882	9.90E-20	202.4846076	Nmetabolism ammonia metabolism glutamate synthase ferredoxin dependent
Sopim03g065340	Phosphorylase	6	0.065481222	0.03357757	4.50E-05	15.27155373	major CHO metabolism degradation starch starch phosphorylase
Sopim03g078290	40S ribosomal protein S18	2	0.37057123	0.1469239	0.001374342	2.698536527	protein synthesis ribosomal protein eukaryotic 40S subunit S18
Sopim03g078400	Actin	2	0.278482771	0.22118338	0.0060829	3.590886418	cell organisation
Sopim03g078570	Rasrelated protein Rab6A	3	0.337521092	0.11533271	0.000839638	2.962777805	signalling Gproteins
Sopim03g082440	G proteincoupled seven transmembrane receptor	2	0.021921189	0.01839026	0.000654928	45.61796351	not assigned unknown
Sopim03g082660	Major facilitator superfamily domain containing protein 5	2	0.139022475	0.0257416	9.61E-07	7.19308155	lipid metabolism phospholipid synthesis
Sopim03g082940	Importin subunit beta	11	0.002690086	0.00222367	3.66E-09	371.7353274	Cofactor and vitamine metabolism
Sopim03g083970	IQ calmodulinbinding motif family protein	2	0.235124877	0.14030918	0.000447486	4.25305911	signalling calcium
Sopim03g096000	Clathrin heavy chain	31	0.000592361	0.00043857	9.90E-20	1688.159754	cell vesicle transport
Sopim03g096850	Genomic DNA chromosome 5 P1 clone MKP11	2	0.371508496	0.17553189	0.002140588	2.691728482	protein assembly and cofactor ligation
Sopim03g096920	Exportin1	4	0.041246917	0.01685356	3.45E-05	24.24423624	protein targeting nucleus
Sopim03g097290	AlanyltRNA synthetase	2	0.018508532	0.02206003	0.003072191	54.0291364	protein aa activation alaninetRNA ligase
Sopim03g097790	Vtype proton ATPase subunit C	3	0.113393006	0.05929557	0.000277706	8.818886061	transport p and vATPases H+transporting twosector ATPase
Sopim03g097840	Mitochondrial phosphate carrier protein	2	0.061064355	0.0529156	0.00154683	16.37616577	RNA processing
Sopim03g097900	40S ribosomal protein S1	2	0.141275541	0.10907486	0.000745869	7.078366099	protein synthesis ribosomal protein eukaryotic 40S subunit S3A
Sopim03g098280	ARGONAUTE 1	4	0.001578169	0.00275894	0.000110418	633.6456995	development unspecified
Sopim03g098700	Cysteine protease inhibitor 8	3	0.007667001	0.00749841	0.000617911	130.4290948	stress biotic PRproteins PR6 proteinase inhibitors
Sopim03g111010	Glyceraldehyde 3 phosphate dehydrogenase	2	0.413386374	0.11032288	0.00120748	2.419044417	glycolysis cytosolic branch glyceraldehyde 3phosphate dehydrogenase GAPDH
Sopim03g111230	60S ribosomal protein L17	3	0.390707642	0.14866828	0.000339451	2.559458512	protein synthesis ribosomal protein eukaryotic 60S subunit L17
Sopim03g111340	Ubiquitin like modifier activating enzyme 5	2	0.302158651	0.16657088	0.001059111	3.309519673	protein degradation ubiquitin E1
Sopim03g111640	Eukaryotic translation initiation factor 4 gamma 2 Fragment	4	0.053416725	0.02641361	0.016151197	18.72072839	DNA unspecified
Sopim03g111810	Sieve element occluding protein 3	2	0.01155318	0.01615801	0.012259689	86.55625551	mitochondrial electron transport / ATP synthesis cytochrome c oxidase
Sopim03g112070	Phosphoglycerate dehydrogenase	5	0.346419981	0.09465054	3.11E-06	2.886669519	PS lightreaction photosystem I LHCI
Sopim03g112150	Elongation factor Tu	3	0.376454174	0.15307558	0.002568052	2.656365818	protein synthesis elongation
Sopim03g112270	Lrr resistance protein fragment	2	0.315519278	0.20307497	0.010912888	3.169378449	RNA regulation of transcription putative transcription regulator
Sopim03g112850	60S ribosomal protein L44	2	0.359858689	0.21286156	0.008492409	2.778868569	protein synthesis ribosomal protein eukaryotic 60S subunit L44
Sopim03g113400	HATPase	12	0.085165506	0.01986401	8.18E-13	11.74184299	tetrapyrrole synthesis ALA dehydratase
Sopim03g113800	Betaine aldehyde dehydrogenase	7	0.182569559	0.03151708	9.05E-12	5.477364384	secondary metabolism N misc betaine betainealdehyde dehydrogenase
Sopim03g114150	Aldehyde dehydrogenase	2	0.14906242	0.05391152	8.89E-05	6.708598988	secondary metabolism N misc betaine
Sopim03g115230	ClpB chaperone	12	0.17276799	0.03210671	2.22E-16	5.788109244	stress abiotic heat
Sopim03g115630	Carbamoyl phosphate synthase small chain	2	0.212623219	0.21457846	0.011485874	4.703155209	protein postranslational modification
Sopim03g116620	Phospholipase D	2	0.026027216	0.02601823	0.000952837	38.42132021	PS lightreaction other electron carrier ox/red plastocyanin
Sopim03g117480	Pyrophosphate energized proton pump- Pyrophosphate energized inorganic pyrophosph	3	0.124422906	0.03362876	0.000209636	8.037105322	PS calvin cycle rubisco small subunit
Sopim03g117630	heat shock protein	2	0.290183679	0.11009535	1.50E-05	3.44609319	transport misc
Sopim03g118020	Tudor / nuclease domaincontaining protein	2	0.377321106	0.22158774	0.006220995	2.650262559	RNA regulation of transcription ZnfingerCCHC
Sopim03g118040	Calcium binding protein Calnexin	10	0.044106676	0.02021342	8.59E-09	22.67230475	signalling calcium
Sopim03g118170	Glycyl tRNA synthetase	2	0.249497212	0.15317093	0.004930049	4.00806082	RNA regulation of transcription orphan family
Sopim03g118340	ATP-dependent clp protease ATPbinding subunit	4	0.355519701	0.09763561	0.000244955	2.812783644	stress abiotic heat
Sopim03g118640	D-tagatose1,6-bisphosphate aldolase subunit gatY	10	0.095071512	0.020817	2.37E-10	10.51839798	OPP oxidative PP 6phosphogluconate dehydrogenase
Sopim03g118760	Tubulin beta chain	6	0.122511543	0.03270243	4.34E-12	8.162496166	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Sopim03g118910	Tcomplex protein 1 subunit delta	4	0.185070601	0.07139428	1.78E-05	5.403343344	protein folding
Sopim03g119080	Betaglucosidase	10	0.040715694	0.01056338	1.83E-11	24.56055397	misc gluco galacto and mannosidases
Sopim03g119090	WD repeat containing protein 1	2	0.083374108	0.06569269	0.001016504	11.99413132	development unspecified
Sopim03g119130	Histone H1	3	0.081006688	0.06229082	0.002403069	12.34465974	DNA synthesis/chromatin structure histone
Sopim03g119360	40S ribosomal protein S7like protein	3	0.400219627	0.10430625	7.32E-05	2.498628085	protein synthesis ribosomal protein eukaryotic 40S subunit S7
Sopim03g120270	Coatomer betaapos subunit	11	0.024531773	0.00470695	3.82E-12	40.76346214	cell vesicle transport
Sopim03g120350	N-alpha-acetyltransferase 16 NatA auxiliary subunit	2	0.057154829	0.06241149	6.52E-05	17.49633439	misc acyl transferases
Sopim03g120850	chaperonin	9	0.144455957	0.05406215	7.62E-10	6.922525182	PS calvin cycle rubisco interacting
Sopim03g121070	Hexokinase	2	0.182114218	0.1654557	0.005175431	5.491059462	signalling receptor kinases leucine rich repeat XI
Sopim03g121570	Transmembrane 9 superfamily protein member 4	2	0.080978897	0.07086688	0.013076461	12.34889628	DNA unspecified
Sopim03g121590	Protein SEY1	5	0.028198008	0.00794952	1.36E-05	35.46349799	signalling Gproteins
Sopim03g121640	chaperonin	4	0.068259844	0.04352909	0.000136476	14.64990163	stress abiotic heat
Sopim03g123630	Pectinesterase	4	0.286885462	0.12439616	1.34E-05	3.48571166	secondary metabolism flavonoids dihydroflavonols
Sopim03g123730	26S protease regulatory subunit 7	2	0.366796081	0.23762548	0.014055265	2.726310481	protein degradation ubiquitin proteasom
Sopim03g123830	Phosphoglycerate dehydrogenase	15	0.123039072	0.01730841	2.22E-16	8.127499531	PS lightreaction photosystem I LHCI
Sopim04g005160	6-phosphogluconate dehydrogenase decarboxylating	2	0.288351769	0.25253859	0.00857495	3.467986354	OPP oxidative PP 6phosphogluconate dehydrogenase
Sopim04g006970	Phosphoenolpyruvate carboxylase	18	0.026628167	0.00940565	2.44E-15	37.55421843	glycolysis cytosolic branch phosphoenolpyruvate carboxylase PEPC
Sopim04g008280	Regulator of ribonuclease activity A	3	0.216282857	0.07624936	4.14E-05	4.623574951	C1metabolism
Sopim04g008310	Glucosyltransferase	3	0.002788214	0.00263258	3.53E-05	358.6525281	transport ABC transporters and multidrug resistance systems
Sopim04g008740	Pyruvate kinase	4	0.189845188	0.09200137	6.73E-05	5.267449813	glycolysis cytosolic branch pyruvate kinase PK
Sopim04g008810	40S ribosomal protein S26	2	0.03606173	0.02931842	0.006550297	27.73022814	protein synthesis ribosomal protein eukaryotic 40S subunit S26
Sopim04g009200	Glutamate-1-semialdehyde-2, 1-aminomutase	2	0.312277904	0.26411353	0.013763208	3.202275881	misc oxidases copper flavone etc
Sopim04g010070	Protein phosphatase 2A regulatory subunit Baposlike protein	2	0.079240722	0.03753144	0.004499047	12.61977396	protein postranslational modification
Sopim04g011350	2oxoglutarate dehydrogenase E1 component	2	0.12056845	0.17108554	0.00121273	8.294043757	lipid metabolism FA synthesis and FA elongation acetyl CoA transacylase
Sopim04g011400	UDPglucose 4 epimerase	3	0.427422387	0.08022891	0.001831006	2.339606044	cell wall precursor synthesis UXS
Sopim04g011440	heat shock protein	11	0.295164035	0.0589209	2.22E-11	3.387946638	protein folding
Sopim04g011500	Actin 4	6	0.260308764	0.06307745	1.57E-07	3.841591749	cell organisation
Sopim04g012040	26S proteasome nonATPase regulatory subunit 12	2	0.053235443	0.03136206	0.010307947	18.78447785	signalling light COP9 signalosome
Sopim04g014510	Glutamine synthetase	3	0.330664222	0.07665564	3.21E-05	3.024215907	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Sopim04g014570	Transmembrane 9 superfamily protein member 1	5	0.058775573	0.01972878	5.64E-09	17.01387071	protein postranslational modification
Sopim04g014600	Universal stress protein family protein	2	0.124744874	0.04965399	0.001005345	8.016361458	RNA regulation of transcription putative transcription regulator
Sopim04g016350	40S ribosomal protein S4like protein	3	0.094345562	0.07821813	0.000740478	10.5993327	protein synthesis ribosomal protein eukaryotic 40S subunit S4
Sopim04g026020	Sieve element occluding protein 3	2	0.038729055	0.01910427	0.00134809	25.82040796	protein postranslational modification
Sopim04g026100	30S ribosomal protein S9	2	0.113323602	0.03889439	0.000566034	8.824287107	protein synthesis ribosome biogenesis
Sopim04g045340	Phosphoglucomutase	7	0.246384539	0.0398204	1.88E-09	4.058696232	glycolysis cytosolic branch phosphoglucomutase PGM
Sopim04g050510	Translational activator gcn1	3	0.057776363	0.03527005	0.000202401	17.30811612	protein synthesis
Sopim04g050520	Translational activator gcn1	3	0.024042617	0.01298231	0.000123697	41.59280997	protein synthesis
Sopim04g051370	26S proteasome nonATPase regulatory subunit 12	4	0.034965097	0.0123849	0.000171491	28.59994926	signalling light COP9 signalosome
Sopim04g053120	4 alphaglucanotransferase	4	0.034059987	0.0261872	8.62E-05	29.35996423	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Sopim04g054480	C2 domain containing proteinlike	5	0.017627614	0.00782508	1.15E-06	56.72917503	not assigned no ontology
Sopim04g055170	Annexin 2	2	0.227964487	0.23726024	0.011673697	4.386648171	misc oxidases copper flavone etc
Sopim04g058070	UDP N-acetylglucosamine pyrophosphorylase	2	0.396337598	0.12629798	0.002010903	2.52310153	cell wall precursor synthesis NDP sugar pyrophosphorylase multiple NDPSugars
Sopim04g063280	Vacuolar protein sortin gassociated protein 27	2	0.346957694	0.17614459	0.005883793	2.882195776	cell vesicle transport
Sopim04g063290	30S ribosomal protein S5	2	0.036439133	0.03776236	0.009776712	27.44302396	protein synthesis ribosome biogenesis
Sopim04g071260	Actin	5	0.250024789	0.07144892	1.86E-06	3.999603415	cell organisation
Sopim04g071340	Fructose 1, 6 bisphosphatase class 1	2	0.309119522	0.19207123	0.010030398	3.23499465	PS calvin cycle FBPase
Sopim04g071350	Exocyst complex component 2	4	0.018730353	0.01177053	0.000136197	53.38927675	transport ammonium
Sopim04g071620	ASR4 Fragment	3	0.001757213	0.00247963	0.001291907	569.082974	stress abiotic drought/salt
Sopim04g072060	Rasrelated protein Rab7a	2	0.251728402	0.06896203	0.000691689	3.972535447	cell wall precursor synthesis UXS
Sopim04g072160	Prostaglandin E synthase 3	2	0.174696188	0.04276133	0.006800888	5.724223359	RNA regulation of transcription AtSR transcription factor family
Sopim04g072240	Oxidoreductase family protein	3	0.18930288	0.040533	0.000130672	5.282539811	not assigned no ontology
Sopim04g073990	Annexin	2	0.040250076	0.03202446	0.013166473	24.84467359	stress abiotic heat
Sopim04g074300	30S ribosomal protein S5	2	0.036439133	0.03776236	0.009776712	27.44302396	protein synthesis ribosomal protein eukaryotic 40S subunit S2
Sopim04g074510	14-3-3 protein beta/alphaB	2	0.207224791	0.08620842	0.00031519	4.825677445	signalling 1433 proteins
Sopim04g076090	Glucose 6 phosphate isomerase 2	3	0.212639036	0.08413872	8.37E-06	4.702805368	glycolysis plastid branch glucose6phosphate isomerase
Sopim04g076230	AP2 complex subunit mu	3	0.031360092	0.02128146	0.000108849	31.88766155	protein targeting secretory pathway unspecified
Sopim04g076380	Cytochrome P450 NADPHreductase	5	0.05952035	0.01357433	3.35E-07	16.80097647	misc cytochrome P450
Sopim04g076790	Serine hydroxymethyltransferase	6	0.129053228	0.06113318	1.03E-08	7.748740698	PS photorespiration serine hydroxymethyltransferase
Sopim04g076890	Ubiquitin fold modifier conjugating enzyme 1	2	0.322149812	0.18454209	0.003027552	3.104145844	not assigned unknown
Sopim04g077020	Tubulin alpha3 chain	5	0.310763735	0.1161178	5.74E-05	3.217878688	RNA regulation of transcription bZIP transcription factor family
Sopim04g077650	Serine carboxypeptidase 1	3	0.270861493	0.08136588	0.000948423	3.691923828	protein degradation serine protease
Sopim04g077670	Serine carboxypeptidase 1	2	0.050564967	0.01863034	0.000438398	19.77653817	protein degradation serine protease
Sopim04g079270	Sorting and assembly machinery component 50 homolog	2	0.008312792	0.01105092	0.01102663	120.2965261	not assigned no ontology
Sopim04g079790	30S ribosomal protein S9	4	0.323922546	0.12623599	0.000671302	3.087157755	protein synthesis ribosomal protein prokaryotic chloroplast 30S subunit S9
Sopim04g080980	Coatomer alpha subunitlike protein	27	0.016504621	0.00328301	9.90E-20	60.58909199	cell vesicle transport
Sopim04g081090	Vtype proton ATPase 16 kDa proteolipid subunit c2	2	0.234332388	0.14588747	0.014925101	4.267442536	transport p and vATPases H+transporting twosector ATPase
Sopim04g081330	Chromosome 11 contig 1 DNA sequence. Fragment	2	0.072234842	0.02837634	0.006600793	13.84373486	not assigned unknown
Sopim04g081440	Neutral invertase like protein	3	0.065666243	0.02557468	0.000119776	15.22852465	protein postranslational modification kinase receptor like cytoplasmatic kinase VII
Sopim04g081490	Tubulin beta1 chain	11	0.169210196	0.02461409	9.90E-20	5.909809359	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Sopim04g081570	Chaperone protein htpG	4	0.003961784	0.00275034	0.000430518	252.4115399	cell wall cell wall proteins proline rich proteins
Sopim04g082140	Laccase22	4	0.15742448	0.09119628	7.23E-06	6.352252204	misc oxidases copper flavone etc
Sopim04g082250	ATP-dependent zinc metalloprotease FTSH chloroplastic Fragment	4	0.313737063	0.07649088	1.05E-06	3.187382423	protein degradation metalloprotease
Sopim04g082460	Catalase	2	0.270357358	0.1186906	0.000236699	3.698808153	redox dismutases and catalases
Sopim04g082630	Glyceraldehyde 3 phosphate dehydrogenase B	3	0.388250185	0.0648472	0.000121855	2.575658786	protein postranslational modification
Sopim04g082670	Dolichyl diphospho oligosaccharide protein glycosyltransferase subunit 1	6	0.00697307	0.00598094	2.35E-08	143.4088572	hormone metabolism cytokinin signal transduction
Sopim04g082700	Solute carrier family 2 facilitated glucose transporter member 12	2	0.121357408	0.03855972	0.000795409	8.240123256	transport sugars
Sopim04g082790	Atp-dependent RNA helicase	3	0.284668518	0.08219339	4.37E-06	3.512857716	protein synthesis initiation
Sopim04g082880	Diphosphate fructose 6 phosphate 1 phosphotransferase	2	0.109074933	0.05184377	0.000222642	9.168009299	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Sopim05g005020	R1 protein alphaglucan water dikinase	11	0.039536065	0.01156571	2.55E-12	25.2933619	major CHO metabolism degradation starch glucan water dikinase
Sopim05g005190	ADP ribosylation factor	2	0.059663858	0.08020281	8.96E-06	16.7605655	protein postranslational modification
Sopim05g005480	Oxido reductase zinc binding dehydrogenase	2	0.265090465	0.21147558	0.003463572	3.772297129	misc oxidases copper flavone etc
Sopim05g005490	Carbonic anhydrase	2	0.272344058	0.19133939	0.005411679	3.671826025	TCA / organic transformation carbonic anhydrases
Sopim05g005690	30S ribosomal protein S9	2	0.117418259	0.03832782	3.30E-05	8.516562999	protein synthesis ribosomal protein eukaryotic 40S subunit S16
Sopim05g005700	Aldehyde dehydrogenase 1	3	0.259271509	0.17630232	0.00101286	3.85696062	secondary metabolism N misc betaine
Sopim05g005780	AP1 complex subunit gamma1	2	0.013750766	0.0092389	0.002097246	72.72322138	cell vesicle transport
Sopim05g005800	Threonyl tRNA synthetase	3	0.052208857	0.02512999	0.002381262	19.15383821	RNA regulation of transcription unclassified
Sopim05g006740	Glutathione S transferase	2	0.159090387	0.08163213	0.000655692	6.285734914	development unspecified
Sopim05g007250	Ribosomal protein	3	0.039689912	0.01583373	0.00222305	25.19531915	protein synthesis ribosomal protein eukaryotic 40S subunit S9
Sopim05g007560	60S ribosomal protein L34	3	0.339801758	0.08288526	0.000245007	2.942892367	protein synthesis ribosome biogenesis
Sopim05g008600	Fructose bisphosphate aldolase	2	0.396857419	0.08382793	8.64E-05	2.519796663	lipid metabolism FA synthesis and FA elongation pyruvate kinase
Sopim05g009600	Phosphatase 2A regulatory A subunit	3	0.16509504	0.11635871	0.001595863	6.057117161	protein postranslational modification
Sopim05g010260	6 phosphogluconate dehydrogenase decarboxylating	2	0.29325729	0.22490903	0.007045469	3.409974906	OPP oxidative PP 6phosphogluconate dehydrogenase
Sopim05g010670	Chaperone protein htpG	3	0.284619715	0.14786785	0.00079336	3.513460057	stress abiotic heat
Sopim05g012480	Mitochondrial processing peptidase beta subunit	6	0.275199016	0.07599457	5.82E-08	3.633733923	protein targeting mitochondria
Sopim05g012510	Phosphorylase	12	0.026300621	0.00839636	1.43E-11	38.02191591	major CHO metabolism degradation starch starch phosphorylase
Sopim05g013850	Sieve element occluding protein 3	6	0.023593847	0.00840513	2.00E-06	42.38393171	protein postranslational modification
Sopim05g013870	Sieve element occluding protein 3	3	0.03130268	0.01080372	0.000105457	31.94614646	protein postranslational modification
Sopim05g013990	Tcomplex protein 1 subunit epsilon	3	0.168679797	0.10651054	0.000221543	5.928392242	protein postranslational modification
Sopim05g014280	Heat shock protein	5	0.081124375	0.04328935	2.98E-06	12.32675136	protein synthesis ribosome biogenesis
Sopim05g014310	Metalloendopeptidase family saccharolysin amp thimet oligopeptidase ISS	3	0.016205657	0.00905168	2.58E-05	61.70684718	protein degradation
Sopim05g014470	Glyceraldehyde 3 phosphate dehydrogenase	4	0.286320175	0.07571375	0.000161401	3.492593562	glycolysis cytosolic branch glyceraldehyde 3phosphate dehydrogenase GAPDH
Sopim05g017950	Bile acid sodium symporter	2	0.079141573	0.04571313	0.000157484	12.63558408	transport unspecified cations
Sopim05g023720	Apocytochrome f	3	0.085787197	0.03536457	0.001335602	11.65675107	PS lightreaction cytochrome b6/f apocytochrome f CYF
Sopim05g025740	SH3 domain containing protein	2	0.016325	0.01391626	0.000470914	61.25574273	not assigned no ontology
Sopim05g026540	Transmembrane protein 214	4	0.115040848	0.04033294	0.000154592	8.692564575	not assigned unknown
Sopim05g032820	Adenosyl homocysteinase	2	0.251138369	0.20078524	0.006530175	3.981868657	not assigned unknown
Sopim05g046330	Dolichyl diphospho oligosaccharide protein glycosyltransferase subunit 2	3	0.09240738	0.04433952	0.000869179	10.8216465	development unspecified
Sopim05g050120	Malic enzyme	10	0.178728996	0.03479154	4.16E-13	5.595063042	TCA / organic transformation other organic acid transformations malic
Sopim05g050600	Dynamin 2	4	0.290359035	0.09474674	0.000100858	3.444011997	minor CHO metabolism myoinositol polyphosphatases
Sopim05g050970	Transketolase 1	2	0.271335789	0.2112954	0.006743034	3.685470331	PS calvin cycle transketolase
Sopim05g051000	40S ribosomal protein S13	4	0.177304138	0.03546934	7.03E-06	5.640026292	protein synthesis ribosome biogenesis
Sopim05g051250	Glutamine synthetase	3	0.330664222	0.07665564	3.21E-05	3.024215907	RNA regulation of transcription squamosa promoter binding protein family SBP
Sopim05g051570	Ras related protein Rab6A	3	0.337521092	0.11533271	0.000839638	2.962777805	signalling Gproteins
Sopim05g052510	Clathrin heavy chain	38	0.000853154	0.00041218	9.90E-20	1172.121329	cell vesicle transport

Sopim05g052600	Fructose 1,6 bisphosphatase class 1	3	0.120483536	0.05345527	0.00025887	8.299889206	PS calvin cycle sedoheptulose bisphosphatase
Sopim05g052780	LIM domain protein	2	0.041286099	0.01843464	0.004541716	24.22122759	RNA regulation of transcription general transcription
Sopim05g052920	Folylpolyglutamate synthase	2	0.045471411	0.04521405	0.000736588	21.9918401	tetrapyrrole synthesis ALA dehydratase
Sopim05g053300	Dihydrolipoyl dehydrogenase	9	0.278277482	0.06742713	5.10E-10	3.593535463	redox ascorbate and glutathione glutathione
Sopim05g053470	chaperonin	15	0.229598009	0.05014968	8.98E-14	4.355438465	stress abiotic heat
Sopim05g053650	26S proteasome regulatory subunit	3	0.048506509	0.01260027	7.07E-06	20.61578993	protein degradation ubiquitin proteasom
Sopim05g053670	60S ribosomal protein L13alike protein	4	0.141813314	0.04372786	1.00E-05	7.05152409	protein synthesis ribosome biogenesis
Sopim05g053830	Protein transport protein Sec23	2	0.027516521	0.02853666	0.000810484	36.34180353	protein targeting secretory pathway golgi
Sopim05g054040	Transmembrane 9 superfamily protein member 1	3	0.064704272	0.02731977	5.73E-05	15.45493009	protein postranslational modification
Sopim05g054050	Glutamate decarboxylase	2	0.165233791	0.1001448	0.002811954	6.052030846	amino acid metabolism synthesis central amino acid metabolism GABA glutamate decarboxylase
Sopim05g054070	60S ribosomal protein L6	2	0.18750757	0.20256207	0.005473385	5.333118018	protein synthesis ribosome biogenesis
Sopim05g054320	Epoxide hydrolase	2	0.318251557	0.15394098	0.003152751	3.142168445	misc misc2
Sopim05g054330	Epoxide hydrolase	2	0.318251557	0.15394098	0.003152751	3.142168445	misc misc2
Sopim05g054350	Epoxide hydrolase	3	0.291713018	0.12702575	0.00099494	3.42802665	misc misc2
Sopim05g054480	Actin	6	0.260308764	0.06307745	1.57E-07	3.841591749	cell organisation
Sopim05g054490	Trans-2-enoylCoA reductase	6	0.031469337	0.01671019	1.03E-05	31.77696435	lipid metabolism exotics steroids squalene etc trans2enoylCoA reductase NADPH
Sopim05g054640	2-oxoglutarate dehydrogenase E1 component	9	0.084173499	0.04723801	8.94E-07	11.88022373	lipid metabolism FA synthesis and FA elongation acetyl CoA transacylase
Sopim05g054760	Dehydroascorbate reductase Fragment	2	0.195690297	0.09544303	0.013465879	5.110115398	redox ascorbate and glutathione ascorbate
Sopim05g055210	Eukaryotic peptide chain release factor subunit 13like	5	0.260516324	0.10872714	1.24E-05	3.838531055	RNA regulation of transcription AtSR transcription factor family
Sopim05g055230	40S ribosomal protein S17like protein	4	0.207582662	0.04697861	8.39E-07	4.817358012	protein synthesis ribosomal protein eukaryotic 40S subunit S17
Sopim05g055400	Cytochrome P450	8	0.075278971	0.02297911	1.53E-09	13.28392228	misc cytochrome P450
Sopim05g055880	Nucleolar protein 5	3	0.195889528	0.07771782	8.34E-06	5.104918115	RNA regulation of transcription putative transcription regulator
Sopim05g056130	Dolichyl diphospho oligosaccharide protein glycosyltransferase subunit 1	2	0.074178207	0.08491251	0.000684	13.48104842	hormone metabolism cytokinin signal transduction
Sopim05g056310	Tcomplex protein 1 subunit gamma	8	0.202441353	0.03171995	4.92E-09	4.939702216	protein folding
Sopim05g056580	Dehydration responsive family protein	3	0.094233464	0.06275206	3.77E-06	10.61194142	tetrapyrrole synthesis ALA dehydratase
Sopim06g005060	Elongation factor 1 alpha	7	0.119974191	0.01838546	6.11E-15	8.335126011	protein synthesis elongation
Sopim06g005080	Vacuolar protein sorting associated protein 18	2	0.019181948	0.0230193	0.004576264	52.1323486	protein targeting secretory pathway vacuole
Sopim06g005910	Tubulin beta chain	9	0.1313913	0.02800225	2.05E-09	7.610853991	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Sopim06g007320	Ubiquitin activating enzyme E1	4	0.119179072	0.06900578	0.00012971	8.39073491	protein degradation ubiquitin E1
Sopim06g007360	40S ribosomal protein S4like protein	4	0.099406678	0.07388077	0.000256157	10.05968633	protein synthesis ribosome biogenesis
Sopim06g007470	40S ribosomal protein S26	2	0.054838514	0.04271639	0.005248869	18.23535919	protein synthesis ribosomal protein eukaryotic 40S subunit S26
Sopim06g009190	Pectinesterase	4	0.066266023	0.02245938	1.30E-05	15.09068984	secondary metabolism flavonoids dihydroflavonols
Sopim06g009750	Importin alpha1b subunit	3	0.213283211	0.09334234	0.000421819	4.68860158	protein targeting nucleus
Sopim06g009960	Elongation factor 1 alpha	3	0.224036575	0.15773682	0.00332821	4.463556899	protein synthesis elongation
Sopim06g011280	Elongation factor 1gamma	9	0.074809174	0.02768322	2.66E-07	13.36734449	protein synthesis elongation
Sopim06g011380	Chaperone ClpB	2	0.180898702	0.10590109	0.007648927	5.52795564	stress abiotic heat
Sopim06g019170	Gammaglutamyl phosphate reductase	2	0.282004577	0.10441339	0.00026707	3.546041737	amino acid metabolism synthesis glutamate family proline delta 1pyrroline5carboxylate synthetase
Sopim06g035970	Tubulin beta chain	12	0.119266592	0.01944845	9.90E-20	8.384577636	cell organisation
Sopim06g036290	Heat shock protein 90 Fragment	4	0.01480378	0.01267392	0.000294015	67.55031485	stress abiotic heat
Sopim06g050120	Ribosomal protein L7a	2	0.223147001	0.17715024	0.001852979	4.481350838	protein synthesis ribosomal protein eukaryotic 60S subunit L7A
Sopim06g050980	Ferritin	5	0.220964656	0.06644931	1.31E-06	4.525610648	metal handling binding chelation and storage
Sopim06g051310	Clathrin heavy chain	35	0.000704924	0.00043446	9.90E-20	1418.592643	cell vesicle transport
Sopim06g052030	Importin subunit beta	6	0.002057551	0.00224047	1.43E-05	486.0146844	protein targeting nucleus
Sopim06g053210	Ubiquitin	2	0.263353471	0.07260891	2.54E-06	3.797177976	protein degradation ubiquitin ubiquitin
Sopim06g053400	2-isopropylmalate synthase 1	2	0.190864498	0.05083945	8.51E-05	5.239319048	amino acid metabolism synthesis branched chain group leucine specific 2isopropylmalate synthase
Sopim06g059740	Alcohol dehydrogenase 2	6	0.228679838	0.0820159	6.74E-08	4.372925959	fermentation ADH
Sopim06g060340	Chloroplast photosystem II-associated protein	2	0.099884565	0.05121778	0.000759426	10.01155684	PS lightreaction photosystem II PSII polypeptide subunits
Sopim06g062590	Transmembrane 9 superfamily protein member 4	4	0.076226501	0.05186454	3.94E-06	13.1187971	DNA unspecified
Sopim06g062800	ATP-dependent RNA helicase eIF4A	2	0.246697655	0.19231179	0.005033273	4.053544814	DNA synthesis/chromatin structure
Sopim06g062840	Threonine synthase	2	0.327208415	0.10955103	0.000200747	3.05615612	amino acid metabolism synthesis aspartate family threonine threonine synthase
Sopim06g063140	26S protease regulatory subunit 7	2	0.366796081	0.23762548	0.014055265	2.726310481	protein degradation ubiquitin proteasom
Sopim06g063330	Vtype ATP synthase alpha chain	8	0.286658694	0.08345199	3.20E-08	3.488469113	PS lightreaction ATP synthase
Sopim06g063370	Chlorophyll ab binding protein 1A chloroplastic	5	0.087596039	0.03480052	5.26E-08	11.41604131	PS lightreaction photosystem II LHCII
Sopim06g064460	Ribosomal protein L7a	2	0.223147001	0.17715024	0.001852979	4.481350838	protein synthesis ribosomal protein eukaryotic 60S subunit L7A
Sopim06g064470	Ribosomal protein L7a	2	0.223147001	0.17715024	0.001852979	4.481350838	protein synthesis ribosomal protein eukaryotic 60S subunit L7A
Sopim06g065270	Adenylate kinase	2	0.284828803	0.12449619	0.000652316	3.510880885	nucleotide metabolism phosphotransfer and pyrophosphatases adenylate kinase
Sopim06g065520	Tcomplex protein eta subunit	6	0.212524312	0.03506613	2.83E-07	4.705344017	protein folding
Sopim06g065590	60S ribosomal protein L18a	8	0.098753517	0.02549095	1.35E-06	10.12622163	protein synthesis ribosome biogenesis
Sopim06g065830	Transmembrane 9 superfamily protein member 2	3	0.010822059	0.00821824	0.000100795	92.40385771	DNA unspecified
Sopim06g066730	Coatomer betaapos subunit	6	0.022674048	0.00583672	1.33E-08	44.10328495	transport sulphate
Sopim06g067920	Cytochrome c1	2	0.255980282	0.14992156	0.003664821	3.906550896	signalling receptor kinases DUF 26
Sopim06g068090	Phospholipase D	9	0.05184226	0.0208738	2.32E-08	19.28928253	lipid metabolism lipid degradation lysophospholipases phospholipase D
Sopim06g068240	Pyrophosphate energized proton pump	2	0.172599141	0.04598034	0.00339873	5.793771592	PS calvin cycle rubisco small subunit
Sopim06g068320	Prolyl tRNA synthetase	2	0.03106986	0.01947885	0.00030169	32.18553286	secondary metabolism isoprenoids mevalonate pathway isopentenyl pyrophosphatedimethyllallyl pyrophosphate isomerase
Sopim06g068860	Alpha mannosidase	2	0.378547936	0.17114558	0.017784878	2.641673365	development unspecified
Sopim06g068950	Phosphoethanolamine N methyltransferase	2	0.178684169	0.11895918	0.003438682	5.596466691	major CHO metabolism degradation starch transporter
Sopim06g069010	Guanine nucleotide-binding protein beta subunitlike protein	2	0.133273807	0.12047647	0.001190461	7.503349852	RNA regulation of transcription unclassified
Sopim06g069090	40S ribosomal protein S7like protein	3	0.400219627	0.10430625	7.32E-05	2.498628085	protein synthesis ribosomal protein eukaryotic 40S subunit S7
Sopim06g069180	Phosphatase 2A regulatory A subunit	3	0.149126476	0.1136643	0.001489787	6.705717367	protein postranslational modification
Sopim06g069860	60S ribosomal protein L34	3	0.339801758	0.08288526	0.000245007	2.942892367	protein synthesis ribosomal protein eukaryotic 60S subunit L34
Sopim06g071100	HATPase	13	0.082013301	0.0190365	1.31E-12	12.19314413	major CHO metabolism degradation sucrose invertases neutral
Sopim06g071310	LIM domain protein	2	0.16141811	0.10686666	0.006084713	6.19509174	RNA regulation of transcription putative transcription regulator
Sopim06g071720	60S ribosomal protein L27A	2	0.27371066	0.08253654	0.000568514	3.653493072	protein synthesis ribosomal protein eukaryotic 60S subunit L27A
Sopim06g071790	Elongation factor Tu	2	0.373466969	0.17231097	0.008869348	2.67761297	protein synthesis elongation
Sopim06g071870	60S ribosomal protein L17	2	0.269424286	0.09504527	0.008866655	3.71161789	protein synthesis ribosomal protein eukaryotic 60S subunit L17
Sopim06g071880	60S ribosomal protein L17	2	0.269424286	0.09504527	0.008866655	3.71161789	protein synthesis ribosome biogenesis
Sopim06g071920	Glyceraldehyde 3 phosphate dehydrogenase	3	0.403446019	0.10583554	0.000486187	2.478646344	glycolysis cytosolic branch glyceraldehyde 3phosphate dehydrogenase GAPDH
Sopim06g072300	ARGONAUTE 1	3	0.102149243	0.07639315	0.001126254	9.789597756	RNA silencing RISC formation AGO
Sopim06g072380	Dihydroxyacetone/glycerone kinaselike protein	2	0.276557215	0.09985733	0.00024234	3.615888307	minor CHO metabolism others
Sopim06g072490	40S ribosomal protein S1	2	0.141275541	0.10907486	0.000745869	7.078366099	protein synthesis ribosome biogenesis
Sopim06g072510	Mitochondrial phosphate carrier protein	2	0.061064355	0.0529156	0.00154683	16.37616577	RNA processing
Sopim06g072540	ATP synthase subunit alpha chloroplastic	2	0.158180352	0.03238409	8.80E-11	6.321897678	PS lightreaction ATP synthase alpha subunit
Sopim06g073370	40S ribosomal protein S18	2	0.37057123	0.1469239	0.001374342	2.698536527	protein synthesis ribosome biogenesis
Sopim06g073790	40S ribosomal protein S11	8	0.270679802	0.04347936	7.40E-10	3.694401993	protein synthesis ribosome biogenesis
Sopim06g073840	Peptidylprolyl cis trans isomerase D	2	0.029585539	0.02631166	0.003038481	33.80029683	DNA synthesis/chromatin structure
Sopim06g074650	AP2 complex subunit alpha	6	0.03333787	0.01201838	5.25E-08	29.99591756	cell vesicle transport
Sopim06g075010	chaperonin	4	0.243324522	0.06521594	1.19E-07	4.109737859	PS calvin cycle rubisco interacting
Sopim06g075340	Carbamoylphosphate synthase large chain	4	0.018035807	0.02075413	2.88E-05	55.44525953	tetrapyrrole synthesis ALA dehydratase
Sopim06g076020	heat shock protein	7	0.211759784	0.04419853	2.04E-07	4.72233198	stress abiotic heat
Sopim06g076090	Actin	6	0.260308764	0.06307745	1.57E-07	3.841591749	cell organisation
Sopim06g076640	Tubulin beta chain	9	0.134866163	0.01834492	9.90E-20	7.414758289	cell organisation
Sopim06g082100	Related to ATP dependent RNA helicase	2	0.005141867	0.00762922	0.000380626	194.4818876	RNA processing RNA helicase
Sopim06g082560	ClpB chaperone	3	0.22027287	0.05741979	1.06E-07	4.53982372	stress abiotic heat
Sopim06g082940	Photosystem I reaction center subunit XI	2	0.42688895	0.06964354	0.000135809	2.342529597	PS lightreaction photosystem I PSI polypeptide subunits
Sopim06g082950	Photosystem I reaction center subunit XI	2	0.42688895	0.06964354	0.000135809	2.342529597	PS lightreaction photosystem I PSI polypeptide subunits
Sopim06g083190	Peptidylprolyl cis trans isomerase	2	0.312659285	0.15098064	0.008070889	3.198369753	protein folding
Sopim06g083580	Pectate lyase 127	5	0.020326295	0.00810723	6.43E-05	49.19735741	cell wall degradation pectate lyases and polygalacturonases
Sopim06g083620	26S protease regulatory subunit 4	2	0.320759487	0.1628954	0.011060935	3.117600696	protein degradation ubiquitin proteasom
Sopim06g083790	SuccinylCoA ligase	2	0.233665799	0.10679809	0.00039921	4.279616462	protein postranslational modification
Sopim06g084210	Transport protein SEC24	3	0.081103208	0.07320185	0.000637792	12.3299685	misc UDP glucosyl and glucoronyl transferases
Sopim07g005040	HATPase	2	0.035818952	0.04550164	0.00065707	27.91818141	transport p and vATPases H+exporting ATPase
Sopim07g005210	Outer membrane lipoprotein blc	2	0.179879093	0.06428145	1.61E-05	5.559289761	transport misc
Sopim07g005600	Transmembrane 9 superfamily protein member 4	3	0.022200062	0.01374777	0.000681361	45.04491924	DNA unspecified
Sopim07g005810	Eukaryotic translation initiation factor 4	3	0.139336126	0.05798557	2.23E-06	7.176889646	protein synthesis initiation
Sopim07g005820	heat shock protein	3	0.289859074	0.10556138	7.18E-06	3.449952372	transport misc
Sopim07g005940	Vacuolar ATPase subunit H protein	6	0.003171384	0.0006972	1.80E-05	315.3197468	tetrapyrrole synthesis ALA dehydratase
Sopim07g006130	Eukaryotic peptide chain release factor subunit 11	3	0.275620226	0.12106066	0.000180488	3.628180756	protein synthesis release
Sopim07g006280	Senescence associated protein	2	0.116638812	0.06839686	0.001113679	8.573475525	development unspecified
Sopim07g006790	Dihydrolipoyl lysine residue acetyltransferase component of pyruvate dehydrogenase co	3	0.301877688	0.19989426	0.003323169	3.312599903	TCA / organic transformation TCA pyruvate DH E2
Sopim07g007030	Transmembrane 9 superfamily protein member 2	5	0.013053525	0.00823866	1.71E-07	76.60765962	DNA unspecified
Sopim07g007600	Pyrophosphate energized proton pump	5	0.0115681	0.00770795	4.43E-06	86.44461925	transport H+ transporting pyrophosphatase
Sopim07g007790	Sucrose phosphate synthase	7	0.037424387	0.01470493	6.42E-06	26.72054455	stress biotic receptors
Sopim07g008160	Nuclear pore complex protein Nup155	2	0.082976328	0.06173527	0.011856932	12.05162995	protein targeting nucleus
Sopim07g008900	Subtilisinlike serine protease	3	0.061454521	0.05192213	0.002460947	16.27219582	redox ascorbate and glutathione glutathione
Sopim07g009140	26S proteasome nonATPase regulatory subunit 6	2	0.032664229	0.02309854	0.006504026	30.61452943	hormone metabolism brassinosteroid synthesisdegradation sterols SMT1
Sopim07g017510	Phosphatidylinositol 4 phosphate 5 kinase family protein	2	0.130112875	0.07113861	0.00200542	7.685634492	signalling phosphinositides phosphatidylinositol4phosphate 5kinase
Sopim07g017610	Saccharopine dehydrogenase NAD L-glutamate forming	4	0.024054631	0.01438347	0.000165876	41.57203659	amino acid metabolism degradation aspartate family lysine
Sopim07g017780	HATPase	4	0.061183977	0.03105932	2.07E-05	16.3441484	transport p and vATPases H+exporting ATPase
Sopim07g018360	Elongation factor Ts	3	0.18150865	0.08060401	0.002465675	5.509379305	protein synthesis elongation
Sopim07g020860	Peroxiredoxin	2	0.224902328	0.16146186	0.006755297	4.446374606	redox peroxiredoxin
Sopim07g032100	Coatomer alpha subunitlike protein	15	0.016841446	0.00509817	1.11E-16	59.37732425	cell vesicle transport
Sopim07g039200	Guanine nucleotide binding protein subunit beta	3	0.241046383	0.09427937	0.001448403	4.148579155	development unspecified
Sopim07g041150	Myosin XI	4	0.059506578	0.02024121	2.67E-07	16.80486483	misc short chain dehydrogenase/reductase SDR
Sopim07g041310	Ribosomal protein	2	0.256032185	0.16370654	0.01158826	3.905758958	protein synthesis ribosomal protein eukaryotic 40S subunit S3
Sopim07g042520	Sucrose synthase 4	5	0.048091212	0.01279585	6.30E-06	20.79381988	major CHO metabolism degradation sucrose Susy
Sopim07g042550	Sucrose synthase	13	0.032026024	0.0069081	2.90E-12	31.22460659	stress abiotic heat
Sopim07g042910	Genomic DNA chromosome 5 TAC clone K21L19	3	0.087808308	0.04988414	0.001039267	11.38844402	RNA regulation of transcription putative transcription regulator
Sopim07g043160	UDP glucosyltransferase	3	0.005539299	0.0060039	3.85E-05	180.5282582	hormone metabolism abscisic acid synthesisdegradation
Sopim07g043320	Unknown Protein	7	0.060401876	0.0240329	4.60E-09	16.55577717	protein synthesis initiation
Sopim07g043570	Aldo/keto reductase family protein	5	0.002452791	0.00285763	1.98E-06	407.6988215	minor CHO metabolism others
Sopim07g044760	ATPdependent RNA helicase	2	0.276604378	0.21329525	0.006344157	3.615271773	RNA processing RNA helicase
Sopim07g044840	2, 3-bisphosphoglycerate-independent phosphoglycerate mutase	9	0.390800297	0.04758803	6.32E-12	2.558851689	glycolysis cytosolic branch phosphoglycerate mutase
Sopim07g045290	Long chain fattyacidCoA ligase 3	4	0.0445583	0.01718419	0.000691283	22.44250791	major CHO metabolism degradation sucrose invertases neutral
Sopim07g047790	Chaperone protein htpG	3	0.243500886	0.13397054	0.00072954	4.106761238	stress abiotic heat
Sopim07g047850	Chlorophyll ab binding protein 4 chloroplastic	4	0.124023713	0.04700891	2.51E-07	8.062974215	PS lightreaction photosystem II LHCII
Sopim07g049690	Cytochrome P450	2	0.185272745	0.1696147	0.004046031	5.397447962	misc cytochrome P450
Sopim07g052350	3-isopropylmalate dehydratase large subunit	5	0.189354263	0.08173642	6.11E-08	5.281106346	TCA / organic transformation TCA aconitase
Sopim07g053280	Ketolacid reductoisomerase	4	0.238867535	0.06693953	1.89E-06	4.186420729	amino acid metabolism synthesis branched chain group common ketolacid reductoisomerase
Sopim07g053650	26S proteasome regulatory subunit	15	0.065971876	0.0127026	3.69E-14	15.15797429	cell wall precursor synthesis UXS
Sopim07g053830	Mitochondrial ADP/ATP carrier protein	3	0.131045926	0.07530624	0.001611529	7.63091254	transport metabolite transporters at the mitochondrial membrane
Sopim07g055060	Phosphoenolpyruvate carboxylase 1	2	0.031080531	0.03093748	0.001038599	32.17448248	glycolysis cytosolic branch phosphoenolpyruvate carboxylase PEPC
Sopim07g055300	Alpha alphatrehalose phosphate synthase UDP-forming	3	0.012068497	0.01307714	9.38E-06	82.8603595	transport ABC transporters and multidrug resistance systems
Sopim07g055320	ATPdependent Zn protease cell division protein FtsH homolog	6	0.422636261	0.07354832	5.86E-07	2.366100811	protein degradation metalloprotease
Sopim07g056420	Glutathione S transferaselike protein	2	0.153615589	0.0189274	0.000115205	6.509755986	misc glutathione S transferases
Sopim07g062130	D-tdpglucose 4, 6 dehydratase	4	0.217531884	0.08448942	9.18E-07	4.597027257	hormone metabolism gibberelin synthesisdegradation
Sopim07g062190	50S ribosomal protein L13	2	0.057755189	0.02537817	0.000182667	17.31446156	protein synthesis ribosome biogenesis
Sopim07g062530	Phosphoenolpyruvate carboxylase 2	45	0.008941153	0.00251155	9.90E-20	111.8423988	glycolysis cytosolic branch phosphoenolpyruvate carboxylase PEPC
Sopim07g062700	Sodium/calcium exchanger family protein	2	0.042799509	0.03586176	0.0003538	23.36475402	signalling calcium
Sopim07g063100	Proton pump interactor 1	2	0.011145432	0.00773137	9.95E-05	89.72285686	transport
Sopim07g063960	50S ribosomal protein L24	2	0.371638688	0.10278628	0.000853168	2.690785519	protein synthesis ribosomal protein prokaryotic unknown organellar
Sopim07g064130	Ubiquitin	5	0.001650129	0.00110703	1.78E-09	606.0132268	protein synthesis ribosomal protein prokaryotic unknown organellar
Sopim07g064170	Pectinesterase	3	0.001670382	0.00235413	0.002316433	598.665455	protein postranslational modification
Sopim07g064180	Pectinesterase	2	0.023524789	0.01307154	0.01434547	42.50835151	cell wall pectinesterases PME
Sopim07g064190	Pectinesterase	2	0.003399892	0.00125613	0.0004248	294.1269899	cell wall pectinesterases PME
Sopim07g064810	Imidazole glycerol phosphate synthase subunit hisF	2	0.268372375	0.16258736	0.001337419	3.726165929	amino acid metabolism synthesis histidine phosphoribosylformimino5aminoimidazole carboxamide ribotide isomerase BBM II
Sopim07g064970	Microtubule associated protein MAP651a	2	0.240651471	0.11564439	0.000320423	4.155387024	misc protease inhibitor/seed storage/lipid transfer protein LTP family protein
Sopim07g065030	Syntaxin 8	3	0.189732137	0.09285537	3.65E-05	5.270588398	protein targeting secretory pathway unspecified
Sopim07g065840	Heat shock protein 90	9	0.190229621	0.05851653	7.50E-12	5.25680488	stress abiotic heat
Sopim07g065950	Enhancer of mRNA decapping protein 4	4	0.024018447	0.01394738	1.88E-06	41.63466522	development unspecified
Sopim07g066030	Proteasome activator subunit 4like	2	0.002248037	0.00290523	0.003505527	444.8325361	not assigned unknown
Sopim07g066310	photosystem II polypeptide	2	0.075093177	0.04550439	0.000728924	13.31678909	RNA regulation of transcription putative transcription regulator
Sopim07g066600	Phosphoglycerate kinase	4	0.424574173	0.06047834	4.08E-07	2.355301061	glycolysis cytosolic branch 3phosphoglycerate kinase PGK
Sopim07g066610	Phosphoglycerate kinase	2	0.092541805	0.06946468	0.001801575	10.80592712	PS calvin cycle phosphoglycerate kinase
Sopim08g005490	Dehydrationresponsive proteinlike	7	0.021467701	0.01598314	1.45E-06	46.58160648	signalling light
Sopim08g005800	Pectinacetylesterase like protein Fragment	3	0.050663848	0.01842287	1.03E-05	19.73794016	RNA regulation of transcription lateral organ boundaries gene family AS2
Sopim08g006040	40S ribosomal protein S6	2	0.001308318	0.00066778	0.000363006	764.3401681	protein synthesis ribosome biogenesis
Sopim08g006890	Tubulin alpha3 chain	5	0.310763735	0.1161178	5.74E-05	3.217878688	RNA regulation of transcription bZIP transcription factor family
Sopim08g006900	Ribosomal protein L32	3	0.334507639	0.09977831	1.83E-05	2.989468351	protein synthesis ribosome biogenesis
Sopim08g007040	Glycine cleavage system H protein 1	2	0.020579993	0.01203295	0.004113048	48.59088144	PS photorespiration glycine cleavage H protein
Sopim08g008590	Ubiquitin	4	0.09121905	0.03297736	1.91E-08	10.96262239	protein degradation ubiquitin ubiquitin
Sopim08g013860	NADdependent malic enzyme 2	4	0.267054798	0.0628865	1.40E-05	3.744549836	major CHO metabolism degradation sucrose hexokinase
Sopim08g014000	Lipoxygenase	2	0.107187139	0.07605787	0.003157167	9.329477485	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim08g014340	Cysteine synthase	2	0.349654882	0.12354206	0.000499585	2.859962928	signalling phosphinositides
Sopim08g014420	Mitogen activated protein kinase 2	2	0.277380285	0.17281794	0.004254181	3.605158889	signalling MAP kinases
Sopim08g015860	Rab GDP dissociation inhibitor	2	0.21582067	0.09083587	0.000314216	4.633476488	signalling Gproteins
Sopim08g016180	60S ribosomal protein L18a	8	0.098753517	0.02549095	1.35E-06	10.12622163	protein synthesis ribosomal protein eukaryotic 60S subunit L18A
Sopim08g023440	Early responsive to dehydration 4	2	0.09133432	0.05100358	0.014219347	10.94878683	stress abiotic drought/salt
Sopim08g041890	Importin alpha1b subunit	3	0.181028186	0.10564098	0.001168837	5.52400166	PS calvin cycle rubisco interacting
Sopim08g061850	Ribosomal protein	3	0.328398138	0.10541007	0.000345801	3.045084257	protein synthesis ribosomal protein eukaryotic 40S subunit S3
Sopim08g061960	Ribosomal protein	3	0.328398138	0.10541007	0.000345801	3.045084257	protein synthesis ribosomal protein eukaryotic 40S subunit S3
Sopim08g062340	Class II small heat shock protein LeHSP17.6	2	0.08515674	0.04875855	0.008771846	11.7430517	stress abiotic heat
Sopim08g062630	Aminopeptidaselike protein	17	0.030249605	0.00420734	1.11E-16	33.05828291	protein degradation metalloprotease
Sopim08g062800	ATP-dependent RNA helicase eIF4A	2	0.214348209	0.15349237	0.00070397	4.665306067	DNA synthesis/chromatin structure
Sopim08g062910	Elongation factor EF2	7	0.021774204	0.0208436	1.20E-07	45.92590388	protein synthesis elongation
Sopim08g062920	Elongation factor EF2	7	0.021774204	0.0208436	1.20E-07	45.92590388	protein synthesis elongation

Sopim08g065220	Glycine dehydrogenase P protein	2	0.179328694	0.12747525	0.000462458	5.576352438	C1metabolism
Sopim08g066750	Major facilitator superfamily domain containing protein 5	2	0.139022475	0.0257416	9.61E-07	7.19308155	lipid metabolism phospholipid synthesis
Sopim08g066790	Phospholipase D	6	0.036495358	0.01569803	1.87E-07	27.40074505	PS lightreaction other electron carrier ox/red plastocyanin
Sopim08g066800	Phospholipase D	16	0.020596276	0.00540588	9.90E-20	48.55246648	RNA regulation of transcription TCP transcription factor family
Sopim08g067030	Os01g0611000 protein Fragment	3	0.110790537	0.06893382	5.67E-07	9.026041637	not assigned unknown
Sopim08g067330	Chlorophyll ab binding protein 3Clike	2	0.183148812	0.1230689	0.000637585	5.460040876	PS lightreaction photosystem II LHCII
Sopim08g068210	AP1 complex subunit beta1	4	0.056494307	0.02030248	2.42E-08	17.70089861	cell vesicle transport
Sopim08g068340	Eukaryotic translation initiation factor 3 subunit 6 interacting protein	3	0.042510965	0.01686691	0.000211091	23.52334274	not assigned unknown
Sopim08g074240	40S ribosomal protein S6	2	0.001308318	0.00066778	0.000363006	764.3401681	protein synthesis ribosomal protein eukaryotic 40S subunit S6
Sopim08g074550	ThreonyltRNA synthetase	3	0.052208857	0.02512999	0.002381262	19.15383821	protein aa activation threoninetRNA ligase
Sopim08g075310	AP1 complex subunit gamma1	4	0.042379119	0.01662923	0.000341988	23.59652639	cell vesicle transport
Sopim08g075390	Isopentenyldiphosphate deltaisomerase family protein	2	0.180832891	0.09724528	0.000156692	5.529967444	nucleotide metabolism salvage NUDIX hydrolases
Sopim08g075870	Dehydrationresponsive family proteinlike	5	0.048689797	0.02736978	9.05E-06	20.5381838	signalling light
Sopim08g076220	Phosphoribulokinase/uridine kinase	8	0.399345543	0.04541678	4.36E-09	2.50409706	PS calvin cycle PRK
Sopim08g076480	Plastid lipidassociated protein 3 chloroplastic	2	0.429332439	0.19844378	0.006047116	2.329197398	cell organisation
Sopim08g076650	Alpha alphatrehalosephosphate synthase UDPforming	7	0.034846578	0.01257805	1.05E-08	28.69722244	minor CHO metabolism trehalose TPS
Sopim08g076970	Acetylornithine deacetylase or succinyldiaminopimelate desuccinylase	9	0.015723428	0.00814099	1.61E-08	63.59936268	protein degradation
Sopim08g076980	Acetylornithine deacetylase or succinyldiaminopimelate desuccinylase	8	0.015334298	0.00814541	5.13E-08	65.21328854	protein degradation
Sopim08g077240	Dehydrationresponsive family protein	4	0.057050325	0.03507324	3.66E-05	17.52838393	signalling light
Sopim08g077360	Dynamin 2	2	0.309700341	0.1736936	0.00295108	3.228927669	minor CHO metabolism myoinositol polyphosphatases
Sopim08g078010	50S ribosomal protein L19	2	0.330026065	0.11636815	0.002159619	3.030063701	protein synthesis ribosomal protein prokaryotic unknown organellar 50S subunit L19
Sopim08g078200	HATPase	2	0.049275167	0.04080137	0.001368199	20.29419809	transport p and vATPases H+exporting ATPase
Sopim08g078390	Acylcoenzyme A oxidase	2	0.237796099	0.11551392	0.001953552	4.205283452	lipid metabolism lipid degradation betaoxidation acyl CoA DH
Sopim08g079020	Adenine phosphoribosyltransferaselike protein	2	0.330610538	0.06993439	0.00011962	3.024706974	redox dismutases and catalases
Sopim08g079090	Laccase22	2	0.413353123	0.18536278	0.003952728	2.41923901	signalling receptor kinases DUF 26
Sopim08g079870	Subtilisinlike protease	6	0.001718291	0.00183454	1.50E-06	581.9736005	cell vesicle transport
Sopim08g080140	dTDP4dehydrorhamnose reductase	2	0.022874453	0.00803625	1.25E-05	43.71689238	cell wall precursor synthesis UER
Sopim08g081190	Aquaporin 1	3	0.080287719	0.01386974	2.88E-06	12.45520501	transport major intrinsic proteins PIP
Sopim08g081250	Aminopeptidase N	5	0.09142416	0.0240621	4.13E-06	10.93802776	protein degradation metalloprotease
Sopim08g081320	AP1 complex subunit beta1	7	0.021003393	0.00609326	7.37E-08	47.61135498	cell vesicle transport
Sopim08g082280	Longchain fattyacidCoA ligase	2	0.042703229	0.03587809	0.01167613	23.41743291	lipid metabolism FA synthesis and FA elongation long chain fatty acid CoA ligase
Sopim09g005010	Importin subunit beta	3	0.017862277	0.01421484	0.00035382	55.98390396	Cofactor and vitamine metabolism
Sopim09g005720	60S ribosomal protein L23a	4	0.245371889	0.06741019	2.06E-05	4.075446475	protein synthesis ribosome biogenesis
Sopim09g007190	C1orf93 homolog	2	0.13154703	0.09067776	0.002055939	7.601843995	protein degradation ubiquitin E3 SCF FBOX
Sopim09g007350	30S ribosomal protein S12	2	0.194943448	0.1335142	0.012600175	5.129692792	protein synthesis ribosomal protein eukaryotic 40S subunit S23
Sopim09g007540	ValyltRNA synthetase	11	0.045719833	0.01082266	3.62E-12	21.87234586	protein aa activation valinetRNA ligase
Sopim09g008280	S-adenosylmethionine synthase	5	0.387865853	0.05869522	1.10E-11	2.578210977	amino acid metabolism synthesis aspartate family methionine Sadenosylmethionine synthetase
Sopim09g008840	Pyruvate kinase	6	0.011688072	0.0040161	1.14E-06	85.55731005	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Sopim09g008970	Unknown Protein	2	0.40627558	0.19105609	0.014902331	2.461383478	not assigned unknown
Sopim09g009020	Enolase	3	0.236206613	0.16578916	0.001516194	4.233581724	glycolysis cytosolic branch enolase
Sopim09g009190	1, 4 alphaglucan branching enzyme II	2	0.003939065	0.00504466	0.014533051	253.8673518	major CHO metabolism synthesis starch starch branching
Sopim09g009260	Fructose bisphosphate aldolase	6	0.385702065	0.10161445	3.02E-06	2.592674737	PS calvin cycle aldolase
Sopim09g009510	Hydrolase alpha/beta fold family protein	3	0.144209396	0.09055945	0.000177533	6.934360921	not assigned no ontology
Sopim09g009530	Hydrolase alpha/beta fold family protein	3	0.144209396	0.09055945	0.000177533	6.934360921	not assigned no ontology
Sopim09g010100	30S ribosomal protein S11	3	0.321879262	0.14199155	0.000607445	3.106754979	protein synthesis ribosomal protein eukaryotic 40S subunit S14
Sopim09g010460	Eukaryotic translation initiation factor 3 subunit A	7	0.018837303	0.0063596	1.23E-06	53.0861557	protein synthesis initiation
Sopim09g010560	5oxoprolinase ATPhydrolyzing	4	0.050473369	0.02766338	2.78E-05	19.81242821	redox ascorbate and glutathione glutathione
Sopim09g010630	heat shock protein	8	0.299815541	0.07171197	4.29E-06	3.335384139	misc cytochrome P450
Sopim09g010860	Expansin	2	0.059757105	0.02861975	0.004144399	16.73441175	major CHO metabolism degradation sucrose invertases neutral
Sopim09g011080	Ribulose1 5bisphosphate carboxylase/oxygenase activase 1	4	0.403541842	0.09500472	0.000619599	2.478057777	PS calvin cycle rubisco interacting
Sopim09g011660	Universal stress protein 1	2	0.354789979	0.11486035	0.001225064	2.818568898	transport peptides and oligopeptides
Sopim09g011670	Universal stress protein family protein	3	0.306236632	0.07510612	1.38E-05	3.265448661	transport peptides and oligopeptides
Sopim09g011810	Fructose 1, 6 bisphosphatase class 1	3	0.158866287	0.0938284	7.06E-05	6.294601699	PS calvin cycle FBPase
Sopim09g013080	Acetylcoenzyme A carboxylase carboxyl transferase subunit alpha	2	0.002800618	0.00329883	1.71E-08	357.064048	lipid metabolism FA synthesis and FA elongation acetyl CoA carboxylation heteromeric complex alpha carboxyltransferase
Sopim09g014350	Glycerol 3 phosphate acyltransferase 6	2	0.033128758	0.02441601	0.00154951	30.18525476	lipid metabolism phospholipid synthesis
Sopim09g014520	Chlorophyll ab binding protein 6A chloroplastic	2	0.303501932	0.13201659	0.003976079	3.294871942	PS lightreaction photosystem II LHCII
Sopim09g015000	class I heat shock protein	4	0.003770808	0.00428457	0.00033481	265.1951518	stress abiotic heat
Sopim09g015020	class I heat shock protein 3	3	0.228941108	0.06716067	0.00072384	4.36793553	hormone metabolism auxin inducedregulatedresponsiveactivated
Sopim09g015490	Phosphoenolpyruvate carboxylase	3	0.083073767	0.09299141	4.11E-05	12.03749434	not assigned unknown
Sopim09g015930	ATPdependent RNA helicase	2	0.292809335	0.21734702	0.007599524	3.415191664	hormone metabolism ethylene inducedregulatedresponsiveactivated
Sopim09g018450	Ubiquitin activating enzyme E1	2	0.016632448	0.02442481	0.009829162	60.12344064	protein degradation ubiquitin E1
Sopim09g018750	Inosine 5 aposmonophosphate dehydrogenase	2	0.373393072	0.09552967	2.53E-05	2.678142887	not assigned no ontology
Sopim09g031780	Tic110 family transporter chloroplast inner envelope protein Tic110	3	0.01112027	0.01616866	0.004262951	89.9258741	protein targeting chloroplast
Sopim09g031970	Phosphorylase	2	0.203708971	0.17692587	0.008125049	4.908963975	major CHO metabolism degradation starch starch phosphorylase
Sopim09g050080	30S ribosomal protein S7 chloroplastic	3	0.382154977	0.14685796	0.000544708	2.616739439	protein synthesis ribosomal protein prokaryotic chloroplast 30S subunit S7
Sopim09g057650	40S ribosomal protein S8	2	0.212872172	0.15855426	0.00098386	4.697654891	protein synthesis ribosome biogenesis
Sopim09g061450	30S ribosomal protein S7 chloroplastic	2	0.365918523	0.20317604	0.004829605	2.73284881	protein synthesis ribosomal protein prokaryotic chloroplast 30S subunit S7
Sopim09g061620	Vesicle associated membrane protein 7B	2	0.073860314	0.05002495	0.003177184	13.53907052	cell vesicle transport
Sopim09g064370	Alcohol dehydrogenase	2	0.269861813	0.22248119	0.005115699	3.705600244	C1metabolism
Sopim09g065180	NAD-dependent epimerase/dehydratase	2	0.350649753	0.19509624	0.004189811	2.85184858	cell vesicle transport
Sopim09g065190	Ran GTPase-activating protein 1	2	0.307361448	0.06224053	0.00077492	3.253498467	signalling Gproteins
Sopim09g065900	Glutathione reductase	2	0.045055282	0.04078773	0.008311166	22.19495597	redox ascorbate and glutathione glutathione
Sopim09g074940	Translocase of chloroplast 90 chloroplastic	3	0.098260534	0.06885543	0.000675252	10.17702591	protein targeting chloroplast
Sopim09g075290	Ribosomal protein L18	4	0.10573448	0.03632783	2.96E-06	9.457652792	protein synthesis ribosome biogenesis
Sopim09g082060	Cysteine synthase	2	0.328809027	0.23318823	0.008271091	3.041279034	signalling phosphinositides
Sopim09g082320	Proteasome subunit beta type	2	0.29205895	0.12330281	0.000939388	3.423966292	protein degradation ubiquitin proteasom
Sopim09g082720	Aldo/keto reductase family protein	3	0.186192271	0.10539938	0.000421538	5.370792217	hormone metabolism auxin inducedregulatedresponsiveactivated
Sopim09g082990	GDP-D-mannose3AC 5AC epimerase 2	6	0.243741948	0.08856714	3.83E-06	4.102699631	cell wall precursor synthesis UXS
Sopim09g083080	Nucleolar protein 5	3	0.195889528	0.07771782	8.34E-06	5.104918115	RNA regulation of transcription putative transcription regulator
Sopim09g083130	Peptidase S9 prolyl oligopeptidase active site domain protein	3	0.022354253	0.01442482	0.002801826	44.7342168	protein degradation
Sopim09g090140	Malate dehydrogenase	2	0.126909893	0.08254404	0.012292646	7.87960636	TCA / organic transformation other organic acid transformations cyt MDH
Sopim09g090190	Dehydrationresponsive proteinlike	2	0.145211313	0.15160908	0.010466274	6.886515791	stress abiotic drought/salt
Sopim09g090660	Guanine nucleotidebinding protein subunit betalike protein	2	0.102293795	0.08113553	0.000757179	9.775764014	hormone metabolism brassinosteroid signal transduction BZR
Sopim09g091180	chaperonin	18	0.214035598	0.04474609	9.90E-20	4.672120009	protein folding
Sopim09g091740	60S ribosomal protein L13alike protein	2	0.126795362	0.05028916	0.002111835	7.886723806	protein synthesis ribosomal protein eukaryotic 60S subunit L13A
Sopim09g091750	26S proteasome regulatory subunit	5	0.049608798	0.01335396	9.54E-06	20.15771477	protein degradation ubiquitin proteasom
Sopim09g092380	Adenosylhomocysteinase	7	0.024974144	0.02095753	2.67E-06	40.04141243	amino acid metabolism degradation aspartate family methionine
Sopim09g092390	Adenosylhomocysteinase	5	0.156702806	0.08019012	3.87E-05	6.381506659	amino acid metabolism degradation aspartate family methionine
Sopim09g092550	Hypothetical salt-inducible protein Fragment	2	0.263862639	0.2008341	0.01192761	3.789850673	not assigned unknown
Sopim09g098150	Metacaspase 7	2	0.001221793	0.00247114	0.023086299	818.4692497	protein degradation
Sopim09g098590	Sucrose synthase	2	0.037534557	0.02566955	0.005771742	26.64211542	major CHO metabolism degradation sucrose Susy
Sopim10g005530	Nuclear capbinding protein subunit 1	2	0.046007139	0.03896721	0.003810994	21.73575714	protein synthesis initiation
Sopim10g005560	Biubiquitin	4	0.09121905	0.03297736	1.91E-08	10.96262239	RNA regulation of transcription ABI3/VP1related B3domaincontaining transcription factor family
Sopim10g005920	Enhancer of mRNAdecapping protein 4	3	0.097965921	0.03966631	0.000223905	10.20763128	development unspecified
Sopim10g006480	Ubiquitin	4	0.09121905	0.03297736	1.91E-08	10.96262239	protein synthesis ribosomal protein prokaryotic unknown organellar
Sopim10g007060	PhenylalanyltRNA synthetase alpha chain	2	0.166083293	0.09279265	0.002475756	6.02107522	protein aa activation phenylalaninetRNA ligase
Sopim10g007290	Phosphoenolpyruvate carboxylase	21	0.013097849	0.00478512	1.28E-14	76.34841416	glycolysis cytosolic branch phosphoenolpyruvate carboxylase PEPC
Sopim10g007480	Dtdpglucose 4,6 dehydratase	2	0.206404975	0.1302362	0.002406436	4.844844462	cell wall precursor synthesis RHM
Sopim10g007600	L-lactate dehydrogenase	2	0.442848858	0.10290134	0.000572528	2.25810676	signalling receptor kinases Catharanthus roseuslike RLK1
Sopim10g008110	AcylCoA oxidase 6	3	0.007559248	0.00640461	0.00204746	132.2882911	lipid metabolism lipid degradation betaoxidation acyl CoA DH
Sopim10g012240	Ubiquitin conjugating enzyme	2	0.310820729	0.14669728	0.004995588	3.217288638	protein degradation ubiquitin E2
Sopim10g017530	ATPdependent RNA Helicase	2	0.178636374	0.1582296	0.000880786	5.597964052	protein synthesis initiation
Sopim10g018300	Transketolase 1	2	0.271335789	0.2112954	0.006743034	3.685470331	PS calvin cycle transketolase
Sopim10g045220	Apocytochrome f	4	0.078860895	0.02463778	0.00042153	12.68055606	PS lightreaction cytochrome b6/f apocytochrome f CYF
Sopim10g047430	Ribulose bisphosphate carboxylase large chain Fragment	3	0.159176719	0.1104773	9.43E-05	6.282325746	PS calvin cycle rubisco large subunit
Sopim10g049620	Progesterone 5 betareductase	3	0.009198245	0.00813258	0.000871104	108.716391	development unspecified
Sopim10g049890	Phosphoglycerate dehydrogenase	3	0.268835415	0.09027217	0.000752755	3.71974801	PS lightreaction photosystem I LHCI
Sopim10g050110	LRR receptorlike serine/threonineprotein kinase RLP	3	0.133155078	0.040393	0.000119811	7.510040286	stress biotic
Sopim10g050890	Nitrite reductase	3	0.308679692	0.07395936	0.000740823	3.239604114	Nmetabolism nitrate metabolism nitrite reductase
Sopim10g051340	Adenylyl cyclase associated protein	4	0.065278476	0.02085001	2.75E-06	15.31898508	DNA unspecified
Sopim10g054560	Vtype proton ATPase 16 kDa proteolipid subunit	2	0.234332388	0.14588747	0.014925101	4.267442536	transport p and vATPases H+transporting twosector ATPase
Sopim10g055670	Vtype ATP synthase beta chain	4	0.090717906	0.04589697	9.21E-05	11.02318213	transport p and vATPases H+transporting twosector ATPase subunit B
Sopim10g074880	Homology to unknown gene Fragment	2	0.251939662	0.13101488	0.004145323	3.969204341	development unspecified
Sopim10g076510	Pyruvate decarboxylase	3	0.03189482	0.03336766	0.000734651	31.35305357	fermentation PDC
Sopim10g078620	Ribosomal protein S5	2	0.382133869	0.18658508	0.003605572	2.61688398	protein synthesis ribosome biogenesis
Sopim10g078930	Activator of heat shock protein ATPase homolog 1	5	0.302984684	0.12210828	0.000115793	3.300496866	redox thioredoxin
Sopim10g078960	60S ribosomal protein L21like protein	2	0.174452525	0.06981665	0.002999824	5.732218551	protein synthesis ribosomal protein eukaryotic 60S subunit L21
Sopim10g079470	L-galactono1,4 lactone dehydrogenase	2	0.262424899	0.07137413	0.006491358	3.810614023	redox ascorbate and glutathione ascorbate Lgalactono1 4lactone dehydrogenase
Sopim10g080500	Actin	6	0.260308764	0.06307745	1.57E-07	3.841591749	cell organisation
Sopim10g080710	AsparaginyltRNA synthetase 2	6	0.078353768	0.03157489	6.81E-06	12.76262808	protein aa activation asparaginetRNA ligase
Sopim10g080940	Tubulin beta chain	11	0.125131787	0.02249435	9.90E-20	7.991574515	cell organisation
Sopim10g081240	Protein grpE	2	0.18156418	0.17398755	0.00853012	5.507694304	transport amino acids
Sopim10g081440	NADH cytochrome b5 reductase	2	0.196928441	0.14696448	0.001412131	5.077986678	redox misc
Sopim10g081510	5methyltetrahydropteroyltriglutamatehomocysteine methyltransferase	2	0.100590131	0.10267189	0.001177675	9.941333111	amino acid metabolism synthesis aspartate family methionine methionine synthase
Sopim10g081610	Ubiquitin carboxylterminal hydrolase family protein expressed	2	0.101586849	0.09780266	0.008999741	9.843793856	protein degradation ubiquitin ubiquitin protease
Sopim10g081920	Coatomer subunit beta1	7	0.032953736	0.00791257	1.58E-10	30.34557296	cell vesicle transport
Sopim10g083440	UDP flavonoid 3Oglucosyltransferase Fragment	3	0.017982639	0.01775045	0.00314523	55.60919062	misc UDP glucosyl and glucoronyl transferases
Sopim10g083570	Fructosebisphosphate aldolase	2	0.403688993	0.18063963	0.003975403	2.477154486	PS calvin cycle aldolase
Sopim10g083720	Pyruvate kinase	6	0.104836107	0.030526	3.16E-07	9.538698342	RNA regulation of transcription MADS box transcription factor family
Sopim10g083760	Threonine dehydratase biosynthetic	2	0.257305064	0.12473533	0.003225927	3.886437307	amino acid metabolism degradation aspartate family threonine
Sopim10g083970	S-adenosylmethionine synthase	4	0.402836079	0.11354939	3.21E-05	2.482399299	amino acid metabolism synthesis aspartate family methionine Sadenosylmethionine synthetase
Sopim10g084610	60S ribosomal protein L23A	2	0.327667105	0.14215871	0.008167237	3.051877911	protein synthesis ribosome biogenesis
Sopim10g085020	Tubulin beta chain	11	0.135339213	0.01827206	9.90E-20	7.388841547	secondary metabolism phenylpropanoids
Sopim10g085550	Enolase	3	0.236206613	0.16578916	0.001516194	4.233581724	glycolysis cytosolic branch enolase
Sopim10g085790	Atpdependent RNA helicase	3	0.284668518	0.08219339	4.37E-06	3.512857716	RNA processing RNA helicase
Sopim10g086010	60S ribosomal protein L4/L1	2	0.283286749	0.22226787	0.013299159	3.529992149	protein synthesis ribosome biogenesis
Sopim10g086330	60S ribosomal protein L23a	2	0.327667105	0.14215871	0.008167237	3.051877911	protein synthesis ribosome biogenesis
Sopim10g086410	Heat shock protein 70	8	0.215592099	0.04346198	2.56E-08	4.638388905	transport misc
Sopim10g086460	Actin	6	0.260308764	0.06307745	1.57E-07	3.841591749	cell organisation
Sopim10g086580	Ribulose1 5bisphosphate carboxylase/oxygenase activase 1	2	0.46031043	0.14604233	0.006631806	2.172446972	PS calvin cycle rubisco interacting
Sopim10g086760	Tubulin beta chain	16	0.139227495	0.01718127	9.90E-20	7.18248935	secondary metabolism phenylpropanoids
Sopim11g005330	Actin	7	0.259605991	0.06163447	5.06E-08	3.851991228	cell organisation
Sopim11g005640	Ubiquitin	4	0.041427872	0.02174946	7.33E-09	24.13833856	protein degradation ubiquitin ubiquitin
Sopim11g005670	Ubiquitin	4	0.09121905	0.03297736	1.91E-08	10.96262239	protein synthesis ribosome biogenesis
Sopim11g005680	40S ribosomal protein S18	2	0.37057123	0.1469239	0.001374342	2.698536527	protein synthesis ribosomal protein eukaryotic 40S subunit S18
Sopim11g006070	Peptidylprolyl cistrans isomerase	3	0.314861532	0.08057719	1.75E-05	3.175999283	cell cycle peptidylprolyl isomerase
Sopim11g006660	Eukaryotic peptide chain release factor subunit 13like	2	0.311961767	0.22045856	0.009358442	3.205521015	RNA regulation of transcription AtSR transcription factor family
Sopim11g006690	40S ribosomal protein S17like protein	2	0.265621315	0.07082499	0.000123708	3.764758111	protein synthesis ribosomal protein eukaryotic 40S subunit S17
Sopim11g007540	Cytochrome P450	6	0.019199935	0.00576035	3.88E-07	52.08350966	misc cytochrome P450
Sopim11g007690	Pyruvate kinase	5	0.09487248	0.03149967	5.82E-07	10.54046442	lipid metabolism FA synthesis and FA elongation pyruvate kinase
Sopim11g007960	Kelch domaincontaining protein 3	2	0.231941505	0.19950366	0.002248258	4.311431885	lipid metabolism FA synthesis and FA elongation acylCoA binding protein
Sopim11g008870	Methylenetetrahydrofolate reductase	7	0.099004485	0.02762766	1.36E-06	10.10055252	C1metabolism methylenetetrahydrofolate reductase
Sopim11g010200	14-3-3 protein beta/alpha1	2	0.28790077	0.17906281	0.003218448	3.473418984	signalling 1433 proteins
Sopim11g010560	Kinesinlike protein	4	0.02821931	0.02456465	0.000522841	35.43672755	cell organisation
Sopim11g011220	Unknown Protein	3	0.107232971	0.06974137	0.001692591	9.325490012	not assigned unknown
Sopim11g011380	Glutamine synthetase	5	0.326742744	0.04653117	1.52E-07	3.060511728	amino acid metabolism synthesis aromatic aa chorismate chorismate synthase
Sopim11g011910	Transmembrane 9 superfamily protein member 1	4	0.073259295	0.01945851	0.000188669	13.65014501	protein postranslational modification
Sopim11g011920	Glutamate decarboxylase	4	0.175805713	0.07753154	0.000237565	5.688097292	amino acid metabolism synthesis central amino acid metabolism GABA glutamate decarboxylase
Sopim11g011960	UTPglucose 1 phosphate uridylyltransferase	7	0.285712582	0.10287322	1.62E-06	3.500020871	glycolysis cytosolic branch UGPase
Sopim11g012140	IsoleucyltRNA synthetase	11	0.024408831	0.00764951	6.62E-13	40.96877888	protein aa activation isoleucinetRNA ligase
Sopim11g012910	Cation transport regulator protein	2	0.143691936	0.09645164	0.004073722	6.959332777	protein synthesis ribosome biogenesis
Sopim11g018550	Thylakoidbound ascorbate peroxidase 6	3	0.138796049	0.04106186	0.001225444	7.204816039	redox ascorbate and glutathione ascorbate
Sopim11g020040	Chaperone DnaK	4	0.285392713	0.12082164	6.61E-05	3.503943704	stress abiotic heat
Sopim11g021130	30S ribosomal protein S7 chloroplastic	3	0.356580668	0.14389891	0.000850326	2.804414512	protein synthesis ribosomal protein prokaryotic chloroplast 30S subunit S7
Sopim11g022460	Phosphoribosylanthranilate transferase like protein	2	0.020233055	0.01445102	0.006908585	49.42407363	amino acid metabolism synthesis aromatic aa tryptophan phosphoribosyanthranilate isomerase
Sopim11g022540	Transmembrane 9 superfamily protein member 3	2	0.04988747	0.03639119	0.000937167	20.04511353	DNA unspecified
Sopim11g028100	Elongation factor 1gamma	6	0.091033341	0.0372687	3.27E-05	10.98498626	protein synthesis elongation
Sopim11g039650	Dynamin2A	2	0.187361844	0.10294444	2.34E-05	5.337266002	misc dynamin
Sopim11g039830	GlycyltRNA synthetase	3	0.129281107	0.08771899	0.000146742	7.735082281	RNA regulation of transcription orphan family
Sopim11g039980	ATP synthase subunit alpha	3	0.140422274	0.07043485	0.000130874	7.121377339	RNA processing ribonucleases
Sopim11g040390	Aspartokinasehomoserine dehydrogenase	3	0.064527339	0.03953921	0.000658191	15.49730727	amino acid metabolism synthesis aspartate family misc homoserine bifunctional aspartate kinase/homoserine dehydrogenase
Sopim11g042610	Ribosomal protein S5	5	0.136052444	0.04814592	9.38E-07	7.350106846	protein synthesis ribosomal protein eukaryotic 40S subunit S5
Sopim11g062130	Mitochondrial ADP/ATP carrier proteins	2	0.068323153	0.04233999	0.001327636	14.63632687	transport unspecified cations
Sopim11g062190	Mitochondrial ADP/ATP carrier proteins	18	0.030511519	0.00426181	9.90E-20	32.77450723	major CHO metabolism synthesis starch transporter
Sopim11g062270	Signal recognition particle protein SRP72	2	0.055556312	0.04013827	0.001833491	17.99975492	protein targeting secretory pathway unspecified
Sopim11g065490	Homology to unknown gene Fragment	3	0.056512418	0.03871538	0.001228457	17.69522585	development unspecified
Sopim11g065920	Xanthine dehydrogenase/oxidase	3	0.069262481	0.0279388	0.000134097	14.43783107	nucleotide metabolism degradation
Sopim11g065990	Actin	6	0.260308764	0.06307745	1.57E-07	3.841591749	cell organisation
Sopim11g066060	heat shock protein	7	0.270688928	0.07846953	5.00E-06	3.69427744	transport misc
Sopim11g066100	heat shock protein	12	0.313312051	0.04792528	2.22E-16	3.19170615	misc cytochrome P450
Sopim11g066720	Bifunctional polymyxin resistance arnA protein	2	0.45409295	0.18810373	0.005962099	2.202192304	cell wall precursor synthesis UXS
Sopim11g066760	AP2 complex subunit alpha	3	0.028413372	0.01550372	0.001270876	35.19469636	cell vesicle transport
Sopim11g067060	Low molecular weight proteintyrosinephosphatase slr0328	2	0.266611441	0.22036151	0.00791848	3.750776772	protein postranslational modification
Sopim11g067160	Aldo/keto reductase family protein	2	0.293162949	0.250557	0.010973209	3.41107225	minor CHO metabolism others
Sopim11g068830	Orotidine 5aposphophate decarboxylase	3	0.210565334	0.16003987	0.00164637	4.749119815	protein targeting mitochondria

Sopim11g069000	Tcomplex protein 1 subunit beta	6	0.121657306	0.01785418	5.82E-11	8.21981049	protein folding	
Sopim11g069050	4-coumarate coA ligase	3	0.135096528	0.07031642	0.000203608	7.402114731	secondary metabolism phenylpropanoids lignin biosynthesis 4CL	
Sopim11g069430	Aquaporin 1	3	0.104947445	0.00895962	5.52E-10	9.528578804	transport major intrinsic proteins PIP	
Sopim11g069490	Serine/threonineprotein phosphatase 6 regulatory subunit 3	2	0.023315675	0.01919972	0.000616011	42.88960109	misc acid and other phosphatases	
Sopim11g069700	Elongation factor 1alpha	2	0.146134998	0.10794797	0.000108961	6.842987742	protein synthesis elongation	
Sopim11g069790	chaperonin	14	0.201499331	0.0256574	9.90E-20	4.962795633	protein folding	
Sopim11g070030	NADHquinone oxidoreductase subunit B	2	0.357877242	0.2568659	0.016530257	2.794254238	mitochondrial electron transport / ATP synthesis NADHDH type I localisation not clear	
Sopim11g071800	Strictosidine synthase family protein	2	0.04219026	0.03531587	0.006987548	23.70215306	secondary metabolism N misc alkaloidlike	
Sopim11g072880	Calcium transporting ATPase	4	0.129811435	0.04357819	2.43E-06	7.703481592	signalling calcium	
Sopim12g005860	3-isopropylmalate dehydratase large subunit	3	0.102553001	0.10667543	0.000628447	9.751055457	TCA / organic transformation TCA aconitase	
Sopim12g006140	Chlorophyll ab binding protein 37	3	0.11139302	0.05918057	5.27E-05	8.977223169	PS lightreaction photosystem II LHCII	
Sopim12g006520	Cycloartenol synthase	2	0.001696935	0.0020487	0.009311995	589.2977633	lipid metabolism exotics steroids squalene etc	
Sopim12g008360	Oligosaccharyl transferase STT3 subunit family protein	2	0.081543985	0.0424076	0.002724154	12.26332022	stress abiotic drought/salt	
Sopim12g008570	ArginyltRNA synthetase	2	0.20251986	0.13997646	0.008039086	4.937787336	protein aa activation argininetRNA ligase	
Sopim12g008630	Mitochondrial processing peptidase alpha subunit	2	0.29226655	0.21577783	0.006142358	3.421534213	protein targeting mitochondria	
Sopim12g008640	Gammaglutamyltransferaselike protein	4	0.108820136	0.05950389	1.75E-06	9.189475742	misc UDP glucosyl and glucoronyl transferases	
Sopim12g009040	LongchainfattyacidCoA ligase 4	3	0.042521169	0.01800195	0.002491615	23.51769774	lipid metabolism FA synthesis and FA elongation long chain fatty acid CoA ligase	
Sopim12g009300	Sucrose synthase	43	0.005504312	0.00123882	9.90E-20	181.675748	stress abiotic heat	
Sopim12g009640	HAT family dimerisation domain containing protein	2	0.02289315	0.02479501	0.002691572	43.68118848	misc cytochrome P450	
Sopim12g009840	Pyrophosphateenergized proton pump	3	0.009161051	0.00795403	0.000549163	109.1577811	transport amino acids	
Sopim12g009960	Eukaryotic translation initiation factor 4	7	0.170371278	0.04338582	2.60E-10	5.869533948	protein synthesis initiation	
Sopim12g010320	Outer membrane lipoprotein blc	4	0.218037527	0.08354104	7.60E-07	4.586366456	transport misc	
Sopim12g010360	HATPase	2	0.133947321	0.05530377	0.005468706	7.465621504	transport p and vATPases H+exporting ATPase	
Sopim12g010380	Adenylate kinaselike protein	4	0.118614143	0.0673307	0.000538406	8.430697847	nucleotide metabolism phosphotransfer and pyrophosphatases adenylate kinase	
Sopim12g010390	Transmembrane 9 superfamily protein member 2 Nonaspanin TM9SF	6	0.016578395	0.00788961	2.08E-08	60.31947001	DNA unspecified	
Sopim12g010520	Eukaryotic peptide chain release factor subunit 11	3	0.275620226	0.12106066	0.000180488	3.628180756	protein synthesis release	
Sopim12g010840	Ketolacid reductoisomerase	2	0.203775013	0.11440683	0.000293058	4.907373015	amino acid metabolism synthesis branched chain group common ketolacid reductoisomerase	
Sopim12g014250	Phosphoenolpyruvate carboxylase 1	3	0.115625136	0.08126714	0.004331253	8.648638476	glycolysis cytosolic branch phosphoenolpyruvate carboxylase PEPC	
Sopim12g014380	Glucose6phosphate isomerase 1	2	0.169958694	0.07241005	0.004052412	5.883782562	glycolysis cytosolic branch glucose6phosphate isomerase	
Sopim12g014390	50S ribosomal protein L13	2	0.25266849	0.10765586	0.009626928	3.957755081	protein synthesis ribosome biogenesis	
Sopim12g015860	Farnesyl pyrophosphate synthase	2	0.055384825	0.03441356	0.003437587	18.05548722	secondary metabolism isoprenoids mevalonate pathway farnesyl pyrophosphate synthetase	
Sopim12g015880	Heat shock protein 90	6	0.222456183	0.07445385	4.37E-07	4.495267277	stress abiotic heat	
Sopim12g017570	Rab GDP dissociation inhibitor	5	0.182648137	0.04741859	2.94E-06	5.475007938	signalling Gproteins	
Sopim12g017830	Sec7 guanine nucleotide exchange factor	7	0.026502965	0.01116253	4.30E-10	37.73162739	signalling Gproteins	
Sopim12g019460	Mitogenactivated protein kinase 1	2	0.277380285	0.17281794	0.004254181	3.605158889	signalling MAP kinases	
Sopim12g038400	Acetylcoenzyme A synthetase	2	0.045924201	0.04019331	0.014401557	21.77501139	lipid metabolism FA synthesis and FA elongation acyl CoA ligase	
Sopim12g040640	Betaglucosidase	3	0.049564161	0.032126	0.000312067	20.17586861	misc gluco galacto and mannosidases	
Sopim12g042060	ATPdependent clp protease ATPbinding subunit	2	0.303586307	0.13516716	0.00219018	3.293956206	stress abiotic heat	
Sopim12g042080	40S ribosomal protein S11	8	0.270679802	0.04347936	7.40E-10	3.694401993	protein synthesis ribosome biogenesis	
Sopim12g042920	Cytochrome c1	5	0.034112963	0.01523825	9.43E-09	29.31436944	signalling receptor kinases DUF 26	
Sopim12g043000	Coatomer betaapos subunit	11	0.023118395	0.00582163	3.83E-12	43.25559798	transport sulphate	
Sopim12g043020	Dihydroxyacid dehydratase	3	0.063961016	0.01059096	1.58E-07	15.63452338	RNA regulation of transcription ABI3/VP1related B3domaincontaining transcription factor family	
Sopim12g043110	Heat shock protein 4	9	0.148742268	0.03939755	2.45E-10	6.723038538	stress abiotic heat	
Sopim12g043120	Heat shock protein 4	5	0.187500023	0.05458141	6.51E-07	5.333332679	stress abiotic heat	
Sopim12g044300	AcylCoA synthetase AMPforming/AMPacid ligase II	5	0.319087094	0.07257116	1.69E-05	3.133940604	lipid metabolism FA synthesis and FA elongation acyl CoA ligase	
Sopim12g044600	NADPdependent malic enzyme chloroplastic	3	0.207994598	0.07411319	0.00063665	4.807817172	TCA / organic transformation other organic acid transformations malic	
Sopim12g044740	Ubiquitin carboxylterminal hydrolase	3	0.30951323	0.096447	0.000388122	3.230879662	protein degradation ubiquitin ubiquitin protease	
Sopim12g044900	Protein SEY1	2	0.019047755	0.02229921	0.001803608	52.49962528	development unspecified	
Sopim12g055800	Vtype ATP synthase alpha chain	11	0.282430871	0.07162422	2.93E-10	3.540689431	transport p and vATPases H+transporting twosector ATPase	
Sopim12g062860	Universal stress protein family protein	3	0.001637064	0.00123855	8.88E-06	610.8496675	stress abiotic unspecified	
Sopim12g088180	Tubulin alpha7 chain	3	0.082917924	0.02101022	4.90E-07	12.06011863	cell organisation	
Sopim12g088990	Exocyst complex component 1	2	0.054240867	0.03643763	0.003828461	18.43628348	RNA regulation of transcription AP2/EREBP APETALA2/ethyleneresponsive element binding protein family	
Sopim12g089310	Tubulin beta1 chain	13	0.128804122	0.01800793	9.90E-20	7.763726692	cell organisation	
Sopim12g089340	Vacuolar protein sorting 35	2	0.023962746	0.02190469	0.00071991	41.7314443	secondary metabolism flavonoids chalcones	
Sopim12g094620	Catalase	5	0.132260951	0.06235019	4.84E-09	7.560810598	redox dismutases and catalases	
Sopim12g095760	Diphosphatefructose6phosphate 1phosphotransferase	3	0.226078569	0.07161162	6.05E-06	4.423241019	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases	
Sopim12g095990	ATPdependent RNA helicase eIF4A	2	0.26805957	0.14457472	0.006872408	3.730514079	protein synthesis initiation	
Sopim12g096000	ATPdependent RNA helicase eIF4A	2	0.26805957	0.14457472	0.006872408	3.730514079	protein synthesis initiation	
Sopim12g096190	Tryptophan synthase beta chain	3	0.297243187	0.18786716	0.003454377	3.364248682	amino acid metabolism synthesis aromatic aa tryptophan tryptophan synthase	
Sopim12g096300	40S ribosomal protein S6	2	0.001308318	0.00066778	0.000363006	764.3401681	protein synthesis ribosome biogenesis	
Sopim12g096540	40S ribosomal protein S10like	2	0.187847324	0.04874566	2.39E-08	5.323472162	protein synthesis ribosomal protein eukaryotic 40S subunit S10	
Sopim12g096550	Pheophorbide a oxygenase family protein	6	0.041186995	0.01531897	1.19E-05	24.27950862	protein targeting chloroplast	
Sopim12g098330	60S ribosomal protein L13alike protein	4	0.195708215	0.02454555	1.26E-08	5.109647543	protein synthesis ribosome biogenesis	
Sopim12g098500	Adenosylhomocysteinase	4	0.156786221	0.08563943	0.000434942	6.378111505	amino acid metabolism degradation aspartate family methionine	
Sopim12g098940	Ubiquitin	4	0.09121905	0.03297736	1.91E-08	10.96262239	protein degradation ubiquitin ubiquitin	
Sopim12g099000	S-adenosylmethionine synthase	4	0.403110785	0.10772213	1.46E-05	2.48070763	amino acid metabolism synthesis aspartate family methionine Sadenosylmethionine synthetase	
Sopim12g099030	Ubiquitin	3	0.077097193	0.03405772	1.21E-07	12.97064084	protein degradation ubiquitin ubiquitin	
Sopim12g099100	Dihydrolipoyl dehydrogenase	4	0.291325216	0.11652795	8.62E-05	3.43258992	redox ascorbate and glutathione glutathione	
Sopim12g099260	ATP citrate lyase asubunit	2	0.28390176	0.20119953	0.003646745	3.522345194	TCA / organic transformation other organic acid transformations atpcitrate lyase	
Sopim12g099360	AcylCoA synthetase/AMPacid ligase II	6	0.055747944	0.02383744	3.08E-08	17.93788126	nucleotide metabolism salvage nucleoside kinases adenosine kinase	
Sopim12g099430	Epoxide hydrolase 1	4	0.075984787	0.03933399	7.05E-05	13.16052909	misc oxidases copper flavone etc	
Sopim12g100160	50S ribosomal protein L6	3	0.125212539	0.05402264	5.74E-05	7.986420593	protein synthesis ribosomal protein prokaryotic unknown organellar	
Sopim01g090190	Nuclear RNA binding protein	2	0.413614749	0.10907885	0.009963093	2.417708755	RNA RNA binding	Nuclear RNA binding protein
Sopim02g083810	Ferredoxin__NADP reductase	2	0.242650637	0.12250617	0.00794287	4.121151349	PS lightreaction other electron	FerredoxinNADP reductase
Sopim03g007890	Heat shock protein 90 (Fragment)	4	0.13764931	0.04079774	0.000493672	7.264838451	stress abiotic heat	FerredoxinNADP reductase
Sopim06g036290	Heat shock protein 90 (Fragment)	3	0.172262984	0.04821004	0.003511481	5.80507766	stress abiotic heat	Heat shock protein 90 Fragment
Sopim06g076520	class I heat shock protein	4	0.379122046	0.05480144	0.000154172	2.637673041	protein folding	Heat shock protein 90 Fragment
Sopim06g076560	class I heat shock protein	4	0.379122046	0.05480144	0.000154172	2.637673041	protein folding	Heat shock protein 90 Fragment
Sopim06g083790	Succinyl_CoA ligase	2	0.217571042	0.09660608	0.005787098	4.596199893	protein postranslational modific	Heat shock protein 90 Fragment
Sopim07g032740	Aspartate aminotransferase	2	0.006172791	0.0035852	0.004400511	162.001273	transport amino acids	class I heat shock protein
Sopim07g064170	Pectinesterase	2	0.016807254	0.01668477	0.019592743	59.49811909	cell wall pectinesterases PME	class I heat shock protein
Sopim07g064180	Pectinesterase	2	0.066418882	0.06973993	0.000979759	15.05595954	cell wall pectinesterases PME	class I heat shock protein
Sopim09g011080	Ribulose_1 5_bisphosphate carboxylase/oxygenase activase 1	2	0.223064236	0.0466916	0.003273191	4.483013584	PS calvin cycle rubisco interact	class I heat shock protein
Sopim09g089580	1_aminocyclopropane_1_carboxylate oxidase_like protein	3	0.006602723	0.00156059	4.51E-05	151.4526658	signalling MAP kinases	class I heat shock protein
Sopim10g086580	Ribulose_1 5_bisphosphate carboxylase/oxygenase activase 1	3	0.251703481	0.0436592	0.00114604	3.972928765	PS calvin cycle rubisco interact	class I heat shock protein
Sopim11g018550	Thylakoid_bound ascorbate peroxidase 6	2	0.028359603	0.03139881	0.004198136	35.2614245	redox ascorbate and glutathion	class I heat shock protein
Sopim11g020040	Chaperone DnaK	3	0.277165243	0.02414276	0.000377673	3.607955995	stress abiotic heat	class I heat shock protein
Sopim00g007270	Translation initiation factor	4	0.000148102	0.00029895	9.21E-05	6752.10328	protein synthesis initiation	Translation initiation factor
Sopim00g007270	Translation initiation factor	4	0.000148102	0.00029895	9.21E-05	6752.10328	cell organisation	Translation initiation factor
Sopim00g009060	Hypoxanthine phosphoribosyltransferase	2	0.183637225	0.19733836	0.003915224	5.445519012	lipid metabolism phospholipid s	Hypoxanthine phosphoribosyltransferase
Sopim01g006280	Formate_tetrahydrofolate ligase	3	0.032819363	0.03166026	1.80E-05	30.46981747	C1metabolism formatetetrahyd	Hypoxanthine phosphoribosyltransferase
Sopim01g006540	Lipoxygenase	3	0.160847987	0.09518641	0.000153911	6.217050139	hormone metabolism jasmonate	Formatetetrahydrofolate ligase
Sopim01g008160	Tetratricopeptide repeat_containing protein	2	0.231630128	0.08363094	0.000347366	4.317227679	DNA synthesis/chromatin struc	Formatetetrahydrofolate ligase
Sopim01g009050	Molybdenum cofactor biosynthesis protein	2	0.06859185	0.07592574	0.00241344	14.57899153	cell wall cell wall proteins	Lipoxygenase
Sopim01g009180	5_methyltetrahydropteroyltriglutamate__homocysteine methyltransferase	2	0.168924871	0.18782214	0.002879363	5.919791408	amino acid metabolism synthes	Tetratricopeptide repeatcontaining protein
Sopim01g059970	Mutator_like transposase	2	0.230455694	0.11745195	0.007304227	4.339228867	development unspecified	Tetratricopeptide repeatcontaining protein
Sopim01g059970	Mutator_like transposase	2	0.230455694	0.11745195	0.007304227	4.339228867	RNA regulation of transcription	Mutatorlike transposase
Sopim01g073650	Serine/threonine_protein phosphatase	2	0.230455694	0.11745195	0.007304227	4.339228867	protein degradation serine prot	Mutatorlike transposase
Sopim01g073740	Citrate synthase	2	0.230455694	0.11745195	0.007304227	4.339228867	DNA unspecified	Mutatorlike transposase
Sopim01g079450	Peptidase S9 prolyl oligopeptidase active site domain protein	3	0.219979804	0.07538415	0.001053573	4.545871856	signalling receptor kinases Cath	Serine/threonineprotein phosphatase
Sopim01g080460	Pyruvate phosphate dikinase	3	0.219979804	0.07538415	0.001053573	4.545871856	protein postranslational modific	Serine/threonineprotein phosphatase
Sopim01g087820	Subtilisin_like protease	2	0.323090872	0.11895195	0.000408604	3.095104463	protein synthesis ribosome biog	Citrate synthase
Sopim01g087850	Subtilisin_like protease	2	0.323090872	0.11895195	0.000408604	3.095104463	TCA / organic transformation T	Citrate synthase
Sopim01g098920	Mitochondrial Rho GTPase 1	2	0.027327773	0.03005121	0.00894125	36.59280981	not assigned unknown	Peptidase S9 prolyl oligopeptidase active site domain protein
Sopim01g099040	GDSL esterase/lipase At5g03980	2	0.086956039	0.08691048	0.002219781	11.50006384	gluconeogenesis / glyoxylate cy	Pyruvate phosphate dikinase
Sopim01g099150	Lipoxygenase	2	0.099929146	0.11905587	0.010923945	10.00709042	protein degradation subtilases	Subtilisinlike protease
Sopim01g099160	Lipoxygenase	2	0.099929146	0.11905587	0.010923945	10.00709042	protein degradation ubiquitin	Subtilisinlike protease
Sopim01g099660	Heat shock protein	4	0.13226532	0.07773528	8.11E-06	7.560560848	protein degradation subtilases	Subtilisinlike protease
Sopim01g108600	Presequence protease_ mitochondrial	4	0.13226532	0.07773528	8.11E-06	7.560560848	protein degradation ubiquitin	Subtilisinlike protease
Sopim01g111120	Triosephosphate isomerase	2	0.284256179	0.20329532	0.003132408	3.51795343	signalling Gproteins	Mitochondrial Rho GTPase 1
Sopim02g065280	Methyl jasmonate esterase	2	0.284256179	0.20329532	0.003132408	3.51795343	protein degradation ubiquitin E	Mitochondrial Rho GTPase 1
Sopim02g067080	UDP_D_glucose dehydrogenase	2	0.284256179	0.20329532	0.003132408	3.51795343	misc cytochrome P450	Mitochondrial Rho GTPase 1
Sopim02g069800	CXE carboxylesterase	2	0.447307345	0.17633862	0.00477653	2.235599328	misc GDSLmotif lipase	GDSL esterase/lipase At5g03980
Sopim02g078120	Eukaryotic translation initiation factor 3 subunit 7	2	0.318698916	0.1817442	0.009474321	3.13775777	hormone metabolism jasmonate	Lipoxygenase
Sopim02g081240	Glutathione S_transferase	4	0.018709671	0.0144962	2.31E-05	53.4482942	hormone metabolism jasmonate	Lipoxygenase
Sopim02g086880	Formate dehydrogenase	2	0.073506602	0.07456258	0.000106244	13.6042202	cell wall hemicellulose synthesi	Heat shock protein
Sopim02g088610	ATP_dependent chaperone ClpB	2	0.073506602	0.07456258	0.000106244	13.6042202	misc cytochrome P450	Heat shock protein
Sopim02g092670	Subtilisin_like protease	2	0.073506602	0.07456258	0.000106244	13.6042202	transport misc	Heat shock protein
Sopim03g007670	SGT1	2	0.073506602	0.07456258	0.000106244	13.6042202	stress abiotic heat	Heat shock protein
Sopim03g007890	Heat shock protein 90 (Fragment)	2	0.073506602	0.07456258	0.000106244	13.6042202	protein folding	Heat shock protein
Sopim03g025720	Long_chain_fatty_acid__CoA ligase	2	0.327946747	0.20193069	0.003506063	3.049275558	protein degradation metalloprot	Presequence protease mitochondrial
Sopim03g082420	Heat shock protein	3	0.17259988	0.04939359	3.17E-07	5.793746786	glycolysis unclear/dually target	Triosephosphate isomerase
Sopim03g082920	Heat shock protein	3	0.17259988	0.04939359	3.17E-07	5.793746786	PS calvin cycle TPI	Triosephosphate isomerase
Sopim03g083090	Glycogen synthase	3	0.311302813	0.07310409	9.88E-07	3.21230634	glycolysis unclear/dually target	Triosephosphate isomerase
Sopim03g096000	Clathrin heavy chain	3	0.311302813	0.07310409	9.88E-07	3.21230634	PS calvin cycle TPI	Triosephosphate isomerase
Sopim03g112590	Cell division protease ftsH homolog	2	0.404008037	0.11215674	0.000562672	2.475198284	misc nitrilases nitrile lyases be	Methyl jasmonate esterase
Sopim03g115230	ClpB chaperone	3	0.095057951	0.04942139	0.000118388	10.51989854	cell wall precursor synthesis U	UDPDglucose dehydrogenase
Sopim03g117630	heat shock protein	2	0.415582093	0.13908691	0.00364834	2.406263448	stress biotic receptors	CXE carboxylesterase
Sopim03g118340	ATP_dependent clp protease ATP_binding subunit	2	0.415582093	0.13908691	0.00364834	2.406263448	biodegradation of xenobiotics	CXE carboxylesterase
Sopim03g120090	Pyridoxal biosynthesis lyase pdxS	3	0.18064458	0.15287919	0.000381212	5.535732099	protein synthesis initiation	Eukaryotic translation initiation factor 3 subunit 7
Sopim04g009630	Alpha_glucosidase 1	2	0.263002577	0.15267938	0.001531422	3.802244113	misc glutathione S transferases	Glutathione Stransferase
Sopim04g011440	heat shock protein	2	0.169203471	0.11893659	0.000102567	5.910044245	C1metabolism formate dehydro	Formate dehydrogenase
Sopim04g045340	Phosphoglucomutase	2	0.169203471	0.11893659	0.000102567	5.910044245	transport amino acids	Formate dehydrogenase
Sopim04g047770	VHS domain_containing protein At3g16270	9	0.013378532	0.0042974	9.90E-20	74.74661644	stress abiotic heat	ATPdependent chaperone ClpB
Sopim04g055200	Asparagine synthase (Glutamine_hydrolyzing)	9	0.013378532	0.0042974	9.90E-20	74.74661644	protein degradation serine prot	ATPdependent chaperone ClpB
Sopim04g072240	Oxidoreductase family protein	2	0.179148584	0.14203764	0.003739977	5.581958716	signalling calcium	Subtilisinlike protease
Sopim04g080880	Cathepsin B_like cysteine proteinase	2	0.179148584	0.14203764	0.003739977	5.581958716	protein degradation ubiquitin E	Subtilisinlike protease
Sopim04g081570	Chaperone protein htpG	2	0.266510431	0.1304971	0.022479389	3.752198352	protein postranslational modific	SGT1
Sopim05g005460	Nucleoredoxin 2	3	0.029671221	0.01366069	0.000511285	33.70269124	not assigned no ontology DC1 domain containing protein	
Sopim05g005480	Oxidoreductase zinc_binding dehydrogenase	2	0.368135918	0.17403744	0.010111741	2.716388027	misc oxidases copper flavone etc	
Sopim05g008450	Oxidoreductase FAD/NAD(P)_binding domain protein	5	0.223089107	0.05519854	1.61E-05	4.482513797	PS lightreaction other electron carrier ox/red ferredoxin oxireductase	
Sopim05g008450	Oxidoreductase FAD/NAD(P)_binding domain protein	2	0.120006181	0.05620433	0.003803922	8.332904119	PS lightreaction other electron carrier ox/red ferredoxin oxireductase	
Sopim05g010670	Chaperone protein htpG	6	0.106846273	0.03927269	5.20E-08	9.359240823	signalling receptor kinases leucine rich repeat III	
Sopim05g010670	Chaperone protein htpG	6	0.106846273	0.03927269	5.20E-08	9.359240823	stress abiotic heat	
Sopim05g014280	Heat shock protein	6	0.409726724	0.03290154	4.80E-09	2.44065115	stress abiotic heat	
Sopim05g014280	Heat shock protein	6	0.409726724	0.03290154	4.80E-09	2.44065115	protein synthesis ribosome biogenesis	
Sopim05g014280	Heat shock protein	6	0.409726724	0.03290154	4.80E-09	2.44065115	cell wall precursor synthesis UXS	
Sopim05g014280	Heat shock protein	6	0.409726724	0.03290154	4.80E-09	2.44065115	RNA regulation of transcription ABI3/VP1related B3domaincontaining transcription factor family	
Sopim05g014280	Heat shock protein	2	0.070218092	0.03408296	0.003181556	14.24134395	stress abiotic heat	
Sopim05g014280	Heat shock protein	2	0.070218092	0.03408296	0.003181556	14.24134395	protein synthesis ribosome biogenesis	
Sopim05g014280	Heat shock protein	2	0.070218092	0.03408296	0.003181556	14.24134395	cell wall precursor synthesis UXS	
Sopim05g014280	Heat shock protein	2	0.070218092	0.03408296	0.003181556	14.24134395	RNA regulation of transcription ABI3/VP1related B3domaincontaining transcription factor family	
Sopim05g052510	Clathrin heavy chain	3	0.029665121	0.02061025	0.000613285	33.70962148	cell vesicle transport	
Sopim05g056310	T_complex protein 1_ gamma subunit	3	0.296089559	0.12596766	0.000212867	3.377356511	protein folding	
Sopim06g005160	Ascorbate peroxidase	2	0.297074043	0.06934137	0.000286577	3.366164172	redox ascorbate and glutathione ascorbate	
Sopim06g005160	Ascorbate peroxidase	2	0.297074043	0.06934137	0.000286577	3.366164172	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases	
Sopim06g005160	Ascorbate peroxidase	2	0.196916883	0.18892623	0.002290944	5.07828473	redox ascorbate and glutathione ascorbate	
Sopim06g005160	Ascorbate peroxidase	2	0.196916883	0.18892623	0.002290944	5.07828473	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases	
Sopim06g005490	Triosephosphate isomerase	2	0.032331427	0.01979046	0.000794734	30.92965863	glycolysis cytosolic branch triosephosphate isomerase TPI	
Sopim06g005490	Triosephosphate isomerase	2	0.032331427	0.01979046	0.000794734	30.92965863	PS calvin cycle TPI	
Sopim06g005490	Triosephosphate isomerase	4	0.169472611	0.08410812	6.29E-06	5.900658485	glycolysis cytosolic branch triosephosphate isomerase TPI	
Sopim06g005490	Triosephosphate isomerase	4	0.169472611	0.08410812	6.29E-06	5.900658485	PS calvin cycle TPI	
Sopim06g007340	Gamma_interferon_inducible lysosomal thiol reductase	2	0.077951071	0.05669845	0.010463964	12.82856011	RNA regulation of transcription C2C2Zn Constanslike zinc finger family COlike	
Sopim06g011400	ATP_dependent chaperone ClpB	2	0.130728381	0.10995981	0.002580689	7.649448363	stress abiotic heat	
Sopim06g011400	ATP_dependent chaperone ClpB	2	0.130728381	0.10995981	0.002580689	7.649448363	protein degradation serine protease	
Sopim06g035960	4_coumarate_CoA ligase_like protein	2	0.240894444	0.14296591	0.005698964	4.151195783	cell organisation	
Sopim06g035960	4_coumarate_CoA ligase_like protein	2	0.240894444	0.14296591	0.005698964	4.151195783	secondary metabolism phenylpropanoids lignin biosynthesis 4CL	
Sopim06g035960	4_coumarate_CoA ligase_like protein	2	0.240894444	0.14296591	0.005698964	4.151195783	lipid metabolism FA synthesis and FA elongation acyl CoA ligase	
Sopim06g036290	Heat shock protein 90 (Fragment)	7	0.047631915	0.02488912	2.36E-11	20.99432702	stress abiotic heat	
Sopim06g036290	Heat shock protein 90 (Fragment)	7	0.047631915	0.02488912	2.36E-11	20.99432702	RNA regulation of transcription MYBrelated transcription factor family	
Sopim06g051310	Clathrin heavy chain	3	0.029665121	0.02061025	0.000613285	33.70962148	cell vesicle transport	
Sopim06g052030	Importin subunit beta	2	0.118492159	0.08445865	0.002181834	8.439376989	Cofactor and vitamine metabolism	
Sopim06g052030	Importin subunit beta	2	0.118492159	0.08445865	0.002181834	8.439376989	protein targeting nucleus	
Sopim06g068320	Prolyl_tRNA synthetase	2	0.044392749	0.02955355	0.000965956	22.52620129	protein aa activation bifunctional aminoacyltRNA synthetase	
Sopim06g068320	Prolyl_tRNA synthetase	2	0.044392749	0.02955355	0.000965956	22.52620129	secondary metabolism isoprenoids mevalonate pathway isopentenyl pyrophosphatedimethyllallyl pyrophosphate isomerase	
Sopim06g068860	Alpha_mannosidase	2	0.169507175	0.23827902	0.01189822	5.899455289	signalling Gproteins	
Sopim06g068860	Alpha_mannosidase	2	0.169507175	0.23827902	0.01189822	5.899455289	development unspecified	
Sopim06g068860	Alpha_mannosidase	2	0.169507175	0.23827902	0.01189822	5.899455289	misc gluco galacto and mannosidases alphamannosidase	
Sopim06g069180	Phosphatase 2A regulatory A subunit	2	0.396241388	0.18675269	0.009802233	2.523714156	protein postranslational modification	
Sopim06g073330	Lysyl_tRNA synthetase	2	0.042978834	0.05158693	0.003851474	23.26726686	protein aa activation lysinetRNA ligase	
Sopim06g074980	26S protease regulatory subunit 6B homolog	6	0.006995811	0.00605996	3.91E-07	142.9426838	cell division	
Sopim06g074980	26S protease regulatory subunit 6B homolog	6	0.006995811	0.00605996	3.91E-07	142.9426838	protein degradation ubiquitin proteasom	
Sopim06g074980	26S protease regulatory subunit 6B homolog	6	0.006995811	0.00605996	3.91E-07	142.9426838	protein degradation AAA type	
Sopim06g075340	Carbamoyl_phosphate synthase large chain	2	0.141124574	0.15567267	0.004287246	7.08593813	tetrapyrrole synthesis ALA dehydratase	
Sopim06g075340	Carbamoyl_phosphate synthase large chain	2	0.141124574	0.15567267	0.004287246	7.08593813	amino acid metabolism synthesis glutamate family arginine carbamoylphosphate synthase	

Sopim06g075340	Carbamoyl_phosphate synthase large chain	2	0.141124574	0.15567267	0.004287246	7.08593813	lipid metabolism FA synthesis and FA elongation pyruvate kinase
Sopim06g075340	Carbamoyl_phosphate synthase large chain	2	0.141124574	0.15567267	0.004287246	7.08593813	nucleotide metabolism synthesis pyrimidine carbamoyl phosphate synthetase
Sopim06g076020	heat shock protein	5	0.220612732	0.11205024	1.70E-06	4.532829955	stress abiotic heat
Sopim06g076020	heat shock protein	5	0.220612732	0.11205024	1.70E-06	4.532829955	misc cytochrome P450
Sopim06g076020	heat shock protein	5	0.220612732	0.11205024	1.70E-06	4.532829955	protein folding
Sopim06g076020	heat shock protein	5	0.220612732	0.11205024	1.70E-06	4.532829955	cell wall hemicellulose synthesis
Sopim06g076020	heat shock protein	5	0.220612732	0.11205024	1.70E-06	4.532829955	transport misc
Sopim06g082560	ClpB chaperone	2	0.344006273	0.22011945	0.010881155	2.906923735	protein degradation serine protease
Sopim06g082560	ClpB chaperone	2	0.344006273	0.22011945	0.010881155	2.906923735	stress abiotic heat
Sopim06g083190	Peptidyl_prolyl cis_trans isomerase	5	0.338849467	0.1325116	0.000121286	2.951162972	cell cycle peptidylprolyl isomerase
Sopim06g083190	Peptidyl_prolyl cis_trans isomerase	5	0.338849467	0.1325116	0.000121286	2.951162972	protein folding
Sopim07g005820	heat shock protein	2	0.323902062	0.22063847	0.012542238	3.087352991	cell wall hemicellulose synthesis
Sopim07g005820	heat shock protein	2	0.323902062	0.22063847	0.012542238	3.087352991	transport misc
Sopim07g005820	heat shock protein	2	0.323902062	0.22063847	0.012542238	3.087352991	protein folding
Sopim07g005820	heat shock protein	2	0.323902062	0.22063847	0.012542238	3.087352991	misc cytochrome P450
Sopim07g005820	heat shock protein	2	0.323902062	0.22063847	0.012542238	3.087352991	stress abiotic heat
Sopim07g007790	Sucrose phosphate synthase	2	0.021528476	0.02280075	0.013236847	46.45010636	major CHO metabolism synthesis sucrose SPS
Sopim07g007790	Sucrose phosphate synthase	2	0.021528476	0.02280075	0.013236847	46.45010636	stress biotic receptors
Sopim07g007790	Sucrose phosphate synthase	2	0.021528476	0.02280075	0.013236847	46.45010636	DNA synthesis/chromatin structure
Sopim07g007790	Sucrose phosphate synthase	2	0.021528476	0.02280075	0.013236847	46.45010636	protein degradation ubiquitin E3 RING
Sopim07g045290	Long_chain_fatty_acid__CoA ligase 3	2	0.052076201	0.04279626	0.004053726	19.20262962	lipid metabolism FA synthesis and FA elongation long chain fatty acid CoA ligase
Sopim07g045290	Long_chain_fatty_acid__CoA ligase 3	2	0.052076201	0.04279626	0.004053726	19.20262962	major CHO metabolism degradation sucrose invertases neutral
Sopim07g047790	Chaperone protein htpG	2	0.001750505	0.0016422	0.00045228	571.263721	signalling receptor kinases leucine rich repeat III
Sopim07g047790	Chaperone protein htpG	2	0.001750505	0.0016422	0.00045228	571.263721	stress abiotic heat
Sopim07g051850	Aspartic proteinase	2	0.257557264	0.26058955	0.012330132	3.882631709	protein degradation aspartate protease
Sopim07g052350	3_isopropylmalate dehydratase large subunit	5	0.020068573	0.01129735	4.49E-07	49.82915327	TCA / organic transformation TCA aconitase
Sopim07g054210	Protochlorophyllide reductase like protein	2	0.260984969	0.11848225	0.009780387	3.831638289	tetrapyrrole synthesis protochlorophyllide reductase
Sopim07g055060	Phosphoenolpyruvate carboxylase 1	5	0.061981348	0.02222005	6.50E-09	16.13388596	glycolysis cytosolic branch phosphoenolpyruvate carboxylase PEPC
Sopim08g007680	Subtilisin_like protease	3	0.0858346	0.09660752	0.005732027	11.65031351	protein degradation subtilases
Sopim08g007680	Subtilisin_like protease	3	0.0858346	0.09660752	0.005732027	11.65031351	cell vesicle transport
Sopim08g007690	Subtilisin_like protease	3	0.0858346	0.09660752	0.005732027	11.65031351	cell vesicle transport
Sopim08g007690	Subtilisin_like protease	3	0.0858346	0.09660752	0.005732027	11.65031351	protein degradation subtilases
Sopim08g007700	Subtilisin_like protease	3	0.0858346	0.09660752	0.005732027	11.65031351	cell vesicle transport
Sopim08g007700	Subtilisin_like protease	3	0.0858346	0.09660752	0.005732027	11.65031351	protein degradation subtilases
Sopim08g014000	Lipoxygenase	5	0.156426278	0.07976038	4.38E-07	6.39278779	hormone metabolism jasmonate synthesisdegradation lipoxygenase
Sopim08g062910	Elongation factor EF_2	4	0.038378372	0.0288419	2.43E-06	26.05634236	protein synthesis elongation
Sopim08g062920	Elongation factor EF_2	4	0.038378372	0.0288419	2.43E-06	26.05634236	protein synthesis elongation
Sopim08g075390	Isopentyl_diphosphate delta_isomerase family protein	2	0.153579976	0.16241197	0.002542062	6.512198363	nucleotide metabolism salvage NUDIX hydrolases
Sopim08g079920	Subtilisin_like protease	3	0.0858346	0.09660752	0.005732027	11.65031351	protein degradation subtilases
Sopim08g079920	Subtilisin_like protease	3	0.0858346	0.09660752	0.005732027	11.65031351	cell vesicle transport
Sopim08g080410	UBX domain_containing protein	3	0.086934524	0.06716422	8.72E-06	11.50290994	cell vesicle transport
Sopim08g080410	UBX domain_containing protein	3	0.086934524	0.06716422	8.72E-06	11.50290994	misc dynamin
Sopim08g080410	UBX domain_containing protein	3	0.086934524	0.06716422	8.72E-06	11.50290994	protein degradation
Sopim08g081010	Glutamate_cysteine ligase	2	0.083955288	0.07839876	0.000824043	11.91110201	redox ascorbate and glutathione glutathione
Sopim08g081250	Aminopeptidase N	4	0.04974593	0.02661515	0.001077681	20.10214705	protein degradation metalloprotease
Sopim08g081910	V_type proton ATPase subunit E	2	0.075420489	0.07058667	0.00293807	13.2589965	protein synthesis initiation
Sopim08g081910	V_type proton ATPase subunit E	2	0.075420489	0.07058667	0.00293807	13.2589965	transport p and vATPases H+transporting twosector ATPase subunit E
Sopim08g082820	Heat shock protein	3	0.301316963	0.166267	0.001401158	3.318764367	cell wall hemicellulose synthesis
Sopim08g082820	Heat shock protein	3	0.301316963	0.166267	0.001401158	3.318764367	misc cytochrome P450
Sopim08g082820	Heat shock protein	3	0.301316963	0.166267	0.001401158	3.318764367	transport misc
Sopim08g082820	Heat shock protein	3	0.301316963	0.166267	0.001401158	3.318764367	protein folding
Sopim08g082820	Heat shock protein	3	0.301316963	0.166267	0.001401158	3.318764367	stress abiotic heat
Sopim09g007270	Ascorbate peroxidase	4	0.423967596	0.03592532	1.55E-06	2.358670826	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Sopim09g007270	Ascorbate peroxidase	4	0.423967596	0.03592532	1.55E-06	2.358670826	redox ascorbate and glutathione ascorbate
Sopim09g007270	Ascorbate peroxidase	3	0.17259988	0.04939359	3.17E-07	5.793746786	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Sopim09g007270	Ascorbate peroxidase	3	0.17259988	0.04939359	3.17E-07	5.793746786	redox ascorbate and glutathione ascorbate
Sopim09g008070	Cell division protease ftsH homolog 3	3	0.006559623	0.00606893	0.000432256	152.4477855	cell division
Sopim09g008070	Cell division protease ftsH homolog 3	3	0.006559623	0.00606893	0.000432256	152.4477855	protein degradation ubiquitin proteasom
Sopim09g008070	Cell division protease ftsH homolog 3	3	0.006559623	0.00606893	0.000432256	152.4477855	protein degradation AAA type
Sopim09g009260	Fructose_bisphosphate aldolase	2	0.374256186	0.22950121	0.007192875	2.671966523	glycolysis cytosolic branch aldolase
Sopim09g009260	Fructose_bisphosphate aldolase	2	0.374256186	0.22950121	0.007192875	2.671966523	RNA regulation of transcription AtSR transcription factor family
Sopim09g009260	Fructose_bisphosphate aldolase	2	0.374256186	0.22950121	0.007192875	2.671966523	PS calvin cycle aldolase
Sopim09g009260	Fructose_bisphosphate aldolase	2	0.374256186	0.22950121	0.007192875	2.671966523	protein postranslational modification
Sopim09g010630	heat shock protein	3	0.000179581	0.00037795	0.004518852	5568.517828	protein folding
Sopim09g010630	heat shock protein	3	0.000179581	0.00037795	0.004518852	5568.517828	stress abiotic heat
Sopim09g010630	heat shock protein	3	0.000179581	0.00037795	0.004518852	5568.517828	misc cytochrome P450
Sopim09g010630	heat shock protein	3	0.000179581	0.00037795	0.004518852	5568.517828	cell wall hemicellulose synthesis
Sopim09g010630	heat shock protein	3	0.000179581	0.00037795	0.004518852	5568.517828	transport misc
Sopim09g018450	Ubiquitin_activating enzyme E1	2	0.023216955	0.02168888	0.001123149	43.07197046	protein degradation ubiquitin E1
Sopim09g057660	Peptidyl_prolyl cis_trans isomerase	2	0.010683881	0.01408194	0.045200209	93.59894593	cell cycle peptidylprolyl isomerase
Sopim09g057660	Peptidyl_prolyl cis_trans isomerase	2	0.010683881	0.01408194	0.045200209	93.59894593	protein folding
Sopim09g075950	Heat shock protein 1	2	0.45371114	0.16915511	0.004081909	2.204045508	stress abiotic heat
Sopim09g091050	Lipase	3	0.071376957	0.03575936	3.10E-13	14.01012374	lipid metabolism lipid degradation lipases triacylglycerol lipase
Sopim09g091050	Lipase	3	0.071376957	0.03575936	3.10E-13	14.01012374	protein targeting mitochondria
Sopim09g091070	Malate dehydrogenase	2	0.229853447	0.16540179	0.003450508	4.350598231	TCA / organic transformation TCA malate DH
Sopim09g091070	Malate dehydrogenase	2	0.229853447	0.16540179	0.003450508	4.350598231	gluconeogenesis / glyoxylate cycle malate dehydrogenase
Sopim09g091070	Malate dehydrogenase	2	0.229853447	0.16540179	0.003450508	4.350598231	TCA / organic transformation other organic acid transformations cyt MDH
Sopim09g091180	chaperonin	3	0.356557896	0.15427846	0.000521078	2.804593619	protein postranslational modification
Sopim09g091180	chaperonin	3	0.356557896	0.15427846	0.000521078	2.804593619	stress abiotic heat
Sopim09g091180	chaperonin	3	0.356557896	0.15427846	0.000521078	2.804593619	protein folding
Sopim09g092380	Adenosylhomocysteinase	4	0.261051581	0.16565873	0.001875013	3.830660577	amino acid metabolism degradation aspartate family methionine
Sopim09g092390	Adenosylhomocysteinase	4	0.261051581	0.16565873	0.001875013	3.830660577	amino acid metabolism degradation aspartate family methionine
Sopim09g092690	Peptidyl_prolyl cis_trans isomerase	3	0.013082365	0.00949644	7.23E-05	76.43877846	protein folding
Sopim09g092690	Peptidyl_prolyl cis_trans isomerase	3	0.013082365	0.00949644	7.23E-05	76.43877846	cell cycle peptidylprolyl isomerase
Sopim10g007480	Dndp_glucose 4 6_dehydratase	3	0.135668312	0.08436771	4.02E-06	7.370917978	hormone metabolism gibberelin synthesisdegradation
Sopim10g007480	Dndp_glucose 4 6_dehydratase	3	0.135668312	0.08436771	4.02E-06	7.370917978	cell wall precursor synthesis RHM
Sopim10g050840	Peptidase S9 prolyl oligopeptidase active site domain protein	3	0.00694573	0.00514846	1.20E-05	143.9733477	major CHO metabolism degradation sucrose invertases neutral
Sopim10g050840	Peptidase S9 prolyl oligopeptidase active site domain protein	3	0.00694573	0.00514846	1.20E-05	143.9733477	RNA regulation of transcription AtSR transcription factor family
Sopim10g050840	Peptidase S9 prolyl oligopeptidase active site domain protein	3	0.00694573	0.00514846	1.20E-05	143.9733477	protein degradation
Sopim10g054280	Haloacid dehalogenase_like hydrolase family protein	2	0.24721522	0.10691787	0.002878337	4.045058391	Nmetabolism ammonia metabolism unspecified
Sopim10g080940	Tubulin beta chain	2	0.132246822	0.17300719	0.001035019	7.561618381	cell organisation
Sopim10g080940	Tubulin beta chain	2	0.132246822	0.17300719	0.001035019	7.561618381	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Sopim10g080940	Tubulin beta chain	2	0.132246822	0.17300719	0.001035019	7.561618381	secondary metabolism phenylpropanoids
Sopim10g081240	Protein grpE	2	0.076629657	0.0331819	0.002405491	13.04977784	PS lightreaction photosystem II PSII polypeptide subunits
Sopim10g081240	Protein grpE	2	0.076629657	0.0331819	0.002405491	13.04977784	transport amino acids
Sopim10g081240	Protein grpE	2	0.076629657	0.0331819	0.002405491	13.04977784	protein folding
Sopim10g081510	5_methyltetrahydropteroyltriglutamate__homocysteine methyltransferase	2	0.091397559	0.08356231	0.002196022	10.94121124	amino acid metabolism synthesis aspartate family methionine methionine synthase
Sopim10g084050	26S protease regulatory subunit 6B homolog	5	0.000853425	0.00082272	7.12E-09	1171.749129	protein degradation AAA type
Sopim10g084050	26S protease regulatory subunit 6B homolog	5	0.000853425	0.00082272	7.12E-09	1171.749129	cell division
Sopim10g084050	26S protease regulatory subunit 6B homolog	5	0.000853425	0.00082272	7.12E-09	1171.749129	protein degradation ubiquitin proteasom
Sopim10g086410	Heat shock protein 70_3	3	0.314786575	0.17061374	0.000986853	3.176755553	stress abiotic heat
Sopim10g086410	Heat shock protein 70_3	3	0.314786575	0.17061374	0.000986853	3.176755553	cell wall hemicellulose synthesis
Sopim10g086410	Heat shock protein 70_3	3	0.314786575	0.17061374	0.000986853	3.176755553	transport misc
Sopim10g086410	Heat shock protein 70_3	3	0.314786575	0.17061374	0.000986853	3.176755553	protein folding
Sopim10g086410	Heat shock protein 70_3	3	0.314786575	0.17061374	0.000986853	3.176755553	misc cytochrome P450
Sopim11g005640	Ubiquitin	3	0.035402443	0.02537829	4.10E-06	28.24663823	protein degradation ubiquitin ubiquitin
Sopim11g006970	Unknown protein DS12 from 2D_PAGE of leaf_ chloroplastic	5	0.265397836	0.0878501	7.32E-05	3.767928236	amino acid metabolism
Sopim11g006970	Unknown protein DS12 from 2D_PAGE of leaf_ chloroplastic	5	0.265397836	0.0878501	7.32E-05	3.767928236	protein postranslational modification
Sopim11g006970	Unknown protein DS12 from 2D_PAGE of leaf_ chloroplastic	5	0.265397836	0.0878501	7.32E-05	3.767928236	signalling Gproteins
Sopim11g006970	Unknown protein DS12 from 2D_PAGE of leaf_ chloroplastic	2	0.212092361	0.13089762	0.000176964	4.714927003	amino acid metabolism
Sopim11g006970	Unknown protein DS12 from 2D_PAGE of leaf_ chloroplastic	2	0.212092361	0.13089762	0.000176964	4.714927003	protein postranslational modification
Sopim11g006970	Unknown protein DS12 from 2D_PAGE of leaf_ chloroplastic	2	0.212092361	0.13089762	0.000176964	4.714927003	signalling Gproteins
Sopim11g011380	Glutamine synthetase	2	0.337400857	0.16336037	0.006175771	2.96383361	RNA regulation of transcription squamosa promoter binding protein family SBP
Sopim11g011380	Glutamine synthetase	2	0.337400857	0.16336037	0.006175771	2.96383361	Nmetabolism ammonia metabolism glutamine synthetase
Sopim11g011380	Glutamine synthetase	2	0.337400857	0.16336037	0.006175771	2.96383361	amino acid metabolism synthesis aromatic as chorismate chorismate synthase
Sopim11g011380	Glutamine synthetase	2	0.337400857	0.16336037	0.006175771	2.96383361	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Sopim11g011470	NADH_ubiquinone oxidoreductase subunit	3	0.009192324	0.00888326	3.56E-05	108.7864179	mitochondrial electron transport / ATP synthesis NADHDH type I localisation not clear
Sopim11g020040	Chaperone DnaK	2	0.136488735	0.09027416	0.000358958	7.326611973	stress abiotic heat
Sopim11g051160	Phosphatidylinositol transfer protein SFH5	5	0.118428859	0.05044355	9.89E-11	8.44388782	DNA unspecified
Sopim11g051160	Phosphatidylinositol transfer protein SFH5	5	0.118428859	0.05044355	9.89E-11	8.44388782	protein targeting secretory pathway unspecified
Sopim11g051160	Phosphatidylinositol transfer protein SFH5	5	0.118428859	0.05044355	9.89E-11	8.44388782	transport misc
Sopim11g066060	heat shock protein	3	0.314786575	0.17061374	0.000986853	3.176755553	misc cytochrome P450
Sopim11g066060	heat shock protein	3	0.314786575	0.17061374	0.000986853	3.176755553	stress abiotic heat
Sopim11g066060	heat shock protein	3	0.314786575	0.17061374	0.000986853	3.176755553	cell wall hemicellulose synthesis
Sopim11g066060	heat shock protein	3	0.314786575	0.17061374	0.000986853	3.176755553	transport misc
Sopim11g066060	heat shock protein	3	0.314786575	0.17061374	0.000986853	3.176755553	protein folding
Sopim11g066100	heat shock protein	4	0.308064943	0.15607751	0.000936251	3.2460688	stress abiotic heat
Sopim11g066100	heat shock protein	4	0.308064943	0.15607751	0.000936251	3.2460688	cell wall hemicellulose synthesis
Sopim11g066100	heat shock protein	4	0.308064943	0.15607751	0.000936251	3.2460688	protein folding
Sopim11g066100	heat shock protein	4	0.308064943	0.15607751	0.000936251	3.2460688	transport misc
Sopim11g066100	heat shock protein	4	0.308064943	0.15607751	0.000936251	3.2460688	misc cytochrome P450
Sopim11g067160	Aldo/keto reductase family protein	2	0.13893552	0.06232949	0.005750897	7.197583455	minor CHO metabolism others
Sopim11g069000	T_complex protein 1 subunit beta	2	0.354388715	0.16902387	0.004453619	2.821760281	protein folding
Sopim11g069720	26S protease regulatory subunit 6B homolog	9	0.007588999	0.00603627	1.72E-11	131.769684	protein degradation ubiquitin proteasom
Sopim11g069720	26S protease regulatory subunit 6B homolog	9	0.007588999	0.00603627	1.72E-11	131.769684	protein degradation AAA type
Sopim11g069720	26S protease regulatory subunit 6B homolog	9	0.007588999	0.00603627	1.72E-11	131.769684	cell division
Sopim12g005860	3_isopropylmalate dehydratase large subunit	9	0.002412895	0.00211028	2.56E-12	414.4399155	TCA / organic transformation TCA aconitase
Sopim12g009250	chaperonin	2	0.070218092	0.03408296	0.003181556	14.24134395	protein folding
Sopim12g009250	chaperonin	2	0.070218092	0.03408296	0.003181556	14.24134395	hormone metabolism auxin inducedregulatedresponsiveactivated
Sopim12g009250	chaperonin	2	0.070218092	0.03408296	0.003181556	14.24134395	stress abiotic heat
Sopim12g009470	Heme oxygenase 1	2	0.207724892	0.14703796	0.006450144	4.814059549	tetrapyrrole synthesis heme oxygenase
Sopim12g011310	Glutathione S_transferase	2	0.067563866	0.07536993	3.20E-06	14.80081084	misc glutathione S transferases
Sopim12g011310	Glutathione S_transferase	7	0.177813251	0.07570489	2.14E-07	5.623877829	misc glutathione S transferases
Sopim12g042060	ATP_dependent clp protease ATP_binding subunit	3	0.257526097	0.17851213	0.002379962	3.883089842	stress abiotic heat
Sopim12g042060	ATP_dependent clp protease ATP_binding subunit	3	0.257526877	0.17851213	0.002379962	3.883089842	protein degradation serine protease
Sopim12g043110	Heat shock protein 4	5	0.062166528	0.03329115	1.32E-06	16.08582677	stress abiotic heat
Sopim12g043110	Heat shock protein 4	5	0.062166528	0.03329115	1.32E-06	16.08582677	major CHO metabolism degradation sucrose invertases neutral
Sopim12g043120	Heat shock protein 4	6	0.008210184	0.00383987	8.62E-08	121.7999499	stress abiotic heat
Sopim12g043120	Heat shock protein 4	6	0.008210184	0.00383987	8.62E-08	121.7999499	major CHO metabolism degradation sucrose invertases neutral
Sopim12g062860	Universal stress protein family protein	2	0.207724892	0.14703796	0.006450144	4.814059549	PS lightreaction other electron carrier ox/red ferredoxin
Sopim12g062860	Universal stress protein family protein	2	0.207724892	0.14703796	0.006450144	4.814059549	stress abiotic unspecified
Sopim12g094620	Catalase	5	0.143391761	0.08880984	9.77E-07	6.973901381	redox dismutases and catalases

Table 5.7. Differentially expressed proteins identified in the fruits of wild species at different developmental stages using nanoLC-MS-MS.

Label-free quantitation was employed by matching retention times of the peaks and measuring area under the matched peaks using Sieve 2.1 software (Thermo Scientific) to identify the differentially expressed proteins in SP-SL, SG-SL, SH-SL pairs. Stringent selection criteria were imposed to identify these proteins (p value≤0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR~1%).

List of upregulated proteins in SH-SL

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO (SH/SL)	STD.DEV	PVALUE	FOLD CHANGE (SH/SL)	MAPMANCLASS
Solyc01g005620.2.	Mitochondrial 2-oxoglutarate/malate carrier protein	3	2.627495068	1.681735318	0.039416532	2.627495068	transport metabolite transporters at the mitochondrial membrane
Solyc01g007320.2.	ATP synthase subunit beta chloroplastic	21	3.021873414	0.545370135	0.001100913	3.021873414	PS lightreaction ATP synthase epsilon chain
Solyc01g059930.2.	Universal stress protein	3	11.8503445	6.995282898	0.013356448	11.8503445	stress abiotic cold
Solyc01g060130.2.	ADP-ribosylation factor-like protein 3	2	7.760095044	1.027597883	0.002715178	7.760095044	cell division
Solyc01g068530.2.	30S ribosomal protein S9	5	4.713974733	0.554064796	0.000175594	4.713974733	protein synthesis ribosomal protein eukaryotic 40S subunit S16
Solyc01g096430.2.	Predicted NADPH-dependent FMN reductase	2	3.512850724	3.593505111	0.017471197	3.512850724	not assigned no ontology
Solyc01g099670.2.	40S ribosomal protein S10-like	5	7.285114204	3.554472865	0.000375628	7.285114204	protein synthesis ribosomal protein eukaryotic 40S subunit S10
Solyc01g100350.2.	ADP-ribosylation factor-like protein 3	4	6.261282405	0.838006659	0.00061965	6.261282405	cell division
Solyc01g105710.2.	Peptidyl-prolyl cis-trans isomerase	3	3.210139451	1.055736742	0.021743961	3.210139451	protein folding
Solyc01g106210.2.	Chaperone DnaK	15	4.336435906	1.270257437	0.000849917	4.336435906	stress abiotic heat
Solyc01g109940.2.	26S protease regulatory subunit	6	2.666520993	1.819101739	1.65E-07	2.666520993	minor CHO metabolism myo-inositol inositol phosphatase
Solyc01g111300.2.	Cold shock protein-1	2	14.58715374	13.10765654	0.029493459	14.58715374	RNA regulation of transcription GRP
Solyc02g020940.2.	Glyceraldehyde-3-phosphate dehydrogenase	7	4.213911658	1.98746107	0.015606912	4.213911658	PS calvin cycle GAP
Solyc02g024050.2.	Ferredoxin--NADP reductase	3	21.2119015	20.19121856	0.031112728	21.2119015	redox ascorbate and glutathione
Solyc02g032940.2.	Aspartic proteinase	2	6.933827775	7.809583306	0.024226381	6.933827775	protein degradation aspartate protease
Solyc02g038690.1.	Histone H2B	2	7.864904471	5.125545936	0.037856591	7.864904471	signalling receptor kinases leucine rich repeat VI
Solyc02g063490.2.	Malate dehydrogenase	4	14.71801684	1.798601655	0.004855938	14.71801684	RNA regulation of transcription ABI3/VP1-related B3-domain-containing transcription factor family
Solyc02g065400.2.	Oxygen-evolving enhancer protein 1 of photosystem II	12	4.326202615	0.83711522	0.028815631	4.326202615	PS lightreaction photosystem II PSII polypeptide subunits
Solyc02g067460.2.	Porin/voltage-dependent anion-selective channel protein	7	3.219798431	2.136604294	0.021517532	3.219798431	Co-factor and vitamine metabolism folate and vitamine K vitamine K isochorismate synthase
Solyc02g071890.2.	Histidinol dehydrogenase	3	5.950637406	3.034332795	0.008905931	5.950637406	amino acid metabolism synthesis histidine histidinol dehydrogenase
Solyc02g079950.2.	Oxygen-evolving enhancer protein 3	3	3.556644047	1.599696886	0.033715175	3.556644047	PS lightreaction photosystem II PSII polypeptide subunits
Solyc02g083590.2.	Dehydroquinate synthase	2	5.883501944	3.42961444	0.034622022	5.883501944	Co-factor and vitamine metabolism folate and vitamine K
Solyc02g085730.2.	Allene oxide cyclase	3	5.182862578	2.983288775	0.005291629	5.182862578	stress abiotic drought/salt
Solyc02g090030.2.	Oxygen-evolving enhancer protein 1 of photosystem II	9	5.779772889	1.084010914	0.025693489	5.779772889	PS lightreaction photosystem II PSII polypeptide subunits
Solyc02g091130.2.	ATP synthase subunit beta	15	6.096493013	1.050840241	1.17E-05	6.096493013	PS lightreaction ATP synthase
Solyc03g006140.2.	Neutral ceramidase	8	2.655010666	1.513229491	0.000302092	2.655010666	lipid metabolism exotics (steroids squalene etc) sphingolipids ceramidase
Solyc03g082920.2.	Heat shock protein	25	2.276907876	0.57701886	0.000584706	2.276907876	misc cytochrome P450
Solyc03g097680.2.	Pyruvate dehydrogenase E1 component subunit beta	3	10.98558769	6.085047571	0.021985353	10.98558769	TCA / organic transformation TCA pyruvate DH E1
Solyc03g098050.2.	Calmodulin 3 protein	4	2.002327761	1.785740434	4.65E-05	2.002327761	signalling calcium
Solyc03g114150.2.	Aldehyde dehydrogenase	11	2.309535902	0.706059984	0.011258991	2.309535902	fermentation aldehyde dehydrogenase
Solyc03g114560.2.	Strictosidine synthase family protein	2	21.43850143	39.15095363	3.45E-05	21.43850143	protein postranslational modification
Solyc03g115360.2.	40S ribosomal protein S19-like	2	5.184620522	4.110920118	0.020469881	5.184620522	protein synthesis ribosome biogenesis
Solyc03g115990.1.	Malate dehydrogenase	7	2.70340284	1.703285445	0.041240854	2.70340284	TCA / organic transformation other organic acid transformations cyt MDH
Solyc03g119130.2.	Histone H1	3	15.54487628	3.883932949	9.28E-08	15.54487628	DNA synthesis/chromatin structure histone
Solyc03g120850.2.	chaperonin	9	5.749480262	1.535228385	9.89E-05	5.749480262	PS calvin cycle rubisco interacting
Solyc04g009030.2.	Glyceraldehyde-3-phosphate dehydrogenase	11	5.672823092	1.380955088	0.002025022	5.672823092	PS calvin cycle GAP
Solyc04g011390.1.	Histone H4	2	6.256906578	3.290631143	0.034778493	6.256906578	cell organisation
Solyc04g026100.1.	30S ribosomal protein S9	4	5.249311	0.596545043	9.22E-05	5.249311	protein synthesis ribosome biogenesis
Solyc04g045340.2.	Phosphoglucomutase	2	2.342920752	1.999014119	0.03186932	2.342920752	glycolysis plastid branch phosphoglucomutase (PGM)
Solyc04g058070.2.	UDP-N-acetylglucosamine-pyrophosphorylase	2	6.393363243	4.270134614	0.017135144	6.393363243	protein postranslational modification
Solyc04g073990.2.	Annexin	14	4.030888224	0.576605199	4.81E-06	4.030888224	transport amino acids
Solyc04g076790.2.	Serine hydroxymethyltransferase	9	3.765038168	1.416476976	0.005030912	3.765038168	amino acid metabolism synthesis serine-glycine-cysteine group glycine
Solyc04g077970.2.	Adenine phosphoribosyltransferase-like	4	4.789516578	2.333036616	0.016222749	4.789516578	redox dismutases and catalases
Solyc04g080550.2.	Phenylcoumaran benzylic ether reductase	2	2.818720501	2.123901291	0.000308866	2.818720501	secondary metabolism flavonoids isoflavonols isoflavone reductase
Solyc04g080570.2.	2 3 4 5-tetrahydropyridine-2 6-dicarboxylate N-acetyltransferase	2	22.03240897	0.696033236	0.006212499	22.03240897	mitochondrial electron transport / ATP synthesis NADH-DH (type I) complex I carbonic anhydrase
Solyc04g082780.2.	Cinnamoyl CoA reductase-like 1	5	4.416185993	2.718257651	0.045524497	4.416185993	secondary metabolism flavonoids dihydroflavonols
Solyc05g005690.1.	30S ribosomal protein S9	4	5.274226455	0.601009068	6.30E-05	5.274226455	protein synthesis ribosomal protein eukaryotic 40S subunit S16
Solyc05g005710.2.	Spermidine synthase	4	4.418805388	2.235990788	0.00571491	4.418805388	polyamine metabolism synthesis spermidine synthase
Solyc05g009030.2.	3-isopropylmalate dehydratase	4	8.810708599	5.937535489	0.01029751	8.810708599	amino acid metabolism synthesis branched chain group leucine specific 3-isopropylmalate dehydrogenase
Solyc05g010260.2.	6-phosphogluconate dehydrogenase decarboxylating	5	2.378166148	1.525617207	0.008239836	2.378166148	OPP oxidative PP 6-phosphogluconate dehydrogenase
Solyc05g018520.2.	NADH-cytochrome b5 reductase-like protein	3	2.180575216	2.284044069	0.000150818	2.180575216	redox misc
Solyc05g053100.2.	Dihydrolipoyl dehydrogenase	4	2.920144566	3.099080019	9.40E-06	2.920144566	redox ascorbate and glutathione glutathione
Solyc06g009660.2.	ADP-ribosylation factor-like protein 3	4	6.455862112	0.849395988	0.000310296	6.455862112	signalling G-proteins
Solyc06g048410.2.	Superoxide dismutase	4	6.66451062	4.245046138	1.24E-06	6.66451062	redox dismutases and catalases
Solyc06g048540.2.	FeS assembly ATPase SufC	6	2.710175868	1.970303056	0.001492431	2.710175868	transport ABC transporters and multidrug resistance systems
Solyc06g051460.2.	ATP-dependent chaperone ClpB	2	99999.9	70710.60741	2.40E-09	99999.9	DNA synthesis/chromatin structure
Solyc06g053200.2.	6-phosphogluconolactonase	2	4.873429152	7.20280922	0.000348644	4.873429152	OPP oxidative PP 6-phosphogluconolactonase
Solyc06g060290.2.	Protein disulfide isomerase	12	6.746382683	2.445911445	0.049271622	6.746382683	redox thioredoxin
Solyc06g071470.2.	Peroxisomal membrane protein PEX14	4	4.337108537	2.893569301	0.03468517	4.337108537	protein targeting peroxisomes
Solyc06g073190.2.	Fructokinase-like	20	2.32040304	0.871633666	8.11E-08	2.32040304	major CHO metabolism degradation sucrose fructokinase
Solyc06g074780.1.	Histone H2B	5	10.00533759	3.538069789	0.029793663	10.00533759	signalling receptor kinases leucine rich repeat VI
Solyc06g074790.1.	Histone H2B	5	10.00533759	3.538069789	0.029793663	10.00533759	protein postranslational modification kinase receptor like cytoplasmatic kinase VII
Solyc06g083190.2.	Peptidyl-prolyl cis-trans isomerase	13	2.364237009	0.515617769	0.027987267	2.364237009	protein folding
Solyc07g005960.2.	Serine carboxypeptidase K10B2.2	3	11.4146031	8.192190083	1.12E-06	11.4146031	cell wall precursor synthesis UXS
Solyc07g006570.2.	S8-RNase (Fragment)	2	6.124338341	6.007504057	0.02039866	6.124338341	hormone metabolism brassinosteroid synthesis-degradation BRs DET2
Solyc07g008370.2.	60S ribosomal protein L7	7	3.055229705	1.353089019	0.024285632	3.055229705	protein synthesis ribosomal protein eukaryotic 60S subunit L7
Solyc07g044840.2.	2 3-bisphosphoglycerate-independent phosphoglycerate mutase	12	2.721103755	1.114382765	0.006099621	2.721103755	glycolysis cytosolic branch phosphoglycerate mutase
Solyc07g062650.2.	Malate dehydrogenase	16	10.62115266	1.242844916	6.40E-07	10.62115266	TCA / organic transformation TCA malate DH
Solyc07g066580.2.	Mercaptopyruvate sulfurtransferase-like protein	4	3.149116656	1.785236375	0.025465893	3.149116656	misc rhodanese
Solyc07g066600.2.	Phosphoglycerate kinase	22	2.525688878	0.495106056	0.038951431	2.525688878	glycolysis cytosolic branch 3-phosphoglycerate kinase (PGK)
Solyc07g066610.2.	Phosphoglycerate kinase	20	2.518380448	0.56291708	1.28E-05	2.518380448	PS calvin cycle phosphoglycerate kinase
Solyc08g006510.2.	NAD dependent epimerase/dehydratase family protein	4	3.619940943	3.170602047	4.34E-06	3.619940943	not assigned unknown
Solyc08g014340.2.	Cysteine synthase	5	4.52880826	2.119126633	0.015981135	4.52880826	amino acid metabolism synthesis serine-glycine-cysteine group cysteine OASTL
Solyc08g014610.2.	Alanine--glyoxylate aminotransferase 2-like 1	2	2.859765366	3.291236178	0.029454825	2.859765366	signalling receptor kinases S-locus glycoprotein like
Solyc08g015690.2.	Late-embryogenesis abundant protein 2	5	2.839716908	1.482277072	0.048972049	2.839716908	development late embryogenesis abundant
Solyc08g016510.2.	Proteasome subunit alpha type	2	5.675222278	4.803454893	0.014695477	5.675222278	protein degradation ubiquitin proteasom
Solyc08g074620.1.	Polyphenol oxidase	26	3.808467107	1.664443512	0.000101761	3.808467107	secondary metabolism simple phenols
Solyc08g079020.2.	Adenine phosphoribosyltransferase-like protein	2	3.378897938	2.432432107	0.016820074	3.378897938	redox dismutases and catalases
Solyc08g079170.2.	Stress-induced protein sti1-like protein	18	3.851194147	0.989683125	0.000468361	3.851194147	stress biotic heat shock proteins
Solyc09g007270.2.	Ascorbate peroxidase	8	2.678852232	1.257253685	0.017800515	2.678852232	redox ascorbate and glutathione ascorbate
Solyc09g009020.2.	Enolase	38	3.173178646	0.493201369	1.74E-06	3.173178646	glycolysis cytosolic branch enolase
Solyc09g010400.2.	Histone H2A	2	33.02602986	2.5426398	0.000723155	33.02602986	development squamosa promoter binding like (SPL)
Solyc09g065620.2.	Chlorophyllase 1	3	16.8110181	10.09560412	9.71E-05	16.8110181	tetrapyrrole synthesis unspecified
Solyc09g075450.2.	Fumarate hydratase class II	4	15.10240745	4.505019717	0.000359842	15.10240745	TCA / organic transformation TCA fumarase
Solyc09g083410.2.	Amidase hydantoinase/carbamoylase family protein expressed	6	5.186500325	2.031229838	0.000234881	5.186500325	protein degradation
Solyc09g091070.1.	Malate dehydrogenase	2	7.829121703	7.463910867	0.032905239	7.829121703	TCA / organic transformation TCA malate DH
Solyc09g091180.2.	chaperonin	12	3.521911022	1.02414183	0.030801109	3.521911022	protein folding
Solyc09g092430.2.	Selenium binding protein	4	3.589630747	2.090819759	0.013142763	3.589630747	metal handling
Solyc10g005510.2.	Glyceraldehyde-3-phosphate dehydrogenase	7	2.80611655	1.789371728	0.015059203	2.80611655	glycolysis cytosolic branch glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc10g047630.1.	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	2	4.091606336	3.660134341	0.026818965	4.091606336	nucleotide metabolism degradation pyrimidine beta-ureidopropionase
Solyc10g050160.1.	Caffeoyl-CoA 3-O-methyltransferase	2	19.69908052	11.10652007	0.002311205	19.69908052	secondary metabolism phenylpropanoids lignin biosynthesis CCoAOMT
Solyc10g074500.1.	Isocitrate dehydrogenase	5	2.411797596	1.453258499	0.017124542	2.411797596	TCA / organic transformation TCA IDH
Solyc10g080770.1.	BZIP transcription factor	2	99999.9	70710.60741	2.40E-09	99999.9	RNA regulation of transcription bZIP transcription factor family
Solyc10g081310.1.	Histidine triad (HIT) protein	2	25.19602	34.25743	0.022559895	25.19602	major CHO metabolism degradation sucrose invertases neutral
Solyc10g082030.1.	Peroxiredoxin	4	2.846116277	1.70066765	0.001358103	2.846116277	redox thioredoxin
Solyc10g083570.1.	Fructose-bisphosphate aldolase	23	3.366019154	0.474140774	0.019033986	3.366019154	RNA regulation of transcription AtSR transcription factor family
Solyc10g085550.1.	Enolase	24	3.120204018	0.556724351	2.02E-06	3.120204018	glycolysis cytosolic branch enolase
Solyc10g086190.1.	Adenosine kinase	4	8.571230318	3.672279907	0.0163905	8.571230318	nucleotide metabolism salvage nucleoside kinases adenosine kinase
Solyc11g010960.1.	Alcohol dehydrogenase	8	3.934981208	1.571310284	0.010272381	3.934981208	secondary metabolism phenylpropanoids lignin biosynthesis CAD
Solyc11g066100.1.	heat shock protein	35	2.276890605	0.336238649	0.006158321	2.276890605	misc cytochrome P450
Solyc11g066160.1.	Histone H4	5	2.975973106	1.233316357	0.038769025	2.975973106	cell organisation
Solyc11g066430.1.	Histone H2B	5	10.00533759	3.538069789	0.029793663	10.00533759	DNA synthesis/chromatin structure histone
Solyc11g067100.1.	60s acidic ribosomal protein-like protein	3	3.543916223	4.030551014	0.00943429	3.543916223	protein synthesis ribosome biogenesis
Solyc11g069150.1.	Proteasome subunit beta type	3	7.180957675	3.635146917	0.001345225	7.180957675	tetrapyrrole synthesis ALA dehydratase
Solyc11g069790.1.	chaperonin	18	5.701417487	0.811263773	1.23E-05	5.701417487	protein folding
Solyc12g006470.1.	Aminotransferase-like protein	4	7.255009219	3.92496615	0.002546385	7.255009219	amino acid metabolism synthesis central amino acid metabolism GABA GABA transaminase
Solyc12g007310.1.	Lactoylglutathione lyase	2	4.881680417	3.80700679	0.03749911	4.881680417	biodegradation of xenobiotics lactoylglutathione lyase
Solyc12g010040.1.	Leucyl aminopeptidase	17	2.899285916	0.778244626	0.003381751	2.899285916	stress abiotic unspecified
Solyc12g014180.1.	Malate dehydrogenase	2	8.194242019	4.272909681	0.003987456	8.194242019	TCA / organic transformation TCA malate DH
Solyc12g014290.1.	Multiprotein bridging factor 1b	2	9.535815731	9.943541068	0.014536108	9.535815731	cell wall precursor synthesis UXS
Solyc12g014380.1.	Glucose-6-phosphate isomerase 1	9	2.107733317	1.171884258	0.00074137	2.107733317	glycolysis cytosolic branch glucose-6-phosphate isomerase
Solyc12g094520.1.	4-coumarate-coa ligase	2	7.270800444	1.747851583	0.011530122	7.270800444	secondary metabolism phenylpropanoids lignin biosynthesis 4CL
Solyc12g094640.1.	Glyceraldehyde-3-phosphate dehydrogenase B	6	5.005650117	2.962531969	0.041861267	5.005650117	protein postranslational modification
Solyc12g095960.1.	Insulin-like growth factor 2 mRNA-binding protein 2	8	3.927876751	1.693982479	0.016444183	3.927876751	protein synthesis ribosome biogenesis
Solyc12g096540.1.	40S ribosomal protein S10-like	4	7.191486278	3.801590037	0.001569255	7.191486278	protein synthesis ribosomal protein eukaryotic 40S subunit S10
Solyc12g099960.1.	Unknown Protein	2	6.283491814	5.446206467	0.018353974	6.283491814	protein synthesis ribosomal protein prokaryotic unknown organellar
Solyc01g010760.2.	Porin/voltage-dependent anion-selective channel protein	4	6.433420558	5.956335608	7.29E-10	6.433420558	transport porins
Solyc01g102330.2.	Acetyl xylan esterase A	2	2.709947712	2.284449223	0.035240681	2.709947712	not assigned unknown
Solyc01g105050.2.	Chlorophyll a-b binding protein chloroplastic	4	4.887453726	2.412468031	0.037209696	4.887453726	PS lightreaction photosystem II LHC-II
Solyc01g106480.2.	Malate dehydrogenase	5	4.924475728	2.893135293	0.021192518	4.924475728	protein synthesis ribosome biogenesis
Solyc02g020940.2.	Glyceraldehyde-3-phosphate dehydrogenase	9	3.822278011	1.296096377	0.003628084	3.822278011	PS calvin cycle GAP
Solyc02g063130.2.	UV excision repair protein RAD23	3	4.109665814	4.32751429	0.020429263	4.109665814	DNA repair
Solyc02g063490.2.	Malate dehydrogenase	6	5.04930253	2.599821792	0.024739707	5.04930253	protein synthesis ribosome biogenesis
Solyc02g067460.2.	Porin/voltage-dependent anion-selective channel protein	5	3.622792869	2.381918298	0.031840889	3.622792869	transport sugars
Solyc02g071890.2.	Histidinol dehydrogenase	5	2.504736712	1.565142333	0.026071818	2.504736712	amino acid metabolism synthesis histidine histidinol dehydrogenase
Solyc02g079950.2.	Oxygen-evolving enhancer protein 3	3	6.498979208	4.073950661	0.035478455	6.498979208	PS lightreaction photosystem II PSII polypeptide subunits
Solyc02g086730.1.	50S ribosomal protein L12-C	4	3.633295653	4.189446766	0.009732752	3.633295653	protein synthesis ribosomal protein prokaryotic unknown organellar
Solyc02g091130.2.	ATP synthase subunit beta	14	3.601449322	0.951024039	0.000164672	3.601449322	mitochondrial electron transport / ATP synthesis F1-ATPase
Solyc03g005580.2.	Legumin 11S-globulin	5	46.39916323	44.16161203	0.028422006	46.39916323	development storage proteins
Solyc03g006140.2.	Neutral ceramidase	7	2.020992244	1.048266071	0.005282445	2.020992244	lipid metabolism exotics (steroids squalene etc) sphingolipids ceramidase
Solyc03g082920.2.	Heat shock protein	29	3.253871003	0.830882775	0.000332367	3.253871003	misc cytochrome P450
Solyc03g098050.2.	Calmodulin 3 protein	4	2.511127273	1.643596176	0.039598936	2.511127273	signalling calcium
Solyc03g120850.2.	chaperonin	9	4.251438143	1.712714648	0.039373603	4.251438143	PS calvin cycle rubisco interacting
Solyc03g121270.2.	IAA-amino acid hydrolase	9	2.399640986	1.31914488	0.006657529	2.399640986	hormone metabolism auxin synthesis-degradation
Solyc04g009030.2.	Glyceraldehyde-3-phosphate dehydrogenase	12	2.758865999	0.785741587	0.000384254	2.758865999	PS calvin cycle GAP
Solyc04g054990.2.	Lipoxygenase homology domain-containing protein 1	4	5.087386426	4.328080556	0.000243401	5.087386426	not assigned no ontology
Solyc04g072850.2.	Alpha-L-arabinofuranosidase/beta-D-xylosidase	10	5.603657142	3.242586923	0.000110808	5.603657142	cell wall degradation cellulases and beta-1 4-glucanases
Solyc04g080550.2.	Phenylcoumaran benzylic ether reductase	10	5.134011294	3.286600527	0.017121574	5.134011294	secondary metabolism flavonoids isoflavonols isoflavone reductase
Solyc06g071960.2.	Nucleoside diphosphate kinase	2	10.36452257	10.46207171	0.041646058	10.36452257	RNA regulation of transcription AtSR transcription factor family
Solyc06g074670.2.	Bifunctional polymyxin resistance arnA protein	3	7.098793427	10.83081888	0.000101829	7.098793427	cell wall precursor synthesis UXS
Solyc07g049450.2.	Thioredoxin/protein disulfide isomerase	10	3.003595253	1.38792404	0.000349581	3.003595253	redox thioredoxin
Solyc07g066470.2.	Porphobilinogen deaminase	3	2.715074019	1.4487712	0.017903966	2.715074019	hormone metabolism brassinosteroid synthesis-degradation sterols SMT1

Solyc08g006510.2.	NAD dependent epimerase/dehydratase family protein	5	7.326756857	4.254485157	0.037632513	7.326756857	not assigned unknown
Solyc09g082340.2.	Vicilin-like protein (Fragment)	2	200.0603176	166.5924384	0.025003155	200.0603176	misc glutathione S transferases
Solyc10g050110.1.	LRR receptor-like serine/threonine-protein kinase RLP	4	6.927080433	4.246426143	3.18E-05	6.927080433	stress biotic
Solyc10g085550.1.	Enolase	27	2.891459466	0.697465895	8.92E-09	2.891459466	glycolysis cytosolic branch enolase
Solyc11g066720.1.	Bifunctional polymyxin resistance arnA protein	4	2.929864211	3.72783146	0.000180903	2.929864211	cell wall precursor synthesis UXS
Solyc12g010320.1.	Outer membrane lipoprotein blc	2	10.91660787	21.57435905	2.55E-05	10.91660787	transport misc
Solyc01g099460.1.	ATP-dependent DNA helicase	4	99999.9	49999.95	2.22E-16	99999.9	protein synthesis ribosome biogenesis
Solyc02g082000.2.	30S ribosomal protein S19	2	3.586960069	0.878170299	0.037505824	3.586960069	protein synthesis ribosomal protein eukaryotic 40S subunit S15
Solyc02g084440.2.	Fructose-bisphosphate aldolase	12	3.533934965	1.693571598	0.032987743	3.533934965	PS calvin cycle aldolase
Solyc02g086730.1.	50S ribosomal protein L12-C	2	4.443596405	8.916821949	3.87E-05	4.443596405	protein synthesis ribosomal protein prokaryotic chloroplast 50S subunit L12
Solyc02g086740.1.	50S ribosomal protein L12-C	2	10.57434288	25.34421774	5.55E-05	10.57434288	protein synthesis ribosomal protein prokaryotic unknown organellar
Solyc02g088260.2.	Latex abundant protein 1	7	5.228763786	3.734299766	0.029129836	5.228763786	RNA regulation of transcription ABI3/VP1-related B3-domain-containing transcription factor family
Solyc03g005220.2.	Histone H2A	3	5.020003622	3.612014721	0.048249977	5.020003622	development squamosa promoter binding like (SPL)
Solyc03g083520.2.	Calmodulin	2	5.086163059	1.730178372	0.01943365	5.086163059	protein postranslational modification
Solyc03e118910.1.	T-complex protein 1 subunit delta	2	5.73908337	3.269778932	0.009821608	5.73908337	protein folding
Solyc04g049330.2.	V-type proton ATPase subunit G 1	8	2.820859373	0.581947854	0.000655422	2.820859373	transport p- and v-ATPases H+-transporting two-sector ATPase
Solyc04g080850.2.	Thioredoxin	3	4.334663734	1.204737274	0.003159079	4.334663734	redox thioredoxin
Solyc06g005260.2.	Cytoplasmic glutaredoxin thioltransferase glutathione-dependent disulfide oxidoreducta	2	3.847876989	2.198674018	0.042147948	3.847876989	redox glutaredoxins
Solyc06g007930.2.	Cytochrome b5	2	3.125937409	0.792786157	2.10E-05	3.125937409	redox ascorbate and glutathione
Solyc06g061070.2.	Glycine cleavage system H protein 1	3	5.248405534	7.706042265	0.00023648	5.248405534	PS photorespiration glycine cleavage H protein
Solyc07g005960.2.	Serine carboxypeptidase K10B2.2	3	4.86516796	6.764417126	0.000192356	4.86516796	misc calcineurin-like phosphoesterase family protein
Solyc07g044860.2.	Oxygen-evolving enhancer protein 2 chloroplastic	5	8.634879978	6.405589106	0.005110189	8.634879978	PS lightreaction photosystem II PSII polypeptide subunits
Solyc08g067020.2.	Ubiquinol-cytochrome c reductase complex protein	5	5.430678028	4.435584457	0.001619083	5.430678028	mitochondrial electron transport / ATP synthesis cytochrome c reductase
Solyc09g014520.2.	Chlorophyll a-b binding protein 6A chloroplastic	9	3.02915307	3.484832647	0.019966419	3.02915307	PS lightreaction photosystem II LHC-II
Solyc09g074300.1.	Histone H2A	3	5.020003622	3.612014721	0.048249977	5.020003622	RNA RNA binding
Solyc10g086580.1.	Ribulose-1 5-bisphosphate carboxylase/oxygenase activase 1	8	4.147673336	2.765071721	0.007974959	4.147673336	PS calvin cycle rubisco interacting

Table 5.7. Differentially expressed proteins identified in the fruits of wild species at different developmental stages using nanoLC-MS-MS.

Label-free quantitation was employed by matching retention times of the peaks and measuring area under the matched peaks using Sieve 2.1 software (Thermo Scientific) to identify the differentially expressed proteins in SP-SL, SG-SL, SH-SL pairs. Stringent selection criteria were imposed to identify these proteins (p value≤0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR=1%).

List of downregulated proteins in SH-SL

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO (SH/SL)	STD.DEV	PVALUE	FOLD CHANGE (SH/SL)	MAPMANCLASS	
Solyc01g005330.2.1	microtubule associated protein Type 1	2	0.064101514	0.08428808	8.55E-05	15.60026	stress abiotic unspec	stress abiotic unspecified
Solyc02g080630.2.1	Lactoylglutathione lyase	10	0.280280683	0.185709766	0.020641872	3.56785	amino acid metaboli	amino acid metabolism degradation aspartate family threonine
Solyc02g086880.2.1	Formate dehydrogenase	17	0.293321929	0.197142384	0.011503691	3.40922	C1-metabolism forn	C1-metabolism formate dehydrogenase
Solyc03g025320.2.1	Hydroxycinnamoyl transferase	12	0.049019614	0.051741181	0.038718934	20.40000	secondary metabolis	secondary metabolism phenylpropanoids
Solyc03g115020.2.1	Unknown Protein	3	0.084913429	0.147552551	0.001223276	11.77670	signalling calcium	signalling calcium
Solyc04g011400.2.1	UDP-glucose 4-epimerase	15	0.171479142	0.114797208	8.82E-05	5.83161	cell wall precursor s	cell wall precursor synthesis UXS
Solyc04g014480.2.1	class I heat shock protein 3	5	0.111107758	0.04730877	0.035915724	9.00027	stress abiotic heat	stress abiotic heat
Solyc04g045340.2.1	Phosphoglucomutase	30	0.189485287	0.132278826	0.000141848	5.27745	glycolysis plastid bra	glycolysis plastid branch phosphoglucomutase (PGM)
Solyc04g055170.2.1	Annexin 2	9	0.231520497	0.12694501	0.028815713	4.31927	stress abiotic heat	stress abiotic heat
Solyc04g081970.2.1	Thioredoxin	2	0.043341926	0.020535211	0.004341864	23.07235	misc UDP glucosyl a	misc UDP glucosyl and glucoronyl transferases
Solyc04g082460.2.1	Catalase	6	0.056395528	0.08422719	0.020245118	17.73190	redox dismutases an	redox dismutases and catalases
Solyc05g017980.2.1	microtubule associated protein Type 1	2	0.093105607	0.215332407	6.17E-05	10.74049	cell organisation	cell organisation
Solyc05g054060.2.1	UTP-glucose 1 phosphate uridylyltransferase	7	0.199617455	0.20315803	0.027565084	5.00958	glycolysis cytosolic l	glycolysis cytosolic branch UGPase
Solyc06g005160.2.1	Ascorbate peroxidase	9	0.069813294	0.067549025	0.027297265	14.32392	misc nitrilases nitril	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Solyc06g052050.2.1	Heat shock protein	6	0.049916335	0.05042831	0.001072255	20.03352	misc cytochrome P4	misc cytochrome P450
Solyc07g044860.2.1	Oxygen-evolving enhancer protein 2 chloroplastic	7	0.40812332	0.358375257	0.00022912	2.45024	PS lightreaction pho	PS lightreaction photosystem II PSII polypeptide subunits
Solyc07g063100.2.1	Proton pump interactor 1	6	0.070316515	0.091715756	0.00020677	14.22141	transport	transport
Solyc07g066150.1.1	Photosystem I reaction center subunit V	2	0.220570441	0.623256902	7.52E-05	4.53370	PS lightreaction pho	PS lightreaction photosystem I PSI polypeptide subunits
Solyc08g082820.2.1	Heat shock protein	28	0.062344808	0.05019783	3.34E-07	16.03983	protein folding	protein folding
Solyc09g008280.1.1	S-adenosylmethionine synthase	15	0.076354511	0.085790383	3.07E-05	13.09680	amino acid metaboli	amino acid metabolism synthesis aspartate family methionine S-adenosylmethionine synthetase
Solyc09g091470.2.1	3-ketoacyl CoA thiolase 2	5	0.214290626	0.256690591	0.01045637	4.66656	lipid metabolism lipi	lipid metabolism lipid degradation beta-oxidation acyl-CoA thioesterase
Solyc10g083970.1.1	S-adenosylmethionine synthase	10	0.062450513	0.085940299	0.015114606	16.01268	amino acid metaboli	amino acid metabolism synthesis aspartate family methionine S-adenosylmethionine synthetase
Solyc10g084400.1.1	Glutathione S-transferase	4	0.372745607	0.412818179	0.001327807	2.68279	misc glutathione S tı	misc glutathione S transferases
Solyc11g011960.1.1	UTP-glucose 1 phosphate uridylyltransferase	32	0.064825851	0.041886232	0.021161216	15.42594	glycolysis cytosolic l	glycolysis cytosolic branch UGPase
Solyc12g006450.1.1	Aminotransferase-like protein	2	0.144726854	0.233551998	0.021554373	6.90957	stress biotic signallii	stress biotic signalling
Solyc00g060810.2.1	Major latex-like protein	3	0.280026183	0.163726004	0.021425515	3.57109	stress abiotic unspec	stress abiotic unspecified
Solyc01g006280.2.1	Formate-tetrahydrofolate ligase	20	0.023042923	0.008216753	1.00E-06	43.39727	C1-metabolism forn	C1-metabolism formate-tetrahydrofolate ligase
Solyc01g007150.2.1	Coatomer subunit beta-1	17	0.05923237	0.035041783	0.048740919	16.88266	cell vesicle transport	cell vesicle transport
Solyc01g008310.2.1	Phenylalanyl-tRNA synthetase beta chain	9	0.041377179	0.026865109	0.001568052	24.16791	protein aa activation	protein aa activation phenylalanine-tRNA ligase
Solyc01g008540.2.1	Cinnamoyl CoA reductase-like protein	2	0.051058436	0.051587381	0.035371984	19.58540	secondary metabolis	secondary metabolism flavonoids dihydroflavonols
Solyc01g008550.2.1	Cinnamoyl CoA reductase-like protein	11	0.003392737	0.002243541	0.000177059	294.74728	protein synthesis rib	protein synthesis ribosome biogenesis
Solyc01g008550.2.1	Cinnamoyl CoA reductase-like protein	2	0.014366917	0.014636809	0.001595904	69.60436	protein synthesis rib	protein synthesis ribosome biogenesis
Solyc01g009280.2.1	Serine/threonine-protein phosphatase	6	0.267201757	0.133289895	0.036583299	3.74249	DNA synthesis/chroı	DNA synthesis/chromatin structure
Solyc01g010700.2.1	AKIN gamma	4	0.080355395	0.063201054	0.022826938	12.44472	cell wall cell wall pr	cell wall cell wall proteins
Solyc01g010820.2.1	Cullin C	2	0.049072622	0.056954644	0.021083323	20.37796	protein degradation ι	protein degradation ubiquitin E3 SCF cullin
Solyc01g044360.2.1	Importin beta-3	31	0.062140937	0.015969776	0.000178338	16.09245	protein targeting nuc	protein targeting nucleus
Solyc01g057830.2.1	30S ribosomal protein S1	4	0.104646989	0.059640936	0.044080852	9.55594	protein synthesis rib	protein synthesis ribosomal protein prokaryotic unknown organellar 30S subunit S1
Solyc01g066520.2.1	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	5	0.06386478	0.052344813	0.022708471	15.65808	amino acid metaboli	amino acid metabolism degradation branched chain group shared
Solyc01g067750.2.1	Shikimate dehydrogenase	6	0.049734091	0.03671444	0.000488272	20.10693	amino acid metaboli	amino acid metabolism synthesis aromatic aa chorismate 3-dehydroquinate dehydratase/shikimate dehydrogenase
Solyc01g073740.2.1	Citrate synthase	18	0.001532573	0.00211579	0.000337296	652.49747	TCA / organic transf	TCA / organic transformation TCA CS
Solyc01g079460.2.1	Unknown Protein	2	0.020101554	0.020588541	4.54E-07	49.74740	RNA processing ribo	RNA processing ribonucleases
Solyc01g079680.2.1	Ran GTPase activating protein (Fragment)	2	0.036356856	0.040693446	0.026469228	27.50513	signalling G-protein:	signalling G-proteins
Solyc01g079860.2.1	Carbohydrate kinase YjeF related protein	2	0.018619051	0.028378695	0.02235041	53.70843	minor CHO metabol	minor CHO metabolism others
Solyc01g080280.2.1	Glutamine synthetase	7	0.044622452	0.024219516	0.017627484	22.41024	RNA regulation of tı	RNA regulation of transcription SET-domain transcriptional regulator family
Solyc01g080460.2.1	Pyruvate phosphate dikinase	56	0.036073898	0.010932692	0.000108815	27.72087	gluconeogenesis / gl	gluconeogenesis / glyoxylate cycle pyruvate dikinase
Solyc01g080460.2.1	Pyruvate phosphate dikinase	37	0.007081365	0.004056427	0.001665326	141.21571	gluconeogenesis / gl	gluconeogenesis / glyoxylate cycle pyruvate dikinase
Solyc01g080840.2.1	Protein translocase subunit secA	5	0.196491902	0.070559277	0.018027937	5.08927	protein targeting chl	protein targeting chloroplast
Solyc01g081300.2.1	Phosphoribosylaminoimidazole-succinocarboxamide synthase	5	0.098174828	0.062101072	0.018264573	10.18591	nucleotide metaboli:	nucleotide metabolism synthesis purine SAICAR synthetase
Solyc01g081310.2.1	Glutathione-S-transferase	4	0.007562543	0.014615504	0.01982253	132.23065	DNA synthesis/chroı	DNA synthesis/chromatin structure
Solyc01g081540.2.1	Myosin XI-F	2	0.154530697	0.131229562	0.020901406	6.47121	hormone metabolism	hormone metabolism brassinosteroid synthesis-degradation BRs DET2
Solyc01g086750.2.1	Protein TIF31 homolog	10	0.096168962	0.068129812	0.042516709	10.39837	protein degradation c	protein degradation cysteine protease
Solyc01g088020.2.1	Protein transport protein sec31	36	0.080772339	0.025644191	0.000322177	12.38048	not assigned no onto	not assigned no ontology
Solyc01g089870.2.1	Pentatricopeptide repeat-containing protein	2	0.094117142	0.088042839	0.009428634	10.62506	mitochondrial electr	mitochondrial electron transport / ATP synthesis F1-ATPase
Solyc01g091160.2.1	Agmatinase	7	0.041490366	0.021154082	0.00798457	24.10198	amino acid metaboli	amino acid metabolism degradation glutamate family arginine
Solyc01g095620.2.1	UDP-glucosyltransferase	4	0.03596526	0.039983467	0.007775432	27.80461	secondary metabolis	secondary metabolism simple phenols
Solyc01g095970.2.1	Dynamin 2	7	0.10583538	0.051311662	0.005049395	9.44864	misc dynamin	misc dynamin
Solyc01g096420.2.1	Predicted NADPH-dependent FMN reductase	2	0.060996891	0.059321133	0.035268555	16.39428	not assigned no onto	not assigned no ontology
Solyc01g098610.2.1	Glutathione synthetase	6	0.117076028	0.068588785	0.016158375	8.54146	redox ascorbate and	redox ascorbate and glutathione glutathione
Solyc01g098920.2.1	Mitochondrial Rho GTPase 1	6	0.047163248	0.050641904	0.046692705	21.20295	protein degradation ι	protein degradation ubiquitin E3 SCF FBOX
Solyc01g099180.2.1	Lipoxygenase	5	0.029099256	0.009869141	0.036974361	34.36514	hormone metabolism	hormone metabolism jasmonate synthesis-degradation lipoxygenase
Solyc01g099190.2.1	Lipoxygenase	32	0.020354063	0.010965239	0.006799683	49.13024	hormone metabolism	hormone metabolism jasmonate synthesis-degradation lipoxygenase
Solyc01g099200.2.1	Lipoxygenase	2	0.028582461	0.028758337	0.016541145	34.98649	hormone metabolism	hormone metabolism jasmonate synthesis-degradation lipoxygenase
Solyc01g099210.2.1	Lipoxygenase	3	0.022221313	0.017861253	0.013778893	45.00184	hormone metabolism	hormone metabolism jasmonate synthesis-degradation lipoxygenase
Solyc01g099280.2.1	5'-AMP-activated protein kinase gamma-1 subunit	2	0.036460927	0.059517553	0.005005394	27.42662	protein postranslatio	protein postranslational modification
Solyc01g100050.2.1	WD-40 repeat protein	10	0.035500725	0.026024394	0.001037642	28.16844	stress biotic	stress biotic
Solyc01g100650.2.1	NHL repeat containing 2	6	0.172142656	0.09661429	0.000209796	5.80914	lipid metabolism lipi	lipid metabolism lipid degradation lysophospholipases
Solyc01g100720.2.1	Importin alpha-1b subunit	7	0.017790003	0.011783034	0.001038323	56.21135	PS calvin cycle rubis	PS calvin cycle rubisco interacting
Solyc01g102510.2.1	Genomic DNA chromosome 5 P1 clone MXC17	15	0.125415422	0.047875551	0.038824678	7.97350	not assigned no onto	not assigned no ontology
Solyc01g102940.2.1	Methionine s-methyltransferase	13	0.025228103	0.020159263	0.013859799	39.63834	amino acid metaboli	amino acid metabolism synthesis aspartate family methionine methionine S-methyltransferase
Solyc01g103010.2.1	Cullin-associated NEDD8-dissociated protein 2	17	0.00463871	0.005484422	0.002871533	215.57718	development unspec	development unspecified
Solyc01g103130.1.1	Dynamin-2A	3	0.117150327	0.07093764	0.002152012	8.53604	misc dynamin	misc dynamin
Solyc01g104070.2.1	Importin beta	21	0.129507149	0.044406794	0.038919054	7.72158	signalling receptor k	signalling receptor kinases DUF 26
Solyc01g105560.2.1	3 4-dihydroxy-2-butanone 4-phosphate synthase	2	0.032559002	0.043107943	0.019029032	30.71347	Co-factor and vitami	Co-factor and vitamine metabolism riboflavin GTP cyclohydrolase II
Solyc01g106450.2.1	L-galactose dehydrogenase	6	0.096832118	0.056274129	0.00437895	10.32715	minor CHO metabol	minor CHO metabolism others
Solyc01g107130.2.1	Vacuolar sorting receptor	2	0.330729391	0.230679797	0.018060099	3.02362	protein targeting sec	protein targeting secretory pathway vacuole
Solyc01g107270.2.1	Phosphoribosylformylglycinamidine synthase	5	0.306821675	0.13649755	0.02743055	3.25922	nucleotide metaboli:	nucleotide metabolism synthesis purine FGAR amidotransferase
Solyc01g107820.2.1	UDP-glucosyltransferase family 1 protein	5	0.012287944	0.012388219	0.032659833	81.38058	misc UDP glucosyl a	misc UDP glucosyl and glucoronyl transferases
Solyc01g108030.2.1	Methylcrotonoyl-CoA carboxylase beta subunit	6	0.039371639	0.033839871	0.017224841	25.39899	amino acid metaboli	amino acid metabolism degradation branched chain group leucine
Solyc01g109300.2.1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	7	0.011117773	0.009970143	0.015683349	89.94607	secondary metabolis	secondary metabolism isoprenoids non-mevalonate pathway HDR
Solyc01g109540.2.1	Coatomer subunit gamma	3	0.029131444	0.03285281	0.048621769	34.32717	cell vesicle transport	cell vesicle transport
Solyc01g109540.2.1	Coatomer subunit gamma	32	0.147810666	0.031758992	0.000306753	6.76541	cell vesicle transport	cell vesicle transport
Solyc01g109850.2.1	Diaminopimelate decarboxylase	11	0.040141183	0.021448314	0.018076116	24.91207	misc nitrilases nitril	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Solyc01g110120.2.1	V-type proton ATPase subunit a	4	0.036302239	0.032257133	0.000771456	27.54651	misc calcineurin-like	misc calcineurin-like phosphoesterase family protein
Solyc01g110120.2.1	V-type proton ATPase subunit a	24	0.107371571	0.028466564	0.000415431	9.31345	misc calcineurin-like	misc calcineurin-like phosphoesterase family protein
Solyc01g111520.2.1	Synaptotagmin	3	0.01523085	0.012931397	0.014932813	65.65622	stress abiotic cold	stress abiotic cold
Solyc01g111710.2.1	26S proteasome non-ATPase regulatory subunit 3	17	0.249064868	0.065548626	0.047924439	4.01502	protein degradation ι	protein degradation ubiquitin proteasom
Solyc01g111780.2.1	Importin beta-2 subunit	7	0.011646262	0.008161925	1.80E-05	85.86446	protein targeting nuc	protein targeting nucleus
Solyc01g112280.2.1	Succinyl-diaminopimelate desuccinylase	8	0.193184002	0.089268233	0.020814604	5.17641	misc nitrilases nitril	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Solyc01g112290.2.1	Glutamyl-tRNA synthetase	5	0.002276166	0.002442802	0.004032824	439.33527	tetrapyrrole synthesi:	tetrapyrrole synthesis glu-tRNA synthetase
Solyc02g020980.2.1	4-alpha-glucanotransferase	21	0.096840886	0.037756321	0.014085559	10.32622	major CHO metabol	major CHO metabolism degradation starch D enzyme
Solyc02g021420.2.1	Gelsolin	19	0.058631842	0.023268484	0.021355241	17.05558	cell organisation	cell organisation
Solyc02g023970.2.1	GTP-binding protein	15	0.004283964	0.004336607	0.003864178	233.42867	signalling G-protein:	signalling G-proteins
Solyc02g031860.2.1	Serine/threonine protein kinase	9	0.163179414	0.083818958	0.046343051	6.12822	protein postranslatio	protein postranslational modification
Solyc02g031910.2.1	Serine/threonine protein kinase	13	0.113816902	0.052503479	0.007744852	8.78604	protein postranslatio	protein postranslational modification
Solyc02g031950.2.1	Pathogenesis-related protein-like protein	2	0.260053941	0.218654002	0.036883346	3.84536	stress biotic PR-prot	stress biotic PR-proteins
Solyc02g062500.2.1	2-oxoglutarate-dependent dioxygenase	6	0.023899841	0.019215913	0.043298072	41.84128	hormone metabolism	hormone metabolism ethylene synthesis-degradation
Solyc02g062970.2.1	Xaa-Pro aminopeptidase 2	6	0.020651185	0.020298708	4.75E-05	48.42337	mitochondrial electr	mitochondrial electron transport / ATP synthesis cytochrome c oxidase
Solyc02g064680.2.1	Calcium-transporting ATPase 1	2	0.159032834	0.100861148	0.019051191	6.28801	signalling calcium	signalling calcium
Solyc02g065300.1.1	Leucyl-tRNA synthetase	40	0.023673477	0.011900857	2.90E-06	42.24137	protein folding	protein folding
Solyc02g067080.2.1	UDP-D-glucose dehydrogenase	7	0.079197346	0.041224974	0.003725635	12.62669	cell wall precursor s	cell wall precursor synthesis UGD
Solyc02g067210.2.1	Nucleic acid binding protein	3	0.097489746	0.062324656	0.004190803	10.25749	RNA RNA binding	RNA RNA binding
Solyc02g068530.2.1	UDP-N-acetylglucosamine pyrophosphorylase	4	0.143948743	0.10487826	0.010827664	6.94692	misc UDP glucosyl a	misc UDP glucosyl and glucoronyl transferases
Solyc02g070770.2.1	NAD-dependent epimerase/dehydratase	7	0.197848167	0.083458547	0.006838921	5.05438	signalling light	signalling light
Solyc02g076720.2.1	Phosphoribosylformylglycinamidine synthase	17	0.200913419	0.064729325	0.015596617	4.97727	nucleotide metaboli:	nucleotide metabolism synthesis purine FGAR amidotransferase
Solyc02g081160.2.1	Diphosphate-fructose-6-phosphate 1-phosphotransferase	18	0.016136192	0.00842958	2.21E-06	61.97249	glycolysis plastid bra	glycolysis plastid branch pyrophosphate-fructose-6-P phosphotransferase
Solyc02g081400.2.1	Intracellular protease PfpI family protein expressed	12	0.001098903	0.001295068	0.021379987	909.99843	development unspec	development unspecified
Solyc02g081880.2.1	Molybdenum cofactor sulfurase protein-like	4	0.022068879	0.025773133	0.02417991	45.31268	Co-factor and vitami	Co-factor and vitamine metabolism molybdenum cofactor
Solyc02g082350.2.1	Lrr resistance protein fragment	3	0.031388566	0.043818238	0.0180489	31.85873	stress biotic	stress biotic
Solyc02g082540.2.1	Actin cytoskeleton-regulatory complex protein pan1	5	0.082323802	0.05442855	0.022375291	12.14716	signalling calcium	signalling calcium
Solyc02g083710.2.1	26S proteasome non-ATPase regulatory subunit 4	8	0.090790541	0.067491003	0.027292487	11.01436	protein degradation ι	protein degradation ubiquitin E2
Solyc02g083860.2.1	Flavanone 3-hydroxylase	9	0.041092074	0.02369208	0.037301189	24.33559	hormone metabolism	hormone metabolism ethylene synthesis-degradation
Solyc02g085220.2.1	Transforming growth factor-beta receptor-associated protein 1	3	0.026581457	0.022887764	0.028906452	37.62021	PS calvin cycle rubis	PS calvin cycle rubisco small subunit
Solyc02g085350.2.1	Succinate dehydrogenase flavoprotein subunit	15	0.000140902	0.000389065	0.003914421	7097.13134	TCA / organic transf	TCA / organic transformation TCA succinate dehydrogenase
Solyc02g085780.2.1	Regulator of chromosome condensation (RCC1)-like protein	2	0.063879488	0.066279975	0.022190072	15.65448	transport misc	transport misc
Solyc02g087240.2.1	NADH-quinone oxidoreductase F subunit family protein	8	0.027951752	0.015772943	0.007620825	35.77593	mitochondrial electr	mitochondrial electron transport / ATP synthesis NADH-DH (type I) localisation not clear
Solyc02g087880.2.1	Tubulin alpha-7 chain	15	0.007422954	0.00465514	0.034355515	134.71726	major CHO metabol	major CHO metabolism degradation sucrose invertases neutral
Solyc02g088690.2.1	UDP-glucose 6-dehydrogenase	4	0.047004927	0.046191945	0.000350221	21.27437	cell wall precursor s	cell wall precursor synthesis UGD
Solyc02g088700.2.1	Mitochondrial processing peptidase beta subunit	13	0.000728159	0.001199288	0.000355493	1373.32643	protein targeting mit	protein targeting mitochondria
Solyc02g089170.2.1	Alpha-1 4-glucan-protein synthase	6	0.073485791	0.032746235	0.008311267	13.60807	signalling receptor k	signalling receptor kinases leucine rich repeat VIII type 2
Solyc02g090860.2.1	Phenylalanyl-tRNA synthetase alpha chain	5	0.083287377	0.07421753	0.039162175	12.00662	protein aa activation	protein aa activation phenylalanine-tRNA ligase
Solyc02g091410.2.1	Pro-apoptotic serine protease nma111-like protein	5	0.316444981	0.185170825	0.04613467	3.16011	protein degradation s	protein degradation serine protease
Solyc02g091490.2.1	Fructokinase 3	9	0.356521961	0.418662351	0.000148178	2.80488	major CHO metabol	major CHO metabolism degradation sucrose fructokinase
Solyc02g092820.2.1	Indole-3-acetic acid-amido synthetase GH3.8	6	0.334138417	0.41046986	0.012029478	2.99277	protein degradation ι	protein degradation ubiquitin proteasom
Solyc03g005080.2.1	Protoporphyrinogen IX oxidase	2	0.092871171	0.098797494	0.02925288	10.76760	tetrapyrrole synthesi:	tetrapyrrole synthesis protoporphyrin IX oxidase
Solyc03g032070.2.1	Holliday junction ATP-dependent DNA helicase ruvB	4	0.041057566	0.048146242	0.039329241	24.35605	protein postranslatio	protein postranslational modification
Solyc03g044150.2.1	Subtilisin-like protease	7	0.064757141	0.044651259	0.026599092	15.44231	protein degradation ι	protein degradation ubiquitin E3 RING
Solyc03g063560.2.1	Glutamate synthase (Ferredoxin)	65	0.154644968	0.025724519	0.001188477	6.46642	N-metabolism ammo	N-metabolism ammonia metabolism glutamate synthase NADH dependent
Solyc03g065340.2.1	Phosphorylase	37	0.025120277	0.008264262	2.52E-06	39.80848	major CHO metabol	major CHO metabolism degradation starch starch phosphorylase
Solyc03g070390.2.1	Alpha-1 4-glucan-protein synthase	8	0.074501754	0.032440548	0.018818936	13.42250	cell wall cell wall pr	cell wall cell wall proteins RGP
Solyc03g071590.2.1	Malate dehydrogenase	3	0.041001275	0.038850045	0.009730779	24.38949	TCA / organic transf	TCA / organic transformation other organic acid transformations cyt MDH
Solyc03g080160.2.1	Nascent polypeptide-associated complex alpha subunit-like protein	6	0.002136692	0.004798306	0.04233388	468.01317	protein synthesis elo	protein synthesis elongation
Solyc03g082940.2.1	Importin subunit beta	15	0.120986839	0.042963256	0.023220257	8.26536	protein targeting nuc	protein targeting nucleus
Solyc03g083970.2.1	IQ calmodulin-binding motif family protein	4	0.024043894	0.020540506	0.041030514	41.59060	signalling calcium	signalling calcium
Solyc03g097470.2.1	3-oxoacyl-	2	0.165794156	0.143295128	0.040853402	6.03158	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation ketoacyl ACP synthase
Solyc03g098240.2.1	Glutamate decarboxylase	12	0.025871654	0.015127035	0.003120044	38.65234	amino acid metaboli	amino acid metabolism synthesis central amino acid metabolism GABA glutamate decarboxylase
Solyc03g111340.2.1	Ubiquitin-like modifier-activating enzyme 5	3	0.002292831	0.005561799	0.044134311	436.14204	RNA regulation of tı	RNA regulation of transcription chromatin remodeling factors
Solyc03g111640.2.1	Eukaryotic translation initiation factor 4 gamma 2 (Fragment)	3	0.021381795	0.026664329	0.028680959	46.76876	misc oxidases - copp	misc oxidases - copper flavone etc
Solyc03g112660.2.1	MOS1	3	0.118490545	0.07039122	0.002192814	8.43949	not assigned unknow	not assigned unknown
Solyc03g113780.2.1	Pyridoxine/pyridoxamine 5'-phosphate oxidase	9	0.063888075	0.037708007	0.002695953	15.65237	Co-factor and vitami	Co-factor and vitamine metabolism
Solyc03g114640.2.1	Signal peptide peptidase SppA type	2	0.063028493	0.072648896	0.029649184	15.86584	protein degradation	protein degradation
Solyc03g114710.2.1	Glucosyltransferase	3	0.10316832	0.074161048	0.020488507	9.69290	misc UDP glucosyl a	misc UDP glucosyl and glucoronyl transferases
Solyc03g115230.2.1	ClpB chaperone	83	0.06873668	0.014272696	7.22E-10	14.54827	stress abiotic heat	stress abiotic heat
Solyc03g115380.1.1	UDP-glucose dehydrogenase	4	0.175052733	0.146641894	0.025307643	5.71256	cell wall precursor s	cell wall precursor synthesis UGD
Solyc03g117430.2.1	Cobalamin synthesis protein P	7	0.004950742	0.007095463	0.011017095	201.98992	cell organisation	cell organisation
Solyc03g117490.2.1	Glycerol kinase	5	0.01676432	0.013574323	0.001665295	59.65050	lipid metabolism gly	lipid metabolism glycerol metabolism glycerol kinase
Solyc03g118030.2.1	Glutamyl-tRNA(Gln) amidotransferase subunit A	5	0.025657915	0.024489922	0.004227245	38.97433	misc nitrilases nitril	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Solyc03g118170.2.1	Glycyl-tRNA synthetase	17	0.000141293	0.000271907	2.17E-06	7077.49145	protein aa activation	protein aa activation glycine-tRNA ligase
Solyc03g118640.2.1	D-tagatose-1 6-bisphosphate aldolase subunit gatY	29	0.170051469	0.049437358	0.019632809	5.88057	OPP oxidative PP 6-	OPP oxidative PP 6-phosphogluconate dehydrogenase
Solyc03g118650.2.1	Aldose 1-epimerase-like protein	6	0.175283295	0.082825312	0.04544495	5.70505	minor CHO metabol	minor CHO metabolism others
Solyc03g118750.2.1	Phosphoethanolamine N-methyltransferase	2	0.05337785	0.055965959	0.005314205	18.73436	lipid metabolism pho	lipid metabolism phospholipid synthesis
Solyc03g120010.2.1	Eukaryotic translation initiation factor 3 subunit 2	4	0.080481668	0.050427973	0.014120658	12.42519	development unspec	development unspecified
Solyc03g120230.2.1	MAR-binding filament-like protein 1	3	0.062617004	0.028201965	0.003944988	15.97010	cell division	cell division
Solyc03g121580.2.1	Histone-binding protein RBBP7	7	0.166361611	0.117067915	0.026438368	6.01100	RNA regulation of tı	RNA regulation of transcription nucleosome/chromatin assembly factor group
Solyc03g121590.2.1	Protein SEY1	4	0.021700189	0.0168868	0.002546511	46.08255	signalling G-protein:	signalling G-proteins
Solyc03g123610.2.1	Alanine aminotransferase	9	0.057093721	0.032609149	4.73E-05	17.51506	amino acid metaboli	amino acid metabolism synthesis central amino acid metabolism alanine alanine aminotransferase
Solyc03g123730.2.1	26S protease regulatory subunit 7	7	0.13770322	0.076265083	0.011356217	7.26199	protein degradation ι	protein degradation ubiquitin proteasom
Solyc04g006970.2.1	Phosphoenolpyruvate carboxylase	90	0.014533157	0.004398469	9.00E-08	68.80817	glycolysis cytosolic l	glycolysis cytosolic branch phospho-enol-pyruvate carboxylase (PEPC)
Solyc04g007980.2.1	1-aminocyclopropane-1-carboxylate oxidase	15	0.031837637	0.013229087	0.00025979	31.40937	hormone metabolism	hormone metabolism ethylene synthesis-degradation
Solyc04g009770.2.1	DNAJ chaperone	6	0.030700832	0.029110479	0.016326562	32.57241	stress abiotic heat	stress abiotic heat
Solyc04g010220.2.1	Unknown Protein	4	0.008381612	0.011312993	0.043152726	119.30879	not assigned no onto	not assigned no ontology
Solyc04g011350.2.1	2-oxoglutarate dehydrogenase E1 component	26	0.153569165	0.037268991	0.000281022	6.51172	TCA / organic transf	TCA / organic transformation TCA 2-oxoglutarate dehydrogenase
Solyc04g011510.2.1	Triosephosphate isomerase	11	0.220164266	0.132293756	0.041086973	4.54206	PS calvin cycle TPI	PS calvin cycle TPI
Solyc04g014270.2.1	Phosphofructokinase family protein	6	0.122680386	0.083767709	0.005444721	8.15126	protein targeting mit	protein targeting mitochondria
Solyc04g014900.2.1	Receptor like kinase RLK	8	0.028480156	0.017007824	0.008236223	35.11217	OPP oxidative PP 6-	OPP oxidative PP 6-phosphogluconolactonase
Solyc04g015100.2.1	Acetyl-CoA C-acetyltransferase protein	8	0.045195861	0.037789727	0.037583096	22.12592	secondary metabolis	secondary metabolism isoprenoids mevalonate pathway acetyl-CoA C-acyltransferase
Solyc04g015830.2.1	Actin-binding protein gelsolin	44	0.111979281	0.023596803	0.00060477	8.93022	cell organisation	cell organisation
Solyc04g016360.2.1	S-formylglutathione hydrolase	9	0.01912222	0.013149705	0.000279441	52.29518	RNA regulation of tı	RNA regulation of transcription ABI3/VP1-related B3-domain-containing transcription factor family
Solyc04g025870.2.1	AP-1 complex subunit gamma-1	5	0.00379134	0.007046401	0.042673017	263.75899	cell vesicle transport	cell vesicle transport
Solyc04g040190.1.1	Lycopene beta-cyclase 1	3	0.01589996	0.016614463	0.034118415	62.89324	secondary metabolis	secondary metabolism isoprenoids carotenoids lycopene beta cyclase
Solyc04g050510.2.1	Translational activator gcn1	2	0.217156568	0.166126849	0.035676722	4.60497	protein synthesis	protein synthesis
Solyc04g054480.2.1	C2 domain-containing protein-like	17	0.005971364	0.005871461	0.009339002	167.46593	not assigned no onto	not assigned no ontology
Solyc04g054710.2.1	Aspartate aminotransferase	5	0.103094955	0.036165798	0.00138219	9.69980	amino acid metaboli	amino acid metabolism degradation aromatic aa tyrosine
Solyc04g055200.2.1	Asparagine synthase (Glutamine-hydrolyzing)	2	0.118289985	0.105898066	0.018381558	8.45380	protein degradation s	protein degradation subtilases
Solyc04g063280.2.1	Vacuolar protein sorting-associated protein 27	5	0.026859625	0.016150501	0.009222522	37.23060	cell vesicle transport	cell vesicle transport
Solyc04g071940.2.1	Xanthoxin dehydrogenase	2	0.290898582	0.174660925	0.040484795	3.43762	transport amino acid	transport amino acids
Solyc04g072240.2.1	Oxidoreductase family protein	3	0.150090741	0.118816432	0.03766459	6.66264	not assigned no onto	not assigned no ontology
Solyc04g077040.2.1	Xylulose kinase	3	0.14884018	0.126471413	0.03901335	6.71862	minor CHO metabol	minor CHO metabolism sugar kinases
Solyc04g080670.2.1	Inositol pentakisphosphate 2-kinase	2	0.000652048	0.001759052	0.028245293	1533.62943	protein degradation ι	protein degradation ubiquitin E3 RING
Solyc04g080980.2.1	Coatomer alpha subunit-like protein	33	0.133081283	0.032347049	0.006954247	7.51420	cell vesicle transport	cell vesicle transport
Solyc04g081490.2.1	Tubulin beta-1 chain	33	0.001230381	0.000940232	2.66E-06	812.75637	secondary metabolis	secondary metabolism phenylpropanoids
Solyc04g081820.2.1	La domain containing protein expressed	3	0.040580963	0.05261641	0.008160228	24.64210	misc protease inhibit	misc protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
Solyc04g082630.2.1	Glyceraldehyde-3-phosphate dehydrogenase B	20	0.003244203	0.002740612	0.002885507	308.24212	protein postranslatio	protein postranslational modification
Solyc04g082880.2.1	Diphosphate--fructose-6-phosphate 1-phosphotransferase	20	0.007131222	0.005074091	9.84E-08	140.22842	misc nitrilases nitril	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Solyc05g005780.2.1	AP-1 complex subunit gamma-1	4	0.092427272	0.095203245	0.032688887	10.81932	RNA regulation of tı	RNA regulation of transcription ABI3/VP1-related B3-domain-containing transcription factor family

Solyc05g006170.2.1	NACHT LRR and PYD domains-containing protein 5	2	0.17774645	0.149799669	0.023301869	5.62599	development unspec	development unspecified
Solyc05g006900.1.1	Unknown Protein	2	0.068362632	0.084167443	0.014900371	14.62787	cell wall precursor s	cell wall precursor synthesis UXS
Solyc05g008870.2.1	Cytidyltransferase-related	2	0.105411931	0.088689141	0.048531991	9.48659	RNA processing spli	RNA processing splicing
Solyc05g009190.2.1	Cysteinyl tRNA synthetase	6	0.015747252	0.018955182	0.000716973	63.50314	redox ascorbate and	redox ascorbate and glutathione
Solyc05g012260.2.1	Purple acid phosphatase	5	0.097524866	0.092407567	0.033842287	10.25380	misc acid and other r	misc acid and other phosphatases
Solyc05g012510.2.1	Phosphorylase	33	0.153673154	0.033440404	0.004590545	6.50732	major CHO metabol	major CHO metabolism degradation starch starch phosphorylase
Solyc05g013070.2.1	Kinase family protein	3	0.021185483	0.021540659	0.03848455	47.20213	protein postranslatio	protein postranslational modification
Solyc05g013990.2.1	T-complex protein 1 subunit epsilon	9	0.015763581	0.011861036	0.01382415	63.43736	protein folding	protein folding
Solyc05g016330.2.1	Cytochrome P450	3	0.022031578	0.026356744	0.034023225	45.38940	RNA regulation of tr	RNA regulation of transcription chromatin remodeling factors
Solyc05g026560.2.1	Catenin beta-1	7	0.037954905	0.020040642	0.001692861	26.34706	protein degradation u	protein degradation ubiquitin E3 RING
Solyc05g050120.2.1	Malic enzyme	43	0.000717564	0.000678567	4.40E-07	1393.60392	TCA / organic transf	TCA / organic transformation other organic acid transformations malic
Solyc05g050600.2.1	Dynamin 2	13	0.027821625	0.018285576	0.001985345	35.94326	misc dynamin	misc dynamin
Solyc05g052510.2.1	Clathrin heavy chain	60	0.090938025	0.018472418	0.004134254	10.99650	cell vesicle transport	cell vesicle transport
Solyc05g054600.2.1	Methionyl-tRNA synthetase	2	0.047860842	0.074454838	0.034887471	20.89391	protein aa activation	protein aa activation methionine-tRNA ligase
Solyc05g054640.2.1	2-oxoglutarate dehydrogenase E1 component	41	0.141704812	0.026219269	6.09E-06	7.05692	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation acetyl CoA transacylase
Solyc05g054980.2.1	Protein phosphatase 2A regulatory subunit B'-like protein	4	0.001795363	0.003162812	0.001024203	556.99042	protein postranslatio	protein postranslational modification
Solyc05g055210.1.1	Eukaryotic peptide chain release factor subunit 1-3-like	7	0.04388096	0.032105897	0.004273787	22.78893	misc cytochrome P4	misc cytochrome P450
Solyc05g056560.2.1	C11orf73 homolog	2	0.152224634	0.230046033	0.04544416	6.56924	protein postranslatio	protein postranslational modification
Solyc06g005370.2.1	Predicted 2 3-bisphosphoglycerate-independent phosphoglycerate mutase	2	0.257734464	0.233490903	0.024078688	3.87996	glycolysis cytosolic b	glycolysis cytosolic branch phosphoglycerate mutase
Solyc06g005970.2.1	Beta-D-glucosidase	11	0.000420022	0.000451827	1.46E-05	2380.82767	misc gluco- galacto	misc gluco- galacto- and mannosidases
Solyc06g006080.2.1	Phosphomethylpyrimidine synthase	5	0.078197878	0.063634797	0.006128922	12.78807	Co-factor and vitami	Co-factor and vitamine metabolism thiamine
Solyc06g007320.2.1	Ubiquitin-activating enzyme E1	25	0.081942273	0.023039691	4.69E-06	12.20371	protein degradation u	protein degradation ubiquitin E1
Solyc06g008090.2.1	Myosin XI-2	2	0.154530697	0.131229562	0.020901406	6.47121	hormone metabolism	hormone metabolism brassinosteroid synthesis-degradation BRs DET2
Solyc06g008530.1.1	Myosin XI	2	0.154530697	0.131229562	0.020901406	6.47121	cell organisation	cell organisation
Solyc06g035970.2.1	Tubulin beta chain	32	0.010295878	0.003828526	1.60E-06	97.12625	secondary metabolis	secondary metabolism phenylpropanoids
Solyc06g048610.2.1	Methionyl-tRNA synthetase-like protein	6	0.031265328	0.023223572	0.030784093	31.98431	protein aa activation	protein aa activation methionine-tRNA ligase
Solyc06g048890.2.1	Protein kinase	3	0.293704947	0.172320662	0.028398314	3.40478	protein postranslatio	protein postranslational modification
Solyc06g050130.2.1	Alpha-galactosidase-like protein	9	0.046266933	0.023764477	0.000422748	21.61371	minor CHO metabol	minor CHO metabolism galactose alpha-galactosidases
Solyc06g050400.1.1	Lysyl-tRNA synthetase	2	0.081101092	0.06881896	0.004543863	12.33029	protein aa activation	protein aa activation lysine-tRNA ligase
Solyc06g052030.2.1	Importin subunit beta	14	0.021807644	0.009965778	5.59E-08	45.85548	Co-factor and vitami	Co-factor and vitamine metabolism
Solyc06g060420.2.1	YbaK/prolyl-tRNA synthetase	6	0.02665248	0.021211261	0.010655539	37.51996	protein aa activation	protein aa activation proline-tRNA ligase
Solyc06g066060.2.1	ATP-dependent RNA helicase	8	0.2218634	0.105494425	0.015226015	4.50728	DNA synthesis/chro	DNA synthesis/chromatin structure
Solyc06g066800.1.1	Glycosyl transferase family 8	3	0.083934013	0.102282745	0.03552881	11.91412	RNA regulation of tr	RNA regulation of transcription bZIP transcription factor family
Solyc06g068950.2.1	Phosphoethanolamine N-methyltransferase	5	0.008411366	0.009846062	0.043451518	118.88675	lipid metabolism pho	lipid metabolism phospholipid synthesis
Solyc06g069020.2.1	Elongation factor 1 alpha	7	0.04814836	0.033184721	0.005483458	20.76914	signalling G-proteins	signalling G-proteins
Solyc06g069180.2.1	Phosphatase 2A regulatory A subunit	13	0.005712087	0.004896777	0.000763015	175.06736	protein postranslatio	protein postranslational modification
Solyc06g069550.1.1	UDP-D-glucose dehydrogenase	4	0.175052733	0.146641894	0.025307643	5.71256	cell wall precursor s	cell wall precursor synthesis UGD
Solyc06g071880.2.1	60S ribosomal protein L17	4	0.038398582	0.067786747	0.025374395	26.04263	protein synthesis ribo	protein synthesis ribosome biogenesis
Solyc06g072380.2.1	Dihydroxyacetone/glycerone kinase-like protein	6	0.060902019	0.022341041	0.016724151	16.41982	minor CHO metabol	minor CHO metabolism others
Solyc06g073960.2.1	Serine/threonine-protein phosphatase	4	0.258469551	0.14619989	0.047381492	3.86893	DNA synthesis/chro	DNA synthesis/chromatin structure
Solyc06g074980.2.1	26S protease regulatory subunit 6B homolog	48	0.274528365	0.047680891	0.020685239	3.64261	cell division	cell division
Solyc06g082560.1.1	ClpB chaperone	30	0.138319377	0.037965295	0.006208559	7.22965	stress abiotic heat	stress abiotic heat
Solyc06g083580.2.1	Pectate lyase 1-27	7	0.077243488	0.03260093	0.004221494	12.94608	cell wall degradation	cell wall degradation pectate lyases and polygalacturonases
Solyc06g083960.1.1	Myosin XI	2	0.154530697	0.131229562	0.020901406	6.47121	hormone metabolism	hormone metabolism brassinosteroid synthesis-degradation BRs DET2
Solyc06g084210.2.1	Transport protein SEC24	15	0.081484711	0.033640242	0.020469324	12.27224	misc UDP glucosyl a	misc UDP glucosyl and glucoronyl transferases
Solyc07g005390.2.1	Aldehyde dehydrogenase	23	0.00406928	0.002649374	2.92E-05	245.74372	glycolysis cytosolic b	glycolysis cytosolic branch non-phosphorylating glyceraldehyde 3-phosphate dehydrogenase (NPGAP-DH)
Solyc07g005760.2.1	Hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase	2	0.02354291	0.025105175	0.034490727	42.47563	transport peptides an	transport peptides and oligopeptides
Solyc07g005940.2.1	Vacuolar ATPase subunit H protein	8	0.004661654	0.003844435	0.002498267	214.51614	tetrapyrrole synthesis	tetrapyrrole synthesis ALA dehydratase
Solyc07g006130.1.1	Eukaryotic peptide chain release factor subunit 1-1	3	0.000677266	0.001518718	0.030382619	1476.52473	protein synthesis rele	protein synthesis release
Solyc07g007790.2.1	Sucrose phosphate synthase	28	0.068993561	0.022246531	2.86E-06	14.49411	DNA synthesis/chro	DNA synthesis/chromatin structure
Solyc07g008610.1.1	ATP-binding cassette protein	4	0.028838695	0.022782796	0.002288947	34.67563	transport ABC trans	transport ABC transporters and multidrug resistance systems
Solyc07g017610.2.1	Saccharopine dehydrogenase (NAD(+) L-glutamate-forming)	21	0.013224821	0.008195223	0.009292247	75.61539	amino acid metaboli	amino acid metabolism degradation aspartate family lysine
Solyc07g017860.2.1	Acetyl-coenzyme A synthetase	3	0.015938498	0.023063233	0.012333099	62.74117	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Solyc07g039330.2.1	Histone-binding protein RBBP7	3	0.025229613	0.021128258	2.09E-07	39.63596	RNA regulation of tr	RNA regulation of transcription nucleosome/chromatin assembly factor group
Solyc07g041150.2.1	Myosin XI	12	0.126135338	0.068293501	0.013706628	7.92799	hormone metabolism	hormone metabolism brassinosteroid synthesis-degradation BRs DET2
Solyc07g043310.2.1	Aminotransferase	14	0.074822915	0.030458409	1.11E-05	13.36489	stress biotic signallin	stress biotic signalling
Solyc07g043320.2.1	Unknown Protein	89	0.039904724	0.007106419	8.40E-09	25.05969	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation long chain fatty acid CoA ligase
Solyc07g053650.2.1	26S proteasome regulatory subunit	10	0.016096023	0.009390691	0.003429703	62.12715	cell wall precursor s	cell wall precursor synthesis UXS
Solyc07g055060.2.1	Phosphoenolpyruvate carboxylase 1	80	0.061698199	0.009629198	1.36E-06	16.20793	glycolysis cytosolic b	glycolysis cytosolic branch phospho-enol-pyruvate carboxylase (PEPC)
Solyc07g056660.2.1	Transforming growth factor-beta receptor-associated protein 1	9	0.036248236	0.021537887	0.014706689	27.58755	misc cytochrome P4	misc cytochrome P450
Solyc07g062530.2.1	Phosphoenolpyruvate carboxylase 2	107	0.022565381	0.003508907	9.90E-20	44.31567	glycolysis cytosolic b	glycolysis cytosolic branch phospho-enol-pyruvate carboxylase (PEPC)
Solyc07g063040.2.1	Enolase-phosphatase E-1	5	0.010513053	0.01220704	0.001990476	95.11985	minor CHO metabol	minor CHO metabolism others
Solyc07g063650.2.1	Ubiquitin carboxyl-terminal hydrolase	6	0.137263583	0.098365629	0.002341017	7.28525	protein degradation u	protein degradation ubiquitin ubiquitin protease
Solyc07g064910.2.1	EH-domain-containing protein 1	2	0.244585755	0.22318312	0.005781589	4.08855	misc nitrilases nitril	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Solyc07g064950.2.1	Trigger factor-like protein	4	0.125967551	0.098514421	0.003382915	7.93855	protein folding	protein folding
Solyc07g065230.1.1	C2 domain-containing protein	3	0.056644564	0.064318354	0.001766467	17.65394	RNA regulation of tr	RNA regulation of transcription CCAAT box binding factor family HAP3
Solyc08g005070.2.1	ADP-ribosylation factor GTPase-activating protein 3	2	0.13528645	0.126065084	0.021559956	7.39172	cell vesicle transport	cell vesicle transport
Solyc08g005630.2.1	Glucose-methanol-choline oxidoreductase	9	0.006090809	0.009629541	0.038289161	164.18180	not assigned no onto	not assigned no ontology
Solyc08g014000.2.1	Lipoxygenase	42	0.017884137	0.004864647	2.09E-06	55.91547	hormone metabolism	hormone metabolism jasmonate synthesis-degradation lipoxygenase
Solyc08g015860.2.1	Rab GDP dissociation inhibitor	24	0.027526371	0.012076823	1.37E-07	36.32880	signalling G-proteins	signalling G-proteins
Solyc08g016080.2.1	NAD-dependent epimerase/dehydratase	2	0.190686638	0.09742019	0.021030393	5.24421	signalling light	signalling light
Solyc08g016170.2.1	3-oxoacyl-(Acyl carrier protein) synthase II	4	0.01279144	0.018341651	0.048192851	78.17728	secondary metabolis	secondary metabolism flavonoids chalcones
Solyc08g042000.2.1	Sucrose phosphate synthase protein 1	3	0.047959927	0.047529282	0.013765071	20.85074	stress biotic receptor	stress biotic receptors
Solyc08g059660.1.1	Phosphatidylinositol binding clathrin assembly protein like	2	0.074067614	0.069786739	0.02846415	13.50118	OPP oxidative PP 6-	OPP oxidative PP 6-phosphogluconolactonase
Solyc08g062910.2.1	Elongation factor EF-2	48	0.027087451	0.009899872	0.016486449	36.91746	protein synthesis elo	protein synthesis elongation
Solyc08g065220.2.1	Glycine dehydrogenase P protein	9	0.032419869	0.025948058	0.019829769	30.84528	amino acid metaboli	amino acid metabolism degradation serine-glycine-cysteine group glycine
Solyc08g065890.2.1	Epsin	2	0.183020945	0.13878107	0.014252264	5.46386	cell wall degradation	cell wall degradation pectate lyases and polygalacturonases
Solyc08g066580.2.1	Nuclear pore complex protein Nup85	3	0.018586012	0.016364621	0.00979288	53.80390	not assigned unknow	not assigned unknown
Solyc08g066600.2.1	Homology to unknown gene	4	0.169889414	0.091752165	0.038651032	5.88618	RNA regulation of tr	RNA regulation of transcription unclassified
Solyc08g066800.2.1	Phospholipase D	24	0.072327035	0.024733879	0.001735403	13.82609	lipid metabolism lipi	lipid metabolism lipid degradation lysophospholipases phospholipase D
Solyc08g067160.2.1	Acyl-protein thioesterase 2	2	0.031012748	0.058384388	0.018080836	32.24480	lipid metabolism lipi	lipid metabolism lipid degradation lysophospholipases carboxylesterase
Solyc08g068210.2.1	AP-1 complex subunit beta-1	6	0.207989085	0.102247037	0.031058	4.80794	cell vesicle transport	cell vesicle transport
Solyc08g068310.2.1	RNA-binding La domain protein	3	0.117465459	0.0760531	0.011200255	8.51314	transport phosphate	transport phosphate
Solyc08g069030.2.1	Delta-aminolevulinic acid dehydratase	2	0.130406349	0.105381719	0.010899002	7.66834	tetrapyrrole synthesis	tetrapyrrole synthesis ALA dehydratase
Solyc08g074550.2.1	Threonyl-tRNA synthetase	6	0.001739918	0.003992588	0.011415437	574.73973	protein aa activation	protein aa activation threonine-tRNA ligase
Solyc08g075100.2.1	Alpha/beta superfamily hydrolase	3	0.001344127	0.002569531	0.017984202	743.97732	PS lightreaction cycl	PS lightreaction cyclic electron flow-chlororespiration
Solyc08g075210.1.1	Acyltransferase-like protein	5	0.005920085	0.005301215	0.001414299	168.91649	secondary metabolis	secondary metabolism phenylpropanoids
Solyc08g075310.2.1	AP-1 complex subunit gamma-1	18	0.031603289	0.020379368	0.000298572	31.64228	cell vesicle transport	cell vesicle transport
Solyc08g075390.2.1	Isopentenyl-diphosphate delta-isomerase family protein	4	0.000399823	0.000978723	0.047036255	2501.10674	nucleotide metabolis	nucleotide metabolism salvage NUDIX hydrolases
Solyc08g075400.2.1	SWIB/MDM2 domain protein	3	0.058024068	0.195430767	0.015898216	17.23423	RNA regulation of tr	RNA regulation of transcription chromatin remodeling factors
Solyc08g076990.2.1	Acetylornithine deacetylase	11	0.002692047	0.002160374	0.000985767	371.46454	protein degradation	protein degradation
Solyc08g077510.2.1	Poly(U)-specific endoribonuclease-A	7	0.106769752	0.057939078	0.006481196	9.36595	protein degradation s	protein degradation serine protease
Solyc08g078700.2.1	Heat shock protein 22	9	0.246489638	0.203547527	0.018678556	4.05697	stress abiotic heat	stress abiotic heat
Solyc08g079180.2.1	Elongation factor G	9	0.083717684	0.045404431	0.044707118	11.94491	protein synthesis elo	protein synthesis elongation
Solyc08g080140.2.1	dTDP-4-dehydrorhamnose reductase	3	0.099984675	0.076172279	0.018322327	10.00153	cell wall precursor s	cell wall precursor synthesis UER
Solyc08g080510.2.1	Replication factor C subunit 4	2	0.178684375	0.128439159	0.014245705	5.59646	DNA synthesis/chro	DNA synthesis/chromatin structure
Solyc08g081910.2.1	V-type proton ATPase subunit E	19	0.010308112	0.008009166	0.015873574	97.01098	transport p- and v-A	transport p- and v-ATPases H+-transporting two-sector ATPase subunit E
Solyc08g082280.2.1	Long-chain-fatty-acid-CoA ligase	2	0.066413132	0.047839775	0.002208187	15.05726	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation long chain fatty acid CoA ligase
Solyc08g083250.2.1	Purple acid phosphatase	2	0.005320387	0.010029018	0.048926806	187.95625	RNA transcription	RNA transcription
Solyc09g005010.2.1	Importin subunit beta	3	0.210071026	0.133609662	0.008376742	4.76029	protein targeting nuc	protein targeting nucleus
Solyc09g008070.2.1	Cell division protease ftsH homolog 3	31	0.272306506	0.054572471	0.017874535	3.67233	cell division	cell division
Solyc09g010560.1.1	5-oxoprolinase (ATP-hydrolyzing)	24	0.054311374	0.0233644	0.016128579	18.41235	protein postranslatio	protein postranslational modification
Solyc09g011490.2.1	Glutathione S-transferase-like protein	2	0.11112128	0.140611837	0.006958435	8.99918	misc glutathione S tr	misc glutathione S transferases
Solyc09g018450.2.1	Ubiquitin-activating enzyme E1	23	0.155638939	0.050815581	0.033086892	6.42513	protein degradation u	protein degradation ubiquitin E1
Solyc09g031650.2.1	Zinc finger protein	2	0.14927202	0.147496605	0.043595135	6.69918	signalling light	signalling light
Solyc09g031780.2.1	Tic110 family transporter chloroplast inner envelope protein Tic110	20	0.01471432	0.013821677	0.003813499	67.96101	protein targeting chlo	protein targeting chloroplast
Solyc09g031970.2.1	Phosphorylase	5	0.049512234	0.030961727	0.010106571	20.19703	major CHO metabol	major CHO metabolism degradation starch starch phosphorylase
Solyc09g065180.2.1	NAD-dependent epimerase/dehydratase	15	0.023267472	0.012536733	0.014260861	42.97846	cell vesicle transport	cell vesicle transport
Solyc09g074660.2.1	Thymidylate kinase	3	0.047090655	0.044810443	0.018885444	21.23564	not assigned unknow	not assigned unknown
Solyc09g082730.2.1	Aldo/keto reductase family protein	13	0.001755186	0.002792649	0.00545357	569.74019	hormone metabolism	hormone metabolism auxin induced-regulated-responsive-activated
Solyc09g089940.1.1	Genomic DNA chromosome 3 TAC clone K7P8	5	0.002934171	0.004255959	0.004993027	340.81177	RNA regulation of tr	RNA regulation of transcription MYB-related transcription factor family
Solyc09g090970.2.1	Major allergen Mal d 1	5	0.026153464	0.034131595	0.040230597	38.23585	RNA processing ribo	RNA processing ribonucleases
Solyc09g091050.2.1	Lipase	8	0.41057101	0.147843156	0.008480193	2.43563	lipid metabolism lipi	lipid metabolism lipid degradation lipases triacylglycerol lipase
Solyc09g091070.1.1	Malate dehydrogenase	3	0.275875119	0.259229526	0.035691899	3.62483	TCA / organic transf	TCA / organic transformation other organic acid transformations cyt MDH
Solyc09g091750.2.1	26S proteasome regulatory subunit	11	0.194647135	0.073372366	0.007008369	5.13750	protein degradation u	protein degradation ubiquitin proteasom
Solyc09g092430.2.1	Selenium binding protein	6	0.305168686	0.303401788	3.93E-05	3.27688	metal handling	metal handling
Solyc09g092550.2.1	Hypothetical salt-inducible protein (Fragment)	2	0.040775857	0.074361063	0.003371837	24.52432	not assigned unknow	not assigned unknown
Solyc09g092680.2.1	Protein transport protein Sec23	3	0.065018952	0.06411804	0.017773496	15.38013	protein targeting sec	protein targeting secretory pathway golgi
Solyc10g005110.2.1	Coproporphyrinogen III oxidase aerobic	15	0.029080225	0.016980827	0.019780021	34.38763	hormone metabolism	hormone metabolism auxin induced-regulated-responsive-activated
Solyc10g006220.2.1	Cell differentiation protein rcd1	3	0.151486417	0.172944674	0.014713144	6.60125	protein degradation u	protein degradation ubiquitin E3 RING
Solyc10g007290.2.1	Phosphoenolpyruvate carboxylase	49	0.044898712	0.008895699	9.06E-08	22.27235	glycolysis cytosolic b	glycolysis cytosolic branch phospho-enol-pyruvate carboxylase (PEPC)
Solyc10g007480.2.1	Dtdp-glucose 4 6-dehydratase	18	0.029884403	0.010544214	1.68E-07	33.46227	hormone metabolism	hormone metabolism gibberelin synthesis-degradation
Solyc10g007600.2.1	L-lactate dehydrogenase	11	0.183546386	0.057408664	0.00884778	5.44821	PS photorespiration	PS photorespiration glycolate oxydase
Solyc10g008640.2.1	Diacylglycerol kinase	4	0.001425994	0.00268917	0.002805236	701.26522	lipid metabolism pho	lipid metabolism phospholipid synthesis diacylglycerol kinase
Solyc10g024320.1.1	Lon protease homolog	3	0.252793665	0.114136701	0.014640155	3.95580	protein degradation s	protein degradation serine protease
Solyc10g037950.1.1	X7 (Fragment)	2	0.054125416	0.04657618	0.005693144	18.47561	not assigned unknow	not assigned unknown
Solyc10g038130.1.1	Pectinacetylesterase like protein (Fragment)	9	0.035861572	0.030239615	0.049505995	27.88500	cell wall pectinester	cell wall pectinesterases acetyl esterase
Solyc10g080100.1.1	Actin-binding protein gelsolin	5	0.111564658	0.053734765	0.015552764	8.96341	cell organisation	cell organisation
Solyc10g080440.1.1	TBCC domain-containing protein 1	5	0.033478054	0.020274259	0.002563051	29.87031	cell organisation	cell organisation
Solyc10g081650.1.1	Carotenoid isomerase chloroplastic	3	0.013877378	0.018764973	0.015805789	72.05972	secondary metabolis	secondary metabolism isoprenoids carotenoids carotenoid isomerase
Solyc10g081920.1.1	Coatomer subunit beta-1	21	0.072272146	0.033728343	0.014538483	13.83659	cell vesicle transport	cell vesicle transport
Solyc10g083440.1.1	UDP flavonoid 3-O-glucosyltransferase (Fragment)	3	0.121910984	0.11184066	0.022230055	8.20271	misc UDP glucosyl a	misc UDP glucosyl and glucoronyl transferases
Solyc10g084050.1.1	26S protease regulatory subunit 6B homolog	43	0.28134314	0.05048912	0.024463088	3.55438	protein degradation u	protein degradation ubiquitin proteasom
Solyc10g084050.1.1	26S protease regulatory subunit 6B homolog	14	0.027208564	0.015084671	0.010948788	36.75313	protein degradation u	protein degradation ubiquitin proteasom
Solyc10g085020.1.1	Tubulin beta chain	31	0.007150603	0.002719708	5.18E-06	139.84835	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Solyc10g086760.1.1	Tubulin beta chain	30	0.007144275	0.002719729	5.67E-06	139.97222	cell organisation	cell organisation
Solyc11g006660.1.1	Eukaryotic peptide chain release factor subunit 1-3-like	7	0.02899519	0.022814049	0.015645199	34.48848	protein synthesis rele	protein synthesis release
Solyc11g007990.1.1	Malate dehydrogenase	11	0.030954622	0.018781738	0.001261374	32.30535	RNA regulation of tr	RNA regulation of transcription NAC domain transcription factor family
Solyc11g008620.1.1	Phosphoglycolate phosphatase	6	0.188300177	0.119177901	0.008533558	5.31067	misc nitrilases nitril	misc nitrilases nitrile lyases berberine bridge enzymes reticuline oxidases troponine reductases
Solyc11g010450.1.1	Phosphofructokinase family protein	6	0.12041755	0.074397324	0.000147408	8.30444	protein targeting mit	protein targeting mitochondria
Solyc11g010560.1.1	Kinesin-like protein	17	0.213754413	0.072866703	0.023597646	4.67827	cell organisation	cell organisation
Solyc11g010580.2.1	Unknown Protein	2	0.075798313	0.079056839	0.003225198	13.19291	not assigned disagree	not assigned disagreeing hits
Solyc11g010740.1.1	UDP-glucosyltransferase	2	0.009218005	0.013536395	0.038254345	108.48334	secondary metabolis	secondary metabolism flavonoids anthocyanins anthocyanidin 3-O-glucosyltransferase
Solyc11g010760.1.1	UDP-glucosyltransferase	2	0.009218005	0.013536395	0.038254345	108.48334	cell wall pectinester	cell wall pectinesterases PME
Solyc11g011420.1.1	Peptidyl-prolyl cis-trans isomerase	7	0.028052705	0.019884549	0.019266146	35.64719	cell cycle peptidylpro	cell cycle peptidylprolyl isomerase
Solyc11g011470.1.1	NADH-ubiquinone oxidoreductase subunit	20	0.004557194	0.003698731	2.21E-08	219.43327	mitochondrial electr	mitochondrial electron transport / ATP synthesis NADH-DH (type I) localisation not clear
Solyc11g011960.1.1	UTP-glucose 1 phosphate uridylyltransferase	35	0.010184121	0.015317685	0.032720944	98.19208	glycolysis cytosolic b	glycolysis cytosolic branch UGPase
Solyc11g012140.1.1	Isoleucyl-tRNA synthetase	31	0.153400111	0.036527516	0.000117666	6.51890	protein aa activation	protein aa activation isoleucine-tRNA ligase
Solyc11g012900.1.1	Small glutamine-rich tetratricopeptide repeat-containing protein A	2	0.016054042	0.03004229	0.049221941	62.28961	protein postranslatio	protein postranslational modification
Solyc11g017300.1.1	COP9 signalosome complex subunit 5b	3	0.044309726	0.054431728	0.000122012	22.56841	RNA regulation of tr	RNA regulation of transcription AtSR transcription factor family
Solyc11g018550.2.1	Thylakoid-bound ascorbate peroxidase 6	14	0.011467713	0.01013364	0.015203558	87.20135	redox ascorbate and	redox ascorbate and glutathione ascorbate
Solyc11g033270.1.1	Serine/threonine-protein kinase 3	10	0.056385225	0.028227275	0.000388321	17.73514	signalling MAP kina	signalling MAP kinases
Solyc11g040390.1.1	Aspartokinase-homoserine dehydrogenase	7	0.039520065	0.039644281	0.032813263	25.30360	amino acid metaboli	amino acid metabolism synthesis aspartate family misc homoserine aspartate kinase
Solyc11g044310.1.1	Proline iminopeptidase	3	0.04459711	0.053161238	0.0482789	22.42298	protein degradation	protein degradation
Solyc11g044530.1.1	PAP fibrillin	3	0.077822283	0.112457552	0.022772721	12.84979	protein postranslatio	protein postranslational modification
Solyc11g045120.1.1	Translation machinery associated protein	2	0.105214252	0.089418877	0.004360131	9.50442	protein synthesis init	protein synthesis initiation
Solyc11g062310.1.1	Proteasome component ECM29	8	0.048320496	0.027907685	0.004949276	20.69515	RNA regulation of tr	RNA regulation of transcription putative transcription regulator
Solyc11g069000.1.1	T-complex protein 1 subunit beta	2	0.027403068	0.017176374	0.048284609	36.49226	protein folding	protein folding
Solyc11g069050.1.1	4-coumarate-coa ligase	2	0.043953508	0.04232657	0.036502209	22.75131	secondary metabolis	secondary metabolism phenylpropanoids lignin biosynthesis 4CL
Solyc11g069090.1.1	ATP-binding cassette protein	2	0.063646158	0.057279703	0.012466638	15.71187	transport ABC trans	transport ABC transporters and multidrug resistance systems
Solyc11g069150.1.1	Proteasome subunit beta type	3	0.312953082	0.30803959	0.045545556	3.19537	protein degradation u	protein degradation ubiquitin proteasom
Solyc11g069490.1.1	Serine/threonine-protein phosphatase 6 regulatory subunit 3	5	0.19403575	0.127032911	0.043184028	5.15369	misc acid and other r	misc acid and other phosphatases
Solyc11g069720.1.1	26S protease regulatory subunit 6B homolog	14	0.027208564	0.015084671	0.010948788	36.75313	protein degradation A	protein degradation AAA type
Solyc11g069800.1.1	cytochrome P450	20	0.000919726	0.001279496	0.000430853	1087.28034	hormone metabolism	hormone metabolism jasmonate synthesis-degradation allene oxidase synthase
Solyc11g072690.1.1	2-dehydro-3-deoxyphosphooctonate aldolase	4	0.01466305	0.018168978	0.019451651	68.19864	minor CHO metabol	minor CHO metabolism others
Solyc12g005860.1.1	3-isopropylmalate dehydratase large subunit	51	0.13513413	0.029232735	0.000274728	7.40006	TCA / organic transf	TCA / organic transformation TCA aconitase
Solyc12g007170.1.1	Fatty acid oxidation complex subunit alpha	2	0.041766616	0.04427679	0.032326194	23.94257	PS lightreaction pho	PS lightreaction photosystem II PSII polypeptide subunits
Solyc12g008570.1.1	Arginyl-tRNA synthetase	6	0.081390503	0.047287099	3.84E-05	12.28645	protein aa activation	protein aa activation arginine-tRNA ligase
Solyc12g009610.1.1	TBC1 domain family member 15	2	0.133747455	0.134505316	0.008556706	7.47678	development unspec	development unspecified
Solyc12g009960.1.1	Eukaryotic translation initiation factor 4	12	0.002956235	0.003927868	3.10E-05	338.26810	protein synthesis init	protein synthesis initiation
Solyc12g010040.1.1	Leucyl aminopeptidase	18	0.031681275	0.014336804	0.001635969	31.56439	protein degradation	protein degradation
Solyc12g010380.1.1	Adenylate kinase-like protein	7	0.017388033	0.01088704	0.004486575	57.51082	nucleotide metabolis	nucleotide metabolism phosphotransfer and pyrophosphatases adenylate kinase
Solyc12g010520.1.1	Eukaryotic peptide chain release factor subunit 1-1	3	0.000677266	0.001518718	0.030382619	1476.52473	protein synthesis rele	protein synthesis release
Solyc12g014100.1.1	Homogentisate 1 2-dioxygenase	2	0.04788314	0.050033648	0.00096092	20.88418	amino acid metaboli	amino acid metabolism degradation aromatic aa tyrosine
Solyc12g014250.1.1	Phosphoenolpyruvate carboxylase 1	78	0.046487129	0.008484541	4.21E-08	21.51133	glycolysis cytosolic b	glycolysis cytosolic branch phospho-enol-pyruvate carboxylase (PEPC)
Solyc12g014400.1.1	Cell differentiation protein rcd1	3	0.151486417	0.172944674	0.014713144	6.60125	misc UDP glucosyl a	misc UDP glucosyl and glucoronyl transferases
Solyc12g014460.1.1	EH-domain-containing protein 1	2	0.244585755	0.22318312	0.005781589	4.08855	signalling calcium	signalling calcium
Solyc12g015740.1.1	Transmembrane emp24 domain-containing protein 3	2	0.25154239	0.714271896	6.22E-05	3.97547	protein targeting sec	protein targeting secretory pathway unspecified
Solyc12g017830.1.1	Sec7 guanine nucleotide exchange factor	9	0.05614098	0.036202997	0.01035914	17.81230	signalling G-proteins	signalling G-proteins
Solyc12g037980.1.1	Actin-like protein 6A	3	0.193779234	0.127907474	0.045562367	5.16051	cell organisation	cell organisation
Solyc12g043110.1.1	Heat shock protein 4	54	0.101035587	0.022859166	0.003101415	9.89750	major CHO metabol	major CHO metabolism degradation sucrose invertases neutral
Solyc12g043120.1.1	Heat shock protein 4	42	0.118830942	0.026520198	0.000670326	8.41532	stress abiotic heat	stress abiotic heat
Solyc12g095800.1.1	Chaperone protein dnaJ 10	7	0.137423469	0.091764521	0.023475323	7.27678	protein postranslatio	protein postranslational modification kinase receptor like cytoplasmatic kinase V
Solyc12g096190.1.1	Tryptophan synthase beta chain	10	0.011675101	0.009187337	8.55E-05	85.65236	amino acid metaboli	amino acid metabolism synthesis aromatic aa tryptophan tryptophan synthase
Solyc12g096650.1.1	Charged multivesicular body protein 6	2	0.197988018	0.181314713	0.04936271	5.05081	RNA regulation of tr	RNA regulation of transcription SNF7
Solyc12g098150.1.1	Voltage-gated potassium channel beta subunit	8	0.012765006	0.014746009	0.045915616	78.33917	signalling receptor k	signalling receptor kinases DUF 26
Solyc12g098420.1.1	Ubiquitin carboxyl-terminal hydrolase	4	0.10524752	0.09150063	0.041671862	9.50141	protein degradation u	protein degradation ubiquitin
Solyc12g098830.1.1	5'-nucleotidase	9	0.110707658	0.070211954	0.008735255	9.03280	not assigned no onto	not assigned no ontology
Solyc12g099110.1.1	30S ribosomal protein S1	4	0.066638794	0.049788887	0.025868071	15.00627	protein synthesis ribo	protein synthesis ribosomal protein prokaryotic unknown organellar 30S subunit S1
Solyc01g006280.2.1	Formate-tetrahydrofolate ligase	11	0.006912188	0.002707312	0.013033792	144.67199	C1-metabolism form	C1-metabolism formate-tetrahydrofolate ligase
Solyc01g007330.2.1	Ribulose bisphosphate carboxylase large chain	20	0.031778518	0.003266111	0.046458232	31.46780	PS calvin cycle rubis	PS calvin cycle rubisco large subunit
Solyc01g008310.2.1	Phenylalanyl-tRNA synthetase beta chain	5	0.033556353	0.017650671	0.001684206	29.80062	protein aa activation	protein aa activation phenylalanine-tRNA ligase
Solyc01g010750.2.1	Stress responsive protein	2	0.003964151	0.003750548	0.016735192	252.26082	protein synthesis ribo	protein synthesis ribosome biogenesis
Solyc01g011100.2.1	Phospholipid-transporting ATPase	2	0.037008919	0.047289165	0.006930281	27.02051	transport p- and v-A	transport p- and v-ATPases
Solyc01g067740.2.1	Superoxide dismutase	2	0.476371131	0.121867831	0.02390494	2.09920	redox dismutases and	redox dismutases and catalases
Solyc01g068400.2.1	Tubulin-specific chaperone A	2	9.51E-05	0.0001344	0.012355549	10515.24711	protein folding	protein folding

Solyc01g079090.2.1	Protoporphyrinogen oxidase	6	0.02121489	0.009604634	0.000617058	47.13670	tetrapyrrole synthesi	tetrapyrrole synthesis protoporphyrin IX oxidase
Solyc01g080140.2.1	Dolichol-phosphate mannosyltransferase	2	0.020601016	0.01573868	0.006910937	48.54130	not assigned unknow	not assigned unknown
Solyc01g080460.2.1	Pyruvate phosphate dikinase	27	0.033744063	0.007984194	2.02E-07	29.63484	gluconeogenesis / gl	gluconeogenesis / glyoxylate cycle pyruvate dikinase
Solyc01g095970.2.1	Dynamin 2	4	0.029221136	0.015575662	0.043725208	34.22180	protein degradation u	protein degradation ubiquitin E3 RING
Solyc01g096450.2.1	Aspartic proteinase nepenthesin-1	13	0.185656291	0.16811235	0.042847405	5.38630	protein degradation a	protein degradation aspartate protease
Solyc01g098610.2.1	Glutathione synthetase	3	0.062315889	0.028809173	0.022373406	16.04727	RNA regulation of tr	RNA regulation of transcription chromatin remodeling factors
Solyc01g098920.2.1	Mitochondrial Rho GTPase 1	10	0.012694138	0.014159097	0.001195085	78.77652	protein degradation u	protein degradation ubiquitin E3 SCF FBOX
Solyc01g098920.2.1	Mitochondrial Rho GTPase 1	2	0.041835062	0.031984249	0.046235305	23.90339	protein degradation u	protein degradation ubiquitin E3 SCF FBOX
Solyc01g099760.2.1	26S protease regulatory subunit 6A homolog	10	0.065520068	0.011776609	0.027468957	15.26250	protein degradation u	protein degradation ubiquitin proteasom
Solyc01g102410.2.1	Glutaminyl-tRNA synthetase	5	0.018293789	0.009366171	0.015559519	54.66336	protein aa activation	protein aa activation glutamate-tRNA ligase
Solyc01g105030.2.1	Chlorophyll a-b binding protein chloroplastic	5	0.147993659	0.159532113	0.001372553	6.75705	PS lightreaction pho	PS lightreaction photosystem II LHC-II
Solyc01g106080.2.1	Methylmalonate-semialdehyde dehydrogenase	3	0.039402331	0.042451191	0.028282171	25.37921	protein degradation m	protein degradation metalloprotease
Solyc01g108030.2.1	Methylcrotonoyl-CoA carboxylase beta subunit	5	0.05244142	0.021925603	0.002539836	19.06890	amino acid metaboli	amino acid metabolism degradation branched chain group leucine
Solyc01g108600.2.1	Presequence protease mitochondrial	5	0.022428113	0.025774493	0.030619378	44.58690	protein degradation m	protein degradation metalloprotease
Solyc01g109540.2.1	Coatomer subunit gamma	9	0.003182271	0.00313402	0.02869401	314.24099	cell vesicle transport	cell vesicle transport
Solyc01g109940.2.1	26S protease regulatory subunit	5	0.005539101	0.004391035	0.019803538	180.53471	minor CHO metabol	minor CHO metabolism myo-inositol inositol phosphatase
Solyc01g111060.2.1	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	2	0.12294055	0.074295815	0.028051773	8.13401	amino acid metaboli	amino acid metabolism synthesis aspartate family methionine
Solyc01g111440.2.1	Senescence-associated protein 12	2	0.160245138	0.092980007	0.028398535	6.24044	protein synthesis rib	protein synthesis ribosome biogenesis
Solyc01g111780.2.1	Importin beta-2 subunit	5	0.011971261	0.009721514	0.000399294	83.53339	protein targeting nuc	protein targeting nucleus
Solyc02g065740.2.1	Alpha-1 4-glucan-protein synthase (UDP-forming)	4	0.114934866	0.026423351	0.018037733	8.70058	signalling receptor k	signalling receptor kinases leucine rich repeat VIII type 2
Solyc02g067180.2.1	Cystathionine gamma synthase	3	0.040219904	0.029725177	0.023041769	24.86331	misc myrosinases-le	misc myrosinases-lectin-jacalin
Solyc02g078840.2.1	Secretory carrier membrane protein	2	0.005103495	0.007004395	0.021960997	195.94415	transport misc	transport misc
Solyc02g080630.2.1	Lactoylglutathione lyase	8	0.013498877	0.023543669	0.003863832	74.08024	amino acid metaboli	amino acid metabolism degradation aspartate family threonine
Solyc02g081160.2.1	Diphosphate-fructose-6-phosphate 1-phosphotransferase	10	0.015296156	0.006442548	0.002347167	65.37590	glycolysis plastid bra	glycolysis plastid branch pyrophosphate-fructose-6-P phosphotransferase
Solyc02g091490.2.1	Fructokinase 3	6	0.490496522	0.431874166	0.002043373	2.03875	major CHO metabol	major CHO metabolism degradation sucrose fructokinase
Solyc02g092430.1.1	Ribosomal protein L26	2	0.109885659	0.048460789	0.015866585	9.10037	protein synthesis rib	protein synthesis ribosomal protein eukaryotic 60S subunit L26
Solyc03g005230.2.1	Menaquinone biosynthesis methyltransferase ubiE	3	0.185014901	0.071027665	5.24E-05	5.40497	secondary metabolis	secondary metabolism isoprenoids tocopherol biosynthesis MPBQ/MSBQ methyltransferase
Solyc03g006870.2.1	Phosphoglucomutase	2	0.024278774	0.015137918	0.0226815	41.18824	glycolysis cytosolic b	glycolysis cytosolic branch phosphoglucomutase (PGM)
Solyc03g007000.2.1	Peptidase M48 Ste24p	2	0.062309448	0.052874683	0.020485817	16.04893	protein degradation	protein degradation
Solyc03g025720.2.1	Long-chain-fatty-acid--CoA ligase	6	0.086852964	0.062315815	0.018871325	11.51371	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Solyc03g052980.2.1	ATP dependent RNA helicase	3	0.053066576	0.013183931	0.015377455	18.84425	RNA processing RN	RNA processing RNA helicase
Solyc03g082500.2.1	Calcium dependent protein kinase-like protein	2	0.010392147	0.007733134	0.041575289	96.22651	secondary metabolis	secondary metabolism isoprenoids terpenoids
Solyc03g093680.2.1	Mago nashi-like protein 2	2	0.000105322	0.000140832	0.037528882	9494.69247	tetrapyrrole synthesi	tetrapyrrole synthesis GSA
Solyc03g095850.1.1	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	3	0.051003805	0.054693658	0.000140642	19.60638	metal handling bindi	metal handling binding chelation and storage
Solyc03g096000.2.1	Clathrin heavy chain	43	0.019587469	0.006864217	0.018359769	51.05305	cell vesicle transport	cell vesicle transport
Solyc03g098230.2.1	Pyridoxal phosphate-dependent enzyme D-cysteine desulfhydrase family	4	0.043790109	0.026347244	0.007975914	22.83621	hormone metabolism	hormone metabolism ethylene synthesis-degradation
Solyc03g112350.2.1	ATP dependent RNA helicase	2	0.072519045	0.004156733	0.007293637	13.78948	protein synthesis rib	protein synthesis ribosome biogenesis
Solyc03g114640.2.1	Signal peptide peptidase SppA type	3	0.021387411	0.01423857	0.002694094	46.75648	protein degradation	protein degradation
Solyc03g114860.2.1	Alpha-1 4-glucan-protein synthase	10	0.109741152	0.023061101	0.029471646	9.11235	signalling receptor k	signalling receptor kinases leucine rich repeat VIII type 2
Solyc03g115230.2.1	ClpB chaperone	5	0.005848683	0.001369145	0.005166373	170.97866	protein degradation s	protein degradation serine protease
Solyc03g120990.2.1	Malic enzyme	7	0.00820186	0.003551418	0.033046055	121.92356	TCA / organic transf	TCA / organic transformation other organic acid transformations malic
Solyc03g122310.2.1	Aldehyde dehydrogenase 7b	6	0.00435731	0.00312153	0.000373313	229.49939	stress abiotic heat	stress abiotic heat
Solyc03g123610.2.1	Alanine aminotransferase	7	0.019650867	0.012257797	0.03510201	50.88834	amino acid metaboli	amino acid metabolism synthesis central amino acid metabolism alanine alanine aminotransferase
Solyc04g005340.2.1	Alpha-1 4-glucan protein synthase	13	0.055445282	0.013020565	0.011573063	18.03580	signalling receptor k	signalling receptor kinases leucine rich repeat VIII type 2
Solyc04g007120.2.1	UV excision repair protein RAD23	3	0.080136854	0.050621736	0.024104292	12.47865	protein degradation u	protein degradation ubiquitin ubiquitin
Solyc04g007260.2.1	Thioesterase superfamily	3	0.000574178	0.000813863	0.000134231	1741.62019	PS lightreaction pho	PS lightreaction photosystem II PSII polypeptide subunits
Solyc04g008520.2.1	Outer envelope protein	3	0.126437719	0.078114443	0.040568326	7.90903	not assigned unknow	not assigned unknown
Solyc04g010080.2.1	ATP-binding domain-containing protein 4	2	0.080273605	0.081203957	0.041787323	12.45739	RNA processing ribo	RNA processing ribonucleases
Solyc04g015750.2.1	Magnesium chelatase H subunit	5	0.023513844	0.011949294	0.001907319	42.52814	tetrapyrrole synthesi	tetrapyrrole synthesis magnesium chelatase
Solyc04g047770.2.1	VHS domain-containing protein At3g16270	3	0.042907193	0.015445204	0.015577191	23.30612	protein synthesis rib	protein synthesis ribosome biogenesis BRIX
Solyc04g071340.2.1	Fructose-1 6-bisphosphatase class 1	2	0.017729997	0.003127557	0.031944742	56.40159	stress biotic receptor	stress biotic receptors
Solyc04g080630.2.1	50S ribosomal protein L31	2	0.001367369	0.000929259	7.66E-05	731.33148	protein synthesis rib	protein synthesis ribosomal protein prokaryotic chloroplast 50S subunit L31
Solyc04g081490.2.1	Tubulin beta-1 chain	7	0.012899212	0.007407106	0.04286608	77.52412	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Solyc04g082670.2.1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	4	0.010038332	0.016365146	0.044523241	99.61814	lipid metabolism FA	lipid metabolism FA desaturation omega 6 desaturase
Solyc05g009020.2.1	Mitochondrial carrier like protein	2	0.057644712	0.021543431	0.026172861	17.34765	transport metabolite	transport metabolite transporters at the mitochondrial membrane
Solyc05g010670.2.1	Chaperone protein htpG	26	0.008802506	0.002498527	3.08E-05	113.60401	stress abiotic heat	stress abiotic heat
Solyc05g010670.2.1	Chaperone protein htpG	24	0.054255068	0.023282659	0.036099675	18.43146	stress abiotic heat	stress abiotic heat
Solyc05g013030.1.1	26S proteasome regulatory subunit	8	0.025527312	0.015577587	0.036826764	39.17373	protein degradation u	protein degradation ubiquitin proteasom
Solyc05g025740.2.1	SH3 domain-containing protein	4	0.00998719	0.007972808	0.033419127	100.12826	not assigned no onto	not assigned no ontology
Solyc05g026050.2.1	Charged multivesicular body protein 4b	2	0.313816069	0.131940276	0.022479466	3.18658	RNA regulation of tr	RNA regulation of transcription SNF7
Solyc05g050120.2.1	Malic enzyme	23	0.009444257	0.001040054	1.16E-05	105.88445	TCA / organic transf	TCA / organic transformation other organic acid transformations malic
Solyc05g050600.2.1	Dynamin 2	7	0.039608621	0.009630965	0.005104221	25.24703	signalling G-protein	signalling G-proteins
Solyc05g050630.2.1	Protein TIF31 homolog	2	0.044245099	0.050917536	0.006440892	22.60137	protein degradation c	protein degradation cysteine protease
Solyc05g050810.2.1	Chaperone dnaJ 3	2	0.09922257	0.092706706	0.028135304	10.07835	stress abiotic heat	stress abiotic heat
Solyc05g052240.2.1	Chalcone--flavonone isomerase	2	0.065224544	0.029852773	0.002774051	15.33165	secondary metabolis	secondary metabolism flavonoids chalcones
Solyc05g052510.2.1	Clathrin heavy chain	54	0.007336849	0.002946085	0.004081636	136.29829	cell vesicle transport	cell vesicle transport
Solyc05g054640.2.1	2-oxoglutarate dehydrogenase E1 component	14	0.030879136	0.015524603	0.04434984	32.38433	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation acetyl CoA transacylase
Solyc05g055160.2.1	DNAJ chaperone	5	0.002625099	0.003305943	0.006066401	380.93801	stress abiotic heat	stress abiotic heat
Solyc05g055210.1.1	Eukaryotic peptide chain release factor subunit 1-3-like	5	0.041029018	0.019908774	0.002316107	24.37299	misc cytochrome P4	misc cytochrome P450
Solyc05g055770.2.1	Basic leucine zipper and W2 domain-containing protein 2	2	0.087754939	0.044294055	0.016457432	11.39537	protein synthesis init	protein synthesis initiation
Solyc06g006100.2.1	Anthranilate synthase component I family protein expressed	3	0.016348557	0.014517892	0.017168498	61.16748	misc calcineurin-like	misc calcineurin-like phosphoesterase family protein
Solyc06g007540.2.1	Cytochrome b-c1 complex subunit 8	3	0.000658857	0.000339812	3.24E-05	1517.78003	mitochondrial electr	mitochondrial electron transport / ATP synthesis cytochrome c reductase
Solyc06g011350.2.1	Aquaporin 2	2	0.228859801	0.125005715	0.041952933	4.36949	transport major intri	transport major intrinsic proteins PIP
Solyc06g011400.2.1	ATP-dependent chaperone ClpB	9	0.012752142	0.002829665	0.000265851	78.41820	protein degradation s	protein degradation serine protease
Solyc06g035970.2.1	Tubulin beta chain	8	0.024589292	0.009506443	0.028070068	40.66811	cell organisation	cell organisation
Solyc06g048890.2.1	Protein kinase	3	0.042085293	0.025539194	0.04253244	23.76127	protein postranslatio	protein postranslational modification
Solyc06g051310.2.1	Clathrin heavy chain	48	0.007559904	0.003407622	0.002953741	132.27681	cell vesicle transport	cell vesicle transport
Solyc06g051620.2.1	1-phosphatidylinositol-4 5-bisphosphate phosphodiesterase (Phosphoinositide-specific phospholipase c)	2	0.35463751	0.027283637	0.005341046	2.81978	signalling phosphino	signalling phosphinositides phosphoinositide phospholipase C
Solyc06g059740.2.1	Alcohol dehydrogenase 2	20	0.012897515	0.000979525	4.95E-10	77.53432	misc alcohol dehydro	misc alcohol dehydrogenases cinnamyl alcohol dehydrogenase
Solyc06g061170.2.1	Solute carrier family 25 (Mitochondrial carrier ornithine transporter) member 15	2	0.15760235	0.091897248	0.035192646	6.34508	transport metabolite	transport metabolite transporters at the mitochondrial membrane
Solyc06g062350.2.1	Holliday junction ATP-dependent DNA helicase ruvB	3	0.01146473	0.007403737	0.000207065	87.22403	development unspec	development unspecified
Solyc06g062500.2.1	60S ribosomal protein L28	2	0.001141366	0.00048092	0.018188793	876.14315	protein synthesis rib	protein synthesis ribosomal protein eukaryotic 60S subunit L28
Solyc06g063290.2.1	Pyridoxamine 5'-phosphate oxidase-related FMN-binding	3	0.121502479	0.069215731	0.003247532	8.23028	protein postranslatio	protein postranslational modification
Solyc06g064810.2.1	Chromosome 06 contig 1 DNA sequence	2	0.001016696	0.001657244	0.000174156	983.57818	protein synthesis rib	protein synthesis ribosome biogenesis
Solyc06g066060.2.1	ATP-dependent RNA helicase	4	0.106482553	0.060817236	0.008591748	9.39121	DNA synthesis/chro	DNA synthesis/chromatin structure
Solyc06g075340.2.1	Carbamoyl-phosphate synthase large chain	10	0.022064758	0.011472332	0.011231681	45.32114	amino acid metaboli	amino acid metabolism synthesis glutamate family arginine carbamoyl-phosphate synthase
Solyc06g076360.2.1	Outer envelope membrane protein	10	0.08208317	0.011236966	0.000868036	12.18277	protein targeting chl	protein targeting chloroplast
Solyc06g076640.2.1	Tubulin beta chain	6	0.023403721	0.009710972	0.04662023	42.72825	secondary metabolis	secondary metabolism phenylpropanoids
Solyc06g082090.2.1	Methionine aminopeptidase	3	0.041721709	0.00588924	0.048489015	23.96834	protein degradation m	protein degradation metalloprotease
Solyc06g082680.2.1	Cytochrome b-c1 complex subunit 8	3	0.000658857	0.000339812	3.24E-05	1517.78003	mitochondrial electr	mitochondrial electron transport / ATP synthesis cytochrome c reductase
Solyc06g083110.1.1	Conserved hypothetical membrane protein	4	0.044759374	0.00700751	0.043716303	22.34169	development unspec	development unspecified
Solyc07g005810.2.1	Eukaryotic translation initiation factor 4	5	0.036822635	0.020599852	0.001607328	27.15721	protein synthesis init	protein synthesis initiation
Solyc07g006030.2.1	Protein TIF31 homolog	4	0.047655711	0.042986971	0.032877248	20.98384	protein degradation c	protein degradation cysteine protease
Solyc07g008610.1.1	ATP-binding cassette protein	5	0.012146183	0.005513783	0.005415589	82.33039	transport ABC transp	transport ABC transporters and multidrug resistance systems
Solyc07g009380.2.1	Xyloglucan endotransglucosylase/hydrolase 2	3	0.342305191	0.521842876	0.000339903	2.92137	cell wall modificatio	cell wall modification
Solyc07g039330.2.1	Histone-binding protein RBBP7	3	0.019540473	0.005651943	0.00993547	51.17583	RNA regulation of tr	RNA regulation of transcription nucleosome/chromatin assembly factor group
Solyc07g053150.2.1	Protein cyaY	2	0.003460024	0.003254824	0.00022705	289.01534	development unspec	development unspecified
Solyc07g053280.2.1	Ketol-acid reductoisomerase	17	0.00165661	0.00107947	0.001352287	603.64238	amino acid metaboli	amino acid metabolism synthesis branched chain group common ketol-acid reductoisomerase
Solyc07g054210.2.1	Protochlorophyllide reductase like protein	3	0.055559235	0.013355863	0.016696766	17.99881	tetrapyrrole synthesi	tetrapyrrole synthesis protochlorophyllide reductase
Solyc07g064600.2.1	Endoribonuclease L-PSP family protein	4	0.01759895	0.000670632	0.00362866	56.82157	RNA processing ribo	RNA processing ribonucleases
Solyc08g014000.2.1	Lipoxygenase	46	0.005432541	0.001643481	0.002089031	184.07592	hormone metabolism	hormone metabolism jasmonate synthesis-degradation lipoxygenase
Solyc08g022000.1.1	26S protease regulatory subunit 6A	2	0.119307726	0.051973964	0.012820033	8.38169	protein degradation u	protein degradation ubiquitin proteasom
Solyc08g029190.2.1	At1g62390-like protein (Fragment)	2	0.109503168	0.141316111	0.040408311	9.13216	RNA processing	RNA processing
Solyc08g061000.2.1	ATP-dependent RNA helicase	4	0.106482553	0.060817236	0.008591748	9.39121	protein synthesis init	protein synthesis initiation
Solyc08g065900.2.1	Charged multivesicular body protein 4b	3	0.305018805	0.126159193	0.047053702	3.27849	RNA regulation of tr	RNA regulation of transcription SNF7
Solyc08g075390.2.1	Isopentenyl-diphosphate delta-isomerase family protein	3	0.030312846	0.016302017	0.020782935	32.98931	nucleotide metabolis	nucleotide metabolism salvage NUDIX hydrolases
Solyc08g077300.2.1	Adenylate kinase	7	0.028024406	0.018065893	0.038184554	35.68318	nucleotide metabolis	nucleotide metabolism phosphotransfer and pyrophosphatases uridylate kinase
Solyc08g079180.2.1	Elongation factor G	4	0.141266284	0.043651855	0.021996207	7.07883	protein synthesis elo	protein synthesis elongation
Solyc08g079280.2.1	cytochrome P450	2	0.14445652	0.012641744	0.015733861	6.92250	secondary metabolis	secondary metabolism flavonoids dihydroflavonols
Solyc09g008920.2.1	Geranylgeranyl pyrophosphate synthase	3	0.040838476	0.03012212	0.011579482	24.48671	RNA regulation of tr	RNA regulation of transcription unclassified
Solyc09g011080.2.1	Ribulose-1 5-bisphosphate carboxylase/oxygenase activase 1	6	0.48351125	0.618429296	0.002742051	2.06820	PS calvin cycle rubis	PS calvin cycle rubisco interacting
Solyc09g059040.2.1	Alcohol dehydrogenase zinc-containing	10	0.03546722	0.020402963	0.049675734	28.19505	misc oxidases - copp	misc oxidases - copper flavone etc
Solyc09g082970.2.1	Pyruvate kinase	3	0.14789849	0.090946834	0.025861855	6.76139	glycolysis plastid bra	glycolysis plastid branch pyruvate kinase (PK)
Solyc09g083420.2.1	CWF19-like 2	2	0.239881756	0.072283594	0.018052673	4.16872	secondary metabolis	secondary metabolism phenylpropanoids
Solyc09g090700.1.1	Succinate semialdehyde dehydrogenase	5	0.030684	0.01932135	0.040042632	32.59028	TCA / organic transf	TCA / organic transformation other organic acid transformations misc
Solyc09g092690.2.1	Peptidyl-prolyl cis-trans isomerase	7	0.025240098	0.011417144	0.001330836	39.61950	cell cycle peptidylpro	cell cycle peptidylprolyl isomerase
Solyc09g098150.2.1	Metacaspase 7	2	0.301646738	0.018165611	0.000555873	3.31514	protein degradation	protein degradation
Solyc10g054040.1.1	26S protease regulatory subunit	2	0.05343778	0.023471836	0.026049984	18.71335	minor CHO metabol	minor CHO metabolism myo-inositol inositol phosphatase
Solyc10g074500.1.1	Isocitrate dehydrogenase	11	0.014316766	0.004606433	0.002395588	69.84818	TCA / organic transf	TCA / organic transformation TCA IDH
Solyc10g076510.1.1	Pyruvate decarboxylase	16	0.010968528	0.005377119	0.005761369	91.16994	fermentation PDC	fermentation PDC
Solyc10g080940.1.1	Tubulin beta chain	7	0.024443209	0.009509646	0.032117463	40.91116	lipid metabolism FA	lipid metabolism FA synthesis and FA elongation acyl CoA ligase
Solyc10g083720.1.1	Pyruvate kinase	18	0.004297477	0.002408628	0.00038933	232.69467	glycolysis cytosolic b	glycolysis cytosolic branch pyruvate kinase (PK)
Solyc10g084050.1.1	26S protease regulatory subunit 6B homolog	3	0.387897029	0.488643807	0.000176298	2.57800	protein degradation u	protein degradation ubiquitin proteasom
Solyc10g085020.1.1	Tubulin beta chain	8	0.013240873	0.00738479	0.032291916	75.52372	secondary metabolis	secondary metabolism phenylpropanoids
Solyc11g006460.1.1	DNAJ chaperone	6	0.002546251	0.00333645	0.013067612	392.73426	stress abiotic heat	stress abiotic heat
Solyc11g006660.1.1	Eukaryotic peptide chain release factor subunit 1-3-like	5	0.041029018	0.019908774	0.002316107	24.37299	misc cytochrome P4	misc cytochrome P450
Solyc11g008340.1.1	Exocyst complex component 4	8	0.021368364	0.017898306	0.018884233	46.79815	cell vesicle transport	cell vesicle transport
Solyc11g012940.1.1	Glutaredoxin 2	2	0.000583172	0.000927369	2.17E-05	1714.75997	not assigned unknow	not assigned unknown
Solyc11g020300.1.1	Translocon Tic40	5	0.117324129	0.060344737	0.017489201	8.52340	RNA regulation of tr	RNA regulation of transcription unclassified
Solyc11g033280.1.1	ATP-dependent RNA helicase FAL1	2	0.080287238	0.020304085	0.006061973	12.45528	protein synthesis init	protein synthesis initiation
Solyc11g051160.1.1	Phosphatidylinositol transfer protein SFH5	30	0.002954081	0.001709708	5.52E-05	338.51475	protein targeting sec	protein targeting secretory pathway unspecified
Solyc11g051160.1.1	Phosphatidylinositol transfer protein SFH5	15	0.005556475	0.003374435	0.045605249	179.97021	protein targeting sec	protein targeting secretory pathway unspecified
Solyc11g064890.1.1	Receptor-like kinase	3	0.166365014	0.075504792	0.033270073	6.01088	protein postranslatio	protein postranslational modification kinase receptor like cytoplasmatic kinase VII
Solyc11g069720.1.1	26S protease regulatory subunit 6B homolog	3	0.387897029	0.488643807	0.000176298	2.57800	protein degradation u	protein degradation ubiquitin proteasom
Solyc11g072640.1.1	Mitochondrial trans-2-enoyl-CoA reductase	7	0.057760041	0.015122036	0.020049551	17.31301	lipid metabolism exo	lipid metabolism exotics (steroids squalene etc) trans-2-enoyl-CoA reductase (NADPH)
Solyc12g006450.1.1	Aminotransferase-like protein	3	0.067087395	0.03939139	0.027818254	14.90593	stress biotic signalli	stress biotic signalling
Solyc12g007170.1.1	Fatty acid oxidation complex subunit alpha	3	0.004939661	0.004233657	0.016654993	202.44304	PS lightreaction pho	PS lightreaction photosystem II PSII polypeptide subunits
Solyc12g008570.1.1	Arginyl-tRNA synthetase	2	0.01783157	0.023066982	0.017586397	56.08031	protein aa activation	protein aa activation arginine-tRNA ligase
Solyc12g015860.1.1	Farnesyl pyrophosphate synthase	2	0.01241696	0.015262751	0.026236219	80.53501	secondary metabolis	secondary metabolism isoprenoids mevalonate pathway farnesyl pyrophosphate synthetase
Solyc12g015880.1.1	Heat shock protein 90	31	0.017487422	0.004159275	0.000177387	57.18396	stress abiotic heat	stress abiotic heat
Solyc12g043110.1.1	Heat shock protein 4	20	0.012423924	0.003656575	0.00932774	80.48987	stress abiotic heat	stress abiotic heat
Solyc12g089310.1.1	Tubulin beta-1 chain	7	0.02421335	0.009525279	0.043018396	41.29953	cell organisation	cell organisation
Solyc12g094620.1.1	Catalase	21	0.011762126	0.002835677	1.38E-06	85.01864	redox dismutases an	redox dismutases and catalases
Solyc12g098150.1.1	Voltage-gated potassium channel beta subunit	6	0.048184302	0.001299113	0.042165138	20.75365	hormone metabolism	hormone metabolism auxin induced-regulated-responsive-activated
Solyc12g099110.1.1	30S ribosomal protein S1	2	0.074317699	0.053869853	0.022526705	13.45574	protein synthesis rib	protein synthesis ribosomal protein prokaryotic unknown organellar 30S subunit S1
Solyc12g100120.1.1	Acetyl-CoA carboxylase-like protein	3	0.408170886	0.43753434	0.000176577	2.44995	protein postranslatio	protein postranslational modification kinase receptor like cytoplasmatic kinase V

Table 5.8. Proteins identified only in wild species but not in tomato.

Label-free quantitation was employed by matching retention times of the peaks and measuring area under the matched peaks using Sieve 2.1 software (Thermo Scientific) to identify the differentially expressed proteins in SH-SL, SP-SL, SG-SL pairs. Stringent selection criteria were imposed to identify these proteins (p value≤0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR=1%). Some of the proteins were found only in the wild species but not in SL and are given here. Even single peptide matches of these proteins could not be detected in SL.

Proteins identified only in SP

PROTEIN ID	DESCRIPTION	PEPTIDES	PValue
Sopim11g007300	ABC transporter G famil	2	2.40259E-09
Sopim03g059310	WD 40 repeat family pro	3	6.3205E-13
Sopim04g081340	Receptor expression_enh	2	2.40259E-09
Sopim08g045730	Unknown Protein	2	2.40259E-09
Sopim06g082420	Peroxidase 3	3	9.9E-20
Sopim03g111720	Peptide methionine sulfo	2	2.40259E-09
Sopim11g066430	Histone H2B	2	2.40259E-09

Proteins identified only in SG

PROTEIN ID	DESCRIPTION	PEPTIDES	PValue
Sopim09g082340	genomic reference:SL2.40ch09 gene region:63490155 63493319 transcript region:SL2.40ch09:63490155..63493319 go terms:GO:0045735 functional description: Vicilin like protein (Fragment) (AHRD V1 Q9SEW4 9ROSI); contains Interpro dor	7	9.9E-20
Sopim08g007620	evidence code:10F0H1E1IEG genomic reference:SL2.40ch08 gene region:2152861 2156967 transcript region:SL2.40ch08:2152861..2156967 go terms:GO:0004252 functional description: Subtilisin like protease (AHRD V1 Q9LWA3 SOLLC); c	6	9.9E-20
Sopim09g090150	genomic reference:SL2.40ch09 gene region:65039694 65042890 transcript region:SL2.40ch09:65039694..65042890 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	2	2.40259E-09
Sopim08g074940	genomic reference:SL2.40ch08 gene region:56237010..56238569 transcript region:SL2.40ch08:56237010..56238569 go terms:GO:0006508 functional description: Aspartic proteinase nepenthesin_2 (AHRD V1 B6SMJ5_MAIZE); contains Interpro c	2	7.77489E-13
Sopim09g025210	genomic reference:SL2.40ch09 gene region:19251698..19253627 transcript region:SL2.40ch09:19251698..19253627 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	2	2.40259E-09
Sopim09g072560	genomic reference:SL2.40ch09 gene region:60593208..60595291 transcript region:SL2.40ch09:60593208..60595291 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	6	9.9E-20
Sopim08g007620	evidence code:10F0H1E1IEG genomic reference:SL2.40ch08 gene region:2152861 2156967 transcript region:SL2.40ch08:2152861..2156967 go terms:GO:0004252 functional description: Subtilisin like protease (AHRD V1 Q9LWA3 SOLLC); c	5	9.9E-20
Sopim09g090150	genomic reference:SL2.40ch09 gene region:65039694 65042890 transcript region:SL2.40ch09:65039694..65042890 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	4	2.22045E-16
Sopim06g017860	evidence code:10F0H1E0IEG genomic reference:SL2.40ch06 gene region:10756897 10760347 transcript region:SL2.40ch06:10756897..10760347 go terms:GO:0042802 GO:0004185 functional description: Serine carboxypeptidase (AHRD V1 Q	3	6.3205E-13
Sopim11g066250	evidence code:10F0H1E0IEG genomic reference:SL2.40ch11 gene region:49045907 49049862 transcript region:SL2.40ch11:49045907..49049862 go terms:GO:0042802 GO:0004185 functional description: Serine carboxypeptidase (AHRD V1 Q	3	6.3205E-13
Sopim09g025210	genomic reference:SL2.40ch09 gene region:19251698..19253627 transcript region:SL2.40ch09:19251698..19253627 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	3	6.3205E-13
Sopim03g005580	genomic reference:SL2.40ch03 gene region:421297 424318 transcript region:SL2.40ch03:421297..424318 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IPR014710	2	2.40259E-09
Sopim08g007660	genomic reference:SL2.40ch08 gene region:2167565 2168849 transcript region:SL2.40ch08:2167565..2168849 go terms:GO:0006508 functional description: Subtilisin like serine protease (AHRD V1 C3VDI0_CARPA); contains Interpro domain(s)	2	2.40259E-09
Sopim08g074940	genomic reference:SL2.40ch08 gene region:56237010..56238569 transcript region:SL2.40ch08:56237010..56238569 go terms:GO:0006508 functional description: Aspartic proteinase nepenthesin_2 (AHRD V1 B6SMJ5_MAIZE); contains Interpro c	2	2.40259E-09
Sopim09g072560	genomic reference:SL2.40ch09 gene region:60593208 60595291 transcript region:SL2.40ch09:60593208..60595291 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	10	9.9E-20
Sopim09g082340	genomic reference:SL2.40ch09 gene region:63490155 63493319 transcript region:SL2.40ch09:63490155..63493319 go terms:GO:0045735 functional description: Vicilin like protein (Fragment) (AHRD V1 Q9SEW4 9ROSI); contains Interpro dor	8	9.9E-20
Sopim09g025210	genomic reference:SL2.40ch09 gene region:19251698 19253627 transcript region:SL2.40ch09:19251698..19253627 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	5	9.9E-20
Sopim09g008770	genomic reference:SL2.40ch09 gene region:2194030 2196459 transcript region:SL2.40ch09:2194030..2196459 functional description: Group 3 late embryogenesis abundant protein (AHRD V1 Q2N1E0 PHAVU); contains Interpro domain(s) IPR00	5	9.9E-20
Sopim09g090150	genomic reference:SL2.40ch09 gene region:65039694 65042890 transcript region:SL2.40ch09:65039694..65042890 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	5	9.9E-20
Sopim06g005940	genomic reference:SL2.40ch06 gene region:921114 925482 transcript region:SL2.40ch06:921114..925482 go terms:GO:0003756 GO:0005515 functional description: Protein disulfide isomerase (AHRD V1 Q6IV17_IPOBA); contains Interpro dom	4	2.22045E-16
Sopim11g066250	evidence code:10F0H1E0IEG genomic reference:SL2.40ch11 gene region:49045907 49049862 transcript region:SL2.40ch11:49045907..49049862 go terms:GO:0042802 GO:0004185 functional description: Serine carboxypeptidase (AHRD V1 Q	4	2.22045E-16
Sopim05g051260	genomic reference:SL2.40ch05 gene region:60688299..60691358 transcript region:SL2.40ch05:60688299..60691358 go terms:GO:0005515 functional description: Endo_1 4 beta_xylanase (AHRD V1 B6SW51_MAIZE); contains Interpro domain(s	3	6.3205E-13
Sopim08g065780	evidence code:10F0H1E1IEG genomic reference:SL2.40ch08 gene region:51300723 51303058 transcript region:SL2.40ch08:51300723..51303058 go terms:GO:0004197 functional description: Vacuolar processing enzyme (AHRD V1 Q9SMD0 S	3	6.3205E-13
Sopim08g074620	evidence code:10F1H1E1IEG genomic reference:SL2.40ch08 gene region:55911248 55913011 transcript region:SL2.40ch08:55911248..55913011 go terms:GO:0008152 GO:0055114 functional description: Polyphenol oxidase (AHRD V1 Q4142	3	6.3205E-13
Sopim06g053510	genomic reference:SL2.40ch06 gene region:32795986 32800783 transcript region:SL2.40ch06:32795986..32800783 go terms:GO:0004766 functional description: Spermidine synthase (AHRD V1 A7DY57 COCOF); contains Interpro domain(s) IP	2	2.40259E-09
Sopim06g017860	evidence code:10F0H1E0IEG genomic reference:SL2.40ch06 gene region:10756897 10760347 transcript region:SL2.40ch06:10756897..10760347 go terms:GO:0042802 GO:0004185 functional description: Serine carboxypeptidase (AHRD V1 Q	2	2.40259E-09
Sopim03g111730	genomic reference:SL2.40ch03 gene region:56432592 56434422 transcript region:SL2.40ch03:56432592..56434422 go terms:GO:0004197 functional description: Cathepsin B like cysteine proteinase (AHRD V1 CYSP SCHMA); contains Interpro	2	2.40259E-09
Sopim10g009410	evidence code:10F0H1E1IEG genomic reference:SL2.40ch10 gene region:3472716 3474092 transcript region:SL2.40ch10:3472716..3474092 go terms:GO:0006508 functional description: Aspartic proteinase nepenthesin I (AHRD V1 A9ZMF9_NI	2	2.40259E-09
Sopim09g065470	genomic reference:SL2.40ch09 gene region:59169265 59174553 transcript region:SL2.40ch09:59169265..59174553 go terms:GO:0045735 GO:0008152 functional description: Vicilin (Fragment) (AHRD V1 B4X640_PISVE); contains Interpro do	2	2.40259E-09
Sopim08g074630	evidence code:10F1H1E1IEG genomic reference:SL2.40ch08 gene region:55921673 55923436 transcript region:SL2.40ch08:55921673..55923436 go terms:GO:0008152 GO:0055114 functional description: Polyphenol oxidase (AHRD V1 Q4142	2	2.40259E-09
Sopim08g074680	genomic reference:SL2.40ch08 gene region:55995940 56008590 transcript region:SL2.40ch08:55995940..56008590 go terms:GO:0008152 functional description: Polyphenol oxidase (AHRD V1 Q41428 SOLTU); contains Interpro domain(s) IPR0	2	2.40259E-09
Sopim05g050120	genomic reference:SL2.40ch05 gene region:59250938 59255250 transcript region:SL2.40ch05:59250938..59255250 go terms:GO:0004473 functional description: Malic enzyme (AHRD V1 O04936 SOLLC); contains Interpro domain(s) IPR01230	2	2.40259E-09
Sopim12g008430	evidence code:10F0H1E0IEG genomic reference:SL2.40ch12 gene region:1860772 1866562 transcript region:SL2.40ch12:1860772..1866562 go terms:GO:0006108 GO:0008152 GO:0051287 GO:0016616 GO:0055114 functional description: Malic	2	2.40259E-09
Sopim01g007940	genomic reference:SL2.40ch01 gene region:2123045 2128114 transcript region:SL2.40ch01:2123045..2128114 go terms:GO:0004021 functional description: Alanine aminotransferase 2 (AHRD V1 A8IKE5 SOYBN); contains Interpro domain(s) II	2	2.40259E-09
Sopim09g072560	genomic reference:SL2.40ch09 gene region:60593208 60595291 transcript region:SL2.40ch09:60593208..60595291 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	30	9.9E-20
Sopim09g025210	genomic reference:SL2.40ch09 gene region:19251698 19253627 transcript region:SL2.40ch09:19251698..19253627 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	26	9.9E-20
Sopim09g090150	genomic reference:SL2.40ch09 gene region:65039694 65042890 transcript region:SL2.40ch09:65039694..65042890 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	10	9.9E-20
Sopim05g051260	genomic reference:SL2.40ch05 gene region:60688299..60691358 transcript region:SL2.40ch05:60688299..60691358 go terms:GO:0005515 functional description: Endo_1 4 beta_xylanase (AHRD V1 B6SW51_MAIZE); contains Interpro domain(s	6	9.9E-20
Sopim01g005820	genomic reference:SL2.40ch01 gene region:537499 541732 transcript region:SL2.40ch01:537499..541732 go terms:GO:0003676 GO:0000166 functional description: Splicing factor arginine/serine rich 4 (AHRD V1 B6U7F9 MAIZE); contains Int	4	2.22045E-16
Sopim09g098120	genomic reference:SL2.40ch09 gene region:67297118 67298585 transcript region:SL2.40ch09:67297118..67298585 functional description: DUF1264 domain protein (AHRD V1 B8NLT6 ASPFN); contains Interpro domain(s) IPR010686 Protein c	4	2.22045E-16
Sopim03g096040	genomic reference:SL2.40ch03 gene region:51304230 51305908 transcript region:SL2.40ch03:51304230..51305908 go terms:GO:0008379 GO:0004672 functional description: Malic enzyme (AHRD V1 O04936 SOLLC); contains Interpro domain(s) IPR01230	3	6.3205E-13
Sopim04g015340	genomic reference:SL2.40ch04 gene region:5526389 5531684 transcript region:SL2.40ch04:5526389..5531684 go terms:GO:0042802 GO:0004185 functional description: Serine carboxypeptidase K10B2.2 (AHRD V1 B6TM29 MAIZE); contains	3	6.3205E-13
Sopim03g111830	genomic reference:SL2.40ch03 gene region:56497562 56502317 transcript region:SL2.40ch03:56497562..56502317 go terms:GO:0004719 GO:0042802 functional description:_Protein_L_isoaspartate O_methyltransferase (AHRD V1 B9I319_POPT	3	6.3205E-13
Sopim09g082340	genomic reference:SL2.40ch09 gene region:63490155 63493319 transcript region:SL2.40ch09:63490155..63493319 go terms:GO:0045735 functional description:_Vicilin_like protein (Fragment) (AHRD V1 Q9SEW4_9ROSI); contains Interpro dor	3	6.3205E-13
Sopim02g032940	genomic reference:SL2.40ch02 gene region:20185974 20192184 transcript region:SL2.40ch02:20185974..20192184 go terms:GO:0004190 functional description:_Aspartic proteinase (AHRD V1 Q8L6A8_THECC); contains Interpro domain(s) IPR	3	9.9E-20
Sopim12g014310	evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch12 gene_region:5129574_5133435 transcript_region:SL2.40ch12:5129574..5133435_ functional_description:_Pathogenesis_related protein_like protein (AHRD V1 ____ Q8L9B0_ARATH)_	2	2.40259E-09
Sopim08g006510	genomic reference:SL2.40ch08 gene region:1108336 1124190 transcript region:SL2.40ch08:1108336..1124190 go terms:GO:0044237 GO:0008152 functional description: NAD dependent epimerase/dehydratase family protein (AHRD V1 B6TVJ7	2	2.40259E-09
Sopim02g081170	genomic reference:SL2.40ch02 gene region:39810752 39812645 transcript region:SL2.40ch02:39810752..39812645 go terms:GO:0005515 functional description: Plastid lipid associated protein chloroplastic (AHRD V1 PAP CITUN); contains Ir	2	2.40259E-09
Sopim01g098850	genomic reference:SL2.40ch01 gene region:81004479 81006268 transcript region:SL2.40ch01:81004479..81006268 go terms:GO:0008152 GO:0055114 functional description: Short chain dehydrogenase/reductase family protein (AHRD V1 D7L3	2	2.40259E-09
Sopim01g109920	genomic reference:SL2.40ch01 gene region:88520599 88521868 transcript region:SL2.40ch01:88520599..88521868 go terms:GO:0009415 functional description: Dehydrin (AHRD V1 Q6YL18 BRAJU); contains Interpro domain(s) IPR000167 L	2	2.40259E-09
Sopim06g075070	genomic reference:SL2.40ch06 gene region:42965938 42968329 transcript region:SL2.40ch06:42965938..42968329 go terms:GO:0004089 functional description: Carbonic anhydrase (Carbonate dehydratase) (AHRD V1 A4Z2G9_BRASO); contain	2	2.40259E-09
Sopim03g033690	evidence_code:10F0H1E0IEG genomic_reference:SL2.40ch03 gene_region:9560339_9562723 transcript_region:SL2.40ch03:9560339..9562723_ go_terms:GO:0055114 functional_description:_Peroxidase (AHRD V1 ____ Q0ZA68_9ROSI); contains Interpr	2	2.40259E-09
Sopim11g043110	evidence_code:10F0H1E1IEG genomic_reference:SL2.40ch11 gene_region:34833475_34835605 transcript_region:SL2.40ch11:34833475..34835605_ go_terms:GO:0006629 functional_description:_GDSL esterase/lipase At1g71250 (AHRD V1 ____ GDL28	2	2.40259E-09
Sopim06g083020	evidence_code:10F0H1E0IEG genomic_reference:SL2.40ch06 gene_region:44872623_44875571 transcript_region:SL2.40ch06:44872623..44875571_ go_terms:GO:0042802 functional_description:_Serine carboxypeptidase 1 (AHRD V1 ____ B6TDA5_MA	2	7.77489E-13
Sopim07g061800	genomic reference:SL2.40ch07 gene region:61967425 61968441 transcript region:SL2.40ch07:61967425..61968441 go terms:GO:0020037 functional description: Heme binding protein 2 (AHRD V1 B6T0C0 MAIZE); contains Interpro domain(s)	2	2.40259E-09
Sopim10g054900	evidence code:10F1H1E1IEG genomic reference:SL2.40ch10 gene region:51531598 51532532 transcript region:SL2.40ch10:51531598..51532532 functional description: Proline rich protein (AHRD V1 Q9M6T7 NICGL); contains Interpro domain(	2	2.40259E-09
Sopim05g054350	genomic reference:SL2.40ch05 gene region:63421809 63424843 transcript region:SL2.40ch05:63421809..63424843 go terms:GO:0004301 functional description: Epoxide hydrolase (AHRD V1 Q41414 SOLTU); contains Interpro domain(s) IPR0	2	2.40259E-09
Sopim09g072560	genomic reference:SL2.40ch09 gene region:60593208 60595291 transcript region:SL2.40ch09:60593208..60595291 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	28	9.9E-20
Sopim09g025210	genomic reference:SL2.40ch09 gene region:19251698 19253627 transcript region:SL2.40ch09:19251698..19253627 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	17	9.9E-20
Sopim09g010930	genomic reference:SL2.40ch09 gene region:4264025 4269432 transcript region:SL2.40ch09:4264025..4269432 go terms:GO:0005507 functional description: NAD_dependent epimerase/dehydratase (AHRD V1 B6T962_MAIZE); contains Interpro c	3	6.3205E-13
Sopim03g005580	genomic reference:SL2.40ch03 gene region:421297 424318 transcript region:SL2.40ch03:421297..424318 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IPR014710	3	6.3205E-13
Sopim06g076540	evidence code:10F0H1E1IEG genomic reference:SL2.40ch06 gene region:43940957 43941421 transcript region:SL2.40ch06:43940957..43941421 functional description: class I heat shock protein (AHRD V1 Q69BI7 CARPA); contains Interpro do	2	2.40259E-09
Sopim02g072050	evidence code:10F0H1E1IEG genomic reference:SL2.40ch02 gene region:35917656 35919451 transcript region:SL2.40ch02:35917656..35919451 functional description: Os05g0272200 protein (Fragment) (AHRD V1 ____ Q0DJJ5_ORYSJ)_	2	2.40259E-09
Sopim03g096040	genomic reference:SL2.40ch03 gene region:51304230 51305908 transcript region:SL2.40ch03:51304230..51305908 go terms:GO:0008379 GO:0004602 functional description: Mitochondrial peroxiredoxin (1 Cys Prx) with thioredoxin peroxidase activit	2	2.40259E-09
Sopim09g098120	genomic reference:SL2.40ch09 gene region:67297118 67298585 transcript region:SL2.40ch09:67297118..67298585 functional description: DUF1264 domain protein (AHRD V1 B8NLT6 ASPFN); contains Interpro domain(s) IPR010686 Protein c	2	2.40259E-09
Sopim12g056390	evidence code:10F0H1E0IEG genomic reference:SL2.40ch12 gene region:47677578 47678261 transcript region:SL2.40ch12:47677578..47678261 functional description: Thaumatin like protein (AHRD V1 Q5DJS5 TOBAC); contains Interpro dor	2	2.40259E-09
Sopim09g057670	genomic reference:SL2.40ch09 gene region:45726675 45731083 transcript region:SL2.40ch09:45726675..45731083 go terms:GO:0005528 functional description: FK506_binding protein 2 (EC 5.2.1.8)(Peptidyl_prolyl cis_trans isomerase)(PPIase)(Rotan	2	2.40259E-09
Sopim02g088100	genomic reference:SL2.40ch02 gene region:44867449 44868915 transcript region:SL2.40ch02:44867449..44868915 go terms:GO:0005199 functional description: Expansin (AHRD V1 Q9ZP31_SOLLC); contains Interpro domain(s) IPR007112 E:	2	2.40259E-09
Sopim09g025210	genomic reference:SL2.40ch09 gene region:19251698 19253627 transcript region:SL2.40ch09:19251698..19253627 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	9	9.9E-20
Sopim09g090150	genomic reference:SL2.40ch09 gene region:65039694 65042890 transcript region:SL2.40ch09:65039694..65042890 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	7	9.9E-20
Sopim12g096930	evidence code:10F1H1E1IEG genomic reference:SL2.40ch12 gene region:63988881 63992407 transcript region:SL2.40ch12:63988881..63992407 functional description: Caleosin (AHRD V1 Q9SQ57 SESIN); contains Interpro domain(s) IPR007	2	7.77489E-13
Sopim09g072560	genomic reference:SL2.40ch09 gene region:60593208 60595291 transcript region:SL2.40ch09:60593208..60595291 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	12	9.9E-20
Sopim09g082340	genomic reference:SL2.40ch09 gene region:63490155 63493319 transcript region:SL2.40ch09:63490155..63493319 go terms:GO:0045735 functional description: Vicilin like protein (Fragment) (AHRD V1 Q9SEW4 9ROSI); contains Interpro dor	5	9.9E-20
Sopim09g008770	genomic reference:SL2.40ch09 gene region:2194030 2196459 transcript region:SL2.40ch09:2194030..2196459 functional description: Group 3 late embryogenesis abundant protein (AHRD V1 Q2N1E0 PHAVU); contains Interpro domain(s) IPR00	4	2.22045E-16
Sopim12g010820	evidence_code:10F0H0E0IEG genomic_reference:SL2.40ch12 gene_region:3763483_3765054 transcript_region:SL2.40ch12:3763483..3765054_ functional_description:_Group 3 late embryogenesis abundant protein (AHRD V1 ____ Q2N1E0_PHAVU); con	3	6.3205E-13
Sopim07g053360	genomic reference:SL2.40ch07 gene region:59144379_59146118 transcript region:SL2.40ch07:59144379..59146118_ functional_description:_Seed biotin_containing protein SBP65 (AHRD V1 ____ SBP65_PEA); contains Interpro domain(s) IPR004238 I	2	2.40259E-09
Sopim07g064170	genomic reference:SL2.40ch07 gene region:63653756 63656317 transcript region:SL2.40ch07:63653756..63656317 go terms:GO:0005618 GO:0030599 functional description:_Pectinesterase (AHRD V1 ____ B9RXQ4_RICCO); contains Interpro domai	2	2.40259E-09
Sopim07g064180	genomic reference:SL2.40ch07 gene region:63663614 63666871 transcript region:SL2.40ch07:63663614..63666871 go terms:GO:0005618 GO:0030599 functional description: Pectinesterase (AHRD V1 B9RXQ4 RICCO); contains Interpro domai	2	2.40259E-09
Sopim09g025210	genomic reference:SL2.40ch09 gene region:19251698 19253627 transcript region:SL2.40ch09:19251698..19253627 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	4	2.22045E-16
Sopim09g090150	genomic reference:SL2.40ch09 gene region:65039694 65042890 transcript region:SL2.40ch09:65039694..65042890 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	3	6.3205E-13
Sopim09g008770	genomic reference:SL2.40ch09 gene region:2194030 2196459 transcript region:SL2.40ch09:2194030..2196459 functional description: Group 3 late embryogenesis abundant protein (AHRD V1 Q2N1E0 PHAVU); contains Interpro domain(s) IPR00	2	2.40259E-09
Sopim09g072560	genomic reference:SL2.40ch09 gene region:60593208 60595291 transcript region:SL2.40ch09:60593208..60595291 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	16	9.9E-20
Sopim09g090150	genomic reference:SL2.40ch09 gene region:65039694 65042890 transcript region:SL2.40ch09:65039694..65042890 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	8	9.9E-20
Sopim05g053350	genomic reference:SL2.40ch05 gene region:62620520 62623062 transcript region:SL2.40ch05:62620520..62623062_ functional description:_Desiccation_related protein PCC13_62 (AHRD V1 ____ B4G1G1_MAIZE)_	5	9.9E-20
Sopim06g076540	evidence code:10F0H1E1IEG genomic reference:SL2.40ch06 gene region:43940957 43941421 transcript region:SL2.40ch06:43940957..43941421 functional description: class I heat shock protein (AHRD V1 Q69BI7 CARPA); contains Interpro do	3	6.3205E-13
Sopim02g032940	genomic reference:SL2.40ch02 gene region:20185974 20192184 transcript region:SL2.40ch02:20185974..20192184 go terms:GO:0004190 functional description: Aspartic proteinase (AHRD V1 Q8L6A8 THECC); contains Interpro domain(s) IPR	3	6.3205E-13
Sopim09g082340	genomic reference:SL2.40ch09 gene region:63490155 63493319 transcript region:SL2.40ch09:63490155..63493319 go terms:GO:0045735 functional description: Vicilin like protein (Fragment) (AHRD V1 Q9SEW4 9ROSI); contains Interpro dor	3	2.22045E-16
Sopim07g064180	genomic reference:SL2.40ch07 gene region:63663614 63666871 transcript region:SL2.40ch07:63663614..63666871 go terms:GO:0005618 GO:0030599 functional description: Pectinesterase (AHRD V1 B9RXQ4 RICCO); contains Interpro domai	3	6.3205E-13
Sopim03g005580	genomic reference:SL2.40ch03 gene region:421297 424318 transcript region:SL2.40ch03:421297..424318 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IPR014710	3	9.9E-20
Sopim08g080620	evidence code:10F0H1E1IEG genomic reference:SL2.40ch08 gene region:61020913 61021593 transcript region:SL2.40ch08:61020913..61021593 go terms:GO:0005515 functional description: Osmotin like protein (Fragment) (AHRD V1 Q8S4L1	2	2.40259E-09
Sopim10g049710	evidence code:10F1H1E1IEG genomic reference:SL2.40ch10 gene region:41900268 41905411 transcript region:SL2.40ch10:41900268..41905411_ go terms:GO:0006508 functional description:_ATP_dependent Clp protease proteolytic subunit (AHRD V	2	2.40259E-09
Sopim02g084840	genomic reference:SL2.40ch02 gene region:42498653 42499621 transcript region:SL2.40ch02:42498653..42499621_ go terms:GO:0009415 functional description:_Dehydrin DHN1 (AHRD V1 ____ DHN1_PEA); contains Interpro domain(s) IPR000167	2	2.40259E-09
Sopim09g090150	genomic reference:SL2.40ch09 gene region:65039694 65042890 transcript region:SL2.40ch09:65039694..65042890 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	12	9.9E-20
Sopim09g072560	genomic reference:SL2.40ch09 gene region:60593208 60595291 transcript region:SL2.40ch09:60593208..60595291 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IP	5	9.9E-20
Sopim03g005580	genomic reference:SL2.40ch03 gene region:421297 424318 transcript region:SL2.40ch03:421297..424318 go terms:GO:0045735 functional description: Legumin 11S globulin (AHRD V1 Q39770 GINBI); contains Interpro domain(s) IPR014710	4	2.22045E-16
Sopim03g116390	genomic reference:SL2.40ch03 gene region:59910675_59911543 transcript region:SL2.40ch03:59910675..59911543_ functional description:_Late embryogenesis abundant protein (AHRD V1 ____ Q2QKE8_CATRO)_	3	6.3205E-13
Solyc09g025210.2.1	functional_description:Legumin 11S_globulin (AHRD V1 __ Q39770_GINBI); contains Interpro domain(s) IPR014710 RmlC_like jelly roll fold	7	9.9E-20
Solyc09g072560.2.1	functional_description:Legumin 11S_globulin (AHRD V1 __ Q39770_GINBI); contains Interpro domain(s) IPR014710 RmlC_like jelly roll fold	7	9.9E-20
Solyc02g070640.2.1	functional_description:60S ribosomal protein L18a (AHRD V1 _ D2D962_9ROSI); contains Interpro domain(s) IPR002670 Ribosomal protein L18ae	3	6.3205E-13
Solyc06g065590.2.1	functional_description:60S ribosomal protein L18a (AHRD V1 _ D2D962_9ROSI); contains Interpro domain(s) IPR002670 Ribosomal protein L18ae	3	6.3205E-13
Solyc08g016180.2.1	functional_description:60S ribosomal protein L18a (AHRD V1 _ D2D962_9ROSI); contains Interpro domain(s) IPR002670 Ribosomal protein L18ae	3	6.3205E-13
Solyc09g082340.2.1	functional_description:Vicilin_like protein (Fragment) (AHRD V1 __ Q9SEW4_9ROSI); contains Interpro domain(s) IPR014710 RmlC_like jelly roll fold	3	9.9E-20

Proteins identified only in SH

PROTEIN ID	DESCRIPTION	PEPTIDES	PValue
Solyc06g051460.2.1	ATP-dependent chaperone ClpB	2	2.40E-09
Solyc10g080770.1.1	BZIP transcription factor	2	2.40E-09
Solyc01g099460.1.1	ATP-dependent DNA helicase	4	2.22E-16

Table 5.9. Differentially expressed proteins identified in the leaves.

Label free quantitation was employed by matching retention times of the peaks and measuring area under the matched peaks using Sieve 2.1 software (Thermo Scientific) to identify the differentially expressed proteins in SP-SL, SG-SL, SH-SL pairs. Stringent criteria were imposed to identify these proteins (P value ≤ 0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR = 1%).

List of upregulated proteins in SP-SL leaf

PROTEIN ID	DESCRIPTION	PEPTIDE	RATIO	STD.DEV	PVALUE	MAPMAN CLASS
Sopim06g076020	genomic reference:SL2.40ch06 gene region:43582389 43585486 transcript region:SL2.40ch06:43582389..43585486 go terms:GO:0051082 GO:0005524 functional description: heat shock protein (AHRD V1 B2D2G5 CAPSN): contains Interpro domain(s) IPR013126 Heat	4	8.95608	4.47181	0.0001	abiotic stress heat
Sopim09g010630	genomic reference:SL2.40ch09 gene region:3965253 3968837 transcript region:SL2.40ch09:3965253..3968837 go terms:GO:0051082 functional description: heat shock protein (AHRD V1 B2D2G5 CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70	4	8.95608	4.47181	0.0001	abiotic stress heat
Sopim10g086410	genomic reference:SL2.40ch10 gene region:64561395 64564764 transcript region:SL2.40ch10:64561395..64564764 go terms:GO:0051082 functional description: Heat shock protein 70 3 (AHRD V1 Q67BD0 TOBAC); contains Interpro domain(s) IPR013126 Heat shock	4	8.95608	4.47181	0.0001	abiotic stress heat
Sopim11g066060	evidence code:10F08I1E1IEG genomic reference:SL2.40ch11 gene region:48824058 48826931 transcript region:SL2.40ch11:48824058..48826931 go terms:GO:0005524 functional description: heat shock protein (AHRD V1 B2D2G5 CAPSN); contains Interpro domain(s) I	4	8.95608	4.47181	0.0001	abiotic stress heat
Sopim08g062910	genomic reference:SL2.40ch08 gene region:49531008 49535044 transcript region:SL2.40ch08:49531008..49535044 go terms:GO:0003746 functional description: Elongation factor EF 2 (AHRD V1 Q9SGT4 ARATH); contains Interpro domain(s) IPR000795 Protein synth	3	7.11207	2.7888	0.00026	protein synthesis
Sopim08g062920	genomic reference:SL2.40ch08 gene region:49546793 49552256 transcript region:SL2.40ch08:49546793..49552256 go terms:GO:0005515 GO:0003746 functional description: Elongation factor EF 2 (AHRD V1 Q9SGT4 ARATH); contains Interpro domain(s) IPR000795	3	7.11207	2.7888	0.00026	protein synthesis
Solyc08g065220.2.1	functional_description:Glycine dehydrogenase P protein (AHRD V1 Q6V9T1_ORYSJ); contains Interpro domain(s) IPR003437 Glycine cleavage system P_protein	2	5.38218	1.04872	0.00067	amino acid metabolism
Sopim08g065220	genomic reference:SL2.40ch08 gene region:50293331 50300381 transcript region:SL2.40ch08:50293331..50300381 go terms:GO:0004375 functional description: Glycine dehydrogenase P protein (AHRD V1 O6V9T1 ORYSJ): contains Interpro domain(s) IPR003437 Glyc	2	5.38218	1.04872	0.00067	amino acid metabolism
Sopim05g050970	genomic reference:SL2.40ch05 gene region:60328753 60332879 transcript region:SL2.40ch05:60328753..60332879 go terms:GO:0004802 GO:0005515 functional description: Transketolase 1 (AHRD V1 O78327 CAPAN); contains Interpro domain(s) IPR005478 Bacteria	2	3.85827	1.08031	0.01324	PS Calvin cycle
Sopim01g108600	genomic reference:SL2.40ch01 gene region:87613555 87626715 transcript region:SL2.40ch01:87613555..87626715 go terms:GO:0004222 functional description: Presequence protease mitochondrial (AHRD V1 PREP DANRE): contains Interpro domain(s) IPR013578 Pe	2	4.94824	0.73698	0.0029	protein degradation
Solyc06g076020.2.1	functional_description:heat shock protein (AHRD V1 _ B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70	2	14.4371	12.6028	0.00365	abiotic stress heat
Solyc09g010630.2.1	functional_description:heat shock protein (AHRD V1 _ B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70	2	14.4371	12.6028	0.00365	abiotic stress heat
Solyc10g086410.2.1	functional_description:Heat shock protein 70 3 (AHRD V1 _ Q67BD0_TOBAC); contains Interpro domain(s) IPR013126 Heat shock protein 70	2	14.4371	12.6028	0.00365	abiotic stress heat
Solyc11g066060.1.1	functional_description:heat shock protein (AHRD V1 _ B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70	2	14.4371	12.6028	0.00365	abiotic stress heat
Sopim04g011440	genomic reference:SL2.40ch04 gene region:3894918 3898067 transcript region:SL2.40ch04:3894918..3898067 go terms:GO:0051082 functional description: heat shock protein (AHRD V1 B2D2G5 CAPSN): contains Interpro domain(s) IPR013126 Heat shock protein 70	2	22.0766	22.327	0.00374	abiotic stress heat
Sopim10g084050	evidence code:10F08I1E1IEG genomic reference:SL2.40ch10 gene region:63048965 63053841 transcript region:SL2.40ch10:63048965..63053841 go terms:GO:0016787 GO:0005524 GO:0017111 GO:0005488 functional description: 26S protease regulatory subunit 6B homolog	2	7.49456	9.08856	0.0013	PS Calvin cycle
Sopim01g110360	genomic reference:SL2.40ch01 gene region:88844597 88847246 transcript region:SL2.40ch01:88844597..88847246 go terms:GO:0005507 functional description: Fructose bisphosphate aldolase (AHRD V1 B0FPD8 SOLTU); contains Interpro domain(s) IPR000741 Fructo	2	8.04743	8.95303	0.01062	PS Calvin cycle
Sopim07g065840	genomic reference:SL2.40ch07 gene region:64658676 64662396 transcript region:SL2.40ch07:64658676..64662396 go terms:GO:0042623 functional description: Heat shock protein 90 (AHRD V1 Q14TBI TOBAC); contains Interpro domain(s) IPR003594 ATP binding m	2	27.4472	19.0678	0.0031	PS Calvin cycle
Sopim05g010670	genomic reference:SL2.40ch05 gene region:4883167 4891847 transcript region:SL2.40ch05:4883167..4891847 go terms:GO:0005524 functional description: Chaperone protein htpG (AHRD V1 HTPG MYXXD); contains Interpro domain(s) IPR001404 Heat shock protein	2	2.38644	1.00511	0.00139	abiotic stress heat
Solyc03g114150.2.1	functional_description:Aldehyde dehydrogenase (AHRD V1 Q1AFT6_9ROSI); contains Interpro domain(s) IPR015590 Aldehyde dehydrogenase	2	8.16336	6.06848	0.00567	fermentation
Solyc05g005700.2.1	functional_description:Aldehyde dehydrogenase 1 (AHRD V1 Q84V96_LOTCO); contains Interpro domain(s) IPR015590 Aldehyde dehydrogenase	2	8.16336	6.06848	0.00567	fermentation
Sopim07g049660	genomic reference:SL2.40ch07 gene region:57349065 57351095 transcript region:SL2.40ch07:57349065..57351095 go terms:GO:0010327 functional description: Acetyl coenzyme A cis 3 hexen 1 ol acetyl transferase (AHRD V1 Q9SRQ2 ARATH); contains Interpro don	2	9.02061	6.80908	0.005	secondary metabolism

List of downregulated proteins in SP-SL leaf

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO	STD.DEV	PVALUE	MAPMAN CLASS
Solyc11g069790.1.1	functional_description:chaperonin (AHRD V1 _ B2IXD2_NOSP7); contains Interpro domain(s) IPR001844 Chaperonin Cpn60	4	0.207663238	0.059006537	0.000115415	protein folding
Solyc01g007500.2.1	functional_description:Photosystem II CP47 chlorophyll apoprotein (AHRD V1 D3WBA3 9BORA); contains Interpro domain(s) IPR017486 Photosystem II	4	0.004132263	0.000659241	2.77E-05	PS Light reaction
Sopim07g052350	genomic reference:SL2.40ch07 gene region:58180514 58188952 transcript region:SL2.40ch07:58180514..58188952 go terms:GO:0005507 functional descr	4	0.117520247	0.041697903	0.000213305	TCA
Sopim11g069790	evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch11 gene_region:51502451_51507359 transcript_region:SL2.40ch11:51502451..51507359_ go_terms	3	0.220799389	0.063736262	0.000523628	protein folding
Solyc10g085020.1.1	functional_description:Tubulin beta chain (AHRD V1 _ B9HP96_POPTR); contains Interpro domain(s) IPR002453 Beta tubulin	3	0.077498278	0.050322825	0.000262892	cell organisation
Solyc10g086760.1.1	functional_description:Tubulin beta chain (AHRD V1 _ B9HP96_POPTR); contains Interpro domain(s) IPR002453 Beta tubulin	3	0.077498278	0.050322825	0.000262892	cell organisation
Solyc12g089310.1.1	functional_description:Tubulin beta_1 chain (AHRD V1 _ D7KT68_ARALY); contains Interpro domain(s) IPR002453 Beta tubulin	3	0.077498278	0.050322825	0.000262892	cell organisation
Solyc02g085950.2.1	functional_description:Ribulose bisphosphate carboxylase small chain (AHRD V1 A9YTZ7 SOLTU); contains Interpro domain(s) IPR000894 Ribulose bisph	2	0.251453949	0.01715706	0.001748472	PS Calvin cycle
Solyc03g034220.2.1	functional_description:Ribulose bisphosphate carboxylase small chain (AHRD V1 A9YTZ7 SOLTU); contains Interpro domain(s) IPR000894 Ribulose bisph	2	0.251453949	0.01715706	0.001748472	PS Calvin cycle
Sopim02g085950	genomic reference:SL2.40ch02 gene region:43293286 43294312 transcript region:SL2.40ch02:43293286..43294312 go terms:GO:0005515 GO:0005507 fu	2	0.251453949	0.01715706	0.001748472	PS Calvin cycle
Sopim09g007540	genomic reference:SL2.40ch09 gene region:1126820 1139864 transcript region:SL2.40ch09:1126820..1139864 go terms:GO:0042802 GO:0004832 functio	2	0.273088518	0.058845082	0.000874878	protein aa activation
Sopim04g071340	genomic_reference:SL2.40ch04 gene_region:55860635_55865238 transcript_region:SL2.40ch04:55860635..55865238_ go_terms:GO:0042132 functional_descr	2	0.244435879	0.045047247	0.001472482	PS Calvin cycle
Solyc12g094620.1.1	functional_description:Catalase (AHRD V1 _ Q2PYW5_SOLTU); contains Interpro domain(s) IPR018028 Catalase related subgroup	2	0.230313947	0.043187836	0.001901821	redox
Solyc12g099000.1.1	functional_description:S_adenosylmethionine synthase (AHRD V1 _ B8LFH4_IPOBA); contains Interpro domain(s) IPR002133 S_adenosylmethionine syntheta	2	0.075834236	0.029122355	0.008951696	Amino acid metabolism
Solyc08g062910.2.1	functional_description:Elongation factor EF 2 (AHRD V1 Q9SGT4 ARATH); contains Interpro domain(s) IPR000795 Protein synthesis factor GTP binding	2	0.160129359	0.022355425	5.82E-05	protein synthesis
Solyc08g062920.2.1	functional_description:Elongation factor EF 2 (AHRD V1 Q9SGT4 ARATH); contains Interpro domain(s) IPR000795 Protein synthesis factor GTP binding	2	0.160129359	0.022355425	5.82E-05	protein synthesis
Solyc02g087880.2.1	functional_description:Tubulin alpha_7 chain (AHRD V1 _ B9IV8_POPTR); contains Interpro domain(s) IPR002452 Alpha tubulin	2	0.05983192	0.000927873	0.002492165	cell organisation
Solyc04g077020.2.1	functional_description:Tubulin alpha_3 chain (AHRD V1 _ B6SPX4_MAIZE); contains Interpro domain(s) IPR002452 Alpha tubulin	2	0.05983192	0.000927873	0.002492165	cell organisation
Solyc08g006890.2.1	functional_description:Tubulin alpha_3 chain (AHRD V1 _ B6SPX4_MAIZE); contains Interpro domain(s) IPR002452 Alpha tubulin	2	0.05983192	0.000927873	0.002492165	cell organisation
Sopim08g065220	genomic_reference:SL2.40ch08 gene_region:50293331_50300381 transcript_region:SL2.40ch08:50293331..50300381_ go_terms:GO:0004375 functional_descr	2	0.312725528	0.042440249	0.010867032	amino acid metabolism
Sopim09g011080	genomic_reference:SL2.40ch09 gene_region:4413327_4416467 transcript_region:SL2.40ch09:4413327..4416467_ go_terms:GO:0046863 functional_descriptio	2	0.050839668	0.020429578	0.003380541	PS Calvin cycle
Solyc10g051110.1.1	functional_description:NAD dependent epimerase/dehydratase family protein (AHRD V1 ___B0CAN3_ACAM1); contains Interpro domain(s) IPR016040 NAI	2	0.015927009	0.006503165	0.007267749	light signaling
Solyc10g080210.1.1	functional_description:Polygalacturonase A (AHRD V1 Q9M6S2_ACTCH); contains Interpro domain(s) IPR000743 Glycoside hydrolase_ family 28	1	0.077550305	0.032475753	0.014972931	Cell wall
Solyc01g110450.2.1	functional_description:NADP dependent sorbitol 6 phosphate dehydrogenase (Fragment) (AHRD V1 Q8S4S2 VAUCA); contains Interpro domain(s) IPR02(	4	0.177609456	0.038535509	6.32E-05	minor CHO metabolism
Solyc10g079860.1.1	functional_description:Beta_1 3 _glucanase (AHRD V1 _ Q68V46_OLEEU); contains Interpro domain(s) IPR000490 Glycoside hydrolase_ family 17	2	0.325037957	0.080690801	0.012669462	misc
Sopim01g105030	genomic reference:SL2.40ch01 gene region:85087662 85089049 transcript region:SL2.40ch01:85087662..85089049 go terms:GO:0016168 functional descr	2	0.27998684	0.106478591	0.016761857	PS Light reaction
Sopim01g105050	genomic reference:SL2.40ch01 gene region:85093521 85094689 transcript region:SL2.40ch01:85093521..85094689 go terms:GO:0016168 functional descr	2	0.27998684	0.106478591	0.016761857	PS Light reaction
Sopim04g011510	genomic_reference:SL2.40ch04 gene_region:3944572_3949105 transcript_region:SL2.40ch04:3944572..3949105_ go_terms:GO:0004807 functional_descriptio	3	0.098935101	0.025776748	7.42E-05	PS Calvin cycle/glycolysis
Solyc12g009250.1.1	functional_description:chaperonin (AHRD V1 __ D1U6H2_9DELT); contains Interpro domain(s) IPR001476 Chaperonin Cpn10	3	0.027429239	0.02941001	0.000601614	protein folding
Solyc02g065400.2.1	functional_description:Oxygen_evolving enhancer protein 1 of photosystem II (AHRD V1 _ A8J0E4_CHLRE); contains Interpro domain(s) IPR002628 Photosy	3	0.080396751	0.05925489	0.000473434	PS Light reaction
Solyc02g090030.2.1	functional_description:Oxygen_evolving enhancer protein 1 of photosystem II (AHRD V1 A8J0E4 CHLRE); contains Interpro domain(s) IPR002628 Photosy	3	0.080396751	0.05925489	0.000473434	PS Light reaction
Sopim07g041720	evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch07 gene_region:51367296_51367931 transcript_region:SL2.40ch07:51367296..51367931 go_terms	3	0.086067802	0.048038417	3.18E-06	abiotic stress heat
Solyc02g038690.1.1	functional_description:Histone H2B (AHRD V1 _ A2IBL2_NICBE); contains Interpro domain(s) IPR000558 Histone H2B	3	0.02532643	0.029512479	0.002987156	DNA synthesis/chromatin structure
Solyc03g071620.1.1	functional_description:Histone H2B (AHRD V1 _ A2IBL2_NICBE); contains Interpro domain(s) IPR000558 Histone H2B	3	0.02532643	0.029512479	0.002987156	DNA synthesis/chromatin structure
Solyc06g075800.1.1	functional_description:Histone H2B (AHRD V1 _ Q2XPW1_SOLTU); contains Interpro domain(s) IPR000558 Histone H2B	3	0.02532643	0.029512479	0.002987156	DNA synthesis/chromatin structure
Solyc11g007920.1.1	functional_description:Histone H2B (AHRD V1 _ A5BCC0_VITVI); contains Interpro domain(s) IPR000558 Histone H2B	3	0.02532643	0.029512479	0.002987156	DNA synthesis/chromatin structure
Solyc11g007930.1.1	functional_description:Histone H2B (AHRD V1 _ D7KHV7_ARALY); contains Interpro domain(s) IPR000558 Histone H2B	3	0.02532643	0.029512479	0.002987156	DNA synthesis/chromatin structure
Solyc02g069450.2.1	functional_description:Photosystem I reaction center subunit III (AHRD V1 _ Q9XQB4_PHAAU); contains Interpro domain(s) IPR003666 Photosystem I reacti	3	0.101920575	0.031141254	0.002490679	PS Light reaction
Solyc02g069460.2.1	functional_description:Photosystem I reaction center subunit III (AHRD V1 Q9XQB4 PHAAU); contains Interpro domain(s) IPR003666 Photosystem I reacti	3	0.094559729	0.028108683	0.000440219	PS Light reaction
Solyc01g097460.2.1	functional_description:Ribose 5 phosphate isomerase (AHRD V1 A8IRQ1 CHLRE); contains Interpro domain(s) IPR004788 Ribose 5 phosphate isomerase	3	0.142660468	0.029975978	0.0001842	PS Calvin cycle
Solyc01g007330.2.1	functional_description:Ribulose bisphosphate carboxylase large chain (AHRD V1 RBL SOLLC); contains Interpro domain(s) IPR000685 Ribulose bisphosphe	3	0.054991665	0.024118379	8.36E-06	PS Calvin cycle
Solyc10g086580.1.1	functional_description:Ribulose 1 5 bisphosphate carboxylase/oxygenase activase 1 (AHRD V1 Q9AXG1 GOSHI); contains Interpro domain(s) IPR003959 .	3	0.052375145	0.039698099	0.001572327	PS Calvin cycle
Solyc11g008990.1.1	functional_description:Phage shock protein A PspA (AHRD V1 _ B7K4B0_CYAP8); contains Interpro domain(s) IPR007157 PspA/IM30	2	0.141983135	0.093034931	0.005533948	RNA regulation of transcription
Sopim10g054870	evidence_code:10F0H1E1IEG genomic_reference:SL2.40ch10 gene_region:51507074_51512787 transcript_region:SL2.40ch10:51507074..51512787_ go_terms	2	0.158390439	0.048510259	0.003586472	PS Calvin cycle
Sopim10g081240	evidence_code:10F0H1E1IEG genomic_reference:SL2.40ch10 gene_region:61667783_61677144 transcript_region:SL2.40ch10:61667783..61677144_ go_terms	2	0.050104273	0.044180227	0.005754192	protein folding
Sopim01g080280	genomic_reference:SL2.40ch01 gene_region:72039739_72045026 transcript_region:SL2.40ch01:72039739..72045026_ go_terms:GO:0004356 functional_descr	2	0.045684869	0.051098922	0.003200157	N metabolism
Solyc03g115820.2.1	functional_description:Ribulose 5 phosphate 3 epimerase (AHRD V1 Q8S4X2 PEA); contains Interpro domain(s) IPR000056 Ribulose phosphate 3 epime	2	0.044380553	0.033688143	0.000613111	PS Calvin cycle
Sopim07g042250	genomic reference:SL2.40ch07 gene region:52684617 52687267 transcript region:SL2.40ch07:52684617..52687267 go terms:GO:0051087 functional descr	2	0.138219958	0.156345188	0.015032975	protein folding
Solyc07g042250.2.1	functional_description:chaperonin (AHRD V1 B4WMS9 9SYNE); contains Interpro domain(s) IPR017416 Chaperonin 21 chloroplast IPR018369 Chapen	2	0.063152387	0.047395954	0.01288456	protein folding
Sopim03g111840	genomic reference:SL2.40ch03 gene region:56501989 56506255 transcript region:SL2.40ch03:56501989..56506255 go terms:GO:0003676 GO:0000166 fu	2	0.072873968	0.06232161	0.000858451	RNA binding
Solyc06g074780.1.1	functional_description:Histone H2B (AHRD V1 _ Q2XTD8_SOLTU); contains Interpro domain(s) IPR000558 Histone H2B	2	0.0157461	0.019810424	0.009737682	DNA synthesis/chromatin structure
Solyc06g074790.1.1	functional_description:Histone H2B (AHRD V1 _ Q2XTD8_SOLTU); contains Interpro domain(s) IPR000558 Histone H2B	2	0.0157461	0.019810424	0.009737682	DNA synthesis/chromatin structure
Solyc11g066430.1.1	functional_description:Histone H2B (AHRD V1 _ B9T301_RICCO); contains Interpro domain(s) IPR000558 Histone H2B	2	0.0157461	0.019810424	0.009737682	DNA synthesis/chromatin structure
Solyc01g087730.2.1	functional_description:50S ribosomal protein L1 (AHRD V1 _ A8YGI8_MICAE); contains Interpro domain(s) IPR005878 Ribosomal protein L1_ bacterial_typ	2	0.071953305	0.047054498	0.006543488	protein synthesis
Solyc03g112150.1.1	functional_description:Elongation factor Tu (AHRD V1 D7MFK2 ARALY); contains Interpro domain(s) IPR004541 Translation elongation factor EFTu/EF1A	2	0.059426109	0.060323287	0.001765114	protein synthesis
Solyc06g071790.2.1	functional_description:Elongation factor Tu (AHRD V1 D7MFK2 ARALY); contains Interpro domain(s) IPR004541 Translation elongation factor EFTu/EF1A	2	0.059426109	0.060323287	0.001765114	protein synthesis
Solyc03g111610.2.1	functional_description:HAD superfamily hydrolase subfamily IA variant 3 containing protein expressed (AHRD V1 Q10I42 ORYSJ); contains Interpro domain(	2	0.20377454	0.08352971	0.013183368	Co- factor and vitamin metabolism
Solyc01g007580.2.1	functional_description:30S ribosomal protein S8 (AHRD V1 _ D4PBE7_PHODC); contains Interpro domain(s) IPR000630 Ribosomal protein S8	2	0.017702245	0.02087067	0.001390657	Protein synthesis
Sopim12g094640	evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch12 gene_region:63152981_63156043 transcript_region:SL2.40ch12:63152981..63156043_ go_terms	2	0.174834492	0.091741872	0.003888059	PS Calvin cycle
Sopim02g070940	evidence_code:10F0H1E1IEG genomic_reference:SL2.40ch02 gene_region:35081036_35081833 transcript_region:SL2.40ch02:35081036..35081833_ go_terms	2	0.11129734	0.049221545	0.003324402	PS Light reaction
Sopim02g070980	evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch02 gene_region:35092891_35093688 transcript_region:SL2.40ch02:35092891..35093688_ go_terms	2	0.11129734	0.049221545	0.003324402	PS Light reaction
Sopim03g005760	evidence_code:10F0H1E1IEG genomic_reference:SL2.40ch03 gene_region:538196_538999 transcript_region:SL2.40ch03:538196..538999_ go_terms:GO:0005	2	0.11129734	0.049221545	0.003324402	PS Light reaction
Sopim03g005770	evidence_code:10F0H1E1IEG genomic_reference:SL2.40ch03 gene_region:540995_541798 transcript_region:SL2.40ch03:540995..541798_ go_terms:GO:0005	2	0.11129734	0.049221545	0.003324402	PS Light reaction
Sopim03g005780	evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch03 gene_region:543035_543838 transcript_region:SL2.40ch03:543035..543838_ go_terms:GO:0016	2	0.11129734	0.049221545	0.003324402	PS Light reaction
Sopim07g047850	genomic reference:SL2.40ch07 gene region:56404445 56405833 transcript region:SL2.40ch07:56404445..56405833 go terms:GO:0016168 functional descr	2	0.11129734	0.049221545	0.003324402	PS Light reaction
Sopim07g065170	genomic reference:SL2.40ch07 gene region:64272755 64275084 transcript region:SL2.40ch07:64272755..64275084 go terms:GO:0003735 GO:0005515 fu	2	0.088632238	0.078026572	0.004208854	protein synthesis
Sopim10g006230	genomic_reference:SL2.40ch10 gene_region:920027_923670 transcript_region:SL2.40ch10:920027..923670_ go_terms:GO:0016020 functional_description:_Cl	2	0.052511316	0.034451832	0.001142722	PS Light reaction
Sopim01g100870	genomic_reference:SL2.40ch01 gene_region:82530325_82533925 transcript_region:SL2.40ch01:82530325..82533925_ go_terms:GO:0005525 functional_descr	2	0.185644666	0.048255507	0.000485138	protein targeting
Sopim04g025560	genomic reference:SL2.40ch04 gene region:21626846_21631497 transcript region:SL2.40ch04:21626846..21631497_ go terms:GO:0005525 functional descr	2	0.185644666	0.048255507	0.000485138	protein targeting
Sopim05g005190	genomic reference:SL2.40ch05 gene region:170330 172998 transcript region:SL2.40ch05:170330..172998 go terms:GO:0042802 functional description: AI	2	0.185644666	0.048255507	0.000485138	protein targeting
Sopim12g005630	evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch12 gene_region:334079_336443 transcript_region:SL2.40ch12:334079..336443_ go_terms:GO:0016	2	0.097348188	0.060203191	0.004627537	PS Light reaction

List of upregulated proteins in SG-SL leaf

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO	STD.DEV	PVALUE	MAPMAN CLASS
Solyc01g007330	aenomic reference:SL2.40ch01 ame reaion:1851938 1853783 transcriot reaion:SL2.40ch01:1851938..1853783 ao terms:GO:0015977 GO:0009536 functional descrintion: Ribulose bisthosnhate carboxylase larae chain (AHRD V1 RBL SOLLC\ contains Interpro domai	4	5.41358	1.07000139	0.0001057	proteinsynthesisribosomal proteinprokaryoticchloroplast30S subunitS15
Solyc01g111510	aenomic reference:SL2.40ch01 ame reaion:89495534 89508705 transcriot reaion:SL2.40ch01:89495534..89508705 ao terms:GO:0016688 functional descrintion: Ascorbate neroxidase (AHRD V1 ORWAV7 CAPAN\ contains Interpro domain\s IPR002207 Plant ascor	2	3.995408	1.594275235	0.01259123	misctmise2
Solyc06g074980	aenomic reference:SL2.40ch06 ame reaion:42868689 42875665 transcriot reaion:SL2.40ch06:42868689..42875665 ao terms:GO:0016787 GO:0005524 GO:0017111 GO:0005488 functional descrintion: 26S nrotease reaulatorv subunit 6B homolow (AHRD V1 PRS6	2	13.85064	14.98563292	0.00860153	proteindegradationubiquitinproteasom
Solyc07g052350	aenomic reference:SL2.40ch07 ame reaion:58180514 58188952 transcriot reaion:SL2.40ch07:58180514..58188952 ao terms:GO:0005507 functional descrintion: 3 isonronvlmalate debvdratase larae subunit (AHRD V1 LEUC NATPD\ contains Interpro domain\s IPR	2	33.65484	57.38193225	0.000996 15	TCA / organic transformation\TCAaconitase
Solyc07g055060	aenomic reference:SL2.40ch07 ame reaion:60510756 60518074 transcriot reaion:SL2.40ch07:60510756..60518074 ao terms:GO:0005515 functional descrintion: Phosnhoenolnvruvate carboxvlase 1 (AHRD V1 O23946 GOSH\ contains Interpro domain\s IPR015813	2	6.232886	4.587880592	0.010157705	glycolysiscytosolic branchphosphe-enol-pyruvate carboxylase (PEPC)
Solyc08g065220	aenomic reference:SL2.40ch08 ame reaion:50293331 50300381 transcriot reaion:SL2.40ch08:50293331..50300381 ao terms:GO:0004375 functional descrintion: Glycine debvdrogenase P nrotein (AHRD V1 O6VVI1 ORYSJ\ contains Interpro domain\s IPR003437 C	2	9.233891	7.479701153	0.00975617	C1-metabolism
Solyc09g065180	aenomic reference:SL2.40ch09 ame reaion:58705860 58708565 transcriot reaion:SL2.40ch09:58705860..58708565 ao terms:GO:0008266 GO:0003729 functional descrintion: NAD denendent enimerase/debvdratase (AHRD V1 B7K7X4 CYAP7\ contains Interpro dor	2	102.0181	106.1391183	0.003139653	cellvesicle transport

List of downregulated proteins in SG-SL leaf

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO	STD.DEV	PVALUE	MAPMAN CLASS
Solyc01g007320	functional_description:ATP synthase subunit beta chloroplastic (AHRD V1 _ Q8MBF8_9SOLA); contains Interpro domain(s) IPR005722 ATPase_ F1 complex_ beta subunit	2	0.100192	0.071661768	0.00691123	mitochondrial electron transport / ATP synthesis.F1-ATPase
Solyc01g007330	genomic_reference:SL2.40ch01 gene_region:1851938 1853783 transcript_region:SL2.40ch01:1851938..1853783 go_terms:GO:0015977 GO:0009536 functional_description: Ribulose bisphosphate carboxyla	2	0.416915	0.011135569	0.00301151	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S15
Solyc01g007380	functional_description:Apocytochrome f (AHRD V1 _ D3WBH0_9AQUA); contains Interpro domain(s) IPR002325 Cytochrome f	2	0.06515	0.073417691	0.00344341	PS.lightreaction.cytochrome b6/f.apocytochrome f (CYF)
Solyc01g007500	functional_description:Photosystem II CP47 chlorophyll apoprotein (AHRD V1 _ D3WBA3_9BORA); contains Interpro domain(s) IPR017486 Photosystem II_ PsbB	4	0.016415	0.008787974	0.00012528	PS.lightreaction.photosystem II.PSII polypeptide subunits
Solyc01g008000	functional_description:ADP_ribosylation factor (AHRD V1 _ Q76ME3_WHEAT); contains Interpro domain(s) IPR006688 ADP_ribosylation factor	2	0.068168	0.012916609	4.56E-05	protein.targeting.secretory pathway.unspecified
Solyc01g008960	functional_description:Argonaute 4_like protein (AHRD V1 _ D5FQ91_PELHO); contains Interpro domain(s) IPR003165 Stem cell self_renewal protein Piwi	2	0.02887	0.022089412	0.00036023	RNA.regulation of transcription.argonaute transcription factor family
Solyc01g087070	functional_description:Mitochondrial ADP/ATP carrier proteins (AHRD V1 Q2UU95_ASPOR); contains Interpro domain(s) IPR002113 Adenine nucleotide translocator 1	2	0.19752	0.011752099	7.12E-05	transport.metabolite transporters at the mitochondrial membrane
Solyc01g087730	functional_description:50S ribosomal protein L1 (AHRD V1 _ A8YGI8_MICAE); contains Interpro domain(s) IPR005878 Ribosomal protein L1_ bacterial_type	2	0.0496	0.039446223	0.00621578	protein.synthesis.ribosomal protein.prokaryotic.unknown organellar
Solyc01g097460	functional_description:Ribose_5_phosphate isomerase (AHRD V1 _ A8IRQ1_CHLRE); contains Interpro domain(s) IPR004788 Ribose 5_phosphate isomerase	2	0.095424	0.026523153	0.00306976	OPP.non-reductive PP.ribose 5-phosphate isomerase
Solyc01g100870	functional_description:ADP_ribosylation factor (AHRD V1 _ Q9M7P4_CAPAN); contains Interpro domain(s) IPR006688 ADP_ribosylation factor	2	0.068168	0.012916609	4.56E-05	protein.postranslational modification
Solyc01g101040	functional_description:ATP_citrate lyase A_3 (AHRD V1 D7KJQ3_ARALY); contains Interpro domain(s) IPR016102 Succinyl_CoA synthetase_like	2	0.037794	0.004409592	0.01162482	TCA / organic transformation.other organic acid transformations.atp-citrate lyase
Solyc01g110360	functional_description:Fructose_bisphosphate aldolase (AHRD V1 _ B0FPD8_SOLTU); contains Interpro domain(s) IPR000741 Fructose_bisphosphate aldolase_ class_I	2	0.03348	0.012965333	0.0050868	lipid metabolism.FA synthesis and FA elongation.pyruvate kinase
Solyc01g110450	functional_description:NADP dependent sorbitol 6_phosphate dehydrogenase (Fragment) (AHRD V1 __ Q8S4S2_VAUCA); contains Interpro domain(s) IPR020471 Aldo/keto reductase subgroup	4	0.20654	0.048020582	2.17E-05	protein.degradation
Solyc02g062340	functional_description:Fructose_bisphosphate aldolase (AHRD V1 _ Q9SXX4_NICPA); contains Interpro domain(s) IPR000741 Fructose_bisphosphate aldolase_ class_I	2	0.03348	0.012965333	0.0050868	PS.calvin cycle.aldolase
Solyc02g063070	functional_description:14_3_3 protein beta/alpha_1 (AHRD V1 __ 143B1_DANRE); contains Interpro domain(s) IPR000308 14_3_3 protein	2	0.040874	0.018800803	0.00315354	signalling.14-3-3 proteins
Solyc02g063150	functional_description:Ribulose bisphosphate carboxylase small chain (AHRD V1 _ Q84QE5_TOBAC); contains Interpro domain(s) IPR000894 Ribulose bisphosphate carboxylase_ small chain	4	0.064167	0.029262916	1.60E-06	PS.calvin cycle.rubisco small subunit
Solyc02g070940	functional_description:Chlorophyll a/b binding protein (AHRD V1 Q41422_SOLTU); contains Interpro domain(s) IPR001344 Chlorophyll A_B binding protein	5	0.152432	0.005665162	5.53E-05	PS.lightreaction.photosystem II.LHC-II
Solyc02g070980	functional_description:Chlorophyll a/b binding protein (AHRD V1 Q41422_SOLTU); contains Interpro domain(s) IPR001344 Chlorophyll A_B binding protein	5	0.152432	0.005665162	5.53E-05	PS.lightreaction.photosystem II.LHC-II
Solyc03g005230	functional_description:Menaquinone biosynthesis methyltransferase ubiE (AHRD V1 _ A1BDQ8_CHLPD); contains Interpro domain(s) IPR013216 Methyltransferase type 11	2	0.006437	0.007690378	0.00283995	secondary metabolism.isoprenoids.tocopherol biosynthesis.MPBQ/MSBQ methyltransferase
Solyc03g005760	functional_description:Chlorophyll a_b binding protein 3C_like (AHRD V1 Q2XTE0_SOLTU); contains Interpro domain(s) IPR001344 Chlorophyll A_B binding protein	5	0.152432	0.005665162	5.53E-05	PS.lightreaction.photosystem II.PSII polypeptide subunits
Solyc03g005770	functional_description:Chlorophyll a_b binding protein 3C_like (AHRD V1 Q2XTE0_SOLTU); contains Interpro domain(s) IPR001344 Chlorophyll A_B binding protein	5	0.152432	0.005665162	5.53E-05	PS.lightreaction.photosystem II.LHC-II
Solyc03g005780	functional_description:Chlorophyll a_b binding protein 3C_like (AHRD V1 Q2XTE0_SOLTU); contains Interpro domain(s) IPR001344 Chlorophyll A_B binding protein	5	0.152432	0.005665162	5.53E-05	PS.lightreaction.photosystem II.LHC-II
Solyc03g034220	functional_description:Ribulose bisphosphate carboxylase small chain (AHRD V1 _ A9YTZ7_SOLTU); contains Interpro domain(s) IPR000894 Ribulose bisphosphate carboxylase_ small chain	4	0.085933	0.029665431	0.00051352	misc.cytochrome P450
Solyc03g063560	functional_description:Glutamate synthase (Ferredoxin) (AHRD V1 _ B8HTZ7_CYAP4); contains Interpro domain(s) IPR002932 Glutamate synthase_ central_C	3	0.025938	0.0061606	0.00053745	N-metabolism.ammonia metabolism.glutamate synthase.ferredoxin dependent
Solyc03g111840	functional_description:Polyadenylate_binding protein 1_like (AHRD V1 __ PAP1L_HUMAN); contains Interpro domain(s) IPR000504 RNA recognition motif_ RNP_1	2	0.046367	0.020464884	0.00563399	RNA.RNA binding
Solyc03g119040	functional_description:Guanine nucleotide_binding protein beta subunit_like protein (AHRD V1 _ B4FKM1_MAIZE); contains Interpro domain(s) IPR020472 G_protein beta WD_40 repeat_ region	2	0.078573	0.090621321	0.01002025	protein.postranslational modification
Solyc04g025560	functional_description:ADP_ribosylation factor (AHRD V1 __ D7KLG4_ARALY); contains Interpro domain(s) IPR006688 ADP_ribosylation factor	2	0.068168	0.012916609	4.56E-05	protein.targeting.secretory pathway.unspecified
Solyc04g077020	functional_description:Tubulin alpha_3 chain (AHRD V1 _ B6SPX4_MAIZE); contains Interpro domain(s) IPR002452 Alpha tubulin	3	0.000169	0.000181893	0.00011876	cell.organisation
Solyc04g082630	functional_description:Glyceraldehyde_3_phosphate dehydrogenase B (AHRD V1 B4F8L7_MAIZE); contains Interpro domain(s) IPR000173 Glyceraldehyde 3_phosphate dehydrogenase	2	0.029274	0.033016236	0.00962778	protein.postranslational modification
Solyc05g005480	genomic_reference:SL2.40ch05 gene_region:352211 355615 transcript_region:SL2.40ch05:352211..355615 go_terms:GO:0004024 functional_description: Oxidoreductase zinc binding dehydrogenase (AHRI	2	0.147572	0.139245049	0.01309993	misc.oxidases - copper flavone etc
Solyc05g055090	functional_description:Ubiquitin carboxyl terminal hydrolase family protein expressed (AHRD V1 Q2R2A3_ORYSJ); contains Interpro domain(s) IPR001394 Peptidase C19 ubiquitin carboxyl terminal hyd	3	0.1135	0.051126399	0.00014868	protein.degradation.ubiquitin.ubiquitin protease
Solyc06g005060	functional_description:Elongation factor 1 alpha (AHRD V1 Q8H9C0_SOLTU); contains Interpro domain(s) IPR004539 Translation elongation factor EF1A eukaryotic and archaeal IPR000795 Protein sy	2	0.055581	0.039972366	0.00023654	protein.synthesis.elongation
Solyc06g054260	functional_description:Photosystem I reaction center subunit II (AHRD V1 _ B4FAW3_MAIZE); contains Interpro domain(s) IPR003685 Photosystem I protein PsaD	2	0.021376	0.009245399	0.00116057	PS.lightreaction.photosystem I.PSI polypeptide subunits
Solyc06g063370	functional_description:Chlorophyll a_b binding protein 1A_ chloroplastic (AHRD V1 _ CB2A_PYRPY); contains Interpro domain(s) IPR001344 Chlorophyll A_B binding protein	2	0.06573	0.067229459	0.00298676	PS.lightreaction.photosystem II.LHC-II
Solyc06g069010	functional_description:Guanine nucleotide_binding protein beta subunit_like protein (AHRD V1 _ B6SJ21_MAIZE); contains Interpro domain(s) IPR020472 G_protein beta WD_40 repeat_ region	2	0.078573	0.090621321	0.01002025	signalling.G-proteins
Solyc06g071920	functional_description:Glyceraldehyde_3_phosphate dehydrogenase (AHRD V1 Q9XG67_TOBAC); contains Interpro domain(s) IPR000173 Glyceraldehyde 3_phosphate dehydrogenase	2	0.080972	0.065997611	0.00107693	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc07g044860	functional_description:Oxygen_evolving enhancer protein 2_ chloroplastic (AHRD V1 _ PSBP_SOLLC); contains Interpro domain(s) IPR002683 Photosystem II oxygen evolving complex protein PsbP	2	0.120841	0.090112311	0.0101735	transport.major intrinsic proteins.NIP
Solyc07g047850	functional_description:Chlorophyll a_b binding protein 4_ chloroplastic (AHRD V1 CB24_SOLLC); contains Interpro domain(s) IPR001344 Chlorophyll A_B binding protein	2	6.94E-05	8.61E-05	0.0007566	PS.lightreaction.photosystem II.LHC-II
Solyc07g052350	functional_description:3_isopropylmalate dehydratase large subunit (AHRD V1 ___ LEUC_NATPD); contains Interpro domain(s) IPR006249 Aconitase/iron regulatory protein 2	2	0.061581	0.065694112	0.00134235	TCA / organic transformation.TCA.aconitase
Solyc07g053830	functional_description:Mitochondrial ADP/ATP carrier proteins (AHRD V1 Q2UU95_ASPOR); contains Interpro domain(s) IPR002113 Adenine nucleotide translocator 1	2	0.19752	0.011752099	7.12E-05	transport.metabolite transporters at the envelope membrane
Solyc07g054210	functional_description:Protochlorophyllide reductase like protein (AHRD V1 _ Q0WVW0_ARATH); contains Interpro domain(s) IPR005979 Light_dependent protochlorophyllide reductase	2	0.031996	0.024880063	7.43E-05	tetrapyrrole synthesis.protochlorophyllide reductase
Solyc07g056540	functional_description:L_lactate dehydrogenase (AHRD V1 _ C0S8Q7_PARBP); contains Interpro domain(s) IPR012133 Alpha_hydroxy acid dehydrogenase_ FMN_dependent	2	0.075766	0.083484239	0.0041514	signalling.receptor kinases.Catharanthus roseus-like RLK1
Solyc07g062060	functional_description:Peptide methionine sulfoxide reductase msrB (AHRD V1 _ B6T2N3_MAIZE); contains Interpro domain(s) IPR002579 Methionine sulphoxide reductase B	2	0.197887	0.100893731	0.00504606	RNA.regulation of transcription.putative transcription regulator
Solyc07g064160	functional_description:Thiazole biosynthetic enzyme (AHRD V1 _ D6N3H1_GOSHI); contains Interpro domain(s) IPR002922 Thiamine biosynthesis Thi4 protein	2	0.003717	0.004191657	0.01129029	Co-factor and vitamine metabolism.thiamine
Solyc07g066610	functional_description:Phosphoglycerate kinase (AHRD V1 _ O81394_SOLTU); contains Interpro domain(s) IPR001576 Phosphoglycerate kinase	4	0.001966	0.001892652	6.99E-07	PS.calvin cycle.phosphoglycerate kinase
Solyc08g006890	functional_description:Tubulin alpha_3 chain (AHRD V1 _ B6SPX4_MAIZE); contains Interpro domain(s) IPR002452 Alpha tubulin	3	0.000169	0.000181893	0.00011876	transport.peptides and oligopeptides
Solyc10g007320	functional_description:Uroporphyrinogen decarboxylase (AHRD V1 D7L387_ARALY); contains Interpro domain(s) IPR006361 Uroporphyrinogen decarboxylase HemE	2	0.175977	0.006683512	7.34E-05	tetrapyrrole synthesis.uroporphyrinogen decarboxylase
Solyc10g018300	functional_description:Transketolase 1 (AHRD V1 O78327_CAPAN); contains Interpro domain(s) IPR005478 Bacterial transketolase	5	0.010609	0.003989794	5.77E-08	PS.calvin cycle.transketolase
Solyc10g081510	functional_description:5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase (AHRD V1 B6UF55_MAIZE); contains Interpro domain(s) IPR006276 5 methyltetrahydropteroyltriglutamat	2	0.002128	0.002944543	0.00732518	amino acid metabolism.synthesis.aspartate family.methionine.methionine synthase
Solyc10g086580	functional_description:Ribulose_1 5_bisphosphate carboxylase/oxygenase activase 1 (AHRD V1 _ Q9AXG1_GOSHI); contains Interpro domain(s) IPR003959 ATPase_ AAA_type_ core	16	0.004767	0.001678118	4.33E-15	PS.calvin cycle.rubisco interacting
Solyc11g005640	functional_description:Ubiquitin (AHRD V1 _ D0EUY5_9POAL); contains Interpro domain(s) IPR019956 Ubiquitin subgroup	3	0.032572	0.012893108	2.11E-05	protein.degradation.ubiquitin.ubiquitin
Solyc11g062190	functional_description:Mitochondrial ADP/ATP carrier proteins (AHRD V1 _ Q2UU95_ASPOR); contains Interpro domain(s) IPR002113 Adenine nucleotide translocator 1	2	0.19752	0.011752099	7.12E-05	transport.metabolite transporters at the envelope membrane
Solyc11g069380	functional_description:4 hydroxy 3 methylbut 2 en 1 yl diphosphate synthase (AHRD V1 A9ZN14_HEVBR); contains Interpro domain(s) IPR017178 4 hydroxy 3 methylbut 2 en 1 yl diphosphate sy	2	0.094886	0.091178627	0.00486578	secondary metabolism.isoprenoids.non-mevalonate pathway.HDS
Solyc12g006140	functional_description:Chlorophyll a_b binding protein 37_ chloroplastic (AHRD V1 _ CB26_PETSP); contains Interpro domain(s) IPR001344 Chlorophyll A_B binding protein	2	0.152282	0.005670311	0.00178999	PS.lightreaction.photosystem II.LHC-II
Solyc12g013710	functional_description:Protochlorophyllide reductase (AHRD V1 _ Q8LAV9_ARATH); contains Interpro domain(s) IPR005979 Light_dependent protochlorophyllide reductase	3	0.010498	0.009733189	7.98E-05	tetrapyrrole synthesis.protochlorophyllide reductase
Solyc12g043120	functional_description:Heat shock protein 4 (AHRD V1 _ B6U237_MAIZE); contains Interpro domain(s) IPR013126 Heat shock protein 70	2	0.13152	0.098613327	0.00645888	major CHO metabolism.degradation.sucrose.invertases.neutral
Solyc12g088180	functional_description:Tubulin alpha_7 chain (AHRD V1 _ B9IJV8_POPTR); contains Interpro domain(s) IPR002452 Alpha tubulin	2	0.019131	0.00356372	0.00027193	cell.organisation
Solyc12g089210	functional_description:Ornithine carbamoyltransferase (AHRD V1 _ Q9SEX4_CANLI); contains Interpro domain(s) IPR002292 Ornithine carbamoyltransferase	2	0.097001	0.084360662	0.00760621	protein.postranslational modification
Solyc12g094620	functional_description:Catalase (AHRD V1 _ Q2PYW5_SOLTU); contains Interpro domain(s) IPR018028 Catalase related subgroup	3	0.037664	0.004263398	0.03338597	redox.dismutases and catalases
Solyc12g094640	functional_description:Glyceraldehyde_3_phosphate dehydrogenase B (AHRD V1 _ B4F8L7_MAIZE); contains Interpro domain(s) IPR000173 Glyceraldehyde 3_phosphate dehydrogenase	2	0.029274	0.033016236	0.00962778	protein.postranslational modification
Solyc12g099080	functional_description:ADP ribosylation factor (AHRD V1 __ Q08IJ1_TOBAC); contains Interpro domain(s) IPR006688 ADP_ribosylation factor	2	0.068168	0.012916609	4.56E-05	protein.targeting.secretory pathway.unspecified

List of upregulated proteins in SH-SL leaf

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO	STD.DEV	PVALUE	MAPMAN CLASS
Solyc01g007320.2.1	ATP synthase subunit beta chloroplastic	2	11.428929	11.37328943	0.002901749	mitochondrial electron transport / ATP synthesis.F1-ATPase
Solyc02g082760.2.1	Catalase	2	4.4770448	2.238692278	0.004440871	redox.dismutases and catalases
Solyc02g091580.2.1	Oligopeptidase A	3	4.2366014	1.263100305	0.001633142	protein.degradation
Solyc03g007890.2.1	Heat shock protein 90 (Fragment)	2	2.9501589	1.377473403	0.014097134	stress.abiotic.heat
Solyc06g036290.2.1	Heat shock protein 90 (Fragment)	2	2.9501589	1.377473403	0.014097134	RNA.regulation of transcription.MYB-related transcription factor family
Solyc06g076020.2.1	heat shock protein	3	6.5913514	2.525821535	0.00089047	transport.misc
Solyc10g081510.1.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2	2.9668184	1.037822351	0.006500767	amino acid metabolism.synthesis.aspartate family.methionine.methionine synthase
Solyc10g086410.2.1	Heat shock protein 70-3	2	6.5024538	2.564180447	0.002381342	protein.folding
Solyc11g069790.1.1	chaperonin	2	15.213297	19.27315477	0.009675311	protein.folding

List of downregulated proteins in SH-SL leaf

PROTEIN ID	DESCRIPTION	PEPTIDES	RATIO	STD.DEV	PVALUE	MAPMAN CLASS
Solyc01g007330.2.1	Ribulose bisphosphate carboxylase large chain	11	22	54	0.003372858	PScalvin cyclerubisco large subunit
Solyc01g007340.2.1	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	2	1	2	0.168998755	not assignedunknown
Solyc01g007500.2.1	Photosystem II CP47 chlorophyll apoprotein	7	11	13	0.004301047	PSlightreactionphotosystem IIPSII polypeptide subunits
Solyc01g008000.2.1	ADP-ribosylation factor	2	1	2	0.153102187	proteintargetingsecretory pathwayunspecified
Solyc01g009990.2.1	Peptidyl-prolyl cis-trans isomerase	3	3	8	0.066798716	cellcyclepeptidylprolyl isomerase
Solyc01g056940.2.1	Ubiquitin	2	3	10	0.004571091	proteindegradationubiquitinubiquitin
Solyc01g080280.2.1	Glutamine synthetase	2	3	9	0.073539101	N-metabolismammonia metabolismglutamine synthase
Solyc01g087730.2.1	50S ribosomal protein L1	2	2	2	0.104460454	proteinsynthesisribosomal proteinprokaryoticchloroplast50S subunitL1
Solyc01g096290.2.1	Ubiquitin	2	3	7	0.004571091	proteindegradationubiquitinubiquitin
Solyc01g097910.2.1	Rubredoxin family protein	2	1	4	0.118355315	proteinassembly and cofactor ligation
Solyc01g098950.1.1	Glyceraldehyde-3-phosphate dehydrogenase	3	5	10	0.051259838	glycolysiscytosolic branchglyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc01g100520.2.1	ATP-dependent Clp protease proteolytic subunit	2	1	2	0.049395173	proteindegradationserine protease
Solyc01g100860.2.1	ADP-ribosylation factor	2	1	2	0.153102187	proteintargetingsecretory pathwayunspecified
Solyc01g105030.2.1	Chlorophyll a-b binding protein chloroplastic	2	2	15	0.1971363	PSlightreactionphotosystem IILHC-II
Solyc01g105050.2.1	Chlorophyll a-b binding protein chloroplastic	2	2	15	0.1971363	PSlightreactionphotosystem IILHC-II
Solyc01g106480.2.1	Malate dehydrogenase	2	3	12	0.116246259	gluconeogenesisMalate DH
Solyc01g110450.2.1	NADP dependent sorbitol 6-phosphate dehydrogenase (Fragment)	4	2	4	0.301310928	minor CHO metabolismothers
Solyc01g111120.2.1	Triosephosphate isomerase	2	2	5	0.006571159	PScalvin cycleTPI
Solyc01g111630.2.1	Glyoxylate/hydroxypyruvate reductase B	2	2	4	0.017614022	PSphotorespirationhydroxypyruvate reductase
Solyc02g062340.2.1	Fructose-bisphosphate aldolase	3	2	9	0.25440467	PScalvin cyclealdolase
Solyc02g063070.2.1	14-3-3 protein beta/alpha-1	2	2	4	0.037873474	signalling14-3-3 proteins
Solyc02g063150.2.1	Ribulose bisphosphate carboxylase small chain	4	8	28	0.002072653	PScalvin cyclerubisco small subunit
Solyc02g063490.2.1	Malate dehydrogenase	2	3	12	0.116246259	gluconeogenesisMalate DH
Solyc02g065400.2.1	Oxygen-evolving enhancer protein 1 of photosystem II	2	1	3	0.12144871	PSlightreactionphotosystem IIPSII polypeptide subunits
Solyc02g070310.2.1	Ribosomal protein L32	2	1	2	0.072647727	proteinsynthesisribosomal proteineukaryotic60S subunitL32
Solyc02g071000.1.1	Chlorophyll a/b binding protein	5	1	5	0.128449339	PSlightreactionphotosystem IILHC-II
Solyc02g080210.2.1	Pectinesterase	3	2	3	0.106910716	cell wallpectin*esterasesPME
Solyc02g085950.2.1	Ribulose bisphosphate carboxylase small chain	4	7	34	0.000355959	PScalvin cyclerubisco small subunit
Solyc02g090030.2.1	Oxygen-evolving enhancer protein 1 of photosystem II	3	3	3	0.074420161	PSlightreactionphotosystem IIPSII polypeptide subunits
Solyc02g091560.2.1	Serine hydroxymethyltransferase	3	1	5	0.020367681	PSphotorespirationserine hydroxymethyltransferase
Solyc03g005230.2.1	Menaquinone biosynthesis methyltransferase ubiE	2	3	6	0.122654432	secondary metabolismisoprenoidstocopherol biosynthesisMPBQ/MSBQ methyltransferase
Solyc03g034220.2.1	Ribulose bisphosphate carboxylase small chain	5	10	31	0.049874535	PScalvin cyclerubisco small subunit
Solyc03g115820.2.1	Ribulose-5-phosphate-3-epimerase	2	2	6	0.169373947	PScalvin cycleRPE
Solyc03g118240.2.1	Magnesium-protoporphyrin ix methyltransferase	2	2	2	0.075350466	tetrapyrrole synthesismagnesium protoporphyrin IX methyltransferase
Solyc03g119040.2.1	Guanine nucleotide-binding protein beta subunit-like protein	2	3	5	0.010816874	signallingG-proteins
Solyc04g009200.2.1	Glutamate-1-semialdehyde-2 1-aminomutase	2	2	2	0.059628509	tetrapyrrole synthesisGSA
Solyc04g025560.2.1	ADP-ribosylation factor	2	1	2	0.153102187	proteintargetingsecretory pathwayunspecified
Solyc04g079790.2.1	30S ribosomal protein S9	2	4	5	0.043042669	proteinsynthesisribosomal proteinprokaryoticchloroplast30S subunitS9
Solyc05g005190.2.1	ADP-ribosylation factor	2	1	2	0.153102187	proteintargetingsecretory pathwayunspecified
Solyc05g052510.2.1	Clathrin heavy chain	3	3	4	0.113496601	cellvesicle transport
Solyc05g055090.2.1	Ubiquitin carboxyl-terminal hydrolase family protein expressed	3	1	3	0.231779155	proteindegradationubiquitinubiquitin protease
Solyc06g007340.2.1	Gamma-interferon-inducible lysosomal thiol reductase	2	1	2	0.128540671	not assignedunknown
Solyc06g009970.2.1	Elongation factor 1-alpha	2	3	8	0.163487688	proteinsynthesiselongation
Solyc06g054260.1.1	Photosystem I reaction center subunit II	2	2	8	40122462	PSlightreactionphotosystem IPSI polypeptide subunits
Solyc06g063330.2.1	V-type ATP synthase alpha chain	2	3	7	0.118284222	transportp- and v-ATPasesH+-transporting two-sector ATPase
Solyc06g063370.2.1	Chlorophyll a-b binding protein 1A chloroplastic	2	4 .1.1		0.004939219	PSlightreactionphotosystem IILHC-II
Solyc06g069010.2.1	Guanine nucleotide-binding protein beta subunit-like protein	2	3	5	0.010816874	signallingG-proteins
Solyc06g071920.2.1	Glyceraldehyde-3-phosphate dehydrogenase	4	6 .1.1		0.05500229	glycolysiscytosolic branchglyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc07g018360.2.1	Elongation factor Ts	2	2	2	0.090074009	proteinsynthesiselongation
Solyc07g041720.1.1	Oxalate oxidase-like germin 171	2	3	6	0.054072951	stressabioticunspecified
Solyc07g052350.2.1	3-isopropylmalate dehydratase large subunit	2	2	2	0.117534835	TCA / org transformationTCAaconitase
Solyc07g056540.2.1	L-lactate dehydrogenase	3	4	27	0.277676769	PSphotorespirationglycolate oxydase
Solyc07g062870.2.1	30S ribosomal protein S20	2	2	7	0.095198621	proteinsynthesisribosomal proteinprokaryoticchloroplast30S subunitS20
Solyc07g064130.1.1	Ubiquitin	2	3	10	0.004571091	proteindegradationubiquitinubiquitin
Solyc07g066610.2.1	Phosphoglycerate kinase	2	2	5	0.117319513	PScalvin cyclephosphoglycerate kinase
Solyc08g006900.2.1	Ribosomal protein L32	2	1	2	0.072647727	proteinsynthesisribosomal proteineukaryotic60S subunitL32
Solyc08g008590.2.1	Ubiquitin	2	3	10	0.004571091	proteindegradationubiquitinubiquitin
Solyc08g062920.2.1	Elongation factor EF-2	3	5	12	0.003377212	proteinsynthesiselongation
Solyc08g065220.2.1	Glycine dehydrogenase P protein	2	2	7	0.115495202	amino acid metabolismdegradationserine-glycine-cysteine groupglycine
Solyc09g011080.2.1	Ribulose-1 5-bisphosphate carboxylase/oxygenase activase 1	3	3	7	0.000122988	PScalvin cyclerubisco interacting
Solyc09g014520.2.1	Chlorophyll a-b binding protein 6A chloroplastic	2	2	3	0.283080257	PSlightreactionphotosystem IILHC-II
Solyc09g063130.2.1	Photosystem I reaction center subunit IV A	3	1	3	0.021219565	PSlightreactionphotosystem IPSI polypeptide subunits
Solyc10g005110.2.1	Coproporphyrinogen III oxidase aerobic	3	1	3	0.23008693	tetrapyrrole synthesiscoproporphyrinogen III oxidase
Solyc10g005560.2.1	Bi-ubiquitin	2	3	10	0.004571091	proteindegradationubiquitinubiquitin
Solyc10g006480.1.1	Ubiquitin	2	3	10	0.004571091	proteindegradationubiquitinubiquitin
Solyc10g006900.2.1	Protochlorophyllide reductase	2	3 .1.1		0.185445138	tetrapyrrole synthesisprotochlorophyllide reductase
Solyc10g054870.1.1	Triosephosphate isomerase	2	2	5	0.006571159	PScalvin cycleTPI
Solyc10g081510.1.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2	4	16	0.134124061	amino acid metabolismsynthesisaspartate familymethionine
Solyc10g086580.1.1	Ribulose-1 5-bisphosphate carboxylase/oxygenase activase 1	14 .1.1		32	0.293246318	PScalvin cyclerubisco interacting
Solyc11g005640.1.1	Ubiquitin	4	3	18	0.004770135	proteindegradationubiquitinubiquitin
Solyc11g006320.1.1	Ubiquitin carboxyl-terminal hydrolase family protein expressed	3	1	3	0.231779155	proteindegradationubiquitinubiquitin protease
Solyc11g011920.1.1	Glutamate decarboxylase	2	1	2	0.051941752	amino acid metabolismsynthesiscentral amino acid metabolismGABAGlutamate decarboxylase
Solyc11g069700.1.1	Elongation factor 1-alpha	2	3	16	0.163487688	proteinsynthesiselongation
Solyc12g005860.1.1	3-isopropylmalate dehydratase large subunit	2	2	2	0.070998831	TCA / org transformationTCAaconitase
Solyc12g013710.1.1	Protochlorophyllide reductase	2	2	2	0.208755019	tetrapyrrole synthesisprotochlorophyllide reductase
Solyc12g014380.1.1	Glucose-6-phosphate isomerase 1	5	1	6	0.164043155	glycolysisplastid branchglucose-6-phosphate isomerase
Solyc12g055800.1.1	V-type ATP synthase alpha chain	2	3	7	0.118284222	transportp- and v-ATPasesH+-transporting two-sector ATPase
Solyc12g098940.1.1	Ubiquitin	2	3	10	0.004571091	proteindegradationubiquitinubiquitin
Solyc12g099030.1.1	Ubiquitin	2	3	10	0.004571091	proteindegradationubiquitinubiquitin

Table 5.10. Proteins identified only in leaves of wild species but not in tomato leaves.

Label-free quantitation was employed by matching retention times of the peaks and measuring area under the matched peaks using Sieve 2.1 software (Thermo Scientific) to identify the differentially expressed proteins in SH-SL, SP-SL, SG-SL pairs. Stringent selection criteria were imposed to identify those proteins (p value≤0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 peptides for identification, FDR=1%). Some of the proteins were found only in the wild species but not in SL and are given here. Even single peptide matches of these proteins could not be detected in SL.

Proteins identified only in SP-SL leaf

PROTEIN ID	DESCRIPTION	PEPTIDES	PValue
Soipen05g005440	automic: reference:SL2.40ch05 area: reinion:341827..347358 transcrint: reinion:SL2.40ch05.341827..347358 : no: terms:GO:0004791 functional: descrintion: Nucleoredoxin 2 (AHRD V1 : A8F934_CHLRE): contains Interpro domain(s): IPR000866: Alkyl hydroperoxide reduc	2	2.40E-09
Soipen09g091840	automic: reference:SL2.40ch09 area: reinion:66389831..66399718 transcrint: reinion:SL2.40ch09.66389831..66399718 : no: terms:GO:0004362 functional: descrintion: Glutathione disulfide reductase (AHRD V1 : O1D9Y5_MYXXD): contains Interpro domain(s): IPR006324	2	2.40E-09
Soipen07g066610	automic: reference:SL2.40ch07 area: reinion:65209792..65212260 transcrint: reinion:SL2.40ch07.65209792..65212260 : no: terms:GO:0005524 functional: descrintion: Phosphoenolpyruvate kinase (AHRD V1 : O81394_SOLTU): contains Interpro domain(s): IPR001576: Phosphoe	2	7.77E-13
Soipen02g086820	automic: reference:SL2.40ch02 area: reinion:44012475..44019926 transcrint: reinion:SL2.40ch02.44012475..44019926 : no: terms:GO:0005515 functional: descrintion: Carbonic anhydrase (AHRD V1 : C8NE20_SOLCU): contains Interpro domain(s): IPR015892: Carbonic anh	6	9.90E-20
Soipen01g011250	evidence: code:10F1H1E1EG automic: reference:SL2.40ch11 area: reinion:4291341..4296684 transcrint: reinion:SL2.40ch11.4291341..4296684 : functional: descrintion: Chloride intracellular channel 6 (AHRD V1 : B6UCX2_MAIZE): contains Interpro domain(s): IPR01793	3	2.22E-16
Soipen09g011300	automic: reference:SL2.40ch09 area: reinion:4641043..4645919 transcrint: reinion:SL2.40ch09.4641043..4645919 : no: terms:GO:0005515 GO:0004845 functional: descrintion: Uracil phosphoribosyltransferase (AHRD V1 : B6U5U2_MAIZE): contains Interpro domain(s): IP	3	6.32E-13
Soipen07g044860	automic: reference:SL2.40ch07 area: reinion:55244985..55247025 transcrint: reinion:SL2.40ch07.55244985..55247025 : no: terms:GO:0008266 functional: descrintion: Oxoneh evolvins enhancer protein 2 : chloroplastic (AHRD V1 : P5IBP_SOLLC): contains Interpro domain	3	6.32E-13
Soipen07g052790	evidence: code:10F1H1E1HEG genomic: reference:SL2.40ch07 area: reginn:58560010..58563287 transcrint: reginn:SL2.40ch07.58560010..58563287 : no: terms:GO:0030275 GO:0000166 functional: descrintion: _Nbs_lrr_ resistance protein	2	2.40E-09
Soipen07g063040	automic: reference:SL2.40ch07 area: reinion:62856775..62862494 transcrint: reinion:SL2.40ch07.62856775..62862494 : no: terms:GO:0046872 GO:0008152 GO:0003737 GO:0015939 functional: descrintion: Enolase : rhoreshaina E 1 (AHRD V1 : A8UON2_9AOUD): cont	2	2.40E-09
Soipen03g044080	evidence: code:10F1H1E1EG automic: reference:SL2.40ch03 area: reinion:11762616..11765056 transcrint: reinion:SL2.40ch03.11762616..11765056 : no: terms:GO:0003735 GO:0003723 functional: descrintion: Ribosomal protein L26 (AHRD V1 : A8HMG7_CHLRE): con	2	2.40E-09
Soipen04g077970	automic: reference:SL2.40ch04 area: reinion:60430505..60453397 transcrint: reinion:SL2.40ch04.60430505..60453397 : no: terms:GO:0016208 GO:0003999 functional: descrintion: Adenine rhonotherhosvltransferase like (AHRD V1 : I2Y997_SOLTU): contains Interpro do	2	7.77E-13
Soipen03g005200	automic: reference:SL2.40ch05 area: reinion:173412..177352 transcrint: reinion:SL2.40ch05.173412..177352 : no: terms:GO:0008233 functional: descrintion: Peptidase rotidase (AHRD V1 : B6SPB9_MAIZE): contains Interpro domain(s): IPR000816: Peptidas	2	2.40E-09
Soipen09g009740	automic: reference:SL2.40ch09 area: reinion:66314629..66317264 transcrint: reinion:SL2.40ch09.66314629..66317264 : no: terms:GO:0003735 GO:0005515 functional: descrintion: 60S ribosomal protein L13a like protein (AHRD V1 : O10BW1_SOLTU): contains Interpro	2	2.40E-09
Soipen01g007670	automic: reference:SL2.40ch01 area: reinion:1893908..1894685 transcrint: reinion:SL2.40ch01.1893908..1894685 : no: terms:GO:0005840 GO:0015935 functional: descrintion: 30S ribosomal protein S7 chloroplastic (AHRD V1 : D3WBE1_9BORA): contains Interpro domai	2	7.77E-13
Soipen09g050080	evidence: code:10F1H1E1EG automic: reference:SL2.40ch09 area: reinion:32305139..32305606 transcrint: reinion:SL2.40ch09.32305139..32305606 : no: terms:GO:0003735 functional: descrintion: 30S ribosomal protein S7 chloroplastic (AHRD V1 : D3WBE1_9BORA): co	2	7.77E-13
Soipen08g082750	automic: reference:SL2.40ch06 area: reinion:44741305..44743095 transcrint: reinion:SL2.40ch06.44741305..44743095 : no: terms:GO:0005840 functional: descrintion: 50S ribosomal protein L17 (AHRD V1 : B4FZB4_MAIZE): contains Interpro domain(s): IPR000456: Ribos	2	2.40E-09
Soipen08g082760	automic: reference:SL2.40ch06 area: reinion:44743556..44745679 transcrint: reinion:SL2.40ch06.44743556..44745679 : no: terms:GO:0005840 functional: descrintion: 50S ribosomal protein L17 (AHRD V1 : B4FZB4_MAIZE): contains Interpro domain(s): IPR000456: Ribos	2	2.40E-09
Soipen09g011580	automic: reference:SL2.40ch09 area: reinion:4859444..4860733 transcrint: reinion:SL2.40ch09.4859444..4860733 : no: terms:GO:0004364 GO:0043295 functional: descrintion: Glutathione S transferase like protein (AHRD V1 : A8DUB9_SOLLC): contains Interpro domain	2	2.40E-09
Soipen03g012360	evidence: code:10F0H1E1EG automic: reference:SL2.40ch03 area: reinion:56836935..56837381 transcrint: reinion:SL2.40ch03.56836935..56837381 : no: terms:GO:0003735 functional: descrintion: 60S ribosomal protein L27A (AHRD V1 : B6VCS4_VERFO): contains Inter	2	2.40E-09
Soipen02g063070	automic: reference:SL2.40ch02 area: reinion:29692418..29699297 transcrint: reinion:SL2.40ch02.29692418..29699297 : no: terms:GO:0050815 functional: descrintion: 14 3 3 protein beta/alpha 1 (AHRD V1 : 143B1_DANRE): contains Interpro domain(s): IPR000308: 14 3	2	2.40E-09
Soipen03g034180	automic: reference:SL2.40ch03 area: reinion:10153209..10155317 transcrint: reinion:SL2.40ch03.10153209..10155317 : no: terms:GO:0050815 functional: descrintion: 14 3 3 protein beta/alpha 1 (AHRD V1 : 143B1_DANRE): contains Interpro domain(s): IPR000308: 14 3	2	2.40E-09
Soipen04g076060	automic: reference:SL2.40ch04 area: reinion:58620807..58625601 transcrint: reinion:SL2.40ch04.58620807..58625601 : no: terms:GO:0050815 functional: descrintion: 14 3 3 protein beta/alpha B (AHRD V1 : 143BB_XENLA): contains Interpro domain(s): IPR000308: 14 3	2	2.40E-09

Proteins identified only in SG leaf

PROTEIN ID	DESCRIPTION	PEPTIDES	PValue	Mapman category
Solyc01g005520	genomic reference:SL2.40ch01 gene region:349916 352687 transcript region:SL2.40ch01:349916..352687 go terms:GO:0005515 GO:0005488 functional description: Tetratricopeptide TPR 2 repeat protein (AHRD V1 A8ZVN6 DESOH): contains Interpro domain(s) IPR00147	2	2.40E-09	RNA.processing.degradation dicer
Solyc01g005560	genomic reference:SL2.40ch01 gene region:394402 399248 transcript region:SL2.40ch01:394402..399248 go terms:GO:0055114 functional description: Isocitrate dehydrogenase (AHRD V1 D2D324 GOSHI): contains Interpro domain(s) IPR004790 Isocitrate dehydrogenase NA	3	6.32E-13	RNA.transcription
Solyc01g007280	genomic reference:SL2.40ch01 gene region:1841683 1842652 transcript region:SL2.40ch01:1841683..1842652 go terms:GO:0015935 GO:0003723 GO:0005622 functional description: 30S ribosomal protein S4 chloroplastic (AHRD V1 B5MF80 PETIN): contains Interpro dom	2	2.40E-09	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S4
Solyc01g007320	genomic reference:SL2.40ch01 gene region:1849252 1851757 transcript region:SL2.40ch01:1849252..1851757 go terms:GO:0045261 GO:0005524 GO:0017111 GO:0033178 GO:0016469 functional description: ATP synthase subunit beta chloroplastic (AHRD V1 Q8MBF8 9	2	2.40E-09	mitochondrial electron transport / ATP synthesis.F1-ATPase
Solyc01g007330	genomic reference:SL2.40ch01 gene region:1851938 1853783 transcript region:SL2.40ch01:1851938..1853783 go terms:GO:0015977 GO:0009536 functional description: Ribulose bisphosphate carboxylase large chain (AHRD V1 RBL SOLLC): contains Interpro domain(s) IPR	3	6.32E-13	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S15
Solyc01g028810	genomic reference:SL2.40ch01 gene region:33327242 33332361 transcript region:SL2.40ch01:33327242..33332361 go terms:GO:0044267 GO:0005737 functional description: chaperonin (AHRD V1 B4VMY1 9CYAN): contains Interpro domain(s) IPR001844 Chaperonin Cpn	2	2.40E-09	protein.folding
Solyc01g087730	genomic reference:SL2.40ch01 gene region:74419417 74424513 transcript region:SL2.40ch01:74419417..74424513 go terms:GO:0006396 GO:0005840 GO:0015934 functional description: 50S ribosomal protein L1 (AHRD V1 A8YGI8 MICAE): contains Interpro domain(s) I	2	2.40E-09	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L1
Solyc01g097340	chloroplast.50S subunit.L1	2	2.40E-09	NAD-dependent epimerase/dehydratase family protei redox.ascorbate and glutathione.ascorbate.GME
Solyc01g099900	Ribosomal protein L18	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc02g063150	genomic reference:SL2.40ch02 gene region:29802717 29803963 transcript region:SL2.40ch02:29802717..29803963 go terms:GO:0005515 GO:0005507 functional description: Ribulose bisphosphate carboxylase small chain (AHRD V1 Q84QE5 TOBAC): contains Interpro dom	2	2.40E-09	transport.amino acids
Solyc02g070320	genomic reference:SL2.40ch02 gene region:34677490 34679867 transcript region:SL2.40ch02:34677490..34679867 go terms:GO:0032183 GO:0003735 functional description: 40S ribosomal protein S4 like protein (AHRD V1 Q2XPX5 SOLTU): contains Interpro domain(s) IP	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc02g065400	Oxygen-evolving enhancer protein 1 of photosystem II	2	2.40E-09	Oxygen-evolving enhancer protein 1 of photosystem II
Solyc02g070310	Ribosomal protein L32	3	2.22E-16	Ribosomal protein L32
Solyc02g070330	genomic reference:SL2.40ch02 gene region:34681390 34683768 transcript region:SL2.40ch02:34681390..34683768 go terms:GO:0032183 GO:0003735 functional description: 40S ribosomal protein S4 like protein (AHRD V1 Q2XPX5 SOLTU): contains Interpro domain(s) IP	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc02g070360	genomic reference:SL2.40ch02 gene region:34691346 34693734 transcript region:SL2.40ch02:34691346..34693734 go terms:GO:0032183 GO:0003735 functional description: 40S ribosomal protein S4 like protein (AHRD V1 Q2XPX5 SOLTU): contains Interpro domain(s) IP	2	2.40E-09	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S4
Solyc02g070940	evidence code:10F0H1E1IEG genomic reference:SL2.40ch02 gene region:35081036 35081833 transcript region:SL2.40ch02:35081036..35081833 go terms:GO:0016168 functional description: Chlorophyll a/b binding protein (AHRD V1 Q41422 SOLTU): contains Interpro dom	2	2.40E-09	PS.lightreaction.photosystem II.LHC-II
Solyc02g070980	evidence code:10F1H1E1IEG genomic reference:SL2.40ch02 gene region:35092891 35093688 transcript region:SL2.40ch02:35092891..35093688 go terms:GO:0005515 GO:0016168 functional description: Chlorophyll a/b binding protein (AHRD V1 Q41422 SOLTU): contains	2	2.40E-09	PS.lightreaction.photosystem II.LHC-II
Solyc02g070990	evidence code:10F0H1E1IEG genomic reference:SL2.40ch02 gene region:35095230 35096027 transcript region:SL2.40ch02:35095230..35096027 go terms:GO:0005515 GO:0016168 functional description: Chlorophyll a/b binding protein (AHRD V1 Q41422 SOLTU): contains	2	2.40E-09	PS.lightreaction.photosystem II.LHC-II
Solyc02g071000	evidence code:10F0H1E1IEG genomic reference:SL2.40ch02 gene region:35097630 35098427 transcript region:SL2.40ch02:35097630..35098427 go terms:GO:0005515 GO:0016168 functional description: Chlorophyll a/b binding protein (AHRD V1 Q41425 SOLTU): contains	2	2.40E-09	PS.lightreaction.photosystem II.LHC-II
Solyc02g072160	genomic reference:SL2.40ch02 gene region:36050355 36058273 transcript region:SL2.40ch02:36050355..36058273 go terms:GO:0008152 functional description: NADH ubiquinone oxidoreductase complex I intermediate associated protein 30 (AHRD V1 B2IZH1 NOSP7): conta	2	2.40E-09	signalling.light
Solyc02g080540	evidence code:10F1H1E1IEG genomic reference:SL2.40ch02 gene region:39325443 39326576 transcript region:SL2.40ch02:39325443..39326576 go terms:GO:0030234 functional description: ATP synthase gamma chain (AHRD V1 B7FIR4 MEDTR): contains Interpro domain(	2	2.40E-09	PS.lightreaction.ATP synthase.gamma chain
Solyc02g080810	genomic reference:SL2.40ch02 gene region:39515754 39519204 transcript region:SL2.40ch02:39515754..39519204 go terms:GO:0004375 GO:0005515 GO:0031405 functional description: Aminomethyltransferase (AHRD V1 C6TF02 SOYBN): contains Interpro domain(s) IP	2	2.40E-09	PS.photorespiration.glycine cleavage.T subunit
Solyc02g085950	genomic reference:SL2.40ch02 gene region:43293286 43294312 transcript region:SL2.40ch02:43293286..43294312 go terms:GO:0005515 GO:0005507 functional description: Ribulose bisphosphate carboxylase small chain (AHRD V1 A9YTZ7 SOLTU): contains Interpro doma	2	2.40E-09	PS.calvin cycle.rubisco small subunit
Solyc02g086820	genomic reference:SL2.40ch02 gene region:44012475 44015926 transcript region:SL2.40ch02:44012475..44015926 go terms:GO:0005515 functional description: Carbonic anhydrase (AHRD V1 Q5NE20 SOLLC): contains Interpro domain(s) IPR015892 Carbonic anhydrase p	5	9.90E-20	TCA / organic transformation.carbonic anhydrases
Solyc02g086910	genomic reference:SL2.40ch02 gene region:44078232 44082017 transcript region:SL2.40ch02:44078232..44082017 go terms:GO:0006457 functional description: Peptidyl prolyl cis trans isomerase cyclophilin type (AHRD V1 A8IRU6 CHLRE): contains Interpro domain(s) IP	2	2.40E-09	protein.folding
Solyc02g091490	genomic reference:SL2.40ch02 gene region:47344370 47349179 transcript region:SL2.40ch02:47344370..47349179 go terms:GO:0008865 GO:0008959 functional description: Fructokinase 3 (AHRD V1 Q6VWJ5 SOLLC): contains Interpro domain(s) IPR011611 Carbohydrate	2	2.40E-09	major CHO metabolism.degradation.sucrose.fructokinase
Solyc03g005260	genomic_reference:SL2.40ch03 gene_region:148411_153101 transcript_region:SL2.40ch03:148411..153101_ go_terms:GO:0004781 functional_description:_Sulfate adenylyltransferase (AHRD V1 ____ Q43183_SOLTU); contains Interpro domain(s) IPR002650 ATP_sulfurylase _	2	2.40E-09	S-assimilation.APS
Solyc03g005760	evidence code:10F0H1E1IEG genomic reference:SL2.40ch03 gene region:538196 538999 transcript region:SL2.40ch03:538196..538999 go terms:GO:0005515 GO:0016168 functional description: Chlorophyll a b binding protein 3C like (AHRD V1 Q2XTE0 SOLTU): contains	2	2.40E-09	PS.lightreaction.photosystem II.LHC-II
Solyc03g005770	evidence code:10F0H1E1IEG genomic reference:SL2.40ch03 gene region:540995 541798 transcript region:SL2.40ch03:540995..541798 go terms:GO:0005515 GO:0016168 functional description: Chlorophyll a b binding protein 3C like (AHRD V1 Q2XTE0 SOLTU): contains	2	2.40E-09	PS.lightreaction.photosystem II.PSII polypeptide subunits
Solyc03g005780	evidence code:10F1H1E1IEG genomic reference:SL2.40ch03 gene region:543035 543838 transcript region:SL2.40ch03:543035..543838 go terms:GO:0016168 functional description: Chlorophyll a b binding protein 3C like (AHRD V1 Q2XTE0 SOLTU): contains Interpro doma	2	2.40E-09	PS.lightreaction.photosystem II.PSII polypeptide subunits
Solyc03g034220	genomic reference:SL2.40ch03 gene region:10202373 10205106 transcript region:SL2.40ch03:10202373..10205106 go terms:GO:0005515 GO:0005507 functional description: Ribulose bisphosphate carboxylase small chain (AHRD V1 A9YTZ7 SOLTU): contains Interpro doma	2	2.40E-09	transport.amino acids
Solyc03g111010	genomic reference:SL2.40ch03 gene region:55761566 55765048 transcript region:SL2.40ch03:55761566..55765048 go terms:GO:0004365 functional description: Glyceraldehyde 3 phosphate dehydrogenase (AHRD V1 Q9XG67 TOBAC): contains Interpro domain(s) IPR00017	2	2.40E-09	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc03g117430	genomic reference:SL2.40ch03 gene region:60652978 60660774 transcript region:SL2.40ch03:60652978..60660774 go terms:GO:0005515 GO:0003824 functional description: Cobalamin synthesis protein P (AHRD V1 D3M8Z8 9ACTO): contains Interpro domain(s) IPR00349	2	2.40E-09	RNA.regulation of transcription.PWWP domain protein
Solyc03g117740	genomic_reference:SL2.40ch03 gene_region:60839793_60842602 transcript_region:SL2.40ch03:60839793..60842602_ functional_description:_Chloroplast At1g16080 protein (Fragment) (AHRD V1 ____ Q1HRY1_SOLLC)_	3	6.32E-13	redox.dismutases and catalases
Solyc03g119040	genomic reference:SL2.40ch03 gene region:61807988 61810035 transcript region:SL2.40ch03:61807988..61810035 go terms:GO:0005080 GO:0000166 functional description: Guanine nucleotide binding protein beta subunit like protein (AHRD V1 B4FKM1 MAIZE): contains	3	6.32E-13	development.unspecified
Solyc04g007550	genomic reference:SL2.40ch04 gene region:1237504 1241655 transcript region:SL2.40ch04:1237504..1241655 go terms:GO:0005507 functional description: ATP synthase subunit beta (AHRD V1 Q82722 NICSY): contains Interpro domain(s) IPR005722 ATPase F1 complex	2	2.40E-09	mitochondrial electron transport / ATP synthesis.F1-ATPase
Solyc04g009200	genomic reference:SL2.40ch04 gene region:2695320 2699163 transcript region:SL2.40ch04:2695320..2699163 go terms:GO:0005515 GO:0042286 functional description: Glutamate 1 semialdehyde 2 1 aminomutase (AHRD V1 D7MPQ2 ARALY): contains Interpro domain(s)	3	6.32E-13	misc.oxidases - copper flavone etc
Solyc04g010240	genomic reference:SL2.40ch04 gene region:3562006 3565042 transcript region:SL2.40ch04:3562006..3565042 go terms:GO:0003735 functional description: 60S ribosomal protein L35 (AHRD V1 D7M7V2 ARALY): contains Interpro domain(s) IPR001854 Ribosomal protein I	2	2.40E-09	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L35
Solyc04g011440	genomic_reference:SL2.40ch04 gene_region:3894918_3898067 transcript_region:SL2.40ch04:3894918..3898067_ go_terms:GO:0051082 functional_description:_heat shock protein (AHRD V1 ____ B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70 _	2	2.40E-09	stress.abiotic.heat
Solyc04g074640	genomic reference:SL2.40ch04 gene region:58163011 58168188 transcript region:SL2.40ch04:58163011..58168188 go terms:GO:0005031 functional description: L ascorbate peroxidase (AHRD V1 A8JG56 CHLRE): contains Interpro domain(s) IPR002207 Plant ascorbate per	2	2.40E-09	redox.ascorbate and glutathione.ascorbate
Solyc04g082310	genomic_reference:SL2.40ch04 gene_region:63614917_63618869 transcript_region:SL2.40ch04:63614917..63618869_ functional_description:_Seed maturation protein PM23 (Fragment) (AHRD V1 ____ Q9SEL1_SOYBN)_	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc04g082630	genomic reference:SL2.40ch04 gene region:63844019 63847151 transcript region:SL2.40ch04:63844019..63847151 go terms:GO:0004365 functional description: Glyceraldehyde 3 phosphate dehydrogenase B (AHRD V1 B4F8L7 MAIZE): contains Interpro domain(s) IPR0001	2	2.40E-09	PS.calvin cycle.GAP
Solyc05g009030	genomic reference:SL2.40ch05 gene region:3194068 3201893 transcript region:SL2.40ch05:3194068..3201893 go terms:GO:0003862 functional description: 3 isopropylmalate dehydrogenase (AHRD V1 B5LAV1 CAPAN): contains Interpro domain(s) IPR004429 Isopropylmal	2	2.40E-09	amino acid metabolism.synthesis.branched chain group.leucine specific.3-isopropylmalate dehydrogenase
Solyc05g012510	genomic reference:SL2.40ch05 gene region:5760758 5767157 transcript region:SL2.40ch05:5760758..5767157 go terms:GO:0008184 functional description: Phosphorylase (AHRD V1 B9HXL0 POPTR): contains Interpro domain(s) IPR011833 Glycogen/starch/alpha glucan ph	2	7.77E-13	major CHO metabolism.degradation.starch.starch phosphorylase
Solyc05g014470	genomic reference:SL2.40ch05 gene region:8322381 8324881 transcript region:SL2.40ch05:8322381..8324881 go terms:GO:0004365 functional description: Glyceraldehyde 3 phosphate dehydrogenase (AHRD V1 Q8LK04 SOLTU): contains Interpro domain(s) IPR000173 Gly	2	2.40E-09	glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc05g053300	genomic reference:SL2.40ch05 gene region:62572547 62577624 transcript region:SL2.40ch05:62572547..62577624 go terms:GO:0005515 functional description: Dihydrolipoyl dehydrogenase (AHRD V1 Q8GT30 SOLLC): contains Interpro domain(s) IPR012999 Pyridine nucl	3	6.32E-13	redox.ascorbate and glutathione.glutathione
Solyc05g054810	genomic reference:SL2.40ch05 gene region:63775298 63777437 transcript region:SL2.40ch05:63775298..63777437 go terms:GO:0003735 functional description: 60S ribosomal protein L35 (AHRD V1 D7M7V2 ARALY): contains Interpro domain(s) IPR001854 Ribosomal pro	2	2.40E-09	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L35
Solyc06g005150	genomic reference:SL2.40ch06 gene region:170218 173338 transcript region:SL2.40ch06:170218..173338 go terms:GO:0055114 functional description: Ascorbate peroxidase (AHRD V1 Q52QQ4 SOLLC): contains Interpro domain(s) IPR019793 Peroxidases heam ligand bindi	2	2.40E-09	redox.ascorbate and glutathione.ascorbate
Solyc06g005160	genomic reference:SL2.40ch06 gene region:182627 185280 transcript region:SL2.40ch06:182627..185280 go terms:GO:0055114 functional description: Ascorbate peroxidase (AHRD V1 Q9SMD3 SOLLC): contains Interpro domain(s) IPR019793 Peroxidases heam ligand bind	2	2.40E-09	redox.ascorbate and glutathione.ascorbate
Solyc06g048730	genomic reference:SL2.40ch06 gene region:28105228 28112767 transcript region:SL2.40ch06:28105228..28112767 go terms:GO:0004853 GO:0042803 functional description: Uroporphyrinogen decarboxylase (AHRD V1 C6TEE8 SOYBN): contains Interpro domain(s) IPR000	2	2.40E-09	cell wall.precursor synthesis.UXS
Solyc06g064470	genomic reference:SL2.40ch06 gene region:36536162 36538759 transcript region:SL2.40ch06:36536162..36538759 go terms:GO:0003735 functional description: Ribosomal protein L7a (AHRD V1 A8J567 CHLRE): contains Interpro domain(s) IPR001921 Ribosomal protein L	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc06g069010	genomic reference:SL2.40ch06 gene region:39208568 39211380 transcript region:SL2.40ch06:39208568..39211380 go terms:GO:0005080 GO:0000166 functional description: Guanine nucleotide binding protein beta subunit like protein (AHRD V1 B6SJ21 MAIZE): contains I	3	6.32E-13	signalling.G-proteins
Solyc06g069090	genomic reference:SL2.40ch06 gene region:39269885 39272377 transcript region:SL2.40ch06:39269885..39272377 go terms:GO:0005840 functional description: 40S ribosomal protein S7 like protein (AHRD V1 Q3HRX6 SOLTU): contains Interpro domain(s) IPR000554 Rib	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc06g071790	genomic reference:SL2.40ch06 gene region:40601620 40603444 transcript region:SL2.40ch06:40601620..40603444 go terms:GO:0003746 functional description: Elongation factor Tu (AHRD V1 D7MFK2 ARALY): contains Interpro domain(s) IPR004541 Translation elongatio	2	2.40E-09	protein.synthesis.elongation
Solyc06g073260	genomic reference:SL2.40ch06 gene region:41530107 41533923 transcript region:SL2.40ch06:41530107..41533923 go terms:GO:0008266 GO:0003729 functional description: NAD dependent epimerase/dehydratase (AHRD V1 C7OWY4 CYAP0): contains Interpro domain(s)	3	6.32E-13	RNA.regulation of transcription.unclassified
Solyc06g073310	genomic reference:SL2.40ch06 gene region:41552819 41554750 transcript region:SL2.40ch06:41552819..41554750 go terms:GO:0032183 GO:0003735 functional description: Ribosomal L9 like protein (AHRD V1 B3TLR1 ELAGV): contains Interpro domain(s) IPR000702 R	2	2.40E-09	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L9
Solyc06g074980	genomic reference:SL2.40ch06 gene region:42868689 42875665 transcript region:SL2.40ch06:42868689..42875665 go terms:GO:0016787 GO:0005524 GO:0017111 GO:0005488 functional description: 26S protease regulatory subunit 6B homolog (AHRD V1 PRS6B ARATH	3	6.32E-13	protein.degradation.ubiquitin.proteasom
Solyc06g075620	genomic reference:SL2.40ch06 gene region:43394530 43397000 transcript region:SL2.40ch06:43394530..43397000 go terms:GO:0003735 functional description: 60S ribosomal protein L35 (AHRD V1 D7M7V2 ARALY): contains Interpro domain(s) IPR001854 Ribosomal pro	2	2.40E-09	RNA.RNA binding
Solyc06g076020	genomic reference:SL2.40ch06 gene region:43582389 43585486 transcript region:SL2.40ch06:43582389..43585486 go terms:GO:0051082 GO:0005524 functional description: heat shock protein (AHRD V1 B2D2G5 CAPSN): contains Interpro domain(s) IPR013126 Heat shoc	2	2.40E-09	transport.misc
Solyc06g076540	evidence code:10F0H1E1IEG genomic reference:SL2.40ch06 gene region:43940957 43941421 transcript region:SL2.40ch06:43940957..43941421 functional description: class I heat shock protein (AHRD V1 Q69BI7 CARPA): contains Interpro domain(s) IPR002068 Heat shocl	2	2.40E-09	stress.abiotic.heat
Solyc07g005390	genomic reference:SL2.40ch07 gene region:296474 302315 transcript region:SL2.40ch07:296474..302315 go terms:GO:0004028 functional description: Aldehyde dehydrogenase (AHRD V1 A7GLM2 BACCN): contains Interpro domain(s) IPR015590 Aldehyde dehydrogenase	2	2.40E-09	glycolysis.cytosolic branch.non-phosphorylating glyceraldehyde 3-phosphate dehydrogenase (NPGAP-DH)
Solyc07g047850	genomic reference:SL2.40ch07 gene region:56404445 56405833 transcript region:SL2.40ch07:56404445..56405833 go terms:GO:0016168 functional description: Chlorophyll a b binding protein 4 chloroplastic (AHRD V1 CB24 SOLLC): contains Interpro domain(s) IPR00134	2	2.40E-09	PS.lightreaction.photosystem II.LHC-II
Solyc07g055060	genomic reference:SL2.40ch07 gene region:60510756 60518074 transcript region:SL2.40ch07:60510756..60518074 go terms:GO:0005515 functional description: Phosphoenolpyruvate carboxylase 1 (AHRD V1 O23946 GOSHI): contains Interpro domain(s) IPR015813 Pyruvat	2	2.40E-09	glycolysis.cytosolic branch.phospho-enol-pyruvate carboxylase (PEPC)
Solyc07g064950	genomic reference:SL2.40ch07 gene region:64125602 64131741 transcript region:SL2.40ch07:64125602..64131741 go terms:GO:0015031 GO:0006457 functional description: Trigger factor like protein (AHRD V1 Q9FLP1 ARATH): contains Interpro domain(s) IPR005215 T	2	2.40E-09	protein.folding
Solyc07g056540	L-lactate dehydrogenase	2	2.40E-09	L-lactate dehydrogenase
Solyc07g066600	genomic reference:SL2.40ch07 gene region:65205704 65208684 transcript region:SL2.40ch07:65205704..65208684 go terms:GO:0005524 functional description: Phosphoglycerate kinase (AHRD V1 Q2VCK2 SOLTU): contains Interpro domain(s) IPR001576 Phosphoglycerate	3	6.32E-13	glycolysis.cytosolic branch.3-phosphoglycerate kinase (PGK)
Solyc07g066610	genomic reference:SL2.40ch07 gene region:65209792 65212260 transcript region:SL2.40ch07:65209792..65212260 go terms:GO:0005524 functional description: Phosphoglycerate kinase (AHRD V1 Q81394 SOLTU): contains Interpro domain(s) IPR001576 Phosphoglycerate k	2	2.40E-09	glycolysis.cytosolic branch.3-phosphoglycerate kinase (PGK)
Solyc08g006900	Ribosomal protein L32	2	7.77E-13	Ribosomal protein L32
Solyc08g014550	genomic reference:SL2.40ch08 gene region:4642663 4644841 transcript region:SL2.40ch08:4642663..4644841 go terms:GO:0003735 functional description: Ribosomal L9 like protein (AHRD V1 B3TLR1 ELAGV): contains Interpro domain(s) IPR000702 Ribosomal protein L	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc08g067330	evidence code:10F1H1E1IEG genomic reference:SL2.40ch08 gene region:53597297 53597593 transcript region:SL2.40ch08:53597297..53597593 go terms:GO:0016020 functional description: Chlorophyll a b binding protein 3C like (AHRD V1 Q2XTE0 SOLTU): contains Int	2	2.40E-09	PS.lightreaction.photosystem II.LHC-II
Solyc09g007560	genomic reference:SL2.40ch09 gene region:1157881 1159523 transcript region:SL2.40ch09:1157881..1159523 go terms:GO:0005840 functional description: 50S ribosomal protein L5 (AHRD V1 B5TV71 CAMSI): contains Interpro domain(s) IPR002132 Ribosomal protein L5	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc09g010630	genomic_reference:SL2.40ch09 gene_region:3965253_3968837 transcript_region:SL2.40ch09:3965253..3968837_ go_terms:GO:0051082 functional_description:_heat shock protein (AHRD V1 ____ B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70 _	3	6.32E-13	cell wall.hemicellulose synthesis
Solyc09g011080	genomic reference:SL2.40ch09 gene region:4413327 4416467 transcript region:SL2.40ch09:4413327..4416467 go terms:GO:0046863 functional description: Ribulose 1 5 bisphosphate carboxylase/oxygenase activase 1 (AHRD V1 Q9AXG1 GOSHI): contains Interpro domain(s	7	9.90E-20	PS.calvin cycle.rubisco interacting
Solyc09g011500	genomic reference:SL2.40ch09 gene region:4812615 4814198 transcript region:SL2.40ch09:4812615..4814198 go terms:GO:0004364 functional description: Glutathione S transferase like protein (AHRD V1 A8DUB0 SOLLC): contains Interpro domain(s) IPR004046 Glutathio	2	2.40E-09	development.unspecified
Solyc09g011810	genomic reference:SL2.40ch09 gene region:5090038 5092652 transcript region:SL2.40ch09:5090038..5092652 go terms:GO:0042132 functional description: Fructose 1 6 bisphosphatase class 1 (AHRD V1 D0MHZ8 RHOM4): contains Interpro domain(s) IPR000146 Fructose	3	6.32E-13	PS.calvin cycle.FBPase
Solyc09g073000	genomic reference:SL2.40ch09 gene region:61156838 61164570 transcript region:SL2.40ch09:61156838..61164570 go terms:GO:0003746 functional description: Elongation factor Tu (AHRD V1 B9SFP0 RICCO): contains Interpro domain(s) IPR004541 Translation elongation	2	2.40E-09	protein.synthesis.elongation
Solyc09g091180	genomic reference:SL2.40ch09 gene region:65848356 65853683 transcript region:SL2.40ch09:65848356..65853683 go terms:GO:0005524 GO:0005507 functional description: chaperonin (AHRD V1 Q6N0B9 9PROT): contains Interpro domain(s) IPR001844 Chaperonin Cpn6	2	2.40E-09	stress.abiotic.heat
Solyc10g007600	genomic reference:SL2.40ch10 gene region:1896939 1901455 transcript region:SL2.40ch10:1896939..1901455 go terms:GO:0008891 functional description: L lactate dehydrogenase (AHRD V1 LLDD VIBPA): contains Interpro domain(s) IPR012133 Alpha hydroxy acid dehy	2	2.22E-16	PS.photorespiration.glycolate oxydase
Solyc10g009570	genomic reference:SL2.40ch10 gene region:3694886 3699858 transcript region:SL2.40ch10:3694886..3699858 go terms:GO:0005515 functional description: Rhodanese related sulfurtransferase (AHRD V1 A4U0O7 9PROT): contains Interpro domain(s) IPR001763 Rhodanese	2	2.40E-09	misc.rhodanese
Solyc10g018300	evidence code:10F0H1E1IEG genomic reference:SL2.40ch10 gene region:7264174 7267205 transcript region:SL2.40ch10:7264174..7267205 go terms:GO:0004802 GO:0005515 functional description: Transketolase 1 (AHRD V1 O78327 CAPAN): contains Interpro domain(s)	3	6.32E-13	OPP.non-reductive PP.transketolase
Solyc10g078930	evidence code:10F0H1E1IEG genomic reference:SL2.40ch10 gene region:59896781 59900058 transcript region:SL2.40ch10:59896781..59900058 go terms:GO:0051087 GO:0001671 functional description: Activator of heat shock protein ATPase homolog 1 (AHRD V1 D3PJW	2	2.40E-09	DNA.synthesis/chromatin structure.histone
Solyc10g081030	evidence code:10F0H1E1IEG genomic reference:SL2.40ch10 gene region:61534917 61538284 transcript region:SL2.40ch10:61534917..61538284 go terms:GO:0051082 functional description: Nascent polypeptide associated complex alpha subunit like protein (AHRD V1 B6T9	2	7.77E-13	cell.unspecified
Solyc10g084050	evidence code:10F0H1E1IEG genomic reference:SL2.40ch10 gene region:63048965 63053841 transcript region:SL2.40ch10:63048965..63053841 go terms:GO:0016787 GO:0005524 GO:0017111 GO:0005488 functional description: 26S protease regulatory subunit 6B homolog (Al	3	6.32E-13	cell.division
Solyc10g086010	evidence code:10F0H1E1IEG genomic reference:SL2.40ch10 gene region:64326308 64329401 transcript region:SL2.40ch10:64326308..64329401 go terms:GO:0005840 functional description: 60S ribosomal protein L4/L1 (AHRD V1 D7L8A9 ARALY): contains Interpro domai	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc10g086410	genomic reference:SL2.40ch10 gene region:64561395 64564764 transcript region:SL2.40ch10:64561395..64564764 go terms:GO:0051082 functional description: Heat shock protein 70 3 (AHRD V1 O67BD0 TOBAC): contains Interpro domain(s) IPR013126 Heat shock protei	2	2.40E-09	protein.folding
Solyc10g086580	evidence code:10F0H1E1IEG genomic reference:SL2.40ch10 gene region:64688483 64690961 transcript region:SL2.40ch10:64688483..64690961 go terms:GO:0005524 functional description: Ribulose 1 5 bisphosphate carboxylase/oxygenase activase 1 (AHRD V1 Q9AXG1	9	9.90E-20	PS.calvin cycle.rubisco interacting
Solyc11g007990	evidence code:10F1H1E1IEG genomic reference:SL2.40ch11 gene region:2198505 2203902 transcript region:SL2.40ch11:2198505..2203902 go terms:GO:0030060 functional description: Malate dehydrogenase (AHRD V1 Q5NE17 SOLLC): contains Interpro domain(s) IPR01	2	2.40E-09	RNA.regulation of transcription.NAC domain transcription factor family
Solyc11g008620	evidence code:10F1H1E1IEG genomic reference:SL2.40ch11 gene region:2807207 2813709 transcript region:SL2.40ch11:2807207..2813709 go terms:GO:0008152 functional description: Phosphoglycolate phosphatase (AHRD V1 C1FHY2 9CHLO): contains Interpro domain(s	2	2.40E-09	minor CHO metabolism.misc
Solyc11g011920	evidence code:10F1H1E1IEG genomic reference:SL2.40ch11 gene region:4848830 4855228 transcript region:SL2.40ch11:4848830..4855228 go terms:GO:0006536 GO:0030170 GO:0019752 functional description: Glutamate decarboxylase (AHRD V1 Q8LKR4 TOBAC): co	3	6.32E-13	amino acid metabolism.synthesis.central amino acid metabolism.GABA.glutamate decarboxylase
Solyc11g066060	evidence code:10F0H1E1IEG genomic reference:SL2.40ch11 gene region:48824058 48826931 transcript region:SL2.40ch11:48824058..48826931 go terms:GO:0005524 functional description: heat shock protein (AHRD V1 B2D2G5 CAPSN): contains Interpro domain(s) IPR0	2	2.40E-09	misc.cytochrome P450
Solyc11g066410	evidence code:10F1H1E1IEG genomic reference:SL2.40ch11 gene region:49273765 49276760 transcript region:SL2.40ch11:49273765..49276760 go terms:GO:0005840 functional description: 50S ribosomal protein L9 (AHRD V1 B4FU53 MAIZE): contains Interpro domain(s)	2	2.40E-09	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L9
Solyc11g069720	evidence code:10F1H1E1IEG genomic reference:SL2.40ch11 gene region:51412028 51417585 transcript region:SL2.40ch11:51412028..51417585 go terms:GO:0016787 GO:0005524 GO:0005975 GO:0017111 GO:0005488 functional description: 26S protease regulatory subunit 6	3	6.32E-13	protein.degradation.ubiquitin.proteasom
Solyc12g005860	3-isopropylmalate dehydratase large subunit	2	2.40E-09	3-isopropylmalate dehydratase large subunit
Solyc12g010840	Ketol-acid reductoisomerase	2	2.40E-09	Ketol-acid reductoisomerase
Solyc12g011280	Chlorophyll a-b binding protein 8 chloroplastic	3	2.22E-16	Chlorophyll a-b binding protein 8 chloroplastic
Solyc12g014390	50S ribosomal protein L13	2	2.40E-09	50S ribosomal protein L13
Solyc12g042060	ATP-dependent clp protease ATP-binding subunit	3	6.32E-13	ATP-dependent clp protease ATP-binding subunit
Solyc12g042080	40S ribosomal protein S11	2	2.40E-09	40S ribosomal protein S11
Solyc11g069790	evidence code:10F1H1E1IEG genomic reference:SL2.40ch11 gene region:51502451 51507359 transcript region:SL2.40ch11:51502451..51507359 go terms:GO:0044267 GO:0005737 functional description: chaperonin (AHRD V1 B2IXD2 NOSP7): contains Interpro domain(s)	2	2.40E-09	PS.calvin cycle.rubisco interacting
Solyc12g006140	evidence code:10F1H1E1IEG genomic reference:SL2.40ch12 gene region:693217 694582 transcript region:SL2.40ch12:693217..694582 go terms:GO:0016020 functional description: Chlorophyll a b binding protein 37 chloroplastic (AHRD V1 CB26 PETSP): contains Interpro	2	2.40E-09	PS.lightreaction.photosystem II.LHC-II
Solyc12g009250	evidence code:10F1H1E1IEG genomic reference:SL2.40ch12 gene region:2529842 2532163 transcript region:SL2.40ch12:2529842..2532163 go terms:GO:0051087 functional description: chaperonin (AHRD V1 D1U6H2 9DELT): contains Interpro domain(s) IPR001476 Chap	3	6.32E-13	protein.folding
Solyc12g040510	evidence code:10F0H1E1IEG genomic reference:SL2.40ch12 gene region:39489012 39490607 transcript region:SL2.40ch12:39489012..39490607 functional description: Guanine nucleotide binding protein beta subunit like protein (AHRD V1 B6SJ21 MAIZE): contains Interpro	3	6.32E-13	signalling.G-proteins
Solyc12g056830	evidence code:10F0H1E1IEG genomic reference:SL2.40ch12 gene region:48264644 48265396 transcript region:SL2.40ch12:48264644..48265396 go terms:GO:0045261 functional description: ATP synthase delta subunit (AHRD V1 Q7XYM8 BIGNA): contains Interpro domain	2	2.40E-09	PS.lightreaction.ATP synthase.delta chain
Solyc12g094640	evidence code:10F0H1E1IEG genomic reference:SL2.40ch12 gene region:63152981 63156043 transcript region:SL2.40ch12:63152981..63156043 go terms:GO:0008152 GO:0055114 functional description: Glyceraldehyde 3 phosphate dehydrogenase B (AHRD V1 B4F8L7 M	3	6.32E-13	protein.postranslational modification
Solyc12g096300	evidence code:10F1H1E1IEG genomic reference:SL2.40ch12 gene region:63621756 63624205 transcript region:SL2.40ch12:63621756..63624205 go terms:GO:0005840 functional description: 40S ribosomal protein S6 (AHRD V1 B6T1H0 MAIZE): contains Interpro domain(s)	2	2.40E-09	protein.synthesis.ribosome biogenesis
Solyc12g096700	evidence code:10F0H1E1IEG genomic reference:SL2.40ch12 gene region:63855944 63857858 transcript region:SL2.40ch12:63855944..63857858 go terms:GO:0005840 functional description: Ribosomal L9 like protein (AHRD V1 B3TLR1 ELAGV): contains Interpro domain(	2	2.40E-09	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L9
Solyc12g100160	evidence code:10F0H1E1IEG genomic reference:SL2.40ch12 gene region:65330773 65334942 transcript region:SL2.40ch12:65330773 65334942 go terms:GO:0005840 functional description: 50S ribosomal protein L6 (AHRD V1 B6SL57 MAIZE): contains Interpro domain(s)	2	2.40E-09	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L6

Proteins identified only in SH leaf

PROTEINID	DESCRIPTION	PEPTIDES	PVALUE	Mapman category
Solyc01g007330.2.1	Ribulose bisphosphate carboxylase large chain	2	2.40E-09	PScalvin cyclerubisco large subunit
Solyc01g028810.2.1	chaperonin	2	2.40E-09	proteinfolding
Solyc01g080280.2.1	Glutamine synthetase	2	2.40E-09	N-metabolismammonia metabolismglutamine synthase
Solyc01g097340.2.1	NAD-dependent epimerase/dehydratase family protein-like protein	2	2.40E-09	cell wallprecursor synthesisUXS
Solyc01g099900.2.1	Ribosomal protein L18	2	2.40E-09	proteinsynthesisribosomal proteineukaryotic60S subunitL18
Solyc01g101060.2.1	S-adenosylmethionine synthase	2	2.40E-09	amino acid metabolismsynthesisaspartate familymethionine
Solyc01g105060.2.1	(3R)-hydroxymyristoyl-	2	2.40E-09	lipid metabolismFA synthesis and FA elongationbeta hydroxyacyl ACP dehydratase
Solyc01g110360.2.1	Fructose-bisphosphate aldolase	2	2.40E-09	PScalvin cyclealdolase
Solyc01g111630.2.1	Glyoxylate/hydroxypyruvate reductase B	2	2.40E-09	PSphotorespirationhydroxypyruvate reductase
Solyc02g065400.2.1	Oxygen-evolving enhancer protein 1 of photosystem II	2	2.40E-09	PSlightreactionphotosystem IIPSII polypeptide subunits
Solyc02g070310.2.1	Ribosomal protein L32	3	2.22E-16	proteinsynthesisribosomal proteineukaryotic60S subunitL32
Solyc03g034220.2.1	Ribulose bisphosphate carboxylase small chain	3	6.32E-13	PScalvin cyclerubisco small subunit
Solyc03g096850.2.1	Genomic DNA chromosome 5 P1 clone MKP11	2	2.40E-09	proteinassembly and cofactor ligation
Solyc03g111010.2.1	Glyceraldehyde-3-phosphate dehydrogenase	5	9.90E-20	glycolysiscytosolic branchglyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc03g111840.2.1	Polyadenylate-binding protein 1-like	2	2.40E-09	RNARNA binding
Solyc03g112150.1.1	Elongation factor Tu	3	6.32E-13	proteinsynthesiselongation
Solyc03g118340.2.1	ATP-dependent clp protease ATP-binding subunit	2	2.40E-09	proteindegradationserine protease
Solyc03g120850.2.1	chaperonin	2	2.40E-09	proteinfolding
Solyc04g011510.2.1	Triosephosphate isomerase	3	6.32E-13	PScalvin cycleTPI
Solyc04g082630.2.1	Glyceraldehyde-3-phosphate dehydrogenase B	2	7.77E-13	PScalvin cycleGAP
Solyc05g010670.2.1	Chaperone protein htpG	2	2.40E-09	stressabioticheat
Solyc05g014470.2.1	Glyceraldehyde 3-phosphate dehydrogenase	6	9.90E-20	glycolysiscytosolic branchglyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc05g052600.2.1	Fructose-1 6-bisphosphatase class 1	2	2.40E-09	PScalvin cycleseduheptulose bisphosphatase
Solyc06g009020.2.1	Glutathione S-transferase	2	2.40E-09	miscglutathione S transferases
Solyc06g071920.2.1	Glyceraldehyde-3-phosphate dehydrogenase	4	2.22E-16	glycolysiscytosolic branchglyceraldehyde 3-phosphate dehydrogenase (GAP-DH)
Solyc06g073310.2.1	Ribosomal L9-like protein	2	2.40E-09	proteinsynthesisribosomal proteineukaryotic60S subunitL9
Solyc06g073790.2.1	40S ribosomal protein S11	2	2.40E-09	proteinsynthesisribosomal proteineukaryotic40S subunitS11
Solyc06g075930.1.1	Histone H4	2	2.40E-09	DNAsynthesis/chromatin structurehistone
Solyc07g053280.2.1	Ketol-acid reductoisomerase	2	2.40E-09	amino acid metabolismsynthesisbranched chain groupcommon
Solyc07g056540.2.1	L-lactate dehydrogenase	2	2.40E-09	PSphotorespirationglycolate oxydase
Solyc08g006900.2.1	Ribosomal protein L32	2	7.77E-13	proteinsynthesisribosomal proteineukaryotic60S subunitL32
Solyc08g014340.2.1	Cysteine synthase	2	2.40E-09	amino acid metabolismsynthesisserine-glycine-cysteine groupcysteineOASTL
Solyc08g062800.2.1	ATP-dependent RNA helicase eIF4A	2	2.40E-09	DNAsynthesis/chromatin structure
Solyc08g076220.2.1	Phosphoribulokinase/uridine kinase	2	2.40E-09	PScalvin cyclePRK
Solyc09g009260.2.1	Fructose-bisphosphate aldolase	2	2.40E-09	PScalvin cyclealdolase
Solyc09g082060.2.1	Cysteine synthase	2	2.40E-09	amino acid metabolismsynthesisserine-glycine-cysteine groupcysteineOASTL
Solyc10g007600.2.1	L-lactate dehydrogenase	2	2.40E-09	PSphotorespirationglycolate oxydase
Solyc10g007690.2.1	Chlorophyll a-b binding protein 8 chloroplastic	4	9.90E-20	PSlightreactionphotosystem IILHC-II
Solyc10g083570.1.1	Fructose-bisphosphate aldolase	2	2.40E-09	PScalvin cyclealdolase
Solyc10g086150.1.1	Single-stranded DNA binding protein	2	2.40E-09	RNARNA binding
Solyc11g066160.1.1	Histone H4	2	2.40E-09	DNAsynthesis/chromatin structurehistone
Solyc11g066410.1.1	50S ribosomal protein L9	2	2.40E-09	proteinsynthesisribosomal proteinprokaryoticchloroplast50S subunitL9
Solyc11g069150.1.1	Proteasome subunit beta type	2	2.40E-09	proteindegradationubiquitinproteasom
Solyc11g072840.1.1	Histone H4	2	2.40E-09	DNAsynthesis/chromatin structurehistone
Solyc12g005860.1.1	3-isopropylmalate dehydratase large subunit	2	2.40E-09	TCA / org transformationTCAaconitase
Solyc12g010840.1.1	Ketol-acid reductoisomerase	2	2.40E-09	amino acid metabolismsynthesisbranched chain groupcommon
Solyc12g011280.1.1	Chlorophyll a-b binding protein 8 chloroplastic	3	2.22E-16	PSlightreactionphotosystem IILHC-II
Solyc12g014390.1.1	50S ribosomal protein L13	2	2.40E-09	proteinsynthesisribosomal proteinprokaryoticchloroplast50S subunitL13
Solyc12g042060.1.1	ATP-dependent clp protease ATP-binding subunit	3	6.32E-13	proteindegradationserine protease
Solyc12g042080.1.1	40S ribosomal protein S11	2	2.40E-09	proteinsynthesisribosomal proteineukaryotic40S subunitS11
Solyc12g094640.1.1	Glyceraldehyde-3-phosphate dehydrogenase B	2	7.77E-13	PScalvin cycleGAP
Solyc12g095990.1.1	ATP-dependent RNA helicase eIF4A	2	2.40E-09	DNAsynthesis/chromatin structure
Solyc12g096000.1.1	ATP-dependent RNA helicase eIF4A	2	2.40E-09	DNAsynthesis/chromatin structure
Solyc12g099000.1.1	S-adenosylmethionine synthase	2	2.40E-09	amino acid metabolismsynthesisaspartate familymethionine

Table 5.11. Percentage of functional categories present at 39 dpa fruits of wild species.

Functional Category	SP		SG		SH	
	Up-regulated proteins (%)	Down-regulated proteins (%)	Up-regulated proteins (%)	Down-regulated proteins (%)	Up-regulated proteins (%)	Down-regulated proteins (%)
Abiotic stress	1.9	21.9	4.1	67.3	0.0	5.1
Amino acid metabolism	2.8	4.2	1.4	18.4	0.0	3.4
Biodegradation of xenobiotics	0.9	0.3	0.0	2.0	0.0	0.0
Biotic stress	0.0	1.5	0.0	6.1	0.0	1.1
C1 metabolism	0.0	1.2	0.0	4.1	0.0	0.6
Cell cycle/Cell division	0.0	1.5	0.0	10.2	0.0	0.6
Cell organisation	0.0	1.8	0.0	8.2	0.0	1.7
Cell wall degradation	3.8	1.2	0.0	34.7	0.0	1.1
Cofactor and vitamin metabolism	0.0	0.0	0.0	6.1	0.0	0.0
Development storage proteins	25.5	0.0	5.5	0.0	0.0	0.0
RNA processing/DNA synthesis/chrot	0.0	0.0	0.0	10.2	4.3	0.6
Fermentation	2.8	0.3	0.0	0.0	0.0	0.6
Gluconeogenesis	0.0	0.6	2.7	4.1	0.0	0.6
Glycolysis	1.9	4.2	0.0	16.3	0.0	2.3
Hormone metabolism	11.3	4.5	9.6	18.4	0.0	1.7
Lipid metabolism	0.9	1.2	2.7	14.3	0.0	4.0
Major CHO metabolism	6.6	0.0	0.0	14.3	0.0	0.6
Metal handling	0.0	0.6	2.7	0.0	0.0	1.1
Minor CHO metabolism	0.9	0.6	1.4	2.0	0.0	1.1
Misc.	9.4	4.0	8.2	53.1	4.3	5.1
Misc.alcohol dehydrogenases	0.0	1.2	0.0	0.0	0.0	0.6
Misc.short chain dehydrogenases	2.8	0.6	1.4	0.0	0.0	0.0
Mitochondrial electron transport	0.9	0.9	0.0	2.0	4.3	1.7
N-metabolism	0.0	1.5	1.4	4.1	0.0	0.0
Nucleotide metabolism	0.0	1.5	1.4	0.0	0.0	2.3
OPP	0.0	0.6	0.0	0.0	0.0	0.0
Post translational modification	0.0	1.5	0.0	14.3	4.3	2.3
Protein degradation	0.9	6.6	9.6	75.5	0.0	13.0
Protein folding	0.0	1.5	0.0	38.8	4.3	1.1
Protein synthesis	1.9	1.5	0.0	18.4	17.4	7.9
Protein targeting	0.0	0.3	1.4	6.1	0.0	2.3
Protein.aa activation	0.0	0.6	0.0	4.1	0.0	2.3
PS calvin cycle	0.0	3.9	1.4	1.6	8.6	1.1
PS light reaction	0.0	0.9	0.0	1.4	8.6	1.7
PS photorespiration	0.0	0.0	4.1	0.0	0.0	0.6
Redox	3.8	5.1	2.7	16.3	13.0	1.1
RNA regulation of transcription	3.8	2.1	2.7	24.5	8.7	7.3
Secondary metabolism	5.7	0.9	6.8	8.2	4.3	5.1
Signaling	0.9	1.2	23.3	18.4	0.0	4.0
TCA	2.8	5.1	0.0	10.2	0.0	1.7
Tetrapyrrole synthesis	0.0	0.6	0.0	6.1	0.0	2.8
Transport	1.9	3.6	4.1	49.0	8.7	6.2
Unknown	5.7	8.4	1.4	6.1	0.0	1.7
Development, unspecified	0.0	0.0	0.0	4.1	0.0	0.0

Table 6.1. Differentially expressed proteins identified in the fruits of *Nps1* and AC at different developmental stages using nanoLC-MS-MS.

Labelled quantitation was used to identify the differentially expressed proteins in *Nps1*. Peptide and protein identifications were performed through Protein Pilot 4.0 software (ABSCIEX) on the basis of the following selection criteria (Pvalue ≤ 0.05, minimum 2-fold change (either up- or down-regulation), minimum 2 unique peptides for identification, FDR=1%).

Accession	Name of the protein	Unused ProtScore	Total Protscore	%Cov(95)	Peptides(95%)	115:114	pvalue 115:114	EF 115:114	116:114	pvalue 116:114	EF 116:114	117:114	pvalue 117:114	EF 117:114
Solyc00g060810.1.1	genomic_reference:SL2.31ch00 evidence_code:10F1H0E1IEG gene_region:14159743-14161838 functional_description:"Major latex-like protein (AHRD V1 **-- B5THI3_PANGI): contains Interpro domain(s) IPF	3.38	3.38	15.07000029	3	15.560	0.038	5.297	4.325	0.049	6.138	25.586	0.033	4.920
Solyc00g060810.1.1	genomic_reference:SL2.31ch00 evidence_code:10F1H0E1IEG gene_region:14159743-14161838 functional_description:"Major latex-like protein (AHRD V1 **-- B5THI3_PANGI): contains Interpro domain(s) IPF	2.21	2.21	13.69999945	2	11.912	0.043	31.623	16.444	0.047	32.211	29.376	0.036	33.419
Solyc01g007330.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:1852121-1853554 functional_description:"Ribulose bisphosphate carboxylase large chain (AHRD V1 ***- RBL_SOLLC): contains Interp	40.94	40.94	38.35999966	29	1.282	0.095	1.191	0.256	0.000	1.977	0.251	0.000	1.941
Solyc01g007330.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:1852121-1853554 functional_description:"Ribulose bisphosphate carboxylase large chain (AHRD V1 ***- RBL_SOLLC): contains Intern	43.82	43.82	36.05999947	35	0.912	0.813	1.127	0.661	0.088	1.318	0.106	0.000	4.130
Solyc01g007500.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:1869775-1871597 functional_description:"Photosystem II CP47 chlorophyll apoprotein (AHRD V1 ***- D3WBA3_9BORA): contains Int	16.81	16.81	17.36000031	14	0.863	0.326	1.393	0.718	0.102	1.486	0.033	0.000	6.427
Solyc01g007500.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:1869775-1871597 functional_description:"Photosystem II CP47 chlorophyll apoprotein (AHRD V1 ***- D3WBA3_9BORA): contains Int	13.51	13.51	10.67000031	8	1.225	0.564	1.500	1.486	0.251	1.528	0.031	0.045	2.704
Solyc01g080460.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:72207323-72214665 functional_description:"Pyruvate phosphate dikinase (AHRD V1 ***- Q84N32_SORBI): contains Interpro domain(s)	37.91	37.91	19.78999972	25	2.032	0.007	1.585	1.556	0.326	1.459	2.208	0.000	1.629
Solyc01g080460.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:72207323-72214665 functional_description:"Pyruvate phosphate dikinase (AHRD V1 ***- Q84N32_SORBI): contains Interpro domain(s)	34.72	34.72	15.23000002	23	1.000	0.725	1.202	1.306	0.182	1.236	2.014	0.003	1.368
Solyc01g099190.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:81252230-81255665 functional_description:"Lipoxygenase (AHRD V1 **** Q42873_SOLLC): contains Interpro domain(s) IPR001246	62.46	62.46	40.09000063	44	1.803	0.102	1.259	7.447	0.018	1.556	19.231	0.001	1.629
Solyc01g099190.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:81252230-81255665 functional_description:"Lipoxygenase (AHRD V1 **** Q42873_SOLLC): contains Interpro domain(s) IPR001246	63.75	63.77	37.65000105	57	1.472	0.163	1.247	2.704	0.047	1.528	25.823	0.000	1.888
Solyc01g008710.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:2755138-2757943 functional_description:"Mannan endo-1 4-beta-mannosidase (AHRD V1 ***- D2S259_HALTV): contains Interpro dom	4.06	4.06	4.510999843	4	0.247	0.016	2.312	13.804	0.019	2.992	53.951	0.006	1.977
Solyc01g008710.1.2	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:2755138-2757943 functional_description:"Mannan endo-1 4-beta-mannosidase (AHRD V1 ***- D2S259_HALTV): contains Interpro dom	3.04	20.23	10.65	4	0.352	0.012	2.405	13.982	0.018	2.888	54.027	0.005	1.864
Solyc02g065400.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:31151211-31153195 functional_description:"Oxygen-evolving enhancer protein 1 of photosystem II (AHRD V1 ***- A8J0E4_CHLRE): c	10.05	10.05	16.11000001	7	0.643	0.573	1.432	0.879	0.910	1.318	0.031	0.016	4.966
Solyc02g065400.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:31151211-31153195 functional_description:"Oxygen-evolving enhancer protein 1 of photosystem II (AHRD V1 ***- A8J0E4_CHLRE): c	8.08	8.4	13.07000071	5	0.855	0.964	1.355	1.067	0.890	1.294	0.205	0.011	1.406
Solyc02g086880.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:44063370-44067505 functional_description:"Formate dehydrogenase (AHRD V1 **** Q5NE18_SOLLC): contains Interpro domain(s) IP	19.69	19.69	29.39999998	14	1.306	0.332	1.486	0.904	0.555	1.445	2.291	0.038	1.722
Solyc02g086880.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:44063370-44067505 functional_description:"Formate dehydrogenase (AHRD V1 **** Q5NE18_SOLLC): contains Interpro domain(s) IP	20.1	20.1	24.93000031	12	0.946	0.523	1.368	1.854	0.254	1.542	4.285	0.000	1.754
Solyc03g083910.1.1	genomic_reference:SL2.31ch03 evidence_code:10F0H1E1IEG gene_region:47398423-47402347 functional_description:"Acid beta-fructofuranosidase (AHRD V1 **-- Q575T1_WHEAT): contains Interpro domain(	17.21	17.21	16.35999978	13	2.938	0.004	2.089	0.370	0.125	2.291	3.631	0.002	2.109
Solyc03g083910.1.1	genomic_reference:SL2.31ch03 evidence_code:10F0H1E1IEG gene_region:47398423-47402347 functional_description:"Acid beta-fructofuranosidase (AHRD V1 **-- Q575T1_WHEAT): contains Interpro domain(	37.79	37.79	26.0800004	28	1.459	0.231	1.368	0.575	0.394	1.644	31.046	0.000	1.738
Solyc03g098240.1.1	genomic_reference:SL2.31ch03 evidence_code:10F1H1E1IEG gene_region:54044225-54048071 functional_description:"Glutamate decarboxylase (AHRD V1 **** B6TV07_MAIZE): contains Interpro domain(s) I	5.89	8.28	8.167000115	6	1.306	0.438	2.109	2.535	0.045	1.854	2.679	0.039	1.380
Solyc03g098240.1.1	genomic_reference:SL2.31ch03 evidence_code:10F1H1E1IEG gene_region:54044225-54048071 functional_description:"Glutamate decarboxylase (AHRD V1 **** B6TV07_MAIZE): contains Interpro domain(s) I	4.09	8.12	5.178999901	4	1.556	0.096	2.911	3.837	0.022	2.965	6.546	0.014	2.911
Solyc03g115230.1.1	genomic_reference:SL2.31ch03 evidence_code:10F0H1E1IEG gene_region:59065622-59068816 functional_description:"ClpB chaperone (AHRD V1 ***- D6QXJ5_TRYCR): contains Interpro domain(s) IPR01309	39.89	40.03	24.80999976	27	1.271	0.414	1.330	2.270	0.011	1.629	4.018	0.000	1.941
Solyc03g115230.1.1	genomic_reference:SL2.31ch03 evidence_code:10F0H1E1IEG gene_region:59065622-59068816 functional_description:"ClpB chaperone (AHRD V1 ***- D6QXJ5_TRYCR): contains Interpro domain(s) IPR01309	32.04	32.32	18.65999997	21	0.560	0.350	1.585	0.863	0.578	1.432	2.188	0.002	1.459
Solyc04g006970.1.1	genomic_reference:SL2.31ch04 evidence_code:10F0H1E1IEG gene_region:663809-674721 functional_description:"Phosphoenolpyruvate carboxylase (AHRD V1 **** A6YM33_RICCO): contains Interpro domain	30.78	33.95	15.71000069	19	1.107	0.849	1.294	0.705	0.026	1.330	0.251	0.000	1.888
Solyc04g006970.1.1	genomic_reference:SL2.31ch04 evidence_code:10F0H1E1IEG gene_region:663809-674721 functional_description:"Phosphoenolpyruvate carboxylase (AHRD V1 **** A6YM33_RICCO): contains Interpro domain	13.94	18.29	7.81000033	9	1.169	0.471	1.247	0.705	0.447	1.271	0.088	0.000	2.938
Solyc04g007770.1.1	genomic_reference:SL2.31ch04 evidence_code:10F1H1E1IEG gene_region:1456882-1458653 functional_description:"Major latex-like protein (AHRD V1 **-- Q9AXU0_PRUPE): contains Interpro domain(s) IPR(	23.41	23.41	39.4600004	24	1.067	0.166	1.368	0.847	0.213	1.419	0.092	0.000	4.920
Solyc04g007770.1.1	genomic_reference:SL2.31ch04 evidence_code:10F1H1E1IEG gene_region:1456882-1458653 functional_description:"Major latex-like protein (AHRD V1 **-- Q9AXU0_PRUPE): contains Interpro domain(s) IPR(	22.55	22.55	44.22000051	18	1.419	0.017	1.294	0.904	0.173	1.306	0.056	0.000	3.981
Solyc04g008740.1.1	genomic_reference:SL2.31ch04 evidence_code:10F1H1E1IEG gene_region:2399524-2402426 functional_description:"Pyruvate kinase (AHRD V1 **** Q3S1N4_SOLTU): contains Interpro domain(s) IPR001697	15.81	15.88	11.76000014	10	0.242	0.156	3.020	0.839	0.258	2.377	5.248	0.003	2.148
Solyc04g008740.1.1	genomic_reference:SL2.31ch04 evidence_code:10F1H1E1IEG gene_region:2399524-2402426 functional_description:"Pyruvate kinase (AHRD V1 **** Q3S1N4_SOLTU): contains Interpro domain(s) IPR001697	9.87	9.95	7.058999687	6	1.318	0.581	1.905	1.306	0.541	2.333	4.529	0.025	2.109
Solyc05g005460.1.1	genomic_reference:SL2.31ch05 evidence_code:10F0H1E1IEG gene_region:341827-347035 functional_description:"Nucleoredoxin 2 (AHRD V1 *--- A8J9J4_CHLRE): contains Interpro domain(s) IPR000866 Alk	9.61	9.91	6.885000318	4	0.453	0.188	2.032	0.535	0.051	1.754	0.474	0.034	1.660
Solyc05g005460.1.1	genomic_reference:SL2.31ch05 evidence_code:10F0H1E1IEG gene_region:341827-347035 functional_description:"Nucleoredoxin 2 (AHRD V1 *--- A8J9J4_CHLRE): contains Interpro domain(s) IPR000866 Alk	12.78	12.93	8.950000256	6	0.759	0.575	1.419	2.559	0.005	1.690	0.294	0.451	2.965
Solyc05g054760.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:63754560-63758454 functional_description:"Dehydroascorbate reductase (Fragment) (AHRD V1 ***- Q1G0W3_SOLLC): contains Interp	14.61	14.61	38.10000122	10	1.127	0.504	1.259	0.773	0.578	1.614	0.325	0.013	1.923
Solyc05g054760.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:63754560-63758454 functional_description:"Dehydroascorbate reductase (Fragment) (AHRD V1 ***- Q1G0W3_SOLLC): contains Interp	18.09	18.09	46.18999958	11	1.629	0.124	1.306	0.855	0.444	1.282	0.211	0.002	2.014
Solyc06g059740.1.1	genomic_reference:SL2.31ch06 evidence_code:10F0H1E1IEG gene_region:33996214-33998056 functional_description:"Alcohol dehydrogenase 2 (AHRD V1 **** Q84UY3_PETHY): contains Interpro domain(s)	48.21	48.21	46.88000083	46	0.718	0.269	1.225	0.863	0.870	1.225	6.792	0.000	1.528
Solyc06g059740.1.1	genomic_reference:SL2.31ch06 evidence_code:10F0H1E1IEG gene_region:33996214-33998056 functional_description:"Alcohol dehydrogenase 2 (AHRD V1 **** Q84UY3_PETHY): contains Interpro domain(s)	39.29	39.29	34.38000083	40	0.673	0.165	1.294	0.429	0.100	1.406	5.105	0.000	1.472
Solyc06g063370.1.1	genomic_reference:SL2.31ch06 evidence_code:10F1H1E1IEG gene_region:36437124-36438771 functional_description:"Chlorophyll a-b binding protein 1A, chloroplastic (AHRD V1 ***- CB2A_PYRPY): contain	13.99	13.99	31.47000074	8	1.368	0.210	1.247	0.855	0.299	1.486	0.029	0.034	2.089
Solyc06g063370.1.1	genomic_reference:SL2.31ch06 evidence_code:10F1H1E1IEG gene_region:36437124-36438771 functional_description:"Chlorophyll a-b binding protein 1A, chloroplastic (AHRD V1 ***- CB2A_PYRPY): contain	13.96	13.99	31.47000074	8	1.343	0.501	1.138	1.871	0.159	1.180	0.029	0.038	2.399
Solyc06g068860.1.1	genomic_reference:SL2.31ch06 evidence_code:10F0H1E1IEG gene_region:39074207-39083962 functional_description:"Alpha-mannosidase (AHRD V1 **** D3TI68_SOLLC): contains Interpro domain(s) IPR011	2.79	3.43	0.680899993	2	0.920	0.468	1.355	1.629	0.075	1.318	2.032	0.019	1.330
Solyc06g068860.1.2	genomic_reference:SL2.31ch06 evidence_code:10F0H1E1IEG gene_region:39074207-39083962 functional_description:"Alpha-mannosidase (AHRD V1 **** D3TI68_SOLLC): contains Interpro domain(s) IPR011	2.84	3.39	0.7201	2	0.898	0.498	1.342	1.616	0.072	1.315	2.035	0.017	1.325
Solyc07g017610.1.1	genomic_reference:SL2.31ch07 evidence_code:10F0H1E1IEG gene_region:7668165-7679799 functional_description:"Saccharopine dehydrogenase (NAD(+) L-glutamate-forming) (AHRD V1 *-** C7PUW7_CHIP	8.87	8.87	3.717999905	4	0.625	0.695	1.923	2.559	0.017	1.472	4.018	0.002	1.786
Solyc07g017610.1.1	genomic_reference:SL2.31ch07 evidence_code:10F0H1E1IEG gene_region:7668165-7679799 functional_description:"Saccharopine dehydrogenase (NAD(+) L-glutamate-forming) (AHRD V1 *-** C7PUW7_CHIP	5.17	5.38	2.287999913	3	0.973	0.943	1.977	0.560	0.772	2.489	2.729	0.037	1.738
Solyc07g044860.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:55247048-55248446 functional_description:"Oxygen-evolving enhancer protein 2, chloroplastic (AHRD V1 ***- PSBP_SOLLC): contain	19.06	19.06	27.91000009	11	1.213	0.162	1.318	0.955	0.576	1.330	0.055	0.002	5.248
Solyc07g044860.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:55247048-55248446 functional_description:"Oxygen-evolving enhancer protein 2, chloroplastic (AHRD V1 ***- PSBP_SOLLC): contain	13.33	13.33	26.73999965	10	0.955	0.840	1.159	1.406	0.129	1.271	0.126	0.027	2.965
Solyc07g062530.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:62455643-62461072 functional_description:"Phosphoenolpyruvate carboxylase 2 (AHRD V1 ***- Q9SCB2_SOLLC): contains Interpro d	64.7	64.7	36.30999923	45	0.904	0.698	1.236	0.787	0.216	1.271	0.319	0.002	1.738
Solyc07g062530.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:62455643-62461072 functional_description:"Phosphoenolpyruvate carboxylase 2 (AHRD V1 ***- Q9SCB2_SOLLC): contains Interpro d	66.8	66.8	31.63999915	47	1.225	0.116	1.117	0.759	0.104	1.138	0.328	0.000	1.556
Solyc07g064170.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:63658087-63660013 functional_description:"Pectinesterase (AHRD V1 ***- B9RXO4_RICCO): contains Interpro domain(s) IPR018040	55.75	55.75	41.38999879	50	1.259	0.262	1.169	0.265	0.000	1.854	0.673	0.001	1.213
Solyc07g064170.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:63658087-63660013 functional_description:"Pectinesterase (AHRD V1 ***- B9RXO4_RICCO): contains Interpro domain(s) IPR018040	97	97	47.62000144	121	1.419	0.603	1.127	0.062	0.000	2.780	2.559	0.000	1.236
Solyc08g005770.1.1	genomic_reference:SL2.31ch08 evidence_code:10F1H1E1IEG gene_region:602701-604754 functional_description:"Alcohol acetyltransferase (AHRD V1 **-* B1A9J8_CUCME): contains Interpro domain(s) IPR(	21.68	21.68	27.14999914	15	1.009	0.668	1.837	10.568	0.006	4.018	18.030	0.000	2.858
Solyc08g005770.1.1	genomic_reference:SL2.31ch08 evidence_code:10F1H1E1IEG gene_region:602701-604754 functional_description:"Alcohol acetyltransferase (AHRD V1 **-* B1A9J8_CUCME): contains Interpro domain(s) IPR(	10.52	10.52	11.08999997	7	4.365	0.225	1.837	9.908	0.156	1.871	40.926	0.032	1.837
Solyc08g006890.1.1	genomic_reference:SL2.31ch08 evidence_code:10F0H1E1IEG gene_region:1457215-1459862 functional_description:"Tubulin alpha-3 chain (AHRD V1 ***- B6SPX4_MAIZE): contains Interpro domain(s) IPR00	20.22	20.22	27.05000043	14	0.474	0.032	1.722	0.356	0.005	1.888	0.288	0.004	2.014
Solyc08g006890.1.1	genomic_reference:SL2.31ch08 evidence_code:10F0H1E1IEG gene_region:1457215-1459862 functional_description:"Tubulin alpha-3 chain (AHRD V1 ***- B6SPX4_MAIZE): contains Interpro domain(s) IPR00	17.43	17.43	16.41000062	10	0.879	1.000	1.236	0.413	0.015	1.318	0.151	0.000	2.188
Solyc08g014000.1.1	genomic_reference:SL2.31ch08 evidence_code:10F1H1E1IEG gene_region:3416509-3422732 functional_description:"Lipoxygenase (AHRD V1 **** Q43190_SOLTU): contains Interpro domain(s) IPR001246 Lip	29.69	36.98	23.72000068	26	1.905	0.219	1.722	2.754	0.039	2.070	2.559	0.085	2.128
Solyc08g014000.1.1	genomic_reference:SL2.31ch08 evidence_code:10F1H1E1IEG gene_region:3416509-3422732 functional_description:"Lipoxygenase (AHRD V1 **** Q43190_SOLTU): contains Interpro domain(s) IPR001246 Lip	38.94	45.41	28.94999981	32	1.159	0.349	1.191	0.380	0.000	1.614	1.614	0.019	1.259
Solyc09g014520.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:6147233-6148853 functional_description:"Chlorophyll a-b binding protein 6A, chloroplastic (AHRD V1 **** CB11_SOLLC): contains Ir	12.85	12.85	28.76999974	7	0.824	0.783	1.500	0.698	0.129	1.191	0.031	0.000	5.058
Solyc09g014520.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:6147233-6148853 functional_description:"Chlorophyll a-b binding protein 6A, chloroplastic (AHRD V1 **** CB11_SOLLC): contains Ir	8.39	8.39	14.04000074	5	0.955	0.985	1.528	1.294	0.329	1.445	0.064	0.004	6.194
Solyc09g089580.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:64647581-64649171 functional_description:"1-aminocyclopropane-1-carboxylate oxidase-like protein (AHRD V1 **-* Q9LTH8_ARATI	30.57	30.57	27.54999995	24	5.702	0.183	1.556	9.120	0.072	1.690	30.200	0.005	1.542
Solyc09g089580.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:64647581-64649171 functional_description:"1-aminocyclopropane-1-carboxylate oxidase-like protein (AHRD V1 **-* Q9LTH8_ARATI	35.26	35.26	38.28999996	28	0.501	0.639	1.486	2.938	0.070	1.500	21.677	0.001	1.600
Solyc09g090980.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:65698825-65700248 functional_description:"Major allergen Mal d 1 (AHRD V1 ***- Q84LA7_MALDO): contains Interpro domain(s) II	48.29	48.29	80.62000275	49	1.159	0.725	1.138	0.824	0.086	1.191	0.196	0.000	2.089
Solyc09g090980.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:65698825-65700248 functional_description:"Major allergen Mal d 1 (AHRD V1 ***- Q84LA7_MALDO): contains Interpro domain(s) II	53.01	53.01	97.50000238	56	1.406	0.136	1.127	0.483	0.001	1.294	0.036	0.000	5.248
Solyc09g092380.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:66844130-66846306 functional_description:"Adenosylhomocysteinase (AHRD V1 **** Q2XTD0_SOLTU): contains Interpro domain(s)	47.7	47.7	42.46999919	38	0.887	0.286	1.754	1.057	0.042	1.306	5.702	0.000	1.528
Solyc09g092380.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:66844130-66846306 functional_description:"Adenosylhomocysteinase (AHRD V1 **** Q2XTD0_SOLTU): contains Interpro domain(s)	54.62	54.62	40.20999968	42	0.809	0.664	1.138	1.445	0.001	1.169	9.550	0.000	1.406
Solyc10g007600.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:1897273-1900788 functional_description:"L-lactate dehydrogenase (AHRD V1 ***- LLDD_VIBPA): contains Interpro domain(s) IPR01	16.62	16.62	22.10000008	9	0.233	0.013	2.148	1.486	0.214	1.629	0.036	0.001	5.861
Solyc10g007600.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:1897273-1900788 functional_description:"L-lactate dehydrogenase (AHRD V1 ***- LLDD_VIBPA): contains Interpro domain(s) IPR01	22.19	22.19	29.64999974	16	0.625	0.120	1.343	2.489	0.002	1.169	0.191	0.002	1.570
Solyc10g080210.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:60882500-60889135 functional_description:"Polygalacturonase A (AHRD V1 **** Q9M6S2_ACTCH): contains Interpro domain(s) IPR(	15.5	15.5	14.44000006	19	1.738	0.124	1.629	4.285	0.033	1.905	44.055	0.000	1.905
Solyc10g080210.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:60882500-60889135 functional_description:"Polygalacturonase A (AHRD V1 **** Q9M6S2_ACTCH): contains Interpro domain(s) IPR(	29.29	29.45	22.31999934	40	0.581	0.003	1.282	0.724	0.107	1.191	52.966	0.000	1.600
Solyc10g081510.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:61889662-61892937 functional_description:"5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (AHRD V1 ***- B6U	36.39	36.39	24.70999956	25	1.282	0.324	1.180	0.759	0.119	1.225	0.429	0.003	1.528
Solyc10g081510.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:61889662-61892937 functional_description:"5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (AHRD V1 ***- B6U	41.56	41.56	23.13999981	28	1.318	0.141	1.148	0.433	0.000	1.343	0.121	0.000	2.630
Solyc10g083720.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:62809938-62815473 functional_description:"Pyruvate kinase (AHRD V1 ***- Q94KE3_ARATH): contains Interpro domain(s) IPR00169	7.76	7.78	10.05999967	5	1.202	0.821	1.923	1.047	0.297	1.770	3.020	0.010	2.128
Solyc10g083720.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:62809938-62815473 functional_description:"Pyruvate kinase (AHRD V1 ***- Q94KE3_ARATH): contains Interpro domain(s) IPR00169	6.12	6.22	4.554000124	4	0.759	0.225	1.770	0.879	0.811	1.570	2.270	0.033	1.318
Solyc10g085880.1.1	genomic_reference:SL2.31ch10 evidence_code:10F0H1E1IEG gene_region:64241098-64242132 functional_description:"UDP-glucosyltransferase family 1 protein (AHRD V1 ***- C6KI43_CITSI): contains Interpro	14.57	14.84	22.6699993	12	1.542	0.590	1.585	13.552	0.003	2.312	14.454	0.007	2.228
Solyc10g085880.1.1	genomic_reference:SL2.31ch10 evidence_code:10F0H1E1IEG gene_region:64241098-64242132 functional_description:"UDP-glucosyltransferase family 1 protein (AHRD V1 ***- C6KI43_CITSI): contains Interpro	12.33	12.33	20.35000026	11	0.313	0.475	2.128	8.017	0.000	2.355	24.660	0.000	2.312
Solyc11g006970.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:1477794-1483280 functional_description:"Unknown protein DS12 from 2D-PAGE of leaf, chloroplastic (AHRD V1 **-- UP12_ORYSJ)"	10.84	10.84	15.45999944	9	0.724	0.128	1.528	1.009	0.769	1.419	0.474	0.012	1.556
Solyc11g006970.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:1477794-1483280 functional_description:"Unknown protein DS12 from 2D-PAGE of leaf, chloroplastic (AHRD V1 **-- UP12_ORYSJ)"	12.07	12.07	19.58999932	10	1.419	0.232	1.355	0.809	0.791	1.528	0.322	0.022	1.837
Solyc11g011960.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:4912765-4919027 functional_description:"UTP-glucose 1 phosphate uridylyltransferase (AHRD V1 ***- B3VDY8_EUCGR): contains Int	37.34	37.34	35.6400013	27	1.117	0.320	1.294	0.698	0.068	1.445	0.603	0.044	1.500
Solyc11g011960.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:4912765-4919027 functional_description:"UTP-glucose 1 phosphate uridylyltransferase (AHRD V1 ***- B3VDY8_EUCGR): contains Int	34.59	34.59	33.32999945	28	1.169	0.328	1.127	0.887	0.177	1.159	0.265	0.000	1.871
Solyc11g051160.1.1	genomic_reference:SL2.31ch11 evidence_code:10F0H1E1IEG gene_region:42742333-42744370 functional_description:"Phosphatidylinositol transfer protein SFH5 (AHRD V1 *--- C5JFB2_AJEDS): contains Inter	12.84	12.85	11.20999977	7	1.247	0.673	1.660	0.673	0.434	2.128	4.656	0.002	2.032
Solyc11g051160.1.1	genomic_reference:SL2.31ch11 evidence_code:10F0H1E1IEG gene_region:42742333-42744370 functional_description:"Phosphatidylinositol transfer protein SFH5 (AHRD V1 *--- C5JFB2_AJEDS): contains Inter	13.04	13.65	7.980000228	6	0.506	0.177	1.585	0.879	0.518	1.977	4.831	0.000	1.472
Solyc11g069790.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:51501731-51506639 functional_description:"chaperonin (AHRD V1 ***- B2IXD2_NOSP7): contains Interpro domain(s) IPR001844 Ch	18.58	20.65	21.25999928	14	0.929	0.640	1.306	1.038	0.998	1.380	1.542	0.034	1.225
Solyc11g069790.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:51501731-51506639 functional_description:"chaperonin (AHRD V1 ***- B2IXD2_NOSP7): contains Interpro domain(s) IPR001844 Ch	22.56	22.76	18.53999943	13	1.271	0.956	1.600	1.629	0.714	1.629	3.436	0.013	1.770
Solyc11g072260.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:52549996-52552681 functional_description:"40S ribosomal protein S13 (AHRD V1 ***- D7LRU2_ARALY): contains Interpro domain(s)	12.14	12.14	35.76000035	7	0.752	0.096	1.306	0.673	0.020	1.343	0.809	0.358	1.406
Solyc11g072260.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:52549996-52552681 functional_description:"40S ribosomal protein S13 (AHRD V1 ***- D7LRU2_ARALY): contains Interpro domain(s)	13.63	13.64	40.40000141	7	0.991	0.750	1.148	0.488	0.015	1.355	0.673	0.460	1.330
Solyc11g072450.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:52704923-52709689 functional_description:"Mitochondrial F0 ATP synthase D chain (AHRD V1 ***- B3TLP5_ELAGV): contains Interp	4.4	4.4	11.30999997	3	1.585	0.255	1.690	2.148	0.114	1.871	0.117	0.031	6.310
Solyc11g072450.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:52704923-52709689 functional_description:"Mitochondrial F0 ATP synthase D chain (AHRD V1 ***- B3TLP5_ELAGV): contains Interp	5.79	5.79	16.06999934	4	1.038	0.884	1.854	0.847	0.696	2.489	0.366	0.045	1.528
Solyc12g005860.1.1	genomic_reference:SL2.31ch12 evidence_code:10F0H1E1IEG gene_region:490745-498964 functional_description:"3-isopropylmalate dehydratase large subunit (AHRD V1 *--- LEUC_BACWK): contains Interpro	39.68	39.68	20.99999934	24	1.086	0.823	1.905	0.738	0.710	1.754	2.535	0.020	1.803
Solyc12g005860.1.1	genomic_reference:SL2.31ch12 evidence_code:10F0H1E1IEG gene_region:490745-498964 functional_description:"3-isopropylmalate dehydratase large subunit (AHRD V1 *--- LEUC_BACWK): contains Interpro	35.78	35.78	17.1299994	22	0.787	0.861	1.294	1.009	0.381	1.236	3.532	0.000	1.528
Solyc12g009300.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:2575133-2579077 functional_description:"Sucrose synthase (AHRD V1 **** Q82693_SOLLC): contains Interpro domain(s) IPR012820	24.61	24.61	18.62999946	19	0.955	0.575	1.380	0.738	0.066	1.225	0.134	0.002	3.532
Solyc12g009300.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:2575133-2579077 functional_description:"Sucrose synthase (AHRD V1 **** Q82693_SOLLC): contains Interpro domain(s) IPR012820	40.92	40.92	26.21000111	27	1.459	0.025	1.086	0.370	0.002	1.393	0.024	0.000	4.742
Solyc12g010320.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:3378861-3381620 functional_description:"Outer membrane lipoprotein blc (AHRD V1 **-- D0RZG9_ACICA): contains Interpro domain(	7.53	7.53	23.78000021	5	2.805	0.164	2.168	3.076	0.070	2.312	9.204	0.003	2.535
Solyc12g010320.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:3378861-3381620 functional_description:"Outer membrane lipoprotein blc (AHRD V1 **-- D0RZG9_ACICA): contains Interpro domain(	13.45	13.45	33.50999951	10	1.000	0.461	1.570	2.679	0.304	1.644	13.932	0.001	1.977
Solyc12g011310.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:4160903-4162115 functional_description:"Glutathione S-transferase (AHRD V1 ***- Q0PN10_9FABA): contains Interpro domain(s) IPF	8.85	8.88	17.81000048	5	1.770	0.946	3.908	23.121	0.000	2.780	28.840	0.000	2.831
Solyc12g011310.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:4160903-4162115 functional_description:"Glutathione S-transferase (AHRD V1 ***- Q0PN10_9FABA): contains Interpro domain(s) IPF	5.83	5.87	9.589000046	3	1.486	0.753	2.443	8.395	0.045	2.535	2.466	0.327	2.466
Solyc12g055800.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:47132509-47140184 functional_description:"V-type ATP synthase alpha chain (AHRD V1 ***- VATA_METTH): contains Interpro doma	42.84	42.84	31.77999854	29	0.938	0.670	1.202	1.067	0.156	1.213	0.166	0.000	3.281
Solyc12g055800.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:47132509-47140184 functional_description:"V-type ATP synthase alpha chain (AHRD V1 ***- VATA_METTH): contains Interpro doma	44.96	44.96	33.86999965	28	0.946	0.871	1.202	1.009	0.340	1.213	0.251	0.001	2.168
Solyc12g094620.1.1	genomic_reference:SL2.31ch12 evidence_code:10F0H1E1IEG gene_region:63143164-63145212 functional_description:"Catalase (AHRD V1 ***- Q2PYW5_SOLTU): contains Interpro domain(s) IPR018028 Cata	19.55	19.55	23.98000062	12	0.445	0.047	1.754	1.282	0.158	1.330	0.370	0.005	1.754
Solyc12g094620.1.1	genomic_reference:SL2.31ch12 evidence_code:10F0H1E1IEG gene_region:63143164-63145212 functional_description:"Catalase (AHRD V1 ***- Q2PYW5_SOLTU): contains Interpro domain(s) IPR018028 Cata	15.06	15.06	14.42999989	8	0.540	0.141	1.472	3.767	0.002	1.406	1.754	0.060	1.306
Solyc12g099430.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:64925323-64928615 functional_description:"Epoxide hydrolase 1 (AHRD V1 ***- D8L7V7_PRUPE): contains Interpro domain(s) IPR0(	24.68	24.68	47.36999869	14	1.247	0.327	1.318	0.738	0.085	1.202	0.113	0.000	3.532
Solyc12g099430.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:64925323-64928615 functional_description:"Epoxide hydrolase 1 (AHRD V1 ***- D8L7V7_PRUPE): contains Interpro domain(s) IPR0(	18.41	18.42	28.16999853	9	0.895	0.770	1.282	1.138	0.407	1.282	0.251	0.007	1.905
Solyc01g088400.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:74964500-74968838 functional_description:"CER1 (AHRD V1 **-- B6TEH3_MAIZE): contains Interpro domain(s) IPR006694 Fatty ac	8.09	8.09	7.802999765	4	0.824	0.671	1.888	4.207	0.020	2.489	9.120	0.002	2.489
Solyc01g100350.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:82174065-82176355 functional_description:"ADP-ribosylation factor-like protein 3 (AHRD V1 **-- ARL3_CAEEL): contains Interpro do	2	10.03	28.49999964	8	78.705	0.023	2.333	80.168	0.023	2.291	87.096	0.022	2.270
Solyc01g101060.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:82680218-82681399 functional_description:"S-adenosylmethionine synthase (AHRD V1 ***- B8LFH4_IPOBA): contains Interpro domair	10.13	10.13	16.7899996	5	0.929	0.666	1.585	0.474	0.046	1.629	0.466	0.127	1.923
Solyc01g105030.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:85088106-85089075 functional_description:"Chlorophyll a-b binding protein, chloroplastic (AHRD V1 ***- CB12_PETHY): contains Int	8	8	8.59400034	4	1.019	0.935	1.330	0.794	0.827	1.706	0.095	0.013	2.805
Solyc01g110120.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:88653701-88663610 functional_description:"V-type proton ATPase subunit a (AHRD V1 **** VPH1_NEUCR): contains Interpro domain	20	20.12	13.05000037	14	1.259	0.697	1.514	1.271	0.996	1.486	0.483	0.042	1.786
Solyc02g020960.1.1	genomic_reference:SL2.31ch02 evidence_code:10F0H1E0IEG gene_region:11444530-11446005 functional_description:"Photosystem I P700 chlorophyll a apoprotein A1 (AHRD V1 ***- D5MAH7_PEA): contains	2.45	2.45	2.827000059	2	0.839	0.754	2.109	0.946	0.923	4.055	0.012	0.046	2.606
Solyc02g062500.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:28749752-28753373 functional_description:"2-oxoglutarate-dependent dioxygenase (AHRD V1 **** B9GL08_POPTR): contains Interpro	23.8	23.83	28.97000015	21	3.373	0.216	2.729	5.012	0.027	3.020	7.178	0.025	2.858
Solyc02g080540.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:39325641-39326774 functional_description:"ATP synthase gamma chain (AHRD V1 ***- B7FIR4_MEDTR): contains Interpro domain(s)	14.34	14.52	18.0399999	8	0.752	0.125	1.393	0.745	0.106	1.368	0.520	0.010	1.486
Solyc02g080630.1.1	genomic_reference:SL2.31ch02 evidence_code:10F0H1E1IEG gene_region:39393072-39397989 functional_description:"Lactoylglutathione lyase (AHRD V1 ***- D2D330_GOSHI): contains Interpro domain(s) IP	17.44	17.44	24.6299997	14	1.213	0.287	1.514	2.535	0.025	1.923	2.355	0.069	1.786
Solyc02g081170.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:39811148-39812759 functional_description:"Plastid-lipid-associated protein, chloroplastic (AHRD V1 **-- PAP_CITUN): contains Inter	18.32	19.08	29.75000143	10	0.912	0.977	1.629	0.655	0.543	1.754	2.992	0.020	1.660
Solyc03g007890.1.1	genomic_reference:SL2.31ch03 evidence_code:10F1H1E1IEG gene_region:2412304-2415022 functional_description:"Heat shock protein 90 (Fragment) (AHRD V1 **-- Q2L3T8_WHEAT): contains Interpro domai	6.14	33.56	23.89000058	21	2.032	0.490	2.228	2.704	0.127	2.377	3.162	0.044	1.614
Solyc03g111010.1.1	genomic_reference:SL2.31ch03 evidence_code:10F0H1E1IEG gene_region:55761844-55764855 functional_description:"Glyceraldehyde-3-phosphate dehydrogenase (AHRD V1 **** Q9XG67_TOBAC): contains I	13.75	37.24	45.98999918	27	1.644	0.341	1.690	2.128	0.050	1.754	2.208	0.073	1.754
Solyc03g113800.1.1	genomic_reference:SL2.31ch03 evidence_code:10F0H1E1IEG gene_region:57895309-57902550 functional_description:"Betaine aldehyde dehydrogenase (AHRD V1 **** D2DEK8_LYCBA): contains Interpro dor	19.28	19.28	19.21000034	14	1.117	0.791	1.368	0.991	0.926	1.380	0.457	0.026	1.614
Solyc04g054310.1.1	genomic_reference:SL2.31ch04 evidence_code:10F0H1E1IEG gene_region:51438134-51443257 functional_description:"Alanine-glyoxylate aminotransferase (AHRD V1 **** D2KZ10_WHEAT): contains Interpro	5.26	5.26	3.804999962	3	1.406	0.589	2.291	2.377	0.343	2.704	9.550	0.002	3.631
Solyc04g072160.1.1	genomic_reference:SL2.31ch04 evidence_code:10F1H1E1IEG gene_region:56773469-56775603 functional_description:"Prostaglandin E synthase 3 (AHRD V1 **-- B4FLE3_MAIZE): contains Interpro domain(s)	3.79	3.79	10.05999967	2	1.180	0.378	2.228	1.837	0.259	2.312	3.499	0.029	1.923
Solyc04g077040.1.1	genomic_reference:SL2.31ch04 evidence_code:10F0H1E1IEG gene_region:59591250-59595247 functional_description:"Xylulose kinase (AHRD V1 ***- D7MPD2_ARALY): contains Interpro domain(s) IPR0005	1.68	1.68	1.431000046	2	0.575	0.598	5.012	4.487	0.066	5.012	7.311	0.035	5.058
Solyc04g081570.1.1	genomic_reference:SL2.31ch04 evidence_code:10F0H1E1IEG gene_region:63109819-63114921 functional_description:"Chaperone protein htpG (AHRD V1 **-- HTPG_MYCA1): contains Interpro domain(s) IPR	7.08	8.12	3.448000178	3	0.802	0.302	1.600	0.474	0.014	1.585	1.213	0.306	1.330
Solyc04g082630.1.1	genomic_reference:SL2.31ch04 evidence_code:10F0H1E1IEG gene_region:63843236-63846005 functional_description:"Glyceraldehyde-3-phosphate dehydrogenase B (AHRD V1 **** B4F8L7_MAIZE): contains	9.98	14.35	15.76000005	9	1.169	0.869	1.432	0.637	0.096	1.706	0.310	0.019	2.051
Solyc05g005700.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:514677-518827 functional_description:"Aldehyde dehydrogenase 1 (AHRD V1 **** Q84V96_LOTCO): contains Interpro domain(s) IPR	9.75	11.14	8.884999901	6	0.904	0.685	1.225	0.752	0.288	1.644	0.322	0.007	1.570
Solyc05g007250.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:1920678-1922827 functional_description:"Ribosomal protein (AHRD V1 ***- B3TM27_ELAGV): contains Interpro domain(s) IPR0019	14.98	14.98	35.53000093	10	0.832	0.542	1.318	0.871	0.972	1.343	0.492	0.039	1.486
Solyc05g009530.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:3737371-3743069 functional_description:"Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (	6.24	6.24	7.190000266	3	0.955	0.716	1.306	0.718	0.027	1.236	0.832	0.202	1.380
Solyc05g050120.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:59250343-59254280 functional_description:"Malic enzyme (AHRD V1 ***- Q04936_SOLLC): contains Interpro domain(s) IPR012302	42.78	42.78	36.26999855	27	1.380	0.035	1.318	1.459	0.010	1.318	1.038	0.473	1.236
Solyc06g007670.1.1	genomic_reference:SL2.31ch06 evidence_code:10F1H1E1IEG gene_region:1672659-1675838 functional_description:"60S ribosomal protein L5-1 (AHRD V1 ***- B6THG9_MAIZE): contains Interpro domain(s)	3.85	4.03	4.983000085	3	0.973	0.806	1.770	1.057	0.957	1.585	0.461	0.028	2.188
Solyc06g060340.1.1	genomic_reference:SL2.31ch06 evidence_code:10F1H1E1IEG gene_region:34711883-34713649 functional_description:"Chloroplast photosystem II-associated protein (AHRD V1 ***- A8HPM2_CHLRE): contains	8.29	8.29	19.20000017	6	0.920	0.957	1.722	0.879	0.383	1.786	0.073	0.007	4.529
Solyc07g007790.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:2439037-2447223 functional_description:"Sucrose phosphate synthase (AHRD V1 **** Q2HYI0_CUCME): contains Interpro domain(s)	5.12	6.67	2.466999926	3	0.711	0.286	1.706	1.459	0.190	1.722	1.600	0.037	1.445
Solyc07g047800.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:56336785-56340363 functional_description:"Short-chain dehydrogenase/reductase family protein (AHRD V1 **-- D7L9J1_ARALY): con	6.34	6.47	14.2900005	4	1.159	0.608	2.559	3.802	0.172	2.208	11.588	0.006	2.582
Solyc07g049530.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:57156095-57160395 functional_description:"1-aminocyclopropane-1-carboxylate oxidase (AHRD V1 ***- Q94F66_SOLTU): contains In	13.31	13.31	18.3799997	10	1.445	0.049	1.318	2.188	0.007	1.107	1.570	0.046	1.236
Solyc07g056420.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:61606450-61607905 functional_description:"Glutathione S-transferase-like protein (AHRD V1 **** Q8GVD1_SOLLC): contains Interpro	12.75	12.75	20.90999931	9	1.722	0.207	1.542	1.306	0.413	1.675	6.855	0.002	2.377
Solyc08g081250.1.1	genomic_reference:SL2.31ch08 evidence_code:10F1H1E1IEG gene_region:61469063-61477559 functional_description:"Aminopeptidase N (AHRD V1 ***- D5C0C8_NITHN): contains Interpro domain(s) IPR012	14.84	15.71	7.306999713	9	2.679	0.152	2.228	2.655	0.084	2.312	4.487	0.002	2.884
Solyc09g063130.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:56787774-56788645 functional_description:"Photosystem I reaction center subunit IV A (AHRD V1 *-*- B6TH55_MAIZE): contains Inter	5.15	5.22	22.85999954	3	1.169	0.836	2.399	0.550	0.156	2.489	0.038	0.013	6.427
Solyc09g066150.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:60174802-60176310 functional_description:"Cytochrome P450 (AHRD V1 ***- B9P4S4_POPTR): contains Interpro domain(s) IPR0024	13.24	13.24	14.33999985	8	0.649	0.969	1.854	6.427	0.025	2.655	11.912	0.001	2.704
Solyc09g075950.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:63079808-63081538 functional_description:"Heat shock protein 1 (AHRD V1 ***- B6SXY0_MAIZE): contains Interpro domain(s) IPR0	2.55	2.56	2.082999982	2	1.854	0.064	25.351	16.444	0.037	33.419	21.281	0.036	34.041
Solyc09g091750.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:66319252-66327875 functional_description:"26S proteasome regulatory subunit (AHRD V1 ***- O48844_ARATH): contains Interpro do	3.65	4.97	2.888000011	4	24.660	0.038	33.113	12.706	0.042	31.915	24.889	0.037	33.113
Solyc10g051020.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:46848063-46853292 functional_description:"Cytochrome P450 (AHRD V1 ***- A9ZT56_COPJA): contains Interpro domain(s) IPR0024	7.64	7.64	6.782999635	4	0.565	0.135	1.660	0.387	0.042	1.923	0.619	0.525	2.377
Solyc10g080900.1.1	genomic_reference:SL2.31ch10 evidence_code:10F1H1E1IEG gene_region:61394239-61396412 functional_description:"3-oxoacyl-reductase (AHRD V1 **-- B6UEX0_MAIZE): contains Interpro domain(s) IPR0(	7.1	7.1	12.89000064	5	0.334	0.394	2.089	7.244	0.011	2.831	3.192	0.233	2.754
Solyc11g010960.1.1	genomic_reference:SL2.31ch11 evidence_code:10F0H1E1IEG gene_region:4006647-4010431 functional_description:"Alcohol dehydrogenase (AHRD V1 ***- ADH2_BACST): contains Interpro domain(s) IPR002	4.05	4.05	3.90000008	2	1.169	0.647	1.556	0.550	0.207	1.406	0.098	0.025	3.802
Solyc11g020330.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:10856076-10856648 functional_description:"class IV heat shock protein (AHRD V1 ***- B6TXB5_MAIZE): contains Interpro domain(s)	8.61	8.61	30.52999973	6	0.156	0.288	3.404	7.112	0.038	2.466	9.462	0.030	2.355
Solyc11g066100.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:48855961-48858259 functional_description:"heat shock protein (AHRD V1 ***- B2D2G5_CAPSN): contains Interpro domain(s) IPR013	5.69	29.78	25.69000125	25	0.920	0.487	2.333	1.393	0.622	2.291	3.698	0.021	1.786
Solyc11g069430.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:51094073-51096743 functional_description:"Aquaporin 1 (AHRD V1 ***- Q9M4T0_ALLCE): contains Interpro domain(s) IPR012269	12.76	12.76	25.78000128	7	1.343	0.426	1.500	0.920	0.817	1.500	2.333	0.045	1.644
Solyc12g044600.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:45081353-45088167 functional_description:"Malic enzyme (AHRD V1 ***- Q04935_SOLLC): contains Interpro domain(s) IPR012302	14.58	20.76	21.04000002	11	1.019	0.702	1.330	0.565	0.015	1.500	0.515	0.008	1.445
Solyc12g056940.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:48363332-48376390 functional_description:"Acetyl-CoA carboxylase (AHRD V1 ***- D2CFN2_9ROSI): contains Interpro domain(s) IF	2.58	2.7	0.814499985	2	1.047	0.009	3.733	1.282	0.006	2.014	1.393	0.006	1.445
Solyc12g099360.1.1	genomic_reference:SL2.31ch12 evidence_code:10F1H1E1IEG gene_region:64880293-64883142 functional_description:"Acyl-CoA synthetase/AMP-acid ligase II (AHRD V1 **** Q2W3Z0_MAGSA): contains Inte	2.06	2.06	1.58699993	2	1.854	0.074	2.582	1.318	0.220	3.373	2.421	0.041	3.281
Solyc01g006540.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:1113939-1123703 functional_description:"Lipoxygenase (AHRD V1 **** Q96573_SOLLC): contains Interpro domain(s) IPR001246 Lip	14.46	16.56	9.598000348	12	0.787	0.832	2.051	1.086	0.981	2.089	31.623	0.000	2.559
Solyc01g007320.1.1	genomic_reference:SL2.31ch01 evidence_code:10F0H1E1IEG gene_region:1849413-1851307 functional_description:"ATP synthase subunit beta chloroplastic (AHRD V1 ***- Q8MBF8_9SOLA): contains Interpro	19.51	21.52	24.95999932	20	0.692	0.454	1.247	1.028	0.792	1.169	0.331	0.007	1.786
Solyc01g028810.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:33327275-33331326 functional_description:"chaperonin (AHRD V1 ***- B4VMY1_9CYAN): contains Interpro domain(s) IPR001844 C	23.49	23.49	18.70000064	12	0.603	0.015	1.472	1.282	0.547	1.318	3.048	0.017	1.542
Solyc01g097520.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:80105972-80107905 functional_description:"Annexin 11 (AHRD V1 ***- D6QX28_SOYBN): contains Interpro domain(s) IPR009118 A	6.4	6.98	7.277999818	3	1.247	0.150	1.738	0.946	0.863	1.706	0.328	0.048	2.291
Solyc01g099160.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:81236889-81243901 functional_description:"Lipoxygenase (AHRD V1 **** Q9FT17_SOLLC): contains Interpro domain(s) IPR001246	4.14	19.01	11.14000008	13	2.780	0.007	2.884	2.965	0.007	2.831	8.551	0.004	2.992
Solyc01g100320.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:82147812-82153647 functional_description:"Thioredoxin/protein disulfide isomerase (AHRD V1 **** Q2U681_ASPOR): contains Interp	18.48	18.58	18.1099996	11	0.619	0.092	1.294	0.855	0.936	1.343	1.905	0.043	1.380
Solyc01g102310.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H0E1IEG gene_region:82889974-82893043 functional_description:"Unknown Protein (AHRD V1)"	4.77	4.8	2.796000056	2	1.159	0.279	1.644	0.433	0.036	1.514	0.661	0.388	1.905
Solyc01g104590.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:84802811-84805383 functional_description:"Ribosomal protein L3 (AHRD V1 ***- Q6SKP4_SOLLC): contains Interpro domain(s) IPR(	22.03	22.15	24.68000054	17	0.802	0.332	1.213	0.637	0.259	1.419	0.394	0.033	1.888
Solyc01g111170.1.1	genomic_reference:SL2.31ch01 evidence_code:10F1H1E1IEG gene_region:89284475-89284990 functional_description:"Peptidyl-prolyl cis-trans isomerase (AHRD V1 ***- Q9XF12_SOLTU): contains Interpro do	13.39	13.39	42.10999906	18	1.459	0.936	1.542	1.236	0.701	1.528	0.201	0.021	2.399
Solyc02g070360.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:34690466-34692550 functional_description:"40S ribosomal protein S4-like protein (AHRD V1 ***- Q2XPX5_SOLTU): contains Interpro	28.87	29.3	46.97000086	21	1.038	0.935	1.247	0.685	0.152	1.318	0.377	0.034	1.722
Solyc02g084440.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:42111522-42113648 functional_description:"Fructose-bisphosphate aldolase (AHRD V1 ***- Q9SXX4_NICPA): contains Interpro domai	15.23	17.25	22.19000012	11	0.718	0.851	1.837	1.368	0.322	1.294	0.137	0.046	5.152
Solyc02g088610.1.1	genomic_reference:SL2.31ch02 evidence_code:10F1H1E1IEG gene_region:45222585-45229209 functional_description:"ATP-dependent chaperone ClpB (AHRD V1 **** B5W0X8_SPIMA): contains Interpro dom	13.19	17.37	8.06099996	10	1.871	0.009	3.311	3.404	0.006	2.729	8.872	0.004	2.754
Solyc03g034220.1.1	genomic_reference:SL2.31ch03 evidence_code:10F1H1E1IEG gene_region:10203724-10205798 functional_description:"Ribulose bisphosphate carboxylase small chain (AHRD V1 ***- A9YTZ7_SOLTU): contain	11.96	12.09	20.55999935	10	1.169	0.360	1.355	1.514	0.130	1.202	0.180	0.044	2.188
Solyc03g123630.1.1	genomic_reference:SL2.31ch03 evidence_code:10F1H1E1IEG gene_region:64478594-64481490 functional_description:"Pectinesterase (AHRD V1 ***- Q564D7_SOLLC): contains Interpro domain(s) IPR000070	18.28	18.29	16.30000025	16	0.685	0.461	1.343	1.191	0.575	1.259	1.959	0.034	1.380
Solyc04g073990.1.1	genomic_reference:SL2.31ch04 evidence_code:10F1H1E1IEG gene_region:57609528-57611510 functional_description:"Annexin (AHRD V1 ***- Q42657_CAPAN): contains Interpro domain(s) IPR009118 Anne	24.18	24.18	35.67000031	15	2.291	0.041	1.738	2.535	0.002	1.770	1.419	0.382	1.393
Solyc04g074300.1.1	genomic_reference:SL2.31ch04 evidence_code:10F1H1E1IEG gene_region:57893335-57895122 functional_description:"30S ribosomal protein S5 (AHRD V1 ***- C5K1T7_AJEDS): contains Interpro domain(s) I	16.52	16.52	28.2099992	10	0.904	0.888	1.107	0.409	0.017	1.614	0.592	0.300	1.294
Solyc04g080980.1.1	genomic_reference:SL2.31ch04 evidence_code:10F0H1E1IEG gene_region:62634837-62639864 functional_description:"Coatomer alpha subunit-like protein (AHRD V1 **-- Q70I39_LOTJA): contains Interpro dor	9.7	9.95	2.95599997	4	1.107	0.734	1.380	0.474	0.033	1.754	0.685	0.353	1.585
Solyc04g082200.1.1	genomic_reference:SL2.31ch04 evidence_code:10F0H1E1IEG gene_region:63550207-63551043 functional_description:"Dehydrin (AHRD V1 *-*- Q1A4H3_COFCA): contains Interpro domain(s) IPR000167 Deh	18.26	18.26	29.12999988	10	0.347	0.013	1.472	0.102	0.100	2.228	2.884	0.000	1.259
Solyc05g005490.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:356257-361232 functional_description:"Carbonic anhydrase (AHRD V1 ***- Q5NE21_SOLLC): contains Interpro domain(s) IPR015892	4.39	4.39	5.970000103	2	0.603	0.639	2.965	1.514	0.327	2.399	6.310	0.007	1.977
Solyc05g014280.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:8089668-8091891 functional_description:"Heat shock protein (AHRD V1 ***- A9QVH3_9FABA): contains Interpro domain(s) IPR0020	4.93	4.93	9.502000362	2	0.525	0.125	1.675	3.162	0.010	1.406	16.596	0.001	1.355
Solyc05g053810.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:62993574-62996701 functional_description:"Serine hydroxymethyltransferase (AHRD V1 **** D2D306_GOSHI): contains Interpro doma	11.81	11.86	12.73999959	7	1.076	0.583	1.368	0.305	0.013	2.188	0.258	0.067	2.858
Solyc05g055440.1.1	genomic_reference:SL2.31ch05 evidence_code:10F1H1E1IEG gene_region:64237680-64238123 functional_description:"Histone H2B (AHRD V1 ***- Q2XPW1_SOLTU): contains Interpro domain(s) IPR000558	12.69	12.69	46.93999887	11	0.982	0.986	1.213	1.057	0.245	1.259	3.048	0.003	1.556
Solyc06g009190.1.1	genomic_reference:SL2.31ch06 evidence_code:10F0H1E1IEG gene_region:3130102-3135541 functional_description:"Pectinesterase (AHRD V1 ***- B9SAU4_RICCO): contains Interpro domain(s) IPR000070 P	6.23	6.92	7.97900036	4	1.754	0.148	1.419	0.575	0.028	1.722	2.466	0.058	1.343
Solyc06g071920.1.1	genomic_reference:SL2.31ch06 evidence_code:10F0H1E1IEG gene_region:40700509-40704055 functional_description:"Glyceraldehyde-3-phosphate dehydrogenase (AHRD V1 **** Q9XG67_TOBAC): contains I	12.43	38.95	44.51000094	37	0.685	0.623	2.377	2.630	0.069	2.208	3.048	0.044	2.168
Solyc06g073190.1.1	genomic_reference:SL2.31ch06 evidence_code:10F1H1E1IEG gene_region:41485353-41487653 functional_description:"Fructokinase-like (AHRD V1 **-* Q307Z3_SOLTU): contains Interpro domain(s) IPR0021	10.08	10.08	18.60000044	6	1.406	0.340	1.169	0.530	0.441	1.556	0.164	0.003	2.805
Solyc06g076570.1.1	genomic_reference:SL2.31ch06 evidence_code:10F1H1E1IEG gene_region:43955837-43956301 functional_description:"class I heat shock protein (AHRD V1 ***- Q69BI7_CARPA): contains Interpro domain(s) II	4.01	24.27	53.25000286	29	1.180	0.051	4.875	8.790	0.039	4.446	16.444	0.034	4.529
Solyc07g006650.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:1517826-1521717 functional_description:"Xylose isomerase (AHRD V1 ***- B9T2F0_RICCO): contains Interpro domain(s) IPR013452	12	12.08	13.81999999	7	1.107	0.374	1.180	1.282	0.085	1.127	1.675	0.009	1.202
Solyc07g051850.1.1	genomic_reference:SL2.31ch07 evidence_code:10F1H1E1IEG gene_region:57715151-57720088 functional_description:"Aspartic proteinase (AHRD V1 **-* Q96383_CENCA): contains Interpro domain(s) IPR00	20	21.8	20.28000057	13	1.585	0.132	1.472	3.873	0.007	2.208	4.018	0.003	2.228
Solyc08g014130.1.1	genomic_reference:SL2.31ch08 evidence_code:10F1H1E1IEG gene_region:3735181-3744282 functional_description:"2-isopropylmalate synthase 1 (AHRD V1 **** Q30DX9_9BRAS): contains Interpro domain(s)	2.24	2.56	2.116999961	2	0.530	0.524	5.495	0.244	0.145	5.200	14.454	0.017	4.920
Solyc08g062920.1.1	genomic_reference:SL2.31ch08 evidence_code:10F0H1E1IEG gene_region:49546658-49549476 functional_description:"Elongation factor EF-2 (AHRD V1 **** Q9SGT4_ARATH): contains Interpro domain(s) IP	35.51	36.02	15.21999985	19	0.545	0.001	1.368	0.685	0.130	1.247	0.570	0.010	1.330
Solyc09g009260.1.1	genomic_reference:SL2.31ch09 evidence_code:10F0H1E1IEG gene_region:2645029-2646904 functional_description:"Fructose-bisphosphate aldolase (AHRD V1 ***- Q2PYX3_SOLTU): contains Interpro domain(	34.96	34.96	37.99000084	31	2.535	0.090	1.738	1.754	0.375	1.542	2.884	0.033	1.871
Solyc09g009390.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:2836565-2841361 functional_description:"Monodehydroascorbate reductase (NADH)-like protein (AHRD V1 **** Q0WUJ1_ARATH): (	30.01	30.01	37.18000054	20	1.445	0.253	1.259	0.991	0.771	1.259	1.542	0.039	1.318
Solyc09g090140.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:65031907-65034895 functional_description:"Malate dehydrogenase (AHRD V1 **** Q2PYY8_SOLTU): contains Interpro domain(s) IPI	22.84	24.88	29.51999903	18	1.117	0.797	1.355	0.824	0.475	1.343	0.063	0.006	5.916
Solyc09g091470.1.1	genomic_reference:SL2.31ch09 evidence_code:10F1H1E1IEG gene_region:66091223-66095670 functional_description:"3-ketoacyl CoA thiolase 2 (AHRD V1 **** C8YNG7_PETHY): contains Interpro domain(s)	8.65	10.7	9.461999685	6	0.555	0.075	2.148	3.162	0.084	2.188	4.875	0.021	2.291
Solyc10g081030.1.1	genomic_reference:SL2.31ch10 evidence_code:10F0H1E1IEG gene_region:61533717-61537084 functional_description:"Nascent polypeptide-associated complex alpha subunit-like protein (AHRD V1 ***- B6T903	4.16	4.16	13.07000071	3	0.752	0.092	1.754	0.929	0.181	1.556	1.528	0.041	1.368
Solyc11g062190.1.1	genomic_reference:SL2.31ch11 evidence_code:10F0H1E1IEG gene_region:46161997-46163624 functional_description:"Mitochondrial ADP/ATP carrier proteins (AHRD V1 ***- Q2UU95_ASPOR): contains Inter	23.12	23.12	27.9399991	18	1.180	0.415	1.138	0.809	0.241	1.138	0.249	0.003	1.905
Solyc11g069720.1.1	genomic_reference:SL2.31ch11 evidence_code:10F1H1E1IEG gene_region:51411308-51416865 functional_description:"26S protease regulatory subunit 6B homolog (AHRD V1 *--- PRS6B_ARATH): contains Inte	11.25	11.3	5.96299991	5	1.247	0.232	1.306	1.318	0.040	1.191	1.514	0.008	1.393
Solyc04g071610.1.1	genomic_reference:SL2.31ch04 evidence_code:10F1H0E1IEG gene_region:56171237-56172257 functional_description:"Water-stress inducible protein 3 (Fragment) (AHRD V1 ---- Q5G1I2_PINTA): contains Inte	37.55	37.55	89.99999762	27	2.780	0.055	1.854	4.529	0.007	2.249	2.014	0.105	1.585

Table 6.2. List of candidate genes associated with high shelf life trait in *Nps1* , identified through MutMap approach.

The probable candidate genes responsible for the high shelf life phenotype in two F_2 segregated lines (obtained from (AC♀x*Nps1*♂ cross) were identified by MutMap approach. The list of SNPs that result in changes in aminoacid sequence (non-synonymous SNPs) and present in coding sequences were given below-

CHRO	POSITIO	REFEI	ALTEF	TRANS	GENE_ID	GENE_NAME	REGIO	VARIANT	REFI	ALTE	AMIN	SIFT_SCORE	NUMBER OF SEQUEN	dbSNP	SIFT_PREDICTION
0	7679740	A	G	Solyc00	Solyc00g008130.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	I	T	144	NA	NA	novel	NA
0	8348718	A	C	Solyc00	Solyc00g008580.1	Unknown Protein (AHRD V1)	CDS	START-LC	M	L	1	NA	NA	novel	NA
0	8348719	T	A	Solyc00	Solyc00g008580.1	Unknown Protein (AHRD V1)	CDS	START-LC	M	K	1	NA	NA	novel	NA
0	8348724	T	G	Solyc00	Solyc00g008580.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	V	3	0.198	2	novel	TOLERATED
0	8348739	T	C	Solyc00	Solyc00g008580.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	Y	H	8	0.561	2	novel	TOLERATED
0	8348740	A	G	Solyc00	Solyc00g008580.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	Y	C	8	0.168	2	novel	TOLERATED
0	8348748	A	C	Solyc00	Solyc00g008580.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	M	L	11	0.418	3	novel	TOLERATED
0	8348749	T	C	Solyc00	Solyc00g008580.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	M	T	11	0.837	3	novel	TOLERATED
0	8348760	T	C	Solyc00	Solyc00g008580.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	W	R	15	0.845	3	novel	TOLERATED
0	9354598	G	C	Solyc00	Solyc00g009770.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	P	53	NA	NA	novel	NA
0	9354604	C	T	Solyc00	Solyc00g009770.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	T	M	55	NA	NA	novel	NA
0	9354625	G	A	Solyc00	Solyc00g009770.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	G	D	62	NA	NA	novel	NA
0	10103487	G	A	Solyc00	Solyc00g011180.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	P	L	11	NA	NA	novel	NA
0	13664043	G	A	Solyc00	Solyc00g050430.2	BHLH transcription factor (AHRD	CDS	NONSYNC	S	N	37	0.585	18	novel	TOLERATED
0	13930415	G	C	Solyc00	Solyc00g055980.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	G	194	NA	NA	novel	NA
0	13930436	A	G	Solyc00	Solyc00g055980.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	L	187	NA	NA	novel	NA
0	14037318	C	T	Solyc00	Solyc00g058280.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	G	R	115	NA	NA	novel	NA
0	14064565	T	TAA	Solyc00	Solyc00g058900.1	GDSL esterase/lipase At2g31540 (.	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
0	14992895	G	C	Solyc00	Solyc00g080550.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	G	A	22	NA	NA	novel	NA
0	14992978	T	A	Solyc00	Solyc00g080550.1	Unknown Protein (AHRD V1)	CDS	STOP-LOS	*	K	50	NA	NA	novel	NA
0	15936807	T	TC	Solyc00	Solyc00g105340.1	Genomic DNA chromosome 5 P1 c	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
0	17326795	A	C	Solyc00	Solyc00g147570.2	Gelsolin (Fragment) (AHRD V1 **	CDS	NONSYNC	I	S	165	0.119	20	novel	TOLERATED
0	18295706	C	A	Solyc00	Solyc00g180440.1	50S ribosomal protein L20 chlorop	CDS	NONSYNC	R	L	18	1	388	novel	TOLERATED
0	18621218	T	A	Solyc00	Solyc00g192150.2	Mutator-like transposase (AHRD V	CDS	NONSYNC	F	Y	395	NA	NA	novel	NA
0	18621223	G	A	Solyc00	Solyc00g192150.2	Mutator-like transposase (AHRD V	CDS	NONSYNC	V	I	397	NA	NA	novel	NA
0	18621440	C	T	Solyc00	Solyc00g192150.2	Mutator-like transposase (AHRD V	CDS	NONSYNC	T	I	469	NA	NA	novel	NA
0	20201696	A	G	Solyc00	Solyc00g254110.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	M	V	20	NA	NA	novel	NA
0	21744587	T	C	Solyc00	Solyc00g322830.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	P	165	NA	NA	novel	NA
0	21744596	T	C	Solyc00	Solyc00g322830.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	S	168	NA	NA	novel	NA
1	259974	C	A	Solyc01	Solyc01g005370.2	Calmodulin-2 (AHRD V1 ***- D7	CDS	NONSYNC	H	Q	36	0.618	29	novel	TOLERATED
1	299280	A	G	Solyc01	Solyc01g005430.2	UBX domain protein 6 (AHRD V1	CDS	NONSYNC	K	E	64	0.312	7	novel	TOLERATED
1	299353	G	A	Solyc01	Solyc01g005430.2	UBX domain protein 6 (AHRD V1	CDS	NONSYNC	G	D	88	0	5	novel	DELETERIOUS
1	299442	G	A	Solyc01	Solyc01g005430.2	UBX domain protein 6 (AHRD V1	CDS	NONSYNC	A	T	118	0.332	7	novel	TOLERATED
1	299550	A	G	Solyc01	Solyc01g005430.2	UBX domain protein 6 (AHRD V1	CDS	NONSYNC	M	V	154	0.313	8	novel	TOLERATED
1	652380	A	AG	Solyc01	Solyc01g005980.2	POT family domain containing prot	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	1049001	C	A	Solyc01	Solyc01g006440.1	Peptide transporter-like protein (AI	CDS	NONSYNC	W	C	233	0.001	51	novel	DELETERIOUS
1	1049002	C	T	Solyc01	Solyc01g006440.1	Peptide transporter-like protein (AI	CDS	STOP-GAI	W	*	233	NA	NA	novel	NA
1	1064992	G	A	Solyc01	Solyc01g006460.1	Non-structural maintenance of chro	CDS	NONSYNC	A	V	312	0.224	8	novel	TOLERATED
1	1070896	G	A	Solyc01	Solyc01g006470.1	Bromodomain protein (AHRD V1 '	CDS	NONSYNC	P	S	227	NA	NA	novel	NA
1	1098080	T	TA	Solyc01	Solyc01g006510.2	L-threonine 3-dehydrogenase (AHR	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	1360031	A	AT	Solyc01	Solyc01g006780.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	1558788	C	CT	Solyc01	Solyc01g006990.2	F-box family protein (AHRD V1 **	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	2118853	T	G	Solyc01	Solyc01g007930.2	Sel1 domain protein repeat-containi	CDS	NONSYNC	N	H	296	0.927	16	novel	TOLERATED
1	2761695	G	A	Solyc01	Solyc01g008720.1	Mannan endo-1 4-beta-mannosidas	CDS	NONSYNC	C	Y	209	0.001	87	novel	DELETERIOUS
1	2834870	C	T	Solyc01	Solyc01g008800.1	Tir-nbs-lrr, resistance protein	CDS	NONSYNC	A	T	514	0.093	33	novel	TOLERATED
1	2900946	G	C	Solyc01	Solyc01g008880.1	Ethylene responsive transcription fa	CDS	NONSYNC	N	K	101	0.901	38	novel	TOLERATED
1	2900951	T	C	Solyc01	Solyc01g008880.1	Ethylene responsive transcription fa	CDS	NONSYNC	K	E	100	0.787	39	novel	TOLERATED
1	2901131	C	T	Solyc01	Solyc01g008880.1	Ethylene responsive transcription fa	CDS	NONSYNC	V	I	40	0.322	20	novel	TOLERATED
1	2953220	C	G	Solyc01	Solyc01g008930.2	Phycoerythrobilin ferredoxin oxidor	CDS	NONSYNC	S	T	116	0.886	18	novel	TOLERATED
1	2955601	A	T	Solyc01	Solyc01g008930.2	Phycoerythrobilin ferredoxin oxidor	CDS	NONSYNC	S	R	44	0.71	5	novel	TOLERATED
1	3830202	T	C	Solyc01	Solyc01g009580.1	Terminal flower 1 (Fragment) (AHI	CDS	NONSYNC	V	A	147	1	211	novel	TOLERATED
1	3883435	G	T	Solyc01	Solyc01g009640.1	Polygalacturonase (AHRD V1 ***-	CDS	NONSYNC	N	K	4	1	9	novel	TOLERATED
1	4000349	A	G	Solyc01	Solyc01g009720.1	Zinc finger family protein (AHRD '	CDS	NONSYNC	S	P	165	0.319	6	novel	TOLERATED
1	4000603	A	G	Solyc01	Solyc01g009720.1	Zinc finger family protein (AHRD '	CDS	NONSYNC	L	S	80	0.12	9	novel	TOLERATED
1	4099930	T	C	Solyc01	Solyc01g009740.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	I	V	574	0.331	4	novel	TOLERATED
1	4253768	T	C	Solyc01	Solyc01g009810.2	LRR receptor-like serine/threonine-	CDS	NONSYNC	L	S	136	1	127	novel	TOLERATED
1	5062009	A	G	Solyc01	Solyc01g010260.2	Cytochrome P450	CDS	NONSYNC	Q	R	344	1	52	novel	TOLERATED
1	5636477	C	T	Solyc01	Solyc01g010630.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	V	I	215	NA	NA	novel	NA
1	8163468	G	A	Solyc01	Solyc01g011250.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	S	N	208	0.431	8	novel	TOLERATED
1	10139332	C	T	Solyc01	Solyc01g013780.1	Dicer-like protein (AHRD V1 ***-	CDS	NONSYNC	R	K	33	1	2	novel	TOLERATED
1	10139338	G	A	Solyc01	Solyc01g013780.1	Dicer-like protein (AHRD V1 ***-	CDS	NONSYNC	S	L	31	0.872	2	novel	TOLERATED
1	10139353	G	T	Solyc01	Solyc01g013780.1	Dicer-like protein (AHRD V1 ***-	CDS	NONSYNC	A	D	26	0	2	novel	DELETERIOUS
1	10139359	C	A	Solyc01	Solyc01g013780.1	Dicer-like protein (AHRD V1 ***-	CDS	NONSYNC	R	I	24	0.049	2	novel	DELETERIOUS
1	11072327	T	A	Solyc01	Solyc01g014040.1	Unknown Protein (AHRD V1)	CDS	STOP-GAI	K	*	123	NA	NA	novel	NA
1	11072329	T	A	Solyc01	Solyc01g014040.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	K	I	122	0.137	2	novel	TOLERATED
1	11072330	T	A	Solyc01	Solyc01g014040.1	Unknown Protein (AHRD V1)	CDS	STOP-GAI	K	*	122	NA	NA	novel	NA
1	11072331	C	A	Solyc01	Solyc01g014040.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	F	121	0.114	2	novel	TOLERATED
1	11072424	C	A	Solyc01	Solyc01g014040.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	F	90	0	3	novel	DELETERIOUS
1	11072432	C	G	Solyc01	Solyc01g014040.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	D	H	88	0	3	novel	DELETERIOUS
1	12554204	C	T	Solyc01	Solyc01g014370.1	Plant synaptotagmin integral membr	CDS	NONSYNC	G	E	129	0.005	21	novel	DELETERIOUS
1	12554355	ACC	A	Solyc01	Solyc01g014370.1	Plant synaptotagmin integral membr	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	14481450	G	T	Solyc01	Solyc01g014650.1	Receptor-like protein kinase (AHRI	CDS	NONSYNC	G	V	15	1	64	novel	TOLERATED
1	22885648	C	T	Solyc01	Solyc01g016910.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	W	10	NA	NA	novel	NA
1	23791101	T	C	Solyc01	Solyc01g017050.1	PG1 protein (Fragment) (AHRD V	CDS	NONSYNC	C	R	9	0.581	2	novel	TOLERATED
1	23791180	A	C	Solyc01	Solyc01g017050.1	PG1 protein (Fragment) (AHRD V	CDS	NONSYNC	Q	P	35	0.202	8	novel	TOLERATED
1	23879361	C	A	Solyc01	Solyc01g017110.1	NADH dehydrogenase subunit 5 (F	CDS	NONSYNC	S	R	264	0.002	24	novel	DELETERIOUS
1	23895591	A	G	Solyc01	Solyc01g017240.1	Ycf1 (Fragment) (AHRD V1 ***- ,	CDS	NONSYNC	F	S	86	1	69	novel	TOLERATED
1	23943367	A	C	Solyc01	Solyc01g017380.1	DNA-directed RNA polymerase sul	CDS	NONSYNC	K	Q	3	0.489	161	novel	TOLERATED
1	26499885	T	C	Solyc01	Solyc01g017930.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	Y	H	482	0.092	18	novel	TOLERATED
1	27929981	A	G	Solyc01	Solyc01g020210.1	Mutator-like transposase (AHRD V	CDS	STOP-LOS	*	W	133	NA	NA	novel	NA
1	36973917	A	G	Solyc01	Solyc01g034220.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	I	V	431	1	21	novel	TOLERATED
1	47056349	A	T	Solyc01	Solyc01g056430.1	Amidohydrolase family (AHRD V1	CDS	STOP-GAI	R	*	315	NA	NA	novel	NA
1	47469648	T	C	Solyc01	Solyc01g056520.2	RAN binding protein 16-like (AHR	CDS	NONSYNC	Y	C	71	0.197	16	novel	TOLERATED
1	49893276	T	C	Solyc01	Solyc01g056850.2	CTP synthase (AHRD V1 ***- B6	CDS	NONSYNC	K	R	54	1	250	novel	TOLERATED
1	50109961	G	A	Solyc01	Solyc01g056860.1	Pol polyprotein (AHRD V1 ***- Q	CDS	NONSYNC	G	R	52	1	137	novel	TOLERATED
1	50394369	A	G	Solyc01	Solyc01g056930.1	Hypothetical chloroplast RF1 (AHF	CDS	NONSYNC	Y	C	77	0.089	2	novel	TOLERATED
1	50394405	G	T	Solyc01	Solyc01g056930.1	Hypothetical chloroplast RF1 (AHF	CDS	STOP-LOS	*	L	89	NA	NA	novel	NA
1	50394406	A	T	Solyc01	Solyc01g056930.1	Hypothetical chloroplast RF1 (AHF	CDS	STOP-LOS	*	C	89	NA	NA	novel	NA
1	51279392	CA	C	Solyc01	Solyc01g057100.1	DNA-directed RNA polymerase sul	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	52746845	T	G	Solyc01	Solyc01g057220.2	Pectinesterase (AHRD V1 ***- B9	CDS	NONSYNC	V	G	512	1	25	novel	TOLERATED
1	52841700	A	G	Solyc01	Solyc01g057240.1	50S ribosomal protein L3-2 (AHRI	CDS	NONSYNC	F	S	24	0.077	16	novel	TOLERATED
1	57858484	CTA	C	Solyc01	Solyc01g058010.2	Neutral invertase (AHRD V1 ***-	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	58392240	C	T	Solyc01	Solyc01g058160.2	Agenet domain-containing protein (	CDS	NONSYNC	T	I	31	0	2	novel	DELETERIOUS
1	59234930	A	G	Solyc01	Solyc01g058360.1	Major facilitator superfamily transp	CDS	NONSYNC	D	G	94	0.085	60	novel	TOLERATED
1	60086454	TTCA	T	Solyc01	Solyc01g058610.1	MuDR family transposase containir	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
1	61177456	T	C	Solyc01	Solyc01g059760.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	S	P	577	NA	NA	novel	NA
1	64181765	C	T	Solyc01	Solyc01g065520.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	G	E	22	NA	NA	novel	NA
1	66676005	T	C	Solyc01	Solyc01g066400.1	Pectinesterase (AHRD V1 ***- Q4	CDS	NONSYNC	H	R	5	0.186	4	novel	TOLERATED
1	66946858	G	T	Solyc01	Solyc01g066530.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	S	R	56	NA	NA	novel	NA
1	68353449	T	C	Solyc01	Solyc01g067410.1	Pectinesterase (AHRD V1 **** D7	CDS	NONSYNC	D	G	68	1	23	novel	TOLERATED
1	69519744	G	GT	Solyc01	Solyc01g068090.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	70626642	T	C	Solyc01	Solyc01g074060.1	Beta-glucosidase 01 (AHRD V1 **	CDS	NONSYNC	S	P	161	0.034	6	novel	DELETERIOUS
1	70789819	C	T	Solyc01	Solyc01g079180.2	Pectinesterase (AHRD V1 **** D8	CDS	NONSYNC	T	I	334	0.172	32	novel	TOLERATED
1	71641292	A	T	Solyc01	Solyc01g080000.1	Xylanase inhibitor (Fragment) (AH	CDS	NONSYNC	N	K	415	0.009	34	novel	DELETERIOUS
1	72410172	G	A	Solyc01	Solyc01g080660.2	Splicing factor arginine/serine-rich	CDS	NONSYNC	R	C	126	0.001	60	novel	DELETERIOUS
1	72431970	G	A	Solyc01	Solyc01g080670.2	Squamosa promoter binding protein	CDS	NONSYNC	S	N	477	0.864	14	novel	TOLERATED

1	72438865	A	G	Solyc01	Solyc01g080680.2	Glucose transporter 8 (AHRD V1 *	CDS	NONSYNC	I	V	204	0.185	76	novel	TOLERATED
1	72444790	T	C	Solyc01	Solyc01g080690.2	Transcription initiation factor TFIII	CDS	NONSYNC	F	S	198	0.739	17	novel	TOLERATED
1	72480062	G	A	Solyc01	Solyc01g080740.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	A	V	1014	1	2	novel	TOLERATED
1	72484385	T	C	Solyc01	Solyc01g080740.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	N	D	250	0.691	2	novel	TOLERATED
1	72497738	T	C	Solyc01	Solyc01g080760.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	Q	R	75	0.572	6	novel	TOLERATED
1	72526553	G	A	Solyc01	Solyc01g080780.2	Translocase of chloroplast 34 (AHF	CDS	NONSYNC	G	R	62	0.175	11	novel	TOLERATED
1	72831305	C	A	Solyc01	Solyc01g081010.2	Nucleolar GTP-binding protein (AI	CDS	NONSYNC	V	L	396	0.065	117	novel	TOLERATED
1	72863483	T	TAGG	Solyc01	Solyc01g081040.2	RING finger protein (AHRD V1 *-	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
1	75741716	A	AT	Solyc01	Solyc01g090320.2	Ethylene responsive transcription fa	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	76897668	T	C	Solyc01	Solyc01g091510.2	Ankyrin repeat and zinc finger dom	CDS	NONSYNC	I	V	368	0.839	11	novel	TOLERATED
1	77109041	A	G	Solyc01	Solyc01g091770.2	Ring H2 finger protein (AHRD V1	CDS	NONSYNC	I	V	45	1	24	novel	TOLERATED
1	77109051	G	T	Solyc01	Solyc01g091770.2	Ring H2 finger protein (AHRD V1	CDS	NONSYNC	G	V	48	0.362	24	novel	TOLERATED
1	77112401	C	T	Solyc01	Solyc01g091780.2	Fructosamine kinase family protein	CDS	NONSYNC	S	F	13	0.048	6	novel	DELETERIOUS
1	77133859	A	G	Solyc01	Solyc01g091820.2	Flap structure-specific endonuclea	CDS	NONSYNC	S	P	133	1	13	novel	TOLERATED
1	77438660	AGG	A	Solyc01	Solyc01g094090.2	Enoyl-CoA-hydratase (AHRD V1 *	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	78823216	G	A	Solyc01	Solyc01g095910.1	Membrane protein-like (AHRD V1	CDS	NONSYNC	P	L	139	NA	NA	novel	NA
1	78823267	A	G	Solyc01	Solyc01g095910.1	Membrane protein-like (AHRD V1	CDS	NONSYNC	L	P	122	NA	NA	novel	NA
1	78890214	A	AT	Solyc01	Solyc01g096040.2	Aspartic proteinase nepenthesin I (/	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	80110068	G	A	Solyc01	Solyc01g097530.1	Photosystem Q(B) protein (AHRD	CDS	NONSYNC	G	D	62	0.001	148	novel	DELETERIOUS
1	80290468	T	A	Solyc01	Solyc01g097830.2	AT5G28150-like protein (Fragmen	CDS	NONSYNC	I	F	71	0.743	19	novel	TOLERATED
1	80489826	A	T	Solyc01	Solyc01g098150.2	Pentatricopeptide repeat-containing	CDS	NONSYNC	I	N	289	0.001	12	novel	DELETERIOUS
1	80563287	A	ACCGC	Solyc01	Solyc01g098210.2	Transmembrane protein adipocyte-(	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
1	80944132	A	G	Solyc01	Solyc01g098750.2	RING finger protein B (AHRD V1	CDS	NONSYNC	T	A	141	1	32	novel	TOLERATED
1	81011808	A	G	Solyc01	Solyc01g098870.2	Nucleolar GTPase (AHRD V1 *-*-	CDS	NONSYNC	D	G	555	0.155	8	novel	TOLERATED
1	81062886	A	G	Solyc01	Solyc01g098930.2	Cyclin (AHRD V1 **** D8UD80_	CDS	NONSYNC	V	A	63	0.874	49	novel	TOLERATED
1	81074550	A	T	Solyc01	Solyc01g098950.1	Glyceraldehyde-3-phosphate dehyd	CDS	NONSYNC	D	V	147	1	396	novel	TOLERATED
1	81082603	T	C	Solyc01	Solyc01g098960.1	Glycogenin-like protein (AHRD V1	CDS	NONSYNC	L	S	150	0.005	32	novel	DELETERIOUS
1	81085511	T	C	Solyc01	Solyc01g098970.1	Glycogenin-like protein (AHRD V1	CDS	NONSYNC	F	S	128	0.203	31	novel	TOLERATED
1	81121928	T	C	Solyc01	Solyc01g099020.2	GDSL esterase/lipase At5g03980 (.	CDS	NONSYNC	K	E	33	0.985	8	novel	TOLERATED
1	81121940	T	C	Solyc01	Solyc01g099020.2	GDSL esterase/lipase At5g03980 (.	CDS	NONSYNC	I	V	29	0.78	9	novel	TOLERATED
1	81121997	A	G	Solyc01	Solyc01g099020.2	GDSL esterase/lipase At5g03980 (.	CDS	NONSYNC	F	L	10	1	7	novel	TOLERATED
1	81229519	C	G	Solyc01	Solyc01g099150.2	Lipoxygenase (AHRD V1 **** Q9	CDS	NONSYNC	Q	E	701	1	172	novel	TOLERATED
1	81229579	G	C	Solyc01	Solyc01g099150.2	Lipoxygenase (AHRD V1 **** Q9	CDS	NONSYNC	V	L	721	1	171	novel	TOLERATED
1	81229589	G	GGTAT	Solyc01	Solyc01g099150.2	Lipoxygenase (AHRD V1 **** Q9	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	81252867	T	C	Solyc01	Solyc01g099190.2	Lipoxygenase (AHRD V1 **** Q4	CDS	NONSYNC	T	A	580	0.175	123	novel	TOLERATED
1	81298876	T	TTCA	Solyc01	Solyc01g099250.1	LRR receptor-like serine/threonine-	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
1	81306629	T	G	Solyc01	Solyc01g099270.2	Microtubule binding protein (AHRI	CDS	NONSYNC	M	L	495	NA	NA	novel	NA
1	81351154	C	G	Solyc01	Solyc01g099300.2	MORC family CW-type zinc finger	CDS	NONSYNC	K	N	342	0.397	18	novel	TOLERATED
1	81369375	G	A	Solyc01	Solyc01g099310.2	RNA polymerase II holoenzyme cy	CDS	NONSYNC	D	N	240	1	19	novel	TOLERATED
1	81714791	A	G	Solyc01	Solyc01g099810.2	Arginine/serine-rich splicing factor	CDS	NONSYNC	F	L	53	0.002	179	novel	DELETERIOUS
1	83621743	GT	G	Solyc01	Solyc01g103200.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	84697987	A	T	Solyc01	Solyc01g104480.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	T	S	222	0.813	12	novel	TOLERATED
1	84697988	C	T	Solyc01	Solyc01g104480.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	T	I	222	0.26	12	novel	TOLERATED
1	85236157	T	A	Solyc01	Solyc01g105230.2	Calmodulin-binding transcription a	CDS	NONSYNC	D	E	1031	0.109	18	novel	TOLERATED
1	86074345	A	T	Solyc01	Solyc01g106410.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	N	K	352	0.522	12	novel	TOLERATED
1	86869784	A	T	Solyc01	Solyc01g107610.2	PRKR interacting protein 1 (AHRD	CDS	NONSYNC	N	Y	150	0.008	22	novel	DELETERIOUS
1	86869785	A	G	Solyc01	Solyc01g107610.2	PRKR interacting protein 1 (AHRD	CDS	NONSYNC	N	S	150	0.197	22	novel	TOLERATED
1	86888582	A	T	Solyc01	Solyc01g107650.2	Receptor like kinase, RLK	CDS	NONSYNC	T	S	9	0.55	9	novel	TOLERATED
1	86912966	TCGG.	T	Solyc01	Solyc01g107690.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	89461235	T	G	Solyc01	Solyc01g111480.1	Mutator-like transposase (AHRD V	CDS	NONSYNC	L	V	103	NA	NA	novel	NA
1	89461253	G	A	Solyc01	Solyc01g111480.1	Mutator-like transposase (AHRD V	CDS	NONSYNC	G	S	109	NA	NA	novel	NA
1	89463061	T	C	Solyc01	Solyc01g111480.1	Mutator-like transposase (AHRD V	CDS	NONSYNC	V	A	507	NA	NA	novel	NA
1	89463567	T	TA	Solyc01	Solyc01g111480.1	Mutator-like transposase (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
1	89463853	C	T	Solyc01	Solyc01g111480.1	Mutator-like transposase (AHRD V	CDS	NONSYNC	P	L	653	0	2	novel	DELETERIOUS
2	5034828	T	C	Solyc02	Solyc02g012010.1	ATP synthase subunit alpha chloro	CDS	NONSYNC	M	V	50	1	336	novel	TOLERATED
2	5034831	G	A	Solyc02	Solyc02g012010.1	ATP synthase subunit alpha chloro	CDS	NONSYNC	P	S	49	0.408	336	novel	TOLERATED
2	5034836	A	G	Solyc02	Solyc02g012010.1	ATP synthase subunit alpha chloro	CDS	NONSYNC	V	A	47	1	337	novel	TOLERATED
2	5034848	T	A	Solyc02	Solyc02g012010.1	ATP synthase subunit alpha chloro	CDS	NONSYNC	N	I	43	1	340	novel	TOLERATED
2	5034851	C	G	Solyc02	Solyc02g012010.1	ATP synthase subunit alpha chloro	CDS	NONSYNC	G	A	42	1	340	novel	TOLERATED
2	6195563	G	A	Solyc02	Solyc02g014060.1	Receptor-like kinase (AHRD V1 *-	CDS	NONSYNC	P	S	29	0.752	50	novel	TOLERATED
2	14306149	C	CT	Solyc02	Solyc02g021740.1	Ulp1 protease family C-terminal cat	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	20599694	T	C	Solyc02	Solyc02g033110.1	Zinc ion binding protein (AHRD V	CDS	NONSYNC	D	G	124	0.701	2	novel	TOLERATED
2	20599731	C	T	Solyc02	Solyc02g033110.1	Zinc ion binding protein (AHRD V	CDS	NONSYNC	V	I	112	0.687	3	novel	TOLERATED
2	27869434	A	C	Solyc02	Solyc02g061770.2	Endochitinase (Chitinase) (AHRD '	CDS	NONSYNC	R	S	226	0.619	277	novel	TOLERATED
2	30860880	C	T	Solyc02	Solyc02g065120.1	Mutator-like transposase (AHRD V	CDS	NONSYNC	A	V	382	0	2	novel	DELETERIOUS
2	31000843	T	G	Solyc02	Solyc02g065250.1	Alpha-hydroxynitrile lyase (AHRD	CDS	NONSYNC	N	K	197	0.289	4	novel	TOLERATED
2	31000844	T	A	Solyc02	Solyc02g065250.1	Alpha-hydroxynitrile lyase (AHRD	CDS	STOP-LOS	*	R	198	NA	NA	novel	NA
2	31019758	T	C	Solyc02	Solyc02g065270.1	Esterase PIR7B (AHRD V1 ***- P	CDS	NONSYNC	M	T	28	0.023	13	novel	DELETERIOUS
2	31566802	T	A	Solyc02	Solyc02g066830.2	Ras GTPase-activating protein-bin	CDS	NONSYNC	Y	N	243	0.025	25	novel	DELETERIOUS
2	31667763	C	T	Solyc02	Solyc02g066880.1	Unknown Protein (AHRD V1)	CDS	STOP-GAI	Q	*	149	NA	NA	novel	NA
2	31765170	ATCG	A	Solyc02	Solyc02g066940.2	Splicing factor -like RNA-binding (	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
2	31778703	T	G	Solyc02	Solyc02g066950.2	Alpha amylase 2 (IC) (AHRD V1 *	CDS	NONSYNC	Y	D	3	0.032	2	novel	DELETERIOUS
2	31868129	A	C	Solyc02	Solyc02g067040.2	cDNA clone J075153F01 full inser	CDS	NONSYNC	E	D	465	0.182	28	novel	TOLERATED
2	31908718	A	T	Solyc02	Solyc02g067100.2	Targeting protein for Xklp2 contain	CDS	NONSYNC	K	M	266	0.003	16	novel	DELETERIOUS
2	31927954	G	A	Solyc02	Solyc02g067140.1	Mutator-like transposase (AHRD V	CDS	NONSYNC	S	F	93	0	4	novel	DELETERIOUS
2	31931014	T	A	Solyc02	Solyc02g067150.2	Pro-resilin (AHRD V1 **-- B6T4C	CDS	NONSYNC	S	R	241	0.516	16	novel	TOLERATED
2	31931433	C	T	Solyc02	Solyc02g067150.2	Pro-resilin (AHRD V1 **-- B6T4C	CDS	NONSYNC	R	C	340	0.007	13	novel	DELETERIOUS
2	31981647	C	CT	Solyc02	Solyc02g067210.2	Nucleic acid binding protein (AHR	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	31981654	A	T	Solyc02	Solyc02g067210.2	Nucleic acid binding protein (AHR	CDS	START-LC	M	K	1	NA	NA	novel	NA
2	32265198	ATGG.	A	Solyc02	Solyc02g067510.2	cDNA clone J023121M11 full inse	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
2	32330703	C	G	Solyc02	Solyc02g067620.1	Zinc transporter like 1 (AHRD V1 '	CDS	NONSYNC	L	F	453	1	46	novel	TOLERATED
2	32356350	A	G	Solyc02	Solyc02g067650.1	Polygalacturonase 1 (AHRD V1 **	CDS	NONSYNC	I	V	204	1	72	novel	TOLERATED
2	33795592	T	G	Solyc02	Solyc02g069270.2	ARGONAUTE 1 (AHRD V1 ***-	CDS	NONSYNC	I	S	902	0.079	23	novel	TOLERATED
2	33916649	A	AT	Solyc02	Solyc02g069450.2	Photosystem I reaction center subur	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	33998331	G	A	Solyc02	Solyc02g069570.2	Pentatricopeptide repeat-containing	CDS	NONSYNC	M	I	395	0.198	12	novel	TOLERATED
2	34195673	C	G	Solyc02	Solyc02g069780.2	Serine/threonine-protein phosphata	CDS	NONSYNC	S	R	620	0.428	28	novel	TOLERATED
2	34195735	A	G	Solyc02	Solyc02g069780.2	Serine/threonine-protein phosphata	CDS	NONSYNC	Q	R	641	0.425	25	novel	TOLERATED
2	34382779	G	A	Solyc02	Solyc02g070000.2	Receptor like kinase, RLK	CDS	NONSYNC	E	K	789	1	33	novel	TOLERATED
2	34382785	A	G	Solyc02	Solyc02g070000.2	Receptor like kinase, RLK	CDS	NONSYNC	T	A	791	0.231	33	novel	TOLERATED
2	34398092	G	A	Solyc02	Solyc02g070030.2	Methyltransferase type 12 (AHRD '	CDS	NONSYNC	P	S	539	0.522	11	novel	TOLERATED
2	34937120	C	T	Solyc02	Solyc02g070700.1	HMG-I and HMG-Y DNA-binding	CDS	NONSYNC	P	S	16	0.73	4	novel	TOLERATED
2	35306122	A	C	Solyc02	Solyc02g071250.2	Protein phosphatase (AHRD V1 *-	CDS	NONSYNC	I	R	282	0.013	17	novel	DELETERIOUS
2	35469294	TG	T	Solyc02	Solyc02g071450.2	1-aminocyclopropane-1-carboxylat	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	35852446	G	C	Solyc02	Solyc02g071900.2	Seipin (AHRD V1 *-*- Q5BIQ8_E	CDS	NONSYNC	R	S	248	0.011	8	novel	DELETERIOUS
2	38750077	A	G	Solyc02	Solyc02g079710.2	Serine/threonine kinase receptor (A	CDS	NONSYNC	S	P	421	0.223	27	novel	TOLERATED
2	39065587	G	T	Solyc02	Solyc02g080210.2	Pectinesterase (AHRD V1 ***- B9	CDS	NONSYNC	T	K	517	0.314	41	novel	TOLERATED
2	39132114	A	T	Solyc02	Solyc02g080290.2	Beta-glucosidase 47 (AHRD V1 **	CDS	NONSYNC	T	S	19	0.434	12	novel	TOLERATED
2	40192383	A	C	Solyc02	Solyc02g081800.1	Acyltransferase (Fragment) (AHRD	CDS	NONSYNC	M	L	112	1	5	novel	TOLERATED
2	40236312	C	T	Solyc02	Solyc02g081870.2	ABC transporter G family member	CDS	NONSYNC	A	V	1376	0.736	225	novel	TOLERATED
2	42591631	A	AT	Solyc02	Solyc02g084980.2	Galactinol synthase (AHRD V1 **'	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	42959779	G	A	Solyc02	Solyc02g085530.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	T	I	114	NA	NA	novel	NA
2	43708392	G	GT	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	43708394	G	GGA	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	43708401	G	A	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	E	K	1126	0.06	9	novel	TOLERATED
2	43708404	T	C	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	L	1127	0.76	9	novel	TOLERATED
2	43708410	T	G	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	V	1129	0.093	8	novel	TOLERATED
2	43708411	T	A	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	STOP-GAI	L	*	1129	NA	NA	novel	NA
2	43708417	C	T	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	S	L	1131	0.299	7	novel	TOLERATED
2	43708423	A	G	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	E	G	1133	0.065	9	novel	TOLERATED
2	43708432	T	C	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	I	T	1136	0.292	9	novel	TOLERATED
2	43708444	A	C	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	K	T	1140	0.2	9	novel	TOLERATED
2	43708467	C	A	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	Q	K	1148	0.351	8	novel	TOLERATED
2	43708468	A	C	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	Q	P	1148	0.076	8	novel	TOLERATED
2	43708471	T	C	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	V	A	1149	0.359	8	novel	TOLERATED
2	43708474	T	C	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	I	T	1150	0.253	8	novel	TOLERATED
2	43708495	T	C	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	P	1157	0.006	8	novel	DELETERIOUS
2	43708497	G	T	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	S	1158	0.075	8	novel	TOLERATED

2	43708500	G	T	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	V	F	1159	0.058	7	novel	TOLERATED
2	43708510	T	A	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	M	K	1162	0.953	8	novel	TOLERATED
2	43708511	G	A	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	M	I	1162	0.229	8	novel	TOLERATED
2	43708517	A	C	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	E	D	1164	0.121	9	novel	TOLERATED
2	43708521	A	C	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	T	P	1166	0.086	9	novel	TOLERATED
2	43708524	G	A	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	T	1167	0.382	9	novel	TOLERATED
2	43712702	T	G	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	V	2187	0.485	7	novel	TOLERATED
2	43712729	T	A	Solyc02	Solyc02g086460.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	S	T	2196	0.634	8	novel	TOLERATED
2	44657947	G	A	Solyc02	Solyc02g087780.2	Aldose-1-epimerase-like protein (A	CDS	NONSYNC	V	M	337	0.01	72	novel	DELETERIOUS
2	44841846	G	A	Solyc02	Solyc02g088060.1	Plasma membrane H+-ATPase (AI	CDS	NONSYNC	L	F	109	0.02	51	novel	DELETERIOUS
2	45010330	C	CA	Solyc02	Solyc02g088290.2	Guanine nucleotide exchange factor	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	45270592	GC	G	Solyc02	Solyc02g088700.2	Mitochondrial processing peptidase	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	45270602	CT	C	Solyc02	Solyc02g088700.2	Mitochondrial processing peptidase	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	45270636	TC	T	Solyc02	Solyc02g088700.2	Mitochondrial processing peptidase	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	45270643	TG	T	Solyc02	Solyc02g088700.2	Mitochondrial processing peptidase	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	45270656	CA	C	Solyc02	Solyc02g088700.2	Mitochondrial processing peptidase	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	45766769	TG	T	Solyc02	Solyc02g089340.2	DNA-directed RNA polymerase (A	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	46871886	A	AT	Solyc02	Solyc02g090790.1	Ethylene responsive transcription fa	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
2	49454188	G	T	Solyc02	Solyc02g094310.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	G	V	361	0.282	7	novel	TOLERATED
2	49454191	A	C	Solyc02	Solyc02g094310.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	N	T	362	0.116	7	novel	TOLERATED
2	49454192	C	A	Solyc02	Solyc02g094310.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	N	K	362	0.048	7	novel	DELETERIOUS
2	49454195	G	T	Solyc02	Solyc02g094310.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	R	S	363	0.334	7	novel	TOLERATED
2	49559523	T	G	Solyc02	Solyc02g094480.2	Pentatricopeptide repeat-containing	CDS	NONSYNC	Y	S	1033	1	76	novel	TOLERATED
2	49559530	T	G	Solyc02	Solyc02g094480.2	Pentatricopeptide repeat-containing	CDS	NONSYNC	I	L	1031	1	76	novel	TOLERATED
3	825470	T	C	Solyc03	Solyc03g006170.2	Pollen allergen Phl p 11 (AHRD V	CDS	NONSYNC	H	R	55	0.264	7	novel	TOLERATED
3	1030619	ACCT	A	Solyc03	Solyc03g006430.2	Os11g0198100 protein (Fragment)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
3	1030920	T	C	Solyc03	Solyc03g006430.2	Os11g0198100 protein (Fragment)	CDS	NONSYNC	S	P	187	1	40	novel	TOLERATED
3	1889647	A	G	Solyc03	Solyc03g007320.2	Polypyrimidine tract-binding protei	CDS	NONSYNC	M	V	222	0.959	35	novel	TOLERATED
3	2004616	C	CTT	Solyc03	Solyc03g007450.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	7581306	G	GA	Solyc03	Solyc03g025800.2	Os03g0111400 protein (Fragment)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	7900082	A	G	Solyc03	Solyc03g026110.2	Calmodulin binding protein (AHRI	CDS	NONSYNC	L	P	382	0.247	18	novel	TOLERATED
3	8708630	C	T	Solyc03	Solyc03g031950.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	Q	108	0.142	11	novel	TOLERATED
3	9047053	C	A	Solyc03	Solyc03g032240.2	Cation/H(+) antiporter 2 (AHRD V	CDS	NONSYNC	R	I	454	1	12	novel	TOLERATED
3	9115271	C	T	Solyc03	Solyc03g033250.1	Tracheary element differentiation-re	CDS	NONSYNC	L	F	83	NA	NA	novel	NA
3	9122734	A	G	Solyc03	Solyc03g033260.2	Maltose excess protein 1, chloropla	CDS	NONSYNC	N	S	48	0.949	6	novel	TOLERATED
3	9481806	G	A	Solyc03	Solyc03g033620.2	Serine carboxypeptidase S28 family	CDS	NONSYNC	S	N	91	1	39	novel	TOLERATED
3	9598177	T	G	Solyc03	Solyc03g033710.2	Peroxidase (AHRD V1 ***- Q0ZA	CDS	NONSYNC	D	E	303	1	141	novel	TOLERATED
3	9662903	G	A	Solyc03	Solyc03g033750.1	BCS1 protein-like protein (AHRD '	CDS	NONSYNC	V	I	46	NA	NA	novel	NA
3	9789911	A	G	Solyc03	Solyc03g033880.1	MADS-box transcription factor 31 (	CDS	NONSYNC	T	A	70	NA	NA	novel	NA
3	10735704	G	A	Solyc03	Solyc03g036480.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	D	N	61	0.082	155	novel	TOLERATED
3	11156986	A	G	Solyc03	Solyc03g043680.1	Gag-Pol polyprotein (AHRD V1 **	CDS	NONSYNC	L	P	214	0.099	10	novel	TOLERATED
3	11598946	G	T	Solyc03	Solyc03g043910.2	BSD domain containing protein (AI	CDS	NONSYNC	H	N	97	0.563	15	novel	TOLERATED
3	11599075	C	A	Solyc03	Solyc03g043910.2	BSD domain containing protein (AI	CDS	NONSYNC	G	C	54	0	19	novel	DELETERIOUS
3	11599083	G	T	Solyc03	Solyc03g043910.2	BSD domain containing protein (AI	CDS	NONSYNC	P	H	51	0.01	14	novel	DELETERIOUS
3	13222899	C	A	Solyc03	Solyc03g044440.1	Ribosomal protein L22 family prote	CDS	NONSYNC	N	K	136	1	12	novel	TOLERATED
3	15466526	G	GA	Solyc03	Solyc03g045080.1	Receptor-like protein kinase 2 (AH	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	28921447	C	A	Solyc03	Solyc03g061650.1	F-box/LRR-repeat protein At3g269	CDS	NONSYNC	W	L	57	0	2	novel	DELETERIOUS
3	29511488	TA	T	Solyc03	Solyc03g062770.1	Ulp1 protease family C-terminal cat	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	32892728	G	A	Solyc03	Solyc03g063690.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	E	K	393	0.727	23	novel	TOLERATED
3	46658395	T	C	Solyc03	Solyc03g083260.1	Unknown Protein (AHRD V1)	CDS	STOP-LOS	*	Q	78	NA	NA	novel	NA
3	48932542	G	A	Solyc03	Solyc03g093800.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	P	L	27	0.699	13	novel	TOLERATED
3	48932546	T	C	Solyc03	Solyc03g093800.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	S	G	26	0.392	13	novel	TOLERATED
3	48953369	G	A	Solyc03	Solyc03g093820.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	K	12	NA	NA	novel	NA
3	48953439	CA	C	Solyc03	Solyc03g093820.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	50117306	A	G	Solyc03	Solyc03g095530.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	T	A	54	NA	NA	novel	NA
3	50211829	C	CA	Solyc03	Solyc03g095580.1	Unknown Protein (AHRD V1); con	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	52902053	T	C	Solyc03	Solyc03g097120.2	Heat stress transcription factor A3 (	CDS	NONSYNC	N	S	477	0.134	21	novel	TOLERATED
3	52902077	C	A	Solyc03	Solyc03g097120.2	Heat stress transcription factor A3 (	CDS	NONSYNC	W	L	469	0.399	20	novel	TOLERATED
3	53034390	C	T	Solyc03	Solyc03g097270.2	Cysteine proteinase inhibitor (AHR	CDS	NONSYNC	S	L	48	0.42	74	novel	TOLERATED
3	53265618	A	ATT	Solyc03	Solyc03g097480.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	56037650	G	A	Solyc03	Solyc03g111390.2	Kelch domain-containing protein 4	CDS	NONSYNC	M	I	555	0.955	14	novel	TOLERATED
3	56178296	T	G	Solyc03	Solyc03g111520.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	E	D	31	NA	NA	novel	NA
3	56478111	C	A	Solyc03	Solyc03g111800.2	Receptor like kinase, RLK	CDS	NONSYNC	R	L	196	0.03	11	novel	DELETERIOUS
3	56821881	A	T	Solyc03	Solyc03g112340.1	Ring H2 finger protein (AHRD V1	CDS	NONSYNC	M	L	389	0.918	5	novel	TOLERATED
3	56843559	G	A	Solyc03	Solyc03g112370.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	F	10	NA	NA	novel	NA
3	56847174	G	T	Solyc03	Solyc03g112390.2	Myb transcription factor (AHRD V	CDS	NONSYNC	H	N	204	1	15	novel	TOLERATED
3	58503971	C	A	Solyc03	Solyc03g114450.2	Extracellular calcium sensing recep	CDS	NONSYNC	P	Q	280	0	13	novel	DELETERIOUS
3	58525687	T	TC	Solyc03	Solyc03g114490.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	58597910	G	A	Solyc03	Solyc03g114610.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	M	I	56	NA	NA	novel	NA
3	58597929	G	T	Solyc03	Solyc03g114610.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	G	C	63	NA	NA	novel	NA
3	58641921	T	G	Solyc03	Solyc03g114690.2	Wd-40 repeat-containing protein (A	CDS	NONSYNC	K	N	917	0.314	8	novel	TOLERATED
3	59127847	T	A	Solyc03	Solyc03g115320.1	Expansin (AHRD V1 ***- Q7X9Q	CDS	NONSYNC	N	I	259	0.002	107	novel	DELETERIOUS
3	59325717	T	C	Solyc03	Solyc03g115620.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	I	V	429	0.954	9	novel	TOLERATED
3	59325975	C	T	Solyc03	Solyc03g115620.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	A	T	343	0.18	10	novel	TOLERATED
3	59326412	G	T	Solyc03	Solyc03g115620.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	T	K	197	0.286	9	novel	TOLERATED
3	59326439	A	G	Solyc03	Solyc03g115620.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	V	A	188	0.764	9	novel	TOLERATED
3	59326521	C	G	Solyc03	Solyc03g115620.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	E	Q	161	0.074	8	novel	TOLERATED
3	59357001	C	T	Solyc03	Solyc03g115660.2	Cell division protein kinase 12 (AH	CDS	NONSYNC	P	L	391	0.165	31	novel	TOLERATED
3	59358671	A	G	Solyc03	Solyc03g115660.2	Cell division protein kinase 12 (AH	CDS	NONSYNC	T	A	616	1	26	novel	TOLERATED
3	59367374	T	C	Solyc03	Solyc03g115670.1	Formin 2B (AHRD V1 ***- C7BG	CDS	NONSYNC	S	P	451	0.304	17	novel	TOLERATED
3	59367383	G	A	Solyc03	Solyc03g115670.1	Formin 2B (AHRD V1 ***- C7BG	CDS	NONSYNC	V	I	454	0.322	14	novel	TOLERATED
3	59405099	T	C	Solyc03	Solyc03g115720.2	ATP-dependent protease La (LON)	CDS	NONSYNC	I	V	317	0.339	24	novel	TOLERATED
3	59420071	C	T	Solyc03	Solyc03g115740.1	Alpha-1 6-xylosyltransferase (AHR	CDS	NONSYNC	E	K	412	1	78	novel	TOLERATED
3	59423272	G	T	Solyc03	Solyc03g115750.1	Galactosyltransferase-like protein (I	CDS	NONSYNC	E	D	132	0.26	19	novel	TOLERATED
3	59423275	G	C	Solyc03	Solyc03g115750.1	Galactosyltransferase-like protein (I	CDS	NONSYNC	K	N	133	0.563	20	novel	TOLERATED
3	59441879	C	T	Solyc03	Solyc03g115780.1	Exonuclease DNA polymerase III e	CDS	NONSYNC	R	H	299	0.193	16	novel	TOLERATED
3	59474888	A	C	Solyc03	Solyc03g115830.1	Fucosyltransferase 7 (AHRD V1 **	CDS	NONSYNC	K	T	85	0.505	33	novel	TOLERATED
3	59475196	A	G	Solyc03	Solyc03g115830.1	Fucosyltransferase 7 (AHRD V1 **	CDS	NONSYNC	I	V	188	0.028	44	novel	DELETERIOUS
3	59475344	G	A	Solyc03	Solyc03g115830.1	Fucosyltransferase 7 (AHRD V1 **	CDS	NONSYNC	R	Q	237	1	37	novel	TOLERATED
3	59531993	T	G	Solyc03	Solyc03g115880.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	V	G	24	NA	NA	novel	NA
3	59532038	T	A	Solyc03	Solyc03g115880.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	Y	39	NA	NA	novel	NA
3	59549046	G	T	Solyc03	Solyc03g115910.1	MADS-box transcription factor 1 (/	CDS	NONSYNC	T	N	95	0.092	39	novel	TOLERATED
3	59584066	G	C	Solyc03	Solyc03g115970.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	E	D	47	NA	NA	novel	NA
3	59598333	G	C	Solyc03	Solyc03g116000.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	T	S	39	0.787	7	novel	TOLERATED
3	59598346	G	A	Solyc03	Solyc03g116000.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	P	S	35	0.161	7	novel	TOLERATED
3	59598355	G	T	Solyc03	Solyc03g116000.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	L	I	32	0.419	4	novel	TOLERATED
3	59598379	G	C	Solyc03	Solyc03g116000.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	R	G	24	NA	NA	novel	NA
3	59598399	A	C	Solyc03	Solyc03g116000.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	L	R	17	NA	NA	novel	NA
3	59598428	A	T	Solyc03	Solyc03g116000.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	H	Q	7	NA	NA	novel	NA
3	59600596	C	G	Solyc03	Solyc03g116010.1	RWP-RK domain-containing protei	CDS	NONSYNC	G	A	121	0.789	14	novel	TOLERATED
3	59603070	G	A	Solyc03	Solyc03g116020.2	DNA-directed RNA polymerase (A	CDS	NONSYNC	P	L	174	0.005	22	novel	DELETERIOUS
3	59697118	A	G	Solyc03	Solyc03g116150.2	Dehydration-responsive family prot	CDS	NONSYNC	I	V	252	1	109	novel	TOLERATED
3	59745105	AG	A	Solyc03	Solyc03g116190.1	Chitinase (AHRD V1 --*- P93327_	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	59819932	A	G	Solyc03	Solyc03g116270.2	Gibberellin 2-beta-dioxygenase 8 (/	CDS	NONSYNC	T	A	302	0.059	10	novel	TOLERATED
3	59821321	A	ACCAT	Solyc03	Solyc03g116280.2	1-aminocyclopropane-1-carboxylat	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
3	59906516	C	T	Solyc03	Solyc03g116380.2	WD-40 repeat protein (AHRD V1 '	CDS	NONSYNC	A	V	88	0.062	4	novel	TOLERATED
3	59930977	C	G	Solyc03	Solyc03g116440.1	PHD finger family protein (AHRD '	CDS	NONSYNC	H	Q	647	0.065	14	novel	TOLERATED
3	59941842	G	A	Solyc03	Solyc03g116480.1	F-box family protein (AHRD V1 **	CDS	NONSYNC	G	S	259	0.694	4	novel	TOLERATED
3	59971512	T	A	Solyc03	Solyc03g116540.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	N	K	16	0.138	6	novel	TOLERATED
3	59971531	G	A	Solyc03	Solyc03g116540.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	V	I	23	1	8	novel	TOLERATED
3	59984688	A	G	Solyc03	Solyc03g116570.2	YuxK (AHRD V1 **-- B4AHQ1_I	CDS	NONSYNC	N	D	88	0.601	25	novel	TOLERATED
3	60015754	A	G	Solyc03	Solyc03g116620.2	Phospholipase D (AHRD V1 ****	CDS	NONSYNC	T	A	603	1	126	novel	TOLERATED
3	60136698	A	T	Solyc03	Solyc03g116820.2	Phox domain-containing protein (A	CDS	NONSYNC	S	T	149	0.506	11	novel	TOLERATED
3	60157333	C	A	Solyc03	Solyc03g116840.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	L	I	274	1	18	novel	TOLERATED
3	60194746	C	CAATT	Solyc03	Solyc03g116890.2	WRKY transcription factor 2 (AHR	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
3	60239020	C	T	Solyc03	Solyc03g116920.1	Sister chromatid cohesion protein P	CDS	NONSYNC	G	D	1155	0.068	3	novel	TOLERATED
3	60239102	A	G	Solyc03	Solyc03g116920.1	Sister chromatid cohesion protein P	CDS	NONSYNC	S	P	1128	0.109	4	novel	TOLERATED

3	60400869	T	G	Solyc03	Solyc03g117090.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	N	T	24	0.625	7	novel	TOLERATED
3	60442838	A	C	Solyc03	Solyc03g117170.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	I	S	166	NA	NA	novel	NA
3	60462327	T	C	Solyc03	Solyc03g117210.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	K	R	186	0.145	15	novel	TOLERATED
3	60500980	T	G	Solyc03	Solyc03g117270.1	F-box family protein (AHRD V1 **-	CDS	NONSYNC	V	G	125	0.185	9	novel	TOLERATED
3	60501031	G	A	Solyc03	Solyc03g117270.1	F-box family protein (AHRD V1 **-	CDS	NONSYNC	S	N	142	0.407	4	novel	TOLERATED
3	60607822	C	G	Solyc03	Solyc03g117420.2	Leucine-rich repeat family protein (	CDS	NONSYNC	A	P	603	NA	NA	novel	NA
3	60656922	T	TCATG	Solyc03	Solyc03g117430.2	Cobalamin synthesis protein P (AH	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
3	60787398	A	AGAT	Solyc03	Solyc03g117650.2	Glycosylphosphatidylinositol ancho	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
3	60787404	A	AGAC	Solyc03	Solyc03g117650.2	Glycosylphosphatidylinositol ancho	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
3	60787435	G	A	Solyc03	Solyc03g117650.2	Glycosylphosphatidylinositol ancho	CDS	NONSYNC	M	I	18	0.523	10	novel	TOLERATED
3	60787466	C	T	Solyc03	Solyc03g117650.2	Glycosylphosphatidylinositol ancho	CDS	NONSYNC	L	F	29	0.03	14	novel	DELETERIOUS
3	60806811	T	A	Solyc03	Solyc03g117680.2	Transcription regulatory protein SN	CDS	NONSYNC	T	S	115	1	25	novel	TOLERATED
3	60817688	A	G	Solyc03	Solyc03g117690.2	Aspartic proteinase nepenthesin-1 (	CDS	NONSYNC	R	G	258	1	25	novel	TOLERATED
3	60819745	A	G	Solyc03	Solyc03g117700.1	Folate/biopterin transporter (AHRE	CDS	NONSYNC	F	S	171	0.006	29	novel	DELETERIOUS
3	60820035	T	C	Solyc03	Solyc03g117700.1	Folate/biopterin transporter (AHRE	CDS	NONSYNC	N	D	132	1	28	novel	TOLERATED
3	60828325	C	G	Solyc03	Solyc03g117720.2	AP2-like ethylene-responsive transc	CDS	NONSYNC	S	C	50	0.062	81	novel	TOLERATED
3	60833352	G	C	Solyc03	Solyc03g117730.2	Tubby-like protein 13 (AHRD V1 *-	CDS	NONSYNC	S	R	349	0.192	32	novel	TOLERATED
3	61667022	A	G	Solyc03	Solyc03g118790.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	N	D	343	0.052	9	novel	TOLERATED
4	359177	T	TG	Solyc04	Solyc04g005540.2	Cc-nbs-lrr, resistance protein	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	359179	T	TGTGC	Solyc04	Solyc04g005540.2	Cc-nbs-lrr, resistance protein	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	776334	G	A	Solyc04	Solyc04g007060.2	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	E	K	342	1	128	novel	TOLERATED
4	776335	A	T	Solyc04	Solyc04g007060.2	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	E	V	342	0.051	128	novel	TOLERATED
4	796855	T	C	Solyc04	Solyc04g007080.2	Lrr, resistance protein fragment	CDS	NONSYNC	T	A	276	0.299	2	novel	TOLERATED
4	796974	T	G	Solyc04	Solyc04g007080.2	Lrr, resistance protein fragment	CDS	NONSYNC	D	A	236	0	2	novel	DELETERIOUS
4	797005	G	C	Solyc04	Solyc04g007080.2	Lrr, resistance protein fragment	CDS	NONSYNC	L	V	226	0.187	2	novel	TOLERATED
4	804398	T	C	Solyc04	Solyc04g007090.1	Lrr, resistance protein fragment	CDS	NONSYNC	R	G	51	NA	NA	novel	NA
4	804400	A	G	Solyc04	Solyc04g007090.1	Lrr, resistance protein fragment	CDS	NONSYNC	F	S	50	NA	NA	novel	NA
4	860874	C	T	Solyc04	Solyc04g007140.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	E	K	20	NA	NA	novel	NA
4	995935	T	G	Solyc04	Solyc04g007280.2	Nup98 protein (Fragment) (AHRD	CDS	NONSYNC	H	Q	571	1	21	novel	TOLERATED
4	1584737	T	C	Solyc04	Solyc04g007920.1	Erwinia induced protein 2 (AHRD '	CDS	NONSYNC	M	V	18	0.948	27	novel	TOLERATED
4	1660163	T	A	Solyc04	Solyc04g008010.2	Protein VAC14 homolog (AHRD V	CDS	NONSYNC	H	L	405	1	36	novel	TOLERATED
4	1797396	T	G	Solyc04	Solyc04g008120.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	I	L	723	1	235	novel	TOLERATED
4	1797499	A	C	Solyc04	Solyc04g008120.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	D	E	688	1	318	novel	TOLERATED
4	1797510	C	T	Solyc04	Solyc04g008120.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	E	K	685	0.531	319	novel	TOLERATED
4	1797515	G	T	Solyc04	Solyc04g008120.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	P	H	683	0.07	316	novel	TOLERATED
4	1797516	G	C	Solyc04	Solyc04g008120.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	P	A	683	0.102	316	novel	TOLERATED
4	1797525	G	C	Solyc04	Solyc04g008120.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	L	V	680	0.484	312	novel	TOLERATED
4	1797528	C	G	Solyc04	Solyc04g008120.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	E	Q	679	0.804	314	novel	TOLERATED
4	1797534	T	C	Solyc04	Solyc04g008120.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	N	D	677	1	304	novel	TOLERATED
4	1797537	G	C	Solyc04	Solyc04g008120.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	L	V	676	0.478	308	novel	TOLERATED
4	2099637	T	G	Solyc04	Solyc04g008480.1	Myb-like DNA-binding domain SH	CDS	NONSYNC	N	H	62	1	14	novel	TOLERATED
4	2128291	G	GTAA	Solyc04	Solyc04g008500.2	C2H2L domain class transcription f	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
4	2129568	A	G	Solyc04	Solyc04g008500.2	C2H2L domain class transcription f	CDS	NONSYNC	S	G	427	0.508	21	novel	TOLERATED
4	2129833	C	CCAAT	Solyc04	Solyc04g008500.2	C2H2L domain class transcription f	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	2225234	C	T	Solyc04	Solyc04g008610.2	Histone acetyltransferase (AHRD V	CDS	NONSYNC	P	L	1416	0.006	27	novel	DELETERIOUS
4	2281755	A	G	Solyc04	Solyc04g008650.2	Receptor like kinase, RLK	CDS	NONSYNC	T	A	149	0.328	31	novel	TOLERATED
4	2281848	G	A	Solyc04	Solyc04g008650.2	Receptor like kinase, RLK	CDS	NONSYNC	E	K	180	0.72	31	novel	TOLERATED
4	2281923	G	A	Solyc04	Solyc04g008650.2	Receptor like kinase, RLK	CDS	NONSYNC	D	N	205	0.521	30	novel	TOLERATED
4	2281930	C	T	Solyc04	Solyc04g008650.2	Receptor like kinase, RLK	CDS	NONSYNC	P	L	207	0.446	25	novel	TOLERATED
4	2314811	G	A	Solyc04	Solyc04g008670.1	Gibberellin 2-beta-dioxygenase 7 (A	CDS	NONSYNC	R	Q	42	0.586	27	novel	TOLERATED
4	2330794	G	A	Solyc04	Solyc04g008680.2	Cell division cycle and apoptosis re	CDS	NONSYNC	D	N	1031	1	12	novel	TOLERATED
4	2389125	T	G	Solyc04	Solyc04g008720.2	WD-repeat protein (AHRD V1 *---	CDS	NONSYNC	H	Q	418	0.682	20	novel	TOLERATED
4	2437446	T	G	Solyc04	Solyc04g008820.2	HMG transcription factor (Fragmen	CDS	NONSYNC	F	L	176	0.661	73	novel	TOLERATED
4	2470460	CCAG	C	Solyc04	Solyc04g008850.1	Aspartic proteinase nepenthesin-1 (	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
4	2470709	G	A	Solyc04	Solyc04g008850.1	Aspartic proteinase nepenthesin-1 (	CDS	NONSYNC	S	F	178	0.008	35	novel	DELETERIOUS
4	2945274	T	G	Solyc04	Solyc04g009530.2	Glutathione S-transferase (AHRD V	CDS	NONSYNC	E	D	239	0.168	43	novel	TOLERATED
4	3231074	T	C	Solyc04	Solyc04g009910.2	Calcium-dependent protein kinase 2	CDS	NONSYNC	M	V	275	1	31	novel	TOLERATED
4	4284375	C	G	Solyc04	Solyc04g011890.1	Nbs, resistance protein fragment	CDS	NONSYNC	R	S	58	0	20	novel	DELETERIOUS
4	4418408	T	TTGA	Solyc04	Solyc04g012110.1	Receptor like kinase, RLK	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
4	4635848	T	C	Solyc04	Solyc04g014380.2	Kinase interacting protein 1 (AHRI	CDS	NONSYNC	V	A	827	0.161	19	novel	TOLERATED
4	4635856	A	C	Solyc04	Solyc04g014380.2	Kinase interacting protein 1 (AHRI	CDS	NONSYNC	I	L	830	1	19	novel	TOLERATED
4	4635914	G	A	Solyc04	Solyc04g014380.2	Kinase interacting protein 1 (AHRI	CDS	NONSYNC	G	E	849	1	19	novel	TOLERATED
4	4635922	T	A	Solyc04	Solyc04g014380.2	Kinase interacting protein 1 (AHRI	CDS	NONSYNC	S	T	852	0.611	19	novel	TOLERATED
4	4642510	G	GT	Solyc04	Solyc04g014400.2	LRR receptor-like serine/threonine-	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	4642556	A	G	Solyc04	Solyc04g014400.2	LRR receptor-like serine/threonine-	CDS	NONSYNC	F	L	1129	1	16	novel	TOLERATED
4	4647789	C	T	Solyc04	Solyc04g014400.2	LRR receptor-like serine/threonine-	CDS	STOP-GAI	W	*	76	NA	NA	novel	NA
4	4674576	T	C	Solyc04	Solyc04g014450.1	Rhamnogalacturonate lyase (AHRE	CDS	NONSYNC	I	V	369	0.358	58	novel	TOLERATED
4	4675644	C	G	Solyc04	Solyc04g014450.1	Rhamnogalacturonate lyase (AHRE	CDS	NONSYNC	C	S	309	1	62	novel	TOLERATED
4	4832005	C	G	Solyc04	Solyc04g014560.2	Pre-mRNA-splicing factor 38B (AI	CDS	NONSYNC	S	R	364	0.062	32	novel	TOLERATED
4	5064643	T	C	Solyc04	Solyc04g014830.1	GRAS family transcription factor (/	CDS	NONSYNC	N	S	533	0.195	49	novel	TOLERATED
4	5674738	C	T	Solyc04	Solyc04g015470.2	Phosphatidylinositol-4-phosphate 5	CDS	STOP-GAI	W	*	290	NA	NA	novel	NA
4	6790023	G	T	Solyc04	Solyc04g016080.1	Kinesin-like protein (AHRD V1 *-'	CDS	NONSYNC	G	C	939	0.075	11	novel	TOLERATED
4	7215418	G	T	Solyc04	Solyc04g016410.2	Chaperone protein dnaJ (AHRD V1	CDS	NONSYNC	F	L	918	1	12	novel	TOLERATED
4	7278212	G	GA	Solyc04	Solyc04g016450.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	10327870	C	T	Solyc04	Solyc04g018190.1	Ycf2 (AHRD V1 ***- A6Y9Y0_H	CDS	NONSYNC	G	S	69	0.83	2	novel	TOLERATED
4	10469876	G	A	Solyc04	Solyc04g018200.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	T	49	NA	NA	novel	NA
4	12793487	C	T	Solyc04	Solyc04g024470.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	G	E	114	1	2	novel	TOLERATED
4	14523185	G	A	Solyc04	Solyc04g024770.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	Q	32	NA	NA	novel	NA
4	16162849	A	G	Solyc04	Solyc04g024950.1	Unknown Protein (AHRD V1)	CDS	START-LC	M	V	1	NA	NA	novel	NA
4	29660884	C	T	Solyc04	Solyc04g039610.1	Ulp1 protease family C-terminal ca	CDS	NONSYNC	D	N	505	NA	NA	novel	NA
4	37772617	A	C	Solyc04	Solyc04g048940.1	Unknown Protein (AHRD V1)	CDS	START-LC	M	R	1	NA	NA	novel	NA
4	37772618	T	G	Solyc04	Solyc04g048940.1	Unknown Protein (AHRD V1)	CDS	START-LC	M	L	1	NA	NA	novel	NA
4	49285127	T	C	Solyc04	Solyc04g051220.1	Protein FAR1-RELATED SEQUEI	CDS	NONSYNC	M	T	87	0.992	5	novel	TOLERATED
4	54172967	C	CAGA1	Solyc04	Solyc04g057910.2	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
4	54547465	G	T	Solyc04	Solyc04g063300.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	V	L	494	0.67	18	novel	TOLERATED
4	56861595	T	A	Solyc04	Solyc04g072260.1	Midasin (AHRD V1 ***- B9MXW	CDS	NONSYNC	I	L	3106	NA	NA	novel	NA
4	57920545	A	C	Solyc04	Solyc04g074320.1	Zinc finger protein (AHRD V1 *---	CDS	NONSYNC	N	T	53	0.156	35	novel	TOLERATED
4	57938741	T	G	Solyc04	Solyc04g074340.2	UDP-glucuronosyltransferase (AHI	CDS	NONSYNC	L	R	192	1	156	novel	TOLERATED
4	57940122	C	A	Solyc04	Solyc04g074350.2	UDP-glucuronosyltransferase (AHI	CDS	NONSYNC	A	S	484	1	82	novel	TOLERATED
4	57953803	C	T	Solyc04	Solyc04g074380.2	UDP-glucuronosyltransferase (AHI	CDS	NONSYNC	A	T	464	0.064	165	novel	TOLERATED
4	57953829	A	G	Solyc04	Solyc04g074380.2	UDP-glucuronosyltransferase (AHI	CDS	NONSYNC	L	S	455	0.736	164	novel	TOLERATED
4	57954178	C	T	Solyc04	Solyc04g074380.2	UDP-glucuronosyltransferase (AHI	CDS	NONSYNC	E	K	339	0.223	173	novel	TOLERATED
4	57954223	C	G	Solyc04	Solyc04g074380.2	UDP-glucuronosyltransferase (AHI	CDS	NONSYNC	E	Q	324	0.076	173	novel	TOLERATED
4	57967945	T	A	Solyc04	Solyc04g074390.2	UDP-glucuronosyltransferase (AHI	CDS	NONSYNC	L	F	328	0.002	170	novel	DELETERIOUS
4	57968521	G	T	Solyc04	Solyc04g074390.2	UDP-glucuronosyltransferase (AHI	CDS	NONSYNC	L	M	158	0.302	164	novel	TOLERATED
4	58000721	T	C	Solyc04	Solyc04g074400.1	Os06g0220000 protein (Fragment)	CDS	NONSYNC	M	V	158	1	82	novel	TOLERATED
4	58000963	C	T	Solyc04	Solyc04g074400.1	Os06g0220000 protein (Fragment)	CDS	NONSYNC	R	Q	77	0.714	78	novel	TOLERATED
4	58025004	C	T	Solyc04	Solyc04g074420.1	Phi-1 protein (Fragment) (AHRD V	CDS	NONSYNC	S	N	68	1	80	novel	TOLERATED
4	58025443	CA	C	Solyc04	Solyc04g074430.1	Phi-1 protein (Fragment) (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58025816	AC	A	Solyc04	Solyc04g074430.1	Phi-1 protein (Fragment) (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58031438	T	A	Solyc04	Solyc04g074450.1	Phi-1 protein (Fragment) (AHRD V	CDS	NONSYNC	T	S	307	0.08	80	novel	TOLERATED
4	58037193	G	GTTT	Solyc04	Solyc04g074460.1	Phi-1 protein (Fragment) (AHRD V	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
4	58037194	CTG	C	Solyc04	Solyc04g074460.1	Phi-1 protein (Fragment) (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58062183	T	A	Solyc04	Solyc04g074480.2	3-deoxy-7-phosphoheptulonate synt	CDS	NONSYNC	S	T	67	0.425	36	novel	TOLERATED
4	58082302	G	T	Solyc04	Solyc04g074490.2	Bifunctional arginine demethylase a	CDS	NONSYNC	R	S	649	0.573	13	novel	TOLERATED
4	58082537	A	T	Solyc04	Solyc04g074490.2	Bifunctional arginine demethylase a	CDS	NONSYNC	T	S	692	0.544	16	novel	TOLERATED
4	58082690	C	G	Solyc04	Solyc04g074490.2	Bifunctional arginine demethylase a	CDS	NONSYNC	H	D	743	0.259	12	novel	TOLERATED
4	58113153	AG	A	Solyc04	Solyc04g074530.2	Alcohol dehydrogenase 1 (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58114138	T	C	Solyc04	Solyc04g074530.2	Alcohol dehydrogenase 1 (AHRD V	CDS	NONSYNC	C	R	129	0.724	381	novel	TOLERATED
4	58151111	C	T	Solyc04	Solyc04g074610.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	R	C	21	NA	NA	novel	NA
4	58177447	T	G	Solyc04	Solyc04g074670.2	Os03g0169000 protein (Fragment)	CDS	NONSYNC	K	T	320	0.223	59	novel	TOLERATED
4	58224904	G	A	Solyc04	Solyc04g074710.2	Queuine tRNA-ribosyltransferase (/	CDS	NONSYNC	H	Y	332	1	137	novel	TOLERATED
4	58317242	C	A	Solyc04	Solyc04g074810.2	BHLH transcription factor (AHRD	CDS	NONSYNC	E	D	260	0.457	16	novel	TOLERATED
4	58320016	G	A	Solyc04	Solyc04g074810.2	BHLH transcription factor (AHRD	CDS	NONSYNC	T	M	3	NA	NA	novel	NA
4	58320023	T	TATTA	Solyc04	Solyc04g074810.2	BHLH transcription factor (AHRD	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58405561	T	C	Solyc04	Solyc04g074880.2	Purine permease family protein (AI	CDS	NONSYNC	V	A	204	0.031	25	novel	DELETERIOUS
4	58409422	C	G	Solyc04	Solyc04g074890.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	G	A	81	0.038	64	novel	DELETERIOUS

4	58409754	G	C	Solyc04	Solyc04g074890.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	L	7	NA	NA	novel	NA
4	58416600	G	A	Solyc04	Solyc04g074920.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	D	N	234	0.71	11	novel	TOLERATED
4	58420922	T	C	Solyc04	Solyc04g074930.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	I	T	135	0.78	15	novel	TOLERATED
4	58433592	C	T	Solyc04	Solyc04g074950.2	Ovarian cancer-associated gene 2 p	CDS	NONSYNC	S	L	207	0.884	30	novel	TOLERATED
4	58433600	A	G	Solyc04	Solyc04g074950.2	Ovarian cancer-associated gene 2 p	CDS	NONSYNC	M	V	210	0.345	30	novel	TOLERATED
4	58648816	C	T	Solyc04	Solyc04g076100.2	Genomic DNA chromosome 5 P1 c	CDS	NONSYNC	T	I	190	0.093	14	novel	TOLERATED
4	58649204	T	C	Solyc04	Solyc04g076100.2	Genomic DNA chromosome 5 P1 c	CDS	NONSYNC	L	P	278	0.131	16	novel	TOLERATED
4	58668718	A	T	Solyc04	Solyc04g076120.2	Serine carboxypeptidase 1 (AHRD	CDS	NONSYNC	E	V	347	0.04	62	novel	DELETERIOUS
4	58669274	C	CCTCA	Solyc04	Solyc04g076130.2	Serine carboxypeptidase 1 (AHRD	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58690924	A	G	Solyc04	Solyc04g076140.2	Rho GTPase activating protein 12 (	CDS	NONSYNC	N	D	818	0.101	8	novel	TOLERATED
4	58694267	C	CT	Solyc04	Solyc04g076150.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58694399	T	TA	Solyc04	Solyc04g076150.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58697906	C	T	Solyc04	Solyc04g076160.1	Helitron helicase-like protein (AHR	CDS	NONSYNC	G	D	362	0.58	29	novel	TOLERATED
4	58697951	G	A	Solyc04	Solyc04g076160.1	Helitron helicase-like protein (AHR	CDS	NONSYNC	T	M	347	1	29	novel	TOLERATED
4	58698221	G	T	Solyc04	Solyc04g076160.1	Helitron helicase-like protein (AHR	CDS	NONSYNC	S	Y	257	0.064	30	novel	TOLERATED
4	58698978	T	C	Solyc04	Solyc04g076160.1	Helitron helicase-like protein (AHR	CDS	NONSYNC	R	G	50	0.384	2	novel	TOLERATED
4	58702712	A	AC	Solyc04	Solyc04g076170.1	ABC transporter G family member	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58703157	T	C	Solyc04	Solyc04g076170.1	ABC transporter G family member	CDS	NONSYNC	K	E	117	0.996	7	novel	TOLERATED
4	58703510	G	A	Solyc04	Solyc04g076170.1	ABC transporter G family member	CDS	NONSYNC	P	L	68	0.725	7	novel	TOLERATED
4	58703601	G	A	Solyc04	Solyc04g076170.1	ABC transporter G family member	CDS	NONSYNC	P	S	38	0	7	novel	DELETERIOUS
4	58745615	G	A	Solyc04	Solyc04g076210.2	Ubiquitin carboxyl-terminal hydrol	CDS	NONSYNC	R	H	1038	0.202	4	novel	TOLERATED
4	58745669	T	C	Solyc04	Solyc04g076210.2	Ubiquitin carboxyl-terminal hydrol	CDS	NONSYNC	L	P	1056	0.07	5	novel	TOLERATED
4	58772489	G	T	Solyc04	Solyc04g076240.1	Transcription factor (AHRD V1 *--	CDS	NONSYNC	D	E	115	0.608	26	novel	TOLERATED
4	58788963	CGAT	C	Solyc04	Solyc04g076260.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
4	58796968	T	C	Solyc04	Solyc04g076280.2	MPF2-like (Fragment) (AHRD V1	CDS	NONSYNC	L	P	17	0.001	68	novel	DELETERIOUS
4	58803706	T	C	Solyc04	Solyc04g076290.2	Os12g0425600 protein (Fragment)	CDS	NONSYNC	I	T	7	0.357	3	novel	TOLERATED
4	58804684	A	G	Solyc04	Solyc04g076290.2	Os12g0425600 protein (Fragment)	CDS	NONSYNC	K	E	70	0.946	31	novel	TOLERATED
4	58804744	T	G	Solyc04	Solyc04g076290.2	Os12g0425600 protein (Fragment)	CDS	NONSYNC	Y	D	90	0.6	35	novel	TOLERATED
4	58808862	A	G	Solyc04	Solyc04g076300.2	Transporter small conductance mec	CDS	NONSYNC	S	P	616	0.161	19	novel	TOLERATED
4	58813104	A	G	Solyc04	Solyc04g076300.2	Transporter small conductance mec	CDS	NONSYNC	S	P	186	0.027	26	novel	DELETERIOUS
4	58832538	T	G	Solyc04	Solyc04g076320.2	Argininosuccinate lyase (AHRD V1	CDS	NONSYNC	E	A	506	0.436	211	novel	TOLERATED
4	58835612	A	G	Solyc04	Solyc04g076320.2	Argininosuccinate lyase (AHRD V1	CDS	NONSYNC	C	R	194	0.703	252	novel	TOLERATED
4	58838439	T	TTGG	Solyc04	Solyc04g076330.1	Pentatricopeptide repeat-containing	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
4	58859790	C	G	Solyc04	Solyc04g076350.1	Kinase interacting protein 1 (AHRI	CDS	NONSYNC	F	L	1371	0.806	17	novel	TOLERATED
4	58861477	A	C	Solyc04	Solyc04g076360.2	Telomeric repeat-binding factor 1 (.	CDS	NONSYNC	C	G	539	0.469	4	novel	TOLERATED
4	58874578	C	G	Solyc04	Solyc04g076380.2	Cytochrome P450 NADPH-reducta	CDS	NONSYNC	D	H	625	0.075	86	novel	TOLERATED
4	58875678	G	A	Solyc04	Solyc04g076380.2	Cytochrome P450 NADPH-reducta	CDS	NONSYNC	A	V	431	0.277	85	novel	TOLERATED
4	58889323	G	C	Solyc04	Solyc04g076390.2	Cysteinyl tRNA synthetase (AHRD	CDS	NONSYNC	S	T	59	0.781	9	novel	TOLERATED
4	58889329	G	T	Solyc04	Solyc04g076390.2	Cysteinyl tRNA synthetase (AHRD	CDS	NONSYNC	G	V	61	0.148	9	novel	TOLERATED
4	58906108	C	CAG	Solyc04	Solyc04g076410.2	Hydroxyproline-rich glycoprotein fa	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	58928251	A	G	Solyc04	Solyc04g076460.2	LRR receptor-like serine/threonine-	CDS	STOP-LOS	*	Q	370	NA	NA	novel	NA
4	58928263	C	T	Solyc04	Solyc04g076460.2	LRR receptor-like serine/threonine-	CDS	NONSYNC	V	I	366	0.572	3	novel	TOLERATED
4	58928281	T	C	Solyc04	Solyc04g076460.2	LRR receptor-like serine/threonine-	CDS	NONSYNC	T	A	360	0.83	4	novel	TOLERATED
4	58971797	T	C	Solyc04	Solyc04g076500.2	BEACH domain-containing protein	CDS	NONSYNC	V	A	413	0.103	12	novel	TOLERATED
4	58985459	C	T	Solyc04	Solyc04g076510.2	Beige/BEACH domain containing p	CDS	NONSYNC	S	F	591	0.115	17	novel	TOLERATED
4	58985498	T	G	Solyc04	Solyc04g076510.2	Beige/BEACH domain containing p	CDS	NONSYNC	I	S	604	0.213	17	novel	TOLERATED
4	59009890	T	C	Solyc04	Solyc04g076530.2	GATA transcription factor 25 (AHI	CDS	NONSYNC	L	S	121	NA	NA	novel	NA
4	59043961	C	T	Solyc04	Solyc04g076550.2	Genomic DNA chromosome 5 TAC	CDS	NONSYNC	R	H	420	0.059	4	novel	TOLERATED
4	59074934	T	C	Solyc04	Solyc04g076570.2	Crt homolog 3 (AHRD V1 ***- CF	CDS	NONSYNC	M	V	45	0.657	19	novel	TOLERATED
4	59097897	C	T	Solyc04	Solyc04g076620.2	Ubiquitin-protein ligase 1 (AHRD '	CDS	NONSYNC	D	N	3434	NA	NA	novel	NA
4	59105125	C	G	Solyc04	Solyc04g076620.2	Ubiquitin-protein ligase 1 (AHRD '	CDS	NONSYNC	L	F	1480	NA	NA	novel	NA
4	59105430	T	C	Solyc04	Solyc04g076620.2	Ubiquitin-protein ligase 1 (AHRD '	CDS	NONSYNC	M	V	1379	NA	NA	novel	NA
4	59108013	C	T	Solyc04	Solyc04g076620.2	Ubiquitin-protein ligase 1 (AHRD '	CDS	NONSYNC	A	T	518	NA	NA	novel	NA
4	59136004	A	G	Solyc04	Solyc04g076640.1	Rhamnogalacturonate lyase (AHRD	CDS	NONSYNC	V	A	60	0.047	59	novel	DELETERIOUS
4	59139102	G	A	Solyc04	Solyc04g076650.1	Rhamnogalacturonate lyase (AHRD	CDS	NONSYNC	T	M	524	0.014	59	novel	DELETERIOUS
4	59250091	T	A	Solyc04	Solyc04g076780.2	Oligopeptide transporter 4 (AHRD	CDS	NONSYNC	K	N	337	0.324	92	novel	TOLERATED
4	59272563	A	C	Solyc04	Solyc04g076800.2	Pentatricopeptide repeat-containing	CDS	NONSYNC	I	L	554	0.364	14	novel	TOLERATED
4	59303997	GTTA	G	Solyc04	Solyc04g076830.2	Phosphoglycerate mutase-like prote	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
4	59304002	TA	T	Solyc04	Solyc04g076830.2	Phosphoglycerate mutase-like prote	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	59304024	G	A	Solyc04	Solyc04g076830.2	Phosphoglycerate mutase-like prote	CDS	NONSYNC	A	V	2	NA	NA	novel	NA
4	59354957	G	T	Solyc04	Solyc04g076850.2	Auxin responsive protein (AHRD \	CDS	NONSYNC	S	I	94	0.213	59	novel	TOLERATED
4	59434376	G	A	Solyc04	Solyc04g076910.2	Symplekin (AHRD V1 *-*- B0WV	CDS	NONSYNC	R	Q	20	0.744	2	novel	TOLERATED
4	59437405	T	C	Solyc04	Solyc04g076910.2	Symplekin (AHRD V1 *-*- B0WV	CDS	NONSYNC	V	A	246	1	18	novel	TOLERATED
4	59468224	ATGC	A	Solyc04	Solyc04g076940.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
4	59517689	A	T	Solyc04	Solyc04g076970.2	BZIP transcription factor (AHRD V	CDS	NONSYNC	Y	F	27	0.368	2	novel	TOLERATED
4	59517709	G	T	Solyc04	Solyc04g076970.2	BZIP transcription factor (AHRD V	CDS	NONSYNC	A	S	34	0.796	2	novel	TOLERATED
4	59518307	G	T	Solyc04	Solyc04g076970.2	BZIP transcription factor (AHRD V	CDS	NONSYNC	G	W	159	0.013	2	novel	DELETERIOUS
4	59539486	A	G	Solyc04	Solyc04g076980.2	LRR receptor-like serine/threonine-	CDS	NONSYNC	I	V	76	0.078	11	novel	TOLERATED
4	59542593	G	A	Solyc04	Solyc04g076990.2	Receptor like kinase, RLK	CDS	NONSYNC	M	I	505	0.984	15	novel	TOLERATED
4	59549002	T	G	Solyc04	Solyc04g077000.2	Predicted E3 ubiquitin ligase (AHR	CDS	NONSYNC	D	E	221	1	9	novel	TOLERATED
4	59549096	A	G	Solyc04	Solyc04g077000.2	Predicted E3 ubiquitin ligase (AHR	CDS	NONSYNC	I	V	253	0.585	9	novel	TOLERATED
4	59563910	T	A	Solyc04	Solyc04g077010.2	Receptor like kinase, RLK	CDS	NONSYNC	L	Q	314	0.342	23	novel	TOLERATED
4	59614471	G	T	Solyc04	Solyc04g077050.2	Amino acid permease 6 (AHRD V1	CDS	NONSYNC	D	Y	407	0.009	149	novel	DELETERIOUS
4	59616375	T	C	Solyc04	Solyc04g077060.2	KH domain-containing protein (AH	CDS	NONSYNC	S	G	433	0.796	15	novel	TOLERATED
4	63089819	A	G	Solyc04	Solyc04g081550.2	Thaumatin-like protein (AHRD V1	CDS	NONSYNC	I	V	299	0.292	20	novel	TOLERATED
4	63451800	C	T	Solyc04	Solyc04g082060.2	F-box family protein (AHRD V1 **	CDS	NONSYNC	S	N	86	0.325	14	novel	TOLERATED
4	63702722	A	G	Solyc04	Solyc04g082470.1	WD repeat 2 (AHRD V1 **-- Q19(	CDS	NONSYNC	M	V	34	0.31	98	novel	TOLERATED
5	2138851	T	C	Solyc05	Solyc05g007610.2	Cc-nbs-lrr, resistance protein with a	CDS	NONSYNC	L	S	901	0.131	25	novel	TOLERATED
5	4066230	C	A	Solyc05	Solyc05g009850.2	Gc-rich sequence DNA-binding fac	CDS	NONSYNC	T	N	97	0.096	11	novel	TOLERATED
5	4067097	T	A	Solyc05	Solyc05g009850.2	Gc-rich sequence DNA-binding fac	CDS	NONSYNC	M	K	386	0.45	13	novel	TOLERATED
5	4125459	A	C	Solyc05	Solyc05g009900.1	CYCLOIDEA-like group 1B protei	CDS	NONSYNC	D	A	94	0.57	8	novel	TOLERATED
5	4225328	T	A	Solyc05	Solyc05g010020.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	N	Y	68	NA	NA	novel	NA
5	5178950	A	G	Solyc05	Solyc05g011960.2	Heat shock protein binding protein	CDS	NONSYNC	R	G	660	0.031	2	novel	DELETERIOUS
5	5178951	G	A	Solyc05	Solyc05g011960.2	Heat shock protein binding protein	CDS	NONSYNC	R	K	660	0.254	2	novel	TOLERATED
5	5973964	T	C	Solyc05	Solyc05g012820.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	I	M	276	0.04	2	novel	DELETERIOUS
5	5998022	T	C	Solyc05	Solyc05g012850.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	I	V	206	NA	NA	novel	NA
5	5998088	C	T	Solyc05	Solyc05g012850.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	V	I	184	NA	NA	novel	NA
5	5998241	A	T	Solyc05	Solyc05g012850.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	S	T	133	NA	NA	novel	NA
5	5998290	C	G	Solyc05	Solyc05g012850.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	K	N	116	NA	NA	novel	NA
5	5998331	C	T	Solyc05	Solyc05g012850.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	T	103	NA	NA	novel	NA
5	5998402	A	G	Solyc05	Solyc05g012850.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	S	79	NA	NA	novel	NA
5	5998457	G	C	Solyc05	Solyc05g012850.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	H	D	61	NA	NA	novel	NA
5	5998577	C	T	Solyc05	Solyc05g012850.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	T	21	NA	NA	novel	NA
5	6722129	A	T	Solyc05	Solyc05g013500.2	Glycosyltransferase-like protein (AI	CDS	NONSYNC	T	S	577	0.134	9	novel	TOLERATED
5	8591468	T	C	Solyc05	Solyc05g014620.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	T	A	6	NA	NA	novel	NA
5	9163611	G	T	Solyc05	Solyc05g014960.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	K	N	889	NA	NA	novel	NA
5	10283623	T	TAAA	Solyc05	Solyc05g015290.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
5	13797938	CGGA	C	Solyc05	Solyc05g016050.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
5	50543829	A	T	Solyc05	Solyc05g041390.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	V	D	92	NA	NA	novel	NA
5	56377896	A	AT	Solyc05	Solyc05g044620.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	56719469	T	TCTAG	Solyc05	Solyc05g045750.1	ORF106 (AHRD V1 *-*- B6VJU5	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	59286262	A	G	Solyc05	Solyc05g050150.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	V	A	148	NA	NA	novel	NA
5	59286298	C	T	Solyc05	Solyc05g050150.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	K	136	NA	NA	novel	NA
5	59335570	T	C	Solyc05	Solyc05g050190.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	G	76	NA	NA	novel	NA
5	59335591	T	C	Solyc05	Solyc05g050190.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	N	D	69	NA	NA	novel	NA
5	59335629	A	G	Solyc05	Solyc05g050190.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	I	T	56	NA	NA	novel	NA
5	59399596	T	C	Solyc05	Solyc05g050210.2	GDSL esterase/lipase At4g01130 (.	CDS	NONSYNC	S	G	151	0.19	24	novel	TOLERATED
5	59418243	A	G	Solyc05	Solyc05g050220.2	G-box binding factor 3 (AHRD V1	CDS	NONSYNC	M	V	183	0.819	29	novel	TOLERATED
5	59443453	AG	A	Solyc05	Solyc05g050260.1	Transposon Ty1-BL Gag-Pol polyp	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	59495740	G	C	Solyc05	Solyc05g050280.2	GH3 family protein (AHRD V1 **	CDS	NONSYNC	G	R	220	0.001	44	novel	DELETERIOUS
5	59616713	A	T	Solyc05	Solyc05g050360.2	Cyclic nucleotide gated channel (AI	CDS	NONSYNC	N	I	24	0.199	31	novel	TOLERATED
5	59616806	G	C	Solyc05	Solyc05g050360.2	Cyclic nucleotide gated channel (AI	CDS	NONSYNC	R	T	55	0.49	36	novel	TOLERATED
5	59754251	G	T	Solyc05	Solyc05g050430.1	Cc-nbs-lrr, resistance protein	CDS	STOP-GAI	E	*	780	NA	NA	novel	NA
5	59754458	T	C	Solyc05	Solyc05g050430.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	S	P	849	0.007	6	novel	DELETERIOUS
5	59755304	A	AT	Solyc05	Solyc05g050430.1	Cc-nbs-lrr, resistance protein	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	59773048	G	C	Solyc05	Solyc05g050470.1	Kinase family protein (AHRD V1 *	CDS	NONSYNC	G	R	19	NA	NA	novel	NA
5	59774110	G	GAAG	Solyc05	Solyc05g050470.1	Kinase family protein (AHRD V1 *	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA

5	59775413	G	A	Solyc05	Solyc05g050480.1	Kinase family protein (AHRD V1 *	CDS	NONSYNC	G	S	8	NA	NA	novel	NA
5	59775818	G	C	Solyc05	Solyc05g050480.1	Kinase family protein (AHRD V1 *	CDS	NONSYNC	E	Q	143	NA	NA	novel	NA
5	59776697	A	ATAAT	Solyc05	Solyc05g050480.1	Kinase family protein (AHRD V1 *	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
5	59778302	T	C	Solyc05	Solyc05g050490.2	ATPase (AHRD V1 *-* D3E0U6_	CDS	NONSYNC	S	P	40	NA	NA	novel	NA
5	59778303	C	T	Solyc05	Solyc05g050490.2	ATPase (AHRD V1 *-* D3E0U6_	CDS	NONSYNC	S	F	40	NA	NA	novel	NA
5	59787643	G	T	Solyc05	Solyc05g050500.1	ATP synthase F1 delta subunit (AH	CDS	NONSYNC	R	M	130	0.215	2	novel	TOLERATED
5	59983494	T	C	Solyc05	Solyc05g050700.1	LRR receptor-like serine/threonine-	CDS	NONSYNC	M	T	182	0.634	14	novel	TOLERATED
5	60020189	A	G	Solyc05	Solyc05g050740.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	T	A	266	NA	NA	novel	NA
5	60020838	C	T	Solyc05	Solyc05g050740.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	V	482	NA	NA	novel	NA
5	60069787	G	C	Solyc05	Solyc05g050770.2	Serine carboxypeptidase 1 (AHRD	CDS	NONSYNC	A	P	38	1	64	novel	TOLERATED
5	60095288	C	T	Solyc05	Solyc05g050780.2	Serine carboxypeptidase 1 (AHRD	CDS	NONSYNC	L	F	5	0.101	33	novel	TOLERATED
5	60126941	T	A	Solyc05	Solyc05g050790.1	Ethylene responsive transcription fa	CDS	NONSYNC	L	M	27	0.237	13	novel	TOLERATED
5	60141218	G	T	Solyc05	Solyc05g050810.2	Chaperone dnaJ 3 (AHRD V1 ****	CDS	NONSYNC	S	I	28	NA	NA	novel	NA
5	60141223	T	C	Solyc05	Solyc05g050810.2	Chaperone dnaJ 3 (AHRD V1 ****	CDS	NONSYNC	S	P	30	NA	NA	novel	NA
5	60145498	AGAA	A	Solyc05	Solyc05g050820.2	DNAJ chaperone (AHRD V1 ***-	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	60224912	T	C	Solyc05	Solyc05g050860.1	Cys2/His2 zinc-finger transcription	CDS	NONSYNC	L	S	121	0.755	13	novel	TOLERATED
5	60225783	TAAC	T	Solyc05	Solyc05g050860.1	Cys2/His2 zinc-finger transcription	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
5	60264899	A	T	Solyc05	Solyc05g050890.1	Peroxidase (AHRD V1 **** Q4W	CDS	NONSYNC	T	S	35	1	317	novel	TOLERATED
5	60279574	C	T	Solyc05	Solyc05g050910.2	Flavin-monooxygenase (AHRD V1	CDS	NONSYNC	E	K	110	0.205	73	novel	TOLERATED
5	60312407	AAAT	A	Solyc05	Solyc05g050940.2	O-sialoglycoprotein endopeptidase	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
5	60318546	T	A	Solyc05	Solyc05g050940.2	O-sialoglycoprotein endopeptidase	CDS	NONSYNC	W	R	364	0.448	33	novel	TOLERATED
5	60381256	T	G	Solyc05	Solyc05g051050.2	Glycogen synthase kinase (AHRD \	CDS	NONSYNC	H	P	290	1	266	novel	TOLERATED
5	60578007	G	GATA	Solyc05	Solyc05g051180.1	Ethylene-responsive transcription fa	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
5	61570080	T	A	Solyc05	Solyc05g052100.2	Glutamate dehydrogenase (AHRD \	CDS	NONSYNC	I	F	56	0.358	129	novel	TOLERATED
5	61570113	TG	T	Solyc05	Solyc05g052100.2	Glutamate dehydrogenase (AHRD \	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	62099795	C	A	Solyc05	Solyc05g052760.2	1-phosphatidylinositol-4 5-bisphosp	CDS	NONSYNC	T	K	3	1	38	novel	TOLERATED
5	62359065	C	T	Solyc05	Solyc05g053090.1	GRAS family transcription factor (/	CDS	NONSYNC	G	D	218	1	38	novel	TOLERATED
5	63091958	G	A	Solyc05	Solyc05g053920.1	Lipase (Fragment) (AHRD V1 ***-	CDS	NONSYNC	R	H	189	0	57	novel	DELETERIOUS
5	63126959	A	C	Solyc05	Solyc05g053990.2	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	N	K	281	1	13	novel	TOLERATED
5	63126962	T	G	Solyc05	Solyc05g053990.2	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	K	N	280	0.279	12	novel	TOLERATED
5	63126985	T	C	Solyc05	Solyc05g053990.2	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	I	V	273	0.227	11	novel	TOLERATED
5	63126988	T	C	Solyc05	Solyc05g053990.2	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	S	G	272	1	11	novel	TOLERATED
5	63127003	G	T	Solyc05	Solyc05g053990.2	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	L	I	267	0.698	12	novel	TOLERATED
5	63127020	T	C	Solyc05	Solyc05g053990.2	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	K	R	261	0.033	11	novel	DELETERIOUS
5	63657105	GA	G	Solyc05	Solyc05g054640.2	2-oxoglutarate dehydrogenase E1 c	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	64412009	T	C	Solyc05	Solyc05g055750.2	WRKY transcription factor-a (AHR	CDS	NONSYNC	K	E	30	0.219	11	novel	TOLERATED
5	64451816	TG	T	Solyc05	Solyc05g055810.2	Catalytic/ hydrolase (AHRD V1 **:	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	64502510	G	C	Solyc05	Solyc05g055900.1	Transcriptional activator TenA fam	CDS	NONSYNC	P	A	106	0.426	10	novel	TOLERATED
5	64502513	A	C	Solyc05	Solyc05g055900.1	Transcriptional activator TenA fam	CDS	NONSYNC	Y	D	105	0.905	10	novel	TOLERATED
5	64682534	TTCA	T	Solyc05	Solyc05g056140.2	Inter-alpha-trypsin inhibitor heavy c	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
5	64876647	TG	T	Solyc05	Solyc05g056430.1	Auxin responsive SAUR protein (A	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	64876683	TG	T	Solyc05	Solyc05g056430.1	Auxin responsive SAUR protein (A	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
5	64876687	TG	T	Solyc05	Solyc05g056430.1	Auxin responsive SAUR protein (A	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	1430144	CT	C	Solyc06	Solyc06g007400.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	2705001	AAT	A	Solyc06	Solyc06g008770.1	Cc-nbs-lrr, resistance protein	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	3544653	C	CA	Solyc06	Solyc06g009560.1	Helitron helicase-like protein (AHR	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	3646472	C	CA	Solyc06	Solyc06g009700.1	Ulp1 protease family C-terminal cat	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	3646491	A	G	Solyc06	Solyc06g009700.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	L	S	486	NA	NA	novel	NA
6	3646521	A	G	Solyc06	Solyc06g009700.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	I	T	476	NA	NA	novel	NA
6	15074831	T	TCCCC	Solyc06	Solyc06g024350.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	22670295	G	C	Solyc06	Solyc06g036430.2	Reticulon family protein (AHRD V	CDS	NONSYNC	D	H	17	0.008	53	novel	DELETERIOUS
6	29448116	A	G	Solyc06	Solyc06g050340.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	P	56	NA	NA	novel	NA
6	29488742	C	CA	Solyc06	Solyc06g050380.1	Mutator-like transposase (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	29490460	GA	G	Solyc06	Solyc06g050380.1	Mutator-like transposase (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	36959813	C	T	Solyc06	Solyc06g065050.1	Transmembrane protein 205 (AHR	CDS	NONSYNC	A	T	13	0.464	6	novel	TOLERATED
6	37227293	G	T	Solyc06	Solyc06g065420.1	Cytochrome P450	CDS	NONSYNC	T	K	227	1	53	novel	TOLERATED
6	37403804	A	G	Solyc06	Solyc06g065630.2	Monooxygenase (AHRD V1 **** I	CDS	NONSYNC	K	R	106	1	114	novel	TOLERATED
6	38323759	T	A	Solyc06	Solyc06g066740.1	Ran binding protein 3 (AHRD V1 *	CDS	NONSYNC	N	K	174	0.942	15	novel	TOLERATED
6	38409578	G	A	Solyc06	Solyc06g066820.2	Gibberellin 3-beta-hydroxylase (Fra	CDS	NONSYNC	V	I	260	0.204	64	novel	TOLERATED
6	38497768	T	C	Solyc06	Solyc06g067930.1	Cytochrome P450	CDS	NONSYNC	I	T	470	0.02	40	novel	DELETERIOUS
6	41361308	A	G	Solyc06	Solyc06g072960.1	Lipid A export ATP-binding/perme	CDS	NONSYNC	T	A	954	0.19	43	novel	TOLERATED
6	41398040	C	A	Solyc06	Solyc06g073050.2	NAC domain protein IPR003441 (/	CDS	NONSYNC	A	D	176	1	9	novel	TOLERATED
6	41751940	A	C	Solyc06	Solyc06g073570.2	Cytochrome P450	CDS	NONSYNC	S	A	494	0.125	61	novel	TOLERATED
6	42880295	TG	T	Solyc06	Solyc06g074990.1	Nitrate transporter (AHRD V1 ***	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	42881815	TA	T	Solyc06	Solyc06g074990.1	Nitrate transporter (AHRD V1 ***	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	43101584	TC	T	Solyc06	Solyc06g075270.2	Convicilin (Fragment) (AHRD V1 '	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	43669138	A	C	Solyc06	Solyc06g076150.2	Eukaryotic translation initiation fact	CDS	NONSYNC	S	A	474	0.857	35	novel	TOLERATED
6	43730566	G	GA	Solyc06	Solyc06g076200.1	X1 (Fragment) (AHRD V1 ***- Q	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
6	45148540	A	AGTTC	Solyc06	Solyc06g083460.2	WD-40 repeat family protein (AHR	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
6	45365613	T	A	Solyc06	Solyc06g083730.2	RNA binding protein (AHRD V1 *	CDS	NONSYNC	F	Y	17	1	19	novel	TOLERATED
6	45566795	T	A	Solyc06	Solyc06g084010.2	Os03g0627500 protein (Fragment)	CDS	NONSYNC	Q	L	91	0.064	12	novel	TOLERATED
7	1876644	CAAT	C	Solyc07	Solyc07g007120.2	Homeobox protein knotted-1-like 3	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
7	1899088	G	A	Solyc07	Solyc07g007140.2	Serine/threonine-protein kinase B-r	CDS	NONSYNC	P	S	52	0.089	5	novel	TOLERATED
7	1957935	C	T	Solyc07	Solyc07g007220.2	Serine/threonine phosphatase famil	CDS	NONSYNC	S	N	255	0.01	69	novel	DELETERIOUS
7	1980018	C	T	Solyc07	Solyc07g007230.2	DNAJ heat shock N-terminal doma	CDS	NONSYNC	S	L	22	0.187	8	novel	TOLERATED
7	2554418	C	G	Solyc07	Solyc07g007880.1	60s acidic ribosomal protein-like pr	CDS	NONSYNC	C	S	101	1	58	novel	TOLERATED
7	2755393	A	C	Solyc07	Solyc07g008040.2	WD-40 repeat protein-like (Fragme	CDS	NONSYNC	I	L	180	0.012	44	novel	DELETERIOUS
7	2755394	T	C	Solyc07	Solyc07g008040.2	WD-40 repeat protein-like (Fragme	CDS	NONSYNC	I	T	180	0.037	44	novel	DELETERIOUS
7	2773652	A	G	Solyc07	Solyc07g008060.1	Phosphatidylinositol binding clathri	CDS	NONSYNC	R	G	530	0.444	21	novel	TOLERATED
7	2797680	G	A	Solyc07	Solyc07g008080.2	WD repeat-containing protein 11 (/	CDS	NONSYNC	A	V	255	1	16	novel	TOLERATED
7	3077621	C	G	Solyc07	Solyc07g008310.2	Rieske (2Fe-2S) domain protein (A	CDS	NONSYNC	H	D	300	1	30	novel	TOLERATED
7	8126459	A	AT	Solyc07	Solyc07g017800.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
7	22797104	G	A	Solyc07	Solyc07g022840.1	Os12g0581300 protein (Fragment)	CDS	NONSYNC	V	M	289	0.052	53	novel	TOLERATED
7	49502410	G	A	Solyc07	Solyc07g041260.1	Histidine decarboxylase (AHRD V	CDS	NONSYNC	R	Q	201	0	2	novel	DELETERIOUS
7	52230105	G	C	Solyc07	Solyc07g042050.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	V	L	207	NA	NA	novel	NA
7	52230115	GAA	G	Solyc07	Solyc07g042050.1	Ulp1 protease family C-terminal cat	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
7	52230118	A	T	Solyc07	Solyc07g042050.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	K	M	211	NA	NA	novel	NA
7	52230120	G	GAT	Solyc07	Solyc07g042050.1	Ulp1 protease family C-terminal cat	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
7	52844462	A	G	Solyc07	Solyc07g042380.2	Ribosomal RNA processing protein	CDS	NONSYNC	V	A	314	1	10	novel	TOLERATED
7	53805708	A	G	Solyc07	Solyc07g042920.1	Pyruvate dehydrogenase E1 compon	CDS	NONSYNC	Y	C	143	0	120	novel	DELETERIOUS
7	54888973	C	T	Solyc07	Solyc07g043620.2	Auxin response factor 6-1 (AHRD '	CDS	STOP-GAI	W	*	180	NA	NA	novel	NA
7	54906281	A	T	Solyc07	Solyc07g043630.1	Acyl-CoA synthetase/AMP-acid lig	CDS	NONSYNC	I	F	230	0.024	266	novel	DELETERIOUS
7	54906959	G	T	Solyc07	Solyc07g043630.1	Acyl-CoA synthetase/AMP-acid lig	CDS	NONSYNC	A	S	456	0.017	265	novel	DELETERIOUS
7	54907028	C	T	Solyc07	Solyc07g043630.1	Acyl-CoA synthetase/AMP-acid lig	CDS	NONSYNC	H	Y	479	1	264	novel	TOLERATED
7	54931382	G	C	Solyc07	Solyc07g043640.2	Acyl-CoA synthetase/AMP-acid lig	CDS	NONSYNC	D	H	65	0.05	243	novel	TOLERATED
7	54935635	G	A	Solyc07	Solyc07g043650.1	AMP-dependent synthetase and liga	CDS	NONSYNC	S	N	72	0.492	99	novel	TOLERATED
7	54935718	G	C	Solyc07	Solyc07g043650.1	AMP-dependent synthetase and liga	CDS	NONSYNC	V	L	100	1	99	novel	TOLERATED
7	54935742	G	A	Solyc07	Solyc07g043650.1	AMP-dependent synthetase and liga	CDS	NONSYNC	G	S	108	0.053	97	novel	TOLERATED
7	54960003	G	T	Solyc07	Solyc07g043670.1	Hydroxycinnamoyl CoA quinate tra	CDS	NONSYNC	T	N	249	0.54	7	novel	TOLERATED
7	54960322	C	G	Solyc07	Solyc07g043670.1	Hydroxycinnamoyl CoA quinate tra	CDS	NONSYNC	V	L	143	0.504	8	novel	TOLERATED
7	55830236	T	C	Solyc07	Solyc07g045400.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	F	S	137	NA	NA	novel	NA
7	55830238	T	A	Solyc07	Solyc07g045400.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	F	I	138	NA	NA	novel	NA
7	55830241	T	G	Solyc07	Solyc07g045400.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	Y	D	139	NA	NA	novel	NA
7	55830406	A	C	Solyc07	Solyc07g045400.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	S	R	194	NA	NA	novel	NA
7	55830413	A	T	Solyc07	Solyc07g045400.1	Pentatricopeptide repeat-containing	CDS	STOP-LOS	*	L	196	NA	NA	novel	NA
7	57353551	C	G	Solyc07	Solyc07g049670.2	Alcohol acetyltransferase (AHRD \	CDS	NONSYNC	N	K	235	1	58	novel	TOLERATED
7	57602731	CAA	C	Solyc07	Solyc07g051800.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
7	58062823	C	CTT	Solyc07	Solyc07g052250.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
7	60040717	T	G	Solyc07	Solyc07g054370.2	F-box/LRR-repeat protein At3g592	CDS	NONSYNC	S	A	286	NA	NA	novel	NA
7	60041912	A	G	Solyc07	Solyc07g054370.2	F-box/LRR-repeat protein At3g592	CDS	NONSYNC	E	G	470	NA	NA	novel	NA
7	60179387	T	C	Solyc07	Solyc07g054580.2	GH3 family protein (AHRD V1 **:	CDS	NONSYNC	M	V	401	1	30	novel	TOLERATED
7	60210978	T	C	Solyc07	Solyc07g054610.2	F-box family protein (AHRD V1 *-	CDS	NONSYNC	L	S	712	NA	NA	novel	NA
7	60248514	T	C	Solyc07	Solyc07g054680.2	Pentatricopeptide repeat-containing	CDS	NONSYNC	S	G	333	0.467	12	novel	TOLERATED
7	60254200	A	G	Solyc07	Solyc07g054690.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	P	34	0.035	8	novel	DELETERIOUS
7	60426793	C	G	Solyc07	Solyc07g054950.1	Cyclin D2 (AHRD V1 **** Q71FH	CDS	NONSYNC	G	A	99	1	19	novel	TOLERATED
7	61088536	T	C	Solyc07	Solyc07g055840.2	Citrate synthase (AHRD V1 **** I	CDS	NONSYNC	D	G	155	0.362	140	novel	TOLERATED
7	61089290	G	A	Solyc07	Solyc07g055840.2	Citrate synthase (AHRD V1 **** I	CDS	NONSYNC	R	W	13	0.001	28	novel	DELETERIOUS

7	61172715	TGGA	T	Solyc07	Solyc07g055920.2	Agamous MADS-box transcription	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	NA	
7	61291785	TCCG	T	Solyc07	Solyc07g056100.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	NA	
7	61294036	T	TCCA	Solyc07	Solyc07g056100.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	NA	
7	61360234	T	C	Solyc07	Solyc07g056180.1	NBS-LRR class disease resistance	CDS	NONSYN	R	G	86	0.029	7	novel	DELETERIOUS		
7	61360273	T	C	Solyc07	Solyc07g056180.1	NBS-LRR class disease resistance	CDS	NONSYN	M	V	73	1	12	novel	TOLERATED		
7	61360351	T	C	Solyc07	Solyc07g056180.1	NBS-LRR class disease resistance	CDS	NONSYN	I	V	47	1	14	novel	TOLERATED		
7	61361359	A	AT	Solyc07	Solyc07g056180.1	NBS-LRR class disease resistance	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
7	61716731	G	A	Solyc07	Solyc07g056580.2	Ethylene receptor (AHRD V1 ****	CDS	NONSYN	E	K	474	1	151	novel	TOLERATED		
7	62300030	G	GT	Solyc07	Solyc07g062310.2	Os03g0825600 protein (Fragment)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
7	62319401	C	A	Solyc07	Solyc07g062340.1	Unknown Protein (AHRD V1)	CDS	NONSYN	L	F	10	0	2	novel	DELETERIOUS		
7	62832522	C	T	Solyc07	Solyc07g063000.2	Receptor like kinase, RLK	CDS	NONSYN	S	N	1013	0.253	14	novel	TOLERATED		
7	62971472	A	G	Solyc07	Solyc07g063220.2	Pentatricopeptide repeat-containing	CDS	NONSYN	T	A	540	NA	NA	novel	NA		
7	62971496	AC	A	Solyc07	Solyc07g063220.2	Pentatricopeptide repeat-containing	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
7	63829330	C	T	Solyc07	Solyc07g064450.2	Cytochrome P450	CDS	NONSYN	V	I	467	1	29	novel	TOLERATED		
7	63829333	T	G	Solyc07	Solyc07g064450.2	Cytochrome P450	CDS	NONSYN	T	P	466	0.937	29	novel	TOLERATED		
7	64550657	G	GT	Solyc07	Solyc07g065630.2	Ubiquitin-protein ligase 1 (AHRD '	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
7	64550688	T	G	Solyc07	Solyc07g065630.2	Ubiquitin-protein ligase 1 (AHRD '	CDS	NONSYN	M	R	2262	1	17	novel	TOLERATED		
7	64593318	AG	A	Solyc07	Solyc07g065700.2	SEC14-like protein 1 (AHRD V1 *	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
7	64593329	AG	A	Solyc07	Solyc07g065700.2	SEC14-like protein 1 (AHRD V1 *	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
7	64593337	C	CA	Solyc07	Solyc07g065700.2	SEC14-like protein 1 (AHRD V1 *	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
7	64632251	C	A	Solyc07	Solyc07g065760.1	Coiled-coil domain-containing prot	CDS	NONSYN	E	D	116	0.576	4	novel	TOLERATED		
7	64632254	T	A	Solyc07	Solyc07g065760.1	Coiled-coil domain-containing prot	CDS	NONSYN	K	N	115	0.172	4	novel	TOLERATED		
7	64632267	T	A	Solyc07	Solyc07g065760.1	Coiled-coil domain-containing prot	CDS	NONSYN	D	V	111	0.145	4	novel	TOLERATED		
7	64976495	A	C	Solyc07	Solyc07g066270.2	Glucosamine-6-phosphate deamina	CDS	NONSYN	D	E	19	1	44	novel	TOLERATED		
7	65046326	A	G	Solyc07	Solyc07g066350.1	Unknown Protein (AHRD V1)	CDS	NONSYN	Y	H	264	0.549	21	novel	TOLERATED		
8	77609	TG	T	Solyc08	Solyc08g005120.2	Cinnamoyl-CoA reductase-like prot	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	219000	T	C	Solyc08	Solyc08g005290.2	BZIP transcription factor 3 (AHRD	CDS	NONSYN	E	G	357	0.007	47	novel	DELETERIOUS		
8	230242	C	G	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONSYN	T	R	272	0.55	15	novel	TOLERATED		
8	230271	A	G	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONSYN	K	E	282	0.93	19	novel	TOLERATED		
8	230326	G	A	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONSYN	R	K	300	0.6	21	novel	TOLERATED		
8	230404	T	TGAA	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA		
8	230545	G	A	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONSYN	R	K	373	0.799	24	novel	TOLERATED		
8	231177	C	T	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONSYN	R	C	556	0.017	23	novel	DELETERIOUS		
8	231193	G	A	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONSYN	G	E	561	0.224	23	novel	TOLERATED		
8	231229	C	T	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONSYN	S	L	573	0.26	23	novel	TOLERATED		
8	231548	G	T	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONSYN	E	D	679	0.571	13	novel	TOLERATED		
8	231621	A	G	Solyc08	Solyc08g005300.1	Chaperone DnaJ (AHRD V1 *-*- /	CDS	NONSYN	I	V	704	1	9	novel	TOLERATED		
8	243295	G	A	Solyc08	Solyc08g005310.2	Guanine nucleotide-binding protein	CDS	NONSYN	G	D	900	NA	NA	novel	NA		
8	511686	C	G	Solyc08	Solyc08g005650.2	Cytochrome P450	CDS	NONSYN	R	P	322	1	55	novel	TOLERATED		
8	711592	A	T	Solyc08	Solyc08g005940.1	Trypsin proteinase inhibitor (AHRI	CDS	NONSYN	I	F	347	0.11	2	novel	TOLERATED		
8	711791	T	A	Solyc08	Solyc08g005940.1	Trypsin proteinase inhibitor (AHRI	CDS	NONSYN	I	N	413	NA	NA	novel	NA		
8	919801	G	A	Solyc08	Solyc08g006230.2	B3 domain-containing transcription	CDS	NONSYN	S	N	326	NA	NA	novel	NA		
8	924287	A	G	Solyc08	Solyc08g006240.1	B3 domain-containing protein LOC	CDS	NONSYN	H	R	276	NA	NA	novel	NA		
8	924778	C	CGAAC	Solyc08	Solyc08g006240.1	B3 domain-containing protein LOC	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA		
8	965134	T	TCCCC	Solyc08	Solyc08g006300.2	Fasciclin-like arabinogalactan prote	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA		
8	2849124	G	C	Solyc08	Solyc08g008460.2	Kinesin light chain (AHRD V1 ***	CDS	NONSYN	N	K	346	0.305	35	novel	TOLERATED		
8	2946599	A	G	Solyc08	Solyc08g008560.1	Mutator-like transposase (AHRD V	CDS	NONSYN	I	V	108	0.739	2	novel	TOLERATED		
8	2956997	A	C	Solyc08	Solyc08g008580.2	Cystathionine gamma-lyase (AHRD	CDS	NONSYN	L	F	104	0.727	51	novel	TOLERATED		
8	3144144	C	T	Solyc08	Solyc08g013800.2	F-box family protein (AHRD V1 **	CDS	NONSYN	G	S	90	0.023	29	novel	DELETERIOUS		
8	3303350	T	C	Solyc08	Solyc08g013930.2	Peroxidase family protein (AHRD '	CDS	NONSYN	T	A	131	0.201	23	novel	TOLERATED		
8	3303376	T	C	Solyc08	Solyc08g013930.2	Peroxidase family protein (AHRD '	CDS	NONSYN	K	R	122	0.557	23	novel	TOLERATED		
8	3370955	T	TG	Solyc08	Solyc08g013970.1	Nbs-lrr, resistance protein	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	3373240	A	T	Solyc08	Solyc08g013970.1	Nbs-lrr, resistance protein	CDS	NONSYN	E	D	780	0.201	14	novel	TOLERATED		
8	3373286	G	T	Solyc08	Solyc08g013970.1	Nbs-lrr, resistance protein	CDS	NONSYN	V	L	796	1	12	novel	TOLERATED		
8	4118381	A	G	Solyc08	Solyc08g014360.1	Cinnamyl alcohol dehydrogenase-li	CDS	NONSYN	L	P	305	0.868	241	novel	TOLERATED		
8	4526443	A	AT	Solyc08	Solyc08g014500.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	7056372	T	A	Solyc08	Solyc08g016280.1	Ulp1 peptidase-like (AHRD V1 *-*	CDS	NONSYN	D	E	801	NA	NA	novel	NA		
8	9837814	C	T	Solyc08	Solyc08g021810.1	Transposon Ty1-A Gag-Pol polypr	CDS	NONSYN	V	M	501	1	32	novel	TOLERATED		
8	37762803	AC	A	Solyc08	Solyc08g048060.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	46026473	T	C	Solyc08	Solyc08g061490.2	MTD1 (AHRD V1 ***- Q9LLM3_	CDS	NONSYN	S	P	82	0.029	29	novel	DELETERIOUS		
8	53558662	C	T	Solyc08	Solyc08g067290.2	RING finger protein 6 (AHRD V1 '	CDS	NONSYN	M	I	188	1	17	novel	TOLERATED		
8	53609840	C	CT	Solyc08	Solyc08g067350.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	53617503	A	G	Solyc08	Solyc08g067360.2	WRKY transcription factor 9 (AHR	CDS	NONSYN	T	A	206	0.75	34	novel	TOLERATED		
8	54637515	C	CATAT	Solyc08	Solyc08g068330.2	Aspartate aminotransferase (AHRD	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	54664162	G	A	Solyc08	Solyc08g068360.1	Ethylene receptor (AHRD V1 ***-	CDS	NONSYN	P	L	101	0.005	17	novel	DELETERIOUS		
8	54664367	T	C	Solyc08	Solyc08g068360.1	Ethylene receptor (AHRD V1 ***-	CDS	NONSYN	T	A	33	1	25	novel	TOLERATED		
8	54664371	C	G	Solyc08	Solyc08g068360.1	Ethylene receptor (AHRD V1 ***-	CDS	NONSYN	R	S	31	1	24	novel	TOLERATED		
8	54747167	G	A	Solyc08	Solyc08g068410.1	Unknown Protein (AHRD V1)	CDS	NONSYN	G	R	316	NA	NA	novel	NA		
8	55103769	T	C	Solyc08	Solyc08g068750.1	Unknown Protein (AHRD V1)	CDS	NONSYN	Q	R	58	NA	NA	novel	NA		
8	55104734	G	A	Solyc08	Solyc08g068760.1	Growth-regulating factor 3 (AHRD	CDS	NONSYN	G	E	146	NA	NA	novel	NA		
8	55122700	T	A	Solyc08	Solyc08g068810.2	Ubiquitin carboxyl-terminal hydrol	CDS	NONSYN	F	I	169	0.348	22	novel	TOLERATED		
8	55124405	T	C	Solyc08	Solyc08g068810.2	Ubiquitin carboxyl-terminal hydrol	CDS	NONSYN	M	T	475	1	31	novel	TOLERATED		
8	55145476	A	G	Solyc08	Solyc08g068860.2	Aspartic proteinase nepenthesin-1 (	CDS	NONSYN	Y	H	230	0.549	11	novel	TOLERATED		
8	55145559	C	T	Solyc08	Solyc08g068860.2	Aspartic proteinase nepenthesin-1 (	CDS	NONSYN	R	Q	202	0.615	10	novel	TOLERATED		
8	56356163	T	C	Solyc08	Solyc08g075030.2	Pectinacetylesterase like protein (Fr	CDS	NONSYN	N	D	95	0.648	78	novel	TOLERATED		
8	56356494	C	T	Solyc08	Solyc08g075030.2	Pectinacetylesterase like protein (Fr	CDS	NONSYN	V	I	45	0.215	73	novel	TOLERATED		
8	56356511	G	A	Solyc08	Solyc08g075030.2	Pectinacetylesterase like protein (Fr	CDS	NONSYN	S	L	39	0.353	42	novel	TOLERATED		
8	56356544	A	G	Solyc08	Solyc08g075030.2	Pectinacetylesterase like protein (Fr	CDS	NONSYN	I	T	28	0.294	37	novel	TOLERATED		
8	56777617	A	AT	Solyc08	Solyc08g075460.2	Nodulin-like protein (AHRD V1 **	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	57874812	A	G	Solyc08	Solyc08g076800.2	Ring H2 finger protein (AHRD V1	CDS	NONSYN	N	D	94	0.808	12	novel	TOLERATED		
8	58690835	G	T	Solyc08	Solyc08g077540.1	Unknown Protein (AHRD V1)	CDS	NONSYN	P	T	49	NA	NA	novel	NA		
8	58893972	AG	A	Solyc08	Solyc08g077820.2	Cationic amino acid transporter (AI	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	59077666	T	C	Solyc08	Solyc08g078040.2	Monooxygenase FAD-binding (AH	CDS	STOP-LOS	*	Q	269	NA	NA	novel	NA		
8	59089069	C	T	Solyc08	Solyc08g078080.2	Pentatricopeptide repeat-containing	CDS	NONSYN	V	M	331	0.27	23	novel	TOLERATED		
8	59794004	A	AT	Solyc08	Solyc08g078970.1	Pleckstrin homology domain-contai	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	59794024	AT	A	Solyc08	Solyc08g078970.1	Pleckstrin homology domain-contai	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	59828808	T	TA	Solyc08	Solyc08g079010.1	Os04g0690100 protein (Fragment)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	60418520	T	A	Solyc08	Solyc08g079770.2	C4-dicarboxylate transporter/malic	CDS	STOP-GAI	K	*	460	NA	NA	novel	NA		
8	61273544	T	TTTCA	Solyc08	Solyc08g080980.2	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA		
8	61281003	T	C	Solyc08	Solyc08g081000.2	Lysine-specific demethylase 5D (AI	CDS	NONSYN	M	V	1687	1	9	novel	TOLERATED		
8	61303467	T	A	Solyc08	Solyc08g081000.2	Lysine-specific demethylase 5D (AI	CDS	NONSYN	S	C	221	0.011	12	novel	DELETERIOUS		
8	61322949	T	C	Solyc08	Solyc08g081020.1	Carboxyl-terminal proteinase (AHR	CDS	NONSYN	I	T	61	0.65	13	novel	TOLERATED		
8	61323507	C	CG	Solyc08	Solyc08g081020.1	Carboxyl-terminal proteinase (AHR	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
8	61356377	T	C	Solyc08	Solyc08g081070.2	Mitochondrial carrier family (AHRI	CDS	NONSYN	N	S	224	0.029	8	novel	DELETERIOUS		
8	61409153	C	A	Solyc08	Solyc08g081170.2	UDP-N-acetylmuramoyl-L-alanyl-I	CDS	NONSYN	H	N	118	0.587	9	novel	TOLERATED		
8	61409221	C	G	Solyc08	Solyc08g081170.2	UDP-N-acetylmuramoyl-L-alanyl-I	CDS	NONSYN	D	E	140	1	9	novel	TOLERATED		
8	61438488	T	C	Solyc08	Solyc08g081210.2	Protein serine/threonine kinase (AH	CDS	NONSYN	K	E	604	1	33	novel	TOLERATED		
8	61438881	G	T	Solyc08	Solyc08g081210.2	Protein serine/threonine kinase (AH	CDS	NONSYN	H	Q	529	0.312	33	novel	TOLERATED		
8	61441782	T	A	Solyc08	Solyc08g081210.2	Protein serine/threonine kinase (AH	CDS	NONSYN	S	C	117	0.192	19	novel	TOLERATED		
8	61475242	T	A	Solyc08	Solyc08g081250.2	Aminopeptidase N (AHRD V1 ***	CDS	NONSYN	H	L	190	0.406	196	novel	TOLERATED		
8	62425409	G	A	Solyc08	Solyc08g082450.2	Lipase class 3 family protein (AHR	CDS	NONSYN	V	I	234	0.272	35	novel	TOLERATED		
8	62440382	G	C	Solyc08	Solyc08g082500.1	GDSL esterase/lipase At1g33811 (.	CDS	NONSYN	Q	E	68	1	13	novel	TOLERATED		
8	62440438	A	G	Solyc08	Solyc08g082500.1	GDSL esterase/lipase At1g33811 (.	CDS	NONSYN	L	S	49	0.443	13	novel	TOLERATED		
8	62541790	G	A	Solyc08	Solyc08g082650.2	Cellulose synthase-like protein H1 (	CDS	NONSYN	A	T	10	1	9	novel	TOLERATED		
8	62568627	G	T	Solyc08	Solyc08g082700.2	26S proteasome non-ATPase regula	CDS	NONSYN	V	F	19	1	26	novel	TOLERATED		
8	62646615	A	G	Solyc08	Solyc08g082810.2	Beta-amylase (AHRD V1 **** B9I	CDS	NONSYN	W	R	262	0.847	63	novel	TOLERATED		
8	62734015	T	C	Solyc08	Solyc08g082910.1	Dof zinc finger protein 2 (AHRD V	CDS	NONSYN	V	A	204	1	24	novel	TOLERATED		
8	62734039	C	CTAA	Solyc08	Solyc08g082910.1	Dof zinc finger protein 2 (AHRD V	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA		
8	62923645	C	A	Solyc08	Solyc08g083240.2	Calmodulin-binding protein family-	CDS	NONSYN	A	S	425	1	27	novel	TOLERATED		
9	7613	C	A	Solyc09	Solyc09g005000.1	Receptor like protein kinase (AHRI	CDS	NONSYN	S	R	527	0.296	48	novel	TOLERATED		
9	14348	A	C	Solyc09	Solyc09g005010.2	Importin subunit beta (AHRD V1 *	CDS	NONSYN	C	W	97	NA	NA	novel	NA		
9	34878	A	AT	Solyc09	Solyc09g005050.1	Unknown Protein (AHRD V1); con	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
9	56696	TC	T	Solyc09	Solyc09g005090.1	LRR receptor-like serine/threonine-	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA		
9	57365	G	A	Solyc09	Solyc09g005090.1	LRR receptor-like serine/threonine-	CDS	NONSYN	D	N	630	0.103	28	novel	TOLERATED		
9	66163	T	A	Solyc09	Solyc09g005110.2	Pyruvate decarboxylase 1 (AHRD '	CDS	NONSYN	T	S	165	0.333	81	novel	TOLERATED		
9	140408	C	T	Solyc09	Solyc09g005140.1	Unknown Protein (AHRD V1)	CDS	NONSYN	G	S	48	0.723	4	novel	TOLERATED		
9	152714	G	A	Solyc09	Solyc09g005160.1	Ubiquitin-protein ligase E3 (AHRI	CDS	NONSYN	E	K	375	0.788	13	novel	TOLERATED		

9	156720	C	T	Solyc09	Solyc09g005170.1	Receptor-like protein kinase At3g2	CDS	NONSYNC	G	R	292	0.048	30	novel	DELETERIOUS
9	158332	C	T	Solyc09	Solyc09g005170.1	Receptor-like protein kinase At3g2	CDS	NONSYNC	G	R	33	0.003	27	novel	DELETERIOUS
9	174491	G	A	Solyc09	Solyc09g005220.1	Potassium channel (AHRD V1 ***	CDS	NONSYNC	A	V	30	0.131	4	novel	TOLERATED
9	174519	G	A	Solyc09	Solyc09g005220.1	Potassium channel (AHRD V1 ***	CDS	NONSYNC	R	W	21	0	3	novel	DELETERIOUS
9	179010	C	T	Solyc09	Solyc09g005230.2	DUF647 domain-containing proteir	CDS	NONSYNC	D	N	115	0.031	15	novel	DELETERIOUS
9	182400	G	A	Solyc09	Solyc09g005240.1	Tobamovirus multiplication protein	CDS	NONSYNC	R	H	92	0.533	34	novel	TOLERATED
9	182420	T	C	Solyc09	Solyc09g005240.1	Tobamovirus multiplication protein	CDS	NONSYNC	Y	H	99	0.652	32	novel	TOLERATED
9	182421	A	G	Solyc09	Solyc09g005240.1	Tobamovirus multiplication protein	CDS	NONSYNC	Y	C	99	0.169	32	novel	TOLERATED
9	182658	T	C	Solyc09	Solyc09g005240.1	Tobamovirus multiplication protein	CDS	NONSYNC	V	A	178	0.042	38	novel	DELETERIOUS
9	193506	GA	G	Solyc09	Solyc09g005260.2	Calcium/proton exchanger (AHRD	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	193552	C	A	Solyc09	Solyc09g005260.2	Calcium/proton exchanger (AHRD	CDS	NONSYNC	K	N	250	0.002	74	novel	DELETERIOUS
9	193554	T	A	Solyc09	Solyc09g005260.2	Calcium/proton exchanger (AHRD	CDS	STOP-GAI	K	*	250	NA	NA	novel	NA
9	193605	G	C	Solyc09	Solyc09g005260.2	Calcium/proton exchanger (AHRD	CDS	NONSYNC	Q	E	233	0.749	66	novel	TOLERATED
9	213603	G	T	Solyc09	Solyc09g005280.2	ATP synthase subunit-like protein (	CDS	NONSYNC	H	Q	278	NA	NA	novel	NA
9	220851	TTGC	T	Solyc09	Solyc09g005290.1	Cc-nbs-lrr, resistance protein	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
9	301226	C	T	Solyc09	Solyc09g005410.1	Major latex-like protein (AHRD V1	CDS	NONSYNC	S	N	84	0.034	16	novel	DELETERIOUS
9	301229	T	A	Solyc09	Solyc09g005410.1	Major latex-like protein (AHRD V1	CDS	NONSYNC	D	V	83	0.007	16	novel	DELETERIOUS
9	301230	C	T	Solyc09	Solyc09g005410.1	Major latex-like protein (AHRD V1	CDS	NONSYNC	D	N	83	0.319	16	novel	TOLERATED
9	301239	C	T	Solyc09	Solyc09g005410.1	Major latex-like protein (AHRD V1	CDS	NONSYNC	D	N	80	0.377	16	novel	TOLERATED
9	344256	A	ATTC	Solyc09	Solyc09g005510.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
9	404763	G	GT	Solyc09	Solyc09g005580.2	SelT-like protein (AHRD V1 ***-	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	405776	T	A	Solyc09	Solyc09g005590.2	SelT-like protein (AHRD V1 ***-	CDS	NONSYNC	S	T	54	0.932	16	novel	TOLERATED
9	460247	A	T	Solyc09	Solyc09g005680.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	M	L	16	NA	NA	novel	NA
9	505251	T	A	Solyc09	Solyc09g005730.2	Plant-specific domain TIGR01589	CDS	STOP-GAI	L	*	91	NA	NA	novel	NA
9	527448	A	C	Solyc09	Solyc09g005760.2	U3 small nucleolar RNA-associatec	CDS	NONSYNC	R	S	8	0.973	6	novel	TOLERATED
9	531336	G	T	Solyc09	Solyc09g005760.2	U3 small nucleolar RNA-associatec	CDS	NONSYNC	G	V	271	0.056	14	novel	TOLERATED
9	541908	A	G	Solyc09	Solyc09g005770.1	F-box family protein (AHRD V1 **	CDS	NONSYNC	N	D	107	0.345	8	novel	TOLERATED
9	619796	G	C	Solyc09	Solyc09g005890.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	I	M	29	NA	NA	novel	NA
9	657214	G	C	Solyc09	Solyc09g005950.2	Pathogenesis-related protein 1a (AI	CDS	NONSYNC	L	V	173	0.057	26	novel	TOLERATED
9	657398	C	A	Solyc09	Solyc09g005950.2	Pathogenesis-related protein 1a (AI	CDS	NONSYNC	K	N	111	0.311	28	novel	TOLERATED
9	746251	A	T	Solyc09	Solyc09g007100.2	BZIP transcription factor (AHRD V	CDS	NONSYNC	Y	F	405	0.144	13	novel	TOLERATED
9	754579	T	C	Solyc09	Solyc09g007110.2	Receptor like kinase, RLK	CDS	NONSYNC	H	R	588	0.182	27	novel	TOLERATED
9	946320	A	T	Solyc09	Solyc09g007340.2	PWWP domain-containing protein (	CDS	NONSYNC	N	I	1317	0.008	103	novel	DELETERIOUS
9	973312	G	A	Solyc09	Solyc09g007380.2	Hydrolase alpha/beta fold family pr	CDS	NONSYNC	V	M	18	0.2	11	novel	TOLERATED
9	975378	A	G	Solyc09	Solyc09g007380.2	Hydrolase alpha/beta fold family pr	CDS	NONSYNC	T	A	303	0.023	17	novel	DELETERIOUS
9	985989	G	C	Solyc09	Solyc09g007410.2	Calmodulin-binding protein (AHRI	CDS	NONSYNC	R	G	338	0.29	24	novel	TOLERATED
9	988190	T	C	Solyc09	Solyc09g007410.2	Calmodulin-binding protein (AHRI	CDS	NONSYNC	E	G	2	1	21	novel	TOLERATED
9	1219907	C	T	Solyc09	Solyc09g007670.2	Wd-repeat protein (AHRD V1 **--	CDS	NONSYNC	A	V	74	0.266	20	novel	TOLERATED
9	1230243	T	C	Solyc09	Solyc09g007680.2	Zinc finger family protein (AHRD '	CDS	NONSYNC	I	V	205	0.037	21	novel	DELETERIOUS
9	1296600	TA	T	Solyc09	Solyc09g007760.2	Aquaporin 2 (AHRD V1 ***- O65	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	1296660	G	GTT	Solyc09	Solyc09g007760.2	Aquaporin 2 (AHRD V1 ***- O65	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	1301281	AT	A	Solyc09	Solyc09g007770.2	Aquaporin 2 (AHRD V1 ***- O65	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	1301458	A	G	Solyc09	Solyc09g007770.2	Aquaporin 2 (AHRD V1 ***- O65	CDS	NONSYNC	I	V	64	0.762	336	novel	TOLERATED
9	1315510	C	T	Solyc09	Solyc09g007790.1	Arabidopsis thaliana genomic DNA	CDS	NONSYNC	P	S	23	0.794	14	novel	TOLERATED
9	1315585	G	T	Solyc09	Solyc09g007790.1	Arabidopsis thaliana genomic DNA	CDS	NONSYNC	V	F	48	0.709	19	novel	TOLERATED
9	1376251	C	A	Solyc09	Solyc09g007840.2	Cyclic nucleotide gated channel (AI	CDS	NONSYNC	L	F	147	1	84	novel	TOLERATED
9	1404334	G	T	Solyc09	Solyc09g007870.2	Manganese transporter mntH (AHR	CDS	NONSYNC	V	F	441	0.11	20	novel	TOLERATED
9	1404566	C	G	Solyc09	Solyc09g007870.2	Manganese transporter mntH (AHR	CDS	NONSYNC	T	S	518	1	18	novel	TOLERATED
9	1406108	T	A	Solyc09	Solyc09g007870.2	Manganese transporter mntH (AHR	CDS	NONSYNC	L	Q	1032	0.604	20	novel	TOLERATED
9	1414945	T	C	Solyc09	Solyc09g007890.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	S	G	251	0.338	170	novel	TOLERATED
9	1414947	G	C	Solyc09	Solyc09g007890.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	T	S	250	0.466	171	novel	TOLERATED
9	1414964	G	C	Solyc09	Solyc09g007890.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	F	L	244	1	176	novel	TOLERATED
9	1414981	T	G	Solyc09	Solyc09g007890.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	N	H	239	0.1	172	novel	TOLERATED
9	1414986	T	C	Solyc09	Solyc09g007890.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	K	R	237	0.492	172	novel	TOLERATED
9	1415009	C	A	Solyc09	Solyc09g007890.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	K	N	229	0.179	174	novel	TOLERATED
9	1415010	T	C	Solyc09	Solyc09g007890.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	K	R	229	0.575	174	novel	TOLERATED
9	1415040	G	A	Solyc09	Solyc09g007890.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	A	V	219	0.103	174	novel	TOLERATED
9	1415044	T	C	Solyc09	Solyc09g007890.1	Phenylalanine ammonia-lyase (AHI	CDS	NONSYNC	I	V	218	0.124	174	novel	TOLERATED
9	1511386	C	A	Solyc09	Solyc09g008040.2	RNA polymerase sigma-70 factor (.	CDS	NONSYNC	H	N	191	1	11	novel	TOLERATED
9	1517931	G	A	Solyc09	Solyc09g008050.2	UDP-glucose glucosyltransferase (/	CDS	NONSYNC	V	I	374	0.894	25	novel	TOLERATED
9	1518079	G	A	Solyc09	Solyc09g008050.2	UDP-glucose glucosyltransferase (/	CDS	NONSYNC	S	N	423	0.486	25	novel	TOLERATED
9	1527588	T	G	Solyc09	Solyc09g008070.2	Cell division protease ftsH homolog	CDS	NONSYNC	S	R	98	1	243	novel	TOLERATED
9	1554724	C	T	Solyc09	Solyc09g008080.2	Unknown Protein (AHRD V1); con	CDS	NONSYNC	S	F	112	NA	NA	novel	NA
9	1566318	AT	A	Solyc09	Solyc09g008090.2	UDP-glucosyltransferase family 1 p	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	1586666	A	G	Solyc09	Solyc09g008110.1	Mutator-like transposase (AHRD V	CDS	NONSYNC	S	P	741	0.024	7	novel	DELETERIOUS
9	2139192	A	G	Solyc09	Solyc09g008700.1	Ubiquitin-protein ligase 7 (AHRD '	CDS	NONSYNC	M	T	956	1	23	novel	TOLERATED
9	2159956	C	A	Solyc09	Solyc09g008720.1	Ethylene receptor (AHRD V1 *--- (	CDS	NONSYNC	D	E	475	0.071	22	novel	TOLERATED
9	4209117	C	T	Solyc09	Solyc09g010870.2	Exoribonuclease R/ribonuclease II (	CDS	NONSYNC	E	K	90	1	10	novel	TOLERATED
9	4259509	T	C	Solyc09	Solyc09g010920.1	GRAS family transcription factor (/	CDS	NONSYNC	L	P	142	0.323	36	novel	TOLERATED
9	4279484	C	T	Solyc09	Solyc09g010940.2	Pyrimidine 5'-nucleotidase (A	CDS	NONSYNC	A	T	172	0.604	24	novel	TOLERATED
9	4504331	T	TA	Solyc09	Solyc09g011150.1	ORF42f (AHRD V1 *-*- Q32989_	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	4516390	G	A	Solyc09	Solyc09g011170.2	Uncharacterized basic helix-loop-h	CDS	NONSYNC	R	C	511	0.048	11	novel	DELETERIOUS
9	4750761	A	AT	Solyc09	Solyc09g011410.2	Plastid RNA-binding protein 1 (AH	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	4799752	T	A	Solyc09	Solyc09g011480.2	Rop guanine nucleotide exchange fi	CDS	NONSYNC	N	I	461	0.002	52	novel	DELETERIOUS
9	5071448	T	C	Solyc09	Solyc09g011780.2	MYB transcription factor (AHRD V	CDS	NONSYNC	Q	R	235	0.48	21	novel	TOLERATED
9	8042896	T	C	Solyc09	Solyc09g015120.2	Kelch-like protein (AHRD V1 *-*-	CDS	NONSYNC	V	A	319	0.719	12	novel	TOLERATED
9	8259199	T	C	Solyc09	Solyc09g015230.1	Receptor-like protein kinase At5g5'	CDS	NONSYNC	L	P	104	0.044	45	novel	DELETERIOUS
9	8551734	AG	A	Solyc09	Solyc09g015340.1	Photosystem I P700 chlorophyll a a	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	12265383	T	G	Solyc09	Solyc09g017990.1	Ubiquitin carboxyl-terminal hydrol	CDS	NONSYNC	K	Q	451	0.481	4	novel	TOLERATED
9	15105762	C	CA	Solyc09	Solyc09g018500.1	DNA binding protein (AHRD V1 *	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	19258968	T	A	Solyc09	Solyc09g025220.1	Legumin 11S-globulin (AHRD V1	CDS	NONSYNC	I	L	154	0.493	20	novel	TOLERATED
9	27300203	G	T	Solyc09	Solyc09g042270.1	Helicase-like protein (AHRD V1 *'	CDS	NONSYNC	P	Q	118	0.004	31	novel	DELETERIOUS
9	28305478	C	A	Solyc09	Solyc09g042460.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	H	N	212	NA	NA	novel	NA
9	29628395	T	G	Solyc09	Solyc09g042720.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	S	A	35	0.787	2	novel	TOLERATED
9	32113116	A	G	Solyc09	Solyc09g050010.1	Polyprotein (AHRD V1 ***- Q9AV	CDS	NONSYNC	I	T	281	0.573	22	novel	TOLERATED
9	42311997	G	A	Solyc09	Solyc09g056020.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	V	43	NA	NA	novel	NA
9	42311998	C	T	Solyc09	Solyc09g056020.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	T	43	NA	NA	novel	NA
9	42312016	A	G	Solyc09	Solyc09g056020.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	W	R	37	NA	NA	novel	NA
9	42680727	A	T	Solyc09	Solyc09g056070.1	Maturase (Fragment) (AHRD V1 *	CDS	NONSYNC	M	K	16	0.003	2	novel	DELETERIOUS
9	45449382	C	G	Solyc09	Solyc09g057600.1	cDNA clone J075118M20 full inse	CDS	NONSYNC	T	R	17	0.003	22	novel	DELETERIOUS
9	50127752	C	T	Solyc09	Solyc09g059460.2	At5g24290 (Fragment) (AHRD V1	CDS	NONSYNC	L	F	389	0.074	7	novel	TOLERATED
9	53127182	G	A	Solyc09	Solyc09g060080.2	Genomic DNA chromosome 3 TAC	CDS	NONSYNC	D	N	719	0.436	15	novel	TOLERATED
9	54754297	TG	T	Solyc09	Solyc09g061460.1	NAD(P)H-quinone oxidoreductase	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	54754299	G	A	Solyc09	Solyc09g061460.1	NAD(P)H-quinone oxidoreductase	CDS	NONSYNC	G	R	139	0	78	novel	DELETERIOUS
9	56712322	CT	C	Solyc09	Solyc09g063110.1	Ulp1 protease family C-terminal cat	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	57319744	T	C	Solyc09	Solyc09g064440.2	ABC transporter C family member :	CDS	NONSYNC	L	P	1490	0.001	58	novel	DELETERIOUS
9	57689099	TG	T	Solyc09	Solyc09g064750.2	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	57689102	AGAC	A	Solyc09	Solyc09g064750.2	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
9	58553818	G	T	Solyc09	Solyc09g065100.1	Transcription factor (AHRD V1 *--	CDS	NONSYNC	A	S	636	1	30	novel	TOLERATED
9	59784378	T	G	Solyc09	Solyc09g065890.2	Lipase (Fragment) (AHRD V1 ***-	CDS	NONSYNC	I	R	450	1	32	novel	TOLERATED
9	59784386	C	G	Solyc09	Solyc09g065890.2	Lipase (Fragment) (AHRD V1 ***-	CDS	NONSYNC	P	A	453	1	29	novel	TOLERATED
9	59784397	CA	C	Solyc09	Solyc09g065890.2	Lipase (Fragment) (AHRD V1 ***-	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	59991977	T	G	Solyc09	Solyc09g066060.1	Homeobox leucine-zipper protein (.	CDS	NONSYNC	L	R	197	0.178	4	novel	TOLERATED
9	59991980	C	A	Solyc09	Solyc09g066060.1	Homeobox leucine-zipper protein (.	CDS	NONSYNC	P	Q	198	0	4	novel	DELETERIOUS
9	59992021	T	A	Solyc09	Solyc09g066060.1	Homeobox leucine-zipper protein (.	CDS	NONSYNC	L	I	212	0.308	3	novel	TOLERATED
9	59992041	C	G	Solyc09	Solyc09g066060.1	Homeobox leucine-zipper protein (.	CDS	NONSYNC	H	Q	218	0.191	2	novel	TOLERATED
9	59992061	T	A	Solyc09	Solyc09g066060.1	Homeobox leucine-zipper protein (.	CDS	NONSYNC	L	H	225	0.043	4	novel	DELETERIOUS
9	60426759	A	G	Solyc09	Solyc09g066410.1	Inorganic phosphate transporter (Al	CDS	NONSYNC	T	A	66	1	164	novel	TOLERATED
9	63038045	A	AT	Solyc09	Solyc09g075900.2	Spermidine synthase (AHRD V1 **	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	63824466	A	AT	Solyc09	Solyc09g082730.2	Aldo/keto reductase family protein (	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
9	64706747	T	C	Solyc09	Solyc09g089610.2	Ethylene receptor (AHRD V1 ****	CDS	NONSYNC	M	T	349	0.238	69	novel	TOLERATED
9	64918562	T	C	Solyc09	Solyc09g089970.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	S	58	0.15	3	novel	TOLERATED
9	65132817	G	T	Solyc09	Solyc09g090250.2	Serine/threonine kinase (AHRD V1	CDS	NONSYNC	L	F	71	1	254	novel	TOLERATED
9	65132857	T	C	Solyc09	Solyc09g090250.2	Serine/threonine kinase (AHRD V1	CDS	NONSYNC	F	L	85	1	252	novel	TOLERATED
9	65132870	G	T	Solyc09	Solyc09g090250.2	Serine/threonine kinase (AHRD V1	CDS	NONSYNC	W	L	89	1	253	novel	TOLERATED
9	65132886	A	C	Solyc09	Solyc09g090250.2	Serine/threonine kinase (AHRD V1	CDS	NONSYNC	K	N	94	1	252	novel	TOLERATED
9	65132896	T	A	Solyc09	Solyc09g090250.2	Serine/threonine kinase (AHRD V1	CDS	NONSYNC	W	R	98	1	253	novel	TOLERATED

9	65563051	GGGA	G	Solyc09	Solyc09g090800.1	Plasma membrane associated protei	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	NA
9	66022293	A	G	Solyc09	Solyc09g091380.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	L	S	79	0.505	165	novel	TOLERATED	
9	66023819	T	TCCAA	Solyc09	Solyc09g091390.2	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	NA
9	66112604	A	AT	Solyc09	Solyc09g091490.1	Transcription factor jumonji domair	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	NA
9	66300691	T	G	Solyc09	Solyc09g091720.1	Monooxygenase (AHRD V1 ***- I	CDS	NONSYNC	L	V	300	1	100	novel	TOLERATED	
9	66388821	G	C	Solyc09	Solyc09g091830.2	Peptidoglycan binding domain cont	CDS	NONSYNC	E	D	259	0.593	14	novel	TOLERATED	
9	66489811	C	T	Solyc09	Solyc09g091940.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	G	S	23	NA	NA	novel	NA	
9	66533786	A	C	Solyc09	Solyc09g091990.2	Receptor-like kinase (AHRD V1 *-	CDS	NONSYNC	Y	S	355	0.84	340	novel	TOLERATED	
9	66667428	G	A	Solyc09	Solyc09g092160.2	Beta-galactosidase (AHRD V1 ***	CDS	NONSYNC	P	S	94	0.002	137	novel	DELETERIOUS	
9	66762794	C	A	Solyc09	Solyc09g092280.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	G	V	634	0.259	7	novel	TOLERATED	
9	66762797	T	C	Solyc09	Solyc09g092280.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	K	R	633	0.654	9	novel	TOLERATED	
9	66762807	G	C	Solyc09	Solyc09g092280.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	L	V	630	0.147	11	novel	TOLERATED	
9	66762836	C	A	Solyc09	Solyc09g092280.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	G	V	620	0.209	11	novel	TOLERATED	
9	66762847	G	T	Solyc09	Solyc09g092280.1	Cc-nbs-lrr, resistance protein	CDS	STOP-GAI	Y	*	616	NA	NA	novel	NA	
9	66762849	A	C	Solyc09	Solyc09g092280.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	Y	D	616	0.447	11	novel	TOLERATED	
9	66762854	G	C	Solyc09	Solyc09g092280.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	S	W	614	0.178	11	novel	TOLERATED	
9	66762873	T	G	Solyc09	Solyc09g092280.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	I	L	608	1	11	novel	TOLERATED	
9	66762882	C	T	Solyc09	Solyc09g092280.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	V	M	605	0.023	11	novel	DELETERIOUS	
9	66794181	A	T	Solyc09	Solyc09g092310.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	V	E	308	1	18	novel	TOLERATED	
9	66799348	A	T	Solyc09	Solyc09g092320.2	RNA binding protein-like protein (/	CDS	NONSYNC	Q	L	24	0.096	251	novel	TOLERATED	
9	66799381	T	A	Solyc09	Solyc09g092320.2	RNA binding protein-like protein (/	CDS	NONSYNC	V	D	35	0.322	251	novel	TOLERATED	
9	66800432	C	CGGAT	Solyc09	Solyc09g092320.2	RNA binding protein-like protein (/	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	
9	66807084	A	T	Solyc09	Solyc09g092330.1	NAD dependent epimerase/dehydra	CDS	NONSYNC	F	Y	403	0.594	94	novel	TOLERATED	
9	66807113	AAT	A	Solyc09	Solyc09g092330.1	NAD dependent epimerase/dehydra	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
9	66807117	A	C	Solyc09	Solyc09g092330.1	NAD dependent epimerase/dehydra	CDS	NONSYNC	F	C	392	0.067	94	novel	TOLERATED	
9	66807120	A	C	Solyc09	Solyc09g092330.1	NAD dependent epimerase/dehydra	CDS	NONSYNC	F	C	391	0.05	94	novel	TOLERATED	
9	66807122	T	TTC	Solyc09	Solyc09g092330.1	NAD dependent epimerase/dehydra	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
9	66825586	C	T	Solyc09	Solyc09g092350.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	D	N	112	NA	NA	novel	NA	
9	66857641	C	G	Solyc09	Solyc09g092400.1	Ectonucleoside triphosphate diphos	CDS	NONSYNC	P	R	409	0.056	68	novel	TOLERATED	
9	67083141	A	G	Solyc09	Solyc09g097820.2	ATP dependent RNA helicase (AH	CDS	NONSYNC	F	L	610	0.135	89	novel	TOLERATED	
9	67173736	A	C	Solyc09	Solyc09g097910.2	Polyribonucleotide nucleotidyltrans	CDS	NONSYNC	K	T	291	0.409	17	novel	TOLERATED	
9	67184371	GTGG.	G	Solyc09	Solyc09g097940.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	
9	67274996	CTCA	C	Solyc09	Solyc09g098100.2	Cc-nbs-lrr, resistance protein	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	
9	67309098	C	T	Solyc09	Solyc09g098140.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	T	I	104	0	13	novel	DELETERIOUS	
9	67421615	G	A	Solyc09	Solyc09g098270.2	Polygalacturonase (AHRD V1 ***-	CDS	START-LC	M	I	1	0.639	3	novel	TOLERATED	
9	67524641	G	A	Solyc09	Solyc09g098450.2	Sn1-specific diacylglycerol lipase a	CDS	NONSYNC	R	H	184	0.143	15	novel	TOLERATED	
9	67557755	G	A	Solyc09	Solyc09g098480.1	Carboxyl-terminal peptidase-like (/	CDS	NONSYNC	E	K	136	0.693	5	novel	TOLERATED	
9	67567437	A	T	Solyc09	Solyc09g098490.2	Epsin 2 (AHRD V1 *-*- Q5NCM7	CDS	NONSYNC	Y	F	672	0.699	16	novel	TOLERATED	
9	67606821	G	T	Solyc09	Solyc09g098530.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	S	I	317	0.21	10	novel	TOLERATED	
9	67633902	T	C	Solyc09	Solyc09g098560.2	Survival motor neuron containing p	CDS	NONSYNC	V	A	441	1	17	novel	TOLERATED	
10	2680746	T	A	Solyc10	Solyc10g008570.2	Pentatricopeptide repeat-containing	CDS	NONSYNC	K	M	649	0.169	13	novel	TOLERATED	
10	2692905	G	T	Solyc10	Solyc10g008600.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	M	I	353	0	7	novel	DELETERIOUS	
10	2857257	G	GT	Solyc10	Solyc10g008780.1	Transcription factor CYCLOIDEA	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
10	4188494	A	T	Solyc10	Solyc10g011910.2	WRKY transcription factor 23 (AH	CDS	NONSYNC	V	E	130	0.001	18	novel	DELETERIOUS	
10	4265841	G	GA	Solyc10	Solyc10g011970.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
10	8753502	C	T	Solyc10	Solyc10g018610.1	50S ribosomal protein L2 chloropla	CDS	NONSYNC	P	S	160	NA	NA	novel	NA	
10	20699399	G	GT	Solyc10	Solyc10g039200.1	Transposase family protein (AHRD	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
10	20979937	G	A	Solyc10	Solyc10g039300.1	Mutator-like transposase (AHRD V	CDS	NONSYNC	G	E	438	0	2	novel	DELETERIOUS	
10	23129558	G	GT	Solyc10	Solyc10g044730.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
10	52872083	T	C	Solyc10	Solyc10g055760.1	NAC domain protein IPR003441 (/	CDS	NONSYNC	L	P	178	0.234	29	novel	TOLERATED	
10	52883186	C	A	Solyc10	Solyc10g055790.1	Chitinase (Fragment) (AHRD V1 --	CDS	NONSYNC	A	S	29	0.061	89	novel	TOLERATED	
10	57057463	G	C	Solyc10	Solyc10g074390.1	Endochitinase (Chitinase) (AHRD '	CDS	NONSYNC	A	G	56	1	172	novel	TOLERATED	
10	57080324	G	A	Solyc10	Solyc10g074430.1	Replication protein A DNA-bindin	CDS	NONSYNC	S	L	445	NA	NA	novel	NA	
10	57234338	C	T	Solyc10	Solyc10g074440.1	Endochitinase (Chitinase) (AHRD '	CDS	NONSYNC	V	I	82	1	261	novel	TOLERATED	
10	57278657	C	CATAT	Solyc10	Solyc10g074460.1	Endochitinase (Chitinase) (AHRD '	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	
10	57486710	C	T	Solyc10	Solyc10g074610.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	V	I	29	NA	NA	novel	NA	
10	57526268	G	C	Solyc10	Solyc10g074650.1	Glycosyl transferase family 8 (AHR	CDS	NONSYNC	H	Q	186	0.572	13	novel	TOLERATED	
10	57557666	G	C	Solyc10	Solyc10g074680.1	SCARECROW (AHRD V1 *--- Q5	CDS	NONSYNC	Q	E	29	0.362	9	novel	TOLERATED	
10	57686396	C	T	Solyc10	Solyc10g074730.1	Harpin-induced 1 (AHRD V1 ***-	CDS	NONSYNC	T	I	101	0	3	novel	DELETERIOUS	
10	57997216	G	C	Solyc10	Solyc10g074950.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	T	S	3	NA	NA	novel	NA	
10	58774696	G	A	Solyc10	Solyc10g076470.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	Q	112	NA	NA	novel	NA	
10	58841041	G	C	Solyc10	Solyc10g076530.1	Receptor-like protein kinase At3g2	CDS	NONSYNC	P	R	192	0.543	36	novel	TOLERATED	
10	58841042	G	C	Solyc10	Solyc10g076530.1	Receptor-like protein kinase At3g2	CDS	NONSYNC	P	A	192	0.775	36	novel	TOLERATED	
10	58841048	C	G	Solyc10	Solyc10g076530.1	Receptor-like protein kinase At3g2	CDS	NONSYNC	E	Q	190	0.559	34	novel	TOLERATED	
10	58841051	C	G	Solyc10	Solyc10g076530.1	Receptor-like protein kinase At3g2	CDS	NONSYNC	D	H	189	0.07	33	novel	TOLERATED	
10	58841060	G	T	Solyc10	Solyc10g076530.1	Receptor-like protein kinase At3g2	CDS	NONSYNC	P	T	186	0.758	26	novel	TOLERATED	
10	58844438	C	CCAAA	Solyc10	Solyc10g076550.1	Receptor-like protein kinase At3g2	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
10	59065474	C	T	Solyc10	Solyc10g076780.1	Alpha-1 4-galactosyltransferase (Al	CDS	NONSYNC	H	Y	73	0.458	10	novel	TOLERATED	
10	59065646	T	C	Solyc10	Solyc10g076780.1	Alpha-1 4-galactosyltransferase (Al	CDS	NONSYNC	L	S	130	0.733	12	novel	TOLERATED	
10	59152321	A	G	Solyc10	Solyc10g076860.1	BTB/POZ domain-containing prote	CDS	NONSYNC	H	R	66	1	25	novel	TOLERATED	
10	59255054	C	A	Solyc10	Solyc10g077000.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	T	K	736	0.611	8	novel	TOLERATED	
10	59829646	G	T	Solyc10	Solyc10g078810.1	Protein phosphatase 2C (AHRD V1	CDS	NONSYNC	T	N	407	NA	NA	novel	NA	
10	59989140	T	A	Solyc10	Solyc10g079010.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	N	K	1163	0.851	12	novel	TOLERATED	
10	59994164	G	A	Solyc10	Solyc10g079020.1	Cc-nbs-lrr resistance protein (AHR	CDS	NONSYNC	E	K	125	NA	NA	novel	NA	
10	62479680	G	T	Solyc10	Solyc10g083320.1	Auxin-induced SAUR-like protein (	CDS	NONSYNC	T	K	77	1	38	novel	TOLERATED	
10	62538782	A	AT	Solyc10	Solyc10g083390.1	Os08g0119500 protein (Fragment)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
10	62658030	GTC	G	Solyc10	Solyc10g083550.1	Glutamine synthetase I (AHRD V1	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
10	62924665	TCC	T	Solyc10	Solyc10g083870.1	Ankyrin repeat domain 1 (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
10	62994457	CTTA	C	Solyc10	Solyc10g083980.1	2-oxoglutarate-dependent dioxygen	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
10	63156754	A	G	Solyc10	Solyc10g084170.1	Bcl-2-associated athanogene-like pı	CDS	NONSYNC	Y	C	15	0.008	5	novel	DELETERIOUS	
10	63156795	T	C	Solyc10	Solyc10g084170.1	Bcl-2-associated athanogene-like pı	CDS	NONSYNC	S	P	29	0.313	5	novel	TOLERATED	
10	63156856	A	T	Solyc10	Solyc10g084170.1	Bcl-2-associated athanogene-like pı	CDS	NONSYNC	D	V	49	0.081	5	novel	TOLERATED	
10	63595126	C	T	Solyc10	Solyc10g084910.1	SUPERMAN-like zinc finger prote	CDS	NONSYNC	D	N	350	0	2	novel	DELETERIOUS	
10	63655031	T	C	Solyc10	Solyc10g084980.1	Copper transporter (AHRD V1 *-*	CDS	NONSYNC	Q	R	119	NA	NA	novel	NA	
10	64716570	G	T	Solyc10	Solyc10g086620.1	Tropinone reductase (AHRD V1 **	CDS	STOP-GAI	G	*	170	NA	NA	novel	NA	
10	64754214	T	G	Solyc10	Solyc10g086650.1	Glyoxal oxidase (AHRD V1 ***- C	CDS	NONSYNC	N	H	296	0.256	56	novel	TOLERATED	
11	2838463	T	TAAAA	Solyc11	Solyc11g008660.1	Flowering locus T (AHRD V1 **--	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA	
11	3550134	G	C	Solyc11	Solyc11g010490.1	Genomic DNA chromosome 5 P1 c	CDS	NONSYNC	A	P	31	0.036	6	novel	DELETERIOUS	
11	3551744	G	T	Solyc11	Solyc11g010490.1	Genomic DNA chromosome 5 P1 c	CDS	NONSYNC	G	V	164	0.531	18	novel	TOLERATED	
11	3613071	G	T	Solyc11	Solyc11g010560.1	Kinesin-like protein (AHRD V1 *-'	CDS	NONSYNC	L	M	911	0.172	12	novel	TOLERATED	
11	3624793	T	G	Solyc11	Solyc11g010560.1	Kinesin-like protein (AHRD V1 *-'	CDS	NONSYNC	E	A	310	0.126	73	novel	TOLERATED	
11	3644740	CTAA	C	Solyc11	Solyc11g010570.1	MADS box transcription factor (AI	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	
11	3644799	C	T	Solyc11	Solyc11g010570.1	MADS box transcription factor (AI	CDS	NONSYNC	P	S	195	0.275	61	novel	TOLERATED	
11	3654634	T	C	Solyc11	Solyc11g010590.1	Protein-tyrosine phosphatase-like m	CDS	NONSYNC	N	D	115	1	28	novel	TOLERATED	
11	3654637	A	T	Solyc11	Solyc11g010590.1	Protein-tyrosine phosphatase-like m	CDS	NONSYNC	F	I	114	0.061	28	novel	TOLERATED	
11	3654651	T	A	Solyc11	Solyc11g010590.1	Protein-tyrosine phosphatase-like m	CDS	NONSYNC	K	I	109	0.084	28	novel	TOLERATED	
11	3655475	A	T	Solyc11	Solyc11g010590.1	Protein-tyrosine phosphatase-like m	CDS	NONSYNC	I	N	64	0.003	25	novel	DELETERIOUS	
11	3655518	T	C	Solyc11	Solyc11g010590.1	Protein-tyrosine phosphatase-like m	CDS	NONSYNC	N	D	50	0.299	25	novel	TOLERATED	
11	3681374	C	A	Solyc11	Solyc11g010620.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	M	359	0.089	11	novel	TOLERATED	
11	3691875	G	A	Solyc11	Solyc11g010630.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	K	50	1	7	novel	TOLERATED	
11	3703218	C	G	Solyc11	Solyc11g010630.2	Unknown Protein (AHRD V1)	CDS	NONSYNC	S	C	830	0.054	25	novel	TOLERATED	
11	3706560	G	A	Solyc11	Solyc11g010650.2	Unknown Protein (AHRD V1); con	CDS	NONSYNC	A	V	19	1	24	novel	TOLERATED	
11	3707839	GGAC	G	Solyc11	Solyc11g010660.1	SGT1 protein (AHRD V1 ***- D3	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	
11	3707899	A	T	Solyc11	Solyc11g010660.1	SGT1 protein (AHRD V1 ***- D3	CDS	NONSYNC	D	E	560	1	19	novel	TOLERATED	
11	3707969	G	C	Solyc11	Solyc11g010660.1	SGT1 protein (AHRD V1 ***- D3	CDS	NONSYNC	A	G	537	0.507	18	novel	TOLERATED	
11	3707992	T	G	Solyc11	Solyc11g010660.1	SGT1 protein (AHRD V1 ***- D3	CDS	NONSYNC	E	D	529	0.935	21	novel	TOLERATED	
11	3708975	G	C	Solyc11	Solyc11g010660.1	SGT1 protein (AHRD V1 ***- D3	CDS	NONSYNC	N	K	462	1	17	novel	TOLERATED	
11	3709117	C	T	Solyc11	Solyc11g010660.1	SGT1 protein (AHRD V1 ***- D3	CDS	NONSYNC	G	D	415	0.671	17	novel	TOLERATED	
11	3709151	T	G	Solyc11	Solyc11g010660.1	SGT1 protein (AHRD V1 ***- D3	CDS	NONSYNC	I	L	404	1	17	novel	TOLERATED	
11	3710253	G	C	Solyc11	Solyc11g010660.1	SGT1 protein (AHRD V1 ***- D3	CDS	NONSYNC	D	E	326	1	19	novel	TOLERATED	
11	3710633	T	C	Solyc11	Solyc11g010660.1	SGT1 protein (AHRD V1 ***- D3	CDS	NONSYNC	N	D	200	0.108	21	novel	TOLERATED	
11	3736357	T	TTGA	Solyc11	Solyc11g010700.1	Receptor-like protein kinase (AHRI	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA	
11	3760343	T	C	Solyc11	Solyc11g010710.1	AP2-like ethylene-responsive transc	CDS	NONSYNC	V	A	239	0.844	18	novel	TOLERATED	
11	3776249	G	A	Solyc11	Solyc11g010730.1	Receptor-like kinase (AHRD V1 **	CDS	NONSYNC	P	L	192	0.335	28	novel	TOLERATED	
11	3791580	T	C	Solyc11	Solyc11g010750.1	UDP-glucosyltransferase (AHRD V	CDS	STOP-LOS	*	Q	126	NA	NA	novel	NA	
11	3795173	T	G	Solyc11	Solyc11g010760.1	UDP-glucosyltransferase (AHRD V	CDS	NONSYNC	L	R	37	0.361	36	novel	TOLERATED	
11	3800051	T	C	Solyc11	Solyc11g010770.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	N	D	17	NA	NA	novel	NA	

11	3800082	G	T	Solyc11	Solyc11g010770.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	L	6	NA	NA	novel	NA
11	3804473	TCA	T	Solyc11	Solyc11g010790.1	Glucosyltransferase (AHRD V1 **-	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	3804476	TTTCC	T	Solyc11	Solyc11g010790.1	Glucosyltransferase (AHRD V1 **-	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	3804502	C	T	Solyc11	Solyc11g010790.1	Glucosyltransferase (AHRD V1 **-	CDS	NONSYNC	L	F	50	0.007	36	novel	DELETERIOUS
11	3853517	C	T	Solyc11	Solyc11g010830.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	T	115	NA	NA	novel	NA
11	3860802	C	G	Solyc11	Solyc11g010840.1	Poly(RC) binding protein 3 (AHRD	CDS	NONSYNC	R	G	530	0.562	9	novel	TOLERATED
11	3890262	G	A	Solyc11	Solyc11g010860.1	RING-finger protein like (AHRD V	CDS	NONSYNC	D	N	25	0.594	2	novel	TOLERATED
11	3959731	C	T	Solyc11	Solyc11g010900.1	RRNA methyltransferase (AHRD V	CDS	NONSYNC	D	N	334	0.424	4	novel	TOLERATED
11	3959808	G	A	Solyc11	Solyc11g010900.1	RRNA methyltransferase (AHRD V	CDS	NONSYNC	T	I	308	0.195	26	novel	TOLERATED
11	3959820	T	C	Solyc11	Solyc11g010900.1	RRNA methyltransferase (AHRD V	CDS	NONSYNC	N	S	304	1	26	novel	TOLERATED
11	3959836	C	T	Solyc11	Solyc11g010900.1	RRNA methyltransferase (AHRD V	CDS	NONSYNC	A	T	299	0.672	26	novel	TOLERATED
11	3959894	A	C	Solyc11	Solyc11g010900.1	RRNA methyltransferase (AHRD V	CDS	NONSYNC	S	R	279	0.514	24	novel	TOLERATED
11	3959914	C	T	Solyc11	Solyc11g010900.1	RRNA methyltransferase (AHRD V	CDS	NONSYNC	A	T	273	0.038	22	novel	DELETERIOUS
11	3959919	T	C	Solyc11	Solyc11g010900.1	RRNA methyltransferase (AHRD V	CDS	NONSYNC	D	G	271	0.428	21	novel	TOLERATED
11	3959959	TTAC	T	Solyc11	Solyc11g010900.1	RRNA methyltransferase (AHRD V	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
11	3963216	G	T	Solyc11	Solyc11g010910.1	WD repeat protein (AHRD V1 ***	CDS	NONSYNC	A	D	356	0.437	20	novel	TOLERATED
11	3963217	C	T	Solyc11	Solyc11g010910.1	WD repeat protein (AHRD V1 ***	CDS	NONSYNC	A	T	356	0.584	20	novel	TOLERATED
11	3966451	C	T	Solyc11	Solyc11g010910.1	WD repeat protein (AHRD V1 ***	CDS	NONSYNC	M	I	144	0.2	15	novel	TOLERATED
11	3966561	A	G	Solyc11	Solyc11g010910.1	WD repeat protein (AHRD V1 ***	CDS	NONSYNC	F	L	108	0.735	19	novel	TOLERATED
11	3970802	T	C	Solyc11	Solyc11g010920.1	Kinesin (AHRD V1 *-*- A6YTD6_	CDS	NONSYNC	I	T	15	NA	NA	novel	NA
11	3971123	T	C	Solyc11	Solyc11g010920.1	Kinesin (AHRD V1 *-*- A6YTD6_	CDS	NONSYNC	V	A	77	0.687	11	novel	TOLERATED
11	3971138	A	T	Solyc11	Solyc11g010920.1	Kinesin (AHRD V1 *-*- A6YTD6_	CDS	NONSYNC	K	I	82	0.078	9	novel	TOLERATED
11	3974043	A	T	Solyc11	Solyc11g010920.1	Kinesin (AHRD V1 *-*- A6YTD6_	CDS	NONSYNC	K	I	390	0.193	36	novel	TOLERATED
11	3977092	C	G	Solyc11	Solyc11g010920.1	Kinesin (AHRD V1 *-*- A6YTD6_	CDS	NONSYNC	D	E	960	1	22	novel	TOLERATED
11	3980600	T	A	Solyc11	Solyc11g010930.1	HVA22-like protein e (AHRD V1 '	CDS	NONSYNC	H	Q	30	1	17	novel	TOLERATED
11	3987754	T	A	Solyc11	Solyc11g010940.1	Dof zinc finger protein 6 (AHRD V	CDS	NONSYNC	Q	H	363	0.251	10	novel	TOLERATED
11	3987787	A	T	Solyc11	Solyc11g010940.1	Dof zinc finger protein 6 (AHRD V	CDS	NONSYNC	D	E	352	0.681	6	novel	TOLERATED
11	3987834	G	T	Solyc11	Solyc11g010940.1	Dof zinc finger protein 6 (AHRD V	CDS	NONSYNC	H	N	337	0.985	10	novel	TOLERATED
11	3987846	A	G	Solyc11	Solyc11g010940.1	Dof zinc finger protein 6 (AHRD V	CDS	NONSYNC	S	P	333	0.323	12	novel	TOLERATED
11	4036451	T	A	Solyc11	Solyc11g011000.1	Cysteine-rich repeat secretory prote	CDS	NONSYNC	H	Q	244	0.181	20	novel	TOLERATED
11	4162754	T	C	Solyc11	Solyc11g011080.1	Tir-nbs-lrr, resistance protein	CDS	NONSYNC	Y	C	904	0.204	13	novel	TOLERATED
11	4166988	C	CTT	Solyc11	Solyc11g011080.1	Tir-nbs-lrr, resistance protein	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	4170926	T	C	Solyc11	Solyc11g011090.1	Tir-nbs-lrr, resistance protein	CDS	NONSYNC	T	A	2789	NA	NA	novel	NA
11	4180193	T	C	Solyc11	Solyc11g011090.1	Tir-nbs-lrr, resistance protein	CDS	NONSYNC	I	V	595	0.009	6	novel	DELETERIOUS
11	4180231	G	T	Solyc11	Solyc11g011090.1	Tir-nbs-lrr, resistance protein	CDS	NONSYNC	S	Y	582	0.14	12	novel	TOLERATED
11	4180252	A	C	Solyc11	Solyc11g011090.1	Tir-nbs-lrr, resistance protein	CDS	NONSYNC	F	C	575	0.012	12	novel	DELETERIOUS
11	4225683	G	A	Solyc11	Solyc11g011150.1	DNA repair protein Rad4 family (A	CDS	NONSYNC	S	N	16	NA	NA	novel	NA
11	4246502	A	T	Solyc11	Solyc11g011180.1	LRR receptor-like serine/threonine-	CDS	NONSYNC	Y	N	550	0.314	18	novel	TOLERATED
11	4264477	G	C	Solyc11	Solyc11g011210.1	Gibberellin regulated protein (AHR	CDS	NONSYNC	T	R	36	0.497	67	novel	TOLERATED
11	4270887	G	A	Solyc11	Solyc11g011220.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	V	479	1	17	novel	TOLERATED
11	4289863	G	A	Solyc11	Solyc11g011240.1	Geranylgeranyl pyrophosphate synt	CDS	NONSYNC	V	I	174	0.079	165	novel	TOLERATED
11	4290097	G	T	Solyc11	Solyc11g011240.1	Geranylgeranyl pyrophosphate synt	CDS	NONSYNC	A	S	252	0.041	165	novel	DELETERIOUS
11	4294802	C	T	Solyc11	Solyc11g011250.1	Chloride intracellular channel 6 (AI	CDS	NONSYNC	V	I	154	0.331	83	novel	TOLERATED
11	4294838	T	C	Solyc11	Solyc11g011250.1	Chloride intracellular channel 6 (AI	CDS	NONSYNC	K	E	142	1	82	novel	TOLERATED
11	4322624	T	C	Solyc11	Solyc11g011270.1	Rhamnogalacturonate lyase (AHRD	CDS	NONSYNC	L	P	189	0.305	45	novel	TOLERATED
11	4343050	A	G	Solyc11	Solyc11g011300.1	Rhamnogalacturonate lyase (AHRD	CDS	NONSYNC	K	R	139	0.852	54	novel	TOLERATED
11	4362140	G	T	Solyc11	Solyc11g011310.1	Rhamnogalacturonate lyase (AHRD	CDS	STOP-GAI	E	*	651	NA	NA	novel	NA
11	4363751	T	A	Solyc11	Solyc11g011320.1	Rhamnogalacturonate lyase (AHRD	CDS	NONSYNC	L	M	5	0.143	3	novel	TOLERATED
11	4363836	A	G	Solyc11	Solyc11g011320.1	Rhamnogalacturonate lyase (AHRD	CDS	NONSYNC	D	G	33	0.418	10	novel	TOLERATED
11	4363976	T	A	Solyc11	Solyc11g011320.1	Rhamnogalacturonate lyase (AHRD	CDS	NONSYNC	N	K	42	0.958	12	novel	TOLERATED
11	4487490	T	C	Solyc11	Solyc11g011420.1	Peptidyl-prolyl cis-trans isomerase (	CDS	NONSYNC	W	R	161	0.354	8	novel	TOLERATED
11	4515569	G	A	Solyc11	Solyc11g011460.1	ATP-dependent RNA helicase (AH	CDS	NONSYNC	R	H	121	0.041	8	novel	DELETERIOUS
11	4555916	C	G	Solyc11	Solyc11g011500.1	Potassium channel (AHRD V1 ***	CDS	NONSYNC	T	S	799	0.955	10	novel	TOLERATED
11	4595077	T	C	Solyc11	Solyc11g011540.1	F-box family protein (AHRD V1 **	CDS	NONSYNC	L	S	159	0.537	4	novel	TOLERATED
11	5123892	G	A	Solyc11	Solyc11g012220.1	Wax synthase isoform 3 (AHRD V	CDS	NONSYNC	G	E	106	0.23	22	novel	TOLERATED
11	6846198	TG	T	Solyc11	Solyc11g013610.1	Zinc finger family protein (AHRD '	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	8243528	T	C	Solyc11	Solyc11g017370.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	N	D	172	0.423	11	novel	TOLERATED
11	9667082	C	CA	Solyc11	Solyc11g018830.1	Ulp1 protease family C-terminal ca	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	9995381	A	T	Solyc11	Solyc11g020000.1	GCN5-related N-acetyltransferase (	CDS	NONSYNC	L	I	171	0.067	9	novel	TOLERATED
11	9995382	T	A	Solyc11	Solyc11g020000.1	GCN5-related N-acetyltransferase (	CDS	NONSYNC	K	N	170	0.08	9	novel	TOLERATED
11	10004129	T	C	Solyc11	Solyc11g020020.1	Serine/threonine-protein phosphata	CDS	NONSYNC	I	V	606	NA	NA	novel	NA
11	10005310	C	T	Solyc11	Solyc11g020020.1	Serine/threonine-protein phosphata	CDS	NONSYNC	G	D	305	0.226	9	novel	TOLERATED
11	10007087	T	A	Solyc11	Solyc11g020030.1	Lysyl-tRNA synthetase (AHRD V1	CDS	NONSYNC	Y	N	61	0.413	38	novel	TOLERATED
11	10007116	T	G	Solyc11	Solyc11g020030.1	Lysyl-tRNA synthetase (AHRD V1	CDS	NONSYNC	N	K	70	1	38	novel	TOLERATED
11	10007183	G	C	Solyc11	Solyc11g020030.1	Lysyl-tRNA synthetase (AHRD V1	CDS	NONSYNC	D	H	93	0.012	17	novel	DELETERIOUS
11	11416182	C	CTTT	Solyc11	Solyc11g020550.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
11	15224056	A	G	Solyc11	Solyc11g027640.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	H	R	29	NA	NA	novel	NA
11	15224065	C	T	Solyc11	Solyc11g027640.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	S	F	32	NA	NA	novel	NA
11	15224069	T	A	Solyc11	Solyc11g027640.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	D	E	33	NA	NA	novel	NA
11	15224085	T	C	Solyc11	Solyc11g027640.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	L	39	NA	NA	novel	NA
11	15224101	C	T	Solyc11	Solyc11g027640.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	P	L	44	NA	NA	novel	NA
11	15224106	C	G	Solyc11	Solyc11g027640.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	Q	E	46	NA	NA	novel	NA
11	15224116	A	G	Solyc11	Solyc11g027640.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	K	R	49	NA	NA	novel	NA
11	15224133	T	A	Solyc11	Solyc11g027640.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	S	T	55	NA	NA	novel	NA
11	15233232	T	C	Solyc11	Solyc11g027650.1	Unknown Protein (AHRD V1)	CDS	STOP-LOS	*	Q	27	NA	NA	novel	NA
11	17022006	A	G	Solyc11	Solyc11g028140.1	Ycf2 (AHRD V1 ***- D2KLP5_O	CDS	NONSYNC	N	D	164	1	33	novel	TOLERATED
11	36000551	C	A	Solyc11	Solyc11g044660.1	Unknown Protein (AHRD V1)	CDS	STOP-GAI	S	*	10	NA	NA	novel	NA
11	42531892	G	GA	Solyc11	Solyc11g051130.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	42966229	C	T	Solyc11	Solyc11g051210.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	A	T	17	NA	NA	novel	NA
11	43032718	G	A	Solyc11	Solyc11g051240.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	C	Y	28	NA	NA	novel	NA
11	43032756	C	T	Solyc11	Solyc11g051240.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	P	S	41	NA	NA	novel	NA
11	43032771	G	T	Solyc11	Solyc11g051240.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	V	F	46	NA	NA	novel	NA
11	43091357	T	G	Solyc11	Solyc11g056290.1	Orf185 protein (AHRD V1 *-*- Q5	CDS	NONSYNC	N	T	75	NA	NA	novel	NA
11	43819503	G	A	Solyc11	Solyc11g056570.1	Gag-pol (AHRD V1 **-- Q8W1D1	CDS	NONSYNC	C	Y	26	0.06	20	novel	TOLERATED
11	45604165	G	T	Solyc11	Solyc11g061790.1	tRNA dimethylallyltransferase (AH	CDS	NONSYNC	E	D	19	0.007	60	novel	DELETERIOUS
11	46945024	T	C	Solyc11	Solyc11g063750.1	Pol polyprotein (AHRD V1 ***- P	CDS	NONSYNC	K	E	38	0.002	74	novel	DELETERIOUS
11	48601969	C	A	Solyc11	Solyc11g065930.1	Xanthine dehydrogenase/oxidase (A	CDS	NONSYNC	A	S	1044	0.018	117	novel	DELETERIOUS
11	48741693	A	G	Solyc11	Solyc11g066020.1	Ankyrin repeat domain-containing p	CDS	NONSYNC	L	S	251	0.839	30	novel	TOLERATED
11	48826912	G	GTT	Solyc11	Solyc11g066060.1	heat shock protein (AHRD V1 ***-	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	48932349	A	T	Solyc11	Solyc11g066150.1	Bifunctional polymyxin resistance p	CDS	NONSYNC	T	S	5	0.555	19	novel	TOLERATED
11	49084831	G	T	Solyc11	Solyc11g066270.1	Xyloglucan endotransglucosylase/h	CDS	NONSYNC	A	S	20	0.443	37	novel	TOLERATED
11	49616531	T	C	Solyc11	Solyc11g066730.1	Phototropic-responsive NPH3 fami	CDS	NONSYNC	F	S	368	0.921	42	novel	TOLERATED
11	49620574	G	T	Solyc11	Solyc11g066740.1	Os12g0283800 protein (Fragment)	CDS	NONSYNC	G	C	28	0.182	4	novel	TOLERATED
11	49630985	C	CTT	Solyc11	Solyc11g066750.1	AP-2 complex subunit alpha-1 (AH	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	49742938	C	CCTT	Solyc11	Solyc11g066860.1	Os02g0448600 protein (Fragment)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
11	50421478	C	CT	Solyc11	Solyc11g068700.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	50421487	C	CA	Solyc11	Solyc11g068700.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	50436090	ATTT	A	Solyc11	Solyc11g068720.1	Os04g0625000 protein (Fragment)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
11	50436096	T	A	Solyc11	Solyc11g068720.1	Os04g0625000 protein (Fragment)	CDS	STOP-GAI	L	*	120	NA	NA	novel	NA
11	50530440	C	CA	Solyc11	Solyc11g068850.1	Mutator-like transposase (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
11	51073674	C	T	Solyc11	Solyc11g069400.1	Protein disulfide isomerase L-2 (AI	CDS	NONSYNC	E	K	500	0	31	novel	DELETERIOUS
11	51211468	G	A	Solyc11	Solyc11g069510.1	GATA transcription factor 9 (AHR	CDS	NONSYNC	P	L	50	0.592	10	novel	TOLERATED
11	51486216	T	C	Solyc11	Solyc11g069770.1	Transcription factor MADS-box (A	CDS	NONSYNC	V	A	83	0.819	25	novel	TOLERATED
11	51643904	C	T	Solyc11	Solyc11g069960.1	Receptor like kinase, RLK	CDS	NONSYNC	G	S	573	1	25	novel	TOLERATED
11	51994401	G	T	Solyc11	Solyc11g071430.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	V	L	215	1	116	novel	TOLERATED
11	52016706	C	G	Solyc11	Solyc11g071480.1	Hydroxycinnamoyl CoA shikimate/c	CDS	NONSYNC	S	T	331	0.032	32	novel	DELETERIOUS
11	52117002	A	G	Solyc11	Solyc11g071610.1	Xanthine dehydrogenase/oxidase (A	CDS	NONSYNC	K	E	1085	0.837	69	novel	TOLERATED
11	52126602	G	A	Solyc11	Solyc11g071620.1	Aldehyde oxidase (AHRD V1 ***-	CDS	NONSYNC	A	T	135	0.231	51	novel	TOLERATED
11	52158083	A	G	Solyc11	Solyc11g071670.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	N	S	119	1	7	novel	TOLERATED
11	52171275	T	C	Solyc11	Solyc11g071680.1	Serine/threonine protein kinase (AI	CDS	NONSYNC	D	G	157	0.402	33	novel	TOLERATED
11	52171296	T	G	Solyc11	Solyc11g071680.1	Serine/threonine protein kinase (AI	CDS	NONSYNC	Q	P	150	0.21	32	novel	TOLERATED
11	52178883	G	C	Solyc11	Solyc11g071690.1	Cellular nucleic acid binding protei	CDS	NONSYNC	Q	E	151	1	12	novel	TOLERATED
11	52187330	T	G	Solyc11	Solyc11g071700.1	Ubiquitin carboxyl-terminal hydrol	CDS	NONSYNC	M	R	187	0.033	43	novel	DELETERIOUS
11	52204819	G	A	Solyc11	Solyc11g071710.1	DnaJ-like zinc-finger protein (AHR	CDS	NONSYNC	R	H	7	0.6	5	novel	TOLERATED
11	52207994	C	T	Solyc11	Solyc11g071720.1	Acetyl esterase (AHRD V1 *--- AE	CDS	NONSYNC	S	L	67	0.243	54	novel	TOLERATED
11	52209265	C	G	Solyc11	Solyc11g071720.1	Acetyl esterase (AHRD V1 *--- AE	CDS	NONSYNC	Q	E	293	1	53	novel	TOLERATED
11	52211394	G	A	Solyc11	Solyc11g071730.1	Kinesin-like protein (AHRD V1 **	CDS	NONSYNC	S	N	93	0.495	17	novel	TOLERATED

11	53109957	T	A	Solyc11	Solyc11g072840.1	Histone H4 (AHRD V1 ***- B6T0	CDS	NONSYNC	L	F	101	1	97	novel	TOLERATED
12	617842	C	T	Solyc12	Solyc12g006000.1	Clathrin assembly protein-like (AH	CDS	NONSYNC	H	Y	598	0.34	4	novel	TOLERATED
12	633529	G	T	Solyc12	Solyc12g006040.1	Nbs, resistance protein fragment	CDS	NONSYNC	T	K	306	NA	NA	novel	NA
12	1874787	G	A	Solyc12	Solyc12g008450.1	tRNA A64-2&apos-O-ribosylphosp	CDS	NONSYNC	T	I	9	1	15	novel	TOLERATED
12	2143881	C	CA	Solyc12	Solyc12g008800.1	MYB transcription factor (AHRD V	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	2240629	GA	G	Solyc12	Solyc12g008920.1	Cytokinin oxidase/dehydrogenase 2	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	3893530	TA	T	Solyc12	Solyc12g011030.1	Xyloglucan endotransglucosylase/h	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	4582132	T	C	Solyc12	Solyc12g013760.1	Mannan endo-1,4-beta-mannosidas	CDS	NONSYNC	E	G	19	1	7	novel	TOLERATED
12	4582307	CG	C	Solyc12	Solyc12g013770.1	Mannan endo-1 4-beta-mannosidas	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	6469768	A	G	Solyc12	Solyc12g017270.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	K	E	48	NA	NA	novel	NA
12	7382657	C	A	Solyc12	Solyc12g017790.1	Protein kinase-like protein (AHRD	CDS	NONSYNC	L	I	99	0.321	3	novel	TOLERATED
12	7382664	T	G	Solyc12	Solyc12g017790.1	Protein kinase-like protein (AHRD	CDS	NONSYNC	F	C	101	0.025	3	novel	DELETERIOUS
12	8579658	G	A	Solyc12	Solyc12g017930.1	Gag polyprotein (Fragment) (AHRI	CDS	NONSYNC	V	M	61	0	2	novel	DELETERIOUS
12	8984821	A	AAG	Solyc12	Solyc12g019020.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	9890482	T	C	Solyc12	Solyc12g019270.1	Ulp1 protease family C-terminal cat	CDS	NONSYNC	K	E	308	NA	NA	novel	NA
12	10206480	T	C	Solyc12	Solyc12g019410.1	Kinase family protein (AHRD V1 *	CDS	NONSYNC	K	E	2	0.164	4	novel	TOLERATED
12	10870687	A	T	Solyc12	Solyc12g019610.1	Os12g0616000 protein (Fragment)	CDS	STOP-GAI	L	*	12	NA	NA	novel	NA
12	11183524	G	C	Solyc12	Solyc12g019720.1	Mutator-like transposase (AHRD V	CDS	NONSYNC	D	H	254	0.26	3	novel	TOLERATED
12	11667067	G	T	Solyc12	Solyc12g019780.1	TNP2 (AHRD V1 *--- C7FDI5_SC	CDS	NONSYNC	V	L	42	0.315	13	novel	TOLERATED
12	14814904	A	C	Solyc12	Solyc12g021210.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	F	L	102	NA	NA	novel	NA
12	14815037	C	G	Solyc12	Solyc12g021210.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	G	A	58	NA	NA	novel	NA
12	16711959	C	G	Solyc12	Solyc12g026430.1	Nucleobase ascorbate transporter (A	CDS	NONSYNC	T	S	154	1	68	novel	TOLERATED
12	26641917	CT	C	Solyc12	Solyc12g035570.1	Unknown Protein (AHRD V1)	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	29008534	A	G	Solyc12	Solyc12g035840.1	50S ribosomal protein L2 chloropla	CDS	NONSYNC	K	E	255	0.126	89	novel	TOLERATED
12	30594998	C	CA	Solyc12	Solyc12g036270.1	Ulp1 protease family C-terminal cat	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	36012474	A	AGTGC	Solyc12	Solyc12g038560.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
12	36012992	T	TAACA	Solyc12	Solyc12g038560.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
12	36013030	G	GCAA	Solyc12	Solyc12g038560.1	Unknown Protein (AHRD V1)	CDS	NONFRAN	NA	NA	NA	NA	NA	NA	NA
12	38476760	G	A	Solyc12	Solyc12g040250.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	T	I	85	0.804	2	novel	TOLERATED
12	42858920	C	CA	Solyc12	Solyc12g042260.1	Low affinity nitrate transporter (AH	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	43657311	T	C	Solyc12	Solyc12g042790.1	Zinc finger RING-type Zinc finger (	CDS	NONSYNC	D	G	82	NA	NA	novel	NA
12	44401072	C	A	Solyc12	Solyc12g044180.1	Cc-nbs-lrr, resistance protein	CDS	NONSYNC	S	I	128	0	3	novel	DELETERIOUS
12	44502600	T	G	Solyc12	Solyc12g044210.1	Pol polyprotein (AHRD V1 ***- P(	CDS	NONSYNC	S	A	125	0.614	399	novel	TOLERATED
12	44717835	A	T	Solyc12	Solyc12g044340.1	Coiled-coil domain-containing prot	CDS	NONSYNC	M	K	210	0.006	17	novel	DELETERIOUS
12	44729692	GA	G	Solyc12	Solyc12g044370.1	Ribonuclease Z (AHRD V1 ***- B	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	44729723	CA	C	Solyc12	Solyc12g044370.1	Ribonuclease Z (AHRD V1 ***- B	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	45732949	A	G	Solyc12	Solyc12g044930.1	F-box protein PP2-B1 (AHRD V1 '	CDS	NONSYNC	I	V	205	0.635	26	novel	TOLERATED
12	45946440	C	A	Solyc12	Solyc12g049080.1	Extensin-like protein Ext1 (AHRD	CDS	NONSYNC	P	H	116	0.002	19	novel	DELETERIOUS
12	46034662	G	A	Solyc12	Solyc12g049170.1	Extensin-like protein Ext1 (AHRD	CDS	NONSYNC	P	S	238	0.108	17	novel	TOLERATED
12	46233697	G	A	Solyc12	Solyc12g049300.1	MYB transcription factor (AHRD V	CDS	NONSYNC	S	N	269	0.41	8	novel	TOLERATED
12	48391257	A	AT	Solyc12	Solyc12g056950.1	Genomic DNA chromosome 5 TAC	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	49333582	T	A	Solyc12	Solyc12g062220.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	C	S	152	1	9	novel	TOLERATED
12	49721935	C	T	Solyc12	Solyc12g062300.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	T	M	93	0.01	4	novel	DELETERIOUS
12	51107560	AAT	A	Solyc12	Solyc12g062470.1	Ycf2 (AHRD V1 ***- C0LEB7_9I	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	51461438	C	G	Solyc12	Solyc12g062510.1	ATPase (AHRD V1 ***- C0SAL8_	CDS	NONSYNC	S	C	140	0.035	40	novel	DELETERIOUS
12	51808276	T	G	Solyc12	Solyc12g062610.1	Photosystem I P700 chlorophyll a a	CDS	NONSYNC	H	Q	102	1	66	novel	TOLERATED
12	52335720	A	G	Solyc12	Solyc12g062720.1	Pentatricopeptide repeat-containing	CDS	NONSYNC	I	V	337	1	14	novel	TOLERATED
12	52342157	G	T	Solyc12	Solyc12g062730.1	Glutathione S-transferase 12 (AHR	CDS	STOP-GAI	Y	*	69	NA	NA	novel	NA
12	52603882	TTC	T	Solyc12	Solyc12g062790.1	Histidine decarboxylase (AHRD V1	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	53957232	G	A	Solyc12	Solyc12g062950.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	V	I	268	0.285	15	novel	TOLERATED
12	53972101	A	G	Solyc12	Solyc12g062960.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	I	V	121	0.617	10	novel	TOLERATED
12	53974233	A	G	Solyc12	Solyc12g062960.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	I	V	338	1	17	novel	TOLERATED
12	53977641	C	CA	Solyc12	Solyc12g062970.1	Unknown Protein (AHRD V1); con	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	53977760	A	G	Solyc12	Solyc12g062970.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	V	A	155	0.03	4	novel	DELETERIOUS
12	54013147	G	A	Solyc12	Solyc12g063000.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	T	I	1791	0.075	21	novel	TOLERATED
12	54013669	G	A	Solyc12	Solyc12g063000.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	A	V	1654	0.186	10	novel	TOLERATED
12	54022346	T	C	Solyc12	Solyc12g063000.1	Unknown Protein (AHRD V1); con	CDS	NONSYNC	I	V	551	0.517	10	novel	TOLERATED
12	55632551	T	C	Solyc12	Solyc12g076310.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	R	G	123	NA	NA	novel	NA
12	56803399	A	T	Solyc12	Solyc12g077350.1	Unknown Protein (AHRD V1)	CDS	NONSYNC	H	L	60	NA	NA	novel	NA
12	57631262	A	G	Solyc12	Solyc12g077490.1	Retroelement pol polyprotein-like (	CDS	STOP-LOS	*	Q	56	NA	NA	novel	NA
12	61744199	C	T	Solyc12	Solyc12g087800.1	Pol polyprotein (AHRD V1 ***- Q	CDS	NONSYNC	T	I	186	0.168	161	novel	TOLERATED
12	62742835	A	AT	Solyc12	Solyc12g089180.1	Glucose transporter 8 (AHRD V1 *	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	62928355	T	C	Solyc12	Solyc12g089360.1	Peroxidase (AHRD V1 ***- B9GQ	CDS	NONSYNC	I	V	103	0.304	52	novel	TOLERATED
12	62930279	T	A	Solyc12	Solyc12g089370.1	Peroxidase (AHRD V1 ***- B9GQ	CDS	NONSYNC	M	L	297	0.026	48	novel	DELETERIOUS
12	63031265	T	C	Solyc12	Solyc12g094470.1	Laccase-2 (AHRD V1 **-- LAC2_	CDS	NONSYNC	F	L	123	0.038	121	novel	DELETERIOUS
12	63086647	G	GCTTT	Solyc12	Solyc12g094540.1	3&apos-5&apos exonuclease (AHF	CDS	FRAMESH	NA	NA	NA	NA	NA	NA	NA
12	63087556	G	A	Solyc12	Solyc12g094550.1	AT1G76250-like protein (Fragmen	CDS	NONSYNC	R	C	306	0.03	15	novel	DELETERIOUS
12	63097327	T	A	Solyc12	Solyc12g094560.1	Ubiquitin-protein ligase (AHRD V	CDS	NONSYNC	S	C	750	0.096	11	novel	TOLERATED
12	63117387	T	A	Solyc12	Solyc12g094600.1	Cyclin B (AHRD V1 **** B6V74(	CDS	NONSYNC	Y	F	111	0.704	36	novel	TOLERATED
12	63117855	C	T	Solyc12	Solyc12g094600.1	Cyclin B (AHRD V1 **** B6V74(	CDS	NONSYNC	R	H	46	0.141	30	novel	TOLERATED
12	63124461	G	A	Solyc12	Solyc12g094610.1	U-box domain-containing protein 1	CDS	NONSYNC	A	T	496	0.413	60	novel	TOLERATED
12	63182533	A	G	Solyc12	Solyc12g094690.1	Ring finger protein (AHRD V1 ***	CDS	NONSYNC	Q	R	93	0.518	40	novel	TOLERATED
12	63330233	T	C	Solyc12	Solyc12g095880.1	Phosphofructokinase family protein	CDS	NONSYNC	D	G	207	1	94	novel	TOLERATED
12	63449872	T	C	Solyc12	Solyc12g096030.1	Mitochondrial carrier-like protein (.	CDS	NONSYNC	V	A	149	0.142	52	novel	TOLERATED

Table 6.3. List of candidate genes associated with high shelf life trait in *Nps1* , identified through MutMap approach.

The probable candidate genes responsible for the high shelf life phenotype in F_3 segregated lines (obtained from (AC♀x*Nps1*♂ cross) were identified by MutMap approach. The list of SNPs that result in changes in aminoacid sequence (non-synonymous SNPs) and only present in coding sequences are given below-

CHRO	POSIT	REFE	ALTE	TRANS	GENE_ID	GENE_NAME	REGION	VARIANT	REFE	ALTE	AMINO	SIFT_SCORE	NUMBER OF SEQUENCES	dbSNP	SIFT_PREDICTION
0	1E+07	A	G	Solyc00	Solyc00g027120.1	Mutator-like transposase	CDS	NONSYNO!	N	D	155	0.69	2	novel	TOLERATED
0	2E+07	A	C	Solyc00	Solyc00g147570.2	Gelsolin (Fragment) (AI	CDS	NONSYNO!	I	S	165	0.119	20	novel	TOLERATED
0	2E+07	C	T	Solyc00	Solyc00g166490.1	Ulp1 protease family C-t	CDS	NONSYNO!	P	L	125	NA	NA	novel	NA
1	7E+07	G	C	Solyc01	Solyc01g068320.1	DNA repair protein (AH	CDS	NONSYNO!	A	G	269	0.484	9	novel	TOLERATED
1	7E+07	C	T	Solyc01	Solyc01g068320.1	DNA repair protein (AH	CDS	NONSYNO!	V	I	186	1	8	novel	TOLERATED
1	7E+07	T	G	Solyc01	Solyc01g068320.1	DNA repair protein (AH	CDS	NONSYNO!	I	L	168	0.05	8	novel	TOLERATED
1	9E+07	G	A	Solyc01	Solyc01g106660.1	Ulp1 protease family C-t	CDS	NONSYNO!	D	N	244	0	2	novel	DELETERIOUS
1	9E+07	C	T	Solyc01	Solyc01g106660.1	Ulp1 protease family C-t	CDS	NONSYNO!	P	L	287	0	2	novel	DELETERIOUS
1	9E+07	A	G	Solyc01	Solyc01g110470.2	GAGA-binding transcrip	CDS	NONSYNO!	D	G	34	0.01	16	novel	DELETERIOUS
2	2E+07	T	A	Solyc02	Solyc02g038750.2	WD repeat-containing pr	CDS	NONSYNO!	H	L	137	0.016	21	novel	DELETERIOUS
2	3E+07	T	A	Solyc02	Solyc02g062310.1	BURP domain-containin	CDS	NONSYNO!	F	L	93	0.308	28	novel	TOLERATED
2	3E+07	A	C	Solyc02	Solyc02g062310.1	BURP domain-containin	CDS	NONSYNO!	N	T	95	0.011	28	novel	DELETERIOUS
2	3E+07	T	A	Solyc02	Solyc02g062310.1	BURP domain-containin	CDS	NONSYNO!	N	K	95	0.014	28	novel	DELETERIOUS
2	3E+07	C	G	Solyc02	Solyc02g068780.2	Genomic DNA chromos	CDS	NONSYNO!	L	V	792	NA	NA	novel	NA
2	3E+07	A	T	Solyc02	Solyc02g068780.2	Genomic DNA chromos	CDS	NONSYNO!	T	S	796	NA	NA	novel	NA
2	4E+07	C	T	Solyc02	Solyc02g086460.2	Unknown Protein (AHR	CDS	NONSYNO!	P	S	1464	0.123	17	novel	TOLERATED
2	4E+07	C	A	Solyc02	Solyc02g086460.2	Unknown Protein (AHR	CDS	NONSYNO!	T	K	1465	0.161	17	novel	TOLERATED
2	5E+07	A	G	Solyc02	Solyc02g091060.1	Unknown Protein (AHR	CDS	NONSYNO!	V	A	64	NA	NA	novel	NA
2	5E+07	G	T	Solyc02	Solyc02g091060.1	Unknown Protein (AHR	CDS	STOP-GAIN	C	*	55	NA	NA	novel	NA
3	6E+07	G	T	Solyc03	Solyc03g111460.1	Nuclear transcription fac	CDS	STOP-GAIN	S	*	77	NA	NA	novel	NA
4	6E+07	A	G	Solyc04	Solyc04g082120.2	Prolyl endopeptidase (AI	CDS	NONSYNO!	K	E	167	1	100	novel	TOLERATED
6	1E+06	C	A	Solyc06	Solyc06g007130.2	Omega-3 fatty acid desat	CDS	NONSYNO!	V	F	217	0.111	148	novel	TOLERATED
6	2E+07	C	T	Solyc06	Solyc06g032760.1	Unknown Protein (AHR	CDS	NONSYNO!	M	I	62	NA	NA	novel	NA
6	4E+07	A	G	Solyc06	Solyc06g065090.1	Mutator-like transposase	CDS	NONSYNO!	Y	H	89	0.649	2	novel	TOLERATED
6	4E+07	G	T	Solyc06	Solyc06g065090.1	Mutator-like transposase	CDS	NONSYNO!	L	I	70	0	2	novel	DELETERIOUS
7	92290	T	C	Solyc07	Solyc07g005040.2	H-ATPase (AHRD V1 *	CDS	NONSYNO!	E	G	46	NA	NA	novel	NA
7	92294	G	T	Solyc07	Solyc07g005040.2	H-ATPase (AHRD V1 *	CDS	NONSYNO!	L	I	45	NA	NA	novel	NA
7	5E+07	A	C	Solyc07	Solyc07g042120.1	Serine/threonine-protein	CDS	NONSYNO!	I	S	149	0.02	2	novel	DELETERIOUS
7	5E+07	T	A	Solyc07	Solyc07g042120.1	Serine/threonine-protein	CDS	NONSYNO!	E	D	103	0.342	2	novel	TOLERATED
7	6E+07	A	G	Solyc07	Solyc07g051900.1	Unknown Protein (AHR	CDS	NONSYNO!	T	A	88	0.004	76	novel	DELETERIOUS
7	6E+07	T	C	Solyc07	Solyc07g054990.1	Unknown Protein (AHR	CDS	NONSYNO!	K	E	74	0.439	8	novel	TOLERATED
7	6E+07	A	T	Solyc07	Solyc07g054990.1	Unknown Protein (AHR	CDS	NONSYNO!	I	N	72	0.47	8	novel	TOLERATED
8	3E+07	A	T	Solyc08	Solyc08g044260.2	CER1 (AHRD V1 **-- E	CDS	NONSYNO!	F	Y	449	1	47	novel	TOLERATED
8	5E+07	A	G	Solyc08	Solyc08g065280.1	Ulp1 protease family C-t	CDS	NONSYNO!	S	P	288	0.358	2	novel	TOLERATED
8	5E+07	G	A	Solyc08	Solyc08g067140.1	Unknown Protein (AHR	CDS	NONSYNO!	A	V	258	NA	NA	novel	NA
8	5E+07	G	T	Solyc08	Solyc08g067140.1	Unknown Protein (AHR	CDS	NONSYNO!	A	D	251	NA	NA	novel	NA
8	5E+07	C	T	Solyc08	Solyc08g067140.1	Unknown Protein (AHR	CDS	NONSYNO!	V	I	232	NA	NA	novel	NA
8	6E+07	A	G	Solyc08	Solyc08g075050.1	Pectinacetylesterase like	CDS	NONSYNO!	T	A	18	0.722	22	novel	TOLERATED
9	3E+06	C	T	Solyc09	Solyc09g009990.2	Transposon protein Mut	CDS	NONSYNO!	G	S	205	0.763	13	novel	TOLERATED
9	4E+07	G	T	Solyc09	Solyc09g056310.1	Maturase (Fragment) (A	CDS	STOP-GAIN	E	*	16	NA	NA	novel	NA
9	6E+07	T	C	Solyc09	Solyc09g075240.1	Ulp1 protease family C-t	CDS	NONSYNO!	F	S	7	NA	NA	novel	NA
10	4E+06	T	C	Solyc10	Solyc10g009620.1	GH3 family protein (AH	CDS	NONSYNO!	I	V	214	1	37	novel	TOLERATED
10	4E+06	G	A	Solyc10	Solyc10g009620.1	GH3 family protein (AH	CDS	NONSYNO!	R	C	211	0.242	36	novel	TOLERATED
10	2E+07	A	T	Solyc10	Solyc10g044440.1	Unknown Protein (AHR	CDS	NONSYNO!	N	K	42	NA	NA	novel	NA
10	6E+07	T	G	Solyc10	Solyc10g076530.1	Receptor-like protein kin	CDS	NONSYNO!	T	P	126	0.217	41	novel	TOLERATED
11	2E+07	C	A	Solyc11	Solyc11g030880.1	Maturase (Fragment) (A	CDS	NONSYNO!	H	N	79	0.002	105	novel	DELETERIOUS
11	4E+07	T	G	Solyc11	Solyc11g050910.1	Pol polyprotein (AHRD	CDS	NONSYNO!	E	D	234	0.21	312	novel	TOLERATED
11	5E+07	A	G	Solyc11	Solyc11g072210.1	Zinc finger protein-like (	CDS	NONSYNO!	N	S	278	0.759	8	novel	TOLERATED
11	5E+07	C	T	Solyc11	Solyc11g072210.1	Zinc finger protein-like (	CDS	NONSYNO!	A	V	283	0.201	9	novel	TOLERATED
12	2E+07	C	A	Solyc12	Solyc12g021300.1	HAT family dimerisatior	CDS	STOP-GAIN	C	*	10	NA	NA	novel	NA
12	3E+07	T	C	Solyc12	Solyc12g036910.1	Unknown Protein (AHR	CDS	NONSYNO!	W	R	92	NA	NA	novel	NA
12	5E+07	C	A	Solyc12	Solyc12g049080.1	Extensin-like protein Ext	CDS	NONSYNO!	P	H	116	0.002	19	novel	DELETERIOUS

Publications from thesis chapters

1. **Kilambi HV**, Manda K, Rai A, Charakana C, Bagri J, Sharma R, Sreelakshmi Y (**2017**) Green-fruited *Solanum habrochaites* lacks fruit-specific carotenogenesis due to blocks at multiple steps. MS ID: **JEXBOT**/2017/193870 (under final and minor revision).

2. **Kilambi HV**, Manda K, Sanivarapu H, Maurya VK, Sharma R, Sreelakshmi Y (**2016**) Shotgun Proteomics of Tomato Fruits: Evaluation, Optimization and Validation of Sample Preparation Methods and Mass Spectrometric Parameters **Front. Plant Sci**. **7:** 969. doi: 10.3389/fpls.2016.00969.

3. **Kilambi HV**, Kumar R, Sharma R, Sreelakshmi Y (**2013**) Chromoplast-specific carotenoid-associated protein appears to be important for enhanced accumulation of carotenoids in *hp1* tomato fruits. **Plant Physiol**. **161:** 2085-2101.

Other publications

1. Mohan V, Gupta S, Thomas S, Mickey H, Charakana C, Chauhan VS, Sharma K, Kumar R, Tyagi K, Sarma S, Gupta SK, **Kilambi HV**, Nongmaithem S, Kumari A, Gupta P, Sreelakshmi Y, Sharma R (**2016**) Tomato Fruits Show Wide Phenomic Diversity but Fruit Developmental Genes show low genomic diversity. **Plos One**. **11:** e0152907.

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3. Santisree P, Nongmaithem S, **Vasuki H**, Sreelakshmi Y, Ivanchenko MG, Sharma R (**2011**) Tomato root penetration in soil requires a coaction between ethylene and auxin signaling. **Plant Physiol**. **156:** 1424-1438.

frontiers in Plant Science

METHODS
published: 29 June 2016
doi: 10.3389/fpls.2016.00969

Shotgun Proteomics of Tomato Fruits: Evaluation, Optimization and Validation of Sample Preparation Methods and Mass Spectrometric Parameters

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Edited by:
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Specialty section:
This article was submitted to Plant Proteomics, a section of the journal Frontiers in Plant Science

Received: *04 May 2016*
Accepted: *17 June 2016*
Published: *29 June 2016*

Citation:
Kilambi HV, Manda K, Sanivarapu H, Maurya VK, Sharma R and Sreelakshmi Y (2016) Shotgun Proteomics of Tomato Fruits: Evaluation, Optimization and Validation of Sample Preparation Methods and Mass Spectrometric Parameters. Front. Plant Sci. 7:969. doi: 10.3389/fpls.2016.00969

An optimized protocol was developed for shotgun proteomics of tomato fruit, which is a recalcitrant tissue due to a high percentage of sugars and secondary metabolites. A number of protein extraction and fractionation techniques were examined for optimal protein extraction from tomato fruits followed by peptide separation on nanoLCMS. Of all evaluated extraction agents, buffer saturated phenol was the most efficient. In-gel digestion [SDS-PAGE followed by separation on LCMS (GeLCMS)] of phenol-extracted sample yielded a maximal number of proteins. For in-solution digested samples, fractionation by strong anion exchange chromatography (SAX) also gave similar high proteome coverage. For shotgun proteomic profiling, optimization of mass spectrometry parameters such as automatic gain control targets (5E+05 for MS, 1E+04 for MS/MS); ion injection times (500 ms for MS, 100 ms for MS/MS); resolution of 30,000; signal threshold of 500; top *N*-value of 20 and fragmentation by collision-induced dissociation yielded the highest number of proteins. Validation of the above protocol in two tomato cultivars demonstrated its reproducibility, consistency, and robustness with a CV of <10%. The protocol facilitated the detection of five-fold higher number of proteins compared to published reports in tomato fruits. The protocol outlined would be useful for high-throughput proteome analysis from tomato fruits and can be applied to other recalcitrant tissues.

Keywords: tomato fruit, shotgun proteomics, proteome coverage, sample preparation, protein fractionation

INTRODUCTION

Tomato is a good model for fleshy fruit ripening due to the availability of a high quality genome sequence, mutant collections, well characterized wild relatives, ease of transformation, etc. It is extensively used for deciphering the molecular basis for fruit ripening at transcriptome and metabolome levels (Gapper et al., 2014; Pesaresi et al., 2014). Proteome is an essential link that

Chromoplast-Specific Carotenoid-Associated Protein Appears to Be Important for Enhanced Accumulation of Carotenoids in *hp1* Tomato Fruits[1][C][W][OA]

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Tomato (*Solanum lycopersicum*) high-pigment mutants with lesions in diverse loci such as DNA Damage-Binding Protein1 (*high pigment1* [*hp1*]), Deetiolated1 (*hp2*), Zeaxanthin Epoxidase (*hp3*), and Intense pigment (*Ip*; gene product unknown) exhibit increased accumulation of fruit carotenoids coupled with an increase in chloroplast number and size. However, little is known about the underlying mechanisms exaggerating the carotenoid accumulation and the chloroplast number in these mutants. A comparison of proteome profiles from the outer pericarp of *hp1* mutant and wild-type (cv Ailsa Craig) fruits at different developmental stages revealed at least 72 differentially expressed proteins during ripening. Hierarchical clustering grouped these proteins into three clusters. We found an increased abundance of chromoplast-specific carotenoid-associated protein (CHRC) in *hp1* fruits at red-ripe stage that is also reflected in its transcript level. Western blotting using CHRC polyclonal antibody from bell pepper (*Capsicum annuum*) revealed a 2-fold increase in the abundance of CHRC protein in the red-ripe stage of *hp1* fruits compared with the wild type. CHRC levels in *hp2* were found to be similar to that of *hp1*, whereas *hp3* and *Ip* showed intermediate levels to those in *hp1*, *hp2*, and wild-type fruits. Both CHRC and carotenoids were present in the isolated plastoglobules. Overall, our results suggest that loss of function of *DDB1*, *DET1*, *Zeaxanthin Epoxidase*, and *Ip* up-regulates CHRC levels. Increase in CHRC levels may contribute to the enhanced carotenoid content in these high-pigment fruits by assisting in the sequestration and stabilization of carotenoids.

Tomato (*Solanum lycopersicum*) high-pigment mutants *hp1* (*hp1*, *hp1*^{w}), *hp2* (*hp2*, *hp2*^{j}, *hp2*^{dg}), *hp3*, and *Intense pigment* (*Ip*) not only share characteristically high lycopene content but also exhibit an increased number and size of chloroplasts in leaves as well as in green fruits. This leads to a higher number of chromoplasts when the fruits ripen (Azari et al., 2010). *HP1* codes for DNA Damage-Binding Protein1 (DDB1; Lieberman et al., 2004; Liu et al., 2004), while *HP2* encodes the Arabidopsis (*Arabidopsis thaliana*) homolog of Deetiolated1 (DET1; Mustilli et al., 1999) and the *hp3* mutant has a lesion in zeaxanthin epoxidase (Galpaz et al., 2008). However, the gene product for *Ip* is still unknown (Lavi et al., 2009). Similar to *hp1* and *hp2* mutants, *Ip* also shows exaggerated photomorphogenesis (Lavi et al., 2009). Due to their high lycopene, flavonoid, and vitamin contents, *hp1* and *hp2* mutations have been introgressed into various breeding populations. One such introgression from *hp2*^{dg} resulted in a 3.5-fold increase in lycopene content in tomato fruits (Levin et al., 2003). Both DDB1 and DET1 seem to interact with Cullin4 (CUL4) and were found to be components of a CUL4-based E3 ubiquitin ligase complex (Wang et al., 2008). CUL4-DDB1 complexes have been shown to affect overall plant development (Bernhardt et al., 2006) and flowering (Chen et al., 2010), where they may affect the epigenetic control of flowering. Double mutants of *ddb1a* and *ddb1b* showed that in Arabidopsis, DDB1 is critical for embryo development (Bernhardt et al., 2010).

Manipulation of light signaling components appears to be a good strategy to improve tomato fruit quality, as shown by fruit-specific RNA interference (RNAi)-mediated suppression of *DET1* and repression of *LeCOP1LIKE* genes, which resulted in increased carotenoid levels (Liu et al., 2004; Davuluri et al., 2005). Similarly, repression of *CUL4* and fruit-specific repression of *HP1/DDB1* by RNAi resulted in increased plastid compartment size and enhanced pigmentation of tomato fruits (Wang et al., 2008). Disrupting the function of all or any of these light signaling components seems to affect plastid biogenesis, leading to an increased number of plastids with greater storage

[1] This work was supported by the Department of Biotechnology, Government of India (grant no. BT/PR10903/GBD/27/123/2008 to Y.S.), the Department of Biotechnology, Tomato Metabolome Network, Government of India (grant no. BT/PR11671/PBD/16/828/2008 to Y.S. and R.S.), the University Grants Commission, New Delhi (junior research fellowship to H.V.K.), and the Council of Scientific and Industrial Research, New Delhi (senior research fellowship to R.K.).

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www.plantphysiol.org/cgi/doi/10.1104/pp.112.212191

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RESEARCH ARTICLE

Tomato Fruits Show Wide Phenomic Diversity but Fruit Developmental Genes Show Low Genomic Diversity

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Citation: Mohan V, Gupta S, Thomas S, Mickey H, Charakana C, Chauhan VS, et al. (2016) Tomato Fruits Show Wide Phenomic Diversity but Fruit Developmental Genes Show Low Genomic Diversity. PLoS ONE 11(4): e0152907. doi:10.1371/journal.pone.0152907

Editor: Monica Scali, Universita degli Studi di Siena, ITALY

Received: December 31, 2015

Accepted: March 21, 2016

Published: April 14, 2016

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Data Availability Statement: All relevant data are within the paper and its Supporting Information files.

Funding: This work was supported by the Department of Biotechnology, India (grant no. BT/PR/5275/AGR/16/465/2004; BT/PR/7002/PBD/16/1009/2012) to RS and YS; University Grants Commission, India to YS and RS; Department of Science and Technology, India (Young Scientist grants to SG and VSC); Council of Scientific and Industrial Research, India (research fellowship to VM, HM, CC, RK, SKG, KT, SN, PG); University Grants Commission, India (research fellowship to ST, KS, SS, HVK) and Indian

Abstract

Domestication of tomato has resulted in large diversity in fruit phenotypes. An intensive phenotyping of 127 tomato accessions from 20 countries revealed extensive morphological diversity in fruit traits. The diversity in fruit traits clustered the accessions into nine classes and identified certain promising lines having desirable traits pertaining to total soluble salts (TSS), carotenoids, ripening index, weight and shape. Factor analysis of the morphometric data from Tomato Analyzer showed that the fruit shape is a complex trait shared by several factors. The 100% variance between round and flat fruit shapes was explained by one discriminant function having a canonical correlation of 0.874 by stepwise discriminant analysis. A set of 10 genes (*ACS2*, *COP1*, *CYC-B*, *RIN*, *MSH2*, *NAC-NOR*, *PHOT1*, *PHYA*, *PHYB* and *PSY1*) involved in various plant developmental processes were screened for SNP polymorphism by EcoTILLING. The genetic diversity in these genes revealed a total of 36 non-synonymous and 18 synonymous changes leading to the identification of 28 haplotypes. The average frequency of polymorphism across the genes was 0.038/Kb. Significant negative Tajima'D statistic in two of the genes, *ACS2* and *PHOT1* indicated the presence of rare alleles in low frequency. Our study indicates that while there is low polymorphic diversity in the genes regulating plant development, the population shows wider phenotype diversity. Nonetheless, morphological and genetic diversity of the present collection can be further exploited as potential resources in future.

Plant, Cell & Environment

Plant, Cell and Environment (2014) **37**, 1688–1702 doi: 10.1111/pce.12279

Original Article

Complex and shifting interactions of phytochromes regulate fruit development in tomato

Suresh Kumar Gupta[1], Sulabha Sharma[1], Parankusam Santisree[1]*, Himabindu Vasuki Kilambi[1], Klaus Appenroth[1,2], Yellamaraju Sreelakshmi[1] & Rameshwar Sharma[1]

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ABSTRACT

Tomato fruit ripening is a complex metabolic process regulated by a genetical hierarchy. A subset of this process is also modulated by light signalling, as mutants encoding negative regulators of phytochrome signal transduction show higher accumulation of carotenoids. In tomato, phytochromes are encoded by a multi-gene family, namely *PHYA*, *PHYB1*, *PHYB2*, *PHYE* and *PHYF*; however, their contribution to fruit development and ripening has not been examined. Using single phytochrome mutants *phyA, phyB1* and *phyB2* and multiple mutants *phyAB1*, *phyB1B2* and *phyAB1B2*, we compared the on-vine transitory phases of ripening until fruit abscission. The *phyAB1B2* mutant showed accelerated transitions during ripening, with shortest time to fruit abscission. Comparison of transition intervals in mutants indicated a phase-specific influence of different phytochrome species either singly or in combination on the ripening process. Examination of off-vine ripened fruits indicated that ripening-specific carotenoid accumulation was not obligatorily dependent upon light and even dark-incubated fruits accumulated carotenoids. The accumulation of transcripts and carotenoids in off-vine and on-vine ripened mutant fruits indicated a complex and shifting phase-dependent modulation by phytochromes. Our results indicate that, in addition to regulating carotenoid levels in tomato fruits, phytochromes also regulate the time required for phase transitions during ripening.

Key-words: carotenoids; fruit ripening; photoreceptors.

INTRODUCTION

Tomato fruit ripening is a fascinating process involving well-orchestrated coordination of several regulatory steps, which transform the green, unpalatable fruit to a fleshy aromatic red fruit, rich in carotenoids and other phytonutrients. The above process involves initiation of multiple genetic and biochemical pathways, the regulation of which has been intensively investigated during the past three decades. These studies have indicated the existence of a molecular hierarchy in regulating the diverse metabolic and cellular responses during fruit ripening. The analysis of naturally occurring tomato mutants impaired in ripening such as *rin* and *cnr* revealed a genetic hierarchy determining initiation of ripening, as fruits of these mutants failed to undergo characteristic changes in colour and aroma. The positional cloning of the above mutant loci indicated that *RIN* and *CNR* loci encode for transcription factors belonging to MADS and SBP box family, respectively, and act as master regulators of ripening (Seymour *et al*. 2013). In addition, other transcription factors such as HB-1, an HD-ZIP homeobox protein (Lin *et al*. 2008), and TAGL1 (Itkin *et al*. 2009; Vrebalov *et al*. 2009) have been shown to be necessary for ripening. Many of the above transcription factors such as RIN are considered to be master regulators of ripening as RIN influences ripening even in non-climacteric fruits such as strawberries (Seymour *et al*. 2011). Recently, developmental modification of epigenome in tomato has also emerged as an additional regulatory step influencing fruit ripening (Zhong *et al*. 2013).

Downstream of genetic regulation of ripening by transcription factors, the climacteric rise of ethylene also plays an important role and mutants defective in perception of ethylene such as *Nr* fail to ripen normally even after exposure to exogenous ethylene. The inhibition of ethylene emission by antisense suppression of genes involved in ethylene biosynthesis such as *ACS2* (Oeller *et al*. 1991) or *ACO1* (Hamilton *et al*. 1990) inhibited ripening, whereas suppression of ethylene receptor genes such *LeETR4* and *LeETR6* elevated ethylene production and accelerated tomato ripening (Tieman *et al*. 2000; Kevany *et al*. 2007). The climacteric regulation of ripening may be assisted by other hormones such as ABA, as exogenous ABA application promoted ethylene synthesis and ripening, and inhibition of ABA synthesis delayed tomato fruit ripening and softening. It has been suggested that onset of tomato ripening is initiated by ABA and the role of ethylene is exerted at later stage of ripening (Zhang *et al*. 2009). In addition to climacteric regulation of ripening by ethylene, an independent non-climacteric pathway also influences ripening process. Hormones such as auxin plays an important role in fruit development, and exogenous application of auxin delays fruit ripening and induces

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Tomato Root Penetration in Soil Requires a Coaction between Ethylene and Auxin Signaling[1][C][W][OA]

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School of Life Sciences, University of Hyderabad, Hyderabad 500046, India (P.S., S.N., H.V., Y.S., R.S.); and Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon 97331 (M.G.I.)

During seed germination, emerging roots display positive gravitropism and penetrate into the soil for nutrition and anchorage. Tomato (*Solanum lycopersicum*) seeds germinated in the presence of 1-methylcyclopropene (1-MCP), an inhibitor of ethylene action, failed to insert roots into Soilrite and grew in the air, forming loops. Time-lapse video imaging showed that 1-MCP-grown root tips retained positive gravitropism and made contact with the surface of Soilrite but failed to penetrate into the Soilrite. Time-course studies revealed that the effect of 1-MCP was most prominent when seed imbibition and germination were carried out in the continual presence of 1-MCP. Conversely, 1-MCP was ineffective when applied postgermination after penetration of roots in the Soilrite. Furthermore, treatment with 1-MCP caused a reduction in *DR5*::*β-glucuronidase* auxin-reporter activity and modified the expression of *SlIAA3* and *SlIAA9* transcripts, indicating interference with auxin signaling. The reduced ethylene perception mutant, *Never-ripe*, displayed decreased ability for root penetration, and the enhanced polar auxin transport mutant, *polycotyledon*, showed a nearly normal root penetration in the presence of 1-MCP, which could be reversed by application of auxin transport inhibitors. Our results indicate that during tomato seed germination, a coaction between ethylene and auxin is required for root penetration into the soil.

Seed germination is a crucial phase in the life cycle of plants, when the emerging seedlings first encounter the external environment and regulate growth to optimize survival. Generally, the primary root is the first organ to emerge from the seed, and its subsequent growth and development are strongly influenced by the local environment. The roots of plants perform multifaceted roles, of which two functions are foremost: to firmly anchor the plant into the soil, and to supply water and nutrients to the aerial parts of the plant (Hodge et al., 2009). To efficiently perform these functions, roots are endowed with a variety of sensory mechanisms for detecting gravity, water, nutrients, and the mechanical resistance of the soil (Arnaud et al., 2010). A large body of physiological experiments in conjunction with surgical dissection have pointed out that the root tip is the site for the perception and integration of many of these signals (Iijima et al., 2008; Arnaud et al., 2010). The root tip harbors the root apical meristem, the quiescent center, and the initial cells that give origin to all cell types of the root. The root tip is surrounded by the root cap covering the apical meristem, which consists of two tissues: columella and lateral root cap cells (Arnaud et al., 2010). The root cap offers physical protection to the root apical meristem against mechanical resistance during penetration of roots into the soil. In addition, the root cap also functions as the site for gravity sensing, and surgical removal and laser or genetic ablation of root cap cells result in a loss of gravitropic response (Blancaflor et al., 1998; Barlow, 2003; Iijima et al., 2003; Morita, 2010).

Consistent with the classic Cholodny-Went hypothesis, a large number of reports have indicated that the differential growth of roots after gravistimulation is initiated by asymmetric redistribution of the plant hormone auxin (Rashotte et al., 2001; Ottenschläger et al., 2003; Muday and Rahman, 2008; Vanneste and Friml, 2009). The reverse-fountain model of auxin transport in the root tip proposes that shoot-derived auxin is acropetally transported to the root cap through the root vascular tissue, and after radial distribution in the root cap, in the epidermal tissues it is basipetally transported back to the elongation zone of the roots, where it regulates growth (Muday

[1] This work was supported by the International Atomic Energy Agency, by the Department of Biotechnology, New Delhi, India (grants to R.S. and Y.S.), by the University Grants Commission, New Delhi, by the Department of Biotechnology-Center for Education and Research in Biology and Biotechnology (fellowship to P.S.), by a University of Hyderabad fellowship to N.S., and by the U.S. Department of Agriculture National Research Initiative Competitive Grants Program (grant no. 2006–03434 to M.G.I.).

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MOLECULAR CHARACTERIZATION OF CAROTENOID ACCUMULATION IN LIGHT SIGNALLING MUTANTS AND WILD RELATIVES OF TOMATO

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(Enfissi et al., 2010). Biochemical analysis of plastoglobules revealed that these are enriched in lipids and also contain several proteins, including enzymes participating in carotenoid metabolism (Austin et al., 2006; Brehélin and Kessler, 2008). Based on the enrichment of lipids in the plastoglobules, it is assumed that carotenoids are also present in them. Since CHRC has been implicated as a protein that assists in the sequestration and

2015). Carotenoid sequestration and accumulation in chromoplasts. Plastoglobules are lipid containing carotenoid sequestering structures associated with thylakoids and contain carotenoid biosynthesis enzymes (Austin et al., 2006; Brehelin and Kessler 2008). In *crtE*, *crtB* and *crtI* carotenogenic lines of tomato, the increased accumulation of carotenoids boosted the development of membranous structures in chromoplasts (Nogueira et al., 2013). In the above lines, the accumulation of carotenoid precursors and biosynthetic enzymes in different compartments in chromoplasts has been identified as an efficient method to sequester and stabilize carotenoids within tomato fruits (Nogueira et al., 2013, Fraser et al., 1994; Fraser and Bramley 2004).

It is now evident that the carotenoid metabolism is regulated at various levels by several factors including environmental cues, developmental signals and phytohormones. But the complete information on the function and underlying molecular mechanisms of the above factors in regulating carotenoid metabolism is still lacking (Liu et al., 2015). A combination of "omics" technologies such as phenomics, genomics, proteomics and metabolomics has been considered as an essential means to understand the molecular events that trigger the carotenoid biosynthesis and degradation (Ricroch et al., 2011; Pirrello et al., 2009). The combination of transcript, protein and metabolite data in fruits of ripening inhibitor mutants such as *rin*, *nor* and *Nr* recognized several interactions that control fruit ripening (Osorio et

Plant Physiology
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First Published on February 11, 2013, doi: http://dx.doi.org/10.1104/pp.112.212191
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Chromoplast-Specific Carotenoid-Associated Protein Appears to Be Important for Enhanced Accumulation of Carotenoids in *hp1* Tomato Fruits[1][C][W][OA]

Himabindu Vasuki Kilambi, Rakesh Kumar, Rameshwar Sharma and Yellamaraju Sreelakshmi*

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First Published on February 11, 2013, doi: http://dx.doi.org/10.1104/pp.112.212191
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Abstract

Tomato (Solanum lycopersicum) high-pigment mutants with lesions in diverse loci such as DNA Damage-Binding Protein1 (high pigment1 [hp1]), Deetiolated1 (hp2), Zeaxanthin Epoxidase (hp3), and Intense pigment (Ip; gene product unknown) exhibit increased accumulation of fruit carotenoids coupled with an increase in chloroplast number and size. However, little is known about the underlying mechanisms exaggerating the carotenoid accumulation and the chloroplast number in these mutants. A comparison of proteome profiles from the outer pericarp of hp1 mutant and wild-type (cv Ailsa Craig) fruits at different developmental stages revealed at least 72 differentially expressed proteins during ripening. Hierarchical clustering grouped these proteins into three clusters. We found an increased abundance of chromoplast-specific carotenoid-associated protein (CHRC) in hp1 fruits at red-ripe stage that is also reflected in its transcript level. Western blotting using CHRC polyclonal antibody from bell pepper (Capsicum annuum) revealed a 2-fold increase in the abundance of CHRC protein in the red-ripe stage of hp1 fruits compared with the wild type. CHRC levels in hp2 were found to be similar to that of hp1, whereas hp3 and Ip showed intermediate levels to those in hp1, hp2, and wild-type fruits. Both CHRC and carotenoids were present in the isolated plastoglobules. Overall, our results suggest that loss of function of DDB1, DET1, Zeaxanthin Epoxidase, and Ip up-regulates CHRC levels. Increase in CHRC levels may contribute to the enhanced carotenoid content in these high-pigment fruits by assisting in the sequestration and stabilization of carotenoids.

Tomato (Solanum lycopersicum) high-pigment mutants hp1 (hp1, $hp1^{w}$), hp2 (hp2, $hp2^{j}$, $hp2^{dg}$), hp3, and Intense pigment (Ip) not only share characteristically high lycopene content but also exhibit an increased number and size of chloroplasts in leaves as well as in green fruits. This leads to a higher number of chromoplasts when the fruits ripen (Azari et al., 2010). HP1 codes for DNA Damage-Binding Protein1 (DDB1; Lieberman et al., 2004; Liu et al., 2004), while HP2 encodes the Arabidopsis (Arabidopsis thaliana) homolog of Deetiolated1 (DET1; Mustilli et al., 1999) and the hp3 mutant has a lesion in zeaxanthin epoxidase (Galpaz et al., 2008). However, the gene product for Ip is still unknown (Lavi et al., 2009). Similar to hp1 and hp2 mutants, Ip also shows exaggerated photomorphogenesis (Lavi et al., 2009). Due to their high lycopene, flavonoid, and vitamin contents, hp1 and hp2 mutations have been introgressed into various breeding populations. One such introgression from $hp2^{dg}$ resulted in a 3.5-fold increase in lycopene content in tomato fruits (Levin et al., 2003). Both DDB1 and DET1 seem to interact with Cullin4 (CUL4) and were found to be components of a CUL4-based E3 ubiquitin ligase complex (Wang et al., 2008). CUL4-DDB1 complexes have been shown to affect overall plant development (Bernhardt et al., 2006) and flowering (Chen et al., 2010), where they may affect the epigenetic control of flowering. Double mutants of ddb1a and ddb1b showed that in Arabidopsis, DDB1 is critical for embryo development (Bernhardt et al., 2010).

Manipulation of light signaling components appears to be a good strategy to improve tomato fruit quality, as shown by fruit-specific RNA interference (RNAi)-mediated suppression of DET1 and repression of LeCOP1LIKE genes, which resulted in increased carotenoid levels (Liu et al., 2004; Davuluri et al., 2005). Similarly, repression of CUL4 and fruit-specific repression of HP1/DDB1 by RNAi resulted in increased plastid compartment size and enhanced pigmentation of tomato fruits (Wang et al., 2008). Disrupting the function of all or any of these light signaling components seems to affect plastid biogenesis, leading to an increased number of plastids with greater storage capacity for the carotenoids

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