

FRANKLIN MAGNUM DE OLIVEIRA SILVA

**INTEGRATIVE ANALYSES OF PHOTOSYNTHESIS, PLANT
GROWTH, METABOLITE LEVELS AND ENZYME ACTIVITIES IN
AN INTROGRESSION LINE POPULATION OF *Solanum pennellii***

Thesis presented to the Universidade
Federal de Viçosa as part of the
requirement of the Plant Physiology
Graduate Program for obtention of the
degree of *Doctor Scientiae*.

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DEDICATIONS

My grandparents, Assis and Guia,
for all love and example of life;

My parents, Francisco Cosmo (*in memoriam*) and Maria José;
for all that represents to me.

I dedicate

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RESUMO

SILVA, Franklin Magnum de Oliveira, D.Sc., Universidade Federal de Viçosa, agosto de 2016. **Integrative analyses of photosynthesis, plant growth, metabolite levels and enzyme activities in an introgression line population of *Solanum pennellii*.** Orientador: Adriano Nunes Nesi.

Para identificar regiões genômicas envolvidas na regulação de processos fisiológicos fundamentais, como fotossíntese, respiração e aqueles relacionados, uma população de ILs de *Solanum pennellii* em fundo genético de *S. lycopersicum* (M82) foi analisada. Foram estudados parâmetros fisiológicos, metabólicos e de crescimento, que vão desde troca gasosa (por exemplo, taxa de assimilação de CO₂ e condutância estomática), fluorescência da clorofila (por exemplo, taxa de transporte de elétrons e de extinção fotoquímica), bem como parâmetros de crescimento (por exemplo, taxa de crescimento relativo, matéria seca da raiz e parte aérea). Em paralelo, nós também analisamos, por meio de uma plataforma robotizada, os principais intermediários metabólicos (por exemplo, açúcares, amido, nitrato, aminoácidos e proteínas), e a atividade de nove enzimas representativas do metabolismo central do C e N. O objetivo do estudo foi: (1) combinar informações sobre as atividades enzimáticas e os níveis de metabólitos de caule, pecíolo e folha com a biomassa e rendimento de frutos; (2) através do estudo desses três órgãos interligados, examinar o quanto há de conectividade entre a atividade das enzimas e os níveis de metabólitos; (3) fornecer informações preditivas sobre as diferenças de particionamento do C e assimilação N inorgânico; (4) investigar a diversidade genética natural e identificar QTLs relacionados ao metabolismo central e a atividade enzimática no caule, pecíolo e folha. As análises dos dados permitiram a identificação de 67 QTL relacionados a parâmetros fisiológicos e metabólicos. Além disso, uma anotação abrangente e detalhada destas regiões permitiu apontar um total de 87 genes candidatos que possam controlar as características investigadas. Desses, 70 genes apresentou variantes alélicas relacionadas inserções de elementos transponíveis entre os dois genótipos parentais. As análises metabólicas e enzimática revelaram alta frequência de correlações positivas entre as enzimas, frequência moderada de correlações entre metabólitos relacionados, e baixa correlações entre a atividade das enzimas e os níveis de metabólitos. Tomados em conjunto,

apresentamos o maior estudo de parâmetros de fotossíntese e crescimento em plantas de tomate até à data. Os resultados permitiram a identificação de genes candidatos que podem estar envolvidos na regulação da fotossíntese, metabolismo primário e crescimento da planta, e fornece um recurso genético valioso para a compreensão dos mecanismos bioquímicos envolvidos na regulação do metabolismo primário em tomateiro.

ABSTRACT

SILVA, Franklin Magnum de Oliveira, D.Sc., Universidade Federal de Viçosa, August, 2016. **Integrative analyses of photosynthesis, plant growth, metabolite levels and enzyme activities in an introgression line population of *Solanum pennellii*.** Adviser: Adriano Nunes Nesi.

To identify genomic regions involved in the regulation of fundamental physiological processes such as photosynthesis, respiration and underlying traits, a population of 71 *Solanum pennellii* introgression lines (ILs) in the genetic background of *S. lycopersicum* (M82) was analyzed. We determined IL phenotypes physiological, metabolic and growth related traits, ranging from gas-exchange parameters (e.g. CO₂ assimilation rates and stomatal conductance), chlorophyll fluorescence parameters (e.g. electron transport rate and photochemical quenching) as well as growth related traits (e.g. relative growth rate, shoot and root dry matter accumulation). In parallel, we also analyzed by robotized platform the major metabolic intermediates (e.g. sugars and starch), and the activities of nine representative enzymes from central C and N metabolism. We aimed: (1) combine information about enzyme activities and metabolite levels from stem, petiole and leaf with biomass and fruit yield; (2) by studying these three interconnected organs, examine how much connectivity exists between enzyme activities and metabolite levels; (3) provide predictive information about differences in C partitioning and inorganic N assimilation; (4) investigate the natural genetic diversity and identify QTL controlling variation of enzyme activities and metabolite levels in stem, petiole and leaf. Data analyses allowed identification of 67 physiological and metabolic QTL. Additionally, a comprehensive and detailed annotation of these regions allowed to point out a total of 87 candidate genes that might control the investigated traits. Out of those, 70 genes showed allelic variants related to differentially transposable element insertions pattern between both parental genotypes. Furthermore, the results revealed high frequency of positive correlations between enzyme activities, moderate frequency of correlations between related metabolites, and few correlations between enzyme activities and metabolite levels. Taken together, we present the largest study of photosynthetic and growth parameters in tomato plants to date. Our results allowed the identification of candidate

genes that might be involved in the regulation of photosynthesis, primary metabolism and plant growth, and provide an valuable genetic resource to understanding of the biochemical mechanisms involved in the regulation of primary metabolism in tomato plants.

OVERVIEW

Biomass accumulation in plants is a remarkably stable function of light intercepted by the canopy and CO₂ transformation into dry matter via photosynthesis. Upon fixation, most of the inorganic carbon is converted into sucrose, which in most plants acts as the major source of organic carbon for further metabolism. Some of the fixed carbon is temporarily stored as starch, and remobilized at night to support respiration or used for continued sucrose synthesis and export to other tissues (Stitt, Lunn, & Usadel, 2010; Zhu et al., 2014)

photosynthesis is genetically controlled, and the genetic blueprint for photosynthesis varies in both within and between species (Arntz & Delph, 2001; Hikosaka, 2010). The adaptive potential of photosynthesis under sub-optimal environments depends on the level of genetic variation for photosynthesis that is present in a population. In recent years, strategies for increasing photosynthesis and how it could positively impact yield have been expertly reviewed (Flood, Harbinson, & Aarts, 2011; Hikosaka, 2010; Lawson, Kramer, & Raines, 2012; Nunes-nesi et al., 2016; Ort et al., 2015). Therefore, we propose that a quantitative genetic approach will be useful in properly assessing the genetic causes of photosynthetic variation at the leaf level and in designing future breeding programs. Thus, a collection of introgression lines (ILs), such as that developed by Zamir et al. (1995), are presented as an important tool to identify genes or the genetic factors underlying the Quantitative trait loci (QTL). This population is composed by a set of 76 introgression lines (ILs) derived from a *S. lycopersicum* cv M82 X *Solanum pennellii* cross. Each of these lines contains a small introgressed region of the *S. pennellii* genome, containing an

estimated 200 to 1,000 genes (Kamenetzky et al., 2010) in a genetic background that otherwise derives from *S. lycopersicum*. So far, several QTL were identified in this population (Alseekh et al., 2013), and whilst many candidate genes have been found only a few of these have been unambiguously cloned (Fridman, Carrari, Liu, Fernie, & Zamir, 2004; Quadrana et al., 2014; Ronen, Carmel-Goren, Zamir, & Hirschberg, 2000). Here, by measuring photosynthetic parameters, selected leaf metabolites and growth-related parameters in the *S. pennellii* IL collection, we identified 67 QTL controlling important determinants of leaf photosynthesis and related processes. In addition, using genomic analysis, we identified a total of 87 candidate genes that may regulate these traits. We also verified lower levels of sucrose and fructoses in leaves as well as several QTL were identified to starch levels. In general, carbohydrate metabolism is more complex in plants than in most other organisms. For example, there are alternative routes for the mobilization and metabolization of diverse components (Carrari et al., 2003). Depending on the tissue, part or all of the glycolytic pathway is present in the plastid and in the cytosol (Lunn, 2007). As a result, a given substrate may be converted into different products, and products can be formed from different substrates and subsequently transported by phloem to different organs. Certain enzymes have been shown to play key roles in those processes (Nunes-Nesi, Fernie, & Stitt, 2010; Stitt et al., 2010). While a great deal of research has focused on the key genes and proteins involved in these processes (Prioul et al., 1999; Takahashi et al., 2009; Wang, Turgeon, Carr, & Berry, 1993), relatively little is known about the natural variation within a species that fine tunes these processes in individual plants, we are just beginning to uncover and understand the functions

of genes responsible for controlling the whole-plant distribution of fixed carbon, particularly in crops (Baker & Braun, 2007; Slewinski, 2011, 2012, Slewinski & Braun, 2010a, 2010b). In this sense, we proposed a quantitative genetic approach to investigate about the relation between the levels of central metabolites, enzyme activities and biomass of three organs (stem, petiole and leaf) directly involved in loading and unloading of source and sink tissues. For this, in partnership with Institut National de la Recherche Agronomique (INRA), the same *S. pennellii* IL collection were grown in a greenhouse in South-West of France and by robotized platform in optimized conditions (Gibon et al., 2004) major metabolic intermediates (sugars, starch, nitrate, amino acids and protein), and the activities of nine representative enzymes from central C and N were evaluated. In total, were analysed 1,065 samples corresponding to 70 ILs, the additional parental control M82 and three organs. I carried out around 9,585 enzymatic reactions corresponding to 9 enzymes and 1,065 samples. Additionally, we also evaluated yield parameters, such as green and red fruit fresh weight, as well as biomass parameters (leaf and stem dry weight). We identified high frequency of positive correlations between enzyme activities, a moderate frequency of correlations between related metabolites, and remarkably few correlations between enzyme activities and metabolite levels. In addition, a large number of QTLs were identified and new strategies will be required to identify and validate the candidate genes underlying these QTL and to uncover their functions.

Finally, based on the studies reported above, we proposed a book chapter. In this chapter we describe the use of ILs population as a tool for the identification of genomic regions involved in the control of photosynthetic

efficiency as well as photorespiration. In this chapter, all the experimental material and procedures, as well as procedures for genomic localization and analyses of the identified QTLs is detailed.

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CHAPTER 1

The Genetic Architecture of Photosynthesis and Plant Growth Related Traits in Tomato

The Genetic Architecture of Photosynthesis and Plant Growth Related Traits in Tomato

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One-sentence Summary: Physiological characterization of a *Solanum pennellii* introgression line population reveals the quantitative genetic basis of photosynthesis and plant growth in tomato plants.

ABSTRACT

To identify genomic regions involved in the regulation of fundamental physiological processes such as photosynthesis, respiration and underlying traits, a population of 71 *Solanum pennellii* introgression lines (ILs) in the genetic background of *S. lycopersicum* (M82) was analyzed. We characterized leaf metabolism and physiology of this population and linked these traits to the different allelic variant harbored by each line. We determined IL phenotypes for physiological, metabolic and growth related traits, ranging from gas-exchange parameters (e.g. CO₂ assimilation rates and stomatal conductance), chlorophyll fluorescence parameters (e.g. electron transport rate and photochemical quenching) as well as growth related traits (e.g. relative growth rate, shoot and root dry matter accumulation) across two independent harvests. Data analyses allowed identification of 67 physiological and metabolic QTL. Nine of the ILs displayed higher assimilation rates in comparison with the recurrent parent, M82. Eleven genomic regions involved in starch levels in addition to seven and sixteen related to shoot and root dry matter, respectively, were identified. Additionally, a comprehensive and detailed annotation of these regions allowed to point out a total of 87 candidate genes that might control the investigated traits. Out of those, 70 genes showed allelic variants related to differentially transposable element insertions pattern between both parental genotypes. Taken together, we present the largest study of photosynthetic and growth parameters in tomato plants to date. Our results allowed the identification of candidate genes that might be involved in the regulation of photosynthesis, primary metabolism and plant growth, and provide new avenues for crop improvement. **Key words:** Photosynthesis, plant growth, quantitative trait loci, tomato.

INTRODUCTION

Plants ability to convert the solar radiation energy into biomass is a paramount importance given that both photoautotrophic and heterotrophic organisms depend on this process. The understanding of molecular, physiological, and developmental determinants of variation in photosynthesis and related processes, such as respiration and photorespiration, as well as plant growth and yield is essential for improving plant performance and production. In this context, the determination of natural variation in physiological as well as metabolic parameters can uncover the molecular basis of key traits associated with plant performance in ecological and agricultural settings, and provide insights into the mechanisms involved into species adaptation to varying environments and bases for prediction of future plant productivity and ecological changes in the context of ongoing global climate changes (Zou et al., 2007; Mozdzer and Ziemann, 2010). Improvement in photosynthetic efficiency can be achieved via different strategies such as improving light capture, light energy conversion, enhancing carbon fixation, carbon conversion, bypassing photorespiration (Ort et al., 2015). However, elevated source of activity if not linked to increase in sugar transport lead to accumulation of carbohydrates in leaves resulting in the downregulation of photosynthesis and the photosynthetic efficiency. In this sense, photosynthesis enhancement should be placed in the context of whole-plant relationships (Rossi et al., 2015). Natural variation in plant photosynthesis exists among and within species (Hikosaka, 2010; Lawson et al., 2012) and can be explored to identify genetic determinants that can be used for further improvement in crop yields (Flood et al., 2011; Lawson et al., 2012). In this context, the genetic variation in chlorophyll *a* fluorescence

parameters has been investigated in several species including *Arabidopsis* (El-Lithy et al., 2005; van Rooijen et al., 2015), wheat (Bertin and Gallais, 2001; Yang et al., 2007; Zhang et al., 2009; Li et al., 2010; Driever et al., 2014), rice (Gu et al., 2012) and soybean (Yin et al., 2010). Interestingly, El-Lithy and co-authors (2005), screening a large set of 127 *Arabidopsis* accessions by using chlorophyll *a* fluorescence as a surrogate for photosynthetic performance, observed that photosynthetic yield is highly conserved and that only severe selection pressure results in marked variations in photosynthetic performance between accessions. Surprisingly, despite the increasing number of natural variation based studies, the genetic factors related to variation in photosynthesis remain largely unknown (Flood et al., 2011). However, studies aimed at identifying genes encoding auxiliary factors or modifiers of photosynthesis, are expected to provide further insight since such factors unlikely have been identified in previous mutant screenings due to potential redundancy and numerous genes involved with small effects (Flood et al., 2011). Natural variation in plant growth has also been observed in *Arabidopsis* (Cross et al., 2006; Meyer et al., 2007; Sulpice et al., 2009) and crop plants (Semel et al., 2006; Liang et al., 2010; Driever et al., 2014; Rosado-Souza et al., 2015). Despite the considerable natural variation in plant growth, relatively little is known about its genetic basis, probably because growth rate is the integrator of numerous inter-dependant factors (Koornneef et al., 2004). As mentioned above, higher rates of photosynthesis do not necessarily lead to increments in biomass and yield (Norby et al. 2006; Rossi et al., 2015). Moreover, analysis of natural genetic variation often reveals a negative correlation between the levels of metabolites and biomass or yield (Cross et al.,

2006; Schauer et al., 2006; Meyer et al., 2007). In this context, a comprehensive study of 94 *A. thaliana* ecotypes indicated that vegetative biomass is negatively correlated with many metabolites including starch, and that the regulatory network that determines metabolite levels contributes to the regulation of biomass production (Sulpice et al., 2009). In the case of tomato, numerous studies using wild species introgression line (ILs) populations have been performed in an attempt to understand tomato fruit composition (Fridman et al. 2000; Frary et al. 2000; Liu et al. 2003; Schauer et al. 2006; Tieman et al. 2006; Do et al. 2010; Schilmiller et al. 2010; Quadrana et al. 2014). Studies with an IL population of *S. pennellii* into a genetic background of *S. lycopersicum* (M82) (Eshed and Zamir, 1995) have allowed the identification of hundreds of QTL related to morphology and fruit yield (Semel et al., 2006), metabolite composition (Causse et al. 2004; Fridman et al. 2004; Baxter et al. 2005; Hackel et al. 2006; Schauer et al. 2006; Quadrana et al. 2014), fruit color (Liu et al., 2003), enzymatic activity (Steinhauser et al., 2011) and organ morphology (Holtan and Hake, 2003; Chitwood et al., 2013; Ron et al., 2013). In addition to determination of morphological and anatomical determinants of mesophyll conductance in wild tomato species (Muir et al. 2014a), the same IL population have been used to map QTL for leaf carbon isotope composition (Xu et al., 2008), leaf traits associated with adaptation to precipitation (Muir et al., 2014b) and stomatal responsiveness and *gs*-related anatomical traits (Fanourakis et al., 2015) and root (Ron et al., 2013) traits. In general, several QTL were identified in this population to date (Alseekh et al., 2013), and have been helpful, bridging the gap between genes and the phenotypic traits that result from them. (Ronen et al., 2000; Fridman et al., 2004; Quadrana et al., 2014).

Thus, this extensively studied collection of ILs, associated with the recent availability of the genome sequence of the parental species (Bolger et al., 2014), configures a powerful tool for identifying and understanding the genetic determinants involved in quantitative traits linked to growth and development in tomato. Here by measuring photosynthetic parameters, selected leaf metabolites and growth-related parameters in the *S. pennellii* IL collection, we identified 67 QTL controlling important determinants of leaf photosynthesis and involved in root and shoot dry matter accumulation. Correlation analysis hinted stomatal conductance as an important factor in determining CO₂ assimilation in tomato and to a less extent photochemical traits. Analyses on the transposable elements (TEs) in the same genomic context of the identified candidate genes indicate that these sequences might be involved in regulatory and structural gene changes observed between *S. pennellii* and *S. lycopersicum*.

MATERIAL AND METHODS

Plant materials and experimental conditions

Solanum pennellii ILs (Eshed and Zamir, 1995) and *S. lycopersicum* cv M82 seeds were kindly donated by Professor Dani Zamir, Hebrew University, Rehovot, Israel. The seeds were germinated on Murashige and Skoog media (Murashige and Skoog, 1962) containing 2% (w/v) sucrose and were grown in a growth chamber (250 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$, 22°C) under a photoperiod of 16-h-light/8-h dark before transfer into the greenhouse. Rooted plantlets were acclimatized and subsequently transferred to 1.16L pots containing commercial substrate Plantmax® supplemented with chemical fertilizer (N: 4; P₂O₅: 14; K₂O: 8). Plants were grown in a greenhouse located in Viçosa (642 m in altitude, 20°45' S latitude and 42°51' W longitude) in southeastern Brazil, with a

minimum of 250 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$. During the growth period, the plants were maintained under naturally fluctuating conditions of light intensity, temperature and relative air humidity. The experiment was repeated in two consecutive years, where plants from 71 ILs and M82 were grown in the spring season. M82 and ILs were arranged in block design with 6 replicates and each blocs was randomized. All sampling procedures were carried out on the first fully expanded source leaves from 4 week-old plants. Leaf samples for starch levels were taken at the end of night, middle and end of day. Plant growth was estimated using plant height and a time-component providing an integrative parameter referred to as relative growth rate (RGR). Plant height was determined (from the base to the tip of the terminal bud), and was employed to estimate the RGR (Hunt, 1982). The dry matter accumulated in shoot and roots was determined at the end of the experiment. After four weeks the plants were harvested in one cut to 1.0 cm above ground level, separating the roots from shoots. The roots, after washed, and shoots were placed in identified paper bags and brought to a forced air circulation oven at 70 °C, after which the dry weight of roots (Root DW) and shoots (Shoot DW) was determined.

Measurements of Photosynthetic Parameters

Gas exchange analyses were performed in the second terminal leaflet of the third leaf from the apex of four week-old plants using a portable open-flow gas exchange system (Li 6400XT, Li-Cor, Inc., Lincoln, NE, USA) equipped with an integrated fluorescence chamber (LI-6400-40; Li-Cor Inc.). The net CO_2 assimilation rate (A), stomatal conductance to water vapor (g_s), internal CO_2 concentration (C_i), and transpiration rate (E) were measured from 08:00 to 12:00 h (solar time) under an external CO_2 concentration of 400 $\mu\text{mol mol}^{-1}$ air

and a flow rate of $300 \mu\text{mol s}^{-1}$. All measurements were conducted under artificial, saturating light of $1000 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ that was provided by a light-emitting diode with 10 % blue light in order to maximize the stomatal opening. The CO_2 concentration and water vapor between the leaf and the reference chamber were automatically matched before the data were recorded. The rates of dark respiration (R_d) were determined from 21:00 to 23:30 h in the same leaf previously used to determine net carbon assimilation. From combined measurements of fluorescence and gas-exchange we estimated the photorespiration rate (Pr) according to Valentini et al. (1995). Previously dark-adapted (1h) leaf tissues were illuminated with weak, modulated measuring beams ($0.03 \mu\text{mol m}^{-2} \text{s}^{-1}$) to obtain the initial fluorescence (F_0). Saturating white light pulses of $8.000 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ were applied for 0.8s to ensure maximum fluorescence emissions (F_m). In light-adapted leaves, the steady-state fluorescence yield (F_s) was measured following a saturating white light pulse ($8,000 \mu\text{mol m}^{-2} \text{s}^{-1}$, 0.8s) that was applied to achieve the light-adapted maximum fluorescence (F_m'). The actinic light was then turned off and far-red illumination was applied ($2 \mu\text{mol m}^{-2} \text{s}^{-1}$) to measure the light-adapted initial fluorescence (F_0') (Aucique-Perez et al., 2014). The obtained values were used to determine the maximum photochemical efficiency of PSII (F_v/F_m), the actual quantum yield of PSII electron transport (δPSII), the coefficients of photochemical quenching (qP) and non-photochemical quenching (NPQ) and the electron transport rate (ETR), as previously described (Schreiber et al., 1995; Aucique-Perez et al., 2014).

Determination of metabolite levels

Leaf samples were harvested at the middle of light period or as indicated in the text, using the same leaf previously used to determine the photosynthetic parameters. Afterwards, the tissue was quickly frozen in liquid nitrogen and stored at - 80 °C until further analysis. Metabolite extraction was performed by grinding the tissue in liquid nitrogen followed by the immediate addition of 80% ethanol as described by Cross et al., (2006). The levels of starch, sucrose, fructose, and glucose in leaf tissue were determined exactly as previously described (Fernie et al., 2001). The levels of malate and fumarate were determined exactly as detailed by Nunes-Nesi et al. (2007), whilst nitrate (NO₃) and chlorophyll *a* and *b* contents were determined as detailed by Sulpice et al. (2009). Total protein and total amino acid contents were quantified as previously reported (Cross et al., 2006).

Statistical analyses

The experiment was designed in randomized blocks with six replicates. The experimental unit was one plant per pot. Statistical analyses were performed using the GENES program (Cruz, 2013) and R statistical software (www.r-project.org). All data were subjected to an analysis of variance (ANOVA), and the means were tested by Dunnett's test at 5 % significance level. Pearson correlation coefficient was used at 5% significance level by T-test for examining the relationships among variables.

Gene and transposable element annotation and analyses

Sequences of the selected region (Table II) were retrieved from M82 and *S. pennellii* genomes (Bolger et al., 2014) by probing the flanking markers (according to the IL genetic map deposited in the sol genomics network portal)

in both genome sequences as indicated in Supplemental Table S5. *De novo* gene prediction was performed by using Augustus software (Stanke et al., 2004). Predicted proteins were functionally annotated by comparison against the SOL Genomics Network (<http://solgenomics.net/>) Heinz protein database and BLASTp engine with cut off value of E-10. Proteins that matched transposable elements were initially removed from the data set. Transposable element (TEs) annotation was then performed with Repeat Masker Open-4.0 (www.repeatmasker.org) against Viridiplantae database with score ≥ 250 in both IL parental genomes, *S. lycopersicum* (cv M82) and *S. pennellii* (LA0716) (Bolger et al., 2014), as well as in the selected trait-associated genomic regions (BINs). Non-redundant gene lists for each BIN were extracted by a dedicated script and Mapman-categorized by using the published Mapman table Solyc ITAG 2.30 (<http://solgenomics.net/>) as subject. This was separately done for both M82 and *S. pennellii* genes. In order to assess over-representation of any Mapman category within the genomic region analyzed, after categorization a contingency table was built between the number of genes assigned to each category and those from the whole gene set of each plant species. Significance ($p < 0.05$) was tested using the Fisher test. For candidate gene selection, the Blast2GO (Conesa et al., 2005) suite was utilized. The previously identified protein entries were used as queries for a BLASTp against the NCBI *A. thaliana* protein dataset with a cut off value of E-3 and a maximum of 20 hits per sequence. Then, the GO terms were associated to each query based on the program annotation algorithm, InterProScan database and ANNEX validation. Candidate genes were surveyed by biological process GO terms associated with the traits under study. The GO terms analysed were: malate

transmembrane transport (GO: 0071423); carbohydrate metabolic process (GO: 0005975); photorespiration (GO: 0009853); photosynthesis (GO: 0015979); root system development (GO: 0022622); growth (GO: 0040007); cellular respiration (GO: 0045333); cell wall organization or biogenesis (GO: 0071554); carbohydrate derivative metabolic process (GO: 1901135). After this selection, TE insertion patterns were manually inspected in a context of $\pm 4,000$ bp around each identified candidate gene for both alleles or until the next *loci* coding sequence. Genes expression based on RNA-seq data of leaf materials of 76 tomato introgression lines from Chitwood et al. (2013) were downloaded and used to compare the expression levels of the selected candidate genes (Supplemental Table S7) across introgression lines and their correlation to phenotypic traits. Genes showed changes in their expression and correlated to phenotypic traits were subjected to sequence analysis of the non-coding region upstream start codon ATG (up to around -1000 bp) from *S. lycopersicum* cv. M82 and *S. pennellii* genome sequences (Bolger et al., 2014).

RESULTS

Natural variation for 24 physiological and metabolic traits across two independent harvests of the *S. pennellii* IL population

The *S. pennellii* IL population was grown in a greenhouse under semi-controlled conditions, in spring of 2012 and 2013. Photosynthetic, metabolic and plant growth related traits were measured prior to flowering. Figure 1 illustrates variation in the 24 evaluated traits. Overall trait variation was largely similar between both experiments. However, as could be expected, by comparing the data sets of the two years (Supplemental Table S1 and S2), large variability within the population and in some cases also between the two experiments was

noted, particularly for total amino acids and chlorophyll a contents, root dry weight (Root DW), electron transport rate (*ETR*) and internal CO₂ concentration (*C_i*).

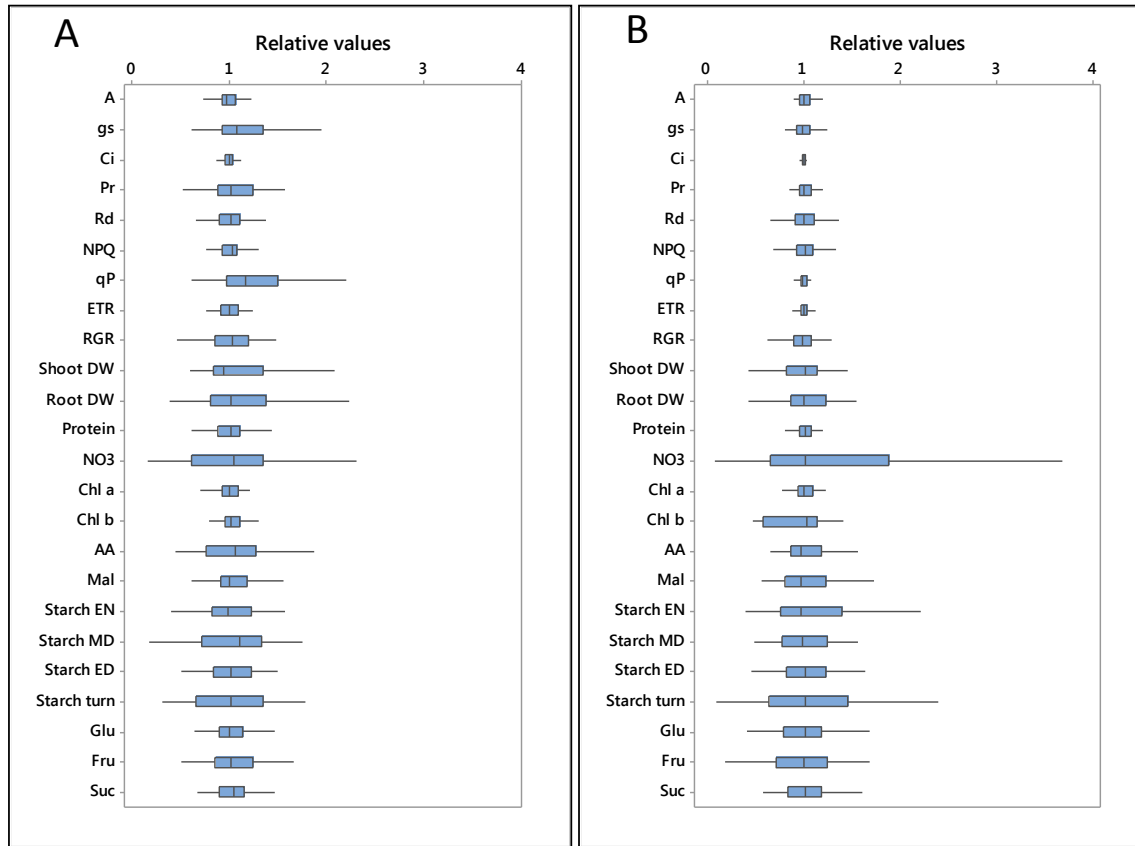


Figure 1. Boxplot graphs illustrating the changes in growth, physiological and metabolic traits from the individual data sets of 2012 (A) and 2013 (B) of a population of 71 introgression lines (ILs) of *Solanum pennellii* into a genetic background of *S. lycopersicum* (M82). Gas exchange and chlorophyll a fluorescence parameters: Photosynthesis (A), stomatal conductance (gs), intercellular CO₂ concentration (*C_i*), photorespiratory rate (Pr), dark respiration (Rd), Non-photochemical quenching (NPQ), photochemical quenching (qP), electron transport rate (*ETR*); Growth related parameters: Relative growth rate (RGR), shoot dry weight (Shoot DW), root dry weight (Root DW); Nitrogen and carbon containing compounds in leaves: malate (Mal), glucose (Glu), fructose (Fru), sucrose (Suc), chlorophyll a (Chl a), chlorophyll b (Chl b), protein, amino acid (AA), nitrate (NO₃), starch levels at the end of the night (Starch EN), middle of the day (Starch MD), end of the day (Starch ED) and starch turnover (Starch turn). Except for the data of starch, samples were harvested at the middle of the light period. The median is indicated by solid lines in each box. Data are normalized to the median of each trait.

Heritability of photosynthetic, plant growth and metabolic traits

We then assessed the heritability (h^2) of the plant growth, photosynthetic and metabolic traits evaluated by correlation analyses in individual and combined data-sets (Table I). This analysis revealed that the measured traits displayed h^2 values ranging between 0.57 and 0.96, for intrinsic water use efficiency (WUE) and shoot DW, respectively. The photosynthetic parameters measured in both experiments displayed h^2 varying between 0.68 and 0.87 for C_i and A , respectively. g_s and dark respiration (R_d) also presented high h^2 values of 0.70 and 0.79 respectively. Non-Photochemical Quenching, Electron Transport Rate, photochemical quenching (qP) and photorespiration (Pr) showed h^2 values of 0.73, 0.75, 0.86, and 0.82, respectively. h^2 values of 0.66, 0.96 and 0.94 were estimated for relative growth rate (RGR), shoot DW and root DW, respectively. The h^2 values were 0.75 for chlorophyll b and 0.92 for total amino acid content whilst chlorophyll a and nitrate contents displayed values of 0.80 and 0.90, respectively. We additionally calculated h^2 for the ratios between nitrate and total chlorophyll (0.87), total amino acids (0.88) and total protein contents (0.90). Heritability of the carbon containing compounds, varied between 0.83 (sucrose) and 0.94 (Starch-ED) at the end of the light period. The estimated starch turnover also presented high h^2 values of 0.94. Since h^2 measures the ratio of the variation between and within the geno-types, it can potentially lead to traits being artificially designated as having a high heritability; we additionally evaluated the correlation between the two experiments exactly as suggested by Schauer et al. (2008). By analyzing the correlation between experiments, this approach compares the averages between experiments and is, therefore, not as likely to be biased by technical factors of data acquisition.

By evaluating the correlation of the trends in physiological, growth and metabolites traits across the population (Table I) we observed that correlation coefficient values were significant only for Rd, NPQ and some of the carbon metabolism related metabolites (malate, glucose and sucrose). Thus, this result suggests that despite some of the evaluated traits are highly heritable caution should be taken with these parameters in *S. lycopersicum*.

Table I. Trait heritability in the population of 71 introgression lines of *Solanum pennellii* into a genetic background of *Solanum lycopersicum* (M82).

Trait	2012 h ²	2013 h ²	Mean h ²	2012/2013 r
Physiological related				
A	0.79	0.95	0.87	0.07
gs	0.67	0.73	0.70	-0.02
Ci	0.61	0.75	0.68	-0.05
WUE	0.57	0.57	0.57	0.03
Pr	0.81	0.84	0.82	0.17
Rd	0.67	0.92	0.79	** -0.40
NPQ	0.55	0.92	0.73	* 0.26
qP	0.73	0.76	0.75	0.08
ETR	0.83	0.90	0.86	0.21
Growth related				
RGR	0.79	0.54	0.66	-0.09
Shoot DW	0.97	0.95	0.96	0.01
Root DW	0.97	0.92	0.94	0.03
Nitrogen metabolism				
Protein	0.89	0.68	0.78	-0.12
Nitrate	0.94	0.85	0.90	0.13
Chl a	0.80	0.81	0.80	0.06
Chl b	0.67	0.83	0.75	0.10
Amino acids	0.91	0.92	0.92	* -0.25
Nitrate/TotalChl	0.92	0.82	0.87	0.20
Nitrate/Amino acids	0.88	0.88	0.88	0.03
Nitrate/Protein	0.93	0.86	0.90	0.04
Carbon metabolism				
Starch-EN	0.89	0.96	0.93	0.21
Starch-MD	0.91	0.95	0.93	0.06
Starch-ED	0.92	0.96	0.94	0.07
Starch turnover	0.93	0.95	0.94	0.10
Glucose	0.83	0.92	0.87	* 0.30
Fructose	0.88	0.93	0.90	0.21
Sucrose	0.75	0.90	0.83	* 0.24
Malate	0.87	0.88	0.87	* 0.29

*** : Significant at 1 and 5% probability by t-test

Pearson correlation analysis between physiological and growth related traits

To assess the level of association between the evaluated traits, we calculated Pearson correlation coefficients for all pairs of physiological, metabolic and growth related traits across the whole set of ILs in 2012 and 2013 data sets. The full data sets of correlation coefficients are presented in heatmaps of Supplemental Fig. S1. In the first year, we observed 60 positive and 44 negative significant correlations while in the second year, 70 positive and 33 negative significant correlations were detected. Probably due to the semi-controlled environmental conditions and a large environmental or environmental x genotype effect for most of the traits under study (see above), only 24 correlations overlapped at a level of significance of 5 % (Figure 2). Despite the presence of expected positive correlations, such as those A and g_s and ETR , C_i and g_s , some were less intuitive, such as the one involving malate negatively correlating with NPQ . Interestingly, no correlations with RGR were observed. However positive correlations were observed between leaf total amino acids content and root DW and shoot DW, as well as a negative correlation between starch levels at the end of the day and amino acids. Fructose, glucose and sucrose correlated positively each others, and also partially correlated with starch levels at the end of the day and midday. Surprisingly sucrose showed a positive correlation with C_i

	2012	2013
A x g _s	0.67	0.39
A x NPQ	-0.37	-0.70
A x ETR	0.35	0.70
C _i x g _s	0.84	0.74
qP x Pr	0.69	0.81
ETR x Pr	0.90	0.93
ETR x qP	0.69	0.90
C _i x Suc	0.23	0.26
Rd x AA	0.35	0.35
Mal x NPQ	-0.40	-0.39
Fru x qP	0.28	0.35
Shoot DW x Root DW	0.85	0.40
AA x Shoot DW	0.55	0.37
AA x Root DW	0.39	0.38
AA x Starch ED	-0.26	-0.29
Starch ED x Starch MD	0.73	0.52
Starch turn x Starch ED	0.93	0.41
Fru x Starch MD	0.56	0.47
Suc x Starch MD	0.40	0.56
Fru x Starch ED	0.52	0.24
Fru x Glu	0.61	0.88
Fru x Suc	0.38	0.56
Suc x Chl a	0.26	0.32
Chl a x Chl b	0.49	0.66

Negative	0.73-0.99	0.5-0.72	0.23-0.49
Positive	0.73-0.99	0.5-0.72	0.23-0.49

Figure 2. Person correlation analysis from the individual data sets of 2012 and 2013 of a population of 71 introgression lines (ILs) of *Solanum pennellii* into a genetic background of *Solanum lycopersicum* (M82). Significant correlation coefficients ($p \leq 0.05$) are indicated by dark, medium, and light shading, with positive and negative correlations being distinguished by green and red respectively. Gas exchange and chlorophyll a fluorescence parameters: Photosynthesis (A), stomatal conductance (g_s), intercellular CO₂ concentration (C_i), photorespiratory rate (Pr), dark respiration (Rd), Non-photochemical quenching (NPQ), photochemical quenching (qP), electron transport rate (ETR); Growth related parameters: Relative growth rate (RGR), shoot dry weight (Shoot DW), root dry weight (Root DW); Nitrogen and carbon containing compounds in leaves: malate (Mal), glucose (Glu), fructose (Fru), sucrose (Suc), chlorophyll a (Chl a), chlorophyll b (Chl b), amino acid (AA), starch levels at the end of the night (Starch EN), middle of the day (Starch MD), end of the day (Starch ED) and starch turnover (Starch turn).

Identification of QTL for leaf photosynthetic and metabolic traits in whole plant growth-related parameters

QTL were determined using analysis of variance and Dunnett's tests, at a significance level of 0.05, to compare statistically each IL with the control (M82). By comparing the two data sets it was observed that only part of the ILs were significantly different from the control M82 in both years of experiments and only these ILs were considered as true QTL. (Supplemental Fig. S2). Using this criterion, we identified 67 single-trait QTL. Of the photosynthetic parameters, net CO₂ assimilation rate (*A*) had the most complex genetic architecture with nine ILs exhibiting higher *A*. In contrast, only two QTL for stomatal conductance (*g_s*) and one QTL for non-photochemical quenching (*NPQ*), photorespiration (*Pr*) and *C_i* were identified. For plant growth related traits, we identified five QTL for higher and two for lower dry matter accumulation in shoots (Shoot DW) and 16 QTL for reduced Root DW. Using the same criterion we identified 29 leaf metabolite QTL. One QTL each for nitrate, chlorophyll *b* and total amino acid levels and 26 QTL for carbon metabolism namely three QTL for malate levels, 15 QTL for starch levels and six QTL for starch turnover. Moreover, we found two QTL for soluble sugars, one for fructose and one for sucrose (Figure 3).

Genomic localization and analyses of the identified QTL

In a next step, we identified the overlap between the introgressed regions of the ILs in order to map the identified QTL to smaller intervals, termed BINs (Figure 3 and Supplemental Table S5). The criteria to select the QTL-associated BINs for further comparative genomic analyses were: (i) that the regions were covered by at least two ILs displaying the same phenotype in both

experimental years or (ii) that the region was spanned by more than two ILs, so that they showed in all overlapping ILs the same phenotype in one harvest. By applying these criteria we identified 11 genomic regions which we further investigated for: (i) detailed gene and transposable elements (TE) prediction and annotation, (ii) candidate gene discovery and (iii) analyses of their genomic contexts (Supplemental Table S3). Out of the 12 BINs, only two, 9C and 11D, displayed the same number of predicted gene *loci* in the two parental species. In contrast, BIN 4DE displayed 12 % variations in the number of gene *loci* (Table II). Gene density was similar within BINs, with approximately 0.09 gene/1,000 nucleotides, with the exception of BIN 4DE that displayed only 0.02 gene/1,000 nucleotides.

Table II. Gene content of analysed BINs

Trait ^a	BIN	# of predicted <i>loci</i> ^b	
		<i>S. lycopersicum</i>	<i>S. pennellii</i>
A	2K	138	150
	11H	62	68
Root DW	1J	202	208
	2L	125	130
	4DE	1140	1292
	7BC	263	262
	9G	74	76
Shoot DW	9C	75	75
Root DW and Shoot DW	9D	54	56
Mal	11D	17	17
Starch ED	11B	100	104

^aTrait abbreviation are according to Figure 2

^bThe complete list of the predicted *loci* and their corresponding gene annotations are presented in Supplemental Table 3

Mapman annotation showed a wide distribution of categories in all of the selected BINs. All categories occurred in more than one analyzed genomic regions with the exception of category 6 (gluconeogenesis/glyoxylate cycle),

which appeared only in BIN 11B, and harbours a QTL for starch content in leaves at the end of the day. Diversity of Mapman categories found in this analysis denotes somehow a broad range of function for the genes spanning these genomic regions. However, when a further contingency analysis followed by a Fisher test was performed, results suggest that a considerable number of categories are over-represented within the genomic region analyzed and that in certain regions functional categories are differentially represented between the two genotypes (Supplemental Table S4).

The analysed regions showed very similar proportion of TEs in both species: 13.86 % in *S. lycopersicum* and 13.61 % in *S. pennellii*. Of note is the under representation of TEs in all regions analyzed when compared to the whole genomes, which correspond to 39 % in *S. lycopersicum* (M82) and 37 % in *S. pennellii* (Bolger et al., 2014) indicating the euchromatic nature of the studied genomic regions. When comparing within BINs, TE content varied from 5.82 to 19.57 % in *S. lycopersicum* and from 5.99 to 17.32 % in *S. pennellii*. Exceptionally, BIN 4DE displayed a high enrichment of retrotransposons; 47.36 % in *S. lycopersicum* and 45.09 % in *S. pennellii*, consistent with its pericentromeric localization on 4 chromosome (The Tomato Genome Consortium, 2012) and the difference in gene number and gene density mentioned above.

Table III. Differentially over-represented Mapman categories in the analyzed genomic regions from *S. pennellii* and *S. lycopersicum*.

BIN	Trait	Over-represented Mapman category (BIN code)	<i>S. pennellii</i>		<i>S. lycopersicum</i>	
			Count	<i>p</i> value ^(*)	Count	<i>p</i> value ^(*)
1J	Root DW	Development (33)			13	0.032
		Polyamine metabolism (22)	2	0.013		
		Miscellaneous (26)	22	0.038		
2L		Biodegradation of xenobiotics (24)			2	0.011
		Miscellaneous (26)	16	0.021		
4DE		Signalling (30)			78	0.047
7BC		Major CHO metabolism (2)			6	0.025
		Lipid metabolism (11)			10	0.036
		Photosynthesis (1)			9	0.049
9G		RNA (27)	18	0.016		
		Stress (20)	8	0.024		
2K	A	Cell wall (10)			7	0.047
		Minor CHO metabolism (3)	4	0.014		
11H		Metal handling (15)	2	0.019		
9D	Root & Shoot DW	TCA / organic transformation (8)	2	0.011		
11B	Starch-ED	Amino acid metabolism (13)	5	0.016		
		Not assigned (35)	12	0.046		
11D	Malate	Metal handling (15)			2	0.001
		RNA (27)	6	0.018		

(*) Over-representation was assessed as described in the Material and Methods section and significance level was tested by a Fisher test ($p < 0.05$).

Abbreviations: DW, dry weight; A, CO₂ assimilation rate; CHO, carbohydrates; TCA, tricarboxylic acid cycle; Starch-ED, starch levels at the end of day.

proportion corresponds to RNA metabolism or transport associated genes. With the exception of BINs 9D (*S. pennellii*) and 11B (both genotypes) more than 50 % of the candidate genes selected belong to one over-represented Mapman category, whilst the only candidate selected from BIN 11D belongs to a non-overrepresented category (34 transport) (Supplemental Fig. S3).

Identity between predicted proteins of *S. lycopersicum* (M82) and *S. pennellii* varied between 80 and 100 % with only four proteins predicted to be identical. Out of the 73 polymorphic proteins, 41 showed differences in length. Interestingly, two and eight genes were exclusively present in *S. lycopersicum* or *S. pennellii*, respectively (Table IV). In order to better understand the origin of the observed protein polymorphisms and support the candidature of the identified genes, the independent prediction of gene structure and TE insertion patterns were compared. More than 50 % of the candidate genes showed contrasted TE insertions within their coding or non-coding flanking regions (Table IV) between genotypes. Four patterns were observed (Figure 4).

The succinate dehydrogenase iron-sulfur protein encoding gene (Soly02g093680) have an insertion of a DNA transposon (TIR_DNA9-6_Stu) in the first exon-intron junction in the wild allele, which leads to a differential predicted splicing pattern between genotypes (Figure 4A). The predicted proteins differ in length and shared 87% identity (Table IV). Expression pattern of this same gene showed no differences between genotypes when leaf tissues were analysed (Chitwood et al., 2013). However, significant higher expression was observed in fruits from *S. pennellii* in comparison with *S. lycopersicum* (Chitwood et al., 2013). The upstream region of a glucose ribitol dehydrogenase encoding gene (Soly04g014670) from *S. lycopersicum* harbors two

retrotransposons (Figure 4B). The orthologous *S. pennellii* loci located in the overlapping region of IL4-2, 4-3 and 4-3-1 is less expressed in these lines in comparison to those observed in the rest of the IL population (Supplemental Table S7). The 1,000 bp upstream region of *S. pennellii* allele has at least 5 InDels ranging in length between 7 to 69 bp in addition to several SNPs.

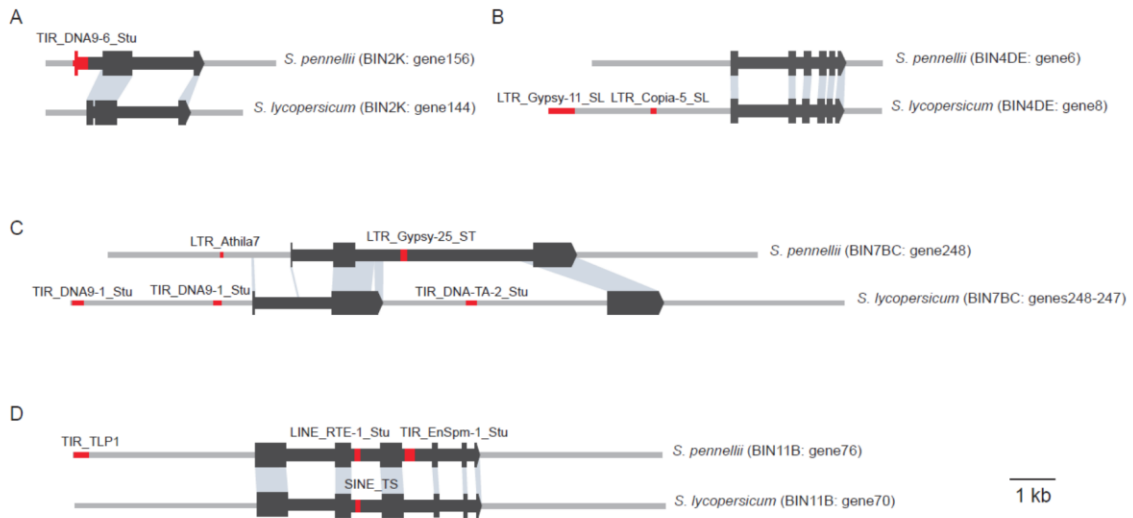


Figure 4. Structure of four candidate genes illustrating differential TE insertions and putative variability in gene and regulatory sequence structure. (A) Succinate dehydrogenase/fumarate reductase. (B) Hydroxycinnamoyl CoA transferase. (C) Glucose ribitol dehydrogenase. (D) 2-Oxoglutarate malate translocator. Red: differential inserted TE between *S. pennellii* and *S. lycopersicum*. Light gray: intergenic regions. Gray boxes: exons. Gray lines: introns. Light gray shades indicate synteny over exons. TE insertion patterns were inspected in a context of $\pm 4,000$ bp around each identified candidate gene for both alleles or until the next *loci* coding sequence.

Gene 248, functionally annotated as a hydroxycinnamoyl CoA transferase (Soly07g008380) presents two condensation domains (Pfam accession cl19241) in the *S. pennellii* allelic form, which correspond to two separately predicted *loci* in *S. lycopersicum* (genes #247 and #248). Although different TEs were identified into the upstream non-coding and intron regions, the difference in gene prediction appears to be the consequence of a deletion of

77 bp in intron 2 of *S. pennellii* allele. Accordingly, structure predicted for M82 cultivar is the same as that reported for the *S. lycopersicum* (cultivar Heinz 1706) allele (Figure 4C). A survey into RNA-seq data reveals lower mRNA levels of this gene in leaf tissue from the IL7-4, 7-4-1 and 7-5, which harbor the *S. pennellii* allele, in comparison to M82 (Supplemental Table S7). The 2-oxoglutarate malate translocator encoding gene presents also differential TE insertion patterns between both genotypes; both in intronic and in the 5' upstream non-coding regions (Figure 4D). Interestingly, this candidate gene is more expressed in the ILs 11-1 and 11-2 harbouring the wild type allele (Supplemental Table S7).

Expression analysis of candidate genes

In order to investigate further on the possible functional mechanisms involved in traits evaluated, we checked the expression levels of the identified candidate genes (Table IV) in the leaf of the ILs based on previously published RNA-seq data (Chitwood et al., 2013). Following this strategy, 30 out of 87 genes showed significant changes in gene expression between the ILs harbouring the *S. pennellii* loci compared to the ILs harbouring the *S. lycopersicum* loci and associated with the phenotypic traits (Supplemental Table S7). For example, in the overlapping region between IL1-4 and IL1-4-18 (BIN 1J), which harbors QTL for starch turnover, root DW, *gs* and *Ci*, four candidate genes showed up-regulation in *S. pennellii* loci compared to the ILs containing *S. lycopersicum* loci, these including three genes involved in hormone metabolism, and one gene involved in Calvin-Benson cycle and photosystem annotated as a triose-phosphate isomerase (Soly01g111120). The gibberellin regulated protein (Soly01g111080) had about 25 fold higher expression in IL1-

4 and IL1-4-18 compared to all other lines. Pairwise analysis of the promoter region revealed a 82 and 32 bp deletion in M82 at positions around 100 and 800 bp, in addition to three InDels ranging in length between 17 to 23 bp. Similarly, Solyc01g110940 and Solyc01g111010 are only expressed in IL1-4 and 4-1-18 and sequence analysis of their promoter regions indicated little similarity with M82. For the triose-phosphate isomerase gene (Solyc01g111120), a 94 bp deletion in M82 at - 25 of ATG was detected, in addition to InDels and SNPs, and was associated to higher expression of this gene in IL1-4 and IL1-4-18.

In BIN 11H, a mitogen-activated protein kinase (Solyc11g072630) orthologue to AT4G01370 in Arabidopsis and located in the overlapping region of the IL11-4 and IL11-4-1, showed changes in gene expression in these two lines compared to other lines. Sequence analysis of the non-coding region, upstream of the start codon ATG (up to around -1000 bp) from *S. lycopersicum* cv. M82 and *S. pennellii* genome sequences (Bolger et al., 2014) showed at least three InDels ranging in length from 14 to 36 bp, in addition to several smaller InDels. In this region a QTL for high A was mapped. Within this region two other genes annotated as mitochondrial electron transport/ATP synthesis, F1-ATPase (Solyc11g072450) and Protein kinase (Solyc11g072710) could also be candidate genes explaining higher A in the lines IL11-4 and IL11-4-1. Even though expression of these genes did not vary in these lines compared to others, analysis of sequence polymorphisms indicates that several consecutive InDels are present between *S. lycopersicum* and *S. pennellii*.

In the IL9-1, changes in the expression of the pyruvate kinase gene (Solyc09g008840) could be associated with higher amino acids and shoot DW,

and sequence alignment between M82 and *S.pennellii* at the promoter region showed six InDels ranging in length between 7 to 26 bp. On the other hand, the expression level of the glucose transporter (Solyc09g074230), located in BIN9G where an association for root DW had been detected, was lower in the overlapping IL9-2 and IL9-2-6 compared to other lines. A very low similarity between M82 and *S. pennellii* sequences upstream of the protein coding region of this gene was observed with a large InDel around -100 bp.

A QTL for higher starch ED, starch MD, starch turnover and malate accumulation was mapped in the BIN 11B. Gene expression of the 2-oxoglutarate/malate translocator (Solyc11g010290) that located in this BIN, which corresponds to the overlapping region of IL11-1 and 11-2, showed about 2 fold higher expression in these two lines compared to the other lines. The sequence alignments of the promoter regions between M82 and *S.pennellii* revealed the presence of 5 InDels ranging in length between 3 bp to 16 bp, in addition to several SNPs.

In addition to the glucose ribitol dehydrogenase encoding gene (Solyc04g014670) located in the overlapping region of IL4-2, 4-3 and 4-3-1 (described above), a 6-phosphofructokinase 2 (Solyc04g015200) had relatively higher expression in IL4-2, 4-3 and 4-3-2 compared to other lines. The sequence comparisons of the upstream region of this gene indicated a deletion of more than 60 bp at around - 250 bp in *S. lycopersicum*. In BIN 7B, located at the top of chromosome 7, three candidate genes encoding for sugar/inositol transporter, serine/threonine protein kinase, and peptide transporter were proposed. Levels of expression of these genes was lower in all overlapping lines IL7-4, 7-4-1 and 7-5 compared to other lines. Comparing the sequences of

the upstream coding region of these genes between M82 and *S. pennellii* showed the presence of several InDels SNPs. The low expression of these genes, in addition to the expression level of hydroxycinnamoyl CoA transferase encoding gene (Soly07g005760) discussed above, is concomitant to a decreased level of several traits mapped to this region, i.e. Root DW, Starch-ED, Starch-EN, *ETR*, *Pr*, *NPQ* and malate content.

DISCUSSION

Variance in gas exchange and fluorescence in the *S. pennellii* IL population

Nine *S. pennellii* ILs (IL2-5, 2-6, 3-1, 3-5, 4-4, 5-1, 9-3-2, 11-4-1 and 11-4) displayed higher *A* for both growth seasons. No ILs with lower *A* than M82 were detected, which is surprising because in previous studies we had observed that *S. pennellii* (Carrari et al., 2003) and *S. lycopersicum* (Nunes-nesi et al., 2005) have *A* values of 9 and 24 $\mu\text{mol m}^{-2} \text{s}^{-1}$ respectively. This suggests a relatively complex genetic architecture of photosynthetic performance in tomato. In the present study, we measured maximal increases in *A* of 19% (first year experiment) and 14% (second year experiment), which are in the range of the increases reported using transgenic approaches with increases in *A* of up to 19% in tobacco (Simkin et al., 2015) and 25% in tomato (Nunes-nesi et al., 2005). A strong positive correlation between *A* and *gs* (Figure 3) was observed, suggesting that the observed increases in *A* were at least partially related to stomata movements. As such, the absence of ILs with changes in the *A/gs* ratio indicates that increases in *A* were the result of lower stomatal limitation in these ILs. Furthermore, it has been reported in transgenic plants that both organic acid and sucrose-dependent modifications of stomatal function greatly influence both the *A* as well as the biomass in *Arabidopsis*, tomato and tobacco (Nunes-

Nesi et al., 2007; Araújo et al., 2011; Tapia et al., 2011; Daloso et al., 2015; Medeiros et al., 2015). In addition, the identification of QTL involved in traits related to *gs* have been reported (Price et al., 1997; Frei et al., 2008; Khowaja and Price, 2008; Xu et al., 2008; Muir et al., 2014b; Fanourakis et al., 2015). Recently, using a subset of the tomato IL population, Fanourakis et al. (2015) assessed variation in stomatal responsiveness to desiccation and *gs*-related anatomical traits under well-watered conditions, observing considerable differences with respect to stomatal size, density, distribution between the leaf adaxial and abaxial sides, as well as pore area per stomatal area. This study revealed that ILs 1- 2, 1-2-4, 2-3, 2-4, 2-6, 2-6-5 and 3-1 displayed significant changes in the characteristic features of *gs*. Given that one of these four ILs (IL 2-6) displayed higher *A* and *gs* in the two independent harvests we analysed, provides support for the conclusion that *gs* has a major influence on photosynthetic rates in tomato. In this sense, most of the photosynthetic variation has been explained by variations in *gs*, previous studies have reported that several segments of the *S. pennellii* genome, when introgressed into the *S. lycopersicum* background, resulted in changes in carbon isotope composition ($\delta^{13}\text{C}$) relative to M82 (Xu et al., 2008). In this study the line IL 5-4 displayed the least negative $\delta^{13}\text{C}$, or the greatest WUE, and other ILs had more negative $\delta^{13}\text{C}$ than M82, including IL2-3, IL2-4, IL12-2, IL3-5, IL7-2 and IL9-2. In the same study, the IL 11-4 also displayed a less negative $\delta^{13}\text{C}$ than M82, which is indicative of a larger photosynthetic potential by that line which corroborates with our data, since both IL 11-4 and its overlapping line (IL 11-4-1) displayed elevated *A*.

Chlorophyll fluorescence is a sensitive indicator of uptake, use and dissipation of photosynthetically active radiation and therefore changes in chlorophyll fluorescence emission may be related to the photosynthetic performance (Baker and Rosenqvist, 2004). Under chilling stress in tomato, two QTL affecting non-photochemical quenching (*NPQ*) were detected and one QTL associated with both photochemical quenching (*qP*) and *Fv/Fm* were identified, all on chromosome 5 (Oyanedel et al., 2000). In the present study, only IL 7-4-1 showed significant changes in fluorescence parameters, but not in *A* (Figure 2). Although no consistent correlation was found between chlorophyll fluorescence and photosynthesis, positive correlation was observed between *ETR* and *A* (Figure 3), thus suggesting that the higher photosynthetic rates observed in some of the ILs might also be associated with changes in photochemical reactions. Interestingly, *NPQ* negatively correlated with malate levels and both traits are collocated in the same genomic region delimited by the IL 7-4-1 (Figure 2). Similar correlation have been observed in *Capsicum chinense* (Rosado-Souza et al., 2015). It has been shown that malate is an essential storage carbon molecule and an intermediate of the TCA cycle in plants (Baxter et al., 2005; Fernie and Martinoia, 2009). Furthermore, malate is a pH regulator and exhibits partial control over the efficacy of nutrient uptake (Fernie and Martinoia 2009) and, additionally, recent evidences indicates that malate (and fumarate) plays key roles as regulator of stomatal function (Nunes-Nesi et al., 2007; Araújo et al., 2011; Medeiros et al., 2015).

Trade-off between leaf metabolism and growth related parameters

Amongst the metabolic parameters measured the set of carbon rich metabolites displayed the highest *h2* (average of 0.90) and the greatest number

of significant correlations between the two seasons (Table I). QTL for sugar content have previously been identified in tomato (Eshed and Zamir, 1995; Fridman et al., 2004; Baxter et al., 2005), however these studies were confined to the fruit. In the present study we identified one negative QTL for sucrose and fructose at IL 9-3-2 (Figure 2). This result is in the line with previous studies reporting that sucrose and fructose levels are considerably lower in leaves of all wild species of tomato (Schauer et al., 2005). Additionally, considering that leaves are the ultimate source of most fruit photoassimilates (Lytovchenko et al., 2011), and overwhelming evidence suggests that sugars are apoplastically unloaded from the phloem into the fruit (Fridman et al., 2004; Hackel et al., 2006), these changes in leaf sugar levels would be expected to influence sugar levels in fruits. Comparing our data with those reported by Schauer et al. (2006) we verified that two ILs having higher *A* (IL2-5 and IL2-6), harboring the genomic region 2K, in fruits showed massive reduction in most of the amino acids and increased levels of sucrose, malate and isocitrate, and the amino acids proline, glutamate and aspartate. On the other hand, another line with higher *A*, IL4-4, displayed in fruits enhanced accumulation in several amino acids, sugars and organic acids in fruits. In contrast, other two lines IL11-4 and 11-4-1, with higher *A* and harboring the genomic region 11H, did not display any significant changes in 74 metabolic traits evaluated by Schauer et al. (2006). We additionally evaluated the fruit metabolic data for other four lines (IL3-1, 3-5, 5-1, 9-3-2) with higher *A* and verified that these lines had significant changes in relatively few metabolites. Taken together these results indicate that an increase in *A* appears to only have a minor effect on fruit composition. Similarly, no consistent correlation between leaf starch levels, biomass production and

plant growth were found in the present study (Supplemental Fig. S2). However, shoot and root DW showed a positive correlation to total amino acids (Figure 3).

Given that large amounts of nitrogen are used in the construction of the photosynthetic machinery and the important link between nitrogen metabolism and photorespiration, optimal CO₂ assimilation through photosynthesis and, as a consequence, biomass production requires an adequate nitrogen supply (Bauwe et al., 2010; Nunes-Nesi et al., 2010). In the present study, only three lines displayed consistent changes in nitrogen metabolism related traits, leaf total amino acids, chlorophyll *b* and nitrate levels in both experiments - lines IL9-1, 10-1 and 11-4-1. Interestingly, the lines IL9-1 and 10-1 showed higher shoot DW without changes in *A* (Figure 2), whilst the line IL11-4-1 which have higher nitrate levels in leaves also displayed higher *A*. These results are somehow surprising because it is well known that photosynthesis plays an important role in nitrogen assimilation providing energy and carbon skeletons (Nunes-Nesi et al., 2010). Thus it would be expected that nitrogen related traits would be colocalized with assimilation rate, shoot and root DW traits. However it has been shown that compromised nitrate assimilation in tomato leaf have no effect on photosynthesis and plant growth (Sienkiewicz-Porzucek et al., 2008; Sulpice et al., 2010). We additionally identified a total of 16 QTL for root DW and seven QTL for shoot DW (Figure 2); however, no consistent co-localisation was found between *A* and shoot DW when all ILs were compared (Supplemental Fig. S2). Given that the experiments were carried out in relatively young plants prior to flowering it is not entirely possible from this study alone to assess the link between *A* and fruit yield. That being said, fruit yield has been measured in several previous studies and is highly robust across

harvests (Semel et al., 2006). Interestingly, this study revealed that the lines IL2-5 (plant weight and fruit number), 2-6 (plant weight and fruit number), 3-5 (biomass, plant weight and fruit number), 9-3-2 (fruit number), 11-4 (plant weight and fruit number) and 11-4-1 (plant weight and fruit number) had significant higher yield related traits and these lines had higher *A* in our study *A*. Regarding root biomass accumulation we found 12 ILs with reduced root DW. This trait was affected by genomic regions of nine out of the 12 chromosomes consistent with the belief that root growth related traits are complex and controlled by many genes with small genetic effect (Sharma et al., 2011). Recently, significant developmental differences between M82 and *S. pennellii* were observed by measuring a large range of root traits including cell number, individual cell types within, cortex-endodermis initial spatiotemporal patterning differences, variability in cell cortex layer and quiescent center cell number, root growth, and the novel gravity set point angle (Ron et al., 2013). Comparing our data with those reported by Ron et al. (2013), we verified that six ILs that displayed reduced DW have also been reported as lines with altered root related traits. IL 1-4-8 has a positive effect on cell number in the second cortex layer, while IL showed a decrease in cell number in the endodermis. In IL4-2, the stele areas and total root area are reported to be larger than their counterparts observed in M82 plants. Another interesting line that displayed reduced root DW in our study was the IL7-5. This line have decreased cell number across several cell layers but root area and area of the first cortex layer were increased. The line IL5-1-1 showed decreased cell number in the pericycle. The line IL9-2 had shorter cell cycle which lead to reduced cell number within the root meristem and increased number of cells in the

elongation zone. Correlation analysis showed that root DW has a positive correlation to shoot DW and to A (season 2012), suggesting that photosynthetic activity and shoot growth are also important determinants of root growth. When considered together, our data in addition to previous published data (Ron et al., 2013), represent an important step toward defining genetic determinants of the natural variation on the regulation of root growth and development between species. In the BIN 1J which is related to root DW one gene encoding Auxin responsive SAUR protein and one related to Gibberellin regulated protein were identified (Supplemental Table S7). Small auxin-up RNAs (SAURs) are the largest family of early auxin response genes, which, due to extensive genetic redundancy, still do not have a clear function (Ren and Gray, 2015). However, it has been proposed that SAURs are key effector outputs of hormonal and environmental signals that regulate plant growth and development (Ren and Gray, 2015). In tomato, genomic analyses revealed 99 SAURs, which are not randomly distributed in the genome but organized in tandem arrays of highly related genes (Wu et al., 2012). In our study, in the BIN 1J, 33 SAURs were found in the *S. pennellii* and 28 in the *S. lycopersicum* genome, indicating that this genomic region represents a hot spot for auxin responses and is possibly related to root growth and development (Supplemental Table S3).

Impact of transposable elements on gene structure and expression.

We further selected genes based on biological processes associated with the traits under study (Table III). The candidate genes were surveyed for their protein sequence identity, TE insertion pattern and gene expression levels in *S. pennellii* and *S. lycopersicum* ortholog loci (Supplemental Table S6). TEs are an

important source of genetic variation in eukaryotic species. They contribute to novelty in gene structure and regulation, at the structural, transcriptional and post-transcriptional levels (Feschotte, 2008). In this work, we identified several candidate genes of *S. pennellii* and *S. lycopersicum* with polymorphic TE insertions in coding and non-coding regions. These TE insertions promoted putative changes in CDSs length and sequence, as well as, in introns, promoters and intergenic regions (Figure 4 and Table III). Most of the insertions were found upstream or downstream of the coding regions, which could affect transcription profiles, by modifying the promoter sequences leading to alternative transcription patterns, new transcription start sites or, disrupting *cis* regulatory sequences (Feschotte, 2008). Five *S. pennellii* and one *S. lycopersicum* genes exhibit exclusive TE insertions upstream of their coding region and were up-regulated in the ILs carrying the corresponding loci, in line with previous observation that TEs are associated with gene enhancer activity and allelic regulatory variation in plant (Makarevitch et al., 2015). On the other hand, TEs inserted close or into genes might also act as targets of RNA-dependent DNA methylation (Castel and Martienssen, 2013; Quadrana et al., 2014). Methylation in plant promoters is well-understood and is associated with transcriptional gene silencing. Additionally, it has been demonstrated that methylation on gene body stimulates transcription elongation (Jones, 2012). Four *S. pennellii* and one *S. lycopersicum* genes with different TE inserted in the upstream coding regions showed down-regulation in the ILs where they were located (Supplemental Table 6).

Table IV. Selected candidate genes.

Trait	BIN	Functional_Description	<i>S. pennellii</i>		<i>S. lycopersicum</i>		Differentially inserted TEs		Protein		
			# Gene	Sense	# Gene	Sense	<i>S. pennellii</i> TE positions	<i>S. lycopersicum</i> TE positions	SP length (aa)	SL length (aa)	% Id
Root DW	1J	Glucose-1-phosphate adenylyltransferase	g1	-	g1	-	NCU (2)	NCU (2)	285	282	98
	1J	26S proteasome subunit P45	g15	-	g14	-	introns	none	398	398	100
	1J	Fructose-bisphosphate aldolase, class-I	g52	+	g51	+	none	none	475	400	92
	1J	Auxin responsive SAUR protein	g70-110 (33)	both	g68-104 (28)	Both	intron-exon	intron (2)	NA	NA	NA
	1J	Gibberellin regulated protein	g115	-	g110	-	none	none	100	100	97
	1J	Plant neutral invertase	g117	-	g112	-	NCU (2)	NCU (5)	568	568	100
	1J	Triosephosphate isomerase	g118	-	g113	-	none	none	323	338	81
	1J	Amino acid transporter, transmembrane	g133	-	g129	-	NCU, NCD	none	400	400	99
	1J	Myb transcription fator	g147	-	g143	-	NCU	NCU (2), NCD	252	237	99
	1J	Glyoxylate_hydroxypyruvate reductase	g159	+	g156	+	none	none	366	366	99
	1J	Cyclin-like F-box	g186	-	g181	-	NCD (2)	intron	475	475	99
	1J	Cyclin-like F-box	g187	-	g182	-	none	none	193	171	98
A	1J	Rop nucleotide exchanger, PRONE	g192	-	g186	-	NCU (2)	NCU (3)	577	577	99
	2K	ATPase, F1 complex, beta subunit	g20	+	g20	+	NCU	none	547	548	99
	2K	Peptidase S14, ClpP	g32	-	g32	-	none	none	117	343	98
	2K	Peptidase S14, ClpP	g33	-	absent	NA	none	NA	228	NA	NA
	2K	Peptidase, trypsin-like serine and cysteine	g44	-	g43	-	NCU (3)	none	1152	1136	98
	2K	Serine hydroxymethyltransferase	g57	+	g55	+	intron (3)	intron (3), NCD	761	761	99
	2K	NADH dehydrogenase, ETC complex I subunit	g120	-	g112	-	none	none	156	156	98
Root DW	2K	Succinate dehydrogenase iron-sulfur protein	g156	-	g144	-	intron-exon	none	279	261	87
	2L	Myb transcription fator	g14	-	g13	-	none	NCU	371	372	97
	2L	Myb transcription fator	g87	-	g80	-	NCU	intron	249	250	99
	2L	Unknown Protein	g88	-	absent	NA	none	NA	385	NA	NA
	2L	DNA-binding WRKY	g131	-	g124	-	NCD (2)	intron	118	117	99
Root DW	2L	Transcription factor, TCP	g133	+	g126	+	none	none	216	175	80
	4DE	Glucose ribitol dehydrogenase	g6	+	g8	+	none	NCU (2)	253	253	99
	4DE	RHO protein GDP dissociation inhibitor	g11	-	g15	-	NCD	none	243	243	99
	4DE	Pyrophosphate-dependent phosphofructokinase	g51	-	g51	-	NCU, NCD (2)	NCU (2), NCD	456	456	99
	4DE	Guanine nucleotide exchange factor-like protein	g1274	-	absent	NA	NCU (6), intron (2), NCD (3)	NA	317	NA	NA
	4DE	Homeobox-leucine zipper protein ROC3	g1494	-	g1300	-	NCU (2), NCD (2)	none	221	246	85
	4DE	Adenylate kinase	g3433	-	g2768	-	NCD	NCU (3), NCD	269	269	99
	4DE	Ammonium transporter	g3813	-	g3075	-	NCU (3)	NCU (4), NCD	514	514	99
	4DE	Myb-like DNA-binding region, SHAQKYF class	g4104	-	g3265	+	none	NCU	542	392	94
	4DE	Myb-like DNA-binding region, SHAQKYF class	g4110	-	absent	NA	NCU (3), NCD (2)	NA	247	NA	NA
Root DW	4DE	Auxin Efflux Carrier	g4584	-	g3686	-	NCU, NCD (2)	intron, NCD (3)	204	204	99
	7BC	Hydroxycinnamoyl CoA transferase	g31	-	g36	-	NCU (3), NCD	none	360	355	97
	7BC	Tetraspanin, Senescence-associated protein	g74	+	g78	+	NCD (2)	NCD (2)	266	266	99
	7BC	Ankyrin	g80	-	g84	-	NCU, NCD	none	339	339	99
	7BC	Trehalose-phosphate synthase	g95	+	g97	+	none	none	876	876	99
	7BC	Auxin efflux carrier	g129	+	g133	+	NCU	none	631	631	99
	7BC	Sugar inositol transporter	g135	-	g138	-	NCU	none	513	513	99
	7BC	Pentatricopeptide repeat	g136	+	g139	+	NCU	none	693	693	99
	7BC	Serine threonine protein kinase	g140	-	g142	-	NCU (3), NCD (3)	NCD	742	768	97
	7BC	Homeobox protein knotted-1-like 3	g146	+	g148	+	none	exon, NCD	478	467	97
	7BC	Ankyrin, Palmitoyltransferase akr1	g170	-	g170	-	none	NCU	663	663	99
	7BC	Adenylate cyclase	g177	-	g177	-	none	none	202	236	98
	7BC	Hydroxycinnamoyl CoA transferase	g248	-	g247	-	NCU, intron	NCU	466	403	85
	7BC	Hydroxycinnamoyl CoA transferase	absent	NA	g248	-	NA	NCU (2)	NA	372	NA
	7BC	Hydroxycinnamoyl CoA transferase	g250	-	absent	NA	NCU (3), NCD	NA	399	NA	NA
	7BC	Pto-like, Serine, threonine kinase protein	g251	+	g249	-	NCU, NCD (5)	NCD (2)	854	772	99
	7BC	Hydroxycinnamoyl CoA transferase	g253	-	absent	NA	NCU (2)	NA	399	NA	NA
	7BC	Multi antimicrobial extrusion protein MatE	g254	+	g250	+	NCU, intron (4)	NCU (2), intron (4)	451	451	98

	7BC	K Homology, type 1, Nucleic acid binding protein	g265	-	g259	-	NCU	NCD (3)	485	482	98
	7BC	TGF-beta receptor, type I_II extracellular region	g272	+	g261	+	NCU (2), NCD	NCU-exon-intron, intron-exon (3), intron	584	2461	99
Shoot DW	9C	Phosphatidylinositol-4-phosphate 5-kinase	g3	-	g3	-	none	none	822	311	87
	9C	Phosphatidylinositol-4-phosphate 5-kinase	absent	NA	g4	-	NA	NCU	NA	411	NA
	9C	Armadillo-like helical, HEAT repeat family protein	g4	+	g5	+	NCU, intron	NCU (3)	341	331	66
	9C	Armadillo-like helical, HEAT repeat family protein	g6	+	g7	+	intron-exon, intron, NCD	NCU, intron-exon, intron (2)	1686	1688	94
	9C	Serine_threonine protein kinase	g17	-	g18	-	NCU, intron, intron-exon	intron	1300	872	90
	9C	Pyruvate kinase	g34	-	g36	-	none	none	564	568	99
	9C	Receptor like kinase, RLK	g36	-	g38	-	NCU	NCU (2)	673	675	99
	9C	Oxoglutarate oxygenase, Gibberellin oxidase	g55	-	g55	-	NCU, intron	NCU	378	365	98
	9C	1,4-alpha-glucan branching enzyme II	g66	+	g61	+	none	NCU, intron	874	852	97
Root DW	9D	Vacuolar protein sorting-associated protein	g1	+	g1	+	intron (2), intron-exon-NCD, NCD	intron	2394	2404	99
Shoot DW	9D	Serine_threonine protein kinase	g2	-	g2	-	NCD (3)	NCU, NCD	1020	1127	99
	9D	APO protein 1, chloroplastic	g4	-	g4	-	NCU (2)	NCU (2)	412	412	98
	9D	Basic leucine zipper	g14	-	g13	-	none	none	442	434	97
	9D	SELF PRUNING 9D	g21	+	g20	+	NCU (5), intron	intron	172	172	99
	9D	Cytochrome P450	g34	-	absent	NA	NCU, NCD (2)	NA	455	NA	NA
	9D	Cytochrome P450	g35	+	absent	NA	none	NA	375	NA	NA
	9D	Lipid A ABC transporter permease	g54	-	g50	-	none	NCU, intron	650	650	98
	9D	Rho GTPase activating protein 2	g60	-	g56	-	NCU (2)	NCU (5)	529	529	99
	9D	Auxin responsive SAUR protein	g61	+	g57	+	none	NCU	150	148	97
Root DW	9G	Cellulose synthase	g26	-	g33	-	intron	none	1048	1048	99
	9G	Glycosyl transferase, family 8	g59	-	g59	-	NCU (2)	NCU	354	354	99
	9G	Sugar_inositol transporter	g84	-	g86	-	NCU	intron-exon	483	480	99
	9G	Aldo_keto reductase	g94	+	g94	+	NCU (4)	NCU	470	470	99
Starch-ED	11B	UDP-galactose transporter-like protein	g10	+	g10	+	none	none	319	315	98
	11B	Nucleotide-sugar transporter	g12	-	g12	-	none	none	397	397	99
	11B	2-phosphoglycolate phosphatase	g13	-	g13	-	none	intron	310	310	99
	11B	Beta-glucosidase G4	g22	+	g21	+	intron	intron (3)	512	514	91
	11B	14-3-3 protein	g68	+	g62	+	none	NCU	258	258	99
	11B	2-oxoglutarate_malate translocator	g76	-	g70	-	NCU, intron (2)	intron	541	544	99
	11B	Pyrophosphate-dependent phosphofructokinase	g90	+	g84	+	NCU, NCD	NCU	532	532	99
Malate	11D	2-oxoglutarate_malate translocator-like protein	g8	-	g8	-	NCU (2)	NCU (2), intron (2)	812	814	99
A	11H	ATPase, F0 complex, subunit D, mitochondrial	g17	-	g18	-	NCU	NCU	168	168	100
	11H	JNK MAP kinase	g35	+	g34	+	NCU, intron, NCD	NCU, intron	372	442	100
	11H	Serine_threonine protein kinase	g41	+	g40	+	intron (3)	NCU (2)	1503	1503	99

Abbreviations: NCU, non-coding upstream; NCD, non-coding downstream; SP, *S. pennellii*; SL, *S. lycopersicum*; DW, dry weight; A, CO₂ assimilation rate; Starch-ED, starch levels at the end of day.

A small number of candidate genes (7%) showed TE insertions in coding gene regions. This kind of mutation can primarily lead to gene disruption. However, if the gene remains transcriptionally active in the presence of TE insertion, two different processes can occur. The first is post-transcriptionally gene silencing by chimeric gene-TE mRNA degradation via RNAi (Feschotte, 2008). The second is exaptation, in which the TE becomes part of a protein

coding sequence, which is the case of the succinate dehydrogenase gene in the BIN 2K of *S. pennellii*. TE exaptation has been recognized in plants (Hoen and Bureau, 2012). Noteworthy, the iron sulfur subunit of the succinate dehydrogenase protein complex has been previously related to higher *A* in tomato and Arabidopsis (Araújo et al. 2011; Fuentes et al. 2011). It has been reported that reduction in the activity of this enzyme enhances *A* via an increased stomatal aperture and indeed, one of the line harboring the region 2K also displayed higher *g_s* and *A*, suggesting stomatal effect on the increased *A* observed in this line.

CONCLUDING REMARKS

The current study is, to our knowledge, the largest study of photosynthetic gas exchange, growth and metabolic parameters in tomato leaves to date. Importantly, our results demonstrates significant natural variation in photosynthetic, growth, and essential metabolites (C and N) between tomato introgression lines. In this study 67 QTLs for *A*, *g_s*, starch metabolism, root and shoot dry matter accumulation and metabolites were identified. Further, genomic analysis allowed us to point out a total of 87 candidate genes that might regulate these traits. Interestingly, there was no direct association between *A*, *g_s*, ETR and biomass suggesting a large complexity in the genetic network involved and/or that other parameters might be equally important. Accordingly, in combination with gene expression, metabolite and enzyme activity related QTLs, which have been previously described for this population, this study might pave the road for the identification of candidate genes regulating photosynthesis related traits in tomato.

The functional consequences of each candidate gene at these intrinsically linked loci remain to be thoroughly investigated and thus future studies should concentrate on the interplay between growth and functional genome organization with a focus on gene regulation. In summary, this study provides an invaluable resource containing a more comprehensive view towards the mechanistic basis of how sequence variants affect photosynthesis and ultimately growth. Furthermore, we provide the basic foundation for the improvement of photosynthetic capacity and yield, aiding in our current understanding of the physiological and biochemical mechanisms involved in the regulation of primary metabolism in tomato leaves.

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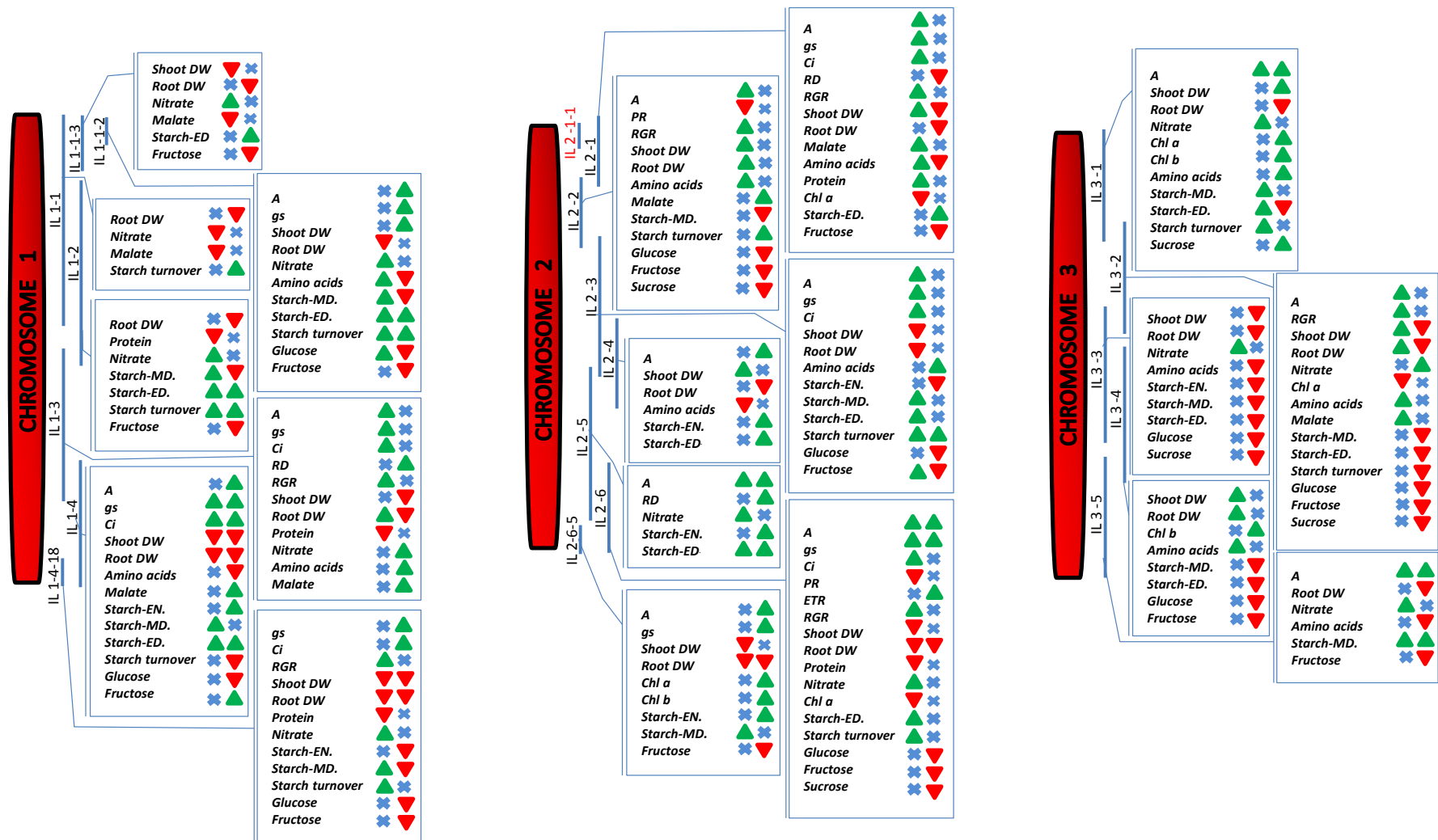
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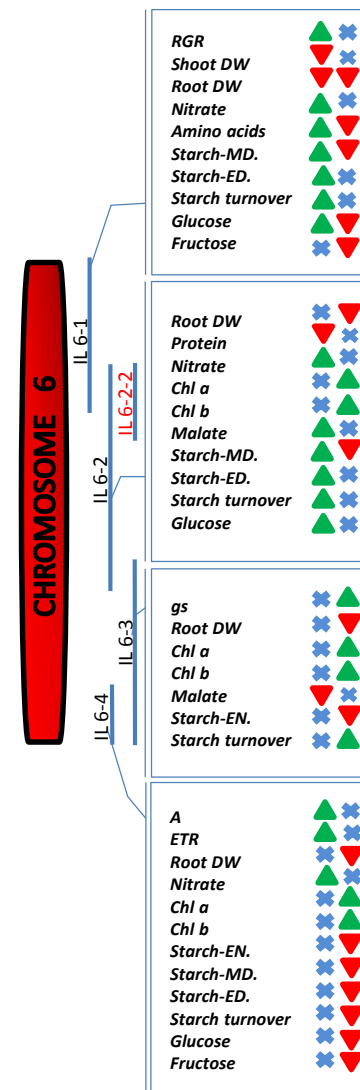
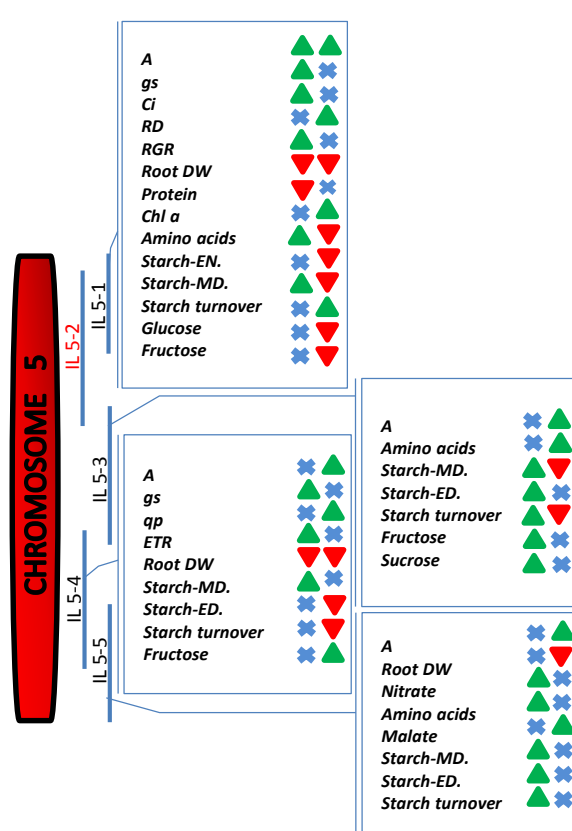
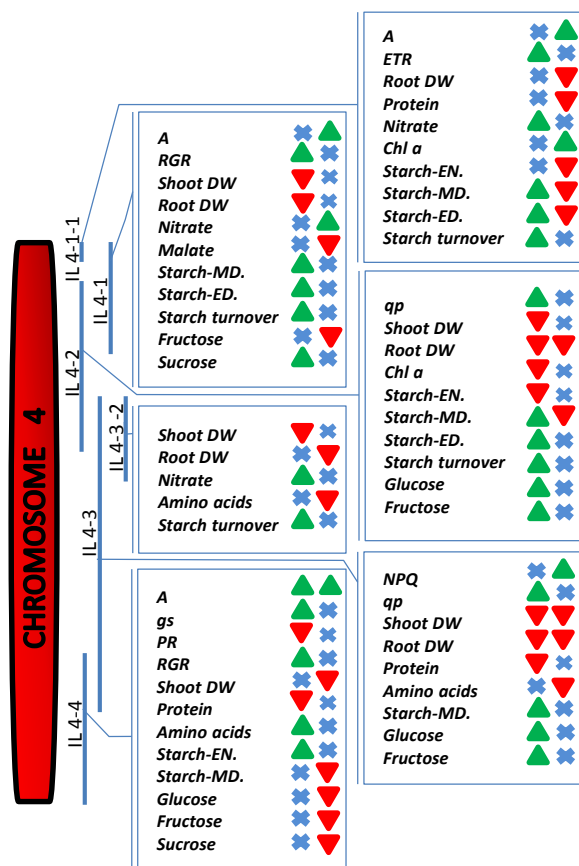
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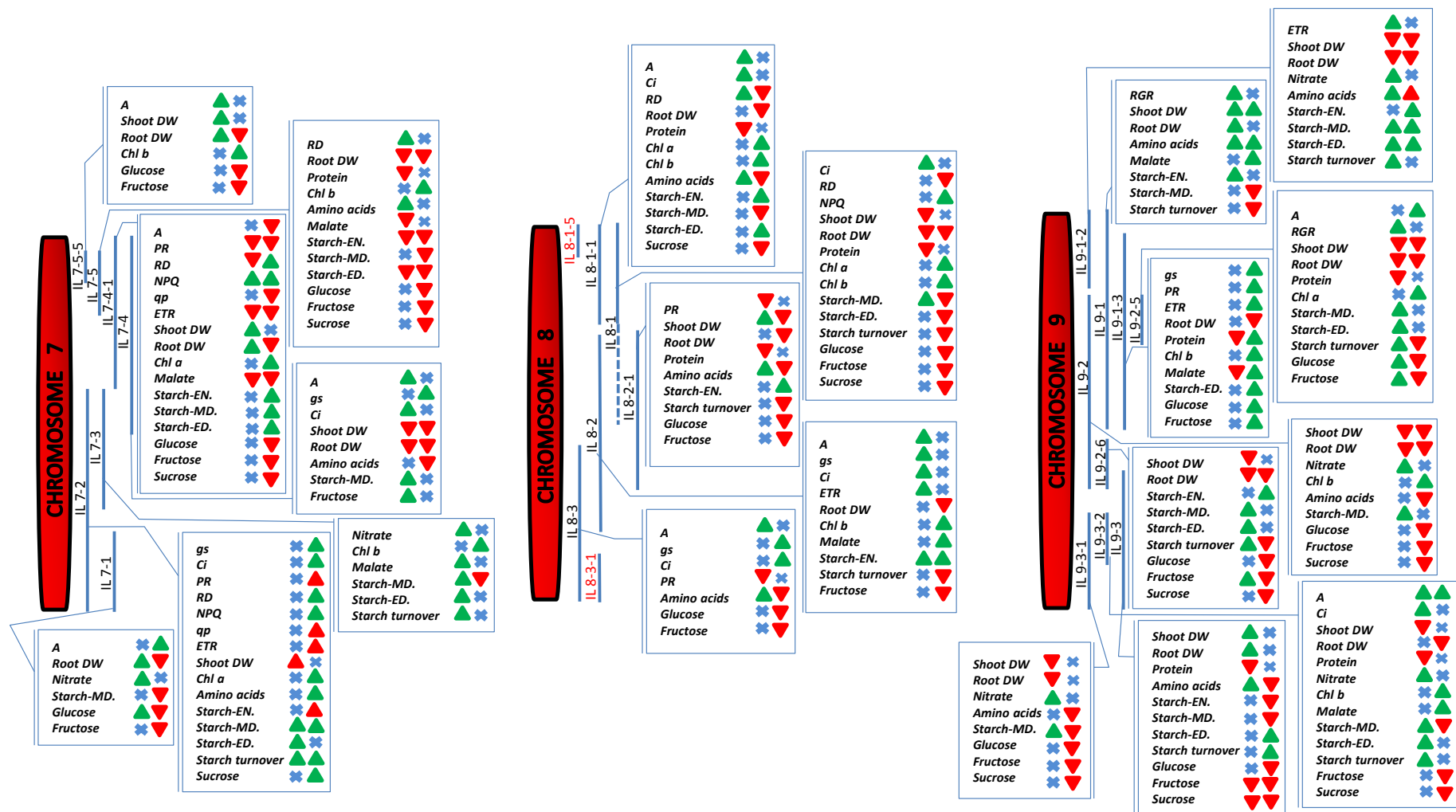
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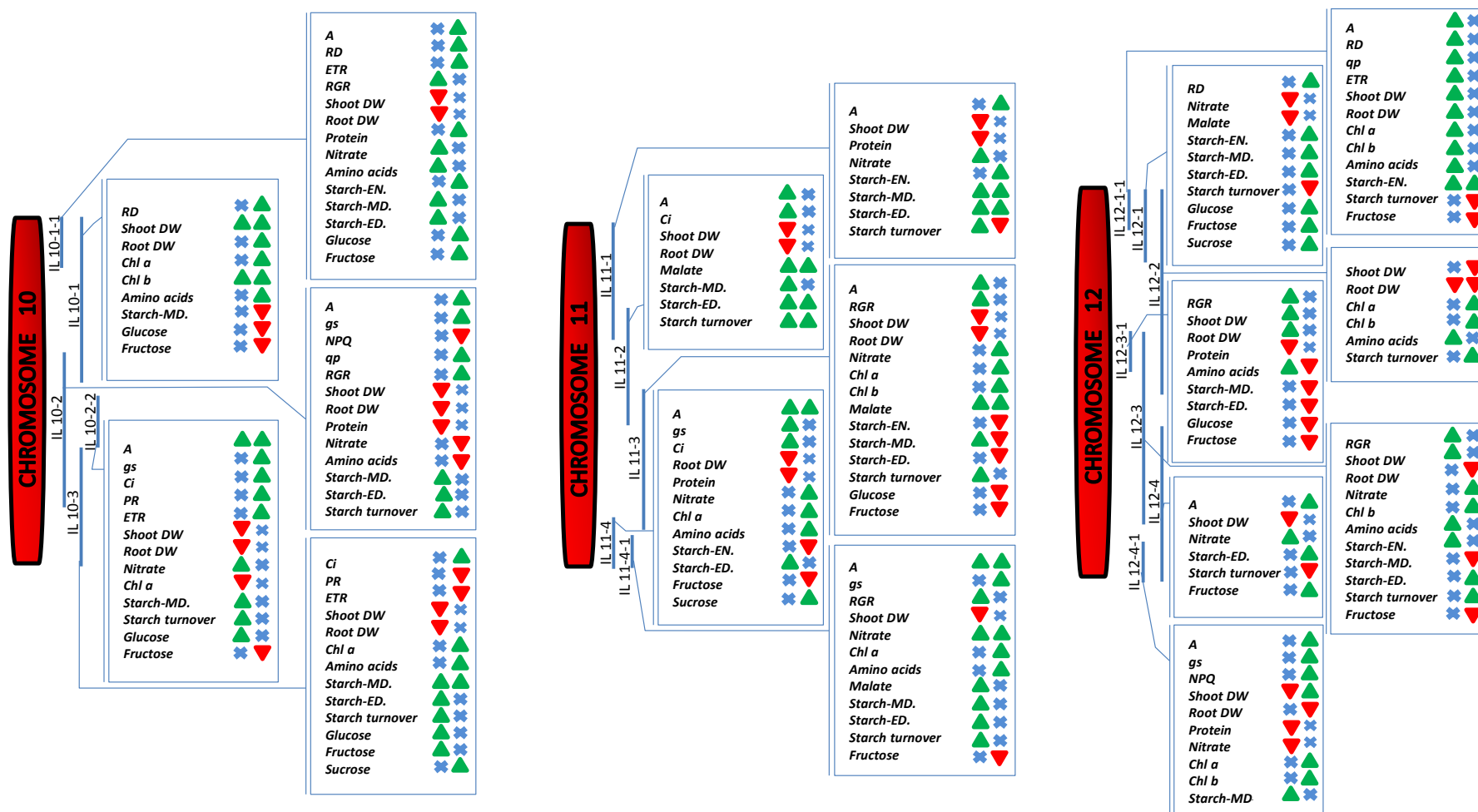
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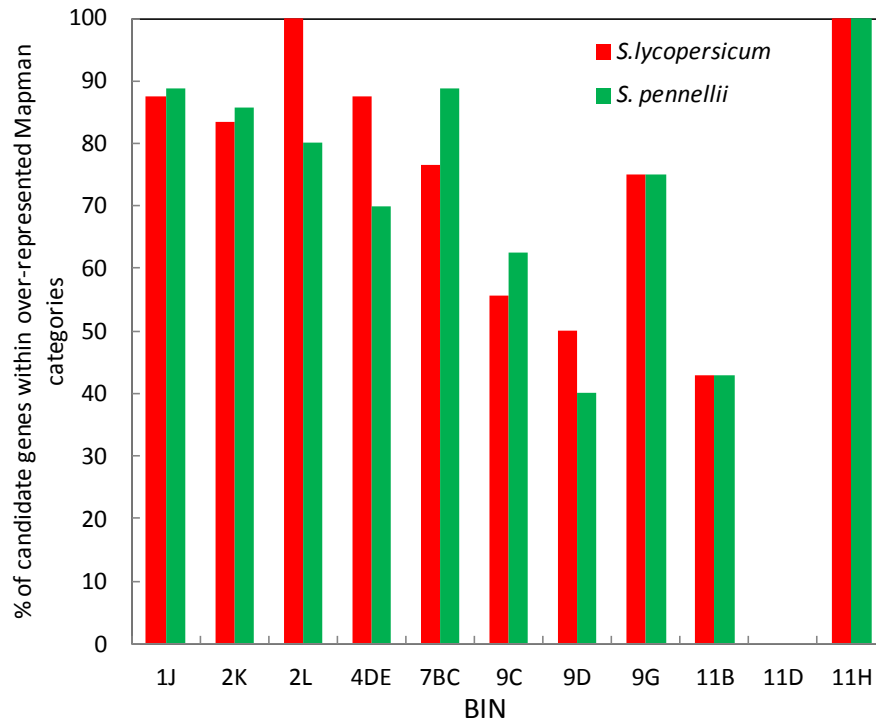








Supplemental Figure S2. Mapping of significant changes in growth, physiological and metabolic traits onto introgressed segments from the individual data sets of 2012 (left column) and 2013 (right column), respectively, of a population of 71 introgression lines (ILs) of *Solanum pennellii* into a genetic background of *Solanum lycopersicum* (M82). Gas exchange and chlorophyll a fluorescence parameters: Photosynthesis (A), stomatal conductance (g_s), stomatal density, intercellular CO₂ concentration (Ci), photorespiratory rate (PR), dark respiration (RD), Non-photochemical quenching (NPQ), photochemical quenching (qp), electron transport rate (ETR); Growth related parameters: Relative growth rate (RGR), shoot dry weight (Shoot DW), root dry weight (Root DW); Nitrogen and carbon containing compounds in leaves: chlorophyll a (Chl a), chlorophyll b (Chl b), starch synthesis at the end of the night (Starch-EN), middle of the day (Starch-MD), end of the day (Starch ED). Except for the data of starch, samples were harvested at the middle of the light period. Symbols ▲, ▼ and ✕ next to traits indicate a positive (green), negative (red) and unaltered (blue) changes. Lines in red have not been evaluated.



Supplemental Figure S3. Percentage of candidate genes selected for each genomic region (BIN) classified within over-represented Mapman categories (as reported in table 4).

Supplemental Table S1. Profiles of the biochemical components, including sugars (fructose, glucose and sucrose), starch, malate, nitrate, total amino acids, total protein, chlorophyll *a* and *b*, physiological parameters as well as growth-related parameters for the 71 ILs grown in the first experiment. Samples for metabolites measurements were harvested at the middle of the light period. Values are presented as mean $\pm$ SE ($n = 5$) and significant changes are indicated in bold. Abbreviations: A, net photosynthesis; g_s , stomatal conductance; C_i , intercellular CO_2 concentration; Pr, photorespiration; Rd, dark respiration; Starch-EN, starch level at end of the night; Starch-MD, starch level at middle of the day; Starch-ED, starch level at end of the day, starch turnover; Starch turn; RGR, relative growth rate; DW, dry weight; qP, photochemical quenching coefficient; NPQ, non-photochemical quenching; ETR, electron transport rate.

ILs	A ($\mu\text{mol } CO_2 \text{ m}^{-2} \text{ s}^{-1}$)	g_s ($\text{mol H}_2\text{O m}^{-2} \text{ s}^{-1}$)	C_i ($\mu\text{mol } CO_2$)	Pr ($\mu\text{mol m}^{-2} \text{ s}^{-1}$)	Rd ($\mu\text{mol } CO_2 \text{ m}^{-2} \text{ s}^{-1}$)	NPQ
IL 1-1	20.66 $\pm$ 0.27	0.31 $\pm$ 0.02	247.36 $\pm$ 5.27	5.18 $\pm$ 0.24	1.60 $\pm$ 0.11	1.80 $\pm$ 0.05
IL 1-1-2	19.08 $\pm$ 1.86	0.42 $\pm$ 0.13	271.23 $\pm$ 21.02	4.35 $\pm$ 0.43	1.76 $\pm$ 0.14	1.61 $\pm$ 0.33
IL 1-1-3	20.10 $\pm$ 0.30	0.34 $\pm$ 0.01	261.78 $\pm$ 1.33	5.10 $\pm$ 0.26	1.34 $\pm$ 0.09	1.71 $\pm$ 0.03
IL 1-2	21.63 $\pm$ 0.87	0.37 $\pm$ 0.06	273.70 $\pm$ 10.98	5.72 $\pm$ 0.51	1.49 $\pm$ 0.09	1.68 $\pm$ 0.19
IL 1-3	24.06 $\pm$ 1.20	0.78 $\pm$ 0.10	315.33 $\pm$ 4.13	5.58 $\pm$ 0.29	1.71 $\pm$ 0.07	1.19 $\pm$ 0.07
IL 1-4	22.15 $\pm$ 0.92	0.62 $\pm$ 0.12	307.36 $\pm$ 11.90	4.53 $\pm$ 0.36	1.69 $\pm$ 0.09	1.67 $\pm$ 0.17
IL 1-4-18	17.93 $\pm$ 1.04	0.38 $\pm$ 0.11	274.68 $\pm$ 19.68	5.73 $\pm$ 0.66	1.69 $\pm$ 0.09	1.79 $\pm$ 0.17
IL 2-1	24.89 $\pm$ 0.96	0.63 $\pm$ 0.11	299.98 $\pm$ 6.17	4.03 $\pm$ 0.56	1.70 $\pm$ 0.17	1.42 $\pm$ 0.24
IL 2-2	24.16 $\pm$ 0.84	0.52 $\pm$ 0.08	289.18 $\pm$ 7.76	2.70 $\pm$ 0.57	1.73 $\pm$ 0.08	1.62 $\pm$ 0.18
IL 2-3	23.66 $\pm$ 0.38	0.60 $\pm$ 0.10	312.47 $\pm$ 10.93	3.94 $\pm$ 0.50	1.86 $\pm$ 0.11	1.77 $\pm$ 0.24
IL 2-4	21.46 $\pm$ 0.58	0.30 $\pm$ 0.02	254.55 $\pm$ 7.35	3.54 $\pm$ 0.20	1.86 $\pm$ 0.10	1.34 $\pm$ 0.12
IL 2-5	24.57 $\pm$ 0.64	0.38 $\pm$ 0.01	250.59 $\pm$ 1.83	5.50 $\pm$ 0.24	1.49 $\pm$ 0.21	1.69 $\pm$ 0.06
IL 2-6	23.76 $\pm$ 0.72	0.65 $\pm$ 0.08	320.34 $\pm$ 11.20	2.13 $\pm$ 0.44	1.69 $\pm$ 0.09	1.68 $\pm$ 0.09
IL 2-6-5	21.84 $\pm$ 0.41	0.41 $\pm$ 0.07	286.82 $\pm$ 13.16	4.53 $\pm$ 0.61	1.71 $\pm$ 0.08	1.73 $\pm$ 0.20
IL 3-1	22.73 $\pm$ 0.91	0.43 $\pm$ 0.06	282.87 $\pm$ 9.93	4.26 $\pm$ 0.46	1.49 $\pm$ 0.06	1.83 $\pm$ 0.21
IL 3-2	24.34 $\pm$ 0.61	0.54 $\pm$ 0.05	293.06 $\pm$ 7.32	4.49 $\pm$ 0.65	1.60 $\pm$ 0.11	1.50 $\pm$ 0.16
IL 3-3	19.28 $\pm$ 0.33	0.33 $\pm$ 0.01	261.88 $\pm$ 5.19	4.95 $\pm$ 0.26	1.42 $\pm$ 0.13	1.98 $\pm$ 0.07
IL 3-4	21.45 $\pm$ 1.53	0.34 $\pm$ 0.06	261.28 $\pm$ 10.39	3.20 $\pm$ 0.41	1.82 $\pm$ 0.14	1.66 $\pm$ 0.09
IL 3-5	22.87 $\pm$ 0.94	0.51 $\pm$ 0.09	288.41 $\pm$ 15.83	4.73 $\pm$ 0.56	1.62 $\pm$ 0.10	1.74 $\pm$ 0.13
IL 4-1	21.26 $\pm$ 0.78	0.58 $\pm$ 0.14	295.31 $\pm$ 17.29	4.42 $\pm$ 0.51	1.66 $\pm$ 0.05	1.55 $\pm$ 0.17
IL 4-1-1	19.70 $\pm$ 0.67	0.39 $\pm$ 0.10	279.85 $\pm$ 14.91	7.18 $\pm$ 0.69	1.75 $\pm$ 0.11	2.22 $\pm$ 0.25
IL 4-2	21.23 $\pm$ 1.26	0.43 $\pm$ 0.07	288.79 $\pm$ 10.39	5.90 $\pm$ 0.64	1.71 $\pm$ 0.10	1.84 $\pm$ 0.17
IL 4-3	21.92 $\pm$ 0.72	0.67 $\pm$ 0.13	294.18 $\pm$ 15.96	5.82 $\pm$ 0.53	1.55 $\pm$ 0.06	1.49 $\pm$ 0.17
IL 4-3-2	20.88 $\pm$ 0.74	0.44 $\pm$ 0.09	288.55 $\pm$ 12.12	4.52 $\pm$ 0.53	1.56 $\pm$ 0.09	1.60 $\pm$ 0.28
IL 4-4	23.57 $\pm$ 1.04	0.54 $\pm$ 0.08	288.43 $\pm$ 11.76	2.10 $\pm$ 0.23	1.75 $\pm$ 0.13	1.51 $\pm$ 0.18
IL 5-1	23.02 $\pm$ 0.25	0.74 $\pm$ 0.08	302.59 $\pm$ 15.89	4.94 $\pm$ 0.39	1.73 $\pm$ 0.07	1.67 $\pm$ 0.15
IL 5-3	19.67 $\pm$ 0.80	0.40 $\pm$ 0.05	295.21 $\pm$ 10.62	4.96 $\pm$ 0.60	1.59 $\pm$ 0.06	1.66 $\pm$ 0.21
IL 5-4	22.21 $\pm$ 0.24	0.64 $\pm$ 0.09	298.22 $\pm$ 17.05	7.07 $\pm$ 0.51	1.40 $\pm$ 0.14	1.47 $\pm$ 0.16
IL 5-5	20.02 $\pm$ 0.79	0.40 $\pm$ 0.06	297.82 $\pm$ 7.06	5.52 $\pm$ 0.42	1.53 $\pm$ 0.08	1.78 $\pm$ 0.18
IL 6-1	19.52 $\pm$ 0.67	0.26 $\pm$ 0.03	251.19 $\pm$ 12.28	5.28 $\pm$ 0.53	1.57 $\pm$ 0.11	1.74 $\pm$ 0.16
IL 6-2	20.97 $\pm$ 0.48	0.50 $\pm$ 0.09	296.96 $\pm$ 13.51	5.62 $\pm$ 0.88	1.53 $\pm$ 0.03	1.88 $\pm$ 0.12
IL 6-3	21.28 $\pm$ 0.91	0.37 $\pm$ 0.02	262.47 $\pm$ 2.74	5.32 $\pm$ 0.27	1.52 $\pm$ 0.10	1.64 $\pm$ 0.10
IL 6-4	22.70 $\pm$ 0.68	0.52 $\pm$ 0.10	292.59 $\pm$ 11.97	6.16 $\pm$ 0.44	1.43 $\pm$ 0.08	1.49 $\pm$ 0.14
IL 7-1	21.51 $\pm$ 0.61	0.35 $\pm$ 0.01	256.60 $\pm$ 4.48	5.04 $\pm$ 0.32	1.54 $\pm$ 0.22	1.69 $\pm$ 0.04
IL 7-2	20.84 $\pm$ 0.77	0.35 $\pm$ 0.06	277.65 $\pm$ 11.58	5.63 $\pm$ 0.86	1.53 $\pm$ 0.09	2.02 $\pm$ 0.23
IL 7-3	21.24 $\pm$ 0.80	0.46 $\pm$ 0.11	278.12 $\pm$ 18.42	6.47 $\pm$ 0.55	1.53 $\pm$ 0.08	1.77 $\pm$ 0.24
IL 7-4	22.75 $\pm$ 0.45	0.57 $\pm$ 0.09	304.51 $\pm$ 12.11	4.31 $\pm$ 0.54	1.72 $\pm$ 0.05	1.54 $\pm$ 0.18
IL 7-4-1	19.03 $\pm$ 0.38	0.43 $\pm$ 0.07	260.63 $\pm$ 7.95	1.93 $\pm$ 0.38	0.56 $\pm$ 0.16	2.57 $\pm$ 0.06
IL 7-5	17.21 $\pm$ 0.66	0.28 $\pm$ 0.02	280.76 $\pm$ 7.28	4.94 $\pm$ 0.30	2.04 $\pm$ 0.15	1.96 $\pm$ 0.07
IL 7-5-5	23.01 $\pm$ 0.47	0.39 $\pm$ 0.05	278.08 $\pm$ 8.79	4.82 $\pm$ 0.36	1.66 $\pm$ 0.14	1.83 $\pm$ 0.17
IL 8-1	21.76 $\pm$ 0.73	0.58 $\pm$ 0.11	305.44 $\pm$ 11.97	5.73 $\pm$ 0.62	1.54 $\pm$ 0.03	1.70 $\pm$ 0.16
IL 8-1-1	23.11 $\pm$ 0.74	0.53 $\pm$ 0.05	301.08 $\pm$ 4.12	4.71 $\pm$ 0.49	2.11 $\pm$ 0.14	1.56 $\pm$ 0.03
IL 8-2	24.77 $\pm$ 0.91	0.68 $\pm$ 0.05	309.00 $\pm$ 2.65	5.94 $\pm$ 0.62	1.83 $\pm$ 0.14	1.73 $\pm$ 0.18
IL 8-2-1	21.36 $\pm$ 1.01	0.38 $\pm$ 0.06	267.98 $\pm$ 14.31	2.42 $\pm$ 0.33	1.62 $\pm$ 0.13	1.80 $\pm$ 0.12
IL 8-3	23.10 $\pm$ 0.46	0.46 $\pm$ 0.04	287.17 $\pm$ 7.08	2.22 $\pm$ 0.21	1.70 $\pm$ 0.10	1.67 $\pm$ 0.06
IL 9-1	20.28 $\pm$ 0.79	0.27 $\pm$ 0.03	249.21 $\pm$ 10.25	3.09 $\pm$ 0.33	1.65 $\pm$ 0.10	2.02 $\pm$ 0.18
IL 9-1-2	21.41 $\pm$ 0.95	0.39 $\pm$ 0.05	283.47 $\pm$ 9.38	6.89 $\pm$ 0.42	1.56 $\pm$ 0.08	1.53 $\pm$ 0.08
IL 9-1-3	21.01 $\pm$ 0.54	0.33 $\pm$ 0.02	252.19 $\pm$ 5.64	5.14 $\pm$ 0.15	1.59 $\pm$ 0.12	1.57 $\pm$ 0.03
IL 9-2	20.15 $\pm$ 0.67	0.40 $\pm$ 0.07	286.36 $\pm$ 14.00	5.28 $\pm$ 0.46	1.67 $\pm$ 0.06	1.69 $\pm$ 0.18
IL 9-2-5	19.87 $\pm$ 0.46	0.34 $\pm$ 0.03	285.22 $\pm$ 4.23	4.90 $\pm$ 0.71	1.50 $\pm$ 0.06	1.26 $\pm$ 0.16
IL 9-2-6	20.15 $\pm$ 0.74	0.36 $\pm$ 0.06	273.72 $\pm$ 11.72	3.92 $\pm$ 0.44	1.70 $\pm$ 0.09	1.89 $\pm$ 0.16
IL 9-3	21.96 $\pm$ 0.75	0.36 $\pm$ 0.07	266.04 $\pm$ 16.61	3.80 $\pm$ 0.44	1.62 $\pm$ 0.13	1.80 $\pm$ 0.25
IL 9-3-1	20.78 $\pm$ 1.01	0.43 $\pm$ 0.08	288.54 $\pm$ 13.45	3.43 $\pm$ 0.44	1.51 $\pm$ 0.04	1.43 $\pm$ 0.24
IL 9-3-2	22.70 $\pm$ 0.84	0.51 $\pm$ 0.04	301.74 $\pm$ 7.00	5.63 $\pm$ 0.50	1.46 $\pm$ 0.08	1.63 $\pm$ 0.09
IL 10-1	20.36 $\pm$ 0.82	0.30 $\pm$ 0.05	254.05 $\pm$ 12.67	3.74 $\pm$ 0.37	1.77 $\pm$ 0.14	1.69 $\pm$ 0.11
IL 10-1-1	21.03 $\pm$ 0.85	0.34 $\pm$ 0.06	253.80 $\pm$ 19.06	4.49 $\pm$ 1.00	1.55 $\pm$ 0.09	2.21 $\pm$ 0.09
IL 10-2	21.14 $\pm$ 0.96	0.47 $\pm$ 0.10	289.04 $\pm$ 14.77	4.43 $\pm$ 0.81	1.54 $\pm$ 0.06	1.72 $\pm$ 0.24
IL 10-2-2	22.71 $\pm$ 0.75	0.53 $\pm$ 0.11	292.69 $\pm$ 15.38	4.66 $\pm$ 0.79	1.48 $\pm$ 0.04	1.85 $\pm$ 0.20
IL 10-3	21.78 $\pm$ 0.79	0.35 $\pm$ 0.08	267.15 $\pm$ 12.06	5.95 $\pm$ 0.62	1.49 $\pm$ 0.05	1.66 $\pm$ 0.18
IL 11-1	21.38 $\pm$ 0.66	0.42 $\pm$ 0.08	283.48 $\pm$ 12.38	3.33 $\pm$ 0.85	1.32 $\pm$ 0.06	1.50 $\pm$ 0.20
IL 11-2	22.65 $\pm$ 0.54	0.56 $\pm$ 0.04	307.51 $\pm$ 6.32	4.40 $\pm$ 0.65	1.59 $\pm$ 0.07	1.52 $\pm$ 0.13
IL 11-3	22.59 $\pm$ 0.40	0.43 $\pm$ 0.04	289.11 $\pm$ 6.13	3.55 $\pm$ 0.69	1.66 $\pm$ 0.07	1.67 $\pm$ 0.11
IL 11-4	23.92 $\pm$ 0.59	0.52 $\pm$ 0.08	291.55 $\pm$ 8.20	5.39 $\pm$ 0.66	1.61 $\pm$ 0.07	1.51 $\pm$ 0.19
IL 11-4-1	23.36 $\pm$ 0.56	0.55 $\pm$ 0.09	295.75 $\pm$ 12.63	3.69 $\pm$ 0.62	1.58 $\pm$ 0.05	1.34 $\pm$ 0.11
IL 12-1	19.31 $\pm$ 0.81	0.34 $\pm$ 0.02	262.08 $\pm$ 8.82	4.75 $\pm$ 0.24	1.37 $\pm$ 0.14	1.70 $\pm$ 0.07
IL 12-1-1	23.25 $\pm$ 1.12	0.48 $\pm$ 0.09	286.16 $\pm$ 10.11	6.41 $\pm$ 0.80	1.99 $\pm$ 0.24	1.32 $\pm$ 0.10
IL 12-2	20.50 $\pm$ 0.77	0.34 $\pm$ 0.05	272.87 $\pm$ 8.53	3.15 $\pm$ 0.40	1.69 $\pm$ 0.04	1.40 $\pm$ 0.07
IL 12-3	21.87 $\pm$ 0.41	0.37 $\pm$ 0.05	278.77 $\pm$ 9.17	3.14 $\pm$ 0.51	1.62 $\pm$ 0.11	1.40 $\pm$ 0.08
IL 12-3-1	21.08 $\pm$ 0.58	0.31 $\pm$ 0.02	263.06 $\pm$ 7.08	4.23 $\pm$ 0.33	1.71 $\pm$ 0.12	1.75 $\pm$ 0.11
IL 12-4	19.65 $\pm$ 0.79	0.35 $\pm$ 0.05	283.75 $\pm$ 13.19	5.96 $\pm$ 0.79	1.58 $\pm$ 0.06	1.46 $\pm$ 0.25
IL 12-4-1	19.39 $\pm$ 0.56	0.41 $\pm$ 0.08	288.74 $\pm$ 10.59	3.69 $\pm$ 0.45	1.68 $\pm$ 0.09	1.47 $\pm$ 0.19
M82	19.35 $\pm$ 0.31	0.32 $\pm$ 0.02	258.12 $\pm$ 7.58	5.05 $\pm$ 0.31	1.56 $\pm$ 0.14	1.73 $\pm$ 0.08

ILs	qP	ETR ($\mu\text{mol e}^- \text{m}^{-2} \text{s}^{-1}$)	RGR ($\text{cm cm}^{-1} \text{day}$)	Shoot DW (g)	Root DW (g)	Protein ($\text{mg g}^{-1} \text{FW}$)
IL 1-1	0.60 ± 0.02	148.04 ± 3.51	0.05 ± 0.00	7.46 ± 0.60	1.37 ± 0.05	1.72 ± 0.10
IL 1-1-2	0.89 ± 0.23	132.02 ± 7.50	0.06 ± 0.01	5.81 ± 0.37	0.68 ± 0.09	1.18 ± 0.12
IL 1-1-3	0.60 ± 0.02	144.24 ± 4.35	0.06 ± 0.00	4.06 ± 0.26	1.00 ± 0.07	1.23 ± 0.09
IL 1-2	0.73 ± 0.10	158.20 ± 5.67	0.06 ± 0.01	5.86 ± 0.31	1.31 ± 0.13	0.81 ± 0.06
IL 1-3	0.52 ± 0.01	166.57 ± 2.94	0.08 ± 0.01	7.15 ± 0.60	1.54 ± 0.10	0.67 ± 0.05
IL 1-4	0.75 ± 0.12	146.31 ± 4.43	0.07 ± 0.00	3.49 ± 0.28	0.50 ± 0.04	1.24 ± 0.06
IL 1-4-18	0.89 ± 0.22	143.88 ± 6.39	0.09 ± 0.00	4.08 ± 0.46	0.59 ± 0.05	0.68 ± 0.08
IL 2-1	0.56 ± 0.01	151.33 ± 5.99	0.08 ± 0.01	9.81 ± 0.52	1.35 ± 0.07	1.81 ± 0.14
IL 2-2	0.49 ± 0.02	132.48 ± 9.26	0.09 ± 0.01	12.05 ± 0.48	1.60 ± 0.25	1.18 ± 0.08
IL 2-3	0.79 ± 0.16	145.67 ± 6.72	0.07 ± 0.01	3.49 ± 0.40	0.32 ± 0.05	1.58 ± 0.17
IL 2-4	0.58 ± 0.06	132.02 ± 3.88	0.06 ± 0.00	11.61 ± 0.76	1.30 ± 0.12	1.32 ± 0.05
IL 2-5	0.67 ± 0.01	167.27 ± 4.16	0.06 ± 0.00	6.78 ± 0.41	1.07 ± 0.05	1.25 ± 0.08
IL 2-6	0.44 ± 0.04	124.02 ± 4.95	0.06 ± 0.00	4.03 ± 0.89	0.38 ± 0.13	1.31 ± 0.04
IL 2-6-5	0.73 ± 0.19	145.20 ± 7.53	0.09 ± 0.01	4.07 ± 0.55	0.31 ± 0.05	0.86 ± 0.11
IL 3-1	0.88 ± 0.15	145.05 ± 7.57	0.05 ± 0.01	4.69 ± 0.25	1.05 ± 0.08	1.15 ± 0.08
IL 3-2	0.73 ± 0.04	154.40 ± 8.31	0.08 ± 0.01	10.86 ± 0.21	2.15 ± 0.15	1.29 ± 0.07
IL 3-3	0.60 ± 0.01	139.39 ± 3.97	0.05 ± 0.00	7.62 ± 0.37	1.09 ± 0.08	1.35 ± 0.11
IL 3-4	0.54 ± 0.06	127.84 ± 4.23	0.07 ± 0.01	11.54 ± 0.52	2.21 ± 0.08	1.14 ± 0.07
IL 3-5	0.72 ± 0.13	151.49 ± 6.94	0.05 ± 0.01	4.85 ± 0.20	0.92 ± 0.13	1.37 ± 0.03
IL 4-1	0.58 ± 0.08	141.36 ± 5.85	0.09 ± 0.01	4.12 ± 0.57	0.54 ± 0.08	1.17 ± 0.06
IL 4-1-1	0.92 ± 0.15	168.41 ± 8.46	0.06 ± 0.00	5.74 ± 0.26	0.98 ± 0.09	1.15 ± 0.03
IL 4-2	1.17 ± 0.30	159.15 ± 7.29	0.06 ± 0.00	4.41 ± 0.25	0.51 ± 0.07	1.44 ± 0.07
IL 4-3	1.30 ± 0.14	160.62 ± 5.20	0.06 ± 0.00	4.16 ± 0.70	0.64 ± 0.09	1.00 ± 0.03
IL 4-3-2	0.90 ± 0.20	140.90 ± 6.96	0.08 ± 0.01	4.45 ± 0.50	0.82 ± 0.12	1.22 ± 0.10
IL 4-4	0.43 ± 0.03	122.92 ± 3.16	0.09 ± 0.02	7.48 ± 0.57	1.24 ± 0.13	1.12 ± 0.09
IL 5-1	0.73 ± 0.07	154.85 ± 4.81	0.08 ± 0.00	4.77 ± 0.26	0.54 ± 0.05	0.91 ± 0.04
IL 5-3	0.87 ± 0.18	141.35 ± 5.73	0.06 ± 0.01	5.43 ± 0.80	0.79 ± 0.08	1.67 ± 0.12
IL 5-4	1.30 ± 0.29	176.52 ± 7.10	0.06 ± 0.00	5.44 ± 0.79	0.78 ± 0.12	1.41 ± 0.04
IL 5-5	0.92 ± 0.24	149.46 ± 4.18	0.05 ± 0.01	5.42 ± 0.36	0.83 ± 0.11	1.47 ± 0.06
IL 6-1	0.87 ± 0.21	144.58 ± 4.19	0.09 ± 0.01	4.53 ± 0.29	0.54 ± 0.15	1.68 ± 0.11
IL 6-2	0.79 ± 0.14	154.35 ± 9.41	0.06 ± 0.01	5.61 ± 0.38	1.10 ± 0.08	1.00 ± 0.03
IL 6-3	0.61 ± 0.01	151.97 ± 2.47	0.05 ± 0.01	7.96 ± 0.48	1.38 ± 0.07	1.45 ± 0.17
IL 6-4	0.95 ± 0.20	167.61 ± 5.71	0.06 ± 0.01	4.79 ± 0.61	0.93 ± 0.09	1.35 ± 0.11
IL 7-1	0.61 ± 0.02	149.57 ± 6.14	0.06 ± 0.00	8.03 ± 0.31	1.78 ± 0.11	1.52 ± 0.12
IL 7-2	0.91 ± 0.21	153.97 ± 9.21	0.06 ± 0.00	4.27 ± 0.16	1.15 ± 0.09	1.29 ± 0.17
IL 7-3	0.98 ± 0.21	165.63 ± 6.48	0.07 ± 0.01	4.66 ± 0.42	0.92 ± 0.08	1.49 ± 0.19
IL 7-4	0.94 ± 0.16	146.09 ± 6.50	0.07 ± 0.00	3.89 ± 0.57	0.49 ± 0.05	1.42 ± 0.10
IL 7-4-1	0.38 ± 0.02	100.45 ± 4.65	0.06 ± 0.01	9.24 ± 0.26	2.16 ± 0.10	1.38 ± 0.11
IL 7-5	0.41 ± 0.01	132.22 ± 3.44	0.05 ± 0.01	6.41 ± 0.38	0.74 ± 0.05	1.09 ± 0.06
IL 7-5-5	0.94 ± 0.18	153.25 ± 4.80	0.06 ± 0.01	13.64 ± 0.91	1.99 ± 0.11	1.19 ± 0.06
IL 8-1	0.89 ± 0.21	158.83 ± 7.04	0.07 ± 0.00	4.32 ± 0.84	0.39 ± 0.02	0.66 ± 0.10
IL 8-1-1	0.38 ± 0.04	153.14 ± 5.49	0.07 ± 0.01	8.04 ± 0.29	1.44 ± 0.06	0.88 ± 0.02
IL 8-2	0.90 ± 0.04	174.00 ± 10.10	0.06 ± 0.01	6.94 ± 0.30	0.98 ± 0.04	1.33 ± 0.08
IL 8-2-1	0.47 ± 0.04	117.66 ± 3.33	0.06 ± 0.01	11.89 ± 0.37	1.39 ± 0.07	1.02 ± 0.07
IL 8-3	0.44 ± 0.03	122.43 ± 2.43	0.07 ± 0.01	7.71 ± 0.74	1.15 ± 0.07	1.54 ± 0.06
IL 9-1	0.47 ± 0.03	121.51 ± 2.00	0.08 ± 0.01	12.75 ± 0.37	2.30 ± 0.13	1.23 ± 0.07
IL 9-1-2	0.98 ± 0.18	171.46 ± 4.75	0.06 ± 0.00	4.41 ± 0.35	0.76 ± 0.06	1.43 ± 0.06
IL 9-1-3	0.61 ± 0.01	148.88 ± 2.03	0.06 ± 0.00	5.99 ± 0.65	1.29 ± 0.04	1.12 ± 0.07
IL 9-2	0.64 ± 0.09	147.28 ± 4.44	0.05 ± 0.00	4.19 ± 0.49	0.50 ± 0.03	1.65 ± 0.09
IL 9-2-5	0.44 ± 0.04	141.27 ± 8.31	0.08 ± 0.01	4.16 ± 0.39	0.63 ± 0.05	0.99 ± 0.09
IL 9-2-6	0.63 ± 0.09	131.05 ± 2.54	0.07 ± 0.00	4.06 ± 0.33	0.50 ± 0.04	1.22 ± 0.16
IL 9-3	0.62 ± 0.03	136.65 ± 7.27	0.06 ± 0.01	9.63 ± 0.69	1.93 ± 0.12	0.98 ± 0.02
IL 9-3-1	0.54 ± 0.04	127.36 ± 2.74	0.06 ± 0.01	3.98 ± 0.74	0.64 ± 0.09	1.34 ± 0.08
IL 9-3-2	1.04 ± 0.23	161.33 ± 3.62	0.07 ± 0.01	4.12 ± 0.24	0.89 ± 0.05	1.02 ± 0.05
IL 10-1	0.59 ± 0.04	129.80 ± 3.96	0.06 ± 0.00	11.20 ± 0.35	1.90 ± 0.04	1.14 ± 0.06
IL 10-1-1	0.45 ± 0.06	141.08 ± 11.66	0.08 ± 0.00	3.69 ± 0.37	0.74 ± 0.04	1.49 ± 0.07
IL 10-2	0.75 ± 0.09	140.79 ± 8.48	0.05 ± 0.00	3.96 ± 0.19	0.72 ± 0.01	1.11 ± 0.04
IL 10-2-2	0.86 ± 0.16	149.65 ± 10.64	0.07 ± 0.01	4.19 ± 0.38	0.50 ± 0.04	1.26 ± 0.07
IL 10-3	0.95 ± 0.19	161.45 ± 7.85	0.05 ± 0.00	3.85 ± 0.33	0.68 ± 0.06	1.31 ± 0.09
IL 11-1	0.60 ± 0.11	128.07 ± 8.46	0.06 ± 0.00	4.21 ± 0.50	0.80 ± 0.09	1.09 ± 0.05
IL 11-2	0.83 ± 0.18	146.55 ± 8.06	0.06 ± 0.00	4.31 ± 0.18	0.63 ± 0.07	1.50 ± 0.14
IL 11-3	0.87 ± 0.27	136.28 ± 8.16	0.10 ± 0.01	3.91 ± 0.53	0.47 ± 0.04	1.57 ± 0.11
IL 11-4	0.83 ± 0.20	163.61 ± 8.11	0.06 ± 0.00	4.35 ± 0.39	0.58 ± 0.04	1.10 ± 0.04
IL 11-4-1	0.59 ± 0.06	140.83 ± 6.77	0.09 ± 0.01	4.29 ± 0.46	0.97 ± 0.13	1.31 ± 0.04
IL 12-1	0.58 ± 0.02	136.95 ± 3.03	0.06 ± 0.00	5.00 ± 0.26	0.85 ± 0.03	1.50 ± 0.10
IL 12-1-1	1.30 ± 0.14	173.92 ± 8.82	0.04 ± 0.00	8.31 ± 0.32	1.73 ± 0.12	1.74 ± 0.06
IL 12-2	0.53 ± 0.03	123.19 ± 5.89	0.07 ± 0.00	5.60 ± 0.39	0.67 ± 0.05	1.33 ± 0.07
IL 12-3	0.51 ± 0.07	128.33 ± 6.77	0.08 ± 0.00	11.37 ± 0.72	1.23 ± 0.06	1.03 ± 0.07
IL 12-3-1	0.62 ± 0.04	138.52 ± 4.90	0.09 ± 0.01	10.37 ± 0.25	1.67 ± 0.05	1.32 ± 0.08
IL 12-4	0.80 ± 0.19	153.34 ± 10.81	0.06 ± 0.01	3.62 ± 0.10	1.08 ± 0.07	1.34 ± 0.09
IL 12-4-1	0.59 ± 0.08	125.18 ± 5.15	0.06 ± 0.00	4.43 ± 0.38	0.80 ± 0.05	1.02 ± 0.03
M82	0.60 ± 0.03	141.17 ± 3.50	0.05 ± 0.00	6.44 ± 0.18	1.15 ± 0.05	1.47 ± 0.06

ILs	Nitrate (mmol g ⁻¹ FW)	Chl a (mg g ⁻¹ FW)	Chl b (mg g ⁻¹ FW)	Amino acids (μmol g ⁻¹ FW)	Malate (μmol g ⁻¹ FW)	Starch-EN (μmol g ⁻¹ FW)
IL 1-1	0.20 ± 0.06	1.49 ± 0.07	0.45 ± 0.02	6.86 ± 0.32	16.90 ± 1.65	25.25 ± 1.21
IL 1-1-2	1.01 ± 0.11	1.29 ± 0.06	0.42 ± 0.05	9.43 ± 1.36	35.31 ± 3.11	17.80 ± 1.68
IL 1-1-3	1.41 ± 0.11	1.25 ± 0.03	0.43 ± 0.01	6.89 ± 0.33	19.26 ± 3.85	22.26 ± 0.79
IL 1-2	0.91 ± 0.07	1.30 ± 0.05	0.46 ± 0.01	5.58 ± 0.36	40.06 ± 2.56	19.79 ± 1.64
IL 1-3	0.72 ± 0.04	1.40 ± 0.09	0.48 ± 0.05	6.47 ± 0.28	44.53 ± 4.84	27.33 ± 2.27
IL 1-4	0.57 ± 0.03	1.45 ± 0.04	0.45 ± 0.03	7.93 ± 0.52	40.15 ± 2.90	16.41 ± 1.24
IL 1-4-18	0.88 ± 0.07	1.47 ± 0.12	0.50 ± 0.05	6.63 ± 0.72	36.61 ± 1.89	16.52 ± 1.41
IL 2-1	0.34 ± 0.01	1.57 ± 0.04	0.53 ± 0.03	9.13 ± 0.29	50.30 ± 3.77	28.88 ± 2.54
IL 2-2	0.47 ± 0.04	1.43 ± 0.07	0.44 ± 0.04	10.13 ± 0.55	46.58 ± 4.19	29.05 ± 2.67
IL 2-3	0.66 ± 0.03	1.49 ± 0.07	0.43 ± 0.05	7.28 ± 0.52	32.00 ± 1.67	15.18 ± 1.52
IL 2-4	0.50 ± 0.01	1.24 ± 0.02	0.41 ± 0.03	9.58 ± 0.65	32.79 ± 1.21	29.41 ± 0.90
IL 2-5	1.04 ± 0.11	1.38 ± 0.05	0.46 ± 0.01	6.56 ± 0.23	32.42 ± 3.43	27.24 ± 2.25
IL 2-6	0.86 ± 0.08	1.56 ± 0.08	0.51 ± 0.03	8.52 ± 1.06	35.11 ± 3.17	18.61 ± 2.27
IL 2-6-5	0.72 ± 0.03	1.30 ± 0.11	0.38 ± 0.03	7.61 ± 0.80	41.76 ± 4.86	27.34 ± 2.10
IL 3-1	0.80 ± 0.04	1.52 ± 0.09	0.55 ± 0.02	5.79 ± 0.55	47.14 ± 5.32	18.57 ± 2.30
IL 3-2	0.74 ± 0.04	1.55 ± 0.06	0.50 ± 0.02	10.22 ± 0.60	61.27 ± 3.48	20.65 ± 1.91
IL 3-3	0.84 ± 0.22	1.37 ± 0.06	0.46 ± 0.02	5.45 ± 0.23	29.28 ± 2.10	24.86 ± 2.17
IL 3-4	0.40 ± 0.01	1.22 ± 0.07	0.42 ± 0.03	10.64 ± 0.26	34.40 ± 1.95	29.47 ± 1.96
IL 3-5	0.82 ± 0.03	1.40 ± 0.04	0.50 ± 0.05	7.06 ± 0.21	39.03 ± 1.77	21.26 ± 3.08
IL 4-1	0.63 ± 0.08	1.18 ± 0.08	0.50 ± 0.05	5.25 ± 0.46	35.78 ± 1.90	18.38 ± 2.09
IL 4-1-1	0.84 ± 0.05	1.27 ± 0.08	0.43 ± 0.05	7.58 ± 0.48	33.69 ± 2.98	14.36 ± 1.13
IL 4-2	0.68 ± 0.04	1.56 ± 0.07	0.41 ± 0.03	6.19 ± 0.75	30.01 ± 0.88	12.60 ± 0.78
IL 4-3	0.46 ± 0.05	1.13 ± 0.05	0.46 ± 0.03	8.76 ± 0.50	36.76 ± 3.51	26.34 ± 2.02
IL 4-3-2	0.83 ± 0.05	1.04 ± 0.05	0.42 ± 0.02	7.80 ± 0.81	35.43 ± 3.75	18.54 ± 2.76
IL 4-4	0.47 ± 0.02	1.36 ± 0.06	0.45 ± 0.03	9.51 ± 0.79	40.47 ± 2.12	34.99 ± 4.19
IL 5-1	0.56 ± 0.03	1.30 ± 0.07	0.43 ± 0.02	9.38 ± 0.57	27.93 ± 1.44	15.73 ± 0.63
IL 5-3	0.56 ± 0.03	1.49 ± 0.06	0.47 ± 0.05	5.30 ± 0.50	38.60 ± 2.29	25.76 ± 1.96
IL 5-4	0.72 ± 0.04	1.36 ± 0.05	0.44 ± 0.04	8.35 ± 0.72	35.21 ± 2.92	16.16 ± 2.62
IL 5-5	1.08 ± 0.03	1.11 ± 0.04	0.45 ± 0.04	10.35 ± 0.31	39.49 ± 3.40	17.00 ± 1.08
IL 6-1	0.75 ± 0.05	1.22 ± 0.11	0.43 ± 0.03	8.83 ± 0.83	35.19 ± 2.40	28.67 ± 2.38
IL 6-2	0.96 ± 0.05	1.12 ± 0.07	0.50 ± 0.03	5.25 ± 0.34	51.56 ± 2.83	26.15 ± 0.83
IL 6-3	0.51 ± 0.07	1.11 ± 0.04	0.40 ± 0.01	5.20 ± 0.36	18.59 ± 1.49	21.07 ± 1.03
IL 6-4	0.79 ± 0.05	1.26 ± 0.08	0.43 ± 0.03	4.79 ± 0.54	31.73 ± 1.67	14.07 ± 1.55
IL 7-1	1.05 ± 0.14	1.42 ± 0.09	0.48 ± 0.03	5.93 ± 0.27	40.95 ± 4.91	25.21 ± 1.70
IL 7-2	0.52 ± 0.02	1.37 ± 0.10	0.41 ± 0.03	4.61 ± 0.57	34.09 ± 2.09	21.45 ± 3.49
IL 7-3	0.79 ± 0.02	1.25 ± 0.09	0.44 ± 0.02	5.17 ± 0.49	49.48 ± 5.26	18.34 ± 2.03
IL 7-4	0.49 ± 0.05	1.30 ± 0.04	0.53 ± 0.04	4.64 ± 0.20	40.65 ± 3.64	19.39 ± 2.17
IL 7-4-1	0.38 ± 0.06	1.47 ± 0.08	0.49 ± 0.01	7.45 ± 0.50	15.04 ± 2.02	28.02 ± 0.60
IL 7-5	0.33 ± 0.02	1.05 ± 0.05	0.33 ± 0.01	9.20 ± 0.52	17.45 ± 0.58	8.89 ± 0.20
IL 7-5-5	0.29 ± 0.01	1.50 ± 0.05	0.44 ± 0.02	7.18 ± 0.71	45.79 ± 2.48	14.54 ± 1.79
IL 8-1	0.47 ± 0.01	1.05 ± 0.03	0.49 ± 0.03	5.97 ± 0.31	24.99 ± 0.85	21.98 ± 2.31
IL 8-1-1	0.35 ± 0.01	1.24 ± 0.03	0.46 ± 0.04	9.97 ± 0.17	34.92 ± 1.35	19.60 ± 1.66
IL 8-2	0.54 ± 0.04	1.37 ± 0.06	0.49 ± 0.03	6.66 ± 0.58	37.04 ± 1.07	32.97 ± 2.07
IL 8-2-1	0.44 ± 0.01	1.48 ± 0.09	0.48 ± 0.02	10.47 ± 0.41	37.01 ± 1.98	27.37 ± 1.20
IL 8-3	0.51 ± 0.02	1.38 ± 0.04	0.53 ± 0.03	9.75 ± 0.45	38.45 ± 4.19	19.79 ± 2.16
IL 9-1	0.36 ± 0.01	1.24 ± 0.07	0.37 ± 0.02	13.27 ± 0.44	38.09 ± 3.11	46.34 ± 2.88
IL 9-1-2	0.84 ± 0.05	1.40 ± 0.06	0.44 ± 0.02	9.65 ± 0.33	42.40 ± 2.30	15.25 ± 1.46
IL 9-1-3	0.39 ± 0.04	1.27 ± 0.06	0.44 ± 0.02	8.31 ± 0.48	12.66 ± 2.72	16.37 ± 0.87
IL 9-2	0.78 ± 0.07	1.37 ± 0.11	0.46 ± 0.07	7.09 ± 0.63	34.26 ± 2.17	19.83 ± 2.87
IL 9-2-5	0.61 ± 0.02	1.41 ± 0.05	0.51 ± 0.04	6.46 ± 0.40	44.33 ± 4.88	15.23 ± 1.94
IL 9-2-6	0.59 ± 0.04	1.20 ± 0.08	0.34 ± 0.02	6.55 ± 0.73	34.41 ± 3.29	23.12 ± 1.45
IL 9-3	0.68 ± 0.04	1.05 ± 0.05	0.43 ± 0.06	9.95 ± 0.62	41.79 ± 4.44	28.04 ± 2.30
IL 9-3-1	0.88 ± 0.04	1.20 ± 0.04	0.41 ± 0.04	5.28 ± 0.62	36.82 ± 2.86	26.37 ± 1.89
IL 9-3-2	0.81 ± 0.05	1.32 ± 0.05	0.48 ± 0.05	6.23 ± 0.27	36.13 ± 2.03	22.75 ± 2.88
IL 10-1	0.50 ± 0.02	1.42 ± 0.07	0.60 ± 0.05	9.02 ± 0.47	40.28 ± 2.88	23.73 ± 2.41
IL 10-1-1	0.82 ± 0.02	1.40 ± 0.08	0.46 ± 0.02	9.14 ± 0.83	32.51 ± 3.28	27.67 ± 2.08
IL 10-2	0.73 ± 0.03	1.18 ± 0.07	0.32 ± 0.03	7.26 ± 0.56	34.85 ± 2.15	20.13 ± 2.01
IL 10-2-2	0.83 ± 0.02	1.58 ± 0.06	0.57 ± 0.04	8.26 ± 0.52	33.34 ± 3.88	15.47 ± 0.76
IL 10-3	0.64 ± 0.03	1.43 ± 0.10	0.43 ± 0.02	5.68 ± 0.28	40.94 ± 3.06	29.24 ± 3.27
IL 11-1	0.90 ± 0.07	1.50 ± 0.10	0.42 ± 0.03	6.38 ± 0.23	35.02 ± 2.07	30.12 ± 3.62
IL 11-2	0.70 ± 0.11	1.37 ± 0.03	0.51 ± 0.02	6.98 ± 0.38	56.65 ± 3.05	22.38 ± 1.39
IL 11-3	0.64 ± 0.06	1.46 ± 0.05	0.55 ± 0.03	6.83 ± 0.40	48.41 ± 3.70	13.36 ± 1.33
IL 11-4	0.65 ± 0.03	1.28 ± 0.09	0.46 ± 0.04	7.59 ± 0.33	49.98 ± 6.41	21.90 ± 1.42
IL 11-4-1	0.92 ± 0.09	1.34 ± 0.10	0.56 ± 0.02	7.04 ± 0.65	47.96 ± 3.47	20.41 ± 1.69
IL 12-1	0.25 ± 0.07	1.23 ± 0.11	0.48 ± 0.02	7.49 ± 0.47	13.43 ± 2.72	25.02 ± 0.87
IL 12-1-1	0.47 ± 0.01	1.60 ± 0.04	0.66 ± 0.04	10.74 ± 0.31	42.23 ± 2.68	31.39 ± 2.06
IL 12-2	0.39 ± 0.01	1.29 ± 0.05	0.41 ± 0.03	9.02 ± 0.53	39.06 ± 3.62	29.25 ± 3.56
IL 12-3	0.39 ± 0.02	1.43 ± 0.03	0.50 ± 0.05	9.07 ± 0.86	40.43 ± 2.70	32.81 ± 2.33
IL 12-3-1	0.42 ± 0.02	1.39 ± 0.07	0.47 ± 0.02	9.46 ± 0.24	39.28 ± 1.46	28.55 ± 2.32
IL 12-4	0.96 ± 0.06	1.33 ± 0.09	0.44 ± 0.03	5.03 ± 0.33	31.25 ± 1.08	20.75 ± 1.96
IL 12-4-1	1.07 ± 0.05	1.36 ± 0.06	0.50 ± 0.03	7.00 ± 0.37	34.11 ± 3.40	25.94 ± 2.13
M82	0.52 ± 0.04	1.29 ± 0.03	0.44 ± 0.01	6.53 ± 0.39	36.55 ± 3.04	21.58 ± 1.59

ILs	Starch-MD ($\mu\text{mol g}^{-1}\text{FW}$)	Starch-ED ($\mu\text{mol g}^{-1}\text{FW}$)	Starch turn ($\mu\text{mol g}^{-1}\text{FW}$)	Glucose ($\mu\text{mol g}^{-1}\text{FW}$)	Fructose ($\mu\text{mol g}^{-1}\text{FW}$)	Sucrose ($\mu\text{mol g}^{-1}\text{FW}$)
IL 1-1	24.39 $\pm$ 1.97	54.75 $\pm$ 3.39	29.51 $\pm$ 3.27	6.85 $\pm$ 0.44	6.01 $\pm$ 0.26	4.54 $\pm$ 0.26
IL 1-1-2	48.71 $\pm$ 2.52	74.92 $\pm$ 3.43	57.12 $\pm$ 4.04	7.85 $\pm$ 0.64	7.36 $\pm$ 0.66	4.04 $\pm$ 0.45
IL 1-1-3	21.72 $\pm$ 2.37	43.07 $\pm$ 2.64	20.80 $\pm$ 3.06	6.75 $\pm$ 0.68	4.76 $\pm$ 0.78	3.81 $\pm$ 0.22
IL 1-2	65.24 $\pm$ 4.74	75.31 $\pm$ 3.18	55.53 $\pm$ 4.51	6.55 $\pm$ 0.63	5.69 $\pm$ 0.58	3.99 $\pm$ 0.47
IL 1-3	21.22 $\pm$ 1.72	38.88 $\pm$ 0.57	11.55 $\pm$ 2.47	4.87 $\pm$ 0.28	4.16 $\pm$ 0.29	4.96 $\pm$ 0.45
IL 1-4	52.03 $\pm$ 4.42	66.77 $\pm$ 6.45	50.35 $\pm$ 7.50	5.48 $\pm$ 0.43	6.91 $\pm$ 0.75	5.12 $\pm$ 0.44
IL 1-4-18	45.53 $\pm$ 3.41	64.71 $\pm$ 4.96	48.20 $\pm$ 4.61	5.16 $\pm$ 0.59	4.71 $\pm$ 0.57	5.27 $\pm$ 0.59
IL 2-1	19.44 $\pm$ 1.45	61.81 $\pm$ 4.47	32.93 $\pm$ 2.75	6.32 $\pm$ 0.24	4.13 $\pm$ 0.38	4.40 $\pm$ 0.38
IL 2-2	28.34 $\pm$ 1.97	53.12 $\pm$ 5.32	24.08 $\pm$ 4.85	5.96 $\pm$ 0.12	3.95 $\pm$ 0.27	3.26 $\pm$ 0.53
IL 2-3	42.91 $\pm$ 3.67	81.19 $\pm$ 4.43	66.00 $\pm$ 4.36	6.98 $\pm$ 0.65	9.15 $\pm$ 0.88	4.42 $\pm$ 0.60
IL 2-4	37.44 $\pm$ 3.49	57.15 $\pm$ 5.63	27.74 $\pm$ 5.43	5.78 $\pm$ 0.43	4.18 $\pm$ 0.39	3.59 $\pm$ 0.20
IL 2-5	35.37 $\pm$ 4.03	69.05 $\pm$ 3.89	41.81 $\pm$ 2.77	5.87 $\pm$ 0.67	4.50 $\pm$ 0.65	4.35 $\pm$ 0.43
IL 2-6	34.37 $\pm$ 7.20	84.19 $\pm$ 6.00	65.58 $\pm$ 5.40	6.34 $\pm$ 0.65	7.40 $\pm$ 0.72	5.27 $\pm$ 0.80
IL 2-6-5	50.93 $\pm$ 6.24	58.87 $\pm$ 4.51	31.54 $\pm$ 3.12	6.28 $\pm$ 0.74	6.26 $\pm$ 0.67	3.13 $\pm$ 0.56
IL 3-1	50.53 $\pm$ 5.68	76.39 $\pm$ 3.84	57.82 $\pm$ 3.29	6.55 $\pm$ 0.36	5.59 $\pm$ 0.19	4.47 $\pm$ 0.65
IL 3-2	17.74 $\pm$ 0.81	36.51 $\pm$ 5.09	15.86 $\pm$ 4.10	6.56 $\pm$ 0.43	5.41 $\pm$ 0.60	3.74 $\pm$ 0.41
IL 3-3	36.30 $\pm$ 2.99	64.94 $\pm$ 4.97	40.07 $\pm$ 5.09	4.27 $\pm$ 0.44	3.47 $\pm$ 0.24	4.23 $\pm$ 0.34
IL 3-4	19.06 $\pm$ 1.21	53.66 $\pm$ 2.64	24.19 $\pm$ 4.43	5.29 $\pm$ 0.36	4.05 $\pm$ 0.28	2.95 $\pm$ 0.45
IL 3-5	55.36 $\pm$ 6.94	56.85 $\pm$ 4.15	35.60 $\pm$ 3.39	6.90 $\pm$ 0.61	6.35 $\pm$ 0.49	4.43 $\pm$ 0.47
IL 4-1	56.05 $\pm$ 6.96	83.77 $\pm$ 4.66	65.39 $\pm$ 4.43	6.32 $\pm$ 0.33	6.62 $\pm$ 0.37	6.23 $\pm$ 0.53
IL 4-1-1	57.40 $\pm$ 4.37	71.45 $\pm$ 3.28	57.09 $\pm$ 2.93	7.71 $\pm$ 0.69	7.42 $\pm$ 0.29	4.68 $\pm$ 0.25
IL 4-2	52.20 $\pm$ 5.53	67.69 $\pm$ 4.12	55.09 $\pm$ 4.27	7.90 $\pm$ 0.54	7.76 $\pm$ 0.58	4.73 $\pm$ 0.35
IL 4-3	46.76 $\pm$ 5.45	66.13 $\pm$ 4.32	39.79 $\pm$ 5.29	8.81 $\pm$ 0.47	7.98 $\pm$ 0.34	3.96 $\pm$ 0.40
IL 4-3-2	41.63 $\pm$ 4.88	64.56 $\pm$ 7.70	46.02 $\pm$ 7.71	7.31 $\pm$ 0.75	6.75 $\pm$ 0.70	3.17 $\pm$ 0.34
IL 4-4	23.52 $\pm$ 1.94	44.77 $\pm$ 4.17	9.77 $\pm$ 3.19	6.00 $\pm$ 0.29	4.99 $\pm$ 0.25	2.95 $\pm$ 0.12
IL 5-1	46.52 $\pm$ 8.53	55.66 $\pm$ 2.58	39.94 $\pm$ 3.06	7.00 $\pm$ 0.61	7.02 $\pm$ 0.63	4.35 $\pm$ 0.36
IL 5-3	48.20 $\pm$ 3.50	77.10 $\pm$ 4.20	51.34 $\pm$ 4.01	7.74 $\pm$ 0.42	7.76 $\pm$ 0.36	6.17 $\pm$ 0.87
IL 5-4	53.13 $\pm$ 7.14	61.76 $\pm$ 3.61	45.60 $\pm$ 4.74	6.78 $\pm$ 0.36	6.06 $\pm$ 0.80	4.40 $\pm$ 0.21
IL 5-5	48.33 $\pm$ 3.64	74.32 $\pm$ 4.20	57.32 $\pm$ 4.36	7.54 $\pm$ 0.15	7.09 $\pm$ 0.64	3.65 $\pm$ 0.43
IL 6-1	49.74 $\pm$ 5.01	78.60 $\pm$ 3.98	49.93 $\pm$ 3.67	7.85 $\pm$ 0.68	6.83 $\pm$ 0.75	4.63 $\pm$ 0.54
IL 6-2	61.83 $\pm$ 5.35	75.24 $\pm$ 3.25	49.09 $\pm$ 3.01	7.95 $\pm$ 0.35	7.46 $\pm$ 0.95	4.85 $\pm$ 0.53
IL 6-3	23.94 $\pm$ 3.65	53.44 $\pm$ 3.29	32.37 $\pm$ 3.38	5.07 $\pm$ 0.62	4.74 $\pm$ 0.47	5.09 $\pm$ 0.31
IL 6-4	40.37 $\pm$ 3.57	49.26 $\pm$ 4.03	35.19 $\pm$ 4.50	5.93 $\pm$ 0.58	4.55 $\pm$ 0.30	4.44 $\pm$ 0.51
IL 7-1	25.61 $\pm$ 2.00	52.78 $\pm$ 4.04	27.57 $\pm$ 3.35	10.53 $\pm$ 0.44	7.52 $\pm$ 0.41	5.04 $\pm$ 0.25
IL 7-2	45.69 $\pm$ 4.00	88.84 $\pm$ 5.27	67.38 $\pm$ 7.51	5.14 $\pm$ 0.62	6.30 $\pm$ 0.34	4.05 $\pm$ 0.35
IL 7-3	43.18 $\pm$ 3.37	79.76 $\pm$ 5.39	61.42 $\pm$ 4.08	5.82 $\pm$ 0.56	6.06 $\pm$ 0.80	4.51 $\pm$ 0.56
IL 7-4	50.01 $\pm$ 8.50	58.53 $\pm$ 3.87	39.14 $\pm$ 5.71	7.73 $\pm$ 0.65	7.82 $\pm$ 0.36	4.80 $\pm$ 0.21
IL 7-4-1	26.70 $\pm$ 4.17	51.02 $\pm$ 3.89	23.00 $\pm$ 4.17	6.83 $\pm$ 0.35	5.13 $\pm$ 0.54	5.54 $\pm$ 0.36
IL 7-5	11.75 $\pm$ 1.93	29.54 $\pm$ 2.95	20.65 $\pm$ 2.80	4.80 $\pm$ 0.38	4.16 $\pm$ 0.35	3.00 $\pm$ 0.17
IL 7-5-5	19.03 $\pm$ 2.71	34.39 $\pm$ 1.17	19.85 $\pm$ 2.00	7.14 $\pm$ 0.27	4.07 $\pm$ 0.39	3.30 $\pm$ 0.20
IL 8-1	43.45 $\pm$ 5.29	59.58 $\pm$ 3.36	37.60 $\pm$ 4.30	4.97 $\pm$ 0.24	4.67 $\pm$ 0.50	5.14 $\pm$ 0.59
IL 8-1-1	28.53 $\pm$ 1.84	63.63 $\pm$ 4.08	44.03 $\pm$ 3.43	6.32 $\pm$ 0.30	4.33 $\pm$ 0.23	3.22 $\pm$ 0.15
IL 8-2	22.91 $\pm$ 1.69	58.21 $\pm$ 2.03	25.24 $\pm$ 2.60	6.64 $\pm$ 0.22	4.75 $\pm$ 0.47	4.18 $\pm$ 0.30
IL 8-2-1	16.00 $\pm$ 1.64	42.67 $\pm$ 3.71	15.30 $\pm$ 3.22	6.76 $\pm$ 0.27	4.90 $\pm$ 0.09	4.21 $\pm$ 0.35
IL 8-3	24.75 $\pm$ 0.75	52.78 $\pm$ 3.00	32.99 $\pm$ 3.15	6.66 $\pm$ 0.53	4.37 $\pm$ 0.49	4.62 $\pm$ 0.38
IL 9-1	33.10 $\pm$ 3.26	58.45 $\pm$ 4.10	12.10 $\pm$ 2.89	7.05 $\pm$ 0.32	4.41 $\pm$ 0.18	3.90 $\pm$ 0.64
IL 9-1-2	60.86 $\pm$ 4.78	111.61 $\pm$ 7.13	96.36 $\pm$ 8.45	7.76 $\pm$ 0.33	6.93 $\pm$ 0.52	5.07 $\pm$ 0.16
IL 9-1-3	24.23 $\pm$ 2.75	42.24 $\pm$ 2.19	25.88 $\pm$ 1.62	10.11 $\pm$ 0.42	8.56 $\pm$ 0.45	4.87 $\pm$ 0.46
IL 9-2	57.52 $\pm$ 4.01	59.64 $\pm$ 6.74	39.82 $\pm$ 6.26	6.22 $\pm$ 0.55	5.58 $\pm$ 0.35	4.87 $\pm$ 0.44
IL 9-2-5	53.19 $\pm$ 4.93	85.22 $\pm$ 4.87	69.99 $\pm$ 3.75	7.99 $\pm$ 0.24	7.69 $\pm$ 0.41	5.10 $\pm$ 0.50
IL 9-2-6	56.80 $\pm$ 4.76	77.74 $\pm$ 3.41	54.62 $\pm$ 3.35	6.80 $\pm$ 0.66	9.40 $\pm$ 0.64	3.89 $\pm$ 0.43
IL 9-3	21.82 $\pm$ 1.06	44.05 $\pm$ 3.45	16.00 $\pm$ 2.45	4.82 $\pm$ 0.27	2.88 $\pm$ 0.29	2.63 $\pm$ 0.32
IL 9-3-1	50.36 $\pm$ 2.73	58.37 $\pm$ 5.57	32.01 $\pm$ 5.11	6.30 $\pm$ 0.64	4.73 $\pm$ 0.56	4.76 $\pm$ 0.53
IL 9-3-2	57.32 $\pm$ 4.24	91.69 $\pm$ 3.25	68.94 $\pm$ 4.70	7.29 $\pm$ 0.65	4.89 $\pm$ 0.64	4.23 $\pm$ 0.33
IL 10-1	26.48 $\pm$ 2.02	42.63 $\pm$ 3.44	18.90 $\pm$ 1.75	7.23 $\pm$ 0.30	4.77 $\pm$ 0.31	2.85 $\pm$ 0.34
IL 10-1-1	48.88 $\pm$ 4.55	71.05 $\pm$ 6.51	43.38 $\pm$ 8.03	6.93 $\pm$ 0.58	6.81 $\pm$ 0.96	5.04 $\pm$ 0.52
IL 10-2	42.72 $\pm$ 2.12	74.55 $\pm$ 1.79	54.42 $\pm$ 3.15	6.14 $\pm$ 0.47	6.83 $\pm$ 0.65	4.38 $\pm$ 0.53
IL 10-2-2	56.32 $\pm$ 2.32	66.07 $\pm$ 2.80	50.60 $\pm$ 2.92	8.07 $\pm$ 0.52	5.96 $\pm$ 1.12	5.04 $\pm$ 0.72
IL 10-3	54.11 $\pm$ 5.48	76.10 $\pm$ 3.16	46.86 $\pm$ 5.83	7.86 $\pm$ 0.30	8.30 $\pm$ 0.49	3.99 $\pm$ 0.36
IL 11-1	53.02 $\pm$ 2.16	82.23 $\pm$ 4.31	52.11 $\pm$ 6.25	6.90 $\pm$ 1.06	6.66 $\pm$ 0.59	4.73 $\pm$ 0.46
IL 11-2	42.24 $\pm$ 3.43	71.81 $\pm$ 8.37	49.43 $\pm$ 8.15	6.66 $\pm$ 0.35	6.75 $\pm$ 0.68	5.86 $\pm$ 0.65
IL 11-3	49.90 $\pm$ 5.09	63.88 $\pm$ 3.58	50.52 $\pm$ 3.53	6.59 $\pm$ 0.51	5.27 $\pm$ 0.38	4.96 $\pm$ 0.32
IL 11-4	43.25 $\pm$ 6.50	67.27 $\pm$ 5.11	45.36 $\pm$ 4.91	7.58 $\pm$ 0.19	6.82 $\pm$ 0.71	4.47 $\pm$ 0.29
IL 11-4-1	37.84 $\pm$ 2.19	73.62 $\pm$ 7.45	53.22 $\pm$ 7.25	6.74 $\pm$ 0.80	6.19 $\pm$ 0.64	4.32 $\pm$ 0.26
IL 12-1	21.79 $\pm$ 2.17	43.34 $\pm$ 2.40	18.32 $\pm$ 2.09	7.67 $\pm$ 0.27	5.50 $\pm$ 0.46	4.76 $\pm$ 0.19
IL 12-1-1	20.67 $\pm$ 1.61	63.15 $\pm$ 6.63	31.76 $\pm$ 5.00	5.91 $\pm$ 0.23	3.57 $\pm$ 0.23	4.26 $\pm$ 0.28
IL 12-2	29.29 $\pm$ 2.23	60.44 $\pm$ 4.89	31.19 $\pm$ 3.11	7.22 $\pm$ 0.44	4.54 $\pm$ 0.31	3.13 $\pm$ 0.12
IL 12-3	23.64 $\pm$ 0.97	52.48 $\pm$ 3.19	19.67 $\pm$ 3.55	7.67 $\pm$ 0.50	4.63 $\pm$ 0.30	3.71 $\pm$ 0.30
IL 12-3-1	29.79 $\pm$ 1.03	45.13 $\pm$ 2.12	16.58 $\pm$ 1.34	7.39 $\pm$ 0.30	4.82 $\pm$ 0.66	3.44 $\pm$ 0.21
IL 12-4	38.97 $\pm$ 6.08	55.83 $\pm$ 6.70	35.09 $\pm$ 5.61	7.15 $\pm$ 0.62	5.15 $\pm$ 0.74	4.48 $\pm$ 0.54
IL 12-4-1	60.49 $\pm$ 6.44	63.69 $\pm$ 2.80	37.75 $\pm$ 4.64	6.86 $\pm$ 0.66	5.55 $\pm$ 0.37	5.04 $\pm$ 0.45
M82	24.99 $\pm$ 2.52	49.31 $\pm$ 3.65	27.72 $\pm$ 4.16	5.87 $\pm$ 0.19	5.47 $\pm$ 0.48	4.35 $\pm$ 0.22

Supplemental Table S2. Profiles of the biochemical components, including sugars (fructose, glucose and sucrose), starch, malate, nitrate, total amino acids, total protein, chlorophyll *a* and *b*, physiological parameters as well as growth-related parameters for the 71 ILs grown in the second experiment. Samples for metabolites measurements were harvested at the middle of the light period. Values are presented as mean $\pm$ SE ($n = 5$) and significant changes are indicated in bold. Abbreviations: A, net photosynthesis; g_s , stomatal conductance; C_i , intercellular CO_2 concentration; Pr, photorespiration; Rd, dark respiration; Starch-EN, starch level at end of the night; Starch-MD, starch level at middle of the day; Starch-ED, starch level at end of the day, starch turnover; Starch turn; RGR, relative growth rate; DW, dry weight; qP, photochemical quenching coefficient; NPQ, non- photochemical quenching; ETR, electron transport rate.

ILs	A ($\mu\text{mol } CO_2 \text{ m}^{-2} \text{ s}^{-1}$)	g_s ($\text{mol H}_2\text{O m}^{-2} \text{ s}^{-1}$)	C_i ($\mu\text{mol } CO_2$)	Pr ($\mu\text{mol m}^{-2} \text{ s}^{-1}$)	Rd ($\mu\text{mol } CO_2 \text{ m}^{-2} \text{ s}^{-1}$)	NPQ
IL 1-1	25.13 $\pm$ 0.35	0.70 $\pm$ 0.06	310.15 $\pm$ 8.35	7.76 $\pm$ 0.27	1.33 $\pm$ 0.07	0.98 $\pm$ 0.05
IL 1-1-2	26.72 $\pm$ 0.43	0.80 $\pm$ 0.03	311.58 $\pm$ 2.34	8.14 $\pm$ 0.48	1.40 $\pm$ 0.08	0.98 $\pm$ 0.03
IL 1-1-3	24.16 $\pm$ 0.21	0.68 $\pm$ 0.03	305.59 $\pm$ 3.44	7.89 $\pm$ 0.11	1.44 $\pm$ 0.05	0.94 $\pm$ 0.02
IL 1-2	23.38 $\pm$ 0.27	0.59 $\pm$ 0.03	304.65 $\pm$ 6.06	7.67 $\pm$ 0.53	1.13 $\pm$ 0.10	1.05 $\pm$ 0.08
IL 1-3	24.06 $\pm$ 0.54	0.49 $\pm$ 0.04	286.82 $\pm$ 4.84	8.20 $\pm$ 0.27	1.82 $\pm$ 0.04	0.86 $\pm$ 0.05
IL 1-4	25.64 $\pm$ 0.27	0.87 $\pm$ 0.04	320.85 $\pm$ 2.35	7.50 $\pm$ 0.13	1.16 $\pm$ 0.05	1.11 $\pm$ 0.05
IL 1-4-18	24.83 $\pm$ 0.19	0.83 $\pm$ 0.05	319.52 $\pm$ 3.84	7.07 $\pm$ 0.18	1.44 $\pm$ 0.07	1.02 $\pm$ 0.03
IL 2-1	23.43 $\pm$ 0.25	0.64 $\pm$ 0.04	307.29 $\pm$ 4.31	8.93 $\pm$ 0.51	0.84 $\pm$ 0.13	1.04 $\pm$ 0.03
IL 2-2	25.36 $\pm$ 0.42	0.55 $\pm$ 0.03	292.60 $\pm$ 2.41	8.13 $\pm$ 0.28	1.55 $\pm$ 0.08	0.77 $\pm$ 0.02
IL 2-3	24.69 $\pm$ 0.42	0.64 $\pm$ 0.05	311.42 $\pm$ 6.69	7.11 $\pm$ 0.36	1.39 $\pm$ 0.03	0.99 $\pm$ 0.04
IL 2-4	25.72 $\pm$ 0.42	0.67 $\pm$ 0.04	306.41 $\pm$ 5.19	8.38 $\pm$ 0.45	1.19 $\pm$ 0.07	0.81 $\pm$ 0.03
IL 2-5	25.68 $\pm$ 0.71	0.62 $\pm$ 0.02	298.96 $\pm$ 3.25	8.63 $\pm$ 0.18	2.05 $\pm$ 0.17	0.96 $\pm$ 0.06
IL 2-6	27.17 $\pm$ 0.31	0.75 $\pm$ 0.04	305.73 $\pm$ 3.77	8.78 $\pm$ 0.28	1.53 $\pm$ 0.17	0.97 $\pm$ 0.06
IL 2-6-5	27.81 $\pm$ 0.42	0.79 $\pm$ 0.03	310.43 $\pm$ 2.72	7.99 $\pm$ 0.39	1.40 $\pm$ 0.09	0.84 $\pm$ 0.03
IL 3-1	26.14 $\pm$ 0.57	0.74 $\pm$ 0.04	310.49 $\pm$ 1.82	7.66 $\pm$ 0.36	1.37 $\pm$ 0.06	0.89 $\pm$ 0.05
IL 3-2	24.62 $\pm$ 0.19	0.69 $\pm$ 0.06	306.10 $\pm$ 5.11	7.86 $\pm$ 0.26	1.12 $\pm$ 0.09	1.05 $\pm$ 0.02
IL 3-3	24.86 $\pm$ 0.38	0.71 $\pm$ 0.03	311.82 $\pm$ 2.71	6.92 $\pm$ 0.26	1.12 $\pm$ 0.04	0.98 $\pm$ 0.05
IL 3-4	23.34 $\pm$ 0.47	0.72 $\pm$ 0.05	315.78 $\pm$ 5.90	6.68 $\pm$ 0.63	1.15 $\pm$ 0.08	0.97 $\pm$ 0.03
IL 3-5	26.15 $\pm$ 0.26	0.67 $\pm$ 0.05	306.29 $\pm$ 3.40	7.98 $\pm$ 0.68	1.24 $\pm$ 0.06	0.80 $\pm$ 0.02
IL 4-1	25.94 $\pm$ 0.36	0.69 $\pm$ 0.06	315.19 $\pm$ 6.88	7.29 $\pm$ 0.51	1.55 $\pm$ 0.05	0.99 $\pm$ 0.03
IL 4-1-1	25.50 $\pm$ 0.27	0.68 $\pm$ 0.02	305.78 $\pm$ 3.24	7.80 $\pm$ 0.22	1.35 $\pm$ 0.08	0.95 $\pm$ 0.03
IL 4-2	23.54 $\pm$ 0.25	0.62 $\pm$ 0.04	301.96 $\pm$ 6.68	7.85 $\pm$ 0.69	1.30 $\pm$ 0.07	0.91 $\pm$ 0.02
IL 4-3	23.06 $\pm$ 0.22	0.65 $\pm$ 0.03	311.22 $\pm$ 3.72	7.83 $\pm$ 0.46	1.22 $\pm$ 0.08	1.15 $\pm$ 0.07
IL 4-3-2	24.14 $\pm$ 0.39	0.67 $\pm$ 0.03	309.87 $\pm$ 3.69	8.18 $\pm$ 0.44	1.20 $\pm$ 0.06	0.96 $\pm$ 0.04
IL 4-4	26.08 $\pm$ 0.30	0.68 $\pm$ 0.02	303.96 $\pm$ 1.14	8.32 $\pm$ 0.24	1.19 $\pm$ 0.04	0.81 $\pm$ 0.03
IL 5-1	26.45 $\pm$ 0.38	0.70 $\pm$ 0.03	303.25 $\pm$ 2.69	8.40 $\pm$ 0.21	2.41 $\pm$ 0.14	0.84 $\pm$ 0.04
IL 5-3	26.21 $\pm$ 0.23	0.68 $\pm$ 0.03	301.63 $\pm$ 1.65	8.09 $\pm$ 0.20	1.62 $\pm$ 0.09	0.81 $\pm$ 0.02
IL 5-4	25.62 $\pm$ 0.28	0.63 $\pm$ 0.05	296.55 $\pm$ 5.28	8.45 $\pm$ 0.29	1.58 $\pm$ 0.04	0.87 $\pm$ 0.03
IL 5-5	25.64 $\pm$ 0.35	0.56 $\pm$ 0.04	292.78 $\pm$ 4.59	8.42 $\pm$ 0.25	1.50 $\pm$ 0.07	0.84 $\pm$ 0.03
IL 6-1	23.73 $\pm$ 0.38	0.70 $\pm$ 0.03	312.59 $\pm$ 3.65	7.68 $\pm$ 0.44	1.49 $\pm$ 0.09	1.01 $\pm$ 0.05
IL 6-2	23.57 $\pm$ 0.46	0.67 $\pm$ 0.05	310.31 $\pm$ 4.76	7.68 $\pm$ 0.38	1.35 $\pm$ 0.05	0.75 $\pm$ 0.04
IL 6-3	24.50 $\pm$ 0.25	0.78 $\pm$ 0.02	317.57 $\pm$ 1.88	7.47 $\pm$ 0.23	1.34 $\pm$ 0.08	0.93 $\pm$ 0.05
IL 6-4	22.60 $\pm$ 0.25	0.62 $\pm$ 0.03	306.67 $\pm$ 2.90	8.70 $\pm$ 0.33	1.16 $\pm$ 0.03	1.01 $\pm$ 0.04
IL 7-1	25.69 $\pm$ 0.17	0.70 $\pm$ 0.06	302.87 $\pm$ 7.83	7.53 $\pm$ 0.32	1.34 $\pm$ 0.05	0.86 $\pm$ 0.03
IL 7-2	23.06 $\pm$ 0.73	0.88 $\pm$ 0.03	365.69 $\pm$ 2.61	4.55 $\pm$ 0.22	2.13 $\pm$ 0.04	1.33 $\pm$ 0.03
IL 7-3	25.27 $\pm$ 0.18	0.63 $\pm$ 0.04	296.44 $\pm$ 6.10	8.27 $\pm$ 0.26	1.48 $\pm$ 0.05	0.88 $\pm$ 0.03
IL 7-4	24.27 $\pm$ 0.34	0.78 $\pm$ 0.06	313.24 $\pm$ 3.90	8.54 $\pm$ 0.56	1.33 $\pm$ 0.08	0.95 $\pm$ 0.04
IL 7-4-1	22.04 $\pm$ 0.37	0.67 $\pm$ 0.02	302.38 $\pm$ 7.65	0.98 $\pm$ 0.45	2.71 $\pm$ 0.09	1.67 $\pm$ 0.10
IL 7-5	24.51 $\pm$ 0.33	0.67 $\pm$ 0.03	305.64 $\pm$ 3.72	7.92 $\pm$ 0.33	1.14 $\pm$ 0.05	0.91 $\pm$ 0.05
IL 7-5-5	25.00 $\pm$ 0.41	0.73 $\pm$ 0.03	310.91 $\pm$ 4.26	8.20 $\pm$ 0.43	1.32 $\pm$ 0.13	0.99 $\pm$ 0.04
IL 8-1	23.09 $\pm$ 0.30	0.71 $\pm$ 0.03	316.29 $\pm$ 3.41	8.03 $\pm$ 0.42	0.92 $\pm$ 0.04	1.13 $\pm$ 0.06
IL 8-1-1	22.82 $\pm$ 0.23	0.70 $\pm$ 0.04	313.13 $\pm$ 5.33	8.77 $\pm$ 0.30	1.03 $\pm$ 0.04	1.04 $\pm$ 0.02
IL 8-2	25.24 $\pm$ 0.45	0.74 $\pm$ 0.03	315.22 $\pm$ 4.28	8.44 $\pm$ 0.22	1.32 $\pm$ 0.06	0.90 $\pm$ 0.03
IL 8-2-1	23.91 $\pm$ 0.39	0.72 $\pm$ 0.04	313.19 $\pm$ 3.97	7.73 $\pm$ 0.36	1.38 $\pm$ 0.04	1.08 $\pm$ 0.06
IL 8-3	23.05 $\pm$ 0.12	0.75 $\pm$ 0.03	318.84 $\pm$ 3.07	7.82 $\pm$ 0.95	1.32 $\pm$ 0.05	1.11 $\pm$ 0.05
IL 9-1	24.59 $\pm$ 0.31	0.61 $\pm$ 0.02	301.40 $\pm$ 3.02	7.87 $\pm$ 0.16	1.50 $\pm$ 0.07	0.90 $\pm$ 0.03
IL 9-1-2	23.32 $\pm$ 0.42	0.62 $\pm$ 0.04	307.64 $\pm$ 2.78	7.65 $\pm$ 0.18	1.34 $\pm$ 0.11	1.03 $\pm$ 0.04
IL 9-1-3	24.98 $\pm$ 0.34	0.75 $\pm$ 0.03	314.20 $\pm$ 1.72	9.79 $\pm$ 0.71	1.19 $\pm$ 0.06	0.83 $\pm$ 0.03
IL 9-2	22.51 $\pm$ 0.32	0.66 $\pm$ 0.03	313.06 $\pm$ 2.14	8.01 $\pm$ 0.53	1.32 $\pm$ 0.08	1.08 $\pm$ 0.02
IL 9-2-5	26.80 $\pm$ 0.29	0.70 $\pm$ 0.01	305.37 $\pm$ 2.37	7.47 $\pm$ 0.40	1.21 $\pm$ 0.05	0.88 $\pm$ 0.07
IL 9-2-6	23.74 $\pm$ 0.25	0.63 $\pm$ 0.02	305.60 $\pm$ 1.43	7.75 $\pm$ 0.25	1.38 $\pm$ 0.11	1.08 $\pm$ 0.05
IL 9-3	25.10 $\pm$ 0.32	0.66 $\pm$ 0.04	304.61 $\pm$ 3.36	7.53 $\pm$ 0.28	1.20 $\pm$ 0.07	0.90 $\pm$ 0.09
IL 9-3-1	25.27 $\pm$ 0.42	0.67 $\pm$ 0.03	305.85 $\pm$ 2.53	7.49 $\pm$ 0.29	1.20 $\pm$ 0.11	1.11 $\pm$ 0.06
IL 9-3-2	25.42 $\pm$ 0.47	0.66 $\pm$ 0.03	304.68 $\pm$ 3.11	7.71 $\pm$ 0.29	1.21 $\pm$ 0.02	0.79 $\pm$ 0.05
IL 10-1	23.97 $\pm$ 0.21	0.64 $\pm$ 0.03	310.83 $\pm$ 5.36	7.32 $\pm$ 0.31	2.36 $\pm$ 0.06	1.10 $\pm$ 0.04
IL 10-1-1	27.06 $\pm$ 0.56	0.67 $\pm$ 0.02	299.63 $\pm$ 4.76	8.78 $\pm$ 0.44	1.86 $\pm$ 0.05	1.18 $\pm$ 0.03
IL 10-2	31.88 $\pm$ 0.28	0.87 $\pm$ 0.02	303.62 $\pm$ 1.09	10.84 $\pm$ 0.34	1.30 $\pm$ 0.05	0.39 $\pm$ 0.06
IL 10-2-2	28.09 $\pm$ 0.47	0.85 $\pm$ 0.02	327.08 $\pm$ 1.41	7.66 $\pm$ 0.55	1.50 $\pm$ 0.07	0.77 $\pm$ 0.03
IL 10-3	23.10 $\pm$ 0.96	0.67 $\pm$ 0.06	326.63 $\pm$ 5.60	6.44 $\pm$ 0.74	1.87 $\pm$ 0.09	1.05 $\pm$ 0.08
IL 11-1	26.69 $\pm$ 0.54	0.64 $\pm$ 0.04	299.87 $\pm$ 5.64	8.48 $\pm$ 0.28	1.51 $\pm$ 0.06	0.82 $\pm$ 0.07
IL 11-2	23.18 $\pm$ 0.20	0.48 $\pm$ 0.02	290.29 $\pm$ 2.45	7.99 $\pm$ 0.29	1.51 $\pm$ 0.07	0.97 $\pm$ 0.03
IL 11-3	23.41 $\pm$ 0.27	0.58 $\pm$ 0.04	302.11 $\pm$ 4.16	8.20 $\pm$ 0.17	1.32 $\pm$ 0.08	1.00 $\pm$ 0.04
IL 11-4	27.61 $\pm$ 0.19	0.85 $\pm$ 0.01	328.01 $\pm$ 1.39	7.29 $\pm$ 0.39	1.69 $\pm$ 0.07	0.77 $\pm$ 0.02
IL 11-4-1	26.74 $\pm$ 0.36	0.75 $\pm$ 0.04	318.18 $\pm$ 3.75	7.57 $\pm$ 0.25	1.54 $\pm$ 0.06	0.80 $\pm$ 0.03
IL 12-1	24.27 $\pm$ 0.43	0.62 $\pm$ 0.02	302.05 $\pm$ 1.33	8.96 $\pm$ 0.54	1.84 $\pm$ 0.08	0.82 $\pm$ 0.03
IL 12-1-1	24.00 $\pm$ 0.22	0.72 $\pm$ 0.03	313.02 $\pm$ 3.00	7.82 $\pm$ 0.32	1.43 $\pm$ 0.05	0.97 $\pm$ 0.05
IL 12-2	24.40 $\pm$ 0.21	0.69 $\pm$ 0.05	314.12 $\pm$ 3.19	7.34 $\pm$ 0.18	1.41 $\pm$ 0.11	0.97 $\pm$ 0.04
IL 12-3	22.90 $\pm$ 0.26	0.68 $\pm$ 0.03	313.09 $\pm$ 1.71	7.44 $\pm$ 0.25	1.44 $\pm$ 0.07	1.04 $\pm$ 0.04
IL 12-3-1	23.47 $\pm$ 0.09	0.73 $\pm$ 0.04	313.91 $\pm$ 3.31	8.45 $\pm$ 0.44	1.31 $\pm$ 0.11	1.05 $\pm$ 0.03
IL 12-4	26.05 $\pm$ 0.61	0.53 $\pm$ 0.02	290.82 $\pm$ 4.67	7.99 $\pm$ 0.27	1.34 $\pm$ 0.06	0.84 $\pm$ 0.03
IL 12-4-1	26.12 $\pm$ 0.65	0.79 $\pm$ 0.09	312.24 $\pm$ 5.76	7.60 $\pm$ 0.42	1.40 $\pm$ 0.13	1.12 $\pm$ 0.06
M82	23.85 $\pm$ 0.66	0.59 $\pm$ 0.04	301.79 $\pm$ 8.33	8.10 $\pm$ 0.76	1.39 $\pm$ 0.08	0.93 $\pm$ 0.09

ILs	qP	ETR ($\mu\text{mol e}^- \text{m}^{-2} \text{s}^{-1}$)	RGR ($\text{cm cm}^{-1} \text{day}$)	Shoot DW (g)	Root DW (g)	Protein ($\text{mg g}^{-1} \text{FW}$)
L 1-1	0.68 ± 0.03	196.31 ± 3.73	0.08 ± 0.00	18.98 ± 0.92	3.06 ± 0.29	4.10 ± 0.24
L 1-1-2	0.70 ± 0.02	207.36 ± 6.62	0.09 ± 0.00	20.59 ± 1.03	3.65 ± 0.21	4.09 ± 0.13
L 1-1-3	0.66 ± 0.02	194.25 ± 1.47	0.09 ± 0.00	16.00 ± 0.65	2.59 ± 0.10	3.42 ± 0.11
L 1-2	0.66 ± 0.04	187.83 ± 7.04	0.09 ± 0.00	15.40 ± 0.21	2.03 ± 0.08	3.80 ± 0.19
L 1-3	0.71 ± 0.02	198.22 ± 4.87	0.06 ± 0.00	13.37 ± 0.56	2.81 ± 0.13	3.80 ± 0.21
L 1-4	0.67 ± 0.01	194.87 ± 1.45	0.12 ± 0.00	14.33 ± 0.50	2.40 ± 0.05	3.55 ± 0.20
L 1-4-18	0.64 ± 0.01	187.00 ± 2.51	0.09 ± 0.00	13.59 ± 0.92	2.24 ± 0.10	4.08 ± 0.03
L 2-1	0.65 ± 0.02	202.50 ± 6.24	0.09 ± 0.00	14.24 ± 0.60	3.02 ± 0.21	3.35 ± 0.17
L 2-2	0.70 ± 0.02	202.08 ± 4.48	0.06 ± 0.00	18.29 ± 0.60	3.27 ± 0.08	3.56 ± 0.16
L 2-3	0.66 ± 0.01	186.87 ± 4.50	0.03 ± 0.00	16.48 ± 0.33	3.58 ± 0.07	3.84 ± 0.13
L 2-4	0.68 ± 0.02	205.87 ± 6.16	0.10 ± 0.00	15.62 ± 0.43	2.63 ± 0.16	3.51 ± 0.28
L 2-5	0.72 ± 0.02	210.44 ± 4.53	0.07 ± 0.00	18.65 ± 0.60	3.28 ± 0.07	3.96 ± 0.17
L 2-6	0.72 ± 0.01	217.07 ± 4.18	0.09 ± 0.00	15.94 ± 0.89	2.91 ± 0.23	3.86 ± 0.18
L 2-6-5	0.69 ± 0.01	209.94 ± 5.42	0.09 ± 0.00	18.42 ± 0.49	2.89 ± 0.14	4.49 ± 0.19
L 3-1	0.63 ± 0.02	199.16 ± 6.18	0.06 ± 0.00	22.36 ± 0.61	3.07 ± 0.09	3.76 ± 0.13
L 3-2	0.67 ± 0.01	195.00 ± 2.76	0.08 ± 0.00	14.51 ± 0.37	2.40 ± 0.19	3.83 ± 0.27
L 3-3	0.62 ± 0.01	184.75 ± 4.07	0.10 ± 0.00	9.34 ± 0.54	2.15 ± 0.16	4.29 ± 0.19
L 3-4	0.63 ± 0.03	175.78 ± 8.88	0.08 ± 0.00	13.02 ± 0.36	2.89 ± 0.06	4.13 ± 0.13
L 3-5	0.71 ± 0.02	202.87 ± 8.29	0.07 ± 0.00	15.44 ± 0.60	2.20 ± 0.14	3.94 ± 0.15
L 4-1	0.65 ± 0.02	194.34 ± 6.09	0.06 ± 0.00	16.91 ± 0.17	3.75 ± 0.02	3.53 ± 0.10
L 4-1-1	0.66 ± 0.01	198.29 ± 2.77	0.08 ± 0.00	18.26 ± 0.63	2.88 ± 0.07	4.73 ± 0.36
L 4-2	0.66 ± 0.04	190.90 ± 8.83	0.08 ± 0.00	15.64 ± 0.87	2.43 ± 0.10	4.41 ± 0.22
L 4-3	0.66 ± 0.02	188.60 ± 6.42	0.10 ± 0.00	8.92 ± 0.55	2.22 ± 0.11	3.97 ± 0.22
L 4-3-2	0.67 ± 0.02	197.11 ± 6.10	0.08 ± 0.00	17.43 ± 0.56	2.77 ± 0.13	4.12 ± 0.14
L 4-4	0.68 ± 0.01	206.47 ± 3.02	0.08 ± 0.00	12.88 ± 0.86	3.75 ± 0.17	4.16 ± 0.29
L 5-1	0.69 ± 0.02	211.48 ± 1.46	0.10 ± 0.00	17.08 ± 0.41	3.04 ± 0.11	3.97 ± 0.35
L 5-3	0.71 ± 0.01	205.17 ± 2.98	0.06 ± 0.00	19.20 ± 0.36	3.28 ± 0.07	4.18 ± 0.17
L 5-4	0.73 ± 0.01	206.97 ± 3.14	0.06 ± 0.00	20.21 ± 0.99	3.14 ± 0.09	3.78 ± 0.18
L 5-5	0.73 ± 0.02	206.58 ± 2.88	0.06 ± 0.00	19.08 ± 1.28	2.91 ± 0.17	2.98 ± 0.20
L 6-1	0.66 ± 0.01	190.03 ± 5.73	0.10 ± 0.00	17.80 ± 0.39	2.17 ± 0.13	3.66 ± 0.11
L 6-2	0.64 ± 0.03	189.13 ± 5.36	0.09 ± 0.00	16.47 ± 0.97	2.73 ± 0.15	4.49 ± 0.42
L 6-3	0.64 ± 0.01	190.35 ± 2.95	0.08 ± 0.00	15.92 ± 0.30	2.69 ± 0.20	4.40 ± 0.13
L 6-4	0.68 ± 0.01	197.09 ± 4.45	0.08 ± 0.00	15.42 ± 0.21	2.77 ± 0.15	3.98 ± 0.11
L 7-1	0.66 ± 0.02	195.83 ± 4.22	0.09 ± 0.00	18.81 ± 0.54	2.49 ± 0.21	4.07 ± 0.23
L 7-2	0.56 ± 0.01	151.11 ± 2.94	0.10 ± 0.00	18.19 ± 0.10	3.95 ± 0.05	3.38 ± 0.16
L 7-3	0.67 ± 0.01	203.23 ± 3.66	0.08 ± 0.00	20.09 ± 0.49	4.13 ± 0.28	4.07 ± 0.22
L 7-4	0.70 ± 0.01	202.16 ± 6.58	0.09 ± 0.00	11.76 ± 0.10	2.87 ± 0.22	4.04 ± 0.28
L 7-4-1	0.50 ± 0.02	105.35 ± 5.01	0.06 ± 0.01	19.08 ± 0.19	2.75 ± 0.02	3.04 ± 0.12
L 7-5	0.68 ± 0.01	195.38 ± 3.16	0.08 ± 0.00	17.10 ± 0.33	2.78 ± 0.15	3.53 ± 0.18
L 7-5-5	0.68 ± 0.02	201.00 ± 6.09	0.08 ± 0.00	16.09 ± 0.53	2.51 ± 0.14	3.94 ± 0.15
L 8-1	0.62 ± 0.03	190.60 ± 4.84	0.07 ± 0.00	20.30 ± 0.61	2.44 ± 0.12	4.48 ± 0.22
L 8-1-1	0.66 ± 0.03	198.62 ± 2.93	0.09 ± 0.00	19.29 ± 0.88	2.24 ± 0.09	3.70 ± 0.15
L 8-2	0.69 ± 0.01	204.87 ± 1.97	0.07 ± 0.00	16.63 ± 0.47	2.23 ± 0.12	3.81 ± 0.20
L 8-2-1	0.66 ± 0.01	191.13 ± 5.07	0.06 ± 0.00	15.12 ± 0.77	2.82 ± 0.25	3.84 ± 0.16
L 8-3	0.60 ± 0.03	188.59 ± 11.54	0.08 ± 0.00	15.50 ± 0.58	3.40 ± 0.26	3.87 ± 0.12
L 9-1	0.69 ± 0.01	195.78 ± 2.76	0.06 ± 0.00	21.38 ± 0.60	4.10 ± 0.04	3.41 ± 0.17
L 9-1-2	0.67 ± 0.01	187.78 ± 3.16	0.09 ± 0.00	11.97 ± 0.28	2.51 ± 0.09	4.52 ± 0.20
L 9-1-3	0.70 ± 0.03	219.82 ± 7.87	0.08 ± 0.00	17.61 ± 0.39	2.46 ± 0.02	4.71 ± 0.27
L 9-2	0.65 ± 0.02	188.84 ± 6.27	0.12 ± 0.01	11.40 ± 0.50	2.32 ± 0.16	4.31 ± 0.22
L 9-2-5	0.66 ± 0.01	199.33 ± 4.61	0.09 ± 0.00	13.47 ± 0.58	2.59 ± 0.15	4.33 ± 0.38
L 9-2-6	0.66 ± 0.01	190.72 ± 3.65	0.06 ± 0.00	15.96 ± 0.52	2.31 ± 0.04	3.75 ± 0.09
L 9-3	0.65 ± 0.01	193.23 ± 2.59	0.13 ± 0.00	18.34 ± 0.87	3.80 ± 0.25	4.01 ± 0.29
L 9-3-1	0.66 ± 0.01	193.34 ± 3.38	0.08 ± 0.00	16.74 ± 0.39	4.16 ± 0.18	3.15 ± 0.13
L 9-3-2	0.66 ± 0.01	196.69 ± 3.67	0.08 ± 0.00	17.88 ± 0.48	2.41 ± 0.13	4.09 ± 0.26
L 10-1	0.63 ± 0.01	188.45 ± 3.86	0.07 ± 0.00	21.60 ± 0.89	3.23 ± 0.28	3.92 ± 0.15
L 10-1-1	0.74 ± 0.01	217.29 ± 4.67	0.06 ± 0.00	18.42 ± 0.89	3.47 ± 0.15	4.80 ± 0.21
L 10-2	0.81 ± 0.01	260.20 ± 4.29	0.24 ± 0.13	18.19 ± 0.16	3.28 ± 0.08	3.94 ± 0.09
L 10-2-2	0.71 ± 0.01	207.34 ± 8.11	0.10 ± 0.01	16.78 ± 0.28	3.74 ± 0.06	3.41 ± 0.17
L 10-3	0.62 ± 0.02	173.35 ± 6.59	0.02 ± 0.00	17.26 ± 0.19	3.62 ± 0.03	3.52 ± 0.23
L 11-1	0.73 ± 0.01	211.49 ± 3.48	0.07 ± 0.00	16.72 ± 0.57	3.34 ± 0.09	3.78 ± 0.28
L 11-2	0.69 ± 0.01	191.61 ± 2.81	0.05 ± 0.00	18.57 ± 0.99	3.68 ± 0.07	4.17 ± 0.39
L 11-3	0.65 ± 0.01	194.65 ± 1.79	0.08 ± 0.00	17.90 ± 0.62	3.27 ± 0.33	3.91 ± 0.24
L 11-4	0.68 ± 0.01	201.25 ± 4.51	0.10 ± 0.01	18.18 ± 0.26	3.96 ± 0.07	3.37 ± 0.16
L 11-4-1	0.68 ± 0.01	200.91 ± 3.26	0.11 ± 0.01	17.65 ± 0.31	3.82 ± 0.03	3.38 ± 0.21
L 12-1	0.73 ± 0.02	208.29 ± 7.08	0.05 ± 0.00	19.79 ± 0.65	3.66 ± 0.07	4.30 ± 0.23
L 12-1-1	0.67 ± 0.02	192.77 ± 4.00	0.09 ± 0.00	17.71 ± 0.30	3.74 ± 0.12	3.68 ± 0.13
L 12-2	0.64 ± 0.01	188.55 ± 2.65	0.09 ± 0.00	15.06 ± 0.45	2.67 ± 0.18	4.18 ± 0.17
L 12-3	0.62 ± 0.01	183.74 ± 2.36	0.08 ± 0.00	17.60 ± 0.98	2.45 ± 0.13	4.13 ± 0.18
L 12-3-1	0.68 ± 0.02	197.89 ± 5.32	0.07 ± 0.00	16.49 ± 0.67	3.25 ± 0.19	3.77 ± 0.07
L 12-4	0.71 ± 0.02	202.81 ± 3.01	0.05 ± 0.00	19.63 ± 0.54	3.81 ± 0.06	4.11 ± 0.13
L 12-4-1	0.69 ± 0.02	198.41 ± 4.55	0.06 ± 0.00	24.05 ± 0.39	2.63 ± 0.10	4.13 ± 0.19
M82	0.67 ± 0.03	195.38 ± 11.09	0.07 ± 0.01	17.84 ± 1.79	3.80 ± 0.54	3.72 ± 0.21

ILs	Nitrate (mmol g ⁻¹ FW)	Chl a (mg g ⁻¹ FW)	Chl b (mg g ⁻¹ FW)	Amino acids (μmol g ⁻¹ FW)	Malate (μmol g ⁻¹ FW)	Starch-EN (μmol g ⁻¹ FW)
IL 1-1	0.15 ± 0.01	1.08 ± 0.11	0.40 ± 0.04	7.02 ± 0.62	49.16 ± 2.39	29.82 ± 3.47
IL 1-1-2	0.13 ± 0.01	1.14 ± 0.04	0.57 ± 0.02	6.00 ± 0.26	45.07 ± 3.10	38.04 ± 3.63
IL 1-1-3	0.13 ± 0.01	1.20 ± 0.04	0.51 ± 0.03	7.83 ± 0.24	48.36 ± 2.52	52.08 ± 5.36
IL 1-2	0.20 ± 0.03	1.16 ± 0.03	0.50 ± 0.06	8.63 ± 0.40	46.85 ± 1.44	27.87 ± 4.08
IL 1-3	0.43 ± 0.04	1.11 ± 0.05	0.43 ± 0.01	13.37 ± 0.35	80.36 ± 2.29	32.26 ± 5.11
IL 1-4	0.12 ± 0.01	1.13 ± 0.05	0.50 ± 0.05	6.48 ± 0.77	60.21 ± 5.38	67.95 ± 4.51
IL 1-4-18	0.24 ± 0.01	1.17 ± 0.05	0.54 ± 0.03	7.86 ± 0.41	49.46 ± 3.71	25.61 ± 2.54
IL 2-1	0.15 ± 0.01	1.16 ± 0.04	0.53 ± 0.03	6.57 ± 0.52	49.08 ± 2.35	57.50 ± 5.54
IL 2-2	0.32 ± 0.02	0.98 ± 0.05	0.40 ± 0.01	9.43 ± 0.32	62.07 ± 3.01	32.47 ± 1.75
IL 2-3	0.26 ± 0.14	1.23 ± 0.01	0.48 ± 0.01	13.08 ± 1.08	44.04 ± 4.31	23.29 ± 0.94
IL 2-4	0.25 ± 0.03	0.92 ± 0.07	0.43 ± 0.03	7.19 ± 0.28	49.15 ± 3.45	80.72 ± 5.05
IL 2-5	0.20 ± 0.00	1.24 ± 0.06	0.46 ± 0.01	9.28 ± 0.64	52.67 ± 2.06	60.09 ± 3.00
IL 2-6	0.16 ± 0.02	1.18 ± 0.09	0.48 ± 0.03	7.07 ± 0.20	47.64 ± 3.84	36.47 ± 2.55
IL 2-6-5	0.17 ± 0.02	1.32 ± 0.08	0.62 ± 0.03	10.09 ± 0.74	56.04 ± 2.97	25.40 ± 1.01
IL 3-1	0.29 ± 0.05	1.37 ± 0.06	0.63 ± 0.04	12.02 ± 0.30	58.97 ± 3.53	36.30 ± 5.21
IL 3-2	0.36 ± 0.06	1.20 ± 0.08	0.53 ± 0.04	7.19 ± 0.24	55.47 ± 3.87	35.35 ± 1.02
IL 3-3	0.27 ± 0.04	1.15 ± 0.04	0.54 ± 0.02	6.85 ± 0.35	44.89 ± 3.02	16.09 ± 2.02
IL 3-4	0.15 ± 0.00	1.14 ± 0.03	0.57 ± 0.02	7.79 ± 0.29	41.09 ± 2.76	29.43 ± 3.58
IL 3-5	0.24 ± 0.03	1.25 ± 0.08	0.52 ± 0.03	6.96 ± 0.29	51.57 ± 3.63	58.00 ± 6.11
IL 4-1	0.48 ± 0.03	1.31 ± 0.03	0.48 ± 0.01	8.58 ± 0.18	25.97 ± 1.72	27.94 ± 1.35
IL 4-1-1	0.20 ± 0.02	1.34 ± 0.11	0.56 ± 0.05	10.63 ± 0.76	54.37 ± 4.41	13.41 ± 2.37
IL 4-2	0.24 ± 0.02	1.27 ± 0.03	0.55 ± 0.01	7.83 ± 0.53	46.54 ± 1.46	43.07 ± 2.96
IL 4-3	0.14 ± 0.01	1.04 ± 0.04	0.42 ± 0.01	5.89 ± 0.60	49.51 ± 1.72	50.58 ± 4.66
IL 4-3-2	0.13 ± 0.01	1.13 ± 0.05	0.50 ± 0.04	6.13 ± 0.43	41.45 ± 2.67	51.70 ± 3.35
IL 4-4	0.24 ± 0.03	1.13 ± 0.05	0.51 ± 0.04	6.97 ± 0.30	45.43 ± 1.99	41.41 ± 4.67
IL 5-1	0.17 ± 0.02	1.32 ± 0.09	0.53 ± 0.04	6.25 ± 0.41	41.31 ± 2.78	15.76 ± 2.56
IL 5-3	0.27 ± 0.02	1.21 ± 0.03	0.49 ± 0.01	10.91 ± 0.41	55.36 ± 2.15	44.11 ± 3.84
IL 5-4	0.33 ± 0.09	1.09 ± 0.07	0.46 ± 0.02	10.35 ± 0.59	50.63 ± 1.46	46.62 ± 3.02
IL 5-5	0.35 ± 0.02	1.00 ± 0.04	0.42 ± 0.01	9.93 ± 0.47	59.94 ± 1.72	45.50 ± 2.93
IL 6-1	0.13 ± 0.01	1.25 ± 0.04	0.55 ± 0.04	6.58 ± 0.45	44.24 ± 2.60	37.06 ± 3.90
IL 6-2	0.16 ± 0.02	1.33 ± 0.08	0.58 ± 0.03	8.14 ± 0.66	42.78 ± 0.78	32.94 ± 3.91
IL 6-3	0.15 ± 0.01	1.38 ± 0.05	0.59 ± 0.04	8.07 ± 0.30	44.28 ± 2.75	22.73 ± 2.03
IL 6-4	0.19 ± 0.01	1.34 ± 0.04	0.67 ± 0.04	10.24 ± 0.71	36.79 ± 1.60	25.46 ± 2.30
IL 7-1	0.12 ± 0.01	1.25 ± 0.05	0.55 ± 0.01	7.06 ± 0.49	49.02 ± 3.57	57.50 ± 8.06
IL 7-2	0.31 ± 0.08	1.39 ± 0.03	0.49 ± 0.01	11.87 ± 0.54	42.75 ± 2.75	21.42 ± 0.81
IL 7-3	0.20 ± 0.02	1.26 ± 0.03	0.57 ± 0.01	9.47 ± 0.43	50.96 ± 1.85	36.47 ± 2.86
IL 7-4	0.11 ± 0.01	1.08 ± 0.06	0.51 ± 0.06	5.69 ± 0.26	42.82 ± 3.37	54.70 ± 2.48
IL 7-4-1	0.18 ± 0.01	1.36 ± 0.12	0.47 ± 0.02	7.06 ± 0.35	8.73 ± 2.56	83.92 ± 7.70
IL 7-5	0.13 ± 0.01	1.25 ± 0.09	0.59 ± 0.04	7.35 ± 0.38	41.44 ± 1.40	22.39 ± 1.85
IL 7-5-5	0.16 ± 0.01	1.27 ± 0.10	0.59 ± 0.05	7.36 ± 0.34	46.38 ± 2.16	55.93 ± 6.47
IL 8-1	0.15 ± 0.01	1.48 ± 0.11	0.75 ± 0.06	7.83 ± 0.63	53.05 ± 4.53	31.49 ± 4.68
IL 8-1-1	0.14 ± 0.01	1.45 ± 0.04	0.71 ± 0.03	5.90 ± 0.31	38.84 ± 2.25	72.39 ± 2.24
IL 8-2	0.17 ± 0.01	1.31 ± 0.08	0.57 ± 0.02	7.86 ± 0.41	64.51 ± 2.32	67.75 ± 2.68
IL 8-2-1	0.15 ± 0.01	1.18 ± 0.03	0.47 ± 0.02	6.81 ± 0.24	42.46 ± 1.81	72.06 ± 4.11
IL 8-3	0.19 ± 0.05	0.99 ± 0.02	0.42 ± 0.03	6.45 ± 0.25	44.33 ± 3.22	54.90 ± 3.22
IL 9-1	0.23 ± 0.01	1.12 ± 0.05	0.44 ± 0.01	11.44 ± 0.41	60.75 ± 5.46	50.25 ± 5.93
IL 9-1-2	0.13 ± 0.01	0.93 ± 0.07	0.43 ± 0.03	5.18 ± 0.30	53.36 ± 2.75	90.65 ± 4.80
IL 9-1-3	0.13 ± 0.01	1.30 ± 0.07	0.59 ± 0.03	7.37 ± 0.35	60.36 ± 4.86	71.02 ± 2.24
IL 9-2	0.18 ± 0.02	1.28 ± 0.07	0.71 ± 0.03	6.62 ± 0.62	50.19 ± 5.48	39.15 ± 3.86
IL 9-2-5	0.21 ± 0.02	1.33 ± 0.07	0.54 ± 0.03	8.86 ± 0.36	53.54 ± 4.66	53.88 ± 2.40
IL 9-2-6	0.21 ± 0.01	1.14 ± 0.07	0.49 ± 0.03	7.31 ± 0.44	42.45 ± 2.07	61.86 ± 3.99
IL 9-3	0.24 ± 0.02	0.96 ± 0.04	0.45 ± 0.02	4.66 ± 0.27	43.86 ± 1.88	22.45 ± 2.79
IL 9-3-1	0.12 ± 0.01	1.00 ± 0.02	0.47 ± 0.02	5.81 ± 0.46	35.51 ± 2.01	35.62 ± 4.70
IL 9-3-2	0.15 ± 0.02	1.21 ± 0.03	0.61 ± 0.04	9.07 ± 0.69	60.71 ± 5.82	27.54 ± 2.81
IL 10-1	0.31 ± 0.04	1.34 ± 0.05	0.60 ± 0.04	9.13 ± 0.17	47.57 ± 3.37	36.63 ± 5.66
IL 10-1-1	0.25 ± 0.01	1.22 ± 0.05	0.46 ± 0.01	9.94 ± 0.41	52.82 ± 1.18	63.17 ± 5.52
IL 10-2	0.08 ± 0.00	1.07 ± 0.03	0.43 ± 0.03	6.81 ± 0.16	42.92 ± 1.47	46.95 ± 2.81
IL 10-2-2	0.33 ± 0.01	1.32 ± 0.04	0.45 ± 0.01	10.45 ± 0.57	35.99 ± 1.33	28.06 ± 1.00
IL 10-3	0.11 ± 0.04	1.35 ± 0.02	0.47 ± 0.01	14.13 ± 0.92	44.41 ± 1.78	40.88 ± 3.29
IL 11-1	0.26 ± 0.04	1.27 ± 0.05	0.44 ± 0.01	9.53 ± 0.55	52.43 ± 4.28	82.83 ± 4.47
IL 11-2	0.23 ± 0.01	1.08 ± 0.04	0.42 ± 0.01	9.08 ± 0.54	58.01 ± 5.33	51.36 ± 1.29
IL 11-3	0.40 ± 0.03	1.34 ± 0.03	0.59 ± 0.03	10.01 ± 0.67	68.00 ± 4.16	11.56 ± 1.32
IL 11-4	0.37 ± 0.04	1.52 ± 0.01	0.50 ± 0.01	13.72 ± 0.36	45.93 ± 2.32	25.82 ± 1.38
IL 11-4-1	0.60 ± 0.07	1.33 ± 0.02	0.47 ± 0.01	10.83 ± 0.52	39.91 ± 3.11	38.16 ± 1.35
IL 12-1	0.22 ± 0.01	1.23 ± 0.10	0.52 ± 0.03	10.36 ± 0.56	52.06 ± 1.44	75.16 ± 5.25
IL 12-1-1	0.13 ± 0.01	1.14 ± 0.06	0.53 ± 0.06	7.28 ± 0.55	52.13 ± 3.62	70.62 ± 0.56
IL 12-2	0.12 ± 0.01	1.44 ± 0.05	0.63 ± 0.03	9.74 ± 0.61	50.36 ± 2.09	29.34 ± 0.72
IL 12-3	0.41 ± 0.06	1.26 ± 0.03	0.63 ± 0.03	8.59 ± 0.50	50.36 ± 2.30	41.30 ± 2.91
IL 12-3-1	0.14 ± 0.01	1.11 ± 0.03	0.45 ± 0.03	6.13 ± 0.34	34.58 ± 1.45	31.70 ± 4.10
IL 12-4	0.27 ± 0.01	1.13 ± 0.07	0.44 ± 0.01	10.10 ± 0.60	55.51 ± 1.75	90.58 ± 8.83
IL 12-4-1	0.24 ± 0.03	1.38 ± 0.05	0.74 ± 0.05	10.27 ± 0.59	43.53 ± 3.02	51.60 ± 4.28
M82	0.22 ± 0.09	1.09 ± 0.05	0.45 ± 0.06	8.84 ± 1.00	45.37 ± 6.32	42.98 ± 3.12

ILs	Starch-MD ($\mu\text{mol g}^{-1}\text{FW}$)	Starch-ED ($\mu\text{mol g}^{-1}\text{FW}$)	Starch turnover ($\mu\text{mol g}^{-1}\text{FW}$)	Glucose ($\mu\text{mol g}^{-1}\text{FW}$)	Fructose ($\mu\text{mol g}^{-1}\text{FW}$)	Sucrose ($\mu\text{mol g}^{-1}\text{FW}$)
IL 1-1	83.13 $\pm$ 6.86	88.69 $\pm$ 6.30	58.87 $\pm$ 5.21	7.52 $\pm$ 0.35	7.47 $\pm$ 0.35	2.86 $\pm$ 0.15
IL 1-1-2	43.85 $\pm$ 6.80	108.05 $\pm$ 6.08	70.02 $\pm$ 7.32	5.42 $\pm$ 0.65	5.22 $\pm$ 0.63	2.32 $\pm$ 0.14
IL 1-1-3	88.92 $\pm$ 4.21	99.98 $\pm$ 3.96	47.90 $\pm$ 3.34	6.66 $\pm$ 0.45	6.87 $\pm$ 0.48	2.69 $\pm$ 0.06
IL 1-2	52.47 $\pm$ 2.83	107.70 $\pm$ 5.64	79.83 $\pm$ 7.71	6.40 $\pm$ 0.71	6.44 $\pm$ 0.77	2.71 $\pm$ 0.19
IL 1-3	60.43 $\pm$ 4.41	67.22 $\pm$ 5.06	34.96 $\pm$ 5.83	7.51 $\pm$ 0.48	8.79 $\pm$ 0.44	3.32 $\pm$ 0.24
IL 1-4	78.55 $\pm$ 5.28	123.24 $\pm$ 5.93	55.29 $\pm$ 5.14	4.70 $\pm$ 0.40	4.23 $\pm$ 0.26	2.42 $\pm$ 0.11
IL 1-4-18	45.40 $\pm$ 1.94	72.23 $\pm$ 3.48	46.62 $\pm$ 2.79	5.81 $\pm$ 0.54	5.12 $\pm$ 0.29	2.63 $\pm$ 0.20
IL 2-1	58.30 $\pm$ 5.36	104.05 $\pm$ 2.34	46.56 $\pm$ 5.10	7.19 $\pm$ 0.60	7.03 $\pm$ 0.56	2.61 $\pm$ 0.16
IL 2-2	47.58 $\pm$ 4.48	88.45 $\pm$ 5.16	55.98 $\pm$ 4.24	4.66 $\pm$ 0.29	5.51 $\pm$ 0.44	1.82 $\pm$ 0.10
IL 2-3	93.14 $\pm$ 2.04	77.93 $\pm$ 2.89	54.64 $\pm$ 3.37	5.10 $\pm$ 0.65	2.04 $\pm$ 0.46	2.60 $\pm$ 0.17
IL 2-4	79.57 $\pm$ 7.54	118.81 $\pm$ 3.93	38.09 $\pm$ 4.41	6.59 $\pm$ 0.50	7.35 $\pm$ 0.71	2.16 $\pm$ 0.08
IL 2-5	92.08 $\pm$ 4.42	101.55 $\pm$ 2.94	41.47 $\pm$ 3.65	8.63 $\pm$ 0.22	10.27 $\pm$ 0.29	3.24 $\pm$ 0.10
IL 2-6	68.87 $\pm$ 4.77	83.20 $\pm$ 3.76	46.73 $\pm$ 2.09	4.27 $\pm$ 0.49	4.47 $\pm$ 0.40	2.02 $\pm$ 0.09
IL 2-6-5	80.09 $\pm$ 5.98	75.29 $\pm$ 2.25	49.88 $\pm$ 2.59	7.02 $\pm$ 0.56	6.88 $\pm$ 0.60	2.51 $\pm$ 0.14
IL 3-1	70.85 $\pm$ 2.95	62.50 $\pm$ 3.71	26.20 $\pm$ 1.89	7.96 $\pm$ 0.26	8.82 $\pm$ 0.49	3.60 $\pm$ 0.19
IL 3-2	23.14 $\pm$ 3.29	52.23 $\pm$ 1.87	16.88 $\pm$ 1.11	4.43 $\pm$ 0.40	3.52 $\pm$ 0.41	2.09 $\pm$ 0.20
IL 3-3	24.50 $\pm$ 2.86	45.27 $\pm$ 3.21	29.18 $\pm$ 1.82	2.51 $\pm$ 0.30	1.49 $\pm$ 0.12	1.78 $\pm$ 0.09
IL 3-4	50.64 $\pm$ 3.26	53.67 $\pm$ 3.22	24.24 $\pm$ 1.08	4.89 $\pm$ 0.43	5.27 $\pm$ 0.48	2.59 $\pm$ 0.24
IL 3-5	98.96 $\pm$ 6.16	88.61 $\pm$ 5.46	30.61 $\pm$ 2.34	6.04 $\pm$ 0.52	5.45 $\pm$ 0.54	2.68 $\pm$ 0.10
IL 4-1	80.44 $\pm$ 3.67	78.91 $\pm$ 3.38	50.97 $\pm$ 2.59	7.09 $\pm$ 0.48	6.06 $\pm$ 0.38	2.67 $\pm$ 0.05
IL 4-1-1	50.06 $\pm$ 5.77	53.98 $\pm$ 2.99	40.57 $\pm$ 3.14	6.25 $\pm$ 0.14	7.22 $\pm$ 0.53	2.49 $\pm$ 0.22
IL 4-2	48.09 $\pm$ 1.79	66.69 $\pm$ 1.73	23.63 $\pm$ 1.56	7.07 $\pm$ 0.77	8.57 $\pm$ 0.67	2.41 $\pm$ 0.11
IL 4-3	63.45 $\pm$ 8.30	85.92 $\pm$ 5.22	35.33 $\pm$ 2.95	7.54 $\pm$ 0.45	8.79 $\pm$ 0.36	2.19 $\pm$ 0.06
IL 4-3-2	59.58 $\pm$ 6.97	86.56 $\pm$ 2.73	34.86 $\pm$ 2.95	8.75 $\pm$ 0.48	8.91 $\pm$ 0.49	2.24 $\pm$ 0.04
IL 4-4	56.28 $\pm$ 3.78	70.03 $\pm$ 4.28	28.62 $\pm$ 2.45	3.59 $\pm$ 0.63	3.81 $\pm$ 0.28	2.08 $\pm$ 0.18
IL 5-1	39.39 $\pm$ 5.30	77.67 $\pm$ 2.69	61.92 $\pm$ 4.15	5.25 $\pm$ 0.47	4.54 $\pm$ 0.57	2.73 $\pm$ 0.08
IL 5-3	50.83 $\pm$ 3.44	53.74 $\pm$ 4.88	9.62 $\pm$ 4.21	8.63 $\pm$ 0.70	11.38 $\pm$ 0.57	2.82 $\pm$ 0.25
IL 5-4	59.63 $\pm$ 3.17	63.95 $\pm$ 3.25	17.33 $\pm$ 3.74	7.95 $\pm$ 0.50	11.87 $\pm$ 0.60	2.84 $\pm$ 0.28
IL 5-5	67.06 $\pm$ 1.16	73.42 $\pm$ 4.47	27.91 $\pm$ 4.94	8.10 $\pm$ 0.50	11.04 $\pm$ 0.37	2.51 $\pm$ 0.25
IL 6-1	34.73 $\pm$ 4.00	74.52 $\pm$ 4.58	37.47 $\pm$ 1.48	4.95 $\pm$ 0.43	4.80 $\pm$ 0.58	2.24 $\pm$ 0.08
IL 6-2	54.15 $\pm$ 2.47	65.80 $\pm$ 3.03	32.86 $\pm$ 1.97	7.25 $\pm$ 0.29	7.44 $\pm$ 0.65	2.40 $\pm$ 0.07
IL 6-3	91.98 $\pm$ 6.15	75.90 $\pm$ 1.99	53.17 $\pm$ 2.99	7.59 $\pm$ 0.33	8.31 $\pm$ 0.35	2.83 $\pm$ 0.13
IL 6-4	35.72 $\pm$ 5.83	41.90 $\pm$ 2.63	16.44 $\pm$ 0.74	4.85 $\pm$ 0.49	5.03 $\pm$ 0.38	2.33 $\pm$ 0.05
IL 7-1	56.34 $\pm$ 4.59	97.55 $\pm$ 7.39	40.05 $\pm$ 2.38	5.59 $\pm$ 0.85	6.86 $\pm$ 0.56	2.88 $\pm$ 0.08
IL 7-2	95.82 $\pm$ 2.24	72.62 $\pm$ 2.90	51.21 $\pm$ 2.71	9.78 $\pm$ 0.36	9.13 $\pm$ 0.50	4.07 $\pm$ 0.19
IL 7-3	50.38 $\pm$ 5.60	83.77 $\pm$ 3.43	47.30 $\pm$ 1.40	6.48 $\pm$ 0.29	8.31 $\pm$ 0.72	2.90 $\pm$ 0.08
IL 7-4	89.41 $\pm$ 8.62	80.50 $\pm$ 2.39	25.80 $\pm$ 1.52	7.60 $\pm$ 0.29	7.78 $\pm$ 0.75	2.52 $\pm$ 0.10
IL 7-4-1	121.53 $\pm$ 8.34	123.98 $\pm$ 4.48	40.06 $\pm$ 4.51	5.42 $\pm$ 0.50	6.91 $\pm$ 0.84	2.03 $\pm$ 0.13
IL 7-5	24.32 $\pm$ 4.07	55.15 $\pm$ 1.56	32.76 $\pm$ 1.63	3.36 $\pm$ 0.11	3.10 $\pm$ 0.20	1.87 $\pm$ 0.08
IL 7-5-5	62.00 $\pm$ 5.74	91.99 $\pm$ 6.05	36.06 $\pm$ 2.11	4.84 $\pm$ 0.56	5.91 $\pm$ 0.49	2.42 $\pm$ 0.11
IL 8-1	45.96 $\pm$ 5.77	48.54 $\pm$ 4.71	17.05 $\pm$ 2.21	4.54 $\pm$ 0.23	5.99 $\pm$ 0.48	2.06 $\pm$ 0.11
IL 8-1-1	44.65 $\pm$ 3.30	102.64 $\pm$ 1.76	30.25 $\pm$ 2.19	7.54 $\pm$ 0.43	7.51 $\pm$ 0.58	2.06 $\pm$ 0.12
IL 8-2	82.91 $\pm$ 2.02	81.74 $\pm$ 2.29	13.99 $\pm$ 0.84	7.08 $\pm$ 0.55	5.30 $\pm$ 0.44	2.98 $\pm$ 0.15
IL 8-2-1	84.88 $\pm$ 8.67	94.09 $\pm$ 3.77	22.03 $\pm$ 1.27	5.28 $\pm$ 0.77	5.47 $\pm$ 0.42	2.69 $\pm$ 0.14
IL 8-3	61.72 $\pm$ 6.08	79.80 $\pm$ 3.05	24.90 $\pm$ 1.39	4.74 $\pm$ 0.35	4.53 $\pm$ 0.25	2.61 $\pm$ 0.06
IL 9-1	47.81 $\pm$ 3.68	66.05 $\pm$ 3.40	15.80 $\pm$ 3.66	8.03 $\pm$ 0.69	9.05 $\pm$ 0.47	2.57 $\pm$ 0.22
IL 9-1-2	97.26 $\pm$ 3.75	118.47 $\pm$ 3.94	27.82 $\pm$ 1.35	7.68 $\pm$ 0.58	7.90 $\pm$ 0.87	2.93 $\pm$ 0.13
IL 9-1-3	89.63 $\pm$ 2.73	107.36 $\pm$ 0.43	36.34 $\pm$ 2.55	7.98 $\pm$ 0.54	8.71 $\pm$ 0.37	3.08 $\pm$ 0.17
IL 9-2	62.85 $\pm$ 3.84	69.82 $\pm$ 3.84	30.67 $\pm$ 3.51	4.71 $\pm$ 0.63	6.23 $\pm$ 0.49	1.79 $\pm$ 0.13
IL 9-2-5	58.35 $\pm$ 3.16	71.43 $\pm$ 2.52	17.55 $\pm$ 1.23	5.46 $\pm$ 0.56	5.97 $\pm$ 0.48	2.17 $\pm$ 0.09
IL 9-2-6	60.53 $\pm$ 3.68	80.75 $\pm$ 4.12	18.89 $\pm$ 0.81	5.01 $\pm$ 0.56	5.52 $\pm$ 0.51	1.88 $\pm$ 0.14
IL 9-3	25.18 $\pm$ 2.70	99.35 $\pm$ 1.44	76.90 $\pm$ 2.08	2.76 $\pm$ 0.20	4.09 $\pm$ 0.52	1.65 $\pm$ 0.06
IL 9-3-1	32.69 $\pm$ 2.55	65.79 $\pm$ 5.70	30.17 $\pm$ 1.54	3.57 $\pm$ 0.47	4.63 $\pm$ 0.37	1.74 $\pm$ 0.05
IL 9-3-2	44.71 $\pm$ 5.10	67.76 $\pm$ 2.12	40.22 $\pm$ 2.40	6.43 $\pm$ 0.52	6.70 $\pm$ 1.07	2.10 $\pm$ 0.07
IL 10-1	39.07 $\pm$ 5.65	76.93 $\pm$ 5.15	40.30 $\pm$ 2.96	4.71 $\pm$ 0.41	5.65 $\pm$ 0.43	2.52 $\pm$ 0.18
IL 10-1-1	86.07 $\pm$ 3.24	88.17 $\pm$ 7.49	24.99 $\pm$ 4.94	9.84 $\pm$ 0.66	12.29 $\pm$ 0.79	3.14 $\pm$ 0.22
IL 10-2	66.91 $\pm$ 2.25	94.12 $\pm$ 2.10	47.18 $\pm$ 2.06	8.49 $\pm$ 0.32	9.15 $\pm$ 0.52	2.71 $\pm$ 0.08
IL 10-2-2	91.25 $\pm$ 4.55	74.15 $\pm$ 2.73	46.09 $\pm$ 2.43	6.67 $\pm$ 0.51	5.27 $\pm$ 0.17	2.75 $\pm$ 0.15
IL 10-3	98.91 $\pm$ 2.50	74.69 $\pm$ 2.15	33.81 $\pm$ 1.62	9.40 $\pm$ 0.51	9.06 $\pm$ 0.72	4.07 $\pm$ 0.29
IL 11-1	103.48 $\pm$ 5.15	101.19 $\pm$ 4.63	18.36 $\pm$ 4.18	9.01 $\pm$ 0.72	11.23 $\pm$ 0.49	2.99 $\pm$ 0.13
IL 11-2	92.50 $\pm$ 1.62	109.14 $\pm$ 4.94	57.78 $\pm$ 4.92	9.30 $\pm$ 0.36	10.54 $\pm$ 0.50	3.21 $\pm$ 0.06
IL 11-3	28.93 $\pm$ 3.24	40.34 $\pm$ 1.94	28.78 $\pm$ 2.29	3.93 $\pm$ 0.57	5.01 $\pm$ 0.37	2.94 $\pm$ 0.30
IL 11-4	82.75 $\pm$ 2.98	75.69 $\pm$ 3.60	49.88 $\pm$ 4.12	8.12 $\pm$ 0.57	6.46 $\pm$ 0.58	3.92 $\pm$ 0.21
IL 11-4-1	60.30 $\pm$ 2.17	71.17 $\pm$ 2.45	33.02 $\pm$ 2.15	6.63 $\pm$ 0.45	5.26 $\pm$ 0.62	2.67 $\pm$ 0.17
IL 12-1	104.36 $\pm$ 5.43	97.15 $\pm$ 4.78	21.99 $\pm$ 6.54	12.34 $\pm$ 0.52	13.34 $\pm$ 0.66	3.69 $\pm$ 0.17
IL 12-1-1	81.33 $\pm$ 2.29	90.88 $\pm$ 1.34	20.26 $\pm$ 1.12	6.74 $\pm$ 0.46	6.37 $\pm$ 0.44	2.82 $\pm$ 0.22
IL 12-2	95.68 $\pm$ 5.11	84.59 $\pm$ 4.31	55.25 $\pm$ 4.26	9.24 $\pm$ 0.28	7.95 $\pm$ 0.44	3.21 $\pm$ 0.13
IL 12-3	35.58 $\pm$ 2.37	100.15 $\pm$ 4.85	58.85 $\pm$ 4.33	7.10 $\pm$ 0.55	4.97 $\pm$ 0.48	2.43 $\pm$ 0.13
IL 12-3-1	48.67 $\pm$ 1.44	55.27 $\pm$ 4.11	23.57 $\pm$ 1.70	4.36 $\pm$ 0.41	4.70 $\pm$ 0.38	2.46 $\pm$ 0.16
IL 12-4	88.47 $\pm$ 10.00	106.39 $\pm$ 7.75	15.82 $\pm$ 4.70	9.61 $\pm$ 0.22	11.47 $\pm$ 0.49	3.04 $\pm$ 0.07
IL 12-4-1	67.11 $\pm$ 6.48	88.35 $\pm$ 4.33	36.75 $\pm$ 1.64	7.77 $\pm$ 0.30	8.62 $\pm$ 0.67	3.15 $\pm$ 0.13
M82	76.36 $\pm$ 5.04	80.25 $\pm$ 5.85	37.27 $\pm$ 7.60	7.84 $\pm$ 0.68	9.27 $\pm$ 0.82	2.72 $\pm$ 0.12

Supplemental Table S3. Complete list of genes in all selected BINs.

ITAG2.4 proteins blastp								SD3 Table Orthologous pairs		Functional Description	
BIN	Augustus ID	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	S.lycopersicum (Heinz)			
1J	g1.t1	1	4987	4986	0	98.25	100	Solyc01g109790.2.1	Glucose-1-phosphate adenylyltransferase IPR011831	Glucose-1-phosphate adenylyltransferase IPR005836	ADP-glucose pyrophosphorylase, conserved site
1J	g2.t1	17866	18734	868	2E-65	57.43	96	Solyc01g109810.2.1	Genomic DNA chromosome 5 TAC clone K1F13		
1J	g3.t1	23906	24812	906	7E-154	75.5	100	Solyc01g109800.2.1	Genomic DNA chromosome 5 TAC clone K1F13		
1J	g4.t1	29656	30699	1043	4E-149	93.36	100	Solyc01g109810.2.1	Genomic DNA chromosome 5 TAC clone K1F13		
1J	g5.t1	32869	33997	1128	0E+00	96.89	100	Solyc01g109820.1.1	Zinc finger (C3HC4 RING finger) protein IPR001841	Zinc finger, RING-type	
1J	g6.t1	36354	42617	6263	0E+00	99.62	100	Solyc01g109830.2.1	Thymidylate synthase IPR012262	Bifunctional dihydrofolate reductase_thymidylate synthase	
1J	g6.t2	36354	42617	6263	0E+00	96.77	100	Solyc01g109830.2.1	Thymidylate synthase IPR012262	Bifunctional dihydrofolate reductase_thymidylate synthase	
1J	g7.t1	45070	50407	5337	0E+00	99.34	92	Solyc01g109850.2.1	Diaminopimelate decarboxylase IPR002986	Diaminopimelate decarboxylase	
1J	g8.t1	53976	57531	3555	0E+00	99.48	100	Solyc01g109860.2.1	Phosphatidylinositol_phosphatidylcholine transfer protein-like IPR001251	Cellular retinaldehyde-binding_triple function, C-terminal	
1J	g9.t1	57833	63177	5344	0E+00	90.08	100	Solyc01g109870.2.1	SEC14-like protein IPR001251	Cellular retinaldehyde-binding_triple function, C-terminal	
1J	g10.t1	90416	91190	774	9E-117	99.39	100	Solyc01g109880.2.1	BZIP transcription factor IPR011700	Basic leucine zipper	
1J	g11.t1	98016	108488	10472	0E+00	99.7	74	Solyc01g109890.2.1	Chaperone protein dnaJ 10 IPR003095	Heat shock protein DnaJ	
1J	g11.t2	98016	108488	10472	0E+00	99.7	77	Solyc01g109890.2.1	Chaperone protein dnaJ 10 IPR003095	Heat shock protein DnaJ	
1J	g12.t1	120646	126385	5739	0E+00	98.37	100	Solyc01g109910.2.1	AT2G21500 protein (Fragment) IPR001841	Zinc finger, RING-type	
1J	g13.t1	128186	129721	1535	9E-107	88.97	100	Solyc01g109920.2.1	Dehydrin IPR000167	Dehydrin	
1J	g14.t1	131466	136201	4735	0E+00	90.88	99	Solyc01g109930.2.1	Inositol monophosphatase family protein IPR011809	Histidinol-phosphate phosphatase, putative, inositol monophosphatase	
1J	g15.t1	136374	141647	5273	0E+00	100	100	Solyc01g109940.2.1	26S protease regulatory subunit IPR005937	26S proteasome subunit P45	
1J	g16.t1	143436	146547	3111	0E+00	98.97	100	Solyc01g109950.2.1	Pto-like, Serine_threonine kinase protein, resistance protein		
1J	g17.t1	146806	155937	9131	0E+00	92.66	100	Solyc01g109960.2.1	Ubiquitin-activating enzyme E1 3 IPR009036	Molybdenum cofactor biosynthesis, MoeB	
1J	g18.t1	157916	166015	8099	0E+00	99.01	98	Solyc01g109970.2.1	DNA repair protein IPR001650	DNA_RNA helicase, C-terminal	
1J	g19.t1	166619	174487	7868	0E+00	98.45	100	Solyc01g109980.2.1	BEL1-like homeodomain protein 6 IPR006563	POX	
1J	g20.t1	177266	189534	12268	0E+00	95.99	59	Solyc01g109990.2.1	RNA-binding protein 28 IPR012677	Nucleotide-binding, alpha-beta plait	
1J	g20.t2	177266	189534	12268	0E+00	95.99	59	Solyc01g109990.2.1	RNA-binding protein 28 IPR012677	Nucleotide-binding, alpha-beta plait	
1J	g21.t1	193183	202017	8834	0E+00	98.07	99	Solyc01g110000.2.1	Beta-galactosidase IPR001944	Glycoside hydrolase, family 35	
1J	g21.t2	193183	202017	8834	0E+00	98.81	99	Solyc01g110000.2.1	Beta-galactosidase IPR001944	Glycoside hydrolase, family 35	
1J	g22.t1	202852	205894	3042	0E+00	98.75	100	Solyc01g110010.2.1	Pentatricopeptide repeat protein IPR002885	Pentatricopeptide repeat	
1J	g23.t1	206163	210164	4001	7E-159	100	98	Solyc01g110020.2.1	BAH-PHD domain-containing protein (Fragment) IPR001025	Bromo adjacent region	
1J	g24.t1	213144	221704	8560	0E+00	100	65	Solyc01g110030.2.1	WD-40 repeat protein IPR017986	WD40 repeat, region	
1J	g25.t1	222804	225274	2470	0E+00	89.6	100	Solyc01g110060.2.1	Purple acid phosphatase IPR015914	Purple acid phosphatase, N-terminal	
1J	g26.t1	226032	230124	4092	0E+00	99.35	99	Solyc01g110060.2.1	Purple acid phosphatase IPR015914	Purple acid phosphatase, N-terminal	
1J	g27.t1	241141	245864	4723	1E-140	96.24	24	Solyc01g110080.1.1	Predicted E3 ubiquitin ligase IPR002867	Zinc finger, C6HC-type	
1J	g28.t1	250352	251424	1072	6E-125	82.57	100	Solyc01g110090.1.1	Predicted E3 ubiquitin ligase IPR002867	Zinc finger, C6HC-type	
1J	g29.t1	255143	258369	3226	4E-147	95.24	74	Solyc01g110100.2.1	Zinc finger family protein IPR002867	Zinc finger, C6HC-type	
1J	g29.t2	255143	258369	3226	3E-141	94.58	81	Solyc01g110100.2.1	Zinc finger family protein IPR002867	Zinc finger, C6HC-type	
1J	g30.t1	260523	262751	2228	0E+00	98.91	100	Solyc01g110110.2.1	Cysteine proteinase cathepsin F IPR013128	Peptidase C1A, papain	
1J	g31.t1	263803	274234	10431	0E+00	99.63	100	Solyc01g110120.2.1	V-type proton ATPase subunit a IPR002490	ATPase, V0_A0 complex, 116-kDa subunit	
1J	g32.t1	276258	282414	6156	0E+00	95.72	100	Solyc01g110130.2.1	DNA replication licensing factor IPR008047	MCM protein 4	
1J	g32.t2	276258	296034	19776	0E+00	95.72	78	Solyc01g110130.2.1	DNA replication licensing factor IPR008047	MCM protein 4	
1J	g33.t1	305434	306894	1460	3E-135	96.94	100	Solyc01g110150.2.1	CM0216.450.nc protein		
1J	g34.t1	308410	314364	5954	0E+00	90.5	100	Solyc01g110160.2.1	Chromosome 11 contig 1 DNA sequence		
1J	g34.t2	308410	314364	5954	0E+00	90.4	98	Solyc01g110160.2.1	Chromosome 11 contig 1 DNA sequence		
1J	g35.t1	316399	318014	1615	2E-120	65.38	79	Solyc01g109730.1.1	Unknown Protein		
1J	g36.t2	324085	338204	14119	0E+00	94.1	95	Solyc01g110190.2.1	Kinesin like protein IPR001752	Kinesin, motor region	
1J	g36.t1	326285	338204	11919	0E+00	95.65	95	Solyc01g110190.2.1	Kinesin like protein IPR001752	Kinesin, motor region	
1J	g38.t1	348443	349814	1371	7E-172	93.14	99	Solyc01g110200.1.1	ME2-like RNA binding protein IPR007201	RNA recognition motif 2	

ITAG2.4 proteins blastp								SD3 Table Orthologous pairs		Functional Description
BIN	Augustus ID	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
1J	g38.i2	348443	349814	1371	7E-162	89.17	99	Solyc01g110200.1.1	MEI2-like RNA binding protein IPR007201	RNA recognition motif 2
1J	g39.i1	352293	353666	1373	6E-152	96.11	100	Solyc01g110210.1.1	Terminal ear1-like 2 protein IPR007201	RNA recognition motif 2
1J	g40.i1	355823	360925	5102	6E-128	90.98	50	Solyc01g110220.1.1	Terminal ear1-like 2 protein IPR007201	RNA recognition motif 2
1J	g41.i1	362863	363996	1133	1E-127	95.5	100	Solyc01g110240.1.1	MEI2-like RNA binding protein IPR007201	RNA recognition motif 2
1J	g41.i2	362863	371844	8981	3E-113	93.65	46	Solyc01g110240.1.1	MEI2-like RNA binding protein IPR007201	RNA recognition motif 2
1J	g42.i1	372833	374245	1412	3E-109	97.37	59	Solyc01g110260.1.1	MEI2-like RNA binding protein IPR007201	RNA recognition motif 2
1J	g43.i1	377392	380162	2770	4E-180	98.8	97	Solyc01g110270.2.1	Crs1_yhby domain containing protein (Fragment) IPR001890	RNA-binding, CRM domain
1J	g44.i1	380206	386693	6487	0E+00	93.54	100	Solyc01g110280.2.1	DNA-damage-inducible protein F IPR002528	Multi antimicrobial extrusion protein MatE
1J	g45.i1	401872	408844	6972	0E+00	99.76	100	Solyc01g110290.2.1	Squalene synthase IPR006449	Farnesyl-diphosphate farnesyltransferase
1J	g46.i1	409282	417753	8471	0E+00	98.64	90	Solyc01g110300.2.1	Clathrin binding protein IPR001452	Src homology-3 domain
1J	g46.i2	409282	417753	8471	0E+00	97.01	90	Solyc01g110300.2.1	Clathrin binding protein IPR001452	Src homology-3 domain
1J	g47.i1	428402	429586	1184	0E+00	98.15	100	Solyc01g110310.2.1	GATA transcription factor 9 IPR016679	Transcription factor, GATA, plant
1J	g48.i1	432398	436473	4075	0E+00	98.08	100	Solyc01g110320.2.1	Coiled-coil domain-containing protein 90B mitochondrial IPR012439	Protein of unknown function DUF1640
1J	g48.i2	432398	436283	3885	2E-167	82.79	100	Solyc01g110320.2.1	Coiled-coil domain-containing protein 90B mitochondrial IPR012439	Protein of unknown function DUF1640
1J	g49.i1	437442	440147	2705	5E-179	80.45	100	Solyc01g110330.1.1	N-acetyltransferase ESCO1 IPR001126	DNA-repair protein, UmuC-like
1J	g50.i1	451322	457220	5898	0E+00	95.77	100	Solyc01g110340.2.1	Endoglucanase 1 IPR001701	Glycoside hydrolase, family 9
1J	g51.i1	458362	462424	4062	8E-163	97.47	98	Solyc01g110350.2.1	Unknown Protein	
1J	g52.i1	463032	466619	3587	0E+00	97.49	79	Solyc01g110360.2.1	Fructose-bisphosphate aldolase IPR000741	Fructose-bisphosphate aldolase, class-I
1J	g52.i2	463032	466619	3587	0E+00	94.36	78	Solyc01g110360.2.1	Fructose-bisphosphate aldolase IPR000741	Fructose-bisphosphate aldolase, class-I
1J	g53.i1	468267	471313	3046	3E-156	99.06	100	Solyc01g110370.2.1	Zinc finger protein CONSTANS-LIKE 3 IPR000315	Zinc finger, B-box
1J	g54.i1	473472	487297	13825	0E+00	94.69	100	Solyc01g110380.2.1	Kinesin like protein IPR001752	Kinesin, motor region
1J	g55.i1	488042	492323	4281	3E-83	100	100	Solyc01g110390.2.1	NADH dehydrogenase IPR008011	Complex 1 LYR protein
1J	g56.i1	494293	495013	720	2E-61	100	100	Solyc01g110400.2.1	Unknown Protein	
1J	g57.i1	495162	501363	6201	0E+00	100	100	Solyc01g110410.2.1	Ubiquitin fusion-degradation protein-like IPR004854	Ubiquitin fusion degradation protein UFD1
1J	g58.i1	524102	526785	2683	0E+00	98.52	84	Solyc01g110440.2.1	Arginine decarboxylase IPR002985	Arginine decarboxylase
1J	g59.i1	527642	531063	3421	0E+00	99.03	100	Solyc01g110450.2.1	NADP dependent sorbitol 6-phosphate dehydrogenase (Fragment) IPR020471	Aldo_keto reductase subgroup
1J	g60.i1	531648	537883	6235	0E+00	84.1	85	Solyc01g110460.2.1	3-oxo-5-alpha-steroid 4-dehydrogenase family protein IPR001104	3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal
1J	g61.i1	546727	549250	2523	0E+00	98.4	96	Solyc01g110470.2.1	GAGA-binding transcriptional activator IPR010409	GAGA binding-like
1J	g62.i1	550337	557132	6795	0E+00	100	100	Solyc01g110480.2.1	BZIP transcription factor family protein expressed IPR011616	bZIP transcription factor, bZIP-1
1J	g63.i1	559747	566721	6974	0E+00	98.43	100	Solyc01g110490.2.1	tRNA-dihydrouridine synthase 3-like IPR001269	tRNA-dihydrouridine synthase
1J	g64.i1	567397	568834	1437	0E+00	97.73	100	Solyc01g110500.2.1	Epsin 2-like protein (Fragment) IPR001026	Epsin, N-terminal
1J	g65.i1	569117	570463	1346	0E+00	95.32	99	Solyc01g110510.2.1	Epsin 1 (Fragment) IPR001026	Epsin, N-terminal
1J	g66.i1	570564	572738	2174	0E+00	98.96	100	Solyc01g110520.2.1	Glucosamine-fructose-6-phosphate aminotransferase IPR005854	Amidophosphoribosyl transferase
1J	g67.i1	575902	578798	2896	7E-83	100	100	Solyc01g110530.2.1	Peptidyl-prolyl cis-trans isomerase C IPR000297	Peptidyl-prolyl cis-trans isomerase, PpiC-type
1J	g68.i1	580637	583218	2581	8E-16	100	31	Solyc01g110540.2.1	Unknown Protein	
1J	g69.i1	583322	588948	5626	3E-145	80.97	72	Solyc01g110550.2.1	Ribosome-binding factor A IPR000238	Ribosome-binding factor A
1J	g70.i1	591837	592578	741	4E-107	98.68	100	Solyc01g110560.2.1	Auxin responsive SAUR protein IPR003676	Auxin responsive SAUR protein
1J	g71.i1	607982	609028	1046	8E-69	98.97	100	Solyc01g110570.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g72.i1	649881	652768	2887	9E-82	70.9	93	Solyc01g111010.2.1	Aquaporin IPR003676	Auxin responsive SAUR protein
1J	g73.i1	654237	656309	2072	7E-29	34.16	79	Solyc03g077970.1.1	Methionine aminopeptidase, related	
1J	g74.i1	656762	657268	506	2E-54	97.59	100	Solyc01g110680.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g75.i2	658098	671168	13070	8E-64	63.48	35	Solyc01g110640.1.1	Unknown Protein	
1J	g75.i1	658151	671168	13017	4E-64	62.84	39	Solyc01g110640.1.1	Unknown Protein	
1J	g76.i1	673385	673888	503	2E-53	93.98	100	Solyc01g110710.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g77.i1	675061	678978	3917	4E-48	98.68	30	Solyc01g110670.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein

ITAG2.4 proteins blastp								SD3 Table Orthologous pairs		Functional Description
BIN	Augustus ID	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
1J	g78.t1	684138	684758	620	9E-49	90.48	98	Solyc01g110920.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g79.t1	685592	686098	506	2E-55	98.8	100	Solyc01g110770.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g80.t1	689411	689978	567	2E-56	100	100	Solyc01g110680.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g81.t1	690885	693758	2873	3E-84	97.58	43	Solyc01g110640.1.1	Unknown Protein	
1J	g82.t1	694551	705118	10567	3E-38	96.97	19	Solyc01g110700.2.1	Unknown Protein	
1J	g82.t2	694551	705118	10567	6E-40	97.1	19	Solyc01g110700.2.1	Unknown Protein	
1J	g83.t1	705458	706008	550	6E-52	93.83	96	Solyc01g110720.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g84.t1	707179	707678	499	2E-54	96.39	100	Solyc01g110710.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g85.t1	709263	709768	505	2E-56	98.81	98	Solyc01g110780.1.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g86.t1	710236	710838	602	1E-28	80.7	84	Solyc01g110920.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g87.t1	711391	711948	557	3E-54	95.29	99	Solyc01g110920.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g88.t1	713087	713598	511	5E-59	100	100	Solyc01g110800.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g89.t1	714661	720998	6337	0E+00	97.86	95	Solyc01g110820.2.1	RNA-binding protein 40 IPR012677	Nucleotide-binding, alpha-beta plait
1J	g91.t1	729874	730378	504	4E-68	97.98	100	Solyc01g110830.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g92.t1	733546	734226	680	2E-62	87.13	100	Solyc01g110860.1.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g93.t1	735937	736726	789	1E-57	87.13	98	Solyc01g110860.1.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g94.t1	739396	740086	690	2E-67	97.03	100	Solyc01g110860.1.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g95.t1	744535	745086	551	7E-68	97	100	Solyc01g110920.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g96.t1	748141	748656	515	2E-66	96.94	100	Solyc01g110880.1.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g97.t1	751307	751956	649	3E-69	99	100	Solyc01g110890.1.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g98.t1	754829	755486	657	2E-70	100	100	Solyc01g110900.1.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g99.t1	759325	759839	514	5E-50	89.16	98	Solyc01g110920.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g100.t1	761235	761788	553	7E-50	87.95	98	Solyc01g110780.1.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g101.t1	763325	763727	402	9E-48	86.75	98	Solyc01g110920.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g102.t1	767445	768004	559	3E-58	98.84	100	Solyc01g110920.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g103.t1	770235	772380	2145	3E-86	72.34	93	Solyc01g111010.2.1	Aquaporin IPR003676	Auxin responsive SAUR protein
1J	g104.t1	772441	773816	1375	0E+00	93.6	100	Solyc01g110950.2.1	Retinoblastoma-binding protein IPR014891	DWNN domain
1J	g105.t1	775445	779103	3658	0E+00	97.41	100	Solyc01g110960.2.1	Glutamic acid-rich protein	
1J	g106.t1	779325	780738	1413	2E-52	90.59	100	Solyc01g110920.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g107.t1	781595	782149	554	1E-50	88.37	100	Solyc01g110920.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g108.t1	782495	786304	3809	0E+00	99.64	95	Solyc01g110990.2.1	ATP-dependent RNA helicase IPR011709	Region of unknown function DUF1605
1J	g109.t2	789095	792916	3821	5E-127	94.82	59	Solyc01g111010.2.1	Aquaporin IPR003676	Auxin responsive SAUR protein
1J	g109.t1	789095	789646	551	7E-50	96.15	95	Solyc01g111000.2.1	Auxin-induced SAUR-like protein IPR003676	Auxin responsive SAUR protein
1J	g110.t1	793455	794819	1364	0E+00	97.87	100	Solyc01g111010.2.1	Aquaporin IPR003676	Auxin responsive SAUR protein
1J	g111.t1	795112	808906	13794	0E+00	83.59	100	Solyc01g111020.2.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
1J	g111.t2	795112	808906	13794	0E+00	83.27	100	Solyc01g111020.2.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
1J	g112.t2	810315	817889	7574	0E+00	87.41	90	Solyc01g111030.1.1	Ribosome biogenesis protein ytm1 IPR020472	G-protein beta WD-40 repeat, region
1J	g112.t3	810315	825113	14798	0E+00	86.55	30	Solyc01g111030.1.1	Ribosome biogenesis protein ytm1 IPR020472	G-protein beta WD-40 repeat, region
1J	g112.t1	818955	825113	6158	0E+00	98.03	46	Solyc01g111040.2.1	EF-Hand containing protein-like IPR018248	EF hand
1J	g113.t1	825685	833183	7498	1E-121	98.37	39	Solyc01g111060.2.1	5_apos-methylthioadenosine_S-adenosylhomocysteine nucleosidase IPR018017	Nucleoside phosphorylase, family 1
1J	g113.t2	825685	833183	7498	4E-121	98.9	36	Solyc01g111060.2.1	5_apos-methylthioadenosine_S-adenosylhomocysteine nucleosidase IPR018017	Nucleoside phosphorylase, family 1
1J	g114.t1	833805	836095	2290	0E+00	99.74	100	Solyc01g111070.2.1	Chalcone synthase family protein IPR011141	Polyketide synthase, type III
1J	g115.t1	836288	837396	1108	9E-69	97.12	100	Solyc01g111080.2.1	Gibberellin-regulated protein 2 IPR003854	Gibberellin regulated protein
1J	g116.t1	842246	848496	6250	0E+00	100	100	Solyc01g111090.2.1	ER lumen protein retaining receptor family protein IPR000133	ER lumen protein retaining receptor
1J	g117.t1	849234	856706	7472	0E+00	100	100	Solyc01g111100.2.1	Neutral invertase like protein IPR006937	Plant neutral invertase

ITAG2.4 proteins blastp								SD3 Table Orthologous pairs	Functional Description
BIN	Augustus ID	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	S.lycopersicum (Heinz)	
1J	g118.t1	862136	868346	6210	0E+00	97.55	100	Solyc01g111120.2.1	Triosephosphate isomerase IPR000652 Triosephosphate isomerase
1J	g119.t1	870213	874086	3873	0E+00	98.5	100	Solyc01g111130.2.1	Transcription factor (Fragment) IPR011598 Helix-loop-helix DNA-binding
1J	g120.t1	876785	888276	11491	0E+00	99.69	56	Solyc01g111140.2.1	Protein FAM50 homolog IPR007005 XAP5 protein
1J	g121.t1	890705	892774	2069	8E-63	53.25	58	Solyc10g054900.1.1	Proline-rich protein IPR010616 Protein of unknown function DUF1210
1J	g122.t1	894245	895016	771	1E-123	99.42	100	Solyc01g111170.2.1	Peptidyl-prolyl cis-trans isomerase IPR002130 Peptidyl-prolyl cis-trans isomerase, cyclophilin-type
1J	g123.t1	908723	915725	7002	0E+00	98.56	59	Solyc01g111200.2.1	Eukaryotic translation initiation factor 4B IPR010433 Plant specific eukaryotic initiation factor 4B
1J	g124.t1	916073	921863	5790	0E+00	98.58	51	Solyc01g111210.2.1	Glutamy-tRNA(Gln) amidotransferase subunit A IPR000120 Amidase signature enzyme
1J	g125.t1	924053	924917	864	6E-128	96.72	100	Solyc01g111230.2.1	Disease resistance response like protein IPR004265 Plant disease resistance response protein
1J	g126.t1	925003	925937	934	3E-69	54.69	100	Solyc02g032040.1.1	Disease resistance response protein IPR004265 Plant disease resistance response protein
1J	g127.t1	927977	934554	6577	0E+00	95.72	99	Solyc01g111240.2.1	Translocase of chloroplast 90, chloroplastic IPR005690 Chloroplast protein import component Toc86_159
1J	g128.t1	936273	937564	1291	0E+00	97.48	100	Solyc01g111250.2.1	Phosphatidylinositol-specific phospholipase c IPR017946 PLC-like phosphodiesterase, TIM beta_alpha-barrel domain
1J	g129.t1	938003	939930	1927	0E+00	97.42	100	Solyc01g111260.2.1	Phosphatidylinositol-specific phospholipase c IPR017946 PLC-like phosphodiesterase, TIM beta_alpha-barrel domain
1J	g130.t1	949513	952183	2670	0E+00	99.23	100	Solyc01g111270.2.1	Armadillo_beta-catenin repeat family protein IPR011989 Armadillo-like helical
1J	g131.t1	952851	953534	683	5E-63	78.61	98	Solyc01g111280.2.1	Cold shock protein-1 IPR002059 Cold-shock protein, DNA-binding
1J	g132.t1	956640	957544	904	3E-113	88.79	100	Solyc01g111300.2.1	Cold shock protein-1 IPR002059 Cold-shock protein, DNA-binding
1J	g133.t1	961760	965224	3464	2E-176	98.39	62	Solyc01g111310.2.1	Transmembrane amino acid transporter protein IPR013057 Amino acid transporter, transmembrane
1J	g134.t1	974233	985878	11645	0E+00	97.04	63	Solyc01g111330.2.1	Thaumatococcus-like protein IPR001938 Thaumatin, pathogenesis-related
1J	g134.t2	974233	985878	11645	0E+00	95.93	54	Solyc01g111330.2.1	Thaumatococcus-like protein IPR001938 Thaumatin, pathogenesis-related
1J	g135.t1	986262	989014	2752	0E+00	98.18	100	Solyc01g111340.2.1	Endo-1 4-beta-xylanase IPR013781 Glycoside hydrolase, subgroup, catalytic core
1J	g136.t1	990178	994134	3956	0E+00	98.92	100	Solyc01g111350.2.1	Nodulin family protein IPR010658 Nodulin-like
1J	g137.t1	1006963	1011512	4549	0E+00	86.38	89	Solyc01g094740.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653 Peptidase C48, SUMO_Sentrin_Ub1
1J	g139.t1	1016643	1020995	4352	1E-167	99.56	100	Solyc01g111360.2.1	Peptidyl-prolyl cis-trans isomerase IPR002130 Peptidyl-prolyl cis-trans isomerase, cyclophilin-type
1J	g140.t1	1022583	1031103	8520	0E+00	99.04	76	Solyc01g111370.2.1	Choline transporter like family IPR007603 Protein of unknown function DUF580
1J	g141.t1	1039483	1042286	2803	0E+00	99.22	100	Solyc01g111400.2.1	Subtilisin-like protease IPR015500 Peptidase S8, subtilisin-related
1J	g142.t2	1046653	1057215	10562	0E+00	98.06	47	Solyc01g111420.2.1	LOC734162 protein (Fragment) IPR002143 Ribosomal protein L1
1J	g142.t1	1046653	1053944	7291	0E+00	91.81	89	Solyc01g111410.2.1	Protein prenyltransferase alpha subunit repeat-containing protein 1 IPR008940 Protein prenyltransferase
1J	g143.t1	1058441	1060454	2013	0E+00	98.03	100	Solyc01g111430.2.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
1J	g144.t1	1060743	1063822	3079	0E+00	99.1	100	Solyc01g111440.2.1	Senescence-associated protein 12 IPR009686 Senescence-associated
1J	g145.t1	1065273	1068037	2764	2E-178	90.88	100	Solyc01g111450.2.1	Proteasome subunit alpha type IPR000426 Proteasome, alpha-subunit, conserved site
1J	g145.t2	1065273	1068037	2764	0E+00	100	100	Solyc01g111450.2.1	Proteasome subunit alpha type IPR000426 Proteasome, alpha-subunit, conserved site
1J	g146.t1	1069812	1075874	6062	0E+00	98.79	80	Solyc01g111470.2.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
1J	g147.t1	1094021	1094951	930	0E+00	99.21	100	Solyc01g111500.2.1	MYB transcription factor IPR015495 Myb transcription factor
1J	g148.t1	1103919	1108621	4702	0E+00	99.3	100	Solyc01g111510.2.1	Ascorbate peroxidase IPR002207 Plant ascorbate peroxidase
1J	g149.t2	1111567	1119111	7544	0E+00	94.67	100	Solyc01g111520.2.1	Synaptotagmin IPR018029 C2 membrane targeting protein
1J	g149.t1	1111618	1119111	7493	0E+00	98.89	100	Solyc01g111520.2.1	Synaptotagmin IPR018029 C2 membrane targeting protein
1J	g150.t1	1123430	1134486	11056	0E+00	96.75	100	Solyc01g111530.2.1	Ubiquitin-protein ligase 4 IPR000569 HECT
1J	g151.t1	1138000	1143640	5640	0E+00	95.31	100	Solyc01g111540.2.1	Beta-galactosidase IPR001944 Glycoside hydrolase, family 35
1J	g151.t2	1138000	1143640	5640	0E+00	98.8	100	Solyc01g111540.2.1	Beta-galactosidase IPR001944 Glycoside hydrolase, family 35
1J	g152.t1	1144310	1158335	14025	0E+00	95.35	68	Solyc01g111550.2.1	Protein MCM10 homolog IPR015408 Zinc finger, Mcm10_DnaG-type
1J	g153.t1	1158950	1166719	7769	0E+00	99.13	100	Solyc01g111570.2.1	Receptor-like kinase IPR002290 Serine_threonine protein kinase
1J	g154.t1	1172840	1177486	4646	0E+00	99.62	82	Solyc01g111580.2.1	BZIP family transcription factor (Fragment) IPR011700 Basic leucine zipper
1J	g155.t1	1177488	1180581	3093	0E+00	98.76	100	Solyc01g111590.2.1	Histone-binding protein RBBP7 IPR020472 G-protein beta WD-40 repeat, region
1J	g155.t2	1177488	1187441	9953	0E+00	98.76	69	Solyc01g111590.2.1	Histone-binding protein RBBP7 IPR020472 G-protein beta WD-40 repeat, region
1J	g156.t1	1192760	1198957	6197	1E-139	96.45	100	Solyc01g111610.2.1	Protein binding protein
1J	g157.t1	1203704	1205511	1807	0E+00	99.63	100	Solyc01g111620.2.1	AT4G35080-like protein (Fragment) IPR011541 Nickel_cobalt transporter, high-affinity

ITAG2.4 proteins blastp								SD3 Table Orthologous pairs	Functional Description
BIN	Augustus ID	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	S.lycopersicum (Heinz)	
1J	g158.t1	1206309	1208471	2162	2E-54	86.73	92	Solyc01g111620.2.1	AT4G35080-like protein (Fragment) IPR011541 Nickel_cobalt transporter, high-affinity
1J	g159.t1	1210630	1214824	4194	0E+00	93.52	100	Solyc01g111630.2.1	Glyoxylate_hydroxypyruvate reductase B IPR006140 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
1J	g159.t2	1210630	1214824	4194	0E+00	87.05	100	Solyc01g111630.2.1	Glyoxylate_hydroxypyruvate reductase B IPR006140 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
1J	g160.t1	1217130	1219021	1891	6E-111	98.73	100	Solyc01g111640.2.1	Skp1 IPR016897 E3 ubiquitin ligase, SCF complex, Skp subunit
1J	g161.t1	1220040	1221944	1904	1E-106	90.17	100	Solyc01g111650.2.1	Skp1 IPR016897 E3 ubiquitin ligase, SCF complex, Skp subunit
1J	g162.t1	1230150	1231336	1186	0E+00	99.65	100	Solyc01g111660.2.1	Aquaporin-like protein IPR012269 Aquaporin
1J	g163.t1	1232940	1233748	808	4E-101	99.32	100	Solyc01g111670.2.1	Unknown Protein IPR009688 Protein of unknown function DUF1279
1J	g164.t1	1234468	1244701	10233	0E+00	98.79	86	Solyc01g111680.2.1	Ubiquitin-conjugating enzyme 22 IPR000608 Ubiquitin-conjugating enzyme, E2
1J	g164.t2	1234468	1244701	10233	0E+00	96.32	82	Solyc01g111680.2.1	Ubiquitin-conjugating enzyme 22 IPR000608 Ubiquitin-conjugating enzyme, E2
1J	g165.t1	1246770	1250503	3733	5E-103	100	100	Solyc01g111690.2.1	Trafficking protein particle complex subunit 2-like protein IPR006722 Sedlin
1J	g166.t1	1250630	1253731	3101	0E+00	98.25	100	Solyc01g111700.1.1	26S proteasome non-ATPase regulatory subunit 3 IPR013143 PCI_PINT associated module
1J	g167.t1	1254851	1259241	4390	0E+00	94.76	100	Solyc01g111710.2.1	26S proteasome non-ATPase regulatory subunit 3 IPR013143 PCI_PINT associated module
1J	g168.t1	1260010	1263801	3791	0E+00	98.27	91	Solyc01g111720.2.1	Translation initiation factor IF-3 IPR001288 Translation initiation factor 3
1J	g169.t1	1264277	1269541	5264	9E-110	99.36	96	Solyc01g111720.2.1	Translation initiation factor IF-3 IPR001288 Translation initiation factor 3
1J	g170.t1	1280360	1287077	6717	0E+00	82.29	100	Solyc01g111730.2.1	Phosphatase 2C family protein IPR015655 Protein phosphatase 2C
1J	g171.t1	1290810	1295204	4394	0E+00	97.67	100	Solyc01g111740.2.1	Bzip-like transcription factor-like IPR006867 Protein of unknown function DUF632
1J	g172.t1	1295601	1298641	3040	0E+00	94.24	100	Solyc01g111750.2.1	Heat shock protein DnaJ domain protein
1J	g172.t2	1295601	1298641	3040	0E+00	95.17	95	Solyc01g111750.2.1	Heat shock protein DnaJ domain protein
1J	g173.t1	1298930	1307165	8235	0E+00	97.29	98	Solyc01g111760.2.1	V-type ATP synthase beta chain IPR005723 ATPase, V1 complex, subunit B
1J	g174.t1	1308100	1312151	4051	0E+00	98.8	100	Solyc01g111770.2.1	Os11g0198100 protein (Fragment) IPR006852 Protein of unknown function DUF616
1J	g175.t1	1313200	1331565	18365	0E+00	97.79	93	Solyc01g111780.2.1	Importin beta-2 subunit IPR011989 Armadillo-like helical
1J	g176.t1	1331711	1333831	2120	0E+00	97.96	98	Solyc01g111790.1.1	Serine_threonine-protein phosphatase 2A regulatory subunit delta 1 isoform IPR002554 Protein phosphatase 2A, regulatory B subunit, B56
1J	g176.t2	1331711	1333831	2120	0E+00	97.7	98	Solyc01g111790.1.1	Serine_threonine-protein phosphatase 2A regulatory subunit delta 1 isoform IPR002554 Protein phosphatase 2A, regulatory B subunit, B56
1J	g177.t1	1334060	1335711	1651	0E+00	97.61	100	Solyc01g111800.2.1	Amino acid permease (Fragment) IPR002293 Amino acid_polyamine transporter I
1J	g178.t1	1336650	1339500	2850	9E-107	99.33	82	Solyc01g111810.2.1	Structural constituent of ribosome IPR005484 Ribosomal protein L18_L5
1J	g179.t1	1342700	1343493	793	9E-68	90.09	100	Solyc01g111820.2.1	Unknown Protein
1J	g180.t1	1352866	1354381	1515	0E+00	99.44	100	Solyc01g111830.2.1	24-sterol C-methyltransferase IPR013705 Sterol methyltransferase C-terminal
1J	g181.t1	1363510	1367678	4168	4E-116	97.67	61	Solyc01g111840.2.1	MFS-type drug efflux transporter P55 IPR016196 Major facilitator superfamily, general substrate transporter
1J	g181.t2	1363630	1367849	4219	1E-115	97.67	56	Solyc01g111840.2.1	MFS-type drug efflux transporter P55 IPR016196 Major facilitator superfamily, general substrate transporter
1J	g182.t1	1367853	1369521	1668	0E+00	97.95	100	Solyc01g111850.2.1	Aspartic proteinase nepenthesin I IPR009007 Peptidase aspartic, catalytic
1J	g183.t1	1370900	1377891	6991	0E+00	98.72	99	Solyc01g111860.2.1	DDB1- and CUL4-associated factor 8-like protein 1 IPR017986 WD40 repeat, region
1J	g184.t1	1380252	1396601	16349	0E+00	97.64	85	Solyc01g111870.1.1	Serine_threonine-protein kinase IPR000403 Phosphatidylinositol 3- and 4-kinase, catalytic
1J	g185.t1	1399125	1407041	7916	0E+00	86.55	100	Solyc01g111880.2.1	Tyrosine-protein kinase transforming protein Src IPR015783 ATMRK serine_threonine protein kinase-like
1J	g185.t2	1399125	1407041	7916	0E+00	95.86	100	Solyc01g111880.2.1	Tyrosine-protein kinase transforming protein Src IPR015783 ATMRK serine_threonine protein kinase-like
1J	g186.t1	1411885	1416571	4686	0E+00	99.79	100	Solyc01g111890.2.1	F-box_LRR-repeat protein 14 IPR001810 Cyclin-like F-box
1J	g187.t1	1418226	1420611	2385	2E-107	98.16	84	Solyc01g111890.2.1	F-box_LRR-repeat protein 14 IPR001810 Cyclin-like F-box
1J	g188.t1	1422225	1423641	1416	0E+00	91.52	99	Solyc01g111900.2.1	O-methyltransferase-like protein IPR016461 O-methyltransferase, COMT, eukaryota
1J	g189.t1	1430716	1432467	1751	0E+00	94.74	100	Solyc01g111900.2.1	O-methyltransferase-like protein IPR016461 O-methyltransferase, COMT, eukaryota
1J	g190.t1	1433916	1444477	10561	0E+00	98.46	100	Solyc01g111910.2.1	RNA polymerase II-associated protein 1 IPR013930 RNA polymerase II-associated protein 1, N-terminal
1J	g190.t2	1433916	1444477	10561	0E+00	97.89	100	Solyc01g111910.2.1	RNA polymerase II-associated protein 1 IPR013930 RNA polymerase II-associated protein 1, N-terminal
1J	g191.t1	1448146	1450511	2365	0E+00	98.77	100	Solyc01g111920.2.1	F-box family protein IPR005174 Protein of unknown function DUF295
1J	g192.t1	1451489	1455167	3678	0E+00	99.13	100	Solyc01g111930.2.1	Rop guanine nucleotide exchange factor 1 IPR005512 Rop nucleotide exchanger, PRONE
1J	g193.t2	1460856	1462343	1487	5E-156	99.56	95	Solyc01g111940.2.1	Coiled-coil domain-containing protein 124 IPR010422 Protein of unknown function DUF1014
1J	g193.t3	1460856	1469394	8538	0E+00	98.75	67	Solyc01g111950.2.1	Receptor-like kinase IPR002290 Serine_threonine protein kinase
1J	g193.t1	1466236	1469394	3158	0E+00	98.76	100	Solyc01g111950.2.1	Receptor-like kinase IPR002290 Serine_threonine protein kinase

ITAG2.4 proteins blastp								SD3 Table Orthologous pairs	Functional Description
BIN	Augustus ID	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	S.lycopersicum (Heinz)	
1J	g194.t1	1469892	1471867	1975	0E+00	97.53	100	Solyc01g111960.2.1	GDSL esterase_lipase At5g55050 IPR001087 Lipase, GDSL
1J	g194.t2	1469892	1471867	1975	0E+00	97.51	100	Solyc01g111960.2.1	GDSL esterase_lipase At5g55050 IPR001087 Lipase, GDSL
1J	g195.t1	1472305	1475877	3572	0E+00	98.13	100	Solyc01g111970.2.1	Laccase 1a IPR001117 Multicopper oxidase, type 1
1J	g195.t2	1472305	1475877	3572	0E+00	98.65	100	Solyc01g111970.2.1	Laccase 1a IPR001117 Multicopper oxidase, type 1
1J	g196.t1	1481054	1483907	2853	0E+00	98.41	100	Solyc01g111980.2.1	Lysine_histidine transporter IPR013057 Amino acid transporter, transmembrane
1J	g197.t2	1496806	1506984	10178	0E+00	99.35	98	Solyc01g111990.2.1	Alanyl-tRNA synthetase IPR002318 Alanyl-tRNA synthetase, class IIc
1J	g197.t1	1498086	1506984	8898	0E+00	94.83	100	Solyc01g111990.2.1	Alanyl-tRNA synthetase IPR002318 Alanyl-tRNA synthetase, class IIc
1J	g198.t1	1510706	1512210	1504	0E+00	98.85	100	Solyc01g112000.2.1	Expansin-like protein IPR007112 Expansin 45, endoglucanase-like IPR007117 Pollen allergen_expansin, C-terminal
1J	g199.t1	1512486	1516037	3551	2E-159	92.71	100	Solyc10g008130.2.1	Pre-rRNA-processing protein ESF2 IPR012677 Nucleotide-binding, alpha-beta plait
1J	g201.t2	1523752	1534317	10565	0E+00	88.96	77	Solyc01g112020.2.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
1J	g201.t1	1523879	1534317	10438	0E+00	88.96	68	Solyc01g112020.2.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
1J	g203.t1	1540303	1548367	8064	0E+00	96.2	58	Solyc01g112050.2.1	Bzip transcription factor-like IPR006867 Protein of unknown function DUF632
1J	g204.t1	1554386	1557827	3441	0E+00	99.74	100	Solyc01g112060.2.1	NmrA family protein-binding domain
1J	g205.t1	1558378	1564887	6509	0E+00	97.97	100	Solyc01g112070.2.1	Os03g0169000 protein (Fragment) IPR004348 Protein of unknown function DUF246, plant
1J	g206.t1	1570486	1572062	1576	0E+00	99.42	100	Solyc01g112080.2.1	LysM-domain GPI-anchored protein IPR002482 Peptidoglycan-binding Lysin subgroup
1J	g207.t1	1572946	1580783	7837	0E+00	83.16	99	Solyc01g112090.2.1	MATE efflux family protein expressed IPR002528 Multi antimicrobial extrusion protein MatE
1J	g208.t1	1581585	1583927	2342	0E+00	97.87	100	Solyc01g112100.2.1	Dimethylaniline monooxygenase 5 IPR012143 Dimethylaniline monooxygenase, N-oxide-forming
1J	g209.t1	1595060	1597877	2817	0E+00	84.32	83	Solyc01g112120.2.1	Dimethylaniline monooxygenase 5
1J	g210.t1	1598623	1601227	2604	0E+00	88.61	100	Solyc01g112140.2.1	Dimethylaniline monooxygenase 5 IPR012143 Dimethylaniline monooxygenase, N-oxide-forming
1J	g211.t1	1601811	1604867	3056	0E+00	99.01	100	Solyc01g112150.2.1	Sec1-1 syntaxin binding protein IPR001619 Sec1-like protein
1J	g212.t1	1605786	1609745	3959	3E-123	95.51	82	Solyc01g112160.2.1	Phosphoglycerate mutase family protein IPR013078 Phosphoglycerate mutase
1J	g213.t1	1610625	1619197	8572	8E-77	74.85	89	Solyc01g112170.2.1	Calcium-dependent protein kinase IPR011992 EF-Hand type
1J	g213.t2	1610625	1620577	9952	2E-94	86.5	69	Solyc01g112170.2.1	Calcium-dependent protein kinase IPR011992 EF-Hand type

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
2K	g2.t1	3964	6397	2433	0E+00	91.59	93	Solyc02g090920.2.1	Lipase IPR002921 Lipase, class 3	
2K	g3.t1	6954	11417	4463	0E+00	98.16	100	Solyc02g090930.2.1	Lipase IPR002921 Lipase, class 3	
2K	g3.t2	6954	11417	4463	0E+00	98.1	100	Solyc02g090930.2.1	Lipase IPR002921 Lipase, class 3	
2K	g4.t1	12804	20827	8023	0E+00	93.02	100	Solyc02g090940.2.1	Lipase IPR002921 Lipase, class 3	
2K	g4.t2	12804	20827	8023	0E+00	98.77	100	Solyc02g090940.2.1	Lipase IPR002921 Lipase, class 3	
2K	g5.t1	22886	26711	3825	6E-123	96.65	55	Solyc02g090950.1.1	BHLH transcription factor-like IPR001092 Basic helix-loop-helix dimerisation region bHLH	
2K	g6.t1	35736	37165	1429	0E+00	96.39	100	Solyc02g090970.1.1	Serine_threonine-protein kinase 24 IPR002290 Serine_threonine protein kinase	
2K	g7.t1	49076	51537	2461	0E+00	96.33	61	Solyc02g090980.1.1	Protein serine_threonine kinase IPR002290 Serine_threonine protein kinase	
2K	g8.t1	59016	60410	1394	0E+00	98.04	100	Solyc02g090990.1.1	Serine_threonine-protein kinase 36 IPR002290 Serine_threonine protein kinase	
2K	g10.t1	66367	68307	1940	0E+00	99.37	100	Solyc02g091000.2.1	Harpin-induced protein IPR010847 Harpin-induced 1	
2K	g11.t1	69681	78647	8966	0E+00	78.1	78	Solyc02g091020.1.1	Nucleoporin autopeptidase family protein expressed	
2K	g11.t2	69681	78647	8966	0E+00	78.63	77	Solyc02g091020.1.1	Nucleoporin autopeptidase family protein expressed	
2K	g12.t1	86216	100046	13830	0E+00	68.08	57	Solyc02g091030.2.1	Nuclear transcription factor Y subunit C-2 IPR003958 Transcription factor CBF_NF-Y_archaeal histone	
2K	g13.t1	104016	113514	9498	0E+00	52	93	Solyc02g091030.2.1	Nuclear transcription factor Y subunit C-2 IPR003958 Transcription factor CBF_NF-Y_archaeal histone	
2K	g13.t2	104016	113646	9630	0E+00	52.69	93	Solyc02g091030.2.1	Nuclear transcription factor Y subunit C-2 IPR003958 Transcription factor CBF_NF-Y_archaeal histone	
2K	g14.t1	116985	127727	10742	0E+00	86.24	47	Solyc02g091070.2.1	Multidrug resistance protein mdtK IPR015521 MATE family transporter related protein	
2K	g15.t1	129837	132697	2860	0E+00	86	100	Solyc02g091080.1.1	Multidrug resistance protein mdtK IPR015521 MATE family transporter related protein	
2K	g16.t1	132886	134137	1251	1E-35	95.24	73	Solyc02g091090.2.1	Mate efflux family protein IPR015521 MATE family transporter related protein	
2K	g17.t1	134309	135697	1388	0E+00	99.73	98	Solyc02g091090.2.1	Mate efflux family protein IPR015521 MATE family transporter related protein	
2K	g18.t1	136424	139887	3463	0E+00	92.26	100	Solyc02g091100.2.1	Oxalyl-CoA decarboxylase IPR012001 Thiamine pyrophosphate enzyme, N-terminal TPP binding region	
2K	g19.t1	141125	165147	24022	0E+00	93.28	88	Solyc02g091120.2.1	DNA ligase IPR000977 ATP-dependent DNA ligase	
2K	g19.t2	141125	144857	3732	7E-137	98.96	100	Solyc02g091110.2.1	Histone chaperone ASF1-like protein IPR006818 Histone chaperone, ASF1-like	
2K	g20.t1	166606	169948	3342	0E+00	98.73	100	Solyc02g091130.2.1	ATP synthase subunit beta IPR005722 ATPase, F1 complex, beta subunit	
2K	g21.t1	170048	171697	1649	0E+00	99.19	100	Solyc02g091140.2.1	S-adenosyl-L-methionine carboxyl methyltransferase family protein IPR005299 SAM dependent carboxyl methyltransferase	
2K	g22.t1	173078	173997	919	2E-51	83.52	100	Solyc02g091150.1.1	Unknown Protein	
2K	g23.t1	180068	180626	558	5E-58	95.6	100	Solyc02g091150.1.1	Unknown Protein	
2K	g24.t1	182325	191571	9246	4E-124	80.97	41	Solyc02g091170.2.1	Kinase family protein IPR002290 Serine_threonine protein kinase	
2K	g24.t2	182325	191571	9246	1E-125	80.31	44	Solyc02g091170.2.1	Kinase family protein IPR002290 Serine_threonine protein kinase	
2K	g25.t1	193165	203539	10374	0E+00	99.09	100	Solyc02g091190.2.1	Methyltransferase-like protein 10 IPR013217 Methyltransferase type 12	
2K	g26.t1	212375	215181	2806	0E+00	98.44	100	Solyc02g091210.1.1	Eukaryotic translation initiation factor 5 IPR002735 Translation initiation factor IF2_IF5	
2K	g27.t1	217765	219993	2228	0E+00	98.22	100	Solyc02g091220.1.1	Eukaryotic translation initiation factor 5 IPR002735 Translation initiation factor IF2_IF5	
2K	g28.t1	220414	222286	1872	2E-109	98.06	72	Solyc02g091230.2.1	E3 ubiquitin-protein ligase MARCH2 IPR011016 Zinc finger, RING-CH-type	
2K	g29.t1	223673	225596	1923	0E+00	98.01	100	Solyc02g091240.1.1	Auxin efflux carrier protein-like IPR004776 Auxin efflux carrier	
2K	g30.t1	233024	233706	682	1E-85	90.65	100	Solyc02g091250.1.1	Predicted by genscan and genefinder	
2K	g31.t1	241705	245369	3664	0E+00	99.11	100	Solyc02g091270.2.1	ELL-associated factor 1 IPR019194 ELL-associated factor	
2K	g32.t1	245763	247026	1263	3E-81	98.29	100	Solyc02g091280.2.1	ATP-dependent Clp protease proteolytic subunit IPR001907 Peptidase S14, ClpP	
2K	g33.t1	247706	250276	2570	1E-136	98.94	83	Solyc02g091280.2.1	ATP-dependent Clp protease proteolytic subunit IPR001907 Peptidase S14, ClpP	
2K	g34.t1	250675	256484	5809	0E+00	91.9	99	Solyc02g091290.2.1	Methionyl-tRNA formyltransferase IPR005794 Methionyl-tRNA formyltransferase	
2K	g34.t2	250675	256506	5831	0E+00	88.68	99	Solyc02g091290.2.1	Methionyl-tRNA formyltransferase IPR005794 Methionyl-tRNA formyltransferase	
2K	g35.t1	266155	267918	1763	0E+00	97.33	99	Solyc02g091310.1.1	Copper chaperone IPR006121 Heavy metal transport detoxification protein	
2K	g36.t1	268315	271676	3361	0E+00	98.74	100	Solyc02g091320.2.1	Unknown Protein	
2K	g37.t1	272320	279866	7546	0E+00	98.16	71	Solyc02g091330.2.1	C20orf4 homolog IPR007946 AAR2	
2K	g37.t2	272320	290236	17916	0E+00	98.16	38	Solyc02g091330.2.1	C20orf4 homolog IPR007946 AAR2	
2K	g37.t3	280191	291316	11125	3E-151	68.48	100	Solyc02g091340.2.1	Pyridoxal kinase biosynthesis, pyridoxal kinase	
2K	g38.t1	295285	297244	1959	0E+00	98.94	99	Solyc02g091350.2.1	Glucosyltransferase-2 IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
2K	g39.t1	299845	300870	1025	6E-118	99.4	100	Solyc02g091360.1.1	Unknown Protein	
2K	g40.t1	302225	304482	2257	0E+00	97.6	92	Solyc02g091370.2.1	Glucosyltransferase-2 IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
2K	g41.t1	305269	305956	687	2E-69	98.1	99	Solyc02g091380.1.1	Unknown Protein	
2K	g42.t1	307190	308186	996	6E-50	100	100	Solyc02g091390.2.1	Little protein 1	
2K	g43.t1	308785	309623	838	2E-56	89.68	100	Solyc02g091400.1.1	Unknown Protein	
2K	g44.t1	309968	335826	25858	0E+00	96.01	100	Solyc02g091410.2.1	Pro-apoptotic serine protease nma111-like protein IPR009003 Peptidase, trypsin-like serine and cysteine	
2K	g45.t1	336130	337596	1466	0E+00	99.25	100	Solyc02g091420.2.1	Aquaporin IPR012269 Aquaporin	
2K	g45.t2	336130	337596	1466	0E+00	99.22	100	Solyc02g091420.2.1	Aquaporin IPR012269 Aquaporin	
2K	g46.t1	341809	344876	3067	0E+00	98.11	95	Solyc02g091430.2.1	Armadillo_beta-catenin repeat family protein IPR011989 Armadillo-like helical	
2K	g47.t1	357545	359524	1979	0E+00	98.74	99	Solyc02g091440.1.1	BHLH transcription factor IPR011598 Helix-loop-helix DNA-binding	
2K	g49.t1	371268	387864	16596	3E-119	96.55	43	Solyc02g091460.2.1	DsRNA-binding protein IPR001159 Double-stranded RNA binding	
2K	g50.t1	394573	397486	2913	0E+00	99.23	100	Solyc02g091470.2.1	Serine_threonine protein kinase-like IPR002290 Serine_threonine protein kinase	
2K	g51.t1	398454	398944	490	2E-54	98.81	100	Solyc02g091480.1.1	Calmodulin 4 IPR011992 EF-Hand type	
2K	g52.t1	399352	406484	7132	0E+00	97.17	100	Solyc02g091490.2.1	Fructokinase 3 IPR011611 Carbohydrate_purine kinase	
2K	g53.t1	413213	413992	779	7E-108	98.08	100	Solyc02g091500.1.1	Calmodulin IPR011992 EF-Hand type	
2K	g54.t1	416437	421514	5077	0E+00	98.41	100	Solyc02g091510.2.1	GDP-L-galactose phosphorylase 2	
2K	g54.t2	416437	421514	5077	0E+00	92.7	100	Solyc02g091510.2.1	GDP-L-galactose phosphorylase 2	
2K	g55.t1	424368	426314	1946	4E-117	98.79	100	Solyc02g091520.2.1	C2 domain-containing protein IPR018029 C2 membrane targeting protein	
2K	g56.t1	434053	443574	9521	3E-134	95.26	52	Solyc02g091530.2.1	5_apos-AMP-activated protein kinase subunit beta-1 (Fragment)	
2K	g57.t1	449713	468891	19178	0E+00	99.42	68	Solyc02g091560.2.1	Serine hydroxymethyltransferase IPR001085 Serine hydroxymethyltransferase	
2K	g57.t2	449713	468891	19178	0E+00	99.42	68	Solyc02g091560.2.1	Serine hydroxymethyltransferase IPR001085 Serine hydroxymethyltransferase	
2K	g58.t1	470568	471844	1276	0E+00	97.33	100	Solyc02g091570.1.1	F-box family protein IPR017451 F-box associated type 1	
2K	g59.t1	473957	489064	15107	0E+00	99.2	49	Solyc02g091580.2.1	Oligopeptidase A IPR001567 Peptidase M3A and M3B, thimet_oligopeptidase F	
2K	g59.t2	473957	489064	15107	0E+00	99.2	49	Solyc02g091580.2.1	Oligopeptidase A IPR001567 Peptidase M3A and M3B, thimet_oligopeptidase F	
2K	g60.t1	490412	495954	5542	2E-171	99.13	100	Solyc02g091600.1.1	Os08g0119500 protein (Fragment)	
2K	g61.t1	508533	509096	563	3E-41	96.92	76	Solyc02g091620.1.1	DNA mismatch repair protein-like IPR002099 DNA mismatch repair protein	
2K	g62.t1	514203	527770	13567	0E+00	99.45	43	Solyc02g091640.2.1	Endoribonuclease E-like protein	
2K	g63.t1	534384	538821	4437	0E+00	91.53	99	Solyc02g091650.2.1	Glycine-rich protein (Fragment) IPR009836 Protein of unknown function DUF1399	
2K	g63.t2	534384	538821	4437	0E+00	97.49	99	Solyc02g091650.2.1	Glycine-rich protein (Fragment) IPR009836 Protein of unknown function DUF1399	
2K	g64.t1	543804	545665	1861	0E+00	95.51	100	Solyc02g091660.2.1	DNA-binding bromodomain-containing protein IPR001487 Bromodomain	
2K	g65.t1	549469	550515	1046	0E+00	99.62	100	Solyc02g091670.1.1	Octicosapeptide_Phox_Bem1p domain-containing protein IPR000270 Octicosapeptide_Phox_Bem1p	
2K	g66.t1	554921	559095	4174	0E+00	98.99	100	Solyc02g091680.2.1	Alpha-L-arabinofuranosidase_beta-D-xylosidase IPR001764 Glycoside hydrolase, family 3, N-terminal	
2K	g67.t1	579143	580235	1092	8E-110	98.08	100	Solyc02g091700.2.1	Hydroxyproline-rich glycoprotein	
2K	g68.t1	600494	603132	2638	0E+00	99.3	100	Solyc02g091710.2.1	von Willebrand factor type A domain-containing protein IPR002035 von Willebrand factor, type A	
2K	g69.t1	605687	607935	2248	0E+00	99.74	100	Solyc02g091720.1.1	Macrophage erythroblast attacher IPR013144 Ran binding protein-like, CRA domain	
2K	g72.t2	618024	649793	31769	0E+00	94.09	36	Solyc02g091780.1.1	Kinesin-like protein IPR001752 Kinesin, motor region	
2K	g72.t3	618024	639732	21708	2E-176	93.73	23	Solyc02g091730.1.1	Os11g0296800 protein (Fragment)	
2K	g72.t1	642624	649793	7169	0E+00	94.21	93	Solyc02g091780.1.1	Kinesin-like protein IPR001752 Kinesin, motor region	
2K	g73.t1	650464	656778	6314	0E+00	99.68	100	Solyc02g091790.2.1	Wd-repeat protein IPR020472 G-protein beta WD-40 repeat, region	
2K	g74.t1	658014	659900	1886	0E+00	94.52	100	Solyc02g091800.2.1	BHLH transcription factor IPR011598 Helix-loop-helix DNA-binding	
2K	g75.t1	670934	672596	1662	0E+00	97.3	100	Solyc02g091810.1.1	Transcription factor IPR011598 Helix-loop-helix DNA-binding	
2K	g76.t1	683684	685941	2257	0E+00	95.78	100	Solyc02g091820.1.1	Transcription factor IPR011598 Helix-loop-helix DNA-binding	
2K	g77.t1	700750	704613	3863	0E+00	95.98	100	Solyc02g091830.2.1	Hexokinase IPR001312 Hexokinase	
2K	g78.t1	707540	715317	7777	0E+00	99.41	100	Solyc02g091840.2.1	Receptor like kinase, RLK	
2K	g79.t1	743320	751986	8666	0E+00	98.48	100	Solyc02g091860.2.1	Receptor like kinase, RLK	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
2K	g80.t1	752260	754567	2307	0E+00	99.78	100	Solyc02g091870.2.1	Tubulin alpha-3 chain IPR002452 Alpha tubulin	
2K	g81.t1	755380	758460	3080	1E-68	100	100	Solyc02g091880.2.1	Cytochrome c oxidase subunit VIa family protein expressed IPR001349 Cytochrome c oxidase, subunit VIa	
2K	g82.t1	761671	765001	3330	0E+00	98.72	100	Solyc02g091890.1.1	MRNA complete cds clone RAFL24-22-E06	
2K	g83.t1	765400	767498	2098	2E-166	84.19	64	Solyc02g091900.2.1	Cysteine desulfurase IPR000192 Amino transferase, class V_Cysteine desulfurase	
2K	g84.i2	772994	780581	7587	6E-56	94.44	44	Solyc02g091910.1.1	EPIDERMAL PATTERNING FACTOR-like protein 2	
2K	g84.t1	778036	780581	2545	4E-57	90.62	83	Solyc06g018030.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
2K	g85.t1	787700	789147	1447	0E+00	99.66	100	Solyc02g091920.2.1	Xyloglucan endotransglucosylase_hydrolase 2 IPR016455 Xyloglucan endotransglucosylase_hydrolase	
2K	g86.t1	808526	809761	1235	0E+00	99.63	100	Solyc02g091930.2.1	Homeobox-leucine zipper protein 22 IPR003106 Leucine zipper, homeobox-associated	
2K	g87.t1	820570	822061	1491	0E+00	98.31	100	Solyc02g091940.2.1	AT5g13970_MAC12_6	
2K	g88.t1	822400	836082	13682	0E+00	98.98	34	Solyc02g091950.2.1	Lysosomal Pro-X carboxypeptidase IPR008758 Peptidase S28	
2K	g89.t1	837045	843871	6826	0E+00	99.46	89	Solyc02g091970.2.1	Branched-chain-amino-acid aminotransferase IPR005786 Branched-chain amino acid aminotransferase II	
2K	g90.t1	849220	851115	1895	0E+00	98.79	100	Solyc02g091980.1.1	MYB transcription factor IPR015495 Myb transcription factor	
2K	g90.i2	849220	868581	19361	0E+00	98.15	59	Solyc02g091980.1.1	MYB transcription factor IPR015495 Myb transcription factor	
2K	g91.t1	875620	877701	2081	0E+00	98.93	100	Solyc02g091990.2.1	1-aminocyclopropane-1-carboxylate synthase IPR004839 Amino transferase, class I and II IPR004838 Amino transferases, class-I, pyridoxal-phosphate-binding site	
2K	g92.t1	886942	890940	3998	0E+00	98.84	100	Solyc02g092000.2.1	Unknown Protein	
2K	g93.t1	892579	901960	9381	0E+00	90.65	95	Solyc02g092010.2.1	GTP-binding protein hflX IPR016496 GTP-binding protein, hflX	
2K	g93.i2	892579	901960	9381	0E+00	92.03	95	Solyc02g092010.2.1	GTP-binding protein hflX IPR016496 GTP-binding protein, hflX	
2K	g94.i2	907209	911525	4316	0E+00	80.59	56	Solyc02g092020.1.1	F-box domain containing protein expressed IPR005174 Protein of unknown function DUF295	
2K	g94.t1	909029	911525	2496	5E-103	98.04	49	Solyc02g092030.1.1	Cbs domain containing protein expressed (Fragment) IPR002550 Protein of unknown function DUF21	
2K	g96.i2	918359	924147	5788	0E+00	99.52	52	Solyc02g092030.1.1	Cbs domain containing protein expressed (Fragment) IPR002550 Protein of unknown function DUF21	
2K	g96.t1	920499	924194	3695	0E+00	99.54	100	Solyc02g092030.1.1	Cbs domain containing protein expressed (Fragment) IPR002550 Protein of unknown function DUF21	
2K	g97.t1	929910	932490	2580	0E+00	100	100	Solyc02g092040.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
2K	g98.t1	939726	943360	3634	0E+00	97.53	100	Solyc02g092050.2.1	AP2-like ethylene-responsive transcription factor At1g16060 IPR001471 Pathogenesis-related transcriptional factor and ERF, DNA-binding	
2K	g99.t1	944992	946260	1268	0E+00	98.58	100	Solyc02g092060.1.1	Short-chain dehydrogenase_reductase family protein IPR002347 Glucose_ribitol dehydrogenase	
2K	g101.t1	962679	970954	8275	0E+00	92.56	95	Solyc02g092070.2.1	Growth regulating factor 1 (Fragment) IPR014977 WRC	
2K	g102.t1	976309	983830	7521	4E-117	97.02	100	Solyc02g092080.1.1	Primary rRNA-binding ribosomal protein component of the large (60S) ribosomal subunit IPR012678 Ribosomal protein L23_L15e, core	
2K	g103.t1	987801	988850	1049	1E-155	99.07	100	Solyc02g092090.1.1	BZIP transcription factor family protein IPR011616 bZIP transcription factor, bZIP-1	
2K	g104.t1	996015	996730	715	1E-81	98.26	100	Solyc02g092100.1.1	Unknown Protein	
2K	g105.t1	1000925	1001390	465	5E-14	60.49	88	Solyc02g092090.1.1	BZIP transcription factor family protein IPR011616 bZIP transcription factor, bZIP-1	
2K	g106.t1	1012799	1013496	697	5E-56	97.59	100	Solyc02g092120.2.1	Phytosulfokines 3 IPR009438 Phytosulfokine	
2K	g107.t1	1018865	1024440	5575	0E+00	97.84	100	Solyc02g092140.1.1	Phloem protein (Fragment)	
2K	g108.t1	1025219	1029427	4208	0E+00	98.76	100	Solyc02g092150.2.1	ACT domain-containing protein IPR002912 Amino acid-binding ACT	
2K	g109.t1	1029551	1033840	4289	0E+00	97.55	100	Solyc02g092160.2.1	BSD domain containing protein IPR005607 BSD	
2K	g110.t1	1037929	1039593	1664	3E-84	96.03	93	Solyc02g092180.1.1	Unknown Protein	
2K	g111.t1	1043189	1044007	818	4E-107	100	100	Solyc02g092190.1.1	Unknown Protein IPR016972 Uncharacterised conserved protein UCP031279	
2K	g112.t1	1046739	1048382	1643	8E-112	98.16	100	Solyc02g092200.2.1	Genomic DNA chromosome 5 TAC clone K9I9	
2K	g113.t1	1050209	1051797	1588	0E+00	98.87	100	Solyc02g092210.1.1	Alpha-6-galactosyltransferase IPR008630 Galactosyl transferase	
2K	g114.t1	1056011	1058830	2819	0E+00	67.05	95	Solyc03g043920.2.1	Alpha-6-galactosyltransferase IPR008630 Galactosyl transferase	
2K	g115.t1	1060499	1064700	4201	0E+00	99.75	100	Solyc02g092230.2.1	Adiponectin receptor 2 IPR004254 Hly-III related	
2K	g116.t1	1073909	1076973	3064	6E-125	98.29	100	Solyc02g092240.2.1	Os10g0352000 protein (Fragment)	
2K	g118.t1	1081120	1083830	2710	0E+00	95.18	100	Solyc02g092250.2.1	Cytochrome P450	
2K	g118.i2	1081120	1083830	2710	0E+00	98.21	100	Solyc02g092250.2.1	Cytochrome P450	
2K	g119.t1	1084979	1091676	6697	0E+00	99.16	100	Solyc02g092260.2.1	Amino-acid N-acetyltransferase	
2K	g120.t1	1092324	1097160	4836	2E-50	98.68	49	Solyc02g092270.2.1	NADH dehydrogenase IPR006885 ETC complex I subunit conserved region	
2K	q121.t1	1099039	1104232	5193	0E+00	97.99	59	Solyc02g092290.2.1	F-box_LRR-repeat protein At5g02910 IPR001810 Cyclin-like F-box	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
2K	g122.t1	1106012	1106850	838	2E-116	100	100	Solyc02g092300.1.1	50S ribosomal protein L12-2 IPR015608 Ribosomal protein L12, chloroplast	
2K	g123.i2	1107191	1115520	8329	0E+00	97.98	56	Solyc02g092310.2.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
2K	g123.t1	1107332	1115170	7838	0E+00	97.98	58	Solyc02g092310.2.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
2K	g124.t1	1124089	1128759	4670	0E+00	86.78	58	Solyc02g092350.2.1	Unknown Protein	
2K	g125.t1	1132399	1137349	4950	0E+00	99.64	50	Solyc02g092360.2.1	Beta-glucanase-like protein IPR006710 Glycoside hydrolase, family 43	
2K	g125.i2	1132399	1137349	4950	0E+00	98.92	100	Solyc02g092360.2.1	Beta-glucanase-like protein IPR006710 Glycoside hydrolase, family 43	
2K	g126.t1	1139963	1143460	3497	0E+00	97.04	100	Solyc02g092370.1.1	GRAS family transcription factor IPR005202 GRAS transcription factor	
2K	g127.t1	1146757	1152220	5463	0E+00	99.33	100	Solyc02g092380.2.1	Peptidyl-prolyl cis-trans isomerase IPR002130 Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	
2K	g128.i2	1156069	1159550	3481	5E-136	98.96	41	Solyc02g092400.1.1	Harpin-induced protein IPR010847 Harpin-induced 1	
2K	g128.t1	1156069	1158409	2340	7E-136	95.59	100	Solyc02g092390.2.1	Unknown Protein	
2K	g129.t1	1159594	1163600	4006	0E+00	99.02	99	Solyc02g092410.2.1	Adenylyl-sulfate kinase IPR002891 Adenylylsulphate kinase, C-terminal	
2K	g129.i2	1159594	1163600	4006	0E+00	91.53	99	Solyc02g092410.2.1	Adenylyl-sulfate kinase IPR002891 Adenylylsulphate kinase, C-terminal	
2K	g130.t1	1176846	1183020	6174	0E+00	97.48	53	Solyc02g092420.2.1	Os07g0587200 protein (Fragment) IPR013069 BTB_POZ	
2K	g130.i2	1176846	1184130	7284	0E+00	97.48	49	Solyc02g092420.2.1	Os07g0587200 protein (Fragment) IPR013069 BTB_POZ	
2K	g131.t1	1184979	1185946	967	3E-102	100	100	Solyc02g092430.1.1	Ribosomal protein L26 IPR005756 Ribosomal protein L26, eukaryotic_archaeal	
2K	g132.t1	1187749	1189960	2211	1E-169	100	96	Solyc02g092440.2.1	Mitochondrial porin (Voltage-dependent anion channel) outer membrane protein IPR001925 Porin, eukaryotic type	
2K	g134.t1	1198649	1209347	10698	0E+00	99.8	73	Solyc02g092450.2.1	Calcium-transporting ATPase 1 IPR006408 ATPase, P-type, calcium-transporting, PMCA-type	
2K	g135.t1	1210792	1215840	5048	0E+00	98.44	100	Solyc02g092470.2.1	Formin 3 IPR015425 Actin-binding FH2	
2K	g136.t1	1229849	1235149	5300	0E+00	97.29	100	Solyc02g092480.2.1	Phototropic-responsive NPH3 family protein IPR004249 NPH3	
2K	g137.t1	1243102	1244893	1791	0E+00	99.28	100	Solyc02g092490.2.1	Acetyltransferase-like protein IPR000182 GCN5-related N-acetyltransferase	
2K	g139.t1	1273692	1289954	16262	0E+00	98.91	33	Solyc02g092510.2.1	UPF0553 protein C9orf64 IPR019438 Protein of unknown function DUF2419	
2K	g139.i2	1273692	1289928	16236	0E+00	98.91	30	Solyc02g092510.2.1	UPF0553 protein C9orf64 IPR019438 Protein of unknown function DUF2419	
2K	g140.t1	1290942	1300243	9301	0E+00	97.67	91	Solyc02g092530.2.1	Formamidase IPR004304 Acetamidase_Formamidase	
2K	g141.t1	1301852	1302925	1073	1E-161	99.08	100	Solyc02g092550.2.1	LOB domain protein 38 IPR004883 Lateral organ boundaries, LOB	
2K	g142.t1	1310980	1318163	7183	0E+00	98.66	100	Solyc02g092560.2.1	Phototropic-responsive NPH3 family protein IPR004249 NPH3	
2K	g143.t1	1321872	1324828	2956	0E+00	98.63	99	Solyc02g092570.1.1	GRAS family transcription factor IPR005202 GRAS transcription factor	
2K	g144.t1	1328544	1330983	2439	0E+00	98.71	100	Solyc02g092580.2.1	Peroxidase IPR002016 Haem peroxidase, plant_fungal_bacterial	
2K	g145.t1	1346822	1347829	1007	7E-154	97.67	100	Solyc02g092590.2.1	Os03g0604500 protein (Fragment)	
2K	g146.t1	1350399	1354213	3814	0E+00	63.86	99	Solyc02g092560.2.1	Phototropic-responsive NPH3 family protein IPR004249 NPH3	
2K	g147.t1	1362392	1369793	7401	0E+00	96.51	100	Solyc02g092640.2.1	Casein kinase IPR002290 Serine_threonine protein kinase	
2K	g147.i2	1362392	1369793	7401	0E+00	100	100	Solyc02g092640.2.1	Casein kinase IPR002290 Serine_threonine protein kinase	
2K	g148.t1	1370089	1372323	2234	2E-47	92.11	99	Solyc02g064730.2.1	Expressed protein having alternate splicing products IPR015023 Protein of unknown function DUF1909	
2K	g149.t1	1373042	1379931	6889	0E+00	98.39	86	Solyc02g092660.2.1	Major facilitator superfamily domain-containing protein IPR008509 Protein of unknown function DUF791	
2K	g150.t1	1383799	1386273	2474	0E+00	97.15	100	Solyc02g092670.1.1	Subtilisin-like protease IPR015500 Peptidase S8, subtilisin-related	
2K	g151.t1	1389712	1392343	2631	0E+00	93.38	100	Solyc02g092680.1.1	Subtilisin-like protease IPR015500 Peptidase S8, subtilisin-related	
2K	g152.t1	1404093	1407207	3114	0E+00	99.36	100	Solyc02g092700.2.1	Ycf36 protein IPR009631 Protein of unknown function DUF1230	
2K	g153.t1	1412236	1419974	7738	6E-154	81.65	72	Solyc02g092710.2.1	Prolyl 4-hydroxylase alpha-2 subunit IPR006620 Prolyl 4-hydroxylase, alpha subunit	
2K	g155.t1	1423326	1424630	1304	0E+00	95.79	100	Solyc02g092720.1.1	Unknown Protein	
2K	g156.t1	1425548	1428817	3269	5E-160	96.79	78	Solyc02g093680.2.1	Succinate dehydrogenase iron-sulfur protein IPR004489 Succinate dehydrogenase_fumarate reductase iron-sulphur protein	
2K	g157.t1	1429256	1432615	3359	0E+00	98.63	100	Solyc02g092750.2.1	Phosphatase 2C family protein IPR015655 Protein phosphatase 2C	
2K	g158.t1	1433766	1435431	1665	0E+00	98.91	100	Solyc02g092760.2.1	Hydrolase_alpha_beta fold family protein expressed IPR000073 Alpha_beta hydrolase fold-1	
2K	g159.t1	1437226	1439135	1909	0E+00	98.9	100	Solyc02g092770.2.1	Hydrolase_alpha_beta fold family protein expressed IPR000073 Alpha_beta hydrolase fold-1	
2K	g160.t1	1447226	1464801	17575	0E+00	88.41	100	Solyc02g092780.1.1	TPR repeat protein IPR011990 Tetatricopeptide-like helical	
2K	g161.t1	1465115	1467957	2842	0E+00	52.22	88	Solyc04g078170.1.1	Tetatricopeptide repeat-containing protein IPR011990 Tetatricopeptide-like helical	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
2L	g2.t1	2958	7047	4089	0E+00	99.8	96	Solyc02g092800.2.1	Manganese transport protein mntH IPR001046	Natural resistance-associated macrophage protein
2L	g3.t1	14278	17897	3619	1E-124	99.43	100	Solyc02g092810.2.1	RNA-binding protein MEX3C IPR001841	Zinc finger, RING-type
2L	g4.t1	34984	37307	2323	0E+00	99.5	100	Solyc02g092820.2.1	Indole-3-acetic acid-amido synthetase GH3.8 IPR004993	GH3 auxin-responsive promoter
2L	g6.t1	57530	59187	1657	1E-43	93.55	72	Solyc02g092830.2.1		Unknown Protein
2L	g7.t1	65096	68206	3110	0E+00	99.42	100	Solyc02g092840.1.1	Galactosyltransferase-like protein (Fragment) IPR004263	Exostosin-like
2L	g8.t1	69216	70604	1388	2E-50	64.03	69	Solyc02g092860.2.1		Cytochrome P450
2L	g8.t2	69216	70534	1318	4E-50	64.03	68	Solyc02g092860.2.1		Cytochrome P450
2L	g9.t1	71053	72747	1694	7E-82	71.5	92	Solyc03g117010.2.1		Sister chromatid cohesion protein PDS5 homolog B
2L	g9.t2	71053	72747	1694	3E-80	67.98	92	Solyc03g117010.2.1		Sister chromatid cohesion protein PDS5 homolog B
2L	g10.t1	79526	81433	1907	0E+00	97.6	100	Solyc02g092860.2.1		Cytochrome P450
2L	g11.t1	81670	87847	6177	0E+00	99.03	100	Solyc02g092870.1.1		Os12g0236050 protein (Fragment)
2L	g12.t1	88569	91057	2488	3E-124	97.69	100	Solyc02g092880.2.1		Unknown Protein
2L	g13.t1	100456	121486	21030	0E+00	98.55	67	Solyc02g092920.2.1		Cadmium-transporting ATPase-translocating
2L	g13.t2	100456	121486	21030	0E+00	98.55	66	Solyc02g092920.2.1		Cadmium-transporting ATPase-translocating
2L	g14.t1	122519	123827	1308	0E+00	96.96	97	Solyc02g092930.1.1		MYB transcription factor IPR015495 Myb transcription factor
2L	g15.t1	155936	159194	3258	0E+00	98.17	100	Solyc02g092940.2.1		Receptor like kinase, RLK
2L	g16.t1	161296	164587	3291	0E+00	84.98	100	Solyc02g092950.2.1		Microtubule plus-end binding protein IPR001715 Calponin-like actin-binding
2L	g16.t2	161296	164587	3291	0E+00	84.38	100	Solyc02g092950.2.1		Microtubule plus-end binding protein IPR001715 Calponin-like actin-binding
2L	g17.t1	165156	165764	608	9E-34	84	85	Solyc02g092960.1.1		Unknown Protein
2L	g18.t1	166126	167704	1578	5E-125	98.27	99	Solyc02g092970.2.1		ADP ribosylation factor IPR006688 ADP-ribosylation factor
2L	g19.t1	170835	172647	1812	0E+00	99.44	100	Solyc02g092980.2.1		Cyclin D-like protein IPR006671 Cyclin, N-terminal
2L	g20.t1	188351	190255	1904	0E+00	97.82	100	Solyc02g092990.1.1		SCF E3 ubiquitin ligase complex F-box protein grrA IPR001810 Cyclin-like F-box
2L	g21.t1	192993	198772	5779	0E+00	93.38	74	Solyc02g093000.2.1		Phosphatase and tensin-like A IPR014020 Tensin phosphatase, C2 domain
2L	g22.t1	201181	203556	2375	5E-85	100	94	Solyc02g093010.2.1		RER1 protein IPR004932 Retrieval of early ER protein Rer1
2L	g24.t1	210641	213678	3037	3E-10	49.02	17	Solyc07g032350.1.1		Unknown Protein
2L	g25.t1	215424	217792	2368	0E+00	99.45	100	Solyc02g093020.2.1		Os06g0524700 protein (Fragment) IPR004158 Protein of unknown function DUF247, plant
2L	g26.t1	219762	226772	7010	6E-85	100	45	Solyc02g093030.2.1		Peptidyl-tRNA hydrolase family protein IPR001328 Peptidyl-tRNA hydrolase
2L	g27.t1	228969	230622	1653	0E+00	97.52	100	Solyc02g093040.2.1		Cathepsin B-like cysteine proteinase IPR013128 Peptidase C1A, papain
2L	g28.t1	238431	246558	8127	0E+00	96.93	100	Solyc02g093050.2.1		WRKY transcription factor 26 IPR003657 DNA-binding WRKY
2L	g29.t1	250331	253429	3098	0E+00	98.49	100	Solyc02g093060.2.1		tRNA-dihydrouridine synthase 1-like protein IPR001269 tRNA-dihydrouridine synthase
2L	g30.t1	253547	263102	9555	0E+00	86.5	56	Solyc02g093080.2.1		1-aminocyclopropane-1-carboxylate oxidase IPR005123 Oxoglutarate and iron-dependent oxygenase
2L	g31.t1	263905	264832	927	7E-168	100	100	Solyc02g093090.1.1		Expressed protein (Fragment) IPR006514 Protein of unknown function DUF579, plant
2L	g32.t1	270041	273251	3210	0E+00	98.05	100	Solyc02g093100.2.1		Receptor like kinase, RLK
2L	g33.t1	274358	276022	1664	3E-78	99.09	74	Solyc02g093110.2.1		Ubiquitin-conjugating enzyme E2 I IPR000608 Ubiquitin-conjugating enzyme, E2
2L	g33.t2	274358	279622	5264	1E-118	100	100	Solyc02g093110.2.1		Ubiquitin-conjugating enzyme E2 I IPR000608 Ubiquitin-conjugating enzyme, E2
2L	g35.t1	304615	315412	10797	4E-124	71.85	82	Solyc02g093140.2.1		CBS domain-containing protein-like IPR000644 Cystathionine beta-synthase, core
2L	g35.t2	304615	315412	10797	7E-127	71.17	85	Solyc02g093140.2.1		CBS domain-containing protein-like IPR000644 Cystathionine beta-synthase, core
2L	g36.t1	326071	329997	3926	0E+00	99.33	87	Solyc02g093150.2.1		AP2-like ethylene-responsive transcription factor At1g16060 IPR001471 Pathogenesis-related transcriptional factor and ERF, DNA-binding
2L	g37.t1	341011	348675	7664	0E+00	98.2	100	Solyc02g093160.2.1		Filament-like plant protein (Fragment) IPR008587 Protein of unknown function DUF869, plant
2L	g38.t1	348769	352232	3463	0E+00	99.42	97	Solyc02g093170.2.1		Cyclin delta-3
2L	g40.t1	373959	375629	1670	0E+00	95.75	99	Solyc02g093180.2.1		N-hydroxycinnamoyl_benzoyltransferase 3 IPR003480 Transferase
2L	g41.t1	382268	410213	27945	0E+00	80.05	24	Solyc02g093200.2.1		Histone-lysine N-methyltransferase MEDEA IPR001214 SET
2L	g42.t1	414718	418516	3798	0E+00	98.59	100	Solyc02g093210.2.1		MAPprotein kinase-like protein IPR017946 PLC-like phosphodiesterase, TIM beta_alpha-barrel domain
2L	g43.t1	418936	421919	2983	2E-166	99.56	100	Solyc02g093220.2.1		F-box_LRR-repeat protein 2 IPR006553 Leucine-rich repeat, cysteine-containing subtype
2L	g43.t2	418936	421919	2983	3E-166	99.56	98	Solyc02g093220.2.1		F-box_LRR-repeat protein 2 IPR006553 Leucine-rich repeat, cysteine-containing subtype

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2L	g44.t1	424714	426059	1345	1E-180	99.59	100	Solyc02g093250.2.1	Caffeoyl-CoA O-methyltransferase IPR002935	O-methyltransferase, family 3
2L	g45.t1	428289	429609	1320	0E+00	100	100	Solyc02g093270.2.1	Caffeoyl-CoA O-methyltransferase IPR002935	O-methyltransferase, family 3
2L	g46.t1	439748	442409	2661	0E+00	91.8	97	Solyc02g093280.2.1	Transcription factor EB IPR011598	Helix-loop-helix DNA-binding
2L	g47.t1	444588	452840	8252	0E+00	99.82	100	Solyc02g093290.2.1	Nicotinate phosphoribosyltransferase-like protein IPR006405	Nicotinate phosphoribosyltransferase putative
2L	g48.t1	452919	465749	12830	0E+00	91.42	100	Solyc02g093300.2.1	DNA polymerase IPR004578	DNA-directed DNA polymerase, family B, pol2
2L	g49.t1	467465	476519	9054	0E+00	99.51	69	Solyc02g093310.2.1	MAP-like protein kinase IPR017946	PLC-like phosphodiesterase, TIM beta_alpha-barrel domain
2L	g50.t1	479808	486864	7056	0E+00	94.56	69	Solyc02g093330.2.1	Nup98 (Fragment) IPR007230	Peptidase S59, nucleoporin
2L	g51.t1	488758	492226	3468	0E+00	98.98	100	Solyc02g093340.2.1	Heterogeneous nuclear ribonucleoprotein A3 IPR012677	Nucleotide-binding, alpha-beta plait
2L	g52.t2	502618	509984	7366	0E+00	99.19	64	Solyc02g093360.2.1	Ribosomal protein S6 kinase alpha-3 IPR002290	Serine_threonine protein kinase
2L	g52.t1	506388	509984	3596	0E+00	99.38	84	Solyc02g093370.2.1	Sucrose cleavage protein-like IPR009737	Sucraseferredoxin-like
2L	g53.t1	510238	512209	1971	0E+00	98.93	100	Solyc02g093380.1.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
2L	g54.t1	512528	518649	6121	0E+00	97.36	30	Solyc06g075420.1.1	Genomic DNA chromosome 5 BAC clone F15L12	
2L	g54.t2	512528	520939	8411	0E+00	97.36	23	Solyc06g075420.1.1	Genomic DNA chromosome 5 BAC clone F15L12	
2L	g55.t1	521988	525076	3088	0E+00	97.82	100	Solyc02g093390.2.1	Ribosomal RNA-processing protein IPR007823	Methyltransferase-related
2L	g56.t3	525355	532139	6784	0E+00	78.59	99	Solyc02g093400.1.1	Integral membrane protein MvIN IPR004268	Flagellin assembly, membrane protein MvIN
2L	g56.t2	525426	529819	4393	0E+00	80.18	99	Solyc02g093400.1.1	Integral membrane protein MvIN IPR004268	Flagellin assembly, membrane protein MvIN
2L	g56.t1	530224	532139	1915	2E-123	93.14	91	Solyc02g093400.1.1	Integral membrane protein MvIN IPR004268	Flagellin assembly, membrane protein MvIN
2L	g57.t1	536008	547767	11759	0E+00	98.73	52	Solyc02g093420.2.1	NAC domain class transcription factor protein	
2L	g58.t1	549057	552219	3162	0E+00	99.72	100	Solyc02g093430.2.1	Glycosyl transferase family 17 protein IPR006813	Glycosyl transferase, family 17
2L	g59.t1	570233	571519	1286	2E-90	92.65	100	Solyc02g093600.2.1	class I heat shock protein IPR008978	HSP20-like chaperone
2L	g60.t1	572226	575839	3613	0E+00	98.12	100	Solyc02g093590.2.1	CONSTANS-like zinc finger protein IPR010402	CCT domain
2L	g60.t2	572226	575839	3613	3E-165	76.56	100	Solyc02g093590.2.1	CONSTANS-like zinc finger protein IPR010402	CCT domain
2L	g61.t1	581508	585968	4460	0E+00	98.25	70	Solyc02g093580.2.1	Pectate lyase IPR002022	Pectate lyase_Amb allergen
2L	g62.t1	592890	593779	889	5E-96	97.16	100	Solyc02g093560.1.1	Unknown Protein IPR013177	Protein of unknown function DUF1713, mitochondria
2L	g63.t1	594357	595809	1452	4E-168	96.54	100	Solyc02g093550.2.1	Methyltransferase type 11 IPR013216	Methyltransferase type 11
2L	g64.t1	601548	609658	8110	0E+00	96.51	63	Solyc02g093540.2.1	Cytochrome P450	
2L	g66.t1	614057	618399	4342	0E+00	98.37	100	Solyc02g093520.2.1	Copine-like protein IPR010734	Copine
2L	g67.t1	623180	626119	2939	0E+00	98.48	100	Solyc02g093510.2.1	cDNA clone J023001A15 full insert sequence IPR008833	Surfeit locus 2
2L	g68.t1	628662	630789	2127	1E-96	61.22	100	Solyc12g040520.1.1	Katanin p60 ATPase-containing subunit IPR003959	ATPase, AAA-type, core
2L	g69.t1	631958	633765	1807	0E+00	79.77	86	Solyc02g093500.2.1	GDSL esterase_lipase At5g14450 IPR001087	Lipase, GDSL
2L	g70.t1	633832	639169	5337	0E+00	100	100	Solyc02g093490.2.1	SAGA-associated factor 29 homolog IPR010750	Protein of unknown function DUF1325
2L	g71.t2	641468	652833	11365	0E+00	100	49	Solyc02g093470.2.1	Lysine ketoglutarate reductase trans-splicing related 1 IPR007877	Protein of unknown function DUF707
2L	g71.t3	641468	646372	4904	0E+00	85.75	94	Solyc02g093480.2.1	Lysine ketoglutarate reductase trans-splicing related 1 IPR007877	Protein of unknown function DUF707
2L	g71.t1	647608	652833	5225	0E+00	100	100	Solyc02g093470.2.1	Lysine ketoglutarate reductase trans-splicing related 1 IPR007877	Protein of unknown function DUF707
2L	g72.t1	652855	659209	6354	0E+00	98.14	100	Solyc02g093460.2.1	tRNA pseudouridine synthase B IPR020103	Pseudouridine synthase, catalytic domain
2L	g73.t1	664338	667177	2839	3E-78	97.44	41	Solyc02g093450.2.1	Genomic DNA chromosome 3 P1 clone MMJ24	
2L	g74.t1	667734	672279	4545	0E+00	98.87	100	Solyc02g093440.2.1	GHMP kinase family protein IPR014721	Ribosomal protein S5 domain 2-type fold
2L	g75.t1	674569	675649	1080	7E-70	71.24	100	Solyc02g093610.2.1	BCL-2 binding anthanogene-1 IPR000626	Ubiquitin
2L	g75.t2	674569	675649	1080	3E-107	96.08	100	Solyc02g093610.2.1	BCL-2 binding anthanogene-1 IPR000626	Ubiquitin
2L	g76.t1	678018	685902	7884	0E+00	98.11	100	Solyc02g093620.1.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
2L	g77.t1	688958	693073	4115	0E+00	99.15	100	Solyc02g093630.2.1	Uncharacterized membrane protein At3g27390	
2L	g78.t1	693326	695759	2433	0E+00	99.06	100	Solyc02g093640.2.1	3-ketoacyl-CoA reductase 1 IPR002347	Glucose_ribitol dehydrogenase
2L	g79.t1	696758	698024	1266	2E-99	99.26	99	Solyc02g093650.2.1	Early nodulin-55-1 (Fragment) IPR003245	Plastocyanin-like
2L	g80.t1	698049	699819	1770	0E+00	98.18	100	Solyc02g093660.1.1	Unknown Protein	
2L	g81.t1	701938	703493	1555	3E-44	100	73	Solyc02g093670.2.1	Nitrate-induced NOLprotein IPR008700	Defence response, Rin4

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2L	g82.t1	705118	708329	3211	0E+00	100	100	Solyc02g093680.2.1	Succinate dehydrogenase iron-sulfur protein IPR004489 Succinate dehydrogenase_fumarate reductase iron-sulphur protein	
2L	g83.t1	709665	713529	3864	0E+00	98.53	100	Solyc02g093690.2.1	ATP12 ATPase IPR011419 ATP12, ATPase F1F0-assembly protein	
2L	g84.t1	721373	723025	1652	0E+00	97.32	97	Solyc02g093700.2.1	Cystine transporter Cystinosin IPR005282 Lysosomal cystine transporter	
2L	g85.t1	727183	728102	919	2E-139	98.43	100	Solyc02g093710.1.1	Genomic DNA chromosome 3 TAC clone K1G2	
2L	g86.t1	728423	736174	7751	0E+00	95.3	85	Solyc02g093720.2.1	Os02g0200800 protein (Fragment) IPR009675 Targeting for Xklp2	
2L	g87.t1	737819	739174	1355	0E+00	99.2	100	Solyc02g093740.2.1	MYB transcription factor IPR015495 Myb transcription factor	
2L	g88.t1	741709	744054	2345	2E-28	34.95	51	Solyc04g025900.1.1	Unknown Protein	
2L	g89.t1	747813	752244	4431	0E+00	98.13	100	Solyc02g093750.2.1	Ring zinc finger protein (Fragment) IPR008166 Protein of unknown function DUF23	
2L	g90.t1	752633	754784	2151	0E+00	96.03	100	Solyc02g093760.2.1	Tripartite motif-containing 25 IPR018957 Zinc finger, C3HC4 RING-type	
2L	g91.t1	755135	767984	12849	0E+00	94.82	100	Solyc02g093770.2.1	GPI inositol-deacylase IPR012908 PGAP1-like	
2L	g92.t1	768693	773163	4470	6E-107	88.36	32	Solyc02g093780.1.1	Unknown Protein	
2L	g93.t1	775519	786654	11135	0E+00	98.62	48	Solyc02g093800.2.1	Serine_threonine-protein phosphatase 2A regulatory subunit delta 1 isoform IPR002554 Protein phosphatase 2A, regulatory B subunit, B56	
2L	g93.t2	775519	786654	11135	0E+00	98.54	46	Solyc02g093800.2.1	Serine_threonine-protein phosphatase 2A regulatory subunit delta 1 isoform IPR002554 Protein phosphatase 2A, regulatory B subunit, B56	
2L	g94.t1	787425	792654	5229	0E+00	98.74	97	Solyc02g093810.2.1	Genomic DNA chromosome 5 P1 clone MNF13	
2L	g95.t1	795783	801063	5280	7E-179	98.01	100	Solyc02g093820.2.1	UBX domain-containing protein IPR001012 UBX	
2L	g96.t1	801463	808480	7017	0E+00	99.8	100	Solyc02g093830.2.1	Glucose-6-phosphate 1-dehydrogenase IPR001282 Glucose-6-phosphate dehydrogenase	
2L	g97.t1	809833	815616	5783	0E+00	94.85	81	Solyc02g093840.2.1	F-box family protein IPR001810 Cyclin-like F-box	
2L	g98.t1	817683	823183	5500	0E+00	98.2	100	Solyc02g093850.2.1	Ankyrin repeat domain-containing protein 50 IPR002110 Ankyrin	
2L	g99.t1	829493	840731	11238	0E+00	99.28	67	Solyc02g093870.2.1	Histidine amino acid transporter IPR013057 Amino acid transporter, transmembrane	
2L	g99.t2	829493	840731	11238	0E+00	96.54	66	Solyc02g093870.2.1	Histidine amino acid transporter IPR013057 Amino acid transporter, transmembrane	
2L	g100.t1	841372	845944	4572	0E+00	98.35	100	Solyc02g093880.2.1	DNA-binding bromodomain-containing protein IPR001487 Bromodomain	
2L	g101.t2	862024	870604	8580	0E+00	97.09	51	Solyc02g093890.1.1	Unknown Protein	
2L	g101.t1	866920	870604	3684	0E+00	100	100	Solyc02g093900.2.1	Cytochrome c1 IPR002326 Cytochrome c1	
2L	g102.t1	872173	875058	2885	0E+00	98.56	100	Solyc02g093910.2.1	Kelch repeat-containing protein-like IPR015915 Kelch-type beta propeller	
2L	g103.t1	875402	880144	4742	0E+00	98.83	100	Solyc02g093920.2.1	COP9 signalosome complex subunit 3 IPR000717 Proteasome component region PCI	
2L	g104.t1	880678	891874	11196	0E+00	91.36	55	Solyc02g093930.2.1	Double-strand-break repair protein rad21 IPR006910 Rad21_Rec8 like protein, N-terminal	
2L	g105.t1	892690	903114	10424	0E+00	98.41	99	Solyc02g093950.2.1	Ankyrin repeat family protein IPR002110 Ankyrin	
2L	g106.t1	905047	907489	2442	0E+00	99.51	100	Solyc02g093960.2.1	Genomic DNA chromosome 5 P1 clone MAC12	
2L	g107.t1	924008	928317	4309	0E+00	98.44	100	Solyc02g093970.2.1	Receptor like kinase, RLK	
2L	g108.t1	930098	937222	7124	0E+00	97.53	100	Solyc02g093980.2.1	Os12g0236050 protein (Fragment)	
2L	g109.t1	937368	942309	4941	0E+00	95.75	100	Solyc02g093990.2.1	Adenylate kinase family-like protein IPR000850 Adenylate kinase	
2L	g109.t2	937368	942309	4941	1E-172	91.89	100	Solyc02g093990.2.1	Adenylate kinase family-like protein IPR000850 Adenylate kinase	
2L	g110.t1	943588	944351	763	2E-98	98.58	100	Solyc02g094000.1.1	Calmodulin-like protein IPR011992 EF-Hand type	
2L	g111.t1	944385	946789	2404	0E+00	98.21	100	Solyc02g094010.1.1	Receptor-like protein kinase IPR002290 Serine_threonine protein kinase	
2L	g112.t1	957628	960377	2749	2E-166	96.62	100	Solyc02g094030.2.1	Unknown Protein	
2L	g113.t1	962008	965333	3325	0E+00	97.23	100	Solyc02g094040.2.1	Lipase IPR006693 AB-hydrolase associated lipase region	
2L	g114.t1	965618	966570	952	3E-120	97.06	100	Solyc02g094050.2.1	Blue copper protein IPR003245 Plastocyanin-like	
2L	g115.t2	966613	1000359	33746	0E+00	92.76	41	Solyc02g094090.2.1	Vacuolar protein sorting 52 IPR007258 Vps52_Sac2	
2L	g115.t1	966613	969859	3246	0E+00	93.49	99	Solyc02g094060.2.1	Voltage-gated chloride channel IPR002251 Chloride channel plant CLC	
2L	g115.t3	979799	1000459	20660	0E+00	91.74	87	Solyc02g094090.2.1	Vacuolar protein sorting 52 IPR007258 Vps52_Sac2	
2L	g116.t1	1001928	1009477	7549	0E+00	98.77	100	Solyc02g094100.2.1	Katanin p60 ATPase-containing subunit IPR003959 ATPase, AAA-type, core	
2L	g117.t1	1012861	1014669	1808	0E+00	97.08	100	Solyc02g094110.1.1	Cytochrome P450	
2L	g118.t1	1018121	1025539	7418	0E+00	96.53	94	Solyc02g094120.2.1	Sulfite oxidase IPR000572 Oxidoreductase, molybdopterin binding	
2L	g119.t1	1027258	1028881	1623	4E-115	37.53	96	Solyc12g096510.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
2L	g120.t1	1029408	1031739	2331	0E+00	98.47	88	Solyc02g094130.2.1	Genomic DNA chromosome 5 P1 clone MJC20 IPR013089 Kelch related	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
2L	g121.i2	1032318	1040232	7914	4E-105	99.32	97	Solyc02g094140.2.1	Mitochondrial import receptor subunit TOM20 IPR010547	Plant specific mitochondrial import receptor subunit TOM20
2L	g121.i3	1032318	1044930	12612	0E+00	86.67	73	Solyc02g094150.2.1	Sua5_YciO_YrdC_YwIC family protein IPR004388	Sua5_YciO_YrdC_YwIC
2L	g121.t1	1040748	1044930	4182	0E+00	86.67	100	Solyc02g094150.2.1	Sua5_YciO_YrdC_YwIC family protein IPR004388	Sua5_YciO_YrdC_YwIC
2L	g122.t1	1045728	1046980	1252	0E+00	99.7	100	Solyc02g094160.1.1	Ribonucleoside-diphosphate reductase small chain IPR000358	Ribonucleotide reductase
2L	g123.t1	1047481	1051329	3848	0E+00	98.43	100	Solyc02g094170.2.1	Zinc finger protein 511 IPR015880	Zinc finger, C2H2-like
2L	g124.t1	1052828	1054695	1867	0E+00	100	100	Solyc02g094180.2.1	Peroxidase 1 IPR002016	Haem peroxidase, plant_fungal_bacterial
2L	g125.t1	1054976	1060989	6013	0E+00	99.13	97	Solyc02g094190.2.1	Nodulin family protein IPR010658	Nodulin-like
2L	g125.i2	1054976	1060989	6013	0E+00	99.28	97	Solyc02g094190.2.1	Nodulin family protein IPR010658	Nodulin-like
2L	g126.t1	1073688	1079815	6127	3E-68	99	60	Solyc02g094200.2.1	Nuclear transport factor 2 IPR018222	Nuclear transport factor 2, Eukaryote
2L	g127.t1	1097025	1097607	582	3E-80	94.57	100	Solyc02g094230.1.1	Unknown Protein	
2L	g128.t1	1100763	1101487	724	9E-73	91.2	100	Solyc02g094240.1.1	Unknown Protein	
2L	g129.t1	1106656	1109340	2684	2E-29	68.67	58	Solyc02g094250.2.1	Unknown Protein	
2L	g130.t1	1111026	1112657	1631	0E+00	98.27	100	Solyc02g094260.1.1	Protein SMG9	
2L	g131.t1	1115152	1117807	2655	5E-85	99.15	99	Solyc02g094270.1.1	WRKY transcription factor IPR003657	DNA-binding WRKY
2L	g132.t1	1124356	1132584	8228	0E+00	97.63	100	Solyc02g094280.2.1	Oligopeptide transporter (Fragment) IPR004813	Oligopeptide transporter OPT superfamily
2L	g132.i2	1124356	1127467	3111	0E+00	95.31	99	Solyc02g094280.2.1	Oligopeptide transporter (Fragment) IPR004813	Oligopeptide transporter OPT superfamily
2L	g133.t1	1132646	1134725	2079	4E-62	93	46	Solyc02g094290.1.1	TCP family transcription factor IPR005333	Transcription factor, TCP
2L	g134.t1	1136856	1139815	2959	0E+00	98.53	77	Solyc02g094300.2.1	Uridyltransferase PII IPR002912	Amino acid-binding ACT
2L	g135.t1	1142206	1149088	6882	0E+00	97.84	81	Solyc02g094310.1.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
2L	g137.t1	1150516	1153209	2693	2E-111	84.34	84	Solyc02g094320.2.1	Actin IPR004000	Actin_actin-like
2L	g137.i2	1150516	1153701	3185	2E-127	85.59	93	Solyc02g094320.2.1	Actin IPR004000	Actin_actin-like

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g1.t1	1	5587	5586	0E+00	93.52	97	Solyc04g014570.2.1	Transmembrane 9 superfamily protein member 1	
4DE	g2.l2	24456	27759	3303	1E-69	90.52	83	Solyc04g014600.2.1	Universal stress protein family protein IPR006016 UspA	
4DE	g2.t1	26026	27759	1733	4E-114	99.38	100	Solyc04g014600.2.1	Universal stress protein family protein IPR006016 UspA	
4DE	g3.t1	28001	31007	3006	6E-123	85.58	100	Solyc04g014610.2.1	Armadillo repeat-containing protein 7 IPR011989 Armadillo-like helical	
4DE	g4.t1	58848	63477	4629	1E-47	51.55	54	Solyc03g078540.1.1	Serine_threonine-protein phosphatase 7 long form homolog IPR019557 Aminotransferase-like, plant mobile domain	
4DE	g5.t1	67506	77320	9814	0E+00	71.81	72	Solyc04g015980.2.1	Receptor like kinase, RLK	
4DE	g5.l2	67506	77320	9814	0E+00	71.81	72	Solyc04g015980.2.1	Receptor like kinase, RLK	
4DE	g6.t1	79866	83155	3289	0E+00	99.6	100	Solyc04g014670.2.1	Short-chain dehydrogenase_reductase SDR IPR002347 Glucose_ribitol dehydrogenase	
4DE	g7.t1	83700	89307	5607	0E+00	99.31	100	Solyc04g014680.2.1	Cysteine-type endopeptidase_ubiquitin thiolesterase	
4DE	g8.t1	99716	103220	3504	0E+00	100	100	Solyc04g014690.2.1	Protein kinase IPR002290 Serine_threonine protein kinase	
4DE	g9.t1	112244	123367	11123	6E-101	84.83	38	Solyc04g014710.2.1	cDNA clone 002-156-B04 full insert sequence	
4DE	g10.l2	128836	143569	14733	0E+00	91.67	49	Solyc04g014730.2.1	Fumarylacetoacetase IPR005959 Fumarylacetoacetase	
4DE	g10.t1	131726	141119	9393	0E+00	91.67	87	Solyc04g014730.2.1	Fumarylacetoacetase IPR005959 Fumarylacetoacetase	
4DE	g11.t1	147990	153337	5347	2E-179	99.18	100	Solyc04g014760.2.1	RHO protein GDP dissociation inhibitor IPR000406 RHO protein GDP dissociation inhibitor	
4DE	g12.t1	155856	156352	496	4E-39	96.97	100	Solyc04g014770.1.1	Unknown Protein	
4DE	g13.t1	168522	170118	1596	1E-19	90.91	22	Solyc04g014780.1.1	Cysteine proteinase inhibitor IPR014756 Immunoglobulin E-set	
4DE	g15.t1	180792	181451	659	3E-76	90.24	100	Solyc04g014780.1.1	Cysteine proteinase inhibitor IPR014756 Immunoglobulin E-set	
4DE	g16.t1	182362	193753	11391	0E+00	99.25	67	Solyc04g014800.2.1	L-galactose-1-phosphate phosphatase 2	
4DE	g17.t1	202162	204568	2406	0E+00	99.11	100	Solyc04g014810.2.1	U-box domain-containing protein 4 IPR011989 Armadillo-like helical	
4DE	g18.t1	206630	214803	8173	8E-179	68.13	85	Solyc11g012470.1.1	Heterogeneous nuclear ribonucleoprotein A3 IPR000504 RNA recognition motif, RNP-1	
4DE	g19.t1	215711	219373	3662	0E+00	96.75	100	Solyc04g014830.1.1	GRAS family transcription factor IPR005202 GRAS transcription factor	
4DE	g20.t1	241172	245903	4731	0E+00	98.18	100	Solyc04g014850.2.1	Unknown Protein	
4DE	g22.t1	266862	271915	5053	0E+00	98.49	98	Solyc04g014870.2.1	RNA-dependent RNA polymerase IPR007855 RNA-dependent RNA polymerase, eukaryotic-type	
4DE	g23.t1	283273	287343	4070	0E+00	82.86	100	Solyc04g015980.2.1	Receptor like kinase, RLK	
4DE	g23.l2	283273	287343	4070	0E+00	82.58	100	Solyc04g015980.2.1	Receptor like kinase, RLK	
4DE	g24.t1	295570	302363	6793	6E-41	30.57	55	Solyc03g062840.1.1	Unknown Protein	
4DE	g25.t1	303544	307613	4069	0E+00	83.52	98	Solyc04g015980.2.1	Receptor like kinase, RLK	
4DE	g25.l2	303544	307613	4069	0E+00	83.52	99	Solyc04g015980.2.1	Receptor like kinase, RLK	
4DE	g26.t1	311239	313793	2554	9E-137	83.33	95	Solyc04g014900.2.1	Receptor like kinase, RLK	
4DE	g27.t1	320172	325148	4976	0E+00	98.97	99	Solyc04g015010.2.1	microtubule associated protein Type 5 IPR009768 Myosin II heavy chain-like	
4DE	g27.l2	320172	324332	4160	0E+00	98.97	100	Solyc04g015010.2.1	microtubule associated protein Type 5 IPR009768 Myosin II heavy chain-like	
4DE	g28.t1	327125	328223	1098	1E-99	86.86	100	Solyc04g015020.2.1	Proline-rich protein IPR006121 Heavy metal transport_detoxification protein	
4DE	g29.t1	336507	341654	5147	1E-177	95.26	100	Solyc04g015030.2.1	Metal ion binding protein IPR006121 Heavy metal transport_detoxification protein	
4DE	g30.t1	342230	344828	2598	7E-85	99.21	99	Solyc04g015040.2.1	Peptidyl-prolyl cis-trans isomerase IPR001179 Peptidyl-prolyl cis-trans isomerase, FKBP-type	
4DE	g31.t1	346671	347418	747	1E-76	99.1	99	Solyc04g015040.2.1	Peptidyl-prolyl cis-trans isomerase IPR001179 Peptidyl-prolyl cis-trans isomerase, FKBP-type	
4DE	g32.t1	349937	355615	5678	1E-115	86.6	100	Solyc04g015050.2.1	Trafficking protein particle complex subunit 5 IPR016696 TRAPP I complex, Trs31	
4DE	g33.t1	358747	361945	3198	0E+00	100	100	Solyc04g015060.1.1	Nuclear transcription factor Y subunit B-6 IPR003957 Transcription factor, CBFA_NFYB, DNA topoisomerase	
4DE	g34.t1	363087	366054	2967	1E-121	100	100	Solyc04g015070.2.1	C2 domain containing protein IPR018029 C2 membrane targeting protein	
4DE	g36.t1	368457	370518	2061	2E-70	97.14	56	Solyc04g015080.2.1	Alkylated DNA repair protein	
4DE	g37.t1	370660	371548	888	7E-155	97.26	99	Solyc04g015090.1.1	DnaJ-like protein IPR015609 Molecular chaperone, heat shock protein, Hsp40, DnaJ	
4DE	g38.t1	376247	385913	9666	0E+00	99.04	61	Solyc04g015110.2.1	Myosin heavy chain-like protein (Fragment) IPR008545 Protein of unknown function DUF827, plant	
4DE	g38.l2	376247	385913	9666	0E+00	99.04	60	Solyc04g015110.2.1	Myosin heavy chain-like protein (Fragment) IPR008545 Protein of unknown function DUF827, plant	
4DE	g39.t1	389817	391914	2097	0E+00	97.8	100	Solyc04g015120.2.1	U-box domain containing protein expressed	
4DE	g40.t1	391981	402118	10137	0E+00	99.51	100	Solyc04g015130.2.1	Ribosomal protein S6 kinase alpha-3 IPR002290 Serine_threonine protein kinase	
4DE	g42.t1	411047	413297	2250	2E-169	82.81	48	Solyc03g062840.1.1	Unknown Protein	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g43.t1	425050	433318	8268	0E+00	95.77	83	Solyc04g015150.2.1	Phosphoglycolate phosphatase IPR006349	2-phosphoglycolate phosphatase, eukaryotic
4DE	g44.t1	438857	452739	13882	0E+00	99.5	69	Solyc04g015160.2.1	C2 domain-containing protein IPR018029	C2 membrane targeting protein
4DE	g46.t1	460177	473226	13049	9E-53	86.87	36	Solyc04g015180.2.1	DNA-directed RNA polymerase II polypeptide	
4DE	g48.t1	483647	485873	2226	1E-53	86.87	61	Solyc04g015180.2.1	DNA-directed RNA polymerase II polypeptide	
4DE	g49.t1	486502	488008	1506	0E+00	99.73	98	Solyc04g015190.2.1	Glucan endo-1 3-beta-glucosidase 5 IPR013781	Glycoside hydrolase, subgroup, catalytic core
4DE	g50.t1	488201	490668	2467	4E-74	100	68	Solyc04g015190.2.1	Glucan endo-1 3-beta-glucosidase 5 IPR013781	Glycoside hydrolase, subgroup, catalytic core
4DE	g51.t1	493526	497118	3592	0E+00	98.9	100	Solyc04g015200.2.1	6-phosphofructokinase 2 IPR012004	Pyrophosphate-dependent phosphofructokinase TP0108
4DE	g52.t1	507100	512348	5248	0E+00	82.11	97	Solyc04g015210.2.1	Cc-nbs-lrr, resistance protein	
4DE	g53.t1	525036	530386	5350	0E+00	85.15	88	Solyc04g015220.2.1	Nbs-lrr, resistance protein	
4DE	g58.t1	558106	568756	10650	3E-29	67.31	30	Solyc04g015220.2.1	Nbs-lrr, resistance protein	
4DE	g60.t1	610815	617526	6711	0E+00	99.41	100	Solyc04g015270.2.1	Glycosyltransferase IPR002495	Glycosyl transferase, family 8
4DE	g61.t1	623655	627637	3982	0E+00	98.31	100	Solyc04g015280.2.1	Zinc finger RING-type IPR018957	Zinc finger, C3HC4 RING-type
4DE	g62.t1	630865	635912	5047	0E+00	99.37	100	Solyc04g015290.2.1	Myb family transcription factor IPR006447	Myb-like DNA-binding region, SHAQKYF class
4DE	g63.t1	636598	647656	11058	0E+00	90.33	100	Solyc04g015300.2.1	Alpha_beta hydrolase IPR000073	Alpha_beta hydrolase fold-1
4DE	g64.t1	651495	659536	8041	0E+00	97.97	100	Solyc04g015330.2.1	Phosphohistidine phosphatase SixA IPR013078	Phosphoglycerate mutase
4DE	g64.t2	651495	659536	8041	9E-173	85.41	100	Solyc04g015330.2.1	Phosphohistidine phosphatase SixA IPR013078	Phosphoglycerate mutase
4DE	g65.t1	659960	665596	5636	0E+00	99.56	100	Solyc04g015340.2.1	Serine carboxypeptidase K10B2.2 IPR001563	Peptidase S10, serine carboxypeptidase
4DE	g67.t1	701707	715822	14115	0E+00	99.14	94	Solyc04g015350.2.1	Phosphatidylinositol 3-kinase IPR008290	Phosphatidylinositol 3-kinase, Vps34 type
4DE	g68.t1	717564	723058	5494	0E+00	98.21	98	Solyc04g015360.2.1	GATA transcription factor 9 IPR000679	Zinc finger, GATA-type
4DE	g69.t1	732843	738008	5165	1E-89	100	100	Solyc04g015370.2.1	Acyl carrier protein	
4DE	g70.t1	739582	742338	2756	0E+00	89.91	100	Solyc04g015380.1.1	Os06g0724200 protein (Fragment)	
4DE	g71.t1	751156	755778	4622	0E+00	96.3	100	Solyc04g015390.2.1	Os06g0724200 protein (Fragment)	
4DE	g72.t1	759113	763138	4025	0E+00	93.19	100	Solyc04g015400.2.1	Os06g0724200 protein (Fragment)	
4DE	g73.t1	768596	772818	4222	0E+00	99.02	100	Solyc04g015430.2.1	Os06g0724200 protein (Fragment)	
4DE	g74.t1	774767	779298	4531	0E+00	94.43	96	Solyc04g015440.2.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
4DE	g75.t1	780450	798138	17688	0E+00	94.43	63	Solyc04g015450.2.1	GTP-binding protein lepA IPR006297	GTP-binding protein LepA
4DE	g75.t2	780450	798138	17688	0E+00	91.84	65	Solyc04g015450.2.1	GTP-binding protein lepA IPR006297	GTP-binding protein LepA
4DE	g76.t1	803327	808350	5023	0E+00	96.93	100	Solyc04g015460.2.1	S-receptor kinase IPR002290	Serine_threonine protein kinase
4DE	g77.t1	809026	813608	4582	0E+00	99.2	100	Solyc04g015470.2.1	Phosphatidylinositol-4-phosphate 5-kinase family protein IPR017163	Phosphatidylinositol-4-phosphate 5-kinase, plant
4DE	g79.t1	819715	822228	2513	2E-73	96.26	63	Solyc05g042140.1.1	Unknown Protein IPR001878	Zinc finger, CCHC-type
4DE	g80.t1	824947	831831	6884	1E-162	76.27	100	Solyc04g015480.2.1	cDNA clone 006-204-H08 full insert sequence	
4DE	g81.t1	833557	849988	16431	0E+00	98.39	69	Solyc04g015490.2.1	Magnesium chelatase subunit D IPR011776	Magnesium chelatase, ATPase subunit D
4DE	g82.t2	853177	864666	11489	2E-134	95.85	28	Solyc04g015500.2.1	B3 domain-containing protein At3g18960 IPR003340	Transcriptional factor B3
4DE	g82.t1	853177	870467	17290	5E-132	95.83	22	Solyc04g015500.2.1	B3 domain-containing protein At3g18960 IPR003340	Transcriptional factor B3
4DE	g83.t1	875387	877570	2183	0E+00	94.59	100	Solyc04g015520.2.1	DNA binding protein IPR005516	Remorin, C-terminal region
4DE	g84.t2	889136	898989	9853	0E+00	84.35	94	Solyc04g015530.1.1	Polygalacturonase A IPR000408	Regulator of chromosome condensation, RCC1 IPR000743
4DE	g84.t1	889136	898989	9853	8E-177	82.11	94	Solyc04g015530.1.1	Polygalacturonase A IPR000408	Regulator of chromosome condensation, RCC1 IPR000743
4DE	g85.t1	914454	915307	853	2E-79	97.5	100	Solyc04g015540.1.1	Unknown Protein	
4DE	g86.t1	938366	947055	8689	0E+00	99.04	99	Solyc04g015560.2.1	Beta-D-glucosidase IPR001764	Glycoside hydrolase, family 3, N-terminal
4DE	g88.t1	955576	959343	3767	0E+00	98.2	100	Solyc04g015570.2.1	AN1-type zinc finger protein 2B IPR000058	Zinc finger, AN1-type
4DE	g89.t1	961236	975849	14613	0E+00	92.52	97	Solyc04g015580.2.1	Protein EFR3 homolog B	
4DE	g89.t2	961236	975849	14613	0E+00	94.42	97	Solyc04g015580.2.1	Protein EFR3 homolog B	
4DE	g90.t1	982596	985992	3396	3E-119	97.04	49	Solyc04g015590.2.1	Dihydroflavonol 4-reductase-binding domain	
4DE	g91.t1	987091	993227	6136	0E+00	98.1	100	Solyc04g015600.2.1	Receptor like kinase, RLK	
4DE	g92.t1	1029436	1031523	2087	0E+00	99.41	96	Solyc04g015610.2.1	Os01g0611000 protein (Fragment) IPR006946	Protein of unknown function DUF642

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g92.t2	1029436	1031523	2087	0E+00	99.41	95	Solyc04g015610.2.1	Os01g0611000 protein (Fragment) IPR006946	Protein of unknown function DUF642
4DE	g93.t1	1032586	1035708	3122	2E-137	99.49	40	Solyc04g015620.2.1	Os01g0611000 protein (Fragment) IPR006946	Protein of unknown function DUF642
4DE	g94.t1	1036017	1038027	2010	0E+00	75.32	99	Solyc04g015630.2.1	Nbs-lrr, resistance protein	
4DE	g94.t2	1036017	1038027	2010	0E+00	75.11	99	Solyc04g015630.2.1	Nbs-lrr, resistance protein	
4DE	g96.t1	1042596	1043557	961	2E-33	79.73	36	Solyc04g015640.1.1	Cc-nbs, resistance protein fragment	
4DE	g96.t2	1042596	1043557	961	4E-32	92.98	31	Solyc04g015640.1.1	Cc-nbs, resistance protein fragment	
4DE	g97.t1	1045364	1048937	3573	9E-63	37.93	56	Solyc04g039990.2.1	Cc-nbs, resistance protein fragment	
4DE	g97.t2	1045364	1048677	3313	6E-58	42.57	54	Solyc04g015630.2.1	Nbs-lrr, resistance protein	
4DE	g98.t1	1050641	1051707	1066	2E-22	73.21	40	Solyc11g012630.1.1	Unknown Protein IPR003656	Zinc finger, BED-type predicted
4DE	g100.t1	1057026	1061374	4348	3E-98	61.32	67	Solyc07g017370.1.1	Serine_threonine-protein phosphatase 7 long form homolog IPR019557	Aminotransferase-like, plant mobile domain
4DE	g102.t1	1067846	1089154	21308	0E+00	95.5	67	Solyc04g015680.2.1	Insulin degrading enzyme IPR011237	Peptidase M16, core
4DE	g102.t2	1067846	1089154	21308	0E+00	88.2	83	Solyc04g015680.2.1	Insulin degrading enzyme IPR011237	Peptidase M16, core
4DE	g103.t1	1090166	1106777	16611	0E+00	97.51	31	Solyc04g015690.2.1	Insulin degrading enzyme IPR011237	Peptidase M16, core
4DE	g104.t1	1109626	1116862	7236	0E+00	91.25	93	Solyc04g015690.2.1	Insulin degrading enzyme IPR011237	Peptidase M16, core
4DE	g104.t2	1109626	1116862	7236	0E+00	92.61	87	Solyc04g015690.2.1	Insulin degrading enzyme IPR011237	Peptidase M16, core
4DE	g105.t1	1118197	1118757	560	2E-60	98.84	100	Solyc04g015700.1.1	Unknown Protein	
4DE	g106.t1	1119856	1124717	4861	0E+00	96.59	100	Solyc04g015710.2.1	Os01g0530300 protein (Fragment) IPR015216	SANT associated
4DE	g107.t1	1125216	1128846	3630	0E+00	65.14	85	Solyc04g015720.1.1	Coiled-coil-containing protein (Fragment)	
4DE	g108.t1	1132665	1135077	2412	4E-164	93.49	100	Solyc04g015730.1.1	Unknown Protein	
4DE	g109.t1	1144096	1149393	5297	0E+00	92.32	71	Solyc04g015740.2.1	DUF288 containing protein	
4DE	g110.t1	1149943	1157657	7714	0E+00	98.36	100	Solyc04g015750.2.1	Magnesium chelatase H subunit IPR011771	Magnesium-chelatase, subunit H
4DE	g111.t1	1160751	1167327	6576	1E-116	91.26	79	Solyc04g015760.2.1	Protein N-terminal glutamine amidohydrolase IPR019161	Protein of unknown function WDYHV
4DE	g113.t1	1183297	1184237	940	6E-97	94.74	95	Solyc04g015780.1.1	Unknown Protein	
4DE	g114.t1	1189627	1190327	700	1E-71	91.23	100	Solyc04g015790.1.1	Unknown Protein	
4DE	g115.t3	1201158	1206347	5189	1E-114	67.45	59	Solyc10g049210.1.1	Serine carboxypeptidase 1 IPR001563	Peptidase S10, serine carboxypeptidase
4DE	g115.t2	1201270	1203037	1767	8E-68	72.99	100	Solyc10g049210.1.1	Serine carboxypeptidase 1 IPR001563	Peptidase S10, serine carboxypeptidase
4DE	g115.t1	1203686	1206347	2661	1E-77	66.29	68	Solyc10g049210.1.1	Serine carboxypeptidase 1 IPR001563	Peptidase S10, serine carboxypeptidase
4DE	g116.t1	1209133	1210317	1184	0E+00	87.61	99	Solyc04g015800.1.1	Unknown Protein	
4DE	g117.t1	1272796	1284550	11754	0E+00	99.14	91	Solyc04g015830.2.1	Actin-binding protein gelsolin IPR007122	Gelsolin
4DE	g118.t1	1299371	1301367	1996	0E+00	96.91	69	Solyc04g015850.2.1	Unknown Protein	
4DE	g119.t1	1351236	1358735	7499	2E-80	85.07	52	Solyc03g096470.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g120.t1	1359211	1360327	1116	6E-64	86.79	77	Solyc04g015880.1.1	Unknown Protein IPR007527	Zinc finger, SWIM-type
4DE	g121.t1	1378396	1382275	3879	1E-89	71.35	58	Solyc10g050120.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g124.t1	1399186	1404479	5293	2E-160	56.06	99	Solyc01g011130.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g127.t1	1424666	1430631	5965	1E-127	61.56	97	Solyc03g046220.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g131.t2	1486616	1510503	23887	0E+00	88.24	25	Solyc04g015940.2.1	Ribosomal RNA-processing protein IPR016024	Armadillo-type fold
4DE	g131.t1	1486676	1510503	23827	0E+00	88.24	26	Solyc04g015940.2.1	Ribosomal RNA-processing protein IPR016024	Armadillo-type fold
4DE	g132.t1	1511316	1521032	9716	0E+00	92.12	100	Solyc04g015950.1.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
4DE	g132.t2	1511316	1521892	10576	0E+00	91.49	98	Solyc04g015950.1.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
4DE	g133.t1	1527886	1562231	34345	0E+00	94.53	88	Solyc04g015970.2.1	ATP-binding cassette 1 IPR003439	ABC transporter-like
4DE	g133.t2	1534816	1562231	27415	0E+00	96.37	100	Solyc04g015970.2.1	ATP-binding cassette 1 IPR003439	ABC transporter-like
4DE	g136.t1	1607273	1610936	3663	0E+00	95.57	99	Solyc04g015980.2.1	Receptor like kinase, RLK	
4DE	g138.t1	1625863	1629229	3366	0E+00	98.99	100	Solyc04g015990.1.1	Cation_H(+) antiporter 28 IPR006153	Cation_H+ exchanger
4DE	g139.t1	1630915	1634684	3769	4E-170	97.89	100	Solyc04g016000.2.1	Heat stress transcription factor-type, DNA-binding	
4DE	g141.t1	1659703	1671464	11761	0E+00	89.36	96	Solyc04g016010.2.1	Thioredoxin reductase IPR000103	Pyridine nucleotide-disulphide oxidoreductase, class-II

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g144.i2	1687603	1695957	8354	1E-19	39.6	10	Solyc11g039450.1.1	Unknown Protein	
4DE	g144.t1	1688493	1695957	7464	8E-20	39.6	10	Solyc11g039450.1.1	Unknown Protein	
4DE	g153.t1	1805822	1812223	6401	0E+00	96.55	84	Solyc04g016050.2.1	GTP-binding family protein IPR002917 GTP-binding protein, HSR1-related	
4DE	g155.t1	1829977	1831233	1256	0E+00	98.58	100	Solyc04g016060.1.1	Plant-specific domain TIGR01570 family protein IPR006460 Protein of unknown function DUF617, plant	
4DE	g156.t1	1836693	1841043	4350	6E-93	95.65	69	Solyc04g016070.2.1	MADS-box protein 9 IPR002487 Transcription factor, K-box	
4DE	g159.i2	1862022	1878521	16499	0E+00	96.69	100	Solyc04g016080.1.1	Kinesin-like protein IPR001752 Kinesin, motor region	
4DE	g159.t1	1865672	1878521	12849	0E+00	96.99	100	Solyc04g016080.1.1	Kinesin-like protein IPR001752 Kinesin, motor region	
4DE	g164.t1	1968474	1982131	13657	0E+00	99.06	100	Solyc04g016130.2.1	F-box_LRR-repeat protein At5g63520 IPR019494 FIST C domain	
4DE	g165.t1	1982480	1983307	827	2E-61	85.58	100	Solyc07g009300.1.1	Unknown Protein	
4DE	g167.t1	1991631	1993891	2260	5E-67	78.79	77	Solyc04g016150.1.1	F-box_LRR-repeat protein At5g63520 IPR019494 FIST C domain	
4DE	g168.t1	2001636	2008861	7225	0E+00	98.16	100	Solyc04g016160.2.1	F-box_LRR-repeat protein At5g63520 IPR019494 FIST C domain	
4DE	g169.t1	2013054	2045041	31987	0E+00	99.55	44	Solyc04g016180.2.1	Glycosyltransferase IPR007657 Glycosyltransferase AER61, uncharacterised	
4DE	g170.t1	2046052	2047831	1779	0E+00	99.36	100	Solyc04g016190.1.1	Glucosyltransferase IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
4DE	g171.t1	2055462	2056421	959	7E-22	58.76	80	Solyc12g027570.1.1	Unknown Protein	
4DE	g174.t1	2085340	2087416	2076	0E+00	91.65	75	Solyc04g016200.1.1	UDP-glucosyltransferase HvUGT5876 IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
4DE	g175.t1	2087809	2095081	7272	0E+00	87.74	29	Solyc04g016210.2.1	UDP-glucosyltransferase IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
4DE	g176.t1	2095141	2095831	690	2E-20	52.05	57	Solyc02g036400.1.1	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence	
4DE	g178.t1	2106625	2109015	2390	0E+00	74.04	100	Solyc04g008310.1.1	Glucosyltransferase IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
4DE	g180.t1	2115495	2119346	3851	3E-166	82.46	36	Solyc03g062840.1.1	Unknown Protein	
4DE	g182.t1	2149714	2151676	1962	0E+00	96.6	100	Solyc04g016230.2.1	Glucosyltransferase IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
4DE	g182.i2	2149714	2151676	1962	0E+00	96.67	100	Solyc04g016230.2.1	Glucosyltransferase IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
4DE	g183.t1	2153752	2163556	9804	0E+00	99.42	100	Solyc04g016240.2.1	Nuclear pore complex protein Nup93-like protein IPR007231 Nucleoporin interacting component Nup93_Nic96	
4DE	g184.t1	2165265	2170173	4908	2E-108	92.22	83	Solyc04g016250.2.1	Mitochondrial glycoprotein expressed IPR003428 Mitochondrial glycoprotein	
4DE	g185.t1	2177795	2187445	9650	0E+00	98.95	100	Solyc04g016260.2.1	Calcium-transporting ATPase 1 IPR006408 ATPase, P-type, calcium-transporting, PMCA-type	
4DE	g186.i2	2187691	2192366	4675	1E-166	98.73	85	Solyc04g016280.2.1	Organic anion transporter IPR004853 Protein of unknown function DUF250	
4DE	g186.t1	2187691	2192366	4675	4E-163	98.71	85	Solyc04g016280.2.1	Organic anion transporter IPR004853 Protein of unknown function DUF250	
4DE	g187.t1	2194485	2199382	4897	0E+00	93.57	100	Solyc04g016290.2.1	Unknown Protein IPR011112 Rho termination factor, N-terminal	
4DE	g189.t1	2206265	2211559	5294	4E-94	90.79	48	Solyc10g050820.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g190.t1	2212056	2216726	4670	1E-76	81.62	55	Solyc11g044490.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
4DE	g191.t1	2218914	2222366	3452	0E+00	99.78	100	Solyc04g016330.2.1	Glycerol-3-phosphate dehydrogenase IPR006168 NAD-dependent glycerol-3-phosphate dehydrogenase	
4DE	g193.t1	2237115	2237671	556	6E-14	58.82	48	Solyc05g018200.1.1	Unknown Protein	
4DE	g194.t1	2239488	2242336	2848	2E-107	72.05	77	Solyc02g070350.2.1	40S ribosomal protein S4-like protein IPR000876 Ribosomal protein S4e	
4DE	g195.t1	2246865	2259513	12648	0E+00	92.41	100	Solyc04g016360.2.1	S-formylglutathione hydrolase IPR014186 S-formylglutathione hydrolase	
4DE	g196.t1	2268161	2272864	4703	0E+00	94.44	68	Solyc04g016370.2.1	DNA ATP-dependent helicase IPR000330 SNF2-related	
4DE	g196.i2	2268161	2272864	4703	0E+00	91.4	68	Solyc04g016370.2.1	DNA ATP-dependent helicase IPR000330 SNF2-related	
4DE	g197.t1	2274919	2291464	16545	0E+00	98.48	75	Solyc04g016370.2.1	DNA ATP-dependent helicase IPR000330 SNF2-related	
4DE	g197.i2	2274919	2285594	10675	0E+00	99.35	96	Solyc04g016370.2.1	DNA ATP-dependent helicase IPR000330 SNF2-related	
4DE	g197.i3	2286995	2291464	4469	0E+00	99.36	100	Solyc04g016380.2.1	Ribosome biogenesis protein BRX1 IPR007109 Brix domain	
4DE	g199.t1	2295347	2297714	2367	0E+00	74.9	96	Solyc01g094740.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1	
4DE	g200.i2	2298686	2308954	10268	5E-87	64.17	33	Solyc08g044310.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g200.t1	2305943	2308954	3011	1E-90	62	82	Solyc08g044310.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g201.t1	2337294	2340064	2770	3E-79	99.13	97	Solyc04g016400.2.1	Calpain-2 catalytic subunit IPR011992 EF-Hand type	
4DE	g203.t1	2348695	2368734	20039	0E+00	95.61	41	Solyc04g016410.2.1	Chaperone protein dnaJ IPR001623 Heat shock protein DnaJ, N-terminal	
4DE	g203.i2	2350165	2368734	18569	0E+00	95.61	42	Solyc04g016410.2.1	Chaperone protein dnaJ IPR001623 Heat shock protein DnaJ, N-terminal	
4DE	g205.t1	2379863	2382357	2494	2E-68	95.15	73	Solyc04g016420.2.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g206.t1	2382519	2385214	2695	0E+00	98.68	100	Solyc04g016430.2.1	Cytokinin oxidase_dehydrogenase 1 IPR015345	Cytokinin dehydrogenase 1, FAD and cytokinin binding
4DE	g207.t1	2413238	2418474	5236	6E-98	98.61	63	Solyc04g016440.2.1	Os06g0301100 protein (Fragment) IPR005349	Uncharacterised protein family UPF0136, Transmembrane
4DE	g207.t2	2413238	2418474	5236	3E-81	88.19	62	Solyc04g016440.2.1	Os06g0301100 protein (Fragment) IPR005349	Uncharacterised protein family UPF0136, Transmembrane
4DE	g209.t1	2442823	2444571	1748	0E+00	95.36	100	Solyc04g016470.2.1	Beta-1 3-glucanase IPR000490	Glycoside hydrolase, family 17
4DE	g210.t1	2444916	2448534	3618	0E+00	88.94	100	Solyc04g016480.2.1	Calmodulin binding protein IPR000048	IQ calmodulin-binding region
4DE	g211.t1	2450795	2456644	5849	0E+00	92.57	91	Solyc04g016490.2.1	lcc family phosphohydrolase IPR011230	Phosphoesterase At2g46880
4DE	g211.t2	2450795	2456644	5849	0E+00	92.57	100	Solyc04g016490.2.1	lcc family phosphohydrolase IPR011230	Phosphoesterase At2g46880
4DE	g212.t1	2460263	2461669	1406	5E-36	59.65	78	Solyc11g065410.1.1		Unknown Protein
4DE	g215.t1	2485923	2489611	3688	0E+00	99.59	82	Solyc04g016510.2.1	Guanine nucleotide-binding protein subunit beta-4 IPR020472	G-protein beta WD-40 repeat, region
4DE	g216.t1	2489627	2497134	7507	0E+00	99.75	89	Solyc04g016520.2.1	UDP-N-acetylglucosamine dolichyl phosphate N-acetylglucosamine-1-phosphate transferase IPR018481	Glycosyl transferase, family 4, conserved region
4DE	g217.t1	2499214	2509814	10600	0E+00	95.25	94	Solyc04g016530.2.1	Exodeoxyribonuclease III IPR000097	AP endonuclease, family 1
4DE	g218.t1	2509982	2512644	2662	0E+00	99.35	100	Solyc04g016540.1.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
4DE	g219.t1	2514091	2525054	10963	3E-133	88.16	33	Solyc04g016550.2.1	Folypolyglutamate synthase IPR001645	Folypolyglutamate synthetase
4DE	g221.t1	2532149	2533514	1365	2E-14	93.94	36	Solyc04g016560.1.1		Unknown Protein
4DE	g222.t1	2553618	2554894	1276	6E-32	68.04	90	Solyc12g013560.1.1	3_apos(2_apos) 5_apos-bisphosphate nucleotidase,5-bisphosphate nucleotidase HAL2	
4DE	g223.t1	2559583	2565737	6154	6E-139	78.06	72	Solyc04g017610.2.1	F-box domain containing protein expressed IPR001810	Cyclin-like F-box
4DE	g228.t1	2641842	2643253	1411	2E-122	63.58	98	Solyc04g017610.2.1	F-box domain containing protein expressed IPR001810	Cyclin-like F-box
4DE	g229.t1	2643279	2647833	4554	8E-24	44.54	44	Solyc02g050170.1.1		Unknown Protein
4DE	g230.t1	2656832	2677723	20891	3E-130	92.5	77	Solyc04g017620.2.1	Phosphatidylinositol-4-phosphate 5-kinase 9 IPR016034	Phosphatidylinositol-4-phosphate 5-kinase, core, subgroup
4DE	g231.t1	2679208	2681003	1795	4E-102	72.07	95	Solyc03g122200.1.1	cDNA clone J013074B07 full insert sequence IPR004332	Transposase, MuDR, plant
4DE	g232.t1	2694842	2696106	1264	2E-37	79.49	57	Solyc05g042140.1.1	Unknown Protein IPR001878	Zinc finger, CCHC-type
4DE	g236.t1	2762488	2765463	2975	3E-34	96.77	24	Solyc04g017650.2.1	Mediator of DNA damage checkpoint protein 1 IPR001357	BRCT
4DE	g236.t2	2762488	2765463	2975	3E-34	96.77	24	Solyc04g017650.2.1	Mediator of DNA damage checkpoint protein 1 IPR001357	BRCT
4DE	g237.t1	2765812	2784031	18219	0E+00	85.71	16	Solyc04g017640.1.1	At1g67150 (Fragment) IPR004158	Protein of unknown function DUF247, plant
4DE	g238.t1	2799303	2807004	7701	0E+00	98.59	100	Solyc04g017650.2.1	Mediator of DNA damage checkpoint protein 1 IPR001357	BRCT
4DE	g239.t3	2817063	2826795	9732	4E-180	93.04	55	Solyc04g017680.2.1	50S ribosomal protein L22-like IPR005727	Ribosomal protein L22, bacterial-type
4DE	g239.t2	2817063	2818693	1630	4E-160	83.88	100	Solyc04g017670.2.1		F-box family protein
4DE	g239.t1	2821303	2826795	5492	0E+00	94.35	100	Solyc04g017680.2.1	50S ribosomal protein L22-like IPR005727	Ribosomal protein L22, bacterial-type
4DE	g240.t1	2831306	2833384	2078	2E-115	98.77	100	Solyc04g017690.2.1	Early response to dehydration 15-like protein (Fragment) IPR009818	Ataxin-2, C-terminal
4DE	g241.t1	2837750	2842724	4974	0E+00	99.24	100	Solyc04g017700.2.1	N-acetylglucosaminyl transferase component Gpi1 IPR007720	N-acetylglucosaminyl transferase component
4DE	g244.t1	2862493	2867898	5405	0E+00	100	99	Solyc04g017710.2.1	Pre-mRNA splicing factor IPR012677	Nucleotide-binding, alpha-beta plait
4DE	g247.t1	2914293	2918023	3730	2E-119	91.11	77	Solyc07g015930.1.1	Methyl binding domain protein IPR001739	Methyl-CpG DNA binding
4DE	g247.t2	2914293	2918023	3730	1E-118	92.09	63	Solyc07g015930.1.1	Methyl binding domain protein IPR001739	Methyl-CpG DNA binding
4DE	g254.t1	2963468	2984935	21467	7E-12	37.27	8	Solyc04g005010.2.1	Phosphoglycerate mutase IPR002156	Ribonuclease H
4DE	g257.t1	3018768	3021241	2473	4E-61	60.71	48	Solyc01g060230.1.1		Unknown Protein
4DE	g258.t1	3021808	3043276	21468	3E-38	52.85	7	Solyc09g055600.1.1	Endonuclease_exonuclease_phosphatase, related	
4DE	g261.t1	3069626	3070109	483	9E-63	98.9	100	Solyc04g017740.1.1		Unknown Protein
4DE	g262.t1	3071420	3075949	4529	0E+00	96.49	62	Solyc04g017750.2.1	Pathogen-induced calmodulin-binding protein (Fragment) IPR012417	Calmodulin-binding, plant
4DE	g264.t1	3118268	3120919	2651	2E-15	88.89	23	Solyc03g044550.1.1		Unknown Protein
4DE	g265.t1	3120969	3122929	1960	2E-25	56.9	19	Solyc05g017810.1.1		Unknown Protein
4DE	g267.t1	3128242	3132039	3797	2E-58	39.95	78	Solyc03g062840.1.1		Unknown Protein
4DE	g289.t1	3310003	3313574	3571	1E-70	91.04	45	Solyc04g017830.1.1		Unknown Protein
4DE	g296.t1	3423043	3423734	691	1E-57	96.74	100	Solyc04g017970.1.1		Unknown Protein
4DE	g297.t1	3436244	3445544	9300	2E-108	47.99	56	Solyc12g036370.1.1		Unknown Protein
4DE	g315.t3	3607868	3637342	29474	2E-111	52.03	45	Solyc07g064380.2.1	Serine threonine-protein phosphatase 7 long form homolog IPR019557	Aminotransferase-like, plant mobile domain

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% Id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g315.i2	3622338	3625887	3549	6E-40	88.57	38	Solyc04g018040.1.1	Unknown Protein	
4DE	g315.t1	3635558	3637342	1784	2E-117	48.53	98	Solyc07g064380.2.1	Serine_threonine-protein phosphatase 7 long form homolog IPR019557	Aminotransferase-like, plant mobile domain
4DE	g321.t1	3714940	3727629	12689	7E-20	57.53	13	Solyc10g046780.1.1	Zinc knuckle family protein IPR001878	Zinc finger, CCHC-type
4DE	g324.i2	3744978	3759477	14499	1E-37	48.26	17	Solyc02g055510.1.1	Helicase-like protein IPR010285	Protein of unknown function DUF889, eukaryote
4DE	g324.t1	3744988	3759477	14489	1E-37	48.26	17	Solyc02g055510.1.1	Helicase-like protein IPR010285	Protein of unknown function DUF889, eukaryote
4DE	g325.t1	3762098	3763720	1622	1E-87	96.9	100	Solyc04g018050.1.1	Unknown Protein	
4DE	g327.t1	3779718	3792877	13159	4E-13	46.99	30	Solyc02g021080.1.1	Unknown Protein	
4DE	g333.t1	3872220	3872983	763	7E-18	59.38	83	Solyc04g018160.1.1	Unknown Protein	
4DE	g334.t1	3877432	3884304	6872	5E-26	51.96	61	Solyc02g021080.1.1	Unknown Protein	
4DE	g338.t1	3908292	3908998	706	1E-23	69.12	62	Solyc04g018240.1.1	Unknown Protein	
4DE	g343.t1	3969903	3981863	11960	7E-46	64.66	33	Solyc04g018220.1.1	Unknown Protein	
4DE	g344.t1	3991832	3993282	1450	4E-18	48.98	31	Solyc03g013330.1.1	Unknown Protein	
4DE	g346.t1	4003212	4004593	1381	1E-25	72.6	45	Solyc04g018210.1.1	Unknown Protein	
4DE	g357.t1	4086514	4089514	3000	2E-54	88.3	79	Solyc04g080570.2.1	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase IPR011004	Trimeric LpxA-like
4DE	g369.t1	4318662	4342877	24215	0E+00	90.36	33	Solyc04g018100.2.1	Sodium_hydrogen exchanger Na+ H+ antiporter IPR018418	Na+_H+ exchanger, isoforms 7_8, conserved region
4DE	g369.i2	4318662	4342596	23934	0E+00	88.12	33	Solyc04g018100.2.1	Sodium_hydrogen exchanger Na+ H+ antiporter IPR018418	Na+_H+ exchanger, isoforms 7_8, conserved region
4DE	g371.t1	4375579	4376777	1198	7E-153	98.6	100	Solyc04g018110.1.1	Calmodulin-like protein 1 IPR011992	EF-Hand type
4DE	g375.i2	4479428	4491140	11712	4E-22	97.5	19	Solyc04g018040.1.1	Unknown Protein	
4DE	g375.t1	4486341	4491140	4799	5E-22	97.5	21	Solyc04g018040.1.1	Unknown Protein	
4DE	g376.t1	4505538	4507320	1782	2E-107	67.86	74	Solyc07g064380.2.1	Serine_threonine-protein phosphatase 7 long form homolog IPR019557	Aminotransferase-like, plant mobile domain
4DE	g377.t1	4521668	4522380	712	1E-96	91.78	100	Solyc04g017860.1.1	Unknown Protein	
4DE	g378.t1	4522536	4524890	2354	7E-120	65.13	99	Solyc07g064380.2.1	Serine_threonine-protein phosphatase 7 long form homolog IPR019557	Aminotransferase-like, plant mobile domain
4DE	g378.i2	4522536	4523650	1114	8E-74	60.26	100	Solyc07g064380.2.1	Serine_threonine-protein phosphatase 7 long form homolog IPR019557	Aminotransferase-like, plant mobile domain
4DE	g383.t1	4560679	4566715	6036	5E-14	88.89	10	Solyc04g018130.1.1	Unknown Protein	
4DE	g395.t1	4640358	4642975	2617	1E-16	62.86	23	Solyc01g022790.1.1	Unknown Protein	
4DE	g399.t1	4664284	4671192	6908	3E-56	65.06	24	Solyc05g017810.1.1	Unknown Protein	
4DE	g399.i2	4664284	4695924	31640	7E-55	65.06	13	Solyc05g017810.1.1	Unknown Protein	
4DE	g402.t1	4740250	4744125	3875	6E-23	83.02	20	Solyc09g042380.1.1	Unknown Protein	
4DE	g403.t1	4749674	4751068	1394	7E-27	71.43	63	Solyc04g018210.1.1	Unknown Protein	
4DE	g410.t1	4833950	4836025	2075	2E-11	64.44	61	Solyc09g042380.1.1	Unknown Protein	
4DE	g411.t1	4836255	4837575	1320	2E-46	56.15	46	Solyc05g017810.1.1	Unknown Protein	
4DE	g413.t1	4846900	4847265	365	3E-27	64.47	99	Solyc09g042380.1.1	Unknown Protein	
4DE	g421.t1	4951425	4956305	4880	7E-45	58.08	30	Solyc05g017810.1.1	Unknown Protein	
4DE	g422.t1	4956884	4982045	25161	1E-68	94.74	8	Solyc05g042010.1.1	Unknown Protein	
4DE	g424.t1	4989404	4992431	3027	1E-36	58.68	47	Solyc04g018230.1.1	Unknown Protein	
4DE	g425.i2	4995886	5000605	4719	2E-38	51.25	26	Solyc05g017810.1.1	Unknown Protein	
4DE	g425.t1	4997616	5000605	2989	2E-38	51.25	27	Solyc05g017810.1.1	Unknown Protein	
4DE	g431.t1	5082323	5085670	3347	5E-27	53.92	43	Solyc02g021080.1.1	Unknown Protein	
4DE	g432.t1	5092079	5102031	9952	9E-18	47.06	43	Solyc04g018220.1.1	Unknown Protein	
4DE	g435.t1	5149520	5155160	5640	9E-18	56.52	34	Solyc02g021080.1.1	Unknown Protein	
4DE	g436.t1	5163459	5165894	2435	1E-103	65.74	100	Solyc04g018230.1.1	Unknown Protein	
4DE	g448.t1	5351101	5353990	2889	1E-10	50	48	Solyc02g021080.1.1	Unknown Protein	
4DE	g449.t1	5360949	5370619	9670	2E-25	68.75	19	Solyc04g018210.1.1	Unknown Protein	
4DE	g450.t1	5375585	5379030	3445	5E-31	70.37	38	Solyc03g013330.1.1	Unknown Protein	
4DE	g453.t1	5435615	5440659	5044	4E-10	37.93	36	Solyc01g038220.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g461.t1	5512284	5512776	492	7E-12	64.44	51	Solyc09g042380.1.1	Unknown Protein	
4DE	g462.l2	5513313	5521906	8593	1E-47	56.38	16	Solyc05g017810.1.1	Unknown Protein	
4DE	g463.t1	5521956	5522606	650	2E-18	67.86	66	Solyc09g042380.1.1	Unknown Protein	
4DE	g464.t1	5530560	5532276	1716	7E-26	51.96	43	Solyc02g021080.1.1	Unknown Protein	
4DE	g467.t1	5599267	5602726	3459	4E-30	58.42	29	Solyc02g021080.1.1	Unknown Protein	
4DE	g467.l2	5599789	5602726	2937	1E-30	58.42	32	Solyc02g021080.1.1	Unknown Protein	
4DE	g472.t1	5711972	5716481	4509	3E-11	51.92	40	Solyc02g021080.1.1	Unknown Protein	
4DE	g473.t1	5717420	5723466	6046	3E-25	79.73	67	Solyc04g018220.1.1	Unknown Protein	
4DE	g477.t1	5827352	5828456	1104	2E-31	64.71	44	Solyc03g013330.1.1	Unknown Protein	
4DE	g479.t1	5836917	5848116	11199	1E-26	67.78	10	Solyc05g017810.1.1	Unknown Protein	
4DE	g486.t1	5933869	5936996	3127	5E-50	65.41	77	Solyc04g018230.1.1	Unknown Protein	
4DE	g493.t1	6029425	6039536	10111	2E-38	71.57	73	Solyc04g018210.1.1	Unknown Protein	
4DE	g494.t1	6052635	6061169	8534	1E-10	39.8	23	Solyc03g013330.1.1	Unknown Protein	
4DE	g497.t1	6081785	6093706	11921	4E-32	80.88	19	Solyc04g018240.1.1	Unknown Protein	
4DE	g497.l2	6081785	6104572	22787	2E-29	58.59	18	Solyc04g018240.1.1	Unknown Protein	
4DE	g508.t1	6293780	6300649	6869	4E-11	48.53	51	Solyc02g021080.1.1	Unknown Protein	
4DE	g515.t1	6383526	6393899	10373	6E-24	50.98	23	Solyc02g021080.1.1	Unknown Protein	
4DE	g523.t1	6524417	6526518	2101	3E-32	47.97	83	Solyc10g012390.1.1	Agamous-like MADS-box protein AGL62 IPR002100 Transcription factor, MADS-box	
4DE	g524.t1	6531225	6531918	693	3E-60	85.37	100	Solyc04g007000.1.1	Ethylene-responsive transcription factor 4 IPR003340 Transcriptional factor B3	
4DE	g527.t1	6549087	6554755	5668	2E-28	64.13	34	Solyc04g018230.1.1	Unknown Protein	
4DE	g529.t1	6582147	6588718	6571	5E-10	68.57	8	Solyc09g042380.1.1	Unknown Protein	
4DE	g530.t1	6589348	6599338	9990	8E-52	63.58	32	Solyc05g017810.1.1	Unknown Protein	
4DE	g531.t1	6633484	6635178	1694	3E-34	86.15	46	Solyc09g042380.1.1	Unknown Protein	
4DE	g532.t1	6635444	6638078	2634	1E-36	81.32	17	Solyc05g017810.1.1	Unknown Protein	
4DE	g537.t1	6678872	6683757	4885	1E-15	71.7	10	Solyc09g042380.1.1	Unknown Protein	
4DE	g543.t1	6739512	6741554	2042	0E+00	97.65	56	Solyc04g019310.1.1	Os06g0524700 protein (Fragment) IPR004158 Protein of unknown function DUF247, plant	
4DE	g547.t1	6783492	6784050	558	4E-36	93.44	60	Solyc04g040230.1.1	Dehydration-responsive protein-like IPR004159 Protein of unknown function DUF248, methyltransferase putative	
4DE	g548.t1	6798902	6801612	2710	0E+00	99.79	100	Solyc04g040220.2.1	NPR1-like protein (Fragment) IPR013069 BTB_POZ	
4DE	g550.t1	6828202	6832301	4099	0E+00	98.4	100	Solyc04g040200.2.1	Cellular retinaldehyde-binding_triple function C-terminal IPR001251 Cellular retinaldehyde-binding_triple function, C-terminal	
4DE	g551.t1	6832910	6834628	1718	0E+00	99	100	Solyc04g040190.1.1	Lycopene beta-cyclase 1	
4DE	g552.t1	6843050	6845550	2500	0E+00	99.62	100	Solyc04g040180.2.1	S-adenosylmethionine-dependent methyltransferase (Fragment) IPR013217 Methyltransferase type 12	
4DE	g553.t1	6856622	6861181	4559	2E-79	100	100	Solyc04g040170.2.1	DNA-directed RNA polymerases I IPR014381 DNA-directed RNA polymerase, RPB5 subunit	
4DE	g555.t1	6864624	6865351	727	1E-60	94.74	66	Solyc04g040170.2.1	DNA-directed RNA polymerases I IPR014381 DNA-directed RNA polymerase, RPB5 subunit	
4DE	g559.t1	6928613	6937331	8718	6E-17	72.73	8	Solyc01g022790.1.1	Unknown Protein	
4DE	g562.t1	6968033	6982059	14026	2E-35	68.69	25	Solyc01g007330.2.1	Ribulose biphosphate carboxylase large chain IPR000685 Ribulose biphosphate carboxylase, large subunit, C-terminal	
4DE	g566.t1	7015180	7017189	2009	0E+00	61.16	95	Solyc03g062840.1.1	Unknown Protein	
4DE	g571.t1	7077385	7081029	3644	0E+00	61.53	100	Solyc01g106660.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g571.l2	7077485	7081029	3544	0E+00	62.73	100	Solyc04g049560.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g572.t1	7085368	7090901	5533	2E-161	75.53	22	Solyc07g043210.1.1	Unknown Protein	
4DE	g573.t1	7094859	7096769	1910	2E-94	59.63	100	Solyc04g039910.1.1	12-oxophytodienoate reductase 1 IPR001155 NADH:flavin oxidoreductase_NADH oxidase, N-terminal	
4DE	g574.l2	7111263	7136659	25396	0E+00	93.15	56	Solyc04g039950.2.1	Mediator of RNA polymerase II transcription subunit 13 IPR009401 Mediator complex, subunit Med13	
4DE	g574.l3	7111263	7115759	4496	0E+00	99.34	70	Solyc04g039940.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
4DE	g574.t1	7116177	7139349	23172	0E+00	95.7	78	Solyc04g039950.2.1	Mediator of RNA polymerase II transcription subunit 13 IPR009401 Mediator complex, subunit Med13	
4DE	g575.t1	7144893	7188821	43928	5E-31	64.89	12	Solyc04g018220.1.1	Unknown Protein	
4DE	g587.t1	7369571	7375468	5897	1E-138	82.73	58	Solyc04g024420.2.1	Proteasome subunit beta type IPR000243 Peptidase T1A, proteasome beta-subunit	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g593.t1	7500777	7513745	12968	5E-63	34.53	30	Solyc00g008000.1.1	Unknown Protein	
4DE	g594.t1	7518627	7540661	22034	4E-57	35.2	10	Solyc00g008110.1.1	Unknown Protein	
4DE	g595.i2	7540717	7551721	11004	1E-54	32.9	27	Solyc00g008000.1.1	Unknown Protein	
4DE	g595.t1	7540717	7543617	2900	1E-53	32.73	82	Solyc00g008000.1.1	Unknown Protein	
4DE	g596.t1	7551728	7554148	2420	2E-24	47.1	34	Solyc12g082760.1.1	Unknown Protein	
4DE	g596.i2	7551728	7554148	2420	5E-23	50.42	31	Solyc12g082760.1.1	Unknown Protein	
4DE	g597.i2	7554507	7584651	30144	9E-54	32.58	11	Solyc00g008000.1.1	Unknown Protein	
4DE	g597.t1	7554777	7558141	3364	1E-43	33.41	57	Solyc00g008110.1.1	Unknown Protein	
4DE	g598.t1	7584485	7585658	1173	6E-25	45.24	100	Solyc12g082760.1.1	Unknown Protein	
4DE	g598.i2	7584668	7585658	990	8E-31	46.48	88	Solyc12g082760.1.1	Unknown Protein	
4DE	g599.t1	7585947	7593840	7893	6E-58	33.33	38	Solyc00g008110.1.1	Unknown Protein	
4DE	g600.t1	7594057	7596240	2183	4E-39	33.41	94	Solyc00g008110.1.1	Unknown Protein	
4DE	g601.t1	7596447	7597900	1453	8E-26	42.27	72	Solyc12g076310.1.1	Unknown Protein	
4DE	g602.i2	7598200	7600568	2368	6E-18	33.33	48	Solyc12g026370.1.1	Unknown Protein	
4DE	g602.t1	7599935	7600568	633	1E-15	39.1	90	Solyc12g082760.1.1	Unknown Protein	
4DE	g603.t1	7600707	7616630	15923	2E-52	30.21	19	Solyc00g008000.1.1	Unknown Protein	
4DE	g604.t1	7619057	7632991	13934	3E-55	31.7	23	Solyc00g008110.1.1	Unknown Protein	
4DE	g605.t1	7632998	7635608	2610	6E-26	36.59	26	Solyc06g016680.1.1	Unknown Protein	
4DE	g607.t1	7638097	7641781	3684	2E-64	34.91	49	Solyc00g008110.1.1	Unknown Protein	
4DE	g608.t1	7641608	7643508	1900	1E-10	44.87	23	Solyc00g005280.1.1	Unknown Protein	
4DE	g608.i2	7641788	7643508	1720	5E-12	71.05	16	Solyc00g008910.1.1	Unknown Protein	
4DE	g609.i2	7643637	7662611	18974	8E-66	36.1	15	Solyc00g008110.1.1	Unknown Protein	
4DE	g609.t1	7643657	7662611	18954	1E-65	36.1	15	Solyc00g008110.1.1	Unknown Protein	
4DE	g610.t1	7662689	7665195	2506	8E-40	35.54	96	Solyc00g008110.1.1	Unknown Protein	
4DE	g611.t1	7665092	7667702	2610	8E-21	64.29	9	Solyc00g010520.1.1	Unknown Protein	
4DE	g612.t1	7667801	7677905	10104	6E-60	35.45	87	Solyc00g008110.1.1	Unknown Protein	
4DE	g613.i2	7699623	7708062	8439	1E-49	90.11	39	Solyc04g024340.2.1	Acid phosphatase_vanadium-dependent haloperoxidase related IPR003832 Acid phosphatase_vanadium-dependent haloperoxidase related	
4DE	g613.t1	7699623	7705022	5399	3E-46	94.87	47	Solyc04g024340.2.1	Acid phosphatase_vanadium-dependent haloperoxidase related IPR003832 Acid phosphatase_vanadium-dependent haloperoxidase related	
4DE	g620.i2	7769911	7774393	4482	5E-146	64.46	43	Solyc06g030440.1.1	N-6 Adenine-specific DNA methylase	
4DE	g620.t1	7769911	7774393	4482	4E-145	64.46	40	Solyc06g030440.1.1	N-6 Adenine-specific DNA methylase	
4DE	g625.t1	7879397	7880197	800	8E-119	94.25	100	Solyc04g045390.1.1	Unknown Protein	
4DE	g633.t1	8012935	8022308	9373	9E-64	81.54	54	Solyc05g013990.2.1	T-complex protein 1 subunit epsilon IPR012718 T-complex protein 1, epsilon subunit	
4DE	g642.t1	8138093	8145918	7825	1E-23	66.67	20	Solyc01g022790.1.1	Unknown Protein	
4DE	g642.i2	8138093	8145918	7825	2E-23	66.67	19	Solyc01g022790.1.1	Unknown Protein	
4DE	g643.t1	8148896	8152674	3778	4E-24	42.34	100	Solyc04g056680.1.1	F-box protein PP2-B1	
4DE	g644.i2	8159016	8169664	10648	3E-169	100	67	Solyc04g024530.2.1	Actin-like protein 3 IPR015623 Actin-related protein 3	
4DE	g644.t1	8163834	8169664	5830	0E+00	99.61	100	Solyc04g024530.2.1	Actin-like protein 3 IPR015623 Actin-related protein 3	
4DE	g645.t1	8173055	8177284	4229	4E-16	45.35	22	Solyc04g039640.2.1	Unknown Protein	
4DE	g646.t1	8180231	8182234	2003	1E-124	100	88	Solyc04g024530.2.1	Actin-like protein 3 IPR015623 Actin-related protein 3	
4DE	g647.i2	8192445	8196548	4103	4E-16	88.89	12	Solyc09g042380.1.1	Unknown Protein	
4DE	g655.i2	8317537	8332535	14998	2E-32	47.57	19	Solyc05g017810.1.1	Unknown Protein	
4DE	g655.t1	8319197	8320802	1605	3E-34	47.57	44	Solyc05g017810.1.1	Unknown Protein	
4DE	g656.t1	8335262	8338728	3466	3E-36	50.29	30	Solyc05g017810.1.1	Unknown Protein	
4DE	g662.i3	8392590	8406103	13513	4E-66	68.48	21	Solyc05g016050.1.1	Unknown Protein	
4DE	g662.t1	8403020	8406103	3083	3E-44	77.42	25	Solyc08g048270.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g666.t1	8486380	8489849	3469	9E-90	92.5	55	Solyc04g024660.1.1		Unknown Protein
4DE	g674.t1	8612482	8614665	2183	0E+00	68.47	72	Solyc12g036370.1.1		Unknown Protein
4DE	g681.t1	8647214	8651023	3809	2E-11	42.22	33	Solyc02g021080.1.1		Unknown Protein
4DE	g685.t1	8678563	8679033	470	1E-12	61.22	59	Solyc09g042380.1.1		Unknown Protein
4DE	g700.t1	8843020	8851169	8149	2E-153	95.13	94	Solyc04g024590.2.1		Dehydrogenase_reductase SDR family member 7 IPR002347 Glucose_ribitol dehydrogenase
4DE	g701.t1	8851344	8857801	6457	5E-10	41.38	52	Solyc01g056820.1.1		Methionine aminopeptidase, related
4DE	g703.t1	8862670	8866815	4145	7E-33	50.41	41	Solyc03g077970.1.1		Methionine aminopeptidase, related
4DE	g713.t1	8981269	8997841	16572	0E+00	95.97	87	Solyc04g024710.2.1		Cysteine-type peptidase IPR003323 Ovarian tumour, otubain
4DE	g713.t2	8985663	8997941	12278	0E+00	98.47	87	Solyc04g024710.2.1		Cysteine-type peptidase IPR003323 Ovarian tumour, otubain
4DE	g716.t1	9038740	9048011	9271	3E-11	35.96	45	Solyc02g021080.1.1		Unknown Protein
4DE	g724.t1	9111513	9115299	3786	4E-11	93.18	31	Solyc03g114170.2.1		Deleted in split hand_splt foot protein 1 IPR007834 DSS1_SEM1
4DE	g728.t1	9146293	9149679	3386	2E-19	47.83	28	Solyc10g046780.1.1		Zinc knuckle family protein IPR001878 Zinc finger, CCHC-type
4DE	g734.t1	9182118	9185134	3016	2E-20	73.58	54	Solyc09g042380.1.1		Unknown Protein
4DE	g742.t1	9321337	9323864	2527	3E-44	63.43	24	Solyc10g017780.1.1		Unknown Protein
4DE	g743.t1	9325295	9330244	4949	0E+00	79.95	26	Solyc00g304030.1.1		Macrolide export ATP-binding_permease protein MacB IPR003439 ABC transporter-like
4DE	g744.t1	9340723	9343327	2604	2E-26	55.84	19	Solyc05g025880.1.1		CTV.20
4DE	g745.t1	9346169	9350644	4475	0E+00	97.06	100	Solyc04g024780.1.1		Unknown Protein IPR012442 Protein of unknown function DUF1645
4DE	g750.t1	9388807	9390044	1237	2E-16	27.61	83	Solyc10g047890.1.1		Ribonuclease H IPR002156 Ribonuclease H
4DE	g755.t1	9425892	9427984	2092	3E-68	49.78	44	Solyc04g017730.1.1		Zinc finger CCHC-type
4DE	g767.t1	9586934	9589930	2996	4E-166	76.62	86	Solyc09g014660.1.1		HGWP repeat containing protein-like
4DE	g769.t1	9599529	9610149	10620	8E-34	74.16	15	Solyc08g067650.1.1		Unknown Protein
4DE	g771.t1	9662392	9668696	6304	3E-109	59.43	33	Solyc03g062840.1.1		Unknown Protein
4DE	g772.t1	9670123	9671363	1240	2E-109	95.65	100	Solyc04g028380.1.1		Sulfotransferase 5b IPR000863 Sulfotransferase
4DE	g781.t1	9777474	9780563	3089	4E-179	88.13	99	Solyc04g028470.1.1		GDSL esterase_lipase 2 IPR001087 Lipase, GDSL
4DE	g784.t1	9816992	9822764	5772	5E-38	51.46	25	Solyc05g017810.1.1		Unknown Protein
4DE	g805.t2	10168026	10173649	5623	2E-43	58.99	20	Solyc05g017810.1.1		Unknown Protein
4DE	g805.t1	10168056	10173649	5593	2E-49	63.19	22	Solyc05g017810.1.1		Unknown Protein
4DE	g821.t2	10396725	10408341	11616	2E-19	54.43	12	Solyc02g021080.1.1		Unknown Protein
4DE	g824.t1	10443580	10447967	4387	2E-30	61.29	28	Solyc02g021080.1.1		Unknown Protein
4DE	g836.t1	10682117	10688853	6736	3E-50	91.57	22	Solyc04g024900.1.1		Unknown Protein
4DE	g841.t1	10761173	10764473	3300	1E-31	80.56	71	Solyc06g068870.2.1		BHLH transcription factor IPR011598 Helix-loop-helix DNA-binding
4DE	g845.t1	10797802	10811774	13972	1E-10	66.67	22	Solyc02g020930.1.1		Unknown Protein
4DE	g858.t2	10961552	10973937	12385	1E-103	84.75	62	Solyc04g025000.1.1		Paired amphipathic helix protein SIN3 IPR003822 Paired amphipathic helix
4DE	g858.t1	10961552	10973937	12385	7E-98	82.49	61	Solyc04g025000.1.1		Paired amphipathic helix protein SIN3 IPR003822 Paired amphipathic helix
4DE	g863.t2	11051484	11073647	22163	2E-95	88.82	19	Solyc04g024990.1.1		Paired amphipathic helix protein SIN3 IPR003822 Paired amphipathic helix
4DE	g863.t1	11071495	11073647	2152	2E-117	90.91	97	Solyc04g024990.1.1		Paired amphipathic helix protein SIN3 IPR003822 Paired amphipathic helix
4DE	g866.t1	11104206	11113870	9664	1E-36	55.62	19	Solyc05g017810.1.1		Unknown Protein
4DE	g874.t1	11215253	11216577	1324	8E-11	39.02	42	Solyc01g058710.1.1		Unknown Protein
4DE	g887.t1	11436809	11439015	2206	1E-15	89.19	21	Solyc03g044550.1.1		Unknown Protein
4DE	g888.t1	11439295	11449855	10560	2E-68	71.94	19	Solyc05g017810.1.1		Unknown Protein
4DE	g889.t1	11450334	11456611	6277	2E-29	50.77	22	Solyc05g017810.1.1		Unknown Protein
4DE	g895.t1	11584934	11599581	14647	3E-16	56.34	17	Solyc02g021080.1.1		Unknown Protein
4DE	g897.t1	11615532	11618710	3178	6E-32	48.11	29	Solyc05g017810.1.1		Unknown Protein
4DE	g899.t1	11633887	11635203	1316	3E-77	92.91	97	Solyc04g024970.1.1		Phosphatidylinositol-4-phosphate 5-kinase IPR002498 Phosphatidylinositol-4-phosphate 5-kinase, core
4DE	g907.t1	11732761	11736433	3672	4E-59	96.94	53	Solyc04g024950.1.1		Unknown Protein

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g910.t1	11763479	11768873	5394	0E+00	98.19	94	Solyc04g024940.2.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g918.t1	11824329	11824948	619	1E-33	63.33	77	Solyc09g042380.1.1	Unknown Protein	
4DE	g920.t1	11837128	11837568	440	2E-26	57.32	75	Solyc09g042380.1.1	Unknown Protein	
4DE	g921.t1	11837667	11846687	9020	4E-112	84.97	45	Solyc04g025000.1.1	Paired amphipathic helix protein SIN3 IPR003822 Paired amphipathic helix	
4DE	g921.t2	11837667	11859807	22140	9E-89	85.21	12	Solyc04g025000.1.1	Paired amphipathic helix protein SIN3 IPR003822 Paired amphipathic helix	
4DE	g930.t1	11957647	11970782	13135	8E-95	78.72	94	Solyc04g025000.1.1	Paired amphipathic helix protein SIN3 IPR003822 Paired amphipathic helix	
4DE	g930.t2	11957647	11977214	19567	1E-89	83.93	25	Solyc04g025000.1.1	Paired amphipathic helix protein SIN3 IPR003822 Paired amphipathic helix	
4DE	g939.t1	12091767	12094721	2954	3E-92	84.15	71	Solyc04g024990.1.1	Paired amphipathic helix protein SIN3 IPR003822 Paired amphipathic helix	
4DE	g952.t1	12256399	12262904	6505	2E-11	35.16	25	Solyc01g058710.1.1	Unknown Protein	
4DE	g964.t1	12403544	12404484	940	9E-147	95.78	100	Solyc04g025040.1.1	Unknown Protein	
4DE	g981.t1	12595195	12599143	3948	3E-17	81.82	36	Solyc04g025090.1.1	Unknown Protein	
4DE	g982.t1	12603172	12603853	681	1E-64	95.05	100	Solyc04g025060.1.1	Unknown Protein	
4DE	g1002.t1	12911500	12914387	2887	2E-23	55.84	18	Solyc05g021350.1.1	Endonuclease_exonuclease_phosphatase	
4DE	g1002.t2	12911500	12914387	2887	2E-23	55.84	18	Solyc05g021350.1.1	Endonuclease_exonuclease_phosphatase	
4DE	g1026.t2	13234589	13237812	3223	0E+00	87.69	96	Solyc04g025160.2.1	Arsenite ATPase transporter (Eurofung) IPR003348 ATPase, anion-transporting	
4DE	g1026.t1	13234589	13237812	3223	2E-179	81.54	95	Solyc04g025160.2.1	Arsenite ATPase transporter (Eurofung) IPR003348 ATPase, anion-transporting	
4DE	g1032.t1	13308096	13315702	7606	0E+00	99	100	Solyc04g025170.2.1	ABC transporter G family member 28 IPR003439 ABC transporter-like	
4DE	g1033.t1	13316021	13317366	1345	1E-77	81.25	59	Solyc12g009620.1.1	CUE domain containing protein	
4DE	g1034.t1	13317384	13320752	3368	0E+00	92.29	98	Solyc04g025170.2.1	ABC transporter G family member 28 IPR003439 ABC transporter-like	
4DE	g1034.t2	13317716	13320752	3036	0E+00	93.51	99	Solyc04g025170.2.1	ABC transporter G family member 28 IPR003439 ABC transporter-like	
4DE	g1036.t1	13324782	13329652	4870	8E-77	98.25	92	Solyc04g025180.2.1	ABC transporter-like	
4DE	g1040.t1	13370911	13384084	13173	0E+00	60.13	89	Solyc11g017000.1.1	Os01g0873900 protein (Fragment) IPR007700 Protein of unknown function DUF668	
4DE	g1041.t1	13392871	13417012	24141	9E-35	57.3	17	Solyc05g017810.1.1	Unknown Protein	
4DE	g1043.t1	13419709	13428412	8703	2E-81	90.77	51	Solyc04g025240.2.1	GCN5-related N-acetyltransferase (GNAT) family protein-like	
4DE	g1044.t1	13440871	13446131	5260	3E-178	92	39	Solyc04g025250.1.1	Unknown Protein IPR017956 AT hook, DNA-binding, conserved site	
4DE	g1049.t1	13540149	13548485	8336	6E-61	65.69	21	Solyc05g017810.1.1	Unknown Protein	
4DE	g1056.t1	13600390	13601775	1385	2E-41	59.68	39	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g1057.t1	13602294	13620981	18687	0E+00	99.16	62	Solyc04g025260.2.1	Endoplasmic reticulum metalloproteinase 1 IPR007484 Peptidase M28	
4DE	g1058.t1	13622075	13626535	4460	9E-29	34.52	27	Solyc03g051940.1.1	Unknown Protein, related	
4DE	g1059.t1	13627024	13631891	4867	0E+00	97.36	97	Solyc04g025260.2.1	Endoplasmic reticulum metalloproteinase 1 IPR007484 Peptidase M28	
4DE	g1066.t1	13724520	13727393	2873	2E-31	50.62	35	Solyc05g017810.1.1	Unknown Protein	
4DE	g1069.t1	13767560	13776792	9232	3E-78	92.16	7	Solyc09g061300.1.1	Unknown Protein	
4DE	g1086.t1	13956746	13966332	9586	2E-52	62.58	16	Solyc05g017810.1.1	Unknown Protein	
4DE	g1096.t1	14080273	14081708	1435	2E-22	82	26	Solyc09g042360.1.1	Unknown Protein	
4DE	g1097.t1	14082066	14085688	3622	2E-26	72.73	22	Solyc05g021430.1.1	Unknown Protein	
4DE	g1099.t1	14123357	14124188	831	4E-62	76.86	77	Solyc00g005420.1.1	Unknown Protein	
4DE	g1101.t1	14165180	14184183	19003	3E-154	67.21	81	Solyc11g050700.1.1	Zinc finger CCHC-type	
4DE	g1103.t1	14217793	14218633	840	1E-10	72.97	41	Solyc09g042380.1.1	Unknown Protein	
4DE	g1117.t1	14460902	14464814	3912	6E-64	98.97	61	Solyc04g025280.2.1	START domain-containing protein IPR009769 Protein of unknown function DUF1336	
4DE	g1119.t1	14472892	14476644	3752	0E+00	96.75	98	Solyc04g025280.2.1	START domain-containing protein IPR009769 Protein of unknown function DUF1336	
4DE	g1119.t2	14472892	14481535	8643	0E+00	96.98	77	Solyc04g025280.2.1	START domain-containing protein IPR009769 Protein of unknown function DUF1336	
4DE	g1121.t1	14525067	14547611	22544	0E+00	90.75	53	Solyc04g025290.2.1	Peptide chain release factor 2 IPR004374 Peptide chain release factor 2	
4DE	g1122.t1	14547872	14551558	3686	0E+00	99.21	100	Solyc04g025300.2.1	Protein SUPPRESSOR OF GENE SILENCING 3	
4DE	g1122.t2	14547872	14551558	3686	0E+00	98.1	100	Solyc04g025300.2.1	Protein SUPPRESSOR OF GENE SILENCING 3	
4DE	g1145.t2	14786207	14794996	8789	7E-104	59.11	54	Solyc03g062840.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g1145.t1	14791817	14794996	3179	5E-40	84.72	47	Solyc05g021120.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g1146.t1	14795077	14798518	3441	2E-117	56.48	83	Solyc07g041560.1.1	Unknown Protein	
4DE	g1148.t1	14819228	14822808	3580	1E-50	97.5	100	Solyc04g025360.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g1158.t1	14909059	14909594	535	8E-29	75	84	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g1161.t2	14939870	14945854	5984	2E-97	74.15	46	Solyc10g049480.1.1	Abc transporter family protein IPR012340 Nucleic acid-binding, OB-fold	
4DE	g1161.t1	14939870	14943084	3214	1E-92	76.06	49	Solyc10g049480.1.1	Abc transporter family protein IPR012340 Nucleic acid-binding, OB-fold	
4DE	g1166.t1	15001183	15017001	15818	2E-19	69.84	23	Solyc07g039630.1.1	Unknown Protein	
4DE	g1170.t1	15043025	15045169	2144	8E-14	42.35	86	Solyc01g058710.1.1	Unknown Protein	
4DE	g1177.t1	15091188	15092959	1771	7E-10	48.44	37	Solyc09g042380.1.1	Unknown Protein	
4DE	g1178.t1	15093235	15095059	1824	7E-66	67.65	41	Solyc05g017810.1.1	Unknown Protein	
4DE	g1179.t1	15095158	15095829	671	5E-16	53.45	44	Solyc07g019470.1.1	Unknown Protein	
4DE	g1182.t2	15123288	15131177	7889	3E-39	86.49	26	Solyc05g045720.1.1	DNA-directed RNA polymerase IPR002092 DNA-directed RNA polymerase, bacteriophage type	
4DE	g1182.t1	15127268	15131177	3909	1E-38	86.49	23	Solyc05g045720.1.1	DNA-directed RNA polymerase IPR002092 DNA-directed RNA polymerase, bacteriophage type	
4DE	g1192.t1	15210703	15218461	7758	3E-41	51.6	19	Solyc05g017810.1.1	Unknown Protein	
4DE	g1206.t1	15417351	15423751	6400	2E-126	85.92	75	Solyc04g025400.2.1	Lipid phosphate phosphatase 3 IPR000326 Phosphatidic acid phosphatase type 2_haloperoxidase	
4DE	g1206.t2	15417351	15423462	6111	2E-98	98.59	71	Solyc04g025400.2.1	Lipid phosphate phosphatase 3 IPR000326 Phosphatidic acid phosphatase type 2_haloperoxidase	
4DE	g1212.t1	15474057	15476702	2645	1E-61	66.18	28	Solyc05g017810.1.1	Unknown Protein	
4DE	g1214.t1	15481753	15484692	2939	9E-16	88.89	28	Solyc03g044550.1.1	Unknown Protein	
4DE	g1222.t1	15620736	15622407	1671	2E-15	40.91	53	Solyc02g021080.1.1	Unknown Protein	
4DE	g1223.t1	15641192	15643757	2565	0E+00	97.76	100	Solyc04g025410.1.1	Cytochrome P450	
4DE	g1231.t1	15752716	15760148	7432	2E-20	71.21	5	Solyc01g058710.1.1	Unknown Protein	
4DE	g1232.t1	15779796	15785794	5998	9E-34	70.65	12	Solyc01g058710.1.1	Unknown Protein	
4DE	g1246.t1	15962974	15964678	1704	0E+00	98.71	100	Solyc04g025430.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
4DE	g1247.t1	15965064	15968449	3385	0E+00	99.57	100	Solyc04g025440.2.1	Polygalacturonase IPR012334 Pectin lyase fold	
4DE	g1258.t1	16115132	16116192	1060	3E-42	92.96	84	Solyc04g025450.1.1	Adenosine monophosphate binding protein 1 AMPBP1	
4DE	g1259.t1	16120842	16129473	8631	0E+00	90.25	94	Solyc10g079300.1.1	Calcium-transporting ATPase 1 IPR006408 ATPase, P-type, calcium-transporting, PMCA-type	
4DE	g1263.t1	16176389	16178183	1794	3E-28	69.12	61	Solyc09g042380.1.1	Unknown Protein	
4DE	g1274.t1	16294385	16301657	7272	6E-82	94.78	42	Solyc04g005560.2.1	Guanine nucleotide exchange factor-like protein contains Interpro domain IPR000904	
4DE	g1276.t1	16321740	16329417	7677	0E+00	86.04	67	Solyc04g025480.1.1	Homeodomain-containing transcription factor FWA IPR002913 Lipid-binding START	
4DE	g1276.t2	16321740	16329417	7677	0E+00	91.3	100	Solyc04g025480.1.1	Homeodomain-containing transcription factor FWA IPR002913 Lipid-binding START	
4DE	g1277.t1	16336831	16347757	10926	2E-97	94.84	47	Solyc04g025480.1.1	Homeodomain-containing transcription factor FWA IPR002913 Lipid-binding START	
4DE	g1287.t1	16436118	16437726	1608	2E-15	70.91	21	Solyc05g017810.1.1	Unknown Protein	
4DE	g1293.t1	16526624	16530619	3995	5E-170	78.26	78	Solyc04g025510.2.1	Os02g0194300 protein (Fragment) IPR014854 Nse4	
4DE	g1295.t1	16539358	16539979	621	1E-62	98.9	100	Solyc04g052970.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein	
4DE	g1296.t1	16540566	16541369	803	3E-92	86.49	100	Solyc11g011640.1.1	Auxin-responsive protein IPR003676 Auxin responsive SAUR protein	
4DE	g1307.t1	16645763	16648936	3173	3E-11	78.57	27	Solyc10g052440.1.1	Unknown Protein	
4DE	g1308.t1	16650330	16654964	4634	0E+00	99.59	100	Solyc04g025530.2.1	Glutamate decarboxylase IPR010107 Glutamate decarboxylase	
4DE	g1315.t1	16769095	16781719	12624	4E-10	51.79	26	Solyc02g021080.1.1	Unknown Protein	
4DE	g1316.t2	16789911	16794756	4845	3E-25	63.41	41	Solyc09g042380.1.1	Unknown Protein	
4DE	g1316.t1	16792306	16794756	2450	1E-25	63.41	67	Solyc09g042380.1.1	Unknown Protein	
4DE	g1317.t1	16796855	16809827	12972	2E-134	74.56	39	Solyc08g044300.1.1	Unknown Protein IPR001878 Zinc finger, CCHC-type	
4DE	g1319.t1	16819235	16823443	4208	3E-38	56.17	24	Solyc05g017810.1.1	Unknown Protein	
4DE	g1319.t2	16819235	16823443	4208	9E-37	55.56	23	Solyc05g017810.1.1	Unknown Protein	
4DE	g1325.t1	16897545	16905396	7851	5E-42	71.43	33	Solyc05g017810.1.1	Unknown Protein	
4DE	g1326.t1	16907255	16911242	3987	1E-39	56.49	52	Solyc05g017810.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.Jycopersicum (Heinz)		
4DE	g1336.t1	16989025	16994360	5335	2E-14	47.5	16	Solyc01g022790.1.1	Unknown Protein	
4DE	g1340.t1	17029855	17041791	11936	0E+00	98.94	55	Solyc04g025540.2.1	Anthranilate phosphoribosyltransferase-like protein IPR000312	Glycosyl transferase, family 3
4DE	g1340.t2	17029855	17041791	11936	0E+00	98.94	54	Solyc04g025540.2.1	Anthranilate phosphoribosyltransferase-like protein IPR000312	Glycosyl transferase, family 3
4DE	g1341.t1	17047881	17055336	7455	3E-80	93.46	8	Solyc09g061300.1.1	Unknown Protein	
4DE	g1349.t1	17122313	17125905	3592	7E-133	98.9	100	Solyc05g005190.2.1	ADP-ribosylation factor IPR006688	ADP-ribosylation factor
4DE	g1364.t2	17297520	17302803	5283	2E-28	64.95	18	Solyc01g058710.1.1	Unknown Protein	
4DE	g1366.t1	17319920	17321631	1711	9E-22	46.53	54	Solyc02g021080.1.1	Unknown Protein	
4DE	g1375.t1	17373000	17374223	1223	2E-44	60.48	47	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g1377.t1	17379100	17381137	2037	5E-108	58.04	99	Solyc05g005220.1.1	Unknown Protein	
4DE	g1381.t1	17420676	17432531	11855	4E-144	52.49	67	Solyc09g092410.2.1	Tir-nbs-lrr, resistance protein	
4DE	g1387.t1	17482984	17484150	1166	9E-11	83.78	21	Solyc00g005170.1.1	Unknown Protein	
4DE	g1389.t1	17532159	17538715	6556	0E+00	71.82	68	Solyc04g071380.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g1389.t2	17532159	17538909	6750	0E+00	59.06	76	Solyc04g071380.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g1400.t1	17679394	17680354	960	5E-58	72.52	89	Solyc03g096330.1.1	Unknown Protein	
4DE	g1409.t2	17725523	17729950	4427	0E+00	49.78	100	Solyc03g078740.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g1409.t1	17728783	17729950	1167	1E-137	76.77	100	Solyc12g070180.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g1413.t1	17771023	17772415	1392	1E-70	88.71	35	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g1417.t1	17803142	17814424	11282	5E-20	69.81	34	Solyc07g064390.1.1	Phosphatase PTC7 homolog IPR010822	Sporulation stage II, protein E C-terminal
4DE	g1429.t2	17972171	17974423	2252	2E-168	60.81	90	Solyc03g062840.1.1	Unknown Protein	
4DE	g1429.t1	17973351	17974423	1072	4E-95	86.25	75	Solyc10g012480.1.1	Unknown Protein	
4DE	g1430.t1	17984031	17987669	3638	2E-23	43.12	92	Solyc11g011230.1.1	F-box family protein IPR001810	Cyclin-like F-box
4DE	g1433.t1	18017338	18018772	1434	1E-144	77.31	99	Solyc09g057700.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g1438.t1	18104915	18105582	667	7E-52	62.31	97	Solyc07g039350.1.1	Unknown Protein	
4DE	g1443.t1	18161346	18162402	1056	4E-123	89.25	99	Solyc06g036270.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g1446.t1	18212441	18215634	3193	3E-39	71.88	51	Solyc03g013330.1.1	Unknown Protein	
4DE	g1447.t3	18221968	18228442	6474	2E-26	55.21	35	Solyc04g018260.1.1	Unknown Protein	
4DE	g1447.t1	18225529	18228442	2913	5E-27	60.67	62	Solyc04g018260.1.1	Unknown Protein	
4DE	g1448.t1	18235591	18248543	12952	3E-21	49.45	44	Solyc02g021080.1.1	Unknown Protein	
4DE	g1451.t1	18293090	18301462	8372	3E-40	64.93	50	Solyc04g018220.1.1	Unknown Protein	
4DE	g1452.t1	18309101	18312038	2937	6E-21	47.37	99	Solyc02g021080.1.1	Unknown Protein	
4DE	g1454.t1	18333065	18336002	2937	4E-96	67.69	83	Solyc07g041560.1.1	Unknown Protein	
4DE	g1454.t2	18333065	18336002	2937	2E-95	66.52	84	Solyc07g041560.1.1	Unknown Protein	
4DE	g1456.t1	18347336	18348002	666	3E-46	84.21	85	Solyc12g040440.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410	Region of unknown function DUF1985
4DE	g1458.t1	18350441	18352752	2311	3E-60	53.14	75	Solyc03g032030.2.1	Mitochondrial phosphate carrier protein IPR001993	Mitochondrial substrate carrier
4DE	g1470.t1	18477841	18479476	1635	7E-34	62.26	91	Solyc06g011500.1.1	Unknown Protein	
4DE	g1480.t1	18539035	18542196	3161	5E-32	48.61	92	Solyc11g011230.1.1	F-box family protein IPR001810	Cyclin-like F-box
4DE	g1484.t1	18603711	18607546	3835	0E+00	98.98	100	Solyc04g025650.2.1	Monoxygenase FAD-binding IPR003042	Aromatic-ring hydroxylase-like
4DE	g1485.t1	18615654	18618896	3242	5E-34	98.25	66	Solyc04g025670.2.1	Os02g0741900 protein (Fragment) IPR019181	RNA-processing, Lsm domain
4DE	g1494.t1	18714916	18720532	5616	8E-91	86.45	70	Solyc04g025740.1.1	Homeobox-leucine zipper protein ROC3 IPR001356	Homeobox
4DE	g1496.t2	18747444	18752522	5078	0E+00	98.62	44	Solyc04g025750.2.1	Nodulin MtN21 family protein IPR000620	Protein of unknown function DUF6, transmembrane
4DE	g1496.t1	18749939	18752522	2583	0E+00	98.64	100	Solyc04g025750.2.1	Nodulin MtN21 family protein IPR000620	Protein of unknown function DUF6, transmembrane
4DE	g1497.t1	18753598	18754572	974	2E-150	96.65	100	Solyc04g025760.1.1	NAC-domain transcription factor protein	
4DE	g1500.t1	18783731	18787725	3994	2E-15	60.34	26	Solyc04g054680.1.1	RING finger protein B IPR001841	Zinc finger, RING-type
4DE	g1506.t1	18865694	18868428	2734	1E-10	52.17	15	Solyc05g017810.1.1	Unknown Protein	
4DE	g1511.t1	18929897	18946038	16141	2E-31	73.61	25	Solyc00g006010.1.1	Unknown Protein	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g1520.t1	19033482	19034333	851	1E-15	76.09	59	Solyc10g074760.1.1	Unknown Protein	
4DE	g1521.t2	19043232	19056999	13767	5E-155	62.36	27	Solyc04g009690.1.1	Cc-nbs-lrr, resistance protein	
4DE	g1521.t1	19044442	19056999	12557	4E-155	62.36	28	Solyc04g009690.1.1	Cc-nbs-lrr, resistance protein	
4DE	g1524.t1	19075716	19086883	11167	3E-177	98.49	55	Solyc04g025870.2.1	AP-1 complex subunit gamma-1 IPR017107 Adaptor protein complex AP-1, gamma subunit	
4DE	g1525.t2	19086934	19095193	8259	4E-60	93.69	29	Solyc04g025870.2.1	AP-1 complex subunit gamma-1 IPR017107 Adaptor protein complex AP-1, gamma subunit	
4DE	g1525.t1	19092858	19095193	2335	3E-49	97.67	45	Solyc04g025870.2.1	AP-1 complex subunit gamma-1 IPR017107 Adaptor protein complex AP-1, gamma subunit	
4DE	g1526.t1	19095747	19106723	10976	0E+00	83.11	76	Solyc04g025870.2.1	AP-1 complex subunit gamma-1 IPR017107 Adaptor protein complex AP-1, gamma subunit	
4DE	g1527.t1	19107412	19111622	4210	2E-16	64.58	42	Solyc09g042380.1.1	Unknown Protein	
4DE	g1528.t1	19114502	19118114	3612	1E-12	80.56	6	Solyc07g019470.1.1	Unknown Protein	
4DE	g1531.t1	19129312	19135791	6479	2E-44	55.03	21	Solyc05g017810.1.1	Unknown Protein	
4DE	g1538.t2	19231275	19257853	26578	0E+00	96.07	29	Solyc04g025880.2.1	Potassium transporter IPR018519 Potassium uptake protein, kup IPR003855 K+ potassium transporter	
4DE	g1538.t1	19232855	19248748	15893	0E+00	96.07	55	Solyc04g025880.2.1	Potassium transporter IPR018519 Potassium uptake protein, kup IPR003855 K+ potassium transporter	
4DE	g1541.t1	19323005	19332238	9233	4E-12	45.24	14	Solyc09g042380.1.1	Unknown Protein	
4DE	g1544.t1	19375220	19378229	3009	0E+00	98.6	100	Solyc04g025940.2.1	Alpha alpha-trehalose-phosphate synthase (UDP-forming) IPR001830 Glycosyl transferase, family 20	
4DE	g1544.t2	19375220	19378229	3009	0E+00	98.13	100	Solyc04g025940.2.1	Alpha alpha-trehalose-phosphate synthase (UDP-forming) IPR001830 Glycosyl transferase, family 20	
4DE	g1551.t1	19503830	19504424	594	7E-13	75	31	Solyc07g019470.1.1	Unknown Protein	
4DE	g1555.t1	19579662	19582066	2404	2E-21	81.63	24	Solyc10g044870.1.1	Enzymatic polypeptide	
4DE	g1555.t2	19579662	19583726	4064	2E-20	81.63	16	Solyc10g044870.1.1	Enzymatic polypeptide	
4DE	g1563.t1	19655274	19663356	8082	2E-74	68.36	50	Solyc03g033560.2.1	Zinc finger protein IPR001876 Zinc finger, RanBP2-type	
4DE	g1564.t1	19681602	19682506	904	1E-48	87.78	87	Solyc07g048070.2.1	Membrane protein IPR017214 Uncharacterised conserved protein UCP037471	
4DE	g1571.t1	19759695	19760676	981	4E-35	76.92	51	Solyc05g017810.1.1	Unknown Protein	
4DE	g1573.t1	19772115	19774626	2511	2E-90	73.53	80	Solyc03g033560.2.1	Zinc finger protein IPR001876 Zinc finger, RanBP2-type	
4DE	g1578.t2	19901090	19912361	11271	2E-15	43.86	14	Solyc05g017810.1.1	Unknown Protein	
4DE	g1578.t1	19907972	19912361	4389	7E-18	44.63	19	Solyc05g017810.1.1	Unknown Protein	
4DE	g1580.t1	19915587	19916221	634	6E-24	66.27	100	Solyc03g063520.1.1	Unknown Protein	
4DE	g1581.t1	19919654	19927031	7377	7E-37	66.34	23	Solyc02g021080.1.1	Unknown Protein	
4DE	g1583.t1	19939465	19942101	2636	7E-12	76.74	10	Solyc05g017810.1.1	Unknown Protein	
4DE	g1586.t1	19974922	19982411	7489	0E+00	99.65	100	Solyc04g025990.2.1	Potassium transporter family protein IPR003855 K+ potassium transporter	
4DE	g1587.t1	20005900	20017107	11207	7E-14	57.63	19	Solyc10g074760.1.1	Unknown Protein	
4DE	g1590.t1	20065978	20068449	2471	3E-52	90	60	Solyc05g013790.2.1	Nucleoporin GLE1 IPR012476 GLE1-like	
4DE	g1593.t1	20092497	20100659	8162	2E-52	70.73	52	Solyc11g042690.1.1	Unknown Protein	
4DE	g1595.t1	20109488	20110405	917	1E-20	42.31	75	Solyc02g014390.1.1	Unknown Protein	
4DE	g1612.t1	20293418	20296905	3487	0E+00	98.35	100	Solyc04g026020.2.1	Sieve element-occluding protein 3	
4DE	g1615.t1	20318118	20324187	6069	2E-10	35.09	33	Solyc02g021080.1.1	Unknown Protein	
4DE	g1621.t1	20391001	20395059	4058	0E+00	100	100	Solyc04g026030.2.1	Spermidine synthase IPR001045 Spermine synthase	
4DE	g1621.t2	20391001	20395059	4058	0E+00	99.03	100	Solyc04g026030.2.1	Spermidine synthase IPR001045 Spermine synthase	
4DE	g1624.t1	20435638	20445948	10310	1E-48	97.56	49	Solyc03g116050.1.1	Pre-mRNA-splicing factor cwc22 IPR003890 MIF4G-like, type 3	
4DE	g1628.t1	20477309	20480749	3440	4E-21	54.93	16	Solyc02g036400.1.1	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence	
4DE	g1632.t1	20568253	20584012	15759	0E+00	86.65	55	Solyc02g038640.1.1	Replication protein A1 IPR012340 Nucleic acid-binding, OB-fold	
4DE	g1632.t3	20568253	20575350	7097	2E-97	69.3	51	Solyc09g015140.2.1	Unknown Protein IPR016027 Nucleic acid-binding, OB-fold-like	
4DE	g1632.t2	20580233	20584012	3779	0E+00	86.65	88	Solyc02g038640.1.1	Replication protein A1 IPR012340 Nucleic acid-binding, OB-fold	
4DE	g1636.t1	20625414	20631754	6340	5E-67	66.25	100	Solyc01g011150.1.1	Unknown Protein IPR006564 Zinc finger, PMZ-type	
4DE	g1641.t1	20675677	20677624	1947	9E-167	60.14	81	Solyc12g036370.1.1	Unknown Protein	
4DE	g1642.t2	20677994	20691924	13930	0E+00	53.65	31	Solyc00g015610.1.1	Unknown Protein	
4DE	g1642.t1	20678164	20691814	13650	0E+00	53.65	32	Solyc00g015610.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g1643.t1	20692093	20696493	4400	6E-52	58.9	68	Solyc04g025820.1.1	Nbs, resistance protein fragment	
4DE	g1647.t1	20749448	20754662	5214	1E-47	73.17	43	Solyc12g038430.1.1	Kinesin-like calmodulin binding protein	
4DE	g1652.t1	20824957	20825489	532	1E-45	75	100	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g1655.t1	20860628	20862403	1775	2E-27	42.38	39	Solyc01g102260.2.1	Pheres1 (Fragment) IPR002100 Transcription factor, MADS-box	
4DE	g1661.t1	20907808	20908918	1110	2E-104	100	100	Solyc04g026100.1.1	30S ribosomal protein S9 IPR000754 Ribosomal protein S9	
4DE	g1665.t1	20945790	20955874	10084	3E-22	53.28	14	Solyc05g017810.1.1	Unknown Protein	
4DE	g1668.t1	20969912	20973384	3472	0E+00	74.06	99	Solyc04g009260.1.1	Cc-nbs-lrr, resistance protein	
4DE	g1673.t1	21034694	21035244	550	3E-73	98.13	100	Solyc04g026140.1.1	Embryo-abundant protein (Fragment)	
4DE	g1675.t1	21059465	21063704	4239	2E-11	43.48	21	Solyc02g021080.1.1	Unknown Protein	
4DE	g1677.t1	21071092	21074204	3112	5E-17	64.81	68	Solyc02g021080.1.1	Unknown Protein	
4DE	g1682.t1	21136294	21137980	1686	8E-42	68.25	39	Solyc05g017810.1.1	Unknown Protein	
4DE	g1689.t1	21240939	21241785	846	3E-15	40.18	78	Solyc01g044510.1.1	Unknown Protein	
4DE	g1690.t1	21246294	21247362	1068	2E-16	38.46	56	Solyc09g074940.1.1	Translocase of chloroplast 90, chloroplastic IPR005690 Chloroplast protein import component Toc86_159	
4DE	g1691.t1	21252824	21255193	2369	6E-53	58.87	96	Solyc02g037570.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1	
4DE	g1714.t1	21536223	21558412	22189	6E-180	96.96	63	Solyc04g026200.2.1	Sentrin-specific protease 2 IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1	
4DE	g1718.t1	21593303	21601831	8528	6E-31	50	38	Solyc06g035600.2.1	Pentatricopeptide repeat-containing protein IPR008991 Translation protein SH3-like	
4DE	g1719.t1	21602757	21603504	747	3E-29	76.06	60	Solyc06g035600.2.1	Pentatricopeptide repeat-containing protein IPR008991 Translation protein SH3-like	
4DE	g1720.t1	21609763	21611453	1690	2E-13	51.85	66	Solyc02g083980.2.1	Endoglucanase 1 IPR001701 Glycoside hydrolase, family 9	
4DE	g1729.t1	21703350	21705875	2525	4E-47	65	85	Solyc04g026210.2.1	Dual serine_threonine and tyrosine protein kinase IPR015783 ATMRK serine_threonine protein kinase-like	
4DE	g1731.t1	21721024	21722675	1651	1E-17	31.43	64	Solyc00g304030.1.1	Macrolide export ATP-binding_permease protein MacB IPR003439 ABC transporter-like	
4DE	g1733.t1	21739324	21744919	5595	4E-21	84.09	35	Solyc04g026200.2.1	Sentrin-specific protease 2 IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1	
4DE	g1734.t1	21747112	21749255	2143	9E-113	48.38	98	Solyc12g062280.1.1	Protein kinase IPR015783 ATMRK serine_threonine protein kinase-like	
4DE	g1738.t1	21792878	21793895	1017	3E-37	55.22	90	Solyc06g009720.1.1	Unknown Protein	
4DE	g1766.t1	22218219	22227404	9185	4E-10	53.7	34	Solyc02g021080.1.1	Unknown Protein	
4DE	g1767.t1	22233663	22238295	4632	5E-54	59.79	22	Solyc05g017810.1.1	Unknown Protein	
4DE	g1776.t1	22329063	22334364	5301	2E-169	98.29	72	Solyc04g026270.2.1	S2 self-incompatibility locus-linked pollen 3.15 protein (Fragment)	
4DE	g1778.t1	22357055	22381655	24600	3E-79	98.41	12	Solyc04g026280.2.1	S1 self-incompatibility locus-linked pollen 3.15 protein (Fragment)	
4DE	g1787.t1	22525359	22526024	665	2E-10	60	50	Solyc09g042380.1.1	Unknown Protein	
4DE	g1788.t1	22527634	22530814	3180	4E-28	42.16	33	Solyc05g017810.1.1	Unknown Protein	
4DE	g1790.t1	22535424	22535864	440	6E-26	65.71	64	Solyc09g042380.1.1	Unknown Protein	
4DE	g1792.t1	22547553	22550164	2611	3E-22	52.17	33	Solyc05g017810.1.1	Unknown Protein	
4DE	g1797.t2	22600033	22602530	2497	3E-15	66.13	12	Solyc01g022790.1.1	Unknown Protein	
4DE	g1797.t1	22600033	22601637	1604	2E-11	71.79	11	Solyc07g019470.1.1	Unknown Protein	
4DE	g1801.t1	22637638	22640254	2616	7E-20	45.06	21	Solyc05g017810.1.1	Unknown Protein	
4DE	g1831.t1	23000153	23004016	3863	2E-19	37.14	100	Solyc12g035290.1.1	Unknown Protein	
4DE	g1832.t1	23007738	23014404	6666	8E-48	75.7	28	Solyc06g074110.2.1	Uncharacterized basic helix-loop-helix protein At1g64625 IPR001092 Basic helix-loop-helix dimerisation region bHLH	
4DE	g1836.t1	23042956	23047154	4198	2E-32	59	39	Solyc02g021080.1.1	Unknown Protein	
4DE	g1851.t1	23291299	23293575	2276	6E-18	44.92	28	Solyc05g017810.1.1	Unknown Protein	
4DE	g1860.t1	23415950	23427275	11325	7E-111	91.43	27	Solyc07g043210.1.1	Unknown Protein	
4DE	g1860.t2	23416082	23427275	11193	5E-111	91.43	26	Solyc07g043210.1.1	Unknown Protein	
4DE	g1863.t1	23449360	23450815	1455	8E-29	87.5	24	Solyc10g044870.1.1	Enzymatic polypeptide	
4DE	g1874.t1	23524014	23525982	1968	2E-129	92.79	52	Solyc07g043210.1.1	Unknown Protein	
4DE	g1880.t1	23582179	23589872	7693	2E-69	69.51	61	Solyc08g028810.1.1	Nucleic acid-binding OB-fold IPR012340 Nucleic acid-binding, OB-fold	
4DE	g1888.t1	23688011	23691292	3281	2E-77	40.19	91	Solyc02g070450.1.1	Glucan endo-1 3-beta-glucosidase 7 IPR013781 Glycoside hydrolase, subgroup, catalytic core	
4DE	g1889.t1	23696041	23696898	857	5E-89	97.69	100	Solyc04g026250.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g1891.i2	23715432	23719162	3730	7E-96	77.95	24	Solyc10g074350.1.1	Unknown Protein	
4DE	g1891.i1	23715432	23724422	8990	6E-93	77.95	15	Solyc10g074350.1.1	Unknown Protein	
4DE	g1893.i1	23732316	23733517	1201	1E-17	40.37	78	Solyc01g058710.1.1	Unknown Protein	
4DE	g1895.i1	23779986	23780905	919	1E-103	96.67	100	Solyc04g028380.1.1	Sulfotransferase 5b IPR000863 Sulfotransferase	
4DE	g1896.i1	23782541	23785547	3006	1E-93	65.53	69	Solyc10g012480.1.1	Unknown Protein	
4DE	g1909.i1	23961404	23963771	2367	8E-25	93.62	34	Solyc04g028430.1.1	Unknown Protein	
4DE	g1913.i1	24037039	24038225	1186	8E-35	41.57	83	Solyc01g056820.1.1	Methionine aminopeptidase, related	
4DE	g1914.i1	24039811	24042645	2834	1E-16	32.67	47	Solyc04g039640.2.1	Unknown Protein	
4DE	g1914.i2	24039811	24042645	2834	2E-16	34.67	42	Solyc04g039640.2.1	Unknown Protein	
4DE	g1920.i1	24128521	24131679	3158	2E-62	71.23	95	Solyc08g041790.1.1	Unknown Protein	
4DE	g1935.i1	24303769	24306810	3041	2E-38	65.35	25	Solyc02g021080.1.1	Unknown Protein	
4DE	g1936.i1	24329789	24338663	8874	3E-13	48.72	96	Solyc01g014490.2.1	Type II DNA topoisomerase VI subunit B IPR015320 DNA topoisomerase VI, subunit B, transducer	
4DE	g1956.i1	24669404	24673375	3971	4E-73	92.31	73	Solyc04g028450.1.1	Unknown Protein	
4DE	g1959.i1	24760884	24774315	13431	1E-13	51.09	27	Solyc10g018960.1.1	Unknown Protein	
4DE	g1974.i1	24999970	25000445	475	7E-12	64.44	53	Solyc09g042380.1.1	Unknown Protein	
4DE	g1975.i1	25001804	25004415	2611	8E-43	53.63	35	Solyc05g017810.1.1	Unknown Protein	
4DE	g1977.i1	25014497	25018695	4198	2E-46	59.87	27	Solyc05g017810.1.1	Unknown Protein	
4DE	g1980.i1	25035314	25036447	1133	1E-11	40.34	85	Solyc01g017560.1.1	Unknown Protein	
4DE	g1981.i2	25045938	25063135	17197	1E-91	97.78	33	Solyc04g028470.1.1	GDSL esterase_lipase 2 IPR001087 Lipase, GDSL	
4DE	g1981.i1	25056680	25063135	6455	2E-100	97.92	99	Solyc04g028470.1.1	GDSL esterase_lipase 2 IPR001087 Lipase, GDSL	
4DE	g1994.i2	25310734	25316185	5451	1E-94	76.88	47	Solyc02g005220.1.1	Unknown Protein	
4DE	g1994.i1	25310734	25316185	5451	5E-94	76.88	45	Solyc02g005220.1.1	Unknown Protein	
4DE	g2006.i1	25532444	25535780	3336	1E-18	41.46	34	Solyc12g070240.1.1	Unknown Protein	
4DE	g2009.i1	25580674	25586400	5726	9E-15	63.93	15	Solyc05g017810.1.1	Unknown Protein	
4DE	g2020.i1	25671278	25691124	19846	1E-18	70.89	25	Solyc05g017810.1.1	Unknown Protein	
4DE	g2021.i1	25729373	25730552	1179	2E-116	94.62	100	Solyc04g039720.1.1	Unknown Protein IPR010666 Zinc finger, GRF-type	
4DE	g2023.i1	25765093	25769294	4201	1E-75	68.09	47	Solyc01g044390.1.1	Unknown Protein	
4DE	g2025.i1	25790262	25794264	4002	0E+00	96.9	96	Solyc04g028560.2.1	Zinc finger transcription factor IPR013087 Zinc finger, C2H2-type_integrase, DNA-binding	
4DE	g2026.i1	25794763	25798318	3555	3E-30	43.92	22	Solyc03g077970.1.1	Methionine aminopeptidase, related	
4DE	g2027.i1	25799364	25800894	1530	3E-171	96.69	93	Solyc04g028570.1.1	Lysine-specific demethylase 4D IPR013129 Transcription factor jumonji	
4DE	g2027.i2	25799364	25808134	8770	3E-170	96.69	77	Solyc04g028570.1.1	Lysine-specific demethylase 4D IPR013129 Transcription factor jumonji	
4DE	g2028.i1	25812938	25814244	1306	0E+00	99.71	100	Solyc04g028580.1.1	Lysine-specific demethylase 5A IPR013129 Transcription factor jumonji	
4DE	g2058.i1	26450945	26473133	22188	6E-29	74.65	16	Solyc02g081160.2.1	Diphosphate-fructose-6-phosphate 1-phosphotransferase IPR011183 Pyrophosphate-dependent phosphofructokinase PfpB	
4DE	g2059.i1	26484575	26494692	10117	1E-120	100	84	Solyc04g026350.2.1	Calmodulin IPR011992 EF-Hand type	
4DE	g2060.i1	26501816	26505405	3589	5E-16	67.31	10	Solyc01g050080.1.1	Unknown Protein	
4DE	g2077.i1	26696089	26698368	2279	1E-15	28.43	52	Solyc10g050070.1.1	HGWP repeat containing protein-like	
4DE	g2113.i1	27284759	27293098	8339	2E-77	94.17	52	Solyc01g007590.2.1	50S ribosomal protein L14 chloroplastic IPR005745 Ribosomal protein L14, bacterial-type	
4DE	g2115.i1	27307868	27308570	702	2E-15	50.62	54	Solyc05g021150.1.1	Unknown Protein	
4DE	g2120.i1	27472019	27475870	3851	7E-13	45.45	61	Solyc05g026510.2.1	Cohesin subunit IPR013721 STAG	
4DE	g2121.i1	27484764	27489560	4796	3E-22	71.01	44	Solyc01g014490.2.1	Type II DNA topoisomerase VI subunit B IPR015320 DNA topoisomerase VI, subunit B, transducer	
4DE	g2128.i1	27541479	27547043	5564	2E-11	47.44	20	Solyc11g039410.1.1	Unknown Protein	
4DE	g2129.i2	27548127	27556320	8193	9E-114	60.47	21	Solyc00g015610.1.1	Unknown Protein	
4DE	g2129.i1	27549513	27556320	6807	3E-114	60.47	22	Solyc00g015610.1.1	Unknown Protein	
4DE	g2136.i1	27616597	27617227	630	6E-13	42.27	99	Solyc10g024450.1.1	Unknown Protein	
4DE	g2139.i1	27621952	27625767	3815	2E-13	23.94	67	Solyc12g077350.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g2147.t1	27688066	27691810	3744	3E-10	24.39	64	Solyc05g016580.1.1	Unknown Protein	
4DE	g2148.t1	27692887	27694677	1790	6E-42	61.54	45	Solyc05g017810.1.1	Unknown Protein	
4DE	g2159.t1	27782058	27787395	5337	2E-11	33.59	18	Solyc11g039420.1.1	Unknown Protein	
4DE	g2186.t1	28024534	28028590	4056	3E-48	85.39	45	Solyc11g039560.1.1	Unknown Protein	
4DE	g2203.t1	28266332	28273204	6872	4E-27	60.23	80	Solyc11g042690.1.1	Unknown Protein	
4DE	g2204.t1	28274020	28275813	1793	1E-93	78.43	81	Solyc06g051580.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g2206.t1	28292341	28300779	8438	2E-148	100	49	Solyc04g026360.2.1	AP-1 complex subunit mu IPR011012	Longin-like
4DE	g2206.t2	28292341	28315692	23351	4E-138	100	14	Solyc04g026360.2.1	AP-1 complex subunit mu IPR011012	Longin-like
4DE	g2219.t1	28470202	28470672	470	3E-12	62.22	54	Solyc09g042380.1.1	Unknown Protein	
4DE	g2224.t1	28532686	28538540	5854	1E-41	56.79	27	Solyc05g017810.1.1	Unknown Protein	
4DE	g2240.t1	28760881	28770421	9540	7E-61	65.2	30	Solyc05g017810.1.1	Unknown Protein	
4DE	g2243.t1	28805989	28808962	2973	0E+00	75.37	79	Solyc02g014550.1.1	Unknown Protein	
4DE	g2244.t1	28809839	28810882	1043	2E-89	86.05	99	Solyc06g051580.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g2245.t2	28811295	28813232	1937	8E-69	47.6	96	Solyc06g036510.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g2245.t1	28812332	28813232	900	1E-19	88.37	37	Solyc11g039510.1.1	Unknown Protein	
4DE	g2246.t1	28813781	28826514	12733	0E+00	87.71	70	Solyc04g039620.2.1	Ribose-phosphate pyrophosphokinase 4 IPR000836	Phosphoribosyltransferase
4DE	g2249.t1	28837345	28849563	12218	0E+00	94.39	36	Solyc04g039640.2.1	Unknown Protein	
4DE	g2251.t1	28869105	28881541	12436	1E-50	59.78	18	Solyc05g017810.1.1	Unknown Protein	
4DE	g2252.t1	28882945	28903692	20747	5E-11	80	7	Solyc09g042380.1.1	Unknown Protein	
4DE	g2253.t1	28905020	28907546	2526	8E-54	64.2	29	Solyc05g017810.1.1	Unknown Protein	
4DE	g2253.t2	28905020	28907546	2526	9E-54	64.2	29	Solyc05g017810.1.1	Unknown Protein	
4DE	g2271.t1	29247299	29257312	10013	6E-34	62.37	46	Solyc02g021080.1.1	Unknown Protein	
4DE	g2272.t1	29258157	29260682	2525	2E-18	75	51	Solyc01g057970.1.1	Unknown Protein	
4DE	g2273.t1	29302431	29303372	941	3E-41	83.33	73	Solyc09g042380.1.1	Unknown Protein	
4DE	g2282.t1	29496014	29501822	5808	9E-48	54.05	40	Solyc05g017810.1.1	Unknown Protein	
4DE	g2284.t1	29509971	29514103	4132	8E-14	56.92	52	Solyc01g044400.1.1	Unknown Protein	
4DE	g2285.t1	29520284	29524492	4208	2E-68	52.87	79	Solyc04g039600.1.1	Unknown Protein	
4DE	g2286.t1	29524848	29526772	1924	2E-26	83.02	38	Solyc02g021750.1.1	Unknown Protein	
4DE	g2296.t1	29679816	29693881	14065	2E-21	49.5	20	Solyc02g021080.1.1	Unknown Protein	
4DE	g2309.t1	29832536	29834840	2304	7E-27	50.71	28	Solyc05g017810.1.1	Unknown Protein	
4DE	g2311.t1	29842203	29845770	3567	2E-18	64.71	11	Solyc01g022790.1.1	Unknown Protein	
4DE	g2320.t1	29929009	29932858	3849	0E+00	94.56	100	Solyc05g005160.2.1	ATP-citrate lyase A-2 IPR016102	Succinyl-CoA synthetase-like
4DE	g2328.t1	30031230	30034678	3448	2E-15	45.98	32	Solyc05g017810.1.1	Unknown Protein	
4DE	g2335.t1	30085007	30088537	3530	2E-40	52.17	31	Solyc05g017810.1.1	Unknown Protein	
4DE	g2343.t2	30131537	30147556	16019	9E-59	64.02	18	Solyc05g017810.1.1	Unknown Protein	
4DE	g2343.t1	30133127	30144442	11315	4E-59	64.02	20	Solyc05g017810.1.1	Unknown Protein	
4DE	g2345.t1	30157780	30160968	3188	3E-66	97.17	49	Solyc04g039690.1.1	Unknown Protein	
4DE	g2345.t2	30157780	30163118	5338	1E-65	97.17	29	Solyc04g039690.1.1	Unknown Protein	
4DE	g2348.t1	30197777	30203480	5703	0E+00	91.15	100	Solyc04g039730.2.1	Receptor like kinase, RLK	
4DE	g2353.t1	30255648	30268610	12962	7E-11	75	9	Solyc07g019470.1.1	Unknown Protein	
4DE	g2356.t1	30326403	30328390	1987	5E-39	37	98	Solyc12g082770.1.1	Unknown Protein	
4DE	g2357.t1	30328489	30331573	3084	2E-19	38.3	26	Solyc00g005280.1.1	Unknown Protein	
4DE	g2358.t1	30332320	30339870	7550	1E-32	35.46	73	Solyc00g008140.1.1	Unknown Protein	
4DE	g2361.t1	30371411	30376630	5219	1E-43	40	87	Solyc12g082770.1.1	Unknown Protein	
4DE	g2362.t1	30376729	30382423	5694	2E-11	34.36	11	Solyc00g005280.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g2363.t1	30397269	30398003	734	7E-16	40.98	65	Solyc06g016680.1.1	Unknown Protein	
4DE	g2364.t1	30447814	30463948	16134	1E-50	31.09	60	Solyc00g008000.1.1	Unknown Protein	
4DE	g2366.t1	30521926	30529165	7239	0E+00	86.71	50	Solyc04g039990.2.1	Cc-ribs, resistance protein fragment	
4DE	g2367.t1	30529813	30530725	912	3E-26	63.95	97	Solyc10g079580.1.1	RNA-binding region RNP-1 IPR000504 RNA recognition motif, RNP-1	
4DE	g2368.t1	30530861	30539555	8694	6E-13	48.44	41	Solyc03g097080.2.1	Unknown Protein IPR006525 Cystatin-related, plant	
4DE	g2371.t1	30584073	30589475	5402	1E-40	84	47	Solyc04g040050.1.1	Unknown Protein	
4DE	g2372.t1	30589551	30595235	5684	2E-21	46.15	60	Solyc03g097080.2.1	Unknown Protein IPR006525 Cystatin-related, plant	
4DE	g2374.t1	30625633	30628276	2643	5E-66	65.03	95	Solyc10g079580.1.1	RNA-binding region RNP-1 IPR000504 RNA recognition motif, RNP-1	
4DE	g2375.t1	30639376	30644706	5330	1E-26	56.82	71	Solyc03g063820.1.1	Unknown Protein	
4DE	g2376.t1	30646125	30648577	2452	2E-22	79.25	71	Solyc09g042380.1.1	Unknown Protein	
4DE	g2382.t1	30732375	30735378	3003	0E+00	97.38	100	Solyc04g040090.2.1	Strictosidine synthase-like protein IPR004141 Strictosidine synthase	
4DE	g2386.t1	30767175	30776454	9279	0E+00	88.82	99	Solyc04g040110.2.1	Kinesin-like protein IPR001752 Kinesin, motor region	
4DE	g2386.t2	30767175	30787810	20635	0E+00	91.79	71	Solyc04g040110.2.1	Kinesin-like protein IPR001752 Kinesin, motor region	
4DE	g2386.t3	30784785	30787810	3025	2E-121	97.97	40	Solyc04g040110.2.1	Kinesin-like protein IPR001752 Kinesin, motor region	
4DE	g2388.t1	30790115	30801339	11224	0E+00	98.03	40	Solyc04g040110.2.1	Kinesin-like protein IPR001752 Kinesin, motor region	
4DE	g2388.t2	30790115	30801499	11384	0E+00	98.03	39	Solyc04g040110.2.1	Kinesin-like protein IPR001752 Kinesin, motor region	
4DE	g2389.t1	30804646	30805986	1340	0E+00	97.6	100	Solyc04g040120.1.1	Omega-6 fatty acid desaturase IPR005804 Fatty acid desaturase, type 1	
4DE	g2390.t1	30813483	30814826	1343	0E+00	99.73	100	Solyc04g040130.1.1	Omega-6 fatty acid desaturase IPR005804 Fatty acid desaturase, type 1	
4DE	g2394.t1	30879945	30880971	1026	2E-120	83.41	79	Solyc03g062840.1.1	Unknown Protein	
4DE	g2395.t1	30901855	30906648	4793	9E-106	52.67	43	Solyc11g050700.1.1	Zinc finger CCHC-type	
4DE	g2396.t1	30907655	30911453	3798	0E+00	87.77	49	Solyc06g030440.1.1	N-6 Adenine-specific DNA methylase	
4DE	g2396.t2	30907655	30911453	3798	0E+00	87.77	55	Solyc06g030440.1.1	N-6 Adenine-specific DNA methylase	
4DE	g2398.t1	30920245	30926911	6666	1E-153	75.32	23	Solyc00g304030.1.1	Macrolide export ATP-binding_permease protein MacB IPR003439 ABC transporter-like	
4DE	g2401.t1	31018390	31023327	4937	0E+00	83.99	99	Solyc04g025950.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g2401.t2	31018390	31023327	4937	0E+00	85.11	99	Solyc12g019730.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g2403.t1	31029351	31033477	4126	0E+00	91.04	100	Solyc12g019730.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g2403.t2	31029351	31040907	11556	0E+00	83	97	Solyc06g069160.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g2415.t1	31204466	31209165	4699	7E-126	50	63	Solyc03g062840.1.1	Unknown Protein	
4DE	g2415.t2	31204466	31209165	4699	1E-125	50	61	Solyc03g062840.1.1	Unknown Protein	
4DE	g2420.t1	31239514	31245271	5757	1E-11	72.09	10	Solyc09g042380.1.1	Unknown Protein	
4DE	g2426.t1	31299814	31306415	6601	0E+00	76.4	94	Solyc04g045310.2.1	Extracellular ligand-gated ion channel	
4DE	g2432.t1	31372668	31373345	677	3E-19	75	42	Solyc09g042380.1.1	Unknown Protein	
4DE	g2433.t1	31374715	31376615	1900	1E-65	67.65	39	Solyc05g017810.1.1	Unknown Protein	
4DE	g2434.t1	31376665	31383455	6790	5E-14	77.78	20	Solyc07g019470.1.1	Unknown Protein	
4DE	g2439.t1	31448351	31450775	2424	3E-22	46.53	41	Solyc03g063820.1.1	Unknown Protein	
4DE	g2454.t1	31654119	31655272	1153	1E-51	54.7	97	Solyc01g066110.1.1	Glucosyltransferase IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
4DE	g2462.t1	31817650	31820100	2450	1E-44	77.01	97	Solyc04g024880.1.1	Unknown Protein	
4DE	g2466.t2	31838699	31851250	12551	2E-19	67.65	20	Solyc01g022790.1.1	Unknown Protein	
4DE	g2466.t1	31838718	31845790	7072	1E-19	67.65	23	Solyc01g022790.1.1	Unknown Protein	
4DE	g2468.t1	31873649	31877556	3907	6E-20	46.08	66	Solyc02g021080.1.1	Unknown Protein	
4DE	g2472.t1	31921091	31936550	15459	4E-39	52.76	20	Solyc05g017810.1.1	Unknown Protein	
4DE	g2484.t1	32083011	32087366	4355	2E-12	39.81	29	Solyc10g046780.1.1	Zinc knuckle family protein IPR001878 Zinc finger, CCHC-type	
4DE	g2485.t1	32097665	32101179	3514	6E-23	53.91	29	Solyc05g017810.1.1	Unknown Protein	
4DE	g2486.t1	32110455	32111444	989	2E-24	85.51	93	Solyc01g105360.2.1	UDP-glucuronosyltransferase IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
4DE	g2489.t1	32131745	32136148	4403	6E-40	56.32	32	Solyc05g017810.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g2495.t1	32168460	32172947	4487	3E-19	70.69	57	Solyc02g021080.1.1	Unknown Protein	
4DE	g2497.t1	32182508	32183037	529	5E-23	75.47	52	Solyc09g042380.1.1	Unknown Protein	
4DE	g2504.t1	32271256	32275322	4066	1E-26	50	23	Solyc11g013210.1.1	Unknown Protein	
4DE	g2505.i2	32279856	32301155	21299	0E+00	91.19	60	Solyc04g045340.2.1	Phosphoglucosyltransferase IPR016055 Alpha-D-phosphohexomutase, alpha_beta_alpha I, II and III	
4DE	g2505.t1	32291406	32301155	9749	0E+00	91.19	99	Solyc04g045340.2.1	Phosphoglucosyltransferase IPR016055 Alpha-D-phosphohexomutase, alpha_beta_alpha I, II and III	
4DE	g2508.t1	32341066	32346971	5905	6E-68	71.58	70	Solyc10g052410.1.1	Unknown Protein	
4DE	g2509.t1	32370320	32381121	10801	1E-126	73.58	29	Solyc01g090330.1.1	Unknown Protein	
4DE	g2510.t1	32390320	32394746	4426	3E-35	58.68	52	Solyc12g100000.1.1	U-box domain-containing protein 4 IPR011989 Armadillo-like helical	
4DE	g2534.t1	32639732	32644531	4799	4E-50	54.3	60	Solyc05g017810.1.1	Unknown Protein	
4DE	g2549.t1	32838711	32840581	1870	6E-36	80.77	66	Solyc02g014760.1.1	Unknown Protein	
4DE	g2557.t1	32939529	32944461	4932	7E-10	60.42	11	Solyc01g050080.1.1	Unknown Protein	
4DE	g2566.t1	33080841	33083781	2940	1E-18	52.17	42	Solyc08g048130.1.1	Unknown Protein	
4DE	g2567.t1	33084760	33091671	6911	4E-10	48.15	12	Solyc09g055600.1.1	Endonuclease_exonuclease_phosphatase, related	
4DE	g2569.t1	33120276	33121971	1695	2E-16	53.66	43	Solyc08g048020.1.1	Unknown Protein	
4DE	g2570.t1	33130067	33131761	1694	9E-17	46.84	43	Solyc09g055600.1.1	Endonuclease_exonuclease_phosphatase, related	
4DE	g2571.t1	33141853	33144241	2388	9E-14	37.5	48	Solyc09g055970.1.1	Unknown Protein	
4DE	g2573.t1	33174336	33182991	8655	6E-63	62.84	38	Solyc08g047940.1.1	Unknown Protein	
4DE	g2578.i2	33278062	33286716	8654	0E+00	93.19	69	Solyc04g024500.2.1	UPF0760 protein C2orf29 homolog	
4DE	g2578.i3	33278062	33298171	20109	0E+00	99.64	45	Solyc04g024500.2.1	UPF0760 protein C2orf29 homolog	
4DE	g2578.t1	33294952	33298171	3219	3E-90	84.15	100	Solyc04g024510.2.1	UPF0760 protein C2orf29 homolog IPR019312 Protein of unknown function DUF2363	
4DE	g2588.t1	33443229	33454104	10875	0E+00	97.9	58	Solyc04g024520.2.1	AT5g13970_MAC12_6	
4DE	g2609.t1	33824016	33836381	12365	2E-31	62.64	25	Solyc04g047780.1.1	DNA glycosylase (Fragment)	
4DE	g2610.t1	33841460	33848039	6579	0E+00	93.86	95	Solyc09g014660.1.1	HGWP repeat containing protein-like	
4DE	g2611.t1	33848058	33849161	1103	0E+00	96.69	96	Solyc02g077250.2.1	Transcription factor CYCLOIDEA (Fragment) IPR005333 Transcription factor, TCP	
4DE	g2615.i2	33883519	33893611	10092	6E-12	77.78	10	Solyc07g019470.1.1	Unknown Protein	
4DE	g2615.t1	33883599	33893611	10012	5E-12	77.78	10	Solyc07g019470.1.1	Unknown Protein	
4DE	g2626.t1	34002491	34004571	2080	2E-28	69.23	97	Solyc09g042380.1.1	Unknown Protein	
4DE	g2627.t1	34020453	34033861	13408	0E+00	81.62	100	Solyc04g045430.2.1	Sh4 homologue protein IPR017877 MYB-like	
4DE	g2647.i3	34284782	34336625	51843	0E+00	87.03	24	Solyc04g045470.2.1	Os01g0841200 protein (Fragment) IPR004348 Protein of unknown function DUF246, plant	
4DE	g2654.t1	34411507	34420039	8532	2E-35	65.31	25	Solyc02g021080.1.1	Unknown Protein	
4DE	g2662.t1	34478687	34493316	14629	2E-169	74.58	95	Solyc04g045480.2.1	Ubiquitin thioesterase otubain-like protein IPR016615 Ubiquitin thioesterase Otubain	
4DE	g2663.i4	34495187	34521509	26322	0E+00	93.5	46	Solyc04g045530.2.1	DNA primase large subunit IPR016558 DNA primase, large subunit, eukaryotic	
4DE	g2663.t1	34512327	34521509	9182	0E+00	93.5	90	Solyc04g045530.2.1	DNA primase large subunit IPR016558 DNA primase, large subunit, eukaryotic	
4DE	g2696.t1	34875108	34893790	18682	0E+00	97.69	87	Solyc04g045560.2.1	Squamosa promoter-binding-like protein 11 IPR004333 Transcription factor, SBP-box	
4DE	g2699.i2	34911613	34923165	11552	6E-68	89.17	35	Solyc04g045580.2.1	Os04g0386500 protein (Fragment) IPR007454 Protein of unknown function DUF493	
4DE	g2707.t1	35099969	35107737	7768	0E+00	99.15	100	Solyc04g045590.2.1	Alpha-ketoglutarate-dependent dioxygenase AlkB IPR005123 Oxoglutarate and iron-dependent oxygenase	
4DE	g2708.t1	35107827	35112800	4973	0E+00	99.67	100	Solyc04g045600.2.1	Serine_threonine kinase IPR002290 Serine_threonine protein kinase	
4DE	g2723.i2	35250165	35255350	5185	2E-25	47.06	35	Solyc05g017810.1.1	Unknown Protein	
4DE	g2723.t1	35250165	35253140	2975	3E-25	47.06	35	Solyc05g017810.1.1	Unknown Protein	
4DE	g2728.t1	35313189	35323075	9886	0E+00	98.8	100	Solyc04g045630.2.1	CTD phosphatase-like protein IPR011948 Dullard-like phosphatase domain	
4DE	g2733.t1	35361637	35369685	8048	1E-21	58.23	6	Solyc09g042380.1.1	Unknown Protein	
4DE	g2749.t1	35618500	35625622	7122	3E-36	79.35	18	Solyc05g017810.1.1	Unknown Protein	
4DE	g2749.i2	35618500	35626022	7522	4E-36	79.35	15	Solyc05g017810.1.1	Unknown Protein	
4DE	g2750.t1	35630731	35646633	15902	0E+00	96.15	71	Solyc04g045650.2.1	Exostosin family protein IPR004263 Exostosin-like	
4DE	g2751.t1	35649215	35652632	3417	2E-84	97.6	60	Solyc04g045660.2.1	DNA mismatch repair protein MutL family protein IPR011186 DNA mismatch repair protein Mlh1	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	Slycopersicum (Heinz)		
4DE	g2753.t1	35660659	35666542	5883	2E-64	100	21	Solyc04g045660.2.1	DNA mismatch repair protein MutL family protein IPR011186	DNA mismatch repair protein Mlh1
4DE	g2754.t1	35672559	35689062	16503	0E+00	95.32	72	Solyc04g045660.2.1	DNA mismatch repair protein MutL family protein IPR011186	DNA mismatch repair protein Mlh1
4DE	g2754.t2	35685598	35689062	3464	0E+00	98.48	86	Solyc04g045660.2.1	DNA mismatch repair protein MutL family protein IPR011186	DNA mismatch repair protein Mlh1
4DE	g2760.t1	35794387	35808276	13889	2E-12	44.55	33	Solyc05g039920.2.1	Unknown Protein	
4DE	g2772.t1	35945617	35949447	3830	2E-10	58	16	Solyc01g050080.1.1	Unknown Protein	
4DE	g2778.t1	35999632	36005192	5560	1E-10	27.5	27	Solyc07g025280.1.1	Zinc knuckle family protein	
4DE	g2778.t2	35999632	36005192	5560	1E-10	27.5	29	Solyc07g025280.1.1	Zinc knuckle family protein	
4DE	g2788.t1	36117111	36128477	11366	2E-60	98.89	62	Solyc04g047670.2.1	Genomic DNA chromosome 5 TAC clone K12G2 IPR011691	SFT2-like
4DE	g2790.t1	36132188	36136472	4284	2E-74	94.67	29	Solyc04g047680.1.1	Os05g0235100 protein (Fragment)	
4DE	g2791.t1	36137891	36140491	2600	2E-44	97.22	72	Solyc04g047690.2.1	SFT2 domain containing 2 IPR011691	SFT2-like
4DE	g2792.t1	36149769	36160587	10818	5E-17	91.67	16	Solyc09g042380.1.1	Unknown Protein	
4DE	g2800.t1	36290553	36294667	4114	1E-12	58	31	Solyc02g021080.1.1	Unknown Protein	
4DE	g2807.t2	36382402	36390465	8063	5E-36	46.49	17	Solyc05g017810.1.1	Unknown Protein	
4DE	g2807.t1	36382709	36390465	7756	5E-36	46.49	17	Solyc05g017810.1.1	Unknown Protein	
4DE	g2812.t1	36417834	36439202	21368	5E-37	81.32	17	Solyc05g017810.1.1	Unknown Protein	
4DE	g2823.t1	36553230	36561031	7801	8E-124	90.91	61	Solyc04g047720.2.1	Unknown Protein	
4DE	g2824.t1	36562382	36579861	17479	1E-65	43.78	22	Solyc03g077970.1.1	Methionine aminopeptidase, related	
4DE	g2838.t1	36936376	36941001	4625	7E-59	64.22	30	Solyc05g017810.1.1	Unknown Protein	
4DE	g2849.t1	37099279	37102494	3215	5E-62	76.98	100	Solyc01g097460.2.1	Ribose-5-phosphate isomerase IPR004788	Ribose 5-phosphate isomerase
4DE	g2865.t2	37309314	37316536	7222	6E-39	52.87	27	Solyc05g017810.1.1	Unknown Protein	
4DE	g2865.t1	37315014	37316536	1522	2E-40	52.87	52	Solyc05g017810.1.1	Unknown Protein	
4DE	g2870.t1	37346026	37348665	2639	7E-12	80.56	12	Solyc07g019470.1.1	Unknown Protein	
4DE	g2875.t1	37418085	37425515	7430	6E-49	54.48	43	Solyc01g060160.1.1	Unknown Protein	
4DE	g2876.t1	37425854	37432880	7026	1E-52	48.95	80	Solyc04g047750.2.1	Alpha-taxilin IPR019132	Taxilin
4DE	g2876.t2	37425854	37432880	7026	3E-30	55.81	36	Solyc04g047750.2.1	Alpha-taxilin IPR019132	Taxilin
4DE	g2900.t1	37807560	37816396	8836	6E-22	47.52	43	Solyc02g021080.1.1	Unknown Protein	
4DE	g2906.t1	37955016	37960637	5621	2E-22	42.35	29	Solyc05g017810.1.1	Unknown Protein	
4DE	g2908.t1	37997246	37999894	2648	2E-37	79.12	51	Solyc05g017810.1.1	Unknown Protein	
4DE	g2911.t1	38029588	38034737	5149	2E-20	45.27	21	Solyc05g017810.1.1	Unknown Protein	
4DE	g2923.t1	38157415	38162091	4676	0E+00	95.05	100	Solyc04g047770.2.1	VHS domain-containing protein At3g16270 IPR018205	VHS subgroup
4DE	g2925.t1	38177835	38193568	15733	0E+00	90.14	57	Solyc04g047780.1.1	DNA glycosylase (Fragment)	
4DE	g2926.t1	38205526	38206226	700	3E-72	94.59	100	Solyc04g047800.1.1	Unknown Protein	
4DE	g2955.t1	38498031	38505467	7436	4E-64	90.57	51	Solyc04g047850.1.1	Unknown Protein	
4DE	g2958.t1	38535956	38543415	7459	1E-11	57.41	11	Solyc02g021080.1.1	Unknown Protein	
4DE	g2965.t1	38640869	38658434	17565	1E-32	81.71	4	Solyc04g047860.1.1	Unknown Protein	
4DE	g2967.t1	38669919	38676160	6241	4E-12	56.45	25	Solyc02g021080.1.1	Unknown Protein	
4DE	g2968.t1	38679669	38680389	720	7E-18	52.05	53	Solyc04g005730.2.1	Os12g0417000 protein (Fragment)	
4DE	g2972.t1	38715249	38717526	2277	4E-178	60.54	69	Solyc12g036370.1.1	Unknown Protein	
4DE	g2975.t1	38759359	38760163	804	2E-140	99.47	100	Solyc04g047870.1.1	MADS box transcription factor 1 IPR002100	Transcription factor, MADS-box
4DE	g2986.t1	38919706	38932563	12857	6E-30	76	34	Solyc12g027500.1.1	Unknown Protein	
4DE	g2987.t1	38948208	38953093	4885	4E-15	47.37	62	Solyc09g090880.1.1	Unknown Protein	
4DE	g2989.t1	38972112	38977949	5837	0E+00	69.04	34	Solyc11g050700.1.1	Zinc finger CCHC-type	
4DE	g2991.t1	39032698	39036268	3570	2E-45	92.41	32	Solyc04g047900.1.1	Unknown Protein	
4DE	g2995.t1	39113809	39120979	7170	7E-10	46.77	47	Solyc10g046780.1.1	Zinc knuckle family protein IPR001878	Zinc finger, CCHC-type
4DE	g2997.t1	39149350	39153656	4306	0E+00	99.17	99	Solyc04g048900.2.1	Calreticulin 2 calcium-binding protein IPR009169	Calreticulin

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g2999.i2	39157440	39168351	10911	5E-53	61.11	24	Solyc05g017810.1.1	Unknown Protein	
4DE	g2999.i1	39162010	39168351	6341	1E-53	61.11	31	Solyc05g017810.1.1	Unknown Protein	
4DE	g3002.i1	39197329	39205631	8302	8E-105	52.33	47	Solyc12g044200.1.1	Cc-nbs-lrr, resistance protein	
4DE	g3005.i1	39280250	39292735	12485	0E+00	98.99	100	Solyc04g048950.2.1	Necrotic spotted lesions 1 (Fragment) IPR001862 Membrane attack complex component_perforin_complement C9	
4DE	g3009.i1	39325959	39328029	2070	5E-87	87.58	72	Solyc04g048960.1.1	Cinnamyl alcohol dehydrogenase-like protein IPR002085 Alcohol dehydrogenase superfamily, zinc-containing	
4DE	g3009.i2	39325959	39328029	2070	6E-87	87.58	72	Solyc04g048960.1.1	Cinnamyl alcohol dehydrogenase-like protein IPR002085 Alcohol dehydrogenase superfamily, zinc-containing	
4DE	g3011.i1	39350782	39351489	707	2E-47	93.42	60	Solyc04g048980.2.1	Unknown Protein	
4DE	g3012.i1	39352896	39355279	2383	1E-59	80.65	88	Solyc04g048990.1.1	Unknown Protein	
4DE	g3020.i1	39423159	39426819	3660	5E-12	62.22	58	Solyc09g042380.1.1	Unknown Protein	
4DE	g3021.i1	39430312	39432639	2327	8E-30	53.92	47	Solyc02g021080.1.1	Unknown Protein	
4DE	g3033.i1	39591123	39592377	1254	1E-12	77.78	10	Solyc07g019470.1.1	Unknown Protein	
4DE	g3034.i1	39601516	39603944	2428	2E-76	61.24	100	Solyc04g049000.1.1	Actin IPR004000 Actin_actin-like	
4DE	g3041.i1	39705677	39735510	29833	1E-27	80.88	9	Solyc04g050270.1.1	Unknown Protein	
4DE	g3047.i1	39794367	39802473	8106	4E-36	71.43	42	Solyc09g042380.1.1	Unknown Protein	
4DE	g3047.i3	39806957	39810565	3608	7E-53	64.2	24	Solyc05g017810.1.1	Unknown Protein	
4DE	g3049.i1	39819017	39824061	5044	3E-11	45.45	32	Solyc02g014390.1.1	Unknown Protein	
4DE	g3054.i1	39861163	39863406	2243	1E-177	61.48	89	Solyc03g062840.1.1	Unknown Protein	
4DE	g3056.i1	39875848	39880344	4496	0E+00	97.6	100	Solyc04g049010.2.1	5_apos-3_apos exoribonuclease 2 IPR017151 5-3 exoribonuclease 2	
4DE	g3058.i1	39885627	39892964	7337	1E-85	87.66	37	Solyc04g049010.2.1	5_apos-3_apos exoribonuclease 2 IPR017151 5-3 exoribonuclease 2	
4DE	g3058.i2	39885627	39901844	16217	7E-84	87.66	26	Solyc04g049010.2.1	5_apos-3_apos exoribonuclease 2 IPR017151 5-3 exoribonuclease 2	
4DE	g3059.i2	39902987	39916054	13067	0E+00	84.25	99	Solyc04g049010.2.1	5_apos-3_apos exoribonuclease 2 IPR017151 5-3 exoribonuclease 2	
4DE	g3059.i1	39903044	39912994	9950	0E+00	92.59	99	Solyc04g049010.2.1	5_apos-3_apos exoribonuclease 2 IPR017151 5-3 exoribonuclease 2	
4DE	g3061.i1	39927798	39940404	12606	3E-21	52.81	70	Solyc09g042380.1.1	Unknown Protein	
4DE	g3063.i1	39972219	39973094	875	5E-48	93.83	45	Solyc04g049050.1.1	Unknown Protein	
4DE	g3064.i1	39973704	39978644	4940	2E-36	88.89	66	Solyc04g049060.1.1	Unknown Protein	
4DE	g3070.i2	40041836	40046314	4478	0E+00	92.15	97	Solyc04g049070.2.1	Alpha glucosidase II IPR000322 Glycoside hydrolase, family 31	
4DE	g3070.i1	40042457	40046314	3857	0E+00	92.15	100	Solyc04g049070.2.1	Alpha glucosidase II IPR000322 Glycoside hydrolase, family 31	
4DE	g3071.i1	40048723	40050654	1931	0E+00	97.58	95	Solyc04g049070.2.1	Alpha glucosidase II IPR000322 Glycoside hydrolase, family 31	
4DE	g3080.i1	40148913	40155929	7016	8E-32	51.27	21	Solyc05g017810.1.1	Unknown Protein	
4DE	g3085.i1	40201092	40206164	5072	6E-117	88.65	65	Solyc04g049080.2.1	Senescence-associated protein-like IPR018499 Tetraspanin	
4DE	g3088.i2	40256939	40265543	8604	0E+00	80.48	99	Solyc04g049090.2.1	MLO-like protein 17 IPR004326 Mlo-related protein	
4DE	g3088.i1	40257793	40265543	7750	0E+00	80.38	98	Solyc04g049090.2.1	MLO-like protein 17 IPR004326 Mlo-related protein	
4DE	g3089.i1	40293280	40295503	2223	0E+00	96.85	71	Solyc12g039050.1.1	PIF-like orf1	
4DE	g3096.i1	40384737	40394925	10188	0E+00	95.42	54	Solyc04g049120.2.1	Nuclear receptor corepressor 2 IPR014778 Myb, DNA-binding	
4DE	g3099.i1	40439777	40462431	22654	3E-107	79.62	28	Solyc04g049130.2.1	At5g03900 (Fragment) IPR000361 FeS cluster biogenesis	
4DE	g3099.i2	40439777	40447681	7904	2E-73	95.49	48	Solyc04g049130.2.1	At5g03900 (Fragment) IPR000361 FeS cluster biogenesis	
4DE	g3102.i1	40505186	40523428	18242	0E+00	98.29	100	Solyc04g049140.2.1	Transcription factor jumonji domain-containing protein IPR013129 Transcription factor jumonji	
4DE	g3108.i1	40640713	40659769	19056	0E+00	100	67	Solyc04g049160.2.1	Calcium dependent protein kinase IPR002290 Serine_threonine protein kinase	
4DE	g3117.i1	40814305	40821805	7500	6E-169	99.16	69	Solyc04g049180.2.1	Transmembrane protein 115 IPR013861 Protein of unknown function DUF1751, integral membrane, eukaryotic	
4DE	g3120.i1	40879225	40879856	631	5E-61	97.85	100	Solyc04g049190.1.1	Unknown Protein	
4DE	g3125.i1	41007648	41019560	11912	8E-79	83.03	34	Solyc12g070240.1.1	Unknown Protein	
4DE	g3126.i1	41019959	41022647	2688	5E-19	67.65	40	Solyc01g022790.1.1	Unknown Protein	
4DE	g3127.i1	41034622	41049960	15338	1E-11	41.57	71	Solyc11g045620.1.1	Unknown Protein	
4DE	g3140.i1	41458172	41460477	2305	8E-23	82.86	69	Solyc01g091470.2.1	AT-hook DNA-binding protein (Fragment) IPR014476 Predicted AT-hook DNA-binding	
4DE	q3164.i1	42044349	42048673	4324	5E-50	55.85	32	Solyc05g017810.1.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g3169.t1	42161334	42161863	529	2E-31	91.67	57	Solyc07g065010.2.1	Bactericidal permeability-increasing protein	IPR017942 Lipid-binding serum glycoprotein, N-terminal
4DE	g3170.t1	42162060	42165335	3275	6E-44	34.46	53	Solyc09g014660.1.1	HGWP repeat containing protein-like	
4DE	g3170.t2	42162719	42165605	2886	4E-44	34.46	53	Solyc09g014660.1.1	HGWP repeat containing protein-like	
4DE	g3194.t1	42904203	42905140	937	1E-65	90.98	81	Solyc01g091470.2.1	AT-hook DNA-binding protein (Fragment)	IPR014476 Predicted AT-hook DNA-binding
4DE	g3204.t1	43250848	43254570	3722	3E-19	74.07	69	Solyc01g074430.1.1	Replication protein A DNA-binding subunit	IPR012340 Nucleic acid-binding, OB-fold
4DE	g3217.t1	43656818	43660259	3441	2E-41	35.4	47	Solyc09g014660.1.1	HGWP repeat containing protein-like	
4DE	g3220.t1	43742648	43748438	5790	7E-49	68.97	25	Solyc05g017810.1.1	Unknown Protein	
4DE	g3223.t2	43852506	43853428	922	2E-47	65.25	97	Solyc10g049480.1.1	Abc transporter family protein	IPR012340 Nucleic acid-binding, OB-fold
4DE	g3223.t1	43852506	43853428	922	2E-44	66.67	97	Solyc10g049480.1.1	Abc transporter family protein	IPR012340 Nucleic acid-binding, OB-fold
4DE	g3228.t1	43922017	43926998	4981	1E-11	55.36	14	Solyc05g017810.1.1	Unknown Protein	
4DE	g3233.t1	44022892	44024540	1648	3E-18	50	44	Solyc02g021080.1.1	Unknown Protein	
4DE	g3238.t1	44147576	44160781	13205	7E-15	67.35	14	Solyc12g035290.1.1	Unknown Protein	
4DE	g3262.t1	44404993	44407998	3005	0E+00	97.48	100	Solyc04g049290.1.1	Prenyltransferase_zinc ion binding protein	IPR001293 Zinc finger, TRAF-type
4DE	g3265.t1	44431177	44432834	1657	2E-50	68.91	70	Solyc10g078290.1.1	BZIP family transcription factor (Fragment)	IPR011616 bZIP transcription factor, bZIP-1
4DE	g3266.t1	44435613	44437183	1570	1E-41	93.33	52	Solyc01g044510.1.1	Unknown Protein	
4DE	g3269.t1	44462783	44463936	1153	1E-10	67.5	28	Solyc10g074760.1.1	Unknown Protein	
4DE	g3275.t1	44533964	44538263	4299	1E-74	100	100	Solyc04g049330.2.1	V-type proton ATPase subunit G 1-ATPase G subunit	
4DE	g3276.t1	44538478	44542425	3947	0E+00	94.08	96	Solyc04g049340.2.1	Tyrosine-specific transport protein	IPR018227 Tryptophan_tyrosine permease
4DE	g3278.t1	44566519	44574065	7546	0E+00	99.77	100	Solyc04g049350.2.1	Chorismate synthase	IPR000453 Chorismate synthase
4DE	g3282.t1	44655473	44665442	9969	7E-99	79.08	67	Solyc12g044170.1.1	RGC2 resistance protein K (Fragment)	
4DE	g3284.t1	44678144	44691434	13290	0E+00	98.77	53	Solyc04g049360.2.1	4-amino-4-deoxychorismate synthase component I	IPR005802 Para-aminobenzoate synthase, component I
4DE	g3296.t1	44841933	44867128	25195	0E+00	84.21	28	Solyc04g049380.2.1	Uncharacterized aarF domain-containing protein kinase 1	IPR004147 ABC-1
4DE	g3298.t1	44881063	44886898	5835	0E+00	94.68	72	Solyc04g049390.2.1	Possible protein kinase ABC1 family	
4DE	g3299.t1	44897898	44902234	4336	0E+00	99.21	99	Solyc04g049400.2.1	Receptor-like protein kinase	IPR002290 Serine_threonine protein kinase
4DE	g3301.t1	44922973	44932982	10009	4E-86	81.41	86	Solyc02g072300.2.1	Glycogen synthase kinase	IPR002290 Serine_threonine protein kinase
4DE	g3302.t2	44945214	44965164	19950	0E+00	97.41	56	Solyc04g049440.1.1	WPP domain-associated protein	
4DE	g3302.t1	44951988	44965164	13176	0E+00	97.41	65	Solyc04g049440.1.1	WPP domain-associated protein	
4DE	g3306.t2	45020384	45032539	12155	0E+00	98.76	78	Solyc04g049450.2.1	Protein disulfide isomerase L-2	IPR005792 Protein disulphide isomerase
4DE	g3306.t1	45027004	45032539	5535	0E+00	98.76	100	Solyc04g049450.2.1	Protein disulfide isomerase L-2	IPR005792 Protein disulphide isomerase
4DE	g3310.t1	45084594	45085145	551	1E-54	66.91	100	Solyc12g056540.1.1	Histone H3	IPR000164 Histone H3
4DE	g3312.t1	45113025	45125575	12550	4E-25	52.43	26	Solyc05g023660.1.1	Unknown Protein	
4DE	g3314.t1	45138014	45170033	32019	0E+00	91.08	43	Solyc04g049490.2.1	Vacuolar protein sorting-associated protein 53	IPR007234 Vps53-like, N-terminal
4DE	g3314.t2	45138014	45170033	32019	0E+00	91.08	42	Solyc04g049490.2.1	Vacuolar protein sorting-associated protein 53	IPR007234 Vps53-like, N-terminal
4DE	g3319.t1	45246914	45248941	2027	2E-11	41.05	43	Solyc11g011540.1.1	F-box family protein	IPR001810 Cyclin-like F-box
4DE	g3321.t1	45266554	45271747	5193	4E-14	25.59	94	Solyc04g005890.1.1	F-box family protein	IPR013596 FBD
4DE	g3323.t1	45280994	45285981	4987	2E-14	37.42	41	Solyc11g011540.1.1	F-box family protein	IPR001810 Cyclin-like F-box
4DE	g3325.t1	45300174	45307505	7331	2E-16	34.73	37	Solyc11g011540.1.1	F-box family protein	IPR001810 Cyclin-like F-box
4DE	g3331.t1	45350004	45359976	9972	3E-31	39.82	57	Solyc11g011540.1.1	F-box family protein	IPR001810 Cyclin-like F-box
4DE	g3333.t1	45370964	45379347	8383	1E-13	46.46	48	Solyc05g010350.2.1	Unknown Protein	
4DE	g3335.t1	45388814	45393539	4725	3E-23	33.56	99	Solyc05g010360.1.1	F-box family protein	IPR001810 Cyclin-like F-box
4DE	g3339.t1	45418274	45419305	1031	9E-12	41.67	42	Solyc05g010370.1.1	F-box_FBD_LRR-repeat protein At1g13570	
4DE	g3357.t1	45640758	45648537	7779	1E-12	75	15	Solyc09g042380.1.1	Unknown Protein	
4DE	g3359.t1	45679609	45680457	848	3E-25	36.02	89	Solyc06g009730.1.1	Unknown Protein	
4DE	g3363.t1	45749776	45751670	1894	1E-16	38.26	54	Solyc05g010350.2.1	Unknown Protein	
4DE	g3371.t2	45839713	45854137	14424	2E-89	99.29	22	Solyc04g049550.2.1	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	IPR004570 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase

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4DE	g3371.11	45845864	45849027	3163	1E-51	100	100	Solyc04g049550.2.1	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	IPR004570 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
4DE	g3372.11	45856469	45860657	4188	2E-88	94.85	82	Solyc04g049550.2.1	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	IPR004570 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
4DE	g3376.11	45904476	45913172	8696	0E+00	64.07	85	Solyc04g009560.2.1	TBC1 domain family member 8B	IPR000195 RabGAP_TBC
4DE	g3376.12	45904476	45913009	8533	0E+00	63.87	85	Solyc04g009560.2.1	TBC1 domain family member 8B	IPR000195 RabGAP_TBC
4DE	g3378.11	45919005	45936398	17393	4E-75	59.76	60	Solyc04g009560.2.1	TBC1 domain family member 8B	IPR000195 RabGAP_TBC
4DE	g3381.11	45967349	45970426	3077	7E-55	74.17	63	Solyc01g057750.1.1	DNAJ heat shock N-terminal domain-containing protein	IPR015609 Molecular chaperone, heat shock protein, Hsp40, DnaJ
4DE	g3382.11	45978524	45981796	3272	2E-29	42.11	23	Solyc04g025900.1.1	Unknown Protein	
4DE	g3389.11	46050885	46074034	23149	2E-141	98.51	35	Solyc04g049580.2.1	Similarity the ORF shows strong similarity to EST 5419 - Aspergillus oryzae	
4DE	g3389.12	46050885	46074034	23149	3E-113	98.79	30	Solyc04g049580.2.1	Similarity the ORF shows strong similarity to EST 5419 - Aspergillus oryzae	
4DE	g3390.11	46074148	46077946	3798	2E-46	77.67	29	Solyc04g049600.2.1	Unknown Protein	
4DE	g3391.11	46078245	46089946	11701	3E-98	80.9	86	Solyc04g049620.2.1	Predicted CDS Pa_1_6620	IPR005123 Oxoglutarate and iron-dependent oxygenase
4DE	g3393.11	46105332	46107638	2306	5E-63	87.96	72	Solyc01g034060.1.1	Unknown Protein	
4DE	g3398.12	46173651	46182128	8477	0E+00	90.85	95	Solyc04g049630.2.1	Peptidase S9 prolyl oligopeptidase active site domain protein	IPR001375 Peptidase S9, prolyl oligopeptidase active site region
4DE	g3398.13	46173651	46190388	16737	0E+00	90.21	52	Solyc04g049630.2.1	Peptidase S9 prolyl oligopeptidase active site domain protein	IPR001375 Peptidase S9, prolyl oligopeptidase active site region
4DE	g3398.11	46186378	46190388	4010	0E+00	89.47	99	Solyc04g049630.2.1	Peptidase S9 prolyl oligopeptidase active site domain protein	IPR001375 Peptidase S9, prolyl oligopeptidase active site region
4DE	g3402.11	46231620	46248408	16788	2E-32	80.49	14	Solyc04g049630.2.1	Peptidase S9 prolyl oligopeptidase active site domain protein	IPR001375 Peptidase S9, prolyl oligopeptidase active site region
4DE	g3403.12	46249160	46260258	11098	8E-56	61.9	23	Solyc05g017810.1.1	Unknown Protein	
4DE	g3406.11	46278081	46280623	2542	0E+00	69.68	75	Solyc12g036370.1.1	Unknown Protein	
4DE	g3409.11	46304737	46306763	2026	9E-121	83.82	99	Solyc09g007170.2.1	Serine_threonine kinase	IPR002290 Serine_threonine protein kinase
4DE	g3412.12	46309333	46315623	6290	9E-41	68.57	19	Solyc04g049650.1.1	Receptor protein kinase-like protein	IPR001245 Tyrosine protein kinase
4DE	g3412.11	46310471	46315623	5152	2E-40	68.57	31	Solyc04g049650.1.1	Receptor protein kinase-like protein	IPR001245 Tyrosine protein kinase
4DE	g3413.11	46316718	46320003	3285	1E-135	97.04	80	Solyc04g049660.1.1	Unknown Protein	
4DE	g3417.11	46385624	46398873	13249	0E+00	93.71	93	Solyc04g049670.2.1	Pseudo response regulator	IPR010402 CCT domain
4DE	g3418.11	46409886	46411003	1117	2E-82	96	99	Solyc04g049680.2.1	Pseudo-response regulator 7	
4DE	g3433.11	46613974	46622238	8264	0E+00	99.63	100	Solyc04g049690.2.1	Adenylate kinase	IPR006259 Adenylate kinase, subfamily
4DE	g3436.11	46658317	46659721	1404	3E-25	92	61	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g3439.11	46688309	46698778	10469	8E-159	98.65	57	Solyc04g049710.2.1	FGFR1 oncogene partner	IPR006594 LisH dimerisation motif
4DE	g3448.11	46782920	46795075	12155	0E+00	99.06	87	Solyc04g049720.2.1	Leukotriene-A4 hydrolase-like protein	IPR001930 Peptidase M1, membrane alanine aminopeptidase
4DE	g3457.11	46887310	46896951	9641	0E+00	95.17	99	Solyc04g049760.2.1	Nonsense-mediated mRNA decay 2 protein	IPR016024 Armadillo-type fold
4DE	g3459.12	46902640	46917268	14628	0E+00	95.51	37	Solyc04g049770.2.1	Nonsense-mediated mRNA decay 2 protein	IPR007193 Up-frameshift suppressor 2
4DE	g3459.11	46902640	46906916	4276	0E+00	99.18	52	Solyc04g049760.2.1	Nonsense-mediated mRNA decay 2 protein	IPR016024 Armadillo-type fold
4DE	g3459.13	46909090	46917268	8178	0E+00	92.06	87	Solyc04g049770.2.1	Nonsense-mediated mRNA decay 2 protein	IPR007193 Up-frameshift suppressor 2
4DE	g3462.11	46936664	46937961	1297	6E-55	91.84	53	Solyc04g024950.1.1	Unknown Protein	
4DE	g3463.11	46952105	46956899	4794	6E-117	99.38	100	Solyc04g049790.2.1	Membrane-associated progesterone receptor component 1	IPR001199 Cytochrome b5
4DE	g3465.11	47004075	47005614	1539	4E-57	49.76	100	Solyc08g028660.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g3466.11	47021585	47026304	4719	8E-45	84.38	13	Solyc04g025900.1.1	Unknown Protein	
4DE	g3469.11	47094225	47097314	3089	0E+00	93.22	100	Solyc04g049800.2.1	AP2-like ethylene-responsive transcription factor At1g79700	IPR001471 Pathogenesis-related transcriptional factor and ERF, DNA-binding
4DE	g3471.11	47114668	47116276	1608	2E-24	60.24	61	Solyc04g011680.1.1	Cytochrome P450	
4DE	g3472.11	47118479	47121696	3217	9E-91	95.89	69	Solyc04g049830.1.1	Unknown Protein	
4DE	g3474.11	47151916	47163009	11093	0E+00	93.82	100	Solyc04g049840.2.1	CCR4-NOT transcription complex subunit 4	IPR003954 RNA recognition, region 1
4DE	g3476.11	47173743	47180629	6886	5E-34	53.98	44	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g3477.11	47186878	47196443	9565	0E+00	97.54	100	Solyc04g049850.2.1	Uncharacterized conserved protein	IPR003734 Protein of unknown function DUF155
4DE	g3487.12	47315273	47321039	5766	3E-13	53.75	35	Solyc00g005170.1.1	Unknown Protein	
4DE	g3487.11	47318602	47321039	2437	2E-12	53.75	54	Solyc00g005170.1.1	Unknown Protein	
4DE	g3490.11	47384948	47387499	2551	0E+00	97.3	100	Solyc04g049860.1.1	Unknown Protein	

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4DE	g3493.t1	47410942	47417679	6737	6E-51	63.98	25	Solyc05g017810.1.1	Unknown Protein	
4DE	g3494.t1	47417891	47420539	2648	3E-68	71.43	27	Solyc05g017810.1.1	Unknown Protein	
4DE	g3495.t1	47425714	47428219	2505	4E-15	88.89	15	Solyc03g044550.1.1	Unknown Protein	
4DE	g3500.t1	47506802	47507742	940	2E-19	79.17	39	Solyc07g019500.2.1	Unknown Protein	
4DE	g3503.t1	47547116	47549992	2876	3E-18	54.21	85	Solyc06g043180.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g3504.i2	47550240	47563242	13002	1E-39	64.22	38	Solyc12g036190.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g3504.t1	47550240	47563362	13122	6E-39	64.22	35	Solyc12g036190.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g3508.t1	47596343	47598152	1809	8E-14	37.98	76	Solyc05g010350.2.1	Unknown Protein	
4DE	g3511.t1	47627690	47628682	992	4E-19	44.85	81	Solyc05g010350.2.1	Unknown Protein	
4DE	g3512.t1	47630403	47632082	1679	2E-16	40.32	90	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3516.t1	47656746	47658642	1896	8E-15	38.51	58	Solyc05g010350.2.1	Unknown Protein	
4DE	g3518.t1	47672346	47677207	4861	4E-10	80.77	13	Solyc10g052440.1.1	Unknown Protein	
4DE	g3524.t1	47728209	47730207	1998	5E-10	43.06	33	Solyc05g010370.1.1	F-box_FBD_LRR-repeat protein At1g13570	
4DE	g3532.i2	47826366	47828247	1881	6E-10	41.67	38	Solyc05g010370.1.1	F-box_FBD_LRR-repeat protein At1g13570	
4DE	g3534.t1	47836102	47837089	987	6E-10	39.62	76	Solyc05g010350.2.1	Unknown Protein	
4DE	g3536.t1	47867297	47869189	1892	1E-10	44.59	34	Solyc05g010350.2.1	Unknown Protein	
4DE	g3537.t1	47878723	47887699	8976	5E-15	37.75	36	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3539.t1	47910956	47917309	6353	3E-11	35.34	96	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3542.t1	47940248	47944084	3836	9E-17	59.38	25	Solyc05g023980.1.1	Unknown Protein	
4DE	g3543.t1	47950077	47952179	2102	1E-16	37.02	74	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3550.t1	48022728	48024622	1894	5E-14	37.21	57	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3552.t1	48034483	48036362	1879	2E-19	36.84	72	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3555.t1	48047478	48049382	1904	1E-17	30.99	80	Solyc04g005890.1.1	F-box family protein IPR013596 FBD	
4DE	g3560.t1	48097894	48099852	1958	7E-15	32.27	98	Solyc04g005890.1.1	F-box family protein IPR013596 FBD	
4DE	g3562.i2	48112864	48114962	2098	1E-11	39.6	41	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3571.t1	48252672	48255612	2940	1E-11	44.29	48	Solyc05g010370.1.1	F-box_FBD_LRR-repeat protein At1g13570	
4DE	g3576.i2	48314905	48316862	1957	1E-12	34.64	59	Solyc05g010350.2.1	Unknown Protein	
4DE	g3589.t1	48463357	48465943	2586	8E-13	45.21	41	Solyc05g010370.1.1	F-box_FBD_LRR-repeat protein At1g13570	
4DE	g3590.t1	48466160	48472843	6683	8E-26	29.33	97	Solyc05g010360.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3592.t1	48491569	48493383	1814	9E-14	30	98	Solyc04g005890.1.1	F-box family protein IPR013596 FBD	
4DE	g3594.t1	48520489	48525337	4848	1E-12	41.1	42	Solyc05g010370.1.1	F-box_FBD_LRR-repeat protein At1g13570	
4DE	g3598.t1	48550792	48552767	1975	1E-42	34.84	83	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3603.i2	48594295	48596277	1982	8E-13	32.18	68	Solyc04g005890.1.1	F-box family protein IPR013596 FBD	
4DE	g3603.t1	48594295	48596277	1982	7E-13	48.65	34	Solyc05g010350.2.1	Unknown Protein	
4DE	g3604.i2	48597656	48628682	31026	0E+00	71.33	31	Solyc07g017550.1.1	Receptor-like protein kinase At3g21340 IPR000719 Protein kinase, core	
4DE	g3604.t1	48609056	48614090	5034	0E+00	98.13	100	Solyc04g049890.2.1	Os02g0252600 protein (Fragment) IPR001544 Aminotransferase, class IV	
4DE	g3605.t1	48633906	48637946	4040	8E-101	97.96	97	Solyc04g049910.2.1	Nuclear transcription factor Y subunit B-3 IPR003957 Transcription factor, CBFA_NFYB, DNA topoisomerase	
4DE	g3606.t1	48643564	48645997	2433	8E-40	43.89	67	Solyc01g056820.1.1	Methionine aminopeptidase, related	
4DE	g3615.t1	48879289	48883478	4189	5E-63	67	35	Solyc05g017810.1.1	Unknown Protein	
4DE	g3619.t1	48939807	48942087	2280	6E-29	48.36	96	Solyc04g054440.1.1	DNA repair protein IPR000330 SNF2-related	
4DE	g3621.t1	48956911	48957818	907	1E-80	94.21	100	Solyc01g094440.1.1	Ripening-related protein 3 IPR009009 Barwin-related endoglucanase	
4DE	g3622.i2	48959467	48962104	2637	2E-85	96.77	54	Solyc05g042010.1.1	Unknown Protein	
4DE	g3622.t1	48960067	48962104	2037	5E-86	96.77	69	Solyc05g042010.1.1	Unknown Protein	
4DE	g3626.t1	49017312	49030106	12794	9E-171	97.89	70	Solyc04g049920.2.1	RNA binding protein-like IPR000504 RNA recognition motif, RNP-1	
4DE	g3626.i2	49017312	49030106	12794	4E-169	97.87	70	Solyc04g049920.2.1	RNA binding protein-like IPR000504 RNA recognition motif, RNP-1	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g3632.t1	49106152	49112598	6446	0E+00	93.67	50	Solyc04g049930.2.1	Unknown Protein	
4DE	g3635.t2	49178652	49187933	9281	1E-56	98.85	33	Solyc04g049970.2.1	Os11g0133900 protein (Fragment) IPR018471 ATP synthase assembly factor FMC1, mitochondrial	
4DE	g3635.t1	49185759	49187933	2174	2E-70	97.12	93	Solyc04g049970.2.1	Os11g0133900 protein (Fragment) IPR018471 ATP synthase assembly factor FMC1, mitochondrial	
4DE	g3637.t1	49208077	49209369	1292	5E-130	73.52	99	Solyc12g100000.1.1	U-box domain-containing protein 4 IPR011989 Armadillo-like helical	
4DE	g3642.t1	49272414	49273518	1104	1E-69	93.46	41	Solyc05g042140.1.1	Unknown Protein IPR001878 Zinc finger, CCHC-type	
4DE	g3643.t1	49284547	49286208	1661	3E-120	97.58	100	Solyc04g050010.1.1	LOB domain protein 1 IPR004883 Lateral organ boundaries, LOB	
4DE	g3644.t1	49296372	49298358	1986	4E-128	88.41	78	Solyc04g050030.1.1	Unknown Protein	
4DE	g3651.t1	49373203	49386674	13471	0E+00	99.66	77	Solyc04g050040.2.1	Mitochondrial carrier C12B10.09 IPR001993 Mitochondrial substrate carrier	
4DE	g3651.t2	49373203	49386674	13471	0E+00	99.66	78	Solyc04g050040.2.1	Mitochondrial carrier C12B10.09 IPR001993 Mitochondrial substrate carrier	
4DE	g3652.t2	49387657	49397564	9907	0E+00	99.22	100	Solyc04g050040.2.1	Mitochondrial carrier C12B10.09 IPR001993 Mitochondrial substrate carrier	
4DE	g3652.t1	49387657	49391934	4277	2E-93	100	93	Solyc04g050040.2.1	Mitochondrial carrier C12B10.09 IPR001993 Mitochondrial substrate carrier	
4DE	g3655.t1	49420803	49422496	1693	4E-26	51.96	72	Solyc10g046780.1.1	Zinc knuckle family protein IPR001878 Zinc finger, CCHC-type	
4DE	g3657.t1	49454509	49460574	6065	0E+00	99.75	86	Solyc04g050050.2.1	Calmodulin-binding protein IPR000048 IQ calmodulin-binding region	
4DE	g3657.t2	49454509	49460574	6065	0E+00	99.49	86	Solyc04g050050.2.1	Calmodulin-binding protein IPR000048 IQ calmodulin-binding region	
4DE	g3659.t1	49492329	49492894	565	7E-53	95.56	80	Solyc04g050060.1.1	Unknown Protein	
4DE	g3660.t1	49493282	49499044	5762	0E+00	83.65	90	Solyc04g050070.1.1	Myb family transcription factor IPR006447 Myb-like DNA-binding region, SHAQKYF class	
4DE	g3660.t2	49493317	49499044	5727	0E+00	83.65	92	Solyc04g050070.1.1	Myb family transcription factor IPR006447 Myb-like DNA-binding region, SHAQKYF class	
4DE	g3669.t1	49589689	49596856	7167	4E-54	57.5	48	Solyc04g050000.1.1	MYB transcription factor IPR015495 Myb transcription factor	
4DE	g3682.t1	49782436	49785163	2727	0E+00	98.75	100	Solyc04g050140.2.1	Genomic DNA chromosome 5 P1 clone MRH10 IPR009291 Protein of unknown function DUF946, plant	
4DE	g3683.t1	49785917	49831277	45360	0E+00	88.87	30	Solyc04g050150.2.1	Chromodomain-helicase-DNA-binding protein 7 IPR000330 SNF2-related	
4DE	g3685.t2	49841537	49850037	8500	1E-52	66.26	10	Solyc05g017810.1.1	Unknown Protein	
4DE	g3685.t3	49841668	49842877	1209	5E-14	60.42	48	Solyc09g042380.1.1	Unknown Protein	
4DE	g3685.t1	49843549	49850037	6488	1E-52	66.26	11	Solyc05g017810.1.1	Unknown Protein	
4DE	g3689.t1	49883912	49890018	6106	1E-29	61.8	55	Solyc01g011150.1.1	Unknown Protein IPR006564 Zinc finger, PMZ-type	
4DE	g3690.t1	49891862	49895528	3666	0E+00	98.77	100	Solyc04g050170.2.1	Receptor like kinase, RLK	
4DE	g3692.t1	49907585	49913428	5843	4E-57	88.89	70	Solyc03g082930.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g3694.t1	49942237	49943748	1511	1E-15	58.62	82	Solyc09g064510.2.1	Transcriptional activator TenA family IPR004305 TENA_THI4 protein_Coenzyme PQQ biosynthesis protein C	
4DE	g3697.t1	49959807	49962729	2922	0E+00	98.47	99	Solyc04g050190.2.1	Transcriptional activator TenA family IPR004305 TENA_THI4 protein_Coenzyme PQQ biosynthesis protein C	
4DE	g3700.t1	50012068	50019398	7330	3E-36	75	53	Solyc09g042380.1.1	Unknown Protein	
4DE	g3703.t2	50039588	50071522	31934	2E-66	86.76	17	Solyc04g050210.1.1	WRKY transcription factor 22 IPR003657 DNA-binding WRKY	
4DE	g3703.t1	50058978	50071522	12544	8E-69	86.76	28	Solyc04g050210.1.1	WRKY transcription factor 22 IPR003657 DNA-binding WRKY	
4DE	g3706.t1	50096697	50098289	1592	6E-132	75.44	87	Solyc04g050210.1.1	WRKY transcription factor 22 IPR003657 DNA-binding WRKY	
4DE	g3713.t1	50218093	50221582	3489	6E-25	48.65	96	Solyc05g045880.1.1	WRKY transcription factor 22 IPR003657 DNA-binding WRKY	
4DE	g3725.t1	50343311	50357985	14674	5E-74	83.1	18	Solyc12g056070.1.1	Unknown Protein	
4DE	g3727.t1	50379769	50382592	2823	0E+00	84.83	99	Solyc04g050210.1.1	WRKY transcription factor 22 IPR003657 DNA-binding WRKY	
4DE	g3734.t1	50498227	50499977	1750	9E-20	63.08	72	Solyc03g098610.2.1	Genomic DNA chromosome 3 P1 clone MV11	
4DE	g3736.t1	50522595	50526747	4152	2E-94	100	100	Solyc04g050240.2.1	Vacuolar protein sorting-associated protein 26-like protein IPR005377 Vacuolar protein sorting-associated protein 26	
4DE	g3738.t1	50535876	50536744	868	2E-48	63.27	87	Solyc07g064130.1.1	Ubiquitin IPR019956 Ubiquitin subgroup	
4DE	g3743.t1	50566476	50571714	5238	2E-60	97.96	55	Solyc04g050260.1.1	G protein-coupled seven transmembrane receptor IPR009637 Transmembrane receptor, eukaryota	
4DE	g3747.t1	50622057	50631127	9070	2E-26	44.3	41	Solyc05g045880.1.1	WRKY transcription factor 22 IPR003657 DNA-binding WRKY	
4DE	g3757.t1	50720263	50722387	2124	5E-18	47.95	73	Solyc09g042380.1.1	Unknown Protein	
4DE	g3758.t1	50724922	50740707	15785	7E-103	98.73	15	Solyc04g050270.1.1	Unknown Protein	
4DE	g3761.t1	50746865	50749817	2952	3E-89	93.43	94	Solyc04g050310.2.1	Unknown Protein	
4DE	g3777.t1	51042460	51043150	690	5E-78	91.41	84	Solyc04g050390.1.1	60S ribosomal protein L12 IPR000911 Ribosomal protein L11	
4DE	g3778.t1	51058363	51059090	727	2E-65	73.76	99	Solyc04g050380.1.1	60S ribosomal protein L12 IPR000911 Ribosomal protein L11	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g3780.t1	51094363	51099210	4847	9E-35	88.41	86	Solyc06g075180.1.1	Ribosomal protein L12 IPR000911 Ribosomal protein L11	
4DE	g3781.t1	51103369	51114100	10731	4E-28	54.24	45	Solyc04g050390.1.1	60S ribosomal protein L12 IPR000911 Ribosomal protein L11	
4DE	g3783.t1	51142721	51143450	729	2E-32	52.31	100	Solyc04g050420.1.1	Phosphoserine aminotransferase IPR000911 Ribosomal protein L11	
4DE	g3784.t1	51150975	51154580	3605	1E-50	89.41	91	Solyc04g050380.1.1	60S ribosomal protein L12 IPR000911 Ribosomal protein L11	
4DE	g3787.t1	51264204	51267151	2947	7E-14	40.28	41	Solyc01g058710.1.1	Unknown Protein	
4DE	g3788.i2	51268324	51273353	5029	6E-37	89.19	17	Solyc09g061300.1.1	Unknown Protein	
4DE	g3788.t1	51268324	51274753	6429	1E-36	89.19	14	Solyc09g061300.1.1	Unknown Protein	
4DE	g3796.t1	51379204	51381395	2191	4E-54	85.57	89	Solyc05g032790.1.1	Ubiquitin	
4DE	g3806.t1	51520818	51521597	779	3E-43	82.14	95	Solyc04g050270.1.1	Unknown Protein	
4DE	g3813.t1	51635779	51639317	3538	0E+00	99.42	100	Solyc04g050440.2.1	Ammonium transporter IPR001905 Ammonium transporter	
4DE	g3818.t1	51699518	51700797	1279	3E-71	95.8	86	Solyc04g050470.2.1	Genomic DNA chromosome 5 P1 clone MNJ8	
4DE	g3819.t1	51705779	51708797	3018	1E-110	98.73	84	Solyc04g050470.2.1	Genomic DNA chromosome 5 P1 clone MNJ8	
4DE	g3820.i2	51712940	51723537	10597	7E-120	99.42	63	Solyc04g050480.2.1	3-5 exoribonuclease CSL4 IPR019495 Exosome complex, component CSL4	
4DE	g3820.t1	51715603	51723537	7934	3E-142	99.48	87	Solyc04g050480.2.1	3-5 exoribonuclease CSL4 IPR019495 Exosome complex, component CSL4	
4DE	g3821.t1	51759636	51760672	1036	1E-41	61.11	98	Solyc05g042140.1.1	Unknown Protein IPR001878 Zinc finger, CCHC-type	
4DE	g3823.t1	51771604	51783437	11833	0E+00	94.94	100	Solyc04g050490.2.1	Carboxyl-terminal proteinase IPR004314 Protein of unknown function DUF239, plant	
4DE	g3827.t1	51825109	51834362	9253	0E+00	99.49	90	Solyc04g050510.2.1	Translational activator gcn1 IPR011989 Armadillo-like helical	
4DE	g3829.t1	51837892	51846252	8360	0E+00	99.33	98	Solyc04g050510.2.1	Translational activator gcn1 IPR011989 Armadillo-like helical	
4DE	g3829.i2	51837892	51847822	9930	0E+00	99.34	92	Solyc04g050510.2.1	Translational activator gcn1 IPR011989 Armadillo-like helical	
4DE	g3830.t1	51847941	51848918	977	2E-40	49.4	61	Solyc10g044430.1.1	Unknown Protein	
4DE	g3831.t1	51849444	51868902	19458	0E+00	98.5	51	Solyc04g050520.2.1	Translational activator gcn1 IPR011989 Armadillo-like helical	
4DE	g3831.i2	51849762	51861442	11680	0E+00	98.5	92	Solyc04g050520.2.1	Translational activator gcn1 IPR011989 Armadillo-like helical	
4DE	g3831.i3	51861800	51868902	7102	0E+00	98.93	89	Solyc04g050520.2.1	Translational activator gcn1 IPR011989 Armadillo-like helical	
4DE	g3833.t1	51906878	51913222	6344	2E-76	91.94	98	Solyc04g050390.1.1	60S ribosomal protein L12 IPR000911 Ribosomal protein L11	
4DE	g3834.t1	51916735	51926562	9827	2E-61	81.67	96	Solyc04g050390.1.1	60S ribosomal protein L12 IPR000911 Ribosomal protein L11	
4DE	g3836.t1	51955615	51956302	687	2E-70	81.25	100	Solyc04g050390.1.1	60S ribosomal protein L12 IPR000911 Ribosomal protein L11	
4DE	g3839.t1	52003213	52007073	3860	6E-42	69.37	100	Solyc04g050390.1.1	60S ribosomal protein L12 IPR000911 Ribosomal protein L11	
4DE	g3844.i2	52091233	52118453	27220	0E+00	99.24	70	Solyc04g050540.2.1	Pentatricopeptide repeat protein IPR003034 DNA-binding SAP	
4DE	g3844.t1	52100981	52115953	14972	0E+00	99.11	88	Solyc04g050540.2.1	Pentatricopeptide repeat protein IPR003034 DNA-binding SAP	
4DE	g3845.t1	52138232	52150950	12718	0E+00	95.6	80	Solyc04g050550.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
4DE	g3846.t1	52155529	52156513	984	1E-56	98.72	80	Solyc04g050570.2.1	GDSL esterase_lipase At5g33370 IPR001087 Lipase, GDSL	
4DE	g3847.t1	52156893	52159813	2920	0E+00	98.61	99	Solyc04g050570.2.1	GDSL esterase_lipase At5g33370 IPR001087 Lipase, GDSL	
4DE	g3855.t1	52252087	52254863	2776	7E-57	73.86	15	Solyc09g061300.1.1	Unknown Protein	
4DE	g3856.t1	52255029	52256373	1344	3E-28	45.04	46	Solyc01g058710.1.1	Unknown Protein	
4DE	g3857.i2	52261956	52268153	6197	1E-176	69.25	97	Solyc04g070980.2.1	Lanosterol synthase IPR018333 Squalene cyclase	
4DE	g3857.t1	52262771	52268153	5382	8E-177	69.25	98	Solyc04g070980.2.1	Lanosterol synthase IPR018333 Squalene cyclase	
4DE	g3861.t1	52292384	52294053	1669	9E-154	90.61	83	Solyc04g050620.2.1	Cytochrome P450	
4DE	g3863.t1	52310924	52312813	1889	0E+00	97.57	100	Solyc04g050620.2.1	Cytochrome P450	
4DE	g3864.t1	52316392	52317832	1440	3E-65	68.18	100	Solyc05g018220.1.1	Unknown Protein	
4DE	g3865.t1	52318292	52319311	1019	6E-92	69.02	100	Solyc09g057700.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1	
4DE	g3869.t1	52362084	52368926	6842	4E-78	91.5	7	Solyc09g061300.1.1	Unknown Protein	
4DE	g3875.t1	52414804	52416392	1588	0E+00	87.73	100	Solyc04g054220.2.1	Cytochrome P450	
4DE	g3875.i2	52414964	52416392	1428	0E+00	86.69	100	Solyc04g054220.2.1	Cytochrome P450	
4DE	g3876.t1	52430184	52431279	1095	3E-76	73.97	99	Solyc04g054220.2.1	Cytochrome P450	
4DE	g3878.t1	52463755	52468125	4370	3E-24	33.2	97	Solyc04g005890.1.1	F-box family protein IPR013596 FBD	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g3879.t1	52472647	52474485	1838	1E-13	35.66	48	Solyc05g010350.2.1	Unknown Protein	
4DE	g3879.t2	52472647	52474485	1838	2E-10	31.33	53	Solyc05g010350.2.1	Unknown Protein	
4DE	g3884.t1	52532294	52536412	4118	2E-21	44.63	27	Solyc05g010360.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3886.t1	52562792	52564222	1430	6E-52	42.4	84	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3888.t1	52593359	52597642	4283	5E-11	29.41	72	Solyc05g010350.2.1	Unknown Protein	
4DE	g3892.t1	52616438	52620442	4004	9E-10	41.67	49	Solyc05g010370.1.1	F-box_FBD_LRR-repeat protein At1g13570	
4DE	g3896.t1	52658412	52660546	2134	3E-22	47.41	49	Solyc06g005050.2.1	F-box_FBD_LRR-repeat protein At1g13570 IPR001810 Cyclin-like F-box	
4DE	g3897.t1	52660917	52662816	1899	2E-65	40	78	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3901.t1	52699776	52702996	3220	3E-30	43.55	49	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3903.t1	52716896	52718806	1910	4E-17	29.01	64	Solyc11g011540.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g3907.t1	52743865	52748236	4371	9E-14	39.78	39	Solyc04g070980.2.1	Lanosterol synthase IPR018333 Squalene cyclase	
4DE	g3909.t1	52758154	52762996	4842	2E-74	73.58	58	Solyc04g050670.1.1	Cycloartenol synthase IPR008930 Terpenoid cylases_protein prenyltransferase alpha-alpha toroid	
4DE	g3911.t1	52771450	52783426	11976	5E-111	71.95	31	Solyc04g050690.1.1	Serine_threonine-protein phosphatase 7 long form homolog IPR019557 Aminotransferase-like, plant mobile domain	
4DE	g3912.t1	52784025	52793846	9821	4E-34	87.32	48	Solyc01g014820.1.1	Inosine-uridine preferring nucleoside hydrolase family protein IPR001910 Inosine_uridine-preferring nucleoside hydrolase	
4DE	g3917.t1	52834013	52839577	5564	0E+00	96.82	96	Solyc04g050720.2.1	PHD-finger family protein expressed	
4DE	g3918.t1	52839864	52844004	4140	0E+00	99.46	100	Solyc04g050730.2.1	GDSL esterase_lipase At5g33370 IPR001087 Lipase, GDSL	
4DE	g3921.t2	52865383	52867404	2021	1E-132	59.63	85	Solyc12g036370.1.1	Unknown Protein	
4DE	g3926.t1	52920363	52921346	983	1E-18	32.89	70	Solyc03g063820.1.1	Unknown Protein	
4DE	g3927.t1	52958883	52960274	1391	1E-29	65.56	49	Solyc11g039800.1.1	Unknown Protein	
4DE	g3930.t1	52976670	52977564	894	3E-101	94.51	100	Solyc04g050750.1.1	Ethylene-responsive transcription factor 1 IPR001471 Pathogenesis-related transcriptional factor and ERF, DNA-binding	
4DE	g3933.t1	53087263	53094506	7243	0E+00	97.37	100	Solyc04g050760.2.1	U11_U12 small nuclear ribonucleoprotein 48 kDa protein	
4DE	g3933.t2	53087263	53094506	7243	0E+00	97.91	100	Solyc04g050760.2.1	U11_U12 small nuclear ribonucleoprotein 48 kDa protein	
4DE	g3934.t1	53098213	53100076	1863	0E+00	97.23	100	Solyc04g050770.1.1	U-box domain-containing protein IPR011989 Armadillo-like helical	
4DE	g3935.t1	53101623	53104846	3223	0E+00	99.53	71	Solyc04g050780.1.1	U-box domain-containing protein IPR011989 Armadillo-like helical	
4DE	g3949.t1	53317358	53320527	3169	0E+00	67.97	100	Solyc04g054740.2.1	Inositol-3-phosphate synthase IPR002587 Myo-inositol-1-phosphate synthase	
4DE	g3954.t1	53389516	53390731	1215	2E-24	36.04	73	Solyc08g048270.1.1	Unknown Protein	
4DE	g3961.t1	53618290	53621510	3220	0E+00	86.88	100	Solyc04g054740.2.1	Inositol-3-phosphate synthase IPR002587 Myo-inositol-1-phosphate synthase	
4DE	g3966.t1	53701240	53704459	3219	0E+00	77.42	100	Solyc04g054740.2.1	Inositol-3-phosphate synthase IPR002587 Myo-inositol-1-phosphate synthase	
4DE	g3967.t1	53707546	53711601	4055	2E-17	73.91	52	Solyc09g042380.1.1	Unknown Protein	
4DE	g3975.t1	53896257	53905651	9394	1E-115	76.29	61	Solyc04g054740.2.1	Inositol-3-phosphate synthase IPR002587 Myo-inositol-1-phosphate synthase	
4DE	g3988.t1	54125780	54126999	1219	4E-15	29.36	69	Solyc08g048270.1.1	Unknown Protein	
4DE	g3992.t1	54184125	54194879	10754	1E-22	35.09	49	Solyc08g048270.1.1	Unknown Protein	
4DE	g3995.t1	54252704	54253918	1214	1E-23	34.71	79	Solyc08g048270.1.1	Unknown Protein	
4DE	g3998.t1	54276227	54282912	6685	1E-52	89.53	100	Solyc10g049480.1.1	Abc transporter family protein IPR012340 Nucleic acid-binding, OB-fold	
4DE	g4000.t1	54296057	54300187	4130	6E-43	70.75	34	Solyc04g050880.1.1	Unknown Protein	
4DE	g4005.t1	54334443	54336808	2365	6E-39	83.12	44	Solyc08g014270.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g4013.t1	54396742	54400030	3288	0E+00	98.98	100	Solyc04g050920.2.1	Os02g0504100 protein (Fragment)	
4DE	g4014.t1	54400104	54403703	3599	0E+00	99.37	100	Solyc04g050930.2.1	Violaxanthin de-epoxidase	
4DE	g4015.t1	54416092	54422798	6706	0E+00	95.8	99	Solyc04g050940.1.1	Receptor protein kinase-like IPR002290 Serine_threonine protein kinase	
4DE	g4020.t1	54465827	54473103	7276	3E-79	92.16	8	Solyc09g061300.1.1	Unknown Protein	
4DE	g4032.t1	54626437	54629181	2744	7E-20	97.62	23	Solyc09g061720.2.1	Unknown Protein	
4DE	g4033.t1	54641473	54643238	1765	6E-104	98.64	100	Solyc04g050950.2.1	Major latex-like protein IPR000916 Bet v I allergen	
4DE	g4046.t1	54717527	54730515	12988	0E+00	96.06	84	Solyc04g050960.2.1	Chromatin remodeling complex subunit IPR012287 Homeodomain-related	
4DE	g4054.t1	54793347	54795574	2227	0E+00	91.58	47	Solyc03g062840.1.1	Unknown Protein	
4DE	g4056.t1	54799773	54802044	2271	5E-100	67.67	98	Solyc04g050960.2.1	Chromatin remodeling complex subunit IPR012287 Homeodomain-related	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g4057.t1	54804953	54805621	668	5E-91	72.07	100	Solyc08g016120.1.1	Unknown Protein IPR006501 Pectinesterase inhibitor	
4DE	g4058.t1	54810333	54811006	673	7E-91	71.51	100	Solyc08g016120.1.1	Unknown Protein IPR006501 Pectinesterase inhibitor	
4DE	g4064.t1	54867722	54874234	6512	0E+00	97.12	100	Solyc04g050970.2.1	Receptor protein kinase-like protein IPR002290 Serine_threonine protein kinase	
4DE	g4064.t2	54867722	54884614	16892	0E+00	97.3	90	Solyc04g050970.2.1	Receptor protein kinase-like protein IPR002290 Serine_threonine protein kinase	
4DE	g4069.t1	54906303	54912744	6441	2E-17	59.02	24	Solyc05g042140.1.1	Unknown Protein IPR001878 Zinc finger, CCHC-type	
4DE	g4070.t2	54926358	54931750	5392	0E+00	98.99	74	Solyc04g050990.2.1	F-box protein PP2-B1 IPR001810 Cyclin-like F-box	
4DE	g4070.t1	54929007	54931750	2743	0E+00	99.33	100	Solyc04g050990.2.1	F-box protein PP2-B1 IPR001810 Cyclin-like F-box	
4DE	g4074.t1	54970849	54975402	4553	3E-65	69.44	39	Solyc04g051010.1.1	Genomic DNA chromosome 3 P1 clone MTO24	
4DE	g4077.t1	55017176	55018650	1474	8E-119	63.17	88	Solyc04g056460.1.1	AtbZIP transcription factor (Fragment) IPR011616 bZIP transcription factor, bZIP-1	
4DE	g4078.t1	55025501	55027570	2069	4E-30	72.73	54	Solyc10g078290.1.1	BZIP family transcription factor (Fragment) IPR011616 bZIP transcription factor, bZIP-1	
4DE	g4081.t1	55065631	55067870	2239	3E-74	47.97	88	Solyc10g078290.1.1	BZIP family transcription factor (Fragment) IPR011616 bZIP transcription factor, bZIP-1	
4DE	g4082.t1	55073475	55074420	945	2E-15	41.43	52	Solyc10g078290.1.1	BZIP family transcription factor (Fragment) IPR011616 bZIP transcription factor, bZIP-1	
4DE	g4083.t1	55078752	55079850	1098	2E-21	47.73	73	Solyc02g062800.2.1	F-box family protein IPR017451 F-box associated type 1	
4DE	g4084.t1	55092074	55094186	2112	8E-48	67.89	100	Solyc04g056500.1.1	Tubulin beta chain IPR019746 Tubulin_FtsZ, N-terminal	
4DE	g4085.t1	55103628	55105826	2198	2E-19	80.39	31	Solyc10g078290.1.1	BZIP family transcription factor (Fragment) IPR011616 bZIP transcription factor, bZIP-1	
4DE	g4086.t1	55113722	55117156	3434	2E-18	56.78	61	Solyc04g056460.1.1	AtbZIP transcription factor (Fragment) IPR011616 bZIP transcription factor, bZIP-1	
4DE	g4087.t2	55119155	55133445	14290	5E-30	46.15	25	Solyc02g062800.2.1	F-box family protein IPR017451 F-box associated type 1	
4DE	g4088.t1	55149635	55154001	4366	2E-25	40.94	32	Solyc02g062800.2.1	F-box family protein IPR017451 F-box associated type 1	
4DE	g4088.t2	55149635	55158711	9076	1E-13	35.04	27	Solyc02g062800.2.1	F-box family protein IPR017451 F-box associated type 1	
4DE	g4090.t1	55174106	55176196	2090	3E-15	35.56	81	Solyc02g062800.2.1	F-box family protein IPR017451 F-box associated type 1	
4DE	g4091.t1	55177475	55197179	19704	2E-10	49.02	16	Solyc02g062800.2.1	F-box family protein IPR017451 F-box associated type 1	
4DE	g4093.t1	55218215	55239346	21131	8E-20	42.48	17	Solyc02g062800.2.1	F-box family protein IPR017451 F-box associated type 1	
4DE	g4094.t1	55242775	55246780	4005	8E-104	91.57	73	Solyc04g039720.1.1	Unknown Protein IPR010666 Zinc finger, GRF-type	
4DE	g4095.t2	55246848	55251946	5098	7E-129	88.64	34	Solyc04g015320.1.1	Unknown Protein IPR017956 AT hook, DNA-binding, conserved site	
4DE	g4096.t1	55257669	55265106	7437	6E-11	84.38	14	Solyc01g097630.1.1	BAC19.2	
4DE	g4102.t2	55326292	55330486	4194	1E-18	42.11	29	Solyc01g057350.1.1	Unknown Protein	
4DE	g4102.t1	55326514	55330486	3972	1E-18	42.11	29	Solyc01g057350.1.1	Unknown Protein	
4DE	g4103.t1	55331335	55336779	5444	8E-17	33.33	47	Solyc10g047550.1.1	Unknown Protein	
4DE	g4104.t1	55339150	55343936	4786	0E+00	94.46	100	Solyc04g051080.1.1	Response regulator 8 IPR006447 Myb-like DNA-binding region, SHAQKYF class	
4DE	g4108.t1	55368185	55370256	2071	7E-25	48.65	47	Solyc01g057350.1.1	Unknown Protein	
4DE	g4110.t1	55378684	55385146	6462	5E-107	77.61	81	Solyc04g051080.1.1	Response regulator 8 IPR006447 Myb-like DNA-binding region, SHAQKYF class	
4DE	g4117.t1	55443854	55447389	3535	2E-17	86.36	27	Solyc04g051100.2.1	Unknown Protein	
4DE	g4125.t1	55508598	55522056	13458	0E+00	98.53	72	Solyc04g051120.2.1	Homology to unknown gene	
4DE	g4126.t1	55533748	55558086	24338	0E+00	84.72	83	Solyc04g051150.2.1	Sterol 3-beta-glucosyltransferase IPR004276 Glycosyl transferase, family 28	
4DE	g4126.t2	55533748	55549485	15737	0E+00	72.09	100	Solyc04g051150.2.1	Sterol 3-beta-glucosyltransferase IPR004276 Glycosyl transferase, family 28	
4DE	g4127.t1	55568419	55593469	25050	1E-31	52.48	20	Solyc05g017810.1.1	Unknown Protein	
4DE	g4133.t1	55648673	55652399	3726	0E+00	80.77	90	Solyc04g051160.1.1	Sugar transporter family protein expressed IPR016196 Major facilitator superfamily, general substrate transporter	
4DE	g4133.t2	55648673	55651269	2596	0E+00	80.65	99	Solyc04g051160.1.1	Sugar transporter family protein expressed IPR016196 Major facilitator superfamily, general substrate transporter	
4DE	g4135.t1	55688368	55690753	2385	3E-73	67.68	100	Solyc01g104820.2.1	Integral membrane protein IPR008217 Protein of unknown function DUF125, transmembrane	
4DE	g4136.t1	55727731	55734319	6588	2E-95	98.51	69	Solyc04g051170.1.1	Carboxyl-terminal proteinase IPR004314 Protein of unknown function DUF239, plant	
4DE	g4138.t1	55765969	55766809	840	4E-78	95.69	100	Solyc07g009300.1.1	Unknown Protein	
4DE	g4149.t1	55870796	55878440	7644	2E-73	60.2	54	Solyc00g153680.1.1	Serine_threonine protein kinase IPR002290 Serine_threonine protein kinase	
4DE	g4151.t1	55885804	55894037	8233	0E+00	99.17	100	Solyc04g051190.2.1	Cytochrome P450	
4DE	g4152.t1	55895478	55899947	4469	0E+00	98.84	76	Solyc04g051200.1.1	Alpha-1 4-glucan-protein synthase IPR004901 Alpha-1,4-glucan-protein synthase, UDP-forming	
4DE	g4153.t1	55914056	55917006	2950	8E-46	56.43	55	Solyc09g010390.2.1	Unknown Protein	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.Jycopersicum (Heinz)		
4DE	g4156.t1	55947611	55959807	12196	1E-48	90.22	31	Solyc11g013370.1.1	E3 ubiquitin-protein ligase bre1	IPR018957 Zinc finger, C3HC4 RING-type
4DE	g4157.t1	55961236	55965738	4502	7E-121	48.42	83	Solyc03g044840.1.1	Helicase-like protein	IPR010285 Protein of unknown function DUF889, eukaryote
4DE	g4160.t1	55995960	55998809	2849	8E-170	73.48	91	Solyc06g065000.1.1	Cc-nbs, resistance protein fragment	
4DE	g4162.t1	56006680	56011419	4739	2E-34	92.31	78	Solyc04g051230.1.1	Unknown Protein	
4DE	g4164.t1	56040506	56044219	3713	0E+00	61.52	99	Solyc04g071780.2.1	Cytochrome P450	
4DE	g4166.t1	56073016	56077319	4303	2E-45	54.5	30	Solyc05g017810.1.1	Unknown Protein	
4DE	g4168.t1	56082891	56089249	6358	3E-17	65.52	64	Solyc10g076470.1.1	Unknown Protein	
4DE	g4171.t1	56148125	56154579	6454	0E+00	98.01	91	Solyc04g051280.2.1	F16G16.9 protein (Fragment)	
4DE	g4172.t1	56159688	56165610	5922	5E-18	39.13	19	Solyc02g094810.1.1	Unknown Protein	
4DE	g4173.t1	56176177	56176823	646	5E-87	100	99	Solyc04g051310.2.1	Genomic DNA chromosome 5 P1 clone MQK4	
4DE	g4175.t1	56183827	56193209	9382	0E+00	89.48	100	Solyc04g051310.2.1	Genomic DNA chromosome 5 P1 clone MQK4	
4DE	g4176.t1	56212297	56213160	863	5E-14	76.19	51	Solyc04g051330.1.1	Unknown Protein	
4DE	g4177.t1	56217064	56224938	7874	4E-163	100	88	Solyc04g051340.2.1	Cov1 (Fragment)	IPR007462 Protein of unknown function DUF502
4DE	g4177.t2	56218637	56225188	6551	2E-162	100	76	Solyc04g051340.2.1	Cov1 (Fragment)	IPR007462 Protein of unknown function DUF502
4DE	g4179.t1	56260397	56266214	5817	0E+00	99.13	100	Solyc04g051350.2.1	Ribonucleoside-diphosphate reductase	IPR013346 Ribonucleoside-diphosphate reductase, alpha subunit
4DE	g4179.t2	56260397	56266214	5817	0E+00	99.26	100	Solyc04g051350.2.1	Ribonucleoside-diphosphate reductase	IPR013346 Ribonucleoside-diphosphate reductase, alpha subunit
4DE	g4180.t1	56274717	56284307	9590	1E-115	90.52	19	Solyc04g051360.2.1	Ethylene responsive transcription factor 2b	IPR001471 Pathogenesis-related transcriptional factor and ERF, DNA-binding
4DE	g4181.t1	56286558	56297268	10710	0E+00	98	100	Solyc04g051370.2.1	26S proteasome non-ATPase regulatory subunit 12	IPR000717 Proteasome component region PCI
4DE	g4181.t2	56286959	56308828	21869	0E+00	98	77	Solyc04g051370.2.1	26S proteasome non-ATPase regulatory subunit 12	IPR000717 Proteasome component region PCI
4DE	g4185.t1	56380199	56392873	12674	0E+00	87.84	73	Solyc04g051410.2.1	Ubiquitin carboxyl-terminal hydrolase	IPR001394 Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2
4DE	g4185.t2	56380199	56392873	12674	0E+00	98.2	75	Solyc04g051410.2.1	Ubiquitin carboxyl-terminal hydrolase	IPR001394 Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2
4DE	g4186.t1	56404289	56412667	8378	0E+00	97.06	99	Solyc04g051450.2.1	Tsl-kinase interacting protein 1	
4DE	g4186.t2	56404289	56437196	32907	0E+00	96.87	55	Solyc04g051450.2.1	Tsl-kinase interacting protein 1	
4DE	g4186.t3	56422119	56437196	15077	5E-113	96.43	36	Solyc09g057700.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1
4DE	g4187.t1	56457982	56462140	4158	0E+00	99.11	100	Solyc04g051480.1.1	Pentatricopeptide repeat-containing protein	IPR002885 Pentatricopeptide repeat
4DE	g4188.t1	56462434	56476980	14546	0E+00	97.61	72	Solyc04g051490.2.1	Essential meiotic endonuclease 1B	IPR006166 DNA repair nuclease, XPF-type_Helicase
4DE	g4188.t2	56462434	56476980	14546	0E+00	97.93	100	Solyc04g051490.2.1	Essential meiotic endonuclease 1B	IPR006166 DNA repair nuclease, XPF-type_Helicase
4DE	g4190.t1	56493999	56499526	5527	0E+00	99.4	99	Solyc04g051500.2.1	Integral membrane protein like	IPR004853 Protein of unknown function DUF250
4DE	g4193.t1	56573500	56577313	3813	0E+00	99.5	100	Solyc04g051510.1.1	Receptor like kinase, RLK	
4DE	g4194.t1	56630784	56635551	4767	2E-174	98.72	100	Solyc04g051540.2.1	WRKY family transcription factor	IPR003657 DNA-binding WRKY
4DE	g4197.t1	56690530	56727863	37333	0E+00	98.16	35	Solyc04g051550.1.1	Unknown Protein	
4DE	g4197.t2	56690530	56727839	37309	0E+00	98.16	35	Solyc04g051550.1.1	Unknown Protein	
4DE	g4198.t1	56729236	56737351	8115	0E+00	83.24	92	Solyc04g051580.2.1	Mitochondrial carrier C12B10.09	IPR002067 Mitochondrial carrier protein
4DE	g4199.t1	56738710	56741559	2849	7E-114	87.96	64	Solyc04g051590.2.1	Glucan endo-1 3-beta-glucosidase 5	IPR013781 Glycoside hydrolase, subgroup, catalytic core
4DE	g4201.t1	56761090	56762200	1110	2E-72	96.26	38	Solyc05g042140.1.1	Unknown Protein	IPR001878 Zinc finger, CCHC-type
4DE	g4202.t1	56762740	56794082	31342	0E+00	89.15	41	Solyc04g051600.2.1	tRNA(His) guanylyltransferase	IPR007537 tRNAHis guanylyltransferase
4DE	g4202.t2	56762740	56794082	31342	0E+00	91.91	42	Solyc04g051600.2.1	tRNA(His) guanylyltransferase	IPR007537 tRNAHis guanylyltransferase
4DE	g4203.t1	56794621	56801291	6670	0E+00	95.22	52	Solyc04g051620.1.1	Alpha-humulene_(-)-(E)-beta-caryophyllene synthase	IPR005630 Terpene synthase, metal-binding domain
4DE	g4204.t1	56819780	56824549	4769	0E+00	61.89	99	Solyc09g091910.1.1	Purple acid phosphatase	IPR015914 Purple acid phosphatase, N-terminal
4DE	g4205.t1	56826029	56828121	2092	1E-91	99.25	100	Solyc04g051660.2.1	TPR repeat	IPR011990 Tetra-trico-peptide-like helical
4DE	g4206.t1	56829367	56830471	1104	2E-146	99.04	84	Solyc04g051660.2.1	TPR repeat	IPR011990 Tetra-trico-peptide-like helical
4DE	g4208.t2	56836630	56877426	40796	0E+00	95.34	40	Solyc04g051670.2.1	N-acetyltransferase 10	IPR007807 Protein of unknown function DUF699, ATPase putative
4DE	g4208.t1	56857550	56877426	19876	0E+00	96.55	100	Solyc04g051670.2.1	N-acetyltransferase 10	IPR007807 Protein of unknown function DUF699, ATPase putative
4DE	g4212.t1	56950970	56953565	2595	3E-89	100	100	Solyc04g051710.1.1	Unknown Protein	
4DE	g4213.t2	56953673	56955261	1588	2E-71	96.33	100	Solyc04g051720.2.1	Genomic DNA chromosome 5 P1 clone MXK3	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g4213.t1	56953673	56960561	6888	1E-46	94.94	68	Solyc04g051720.2.1	Genomic DNA chromosome 5 P1 clone MXK3	
4DE	g4214.t1	56963170	56971899	8729	0E+00	97.34	36	Solyc04g051730.1.1	Cytochrome P450	
4DE	g4215.t1	56973030	56976953	3923	1E-157	71.99	99	Solyc04g011920.1.1	Cytochrome P450	
4DE	g4216.t1	56978906	56983961	5055	0E+00	93.59	98	Solyc04g051780.2.1	Programmed cell death protein 2 IPR007320 Programmed cell death protein 2, C-terminal	
4DE	g4216.t2	56978906	56993131	14225	0E+00	93.59	46	Solyc04g051780.2.1	Programmed cell death protein 2 IPR007320 Programmed cell death protein 2, C-terminal	
4DE	g4220.t1	57022611	57027790	5179	0E+00	99.42	100	Solyc04g051800.2.1	ABC transporter ATP-binding protein IPR003439 ABC transporter-like	
4DE	g4221.t1	57041709	57045156	3447	3E-67	96.94	100	Solyc04g051820.2.1	Os03g0169900 protein (Fragment)	
4DE	g4222.t2	57048804	57068760	19956	0E+00	79.59	69	Solyc04g051830.2.1	Developmentally regulated GTP binding protein 1 IPR004095 TGS	
4DE	g4222.t1	57048892	57062460	13568	0E+00	81	98	Solyc04g051830.2.1	Developmentally regulated GTP binding protein 1 IPR004095 TGS	
4DE	g4223.t1	57071049	57073605	2556	8E-97	77.6	96	Solyc04g051850.2.1	Unknown Protein	
4DE	g4224.t1	57074949	57083602	8653	0E+00	86.46	89	Solyc04g051860.2.1	Shikimate kinase IPR000623 Shikimate kinase	
4DE	g4225.t1	57084453	57090640	6187	0E+00	99.7	46	Solyc04g051870.1.1	Kelch repeat-containing F-box family protein IPR015915 Kelch-type beta propeller	
4DE	g4226.t1	57091902	57092600	698	2E-11	63.89	35	Solyc11g011720.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein	
4DE	g4227.t1	57094920	57097700	2780	8E-79	47.77	91	Solyc07g042790.1.1	Helicase-like protein IPR010285 Protein of unknown function DUF889, eukaryote	
4DE	g4230.t1	57110442	57111630	1188	3E-75	78.87	78	Solyc04g052900.1.1	Unknown Protein	
4DE	g4230.t2	57110442	57121450	11008	1E-70	78.32	23	Solyc04g052900.1.1	Unknown Protein	
4DE	g4231.t1	57123189	57125343	2154	4E-145	91.11	66	Solyc00g024570.1.1	F-box family protein IPR001810 Cyclin-like F-box	
4DE	g4233.t2	57155718	57162710	6992	4E-71	59.85	32	Solyc04g052940.1.1	Unknown Protein	
4DE	g4233.t1	57159541	57162710	3169	1E-71	59.85	35	Solyc04g052940.1.1	Unknown Protein	
4DE	g4234.t1	57163559	57173427	9868	5E-96	97.97	10	Solyc04g052960.1.1	Auxin-responsive protein IPR003676 Auxin responsive SAUR protein	
4DE	g4234.t2	57163559	57169469	5910	4E-43	51.15	20	Solyc04g052940.1.1	Unknown Protein	
4DE	g4235.t1	57174243	57174860	617	2E-60	100	100	Solyc04g052970.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein	
4DE	g4236.t1	57175429	57176191	762	1E-102	95.27	100	Solyc04g052980.1.1	Auxin-responsive protein IPR003676 Auxin responsive SAUR protein	
4DE	g4238.t1	57184769	57185614	845	6E-96	93.66	100	Solyc04g052990.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein	
4DE	g4240.t1	57192139	57194918	2779	2E-91	85.14	100	Solyc11g011640.1.1	Auxin-responsive protein IPR003676 Auxin responsive SAUR protein	
4DE	g4241.t1	57196619	57197406	787	2E-96	94.37	100	Solyc04g052990.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein	
4DE	g4242.t1	57197755	57198440	685	1E-59	96.74	100	Solyc04g053000.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein	
4DE	g4243.t1	57198989	57199718	729	5E-93	87.84	100	Solyc04g053020.1.1	Auxin-responsive protein IPR003676 Auxin responsive SAUR protein	
4DE	g4244.t1	57204074	57204983	909	5E-85	80.95	99	Solyc04g053020.1.1	Auxin-responsive protein IPR003676 Auxin responsive SAUR protein	
4DE	g4245.t1	57205464	57206235	771	4E-105	97.97	100	Solyc04g053020.1.1	Auxin-responsive protein IPR003676 Auxin responsive SAUR protein	
4DE	g4246.t1	57209254	57210007	753	1E-104	99.32	99	Solyc04g053030.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein	
4DE	g4252.t1	57246798	57248725	1927	0E+00	98.71	93	Solyc04g053080.2.1	OTU domain-containing protein 6B IPR003323 Ovarian tumour, otubain	
4DE	g4255.t1	57288324	57288984	660	2E-69	99.03	100	Solyc00g028960.1.1	Glutaredoxin family protein IPR011905 Glutaredoxin-like, plant II	
4DE	g4259.t1	57321604	57327143	5539	2E-111	98.17	69	Solyc04g053090.1.1	AT-hook motif nuclear localized protein 2 IPR005175 Protein of unknown function DUF296	
4DE	g4259.t2	57321604	57328521	6917	2E-105	97.45	70	Solyc04g053090.1.1	AT-hook motif nuclear localized protein 2 IPR005175 Protein of unknown function DUF296	
4DE	g4261.t1	57343454	57346011	2557	6E-80	93.7	100	Solyc04g053100.1.1	AT-hook motif nuclear localized protein 2 IPR005175 Protein of unknown function DUF296	
4DE	g4263.t1	57369764	57371726	1962	2E-113	96.45	100	Solyc04g053090.1.1	AT-hook motif nuclear localized protein 2 IPR005175 Protein of unknown function DUF296	
4DE	g4263.t2	57369764	57371726	1962	4E-110	95.27	100	Solyc04g053090.1.1	AT-hook motif nuclear localized protein 2 IPR005175 Protein of unknown function DUF296	
4DE	g4264.t1	57390288	57393361	3073	1E-63	64.5	100	Solyc04g053090.1.1	AT-hook motif nuclear localized protein 2 IPR005175 Protein of unknown function DUF296	
4DE	g4268.t1	57413138	57426575	13437	2E-90	89.47	71	Solyc04g053090.1.1	AT-hook motif nuclear localized protein 2 IPR005175 Protein of unknown function DUF296	
4DE	g4268.t2	57423478	57426575	3097	2E-108	92.9	100	Solyc04g053090.1.1	AT-hook motif nuclear localized protein 2 IPR005175 Protein of unknown function DUF296	
4DE	g4272.t1	57473808	57474423	615	4E-70	100	100	Solyc04g053110.1.1	Glutaredoxin IPR011905 Glutaredoxin-like, plant II	
4DE	g4273.t1	57478072	57485259	7187	0E+00	99.48	100	Solyc04g053120.2.1	4-alpha-glucanotransferase IPR003385 Glycoside hydrolase, family 77	
4DE	g4277.t1	57521507	57523959	2452	3E-141	97.95	100	Solyc04g053130.2.1	LHC-related protein	
4DE	g4279.t1	57576014	57577154	1140	2E-165	97.03	100	Solyc04g053140.1.1	Plant-specific domain TIGR01570 family protein IPR006460 Protein of unknown function DUF617, plant	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g4280.t1	57579763	57584786	5023	5E-12	60.56	51	Solyc00g005170.1.1	Unknown Protein	
4DE	g4283.t1	57634468	57645354	10886	0E+00	96.07	100	Solyc04g054140.2.1	Ryanodine receptor IPR018355 SPla_Ryanodine receptor subgroup	
4DE	g4284.t1	57647593	57649500	1907	2E-60	63.98	73	Solyc03g096700.1.1	Unknown Protein	
4DE	g4290.t2	57708583	57717307	8724	0E+00	80.2	100	Solyc04g054170.2.1	CPR5 (Fragment)	
4DE	g4290.t1	57708583	57713777	5194	2E-79	99.17	59	Solyc04g054170.2.1	CPR5 (Fragment)	
4DE	g4291.t1	57718752	57726744	7992	0E+00	94.52	90	Solyc04g054180.2.1	Os02g0519300 protein (Fragment)	
4DE	g4291.t2	57718752	57726744	7992	0E+00	91.88	91	Solyc04g054180.2.1	Os02g0519300 protein (Fragment)	
4DE	g4293.t1	57761113	57771487	10374	0E+00	99.73	100	Solyc04g054190.2.1	ABC-1 domain protein IPR004147 ABC-1	
4DE	g4294.t1	57776678	57788384	11706	2E-14	62.26	45	Solyc01g057970.1.1	Unknown Protein	
4DE	g4295.t1	57793563	57801795	8232	0E+00	95.72	100	Solyc04g054200.2.1	Receptor like kinase, RLK	
4DE	g4295.t3	57793563	57814374	20811	0E+00	95.62	50	Solyc04g054200.2.1	Receptor like kinase, RLK	
4DE	g4300.t2	57857922	57864864	6942	3E-40	64.06	56	Solyc03g096700.1.1	Unknown Protein	
4DE	g4301.t1	57902625	57905218	2593	0E+00	85.9	100	Solyc04g054220.2.1	Cytochrome P450	
4DE	g4308.t1	57984187	57986025	1838	0E+00	80.85	100	Solyc04g050620.2.1	Cytochrome P450	
4DE	g4310.t2	57996237	57998591	2354	0E+00	97.14	93	Solyc04g054250.2.1	Cytochrome P450	
4DE	g4310.t1	57996757	57998591	1834	0E+00	97.14	98	Solyc04g054250.2.1	Cytochrome P450	
4DE	g4313.t1	58014217	58020714	6497	1E-89	78.03	34	Solyc12g070190.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR015410 Region of unknown function DUF1985	
4DE	g4315.t1	58035252	58053038	17786	7E-101	97.99	83	Solyc00g247300.2.1	Cytochrome P450	
4DE	g4319.t1	58121697	58124265	2568	0E+00	97.48	100	Solyc00g247300.2.1	Cytochrome P450	
4DE	g4320.t1	58126027	58127653	1626	0E+00	97.33	100	Solyc00g247300.2.1	Cytochrome P450	
4DE	g4323.t1	58151915	58152478	563	3E-70	95.54	99	Solyc04g054260.2.1	Cytochrome P450	
4DE	g4324.t1	58152625	58158078	5453	2E-137	98.96	95	Solyc04g054260.2.1	Cytochrome P450	
4DE	g4325.t1	58171047	58174207	3160	0E+00	89.96	100	Solyc04g054270.2.1	Pentatricopeptide repeat protein 5 IPR002885 Pentatricopeptide repeat	
4DE	g4327.t2	58183807	58203919	20112	0E+00	97.81	50	Solyc04g054290.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
4DE	g4327.t1	58198547	58203919	5372	0E+00	98.1	100	Solyc04g054310.2.1	Alanine-glyoxylate aminotransferase IPR005814 Aminotransferase class-III	
4DE	g4328.t1	58204214	58210828	6614	0E+00	98.11	100	Solyc04g054320.2.1	BZIP transcription factor IPR011616 bZIP transcription factor, bZIP-1	
4DE	g4328.t2	58204214	58210828	6614	0E+00	98.11	100	Solyc04g054320.2.1	BZIP transcription factor IPR011616 bZIP transcription factor, bZIP-1	
4DE	g4330.t1	58222094	58224298	2204	1E-25	60.27	12	Solyc02g036400.1.1	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence	
4DE	g4333.t1	58275304	58284553	9249	8E-83	100	34	Solyc04g054330.2.1	Zinc finger C3HC4 type family protein IPR011016 Zinc finger, RING-CH-type	
4DE	g4333.t2	58275304	58284553	9249	2E-79	91.11	36	Solyc04g054330.2.1	Zinc finger C3HC4 type family protein IPR011016 Zinc finger, RING-CH-type	
4DE	g4340.t1	58366464	58368343	1879	6E-16	76.74	25	Solyc09g042380.1.1	Unknown Protein	
4DE	g4341.t1	58388924	58389915	991	3E-84	77.27	73	Solyc10g012480.1.1	Unknown Protein	
4DE	g4342.t1	58390144	58391135	991	3E-89	64.49	88	Solyc10g012470.1.1	Unknown Protein	
4DE	g4367.t1	58671857	58677802	5945	4E-20	49.5	29	Solyc02g021080.1.1	Unknown Protein	
4DE	g4371.t2	58717770	58741218	23448	2E-54	34.2	15	Solyc00g008110.1.1	Unknown Protein	
4DE	g4371.t1	58720078	58724248	4170	1E-38	31.4	62	Solyc00g008000.1.1	Unknown Protein	
4DE	g4372.t1	58744578	58746388	1810	3E-33	31.61	89	Solyc00g008110.1.1	Unknown Protein	
4DE	g4381.t1	58860421	58865745	5324	3E-24	42.03	28	Solyc10g046780.1.1	Zinc knuckle family protein IPR001878 Zinc finger, CCHC-type	
4DE	g4385.t1	58918762	58921035	2273	2E-92	40.81	77	Solyc03g062840.1.1	Unknown Protein	
4DE	g4389.t1	58955279	58961629	6350	3E-72	39.25	75	Solyc10g077140.1.1	cDNA clone J013074B07 full insert sequence IPR018289 MULE transposase, conserved domain	
4DE	g4390.t1	58966944	58967609	665	1E-116	96.97	100	Solyc04g054370.1.1	RING finger protein 13 IPR018957 Zinc finger, C3HC4 RING-type	
4DE	g4391.t1	58972088	58979282	7194	5E-61	90	10	Solyc09g061300.1.1	Unknown Protein	
4DE	g4399.t1	59046608	59048889	2281	0E+00	61.38	87	Solyc03g062840.1.1	Unknown Protein	
4DE	g4403.t1	59062614	59065409	2795	0E+00	98.19	100	Solyc04g054380.1.1	Alpha-humulene_(-)(E)-beta-caryophyllene synthase IPR005630 Terpene synthase, metal-binding domain	
4DE	g4403.t2	59062614	59066069	3455	0E+00	98.01	100	Solyc04g054380.1.1	Alpha-humulene_(-)(E)-beta-caryophyllene synthase IPR005630 Terpene synthase, metal-binding domain	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g4408.t1	59127778	59135329	7551	0E+00	97.82	99	Solyc04g054400.2.1	Short-chain dehydrogenase_reductase SDR IPR002347	Glucose_ribitol dehydrogenase
4DE	g4409.t1	59136629	59148829	12200	0E+00	96.19	51	Solyc04g054410.2.1	Regulation of nuclear pre-mRNA domain containing 1B IPR006903	Protein of unknown function DUF618
4DE	g4409.t2	59136629	59148829	12200	0E+00	85.49	60	Solyc04g054410.2.1	Regulation of nuclear pre-mRNA domain containing 1B IPR006903	Protein of unknown function DUF618
4DE	g4411.t1	59209238	59211403	2165	1E-29	50.76	38	Solyc10g049340.1.1	CCHC-type integrase (Fragment)	
4DE	g4414.t1	59227018	59232095	5077	0E+00	98.93	50	Solyc04g054440.1.1	DNA repair protein IPR000330	SNF2-related
4DE	g4415.t1	59249934	59251759	1825	3E-98	92.99	100	Solyc04g054460.2.1	Glycine-rich protein	
4DE	g4416.t1	59252738	59269131	16393	0E+00	95.62	75	Solyc04g054470.2.1	Myosin class II heavy chain (ISS)	
4DE	g4418.t1	59285618	59296744	11126	0E+00	99.62	60	Solyc04g054480.2.1	C2 domain-containing protein-like IPR011989	Armadillo-like helical
4DE	g4419.t1	59309424	59317088	7664	0E+00	92.86	100	Solyc04g054490.2.1	Aspartyl protease family protein IPR001461	Peptidase A1
4DE	g4419.t2	59309424	59317088	7664	0E+00	87.11	100	Solyc04g054490.2.1	Aspartyl protease family protein IPR001461	Peptidase A1
4DE	g4420.t1	59327284	59328396	1112	2E-99	97.86	100	Solyc04g054500.2.1	Metal ion binding protein IPR006121	Heavy metal transport detoxification protein
4DE	g4421.t1	59329975	59338015	8040	3E-43	100	37	Solyc04g054510.2.1	DNA-directed RNA polymerase I subunit RPA12 IPR001222	Zinc finger, TFIIIS-type
4DE	g4422.t1	59345474	59346115	641	4E-49	97.47	82	Solyc11g065580.1.1	Unknown Protein	
4DE	g4423.t1	59348001	59355225	7224	6E-132	100	64	Solyc04g054520.2.1	Peptidyl-prolyl cis-trans isomerase IPR001179	Peptidyl-prolyl cis-trans isomerase, FKBP-type
4DE	g4425.t1	59381931	59388255	6324	1E-95	78.69	71	Solyc00g045570.1.1	Unknown Protein	
4DE	g4427.t2	59405471	59410945	5474	4E-17	37.86	32	Solyc05g051830.2.1	MADS-box transcription factor 1 IPR002100	Transcription factor, MADS-box
4DE	g4427.t1	59405471	59410945	5474	5E-17	31.69	38	Solyc05g051830.2.1	MADS-box transcription factor 1 IPR002100	Transcription factor, MADS-box
4DE	g4429.t1	59418201	59423485	5284	8E-21	31.25	39	Solyc05g051830.2.1	MADS-box transcription factor 1 IPR002100	Transcription factor, MADS-box
4DE	g4431.t1	59436204	59436915	711	1E-18	46.15	94	Solyc04g078300.2.1	MADS-box transcription factor 1 IPR002100	Transcription factor, MADS-box
4DE	g4437.t1	59491671	59494567	2896	2E-28	57.14	100	Solyc11g044210.1.1	Unknown Protein	
4DE	g4438.t1	59494796	59500602	5806	6E-39	93.33	37	Solyc04g054680.1.1	RING finger protein B IPR001841	Zinc finger, RING-type
4DE	g4440.t1	59505902	59506597	695	1E-20	57.53	88	Solyc04g078300.2.1	MADS-box transcription factor 1 IPR002100	Transcription factor, MADS-box
4DE	g4443.t1	59518326	59519249	923	2E-69	94.69	79	Solyc04g054680.1.1	RING finger protein B IPR001841	Zinc finger, RING-type
4DE	g4445.t1	59526109	59526807	698	1E-20	57.53	88	Solyc04g078300.2.1	MADS-box transcription factor 1 IPR002100	Transcription factor, MADS-box
4DE	g4447.t1	59538168	59539657	1489	2E-65	69.9	89	Solyc04g054600.1.1	Unknown Protein	
4DE	g4448.t1	59545766	59548391	2625	4E-69	93.81	57	Solyc04g054680.1.1	RING finger protein B IPR001841	Zinc finger, RING-type
4DE	g4449.t2	59549662	59555857	6195	2E-20	58.11	21	Solyc04g078300.2.1	MADS-box transcription factor 1 IPR002100	Transcription factor, MADS-box
4DE	g4453.t1	59593087	59595437	2350	0E+00	99.31	100	Solyc04g054690.2.1	Laccase 1a IPR017760	L-ascorbate oxidase, plants
4DE	g4454.t2	59607829	59614237	6408	0E+00	98.88	67	Solyc04g054700.2.1	General transcription factor IIH subunit 2 IPR007198	Ssl1-like
4DE	g4454.t1	59610508	59614237	3729	0E+00	98.51	71	Solyc04g054700.2.1	General transcription factor IIH subunit 2 IPR007198	Ssl1-like
4DE	g4455.t1	59625586	59631977	6391	0E+00	96.04	100	Solyc04g054710.2.1	Aspartate aminotransferase IPR004839	Aminotransferase, class I and II
4DE	g4456.t1	59634706	59636340	1634	0E+00	98.34	99	Solyc04g054720.2.1	Exonuclease DNA polymerase III epsilon subunit family IPR006055	Exonuclease
4DE	g4456.t2	59634706	59641183	6477	0E+00	98.18	57	Solyc04g054720.2.1	Exonuclease DNA polymerase III epsilon subunit family IPR006055	Exonuclease
4DE	g4457.t1	59644008	59650087	6079	0E+00	95.65	100	Solyc04g054730.2.1	High affinity sulfate transporter 2 IPR001902	Sulphate anion transporter
4DE	g4461.t2	59729849	59733483	3634	2E-27	68.66	39	Solyc09g042380.1.1	Unknown Protein	
4DE	g4462.t1	59741772	59742925	1153	5E-45	61.29	37	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g4465.t2	59783492	59789633	6141	0E+00	99.32	45	Solyc04g054740.2.1	Inositol-3-phosphate synthase IPR002587	Myo-inositol-1-phosphate synthase
4DE	g4465.t1	59786712	59789633	2921	0E+00	99.32	73	Solyc04g054740.2.1	Inositol-3-phosphate synthase IPR002587	Myo-inositol-1-phosphate synthase
4DE	g4466.t1	59789812	59795795	5983	5E-50	40.71	51	Solyc12g0006040.1.1	Nbs, resistance protein fragment	
4DE	g4466.t2	59789812	59795795	5983	7E-50	40.71	49	Solyc12g0006040.1.1	Nbs, resistance protein fragment	
4DE	g4467.t1	59806662	59809990	3328	0E+00	99.61	100	Solyc04g054740.2.1	Inositol-3-phosphate synthase IPR002587	Myo-inositol-1-phosphate synthase
4DE	g4468.t1	59832781	59837412	4631	4E-106	98.64	100	Solyc04g054760.2.1	Os10g0422600 protein (Fragment) IPR007650	Protein of unknown function DUF581
4DE	g4469.t2	59860621	59874772	14151	1E-14	45.65	17	Solyc02g071230.1.1	Pre-mRNA-processing factor 39 IPR003107	RNA-processing protein, HAT helix
4DE	g4471.t1	59907961	59911210	3249	1E-144	91.11	79	Solyc04g054800.2.1	Unknown Protein IPR010369	Protein of unknown function DUF966
4DE	g4471.t2	59907961	59911210	3249	5E-143	91.11	64	Solyc04g054800.2.1	Unknown Protein IPR010369	Protein of unknown function DUF966

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g4472.t1	59921841	59923041	1200	2E-112	97.48	100	Solyc04g054810.2.1	Pollen allergen Phi p 11 IPR006041 Pollen Ole e 1 allergen and extensin	
4DE	g4473.t1	59926371	59938148	11777	0E+00	92.24	61	Solyc04g054830.2.1	Inositol-1 4 5-trisphosphate 5-phosphatase-like protein IPR000300 Inositol polyphosphate related phosphatase	
4DE	g4473.t2	59926371	59938148	11777	0E+00	92.07	61	Solyc04g054830.2.1	Inositol-1 4 5-trisphosphate 5-phosphatase-like protein IPR000300 Inositol polyphosphate related phosphatase	
4DE	g4474.t1	59938391	59940112	1721	0E+00	93.08	99	Solyc04g054840.1.1	Ethylene insensitive 3 class transcription factor IPR006957 Ethylene insensitive 3	
4DE	g4478.t1	59992716	59999324	6608	0E+00	99.72	100	Solyc04g054880.2.1	BZIP transcription factor IPR006867 Protein of unknown function DUF632	
4DE	g4481.t2	60025986	60033782	7796	0E+00	98.05	35	Solyc04g054900.2.1	Genomic DNA chromosome 5 P1 clone MQN23	
4DE	g4482.t1	60056166	60058106	1940	1E-173	90.71	73	Solyc04g054910.2.1	Ethylene-responsive transcription factor 13 IPR001471 Pathogenesis-related transcriptional factor and ERF, DNA-binding	
4DE	g4485.t1	60090596	60097206	6610	1E-88	83.33	62	Solyc12g019090.1.1	Serine_threonine-protein phosphatase 7 long form homolog IPR019557 Aminotransferase-like, plant mobile domain	
4DE	g4488.t1	60105925	60112617	6692	0E+00	99.68	82	Solyc04g054930.2.1	Trehalose-6-phosphate phosphatase-like protein IPR003337 Trehalose-phosphatase	
4DE	g4490.t1	60151420	60153087	1667	0E+00	97.34	100	Solyc04g054950.2.1	Tropinone reductase I IPR002347 Glucose_ribitol dehydrogenase	
4DE	g4491.t1	60161604	60162884	1280	0E+00	93.82	100	Solyc04g054960.1.1	Harpin-induced protein 1 containing protein expressed	
4DE	g4493.t1	60171223	60180458	9235	4E-130	97.3	51	Solyc04g054990.2.1	Lipoxygenase homology domain-containing protein 1 IPR001024 Lipoxygenase, LH2	
4DE	g4496.t1	60202650	60205974	3324	0E+00	98.06	100	Solyc04g055020.1.1	Iron sulfur subunit of succinate dehydrogenase IPR004489 Succinate dehydrogenase_fumarate reductase iron-sulphur protein	
4DE	g4498.t1	60213467	60215424	1957	4E-26	35.05	71	Solyc04g025900.1.1	Unknown Protein	
4DE	g4500.t1	60217405	60219494	2089	3E-28	92.31	54	Solyc07g052280.1.1	Unknown Protein	
4DE	g4501.t1	60234723	60241021	6298	4E-66	98.97	42	Solyc01g099610.1.1	F-box-containing protein 1	
4DE	g4503.t1	60286883	60289485	2602	0E+00	97.83	100	Solyc04g055080.2.1	Transporter major facilitator family IPR016196 Major facilitator superfamily, general substrate transporter	
4DE	g4505.t1	60303563	60310293	6730	0E+00	95.12	78	Solyc04g055090.1.1	Unknown Protein	
4DE	g4506.t1	60311265	60312324	1059	0E+00	96.58	100	Solyc04g055100.1.1	Unknown Protein IPR010605 Protein of unknown function DUF1191	
4DE	g4509.t1	60357958	60370468	12510	0E+00	100	99	Solyc04g055110.2.1	Mitochondrial import receptor subunit TOM34 IPR011990 Tetratricopeptide-like helical	
4DE	g4511.t1	60394798	60419382	24584	0E+00	93.92	100	Solyc04g055120.2.1	Uncharacterized ABC transporter ATP-binding protein sl0182 IPR010509 ABC transporter, N-terminal	
4DE	g4513.t1	60430168	60430986	818	2E-89	96.88	100	Solyc04g055130.1.1	Unknown Protein	
4DE	g4514.t1	60432458	60433336	878	6E-90	94.81	100	Solyc04g055140.1.1	Unknown Protein	
4DE	g4515.t2	60437308	60440620	3312	0E+00	88.83	100	Solyc04g055160.2.1	cDNA clone J033025P19 full insert sequence	
4DE	g4515.t1	60439198	60440620	1422	4E-173	100	89	Solyc04g055160.2.1	cDNA clone J033025P19 full insert sequence	
4DE	g4516.t1	60441212	60445249	4037	0E+00	94.48	100	Solyc04g055170.2.1	Annexin 2 IPR009118 Annexin, type plant	
4DE	g4517.t1	60448528	60467325	18797	0E+00	95.36	47	Solyc04g055190.2.1	Glycerol uptake protein 1 IPR004299 Membrane bound O-acyl transferase, MBOAT	
4DE	g4518.t1	60490522	60507479	16957	0E+00	74.52	91	Solyc06g007180.2.1	Asparagine synthase (Glutamine-hydrolyzing) IPR006426 Asparagine synthase, glutamine-hydrolyzing	
4DE	g4519.t2	60516483	60540082	23599	0E+00	94.74	41	Solyc04g055240.1.1	F-box family protein IPR005174 Protein of unknown function DUF295	
4DE	g4520.t1	60542803	60550457	7654	0E+00	87.39	85	Solyc04g055240.1.1	F-box family protein IPR005174 Protein of unknown function DUF295	
4DE	g4524.t1	60596135	60597994	1859	3E-106	96.71	100	Solyc04g055260.2.1	Carboxyl methyltransferase IPR005299 SAM dependent carboxyl methyltransferase	
4DE	g4526.t1	60613276	60626764	13488	0E+00	97.98	53	Solyc04g056270.2.1	Calmodulin-binding transcription activator 3 IPR005559 CG-1	
4DE	g4528.t1	60645993	60658050	12057	0E+00	100	100	Solyc04g056280.2.1	Cell division protein kinase 9 IPR002290 Serine_threonine protein kinase	
4DE	g4528.t2	60645993	60658050	12057	0E+00	95.52	100	Solyc04g056280.2.1	Cell division protein kinase 9 IPR002290 Serine_threonine protein kinase	
4DE	g4529.t1	60658977	60673924	14947	4E-137	100	30	Solyc04g056290.2.1	Ubiquitin carboxyl-terminal hydrolase IPR001394 Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	
4DE	g4530.t1	60675376	60678084	2708	2E-11	36.79	34	Solyc04g025900.1.1	Unknown Protein	
4DE	g4533.t1	60722968	60724790	1822	0E+00	98.1	99	Solyc04g056310.2.1	MYB transcription factor IPR015495 Myb transcription factor	
4DE	g4535.t1	60741028	60742074	1046	5E-52	78.38	55	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g4537.t1	60773888	60775242	1354	0E+00	97.05	100	Solyc04g056320.1.1	Zinc finger family protein IPR007087 Zinc finger, C2H2-type	
4DE	g4538.t1	60779141	60780039	898	1E-119	95.32	100	Solyc04g056330.1.1	Protein containing AIG2-like domain IPR013024 Butirosin biosynthesis, BtrG-like	
4DE	g4539.t1	60798018	60800115	2097	2E-148	98.01	100	Solyc04g056340.2.1	Tyrosine phosphatase family protein IPR020428 Protein-tyrosine phosphatase, dual specificity phosphatase, eukaryotic	
4DE	g4541.t1	60815178	60816015	837	2E-69	99.04	81	Solyc04g056350.1.1	Zinc finger family protein	
4DE	g4542.t1	60824337	60827449	3112	7E-126	83.47	84	Solyc04g056360.2.1	WRKY transcription factor 78 IPR003657 DNA-binding WRKY	
4DE	g4545.t1	60854958	60857493	2535	0E+00	93.44	91	Solyc04g056380.2.1	Genomic DNA chromosome 5 P1 clone MQK4 IPR009617 Adipose-regulatory protein, Seipin	
4DE	g4546.t1	60858749	60862769	4020	0E+00	97.62	100	Solyc04g056390.2.1	Isopentenyl-diphosphate delta-isomerase IPR011876 Isopentenyl-diphosphate delta-isomerase, type 1	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.Jycopersicum (Heinz)		
4DE	g4547.t1	60875298	60889606	14308	0E+00	97.8	57	Solyc04g056410.2.1	DNA repair and recombination protein RAD54	IPR000330 SNF2-related
4DE	g4548.t1	60894268	60896222	1954	0E+00	93.05	100	Solyc07g047740.2.1	Peroxidase	IPR002016 Haem peroxidase, plant_fungal_bacterial
4DE	g4548.t2	60894268	60901029	6761	0E+00	92.81	73	Solyc07g047740.2.1	Peroxidase	IPR002016 Haem peroxidase, plant_fungal_bacterial
4DE	g4549.t2	60913518	60924578	11060	0E+00	68.21	74	Solyc03g045140.2.1	Cyclopropane-fatty-acyl-phospholipid synthase	IPR003333 Cyclopropane-fatty-acyl-phospholipid synthase
4DE	g4550.t1	60930238	60942139	11901	0E+00	78.49	99	Solyc09g090510.2.1	Cyclopropane-fatty-acyl-phospholipid synthase	IPR003333 Cyclopropane-fatty-acyl-phospholipid synthase
4DE	g4551.t1	60952206	60952849	643	3E-22	53.42	45	Solyc02g036400.1.1	SLG-Sc and SLA-Sc genes and Melmoth retrotransposon sequence	
4DE	g4552.t1	60956248	60959049	2801	0E+00	90.42	74	Solyc04g056460.1.1	AtbZIP transcription factor (Fragment)	IPR011616 bZIP transcription factor, bZIP-1
4DE	g4554.t1	60971883	60973839	1956	0E+00	91.58	47	Solyc03g062840.1.1	Unknown Protein	
4DE	g4558.t1	60999838	61002074	2236	0E+00	61.49	79	Solyc10g078290.1.1	BZIP family transcription factor (Fragment)	IPR011616 bZIP transcription factor, bZIP-1
4DE	g4561.t1	61010303	61011879	1576	6E-27	43.59	50	Solyc02g062800.2.1	F-box family protein	IPR017451 F-box associated type 1
4DE	g4562.t1	61018828	61019738	910	3E-11	57.89	34	Solyc08g068750.1.1	Unknown Protein	
4DE	g4568.t1	61103885	61107635	3750	1E-11	34.31	72	Solyc02g062800.2.1	F-box family protein	IPR017451 F-box associated type 1
4DE	g4570.t1	61118064	61129585	11521	8E-21	44.64	26	Solyc02g062800.2.1	F-box family protein	IPR017451 F-box associated type 1
4DE	g4572.t1	61159694	61161422	1728	2E-41	55.71	78	Solyc10g078290.1.1	BZIP family transcription factor (Fragment)	IPR011616 bZIP transcription factor, bZIP-1
4DE	g4575.t1	61215814	61225892	10078	0E+00	95.72	58	Solyc04g056540.2.1	Riboflavin biosynthesis protein RibD	IPR004794 Riboflavin biosynthesis protein RibD
4DE	g4576.t1	61226142	61227035	893	2E-124	96.59	96	Solyc04g056550.1.1	MADS-box transcription factor 25	IPR002100 Transcription factor, MADS-box
4DE	g4578.t1	61246839	61253011	6172	0E+00	99.25	81	Solyc04g056560.2.1	Protein phosphatase 2c	IPR015655 Protein phosphatase 2C
4DE	g4579.t1	61253101	61257130	4029	0E+00	96.01	100	Solyc04g056570.2.1	Tir-nbs-lrr, resistance protein	
4DE	g4580.t1	61258539	61260376	1837	0E+00	96.89	97	Solyc04g056580.2.1	Homology to unknown gene	
4DE	g4581.t1	61261463	61271590	10127	0E+00	96.81	91	Solyc04g056590.2.1	Aspartyl protease family protein	IPR001461 Peptidase A1
4DE	g4581.t2	61261463	61290990	29527	0E+00	97.04	50	Solyc04g056590.2.1	Aspartyl protease family protein	IPR001461 Peptidase A1
4DE	g4581.t4	61278775	61280280	1505	8E-72	96.4	76	Solyc04g056600.2.1	Sodium_hydrogen exchanger	IPR018409 Na+_H+ exchanger, isoform 5_6_8, conserved region
4DE	g4581.t3	61284707	61287580	2873	2E-155	95.28	94	Solyc04g056600.2.1	Sodium_hydrogen exchanger	IPR018409 Na+_H+ exchanger, isoform 5_6_8, conserved region
4DE	g4583.t1	61300572	61307640	7068	0E+00	99.09	100	Solyc04g056610.2.1	Genomic DNA chromosome 5 P1 clone MDF20	
4DE	g4584.t2	61313582	61316810	3228	1E-137	86.64	100	Solyc04g056620.1.1	Auxin Efflux Carrier	IPR004776 Auxin efflux carrier
4DE	g4584.t1	61313622	61316810	3188	7E-134	86.34	100	Solyc04g056620.1.1	Auxin Efflux Carrier	IPR004776 Auxin efflux carrier
4DE	g4586.t1	61342949	61345739	2790	0E+00	99.06	99	Solyc04g056640.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
4DE	g4587.t1	61346206	61355810	9604	0E+00	99.26	61	Solyc04g056650.2.1	ABC transporter ATP-binding protein	IPR003439 ABC transporter-like
4DE	g4588.t1	61360157	61366800	6643	1E-15	69.81	19	Solyc09g042380.1.1	Unknown Protein	
4DE	g4592.t1	61388587	61395710	7123	4E-123	97.67	67	Solyc04g056680.1.1	F-box protein PP2-B1	
4DE	g4592.t2	61388587	61395480	6893	4E-123	97.67	76	Solyc04g056680.1.1	F-box protein PP2-B1	
4DE	g4602.t1	61476274	61477069	795	2E-10	34.65	85	Solyc11g039800.1.1	Unknown Protein	
4DE	g4606.t1	61498692	61499585	893	2E-117	96.95	100	Solyc04g056740.1.1	MADS-box protein	IPR002100 Transcription factor, MADS-box
4DE	g4607.t1	61504558	61505645	1087	4E-35	49.01	89	Solyc04g083140.1.1	cytochrome P450	
4DE	g4611.t1	61541434	61544111	2677	0E+00	70.11	64	Solyc02g088140.1.1	Pentatricopeptide repeat-containing protein	IPR002885 Pentatricopeptide repeat
4DE	g4613.t1	61551644	61555250	3606	0E+00	94.82	100	Solyc04g083150.1.1	cytochrome P450	
4DE	g4614.t1	61568884	61569674	790	1E-151	97.57	100	Solyc04g057830.1.1	Unknown Protein	
4DE	g4615.t1	61570484	61574305	3821	1E-149	65.17	90	Solyc04g005540.2.1	Cc-nbs-lrr, resistance protein	
4DE	g4616.t1	61574741	61583665	8924	9E-57	75.37	70	Solyc04g005550.1.1	Cc-nbs-lrr, resistance protein	
4DE	g4617.t1	61593750	61594590	840	2E-82	92.97	97	Solyc04g057860.1.1	60S ribosomal protein L27	IPR001141 Ribosomal protein L27e
4DE	g4618.t1	61599799	61605838	6039	0E+00	91.69	89	Solyc04g057870.2.1	Os11g0110100 protein (Fragment)	
4DE	g4620.t1	61635709	61653706	17997	0E+00	98.41	95	Solyc04g057880.2.1	Histone-lysine N-methyltransferase	IPR001214 SET
4DE	g4620.t2	61635709	61656944	21235	0E+00	98.41	76	Solyc04g057880.2.1	Histone-lysine N-methyltransferase	IPR001214 SET
4DE	g4621.t1	61657578	61661000	3422	0E+00	99.25	100	Solyc04g057890.2.1	Ganglioside-induced differentiation-associated protein 1	IPR004045 Glutathione S-transferase, N-terminal
4DE	g4624.t1	61675919	61677604	1685	1E-144	89.32	78	Solyc04g057900.1.1	Unknown Protein	IPR004910 Yippee-like protein

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
4DE	g4625.t1	61679339	61680877	1538	0E+00	94.93	100	Solyc04g057910.2.1	Unknown Protein	
4DE	g4626.t1	61681219	61682980	1761	2E-132	92.46	82	Solyc04g057920.1.1	Unknown Protein IPR004910 Yippee-like protein	
4DE	g4627.t1	61708269	61712561	4292	0E+00	98.57	100	Solyc04g057930.2.1	Receptor-like kinase IPR002290 Serine_threonine protein kinase	
4DE	g4628.t1	61716579	61733135	16556	0E+00	98.32	100	Solyc04g057940.2.1	U-box domain-containing protein IPR017986 WD40 repeat, region	
4DE	g4629.t1	61750459	61752850	2391	0E+00	94.94	74	Solyc04g057950.1.1	F-box family protein IPR013101 Leucine-rich repeat 2	
4DE	g4630.t1	61753674	61774920	21246	0E+00	94.21	100	Solyc04g057960.2.1	Cell division protease ftsH homolog 1 IPR003959 ATPase, AAA-type, core	
4DE	g4631.t1	61785739	61787526	1787	0E+00	95.37	93	Solyc04g057970.2.1	Unknown Protein	
4DE	g4632.t1	61791801	61792940	1139	4E-158	98.1	100	Solyc04g057980.2.1	NAD(P)H-quinone oxidoreductase subunit MH-quinone oxidoreductase subunit M	
4DE	g4633.t1	61793260	61806330	13070	0E+00	94.88	79	Solyc04g057990.2.1	mRNA 3_apos-end-processing protein YTH1 IPR000571 Zinc finger, CCCH-type	
4DE	g4634.t1	61809189	61811952	2763	4E-43	51.2	96	Solyc03g121370.2.1	30S ribosomal protein S8 IPR000630 Ribosomal protein S8	
4DE	g4635.t1	61813032	61816410	3378	1E-29	67.44	33	Solyc05g042130.1.1	Zinc knuckle containing protein	
4DE	g4636.t1	61827498	61830380	2882	6E-26	92.16	47	Solyc08g044340.1.1	Glutamate receptor 3.6 IPR015683 Glutamate receptor-related	
4DE	g4637.t1	61833339	61834545	1206	3E-48	67.86	60	Solyc02g020930.1.1	Unknown Protein	
4DE	g4638.t1	61834769	61837152	2383	7E-16	88.89	8	Solyc04g058120.1.1	Cysteine synthase	
4DE	g4639.t1	61838029	61842420	4391	0E+00	95.4	99	Solyc04g058110.2.1	Serine_threonine-protein kinase receptor IPR002290 Serine_threonine protein kinase	
4DE	g4640.t1	61856246	61857390	1144	7E-43	98.61	100	Solyc04g058100.2.1	Type 2 metallothionein IPR000347 Plant metallothionein, family 15	
4DE	g4641.t1	61864159	61869981	5822	0E+00	97.03	99	Solyc04g058090.2.1	Phosphoribosylformylglycinamide cyclo-ligase IPR004733 Phosphoribosylformylglycinamide cyclo-ligase	
4DE	g4642.t1	61872499	61873743	1244	2E-110	96.75	100	Solyc04g058080.2.1	Glucan endo-1 3-beta-glucosidase IPR012946 X8	
4DE	g4643.t1	61876720	61880840	4120	3E-123	80.79	72	Solyc04g058070.2.1	UDP-N-acetylglucosamine-pyrophosphorylase IPR002618 UTP-glucose-1-phosphate uridylyltransferase	
4DE	g4644.t1	61880991	61889760	8769	0E+00	98.02	100	Solyc04g058070.2.1	UDP-N-acetylglucosamine-pyrophosphorylase IPR002618 UTP-glucose-1-phosphate uridylyltransferase	
4DE	g4645.t1	61893253	61903900	10647	5E-175	97.49	52	Solyc04g058060.1.1	30S ribosomal protein S8P IPR004314 Protein of unknown function DUF239, plant	
4DE	g4647.i2	61912170	61915890	3720	1E-99	95.51	95	Solyc04g058070.2.1	UDP-N-acetylglucosamine-pyrophosphorylase IPR002618 UTP-glucose-1-phosphate uridylyltransferase	
4DE	g4647.t1	61912543	61915890	3347	1E-99	82.26	99	Solyc04g058070.2.1	UDP-N-acetylglucosamine-pyrophosphorylase IPR002618 UTP-glucose-1-phosphate uridylyltransferase	
4DE	g4648.t1	61919375	61926050	6675	5E-135	82.83	66	Solyc04g058060.1.1	30S ribosomal protein S8P IPR004314 Protein of unknown function DUF239, plant	
4DE	g4649.t1	61926969	61933282	6313	1E-52	81.08	62	Solyc08g063100.1.1	Ulp1 protease family C-terminal catalytic domain containing protein	
4DE	g4650.t1	61940995	61942645	1650	0E+00	90.22	99	Solyc04g058000.1.1	Laccase IPR001117 Multicopper oxidase, type 1	
4DE	g4651.t1	61944702	61949635	4933	4E-43	51.2	96	Solyc03g121370.2.1	30S ribosomal protein S8 IPR000630 Ribosomal protein S8	
4DE	g4652.t1	61970144	61972015	1871	4E-43	51.2	96	Solyc03g121370.2.1	30S ribosomal protein S8 IPR000630 Ribosomal protein S8	
4DE	g4654.t1	61991044	62001963	10919	0E+00	98.41	56	Solyc04g058110.2.1	Serine_threonine-protein kinase receptor IPR002290 Serine_threonine protein kinase	
4DE	g4655.t1	62003704	62004571	867	6E-43	100	100	Solyc04g058150.2.1	Type 2 metallothionein IPR000347 Plant metallothionein, family 15	
4DE	g4656.t1	62010514	62011775	1261	2E-107	98.73	100	Solyc04g058160.1.1	Calmodulin IPR011992 EF-Hand type	
4DE	g4657.t1	62017044	62017853	809	5E-108	99.36	100	Solyc04g058170.1.1	Calmodulin-like protein IPR011992 EF-Hand type	
4DE	g4658.t1	62018313	62023945	5632	0E+00	95.9	100	Solyc04g058180.2.1	Dehydration-responsive family protein IPR004159 Protein of unknown function DUF248, methyltransferase putative	
4DE	g4659.t1	62029994	62046208	16214	0E+00	77.63	100	Solyc04g058190.2.1	Lysine-specific demethylase 5D IPR019787 Zinc finger, PHD-finger	
4DE	g4659.i2	62029994	62046398	16404	0E+00	74.26	100	Solyc04g058190.2.1	Lysine-specific demethylase 5D IPR019787 Zinc finger, PHD-finger	
4DE	g4660.t1	62047040	62052195	5155	7E-144	98	100	Solyc04g058200.2.1	TPR repeat protein IPR011990 Tetratricopeptide-like helical	
4DE	g4661.t1	62072444	62072902	458	6E-23	90	100	Solyc04g063200.1.1	Unknown Protein	
4DE	g4662.t1	62078553	62080004	1451	0E+00	97.16	100	Solyc04g063210.2.1	Caffeoyl-CoA O-methyltransferase IPR002935 O-methyltransferase, family 3	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
7BC	g2.t1	11606	15228	3622	5E-10	95.83	13	Solyc07g005290.1.1	Unknown Protein	
7BC	g5.t1	28066	34335	6269	6E-31	62.38	21	Solyc07g005230.2.1	Unknown Protein	
7BC	g6.t1	36516	37655	1139	7E-135	99.46	100	Solyc07g0005210.2.1	Outer membrane lipoprotein blc IPR002345 Lipocalin	
7BC	g7.t1	39370	42867	3497	1E-135	97.84	91	Solyc07g0005200.2.1	Synaptobrevin homolog YKT6 IPR010908 Longin	
7BC	g8.t1	43036	56337	13301	0E+00	98.76	68	Solyc07g0005190.2.1	Lysosomal Pro-X carboxypeptidase IPR008758 Peptidase S28	
7BC	g8.t2	43036	56337	13301	0E+00	98.76	68	Solyc07g0005190.2.1	Lysosomal Pro-X carboxypeptidase IPR008758 Peptidase S28	
7BC	g9.t1	78047	92827	14780	0E+00	93.91	59	Solyc07g0005480.2.1	Fomin 2B IPR015425 Actin-binding FH2	
7BC	g10.t1	96156	101886	5730	0E+00	97.76	100	Solyc07g0005510.2.1	Omega-6 fatty acid desaturase IPR005804 Fatty acid desaturase, type 1	
7BC	g10.t2	96156	101886	5730	0E+00	99.55	100	Solyc07g0005510.2.1	Omega-6 fatty acid desaturase IPR005804 Fatty acid desaturase, type 1	
7BC	g11.t1	103744	110637	6893	0E+00	99.55	100	Solyc07g0005520.1.1	Potassium channel tetramerization domain-containing protein IPR003131 Potassium channel, voltage dependent, Kv, tetramerisation	
7BC	g12.t1	113096	121189	8093	0E+00	98.37	100	Solyc07g0005530.2.1	Ubiquitin carboxyl-terminal hydrolase IPR001394 Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	
7BC	g12.t2	113096	132959	19863	0E+00	98.23	51	Solyc07g0005530.2.1	Ubiquitin carboxyl-terminal hydrolase IPR001394 Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	
7BC	g13.t1	134997	139277	4280	0E+00	98.39	100	Solyc07g0005550.2.1	Unknown Protein	
7BC	g14.t1	141096	144984	3888	2E-116	100	100	Solyc07g0005560.2.1	Eukaryotic translation initiation factor 5A IPR019769 Translation elongation factor, IF5A, hypusine site	
7BC	g15.t1	146408	150117	3709	0E+00	98.85	100	Solyc07g0005570.2.1	AP0 protein 2, chloroplastic IPR008512 Protein of unknown function DUF794, plant	
7BC	g16.t1	151166	159055	7889	0E+00	98.08	72	Solyc07g0005580.2.1	1-acyl-sn-glycerol-3-phosphate acyltransferase IPR004552 1-acyl-sn-glycerol-3-phosphate acyltransferase	
7BC	g17.t1	191308	200019	8711	0E+00	99.86	100	Solyc07g0005590.2.1	Cyclic nucleotide gated channel IPR000595 Cyclic nucleotide-binding	
7BC	g18.t1	200514	205029	4515	0E+00	99.84	100	Solyc07g0005600.2.1	Transmembrane 9 superfamily protein member 4	
7BC	g19.t2	206545	212299	5754	6E-108	75.47	67	Solyc07g0005610.2.1	Endonuclease_exonuclease_phosphatase family	
7BC	g19.t1	206667	222719	16052	1E-107	75.47	76	Solyc07g0005610.2.1	Endonuclease_exonuclease_phosphatase family	
7BC	g20.t1	218428	231505	13077	1E-127	86.4	94	Solyc07g0005640.2.1	26S proteasome non-ATPase regulatory subunit 9 IPR001478 PDZ_DHR_GLGF	
7BC	g21.t1	231721	238059	6338	0E+00	91.62	100	Solyc07g0005650.2.1	WRKY transcription factor IPR003657 DNA-binding WRKY	
7BC	g22.t1	250428	251805	1377	0E+00	86.8	100	Solyc07g0005660.2.1	Purine permease family protein IPR004853 Protein of unknown function DUF250	
7BC	g23.t1	267892	270639	2747	5E-170	88.76	100	Solyc07g0005670.1.1	Transport protein YIF1 IPR005578 Hrf1	
7BC	g24.t1	277428	286871	9443	2E-129	98.9	63	Solyc07g0005680.2.1	Serine carboxypeptidase K10B2.2 IPR001563 Peptidase S10, serine carboxypeptidase	
7BC	g25.t1	292168	295335	3167	0E+00	97.99	99	Solyc07g0005690.2.1	Unknown Protein	
7BC	g26.t1	295734	302859	7125	0E+00	97.25	100	Solyc07g0005700.2.1	Unknown Protein IPR003604 Zinc finger, U1-type	
7BC	g27.t1	305040	311199	6159	8E-56	95.1	80	Solyc07g0005710.2.1	Unknown Protein	
7BC	g28.t1	311348	316407	5059	9E-43	98.59	68	Solyc07g0005730.2.1	Plasma membrane protein 3 IPR000612 Uncharacterised protein family UPF0057	
7BC	g29.t1	318488	320155	1667	0E+00	97.27	100	Solyc07g0005740.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
7BC	g30.t1	320618	324550	3932	0E+00	95.19	100	Solyc07g0005750.2.1	F-box_LRR-repeat protein 17 IPR001810 Cyclin-like F-box	
7BC	g31.t1	327394	331049	3655	0E+00	96.67	100	Solyc07g0005760.2.1	Hydroxycinnamoyl CoA shikimate_quinate hydroxycinnamoyltransferase IPR003480 Transferase	
7BC	g32.t1	343673	353340	9667	0E+00	77.38	34	Solyc07g0005770.2.1	Cc-nbs-lrr, resistance protein	
7BC	g33.t1	355873	364730	8857	0E+00	70.77	75	Solyc07g0005780.1.1	Eukaryotic translation initiation factor 4 gamma 3 IPR016021 MIF4-like, type 1_2_3	
7BC	g33.t2	355873	364730	8857	0E+00	73.07	75	Solyc07g0005780.1.1	Eukaryotic translation initiation factor 4 gamma 3 IPR016021 MIF4-like, type 1_2_3	
7BC	g34.t1	367730	370360	2630	3E-12	53.97	8	Solyc05g021410.1.1	Unknown Protein	
7BC	g35.t1	402707	409930	7223	9E-70	66.13	43	Solyc07g0005800.2.1	Genomic DNA chromosome 5 P1 clone MTI20	
7BC	g35.t2	402707	409930	7223	2E-69	66.13	39	Solyc07g0005800.2.1	Genomic DNA chromosome 5 P1 clone MTI20	
7BC	g36.t1	410295	415680	5385	0E+00	99.1	100	Solyc07g0005810.2.1	Eukaryotic translation initiation factor 4 IPR016021 MIF4-like, type 1_2_3	
7BC	g37.t1	418167	421590	3423	0E+00	97.88	100	Solyc07g0005820.2.1	heat shock protein IPR013126 Heat shock protein 70	
7BC	g38.t1	424049	428919	4870	0E+00	91.41	100	Solyc07g0005830.2.1	Translation initiation factor IF-3 IPR001288 Translation initiation factor 3	
7BC	g39.t1	430179	436145	5966	0E+00	99.81	100	Solyc07g0005840.2.1	Cellulose synthase 3 IPR005150 Cellulose synthase	
7BC	g40.t1	436876	439520	2644	0E+00	98.74	100	Solyc07g0005850.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
7BC	g41.t1	440436	448270	7834	0E+00	96.57	100	Solyc07g0005860.2.1	Os02g0794300 protein (Fragment) IPR007573 Protein of unknown function DUF566	
7BC	g41.t2	440436	448270	7834	0E+00	99.33	100	Solyc07g0005860.2.1	Os02g0794300 protein (Fragment) IPR007573 Protein of unknown function DUF566	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
7BC	g42.t1	460856	469550	8694	0E+00	84.89	100	Solyc07g005870.2.1	FAD dependent oxidoreductase IPR002938 Monooxygenase, FAD-binding	
7BC	g43.t1	470000	483220	13220	0E+00	99.21	100	Solyc07g005880.2.1	DNA REPLICATION FACTOR C SUBUNIT IPR012178 DNA replication factor C, large subunit	
7BC	g43.t3	470000	499340	29340	0E+00	99.21	63	Solyc07g005880.2.1	DNA REPLICATION FACTOR C SUBUNIT IPR012178 DNA replication factor C, large subunit	
7BC	g43.t2	490289	499340	9051	0E+00	98.43	88	Solyc07g005890.2.1	ATP-dependent RNA helicase IPR011545 DNA_RNA helicase, DEAD_DEAH box type, N-terminal	
7BC	g44.t1	500559	506238	5679	6E-126	100	100	Solyc07g005900.2.1	Calcineurin subunit B IPR011992 EF-Hand type	
7BC	g45.t1	509849	512360	2511	0E+00	98.66	92	Solyc07g005910.2.1	IFA-binding protein IPR007656 Protein of unknown function DUF593	
7BC	g46.t1	513664	517030	3366	0E+00	85.34	67	Solyc07g005920.1.1	Receptor like kinase, RLK	
7BC	g47.t1	525694	536672	10978	0E+00	97.39	95	Solyc07g005930.2.1	DNA-directed RNA polymerase IPR002092 DNA-directed RNA polymerase, bacteriophage type	
7BC	g48.t1	537752	545815	8063	0E+00	93.17	100	Solyc07g005940.2.1	Vacuolar ATPase subunit H protein IPR004908 ATPase, V1 complex, subunit H	
7BC	g48.t2	537752	540895	3143	0E+00	99.69	97	Solyc07g005940.2.1	Vacuolar ATPase subunit H protein IPR004908 ATPase, V1 complex, subunit H	
7BC	g49.t1	546379	551295	4916	0E+00	97.96	99	Solyc07g005950.2.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
7BC	g50.t1	556239	563845	7606	0E+00	98.92	100	Solyc07g005960.2.1	Serine carboxypeptidase K10B2.2 IPR001563 Peptidase S10, serine carboxypeptidase	
7BC	g51.t1	571364	581825	10461	0E+00	98.61	100	Solyc07g005970.2.1	Unknown Protein IPR019460 Autophagy-related protein 11	
7BC	g52.t1	583174	586273	3099	4E-162	95.45	100	Solyc07g005980.1.1	Unknown Protein IPR001841 Zinc finger, RING-type	
7BC	g53.t1	611887	618365	6478	0E+00	96.36	100	Solyc07g005990.2.1	Transcription regulatory protein SNF5	
7BC	g54.t1	620301	624265	3964	1E-70	89.4	67	Solyc07g006000.2.1	50S ribosomal protein L35 IPR001706 Ribosomal protein L35	
7BC	g55.t1	625472	629065	3593	0E+00	98.83	94	Solyc07g006010.2.1	Nucleoporin Nup43 IPR011046 WD40 repeat-like	
7BC	g56.t1	635264	638488	3224	0E+00	98.06	99	Solyc07g006020.2.1	Adiponectin receptor IPR004254 Hly-III related	
7BC	g56.t2	635264	638488	3224	0E+00	99.44	99	Solyc07g006020.2.1	Adiponectin receptor IPR004254 Hly-III related	
7BC	g57.t1	638908	653725	14817	0E+00	97.09	96	Solyc07g006030.2.1	Protein TIF31 homolog IPR011990 Tetratricopeptide-like helical	
7BC	g58.t1	665454	680765	15311	0E+00	86.02	49	Solyc07g006050.1.1	Histone-lysine N-methyltransferase ASHR3 IPR014857 Zinc finger, RING-like	
7BC	g58.t2	665454	683887	18433	0E+00	86.02	36	Solyc07g006050.1.1	Histone-lysine N-methyltransferase ASHR3 IPR014857 Zinc finger, RING-like	
7BC	g59.t1	708578	712009	3431	1E-126	73.56	100	Solyc07g006090.1.1	GMP synthase IPR000991 Glutamine amidotransferase class-I, C-terminal	
7BC	g60.t1	713003	722679	9676	0E+00	99.35	100	Solyc07g006100.2.1	Oxysterol-binding protein IPR000648 Oxysterol-binding protein	
7BC	g60.t2	713003	722679	9676	0E+00	96.85	100	Solyc07g006100.2.1	Oxysterol-binding protein IPR000648 Oxysterol-binding protein	
7BC	g61.t1	744178	749066	4888	0E+00	99.37	100	Solyc07g006110.2.1	Receptor like kinase, RLK	
7BC	g62.t1	753368	759816	6448	0E+00	97.56	100	Solyc07g006120.2.1	WD repeat domain phosphoinositide-interacting protein IPR011046 WD40 repeat-like	
7BC	g62.t2	753368	759816	6448	0E+00	96.71	100	Solyc07g006120.2.1	WD repeat domain phosphoinositide-interacting protein IPR011046 WD40 repeat-like	
7BC	g63.t1	760558	764567	4009	0E+00	100	72	Solyc07g006130.1.1	Eukaryotic peptide chain release factor subunit 1-1 IPR004403 Peptide chain release factor eRF_aRF subunit 1	
7BC	g64.t1	764608	767629	3021	7E-97	99.28	100	Solyc07g006140.2.1	Cytochrome P450	
7BC	g65.t2	771247	775819	4572	2E-127	100	100	Solyc07g006150.2.1	Transmembrane protein 208 IPR008506 Protein of unknown function DUF788	
7BC	g65.t1	771247	775869	4622	2E-74	100	100	Solyc07g006150.2.1	Transmembrane protein 208 IPR008506 Protein of unknown function DUF788	
7BC	g66.t1	778208	784079	5871	0E+00	99.2	100	Solyc07g006160.2.1	AFG1-family ATPase IPR005654 ATPase, AFG1-like	
7BC	g67.t1	785428	788275	2847	0E+00	97.79	100	Solyc07g006170.2.1	Exostosin-like IPR004263 Exostosin-like	
7BC	g68.t1	789118	794329	5211	0E+00	91.4	100	Solyc07g006180.2.1	Tetratricopeptide repeat protein 4 homolog IPR011990 Tetratricopeptide-like helical	
7BC	g68.t2	789118	794329	5211	0E+00	97.7	100	Solyc07g006180.2.1	Tetratricopeptide repeat protein 4 homolog IPR011990 Tetratricopeptide-like helical	
7BC	g69.t1	797032	814209	17177	0E+00	99.23	70	Solyc07g006190.2.1	5_apos-nucleotidase IPR016695 Purine 5-nucleotidase	
7BC	g70.t1	814715	815419	704	1E-111	98.15	100	Solyc07g006210.1.1	Unknown Protein	
7BC	g71.t1	822590	824089	1499	0E+00	99.76	100	Solyc07g006220.1.1	UDP-D-glucuronate 4-epimerase 1-binding domain	
7BC	g72.t1	829824	830389	565	6E-67	97.74	100	Solyc07g006230.1.1	Unknown Protein	
7BC	g73.t1	834648	838445	3797	6E-64	98.95	49	Solyc07g006250.2.1	DNA-directed RNA polymerase III subunit RPC8 IPR013238 RNA polymerase III, subunit Rpc25	
7BC	g73.t2	834648	851070	16422	0E+00	97.43	47	Solyc07g006260.2.1	Myosin-like protein	
7BC	g74.t1	853978	856980	3002	0E+00	99.62	100	Solyc07g006280.2.1	Senescence-associated protein IPR000301 Tetraspanin, subgroup	
7BC	g75.t1	862923	864279	1356	2E-48	79.51	100	Solyc07g006290.1.1	Nodulin-like protein IPR000620 Protein of unknown function DUF6, transmembrane	
7BC	g76.t1	868348	869882	1534	1E-111	50.64	99	Solyc08g082510.1.1	F-box family protein IPR005174 Protein of unknown function DUF295	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
7BC	g77.t1	876403	890023	13620	1E-151	85	94	Solyc07g006300.2.1	CER1 protein (Fragment) IPR006694 Fatty acid hydroxylase	
7BC	g78.t1	922273	925887	3614	0E+00	93.44	97	Solyc07g006320.2.1	Genomic DNA chromosome 5 P1 clone MR1I IPR008546 Protein of unknown function DUF828, plant	
7BC	g79.t1	927385	934264	6879	0E+00	86.68	76	Solyc07g006330.1.1	Dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase-like IPR005599 Alg9-like mannosyltransferase	
7BC	g79.t2	927385	934264	6879	0E+00	90.06	77	Solyc07g006330.1.1	Dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase-like IPR005599 Alg9-like mannosyltransferase	
7BC	g80.t2	944325	955624	11299	0E+00	98.81	100	Solyc07g006350.2.1	Ankyrin repeat-rich protein IPR002110 Ankyrin	
7BC	g80.t1	945613	955624	10011	0E+00	99.4	99	Solyc07g006350.2.1	Ankyrin repeat-rich protein IPR002110 Ankyrin	
7BC	g82.t1	972563	974214	1651	0E+00	97.91	100	Solyc07g006360.1.1	RING finger protein IPR018957 Zinc finger, C3HC4 RING-type	
7BC	g83.t1	978778	980584	1806	0E+00	97.74	100	Solyc07g006370.1.1	Sodium_calcium exchanger protein IPR004837 Sodium_calcium exchanger membrane region	
7BC	g84.t1	990643	991605	962	7E-69	95.24	100	Solyc07g006380.2.1	Defensin-like protein IPR008177 Gamma Purothionin	
7BC	g85.t1	1002503	1003189	686	1E-96	97.14	100	Solyc07g006400.1.1	Ring H2 finger protein IPR018957 Zinc finger, C3HC4 RING-type	
7BC	g87.t1	1022893	1027441	4548	0E+00	92.05	63	Solyc07g006430.1.1	Aspartic proteinase nepenthesin I IPR001461 Peptidase A1	
7BC	g88.t1	1027993	1029589	1596	0E+00	96.32	100	Solyc07g006440.1.1	Aspartic proteinase nepenthesin I IPR001461 Peptidase A1	
7BC	g89.t1	1032123	1033708	1585	0E+00	98.16	100	Solyc07g006450.1.1	Aspartic proteinase nepenthesin I IPR001461 Peptidase A1	
7BC	g91.t1	1042163	1044154	1991	0E+00	95.06	100	Solyc07g006460.1.1	Aspartic proteinase nepenthesin I IPR001461 Peptidase A1	
7BC	g92.t1	1045733	1047250	1517	0E+00	97.14	100	Solyc07g006470.1.1	Aspartic proteinase nepenthesin I IPR001461 Peptidase A1	
7BC	g93.t1	1047290	1049534	2244	0E+00	94.01	98	Solyc07g006480.2.1	LRR receptor-like serine_threonine-protein kinase FEI1 IPR002290 Serine_threonine protein kinase	
7BC	g94.t1	1054253	1058759	4506	1E-89	97.67	87	Solyc07g006490.2.1	Unknown Protein	
7BC	g95.t1	1091843	1095049	3206	0E+00	99.2	100	Solyc07g006500.2.1	Alpha alpha-trehalose-phosphate synthase (UDP-forming) IPR001830 Glycosyl transferase, family 20	
7BC	g96.t1	1101173	1110235	9062	0E+00	99.72	100	Solyc07g006510.2.1	Cyclic nucleotide-gated ion channel 18 IPR000595 Cyclic nucleotide-binding	
7BC	g97.t1	1110704	1118344	7640	0E+00	99.81	100	Solyc07g006520.2.1	Preprotein translocase secY subunit IPR002208 SecY protein	
7BC	g98.t1	1118863	1124992	6129	0E+00	86.87	100	Solyc07g006530.2.1	Adenylosuccinate lyase IPR004769 Adenylosuccinate lyase	
7BC	g99.t1	1138509	1142854	4345	0E+00	98.38	100	Solyc07g006540.2.1	Chaperone protein ClpB	
7BC	g100.t1	1174083	1175314	1231	9E-98	93.79	100	Solyc07g006570.2.1	S8-RNase (Fragment) IPR001568 Ribonuclease T2	
7BC	g101.t1	1182293	1201663	19370	0E+00	98.62	91	Solyc07g006580.2.1	Diacylglycerol kinase 7 IPR016961 Diacylglycerol kinase, plant	
7BC	g101.t2	1182293	1201663	19370	0E+00	92.63	90	Solyc07g006580.2.1	Diacylglycerol kinase 7 IPR016961 Diacylglycerol kinase, plant	
7BC	g102.t1	1243986	1247661	3675	1E-125	96.79	100	Solyc07g006600.1.1	GDU1	
7BC	g106.t1	1272926	1277543	4617	0E+00	95.34	100	Solyc07g006610.2.1	Serine_threonine protein kinase IPR002290 Serine_threonine protein kinase	
7BC	g107.t1	1293066	1300514	7448	0E+00	98.5	76	Solyc07g006620.2.1	Receptor-like kinase IPR002290 Serine_threonine protein kinase	
7BC	g108.t1	1305260	1307717	2457	0E+00	97.15	100	Solyc07g006630.2.1	CONSTANS-like protein IPR010402 CCT domain	
7BC	g109.t1	1314806	1326091	11285	5E-119	75.97	100	Solyc07g006640.2.1	ADP-ribosylation factor 3 IPR006688 ADP-ribosylation factor	
7BC	g110.t1	1326563	1331757	5194	0E+00	99.5	83	Solyc07g006650.2.1	Xylose isomerase IPR013452 Xylose isomerase, bacterial type	
7BC	g111.t1	1333607	1336247	2640	0E+00	99.24	100	Solyc07g006660.1.1	Glyoxal oxidase IPR009880 Glyoxal oxidase, N-terminal	
7BC	g112.t1	1350116	1351708	1592	0E+00	94.24	100	Solyc07g006680.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase	
7BC	g113.t2	1369907	1373047	3140	8E-62	91.67	40	Solyc07g006690.2.1	Potential lipid particle serine esterase IPR007751 Protein of unknown function DUF676, hydrolase-like	
7BC	g113.t1	1369907	1373177	3270	1E-61	91.67	40	Solyc07g006690.2.1	Potential lipid particle serine esterase IPR007751 Protein of unknown function DUF676, hydrolase-like	
7BC	g114.t1	1373641	1380097	6456	0E+00	98.18	100	Solyc07g006690.2.1	Potential lipid particle serine esterase IPR007751 Protein of unknown function DUF676, hydrolase-like	
7BC	g115.t1	1386447	1387307	860	2E-90	100	100	Solyc07g006710.1.1	Pathogenesis-related protein PR-1 IPR002413 Ves allergen	
7BC	g116.t1	1400656	1408534	7878	0E+00	98.44	51	Solyc07g006720.2.1	UDP flavonoid 3-O-glucosyltransferase (Fragment) IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
7BC	g117.t1	1408648	1413067	4419	0E+00	99.13	94	Solyc07g006740.2.1	Multidrug resistance protein mdrK IPR015521 MATE family transporter related protein	
7BC	g118.t1	1419561	1421957	2396	0E+00	98.91	100	Solyc07g006750.2.1	MYB transcription factor IPR015495 Myb transcription factor	
7BC	g119.t1	1430473	1437027	6554	0E+00	96.83	100	Solyc07g006760.2.1	Serine_threonine protein kinase IPR001245 Tyrosine protein kinase	
7BC	g120.t1	1447383	1450697	3314	0E+00	98.2	99	Solyc07g006770.2.1	Receptor like kinase, RLK	
7BC	g121.t2	1451697	1462617	10920	0E+00	80.09	100	Solyc07g006780.2.1	Glycerol kinase IPR006003 Carbohydrate kinase, FGGY-related	
7BC	g121.t1	1456966	1462617	5651	0E+00	85.66	97	Solyc07g006780.2.1	Glycerol kinase IPR006003 Carbohydrate kinase, FGGY-related	
7BC	g122.t1	1463576	1471351	7775	0E+00	99.64	100	Solyc07g006790.2.1	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex IPR006257 Dihydrolipoamide acetyltransferase, long form	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
7BC	g123.t1	1472090	1473597	1507	0E+00	97.57	100	Solyc07g006800.1.1	UDP-glucosyltransferase HvUGT5876 IPR002213	UDP-glucuronosyl-UDP-glucosyltransferase
7BC	g124.t1	1474256	1519854	45598	0E+00	92.23	59	Solyc07g006820.2.1	Transcription initiation factor TFIIID subunit 1 IPR001487	Bromodomain
7BC	g124.t2	1474556	1519854	45298	0E+00	91.98	59	Solyc07g006820.2.1	Transcription initiation factor TFIIID subunit 1 IPR001487	Bromodomain
7BC	g125.t1	1521066	1529306	8240	0E+00	97.54	100	Solyc07g006830.2.1	Calmodulin-binding protein (Fragment) IPR012416	Calmodulin binding protein-like
7BC	g126.t2	1535056	1544775	9719	0E+00	96.18	60	Solyc07g006840.1.1	NAC domain protein IPR003441	protein
7BC	g126.t1	1535366	1538719	3353	0E+00	93.79	100	Solyc07g006840.1.1	NAC domain protein IPR003441	protein
7BC	g127.t1	1546866	1548681	1815	0E+00	98.94	99	Solyc07g006860.2.1	Xyloglucan endotransglucosylase_hydrolase 3 IPR016455	Xyloglucan endotransglucosylase_hydrolase
7BC	g128.t1	1571846	1578584	6738	0E+00	98.62	78	Solyc07g006890.1.1	Cytochrome P450	
7BC	g129.t1	1584196	1588316	4120	0E+00	99.84	100	Solyc07g006900.1.1	Auxin efflux carrier protein IPR014024	Auxin efflux carrier, subgroup
7BC	g130.t1	1591791	1594937	3146	0E+00	99.7	90	Solyc07g006910.2.1	Solute carrier family 35 member E3 IPR004853	Protein of unknown function DUF250
7BC	g131.t1	1596040	1600127	4087	0E+00	91.17	99	Solyc07g006920.2.1	Os06g0207500 protein (Fragment) IPR004253	Protein of unknown function DUF231, plant
7BC	g131.t2	1596040	1600127	4087	0E+00	91.39	99	Solyc07g006920.2.1	Os06g0207500 protein (Fragment) IPR004253	Protein of unknown function DUF231, plant
7BC	g132.t1	1601016	1605626	4610	0E+00	97.45	60	Solyc07g006930.1.1	Pentatricopeptide (PPR) repeat-containing protein-like IPR004158	Protein of unknown function DUF247, plant
7BC	g133.t1	1606306	1608455	2149	1E-62	96	70	Solyc07g006950.2.1	UPF0414 transmembrane protein C20orf30 homolog IPR008590	Uncharacterised protein family UPF0414
7BC	g134.t1	1608874	1613117	4243	1E-91	97.06	76	Solyc07g006960.2.1	Actin associated protein	
7BC	g135.t1	1614022	1619167	5145	0E+00	98.83	100	Solyc07g006970.2.1	Solute carrier family 2, facilitated glucose transporter member 5 IPR003663	Sugar_inositol transporter
7BC	g136.t1	1624216	1626754	2538	0E+00	99.27	99	Solyc07g006990.1.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
7BC	g137.t1	1629886	1630361	475	1E-68	76.8	100	Solyc10g051210.1.1	Unknown Protein	
7BC	g138.t1	1639986	1640603	617	3E-68	78.69	98	Solyc10g051210.1.1	Unknown Protein	
7BC	g139.t1	1641863	1643737	1874	0E+00	98.66	100	Solyc07g007010.1.1	Pentatricopeptide (PPR) repeat-containing protein-like IPR004158	Protein of unknown function DUF247, plant
7BC	g140.t1	1648379	1655597	7218	0E+00	91.88	99	Solyc07g007020.2.1	Receptor-like protein kinase At3g21340 IPR002290	Serine_threonine protein kinase
7BC	g141.t2	1655839	1658187	2348	0E+00	99.7	100	Solyc07g007030.1.1	Transmembrane 9 superfamily protein member 2	
7BC	g141.t3	1655839	1668427	12588	0E+00	99.7	45	Solyc07g007030.1.1	Transmembrane 9 superfamily protein member 2	
7BC	g141.t1	1659726	1668427	8701	0E+00	93.4	99	Solyc07g007040.2.1	Zinc finger CCCH-type with G patch domain-containing protein IPR000467	D111_G-patch
7BC	g142.t1	1674506	1675398	892	6E-82	98.32	100	Solyc07g007050.1.1	Unknown Protein	
7BC	g143.t1	1679353	1683457	4104	0E+00	98.67	90	Solyc07g007060.1.1	Zinc transporter IPR002524	Cation efflux protein
7BC	g144.t1	1693507	1694967	1460	2E-11	48.15	58	Solyc01g008800.1.1	Tir-nbs-lrr, resistance protein	
7BC	g145.t1	1697976	1707364	9388	0E+00	97.64	64	Solyc07g007110.2.1	Peptidyl-prolyl cis-trans isomerase IPR002130	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type
7BC	g146.t1	1721296	1726820	5524	0E+00	81.7	99	Solyc07g007120.2.1	Homeobox protein knotted-1-like 3 IPR005541	KNOX2
7BC	g146.t2	1721296	1726820	5524	0E+00	84.42	99	Solyc07g007120.2.1	Homeobox protein knotted-1-like 3 IPR005541	KNOX2
7BC	g147.t1	1732011	1733127	1116	5E-108	96.2	99	Solyc07g007130.1.1	NHL repeat-containing protein	
7BC	g148.t1	1735110	1745027	9917	0E+00	98.52	100	Solyc07g007140.2.1	Serine_threonine-protein kinase B-raf IPR002290	Serine_threonine protein kinase
7BC	g148.t2	1735110	1745027	9917	0E+00	96.6	100	Solyc07g007140.2.1	Serine_threonine-protein kinase B-raf IPR002290	Serine_threonine protein kinase
7BC	g149.t1	1758032	1758688	656	4E-95	97.14	100	Solyc07g007150.1.1	Unknown Protein	
7BC	g150.t1	1775517	1782405	6888	0E+00	95.45	82	Solyc07g007190.2.1	Unknown Protein	
7BC	g151.t1	1783551	1788928	5377	0E+00	89.4	100	Solyc07g007200.2.1	Ring finger protein 12 IPR018957	Zinc finger, C3HC4 RING-type
7BC	g152.t1	1791567	1799222	7655	0E+00	97.47	94	Solyc07g007210.2.1	Elongation factor like protein IPR001841	Zinc finger, RING-type
7BC	g152.t2	1791567	1799222	7655	0E+00	99.89	94	Solyc07g007210.2.1	Elongation factor like protein IPR001841	Zinc finger, RING-type
7BC	g153.t1	1799998	1804808	4810	0E+00	98.69	100	Solyc07g007220.2.1	Serine_threonine phosphatase family protein IPR015655	Protein phosphatase 2C
7BC	g155.t1	1823807	1825826	2019	0E+00	70.59	95	Solyc11g006170.1.1	DnaJ (Fragment) IPR015609	Molecular chaperone, heat shock protein, Hsp40, DnaJ
7BC	g156.t2	1839467	1840748	1281	2E-96	97.81	100	Solyc07g007270.2.1	Unknown Protein	
7BC	g156.t1	1839467	1841428	1961	2E-53	97.59	100	Solyc07g007270.2.1	Unknown Protein	
7BC	g157.t1	1855524	1857228	1704	5E-125	98.85	100	Solyc07g007280.2.1	Conserved domain protein IPR014946	Protein of unknown function DUF1817
7BC	g158.t1	1864857	1868681	3824	0E+00	98.47	99	Solyc07g007290.1.1	Dimethylaniline monooxygenase 5 IPR012143	Dimethylaniline monooxygenase, N-oxide-forming
7BC	g159.t1	1869667	1873820	4153	0E+00	98.22	99	Solyc07g007300.2.1	Menadiquinone biosynthesis methyltransferase ubiE IPR013216	Methyltransferase type 11

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7BC	g160.t1	1875457	1890201	14744	0E+00	97.66	54	Solyc07g007310.2.1	Menaquinone biosynthesis methyltransferase ubiE	IPR013216 Methyltransferase type 11
7BC	g161.t1	1915527	1916539	1012	3E-139	97.57	100	Solyc07g007330.1.1	Serine-rich protein	
7BC	g162.t1	1954971	1959695	4724	0E+00	99.28	100	Solyc07g007340.2.1	Nodulin-like protein	IPR010658 Nodulin-like
7BC	g163.t1	1960816	1962902	2086	0E+00	98.41	100	Solyc07g007350.1.1	Jp18	IPR010993 Sterile alpha motif homology
7BC	g164.t1	1973186	1975712	2526	0E+00	98.87	82	Solyc07g007360.1.1	Os07g0175100 protein (Fragment)	
7BC	g165.t1	1977139	1977852	713	1E-79	96.55	100	Solyc07g009300.1.1	Unknown Protein	
7BC	g166.t1	1980431	1987098	6667	0E+00	92.46	100	Solyc07g007370.2.1	NEDD8 ultimate buster 1	IPR009060 UBA-like
7BC	g167.t1	1987353	1993472	6119	0E+00	90.41	100	Solyc07g007380.2.1	Endoplasmic reticulum lectin 1	IPR012913 Glucosidase II beta subunit-like
7BC	g168.t1	1995261	2001170	5909	0E+00	99.1	100	Solyc07g007390.2.1	At1g62390-like protein (Fragment)	IPR011990 Tetratricopeptide-like helical
7BC	g169.t1	2001805	2013012	11207	0E+00	65.38	99	Solyc12g009870.1.1	Leucine-rich repeat-like protein	IPR006553 Leucine-rich repeat, cysteine-containing subtype
7BC	g170.t1	2016895	2025242	8347	0E+00	95.02	100	Solyc07g007430.2.1	Palmitoyltransferase akr1 (EC 2.3.1.-)(Ankyrin repeat-containing protein akr1)	IPR002110 Ankyrin
7BC	g171.t1	2029561	2031145	1584	0E+00	94.8	100	Solyc07g007440.1.1	Ring H2 finger protein	IPR018957 Zinc finger, C3HC4 RING-type
7BC	g172.t1	2032921	2036410	3489	2E-118	96.95	100	Solyc07g007450.2.1	Iron-sulfur cluster assembly scaffold protein lscU	IPR002871 NIF system FeS cluster assembly, NifU, N-terminal
7BC	g172.t2	2032921	2036410	3489	5E-110	77.56	100	Solyc07g007450.2.1	Iron-sulfur cluster assembly scaffold protein lscU	IPR002871 NIF system FeS cluster assembly, NifU, N-terminal
7BC	g174.t1	2060300	2062522	2222	1E-88	82.93	100	Solyc07g006730.2.1	Multidrug resistance protein mdtK	IPR015521 MATE family transporter related protein
7BC	g174.t2	2060300	2062522	2222	4E-73	71.71	100	Solyc07g006730.2.1	Multidrug resistance protein mdtK	IPR015521 MATE family transporter related protein
7BC	g175.t1	2065541	2070858	5317	4E-95	97.47	53	Solyc07g007500.2.1	Unknown Protein	
7BC	g175.t2	2065541	2070858	5317	1E-94	93.45	60	Solyc07g007500.2.1	Unknown Protein	
7BC	g176.t1	2072451	2073428	977	7E-35	49.63	63	Solyc04g0071270.1.1	F-box family protein	IPR001810 Cyclin-like F-box
7BC	g177.t1	2074782	2075802	1020	1E-144	99	99	Solyc07g007510.2.1	Adenylate cyclase	IPR008172 Adenylate cyclase
7BC	g178.t1	2077961	2084198	6237	6E-140	92.92	48	Solyc07g007520.1.1	Unknown Protein	
7BC	g179.t2	2091891	2097046	5155	0E+00	98.43	99	Solyc07g007550.2.1	Heparanase	IPR005199 Glycoside hydrolase family 79, N-terminal
7BC	g179.t1	2092191	2097046	4855	0E+00	98.32	100	Solyc07g007550.2.1	Heparanase	IPR005199 Glycoside hydrolase family 79, N-terminal
7BC	g180.t1	2097130	2108522	11392	0E+00	98.88	71	Solyc07g007560.2.1	Vesicular glutamate transporter 3	IPR016196 Major facilitator superfamily, general substrate transporter
7BC	g181.t1	2110072	2111502	1430	0E+00	99.47	100	Solyc07g007590.1.1	Prephenate dehydrogenase family protein	IPR012070 Arogenate_prephenate dehydrogenase, plant
7BC	g182.t1	2118229	2122834	4605	0E+00	99.87	100	Solyc07g007600.2.1	Pyrophosphate-energized proton pump	IPR004131 Inorganic H+ pyrophosphatase
7BC	g183.t1	2140913	2145782	4869	2E-176	99.58	100	Solyc07g007610.2.1	AT2G21500 protein (Fragment)	IPR001841 Zinc finger, RING-type
7BC	g184.t3	2150973	2162941	11968	0E+00	92.55	68	Solyc07g007620.2.1	Processive diacylglycerol glucosyltransferase	IPR009695 Monogalactosyldiacylglycerol synthase
7BC	g184.t1	2150973	2179407	28434	0E+00	98.9	25	Solyc07g007650.1.1	Translocase of chloroplast 90, chloroplastic	
7BC	g184.t2	2166413	2179180	12767	0E+00	98.9	37	Solyc07g007650.1.1	Translocase of chloroplast 90, chloroplastic	
7BC	g185.t1	2182116	2183714	1598	0E+00	98.28	100	Solyc07g007660.1.1	Unknown Protein	
7BC	g186.t1	2190013	2197484	7471	0E+00	98.32	100	Solyc07g007670.2.1	Purple acid phosphatase 3	IPR015914 Purple acid phosphatase, N-terminal
7BC	g187.t1	2197794	2209304	11510	0E+00	98.58	100	Solyc07g007680.2.1	Plant synaptotagmin	IPR018029 C2 membrane targeting protein
7BC	g188.t1	2220943	2229822	8879	0E+00	98.98	100	Solyc07g007690.2.1	Voltage-gated chloride channel	IPR002251 Chloride channel plant CLC
7BC	g189.t1	2232533	2234149	1616	0E+00	98.75	100	Solyc07g007700.1.1	Isoprenylcysteine carboxyl methyltransferase	
7BC	g191.t1	2259003	2270070	11067	0E+00	98.74	100	Solyc07g007820.2.1	Phosphatidylinositol binding clathrin assembly protein like	IPR011417 ANTH
7BC	g192.t1	2273383	2278591	5208	0E+00	88.89	100	Solyc07g007830.2.1	BSD domain containing protein	IPR005607 BSD
7BC	g193.t1	2283227	2285624	2397	0E+00	97.72	93	Solyc07g007840.1.1	Unknown Protein	
7BC	g195.t1	2302697	2306762	4065	0E+00	95.08	98	Solyc07g007850.2.1	Os02g0208600 protein (Fragment)	
7BC	g196.t1	2321061	2321665	604	6E-80	99.19	100	Solyc07g007860.1.1	Proline rich protein (Fragment)	IPR013770 Plant lipid transfer protein and hydrophobic protein, helical
7BC	g197.t1	2327421	2331665	4244	0E+00	99.24	100	Solyc07g007870.2.1	NADH flavin oxidoreductase_12-oxophytodienoate reductase	IPR001155 NADH:flavin oxidoreductase_NADH oxidase, N-terminal
7BC	g198.t1	2332253	2332772	519	2E-47	92.98	100	Solyc07g007880.1.1	60s acidic ribosomal protein-like protein	IPR001813 Ribosomal protein 60S
7BC	g199.t1	2334208	2350282	16074	0E+00	99.3	100	Solyc07g007890.2.1	CCR4-NOT transcription complex subunit 10	IPR011990 Tetratricopeptide-like helical
7BC	g200.t1	2350955	2359752	8797	0E+00	97.72	100	Solyc07g007920.1.1	Telomere-associated protein RIF1	IPR016024 Armadillo-type fold
7BC	g200.t2	2350955	2359752	8797	0E+00	96.23	100	Solyc07g007920.1.1	Telomere-associated protein RIF1	IPR016024 Armadillo-type fold

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7BC	g201.t1	2362701	2370387	7686	0E+00	98.51	100	Solyc07g007930.2.1	Alkaline alpha galactosidase 2	IPR008811 Raffinose synthase
7BC	g201.t2	2365891	2370387	4496	0E+00	98.87	98	Solyc07g007930.2.1	Alkaline alpha galactosidase 2	IPR008811 Raffinose synthase
7BC	g202.t1	2370778	2379672	8894	0E+00	87.73	100	Solyc07g007940.2.1	Unknown Protein, subunit SNAP43	
7BC	g202.t2	2370778	2379672	8894	0E+00	81.95	100	Solyc07g007940.2.1	Unknown Protein, subunit SNAP43	
7BC	g204.t1	2433331	2434577	1246	9E-152	97.3	100	Solyc07g007950.1.1	Calmodulin-like protein	IPR011992 EF-Hand type
7BC	g205.t1	2437409	2444782	7373	0E+00	98.87	100	Solyc07g007960.2.1	CUE domain containing protein	IPR003892 Ubiquitin system component Cue
7BC	g206.t2	2446091	2463869	17778	0E+00	99.55	50	Solyc07g007980.2.1	ATP binding _serine-threonine kinase	IPR002290 Serine_threonine protein kinase
7BC	g206.t1	2446091	2456254	10163	0E+00	98.89	99	Solyc07g007970.2.1	Conserved membrane protein Yjcl	IPR008537 Protein of unknown function DUF819
7BC	g206.t3	2460391	2463818	3427	0E+00	99.55	100	Solyc07g007980.2.1	ATP binding _serine-threonine kinase	IPR002290 Serine_threonine protein kinase
7BC	g207.t1	2474055	2478541	4486	0E+00	97.93	100	Solyc01g009830.2.1	UDP-glucuronic acid_UDP-N-acetylglactosamine transporter	IPR004853 Protein of unknown function DUF250
7BC	g208.t1	2481960	2497887	15927	0E+00	88.54	74	Solyc07g008000.2.1	TBC1 domain family member 15	IPR000195 RabGAP_TBC
7BC	g208.t2	2485470	2498087	12617	0E+00	88.54	72	Solyc07g008000.2.1	TBC1 domain family member 15	IPR000195 RabGAP_TBC
7BC	g209.t1	2498183	2499251	1068	8E-150	99.5	100	Solyc07g008010.2.1	Myb transcription factor	IPR015495 Myb transcription factor
7BC	g210.t1	2519880	2523354	3474	1E-121	93	100	Solyc07g008020.2.1	Auxin response factor 16	IPR003311 AUX_IAA protein
7BC	g211.t1	2528970	2532816	3846	0E+00	98.07	100	Solyc07g008030.1.1	Glycosyl transferase family 17 protein	IPR006813 Glycosyl transferase, family 17
7BC	g212.t1	2545460	2553004	7544	0E+00	98.02	97	Solyc07g008040.2.1	WD-40 repeat protein-like (Fragment)	IPR017986 WD40 repeat, region
7BC	g213.t1	2554280	2559031	4751	0E+00	91.6	98	Solyc07g008050.2.1	RING finger protein	IPR001607 Zinc finger, UBP-type
7BC	g214.t1	2562250	2566026	3776	0E+00	97.88	100	Solyc07g008060.1.1	Phosphatidylinositol binding clathrin assembly protein like	IPR011417 ANTH
7BC	g215.t1	2566765	2571751	4986	0E+00	97.35	62	Solyc07g008070.1.1	C2 domain-containing protein	IPR000008 C2 calcium-dependent membrane targeting
7BC	g215.t2	2566765	2571751	4986	0E+00	97.35	63	Solyc07g008070.1.1	C2 domain-containing protein	IPR000008 C2 calcium-dependent membrane targeting
7BC	g218.t1	2589831	2590411	580	5E-14	48.65	70	Solyc05g021410.1.1	Unknown Protein	
7BC	g219.t2	2593381	2614961	21580	0E+00	97.53	76	Solyc07g008080.2.1	WD repeat-containing protein 11	IPR011046 WD40 repeat-like
7BC	g219.t1	2593453	2614961	21508	0E+00	96.95	76	Solyc07g008080.2.1	WD repeat-containing protein 11	IPR011046 WD40 repeat-like
7BC	g220.t1	2628140	2632722	4582	0E+00	98.39	97	Solyc07g008100.2.1	Genomic DNA chromosome 3 P1 clone MUJ8	
7BC	g221.t1	2642503	2644918	2415	2E-93	98.55	42	Solyc07g008110.2.1	Blue copper protein (Fragment)	IPR003245 Plastocyanin-like
7BC	g222.t1	2648257	2650269	2012	7E-91	94.2	42	Solyc07g008110.2.1	Blue copper protein (Fragment)	IPR003245 Plastocyanin-like
7BC	g223.t1	2650952	2653078	2126	8E-94	92.19	100	Solyc07g008130.2.1	Blue copper protein (Fragment)	IPR003245 Plastocyanin-like
7BC	g224.t1	2656459	2658008	1549	5E-122	93.28	100	Solyc07g008140.2.1	Blue copper protein (Fragment)	IPR003245 Plastocyanin-like
7BC	g225.t1	2662972	2666728	3756	0E+00	97.77	89	Solyc07g008150.2.1	Glucan endo-1 3-beta-glucosidase 7	IPR000490 Glycoside hydrolase, family 17
7BC	g225.t2	2662972	2666728	3756	0E+00	97.77	85	Solyc07g008150.2.1	Glucan endo-1 3-beta-glucosidase 7	IPR000490 Glycoside hydrolase, family 17
7BC	g226.t1	2673317	2689887	16570	0E+00	99.01	82	Solyc07g008160.2.1	Nuclear pore complex protein Nup155	IPR004870 Nucleoporin, non-repetitive_WGA-negative
7BC	g227.t1	2690930	2705728	14798	0E+00	75.63	100	Solyc07g008170.2.1	Methyl binding domain protein (Fragment)	IPR001739 Methyl-CpG DNA binding
7BC	g228.t1	2706667	2710282	3615	9E-69	94.39	84	Solyc03g006430.2.1	Os11g0198100 protein (Fragment)	IPR006852 Protein of unknown function DUF616
7BC	g229.t1	2746826	2750628	3802	0E+00	97.38	93	Solyc07g008190.2.1	Unknown Protein	
7BC	g230.t1	2754778	2757218	2440	1E-55	96.7	52	Solyc07g008190.2.1	Unknown Protein	
7BC	g231.t1	2762267	2765021	2754	5E-121	96.67	59	Solyc07g008200.2.1	Equilibrative nucleoside transporter	IPR002259 Delayed-early response protein_equilibrative nucleoside transporter
7BC	g232.t1	2766765	2768078	1313	3E-83	97.28	99	Solyc07g008210.2.1	TPR domain protein	IPR011990 Tetrahricopeptide-like helical
7BC	g234.t1	2783826	2785538	1712	0E+00	97.33	100	Solyc07g008230.1.1	UDP-glucosyltransferase family 1 protein	IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase
7BC	g235.t1	2788518	2790708	2190	2E-107	98.68	100	Solyc07g008240.2.1	Non-symbiotic hemoglobin protein	IPR001032 Leghaemoglobin
7BC	g236.t1	2798556	2802578	4022	0E+00	97.16	90	Solyc07g008250.2.1	SCF E3 ubiquitin ligase complex F-box protein grrA	IPR006553 Leucine-rich repeat, cysteine-containing subtype
7BC	g237.t1	2827922	2834989	7067	7E-112	99.35	72	Solyc07g008260.2.1	Genomic DNA chromosome 3 P1 clone MSJ11	
7BC	g238.t1	2853921	2856559	2638	8E-32	66.67	75	Solyc07g008270.2.1	50S ribosomal protein L36	IPR000473 Ribosomal protein L36
7BC	g239.t1	2872974	2874099	1125	1E-99	97.24	100	Solyc07g008280.2.1	Unknown Protein	
7BC	g240.t1	2879127	2885499	6372	0E+00	98.45	91	Solyc07g008290.2.1	Growth regulator like protein	IPR004348 Protein of unknown function DUF246, plant
7BC	g241.t1	2889758	2899675	9917	0E+00	98.42	46	Solyc07g008300.1.1	Rieske (2Fe-2S) domain protein	IPR001663 Aromatic-ring-hydroxylating dioxygenase, alpha subunit

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
7BC	g241.i2	2892308	2899675	7367	0E+00	98.14	49	Solyc07g008310.2.1	Rieske (2Fe-2S) domain protein IPR001663	Aromatic-ring-hydroxylating dioxygenase, alpha subunit
7BC	g242.i1	2900883	2918819	17936	0E+00	96.9	100	Solyc07g008320.2.1	Calcium-transporting ATPase 1 IPR006408	ATPase, P-type, calcium-transporting, PMCA-type
7BC	g243.i1	2936226	2941789	5563	0E+00	98.54	100	Solyc07g008330.2.1	Nucleolar and coiled-body phosphoprotein 1-like IPR007718	SRP40, C-terminal
7BC	g244.i1	2942828	2955687	12859	0E+00	99.65	56	Solyc07g008340.2.1	Zinc import ATP-binding protein ZnuC IPR013283	ABC transporter, ABCE
7BC	g246.i2	2960108	2971268	11160	0E+00	99.28	96	Solyc07g008350.2.1	Porin_voltage-dependent anion-selective channel protein IPR001925	Porin, eukaryotic type
7BC	g246.i1	2961388	2971268	9880	0E+00	99.28	100	Solyc07g008350.2.1	Porin_voltage-dependent anion-selective channel protein IPR001925	Porin, eukaryotic type
7BC	g247.i1	2976338	2986579	10241	0E+00	99.09	63	Solyc07g008360.1.1	p-coumarate CoA-ligase 2 IPR000873	AMP-dependent synthetase and ligase
7BC	g247.i2	2976338	2986585	10247	0E+00	98.31	67	Solyc07g008360.1.1	p-coumarate CoA-ligase 2 IPR000873	AMP-dependent synthetase and ligase
7BC	g248.i1	3009997	3016598	6601	0E+00	85.25	79	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480	Transferase
7BC	g249.i1	3021517	3027089	5572	0E+00	98.62	99	Solyc07g008410.2.1	Multidrug and toxin extrusion protein 1 IPR002528	Multi antimicrobial extrusion protein MatE
7BC	g250.i1	3043120	3044528	1408	0E+00	88.83	100	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480	Transferase
7BC	g251.i1	3048807	3051706	2899	0E+00	99.06	100	Solyc07g008400.1.1	Pto-like, Serine_threonine kinase protein, resistance protein	
7BC	g253.i1	3060933	3062508	1575	0E+00	91.32	100	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480	Transferase
7BC	g254.i1	3078897	3087088	8191	0E+00	92.29	100	Solyc07g008410.2.1	Multidrug and toxin extrusion protein 1 IPR002528	Multi antimicrobial extrusion protein MatE
7BC	g255.i1	3088104	3089488	1384	1E-73	98.11	100	Solyc07g008420.2.1	Blue copper-like protein IPR008972	Cupredoxin
7BC	g258.i1	3189096	3190203	1107	2E-165	92.83	97	Solyc07g008440.2.1	Purine permease family protein IPR004853	Protein of unknown function DUF250
7BC	g259.i1	3198149	3216703	18554	0E+00	85.53	60	Solyc07g008450.2.1	HEAT repeat-containing protein IPR011989	Armadillo-like helical
7BC	g259.i2	3198262	3216283	18021	0E+00	85.43	62	Solyc07g008450.2.1	HEAT repeat-containing protein IPR011989	Armadillo-like helical
7BC	g261.i1	3223463	3228663	5200	0E+00	99.47	96	Solyc07g008450.2.1	HEAT repeat-containing protein IPR011989	Armadillo-like helical
7BC	g261.i2	3223463	3228663	5200	0E+00	99.47	98	Solyc07g008450.2.1	HEAT repeat-containing protein IPR011989	Armadillo-like helical
7BC	g262.i2	3231782	3245907	14125	0E+00	89	100	Solyc07g008460.2.1	Histone-lysine N-methyltransferase IPR001214	SET
7BC	g262.i1	3237792	3245907	8115	0E+00	86.84	99	Solyc07g008460.2.1	Histone-lysine N-methyltransferase IPR001214	SET
7BC	g263.i1	3246148	3250143	3995	7E-70	98.13	81	Solyc07g008470.2.1	Macrophage migration inhibitory factor family protein IPR001398	Macrophage migration inhibitory factor
7BC	g264.i1	3258294	3260613	2319	0E+00	99.8	80	Solyc07g008480.1.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
7BC	g265.i1	3265117	3269213	4096	0E+00	97.65	93	Solyc07g008490.2.1	Nucleic acid binding protein IPR018111	K Homology, type 1, subgroup
7BC	g265.i2	3265117	3270883	5766	0E+00	98.13	99	Solyc07g008490.2.1	Nucleic acid binding protein IPR018111	K Homology, type 1, subgroup
7BC	g269.i1	3324372	3330409	6037	5E-18	65.38	8	Solyc07g008580.1.1	Histone-lysine N-methyltransferase, H3 lysine-36 specific IPR001214	SET
7BC	g270.i1	3331802	3341461	9659	2E-144	90.99	21	Solyc07g008500.1.1	Histone-lysine N-methyltransferase IPR001214	SET
7BC	g270.i2	3331802	3341461	9659	2E-144	90.99	21	Solyc07g008500.1.1	Histone-lysine N-methyltransferase IPR001214	SET
7BC	g272.i1	3366259	3373511	7252	0E+00	99.32	100	Solyc07g008520.2.1	Peptide transporter IPR000109	TGF-beta receptor, type II extracellular region
7BC	g273.i1	3376029	3381571	5542	0E+00	99.04	99	Solyc07g008530.1.1	Tyrosyl-tRNA synthetase IPR002307	Tyrosyl-tRNA synthetase, class b, bacterial_mitochondrial
7BC	g274.i1	3383780	3388090	4310	0E+00	86.57	100	Solyc07g008540.2.1	CONSTANS-like zinc finger protein IPR010402	CCT domain
7BC	g275.i2	3423159	3436251	13092	0E+00	97.97	100	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g275.i3	3423159	3439850	16691	0E+00	97.87	57	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g275.i1	3437609	3439850	2241	0E+00	99.07	100	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g276.i1	3441627	3446350	4723	0E+00	95.37	100	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g276.i2	3441627	3445970	4343	0E+00	96.77	98	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g278.i1	3462059	3469543	7484	0E+00	99.06	100	Solyc07g008560.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g279.i1	3483079	3490750	7671	0E+00	97.48	100	Solyc07g008570.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g280.i1	3494243	3496380	2137	3E-131	94.85	33	Solyc10g074350.1.1	Unknown Protein	
7BC	g282.i1	3506014	3509010	2996	7E-137	79.5	74	Solyc07g008580.1.1	Histone-lysine N-methyltransferase, H3 lysine-36 specific IPR001214	SET
7BC	g284.i1	3517189	3520446	3257	0E+00	96.12	100	Solyc07g008590.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
7BC	g285.i1	3520485	3523750	3265	0E+00	97.2	100	Solyc07g008600.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
7BC	g286.i1	3528744	3532547	3803	0E+00	99.71	95	Solyc07g008610.1.1	ATP-binding cassette protein IPR003439	ABC transporter-like
7BC	g287.i1	3533628	3537465	3837	0E+00	87.88	100	Solyc07g008620.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
7BC	g241.12	2892308	2899675	7367	0E+00	98.14	49	Solyc07g008310.2.1	Rieske (2Fe-2S) domain protein IPR001663	Aromatic-ring-hydroxylating dioxygenase, alpha subunit
7BC	g242.11	2900883	2918819	17936	0E+00	96.9	100	Solyc07g008320.2.1	Calcium-transporting ATPase 1 IPR006408	ATPase, P-type, calcium-transporting, PMCA-type
7BC	g243.11	2936226	2941789	5563	0E+00	98.54	100	Solyc07g008330.2.1	Nucleolar and coiled-body phosphoprotein 1-like IPR007718	SRP40, C-terminal
7BC	g244.11	2942828	2955687	12859	0E+00	99.65	56	Solyc07g008340.2.1	Zinc import ATP-binding protein ZnuC IPR013283	ABC transporter, ABCE
7BC	g246.12	2960108	2971268	11160	0E+00	99.28	96	Solyc07g008350.2.1	Porin_voltage-dependent anion-selective channel protein IPR001925	Porin, eukaryotic type
7BC	g246.11	2961388	2971268	9880	0E+00	99.28	100	Solyc07g008350.2.1	Porin_voltage-dependent anion-selective channel protein IPR001925	Porin, eukaryotic type
7BC	g247.11	2976338	2986579	10241	0E+00	99.09	63	Solyc07g008360.1.1	p-coumarate CoA-ligase 2 IPR000873	AMP-dependent synthetase and ligase
7BC	g247.12	2976338	2986585	10247	0E+00	98.31	67	Solyc07g008360.1.1	p-coumarate CoA-ligase 2 IPR000873	AMP-dependent synthetase and ligase
7BC	g248.11	3009997	3016598	6601	0E+00	85.25	79	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480	Transferase
7BC	g249.11	3021517	3027089	5572	0E+00	98.62	99	Solyc07g008410.2.1	Multidrug and toxin extrusion protein 1 IPR002528	Multi antimicrobial extrusion protein MatE
7BC	g250.11	3043120	3044528	1408	0E+00	88.83	100	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480	Transferase
7BC	g251.11	3048807	3051706	2899	0E+00	99.06	100	Solyc07g008400.1.1	Pto-like, Serine_threonine kinase protein, resistance protein	
7BC	g253.11	3060933	3062508	1575	0E+00	91.32	100	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480	Transferase
7BC	g254.11	3078897	3087088	8191	0E+00	92.29	100	Solyc07g008410.2.1	Multidrug and toxin extrusion protein 1 IPR002528	Multi antimicrobial extrusion protein MatE
7BC	g255.11	3088104	3089488	1384	1E-73	98.11	100	Solyc07g008420.2.1	Blue copper-like protein IPR008972	Cupredoxin
7BC	g258.11	3189096	3190203	1107	2E-165	92.83	97	Solyc07g008440.2.1	Purine permease family protein IPR004853	Protein of unknown function DUF250
7BC	g259.11	3198149	3216703	18554	0E+00	85.53	60	Solyc07g008450.2.1	HEAT repeat-containing protein IPR011989	Armadillo-like helical
7BC	g259.12	3198262	3216283	18021	0E+00	85.43	62	Solyc07g008450.2.1	HEAT repeat-containing protein IPR011989	Armadillo-like helical
7BC	g261.11	3223463	3228663	5200	0E+00	99.47	96	Solyc07g008450.2.1	HEAT repeat-containing protein IPR011989	Armadillo-like helical
7BC	g261.12	3223463	3228663	5200	0E+00	99.47	98	Solyc07g008450.2.1	HEAT repeat-containing protein IPR011989	Armadillo-like helical
7BC	g262.12	3231782	3245907	14125	0E+00	89	100	Solyc07g008460.2.1	Histone-lysine N-methyltransferase IPR001214	SET
7BC	g262.11	3237792	3245907	8115	0E+00	86.84	99	Solyc07g008460.2.1	Histone-lysine N-methyltransferase IPR001214	SET
7BC	g263.11	3246148	3250143	3995	7E-70	98.13	81	Solyc07g008470.2.1	Macrophage migration inhibitory factor family protein IPR001398	Macrophage migration inhibitory factor
7BC	g264.11	3258294	3260613	2319	0E+00	99.8	80	Solyc07g008480.1.1	Pentatricopeptide repeat-containing protein IPR002885	Pentatricopeptide repeat
7BC	g265.11	3265117	3269213	4096	0E+00	97.65	93	Solyc07g008490.2.1	Nucleic acid binding protein IPR018111	K Homology, type 1, subgroup
7BC	g265.12	3265117	3270883	5766	0E+00	98.13	99	Solyc07g008490.2.1	Nucleic acid binding protein IPR018111	K Homology, type 1, subgroup
7BC	g269.11	3324372	3330409	6037	5E-18	65.38	8	Solyc07g008580.1.1	Histone-lysine N-methyltransferase, H3 lysine-36 specific IPR001214	SET
7BC	g270.11	3331802	3341461	9659	2E-144	90.99	21	Solyc07g008500.1.1	Histone-lysine N-methyltransferase IPR001214	SET
7BC	g270.12	3331802	3341461	9659	2E-144	90.99	21	Solyc07g008500.1.1	Histone-lysine N-methyltransferase IPR001214	SET
7BC	g272.11	3366259	3373511	7252	0E+00	99.32	100	Solyc07g008520.2.1	Peptide transporter IPR000109	TGF-beta receptor, type I_II extracellular region
7BC	g273.11	3376029	3381571	5542	0E+00	99.04	99	Solyc07g008530.1.1	Tyrosyl-tRNA synthetase IPR002307	Tyrosyl-tRNA synthetase, class Ib, bacterial_mitochondrial
7BC	g274.11	3383780	3388090	4310	0E+00	86.57	100	Solyc07g008540.2.1	CONSTANS-like zinc finger protein IPR010402	CCT domain
7BC	g275.12	3423159	3436251	13092	0E+00	97.97	100	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g275.13	3423159	3439850	16691	0E+00	97.87	57	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g275.11	3437609	3439850	2241	0E+00	99.07	100	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g276.11	3441627	3446350	4723	0E+00	95.37	100	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g276.12	3441627	3445970	4343	0E+00	96.77	98	Solyc07g008550.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g278.11	3462059	3469543	7484	0E+00	99.06	100	Solyc07g008560.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g279.11	3483079	3490750	7671	0E+00	97.48	100	Solyc07g008570.2.1	Purple acid phosphatase IPR008963	Purple acid phosphatase-like, N-terminal
7BC	g280.11	3494243	3496380	2137	3E-131	94.85	33	Solyc10g074350.1.1	Unknown Protein	
7BC	g282.11	3506014	3509010	2996	7E-137	79.5	74	Solyc07g008580.1.1	Histone-lysine N-methyltransferase, H3 lysine-36 specific IPR001214	SET
7BC	g284.11	3517189	3520446	3257	0E+00	96.12	100	Solyc07g008590.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
7BC	g285.11	3520485	3523750	3265	0E+00	97.2	100	Solyc07g008600.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
7BC	g286.11	3528744	3532547	3803	0E+00	99.71	95	Solyc07g008610.1.1	ATP-binding cassette protein IPR003439	ABC transporter-like
7BC	g287.11	3533628	3537465	3837	0E+00	87.88	100	Solyc07g008620.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
7BC	g288.11	3538758	3542075	3317	0E+00	97.75	100	Solyc07g008630.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
7BC	g289.11	3542527	3549375	6848	0E+00	52.79	64	Solyc07g008640.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
7BC	g290.11	3550134	3556542	6408	2E-147	98.51	98	Solyc07g008650.2.1	tRNA-specific adenosine deaminase IPR016193	Cytidine deaminase-like
7BC	g290.12	3550134	3556542	6408	3E-135	77.25	98	Solyc07g008650.2.1	tRNA-specific adenosine deaminase IPR016193	Cytidine deaminase-like
7BC	g291.11	3558692	3560745	2053	1E-44	88.1	66	Solyc07g008660.2.1	30S ribosomal protein S16 IPR000307	Ribosomal protein S16

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
9C	g1.t1	1	2417	2416	9E-45	100	100	Solyc09g008460.2.1	Ras-related protein Rab-18 IPR015598 Rab18	
9C	g2.t1	7616	12541	4925	0E+00	99.42	100	Solyc09g008470.2.1	Splicing factor 3a subunit 2 IPR000690 Zinc finger, C2H2-type matr	
9C	g2.t2	7616	12541	4925	0E+00	99.42	92	Solyc09g008470.2.1	Splicing factor 3a subunit 2 IPR000690 Zinc finger, C2H2-type matr	
9C	g3.t1	12694	19817	7123	0E+00	88.47	100	Solyc09g008480.2.1	Phosphatidylinositol-4-phosphate 5-kinase 9 IPR017163 Phosphatidylinositol-4-phosphate 5-kinase, plant	
9C	g3.t2	12694	24267	11573	0E+00	93.61	100	Solyc09g008480.2.1	Phosphatidylinositol-4-phosphate 5-kinase 9 IPR017163 Phosphatidylinositol-4-phosphate 5-kinase, plant	
9C	g3.t3	20891	24267	3376	0E+00	98.52	99	Solyc09g008480.2.1	Phosphatidylinositol-4-phosphate 5-kinase 9 IPR017163 Phosphatidylinositol-4-phosphate 5-kinase, plant	
9C	g4.t1	35706	45370	9664	6E-91	96.88	45	Solyc09g008490.2.1	HEAT repeat family protein expressed IPR011989 Armadillo-like helical	
9C	g6.t1	48046	75328	27282	0E+00	96.38	84	Solyc09g008490.2.1	HEAT repeat family protein expressed IPR011989 Armadillo-like helical	
9C	g6.t2	48046	75514	27468	0E+00	94.43	84	Solyc09g008490.2.1	HEAT repeat family protein expressed IPR011989 Armadillo-like helical	
9C	g7.t1	87710	89577	1867	0E+00	96.56	99	Solyc09g008510.1.1	UDP-glucosyltransferase family 1 protein IPR002213 UDP-glucuronosyl_UDP-glucosyltransferase	
9C	g8.t1	94796	104107	9311	0E+00	84.16	100	Solyc09g008520.2.1	Chromodomain helicase DNA binding protein 3 (Fragment) IPR019787 Zinc finger, PHD-finger	
9C	g8.t2	94796	104117	9321	0E+00	84.75	100	Solyc09g008520.2.1	Chromodomain helicase DNA binding protein 3 (Fragment) IPR019787 Zinc finger, PHD-finger	
9C	g9.t1	112390	119897	7507	0E+00	94.29	100	Solyc09g008530.1.1	RRP1 IPR009053 Prefoldin	
9C	g10.t1	124406	127257	2851	5E-101	61.67	96	Solyc12g057020.1.1	Acetyl xylan esterase A IPR005181 Protein of unknown function DUF303, acetyl	
9C	g11.t1	128756	133631	4875	0E+00	96.31	49	Solyc09g008550.2.1	NCS1 family transporter cytosine_purines_uracil_thiamine_allantoin IPR001248 Permease, cytosine_purines, uracil, thiamine, allantoin	
9C	g12.t1	156979	157577	598	2E-64	97.92	99	Solyc11g039970.1.1	Unknown Protein	
9C	g13.t1	158836	167220	8384	0E+00	99	100	Solyc09g008600.2.1	Aspartyl protease family protein IPR001461 Peptidase A1	
9C	g14.t1	167551	175347	7796	0E+00	95.52	100	Solyc09g008610.2.1	KIAA0090 homolog IPR011678 Protein of unknown function DUF1620	
9C	g14.t2	167551	175347	7796	0E+00	98.78	100	Solyc09g008610.2.1	KIAA0090 homolog IPR011678 Protein of unknown function DUF1620	
9C	g15.t1	177186	183538	6352	0E+00	98.84	100	Solyc09g008620.1.1	Polyadenylate binding protein IPR006515 Polyadenylate binding protein, human types 1, 2, 3, 4	
9C	g16.t1	183968	189517	5549	1E-122	97.69	68	Solyc09g008630.2.1	DNA replication complex GNS protein PSF1 IPR005339 GNS complex, Psf1 component	
9C	g17.t1	192097	205846	13749	0E+00	98.24	48	Solyc09g008640.1.1	Receptor-like protein kinase At3g21340 IPR002290 Serine_threonine protein kinase	
9C	g18.t1	213795	219238	5443	0E+00	97.49	100	Solyc09g008670.2.1	Threonine ammonia-lyase biosynthetic IPR000634 Serine_threonine dehydratase, pyridoxal-phosphate-binding site IPR005787 Threonine dehydratase I	
9C	g19.t1	219643	223516	3873	6E-135	86.92	99	Solyc09g008680.2.1	FAD binding protein	
9C	g20.t1	224615	225672	1057	3E-170	97.86	100	Solyc09g008690.1.1	GDSL esterase_lipase At3g53100 IPR001087 Lipase, GDSL	
9C	g20.t2	224615	226849	2234	0E+00	82.18	95	Solyc10g085740.1.1	GDSL esterase_lipase At5g03820 IPR001087 Lipase, GDSL	
9C	g20.t3	225865	226849	984	3E-94	83.44	95	Solyc10g085740.1.1	GDSL esterase_lipase At5g03820 IPR001087 Lipase, GDSL	
9C	g21.t1	226920	236826	9906	0E+00	98.9	97	Solyc09g008700.1.1	Ubiquitin-protein ligase 7 IPR000569 HECT	
9C	g22.t2	246035	257909	11874	0E+00	98	43	Solyc09g008720.1.1	Ethylene receptor IPR004263 Exostosin-like	
9C	g22.t1	246825	257909	11084	0E+00	98	41	Solyc09g008720.1.1	Ethylene receptor IPR004263 Exostosin-like	
9C	g23.t1	261986	263116	1130	4E-115	93.92	100	Solyc09g008740.1.1	Unknown Protein IPR008889 VQ	
9C	g24.t1	271152	272116	964	4E-79	90.74	100	Solyc09g008750.1.1	Unknown Protein	
9C	g25.t1	280635	281711	1076	2E-80	90.53	100	Solyc09g008760.1.1	Unknown Protein IPR008889 VQ	
9C	g26.t1	283395	285575	2180	0E+00	88.67	100	Solyc09g008770.2.1	Group 3 late embryogenesis abundant protein IPR004238 Late embryogenesis abundant protein	
9C	g27.t1	293345	299564	6219	0E+00	91.56	100	Solyc09g008780.2.1	Os01g0786800 protein (Fragment) IPR002781 Protein of unknown function DUF81	
9C	g28.t1	303060	303906	846	1E-98	96.58	100	Solyc09g008790.2.1	Serine_threonine protein kinase IPR002290 Serine_threonine protein kinase	
9C	g29.t1	306025	309476	3451	0E+00	99.5	99	Solyc09g008790.2.1	Serine_threonine protein kinase IPR002290 Serine_threonine protein kinase	
9C	g30.t1	310295	312699	2404	2E-114	100	100	Solyc09g008800.2.1	60S ribosomal protein L24 IPR000988 Ribosomal protein L24e	
9C	g31.t1	316311	317926	1615	4E-76	98.26	95	Solyc09g008810.2.1	Homeobox-leucine zipper-like protein IPR001356 Homeobox	
9C	g32.t1	330297	337966	7669	0E+00	100	80	Solyc09g008820.2.1	F-box protein PP2-B1 IPR001810 Cyclin-like F-box	
9C	g33.t1	342035	346660	4625	9E-103	99.35	31	Solyc09g008830.2.1	Os01g0318400 protein (Fragment)	
9C	g34.t1	348000	356066	8066	0E+00	95.96	96	Solyc09g008840.2.1	Pyruvate kinase IPR001697 Pyruvate kinase	
9C	g34.t2	348000	356066	8066	0E+00	99.24	96	Solyc09g008840.2.1	Pyruvate kinase IPR001697 Pyruvate kinase	
9C	g35.t1	358075	365272	7197	0E+00	99.25	100	Solyc09g008850.2.1	Uridylate kinase IPR001048 Aspartate_glutamate_uridylate kinase	
9C	g36.t1	367200	370176	2976	0E+00	99.11	100	Solyc09g008860.2.1	Receptor like kinase, RLK	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
9C	g37.t1	384425	389575	5150	0E+00	97.61	95	Solyc09g098620.1.1		cytochrome P450
9C	g38.t1	390752	392526	1774	2E-119	80	100	Solyc10g083690.2.1		Cytochrome P450
9C	g39.t1	395985	397855	1870	0E+00	98.83	100	Solyc09g008910.1.1		Cytochrome P450
9C	g40.t1	398397	403646	5249	0E+00	92.96	100	Solyc09g008920.2.1		Geranylgeranyl pyrophosphate synthase IPR000092 Polyisoprenyl synthetase
9C	g41.t1	404753	408136	3383	0E+00	81.76	99	Solyc09g008930.2.1		Os03g0270500 protein (Fragment) IPR007700 Protein of unknown function DUF668
9C	g42.t2	421505	429517	8012	0E+00	95.78	99	Solyc09g008940.2.1		AT-hook motif nuclear localized protein 1 IPR005175 Protein of unknown function DUF296
9C	g42.t1	428445	429517	1072	4E-114	98.18	99	Solyc09g008940.2.1		AT-hook motif nuclear localized protein 1 IPR005175 Protein of unknown function DUF296
9C	g43.t1	429804	432316	2512	2E-56	92.39	100	Solyc09g008950.1.1		Homology to unknown gene IPR004274 NLI interacting factor
9C	g44.t1	433572	435326	1754	5E-112	95.15	91	Solyc09g008960.1.1		Homology to unknown gene IPR004274 NLI interacting factor
9C	g45.t1	438255	438842	587	1E-83	91.91	100	Solyc09g008970.1.1		Unknown Protein
9C	g46.t1	440765	441541	776	1E-101	96.08	100	Solyc09g008980.1.1		Unknown Protein
9C	g47.t3	451125	458247	7122	0E+00	80.08	100	Solyc10g083670.1.1		Cellulose synthase-like C2 glycosyltransferase family 2 IPR001173 Glycosyl transferase, family 2
9C	g47.t2	451125	468657	17532	0E+00	93.69	49	Solyc09g009020.2.1		Enolase IPR000941 Enolase
9C	g47.t1	463955	468657	4702	0E+00	93.69	100	Solyc09g009020.2.1		Enolase IPR000941 Enolase
9C	g49.t2	477223	481816	4593	1E-146	92.06	100	Solyc09g009030.2.1		Histone deacetylase 2a-like IPR007087 Zinc finger, C2H2-type
9C	g49.t1	477223	481816	4593	4E-141	91.94	92	Solyc09g009030.2.1		Histone deacetylase 2a-like IPR007087 Zinc finger, C2H2-type
9C	g50.t1	484175	492195	8020	0E+00	86.69	63	Solyc09g009040.2.1		Delta14-sterol reductase IPR001171 Ergosterol biosynthesis ERG4_ERG24
9C	g50.t2	484195	492195	8000	0E+00	86.69	61	Solyc09g009040.2.1		Delta14-sterol reductase IPR001171 Ergosterol biosynthesis ERG4_ERG24
9C	g51.t1	504655	519114	14459	0E+00	96.22	94	Solyc09g009080.2.1		Repressor of silencing 1 IPR003265 HhH-GPD domain
9C	g53.t1	529295	544878	15583	0E+00	99.4	100	Solyc09g009090.2.1		Protein kinase IPR002290 Serine_threonine protein kinase
9C	g54.t1	548266	550826	2560	0E+00	96.27	100	Solyc09g009100.2.1		Heat stress transcription factor A3-type, DNA-binding
9C	g55.t1	551845	553766	1921	0E+00	97.62	100	Solyc09g009110.2.1		Gibberellin 20-oxidase IPR005123 Oxoglutarate and iron-dependent oxygenase
9C	g56.t1	556215	564095	7880	0E+00	96.86	100	Solyc09g009120.2.1		mRNA cleavage factor complex component Pcf11 IPR006903 Protein of unknown function DUF618
9C	g56.t2	556215	564095	7880	0E+00	96.87	100	Solyc09g009120.2.1		mRNA cleavage factor complex component Pcf11 IPR006903 Protein of unknown function DUF618
9C	g58.t1	588073	591583	3510	0E+00	98.92	93	Solyc09g009140.2.1		Gamma-tubulin complex component 3 IPR015697 Gamma tubulin complex protein 3
9C	g58.t2	588073	598219	10146	0E+00	98.92	65	Solyc09g009140.2.1		Gamma-tubulin complex component 3 IPR015697 Gamma tubulin complex protein 3
9C	g63.t1	620773	622264	1491	3E-132	97.77	99	Solyc09g009170.2.1		Serine_threonine protein phosphatase family protein-tetraphosphatase
9C	g65.t1	654833	664694	9861	0E+00	93.66	100	Solyc09g009180.2.1		Chaperone protein dnaJ IPR003095 Heat shock protein DnaJ
9C	g66.t1	670223	688344	18121	0E+00	92.52	98	Solyc09g009190.2.1		1 4-alpha-glucan branching enzyme II IPR006589 Glycosyl hydrolase, family 13, subfamily, catalytic region
9C	g66.t2	670223	688344	18121	0E+00	96.25	100	Solyc09g009190.2.1		1 4-alpha-glucan branching enzyme II IPR006589 Glycosyl hydrolase, family 13, subfamily, catalytic region
9C	g67.t1	689043	691924	2881	2E-133	86.75	100	Solyc09g009200.1.1		Growth-regulating factor 10 IPR014977 WRC
9C	g68.t1	706743	709817	3074	1E-113	100	100	Solyc09g009210.2.1		cDNA clone J033118E13 full insert sequence IPR007033 Protein of unknown function DUF662
9C	g69.t1	722375	727074	4699	0E+00	97.04	100	Solyc09g009220.2.1		Unknown Protein
9C	g71.t1	744774	746714	1940	0E+00	98.65	100	Solyc09g009230.1.1		AT5g22550_MQJ16_9 IPR004158 Protein of unknown function DUF247, plant
9C	g72.t1	747826	749004	1178	2E-147	98.02	100	Solyc09g009240.1.1		Ethylene-responsive transcription factor 13 IPR001471 Pathogenesis-related transcriptional factor and ERF, DNA-binding
9C	g73.t1	766793	770204	3411	0E+00	98.53	100	Solyc09g009250.2.1		Trihelix transcription factor IPR017877 MYB-like
9C	g74.t1	775933	778084	2151	0E+00	99.72	100	Solyc09g009260.2.1		Fructose-bisphosphate aldolase IPR000741 Fructose-bisphosphate aldolase, class-I
9C	g75.t1	786251	787674	1423	0E+00	99.26	100	Solyc09g009270.1.1		Tumor susceptibility protein 101 (Fragment) IPR008883 Tumour susceptibility gene 101
9C	g76.t1	792073	793329	1256	1E-157	68.7	99	Solyc09g010310.1.1		Unknown Protein IPR005174 Protein of unknown function DUF295
9C	g77.t1	795754	805554	9800	3E-161	100	52	Solyc09g009280.1.1		AT5G28150-like protein (Fragment) IPR008586 Protein of unknown function DUF868, plant
9C	g78.t1	806423	811763	5340	0E+00	98.59	49	Solyc09g009290.2.1		Ankyrin repeat protein IPR002110 Ankyrin
9C	g79.t1	812023	822684	10661	1E-104	98.65	25	Solyc09g009300.2.1		BUD31 homolog IPR001748 G10 protein
9C	g80.t1	851843	857588	5745	7E-162	90.53	59	Solyc09g009310.1.1		Unknown Protein IPR005174 Protein of unknown function DUF295
9C	g81.t1	863789	871314	7525	6E-107	96.75	61	Solyc09g009320.1.1		F-box protein family-like IPR001810 Cyclin-like F-box
9C	g82.t1	872770	875964	3194	0E+00	90	100	Solyc09g009310.1.1		Unknown Protein IPR005174 Protein of unknown function DUF295
9C	g83.t1	879394	884554	5160	4E-38	98.53	73	Solyc09g009340.1.1		DNA double-strand break repair protein mre11 IPR003701 DNA repair exonuclease
9C	g84.t1	884895	896384	11489	0E+00	93.91	99	Solyc09g009340.1.1		DNA double-strand break repair protein mre11 IPR003701 DNA repair exonuclease
9C	g84.t2	884895	896384	11489	0E+00	95.85	99	Solyc09g009340.1.1		DNA double-strand break repair protein mre11 IPR003701 DNA repair exonuclease
9C	g85.t1	905593	955707	50114	0E+00	93.98	50	Solyc09g009370.2.1		Vacuolar protein sorting-associated protein IPR009291 Protein of unknown function DUF946, plant

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
9D	g1.t1	1	23841	23840	0E+00	97.59	99	Solyc09g009370.2.1	Vacuolar protein sorting-associated protein IPR009291 Protein of unknown function DUF946, plant	
9D	g1.t2	1	27042	27041	0E+00	97.5	91	Solyc09g009370.2.1	Vacuolar protein sorting-associated protein IPR009291 Protein of unknown function DUF946, plant	
9D	g2.t1	37386	48397	11011	0E+00	98.82	100	Solyc09g009380.2.1	Protein kinase-like protein IPR002290 Serine_threonine protein kinase	
9D	g3.t1	57046	62106	5060	0E+00	96.07	100	Solyc09g009390.2.1	Monodehydroascorbate reductase (NADH)-like protein IPR013027 FAD-dependent pyridine nucleotide-disulphide oxidoreductase	
9D	g3.t2	57046	62106	5060	0E+00	95.84	100	Solyc09g009390.2.1	Monodehydroascorbate reductase (NADH)-like protein IPR013027 FAD-dependent pyridine nucleotide-disulphide oxidoreductase	
9D	g4.t1	62193	65087	2894	0E+00	98.23	96	Solyc09g009400.2.1	APO protein 1, chloroplastic IPR008512 Protein of unknown function DUF794, plant	
9D	g6.t2	69046	81812	12766	0E+00	96.88	75	Solyc09g009410.2.1	WD repeat protein 39 IPR020472 G-protein beta WD-40 repeat, region	
9D	g6.t1	75856	81812	5956	0E+00	96.88	100	Solyc09g009410.2.1	WD repeat protein 39 IPR020472 G-protein beta WD-40 repeat, region	
9D	g7.t1	90346	97517	7171	2E-86	80.35	92	Solyc09g009430.2.1	Cell division protein ftsZ IPR000158 Cell division protein FtsZ, N-terminal	
9D	g8.t1	97765	98457	692	5E-20	49.02	72	Solyc03g114270.1.1	Unknown Protein	
9D	g10.t1	104478	111137	6659	0E+00	99.36	100	Solyc09g009430.2.1	Cell division protein ftsZ IPR000158 Cell division protein FtsZ, N-terminal	
9D	g11.t1	112766	127881	15115	0E+00	98.57	60	Solyc09g009470.1.1	F-box family protein IPR001810 Cyclin-like F-box	
9D	g12.t1	114653	121667	7014	2E-98	95.71	62	Solyc09g009450.1.1	Unknown Protein	
9D	g13.t1	132246	133848	1602	3E-118	96.49	45	Solyc09g009480.1.1	S-locus F-box-like protein b	
9D	g14.t1	140331	143217	2886	0E+00	97.99	90	Solyc09g009490.2.1	Bzip transcription factor IPR011700 Basic leucine zipper	
9D	g15.t1	146566	151477	4911	0E+00	94.59	100	Solyc09g009500.2.1	Hydrolase alpha_beta fold family protein IPR000073 Alpha_beta hydrolase fold-1	
9D	g15.t2	146566	151477	4911	0E+00	99.19	100	Solyc09g009500.2.1	Hydrolase alpha_beta fold family protein IPR000073 Alpha_beta hydrolase fold-1	
9D	g16.t1	151684	154597	2913	0E+00	98.28	100	Solyc09g009510.2.1	Hydrolase alpha_beta fold family protein IPR000073 Alpha_beta hydrolase fold-1	
9D	g17.t1	155634	161317	5683	0E+00	96.6	87	Solyc09g009520.2.1	Hydrolase alpha_beta fold family protein IPR000073 Alpha_beta hydrolase fold-1	
9D	g18.t1	164483	167427	2944	0E+00	98.85	100	Solyc09g009530.2.1	Hydrolase alpha_beta fold family protein IPR000073 Alpha_beta hydrolase fold-1	
9D	g19.t1	178028	187126	9098	0E+00	98.28	100	Solyc09g009540.2.1	Hydrolase alpha_beta fold family protein IPR000073 Alpha_beta hydrolase fold-1	
9D	g20.t1	190229	193116	2887	0E+00	97.99	100	Solyc09g009550.2.1	Hydrolase alpha_beta fold family protein IPR000073 Alpha_beta hydrolase fold-1	
9D	g21.t1	198165	201148	2983	4E-125	98.84	100	Solyc09g009560.1.1	SELF PRUNING 9D	
9D	g23.t1	235245	239915	4670	7E-117	97.66	77	Solyc09g009580.2.1	Fatty acyl coA reductase IPR013120 Male sterility, NAD-binding	
9D	g23.t2	235245	239915	4670	1E-111	71.11	82	Solyc09g009590.2.1	Fatty acyl coA reductase IPR013120 Male sterility, NAD-binding	
9D	g24.t1	249713	254256	4543	0E+00	98.43	100	Solyc09g009600.1.1	Purple acid phosphatase IPR008963 Purple acid phosphatase-like, N-terminal	
9D	g25.t1	259745	263720	3975	0E+00	98.66	100	Solyc09g009610.1.1	Purple acid phosphatase IPR008963 Purple acid phosphatase-like, N-terminal	
9D	g26.t1	271725	273136	1411	5E-41	98.65	83	Solyc09g009620.1.1	Unknown Protein	
9D	g27.t1	279419	286356	6937	3E-174	96.06	94	Solyc09g009630.2.1	CAAX prenyl protease 2 IPR003675 Abortive infection protein	
9D	g29.t1	292992	298416	5424	0E+00	74.3	100	Solyc08g065200.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1	
9D	g30.t1	308915	322573	13658	0E+00	99.67	73	Solyc09g009660.2.1	Solute carrier family 35 member F1 IPR009262 Protein of unknown function DUF914, eukaryotic	
9D	g30.t3	308915	312935	4020	7E-61	77.95	100	Solyc09g009640.2.1	U6 snRNA-associated Sm-like protein LSM7 IPR017132 U6 snRNA-associated Sm-like protein LSM7	
9D	g30.t2	317825	322350	4525	0E+00	99.68	100	Solyc09g009660.2.1	Solute carrier family 35 member F1 IPR009262 Protein of unknown function DUF914, eukaryotic	
9D	g31.t1	322975	325285	2310	0E+00	86.13	100	Solyc09g009670.2.1	Solute carrier family 35 member F1 IPR009262 Protein of unknown function DUF914, eukaryotic	
9D	g31.t2	322975	325285	2310	0E+00	95.81	100	Solyc09g009670.2.1	Solute carrier family 35 member F1 IPR009262 Protein of unknown function DUF914, eukaryotic	
9D	g32.t1	326465	332888	6423	0E+00	98.23	100	Solyc09g009680.2.1	Transcription initiation factor TFIIID subunit 12 IPR003228 Transcription initiation factor TFIIID	
9D	g33.t1	334915	350501	15586	0E+00	95.22	52	Solyc09g009700.2.1	GDSL esterase_lipase At5g03610 IPR001087 Lipase, GDSL	
9D	g34.t1	353526	355286	1760	0E+00	76.16	99	Solyc10g083400.1.1	Cytochrome P450	
9D	g35.t1	362750	364187	1437	2E-105	74.63	55	Solyc10g083400.1.1	Cytochrome P450	
9D	g36.t1	365340	377057	11717	0E+00	95.08	100	Solyc09g009710.2.1	General transcription factor 3C polypeptide 2 IPR011046 WD40 repeat-like	
9D	g36.t2	365340	377057	11717	0E+00	94.37	100	Solyc09g009710.2.1	General transcription factor 3C polypeptide 2 IPR011046 WD40 repeat-like	
9D	g37.t1	378060	378728	668	1E-123	99.4	100	Solyc09g009720.1.1	Ubiquitin-conjugating enzyme 13 E2 IPR000608 Ubiquitin-conjugating enzyme, E2	
9D	g38.t1	404320	406494	2174	5E-16	79.49	11	Solyc10g044870.1.1	Enzymatic polyprotein	
9D	g39.t2	407210	431897	24687	0E+00	99.37	43	Solyc09g009750.1.1	Subtilisin-like serine protease IPR015500 Peptidase S8, subtilisin-related	
9D	g39.t1	420850	431922	11072	0E+00	98.92	100	Solyc09g009750.1.1	Subtilisin-like serine protease IPR015500 Peptidase S8, subtilisin-related	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
9D	g40.t1	432187	437101	4914	0E+00	95.9	86	Solyc09g009760.1.1	Z-box binding factor 2 protein IPR011616	bZIP transcription factor, bZIP-1
9D	g41.t1	439962	443811	3849	0E+00	98.67	100	Solyc09g009770.2.1	Calmodulin binding protein	
9D	g42.t1	450170	452137	1967	2E-109	98.72	100	Solyc09g009780.2.1	Glucosamine 6-phosphate N-acetyltransferase IPR000182 GCN5-related N-acetyltransferase	
9D	g43.t1	452287	454681	2394	0E+00	90.17	75	Solyc09g009790.2.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
9D	g44.t1	454743	476611	21868	0E+00	91.89	100	Solyc09g009800.2.1	Transcription factor (Fragment) IPR007309 B-block binding subunit of TFIIIC	
9D	g44.t2	454743	476611	21868	0E+00	91.61	100	Solyc09g009800.2.1	Transcription factor (Fragment) IPR007309 B-block binding subunit of TFIIIC	
9D	g45.t1	484690	485921	1231	1E-120	97.71	98	Solyc09g009810.1.1	Unknown Protein	
9D	g46.t1	495120	501824	6704	0E+00	89.85	92	Solyc09g009820.2.1	Glutathione S-transferase domain protein IPR004045 Glutathione S-transferase, N-terminal	
9D	g46.t2	495120	501824	6704	0E+00	87.99	92	Solyc09g009820.2.1	Glutathione S-transferase domain protein IPR004045 Glutathione S-transferase, N-terminal	
9D	g47.t1	507490	510497	3007	4E-61	92.93	51	Solyc09g009830.2.1	Carbonic anhydrase (Carbonate dehydratase) IPR018340 Carbonic anhydrase, CAH1-like	
9D	g48.t1	515022	520171	5149	0E+00	97.92	100	Solyc09g009840.1.1	Calcium_calmodulin protein kinase	
9D	g49.t1	520560	528096	7536	4E-97	96	72	Solyc09g009850.2.1	Genomic DNA chromosome 5 P1 clone MUB3	
9D	g51.t1	533636	544025	10389	0E+00	98.28	47	Solyc09g009860.1.1	Glutaredoxin family protein IPR012335 Thioredoxin fold	
9D	g52.t1	571988	580877	8889	0E+00	99.18	100	Solyc09g009890.2.1	Polyadenylate-binding protein IPR012677 Nucleotide-binding, alpha-beta plait	
9D	g53.t1	582784	585437	2653	1E-74	100	100	Solyc09g009900.2.1	Pollen-specific protein - like IPR013970 Replication factor A protein 3	
9D	g54.t1	586049	595287	9238	0E+00	91.24	100	Solyc09g009910.2.1	Lipid A ABC transporter permease_ATP-binding protein IPR003439 ABC transporter-like	
9D	g54.t2	586049	595287	9238	0E+00	96.15	100	Solyc09g009910.2.1	Lipid A ABC transporter permease_ATP-binding protein IPR003439 ABC transporter-like	
9D	g55.t1	596257	598227	1970	0E+00	98.96	100	Solyc09g009920.1.1	F-box family protein IPR013596 FBD	
9D	g56.t1	599690	601037	1347	1E-58	98.9	100	Solyc09g009930.1.1	Unknown Protein	
9D	g57.t1	602004	609117	7113	0E+00	99.47	100	Solyc09g009940.2.1	Signal recognition particle protein IPR004780 Signal recognition particle, SRP	
9D	g58.t1	609906	612187	2281	0E+00	93.13	100	Solyc09g009950.2.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat	
9D	g59.t1	612637	617157	4520	0E+00	87.26	98	Solyc09g009960.2.1	4_apos-phosphopantetheinyl transferase family protein IPR008278 4-phosphopantetheinyl transferase	
9D	g60.t1	618670	623217	4547	0E+00	99.24	100	Solyc09g009970.2.1	Rho GTPase activating protein 2 IPR000198 RhoGAP	
9D	g61.t1	633396	635546	2150	4E-104	96.67	100	Solyc09g009980.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
9G	g1.t1	1	1567	1566	0E+00	99.74	100	Solyc09g072560.2.1	Legumin 11S-globulin IPR014710 RmIC-like jelly roll fold	
9G	g2.t1	6445	13147	6702	0E+00	100	100	Solyc09g072570.2.1	Pre-mRNA-splicing factor SLU7-A	
9G	g3.t1	15886	22828	6942	1E-100	99.31	49	Solyc09g072580.2.1	Chromatin modification-related protein MEAF6 IPR015418 Histone H4 acetyltransferase, NuA4 complex, Eaf6	
9G	g5.t1	71886	76308	4422	9E-60	96.63	64	Solyc09g072590.2.1	Actin-depolymerizing factor 6 IPR002108 Actin-binding, cofilin_tropomyosin type	
9G	g6.t1	105436	108627	3191	0E+00	98.08	100	Solyc09g072610.2.1	Glucose-methanol-choline oxidoreductase IPR012400 Long-chain fatty alcohol dehydrogenase	
9G	g8.t1	135594	141387	5793	0E+00	99.6	100	Solyc09g072620.2.1	Phytochelatin synthase IPR015407 Phytochelatin synthase, C-terminal	
9G	g9.t1	148596	150979	2383	0E+00	99.02	90	Solyc09g072630.2.1	LRR receptor-like serine_threonine-protein kinase, RLP	
9G	g10.t1	150982	159177	8195	4E-147	95.52	100	Solyc09g072640.2.1	Rop-interactive crib motif-containing protein 1 IPR000095 PAK-box_P21-Rho-binding	
9G	g10.t2	150982	155047	4065	2E-128	95.96	100	Solyc09g072640.2.1	Rop-interactive crib motif-containing protein 1 IPR000095 PAK-box_P21-Rho-binding	
9G	g11.t1	160486	165559	5073	0E+00	93.98	100	Solyc09g072650.2.1	Calmodulin-binding protein MPCBP IPR011990 Tetratricopeptide-like helical	
9G	g12.t1	166060	168337	2277	0E+00	99.08	100	Solyc09g072660.2.1	FAD-binding domain-containing protein IPR006094 FAD linked oxidase, N-terminal	
9G	g13.t2	174286	186004	11718	5E-126	77.96	82	Solyc09g072670.2.1	Rho GDP dissociation inhibitor 1 IPR000406 RHO protein GDP dissociation inhibitor	
9G	g13.t1	174286	178003	3717	2E-111	96.91	96	Solyc09g072670.2.1	Rho GDP dissociation inhibitor 1 IPR000406 RHO protein GDP dissociation inhibitor	
9G	g14.t1	186007	188527	2520	0E+00	98.98	99	Solyc09g072680.1.1	F-box family protein IPR017451 F-box associated type 1	
9G	g15.t1	210402	212287	1885	0E+00	98.62	100	Solyc09g072690.1.1	Sodium_calcium exchanger protein (Fragment) IPR004837 Sodium_calcium exchanger membrane region	
9G	g16.t2	215357	236487	21130	0E+00	81.93	61	Solyc09g072710.2.1	Phosphatidylcholine-sterol O-acyltransferase IPR003386 Lecithin:cholesterol acyltransferase	
9G	g16.t1	223718	236477	12759	0E+00	81.93	86	Solyc09g072710.2.1	Phosphatidylcholine-sterol O-acyltransferase IPR003386 Lecithin:cholesterol acyltransferase	
9G	g17.t1	237716	242420	4704	0E+00	96.56	100	Solyc09g072720.1.1	AT1G10385-like protein (Fragment) IPR014812 Vps51_Vps67	
9G	g18.t1	248996	256480	7484	4E-112	85.99	79	Solyc09g072770.1.1	mRNA clone RAFL22-93-M12 (Fragment)	
9G	g19.t1	267416	270306	2890	6E-39	92.21	37	Solyc02g005530.1.1	Helitron helicase-like protein IPR010285 Protein of unknown function DUF889, eukaryote	
9G	g20.t1	278615	282447	3832	0E+00	98.9	100	Solyc09g072780.1.1	Peptide transporter IPR000109 TGF-beta receptor, type II extracellular region	
9G	g22.t2	292661	302257	9596	0E+00	98.86	28	Solyc09g072790.2.1	RNA-binding protein-like IPR000504 RNA recognition motif, RNP-1	
9G	g22.t1	299131	302257	3126	0E+00	98.86	99	Solyc09g072790.2.1	RNA-binding protein-like IPR000504 RNA recognition motif, RNP-1	
9G	g24.t1	309806	315153	5347	0E+00	88.94	100	Solyc09g072800.2.1	At1g04030 (Fragment)	
9G	g25.t1	320806	324689	3883	0E+00	97.95	100	Solyc09g072810.2.1	Receptor like kinase, RLK	
9G	g26.t1	324800	332047	7247	0E+00	99.52	100	Solyc09g072820.2.1	Cellulose synthase IPR005150 Cellulose synthase	
9G	g27.t1	332526	335757	3231	2E-161	98.37	58	Solyc01g088700.2.1	Eukaryotic translation initiation factor 4 gamma 1 IPR016021 MIF4-like, type 1_2_3	
9G	g28.t1	336466	345407	8941	0E+00	97.01	100	Solyc09g072830.2.1	Myb family transcription factor IPR006447 Myb-like DNA-binding region, SHAQKYF class	
9G	g29.t1	348143	352994	4851	4E-126	78.17	69	Solyc09g072840.1.1	Unknown Protein	
9G	g30.t1	353538	360864	7326	0E+00	91.94	100	Solyc09g072860.1.1	Genomic DNA chromosome 5 P1 clone MRH10	
9G	g30.t2	353538	360864	7326	2E-160	94.96	66	Solyc09g072860.1.1	Genomic DNA chromosome 5 P1 clone MRH10	
9G	g31.t2	361672	363474	1802	5E-98	100	100	Solyc09g090610.2.1	50S ribosomal protein L14 IPR000218 Ribosomal protein L14b_L23e	
9G	g31.t1	361672	363474	1802	6E-94	87.5	100	Solyc09g090610.2.1	50S ribosomal protein L14 IPR000218 Ribosomal protein L14b_L23e	
9G	g32.t1	366543	370561	4018	0E+00	98.28	100	Solyc09g072880.2.1	Chloroplast FLU-like protein (Fragment) IPR011990 Tetratricopeptide-like helical	
9G	g32.t2	366543	380901	14358	0E+00	98.28	55	Solyc09g072880.2.1	Chloroplast FLU-like protein (Fragment) IPR011990 Tetratricopeptide-like helical	
9G	g33.t1	381560	389794	8234	0E+00	97.46	87	Solyc09g072890.1.1	Histone-lysine n-methyltransferase IPR001214 SET	
9G	g34.t1	394813	398419	3606	0E+00	98.28	100	Solyc09g072880.2.1	Chloroplast FLU-like protein (Fragment) IPR011990 Tetratricopeptide-like helical	
9G	g34.t2	394813	402999	8186	0E+00	98.28	79	Solyc09g072880.2.1	Chloroplast FLU-like protein (Fragment) IPR011990 Tetratricopeptide-like helical	
9G	g35.t1	413197	421114	7917	0E+00	93.21	48	Solyc09g072890.1.1	Histone-lysine n-methyltransferase IPR001214 SET	
9G	g37.t1	438183	443567	5384	9E-174	98.74	100	Solyc09g072900.2.1	Dienelactone hydrolase family protein IPR002925 Dienelactone hydrolase	
9G	g38.t1	446663	448144	1481	0E+00	95.06	100	Solyc09g072910.1.1	F-box family protein IPR017451 F-box associated type 1	
9G	g39.t1	450379	452234	1855	2E-95	89.63	30	Solyc09g072920.1.1	Zinc finger-homeodomain protein 1 (Fragment) IPR012287 Homeodomain-related	
9G	g40.t1	454899	456344	1445	0E+00	91.56	100	Solyc09g072930.1.1	F-box family protein IPR017451 F-box associated type 1	
9G	g41.t1	458432	460904	2472	8E-13	93.75	16	Solyc09g072940.1.1	Nbs-Irr resistance protein (Fragment) IPR001810 Cyclin-like F-box	
9G	g42.t1	461009	462394	1385	8E-155	95.15	96	Solyc09g072940.1.1	Nbs-Irr resistance protein (Fragment) IPR001810 Cyclin-like F-box	

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					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
9G	g43.t1	469393	470861	1468	2E-67	60.53	55	Solyc09g072940.1.1	Nbs-Irr resistance protein (Fragment) IPR001810	Cyclin-like F-box
9G	g45.t1	479793	485864	6071	6E-106	89.14	49	Solyc09g072960.1.1	F-box family protein IPR013101	Leucine-rich repeat 2
9G	g47.t1	494175	495584	1409	2E-61	53.45	49	Solyc09g072940.1.1	Nbs-Irr resistance protein (Fragment) IPR001810	Cyclin-like F-box
9G	g48.t1	497973	502044	4071	5E-63	98.91	84	Solyc09g072970.2.1	U6 snRNA-associated Sm-like protein LSM2 IPR016654	U6 snRNA-associated Sm-like protein LSM2
9G	g49.t1	504524	510484	5960	0E+00	93.41	100	Solyc09g072980.2.1	BTB_POZ domain containing protein expressed IPR013089	Kelch related
9G	g50.t1	514613	520111	5498	5E-163	95.8	41	Solyc09g072990.2.1	Unknown Protein	
9G	g51.t1	520748	527314	6566	0E+00	99.56	100	Solyc09g073000.2.1	Elongation factor Tu IPR004541	Translation elongation factor EFTu_EF1A, bacterial and organelle
9G	g52.t1	531738	540940	9202	2E-116	81.9	100	Solyc09g073010.1.1	Inorganic phosphate transporter 1 IPR016196	Major facilitator superfamily, general substrate transporter
9G	g54.t1	564719	571402	6683	1E-57	50.43	42	Solyc09g072940.1.1	Nbs-Irr resistance protein (Fragment) IPR001810	Cyclin-like F-box
9G	g56.t1	591919	592721	802	4E-132	94.23	100	Solyc09g074040.1.1	Unknown Protein	
9G	g57.t1	613639	620468	6829	0E+00	98.55	100	Solyc09g074050.2.1	Oxidoreductase	
9G	g58.t1	621898	624170	2272	0E+00	95.99	82	Solyc09g074060.2.1	BSD domain containing 1 IPR005607	BSD
9G	g59.t1	627012	628620	1608	0E+00	98.87	100	Solyc09g074080.1.1	Glycosyltransferase family GT8 protein IPR002495	Glycosyl transferase, family 8
9G	g60.t1	633059	640828	7769	0E+00	98.77	100	Solyc09g074090.2.1	Exosome complex exonuclease RRP4	
9G	g61.t1	642023	648460	6437	0E+00	98.76	100	Solyc09g074100.2.1	tRNA-specific 2-thiouridylyase mmmA IPR018318	tRNA methyl transferase-like
9G	g63.t2	665389	696048	30659	0E+00	97.87	76	Solyc09g074110.2.1	AGAP009276-PA (Fragment)	
9G	g63.t1	678839	696048	17209	0E+00	99.33	79	Solyc09g074110.2.1	AGAP009276-PA (Fragment)	
9G	g65.t1	718479	723938	5459	0E+00	93.03	100	Solyc09g074140.1.1	Baculoviral IAP repeat-containing 2 IPR001841	Zinc finger, RING-type
9G	g66.t1	728064	734902	6838	0E+00	91.06	100	Solyc09g074140.1.1	Baculoviral IAP repeat-containing 2 IPR001841	Zinc finger, RING-type
9G	g67.t1	737564	741871	4307	0E+00	92.29	100	Solyc09g074140.1.1	Baculoviral IAP repeat-containing 2 IPR001841	Zinc finger, RING-type
9G	g68.t1	746714	752736	6022	1E-112	52.15	81	Solyc09g074200.1.1	Baculoviral IAP repeat-containing 3 IPR001841	Zinc finger, RING-type
9G	g71.t1	758734	759369	635	2E-45	97.22	71	Solyc09g074180.2.1	Unknown Protein	
9G	g75.t1	790114	794673	4559	2E-88	61.15	63	Solyc09g074200.1.1	Baculoviral IAP repeat-containing 3 IPR001841	Zinc finger, RING-type
9G	g77.t1	808624	812691	4067	0E+00	96.01	100	Solyc09g074190.1.1	Baculoviral IAP repeat-containing 2 IPR001841	Zinc finger, RING-type
9G	g78.t1	826914	830984	4070	0E+00	94.92	100	Solyc09g074200.1.1	Baculoviral IAP repeat-containing 3 IPR001841	Zinc finger, RING-type
9G	g80.t1	840686	853765	13079	4E-117	92.27	100	Solyc04g051520.1.1	Ulp1 protease family C-terminal catalytic domain containing protein IPR003653	Peptidase C48, SUMO_Sentrin_Ubl1
9G	g82.t1	859714	862481	2767	0E+00	99.8	100	Solyc09g074210.2.1	Endonuclease_exonuclease_phosphatase family protein IPR005135	Endonuclease_exonuclease_phosphatase
9G	g84.t1	866842	870955	4113	0E+00	98.96	100	Solyc09g074230.2.1	Glucose transporter 8 IPR003663	Sugar_inositol transporter
9G	g84.t2	866842	870955	4113	0E+00	93.37	100	Solyc09g074230.2.1	Glucose transporter 8 IPR003663	Sugar_inositol transporter
9G	g86.t1	878234	884805	6571	0E+00	98.43	100	Solyc09g074240.1.1	Receptor-like serine_threonine kinase IPR002290	Serine_threonine protein kinase
9G	g87.t1	889759	895838	6079	0E+00	92.07	69	Solyc09g074250.2.1	Receptor-like kinase IPR002290	Serine_threonine protein kinase
9G	g89.t1	927999	929475	1476	0E+00	99.46	100	Solyc09g074260.1.1	LRR receptor-like serine_threonine-protein kinase, RLP	
9G	g90.t1	940243	947830	7587	0E+00	98.8	99	Solyc09g074270.2.1	Acetyl esterase IPR013094	Alpha_beta hydrolase fold-3
9G	g92.t1	964509	968571	4062	0E+00	97.17	100	Solyc09g074280.1.1	Ankyrin repeat-containing protein IPR002110	Ankyrin
9G	g93.t1	968658	971790	3132	0E+00	97.05	100	Solyc09g074290.1.1	Ankyrin repeat-containing protein IPR002110	Ankyrin
9G	g94.t1	975609	980496	4887	0E+00	98.22	72	Solyc09g074310.2.1	Oxidoreductase aldo_keto reductase family protein expressed IPR001395	Aldo_keto reductase
9G	g96.t2	989539	1002993	13454	0E+00	90.77	100	Solyc09g074320.2.1	Serine_threonine-protein phosphatase IPR012391	Serine_threonine protein phosphatase, BSU1
9G	g96.t1	990049	1002993	12944	0E+00	93.33	100	Solyc09g074320.2.1	Serine_threonine-protein phosphatase IPR012391	Serine_threonine protein phosphatase, BSU1
9G	g97.t1	1003702	1019460	15758	0E+00	91.38	100	Solyc09g074330.2.1	NDX1 homeobox protein (Fragment) IPR001356	Homeobox
9G	g98.t1	1045479	1050774	5295	0E+00	97.62	100	Solyc09g074340.2.1	Rho GTPase activating protein 2 IPR000198	RhoGAP
9G	g99.t1	1052753	1053530	777	4E-74	90.53	99	Solyc09g074350.1.1	Unknown Protein	
9G	q100.t1	1062912	1063950	1038	1E-38	75.28	79	Solyc09g074360.2.1	RNA binding protein IPR015903	Ribonucleoprotein, BRUNO-like

ITAG2.4 proteins blastp								SD3 Table Orthologous pairs	Functional Description
BIN	Augustus ID	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	S.lycopersicum (Heinz)	
11B	g1.t1	2	22455	22453	0E+00	98.8	43	Solyc11g008490.1.1	Pumilio-like IPR011989 Armadillo-like helical
11B	g1.t2	2	31168	31166	0E+00	98.77	36	Solyc11g008490.1.1	Pumilio-like IPR011989 Armadillo-like helical
11B	g1.t3	24276	31168	6892	0E+00	95.97	100	Solyc11g008500.1.1	Actin IPR004000 Actin_actin-like
11B	g3.t1	34956	36182	1226	3E-44	100	100	Solyc11g008510.1.1	60S ribosomal protein L38 IPR002675 Ribosomal protein L38e
11B	g4.t2	46846	61056	14210	0E+00	97.2	93	Solyc11g008520.1.1	Ribonuclease 3-like protein 3 IPR000999 Ribonuclease III
11B	g4.t3	46846	61003	4157	3E-56	96.88	83	Solyc11g005690.1.1	Tetratricopeptide repeat family IPR011990 Tetratricopeptide-like helical
11B	g4.t1	54076	61056	6980	0E+00	97.2	100	Solyc11g008520.1.1	Ribonuclease 3-like protein 3 IPR000999 Ribonuclease III
11B	g5.t1	62136	70305	8169	0E+00	89.44	96	Solyc11g008530.1.1	Ribonuclease 3-like protein 3 IPR000999 Ribonuclease III
11B	g5.t2	62136	70305	8169	0E+00	88.83	96	Solyc11g008530.1.1	Ribonuclease 3-like protein 3 IPR000999 Ribonuclease III
11B	g6.t1	76336	87293	10957	0E+00	94.9	96	Solyc11g008540.1.1	Ribonuclease 3-like protein 3 IPR000999 Ribonuclease III
11B	g7.t1	89126	100124	10998	0E+00	90.62	95	Solyc11g008550.1.1	Lecithin cholesterol acyltransferase family protein IPR003386 Lecithin:cholesterol acyltransferase
11B	g7.t2	89126	98023	8897	0E+00	98.44	100	Solyc11g008550.1.1	Lecithin cholesterol acyltransferase family protein IPR003386 Lecithin:cholesterol acyltransferase
11B	g8.t1	110916	124495	13579	0E+00	93.97	55	Solyc11g008570.1.1	Calcineurin-related phosphoesterase-like IPR004843 Metallophosphoesterase
11B	g8.t2	110916	124495	13579	0E+00	92.47	53	Solyc11g008570.1.1	Calcineurin-related phosphoesterase-like IPR004843 Metallophosphoesterase
11B	g9.t1	125188	136257	11069	0E+00	95.47	100	Solyc11g008580.1.1	Ariadne-like ubiquitin ligase IPR002867 Zinc finger, C6HC-type
11B	g9.t2	125188	136257	11069	0E+00	90.61	100	Solyc11g008580.1.1	Ariadne-like ubiquitin ligase IPR002867 Zinc finger, C6HC-type
11B	g10.t1	139036	146247	7211	0E+00	96.31	100	Solyc11g008590.1.1	UDP-galactose transporter-like protein IPR007271 Nucleotide-sugar transporter
11B	g11.t1	149537	150417	880	7E-92	97.76	100	Solyc11g008600.1.1	Genomic DNA chromosome 5 P1 clone MUA2
11B	g12.t1	155752	165577	9825	0E+00	94.12	93	Solyc11g008610.1.1	Nucleotide-sugar transporter UDP N-acetylglucosamine-like signal peptide 9 or more transmembrane domains (Fragment) IPR007271 Nucleotide-sugar transporter
11B	g12.t2	156845	165577	8732	0E+00	99.23	97	Solyc11g008610.1.1	Nucleotide-sugar transporter UDP N-acetylglucosamine-like signal peptide 9 or more transmembrane domains (Fragment) IPR007271 Nucleotide-sugar transporter
11B	g13.t1	167460	174097	6637	0E+00	96.56	100	Solyc11g008620.1.1	Phosphoglycolate phosphatase IPR006349 2-phosphoglycolate phosphatase, eukaryotic
11B	g13.t2	167460	174097	6637	0E+00	99.68	100	Solyc11g008620.1.1	Phosphoglycolate phosphatase IPR006349 2-phosphoglycolate phosphatase, eukaryotic
11B	g14.t1	181521	184367	2846	0E+00	99.53	100	Solyc11g008630.1.1	Hydroxycinnamoyl CoA shikimate_quinatase hydroxycinnamoyltransferase-like protein (Fragment) IPR003480 Transferase
11B	g15.t1	184974	187522	2548	2E-127	99.43	100	Solyc11g008640.1.1	Flowering locus T IPR008914 Phosphatidylethanolamine-binding protein PEBP
11B	g16.t1	197115	200642	3527	8E-98	77.78	97	Solyc03g063100.1.1	SELF PRUNING 3D
11B	g16.t2	197115	203052	5937	2E-84	82.14	86	Solyc03g063100.1.1	SELF PRUNING 3D
11B	g17.t1	211111	219064	7953	0E+00	98.08	100	Solyc11g008670.1.1	At1g65470_F5114_33 (Fragment)
11B	g17.t2	211111	225693	14582	0E+00	94.82	68	Solyc11g008670.1.1	At1g65470_F5114_33 (Fragment)
11B	g17.t3	220511	225693	5182	0E+00	100	100	Solyc11g008680.1.1	Acyl- IPR005067 Fatty acid desaturase, type 2
11B	g19.t1	247753	248572	819	3E-137	100	100	Solyc11g008690.1.1	TO23-3 (Fragment)
11B	g20.t1	249322	259212	9890	0E+00	94.88	100	Solyc11g008700.1.1	Splicing factor U2AF-associated protein IPR012677 Nucleotide-binding, alpha-beta plait
11B	g21.t1	260891	266152	5261	0E+00	92.83	100	Solyc11g008710.1.1	30S ribosomal protein S5 IPR000851 Ribosomal protein S5
11B	g22.t1	267511	274730	7219	0E+00	92.57	100	Solyc11g008720.1.1	Beta-glucosidase G4 IPR001360 Glycoside hydrolase, family 1
11B	g22.t2	267511	274698	7187	0E+00	96.63	100	Solyc11g008720.1.1	Beta-glucosidase G4 IPR001360 Glycoside hydrolase, family 1
11B	g23.t1	277891	287156	9265	0E+00	89.8	100	Solyc11g008730.1.1	U11_U12 small nuclear ribonucleoprotein protein IPR019955 Ubiquitin supergroup
11B	g24.t1	288474	302382	13908	0E+00	92.58	100	Solyc11g008740.1.1	Double-strand-break repair protein rad21 IPR006910 Rad21_Rec8 like protein, N-terminal
11B	g24.t2	288474	302382	13908	0E+00	95.96	100	Solyc11g008740.1.1	Double-strand-break repair protein rad21 IPR006910 Rad21_Rec8 like protein, N-terminal
11B	g25.t1	307461	308607	1146	2E-68	95.54	100	Solyc11g008750.1.1	Unknown Protein
11B	g26.t1	311114	313842	2728	0E+00	98.66	100	Solyc11g008760.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
11B	g27.t1	315188	329642	14454	0E+00	94.95	100	Solyc11g008770.1.1	LETM1 and EF-hand domain-containing protein 1, mitochondrial IPR011685 LETM1-like
11B	g28.t1	341371	355512	14141	0E+00	94.09	73	Solyc11g008780.1.1	Acetolactate synthase small subunit IPR004789 Acetolactate synthase, small subunit
11B	g28.t2	341371	355512	14141	0E+00	98.91	74	Solyc11g008780.1.1	Acetolactate synthase small subunit IPR004789 Acetolactate synthase, small subunit
11B	g29.t1	356139	366735	10596	0E+00	96.14	100	Solyc11g008800.1.1	Inositol 1 4 5-trisphosphate 5-phosphatase-like protein IPR000300 Inositol polyphosphate related phosphatase
11B	g30.t1	376624	385545	8921	0E+00	97.18	94	Solyc11g008810.1.1	Beta-hexosaminidase b IPR001540 Glycoside hydrolase, family 20
11B	g31.t1	385885	392705	6820	0E+00	99.2	79	Solyc11g008820.1.1	Endoglucanase IPR001701 Glycoside hydrolase, family 9

ITAG2.4 proteins blastp								SD3 Table Orthologous pairs	Functional Description
BIN	Augustus ID	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	S.lycopersicum (Heinz)	
11B	g32.t1	400864	403054	2190	1E-169	99.57	100	Solyc11g008830.1.1	LOB domain protein IPR004883 Lateral organ boundaries, LOB
11B	g34.t1	414374	421296	6922	0E+00	88.5	100	Solyc11g008850.1.1	Serine protease IPR015724 Serine endopeptidase DegP2
11B	g35.t1	422154	424526	2372	0E+00	97.13	100	Solyc11g008860.1.1	Laccase-2 IPR001117 Multicopper oxidase, type 1
11B	g36.t1	427406	431815	4409	0E+00	99.66	100	Solyc11g008870.1.1	Methylenetetrahydrofolate reductase IPR004621 Eukaryotic-type methylenetetrahydrofolate reductase
11B	g37.t1	436033	436865	832	2E-58	98.86	79	Solyc11g008880.1.1	Wiscott-Aldrich syndrome C-terminal IPR000095 PAK-box_P21-Rho-binding
11B	g38.t1	440928	445785	4857	0E+00	99.66	100	Solyc11g008890.1.1	Predicted membrane protein (Fragment) IPR001727 Uncharacterised protein family UPF0016
11B	g39.t1	449674	457804	8130	0E+00	96.44	100	Solyc11g008900.1.1	Zinc finger CCCH domain-containing protein 66 IPR000571 Zinc finger, CCCH-type
11B	g39.t2	451404	464663	13259	0E+00	100	64	Solyc11g008900.1.1	Zinc finger CCCH domain-containing protein 66 IPR000571 Zinc finger, CCCH-type
11B	g40.t1	468528	472485	3957	4E-132	95.85	52	Solyc11g008930.1.1	Lysine ketoglutarate reductase trans-splicing related 1-like IPR007877 Protein of unknown function DUF707
11B	g41.t1	474684	477032	2348	0E+00	98.01	100	Solyc11g008940.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
11B	g43.t1	493103	500385	7282	0E+00	97.65	96	Solyc11g008960.1.1	Receptor like kinase, RLK
11B	g45.t1	522974	526070	3096	0E+00	98.03	100	Solyc11g008970.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
11B	g46.t1	526501	527525	1024	7E-143	99.02	100	Solyc11g008980.1.1	Os02g0726600 protein (Fragment)
11B	g47.t1	528800	536715	7915	0E+00	97.05	100	Solyc11g008990.1.1	Phage shock protein A PspA IPR007157 PspA_IM30
11B	g48.t1	542474	544051	1577	1E-68	99.02	97	Solyc11g009000.1.1	Carboxylesterase bioH IPR000073 Alpha_beta hydrolase fold-1
11B	g49.t1	549164	557264	8100	2E-86	65.19	96	Solyc10g047340.1.1	Hydrolase IPR000639 Epoxide hydrolase-like
11B	g50.t1	558487	561755	3268	0E+00	98.67	98	Solyc11g009020.1.1	HAD-superfamily hydrolase subfamily IA variant 3 containing protein expressed IPR005834 Haloacid dehalogenase-like hydrolase
11B	g51.t1	562374	562955	581	2E-65	93.33	100	Solyc11g009030.1.1	Ribosomal protein L37
11B	g52.t1	564998	568485	3487	1E-25	93.33	54	Solyc11g009040.1.1	EPIDERMAL PATTERNING FACTOR-like protein 1
11B	g53.t1	573534	577631	4097	0E+00	99.69	100	Solyc11g009050.1.1	F-box protein-like IPR001810 Cyclin-like F-box
11B	g54.t1	581502	589645	8143	0E+00	74.63	100	Solyc11g009060.1.1	Unknown Protein
11B	g54.t2	581502	588185	6683	5E-165	69.34	99	Solyc11g009060.1.1	Unknown Protein
11B	g55.t1	590198	596375	6177	0E+00	97.09	99	Solyc11g009070.1.1	Genomic DNA chromosome 5 P1 clone MQN23
11B	g56.t1	596784	601522	4738	0E+00	72.54	80	Solyc11g009080.1.1	Phospho-2-dehydro-3-deoxyheptonate aldolase 1 IPR002480 DAHP synthetase, class II
11B	g57.t1	604614	608117	3503	0E+00	99.61	100	Solyc11g009080.1.1	Phospho-2-dehydro-3-deoxyheptonate aldolase 1 IPR002480 DAHP synthetase, class II
11B	g58.t1	608803	614545	5742	1E-155	86.17	100	Solyc11g009090.1.1	Polyadenylate-binding protein family protein IPR012677 Nucleotide-binding, alpha-beta plait
11B	g59.t1	615604	624538	8934	0E+00	96.79	84	Solyc11g009100.1.1	ABC transporter G family member 11 IPR013525 ABC-2 type transporter
11B	g59.t2	615604	624538	8934	0E+00	97.16	88	Solyc11g009100.1.1	ABC transporter G family member 11 IPR013525 ABC-2 type transporter
11B	g60.t1	637554	639775	2221	1E-165	98.66	100	Solyc11g010100.1.1	Ras-related protein Rab-25 IPR015595 Rab11-related
11B	g61.t1	640114	650315	10201	0E+00	98.75	100	Solyc11g010110.1.1	Ribosomal RNA small subunit methyltransferase F_eukaryotic nucleolar NOL1_Nop2p
11B	g62.t1	654644	663311	8667	5E-149	85.1	100	Solyc11g010120.1.1	Peroxidase 17 IPR002016 Haem peroxidase, plant_fungal_bacterial
11B	g63.t1	666604	669815	3211	2E-163	71.18	100	Solyc04g012160.2.1	Serine-threonine protein kinase IPR002290 Serine_threonine protein kinase
11B	g64.t1	670554	675901	5347	0E+00	97.11	100	Solyc11g010160.1.1	Cc-nbs-irr, resistance protein
11B	g65.t1	675958	681165	5207	0E+00	97.64	100	Solyc11g010170.1.1	LanC-like protein 2 IPR020464 LanC-like protein, eukaryotic
11B	g66.t1	683561	687305	3744	1E-91	100	100	Solyc11g010180.1.1	Mitochondrial_chloroplast ribosomal protein L54_L37 (ISS) IPR013870 Ribosomal protein L37, mitochondrial
11B	g67.t1	688824	689887	1063	0E+00	99.64	100	Solyc11g010190.1.1	Prohibitin IPR000163 Prohibitin
11B	g68.t1	692684	693997	1313	2E-176	100	93	Solyc11g010200.1.1	14-3-3 protein beta_alpha-1 IPR000308 14-3-3 protein
11B	g69.t1	697188	700085	2897	0E+00	98.45	100	Solyc11g010210.1.1	SKIP interacting protein 3 (Fragment)
11B	g70.t2	705625	710244	4619	0E+00	97.04	80	Solyc11g010220.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
11B	g70.t1	708445	710244	1799	4E-95	100	100	Solyc11g010230.1.1	Histone H3 IPR000164 Histone H3
11B	g71.t1	711858	718144	6286	0E+00	98.48	100	Solyc11g010240.1.1	Protein SCAI
11B	g71.t2	711858	718144	6286	0E+00	98	100	Solyc11g010240.1.1	Protein SCAI
11B	g72.t1	729389	730234	845	2E-93	97.87	100	Solyc11g010250.1.1	Avr9_Cf9 rapidly elicited protein 75
11B	g73.t1	733573	738138	4565	0E+00	98.77	99	Solyc11g010260.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
11B	g75.t1	772812	779254	6442	0E+00	98.02	100	Solyc11g010270.1.1	Homeobox-leucine zipper protein IPR001356 Homeobox

ITAG2.4 proteins blastp								SD3 Table Orthologous pairs	Functional Description
BIN	Augustus ID	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	S.lycopersicum (Heinz)	
11B	g75.i2	772812	774944	2132	0E+00	97.89	97	Solyc11g010270.1.1	Homeobox-leucine zipper protein IPR001356 Homeobox
11B	g76.t1	784240	789494	5254	0E+00	98.8	92	Solyc11g010290.1.1	2-oxoglutarate_malate translocator IPR001898 Sodium_sulphate symporter
11B	g77.t1	795563	801285	5722	0E+00	98.89	95	Solyc11g010300.1.1	3 4-dihydroxy-2-butanone 4-phosphate synthase IPR000422 DHBP synthase RibB
11B	g78.t1	807313	814558	7245	0E+00	98.94	100	Solyc11g010310.1.1	ATP dependent RNA helicase IPR014001 DEAD-like helicase, N-terminal
11B	g79.t1	814601	815614	1013	2E-129	95.74	99	Solyc11g010320.1.1	AT2G46550 protein (Fragment)
11B	g80.t1	818873	820102	1229	0E+00	96.36	100	Solyc11g010330.1.1	RING finger protein IPR018957 Zinc finger, C3HC4 RING-type
11B	g81.t1	825757	828784	3027	0E+00	96.64	100	Solyc11g010340.1.1	BHLH transcription factor IPR001092 Basic helix-loop-helix dimerisation region bHLH
11B	g82.i2	836353	841240	4887	0E+00	98.65	84	Solyc11g010350.1.1	Glucan 1 3-beta-glucosidase IPR001547 Glycoside hydrolase, family 5
11B	g82.t1	836883	840853	3970	0E+00	98.65	84	Solyc11g010350.1.1	Glucan 1 3-beta-glucosidase IPR001547 Glycoside hydrolase, family 5
11B	g83.t1	843435	844654	1219	4E-173	97.9	100	Solyc11g010360.1.1	Plant-specific domain TIGR01570 family protein IPR006460 Protein of unknown function DUF617, plant
11B	g84.t1	855903	857278	1375	0E+00	97.42	100	Solyc11g010370.1.1	At4g40080-like protein (Fragment) IPR013809 Epsin-like, N-terminal
11B	g85.t1	859770	865664	5894	0E+00	98.92	89	Solyc11g010380.1.1	Mate efflux family protein IPR002528 Multi antimicrobial extrusion protein MatE
11B	g86.t1	874194	874924	730	1E-42	81.29	100	Solyc11g010390.1.1	Unknown Protein
11B	g87.t1	883518	885963	2445	2E-75	95.76	100	Solyc11g010400.1.1	1-aminocyclopropane-1-carboxylate oxidase IPR005123 Oxoglutarate and iron-dependent oxygenase
11B	g88.t1	889718	892116	2398	7E-116	95.83	100	Solyc11g010410.1.1	1-aminocyclopropane-1-carboxylate oxidase IPR005123 Oxoglutarate and iron-dependent oxygenase
11B	g89.i3	895908	907350	11442	6E-172	81.97	53	Solyc11g010440.1.1	FIP1 IPR004182 GRAM
11B	g89.i2	895908	903936	8028	4E-128	71.27	98	Solyc11g010430.1.1	Ovarian cancer-associated gene 2 protein homolog IPR005645 Protein of unknown function DUF341
11B	g89.t1	904728	907350	2622	5E-178	81.97	100	Solyc11g010440.1.1	FIP1 IPR004182 GRAM
11B	g90.t1	908628	914434	5806	0E+00	99.25	100	Solyc11g010450.1.1	Phosphofructokinase family protein IPR012004 Pyrophosphate-dependent phosphofructokinase TP0108
11B	g91.t1	922424	925749	3325	0E+00	90.35	100	Solyc11g010460.1.1	Cyclin D2 IPR015451 Cyclin D
11B	g92.t1	934167	939919	5752	0E+00	100	100	Solyc11g010470.1.1	14-3-3 protein beta_alpha IPR000308 14-3-3 protein
11B	g93.t1	943938	949730	5792	0E+00	74.4	100	Solyc11g010480.1.1	Threonine endopeptidase
11B	g94.t1	949788	961489	11701	0E+00	96.91	86	Solyc11g010490.1.1	Genomic DNA chromosome 5 P1 clone MNA5
11B	g95.t1	964456	965809	1353	0E+00	99.69	100	Solyc11g010500.1.1	Mitochondrial carrier family IPR001993 Mitochondrial substrate carrier
11B	g96.t1	971178	974022	2844	0E+00	98.41	100	Solyc11g010510.1.1	Thymidylate synthase (Fragment) IPR001498 Uncharacterised protein family UPF0029, N-terminal
11B	g96.i2	971178	974022	2844	7E-180	90.15	100	Solyc11g010510.1.1	Thymidylate synthase (Fragment) IPR001498 Uncharacterised protein family UPF0029, N-terminal
11B	g97.t1	976868	982704	5836	3E-30	86.59	53	Solyc11g010530.1.1	Unknown Protein IPR010800 Glycine rich
11B	g98.t1	984602	986619	2017	3E-33	40.61	59	Solyc11g010540.1.1	DnaJ domain containing protein expressed IPR015609 Molecular chaperone, heat shock protein, Hsp40, DnaJ
11B	g99.t1	987178	988899	1721	9E-80	47.46	66	Solyc11g010540.1.1	DnaJ domain containing protein expressed IPR015609 Molecular chaperone, heat shock protein, Hsp40, DnaJ
11B	g100.t1	994258	995817	1559	0E+00	92.78	100	Solyc11g010540.1.1	DnaJ domain containing protein expressed IPR015609 Molecular chaperone, heat shock protein, Hsp40, DnaJ
11B	g101.t1	998048	1008799	10751	0E+00	99.38	100	Solyc11g010550.1.1	GPI ethanolamine phosphate transferase IPR017850 Alkaline-phosphatase-like, core domain
11B	g102.t1	1009523	1031789	22266	0E+00	94.66	77	Solyc11g010560.1.1	Kinesin-like protein IPR001752 Kinesin, motor region
11B	g102.i2	1009523	1031789	22266	0E+00	94.66	73	Solyc11g010560.1.1	Kinesin-like protein IPR001752 Kinesin, motor region
11B	g103.t1	1055688	1057551	1863	0E+00	99.7	79	Solyc11g010580.2.1	Unknown Protein
11B	g104.t1	1057676	1061679	4003	3E-63	57.36	93	Solyc04g014370.2.1	Tyrosine phosphatase-like IPR007482 Protein-tyrosine phosphatase-like, PTPLA
11B	g104.i2	1057676	1061679	4003	1E-43	47.21	92	Solyc04g014370.2.1	Tyrosine phosphatase-like IPR007482 Protein-tyrosine phosphatase-like, PTPLA
11B	g105.i2	1066578	1072159	5581	0E+00	88.27	100	Solyc11g010600.1.1	Os01g0841200 protein (Fragment) IPR004348 Protein of unknown function DUF246, plant
11B	g105.t1	1066718	1072159	5441	0E+00	93.86	100	Solyc11g010600.1.1	Os01g0841200 protein (Fragment) IPR004348 Protein of unknown function DUF246, plant
11B	g106.t1	1072506	1080802	8296	0E+00	95.23	100	Solyc11g010610.1.1	Small conductance mechanosensitive (MscS-family) ion channel IPR006685 Mechanosensitive ion channel MscS
11B	g107.t1	1081897	1086352	4455	0E+00	90.49	96	Solyc11g010620.1.1	Unknown Protein
11B	g109.t1	1100881	1102394	1513	1E-109	99.36	85	Solyc11g010630.2.1	Unknown Protein
11B	g110.t1	1109661	1114057	4396	0E+00	98.94	100	Solyc11g010630.2.1	Unknown Protein
11B	g111.t1	1114174	1116682	2508	3E-166	98.26	100	Solyc11g010650.2.1	Unknown Protein IPR000868 Isochorismatase-like
11B	g111.i2	1114174	1116682	2508	2E-159	95.59	90	Solyc11g010650.2.1	Unknown Protein IPR000868 Isochorismatase-like

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
11D	g1.t1	1	7047	7046	0.0	98.6	61	Solyc11g065750.1.1	Armadillo repeat-containing protein IPR011989	Armadillo-like helical
11D	g1.t2	788	7047	6259	0.0	98.35	69	Solyc11g065750.1.1	Armadillo repeat-containing protein IPR011989	Armadillo-like helical
11D	g2.t1	7576	15357	7781	0.0	97.08	94	Solyc11g065750.1.1	Armadillo repeat-containing protein IPR011989	Armadillo-like helical
11D	g3.t1	17370	18257	887	6E-95	81.64	100	Solyc00g084760.1.1	RNase H family protein	
11D	g4.t1	18711	24137	5426	5E-155	99.53	52	Solyc11g065760.1.1	Thymidine kinase IPR001267	Thymidine kinase
11D	g5.t1	31676	46438	14762	0.0	94.41	43	Solyc11g065770.1.1	Cytochrome P450	
11D	g6.t1	46766	48474	1708	5E-109	51.36	99	Solyc11g071430.1.1	Cc-nbs-lrr, resistance protein	
11D	g7.t1	48729	50907	2178	2E-136	97.04	99	Solyc11g065820.1.1	Mate efflux family protein IPR002528	Multi antimicrobial extrusion protein MatE
11D	g8.t1	50993	61767	10774	0.0	99.46	68	Solyc11g065830.1.1	2-oxoglutarate_malate translocator-like protein IPR001898	Sodium_sulphate symporter
11D	g9.t1	78845	82327	3482	0.0	98.59	100	Solyc11g065840.1.1	MYB transcription factor IPR015495	Myb transcription factor
11D	g10.t1	97446	114486	17040	0.0	90.91	70	Solyc11g065870.1.1	GTP-binding protein engA IPR016484	GTP-binding, EngA
11D	g11.t1	115689	116797	1108	9E-37	96.77	87	Solyc11g065880.1.1	Polyadenylate-binding protein 4 IPR012677	Nucleotide-binding, alpha-beta plait
11D	g12.t1	117035	122497	5462	0.0	100	92	Solyc11g065880.1.1	Polyadenylate-binding protein 4 IPR012677	Nucleotide-binding, alpha-beta plait
11D	g12.t2	117035	122497	5462	0.0	99.72	92	Solyc11g065880.1.1	Polyadenylate-binding protein 4 IPR012677	Nucleotide-binding, alpha-beta plait
11D	g14.t1	125827	126697	870	6E-61	91.75	87	Solyc01g111490.1.1	Unknown Protein IPR010666	Zinc finger, GRF-type
11D	g15.t2	131626	143868	12242	0.0	84.97	100	Solyc11g065890.1.1	1-acyl-sn-glycerol-3-phosphate acyltransferase IPR002123	Phospholipid_glycerol acyltransferase
11D	g15.t3	131626	153381	21755	0.0	82.61	59	Solyc11g065890.1.1	1-acyl-sn-glycerol-3-phosphate acyltransferase IPR002123	Phospholipid_glycerol acyltransferase
11D	g15.t1	148136	153381	5245	4E-165	100	100	Solyc11g065900.1.1	DNA replication complex GINS protein SLD5 IPR008591	GINS complex, Sld5 component
11D	g16.t1	153729	155257	1528	1E-46	80.75	52	Solyc11g065910.1.1	Unknown Protein IPR006706	Extensin-like region
11D	g17.t1	155852	170247	14395	0.0	96.57	100	Solyc11g065920.1.1	Xanthine dehydrogenase_oxidase IPR016208	Aldehyde oxidase_xanthine dehydrogenase
11D	g18.t1	175823	187894	12071	0.0	96.61	98	Solyc11g065930.1.1	Xanthine dehydrogenase_oxidase IPR016208	Aldehyde oxidase_xanthine dehydrogenase

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.Jycopersicum (Heinz)		
11H	g1.t1	1	2587	2586	0E+00	91.75	100	Solyc11g072220.1.1	Sentrin specific protease 1b IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1	
11H	g1.t2	1	2587	2586	0E+00	94.48	100	Solyc11g072220.1.1	Sentrin specific protease 1b IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1	
11H	g2.t1	2724	4427	1703	0E+00	98.78	99	Solyc11g072230.1.1	Glucan endo-1 3-beta-glucosidase 3 IPR013781 Glycoside hydrolase, subgroup, catalytic core	
11H	g3.t1	7061	10537	3476	1E-104	100	79	Solyc12g099990.1.1	Calmodulin 2 IPR011992 EF-Hand type	
11H	g4.t1	11750	17507	5757	0E+00	86.91	100	Solyc11g072250.1.1	Unknown Protein	
11H	g5.t1	21890	24387	2497	1E-98	100	100	Solyc11g072260.1.1	40S ribosomal protein S13 IPR000589 Ribosomal protein S15	
11H	g6.t1	26926	27767	841	1E-103	99.32	100	Solyc11g072270.1.1	Calmodulin IPR011992 EF-Hand type	
11H	g7.t2	28744	33767	5023	0E+00	98.5	98	Solyc11g072280.1.1	Microtubule-associated protein MAP65-1a IPR007145 MAP65_ASE1	
11H	g7.t1	29084	33767	4683	0E+00	98.5	100	Solyc11g072280.1.1	Microtubule-associated protein MAP65-1a IPR007145 MAP65_ASE1	
11H	g8.t1	36034	39117	3083	3E-117	96.99	88	Solyc11g072290.1.1	Cysteine and histidine-rich domain-containing protein 1 IPR007051 CHORD	
11H	g9.t1	41171	52477	11306	5E-175	85.52	100	Solyc11g072300.1.1	Os10g0188400 protein (Fragment)	
11H	g9.t2	41171	52477	11306	2E-172	81.15	100	Solyc11g072300.1.1	Os10g0188400 protein (Fragment)	
11H	g10.t1	62046	103464	41418	0E+00	98.11	29	Solyc11g072320.1.1	Something about silencing protein 10, C-terminal	
11H	g10.t2	70006	103600	33594	0E+00	98.16	34	Solyc11g072320.1.1	Something about silencing protein 10, C-terminal	
11H	g11.t1	104303	107947	3644	0E+00	97.65	100	Solyc11g072380.1.1	Vicilin-like protein (Fragment) IPR011051 Cupin, RmlC-type	
11H	g12.t1	108486	116719	8233	0E+00	93.99	98	Solyc11g072390.1.1	Something about silencing protein 10, C-terminal	
11H	g12.t2	108486	118124	9638	0E+00	90.61	78	Solyc11g072390.1.1	Something about silencing protein 10, C-terminal	
11H	g13.t1	120076	121978	1902	2E-120	96.67	67	Solyc11g072390.1.1	Something about silencing protein 10, C-terminal	
11H	g14.t1	122966	132021	9055	0E+00	97.28	59	Solyc11g072400.1.1	Defects in morphology protein 1 homolog IPR019190 Defects in morphology protein 1-like	
11H	g14.t2	122966	132021	9055	0E+00	97.28	58	Solyc11g072400.1.1	Defects in morphology protein 1 homolog IPR019190 Defects in morphology protein 1-like	
11H	g15.t1	132387	162547	30160	0E+00	91.89	62	Solyc11g072420.1.1	RNA ligase isoform 2 (Fragment)	
11H	g15.t2	132438	142777	10339	0E+00	98.86	100	Solyc11g072420.1.1	RNA ligase isoform 2 (Fragment)	
11H	g16.t1	163869	167877	4008	0E+00	97.06	100	Solyc11g072440.1.1	Hydrolase alpha_beta fold family protein IPR000073 Alpha_beta hydrolase fold-1	
11H	g17.t1	171704	180579	8875	8E-121	100	100	Solyc11g072450.1.1	Mitochondrial F0 ATP synthase D chain IPR008689 ATPase, F0 complex, subunit D, mitochondrial	
11H	g18.t1	183348	195601	12253	0E+00	93.85	72	Solyc11g072460.1.1	Nedd8 activating enzyme E1 subunit 1 IPR009036 Molybdenum cofactor biosynthesis, MoeB	
11H	g19.t1	202463	204799	2336	2E-134	97.88	100	Solyc11g072470.1.1	LOB domain protein 1 IPR004883 Lateral organ boundaries, LOB	
11H	g20.t1	220079	222449	2370	2E-143	66.67	87	Solyc11g071430.1.1	Cc-nbs-lrr, resistance protein	
11H	g21.t1	223233	230329	7096	7E-158	98.6	100	Solyc11g072480.1.1	Senescence-associated protein IPR000301 Tetraspanin, subgroup	
11H	g22.t1	234788	239156	4368	0E+00	98.74	99	Solyc11g072490.1.1	Interactor of constitutive active ROPs 3	
11H	g23.t1	249828	252012	2184	3E-161	89.53	100	Solyc11g072500.1.1	Dof zinc finger protein 12 IPR003851 Zinc finger, Dof-type	
11H	g24.t1	255848	259978	4130	0E+00	99.69	100	Solyc11g072510.1.1	Cinnamoyl-CoA reductase-binding domain	
11H	g25.t1	260638	268043	7405	0E+00	81.46	96	Solyc11g072520.1.1	Prephenate dehydratase IPR001086 Prephenate dehydratase	
11H	g26.t1	268248	280908	12660	0E+00	97.7	100	Solyc11g072530.1.1	V-type proton ATPase subunit a IPR002490 ATPase, V0_A0 complex, 116-kDa subunit	
11H	g26.t2	268248	280908	12660	0E+00	92.66	97	Solyc11g072530.1.1	V-type proton ATPase subunit a IPR002490 ATPase, V0_A0 complex, 116-kDa subunit	
11H	g27.t1	281578	291437	9859	0E+00	99.35	68	Solyc11g072540.1.1	DDB1- and CUL4-associated factor 8-like protein 1 IPR017986 WD40 repeat, region	
11H	g28.t1	291444	294219	2775	0E+00	98.25	87	Solyc11g072560.1.1	Solute carrier family 15 member 4 IPR000109 TGF-beta receptor, type I_II extracellular region	
11H	g29.t1	296206	299129	2923	0E+00	97.5	100	Solyc11g072570.1.1	Proton-dependent oligopeptide transport family protein IPR000109 TGF-beta receptor, type I_II extracellular region	
11H	g29.t2	296206	301659	5453	0E+00	97.71	100	Solyc11g072570.1.1	Proton-dependent oligopeptide transport family protein IPR000109 TGF-beta receptor, type I_II extracellular region	
11H	g30.t1	302449	305809	3360	0E+00	96.99	100	Solyc11g072580.1.1	Proton-dependent oligopeptide transport family protein IPR000109 TGF-beta receptor, type I_II extracellular region	
11H	g31.t1	306758	322101	15343	0E+00	97.21	99	Solyc11g072590.1.1	CCR4-NOT transcription complex subunit 4 IPR003954 RNA recognition, region 1	
11H	g32.t1	327790	331029	3239	0E+00	94.01	100	Solyc11g072600.1.1	AP2-like ethylene-responsive transcription factor At1g79700 IPR001471 Pathogenesis-related transcriptional factor and ERF, DNA-binding	
11H	g32.t2	327790	331029	3239	0E+00	96.91	100	Solyc11g072600.1.1	AP2-like ethylene-responsive transcription factor At1g79700 IPR001471 Pathogenesis-related transcriptional factor and ERF, DNA-binding	
11H	g33.t1	383128	392875	9747	0E+00	93.02	67	Solyc11g072610.1.1	DNA recombination and repair protein IPR016467 DNA repair and recombination, RecA-like	
11H	g34.t1	399514	399956	442	4E-47	96.1	100	Solyc11g072620.1.1	Unknown Protein	
11H	g35.t1	429554	434044	4490	0E+00	100	100	Solyc11g072630.1.1	Mitogen-activated protein kinase IPR008351 JNK MAP kinase	

BIN	Augustus ID	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			SD3 Table Orthologous pairs		Functional Description
					e-value	% id	% qcoverage	S.lycopersicum (Heinz)		
11H	g36.t1	439512	444585	5073	0E+00	96.3	100	Solyc11g072640.1.1	Mitochondrial trans-2-enoyl-CoA reductase	IPR002085 Alcohol dehydrogenase superfamily, zinc-containing
11H	g37.t1	446708	450055	3347	0E+00	97.68	100	Solyc11g072650.1.1	Trans-2-enoyl CoA reductase	IPR002085 Alcohol dehydrogenase superfamily, zinc-containing
11H	g38.t1	457434	462001	4567	0E+00	93.7	100	Solyc11g072660.1.1	Receptor protein kinase-like protein	IPR002290 Serine_threonine protein kinase
11H	g38.t2	457434	463862	6428	0E+00	93.56	72	Solyc11g072660.1.1	Receptor protein kinase-like protein	IPR002290 Serine_threonine protein kinase
11H	g39.t1	464974	472025	7051	0E+00	95.62	59	Solyc11g072680.1.1	Fasciclin-like arabinogalactan protein 21	IPR000782 FAS1 domain
11H	g39.t2	464974	472778	7804	0E+00	95.62	57	Solyc11g072680.1.1	Fasciclin-like arabinogalactan protein 21	IPR000782 FAS1 domain
11H	g40.t1	473570	476535	2965	0E+00	98.82	100	Solyc11g072700.1.1	Glycosyltransferase-like protein	IPR006740 Protein of unknown function DUF604
11H	g41.t1	479484	497046	17562	0E+00	99.08	65	Solyc11g072710.1.1	Protein kinase	IPR002290 Serine_threonine protein kinase
11H	g42.t2	499693	529995	30302	0E+00	93.28	100	Solyc11g072730.1.1	DNA-directed RNA polymerase	IPR015700 DNA-directed RNA polymerase III largest subunit
11H	g42.t1	500924	506835	5911	0E+00	99.64	90	Solyc11g072730.1.1	DNA-directed RNA polymerase	IPR015700 DNA-directed RNA polymerase III largest subunit
11H	g42.t3	508742	530005	21263	0E+00	82.26	95	Solyc11g072730.1.1	DNA-directed RNA polymerase	IPR015700 DNA-directed RNA polymerase III largest subunit
11H	g43.t1	531744	532708	964	9E-122	93.09	100	Solyc11g072740.1.1	Unknown Protein	
11H	g44.t1	534869	536685	1816	0E+00	99.35	100	Solyc11g072750.1.1	Chitinase a	IPR001223 Glycoside hydrolase, family 18, catalytic domain
11H	g45.t1	536950	538285	1335	0E+00	98.37	100	Solyc11g072760.1.1	Chitinase a	IPR001223 Glycoside hydrolase, family 18, catalytic domain
11H	g46.t1	539444	540399	955	1E-11	35.9	64	Solyc01g104020.2.1	Embryo-specific 3	IPR010417 Embryo-specific 3
11H	g48.t1	549864	551548	1684	1E-84	94.53	100	Solyc11g072770.1.1	WUSCHEL-related homeobox 3B	IPR001356 Homeobox
11H	g49.t1	566144	567649	1505	6E-152	98.09	100	Solyc11g072790.1.1	WUSCHEL-related homeobox 3B	IPR001356 Homeobox
11H	g50.t1	572117	576695	4578	0E+00	93.09	97	Solyc11g072800.1.1	NADPH oxidase	IPR013121 Ferric reductase, NAD binding
11H	g51.t1	580344	584911	4567	0E+00	96.4	100	Solyc11g072810.1.1	Nuclear factor related to kappa-B-binding protein related	
11H	g52.t1	585663	592495	6832	0E+00	99.05	100	Solyc11g072820.1.1	Kinesin-5	IPR001752 Kinesin, motor region
11H	g53.t1	598374	599890	1516	0E+00	99.67	100	Solyc11g072830.1.1	Chitinase 2	IPR001223 Glycoside hydrolase, family 18, catalytic domain
11H	g54.t1	600683	602245	1562	5E-67	100	100	Solyc11g072860.1.1	Histone H4	IPR001951 Histone H4
11H	g55.t1	614444	615130	686	5E-67	100	100	Solyc11g072860.1.1	Histone H4	IPR001951 Histone H4
11H	g56.t2	615867	618575	2708	1E-69	96.43	38	Solyc11g072870.1.1	S-adenosyl-L-methionine salicylic acid carboxyl methyltransferase	IPR005299 SAM dependent carboxyl methyltransferase
11H	g56.t1	615931	618575	2644	7E-87	40.28	96	Solyc01g005360.2.1	S-adenosyl-L-methionine salicylic acid carboxyl methyltransferase	IPR005299 SAM dependent carboxyl methyltransferase
11H	g57.t1	620540	627305	6765	0E+00	98.49	100	Solyc11g072880.1.1	Calcium-transporting ATPase	IPR005782 ATPase, P-type, calcium-transporting
11H	g58.t1	636104	637073	969	3E-103	94.94	100	Solyc11g072890.1.1	Unknown Protein	
11H	g59.t1	642837	648975	6138	0E+00	98.68	81	Solyc11g072910.1.1	Pto-like, Serine_threonine kinase protein, resistance protein	
11H	g60.t1	650761	654455	3694	0E+00	98.07	97	Solyc11g072920.1.1	Peroxidase 5	IPR002016 Haem peroxidase, plant_fungal_bacterial
11H	g61.t1	655574	669066	13492	0E+00	91.76	58	Solyc11g072940.1.1	CCR4-NOT transcription complex subunit 2	IPR007282 NOT2_NOT3_NOT5
11H	g61.t2	655574	669053	13479	0E+00	89.71	58	Solyc11g072940.1.1	CCR4-NOT transcription complex subunit 2	IPR007282 NOT2_NOT3_NOT5
11H	g62.t1	669309	676475	7166	0E+00	98.9	100	Solyc11g072950.1.1	E3 UFM1-protein ligase 1 homolog	IPR018611 Protein of unknown function DUF2042
11H	g62.t2	669309	676475	7166	0E+00	95.96	100	Solyc11g072950.1.1	E3 UFM1-protein ligase 1 homolog	IPR018611 Protein of unknown function DUF2042
11H	g63.t1	677032	680045	3013	0E+00	99.62	100	Solyc11g072960.1.1	Ankyrin repeat family protein	IPR002110 Ankyrin
11H	g64.t1	681234	687845	6611	0E+00	91.61	100	Solyc11g072970.1.1	Nucleoside diphosphate-linked moiety X motif 22	IPR000086 NUDIX hydrolase domain
11H	g64.t2	681234	687845	6611	0E+00	85.71	100	Solyc11g072970.1.1	Nucleoside diphosphate-linked moiety X motif 22	IPR000086 NUDIX hydrolase domain
11H	g66.t1	703253	704835	1582	0E+00	98.8	100	Solyc11g072980.1.1	3-ketoacyl-CoA synthase 6	IPR012392 Very-long-chain 3-ketoacyl-CoA synthase
11H	g67.t1	707630	709985	2355	0E+00	100	100	Solyc11g072990.1.1	Fatty acid elongase 3-ketoacyl-CoA synthase	IPR012392 Very-long-chain 3-ketoacyl-CoA synthase
11H	g68.t1	730642	732847	2205	0E+00	97.48	100	Solyc11g073010.1.1	Exocyst complex protein EXO70	IPR004140 Exo70 exocyst complex subunit
11H	g69.t1	741768	746837	5069	1E-166	90.7	100	Solyc11g073020.1.1	Metal ion binding protein	IPR006121 Heavy metal transport_detoxification protein
11H	q70.t1	750750	751657	907	3E-118	81.06	94	Solyc06g075630.2.1	Dirigent-like protein	IPR004265 Plant disease resistance response protein

Genes informations and functional description are those assigned in Sol Genomics Network. M82: *Solanum lycopersicum* and Spenn: *Solanum pennellii*
Coordinates are given according the genome versions 1.0 and 2.0 for M82 and Spenn, respectively.

Supplemental Table S4. MAPMAN contingency table Fisher test

MAPMAN CONTINGENCY TABLE FISHER TEST (M82)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
1J	29	protein	91	1E-24
1J	27	RNA	56	6E-08
1J	34	transport	46	4E-18
1J	17	hormone metabolism	39	3E-16
1J	35	not assigned	22	2E-03
1J	20	stress	17	2E-02
1J	33	development	13	3E-02
1J	10	cell wall	12	3E-03
1J	13	amino acid metabolism	10	7E-04
1J	3	minor CHO metabolism	6	2E-03
1J	23	nucleotide metabolism	4	3E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (<i>S.penn</i>)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
1J	29	protein	96	6E-27
1J	27	RNA	58	3E-08
1J	34	transport	49	7E-20
1J	17	hormone metabolism	43	7E-19
1J	26	misc	22	4E-02
1J	35	not assigned	20	2E-04
1J	20	stress	18	1E-02
1J	10	cell wall	11	2E-02
1J	13	amino acid metabolism	10	9E-04
1J	3	minor CHO metabolism	6	2E-03
1J	23	nucleotide metabolism	5	7E-03
1J	22	polyamine metabolism	2	1E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (M82)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
2K	29	protein	33	5E-03
2K	27	RNA	30	8E-03
2K	30	signalling	20	6E-05
2K	26	misc	17	2E-02
2K	34	transport	14	1E-02
2K	33	development	12	3E-03
2K	17	hormone metabolism	12	1E-02
2K	13	amino acid metabolism	10	3E-05
2K	10	cell wall	7	5E-02
2K	9	mitochondrial electron transport / ATP synthesis	5	3E-03
2K	14	S-assimilation	2	7E-04
2K	5	fermentation	2	1E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (<i>S.penn</i>)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
2K	29	protein	36	4E-03
2K	27	RNA	33	4E-03
2K	30	signalling	20	2E-04
2K	26	misc	17	3E-02
2K	17	hormone metabolism	15	1E-03
2K	34	transport	15	1E-02
2K	33	development	11	2E-02
2K	13	amino acid metabolism	10	7E-05
2K	9	mitochondrial electron transport / ATP synthesis	5	4E-03
2K	3	minor CHO metabolism	4	1E-02
2K	14	S-assimilation	2	8E-04
2K	5	fermentation	2	1E-02

MAPMAN CONTINGENCY TABLE FISHER TEST (M82)

BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
2L	29	protein	38	1E-05
2L	27	RNA	30	1E-03
2L	30	signalling	15	4E-03
2L	31	cell	13	1E-04
2L	16	secondary metabolism	10	2E-03
2L	28	DNA	9	4E-02
2L	23	nucleotide metabolism	4	6E-03
2L	2	major CHO metabolism	4	2E-02
2L	24	biodegradation of xenobiotics	2	1E-02
2L	12	N-metabolism	2	4E-02

MAPMAN CONTINGENCY TABLE FISHER TEST (S.penn)

BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
2L	29	protein	40	5E-06
2L	27	RNA	31	1E-03
2L	26	misc	16	2E-02
2L	30	signalling	15	6E-03
2L	31	cell	12	6E-04
2L	28	DNA	9	5E-02
2L	16	secondary metabolism	8	2E-02
2L	23	nucleotide metabolism	4	7E-03
2L	2	major CHO metabolism	4	3E-02
2L	12	N-metabolism	2	4E-02

MAPMAN CONTINGENCY TABLE FISHER TEST (M82)

BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
4DE	35	not assigned	416	9E-43
4DE	29	protein	317	1E-29
4DE	12	N-metabolism	27	6E-19
4DE	28	DNA	90	5E-13
4DE	31	cell	80	9E-12
4DE	26	misc	129	3E-08
4DE	17	hormone metabolism	80	2E-06
4DE	20	stress	89	2E-06
4DE	27	RNA	205	9E-06
4DE	16	secondary metabolism	52	1E-04
4DE	3	minor CHO metabolism	18	4E-04
4DE	1	PS	7	2E-03
4DE	4	glycolysis	10	9E-03
4DE	34	transport	75	2E-02
4DE	25	C1-metabolism	4	3E-02
4DE	7	OPP	5	4E-02
4DE	30	signalling	78	5E-02

MAPMAN CONTINGENCY TABLE FISHER TEST (S.penn)

BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
4DE	29	protein	392	4E-46
4DE	12	N-metabolism	49	1E-44
4DE	35	not assigned	458	2E-43
4DE	28	DNA	126	2E-25
4DE	31	cell	101	1E-17
4DE	26	misc	163	4E-14
4DE	17	hormone metabolism	110	2E-13
4DE	27	RNA	266	3E-13
4DE	20	stress	121	4E-13
4DE	3	minor CHO metabolism	24	3E-06
4DE	16	secondary metabolism	61	1E-05
4DE	4	glycolysis	13	9E-04
4DE	34	transport	88	4E-03
4DE	1	PS	10	6E-03
4DE	7	OPP	6	2E-02
4DE	25	C1-metabolism	4	5E-02

MAPMAN CONTINGENCY TABLE FISHER TEST (M82)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
7BC	29	protein	92	5E-16
7BC	34	transport	41	1E-10
7BC	26	misc	38	1E-05
7BC	27	RNA	60	3E-05
7BC	3	minor CHO metabolism	9	5E-05
7BC	30	signalling	26	4E-03
7BC	20	stress	23	5E-03
7BC	33	development	17	2E-02
7BC	2	major CHO metabolism	6	3E-02
7BC	11	lipid metabolism	10	4E-02
7BC	19	tetrapyrrole synthesis	4	4E-02
7BC	1	PS	9	5E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (S.penn)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
7BC	29	protein	87	9E-14
7BC	34	transport	43	8E-12
7BC	27	RNA	61	1E-05
7BC	26	misc	36	7E-05
7BC	3	minor CHO metabolism	8	3E-04
7BC	19	tetrapyrrole synthesis	6	2E-03
7BC	30	signalling	26	4E-03
7BC	33	development	17	2E-02
7BC	20	stress	20	3E-02
7BC	16	secondary metabolism	13	3E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (M82)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
9C	27	RNA	20	2E-03
9C	4	glycolysis	3	3E-03
9C	18	Co-factor and vitamine metabolism	3	3E-03
9C	11	lipid metabolism	5	1E-02
9C	26	misc	11	2E-02
9C	17	hormone metabolism	7	3E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (S.penn)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
9C	27	RNA	21	9E-04
9C	4	glycolysis	3	3E-03
9C	17	hormone metabolism	8	1E-02
9C	11	lipid metabolism	5	1E-02
9C	18	Co-factor and vitamine metabolism	2	3E-02
9C	26	misc	10	4E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (M82)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
9D	29	protein	15	1E-02
9D	15	metal handling	2	1E-02
9D	21	redox	3	2E-02
9D	27	RNA	13	3E-02
9D	13	amino acid metabolism	3	4E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (S.penn)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
9D	8	TCA / organic transformation	2	1E-02
9D	15	metal handling	2	1E-02
9D	27	RNA	14	2E-02
9D	29	protein	15	2E-02
9D	21	redox	3	2E-02
9D	13	amino acid metabolism	3	5E-02

MAPMAN CONTINGENCY TABLE FISHER TEST (M82)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
9G	29	protein	25	5E-05
9G	30	signalling	11	2E-03
9G	34	transport	10	4E-03
9G	26	misc	12	4E-03
9G	2	major CHO metabolism	3	3E-02
9G	21	redox	3	4E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (S.penn)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
9G	29	protein	28	2E-06
9G	34	transport	11	1E-03
9G	30	signalling	11	3E-03
9G	2	major CHO metabolism	4	4E-03
9G	26	misc	12	5E-03
9G	27	RNA	18	2E-02
9G	20	stress	8	2E-02
9G	21	redox	3	5E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (M82)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
11B	27	RNA	31	4E-06
11B	34	transport	15	1E-04
11B	29	protein	29	3E-04
11B	26	misc	16	1E-03
11B	33	development	9	9E-03
11B	28	DNA	8	2E-02
11B	11	lipid metabolism	5	4E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (S.penn)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
11B	27	RNA	31	2E-05
11B	34	transport	17	2E-05
11B	29	protein	30	3E-04
11B	26	misc	17	7E-04
11B	13	amino acid metabolism	5	2E-02
11B	28	DNA	8	3E-02
11B	33	development	8	3E-02
11B	35	not assigned	12	5E-02
11B	11	lipid metabolism	5	5E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (M82)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
11D	23	nucleotide metabolism	3	1E-04
11D	15	metal handling	2	1E-03
MAPMAN CONTINGENCY TABLE FISHER TEST (S.penn)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
11D	23	nucleotide metabolism	3	1E-04
11D	27	RNA	6	2E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (M82)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
11H	27	RNA	20	1E-04
11H	31	cell	7	3E-03
11H	1	PS	5	5E-03
11H	29	protein	18	7E-03
11H	11	lipid metabolism	5	7E-03
11H	34	transport	8	1E-02
11H	30	signalling	8	2E-02
MAPMAN CONTINGENCY TABLE FISHER TEST (S.penn)				
BIN	BIN CODE	BIN NAME	COUNT	P-VALUE <0.05
11H	27	RNA	21	2E-04
11H	29	protein	18	2E-02
11H	31	cell	10	4E-05
11H	34	transport	9	7E-03
11H	30	signalling	8	3E-02
11H	1	PS	5	6E-03
11H	11	lipid metabolism	5	1E-02
11H	15	metal handling	2	2E-02

Supplemental Table 5. Summary of the genomic regions retrieved by the corresponding markers and analyzed in this work.

BIN	MARKER ⁽¹⁾		pseudomolecule	Species ⁽²⁾	COORDINATES (nt) ⁽³⁾		BIN LENGTH (bp)
	NORTH	SOUTH			NORTH	SOUTH	
1J	SGN-M339	SGN-M179	ch01	M82	88,405,992	90,012,404	1,606,412
				Spenn	107,469,899	109,091,436	1,621,537
2K	SGN-M122	SGN-M46	ch02	M82	46,972,754	48,343,617	1,370,863
				Spenn	56,708,671	58,184,832	1,476,161
2L	SGN-M46	SGN-M100	ch02	M82	48,343,094	49,466,629	1,123,535
				Spenn	58,184,286	59,337,992	1,153,706
4DE	SGN-M169	SGN-M399	ch04	M82	4,835,317	54,473,808	49,638,491
				Spenn	5,052,493	67,132,547	62,080,054
7BC	SGN-M604	SGN-M85	ch07	M82	243,493	3,597,081	3,353,588
				Spenn	474,483	4,036,295	3,561,812
9C	SGN-M82	SGN-M89	ch09	M82	1,908,874	2,780,571	871,697
				Spenn	1,959,093	2,914,799	955,706
9D	SGN-M89	SGN-M8002	ch09	M82	2,779,816	3,442,909	663,093
				Spenn	2,914,068	3,554,228	640,16
9G	SGN-M310	SGN-M193	ch09	M82	60,595,984	61,658,753	1,062,769
				Spenn	76,506,918	77,571,165	1,064,247
11B	SGN-M582	SGN-M121	ch11	M82	2,651,274	3,708,436	1,057,162
				Spenn	2,718,613	3,836,493	1,117,880
11D	SGN-M125	SGN-M565	ch11	M82	48,434,778	48,609,237	174,459
				Spenn	61,071,210	61,271,448	200,238
11H	SGN-M34	SGN-M151	ch11	M82	52,536,512	53,256,293	719,781
				Spenn	65,305,916	66,065,401	759,485

(1) Marker codes are those assigned in Sol Genomics Network

(2) M82: *Solanum lycopersicum* and Spenn: *Solanum pennellii*

(3) Coordinates are given according the genome versions 1.0 and 2.0 for M82 and Spenn, respectively.

Supplemental Table S6. List of candidate genes and TEs information.

										<i>S. pennellii</i>	
Trait	BIN	# Gene	Sense	Gene Start	Gene End	Gene Size	ITAG2.4 proteins blastp			ITAG2.4 Orthologous for <i>S.lycopersicum</i> (Heinz)	Functional Description
							e-value	% id	% qcoverage		
Root DW	1J	g1	-	4987	1	4987	0	98.25	100	Solyc01g109790.2.1	Glucose-1-phosphate adenyltransferase IPR011831 Glucose-1-phosphate adenyltransferase IPR005836 ADP-glucose pyrophosphorylase, conserved s
Root DW	1J	g15	-	141647	136374	5273	0	99.44	100	Solyc01g109940.2.1	26S protease regulatory subunit IPR005937 26S proteasome subunit P45
Root DW	1J	g52	+	463032	466619	3587	0	94.36	78	Solyc01g110360.2.1	Fructose-bisphosphate aldolase IPR000741 Fructose-bisphosphate aldolase, class-I
Root DW	1J	g70-g110 (33)	both	591837	794819	NA	NA	NA	NA	NA	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein
Root DW	1J	g115	-	837396	836288	1108	9E-69	97.12	100	Solyc01g111080.2.1	Gibberellin-regulated protein 2 IPR003854 Gibberellin regulated protein
Root DW	1J	g117	-	856706	849234	7472	0	100	100	Solyc01g111100.2.1	Neutral invertase like protein IPR006937 Plant neutral invertase
Root DW	1J	g118	-	868346	862136	6210	0	97.55	100	Solyc01g111120.2.1	Triosephosphate isomerase IPR000652 Triosephosphate isomerase
Root DW	1J	g133	-	965224	961760	3464	2E-176	98.39	62	Solyc01g111310.2.1	Transmembrane amino acid transporter protein IPR013057 Amino acid transporter, transmembrane
Root DW	1J	g147	-	1094951	1094021	930	0	99.21	100	Solyc01g111500.2.1	MYB transcription factor IPR015495 Myb transcription factor
Root DW	1J	g159	+	1210630	1214824	4194	0	93.52	100	Solyc01g111630.2.1	Glyoxylate_hydroxypyruvate reductase B IPR006140 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
Root DW	1J	g186	-	1416571	1411885	4686	0	99.79	100	Solyc01g111890.2.1	F-box_LRR-repeat protein 14 IPR001810 Cyclin-like F-box
Root DW	1J	g187	-	1420611	1418226	2385	2E-107	98.16	84	Solyc01g111890.2.1	F-box_LRR-repeat protein 14 IPR001810 Cyclin-like F-box
Root DW	1J	g192	-	1455167	1451489	3678	0	99.13	100	Solyc01g111930.2.1	Rop guanine nucleotide exchange factor 1 IPR005512 Rop nucleotide exchanger, PRONE
A	2K	g20	+	166606	169948	3342	0	98.73	100	Solyc02g091130.2.1	ATP synthase subunit beta IPR005722 ATPase, F1 complex, beta subunit
A	2K	g32	-	247026	245763	1263	3E-81	98.29	100	Solyc02g091280.2.1 (broken)	ATP-dependent Clp protease proteolytic subunit IPR001907 Peptidase S14, ClpP
A	2K	g33	-	250276	247706	2570	1E-136	98.94	83	Solyc02g091280.2.1 (broken)	ATP-dependent Clp protease proteolytic subunit IPR001907 Peptidase S14, ClpP
A	2K	g44	-	335826	309968	25858	0	96.01	100	Solyc02g091410.2.1	Pro-apoptotic serine protease nma111-like protein IPR009003 Peptidase, trypsin-like serine and cysteine
A	2K	g57	+	449713	468891	19178	0	99.42	68	Solyc02g091560.2.1	Serine hydroxymethyltransferase IPR001085 Serine hydroxymethyltransferase
A	2K	g120	-	1097160	1092324	4836	2E-50	98.68	49	Solyc02g092270.2.1	NADH dehydrogenase IPR006885 ETC complex I subunit conserved region
A	2K	g156	-	1428817	1425548	3269	5E-160	96.79	78	Solyc02g093680.2.1	Succinate dehydrogenase iron-sulfur protein IPR004489 Succinate dehydrogenase_fumarate reductase iron-sulphur protein
Root DW	2L	g14	-	123827	122519	1308	0	96.96	97	Solyc02g092930.1.1	MYB transcription factor IPR015495 Myb transcription factor
Root DW	2L	g87	-	739174	737819	1355	0	99.2	100	Solyc02g093740.2.1 (broken)	MYB transcription factor IPR015495 Myb transcription factor
Root DW	2L	g88	-	744054	741709	2345	2E-28	34.95	51	Solyc04g025900.1.1 (broken)	Unknown Protein
Root DW	2L	g131	-	1117807	1115152	2655	5E-85	99.15	99	Solyc02g094270.1.1	WRKY transcription factor IPR003657 DNA-binding WRKY
Root DW	2L	g133	+	1132646	1134725	2079	4E-62	93	46	Solyc02g094290.1.1	TCP family transcription factor IPR005333 Transcription factor, TCP
Root DW	4DE	g6	+	79866	83155	3289	0	99.6	100	Solyc04g014670.2.1	Short-chain dehydrogenase_reductase SDR IPR002347 Glucose_ribitol dehydrogenase
Root DW	4DE	g11	-	153337	147990	5347	2E-179	99.18	100	Solyc04g014760.2.1	RHO protein GDP dissociation inhibitor IPR000406 RHO protein GDP dissociation inhibitor
Root DW	4DE	g51	-	497118	493526	3592	0	98.9	100	Solyc04g015200.2.1	6-phosphofructokinase 2 IPR012004 Pyrophosphate-dependent phosphofructokinase TP0108
Root DW	4DE	g1274	-	16301657	16294385	7272	6E-82	94.78	42	Solyc04g005560.2.1	Guanine nucleotide exchange factor-like protein contains Interpro domain IPR000904
Root DW	4DE	g1494	-	18720532	18714916	5616	8E-91	86.45	70	Solyc04g025740.1.1	Homeobox-leucine zipper protein ROC3 IPR001356 Homeobox
Root DW	4DE	g3433	-	46622238	46613974	8264	0	99.63	100	Solyc04g049690.2.1	Adenylate kinase IPR006259 Adenylate kinase, subfamily
Root DW	4DE	g3813	-	51639317	51635779	3538	0	99.42	100	Solyc04g050440.2.1	Ammonium transporter IPR001905 Ammonium transporter
Root DW	4DE	g4104	-	55343936	55339150	4786	0	94.46	100	Solyc04g051080.1.1	Response regulator 8 IPR006447 Myb-like DNA-binding region, SHAQKYF class
Root DW	4DE	g4110	-	55385146	55378684	6462	5E-107	77.61	81	Solyc04g051080.1.1	Response regulator 8 IPR006447 Myb-like DNA-binding region, SHAQKYF class
Root DW	4DE	g4584	-	61316810	61313622	3188	7E-134	86.34	100	Solyc04g056620.1.1	Auxin Efflux Carrier IPR004776 Auxin efflux carrier
Root DW	78C	g31	-	331049	327394	3655	0	96.67	100	Solyc07g005760.2.1	Hydroxycinnamoyl CoA shikimate_quinate hydroxycinnamoyltransferase IPR003480 Transferase
Root DW	78C	g74	+	853978	856980	3002	0	99.62	100	Solyc07g006280.2.1	Senescence-associated protein IPR000301 Tetraspanin, subgroup
Root DW	78C	g80	-	955624	945613	10011	0	99.4	99	Solyc07g006350.2.1	Ankyrin repeat-rich protein IPR002110 Ankyrin
Root DW	78C	g95	+	1091843	1095049	3206	0	99.2	100	Solyc07g006500.2.1	Alpha alpha-trehalose-phosphate synthase (UDP-forming) IPR001830 Glycosyl transferase, family 20
Root DW	78C	g129	+	1584196	1588316	4120	0	99.84	100	Solyc07g006900.1.1	Auxin efflux carrier protein IPR014024 Auxin efflux carrier, subgroup
Root DW	78C	g135	-	1619167	1614022	5145	0	98.83	100	Solyc07g006970.2.1	Solute carrier family 2, facilitated glucose transporter member 5 IPR003663 Sugar_inositol transporter
Root DW	78C	g136	+	1624216	1626754	2538	0	99.27	99	Solyc07g006990.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
Root DW	78C	g140	-	1655597	1648379	7218	0	91.88	99	Solyc07g007020.2.1	Receptor-like protein kinase At3g21340 IPR002290 Serine_threonine protein kinase
Root DW	78C	g146	+	1721296	1726820	5524	0	81.7	99	Solyc07g007120.2.1	Homeobox protein knotted-1-like 3 IPR005541 KNOX2
Root DW	78C	g170	-	2025242	2016895	8347	0	95.02	100	Solyc07g007430.2.1	Palmitoyltransferase akr1 (EC 2.3.1.-)[Ankyrin repeat-containing protein akr1] IPR002110 Ankyrin
Root DW	78C	g177	-	2075802	2074782	1020	1E-144	99	99	Solyc07g007510.2.1	Adenylate cyclase IPR008172 Adenylate cyclase

<i>S. pennellii</i>										
ITAG2.4 proteins blastp										
ITAG2.4 Orthologous for <i>S. lycopersicum</i>										
Trait	BIN	# Gene	Sense	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	Functional_Description
Root DW	78C	g248	-	3016598	3009997	6601	0	85.25	79	Solyc07g008380.1.1 Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	78C	absent	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	78C	g250	-	3044528	3043120	1408	0	88.83	100	Solyc07g008380.1.1 Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	78C	g251	+	3048807	3051706	2899	0	99.06	100	Solyc07g008400.1.1 Pto-like, Serine_threonine kinase protein, resistance protein
Root DW	78C	g253	-	3062508	3060933	1575	0	91.32	100	Solyc07g008380.1.1 Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	78C	g254	+	3078897	3087088	8191	0	92.29	100	Solyc07g008410.2.1 Multidrug and toxin extrusion protein 1 IPR002528 Multi antimicrobial extrusion protein MatE
Root DW	78C	g265	-	3269213	3265117	4096	0	97.65	93	Solyc07g008490.2.1 Nucleic acid binding protein IPR018111 K Homology, type 1, subgroup
Root DW	78C	g272	+	3366259	3373511	7252	0	99.32	100	Solyc07g008520.2.1 Peptide transporter IPR000109 TGF-beta receptor, type I, extracellular region
Shoot DW	9C	g3	-	19817	12694	7123	0	88.47	100	Solyc09g008480.2.1 Phosphatidylinositol-4-phosphate 5-kinase 9 IPR017163 Phosphatidylinositol-4-phosphate 5-kinase, plant
Shoot DW	9C	absent	NA	NA	NA	NA	NA	NA	NA	NA
Shoot DW	9C	g4	+	35706	45370	9664	6E-91	96.88	45	Solyc09g008490.2.1 HEAT repeat family protein expressed IPR011989 Armadillo-like helical
Shoot DW	9C	g6	+	48046	75328	27282	0	96.38	84	Solyc09g008490.2.1 HEAT repeat family protein expressed IPR011989 Armadillo-like helical
Shoot DW	9C	g17	-	205846	192097	13749	0	98.24	48	Solyc09g008640.1.1 Receptor-like protein kinase At3g21340 IPR002290 Serine_threonine protein kinase
Shoot DW	9C	g34	-	356066	348000	8066	0	95.96	96	Solyc09g008840.2.1 Pyruvate kinase IPR001697 Pyruvate kinase
Shoot DW	9C	g36	-	370176	367200	2976	0	99.11	100	Solyc09g008860.2.1 Receptor like kinase, RLK
Shoot DW	9C	g55	-	553766	551845	1921	0	97.62	100	Solyc09g009110.2.1 Gibberellin 20-oxidase IPR005123 Oxoglutarate and iron-dependent oxygenase
Shoot DW	9C	g66	+	670223	688344	18121	0	92.52	98	Solyc09g009190.2.1 1,4-alpha-glucan branching enzyme II IPR006589 Glycosyl hydrolase, family 13, subfamily, catalytic region
Root DW	9D	g1	+	1	23841	23840	0	97.59	99	Solyc09g009370.2.1 Vacuolar protein sorting-associated protein IPR009291 Protein of unknown function DUF946, plant
ShootDW	9D	g2	-	48397	37386	11011	0	98.82	100	Solyc09g009380.2.1 Protein kinase-like protein IPR002290 Serine_threonine protein kinase
ShootDW	9D	g4	-	65087	62193	2894	0	98.23	96	Solyc09g009400.2.1 APO protein 1, chloroplastic IPR008512 Protein of unknown function DUF794, plant
ShootDW	9D	g14	-	143217	140331	2886	0	97.99	90	Solyc09g009490.2.1 Bzip transcription factor IPR011700 Basic leucine zipper
ShootDW	9D	g21	+	198165	201148	2983	4E-125	98.84	100	Solyc09g009560.1.1 SELF PRUNING 9D
ShootDW	9D	g34	-	355286	353526	1760	0	76.16	99	Solyc10g083400.1.1 (duplicated) Cytochrome P450
ShootDW	9D	g35	+	362750	364187	1437	2E-105	74.63	55	Solyc10g083400.1.1 (duplicated) Cytochrome P450
ShootDW	9D	g54	-	595287	586049	9238	0	91.24	100	Solyc09g009910.2.1 Lipid A ABC transporter permease_ATP-binding protein IPR003439 ABC transporter-like
ShootDW	9D	g60	-	623217	618670	4547	0	99.24	100	Solyc09g009970.2.1 Rho GTPase activating protein 2 IPR000198 RhoGAP
ShootDW	9D	g61	+	633396	635546	2150	4E-104	96.67	100	Solyc09g009980.1.1 Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein
Root DW	9G	g26	-	332047	324800	7247	0	99.52	100	Solyc09g072820.2.1 Cellulose synthase IPR005150 Cellulose synthase
Root DW	9G	g59	-	628620	627012	1608	0	98.87	100	Solyc09g074080.1.1 Glycosyltransferase family GT8 protein IPR002495 Glycosyl transferase, family 8
Root DW	9G	g84	-	870955	866842	4113	0	98.96	100	Solyc09g074230.2.1 Glucose transporter 8 IPR003663 Sugar_inositol transporter
Root DW	9G	g94	+	975609	980496	4887	0	98.22	72	Solyc09g074310.2.1 Oxidoreductase aldo_keto reductase family protein expressed IPR001395 Aldo_keto reductase
Starch/ED	11B	g10	+	139036	146247	7211	0	96.31	100	Solyc11g008590.1.1 UDP-galactose transporter-like protein IPR007271 Nucleotide-sugar transporter
Starch/ED	11B	g12	-	165577	155752	9825	0	94.12	93	Solyc11g008610.1.1 Nucleotide-sugar transporter UDP N-acetylglucosamine-like signal peptide 9 or more transmembrane domains (Fragment) IPR007271 Nucleotide-sugar tr
Starch/ED	11B	g13	-	174097	167460	6637	0	96.56	100	Solyc11g008620.1.1 Phosphoglycolate phosphatase IPR006349 2-phosphoglycolate phosphatase, eukaryotic
Starch/ED	11B	g22	+	267511	274730	7219	0	92.57	100	Solyc11g008720.1.1 Beta-glucosidase G4 IPR001360 Glycoside hydrolase, family 1
Starch/ED	11B	g68	+	692684	693997	1313	2E-176	100	93	Solyc11g010200.1.1 14-3-3 protein beta_alpha-1 IPR000308 14-3-3 protein
Starch/ED	11B	g76	-	789494	784240	5254	0	98.8	92	Solyc11g010290.1.1 2-oxoglutarate_malate translocator IPR001898 Sodium_sulphate symporter
Starch/ED	11B	g90	+	908628	914434	5806	0	99.25	100	Solyc11g010450.1.1 Phosphofructokinase family protein IPR012004 Pyrophosphate-dependent phosphofructokinase TP0108
Malate	11D	g8	-	61767	50993	10774	0.0	99.46	68	Solyc11g065830.1.1 2-oxoglutarate_malate translocator-like protein IPR001898 Sodium_sulphate symporter
A	11H	g17	-	180579	171704	8875	8E-121	100	100	Mitochondrial F0 ATP synthase D chain IPR008689 ATPase, F0 complex, subunit D, mitochondrial
A	11H	g35	+	429554	434044	4490	0	100	100	Solyc11g072630.1.1 Mitogen-activated protein kinase IPR008351 JNK MAP kinase
A	11H	g41	+	479484	497046	17562	0	99.08	65	Solyc11g072710.1.1 Protein kinase IPR002290 Serine_threonine protein kinase

NCU: non-conding upstream region: intergenic, promoter or 5' UTR

NCD: non-conding downstream region: 3' UTR or intergenic region

intron

exon

intron-exon: intron-exon junction

NA: non applicable

Numbers in brackets indicate the number of elements in the corresponding position

										<i>S. lycopersicum</i>	
										ITAG2.4 Orthologous for <i>S. lycopersicum</i>	
Trait	BIN	# Gene	Sense	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	(Heinz)	Functional_Description
Root DW	1J	g1	-	5327	1	5326	0	100	100	Solyc01g109790.2.1	Glucose-1-phosphate adenylyltransferase IPR011831 Glucose-1-phosphate adenylyltransferase IPR005836 ADP-glucose pyrophosphorylase, conserved site
Root DW	1J	g14	-	1358137	1356650	1487	0	100	100	Solyc01g109940.2.1	26S protease regulatory subunit IPR005937 26S proteasome subunit P45
Root DW	1J	g51	+	445655	448174	2519	0	97.78	100	Solyc01g110360.2.1	Fructose-bisphosphate aldolase IPR000741 Fructose-bisphosphate aldolase, class-I
Root DW	1J	g68-g104 (28)	both	575070	789329	NA	NA	NA	NA	NA	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein
Root DW	1J	g110	-	828076	826922	1154	5E-71	100	100	Solyc01g111080.2.1	Gibberellin-regulated protein 2 IPR003854 Gibberellin regulated protein
Root DW	1J	g112	-	844486	839544	4942	0	100	100	Solyc01g111100.2.1/	Neutral invertase like protein IPR006937 Plant neutral invertase/
Root DW	1J	g113	-	861350	855257	6093	0	82.14	100	Solyc01g111120.2.1	Triosephosphate isomerase IPR000652 Triosephosphate isomerase
Root DW	1J	g129	-	957880	954392	3488	2E-177	98.79	62	Solyc01g111310.2.1	Transmembrane amino acid transporter protein IPR013057 Amino acid transporter, transmembrane
Root DW	1J	g143	-	1083187	1081049	2138	1E-160	100	91	Solyc01g111500.2.1	MYB transcription factor IPR015495 Myb transcription factor
Root DW	1J	g156	+	1209971	1214092	4121	0	93.78	100	Solyc01g111630.2.1	Glyoxylate_hydroxypyruvate reductase B IPR006140 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
Root DW	1J	g181	-	1423547	1417145	6402	0	100	100	Solyc01g111890.2.1	F-box_LRR-repeat protein 14 IPR001810 Cyclin-like F-box
Root DW	1J	g182	-	1425957	1424890	1067	3E-111	98.2	98	Solyc01g111890.2.2	F-box_LRR-repeat protein 14 IPR001810 Cyclin-like F-box
Root DW	1J	g186	#REF!	1453127	1449337	3790	0	100	100	Solyc01g111930.2.1	Rop guanine nucleotide exchange factor 1 IPR005512 Rop nucleotide exchanger, PRONE
A	2K	g20	+	152316	155738	3422	0	99.27	100	Solyc02g091130.2.1	ATP synthase subunit beta IPR005722 ATPase, F1 complex, beta subunit
A	2K	g32	-	234703	230019	4684	0	90.09	100	Solyc02g091280.2.1	ATP-dependent Clp protease proteolytic subunit IPR001907 Peptidase S14, ClpP
A	2K	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
A	2K	g43	-	320583	298599	21984	0	97.71	100	Solyc02g091410.2.1	Pro-apoptotic serine protease nma111-like protein IPR009003 Peptidase, trypsin-like serine and cysteine
A	2K	g55	+	430422	436960	6538	0	100	100	Solyc02g091560.2.1	Serine hydroxymethyltransferase IPR001085 Serine hydroxymethyltransferase
A	2K	g112	-	1017394	1013194	4200	7E-29	73.61	40	Solyc02g092270.2.1	NADH dehydrogenase IPR006885 ETC complex I subunit conserved region
A	2K	g144	-	1324414	1321722	2692	9E-165	100	85	Solyc02g092730.2.1	Iron sulfur subunit of succinate dehydrogenase IPR004489 Succinate dehydrogenase_fumarate reductase iron-sulphur protein
Root DW	2L	g13	-	115827	114521	1306	0	99.72	97	Solyc02g092930.1.1	MYB transcription factor IPR015495 Myb transcription factor
Root DW	2L	g80	-	712154	710861	1293	0	100	100	Solyc02g093740.2.1	MYB transcription factor IPR015495 Myb transcription factor
Root DW	2L	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	2L	g124	-	1088676	1085931	2745	2E-85	100	100	Solyc02g094270.1.1	WRKY transcription factor IPR003657 DNA-binding WRKY
Root DW	2L	g126	+	1106165	1108032	1867	3E-44	100	39	Solyc02g094290.1.1	TCP family transcription factor IPR005333 Transcription factor, TCP
Root DW	4DE	g8	+	100106	102975	2869	0	100	100	Solyc04g014670.2.1	Short-chain dehydrogenase_reductase SDR IPR002347 Glucose_ribitol dehydrogenase
Root DW	4DE	g15	-	176107	170922	5185	0	100	100	Solyc04g014760.2.1	RHO protein GDP dissociation inhibitor IPR000406 RHO protein GDP dissociation inhibitor
Root DW	4DE	g51	-	549814	546714	3100	0	100	100	Solyc04g015200.2.1	6-phosphofructokinase 2 IPR012004 Pyrophosphate-dependent phosphofructokinase TP0108
Root DW	4DE	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	4DE	g1300	-	17447365	17442124	5241	9E-93	97.12	57	Solyc04g025740.1.1	Homeobox-leucine zipper protein ROC3 IPR001356 Homeobox
Root DW	4DE	g2768	-	37377760	37369442	8318	0	99.63	100	Solyc04g049690.2.1	Adenylate kinase IPR006259 Adenylate kinase, subfamily
Root DW	4DE	g3075	-	41549616	41546792	2824	0	100	100	Solyc04g050440.2.1	Ammonium transporter IPR001905 Ammonium transporter
Root DW	4DE	g3265	+	43800306	43805862	5556	0	99.34	78	Solyc04g051080.1.1	Response regulator 8 IPR006447 Myb-like DNA-binding region, SHAQKYF class
Root DW	4DE	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	4DE	g3686	-	48916526	48912990	3536	4E-134	86.34	100	Solyc04g056620.1.1	Auxin Efflux Carrier IPR004776 Auxin efflux carrier
Root DW	7BC	g36	-	368287	364567	3720	0	100	100	Solyc07g005760.2.1	Hydroxycinnamoyl CoA shikimate_quinate hydroxycinnamoyltransferase IPR003480 Transferase
Root DW	7BC	g78	+	826231	829281	3050	0	100	100	Solyc07g006280.2.1	Senescence-associated protein IPR000301 Tetraspanin, subgroup
Root DW	7BC	g84	-	931477	924649	6828	0	100	99	Solyc07g006350.2.1	Ankyrin repeat-rich protein IPR002110 Ankyrin
Root DW	7BC	g97	+	1057911	1061119	3208	0	100	100	Solyc07g006500.2.1	Alpha alpha-trehalose-phosphate synthase (UDP-forming) IPR001830 Glycosyl transferase, family 20
Root DW	7BC	g133	+	1511886	1515103	3217	0	100	100	Solyc07g006900.1.1	Auxin efflux carrier protein IPR014024 Auxin efflux carrier, subgroup
Root DW	7BC	g138	-	1545017	1540284	4733	0	100	100	Solyc07g006970.2.1	Solute carrier family 2, facilitated glucose transporter member 5 IPR003663 Sugar_inositol transporter
Root DW	7BC	g139	+	1549771	1552312	2541	0	100	99	Solyc07g006990.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
Root DW	7BC	g142	-	1571572	1564868	6704	0	94.49	96	Solyc07g007020.2.1	Receptor-like protein kinase At3g21340 IPR002290 Serine_threonine protein kinase
Root DW	7BC	g148	+	1632991	1638889	5898	0	100	89	Solyc07g007120.2.1	Homeobox protein knotted-1-like 3 IPR005541 KNOX2
Root DW	7BC	g170	-	1910377	1902138	8239	0	95.17	100	Solyc07g007430.2.1	Palmitoyltransferase akr1 (EC 2.3.1.)-(Ankyrin repeat-containing protein akr1) IPR002110 Ankyrin
Root DW	7BC	g177	-	1960492	1959458	1034	1E-138	98.95	81	Solyc07g007510.2.1	Adenylate cyclase IPR008172 Adenylate cyclase

Root DW	7BC	g247	-	2940831	2938989	1842	0	100	100	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	7BC	g248	-	2948361	2945147	3214	0	100	98	Solyc07g008390.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	7BC	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	7BC	g249	-	2957871	2955136	2735	0	100	100	Solyc07g008400.1.1	Pto-like, Serine_threonine kinase protein, resistance protein
Root DW	7BC	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	7BC	g250	+	2962640	2970025	7385	0	93.96	100	Solyc07g008410.2.1	Multidrug and toxin extrusion protein 1 IPR002528 Multi antimicrobial extrusion protein MatE
Root DW	7BC	g259	-	3156598	3150659	5939	0	100	100	Solyc07g008490.2.1	Nucleic acid binding protein IPR018111 K Homology, type 1, subgroup
Root DW	7BC	g261	+	3180057	3204832	24775	0	99.83	24	Solyc07g008520.2.1	Peptide transporter IPR000109 TGF-beta receptor, type I, II extracellular region
Shoot DW	9C	g3	-	18297	12607	5690	0	89.37	100	Solyc09g008480.2.1 (broken)	Phosphatidylinositol-4-phosphate 5-kinase 9 IPR017163 Phosphatidylinositol-4-phosphate 5-kinase, plant
Shoot DW	9C	g4	-	24707	19363	5344	0	100	99	Solyc09g008480.2.1 (broken)	Phosphatidylinositol-4-phosphate 5-kinase 9 IPR017163 Phosphatidylinositol-4-phosphate 5-kinase, plant
Shoot DW	9C	g5	+	34056	43890	9834	4E-115	96.89	57	Solyc09g008490.2.1	HEAT repeat family protein expressed IPR011989 Armadillo-like helical
Shoot DW	9C	g7	+	56106	74343	18237	0	95	99	Solyc09g008490.2.1	HEAT repeat family protein expressed IPR011989 Armadillo-like helical
Shoot DW	9C	g18	-	203938	192202	11736	0	100	71	Solyc09g008640.1.1	Receptor-like protein kinase At3g21340 IPR002290 Serine_threonine protein kinase
Shoot DW	9C	g36	-	357688	349932	7756	0	90.81	96	Solyc09g008840.2.1	Pyruvate kinase IPR001697 Pyruvate kinase
Shoot DW	9C	g38	-	373368	370500	2868	0	100	100	Solyc09g008860.2.1	Receptor like kinase, RLK
Shoot DW	9C	g55	-	542623	540713	1910	0	99.18	100	Solyc09g009110.2.1	Gibberellin 20-oxidase IPR005123 Oxoglutarate and iron-dependent oxygenase
Shoot DW	9C	g61	+	631165	649298	18133	0	95.57	100	Solyc09g009190.2.1	1,4-alpha-glucan branching enzyme II IPR006589 Glycosyl hydrolase, family 13, subfamily, catalytic region
Root DW	9D	g1	+	763	24025	23262	0	98.85	98	Solyc09g009370.2.1	Vacuolar protein sorting-associated protein IPR009291 Protein of unknown function DUF946, plant
ShootDW	9D	g2	-	37827	29641	8186	0	100	86	Solyc09g009380.2.1	Protein kinase-like protein IPR002290 Serine_threonine protein kinase
ShootDW	9D	g4	-	63907	60898	3009	0	99.75	96	Solyc09g009400.2.1	AP0 protein 1, chloroplastic IPR008512 Protein of unknown function DUF794, plant
ShootDW	9D	g13	-	137207	132737	4470	0	99.5	92	Solyc09g009490.2.1	Bzip transcription factor IPR011700 Basic leucine zipper
ShootDW	9D	g20	+	188974	191913	2939	3E-126	100	100	Solyc09g009560.1.1	SELF PRUNING 9D
ShootDW	9D	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
ShootDW	9D	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
ShootDW	9D	g50	-	615874	606800	9074	0	98.31	100	Solyc09g009910.2.1	Lipid A ABC transporter permease_ATP-binding protein IPR003439 ABC transporter-like
ShootDW	9D	g56	-	643774	639156	4618	0	100	100	Solyc09g009970.2.1	Rho GTPase activating protein 2 IPR000198 RhoGAP
ShootDW	9D	g57	+	657313	658289	976	7E-108	100	100	Solyc09g009980.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein
Root DW	9G	g33	-	424467	417955	6512	0	100	100	Solyc09g072820.2.1	Cellulose synthase IPR005150 Cellulose synthase
Root DW	9G	g59	-	667908	666268	1640	0	100	100	Solyc09g074080.1.1	Glycosyltransferase family GT8 protein IPR002495 Glycosyl transferase, family 8
Root DW	9G	g86	-	911642	907562	4080	0	100	100	Solyc09g074230.2.1	Glucose transporter 8 IPR003663 Sugar_inositol transporter
Root DW	9G	g94	+	991941	997157	5216	0	92.18	75	Solyc09g074310.2.1	Oxidoreductase aldo_keto reductase family protein expressed IPR001395 Aldo_keto reductase
Starchy/ED	11B	g10	+	127566	135024	7458	0	97.39	90	Solyc11g008590.1.1	UDP-galactose transporter-like protein IPR007271 Nucleotide-sugar transporter
Starchy/ED	11B	g12	-	153977	144117	9860	0	94.37	93	Solyc11g008610.1.1	Nucleotide-sugar transporter UDP N-acetylglucosamine-like signal peptide 9 or more transmembrane domains (Fragment) IPR007271 Nucleotide-sugar transporter
Starchy/ED	11B	g13	-	163127	156304	6823	0	100	100	Solyc11g008620.1.1	Phosphoglycolate phosphatase IPR006349 2-phosphoglycolate phosphatase, eukaryotic
Starchy/ED	11B	g21	+	243591	250622	7031	0	93.17	100	Solyc11g008720.1.1	Beta-glucosidase G4 IPR001360 Glycoside hydrolase, family 1
Starchy/ED	11B	g62	+	624048	625356	1308	1E-176	100	93	Solyc11g010200.1.1	14-3-3 protein beta_alpha-1 IPR000308 14-3-3 protein
Starchy/ED	11B	g70	-	721572	715854	5718	0	100	92	Solyc11g010290.1.1	2-oxoglutarate_malate translocator IPR001898 Sodium_sulphate symporter
Starchy/ED	11B	g84	+	848921	855471	6550	0	100	100	Solyc11g010450.1.1	Phosphofructokinase family protein IPR012004 Pyrophosphate-dependent phosphofructokinase TP0108
Malate	11D	g8	-	55707	43507	12200	0.0	100	68	Solyc11g065830.1.1	2-oxoglutarate_malate translocator-like protein IPR001898 Sodium_sulphate symporter
A	11H	g18	-	179687	174524	5163	8E-121	100	100	Solyc11g072450.1.1	Mitochondrial FO ATP synthase D chain IPR008689 ATPase, FO complex, subunit D, mitochondrial
A	11H	g34	+	409878	418820	8942	0	100	85	Solyc11g072630.1.1	Mitogen-activated protein kinase IPR008351 JNK MAP kinase
A	11H	g40	+	460998	471130	10132	0	100	100	Solyc11g072710.1.1	Protein kinase IPR002290 Serine_threonine protein kinase

NCU: non-conding upstream region: intergenic, promoter or 5' UTR

NCD: non-conding downstream region: 3' UTR or intergenic region

intron

exon

intron-exon: intron-exon junction

NA: non applicable

Numbers in brackets indicate the number of elements in the corresponding position

Trait	BIN	<i>S. pennellii</i> TE positions	<i>S. pennellii</i> TE type	<i>S. lycopersicum</i> TE positions	<i>S. lycopersicum</i> TE type
Root DW	1J	NCU (2)	TIR_DNA3-8_Stu, TIR_DNA9-6_Stu	NCU (2)	TIR_DNA9-1_Stu, TIR_TLP1
Root DW	1J	intron	TIR_MuDR-4_Stu	none	none
Root DW	1J	none	none	none	none
Root DW	1J	intron-exon	LINE_L1-5_Stu	intron (2)	TIR_DNA-TA-1_Stu, TIR_DNA9-5_Stu
Root DW	1J	none	none	none	none
Root DW	1J	NCU (2)	LTR_TLC1, TIR_TLP2	NCU (5)	TIR_DNA9-3_Stu, TIR_DNA9-6_Stu, TIR_TLP1, TIR_MUDRAV12, TIR_EnSpm-3_VV
Root DW	1J	none	none	none	none
Root DW	1J	NCU, NCD	TIR_HATSOD1, LTR_Copia-1_ST	none	none
Root DW	1J	NCU	LTR_SONATA2	NCU (2), NCD	LTR_Copia-3_SL, TIR_DNA9-4_Stu, TIR_DNA3-8_Stu
Root DW	1J	none	none	none	none
Root DW	1J	NCD (2)	TIR_SHAAMUDRAV_MT, LTR_Copia-75_ST	intron	RC_Helitron-2_Stu
Root DW	1J	none	none	none	none
Root DW	1J	NCU (2)	TIR_SONATA1, TIR_DNA-TA-1_Stu	NCU (3)	TIR_EnSpm-11_OS, TIR_MuDR-21_VV, TIR_SONATA1
A	2K	NCU	TIR_hAT-4_PTr	none	none
A	2K	none	none	none	none
A	2K	none	none	NA	NA
A	2K	NCU (3)	TIR_DNA9-4_Stu, TIR_hAT-N3_Stu, TIR_HARB-N1_Stu	none	none
A	2K	intron (3)	TIR_hAT-1_Stu, TIR_STOWAWAYSO_OS, TIR_MuDR-21_VV	intron (3), NCD	TIR_MuDR-1_Stu, TIR_MuDR-1_Stu, TIR_DNA9-5, TIR_DNA3-8_Stu
A	2K	none	none	none	none
A	2K	intron-exon	TIR_DNA9-6_Stu	none	none
Root DW	2L	none	none	NCU	RC_HELITRON7_OS
Root DW	2L	NCU	TIR_DNA9-4_Stu	intron	LTR_TOTO1_LP
Root DW	2L	none	none	NA	NA
Root DW	2L	NCD (2)	TIR_MuDR-8_Mad, LTR_Gypsy-31_ST	intron	TIR_EnSpm-5_HV
Root DW	2L	none	none	none	none
Root DW	4DE	none	none	NCU (2)	LTR_Gypsy-11_SL, LTR_Copia-5_SL
Root DW	4DE	NCD	TIR_DNA3-6_Stu	none	none
Root DW	4DE	NCU, NCD (2)	TIR_DNA9-4_Stu, TIR_SONATA2, TIR_DNA3-7_Stu	NCU (2), NCD	LTR_Gypsy-40_Mad, TIR_DNA-TA-2_Stu, LTR_TOTO1_LP
Root DW	4DE	NCU (6), intron (2), NCD (3)	LTR_Gypsy-21_ST, LTR_Gypsy-39_Stu, LTR_Gypsy-43_Stu, LTR_Gypsy-41_Stu, LTR_Gypsy-41_Stu, TIR_HARB-1_Stu, TIR_EnSpm-34_Sbi, EnSpm-3_TA, LTR_Gypsy-45_Stu, LTR_G NA	none	NA
Root DW	4DE	NCU (2), NCD (2)	LTR_Gypsy-27_ST, TIR_DNA3-6_Stu, LTR_Gypsy-45_Stu, LTR_Gypsy-41_Stu	none	none
Root DW	4DE	NCD	TIR_TLP1	NCU (3), NCD	LTR_Gypsy-24_ST, TIR_MuDR-7_Stu, TIR_hAT-N4_Stu, TIR_DNA9-1_Stu
Root DW	4DE	NCU (3)	LTR_Gypsy-120_SB, TIR_MuDR-11N_VV, TIR_MuDR-11N_VV	NCU (4), NCD	LTR_Gypsy-11_SL, TIR_EnSpm-12_OS, TIR_MuDR-8_VV, TIR_EnSpm-5_HV, TIR_hAT-N4_Stu
Root DW	4DE	none	none	NCU	LTR_Gypsy-41_Stu
Root DW	4DE	NCU (3), NCD (2)	LTR_Gypsy-41_Stu, LTR_Gypsy-44_Stu, LTR_Gypsy-27_ST, LTR_Copia-18_ST, TIR_EnSpm-1_Stu	NA	NA
Root DW	4DE	NCU, NCD (2)	TIR_hAT-N6_Stu, TIR_DNA3-8_Stu, SINE_SO	intron, NCD (3)	TIR_DNA3-8_Stu, LTR_Copia11-VV, TIR_EnSpm-5_HV, RC_Helitron-4n1_Smo
Root DW	7BC	NCU (3), NCD	TIR_MtPH-A6-3-Ta, LTR_Copia11-VV, TIR_MuDR-8_VV, TIR_DNA3-3_Stu	none	none
Root DW	7BC	NCD (2)	LTR_Gypsy-28_ST, TIR_LTP1	NCD (2)	TIR_TLP2, TIR_DNA3-8_Stu
Root DW	7BC	NCU, NCD	LTR_Copia-1_ST, TIR_hAT-N4_Stu	none	none
Root DW	7BC	none	none	none	none
Root DW	7BC	NCU	TIR_DNA9-6_Stu	none	none
Root DW	7BC	NCU	TIR_DNA3-4_Stu	none	none
Root DW	7BC	NCU	TIR_EnSpm-2_SB	none	none
Root DW	7BC	NCU (3), NCD (3)	SINE_TS2, LINE RTE-1_Stu, LTR_Copia4-VV, LINE RTE-1_Stu, TIR_hAT-N3_Stu, LINE RTE-1_Stu	NCD	TIR_EnSpm-1_Stu
Root DW	7BC	none	none	exon, NCD	TIR_EnSpm-34_Sbi, LTR_Copia-1_ST
Root DW	7BC	none	none	NCU	TIR_HARB-3_Stu
Root DW	7BC	none	none	none	none

Differentially inserted Tes						
Trait	BIN	<i>S. pennellii</i> TE positions	<i>S. pennellii</i> TE type		<i>S. lycopersicum</i> TE positions	<i>S. lycopersicum</i> TE type
Root DW	7BC	NCU, intron	LTR_Athila7, LTR_Gypsy-25_ST		NCU	TIR_DNA9-1_Stu
Root DW	7BC	NA	NA		NCU (2)	TIR_DNA9-1_Stu, TIR_DNA-TA-2_Stu
Root DW	7BC	NCU (3), NCD	SINE_SINE_SO, TIR_DNA3-6_Stu, TIR_DNA3-6_Stu, LTR_Gypsy-11_SL		NA	NA
Root DW	7BC	NCU, NCD (5)	SINE_SO, TIR_DNA9-4_Stu, TIR_DNA9-5_Stu, TIR_DNA9-6_Stu, TIR_DNA-TA-1_Stu, TIR_DNA3-8_Stu		NCD (2)	TIR_DNA9-4_Stu, TIR_DNA9-1_Stu
Root DW	7BC	NCU (2)	TIR_DNA3-6_Stu, LTR_Gypsy-11_SL		NA	NA
Root DW	7BC	NCU, intron (4)	SINE_SO, TIR_SONATA1, TIR_DNA9-1_Stu, TIR_DNA9-5_Stu, TIR_DNA-TA-1_Stu		NCU (2), intron (4)	TIR_EnSpm-2_TD, TIR_DNA-TA-2_Stu, TIR_SONATA2, TIR_TLP1, TIR_TPL3, TIR_DNA9-6_Stu
Root DW	7BC	NCU	LTR_TLP1		NCD (3)	LINE_L1-14_Stu, TIR_DNA-TA-2_Stu, TIR_DNA3-5_Stu
Root DW	7BC	NCU (2), NCD	TIR_EnSpm-3_TA, TIR_SONATA2, TIR_hAT-N4_Stu		NCU-exon-intron, intron-exon (3), intron	LTR_Copia-59_ST, LTR_Copia-56_ST, LTR_Gypsy-6_ST, LTR_Copia-45_GM, TIR_DNA9-4_Stu
Shoot DW	9C	none	none		none	none
Shoot DW	9C	NA	NA		NCU	TIR_DNA9-1_Stu
Shoot DW	9C	NCU, intron	TIR_DNA9-6_Stu, TIR_EnSpm-10_Stu		NCU (3)	TIR_DNA9-6_Stu, LINE RTE-1_Stu, TIR_DNA3-8_Stu
Shoot DW	9C	intron-exon, intron, NCD	LINE_L1-15_Stu, LTR_Copia 11-VV, TIR_EnSpm-6_Stu		NCU, intron-exon, intron (2)	LINE_L1-12_Stu, LINE_L1-15_Stu, LTR_Copia-97_GM, TIR_EnSpm-6_Stu
Shoot DW	9C	NCU, intron, intron-exon	TIR_POTTEN1, TIR_SONATA 2, LINE_L1-11_Stu		intron	LTR_NonLTR-1_Stu
Shoot DW	9C	none	none		none	none
Shoot DW	9C	NCU	TIR_DNA8-1_Stu		NCU (2)	TIR_DNA-TA-2_Stu, TIR_DNA3-7_Stu
Shoot DW	9C	NCU, intron	TIR_ATHPOGON3, TIR_EnSpm-1_Stu		NCU	TIR_ATHPOGO
Shoot DW	9C	none	none		NCU, intron	TIR_EnSpm-5_VV, SINE_TS
Root DW	9D	intron (2), intron-exon-NCD, NCD	TIR_DNA3-3_Stu, TIR_MUDRAV1, LTR_Copia-1_ST, LTR_TOT01_LP		intron	TIR_EnSpm-34_Sbi
ShootDW	9D	NCD (3)	TIR_hAT-6_Stu, TIR_MuDR-1_Stu, TIR_DNA3-8_Stu		NCU, NCD	LTR_Gypsy-11_SL, LTR_Copia-1_ST
ShootDW	9D	NCU (2)	TIR_TLP1, TIR_HATSOD1		NCU (2)	TIR_SONATA2, TIR_HATSOD1
ShootDW	9D	none	none		none	none
ShootDW	9D	NCU (5), intron	LTR_Gypsy-25_ST, RC_HELITRON7_OS, TIR_MUDRAV1, TIR_DNA9-1_Stu, TIR_EnSpm-16_Sbi, TIR_DNA9-6_Stu		intron	LINE RTE-1_Stu
ShootDW	9D	NCU, NCD (2)	SINE_SO, TIR_DNA9-1_Stu, LTR_Copia-75_ST		NA	NA
ShootDW	9D	none	none		NA	NA
ShootDW	9D	none	none		NCU, intron	LTR_GYLES1, SINE_TS2
ShootDW	9D	NCU (2)	TIR_DNA9-5_Stu, TIR_DNA-TA-2_Stu		NCU (5)	TIR_DNA-TA-2_Stu, TIR_POTTEN2, TIR_POTTEN2, TIR_POTTEN1, TIR_DNA-TA-2_Stu
ShootDW	9D	none	none		NCU	LTR_Gypsy-11_SL
Root DW	9G	intron	LTR_Copia-1_ST		none	none
Root DW	9G	NCU (2)	TIR_hAT-N3_Stu, LTR_Gypsy-40_Stu		NCU	LTR_Copia-1_ST
Root DW	9G	NCU	TIR_DNA3-8_Stu		intron-exon	TIR_hAT-6_VV
Root DW	9G	NCU (4)	TIR_hAT-N1_Stu, TIR_DNA9-2_Stu, TIR_hAT-N4_Stu, LINE RTE-1_Stu		NCU	TIR_EnSpm-1_Stu
Starch/ED	11B	none	none		none	none
Starch/ED	11B	none	none		none	none
Starch/ED	11B	none	none		intron	LTR_Copia-75_ST
Starch/ED	11B	intron	LINE RTE-1_Stu		intron (3)	TIR_SONATA3, TIR_EnSpm-1_Stu, LINE RTE-1_STu
Starch/ED	11B	none	none		NCU	TIR_DNA-TA-1_Stu
Starch/ED	11B	NCU, intron (2)	TIR_TLP1, LINE RTE-1_Stu, TIR_EnSpm-1_Stu		intron	SINE_TS
Starch/ED	11B	NCU, NCD	LINE RTE-1_Stu, TIR_DNA-TA-2_Stu		NCU	SINE_TS2
Malate	11D	NCU (2)	LTR_Copia-96_ST, LTR_Copia-3_SL		NCU (2), intron (2)	SINE_TS2, SINE_TS2, TIR_EnSpm-17_ZM, TIR_EnSpm-5_HV
A	11H	NCU	TIR_MUDSOLD1		NCU	TIR_MUDSOLD1
A	11H	NCU, intron, NCD	TIR_DNA9-2_Stu, TIR_SONATA2, LTR_Copia-2_SL		NCU, intron	LTR_Ogre-SD1, TIR_DNA9-2_Stu
A	11H	intron (3)	TIR_DNA9-4_Stu, TIR_EnSpm-4_VV, TIR_EnSpm-1_Stu		NCU (2)	TIR_EnSpm-34_Sbi, LTR_Copia-75_ST

NCU: non-conding upstream region:intergenic, promoter or 5' UTR

NCD: non-conding downstream region: 3' UTR or intergenic region

intron

exon

intron-exon: intron-exon junction

NA: non applicable

Numbers in brackets indicate the number of elements in the corresponding position

Supplemental Table S7. Genes expression based on RNA-seq data of leaf materials of 76 tomato introgression lines from Chitwood et al. (2013)

S. lycopersicum											
ITAG2.4 proteins blastp							ITAG2.4 Orthologous for S.lycopersicum		Functional_Description		
Trait	BIN	# Gene	Sense	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	(Heinz)	
Root DW	1J	g1	-	4987	1	4987	0	98.25	100	Solyc01g109790.2.1	Glucose-1-phosphate adenylyltransferase IPR011831 Glucose-1-phosphate adenylyltransferase IPR005836 ADP-glucose pyrophosphorylase, conserved site
Root DW	1J	g15	-	141647	136374	5273	0	99.44	100	Solyc01g109940.2.1	26S protease regulatory subunit IPR005937 26S proteasome subunit P45
Root DW	1J	g52	+	463032	466619	3587	0	94.36	78	Solyc01g110360.2.1	Fructose-bisphosphate aldolase IPR000741 Fructose-bisphosphate aldolase, class-I
Root DW	1J	g70-g110 (33)	both	591837	794819	NA	NA	NA	NA	NA	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein
Root DW	1J	g115	-	837396	836288	1108	9E-69	97.12	100	Solyc01g111080.2.1	Gibberellin-regulated protein 2 IPR003854 Gibberellin regulated protein
Root DW	1J	g117	-	856706	849234	7472	0	100	100	Solyc01g111100.2.1	Neutral invertase like protein IPR006937 Plant neutral invertase
Root DW	1J	g118	-	868346	862136	6210	0	97.55	100	Solyc01g111120.2.1	Triosephosphate isomerase IPR000652 Triosephosphate isomerase
Root DW	1J	g133	-	965224	961760	3464	2E-176	98.39	62	Solyc01g111310.2.1	Transmembrane amino acid transporter protein IPR013057 Amino acid transporter, transmembrane
Root DW	1J	g147	-	1094951	1094021	930	0	99.21	100	Solyc01g111500.2.1	MYB transcription factor IPR015495 Myb transcription factor
Root DW	1J	g159	+	1210630	1214824	4194	0	93.52	100	Solyc01g111630.2.1	Glyoxylate_hydroxypyruvate reductase B IPR006140 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
Root DW	1J	g186	-	1416571	1411885	4686	0	99.79	100	Solyc01g111890.2.1	F-box_LRR-repeat protein 14 IPR001810 Cyclin-like F-box
Root DW	1J	g187	-	1420611	1418226	2385	2E-107	98.16	84	Solyc01g111890.2.1	F-box_LRR-repeat protein 14 IPR001810 Cyclin-like F-box
Root DW	1J	g192	-	1455167	1451489	3678	0	99.13	100	Solyc01g111930.2.1	Rop guanine nucleotide exchange factor 1 IPR005512 Rop nucleotide exchanger, PRONE
A	2K	g20	+	166606	169948	3342	0	98.73	100	Solyc02g091130.2.1	ATP synthase subunit beta IPR005722 ATPase, F1 complex, beta subunit
A	2K	g32	-	247026	245763	1263	3E-81	98.29	100	Solyc02g091280.2.1 (broken)	ATP-dependent Clp protease proteolytic subunit IPR001907 Peptidase S14, ClpP
A	2K	g33	-	250276	247706	2570	1E-136	98.94	83	Solyc02g091280.2.1 (broken)	ATP-dependent Clp protease proteolytic subunit IPR001907 Peptidase S14, ClpP
A	2K	g44	-	335826	309968	25858	0	96.01	100	Solyc02g091410.2.1	Pro-apoptotic serine protease nma111-like protein IPR009003 Peptidase, trypsin-like serine and cysteine
A	2K	g57	+	449713	468891	19178	0	99.42	68	Solyc02g091560.2.1	Serine hydroxymethyltransferase IPR001085 Serine hydroxymethyltransferase
A	2K	g120	-	1097160	1092324	4836	2E-50	98.68	49	Solyc02g092270.2.1	NADH dehydrogenase IPR006885 ETC complex I subunit conserved region
A	2K	g156	-	1428817	1425548	3269	5E-160	96.79	78	Solyc02g093680.2.1	Succinate dehydrogenase iron-sulfur protein IPR004489 Succinate dehydrogenase_fumarate reductase iron-sulphur protein
Root DW	2L	g14	-	123827	122519	1308	0	96.96	97	Solyc02g092930.1.1	MYB transcription factor IPR015495 Myb transcription factor
Root DW	2L	g87	-	739174	737819	1355	0	99.2	100	Solyc02g093740.2.1 (broken)	MYB transcription factor IPR015495 Myb transcription factor
Root DW	2L	g88	-	744054	741709	2345	2E-28	34.95	51	Solyc04g025900.1.1 (broken)	Unknown Protein
Root DW	2L	g131	-	1117807	1115152	2655	5E-85	99.15	99	Solyc02g094270.1.1	WRKY transcription factor IPR003657 DNA-binding WRKY
Root DW	2L	g133	+	1132646	1134725	2079	4E-62	93	46	Solyc02g094290.1.1	TCP family transcription factor IPR005333 Transcription factor, TCP
Root DW	4DE	g6	+	79866	83155	3289	0	99.6	100	Solyc04g014670.2.1	Short-chain dehydrogenase_reductase SDR IPR002347 Glucose_ribitol dehydrogenase
Root DW	4DE	g11	-	153337	147990	5347	2E-179	99.18	100	Solyc04g014760.2.1	RHO protein GDP dissociation inhibitor IPR000406 RHO protein GDP dissociation inhibitor
Root DW	4DE	g51	-	497118	493526	3592	0	98.9	100	Solyc04g015200.2.1	6-phosphofructokinase 2 IPR012004 Pyrophosphate-dependent phosphofructokinase TP0108
Root DW	4DE	g1274	-	16301657	16294385	7272	6E-82	94.78	42	Solyc04g005560.2.1	Guanine nucleotide exchange factor-like protein contains Interpro domain IPR000904
Root DW	4DE	g1494	-	18720532	18714916	5616	8E-91	86.45	70	Solyc04g025740.1.1	Homeobox-leucine zipper protein ROC3 IPR001356 Homeobox
Root DW	4DE	g3433	-	46622238	46613974	8264	0	99.63	100	Solyc04g049690.2.1	Adenylate kinase IPR006259 Adenylate kinase, subfamily
Root DW	4DE	g3813	-	51639317	51635779	3538	0	99.42	100	Solyc04g050440.2.1	Ammonium transporter IPR001905 Ammonium transporter
Root DW	4DE	g4104	-	55343936	55339150	4786	0	94.46	100	Solyc04g051080.1.1	Response regulator 8 IPR006447 Myb-like DNA-binding region, SHAKYF class
Root DW	4DE	g4110	-	55385146	55378684	6462	5E-107	77.61	81	Solyc04g051080.1.1	Response regulator 8 IPR006447 Myb-like DNA-binding region, SHAKYF class
Root DW	4DE	g4584	-	61316810	61313622	3188	7E-134	86.34	100	Solyc04g055620.1.1	Auxin Efflux Carrier IPR004776 Auxin efflux carrier
Root DW	7BC	g31	-	331049	327394	3655	0	96.67	100	Solyc07g005760.2.1	Hydroxycinnamoyl CoA shikimate_ quinate hydroxycinnamoyltransferase IPR003480 Transferase
Root DW	7BC	g74	+	853978	856980	3002	0	99.62	100	Solyc07g006280.2.1	Senescence-associated protein IPR000301 Tetraspanin, subgroup
Root DW	7BC	g80	-	955624	945613	10011	0	99.4	99	Solyc07g006350.2.1	Ankyrin repeat-rich protein IPR002110 Ankyrin
Root DW	7BC	g95	+	1091843	1095049	3206	0	99.2	100	Solyc07g006500.2.1	Alpha alpha-trehalose-phosphate synthase (UDP-forming) IPR001830 Glycosyl transferase, family 20
Root DW	7BC	g129	+	1584196	1588316	4120	0	99.84	100	Solyc07g006900.1.1	Auxin efflux carrier protein IPR014024 Auxin efflux carrier, subgroup
Root DW	7BC	g135	-	1619167	1614022	5145	0	98.83	100	Solyc07g006970.2.1	Solute carrier family 2, facilitated glucose transporter member 5 IPR003663 Sugar_inositol transporter
Root DW	7BC	g136	+	1624216	1626754	2538	0	99.27	99	Solyc07g006990.1.1	Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat
Root DW	7BC	g140	-	1655597	1648379	7218	0	91.88	99	Solyc07g007020.2.1	Receptor-like protein kinase At3g21340 IPR002290 Serine_threonine protein kinase
Root DW	7BC	g146	+	1721296	1726820	5524	0	81.7	99	Solyc07g007120.2.1	Homeobox protein knotted-1-like 3 IPR005541 KNOX2

<i>S. lycopersicum</i>										
ITAG2.4 proteins blastp										
ITAG2.4 Orthologous for <i>S. lycopersicum</i>										
Trait	BIN	# Gene	Sense	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	Functional_Description
Root DW	7BC	g170	-	2025242	2016895	8347	0	95.02	100	Solyc07g007430.2.1 Palmitoyltransferase akr1 [EC 2.3.1.-](Ankyrin repeat-containing protein akr1) IPR002110 Ankyrin
Root DW	7BC	g177	-	2075802	2074782	1020	1E-144	99	99	Solyc07g0007510.2.1 Adenylate cyclase IPR008172 Adenylate cyclase
Root DW	7BC	g248	-	3016598	3009997	6601	0	85.25	79	Solyc07g008380.1.1 Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	7BC	absent	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	7BC	g250	-	3044528	3043120	1408	0	88.83	100	Solyc07g008380.1.1 Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	7BC	g251	+	3048807	3051706	2899	0	99.06	100	Solyc07g008400.1.1 Pto-like, Serine_threonine kinase protein, resistance protein
Root DW	7BC	g253	-	3062508	3060933	1575	0	91.32	100	Solyc07g008380.1.1 Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	7BC	g254	+	3078897	3087088	8191	0	92.29	100	Solyc07g008410.2.1 Multidrug and toxin extrusion protein 1 IPR002528 Multi antimicrobial extrusion protein MatE
Root DW	7BC	g265	-	3269213	3265117	4096	0	97.65	93	Solyc07g008490.2.1 Nucleic acid binding protein IPR018111 K Homology, type 1, subgroup
Root DW	7BC	g272	+	3366259	3373511	7252	0	99.32	100	Solyc07g008520.2.1 Peptide transporter IPR000109 TGF-beta receptor, type I, II extracellular region
Shoot DW	9C	g3	-	19817	12694	7123	0	88.47	100	Solyc09g008480.2.1 Phosphatidylinositol-4-phosphate 5-kinase 9 IPR017163 Phosphatidylinositol-4-phosphate 5-kinase, plant
Shoot DW	9C	absent	NA	NA	NA	NA	NA	NA	NA	NA
Shoot DW	9C	g4	+	35706	45370	9664	6E-91	96.88	45	Solyc09g008490.2.1 HEAT repeat family protein expressed IPR011989 Armadillo-like helical
Shoot DW	9C	g6	+	48046	75328	27282	0	96.38	84	Solyc09g008490.2.1 HEAT repeat family protein expressed IPR011989 Armadillo-like helical
Shoot DW	9C	g17	-	205846	192097	13749	0	98.24	48	Solyc09g008640.1.1 Receptor-like protein kinase At3g21340 IPR002290 Serine_threonine protein kinase
Shoot DW	9C	g34	-	356066	348000	8066	0	95.96	96	Solyc09g008840.2.1 Pyruvate kinase IPR001697 Pyruvate kinase
Shoot DW	9C	g36	-	370176	367200	2976	0	99.11	100	Solyc09g008860.2.1 Receptor like kinase, RLK
Shoot DW	9C	g55	-	553766	551845	1921	0	97.62	100	Solyc09g009110.2.1 Gibberellin 20-oxidase IPR005123 Oxoglutarate and iron-dependent oxygenase
Shoot DW	9C	g66	+	670223	688344	18121	0	92.52	98	Solyc09g009190.2.1 1,4-alpha-glucan branching enzyme II IPR006589 Glycosyl hydrolase, family 13, subfamily, catalytic region
Root DW	9D	g1	+	1	23841	23840	0	97.59	99	Solyc09g009370.2.1 Vacuolar protein sorting-associated protein IPR009291 Protein of unknown function DUF946, plant
ShootDW	9D	g2	-	48397	37386	11011	0	98.82	100	Solyc09g009380.2.1 Protein kinase-like protein IPR002290 Serine_threonine protein kinase
ShootDW	9D	g4	-	65087	62193	2894	0	98.23	96	Solyc09g009400.2.1 APO protein 1, chloroplastic IPR008512 Protein of unknown function DUF794, plant
ShootDW	9D	g14	-	143217	140331	2886	0	97.99	90	Solyc09g009490.2.1 Bzip transcription factor IPR011700 Basic leucine zipper
ShootDW	9D	g21	+	198165	201148	2983	4E-125	98.84	100	Solyc09g009560.1.1 SELF PRUNING 9D
ShootDW	9D	g34	-	355286	353526	1760	0	76.16	99	Solyc10g083400.1.1 (duplicated) Cytochrome P450
ShootDW	9D	g35	+	362750	364187	1437	2E-105	74.63	55	Solyc10g083400.1.1 (duplicated) Cytochrome P450
ShootDW	9D	g54	-	595287	586049	9238	0	91.24	100	Solyc09g009910.2.1 Lipid A ABC transporter permease_ATP-binding protein IPR003439 ABC transporter-like
ShootDW	9D	g60	-	623217	618670	4547	0	99.24	100	Solyc09g009970.2.1 Rho GTPase activating protein 2 IPR000198 RhoGAP
ShootDW	9D	g61	+	633396	635546	2150	4E-104	96.67	100	Solyc09g009980.1.1 Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein
Root DW	9G	g26	-	332047	324800	7247	0	99.52	100	Solyc09g072820.2.1 Cellulose synthase IPR005150 Cellulose synthase
Root DW	9G	g59	-	628620	627012	1608	0	98.87	100	Solyc09g074080.1.1 Glycosyltransferase family GT8 protein IPR002495 Glycosyl transferase, family 8
Root DW	9G	g84	-	870955	866842	4113	0	98.96	100	Solyc09g074230.2.1 Glucose transporter 8 IPR003663 Sugar_inositol transporter
Root DW	9G	g94	+	975609	980496	4887	0	98.22	72	Solyc09g074310.2.1 Oxidoreductase aldo_keto reductase family protein expressed IPR001395 Aldo_keto reductase
Starch/ED	11B	g10	+	139036	146247	7211	0	96.31	100	Solyc11g008590.1.1 UDP-galactose transporter-like protein IPR007271 Nucleotide-sugar transporter
Starch/ED	11B	g12	-	165577	155752	9825	0	94.12	93	Solyc11g008610.1.1 Nucleotide-sugar transporter UDP N-acetylglucosamine-like signal peptide 9 or more transmembrane domains (Fragment) IPR007271 Nucleotide-sugar transporter
Starch/ED	11B	g13	-	174097	167460	6637	0	96.56	100	Solyc11g008620.1.1 Phosphoglycolate phosphatase IPR006349 2-phosphoglycolate phosphatase, eukaryotic
Starch/ED	11B	g22	+	267511	274730	7219	0	92.57	100	Solyc11g008720.1.1 Beta-glucosidase G4 IPR001360 Glycoside hydrolase, family 1
Starch/ED	11B	g68	+	692684	693997	1313	2E-176	100	93	Solyc11g010200.1.1 14-3-3 protein beta_alpha-1 IPR000308 14-3-3 protein
Starch/ED	11B	g76	-	789494	784240	5254	0	98.8	92	Solyc11g010290.1.1 2-oxoglutarate_malate translocator IPR001898 Sodium_sulphate symporter
Starch/ED	11B	g90	+	908628	914434	5806	0	99.25	100	Solyc11g010450.1.1 Phosphofructokinase family protein IPR012004 Pyrophosphate-dependent phosphofructokinase TP0108
Malate	11D	g8	-	61767	50993	10774	0.0	99.46	68	Solyc11g065830.1.1 2-oxoglutarate_malate translocator-like protein IPR001898 Sodium_sulphate symporter
A	11H	g17	-	180579	171704	8875	8E-121	100	100	Solyc11g072450.1.1 Mitochondrial FO ATP synthase D chain IPR008689 ATPase, FO complex, subunit D, mitochondrial
A	11H	g35	+	429554	434044	4490	0	100	100	Solyc11g072630.1.1 Mitogen-activated protein kinase IPR008351 JNK MAP kinase
A	11H	g41	+	479484	497046	17562	0	99.08	65	Solyc11g072710.1.1 Protein kinase IPR002290 Serine_threonine protein kinase

NCU: non-conding upstream region:intergenic, promoter or 5' UTR

NCD: non-conding downstream region: 3' UTR or intergenic region

intron

exon

intron-exon: intron-exon junction

NA: non applicable

Numbers in brackets indicate the number of elements in the corresponding position

										<i>S. pennellii</i>		
ITAG2.4 proteins blastp										ITAG2.4 Orthologous for <i>S.lycopersicum</i>	Functional_Description	
Trait	BIN	# Gene	Sense	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	(Heinz)		
Root DW	1J	g1	-	5327	1	5326	0	100	100	Solyc01g109790.2.1	Glucose-1-phosphate adenylyltransferase	IPR011831 Glucose-1-phosphate adenylyltransferase IPR005836 ADP-glucose pyrophosphorylase, conserved site
Root DW	1J	g14	-	1358137	1356650	1487	0	100	100	Solyc01g109940.2.1	26S protease regulatory subunit	IPR005937 26S proteasome subunit P45
Root DW	1J	g51	+	445655	448174	2519	0	97.78	100	Solyc01g110360.2.1	Fructose-bisphosphate aldolase	IPR000741 Fructose-bisphosphate aldolase, class-I
Root DW	1J	g68-g104 (28)	both	575070	789329	NA	NA	NA	NA	NA	Auxin-induced SAUR-like protein	IPR003676 Auxin responsive SAUR protein
Root DW	1J	g110	-	828076	826922	1154	5E-71	100	100	Solyc01g111080.2.1	Gibberellin-regulated protein 2	IPR003854 Gibberellin regulated protein
Root DW	1J	g112	-	844486	839544	4942	0	100	100	Solyc01g111100.2.1/	Neutral invertase like protein	IPR006937 Plant neutral invertase/
Root DW	1J	g113	-	861350	855257	6093	0	82.14	100	Solyc01g111120.2.1	Triosephosphate isomerase	IPR000652 Triosephosphate isomerase
Root DW	1J	g129	-	957880	954392	3488	2E-177	98.79	62	Solyc01g111310.2.1	Transmembrane amino acid transporter protein	IPR013057 Amino acid transporter, transmembrane
Root DW	1J	g143	-	1083187	1081049	2138	1E-160	100	91	Solyc01g111500.2.1	MYB transcription factor	IPR015495 Myb transcription factor
Root DW	1J	g156	+	1209971	1214092	4121	0	93.78	100	Solyc01g111630.2.1	Glyoxylate_hydroxypyruvate reductase B	IPR006140 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding
Root DW	1J	g181	-	1423547	1417145	6402	0	100	100	Solyc01g111890.2.1	F-box_LRR-repeat protein 14	IPR001810 Cyclin-like F-box
Root DW	1J	g182	-	1425957	1424890	1067	3E-111	98.2	98	Solyc01g111890.2.2	F-box_LRR-repeat protein 14	IPR001810 Cyclin-like F-box
Root DW	1J	g186	-	1453127	1449337	3790	0	100	100	Solyc01g111930.2.1	Rop guanine nucleotide exchange factor 1	IPR005512 Rop nucleotide exchanger, PRONE
A	2K	g20	+	152316	155738	3422	0	99.27	100	Solyc02g091130.2.1	ATP synthase subunit beta	IPR005722 ATPase, F1 complex, beta subunit
A	2K	g32	-	234703	230019	4684	0	90.09	100	Solyc02g091280.2.1	ATP-dependent Clp protease proteolytic subunit	IPR001907 Peptidase S14, ClpP
A	2K	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A	2K	g43	-	320583	298599	21984	0	97.71	100	Solyc02g091410.2.1	Pro-apoptotic serine protease nma111-like protein	IPR009003 Peptidase, trypsin-like serine and cysteine
A	2K	g55	+	430422	436960	6538	0	100	100	Solyc02g091560.2.1	Serine hydroxymethyltransferase	IPR001085 Serine hydroxymethyltransferase
A	2K	g112	-	1017394	1013194	4200	7E-29	73.61	40	Solyc02g092270.2.1	NADH dehydrogenase	IPR006885 ETC complex I subunit conserved region
A	2K	g144	-	1324414	1321722	2692	9E-165	100	85	Solyc02g092730.2.1	Iron sulfur subunit of succinate dehydrogenase	IPR004489 Succinate dehydrogenase_fumarate reductase iron-sulphur protein
Root DW	2L	g13	-	115827	114521	1306	0	99.72	97	Solyc02g092930.2.1	MYB transcription factor	IPR015495 Myb transcription factor
Root DW	2L	g80	-	712154	710861	1293	0	100	100	Solyc02g093740.2.1	MYB transcription factor	IPR015495 Myb transcription factor
Root DW	2L	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	2L	g124	-	1088676	1085931	2745	2E-85	100	100	Solyc02g094270.1.1	WRKY transcription factor	IPR003657 DNA-binding WRKY
Root DW	2L	g126	+	1106165	1108032	1867	3E-44	100	39	Solyc02g094290.1.1	TCP family transcription factor	IPR005333 Transcription factor, TCP
Root DW	4DE	g8	+	100106	102975	2869	0	100	100	Solyc04g014670.2.1	Short-chain dehydrogenase_reductase SDR	IPR002347 Glucose_ribitol dehydrogenase
Root DW	4DE	g15	-	176107	170922	5185	0	100	100	Solyc04g014760.2.1	RHO protein GDP dissociation inhibitor	IPR000406 RHO protein GDP dissociation inhibitor
Root DW	4DE	g51	-	549814	546714	3100	0	100	100	Solyc04g015200.2.1	6-phosphofructokinase 2	IPR012004 Pyrophosphate-dependent phosphofructokinase TP0108
Root DW	4DE	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	4DE	g1300	-	17447365	17442124	5241	9E-93	97.12	57	Solyc04g025740.1.1	Homeobox-leucine zipper protein ROC3	IPR001356 Homeobox
Root DW	4DE	g2768	-	37377760	37369442	8318	0	99.63	100	Solyc04g049690.2.1	Adenylate kinase	IPR006259 Adenylate kinase, subfamily
Root DW	4DE	g3075	-	41549616	41546792	2824	0	100	100	Solyc04g050440.2.1	Ammonium transporter	IPR001905 Ammonium transporter
Root DW	4DE	g3265	+	43800306	43805862	5556	0	99.34	78	Solyc04g051080.1.1	Response regulator 8	IPR006447 Myb-like DNA-binding region, SHAKYF class
Root DW	4DE	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	4DE	g3686	-	48916526	48912990	3536	4E-134	86.34	100	Solyc04g056620.1.1	Auxin Efflux Carrier	IPR004776 Auxin efflux carrier
Root DW	7BC	g36	-	368287	364567	3720	0	100	100	Solyc07g005760.2.1	Hydroxycinnamoyl CoA shikimate_quinase	hydroxycinnamoyltransferase IPR003480 Transferase
Root DW	7BC	g78	+	826231	829281	3050	0	100	100	Solyc07g006280.2.1	Senescence-associated protein	IPR000301 Tetraspanin, subgroup
Root DW	7BC	g84	-	931477	924649	6828	0	100	99	Solyc07g006350.2.1	Ankyrin repeat-rich protein	IPR002110 Ankyrin
Root DW	7BC	g97	+	1057911	1061119	3208	0	100	100	Solyc07g006500.2.1	Alpha alpha-trehalose-phosphate synthase (UDP-forming)	IPR001830 Glycosyl transferase, family 20
Root DW	7BC	g133	+	1511886	1515103	3217	0	100	100	Solyc07g006900.1.1	Auxin efflux carrier protein	IPR014024 Auxin efflux carrier, subgroup
Root DW	7BC	g138	-	1545017	1540284	4733	0	100	100	Solyc07g006970.2.1	Solute carrier family 2, facilitated glucose transporter member 5	IPR003663 Sugar_inositol transporter
Root DW	7BC	g139	+	1549771	1552312	2541	0	100	99	Solyc07g006990.1.1	Pentatricopeptide repeat-containing protein	IPR002885 Pentatricopeptide repeat
Root DW	7BC	g142	-	1571572	1564868	6704	0	94.49	96	Solyc07g007020.2.1	Receptor-like protein kinase At3g21340	IPR002290 Serine_threonine protein kinase
Root DW	7BC	g148	+	1632991	1638889	5898	0	100	89	Solyc07g007120.2.1	Homeobox protein knotted-1-like 3	IPR005541 KNOX2

										<i>S. pennellii</i>	
										ITAG2.4 proteins blastp	
										ITAG2.4 Orthologous for <i>S.lycopersicum</i>	
Trait	BIN	# Gene	Sense	Gene Start	Gene End	Gene Size	e-value	% id	% qcoverage	(Heinz)	Functional_Description
Root DW	78C	g170	-	2025242	2016895	8347	0	95.02	100	Solyc07g007430.2.1	Palmitoyltransferase akr1 (EC 2.3.1.-)[Ankyrin repeat-containing protein akr1] IPR002110 Ankyrin
Root DW	78C	g177	-	2075802	2074782	1020	1E-144	99	99	Solyc07g007510.2.1	Adenylate cyclase IPR008172 Adenylate cyclase
Root DW	78C	g248	-	3016598	3009997	6601	0	85.25	79	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	78C	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
Root DW	78C	g250	-	3044528	3043120	1408	0	88.83	100	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	78C	g251	+	3048807	3051706	2899	0	99.06	100	Solyc07g008400.1.1	Pto-like, Serine_threonine kinase protein, resistance protein
Root DW	78C	g253	-	3062508	3060933	1575	0	91.32	100	Solyc07g008380.1.1	Hydroxycinnamoyl CoA quinate transferase IPR003480 Transferase
Root DW	78C	g254	+	3078897	3087088	8191	0	92.29	100	Solyc07g008410.2.1	Multidrug and toxin extrusion protein 1 IPR002528 Multi antimicrobial extrusion protein MatE
Root DW	78C	g265	-	3269213	3265117	4096	0	97.65	93	Solyc07g008490.2.1	Nucleic acid binding protein IPR018111 K Homology, type 1, subgroup
Root DW	78C	g272	+	3366259	3373511	7252	0	99.32	100	Solyc07g008520.2.1	Peptide transporter IPR000109 TGF-beta receptor, type I, II extracellular region
Shoot DW	9C	g3	-	19817	12694	7123	0	88.47	100	Solyc09g008480.2.1	Phosphatidylinositol-4-phosphate 5-kinase 9 IPR017163 Phosphatidylinositol-4-phosphate 5-kinase, plant
Shoot DW	9C	absent	NA	NA	NA	NA	NA	NA	NA	NA	NA
Shoot DW	9C	g4	+	35706	45370	9664	6E-91	96.88	45	Solyc09g008490.2.1	HEAT repeat family protein expressed IPR011989 Armadillo-like helical
Shoot DW	9C	g6	+	48046	75328	27282	0	96.38	84	Solyc09g008490.2.1	HEAT repeat family protein expressed IPR011989 Armadillo-like helical
Shoot DW	9C	g17	-	205846	192097	13749	0	98.24	48	Solyc09g008640.1.1	Receptor-like protein kinase At3g21340 IPR002290 Serine_threonine protein kinase
Shoot DW	9C	g34	-	356066	348000	8066	0	95.96	96	Solyc09g008840.2.1	Pyruvate kinase IPR001697 Pyruvate kinase
Shoot DW	9C	g36	-	370176	367200	2976	0	99.11	100	Solyc09g008860.2.1	Receptor like kinase, RLK
Shoot DW	9C	g55	-	553766	551845	1921	0	97.62	100	Solyc09g009110.2.1	Gibberellin 20-oxidase IPR005123 Oxoglutarate and iron-dependent oxygenase
Shoot DW	9C	g66	+	670223	688344	18121	0	92.52	98	Solyc09g009190.2.1	1,4-alpha-glucan branching enzyme II IPR006589 Glycosyl hydrolase, family 13, subfamily, catalytic region
Root DW	9D	g1	+	1	23841	23840	0	97.59	99	Solyc09g009370.2.1	Vacuolar protein sorting-associated protein IPR009291 Protein of unknown function DUF946, plant
ShootDW	9D	g2	-	48397	37386	11011	0	98.82	100	Solyc09g009380.2.1	Protein kinase-like protein IPR002290 Serine_threonine protein kinase
ShootDW	9D	g4	-	65087	62193	2894	0	98.23	96	Solyc09g009400.2.1	APO protein 1, chloroplastic IPR008512 Protein of unknown function DUF794, plant
ShootDW	9D	g14	-	143217	140331	2886	0	97.99	90	Solyc09g009490.2.1	Bzip transcription factor IPR011700 Basic leucine zipper
ShootDW	9D	g21	+	198165	201148	2983	4E-125	98.84	100	Solyc09g009560.1.1	SELF PRUNING 9D
ShootDW	9D	g34	-	355286	353526	1760	0	76.16	99	Solyc10g083400.1.1 (duplicated)	Cytochrome P450
ShootDW	9D	g35	+	362750	364187	1437	2E-105	74.63	55	Solyc10g083400.1.1 (duplicated)	Cytochrome P450
ShootDW	9D	g54	-	595287	586049	9238	0	91.24	100	Solyc09g009910.2.1	Lipid A ABC transporter permease_ATP-binding protein IPR003439 ABC transporter-like
ShootDW	9D	g60	-	623217	618670	4547	0	99.24	100	Solyc09g009970.2.1	Rho GTPase activating protein 2 IPR000198 RhoGAP
ShootDW	9D	g61	+	633396	635546	2150	4E-104	96.67	100	Solyc09g009980.1.1	Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein
Root DW	9G	g26	-	332047	324800	7247	0	99.52	100	Solyc09g072820.2.1	Cellulose synthase IPR005150 Cellulose synthase
Root DW	9G	g59	-	628620	627012	1608	0	98.87	100	Solyc09g074080.1.1	Glycosyltransferase family GT8 protein IPR002495 Glycosyl transferase, family 8
Root DW	9G	g84	-	870955	866842	4113	0	98.96	100	Solyc09g074230.2.1	Glucose transporter 8 IPR003663 Sugar_inositol transporter
Root DW	9G	g94	+	975609	980496	4887	0	98.22	72	Solyc09g074310.2.1	Oxidoreductase aldo_keto reductase family protein expressed IPR001395 Aldo_keto reductase
Starch/ED	11B	g10	+	139036	146247	7211	0	96.31	100	Solyc11g008590.1.1	UDP-galactose transporter-like protein IPR007271 Nucleotide-sugar transporter
Starch/ED	11B	g12	-	165577	155752	9825	0	94.12	93	Solyc11g008610.1.1	Nucleotide-sugar transporter UDP N-acetylglucosamine-like signal peptide 9 or more transmembrane domains (Fragment) IPR007271 Nucleotide-sugar transporter
Starch/ED	11B	g13	-	174097	167460	6637	0	96.56	100	Solyc11g008620.1.1	Phosphoglycolate phosphatase IPR006349 2-phosphoglycolate phosphatase, eukaryotic
Starch/ED	11B	g22	+	267511	274730	7219	0	92.57	100	Solyc11g008720.1.1	Beta-glucosidase G4 IPR001360 Glycoside hydrolase, family 1
Starch/ED	11B	g68	+	692684	693997	1313	2E-176	100	93	Solyc11g010200.1.1	14-3-3 protein beta_alpha-1 IPR000308 14-3-3 protein
Starch/ED	11B	g76	-	789494	784240	5254	0	98.8	92	Solyc11g010290.1.1	2-oxoglutarate_malate translocator IPR001898 Sodium_sulphate symporter
Starch/ED	11B	g90	+	908628	914434	5806	0	99.25	100	Solyc11g010450.1.1	Phosphofructokinase family protein IPR012004 Pyrophosphate-dependent phosphofructokinase TP0108
Malate	11D	g8	-	61767	50993	10774	0.0	99.46	68	Solyc11g065830.1.1	2-oxoglutarate_malate translocator-like protein IPR001898 Sodium_sulphate symporter
A	11H	g17	-	180579	171704	8875	8E-121	100	100	Solyc11g072450.1.1	Mitochondrial FO ATP synthase D chain IPR008689 ATPase, FO complex, subunit D, mitochondrial
A	11H	g35	+	429554	434044	4490	0	100	100	Solyc11g072630.1.1	Mitogen-activated protein kinase IPR008351 JNK MAP kinase
A	11H	g41	+	479484	497046	17562	0	99.08	65	Solyc11g072710.1.1	Protein kinase IPR002290 Serine_threonine protein kinase

NCU: non-conding upstream region: intergenic, promoter or 5' UTR

NCD: non-conding downstream region: 3' UTR or intergenic region

intron

exon

intron-exon: intron-exon junction

NA: non applicable

Numbers in brackets indicate the number of elements in the corresponding position

Differentially inserted TEs							
Trait	BIN	<i>S. pennellii</i> TE positions		<i>S. pennellii</i> TE type	<i>S. lycopersicum</i> TE positions		<i>S. lycopersicum</i> TE type
Root DW	1J	NCU (2)	TIR_DNA3-8_Stu, TIR_DNA9-6_Stu		NCU (2)	TIR_DNA9-1_Stu, TIR_TLP1	
Root DW	1J	intron	TIR_MuDR-4_Stu		none	none	
Root DW	1J	none	none		none	none	
Root DW	1J	intron-exon	LINE_L1-5_Stu		intron (2)	TIR_DNA-TA-1_Stu, TIR_DNA9-5_Stu	
Root DW	1J	none	none		none	none	
Root DW	1J	NCU (2)	LTR_TLC1, TIR_TLP2		NCU (5)	TIR_DNA9-3_Stu, TIR_DNA9-6_Stu, TIR_TLP1, TIR_MUDRAV12, TIR_EnSpm-3_VV	
Root DW	1J	none	none		none	none	
Root DW	1J	NCU, NCD	TIR_HATSOD1, LTR_Copia-1_ST		none	none	
Root DW	1J	NCU	LTR_SONATA2		NCU (2), NCD	LTR_Copia-3_SL, TIR_DNA9-4_Stu, TIR_DNA3-8_Stu	
Root DW	1J	none	none		none	none	
Root DW	1J	NCD (2)	TIR_SHAAMUDRAV_MT, LTR_Copia-75_ST		intron	RC_Helitron-2_Stu	
Root DW	1J	none	none		none	none	
Root DW	1J	NCU (2)	TIR_SONATA1, TIR_DNA-TA-1_Stu		NCU (3)	TIR_EnSpm-11_OS, TIR_MuDR-21_VV, TIR_SONATA1	
A	2K	NCU	TIR_hAT-4_PTr		none	none	
A	2K	none	none		none	none	
A	2K	none	none		NA	NA	
A	2K	NCU (3)	TIR_DNA9-4_Stu, TIR_hAT-N3_Stu, TIR_HARB-N1_Stu		none	none	
A	2K	intron (3)	TIR_hAT-1_Stu, TIR_STOWAWAY50_OS, TIR_MuDR-21_VV		intron (3), NCD	TIR_MuDR-1_Stu, TIR_MuDR-1_Stu, TIR_DNA9-5, TIR_DNA3-8_Stu	
A	2K	none	none		none	none	
A	2K	intron-exon	TIR_DNA9-6_Stu		none	none	
Root DW	2L	none	none		NCU	RC_HEUTRON7_OS	
Root DW	2L	NCU	TIR_DNA9-4_Stu		intron	LTR_TOTO1_LP	
Root DW	2L	none	none		NA	NA	
Root DW	2L	NCD (2)	TIR_MuDR-8_Mad, LTR_Gypsy-31_ST		intron	TIR_EnSpm-5_HV	
Root DW	2L	none	none		none	none	
Root DW	4DE	none	none		NCU (2)	LTR_Gypsy-11_SL, LTR_Copia-5_SL	
Root DW	4DE	NCD	TIR_DNA3-6_Stu		none	none	
Root DW	4DE	NCU, NCD (2)	TIR_DNA9-4_Stu, TIR_SONATA2, TIR_DNA3-7_Stu		NCU (2), NCD	LTR_Gypsy-40_Mad, TIR_DNA-TA-2_Stu, LTR_TOTO1_LP	
Root DW	4DE	NCU (6), intron (2), NCD (3)	LTR_Gypsy-21_ST, LTR_Gypsy-39_Stu, LTR_Gypsy-43_Stu, LTR_Gypsy-41_Stu, LTR_Gypsy-41_Stu, TIR_HARB-1_Stu, TIR_EnSpm-34_Sbi, EnSpm-3_TA, LTR_Gypsy-45_Stu, LTR_G		NA	NA	
Root DW	4DE	NCU (2), NCD (2)	LTR_Gypsy-27_ST, TIR_DNA3-6_Stu, LTR_Gypsy-45_Stu, LTR_Gypsy-41_Stu		none	none	
Root DW	4DE	NCD	TIR_TLP1		NCU (3), NCD	LTR_Gypsy-24_ST, TIR_MuDR-7_Stu, TIR_hAT-N4_Stu, TIR_DNA9-1_Stu	
Root DW	4DE	NCU (3)	LTR_Gypsy-120_SB, TIR_MuDR-11N_VV, TIR_MuDR-11N_VV		NCU (4), NCD	LTR_Gypsy-11_SL, TIR_EnSpm-12_OS, TIR_MuDR-8_VV, TIR_EnSpm-5_HV, TIR_hAT-N4_Stu	
Root DW	4DE	none	none		NCU	LTR_Gypsy-41_Stu	
Root DW	4DE	NCU (3), NCD (2)	LTR_Gypsy-41_Stu, LTR_Gypsy-44_Stu, LTR_Gypsy-27_ST, LTR_Copia-18_ST, TIR_EnSpm-1_Stu		NA	NA	
Root DW	4DE	NCU, NCD (2)	TIR_hAT-N6_Stu, TIR_DNA3-8_Stu, SINE_SO		intron, NCD (3)	TIR_DNA3-8_Stu, LTR_Copia11-VV, TIR_EnSpm-5_HV, RC_Helitron-4n1_Smo	
Root DW	78C	NCU (3), NCD	TIR_MPH-A6-3-Ta, LTR_Copia11-VV, TIR_MuDR-8_VV, TIR_DNA3-3_Stu		none	none	
Root DW	78C	NCD (2)	LTR_Gypsy-28_ST, TIR_LTP1		NCD (2)	TIR_TLP2, TIR_DNA3-8_Stu	
Root DW	78C	NCU, NCD	LTR_Copia-1_ST, TIR_hAT-N4_Stu		none	none	
Root DW	78C	none	none		none	none	
Root DW	78C	NCU	TIR_DNA9-6_Stu		none	none	
Root DW	78C	NCU	TIR_DNA3-4_Stu		none	none	
Root DW	78C	NCU	TIR_EnSpm-2_SB		none	none	
Root DW	78C	NCU (3), NCD (3)	SINE_TS2, LINE_RTE-1_Stu, LTR_Copia4-VV, LINE_RTE-1_Stu, TIR_hAT-N3_Stu, LINE_RTE-1_Stu		NCD	TIR_EnSpm-1_Stu	
Root DW	78C	none	none		exon, NCD	TIR_EnSpm-34_Sbi, LTR_Copia-1_ST	

Trait	BIN	<i>S. pennellii</i> TE positions		<i>S. pennellii</i> TE type	<i>S. lycopersicum</i> TE positions		<i>S. lycopersicum</i> TE type
Root DW	78C	none	none		NCU	TIR_HARB-3_Stu	
Root DW	78C	none	none		none	none	
Root DW	78C	NCU, intron	LTR_Athila7, LTR_Gypsy-25_ST		NCU	TIR_DNA9-1_Stu	
Root DW	78C	NA	NA		NCU (2)	TIR_DNA9-1_Stu, TIR_DNA-TA-2_Stu	
Root DW	78C	NCU (3), NCD	SINE_SINE_S0, TIR_DNA3-6_Stu, TIR_DNA3-6_Stu, LTR_Gypsy-11_SL		NA	NA	
Root DW	78C	NCU, NCD (5)	SINE_S0, TIR_DNA9-4_Stu, TIR_DNA9-5_Stu, TIR_DNA9-6_Stu, TIR_DNA-TA-1_Stu, TIR_DNA3-8_Stu		NCD (2)	TIR_DNA9-4_Stu, TIR_DNA9-1_Stu	
Root DW	78C	NCU (2)	TIR_DNA3-6_Stu, LTR_Gypsy-11_SL		NA	NA	
Root DW	78C	NCU, intron (4)	SINE_S0, TIR_SONATA1, TIR_DNA9-1_Stu, TIR_DNA9-5_Stu, TIR_DNA-TA-1_Stu		NCU (2), intron (4)	TIR_EnSpm-2_TD, TIR_DNA-TA-2_Stu, TIR_SONATA2, TIR_TLP1, TIR_TPL3, TIR_DNA9-6_Stu	
Root DW	78C	NCU	LTR_TLP1		NCD (3)	LINE_L1-14_Stu, TIR_DNA-TA-2_Stu, TIR_DNA3-5_Stu	
Root DW	78C	NCU (2), NCD	TIR_EnSpm-3_TA, TIR_SONATA2, TIR_hAT-N4_Stu		U-exon-intron, intron-exon (3), int	LTR_Copia-59_ST, LTR_Copia-56_ST, LTR_Gypsy-6_ST, LTR_Copia-45_GM, TIR_DNA9-4_Stu	
Shoot DW	9C	none	none		none	none	
Shoot DW	9C	NA	NA		NCU	TIR_DNA9-1_Stu	
Shoot DW	9C	NCU, intron	TIR_DNA9-6_Stu, TIR_EnSpm-10_Stu		NCU (3)	TIR_DNA9-6_Stu, LINE_RTE-1_Stu, TIR_DNA3-8_Stu	
Shoot DW	9C	intron-exon, intron, NCD	LINE_L1-15_Stu, LTR_Copia 11-VV, TIR_EnSpm-6_Stu		NCU, intron-exon, intron (2)	LINE_L1-12_Stu, LINE_L1-15_Stu, LTR_Copia-97_GM, TIR_EnSpm-6_Stu	
Shoot DW	9C	NCU, intron, intron-exon	TIR_POTTEN1, TIR_SONATA 2, LINE_L1-11_Stu		intron	LTR_NonLTR-1_Stu	
Shoot DW	9C	none	none		none	none	
Shoot DW	9C	NCU	TIR_DNA8-1_Stu		NCU (2)	TIR_DNA-TA-2_Stu, TIR_DNA3-7_Stu	
Shoot DW	9C	NCU, intron	TIR_ATHPOGON3, TIR_EnSpm-1_Stu		NCU	TIR_ATHPOGO	
Shoot DW	9C	none	none		NCU, intron	TIR_EnSpm-5_VV, SINE_TS	
Root DW	9D	intron (2), intron-exon-NCD, NCD	TIR_DNA3-3_Stu, TIR_MUDRAV1, LTR_Copia-1_ST, LTR_TOT01_LP		intron	TIR_EnSpm-34_Sbi	
ShootDW	9D	NCD (3)	TIR_hAT-6_Stu, TIR_MuDR-1_Stu, TIR_DNA3-8_Stu		NCU, NCD	LTR_Gypsy-11_SL, LTR_Copia-1_ST	
ShootDW	9D	NCU (2)	TIR_TLP1, TIR_HATSOD1		NCU (2)	TIR_SONATA2, TIR_HATSOD1	
ShootDW	9D	none	none		none	none	
ShootDW	9D	NCU (5), intron	LTR_Gypsy-25_ST, RC_HEUTRON7_OS, TIR_MUDRAV1, TIR_DNA9-1_Stu, TIR_EnSpm-16_Sbi, TIR_DNA9-6_Stu		intron	LINE_RTE-1_Stu	
ShootDW	9D	NCU, NCD (2)	SINE_S0, TIR_DNA9-1_Stu, LTR_Copia-75_ST		NA	NA	
ShootDW	9D	none	none		NA	NA	
ShootDW	9D	none	none		NCU, intron	LTR_GYLES1, SINE_TS2	
ShootDW	9D	NCU (2)	TIR_DNA9-5_Stu, TIR_DNA-TA-2_Stu		NCU (5)	TIR_DNA-TA-2_Stu, TIR_POTTEN2, TIR_POTTEN2, TIR_POTTEN1, TIR_DNA-TA-2_Stu	
ShootDW	9D	none	none		NCU	LTR_Gypsy-11_SL	
Root DW	9G	intron	LTR_Copia-1_ST		none	none	
Root DW	9G	NCU (2)	TIR_hAT-N3_Stu, LTR_Gypsy-40_Stu		NCU	LTR_Copia-1_ST	
Root DW	9G	NCU	TIR_DNA3-8_Stu		intron-exon	TIR_hAT-6_VV	
Root DW	9G	NCU (4)	TIR_hAT-N1_Stu, TIR_DNA9-2_Stu, TIR_hAT-N4_Stu, LINE_RTE-1_Stu		NCU	TIR_EnSpm-1_Stu	
Starchy/ED	11B	none	none		none	none	
Starchy/ED	11B	none	none		none	none	
Starchy/ED	11B	none	none		intron	LTR_Copia-75_ST	
Starchy/ED	11B	intron	LINE_RTE-1_Stu		intron (3)	TIR_SONATA3, TIR_EnSpm-1_Stu, LINE_RTE-1_Stu	
Starchy/ED	11B	none	none		NCU	TIR_DNA-TA-1_Stu	
Starchy/ED	11B	NCU, intron (2)	TIR_TLP1, LINE_RTE-1_Stu, TIR_EnSpm-1_Stu		intron	SINE_TS	
Starchy/ED	11B	NCU, NCD	LINE_RTE-1_Stu, TIR_DNA-TA-2_Stu		NCU	SINE_TS2	
Malate	11D	NCU (2)	LTR_Copia-96_ST, LTR_Copia-3_SL		NCU (2), intron (2)	SINE_TS2, SINE_TS2, TIR_EnSpm-17_ZM, TIR_EnSpm-5_HV	
A	11H	NCU	TIR_MUDSOLD1		NCU	TIR_MUDSOLD1	
A	11H	NCU, intron, NCD	TIR_DNA9-2_Stu, TIR_SONATA2, LTR_Copia-2_SL		NCU, intron	LTR_Ogre-SD1, TIR_DNA9-2_Stu	
A	11H	intron (3)	TIR_DNA9-4_Stu, TIR_EnSpm-4_VV, TIR_EnSpm-1_Stu		NCU (2)	TIR_EnSpm-34_Sbi, LTR_Copia-75_ST	

NCU: non-conding upstream region: intergenic, promoter or 5' UTR

NCD: non-conding downstream region: 3' UTR or intergenic region

intron

exon

intron-exon: intron-exon junction

NA: non applicable

Numbers in brackets indicate the number of elements in the corresponding position

Trait	BIN	ILs with <i>S. pennellii</i> loci	Mean RPKM for ILs with <i>S. pennellii</i> loci	SD RPKM for ILs with <i>S. pennellii</i> loci	Mean RPKM for other ILs	SD RPKM for other ILs	P value (T-test)
Root DW	1J	IL 1-4, IL 1-4-18	64.193	13.348	59.040	6.492	2.82E-01
Root DW	1J		292.540	48.996	238.033	14.543	5.51E-06
Root DW	1J		317.664	5.194	412.038	99.869	1.88E-01
Root DW	1J		NA	NA	NA	NA	NA
Root DW	1J		25.330	0.230	1.357	0.544	1.79E-65
Root DW	1J		1.671	0.361	1.008	0.265	8.78E-04
Root DW	1J		160.521	6.254	110.521	13.145	9.98E-07
Root DW	1J		86.264	13.100	75.433	10.236	1.46E-01
Root DW	1J		9.795	1.805	7.815	1.435	5.90E-02
Root DW	1J		508.715	8.954	443.041	56.496	1.07E-01
Root DW	1J		55.053	2.034	61.504	4.773	6.18E-02
Root DW	1J		65.591	0.978	62.629	4.611	3.70E-01
A	2K		NA	NA	NA	NA	NA
A	2K		262.662	12.400	230.429	17.142	1.03E-02
A	2K		48.636	4.329	44.374	3.451	9.02E-02
A	2K	IL 2-5, IL 2-6	1055.926	345.005	1011.969	170.594	7.26E-01
A	2K		132.539	3.689	154.461	15.678	5.33E-02
A	2K		119.073	12.478	123.338	12.122	6.25E-01
A	2K		36.079	12.551	28.235	3.521	5.07E-03
Root DW	2L	IL 2-6, IL2-6-5	5.252	0.649	4.527	0.891	2.58E-01
Root DW	2L		NA	NA	NA	NA	NA
Root DW	2L		NA	NA	NA	NA	NA
Root DW	2L		NA	NA	NA	NA	NA
Root DW	4DE	IL 4-1, IL 4-2, IL 4-3, IL 4-3-2	49.510	5.774	93.783	9.468	6.36E-14
Root DW	4DE		40.527	10.334	51.736	5.253	1.89E-04
Root DW	4DE		4.010	0.966	2.605	0.464	4.43E-07
Root DW	4DE		NA	NA	NA	NA	NA
Root DW	4DE		NA	NA	NA	NA	NA
Root DW	4DE		26.033	3.484	22.550	2.036	1.98E-03
Root DW	4DE		12.014	2.608	8.675	1.866	1.03E-03
Root DW	4DE		NA	NA	NA	NA	NA
Root DW	4DE		NA	NA	NA	NA	NA
Root DW	4DE		NA	NA	NA	NA	NA
Root DW	7BC		30.457	4.455	67.829	7.094	4.27E-16
Root DW	7BC		86.516	3.493	99.163	8.340	3.65E-03
Root DW	7BC	IL 7-4, IL 7-4-1, IL 7-5, IL 7-5-5	17.457	1.155	13.455	1.226	1.44E-08
Root DW	7BC		5.880	1.072	6.047	1.486	8.25E-01
Root DW	7BC		NA	NA	NA	NA	NA
Root DW	7BC		1.774	0.558	3.113	0.518	3.50E-06
Root DW	7BC		3.269	0.484	2.530	0.520	6.96E-03
Root DW	7BC		8.920	0.683	17.233	1.753	2.99E-14
Root DW	7BC		229.879	14.495	228.989	18.174	9.24E-01
Root DW	7BC		39.904	2.165	39.381	3.138	7.44E-01
Root DW	7BC		33.515	1.664	48.104	6.981	8.84E-05
Root DW	7BC		NA	NA	NA	NA	NA
Root DW	7BC		NA	NA	NA	NA	NA
Root DW	7BC		NA	NA	NA	NA	NA
Root DW	7BC		0.126	0.212	0.643	0.212	9.68E-06
Root DW	7BC		NA	NA	NA	NA	NA
Root DW	7BC		NA	NA	NA	NA	NA
Root DW	7BC		78.845	4.929	79.669	5.180	7.57E-01
Root DW	7BC		0.382	0.438	1.272	0.400	5.02E-05

Trait	BIN	ILs with <i>S. pennellii</i> loci	Mean RPKM for ILs with <i>S. pennellii</i> loci	SD RPKM for ILs with <i>S. pennellii</i> loci	Mean RPKM for other ILs	SD RPKM for other ILs	P value (T-test)
Shoot DW	9C		27.138	1.811	30.763	2.201	2.41E-02
Shoot DW	9C						
Shoot DW	9C		23.248	1.268	28.720	2.087	4.48E-04
Shoot DW	9C	IL 9-1, IL 9-1-3	12.686	0.217	6.745	1.100	7.81E-11
Shoot DW	9C		29.275	2.855	16.091	2.619	9.22E-10
Shoot DW	9C		38.764	5.008	40.247	4.454	6.44E-01
Shoot DW	9C		NA	NA	NA	NA	NA
Shoot DW	9C		149.817	18.386	149.212	15.507	9.57E-01
Root DW	9D		28.195	2.655	26.843	2.967	3.76E-01
ShootDW	9D		9.172	1.245	11.089	1.529	1.63E-02
ShootDW	9D		15.664	1.512	20.960	1.898	5.79E-07
ShootDW	9D		NA	NA	NA	NA	NA
ShootDW	9D	IL 9-1, IL 9-1-3, IL 9-2, IL 9-2-5	NA	NA	NA	NA	NA
ShootDW	9D		NA	NA	NA	NA	NA
ShootDW	9D		8.993	1.265	7.403	1.057	4.85E-03
ShootDW	9D		27.509	2.199	27.803	1.894	7.65E-01
ShootDW	9D		NA	NA	NA	NA	NA
Root DW	9G		22.898	2.333	23.932	2.730	5.98E-01
Root DW	9G	IL 9-2, IL 9-2-6	NA	NA	NA	NA	NA
Root DW	9G		23.048	1.579	45.141	4.892	1.62E-08
Root DW	9G		8.495	1.808	6.442	0.711	2.17E-04
Starch/ED	11B		14.806	1.439	16.791	1.345	4.31E-02
Starch/ED	11B		5.505	0.245	6.044	0.810	3.53E-01
Starch/ED	11B		96.732	3.136	74.191	16.312	5.61E-02
Starch/ED	11B	IL 11-1, IL 11-2	4.732	0.356	5.733	0.682	4.30E-02
Starch/ED	11B		282.549	37.779	260.280	15.150	5.11E-02
Starch/ED	11B		9.567	2.225	4.311	0.765	9.15E-14
Starch/ED	11B		9.391	0.622	14.740	1.765	6.05E-05
Malate	11D	IL 11-2, IL 11-3	237.153	8.690	141.720	21.688	3.24E-08
A	11H		62.562	8.307	66.546	6.089	3.67E-01
A	11H	IL 11-4, IL 11-4-1	21.206	3.181	32.199	2.262	3.02E-09
A	11H		113.932	12.480	122.507	19.285	5.35E-01

Significant changes are indicated in bold

CHAPTER 2

Natural Diversity of Metabolites and Enzyme Activities In Leaves Petioles and Stems Using Tomato Interspecific Introgression Lines

Natural Diversity of Metabolites and Enzyme Activities In Leaves Petioles and Stems Using Tomato Interspecific Introgression Lines

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ABSTRACT

Natural genetic diversity provides a powerful and complementary resource to analyze complex metabolic networks. To identify QTLs and eventually genes that affect metabolic parameter, enzyme activities and traits related to biomass production and fruit yield, a collection of introgression lines (ILs) derived from a *Solanum lycopersicum* cv M82 X *Solanum pennellii* cross was grown in greenhouse and after four weeks growth stem, petiole and leaves were sampled in order to understand the role of stem and petiole during the export photosynthate from sink to source a leaf. We analyzed by robotized platform the major metabolic intermediates (sugars, starch, nitrate, amino acids and protein), and the activities of nine representative enzymes from central C and N metabolism. The results revealed high frequency of positive correlations between enzyme activities, moderate frequency of correlations between related metabolites, and few correlations between enzyme activities and metabolite levels. The majority of enzymatic QTLs were identified for FBP Ald and GIDH,

while for metabolic QTLs, Glucose and Fructose were highlights. Relative to biomass and yield, a large number of genomic regions involved with stem dry weight and green fruit fresh weight, respectively, were identified. Here, we provide an valuable genetic resource to understanding of the biochemical mechanisms involved in the regulation of primary metabolism in tomato plants.

INTRODUCTION

Plant biomass is largely derived from photosynthetically captured carbon and in this sense, variation in the efficiency or capacity of photosynthesis can lead to variation in growth rate and productivity, which are important factors in species competition and crop yield (Flood et al., 2011).

Carbon metabolism provides energy and carbon building blocks for nitrogen assimilation, and amino acid biosynthesis. Certain enzymes have been shown to play key roles in these processes (Nunes-Nesi et al., 2010; Stitt et al., 2010), among them are ADP-Glc pyrophosphorylase (AGPase) for starch synthesis (Preiss, 1982; Neuhaus and Stitt, 1990), aldolase (ALD; Haake et al., 1999), phosphoglucomutase (PGM; Gibon et al., 2004a) in glycolysis and citrate synthase (CS; Sienkiewicz-Porzucek et al., 2008) in the tricarboxylic acid (TCA) cycle.

Our understanding of the impact of the C supply on allocation, N metabolism and growth essentially derives from studies of experimentally induced environmental transitions, characterization of mutant plants and transformants with altered enzyme activities from central metabolism, and investigations of signaling pathway mutants, although studies involving genetic diversity might prove very informative too (Cross et al., 2006). Indeed, given the existing diversity among plant species, with large differences in their energy

metabolism, growth and storage of reserves (Keurentjes et al., 2008), it can be expected that there will be considerable variation in primary carbohydrate metabolism between species, and most likely also within species.

Large differences between *Arabidopsis* accessions have been observed for many enzyme activities and metabolite contents (Fiehn O et al., 2000; Sumner et al., 2003; Cross et al., 2006). These differences are influenced by several factors including growth conditions (Stitt and Fernie, 2003; Roessner et al., 2000), developmental stages (Roessner U et al., 2001), time period (von Roepenack-Lahaye et al., 2004) and tissues (Ratcliffe and Shachar-Hill, 2001; Krishnan et al., 2005). The role of natural variation is important for understanding the regulation of primary metabolism and development because it provides the possibility to associate metabolic traits with plant performance (e.g., what metabolic traits are correlated with biomass?), and then to identify the genetic bases of the variations in metabolic pathways and related processes that control such traits. Thus, natural variation can be used to identify quantitative trait loci (QTL) for metabolites or enzymes, and ultimately the genes that control a given metabolic trait of interest (Soltis et al., 2015). It can also be used to uncover correlations between parameters across a large set of genotypes, which may provide insights into the structure of physiological, metabolic, or regulatory networks (Poorter et al., 2005).

In this context, a collection of introgression lines (ILs) are presented as powerful tools to identify QTL for a range of traits, and ultimately the responsible genes or genetic factors (Fridman et al., 2006; Alseekh et al., 2013). The population developed by Zamir et al. (1995) is composed by a set of 76 ILs derived from a *Solanum lycopersicum* cv M82 versus *Solanum pennellii* cross.

Each of these lines contains a small introgressed region of the *S. pennellii* genome, which harbours 200 to 1,000 genes (Kamenetzky et al., 2010) in a genetic background of *S. lycopersicum*. Studies performed by various research groups with this population have allowed the identification of several QTL related to morphology and fruit yield (Semel et al., 2006), metabolite composition (Causse et al., 2004; Fridman et al, 2004; Baxter et al, 2005; Schauer et al, 2006), fruit color (Liu et al, 2003), enzymatic activity (Steinhauser et al, 2010), volatile metabolites and antioxidants (Tieman et al, 2006; Rousseaux et al, 2005), various organ morphology traits (Chitwood et al, 2013; Holtan and Hake 2003; Ron et al., 2013), cell development and tolerance to abiotic and biotic stress (Lippman et al., 2007; Bolger et al., 2014), photosynthesis and starch levels (de Oliveira et al., *unpublished*). Over 3069 QTL have been identified in this population to date (Alseekh et al., 2013) and some genes have been unambiguously identified and cloned (Ronen et al., 2000; Fridman et al., 2004).

The metabolic interconversions are catalyzed by enzymes; however it remains unclear whether the genetic variation in metabolite levels can be explained by changes in the activities of one or several enzymes. In this sense, an enzymatic and metabolic approach can provide an attractive strategy to link the changes in metabolite levels to genetic variations at loci that encode enzymes or are involved in the regulation of their expression and/or their activity. It has been shown that enzyme activities exhibit considerable natural genetic variation (Zhang et al., 2010; Sulpice et al., 2010). Analyses of a maize (*Zea mays*) IL population identified a QTL for sucrose phosphate synthase (SPS) and invertase activities that was colocated with genes encoding these

two enzymes (Causse et al., 1995; Prioul et al., 1999; Thevenot et al., 2005). In a study of six enzymes from primary metabolism and four enzymes from secondary metabolism in an *Arabidopsis* recombinant inbred line (RIL) population, several QTL were identified for each enzyme activity (Mitchell-Olds and Pedersen, 1998). Interestingly in this study a colocalization with structural genes and a trans QTL (i.e. a QTL that does not colocate with a structural gene) for three glycolytic enzymes was observed. They also found strong correlations between the activities of five glycolytic enzymes (phosphoglucose isomerase, glucose-6-phosphate dehydrogenase, fructose-1,6-bisphosphatase, and glucose-6-phosphatase), and coarse mapping detected a trans-QTL for three of the enzymes, which did not colocate with their structural genes and might represent a joint regulator of these enzymes. Afterwards, a study of 15 enzymes from central carbon and nitrogen metabolism in a Landsberg *erecta* versus Cape verde islands *Arabidopsis* RIL population, a total of 15 enzyme activity QTL were identified (Keurentjes et al., 2008). Despite the fact that the majority was in trans to structural genes, five QTL colocated with structural genes for the corresponding enzyme, of which three also showed a strong correlation with transcript levels from the structural gene. The fact that most activity QTL are in trans has also been found in Maize (Zhang et al., 2010).

A number of studies dealing with the variation in enzyme activities have been performed, but fewer studies have investigated enzyme activities and metabolites from central metabolism in parallel. The latter only investigated a small number of traits (Keurentjes et al., 2008) and in a single organ (Schauer et al., 2006; Meyer et al., 2007). Thus, the extent of the connectivity between enzyme activities and metabolites needs further investigation. It probably

depends on the complexity of the pathway and the extent to which genetic variation generates coordinated or noncoordinated changes in enzyme activities (Sulpice et al., 2010). In this sense, the aim of this work was to investigate in parallel the major metabolic intermediates (sugars, starch, nitrate, amino acids and protein) and the activities of nine representative enzymes from central C and N metabolism as well as performance traits in the IL population developed by Zamir and colleagues (1995). Given the differences in C partitioning and inorganic N assimilation and the role of stem and petiole during the export photosynthate from sink to source a leaf, in the following study, we aimed: (1) combine information about enzyme activities and metabolite levels from stem, petiole and leaf with biomass and fruit yield; (2) by studying these three interconnected organs, examine how much connectivity exists between enzyme activities and metabolite levels; (3) provide predictive information about differences in C partitioning and inorganic N assimilation; (4) investigate the natural genetic diversity and identify QTL controlling variation of enzyme activities and metabolite levels in stem, petiole and leaf.

MATERIALS AND METHODS

Plant materials and experimental conditions

Solanum pennellii ILs (Eshed and Zamir, 1995) and *S. lycopersicum* cv M82 seeds were kindly donated by Professor Dani Zamir, Hebrew University, Rehovot, Israel. The *Solanum pennellii* ILs population composed of 76 ILs containing a defined genomic segment of the *S. pennellii* (LA0716) genome replacing homologous regions in a tomato (*S. lycopersicum* cv. M82) background. This IL population is a set of nearly isogenic lines developed

through a succession of backcrosses, where each line carries a single genetically defined chromosome segment from a divergent genome (Zamir, 2001) The IL map is linked to the high-resolution F2 map composed of 1500 markers achieved by probing all of the specific chromosome lines with the Restriction Fragment Length Polymorphism (RFLP) markers from the framework F2 map. A total of 614 markers were probed and the ends of the introgressions were mapped with the resolution of the F2 map (Eshed Y et al., 1992).

Plant Growth and Sampling

Tomato plants were grown in a greenhouse in South-West of France (44°23'56"N, 0°35'25"E) from July to September with a room temperature between 25-30 °C during the day, and 18-22 °C at night, humidity 60% and irradiance of ~ 600 W m⁻² outside the greenhouse. In early June 2015, seeds were germinated and grown for the first 7 days in peat . Subsequently, rooted plantlets were acclimatized and transferred to 1 L pots containing commercial substrate. The nutrient solutions described previously (Bénard et al., 2015) were adapted to plant growth, and the water supply was adjusted to the climate (at least 30% drainage, pH adjusted to 5.9, electrical conductivity to 2.2 mS cm⁻¹). The population was grown in a randomized design composed of five blocks, each of them containing one plant of the 76 ILs and at least one M82 control plant per block.

After four weeks growth, the plants were harvested in one cut to 1.0 cm above ground level, separating the roots from shoots. The shoots were placed in paper bags identified and brought to a forced-air circulation oven at 70 °C to determine dry weight. For determination of metabolite levels and

enzyme activities, five independent samples from stem, petiole and leaves were harvested at the middle of the day and immediately frozen in liquid N and stored at -80 °C until further analysis.

Enzyme and Metabolite Assays

Aliquots of ~20 mg of fresh frozen powder were weighed in 1.1 mL MicronicTM tubes (Lelystad, The Netherlands) and stored at -80 °C until analysis. Metabolites were extracted twice with 80% (v/v) ethanol and once with 50% ethanol (Geigenberger et al., 1996). The sum of free amino acids, glucose, fructose, sucrose and nitrate were determined in the ethanolic supernatant. Starch and protein contents were determined in the pellet. Chemicals were purchased as described (Gibon et al., 2004a). Total protein, starch, glucose, fructose, sucrose, nitrate (Cross et al., 2006) and total amino acids (Bantan-Polak et al., 2001) were determined as previously described using 96-well polystyrene microplates (Sarstedt, Marnay, France). Extractions and assays were performed using a robotised Starlet platform (Hamilton, Villebon sur Yvette, France) and absorbancies were respectively read at 340 (carbohydrates) or 600 nm (protein content) in MP96 readers (SAFAS, Monaco). Fluorescamine fluorescence for amino acids was determined using a Xenius reader (SAFAS, Monaco) with excitation at 405 nm and detection at 485 nm.

For all enzymes the extraction and assays were performed exactly as described previously (Gibon et al., 2004a). In this study the enzyme activities of nine enzymes associated with carbon metabolism were determined: FBP Ald, Fructose-bisphosphate aldolase; G6PDH, Glucose-6-phosphate dehydrogenase; PGM, Phosphoglucomutase; PGI, Phosphoglucose Isomerase

total; PFK, ATP dependent Phosphofructokinase; Frk, Fructokinase; AGPase, ADP-glucose pyrophosphorylase; GK, Glucokinase; GIDH, NAD dependent Glutamate Dehydrogenase. For all assays, standard samples were assayed on each microplate and samples were randomized during extraction and analysis to avoid evaluation of a given parameter for all extracts of a particular accession on a single microplate. Standards were included on each microplate as measuring references.

Harvest data

After 105 days of growth, green and red fruits from all ILs were harvested and the following measurements were performed: fresh weight and number of green and red fruit, stem and truss number and leaf and stem dry weight.

Statistic analyses

The experiment was designed in randomized blocks with five replicates. The experimental unit was one plant per pot. Statistical analyses were performed using the GENES program (Cruz, 2013) and Minitab software. All data were subjected to an analysis of variance (ANOVA), and the means were tested by Dunnett's test at 5 % significance level. Pearson correlation coefficient was used at 5% significance level by T-test for examining the relationships among variables. In order to reduce the dimensionality of the data set and identify the variables that explain higher proportion of the total variance which may provide insights into the structure of enzymatic, metabolic, or regulatory networks, multivariate analysis technique by Principal Components Analysis (PCA) were used.

QTL Mapping

The chromosomal locations of putative QTL were determined first by ANOVA. Thereafter, QTL localization was determined using Dunnett's test to compare statistically each IL with the control M82. Once identified the QTL, BIN mapping was performed. The criteria to select the QTL-associated BINs for further comparative genomic was selection of regions spanned by more than two ILs (overlapping region), which showed the same phenotype. For each IL, where an QTL was identified, we first mapped the genetic markers that defined the IL to the physical map. To this end, flanking markers were extracted from the SOL Genomics Network Web site (Mueller et al., 2005). The phenotypic effect of QTL was considered to be the effect of the significant line and was expressed by using text colors to indicate a positive (red) or negative (green) significant changes as compared to M82 as identified by Dunnett's test (Figure 1,2 and 3)

RESULTS

Evaluation of yield related parameters

The leaves and stem dry weight were analyzed as an estimate of plant growth, while truss number and green and red fruit fresh weight, as an estimate of yield. In terms of leaf and stem dry weight, 23 and 21 ILs, respectively showed significant changes as compared to M82. Then, six and five ILs increase (red) and 18 and 16 ILs decrease (green), respectively for leaf and stem dry weight (Figure 1). In relation to yield parameters, 25 and 32 ILs, in this order, displayed significant changes. Of these, when compared to M82, seven and 17 showed increase and 18 and 14 decreases. Regarding the number of truss, only eight ILs decreased and four ILs displayed significant changes (one increase and three decreased) (Figure 1). The mean values, calculated for each

parameter and IL for all three organs, are presented in the supplemental tables S1, S2 and S3.

Determination of metabolite levels in stem petiole and leaf blade of plants from IL population

In this study we analyzed the metabolite levels and enzyme activities of leaf, petiole and stem of 71 ILs. To provide information about differences in C partitioning, we evaluated the levels of starch, glucose, fructose and sucrose at the middle of the light period. In stem, 15, 3, 7 and 5 ILs, respectively displayed higher levels for starch, glucose, fructose and sucrose when compared with M82, respectively (Figure 1). 16 and 3 ILs presented reduced levels of fructose and sucrose as compared to M82, respectively (Figure 1). In the same samples, harvested at the middle of the light period, we analysed the levels of amino acids, nitrate and protein to provide an indirect measure of the rate of inorganic N assimilation. For these variables, only ILs 8-2 and 12-4-1 displayed higher amino acids levels while the ILs 4-3 and 3-2 reduced levels of nitrate as compared to M82 control (Figure 1). It was also found one IL that displayed reduced levels of protein as compared to M82.

Similar to that observed in stem, for starch 16 ILs presented increase and only one ILs (IL 3-2) decrease when compared to M82 (Supplemental Figure S2). We verified that for starch, 10 ILs that displayed higher levels in stem have also been reported as lines with higher starch levels in petiole. This corresponds to one overlap of 63%. On the other hand, when we analyzed the levels of glucose, fructose and sucrose in petiole, glucose showed a larger number of ILs (30 ILs) with increased levels when compared with control. While in stem a larger number was observed for fructose. Within the variables

10-1-1), fructose (IL 11-3) and starch (ILs 1-1-3 and IL 3-2) showed decrease as compared to M82. For traits associated with the N assimilation, two ILs showed decrease for nitrate and three for protein, while increased levels of nitrate, amino acids and protein were observed in two (IL 9-2 and IL 9-3-1), one (IL 9-1-3) and one (IL 10-1-1) ILs, respectively (Figure 3).

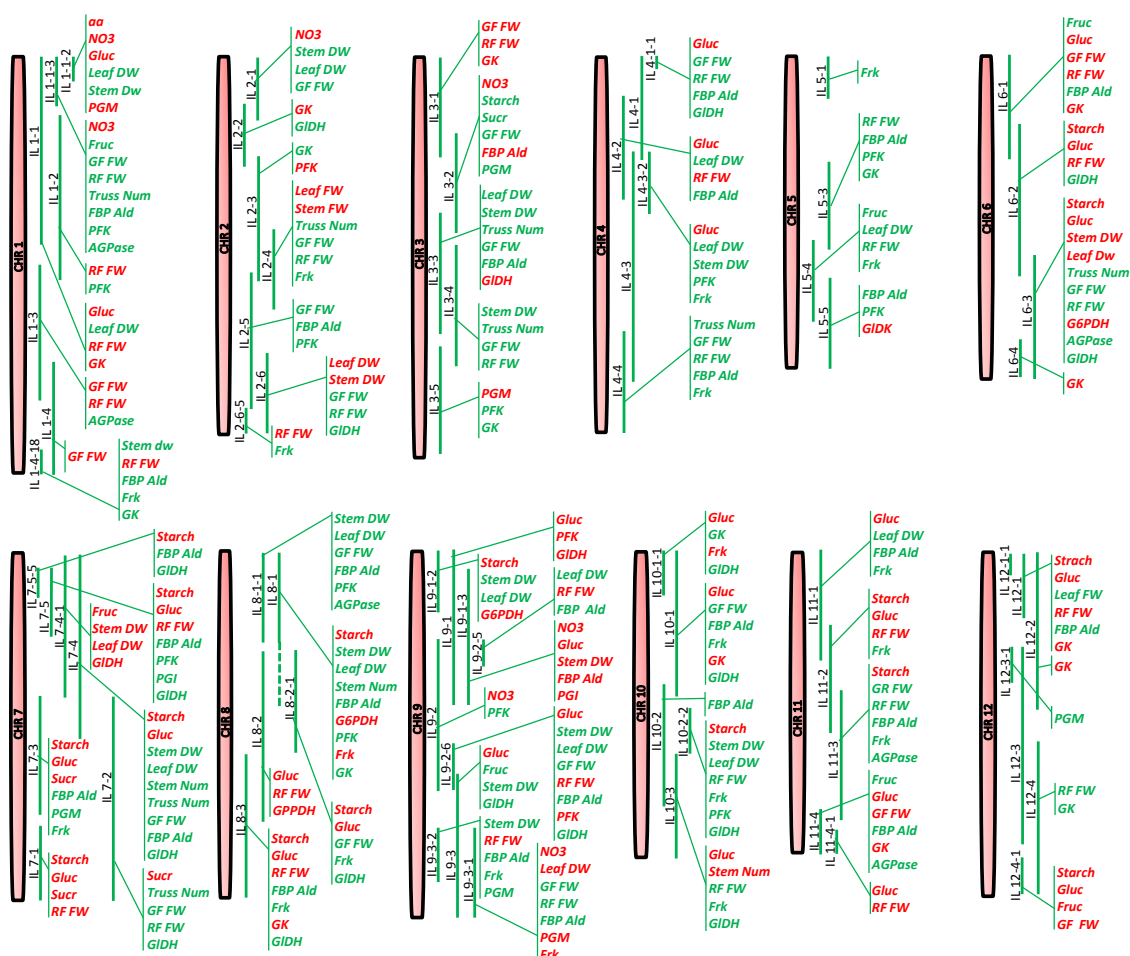


Figure 2. Petiole QTL map of significant changes in the metabolites, enzymes and harvest traits of a population of 71 introgression lines (ILs) of *Solanum pennellii* (green bar) into a genetic background of *Solanum lycopersicum* (M82). Metabolites: aa, Amino acid; NO₃, Nitrate; Starch; Protein; Gluc, Glucose; Fruc, Fructose; Sucr, Sucrose. Harvest data: GF FW, Green fruit fresh weight; RD FW, Red fruit fresh weight; Stem Num, Stem number; Truss Num, Truss number; Leaf DW, Leaf dry weight; Stem DW, Stem dry weight. Enzymes: FBP Ald, Fructose-bisphosphate aldolase; G6PDH, Glucose-6-phosphate dehydrogenase; PGM, Phosphoglucumutase; PGI, Phosphoglucose Isomerase total; PFK, Phosphofructokinase (ATP); Frk, Fructokinase, AGPase, ADP-glucose pyrophosphorylase; GK, Glucokinase; GIDH, Glutamate DH (NAD). Traits indicate a positive (red) or negative (green) significant changes as compared to M82 as identified by Dunnett's test.

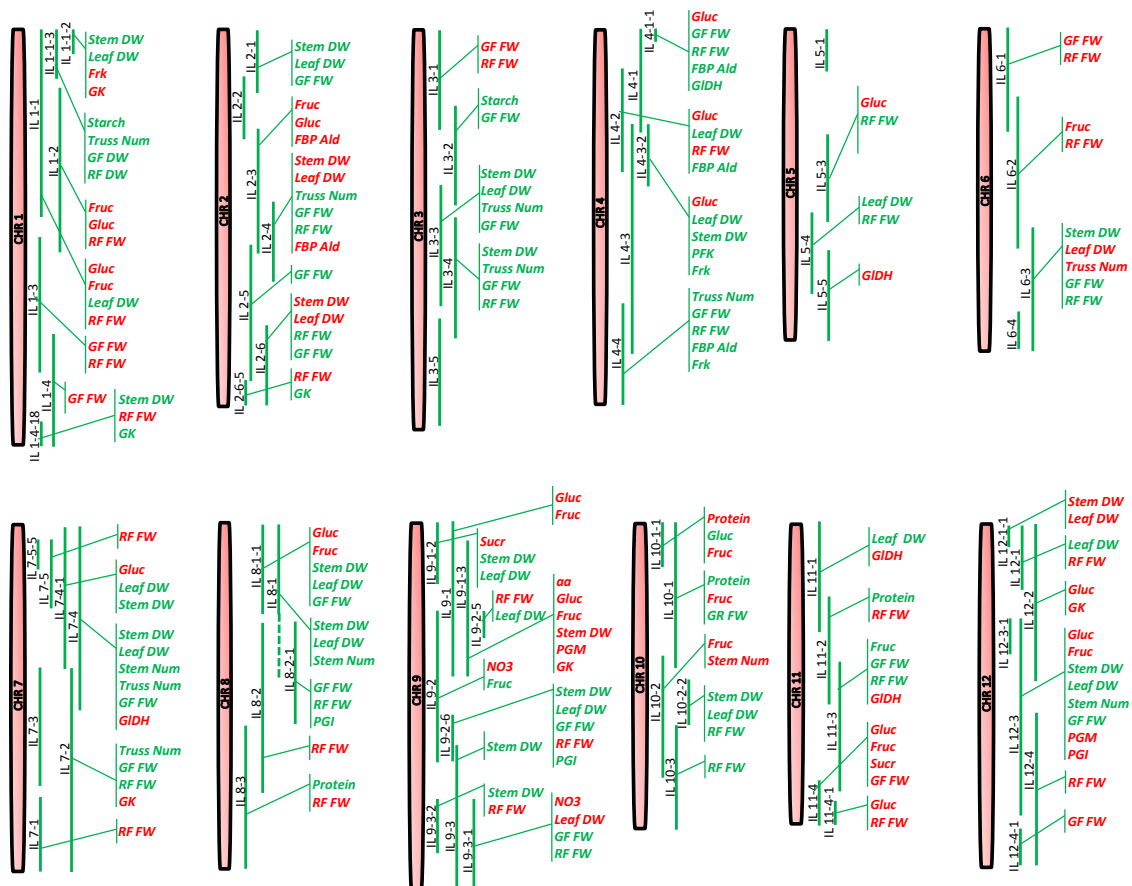


Figure 3. Leaf QTL map of significant changes in the metabolites, enzymes and harvest traits of a population of 71 introgression lines (ILs) of *Solanum pennellii* (green bar) into a genetic background of *Solanum lycopersicum* (M82). Metabolites: aa, Amino acid; NO₃, Nitrate; Starch; Protein; Gluc, Glucose; Fruc, Fructose; Sucr, Sucrose. Harvest data: GF FW, Green fruit fresh weight; RD FW, Red fruit fresh weight; Stem Num, Stem number; Truss Num, Truss number; Leaf DW, Leaf dry weight; Stem DW, Stem dry weight. Enzymes: FBP Ald, Fructose-bisphosphate aldolase; G6PDH, Glucose-6-phosphate dehydrogenase; PGM, Phosphoglucomutase; PGI, Phosphoglucose Isomerase total; PFK, Phosphofructokinase (ATP); Frk, Fructokinase, AGPase, ADP-glucose pyrophosphorylase; GK, Glucokinase; GIDH, Glutamate DH (NAD). Traits indicate a positive (red) or negative (green) significant changes as compared to M82 as identified by Dunnett's test.

Determination of enzyme activities in stem petiole and leaf blade

We analysed 1,065 samples corresponding to 71 ILs, the additional parental control M82 and three organs. Were carried out around of 9,585 enzymatic reactions corresponding to 9 enzymes and 1,065 samples By analyzing the stem data, we observed a large number of ILs with increase in enzyme activities associated with glycolysis/ gluconeogenesis, sucrose and starch metabolism (Figure 1). A great number of ILs with variation in enzyme

activity was observed for PGM (15 ILs) and PGI (16 ILs), of which seven ILs are common to both. In addition, we also verified that GDH displayed a large number of ILs (22 ILs) with high activity as compared to M82 (Supplemental Figure S1). On the other hand, in petiole, a large number of ILs displayed reduction in the activity of enzymes involved in glycolysis / gluconeogenesis pathways, sucrose and starch metabolism. We observed that FBP Ald and PFK, 27 and 12 ILs, respectively, presented significant changes when compared with M82. Concerning Frk activity, 17 ILs differed from M82 (Figure 2). In general, stem presented a larger number of lines with higher enzyme activity, while petiole these numbers were minor and associated to reduction in the activity of enzymes.

In leaves, as observed for metabolite levels, we identified a small number of ILs with changes as compared to stem and petiole. A total of 25 ILs differed from the M82 (Figure 3). The enzymes GK (5 ILs) and GIDH (4 ILs) displayed a larger number of ILs higher activities while the FBP Ald and PGI, both with 2 ILs, with lower activity with relation to M82.

Identification of genomic regions associated with enzyme activities and metabolites in stem, petiole and leaf blade

ILs that displayed traits increased or decreased when compared with M82 were considered as putative QTLs and indicated in the chromosomal map as positive (red) or negative (green) changes, respectively (Figure 1, 2 and 3). Based on these map, we identified the overlapping region between the introgressed regions of the ILs in order to map the identified putative QTL to smaller intervals, termed as BINs. The criterion to select the QTL-associated BINs as the region spanned by more than two ILs with significant changes in

relation to M82, so that they showed in all overlapping ILs the same phenotype. Thus, the smallest common region between the QTL was kept to define the associated confidence interval. By applying these criteria, we identified for stem 6 BINs related to metabolites trait and 13 BINs to enzymatic activities (Supplemental Table S4) For petiole, 34 BINs were identified, of which, 18 BINs were to metabolites trait and 16 BINs to enzymatic activities. To this organs, most of the BINs associated C metabolites were to glucose (11 BINs), while to BINs associated to enzymatic activities was to fructose-bisphosphate aldolase (7 BINs). On the other hand, in the case of leaf, this showed a low number of BINs (Supplemental Table S4). Only 10 BINs were identified to this organ, of which, 9 BINs were associated to metabolite levels of glucose and fructose and only 1 BIN (FBP Ald) to enzymatic activities. In general, to stem, petiole and leaf, we indentified 62 BINs to several different traits associated to metabolite levels and enzymatic activities. Additionally, in the present study, we indentified others 22 BINs related to harvest and biomass data. Of these, five BINs related to fresh weight in green fruit, three to leaf dry weight, five to fresh weight in red fruit, stem dry weight and two related to truss number (Supplemental Table S4).

Correlation Analysis of Parameters across the Entire Data Set.

The study of correlation analysis in stem showed that glucose and sucrose were strongly and positively correlated with starch (Gluc x Starch, $R=0.598$; Fruc x Starch, $R=0.608$) (Figure 4A). On the other hand, the traits associated with N assimilation, such as nitrate (NO_3), this displayed negative correlation with starch and glucose (NO_3 x starch, $R= -0.492$; NO_3 x Gluc, $R= -0.463$). While to amino acids (aa), the correlation with metabolites associated with C partitioning were positive (aa x Starch, $R=0.370$; aa x Fruc, $R=0.335$; aa

x Sucr, $R=0.368$). In relation to harvest traits, a large number of correlations were among themselves, emphasizing the strong and positive correlation between leaf dry weight and stem dry weight ($R=0.851$), green fruit fresh weight versus red fruit fresh weight ($R=0.566$) and green fruit fresh weight versus truss number ($R=0.693$) (Figure 4A). Regarding to correlations existing across enzymes and the entire data set, PGM showed a striking positive correlation between the activities of PGI ($R=0.719$) and Frk ($R=0.412$). In general, a large number of correlations involving the enzymatic activities were positive and among themselves (Figure 4A).

Correlation analysis performed with petiole data set, likewise of stem, indicated a positive correlation between glucose and sucrose with starch (Gluc x Starch, $R=0.44$; Fruc x Starch, $R=0.44$) and negative correlation between nitrate versus starch ($R= -0.49$) and nitrate versus glucose ($R= -0.39$) (Figure 4B). On the other hand, in petiole correlations between amino acids and metabolites associated to C partitioning, such as glucose, fructose, sucrose and starch were not observed. Although, amino acids displayed positive correlations between the activities of enzymes G6PDH, Frk, PGM and PGI. Interestingly a positive correlation of the amino acids versus PGM ($R=0.464$) and amino acids versus PGI ($R=0.436$) was verified. Unlike of stem, the enzymes analyzed in petiole showed a lower number of correlations among themselves and the activities of G6PDH displayed strong and positive correlation with PGI ($R=0.40$) (Figure 4B)

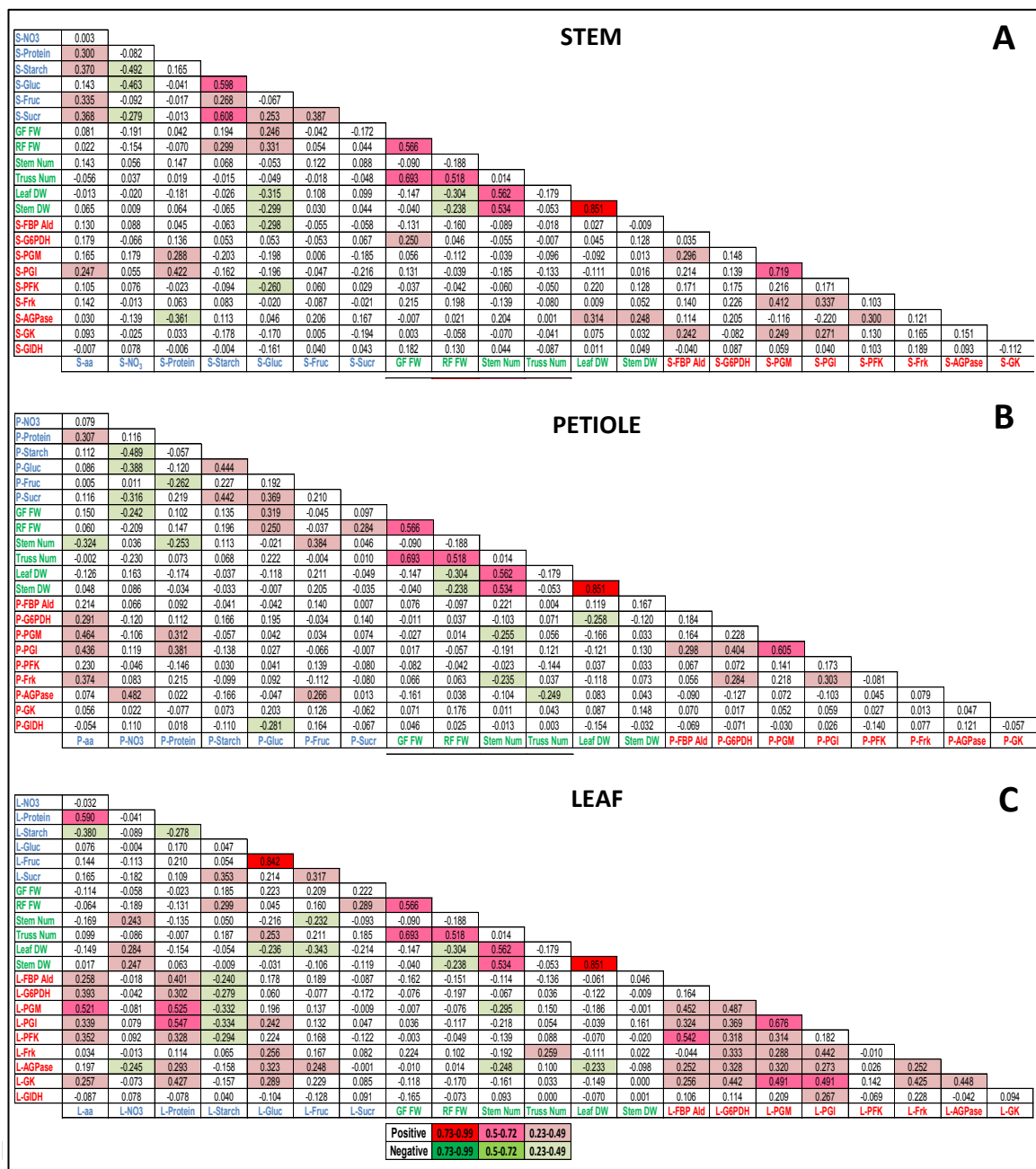


Figure 4. Pearson correlation analysis of three organ; stem (Figure A), petiole (Figure B) and leaf (Figure C) of a population of 71 introgression lines (ILs) of *Solanum pennellii* into a genetic background of *S. lycopersicum* (M82). Significant correlation coefficients ($p \leq 0.05$) are indicated by dark, medium, and light shading, with positive and negative correlations being distinguished by red and green respectively. Metabolites: aa, Amino acid; NO3, Nitrate; Starch; Gluc, Glucose; Fru, Fructose; Sucr, Sucrose. Harvest data: GF FW, Green fruit fresh weight; RD FW, Red fruit fresh weight; Stem Num, Stem number; Truss Num, Truss number; Leaf DW, Leaf dry weight; Stem DW, Stem dry weight. Enzymes: FBP Ald, Fructose-bisphosphate aldolase; G6PDH, Glucose-6-phosphate dehydrogenase; PGM, Phosphoglucomutase; PGI, Phosphoglucose Isomerase total; PFK, Phosphofructokinase (ATP); Frk, Fructokinase, AGPase, ADP-glucose pyrophosphorylase; GK, Glucokinase; GIDH, Glutamate DH (NAD). The letters S, P and L that precede the variables correspond to stem, petiole and leaf respectively. Relations that are significant at $P < 0.05$ are indicated with positive (red) and negative (green) box color. Text colors indicate the cluster to which variable have been assigned using hierarchical clustering (blue, metabolite; red, enzymes; green, harvest data).

Among the analyzed organs, the correlation analysis in leaf was the most complex and with higher number of correlations (74 correlations). For traits associated with N assimilation, amino acids showed a large number of positive correlations between most of the analysed enzymes, such as FBP Ald, G6PDH, PGM, PGI, PFK and GK (Figure 4C). There was a striking positive correlation between the activities of PGM and amino acids ($R=0.521$) and likewise of observed for amino acids, protein displayed a large and positive correlation between the majority of the enzymes, though with an emphasis to positive correlation between the activities of PGM ($R=0.525$) and PGI ($R=0.547$). For metabolites associated with C partitioning, glucose is strongly and positively correlated with fructose ($R=0.842$) and starch showed a large number of negative correlation with the majority of the analysed enzymes involved in glycolysis/gluconeogenesis pathways and on branch between glycolysis /gluconeogenesis, sucrose and starch metabolism. Nevertheless, correlation analysis in leaf data set revealed higher complexity of correlations among the studied enzymes. In general, the enzymes displayed positive correlation among themselves, which indicates that enzyme activities in leaf might be more complex than in stem and petiole. It is worth mention that there was a strong positive correlation between the activities of FBP, Ald and PFK ($R=0.542$; Figure 4C) and two others enzymes (PGI and GK) with PGM ($R=0.676$ and $R=0.491$).

Principal Components Analysis

To determine a possible common factor that explains the observed correlations, we performed a principal component analysis (PCA) based on all analyzed traits (Figure 5). For this comparison, a PCA was first performed on

averaged data obtained from all traits. For stem, petiole and leaf, the distribution of metabolites, enzyme activities, and harvest data in the first and second components are shown in Figure 5.

In stem, the first principal component (PC1), which explains 15.4% of total variance, separates the metabolites associated to C partitioning of the vast majority of enzymes. Secondly, the traits associated with N assimilation displayed a grouping remarkable with majority of enzymes. In contrast, the second principal component (PC2), which explains 14% of total variance, separated the yield associated traits, such as, trusses number, red and green fruit fresh weight, of the trait to biomass (stem number, leaf DW and stem DW; Figure 5B). Thus evidencing antagonistic correlation between yield and vegetative growth. In petiole, the PC1 and PC2 explained 15% and 13%, respectively of total variance. Different from the one observed in stem, in the PC2, glucose, sucrose and starch were grouped closely with several traits associated to yield. On the other hand, as observed previously to stem, protein and amino acids were grouped with enzymes, especially PGM, PGI and Frk. (Figure 5D). In leaf, the PC1 explains 21.6% and PC2 explains 15.3%. Among the analyzed organs, leaf was the one that presented the highest value for the sum of two components (36.9%). In general, the PCA in leaf showed a result that mixes characteristics of grouping already observed in stem and petiole (Figure 5F).

Likewise PC2 in petiole, protein and amino acids were grouped with enzymes and again with PGM and PGI. Although glucose, sucrose and starch were not grouped closely with several traits associated to yield (Figure 5F). For the PCA analysis in leaf, we highlight: (1) a remarkable opposite separation of

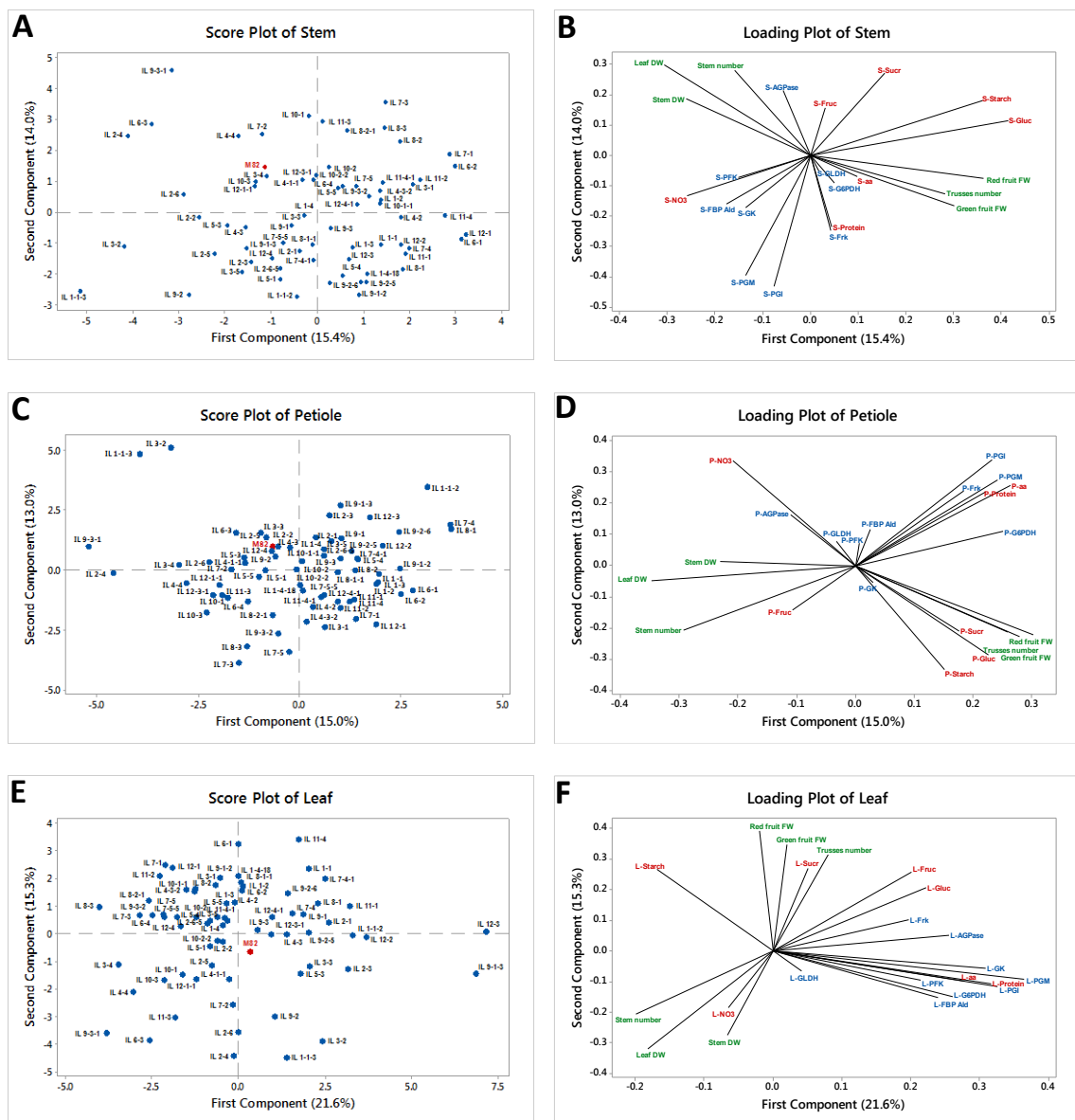


Figure 5. Principal components analysis of three organ; stem (Figure A e B), petiole (Figure C e D) and leaf (Figure E e F) of a population of 71 introgression lines (ILs) of *Solanum pennellii* into a genetic background of *S. lycopersicum* (M82). Principal components analysis was performed on the correlation matrix of least square means of accessions averaged. Numbers in parentheses give the percent variation explained by the first and the second principal component. The figure A, C and E shows the scores plot obtained for resulting distribution of ILs and figure B, D and F the corresponding loadings plot of metabolites, enzyme activities and harvest data distribution. Text colors indicate the cluster to which variable have been assigned using hierarchical clustering (blue, enzymes; red, metabolites; green, harvest data). Abbreviations for enzymes and metabolites are the same as in **Figure 1**.

traits associated to biomass of the metabolites glucose, fructose and sucrose (see CP1) and (2) antagonistic correlation between glucose and starch not observed in stem and petiole (see CP2). In relation to score plot of stem, petiole and leaf, there is no clear grouping of ILs. Although, was possible to identify, with a complementary overview of the enzyme-metabolite-biomass-yield, ILs that displayed highlighted changes when compared to M82 (Figure 5A, 5C and 5E).

DISCUSSION

QTLs study

Natural genetic diversity is a powerful and complementary resource to analyze complex metabolic networks (Kamenetzky et al., 2010; Stitt et al., 2010). It provides a complementary approach to uncover features of regulatory networks, which may have been overlooked in studies of physiological responses or individual mutants (Cross et al., 2006). In the last two decades, QTL mapping, first with linkage analysis and later with association mapping, has been used to dissect C and N metabolism in several species, including *Arabidopsis* (*Arabidopsis thaliana*; Mitchell-Olds and Pedersen, 1998; Keurentjes et al., 2008; Lisec et al., 2008; Sulpice et al., 2009), tomato (*Solanum lycopersicum*; Schauer et al., 2006), and maize (Hirel et al., 2001; Limami et al., 2002; Zhang et al., 2006, 2010a, 2010b, 2015). In general, these studies identified key genetic regions underlying variation in core C and N metabolism, many of which include candidate genes known to be involved in these processes. For example, in tomato fruits, the genomic region denominated by IL-4-4, were identified three positive enzyme activity QTLs for the enzymes in the glycolysis/gluconeogenesis pathway (NAD-GAPDH, UGP,

and FruK; Steinhauser et al (2001). For two of these enzymes, Baxter et al. (2005) reported increased levels of the corresponding transcripts (NAD-GAPDH, fructokinase). Furthermore, Schauer et al. (2006) described positive metabolite QTLs at this same locus for Fru, Suc, Glc, Fru-6-P, glycerate-3-phosphate, citrate, isocitrate, Asp, Glu, and succinate, including metabolites that are direct substrates or products of NAD-GAPDH, UGP, and FruK or metabolites farther upstream or downstream in the glycolysis/gluconeogenesis pathway.

In this work, to provide new insights into the mechanistic structures that influence how plant metabolism functions within a broader context, stem, petiole and leaf blade were investigated in relation to the variation of soluble sugars and starch, nitrate and amino acids, structural components, plant weight, and the activities of nine representative enzymes from central metabolism in a *Solanum pennellii* IL population. This approach allowed a better understanding of how information about variation in enzyme activities can be combined with information about biomass and metabolites to explore network structures in metabolism and the connectivity between metabolism and natural diversity.

The first aim was to identify metabolites and key enzymes that show larger variation and can subsequently be useful for studies exploiting natural diversity to identify genes and dissect regulatory networks that regulate C and N allocation. In this work, 19 QTL were identified in stem, and a large number of QTL were tagged to conserved changes in enzyme activities, principally of PGM and GIDH (Supplemental Table S4). The role of PGM has been studied in both photosynthetic and non-photosynthetic plants systems (Fernie et al., 2002). In potato plants, Fernie et al (2002) observed that plants with lower cytosolic PGM

activity showed the leaves of these plants were inhibited in sucrose synthesis whereas the tubers exhibited decreased levels of sucrose and starch as well as decreased levels of glycolytic intermediates. Complementarity, in tomato plants, Gibon et al (2004) verified via starchless *pgm* mutant, which lacks plastidic phosphoglucomutase, that PGM is essential for starch synthesis in the leaf. Interestingly, in our previous study presented in the chapter 1, about genetic basis of photosynthetic traits in tomato leaves, we verified that all BINs (BIN 1A, 5H, 9D and 9G) that displayed significant changes to PGM activity, also showed significant changes in metabolites associated with C partitioning, with starch. Thus, the results presented here reinforce the importance of that PGM plays as crucial role in the maintaining of starch levels in tomato plants (Supplemental Table S4).

Another enzyme that seems to be important in stem, was the GIDH. Altogether, five BINs (2C, 3B, 3H, 4D and 6G) were located in overlapping region (Supplemental Table S4). Although the physiological role of GIDH still needs to be fully assessed, it is becoming more and more likely that the enzyme plays a pivotal role at the interface between C and N metabolism through its metabolic activity or sensing function restricted to the vascular tissues. This pivotal role of GIDH by virtue of its tissue-specific expression may be essential for regulating the plant C and N balance and thus resource allocation at particular stages of plant growth and development (Tercé-Laforgue et al. 2004a,b). By means of GIDH-deficient mutants of *Arabidopsis thaliana*, was demonstrated that the enzyme serves as a major link between carbohydrate and amino acid metabolism (Miyashita and Good 2008) In particular, several co-localizations between QTLs related to yield, physiological traits related to

nitrogen use efficiency and enzyme activities involved in the control of N assimilation and recycling were detected for GIDH in maize (Gallais and Hirel 2004). In our studies, we verified by PCA analysis (Figure 5A) that ILs displaying a close relation with GIDH enzyme also showed a close link with amino acids levels. Thus, genetic characterization of the identified QTLs through sequence analysis of this ILs will certainly allow the identification of possible structural or regulatory genes controlling N assimilation and partitioning at specific organ.

Different from stem, petiole presented a large number of overlapping regions, for the analysed metabolites as well as for enzymes. Regarding the metabolites, QTL for high glucose levels were majority (Supplemental Table S4). In most plant species, it is now well established that sucrose is the principal form of carbohydrate translocated through the petiole from carbon-exporting source leave to carbon-importing sink tissues. In addition to sucrose, polyols (mainly sorbitol and mannitol) and oligosaccharides of the raffinose family can also be found. In some species, both polyols and raffinose are found in the phloem (Rennie and Turgeon, 2009). Mannitol and sucrose are produced photosynthetically in the mesophyll cells and translocated into the phloem. Keller and Matile (1989) verified that thick and fleshy petioles of celery leaves act as reversible carbohydrate sinks, storing mainly mannitol, glucose and fructose but very little sucrose in their parenchyma. In addition, the concentrations of soluble carbohydrates and the activities of enzymes sucrose cleavage were assayed in the parenchyma of petiole during leaf development. The authors verified that, mannitol (about 20 mg ml⁻¹ sap), glucose and fructose (about 10 to 15 mg ml⁻¹ sap each), changed little with development and

enzymatic activity was closely related to development with a sharp decrease during leaf maturation. As previously reported, in our studies higher concentration of glucose is observed in this tissue, which corroborates the findings of other authors.

In relation to enzymes, we observed a large number of QTL for FBP Ald, which shows that this enzyme plays an important role in petiole (Supplemental Table S4). FBP Ald is a key enzyme in plants, which is involved not only in glycolysis and gluconeogenesis in the cytoplasm, but also in the Calvin cycle in plastids. Extensive studies of the FBA genes in various plant species have provided a better understanding of this gene family. Thus far, different members of the FBA family have been identified and characterized by functional genomics approaches in a variety of plant species, including Arabidopsis and rice (Lu et al., 2012; Zhang, 2014). Despite extensive studies of FBAs in many other species, little is known about this gene family in tomato (*Solanum lycopersicum*). In a recent study, Bingbing et al (2016), by expression profiles of SIFBA genes at five different tissues (roots, stems, leaves, flowers, and fruits) verified that the 8 SIFBA genes showed different tissue-specific expression patterns. Interestingly, for non-photosynthetic tissues the authors verified undetectable or low expression to all SIFBA genes, as well as already verified in Arabidopsis. This is similar with our studies, since only QTLs showing reduction in the FBP Ald activity were identified in petiole and stem, while in leaves, only higher activities QTL were identified for this enzyme.

In leaves, QTL associated with aspects of carbohydrate metabolism (Chen et al., 2001; Sergeeva et al., 2004, Gibon et al., 2006, Sulpice et al., 2009, 2010), N metabolism (Hirel et al., 2001; Rauh et al., 2002; Loudet et

al., 2003a; Harrison et al., 2004), and C-N interactions (Rauh et al., 2002; Loudet et al., 2003ab; Krapp et al., 2005,) have been identified in Arabidopsis and other crop plants. In our study, out of 10 QTLs that were identified in leaves, nine were related to metabolite traits, glucose and fructose (Supplemental Table S4). Interestingly, in our previous studies about genetic basis of photosynthetic traits in tomato leaves (Chapter 1), we verified that BIN 11H, that in present study represent a positive QTL for glucose, also lead to higher CO₂ assimilation rate. Moreover, accumulation of glucose, fructose, and mainly sucrose in leaves as well as in ripe tomato fruits can also lead to a decrease in photosynthesis by feedback inhibition mechanisms (Poljakoff-Mayber and Lerner, 1994; Gautier et al., 2010; Osorio S et al., 2014), however this relationship was not observed here probably due to different growth conditions. In addition, we also find an overlap of informations retained in the BINs 9B, to higher glucose as well as fructose levels. Interestingly, in study to QTL regulating leaf shape, Chitwood et al (2013) verified that IL 9-1-2, which overlaps the region of BIN 9B, displayed transgressively narrower leaflets than cv M82. In addition, the leaf phenotype data were placed within the context of previously reported metabolic, enzymatic, and whole-plant phenotypes. Wondrously, this analysis revealed an interesting association between leaf morphology and sugar accumulation.

Relationship between Enzyme Activities, Metabolite Levels, Biomass and Yield

The central metabolism is characterized by a complex and multilevel regulation, presence of redundant pathways in multiple cellular compartments, in addition to futile cycles and enzyme promiscuity (Collakova et al., 2012). However this complexity of plant metabolism is essential for metabolic stability

(Rontein et al., 2002). Thus, the relationship between enzyme activities and metabolite levels could be rather nonintuitive. As already outlined, empirical studies show that a change in the activity of a single enzyme can result in complex changes in the levels of metabolites and fluxes. Theoretical considerations point to the same conclusion. Seen in these terms, statistical techniques such as PCA and correlation analysis are then used to guide the interpretation of detectable changes between enzyme activities and metabolite levels (Figure 4 and 5).

For traits associated with N assimilation, we verified negative correlation between NO_3 levels and metabolites associated with C partitioning (Glucose, fructose and starch) in stem and petiole (Figure 4). In most plant species, it is now well established that nitrate assimilation is closely integrated with changes in organic carbon metabolism (Stitt, M et al., 2002; Nunes-Nesi et al., 2010). During nitrate assimilation, significant amounts of fixed C are required to provide the C skeletons that act as acceptors during N assimilation and use, as evidenced in our previous study (See chapter 1). Thus, this negative correlation is not unexpected. In leaves, protein levels correlated positively with enzyme activities. A probable explanation for this correlation may be due to coordinated changes of enzyme activities or simply due to a change in the overall protein content. According to Sulpice et al, 2010, this high frequency of positive correlations between enzyme activities is retained when the activities are expressed on a protein basis. This, excludes a trivial explanation for the coordinated changes of enzyme activities.

This work also shows that, stem and petiole enzymes are highly connected with enzymes in the same pathway than with enzymes of other

pathways (Figure 4). For instance, PGM, PGI and GK, all of them involved in branching between glycolysis/ gluconeogenesis, sucrose and starch metabolism, displayed coordinated changes. However, the enzyme activities in leaves showed a highest connectivity to other enzymes, independent of the pathway. The same aspect was not observed by Sulpice and collaborators, (2010) in a network analysis to enzyme activities and metabolite in *Arabidopsis* leaves. A probable explanation for the lack of coordinated changes may be determined by several enzymes evaluated by the authors.

As a complement to that analysis, we performed PCA analysis on all traits analyzed to determine a possible common factor that explains the observed correlations. In this analysis, independently of the tissue, the metabolites correlate most frequently with metabolites from the same sector of metabolism, as seen previously (Galili and Hofgen, 2002; Foyer et al., 2003; Lu et al., 2008). For exemple, protein and amino acid showed strictly relation in all organs, the same was observed to glucose, sucrose and starch (Figure 5).

Another important issue is the fact that metabolites were less connected to each other than enzymes. In leaves, this becomes even more evidente to enzymes. The lower connectivity is not due to noise. Genetic variance actually explains a larger proportion of the total variation in metabolite levels than in enzyme activities (Sulpice et al., 2006, Meyer et al., 2007; Sulpice et al., 2009).

Finally, there were few correlations between enzyme activities and metabolites. Several explanations can be advanced for this lack of connectivity (Figure 4). A trivial explanation would be that many of the enzymes and metabolites come from different pathways. Another explanation for the lack of

connectivity would be that the level of a metabolite may be determined by several enzymes (Sulpice et al.,2010)

CONCLUDING REMARKS

The Integrated view of metabolite with enzyme activity reveals a very high frequency of positive correlations between enzyme activities, a moderate frequency of correlations between related metabolites, and remarkably few correlations between enzyme activities and metabolite levels. In addition, 85 QTLs related to metabolic levels, enzyme activities and biomass were identified ,thus new strategies will be required to identify and validate the candidate genes underlying these QTL and to uncover their functions.

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Supplemental Table S1: Averages and standard deviation of Stem (mean $\pm$ SD, n = 5) for each parameter and accessionin of a population of 71 introgression lines (ILs) of *Solanum pennellii* into a genetic background of *Solanum lycopersicum* (M82). Metabolites: aa, Amino acid; NO₃, Nitrate; Starch; Protein; Glucose; Fructose; Sucrose. Harvest data: Green fruit fresh weight; Red fruit fresh weight; Stem number; Truss number; Leaf dry weight; Stem dry weight. Enzymes: FBP Ald, Fructose-bisphosphate aldolase; G6PDH, Glucose-6-phosphate dehydrogenase; PGM, Phosphoglucomutase; PGI, Phosphoglucose Isomerase total; PFK, Phosphofructokinase (ATP); Frk, Fructokinase, AGPase, ADP-glucose pyrophosphorylase; GK, Glucokinase; GIDH, Glutamate DH (NAD).

IL	aa ($\mu\text{mol mg}^{-1}$ FW)	NO ₃ ($\mu\text{mol g}^{-1}$ FW)	Protein (mg mg ⁻¹ FW)	Starch (mmol eq Glucose g ⁻¹ FW)	Glucose ($\mu\text{mol g}^{-1}$ FW)
IL 10-1	0.0520 $\pm$ 0.0119	0.0420 $\pm$ 0.0072	3.6379 $\pm$ 0.1212	22.3009 $\pm$ 2.3571	33.7645 $\pm$ 4.0436
IL 10-1-1	0.0910 $\pm$ 0.0117	0.0685 $\pm$ 0.0086	3.9346 $\pm$ 0.2237	29.0471 $\pm$ 5.1714	36.7069 $\pm$ 4.4014
IL 10-2	0.0494 $\pm$ 0.0068	0.0416 $\pm$ 0.0081	3.9957 $\pm$ 0.1830	18.2845 $\pm$ 1.8144	31.7050 $\pm$ 2.8003
IL 10-2-2	0.0468 $\pm$ 0.0057	0.0908 $\pm$ 0.0318	3.5226 $\pm$ 0.3281	15.7778 $\pm$ 4.2853	32.7070 $\pm$ 3.7919
IL 10-3	0.0586 $\pm$ 0.0102	0.0757 $\pm$ 0.0048	4.1150 $\pm$ 0.1554	22.1426 $\pm$ 1.8464	29.2543 $\pm$ 1.8607
IL 1-1	0.0632 $\pm$ 0.0102	0.0440 $\pm$ 0.0073	4.6421 $\pm$ 0.2880	17.5423 $\pm$ 2.4308	29.6369 $\pm$ 2.1166
IL 11-1	0.0696 $\pm$ 0.0096	0.0527 $\pm$ 0.0054	3.9969 $\pm$ 0.3193	20.9526 $\pm$ 4.1973	34.1139 $\pm$ 2.2063
IL 11-2	0.0855 $\pm$ 0.0091	0.0525 $\pm$ 0.0039	3.9335 $\pm$ 0.1359	34.2218 $\pm$ 1.5678	39.9824 $\pm$ 2.5447
IL 1-1-2	0.0841 $\pm$ 0.0030	0.1745 $\pm$ 0.0816	3.4479 $\pm$ 0.0902	7.3262 $\pm$ 1.4146	33.5507 $\pm$ 5.2880
IL 11-3	0.0669 $\pm$ 0.0048	0.2261 $\pm$ 0.1098	3.7384 $\pm$ 0.0908	25.8267 $\pm$ 3.9623	35.2131 $\pm$ 4.9897
IL 1-1-3	0.0545 $\pm$ 0.0062	0.5486 $\pm$ 0.1715	3.9019 $\pm$ 0.5076	4.5988 $\pm$ 1.0241	23.0333 $\pm$ 2.8224
IL 11-4	0.0736 $\pm$ 0.0063	0.0580 $\pm$ 0.0201	3.9710 $\pm$ 0.2573	22.7748 $\pm$ 2.7869	41.4940 $\pm$ 4.0683
IL 11-4-1	0.0629 $\pm$ 0.0069	0.1020 $\pm$ 0.0349	4.2138 $\pm$ 0.2385	21.2656 $\pm$ 3.0253	33.6097 $\pm$ 1.8557
IL 1-2	0.0759 $\pm$ 0.0178	0.0814 $\pm$ 0.0216	3.2672 $\pm$ 0.3275	18.6011 $\pm$ 2.2097	35.3373 $\pm$ 1.4362
IL 12-1	0.0871 $\pm$ 0.0070	0.0625 $\pm$ 0.0200	4.7418 $\pm$ 0.2680	37.5198 $\pm$ 5.8899	37.3510 $\pm$ 2.6183
IL 12-1-1	0.0707 $\pm$ 0.0131	0.0487 $\pm$ 0.0084	4.2386 $\pm$ 0.2926	25.9810 $\pm$ 1.7913	27.7410 $\pm$ 3.0996
IL 12-2	0.0767 $\pm$ 0.0128	0.0638 $\pm$ 0.0343	4.2475 $\pm$ 0.2282	29.9368 $\pm$ 6.0218	37.0235 $\pm$ 6.1423
IL 12-3	0.0883 $\pm$ 0.0175	0.1601 $\pm$ 0.1246	3.6714 $\pm$ 0.6710	17.1868 $\pm$ 2.8815	34.9563 $\pm$ 1.7206
IL 12-3-1	0.0622 $\pm$ 0.0042	0.1069 $\pm$ 0.0165	3.4260 $\pm$ 0.1744	9.1370 $\pm$ 1.0501	29.5560 $\pm$ 2.2509
IL 12-4	0.0920 $\pm$ 0.0021	0.1406 $\pm$ 0.0187	4.3810 $\pm$ 0.1960	13.0239 $\pm$ 0.7007	23.8601 $\pm$ 1.1818
IL 12-4-1	0.0995 $\pm$ 0.0103	0.0641 $\pm$ 0.0174	4.3390 $\pm$ 0.8541	27.4699 $\pm$ 4.1461	28.1367 $\pm$ 2.7954
IL 1-3	0.0720 $\pm$ 0.0060	0.0639 $\pm$ 0.0048	4.2108 $\pm$ 0.2682	21.1161 $\pm$ 2.7836	30.1589 $\pm$ 1.8969
IL 1-4	0.0473 $\pm$ 0.0057	0.0684 $\pm$ 0.0066	3.8169 $\pm$ 0.3139	14.1438 $\pm$ 1.1045	31.7264 $\pm$ 5.4417
IL 1-4-18	0.0501 $\pm$ 0.0038	0.0528 $\pm$ 0.0105	4.1000 $\pm$ 0.3801	15.6818 $\pm$ 2.5417	29.8742 $\pm$ 3.8833
IL 2-1	0.0572 $\pm$ 0.0092	0.1365 $\pm$ 0.0472	3.3879 $\pm$ 0.3826	6.7313 $\pm$ 0.5712	27.1062 $\pm$ 3.8406
IL 2-2	0.0467 $\pm$ 0.0008	0.3694 $\pm$ 0.1582	3.6292 $\pm$ 0.1602	7.5800 $\pm$ 1.5867	22.2869 $\pm$ 3.4738
IL 2-3	0.0926 $\pm$ 0.0067	0.4814 $\pm$ 0.2150	4.3198 $\pm$ 0.4484	19.4751 $\pm$ 3.0631	26.0611 $\pm$ 2.2926
IL 2-4	0.0680 $\pm$ 0.0050	0.0893 $\pm$ 0.0104	3.9581 $\pm$ 0.2624	8.4887 $\pm$ 1.5408	20.9365 $\pm$ 2.9272
IL 2-5	0.0626 $\pm$ 0.0075	0.0409 $\pm$ 0.0125	4.9572 $\pm$ 0.2636	12.6806 $\pm$ 0.8427	24.5013 $\pm$ 1.7229
IL 2-6	0.0696 $\pm$ 0.0174	0.0946 $\pm$ 0.0267	3.8794 $\pm$ 0.2990	11.6541 $\pm$ 0.6391	26.3699 $\pm$ 3.6314
IL 2-6-5	0.0674 $\pm$ 0.0098	0.3069 $\pm$ 0.1275	3.7980 $\pm$ 0.3837	13.7373 $\pm$ 1.1537	20.4453 $\pm$ 2.6076
IL 3-1	0.0530 $\pm$ 0.0129	0.0451 $\pm$ 0.0069	3.4168 $\pm$ 0.5366	18.0836 $\pm$ 1.2869	33.9891 $\pm$ 3.5482
IL 3-2	0.0625 $\pm$ 0.0111	1.2886 $\pm$ 0.2072	3.8951 $\pm$ 0.2084	3.3962 $\pm$ 0.7674	16.1660 $\pm$ 1.8462
IL 3-3	0.0718 $\pm$ 0.0092	0.2893 $\pm$ 0.0910	4.0482 $\pm$ 0.2863	18.1563 $\pm$ 2.5311	30.0870 $\pm$ 4.6622
IL 3-4	0.0573 $\pm$ 0.0054	0.0775 $\pm$ 0.0144	3.760 $\pm$ 0.2039	14.7856 $\pm$ 0.8472	35.5928 $\pm$ 3.7012
IL 3-5	0.0555 $\pm$ 0.0067	0.2257 $\pm$ 0.1423	4.2712 $\pm$ 0.2126	12.8943 $\pm$ 1.4331	19.9311 $\pm$ 1.5647
IL 4-1-1	0.0550 $\pm$ 0.0036	0.0613 $\pm$ 0.0054	4.1667 $\pm$ 0.1488	22.7184 $\pm$ 2.2160	33.5452 $\pm$ 3.4651
IL 4-2	0.0532 $\pm$ 0.0108	0.0863 $\pm$ 0.0103	4.0225 $\pm$ 0.2449	13.8916 $\pm$ 0.7930	35.5717 $\pm$ 4.7530
IL 4-3	0.0718 $\pm$ 0.0053	0.6568 $\pm$ 0.3346	3.4763 $\pm$ 0.1899	5.0907 $\pm$ 1.2226	24.9891 $\pm$ 2.0778
IL 4-3-2	0.0408 $\pm$ 0.0065	0.0478 $\pm$ 0.0095	3.4860 $\pm$ 0.1452	16.2720 $\pm$ 1.9262	30.1625 $\pm$ 1.6995
IL 4-4	0.0614 $\pm$ 0.0074	0.1374 $\pm$ 0.0316	3.8992 $\pm$ 0.2201	16.3213 $\pm$ 1.5661	29.0593 $\pm$ 1.9144
IL 5-1	0.0719 $\pm$ 0.0112	0.0904 $\pm$ 0.0197	4.2335 $\pm$ 0.2712	16.4449 $\pm$ 1.8526	23.4750 $\pm$ 2.6319
IL 5-3	0.0649 $\pm$ 0.0055	0.0571 $\pm$ 0.0090	4.3708 $\pm$ 0.2824	14.8710 $\pm$ 1.5418	23.5781 $\pm$ 5.0142
IL 5-4	0.0742 $\pm$ 0.0176	0.0725 $\pm$ 0.0219	4.5392 $\pm$ 0.2862	25.1059 $\pm$ 2.0250	36.3011 $\pm$ 4.8533
IL 5-5	0.0485 $\pm$ 0.0036	0.0864 $\pm$ 0.0279	3.9349 $\pm$ 0.3186	15.2329 $\pm$ 0.9618	31.1116 $\pm$ 5.9161
IL 6-1	0.0713 $\pm$ 0.0124	0.0439 $\pm$ 0.0054	4.2466 $\pm$ 0.2659	22.6270 $\pm$ 4.4712	36.7740 $\pm$ 4.4399
IL 6-2	0.0724 $\pm$ 0.0031	0.0446 $\pm$ 0.0102	3.9495 $\pm$ 0.2734	25.3254 $\pm$ 3.6871	40.1398 $\pm$ 5.2080
IL 6-3	0.0726 $\pm$ 0.0068	0.0748 $\pm$ 0.0173	4.2383 $\pm$ 0.2301	19.3394 $\pm$ 1.4300	27.9465 $\pm$ 3.1612
IL 6-4	0.0535 $\pm$ 0.0147	0.0648 $\pm$ 0.0152	3.8258 $\pm$ 0.3530	16.3278 $\pm$ 2.1704	25.9416 $\pm$ 2.6615
IL 7-1	0.0802 $\pm$ 0.0179	0.0358 $\pm$ 0.0048	4.2799 $\pm$ 0.2081	33.3569 $\pm$ 2.9702	34.3830 $\pm$ 1.2607
IL 7-2	0.0710 $\pm$ 0.0079	0.0442 $\pm$ 0.0135	4.0650 $\pm$ 0.2262	14.2351 $\pm$ 1.6211	30.7433 $\pm$ 0.6508
IL 7-3	0.0580 $\pm$ 0.0076	0.0605 $\pm$ 0.0074	3.4647 $\pm$ 0.1089	27.2954 $\pm$ 1.6418	34.3960 $\pm$ 1.3299
IL 7-4	0.0790 $\pm$ 0.0114	0.0435 $\pm$ 0.0077	4.5584 $\pm$ 0.1831	19.2460 $\pm$ 2.6228	36.0682 $\pm$ 3.0932
IL 7-4-1	0.0480 $\pm$ 0.0036	0.1102 $\pm$ 0.0184	4.2703 $\pm$ 0.3081	11.4137 $\pm$ 1.0856	30.0606 $\pm$ 4.4225
IL 7-5	0.0601 $\pm$ 0.0085	0.0881 $\pm$ 0.0240	3.2676 $\pm$ 0.3383	20.4630 $\pm$ 2.5639	34.0194 $\pm$ 1.2362
IL 7-5-5	0.0683 $\pm$ 0.0126	0.0714 $\pm$ 0.0197	3.5399 $\pm$ 0.2666	17.4396 $\pm$ 1.5367	32.9068 $\pm$ 2.8263
IL 8-1	0.0801 $\pm$ 0.0060	0.0603 $\pm$ 0.0223	4.7139 $\pm$ 0.3330	23.3398 $\pm$ 3.6881	27.7174 $\pm$ 2.2640
IL 8-1-1	0.0690 $\pm$ 0.0088	0.2096 $\pm$ 0.1331	3.7802 $\pm$ 0.3031	14.9998 $\pm$ 1.4287	33.3913 $\pm$ 3.0149
IL 8-2	0.1003 $\pm$ 0.0140	0.1054 $\pm$ 0.0327	3.9480 $\pm$ 0.1735	21.7058 $\pm$ 1.8415	31.8867 $\pm$ 0.4765
IL 8-2-1	0.0647 $\pm$ 0.0051	0.1056 $\pm$ 0.0220	3.9098 $\pm$ 0.0878	28.2484 $\pm$ 5.3368	32.6470 $\pm$ 2.0964
IL 8-3	0.0600 $\pm$ 0.0083	0.0864 $\pm$ 0.0196	3.3695 $\pm$ 0.3370	24.3258 $\pm$ 2.1336	35.9893 $\pm$ 2.5970
IL 9-1	0.0502 $\pm$ 0.0047	0.0435 $\pm$ 0.0096	3.7290 $\pm$ 0.2803	15.7359 $\pm$ 0.7858	33.4415 $\pm$ 2.8690
IL 9-1-2	0.0929 $\pm$ 0.0124	0.0639 $\pm$ 0.0041	4.7713 $\pm$ 0.1625	24.2102 $\pm$ 1.7856	31.7646 $\pm$ 3.0080
IL 9-1-3	0.0808 $\pm$ 0.0142	0.3815 $\pm$ 0.1447	4.5125 $\pm$ 0.3020	8.2928 $\pm$ 2.0260	30.4950 $\pm$ 3.5027
IL 9-2	0.0660 $\pm$ 0.0131	0.1547 $\pm$ 0.0551	4.3662 $\pm$ 0.4025	9.1618 $\pm$ 1.4369	21.1197 $\pm$ 3.5145
IL 9-2-5	0.0636 $\pm$ 0.0054	0.2059 $\pm$ 0.0709	3.2811 $\pm$ 0.4479	19.5572 $\pm$ 2.0402	29.8902 $\pm$ 3.6609
IL 9-2-6	0.0617 $\pm$ 0.0082	0.0448 $\pm$ 0.0042	4.5076 $\pm$ 0.1893	18.6149 $\pm$ 0.6826	20.0646 $\pm$ 2.4163
IL 9-3	0.0641 $\pm$ 0.0099	0.0947 $\pm$ 0.0231	3.9376 $\pm$ 0.0672	18.1263 $\pm$ 2.6269	33.6628 $\pm$ 3.4215
IL 9-3-1	0.0737 $\pm$ 0.0010	0.0260 $\pm$ 0.0043	2.3631 $\pm$ 0.2156	21.2656 $\pm$ 3.0253	20.0170 $\pm$ 2.7113
IL 9-3-2	0.0579 $\pm$ 0.0077	0.1652 $\pm$ 0.0787	3.5369 $\pm$ 0.1515	24.4211 $\pm$ 5.1948	31.1494 $\pm$ 3.4145
M82	0.0613 $\pm$ 0.0033	0.2572 $\pm$ 0.0810	3.9778 $\pm$ 0.0805	13.5444 $\pm$ 0.8455	25.2407 $\pm$ 1.3657

IL	Fructose ($\mu\text{mol g}^{-1}\text{FW}$)	Sucrose ($\mu\text{mol g}^{-1}\text{FW}$)	Green fruit FW (g)	Red fruit FW (g)	Stem number (unit)
IL 10-1	0.4809 $\pm$ 0.0928	11.5401 $\pm$ 0.6973	55.3900 $\pm$ 12.5104	45.8450 $\pm$ 7.2530	3.2500 $\pm$ 0.1936
IL 10-1-1	0.0288 $\pm$ 0.0066	11.3777 $\pm$ 0.6296	174.2750 $\pm$ 21.0464	53.7000 $\pm$ 9.1516	2.5000 $\pm$ 0.2236
IL 10-2	0.0463 $\pm$ 0.0047	8.7034 $\pm$ 0.8234	218.6600 $\pm$ 27.2375	123.7700 $\pm$ 2.0066	2.5000 $\pm$ 0.2236
IL 10-2-2	0.0242 $\pm$ 0.0038	8.1546 $\pm$ 0.6802	160.6180 $\pm$ 8.3407	0.0000 $\pm$ 0.0000	2.5000 $\pm$ 0.2236
IL 10-3	0.4366 $\pm$ 0.0444	8.9621 $\pm$ 0.5635	179.7000 $\pm$ 23.2313	0.0000 $\pm$ 0.0000	4.0000 $\pm$ 0.0000
IL 1-1	0.5586 $\pm$ 0.1155	11.3846 $\pm$ 1.1152	244.1750 $\pm$ 30.9156	170.6750 $\pm$ 38.3234	2.2500 $\pm$ 0.1936
IL 11-1	0.0463 $\pm$ 0.0047	11.7875 $\pm$ 1.2260	281.2200 $\pm$ 28.9185	58.1650 $\pm$ 3.5972	2.2500 $\pm$ 0.1936
IL 11-2	0.8361 $\pm$ 0.0655	14.3866 $\pm$ 2.0965	170.6250 $\pm$ 22.1564	187.7000 $\pm$ 25.4187	3.0000 $\pm$ 0.3162
IL 1-1-2	0.6218 $\pm$ 0.0668	7.3087 $\pm$ 0.4936	224.6000 $\pm$ 18.2466	133.4150 $\pm$ 7.5232	2.7500 $\pm$ 0.1936
IL 11-3	0.9480 $\pm$ 0.1216	12.8178 $\pm$ 1.4171	35.3100 $\pm$ 4.5280	0.0000 $\pm$ 0.0000	3.2500 $\pm$ 0.1936
IL 1-1-3	0.4193 $\pm$ 0.0889	8.6267 $\pm$ 0.5572	0.0000 $\pm$ 0.0000	0.0000 $\pm$ 0.0000	2.8000 $\pm$ 0.2000
IL 11-4	0.3564 $\pm$ 0.1160	8.6129 $\pm$ 0.7008	296.7250 $\pm$ 24.8374	133.2050 $\pm$ 13.7229	2.5000 $\pm$ 0.2236
IL 11-4-1	0.4394 $\pm$ 0.0599	11.4812 $\pm$ 0.3568	201.5000 $\pm$ 24.2540	176.7250 $\pm$ 22.8275	3.0000 $\pm$ 0.3162
IL 1-2	0.0271 $\pm$ 0.0068	11.5202 $\pm$ 0.3279	246.5250 $\pm$ 10.9977	184.0500 $\pm$ 24.9842	2.7500 $\pm$ 0.1936
IL 12-1	1.0818 $\pm$ 0.0874	12.8230 $\pm$ 0.3499	264.7750 $\pm$ 13.5314	216.0000 $\pm$ 32.8555	2.9000 $\pm$ 0.1000
IL 12-1-1	0.1482 $\pm$ 0.0718	14.3042 $\pm$ 1.0838	166.7500 $\pm$ 14.2728	48.5250 $\pm$ 10.4611	3.2500 $\pm$ 0.3708
IL 12-2	1.2166 $\pm$ 0.2199	12.3576 $\pm$ 1.2784	186.2250 $\pm$ 31.5059	108.5000 $\pm$ 12.8193	2.5000 $\pm$ 0.2236
IL 12-3	0.6885 $\pm$ 0.0941	11.8247 $\pm$ 1.2411	86.8500 $\pm$ 15.5325	50.6450 $\pm$ 6.4328	1.7500 $\pm$ 0.1936
IL 12-3-1	0.7737 $\pm$ 0.1758	11.7042 $\pm$ 0.9067	201.4000 $\pm$ 19.7120	136.4050 $\pm$ 17.7082	3.2500 $\pm$ 0.1936
IL 12-4	0.5710 $\pm$ 0.0752	9.4577 $\pm$ 0.2832	277.9100 $\pm$ 30.8604	0.0000 $\pm$ 0.0000	2.0000 $\pm$ 0.0000
IL 12-4-1	2.1130 $\pm$ 0.3540	14.2518 $\pm$ 1.5243	299.0750 $\pm$ 29.8522	48.9500 $\pm$ 6.0051	3.0000 $\pm$ 0.0000
IL 1-3	0.4788 $\pm$ 0.1057	8.1054 $\pm$ 0.8071	310.7250 $\pm$ 35.2472	153.0000 $\pm$ 9.9977	3.0000 $\pm$ 0.0000
IL 1-4	0.4482 $\pm$ 0.0441	10.8529 $\pm$ 1.1684	212.5250 $\pm$ 45.8572	80.8200 $\pm$ 10.8288	2.2500 $\pm$ 0.3708
IL 1-4-18	0.6771 $\pm$ 0.1061	8.3044 $\pm$ 0.6890	227.9000 $\pm$ 44.7070	227.4750 $\pm$ 27.7731	2.2500 $\pm$ 0.1936
IL 2-1	0.3658 $\pm$ 0.0575	9.0160 $\pm$ 0.8888	51.8350 $\pm$ 3.5180	122.7750 $\pm$ 10.6394	1.9500 $\pm$ 0.0500
IL 2-2	0.3310 $\pm$ 0.0726	6.6843 $\pm$ 0.7186	154.3700 $\pm$ 15.4588	122.1500 $\pm$ 9.3097	2.7000 $\pm$ 0.2000
IL 2-3	0.8170 $\pm$ 0.0928	15.7553 $\pm$ 0.1623	125.7850 $\pm$ 7.3037	62.2700 $\pm$ 5.0057	2.5000 $\pm$ 0.2236
IL 2-4	0.6788 $\pm$ 0.0874	14.5514 $\pm$ 1.5811	6.2150 $\pm$ 1.0017	0.0000 $\pm$ 0.0000	3.5000 $\pm$ 0.2236
IL 2-5	0.7553 $\pm$ 0.0720	8.2612 $\pm$ 0.6755	39.3050 $\pm$ 4.7901	39.2250 $\pm$ 4.1184	2.7500 $\pm$ 0.1936
IL 2-6	0.3912 $\pm$ 0.0771	8.1629 $\pm$ 0.3415	68.4500 $\pm$ 6.9368	7.4700 $\pm$ 0.3986	3.2500 $\pm$ 0.3708
IL 2-6-5	0.5081 $\pm$ 0.0645	8.1319 $\pm$ 0.7784	241.1500 $\pm$ 19.1384	185.2600 $\pm$ 29.4311	2.2500 $\pm$ 0.1936
IL 3-1	0.5296 $\pm$ 0.1143	10.7419 $\pm$ 1.4422	425.3750 $\pm$ 45.3629	223.9100 $\pm$ 24.0168	3.0000 $\pm$ 0.3162
IL 3-2	0.5336 $\pm$ 0.1316	6.8299 $\pm$ 0.2606	84.5700 $\pm$ 6.7718	59.7300 $\pm$ 6.1437	3.0000 $\pm$ 0.0000
IL 3-3	0.4892 $\pm$ 0.0826	13.2793 $\pm$ 0.6822	0.0000 $\pm$ 0.0000	28.4050 $\pm$ 2.6174	2.2500 $\pm$ 0.1936
IL 3-4	1.3201 $\pm$ 0.1377	11.6642 $\pm$ 0.6906	0.0000 $\pm$ 0.0000	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.3162
IL 3-5	0.0317 $\pm$ 0.0045	7.7455 $\pm$ 0.3126	193.0500 $\pm$ 8.2012	128.0750 $\pm$ 16.8745	3.0000 $\pm$ 0.0000
IL 4-1-1	0.0213 $\pm$ 0.0045	14.5701 $\pm$ 0.3140	0.0000 $\pm$ 0.0000	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.0000
IL 4-2	0.5157 $\pm$ 0.0570	7.7157 $\pm$ 0.8189	275.3000 $\pm$ 28.0175	154.1500 $\pm$ 19.1485	2.7500 $\pm$ 0.1936
IL 4-3	0.0332 $\pm$ 0.0051	7.7778 $\pm$ 0.2431	175.7000 $\pm$ 21.9478	56.2950 $\pm$ 8.8400	3.0000 $\pm$ 0.3162
IL 4-3-2	0.5706 $\pm$ 0.0924	10.0100 $\pm$ 0.4224	216.0450 $\pm$ 31.1439	86.6400 $\pm$ 6.4367	3.2500 $\pm$ 0.3708
IL 4-4	0.6809 $\pm$ 0.1540	10.0014 $\pm$ 0.6883	43.5850 $\pm$ 4.5427	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.3162
IL 5-1	0.3610 $\pm$ 0.0638	12.5113 $\pm$ 1.2789	201.1000 $\pm$ 24.1758	76.7600 $\pm$ 5.7822	2.5000 $\pm$ 0.2236
IL 5-3	0.4879 $\pm$ 0.0936	9.1574 $\pm$ 0.8385	154.3120 $\pm$ 7.4330	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.3162
IL 5-4	0.0656 $\pm$ 0.0101	10.2558 $\pm$ 1.4394	266.9200 $\pm$ 52.7811	0.0000 $\pm$ 0.0000	2.8000 $\pm$ 0.2000
IL 5-5	0.3303 $\pm$ 0.1429	9.3538 $\pm$ 0.6477	161.6750 $\pm$ 10.0421	133.1800 $\pm$ 19.3132	2.5000 $\pm$ 0.2236
IL 6-1	0.3907 $\pm$ 0.0285	9.8954 $\pm$ 0.7805	320.6750 $\pm$ 37.0737	268.9850 $\pm$ 32.3782	2.2500 $\pm$ 0.1936
IL 6-2	0.4582 $\pm$ 0.1267	11.6887 $\pm$ 0.6590	184.4250 $\pm$ 28.9173	255.2750 $\pm$ 22.2530	2.7500 $\pm$ 0.1936
IL 6-3	0.0242 $\pm$ 0.0038	10.3013 $\pm$ 0.8886	5.0950 $\pm$ 1.1981	0.0000 $\pm$ 0.0000	3.2500 $\pm$ 0.1936
IL 6-4	0.6708 $\pm$ 0.1292	12.5736 $\pm$ 0.5591	177.9550 $\pm$ 22.2613	97.3050 $\pm$ 10.1646	2.7500 $\pm$ 0.1936
IL 7-1	1.7946 $\pm$ 0.2710	13.9923 $\pm$ 0.9197	200.0950 $\pm$ 43.9129	234.5000 $\pm$ 27.2390	2.7500 $\pm$ 0.3708
IL 7-2	0.5641 $\pm$ 0.1181	13.4530 $\pm$ 1.0431	3.5900 $\pm$ 0.3894	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.4472
IL 7-3	0.6095 $\pm$ 0.0235	15.7696 $\pm$ 1.4814	146.9000 $\pm$ 12.7553	135.5950 $\pm$ 15.0422	3.7500 $\pm$ 0.1936
IL 7-4	0.3406 $\pm$ 0.1570	13.7135 $\pm$ 1.0018	79.2000 $\pm$ 4.6161	80.5850 $\pm$ 5.2083	1.0000 $\pm$ 0.0000
IL 7-4-1	0.0230 $\pm$ 0.0035	5.9138 $\pm$ 0.6608	216.7250 $\pm$ 14.0708	63.2700 $\pm$ 5.3897	1.9500 $\pm$ 0.0500
IL 7-5	0.4165 $\pm$ 0.1488	13.4459 $\pm$ 1.3004	249.4750 $\pm$ 29.1521	195.5750 $\pm$ 20.2970	2.7500 $\pm$ 0.1936
IL 7-5-5	0.3446 $\pm$ 0.0505	12.0739 $\pm$ 1.0311	259.9250 $\pm$ 15.1216	134.6900 $\pm$ 4.6672	3.0000 $\pm$ 0.0000
IL 8-1	0.0522 $\pm$ 0.0293	12.8552 $\pm$ 2.0316	187.8200 $\pm$ 26.2024	120.9100 $\pm$ 11.8994	1.8000 $\pm$ 0.2000
IL 8-1-1	0.0439 $\pm$ 0.0063	8.3110 $\pm$ 0.8060	49.8350 $\pm$ 5.1702	85.6500 $\pm$ 5.1646	2.5000 $\pm$ 0.2236
IL 8-2	1.3229 $\pm$ 0.1161	14.5043 $\pm$ 1.0092	185.8750 $\pm$ 18.8275	160.6500 $\pm$ 14.1456	2.5000 $\pm$ 0.2236
IL 8-2-1	0.3304 $\pm$ 0.0994	15.4131 $\pm$ 0.5772	61.6450 $\pm$ 7.7380	50.6050 $\pm$ 3.4740	2.7500 $\pm$ 0.1936
IL 8-3	0.2355 $\pm$ 0.0629	12.4860 $\pm$ 0.8156	181.6000 $\pm$ 30.8467	189.5750 $\pm$ 9.6210	2.7500 $\pm$ 0.3708
IL 9-1	0.0362 $\pm$ 0.0133	6.9709 $\pm$ 0.5149	184.5600 $\pm$ 33.9026	48.4500 $\pm$ 3.8218	2.2500 $\pm$ 0.1936
IL 9-1-2	0.2449 $\pm$ 0.0403	9.5136 $\pm$ 0.7131	160.1900 $\pm$ 37.3474	138.9100 $\pm$ 6.4330	2.7500 $\pm$ 0.3708
IL 9-1-3	0.1232 $\pm$ 0.0154	9.7455 $\pm$ 0.8322	195.5000 $\pm$ 21.7955	50.7400 $\pm$ 3.3427	2.7500 $\pm$ 0.1936
IL 9-2	0.5433 $\pm$ 0.0581	7.4133 $\pm$ 0.3466	229.8000 $\pm$ 35.8837	26.9600 $\pm$ 5.0105	2.7500 $\pm$ 0.1936
IL 9-2-5	0.0242 $\pm$ 0.0038	9.5945 $\pm$ 0.7836	170.6750 $\pm$ 21.8058	228.1500 $\pm$ 62.2920	2.2500 $\pm$ 0.1936
IL 9-2-6	0.9303 $\pm$ 0.1574	12.0507 $\pm$ 1.3154	77.3300 $\pm$ 8.4810	156.9800 $\pm$ 10.3476	2.0000 $\pm$ 0.4472
IL 9-3	0.0496 $\pm$ 0.0085	9.7343 $\pm$ 0.2234	168.3750 $\pm$ 29.2778	75.5250 $\pm$ 6.1160	2.5000 $\pm$ 0.2236
IL 9-3-1	1.7461 $\pm$ 0.1663	12.9463 $\pm$ 1.2927	56.1000 $\pm$ 8.5511	0.0000 $\pm$ 0.0000	2.5000 $\pm$ 0.2236
IL 9-3-2	0.3566 $\pm$ 0.0563	14.1611 $\pm$ 1.6534	242.8400 $\pm$ 40.7823	146.6000 $\pm$ 19.4105	2.5000 $\pm$ 0.2236
M82	0.5908 $\pm$ 0.0257	10.9414 $\pm$ 0.3604	187.5860 $\pm$ 7.9228	79.7290 $\pm$ 5.2965	2.8500 $\pm$ 0.0742

IL	Trusses number (unit)	Leaf DW (g)	Stem DW (g)	FBP Ald (nmol g ⁻¹ FW min ⁻¹)	G6PDH (nmol g ⁻¹ FW min ⁻¹)
IL 10-1	2.2500 ± 0.6614	39.5250 ± 2.3046	11.4500 ± 0.7684	6201.2492 ± 497.0646	786.7200 ± 55.7109
IL 10-1-1	4.2500 ± 0.9152	37.6500 ± 1.4699	12.1475 ± 0.5494	9742.3170 ± 522.3496	1632.1040 ± 155.1652
IL 10-2	3.7500 ± 1.1124	42.8250 ± 1.2066	18.0750 ± 1.0317	4124.3580 ± 782.7188	609.6724 ± 83.0939
IL 10-2-2	4.0500 ± 0.5268	30.5500 ± 2.6043	8.2000 ± 0.4919	5931.6600 ± 509.7808	1721.6003 ± 245.1205
IL 10-3	4.0000 ± 0.8367	45.3500 ± 4.2372	16.1000 ± 1.0766	5080.7760 ± 1107.0279	984.4225 ± 72.1200
IL 1-1	5.7500 ± 0.6614	30.0750 ± 1.7130	10.9250 ± 0.8387	5188.8575 ± 529.1716	1306.7308 ± 167.5996
IL 11-1	6.0500 ± 0.5268	25.7000 ± 1.4960	10.1250 ± 0.7876	4510.4480 ± 871.4359	1136.0204 ± 60.1650
IL 11-2	4.2500 ± 0.4873	34.1500 ± 1.5506	13.1750 ± 0.8511	6845.5600 ± 1005.7592	1542.3720 ± 231.1313
IL 1-1-2	3.5000 ± 0.5477	25.1550 ± 1.9079	9.1175 ± 0.5851	6034.1400 ± 970.0866	1396.5300 ± 106.8267
IL 11-3	4.7500 ± 0.9811	43.5907 ± 3.8789	11.9467 ± 0.9900	5556.4520 ± 816.4977	939.3700 ± 30.2946
IL 1-1-3	1.6000 ± 0.6000	41.1000 ± 3.9891	13.5500 ± 1.6277	14264.6700 ± 1219.1652	1955.9000 ± 171.4144
IL 11-4	5.5000 ± 0.3873	32.2500 ± 2.8267	11.2250 ± 0.5589	5053.1525 ± 765.5210	1613.6525 ± 102.8998
IL 11-4-1	5.2500 ± 0.7331	42.4000 ± 1.8509	16.1700 ± 0.6785	4752.7884 ± 754.9477	2338.3836 ± 536.5921
IL 1-2	6.4000 ± 0.5099	38.3875 ± 1.1602	13.2850 ± 0.4356	10023.4656 ± 625.8497	1241.5575 ± 219.8244
IL 12-1	5.0000 ± 0.9487	25.9650 ± 1.8221	10.2250 ± 0.3836	6974.8140 ± 750.4032	1117.1104 ± 95.7185
IL 12-1-1	4.0500 ± 0.4213	60.9200 ± 1.9683	29.3050 ± 2.3354	6212.9975 ± 1395.7399	1280.5280 ± 181.4855
IL 12-2	3.7500 ± 0.1936	32.2850 ± 0.6081	12.6150 ± 0.7085	3722.3540 ± 657.8052	1936.3450 ± 240.5099
IL 12-3	3.2500 ± 0.7331	24.5050 ± 2.5950	7.7525 ± 1.1328	3355.9588 ± 612.1199	1511.9067 ± 93.3671
IL 12-3-1	5.4000 ± 0.5099	39.1250 ± 3.5311	10.8500 ± 0.6961	4576.0625 ± 877.5777	1020.9700 ± 59.0004
IL 12-4	2.4000 ± 0.6782	41.2750 ± 1.1389	9.8225 ± 0.7462	8317.7785 ± 498.5405	1340.5590 ± 54.1357
IL 12-4-1	6.2000 ± 0.4899	44.1000 ± 4.2541	16.8000 ± 1.5281	7234.6944 ± 923.7453	1322.0860 ± 104.8913
IL 1-3	6.5000 ± 0.5000	40.5750 ± 2.7679	14.6250 ± 1.0504	7144.9070 ± 456.7276	1094.9475 ± 39.1362
IL 1-4	3.2500 ± 0.7331	36.8520 ± 3.0089	12.5800 ± 1.2155	3918.1732 ± 1017.7382	1160.9075 ± 56.0824
IL 1-4-18	4.6500 ± 0.8047	31.6250 ± 1.1770	9.7250 ± 0.6460	4382.9750 ± 603.1990	1212.2500 ± 94.1808
IL 2-1	4.4000 ± 0.4000	19.2500 ± 1.9810	7.2250 ± 1.0072	5998.1225 ± 775.1241	1165.8040 ± 88.1376
IL 2-2	4.3500 ± 0.5220	43.8750 ± 2.9805	13.2500 ± 1.9785	9238.9600 ± 923.5193	658.4710 ± 49.5710
IL 2-3	3.6000 ± 0.6000	40.9500 ± 0.8953	16.1500 ± 1.3366	8897.9552 ± 1509.5066	1392.1475 ± 88.8177
IL 2-4	0.9500 ± 0.0500	62.5250 ± 4.6058	27.5000 ± 1.9867	5821.6504 ± 513.0880	1351.5587 ± 92.4150
IL 2-5	3.3500 ± 0.5895	40.0250 ± 3.7516	15.3000 ± 1.5732	7185.3356 ± 573.8082	1156.6552 ± 121.1438
IL 2-6	2.9500 ± 0.8231	54.3500 ± 1.6913	20.4500 ± 2.3252	6865.5175 ± 989.3395	1642.8375 ± 371.0496
IL 2-6-5	4.2500 ± 0.8588	39.5500 ± 2.4579	11.1000 ± 1.0010	7457.6380 ± 1002.3564	1236.9940 ± 52.7962
IL 3-1	5.8000 ± 0.7348	43.5725 ± 2.9498	16.9225 ± 1.4319	5685.0248 ± 969.8167	2909.9700 ± 351.5087
IL 3-2	2.8500 ± 0.3500	38.7000 ± 2.2034	12.5400 ± 1.0012	4353.0784 ± 646.1263	889.4312 ± 124.5407
IL 3-3	1.1500 ± 0.2179	14.8000 ± 3.3029	3.9750 ± 0.9254	11968.8540 ± 746.8183	685.9720 ± 38.2514
IL 3-4	0.0500 ± 0.0500	33.0400 ± 0.9899	8.7275 ± 0.5120	5509.3992 ± 1179.0927	601.2734 ± 77.6261
IL 3-5	5.5000 ± 0.6708	44.4250 ± 2.2001	15.8625 ± 1.2733	6432.2500 ± 555.1133	1705.3412 ± 141.8258
IL 4-1-1	4.8000 ± 0.4899	37.7500 ± 2.1457	11.7200 ± 1.3051	6283.9130 ± 310.6071	1375.6750 ± 96.1636
IL 4-2	4.7500 ± 0.3708	25.7750 ± 2.1453	9.9750 ± 0.7290	3480.4400 ± 1013.7131	1404.6510 ± 136.1439
IL 4-3	5.7500 ± 0.7984	39.2875 ± 1.9138	14.7475 ± 0.7257	3071.6840 ± 647.1484	1470.5350 ± 284.8115
IL 4-3-2	5.5500 ± 0.6910	23.4825 ± 2.2869	8.4650 ± 0.6783	6405.1272 ± 294.0837	1122.1175 ± 92.0820
IL 4-4	1.9500 ± 0.3571	50.2500 ± 3.8849	16.2025 ± 1.3905	3015.5850 ± 564.6628	1192.6700 ± 162.1448
IL 5-1	4.2500 ± 0.6614	40.1500 ± 3.6653	14.1750 ± 0.6748	6718.4625 ± 846.8901	1155.2613 ± 106.6920
IL 5-3	5.6000 ± 0.8124	46.8000 ± 5.1530	17.2250 ± 2.1960	6766.8225 ± 326.3336	689.1670 ± 57.5013
IL 5-4	5.2000 ± 0.5831	29.3250 ± 2.0053	12.3250 ± 0.5757	6531.6668 ± 1106.3064	2145.9968 ± 336.2931
IL 5-5	5.4000 ± 1.1225	35.9000 ± 2.9036	14.0500 ± 0.9599	6325.5732 ± 1346.5292	839.4173 ± 57.0443
IL 6-1	6.0000 ± 0.7071	32.5500 ± 3.6444	14.5750 ± 0.5458	5758.0928 ± 1154.8951	1414.5513 ± 227.8043
IL 6-2	5.6500 ± 0.5895	34.4500 ± 1.4080	11.9100 ± 1.0274	4461.9300 ± 662.2365	620.0725 ± 120.3878
IL 6-3	1.7000 ± 0.3742	66.2200 ± 3.8131	29.3125 ± 2.2987	8203.5048 ± 611.6831	1485.0650 ± 210.2387
IL 6-4	3.1000 ± 0.6782	38.7500 ± 3.2278	10.7000 ± 1.5547	7186.1600 ± 1056.3033	1782.8000 ± 409.2852
IL 7-1	5.0000 ± 0.6325	36.1000 ± 3.5826	13.7925 ± 1.4949	5680.6416 ± 892.9059	1671.5760 ± 387.1363
IL 7-2	1.9000 ± 0.4583	47.1533 ± 2.9573	14.5140 ± 1.2562	3393.2033 ± 498.9627	1768.5593 ± 365.8870
IL 7-3	4.5000 ± 1.0247	38.6500 ± 1.5312	11.3100 ± 0.5066	3530.2200 ± 1042.1934	678.5048 ± 126.5267
IL 7-4	1.4000 ± 0.4000	15.3250 ± 1.4644	3.2250 ± 0.3397	6602.6160 ± 926.8763	1211.2656 ± 88.7682
IL 7-4-1	6.6000 ± 0.4000	26.1250 ± 1.2543	8.0750 ± 0.3527	6183.8012 ± 710.6549	1610.3892 ± 224.8723
IL 7-5	5.0000 ± 0.3162	52.6500 ± 4.4721	13.2000 ± 0.7259	5654.7650 ± 995.6585	558.9080 ± 99.6175
IL 7-5-5	3.5000 ± 0.5000	38.3250 ± 2.9030	12.1500 ± 1.2757	8509.9100 ± 516.8493	2737.6275 ± 304.9895
IL 8-1	4.6000 ± 0.2449	23.1750 ± 1.4218	8.6000 ± 0.6075	6477.0972 ± 968.6800	2458.4650 ± 608.6559
IL 8-1-1	4.0500 ± 0.2784	18.6500 ± 1.9459	7.3350 ± 0.3282	6555.3452 ± 1007.1762	690.9287 ± 35.7341
IL 8-2	3.7500 ± 0.1936	35.1500 ± 2.5362	13.8575 ± 1.0736	3944.2780 ± 449.3148	1279.0525 ± 155.7175
IL 8-2-1	3.4500 ± 0.6344	42.3637 ± 4.2321	9.9223 ± 1.0978	5568.5692 ± 518.1725	1467.2164 ± 248.5817
IL 8-3	4.2500 ± 0.7984	42.5250 ± 2.1616	10.0250 ± 0.4872	4733.3500 ± 586.8262	1485.6300 ± 206.6545
IL 9-1	3.5000 ± 0.5000	38.9750 ± 3.0312	13.2450 ± 0.7517	6415.8368 ± 548.7871	866.5688 ± 103.5421
IL 9-1-2	4.3500 ± 0.4153	28.3200 ± 2.6973	7.4500 ± 1.1741	9207.5295 ± 729.3537	1279.1648 ± 94.4673
IL 9-1-3	5.0000 ± 0.7071	41.1750 ± 3.4261	20.8750 ± 1.9247	4067.4600 ± 688.2613	2164.2420 ± 471.1157
IL 9-2	4.7500 ± 0.4873	45.3750 ± 3.1557	18.2000 ± 1.1866	10691.7604 ± 424.3606	1209.3995 ± 56.5403
IL 9-2-5	5.2500 ± 0.3708	30.8300 ± 2.7217	9.9900 ± 0.6755	7424.9675 ± 578.7267	1070.5483 ± 72.1708
IL 9-2-6	4.2000 ± 0.7348	25.7940 ± 2.1272	6.1420 ± 0.8452	6835.1870 ± 495.4732	1482.9730 ± 234.3346
IL 9-3	2.7500 ± 0.6614	34.1250 ± 3.2632	9.6450 ± 0.7978	6141.3160 ± 1021.7605	1177.6450 ± 159.1185
IL 9-3-1	2.5000 ± 0.6708	67.2940 ± 0.6131	17.8600 ± 0.4238	8732.1100 ± 896.2541	1375.4623 ± 139.1119
IL 9-3-2	4.5000 ± 1.1619	31.2750 ± 2.5234	9.4500 ± 0.7928	6931.4512 ± 721.0660	1131.9073 ± 23.1284
M82	42.1240 ± 1.1670	4.5900 ± 0.4220	14.3115 ± 0.4386	6882.8060 ± 505.6856	1184.7341 ± 48.0060

IL	PGM (nmol g ⁻¹ FW min ⁻¹)	PGI (nmol g ⁻¹ FW min ⁻¹)	PFK (nmol g ⁻¹ FW min ⁻¹)	Frk (nmol g ⁻¹ FW min ⁻¹)	AGPase (nmol g ⁻¹ FW min ⁻¹)
IL 10-1	640.2256 ± 96.6890	289.1125 ± 17.9683	745.8850 ± 46.6655	202.8888 ± 44.6831	134.9108 ± 22.91042
IL 10-1-1	656.0532 ± 52.8257	411.8914 ± 60.9579	1631.2706 ± 215.4812	184.3786 ± 19.7063	73.3462 ± 11.69511
IL 10-2	703.2736 ± 102.0570	352.0860 ± 33.7351	1192.0336 ± 139.6766	134.3508 ± 10.9692	109.1325 ± 10.56870
IL 10-2-2	620.6375 ± 115.5066	270.9513 ± 4.1454	1146.1200 ± 228.0247	192.0900 ± 10.7690	52.8053 ± 7.20874
IL 10-3	845.2608 ± 74.7766	427.4150 ± 28.9355	2466.0417 ± 461.4701	186.0272 ± 21.4230	87.1540 ± 8.58056
IL 1-1	780.5100 ± 75.4782	417.3750 ± 37.0244	2013.0793 ± 304.2170	163.1232 ± 17.6854	103.0756 ± 6.81685
IL 11-1	1067.0504 ± 87.2911	404.2460 ± 33.8022	1273.9724 ± 222.0443	224.7020 ± 32.8577	93.1156 ± 7.03904
IL 11-2	874.5680 ± 32.7117	379.5420 ± 15.5132	2101.7620 ± 225.8735	249.6160 ± 23.1759	161.4700 ± 33.74023
IL 1-1-2	1244.1348 ± 148.1657	483.9020 ± 25.7351	2469.4800 ± 201.3503	251.4368 ± 25.1234	112.3956 ± 11.62966
IL 11-3	751.8005 ± 21.6176	273.8947 ± 12.7851	1657.4760 ± 83.1009	239.7453 ± 8.1399	136.8703 ± 8.32169
IL 1-1-3	1277.2988 ± 118.7686	444.8524 ± 37.8047	2661.2192 ± 185.0247	229.9300 ± 19.9279	83.3093 ± 8.00339
IL 11-4	712.6692 ± 76.8091	386.2440 ± 22.3321	609.1633 ± 60.9090	192.0975 ± 24.0695	82.6464 ± 7.38157
IL 11-4-1	726.1880 ± 24.9762	327.1608 ± 32.0534	1437.2073 ± 137.8792	310.5000 ± 74.3736	134.9280 ± 12.74745
IL 1-2	707.8152 ± 88.3839	294.0150 ± 28.7683	1683.9840 ± 139.3156	346.5750 ± 70.2872	147.5600 ± 15.23479
IL 12-1	973.2612 ± 79.9988	418.1524 ± 21.5272	1823.5813 ± 380.0125	205.6668 ± 41.1033	91.5475 ± 16.99844
IL 12-1-1	910.4616 ± 71.2439	467.0448 ± 36.9627	2063.4025 ± 315.9105	363.9984 ± 105.6570	100.8780 ± 9.24533
IL 12-2	974.4812 ± 98.2464	514.8100 ± 67.4020	1790.3096 ± 176.1563	316.1080 ± 113.2877	89.6216 ± 13.41815
IL 12-3	894.9520 ± 42.7679	509.9040 ± 71.7530	2052.1525 ± 204.5784	204.0700 ± 7.7848	71.0475 ± 9.70555
IL 12-3-1	718.4640 ± 44.8629	352.8728 ± 35.1363	1642.3052 ± 139.3139	178.2800 ± 6.0368	117.3528 ± 12.30431
IL 12-4	787.6080 ± 49.9780	370.1270 ± 3.5079	1675.2960 ± 56.9977	222.8430 ± 17.3338	51.2120 ± 6.88555
IL 12-4-1	1081.0775 ± 91.8942	379.5980 ± 57.1139	2376.5360 ± 254.1527	264.2940 ± 71.4061	102.2296 ± 9.31051
IL 1-3	915.4268 ± 32.0573	420.2700 ± 20.5828	2017.5514 ± 225.4327	226.3232 ± 15.4914	89.1170 ± 11.90853
IL 1-4	984.0204 ± 139.9304	345.0050 ± 31.2850	2331.4825 ± 209.5489	167.4588 ± 23.4711	92.7900 ± 16.57435
IL 1-4-18	1015.1492 ± 90.1490	446.2620 ± 27.6569	2340.5224 ± 215.8326	287.0100 ± 52.2140	77.7476 ± 11.03717
IL 2-1	884.0996 ± 69.9384	426.2472 ± 28.7686	1689.4476 ± 199.6185	172.2200 ± 18.6393	52.8125 ± 9.72088
IL 2-2	863.5850 ± 61.9601	340.2967 ± 23.6625	2699.8887 ± 140.0179	194.6425 ± 20.1214	161.0975 ± 11.04510
IL 2-3	1094.8624 ± 73.8385	416.1212 ± 43.2602	2048.0576 ± 411.2278	306.1868 ± 85.3203	70.2688 ± 4.33797
IL 2-4	851.2900 ± 74.1118	387.1575 ± 41.7001	1830.7475 ± 308.4746	193.3225 ± 25.0931	73.6500 ± 6.62791
IL 2-5	896.8268 ± 79.9500	481.3800 ± 45.7701	2064.1400 ± 301.6101	196.4256 ± 29.5841	85.5364 ± 6.38877
IL 2-6	989.6788 ± 50.7494	393.2692 ± 24.0772	1865.9593 ± 301.2824	235.2075 ± 39.8642	121.5853 ± 11.15451
IL 2-6-5	815.7240 ± 40.8550	445.4927 ± 12.4681	2711.8940 ± 369.1404	239.8840 ± 40.8852	75.2120 ± 9.83364
IL 3-1	615.5200 ± 57.2251	352.9356 ± 36.7588	1719.8813 ± 229.7965	211.4884 ± 18.7104	102.1740 ± 6.03941
IL 3-2	870.9104 ± 20.1753	372.2900 ± 17.9603	1573.3425 ± 250.3729	191.0840 ± 16.8967	65.4672 ± 6.32285
IL 3-3	793.9875 ± 71.1834	370.0000 ± 47.8694	1616.9625 ± 85.9997	156.6000 ± 19.1520	73.1650 ± 6.84649
IL 3-4	914.2742 ± 130.7440	408.7352 ± 32.6899	1241.1950 ± 271.4164	218.8270 ± 21.2312	95.5980 ± 12.02378
IL 3-5	851.4212 ± 39.7578	435.0260 ± 19.7359	2093.1160 ± 589.2804	288.7104 ± 53.6428	74.2040 ± 10.96545
IL 4-1-1	1036.1720 ± 29.1154	358.1070 ± 21.8352	2253.2400 ± 109.7253	121.5330 ± 9.1263	65.2120 ± 2.21489
IL 4-2	806.9432 ± 37.1430	302.5000 ± 33.8849	1517.8328 ± 122.5312	242.4472 ± 31.8511	78.7560 ± 13.12162
IL 4-3	880.8748 ± 99.1445	339.2900 ± 34.7626	1495.4500 ± 84.1675	186.4575 ± 20.9623	53.0775 ± 6.83608
IL 4-3-2	744.8276 ± 66.6879	354.2407 ± 13.4152	615.5050 ± 85.0128	212.2192 ± 17.3229	88.4650 ± 5.18690
IL 4-4	720.6638 ± 32.9041	278.4080 ± 22.3424	2002.4516 ± 183.7474	193.2036 ± 13.5296	81.2750 ± 7.20924
IL 5-1	1158.9240 ± 79.9660	480.3200 ± 36.0666	2219.1440 ± 110.6351	288.9104 ± 55.8759	72.8850 ± 7.68571
IL 5-3	731.9575 ± 49.5138	418.6073 ± 27.6331	1866.6425 ± 254.8141	206.3750 ± 47.2278	86.1147 ± 8.80707
IL 5-4	1105.1096 ± 72.5373	419.0400 ± 36.5300	2566.1280 ± 265.3154	272.6408 ± 46.3764	61.8796 ± 6.10333
IL 5-5	659.2536 ± 42.9513	324.7920 ± 25.7963	1884.7580 ± 311.2037	168.3860 ± 7.5491	82.4250 ± 3.41469
IL 6-1	821.9616 ± 24.3173	361.9250 ± 18.9547	1433.3125 ± 176.4800	218.9340 ± 19.8033	52.9596 ± 3.32974
IL 6-2	621.7316 ± 78.7273	333.7600 ± 45.6536	1867.1900 ± 390.3349	170.9232 ± 24.4857	72.8893 ± 4.60123
IL 6-3	710.3740 ± 108.7641	284.2920 ± 29.1820	1732.7932 ± 250.5545	183.0950 ± 9.0421	126.8350 ± 18.15840
IL 6-4	651.6200 ± 88.6733	312.9500 ± 12.5715	1903.7725 ± 112.7812	213.1712 ± 44.4361	95.9396 ± 14.95634
IL 7-1	765.9280 ± 69.4055	277.6400 ± 23.1840	1654.1520 ± 204.2239	179.9360 ± 25.8872	89.4775 ± 10.72487
IL 7-2	713.0093 ± 84.6918	305.8307 ± 19.2745	2102.9233 ± 384.3690	156.5313 ± 8.8843	86.7913 ± 12.03463
IL 7-3	628.0100 ± 37.9553	283.8325 ± 14.3953	1912.2412 ± 140.3255	155.8140 ± 14.3717	75.7260 ± 5.39270
IL 7-4	670.4512 ± 84.4027	385.7768 ± 45.7942	1972.8780 ± 107.3358	230.6550 ± 21.7904	72.5948 ± 3.88420
IL 7-4-1	845.3788 ± 57.3639	373.0193 ± 16.9924	2212.1787 ± 199.4090	187.1075 ± 24.1489	77.9084 ± 7.23910
IL 7-5	827.3860 ± 110.5368	383.2075 ± 36.6856	1816.7132 ± 146.0906	250.9588 ± 37.6895	84.9316 ± 8.99499
IL 7-5-5	1218.9320 ± 110.1309	450.6660 ± 20.3351	2600.7750 ± 421.2638	288.0684 ± 26.9015	219.4975 ± 46.59761
IL 8-1	837.0700 ± 42.1067	406.1000 ± 51.8249	1703.3892 ± 270.4069	270.9475 ± 57.9048	122.6364 ± 24.91002
IL 8-1-1	784.0060 ± 101.1144	340.2320 ± 31.1865	2125.3113 ± 215.5382	228.7100 ± 38.2047	98.6850 ± 14.97556
IL 8-2	580.1400 ± 65.3225	293.3800 ± 41.8931	1941.4840 ± 180.8789	175.9356 ± 32.5548	118.9400 ± 7.20377
IL 8-2-1	583.3220 ± 95.2047	308.9392 ± 22.3838	1999.1773 ± 199.8417	163.0975 ± 11.4606	102.1900 ± 13.11241
IL 8-3	502.3812 ± 85.6502	232.5300 ± 10.5734	3565.8696 ± 785.3664	164.9575 ± 19.9175	114.7060 ± 9.78321
IL 9-1	842.7850 ± 36.7007	350.1520 ± 15.3599	2300.3950 ± 332.6105	338.3936 ± 53.7260	115.5816 ± 16.21242
IL 9-1-2	1027.4322 ± 20.0857	467.4115 ± 27.5470	1947.9650 ± 242.6591	211.3000 ± 16.7222	45.9575 ± 9.90987
IL 9-1-3	852.6540 ± 60.3378	453.8525 ± 31.0364	3591.6400 ± 643.5040	268.6904 ± 68.7082	150.6500 ± 22.82568
IL 9-2	1154.9280 ± 122.0378	548.5333 ± 45.1273	2368.9000 ± 330.9442	179.7180 ± 17.7368	73.6316 ± 5.47696
IL 9-2-5	1030.9425 ± 73.4039	398.7396 ± 36.8158	1727.0000 ± 179.1018	416.2150 ± 130.3643	76.8200 ± 7.07028
IL 9-2-6	1005.6658 ± 25.3743	417.6100 ± 11.1396	2365.2790 ± 156.1016	345.5560 ± 17.4239	75.4072 ± 4.95864
IL 9-3	871.5388 ± 39.1845	357.4340 ± 21.3002	2031.6060 ± 235.3371	287.5684 ± 37.0833	80.0556 ± 13.51786
IL 9-3-1	566.2706 ± 22.5762	274.1830 ± 7.3355	3252.5637 ± 213.3805	173.9730 ± 13.6315	224.1040 ± 17.40847
IL 9-3-2	672.7796 ± 59.1726	328.3800 ± 19.4930	2634.0852 ± 444.3958	229.1340 ± 43.2117	94.7525 ± 9.51071
M82	688.1519 ± 40.4165	288.7068 ± 23.0036	1790.6947 ± 115.2455	160.6228 ± 7.2645	100.8074 ± 4.98106

IL	GK (nmol g ⁻¹ FW min ⁻¹)	GIDH (nmol g ⁻¹ FW min ⁻¹)
IL 10-1	85.4547 ± 7.1294	193.5500 ± 26.8427
IL 10-1-1	33.5995 ± 4.8077	566.0468 ± 35.1402
IL 10-2	62.0260 ± 4.1379	379.3550 ± 52.7014
IL 10-2-2	69.1987 ± 2.3710	404.8450 ± 37.7645
IL 10-3	81.5900 ± 5.6716	514.8433 ± 28.1341
IL 1-1	154.3607 ± 10.0043	495.4340 ± 90.5038
IL 11-1	96.9907 ± 9.8917	488.3160 ± 18.4842
IL 11-2	126.0588 ± 18.5864	634.5540 ± 46.6769
IL 1-1-2	155.2525 ± 17.9122	381.6325 ± 72.2491
IL 11-3	26.9100 ± 2.1135	459.9700 ± 19.1812
IL 1-1-3	158.7375 ± 29.6633	91.6340 ± 9.3140
IL 11-4	115.9572 ± 20.1591	303.5430 ± 8.7423
IL 11-4-1	49.6250 ± 5.7502	478.1705 ± 29.8542
IL 1-2	131.1836 ± 20.6399	330.1250 ± 19.9735
IL 12-1	121.4700 ± 12.7378	647.1520 ± 81.1907
IL 12-1-1	45.0150 ± 11.4003	572.7367 ± 64.6985
IL 12-2	107.7080 ± 4.3688	367.8640 ± 29.9638
IL 12-3	151.8050 ± 16.8214	287.8040 ± 13.2081
IL 12-3-1	172.2775 ± 28.0219	314.0480 ± 31.0085
IL 12-4	174.1170 ± 11.0368	259.3880 ± 25.7552
IL 12-4-1	57.3667 ± 5.1013	738.9853 ± 19.2165
IL 1-3	124.3465 ± 7.8592	502.0330 ± 20.8184
IL 1-4	163.2050 ± 16.1852	540.5093 ± 8.0140
IL 1-4-18	132.4976 ± 18.8145	564.8290 ± 14.7396
IL 2-1	72.7780 ± 6.1167	622.5775 ± 6.1268
IL 2-2	81.2200 ± 6.5999	745.5240 ± 42.6222
IL 2-3	192.0824 ± 43.2745	571.7550 ± 76.7405
IL 2-4	73.6640 ± 11.5102	614.2207 ± 52.2642
IL 2-5	175.8650 ± 13.0829	439.9617 ± 47.4617
IL 2-6	84.8493 ± 8.2954	551.4123 ± 38.2176
IL 2-6-5	79.2480 ± 5.4786	513.9213 ± 46.5916
IL 3-1	67.7867 ± 5.3081	647.1520 ± 81.1907
IL 3-2	61.6400 ± 5.9763	675.9253 ± 91.1080
IL 3-3	75.8813 ± 2.4940	553.7513 ± 61.7102
IL 3-4	92.3940 ± 9.4576	594.7067 ± 72.9543
IL 3-5	180.5104 ± 21.4111	606.9440 ± 67.3631
IL 4-1-1	43.2410 ± 4.5498	246.5980 ± 21.4284
IL 4-2	54.4750 ± 5.9496	458.1430 ± 31.9754
IL 4-3	63.9867 ± 8.5816	630.8775 ± 12.5393
IL 4-3-2	67.6122 ± 8.7183	775.0100 ± 73.3697
IL 4-4	76.4755 ± 7.2904	412.1350 ± 42.8239
IL 5-1	98.3450 ± 8.1220	810.8267 ± 38.7067
IL 5-3	265.4080 ± 25.2994	557.4960 ± 11.5737
IL 5-4	59.2820 ± 4.8195	562.1570 ± 40.6423
IL 5-5	26.1380 ± 3.2311	553.3520 ± 19.7185
IL 6-1	62.7520 ± 8.8938	618.3913 ± 46.3602
IL 6-2	51.6920 ± 4.5678	262.3280 ± 18.2634
IL 6-3	184.1775 ± 25.9801	393.3200 ± 60.8326
IL 6-4	69.9192 ± 6.5827	974.4650 ± 213.0407
IL 7-1	93.9172 ± 8.1937	469.3153 ± 16.5612
IL 7-2	54.8527 ± 6.1454	594.9880 ± 53.9640
IL 7-3	63.8776 ± 5.3728	388.1025 ± 67.1666
IL 7-4	59.0988 ± 9.8937	484.7137 ± 15.5164
IL 7-4-1	83.6700 ± 9.0580	400.1510 ± 26.1437
IL 7-5	148.5925 ± 21.6338	479.3427 ± 69.6443
IL 7-5-5	174.8575 ± 31.2795	718.4427 ± 93.5716
IL 8-1	77.8300 ± 9.5375	640.8153 ± 44.0217
IL 8-1-1	211.3850 ± 22.8580	669.7533 ± 73.0181
IL 8-2	50.9700 ± 8.8571	555.5850 ± 86.1171
IL 8-2-1	68.7788 ± 7.8056	427.5873 ± 86.2572
IL 8-3	61.2550 ± 10.0181	591.1267 ± 112.5045
IL 9-1	205.1160 ± 28.7987	594.9520 ± 42.4701
IL 9-1-2	142.9867 ± 14.1370	489.0195 ± 66.7100
IL 9-1-3	71.5020 ± 6.7159	548.6025 ± 44.9145
IL 9-2	80.2932 ± 10.5155	403.3575 ± 7.7679
IL 9-2-5	90.7930 ± 2.3707	635.3020 ± 24.8447
IL 9-2-6	83.4412 ± 3.6295	357.5110 ± 17.1594
IL 9-3	69.4375 ± 7.1960	532.9975 ± 55.0286
IL 9-3-1	145.3520 ± 11.4797	453.9320 ± 11.3337
IL 9-3-2	89.1525 ± 13.2911	546.2647 ± 39.3344
M82	91.2903 ± 2.8887	358.7461 ± 20.8885

Supplemental Table S2: Averages and standard deviation of Petiole (mean $\pm$ SD, n = 5) for each parameter and accessionin of a population of 71 introgression lines (ILs) of *Solanum pennellii* into a genetic background of *Solanum lycopersicum* (M82). Metabolites: aa, Amino acid; NO₃, Nitrate; Starch; Protein; Glucose; Fructose; Sucrose. Harvest data: Green fruit fresh weight; Red fruit fresh weight; Stem number; Truss number; Leaf dry weight; Stem dry weight. Enzymes: FBP Ald, Fructose-bisphosphate aldolase; G6PDH, Glucose-6-phosphate dehydrogenase; PGM, Phosphoglucomutase; PGI, Phosphoglucose Isomerase total; PFK, Phosphofructokinase (ATP); Frk, Fructokinase, AGPase, ADP-glucose pyrophosphorylase; GK, Glucokinase; GIDH, Glutamate DH (NAD).

IL	aa ($\mu\text{mol mg}^{-1}$ FW)	NO ₃ ($\mu\text{mol g}^{-1}$ FW)	Protein (mg mg ⁻¹ FW)	Starch (mmol eq Glucose g ⁻¹ FW)	Glucose ($\mu\text{mol g}^{-1}$ FW)
IL 10-1	0.0412 $\pm$ 0.0069	0.0600 $\pm$ 0.0100	3.5241 $\pm$ 0.0512	20.9782 $\pm$ 2.2040	20.1121 $\pm$ 0.9191
IL 10-1-1	0.0498 $\pm$ 0.0035	0.0640 $\pm$ 0.0126	3.1832 $\pm$ 0.2416	22.9311 $\pm$ 4.0785	21.9799 $\pm$ 1.5047
IL 10-2	0.0540 $\pm$ 0.0066	0.0696 $\pm$ 0.0072	3.6970 $\pm$ 0.2599	22.2079 $\pm$ 2.3149	17.0779 $\pm$ 1.4775
IL 10-2-2	0.0521 $\pm$ 0.0070	0.0343 $\pm$ 0.0024	3.3263 $\pm$ 0.1990	24.7813 $\pm$ 3.3623	17.9056 $\pm$ 0.4862
IL 10-3	0.0476 $\pm$ 0.0076	0.0754 $\pm$ 0.0119	3.3015 $\pm$ 0.5178	22.2544 $\pm$ 3.7052	20.0132 $\pm$ 1.9359
IL 1-1	0.0648 $\pm$ 0.0085	0.0433 $\pm$ 0.0095	3.3590 $\pm$ 0.1963	17.8923 $\pm$ 1.7109	20.5831 $\pm$ 3.2673
IL 11-1	0.0469 $\pm$ 0.0018	0.0598 $\pm$ 0.0091	4.3164 $\pm$ 0.3010	23.6795 $\pm$ 3.2522	24.3636 $\pm$ 0.9749
IL 11-2	0.0569 $\pm$ 0.0040	0.0547 $\pm$ 0.0114	3.7571 $\pm$ 0.3837	34.3197 $\pm$ 4.0094	23.7465 $\pm$ 2.2923
IL 1-1-2	0.0830 $\pm$ 0.0124	0.4717 $\pm$ 0.1187	4.5219 $\pm$ 0.2540	21.4516 $\pm$ 4.3923	13.3467 $\pm$ 5.1538
IL 11-3	0.0390 $\pm$ 0.0034	0.0437 $\pm$ 0.0042	3.2898 $\pm$ 0.2962	37.2390 $\pm$ 3.2898	5.3161 $\pm$ 1.1930
IL 1-1-3	0.0548 $\pm$ 0.0102	1.4757 $\pm$ 0.2785	3.8662 $\pm$ 0.1193	5.2243 $\pm$ 0.8775	5.4181 $\pm$ 1.0391
IL 11-4	0.0458 $\pm$ 0.0026	0.0587 $\pm$ 0.0148	3.1001 $\pm$ 0.4855	16.6191 $\pm$ 1.3929	23.6795 $\pm$ 1.9443
IL 11-4-1	0.0404 $\pm$ 0.0012	0.0529 $\pm$ 0.0061	3.3198 $\pm$ 0.4356	23.7263 $\pm$ 1.9846	23.5262 $\pm$ 1.3643
IL 1-2	0.0529 $\pm$ 0.0052	0.0643 $\pm$ 0.0095	3.5425 $\pm$ 0.2923	18.4899 $\pm$ 1.5778	24.0985 $\pm$ 1.4048
IL 12-1	0.0566 $\pm$ 0.0097	0.0533 $\pm$ 0.0103	3.3208 $\pm$ 0.1778	37.6485 $\pm$ 2.5826	25.8909 $\pm$ 1.0885
IL 12-1-1	0.0577 $\pm$ 0.0101	0.0772 $\pm$ 0.0075	3.4923 $\pm$ 0.3887	22.9742 $\pm$ 2.5053	23.2203 $\pm$ 1.2320
IL 12-2	0.0716 $\pm$ 0.0075	0.0548 $\pm$ 0.0112	3.6033 $\pm$ 0.2536	22.4154 $\pm$ 2.9966	21.7737 $\pm$ 2.5415
IL 12-3	0.0570 $\pm$ 0.0109	0.0582 $\pm$ 0.0038	3.3665 $\pm$ 0.5449	18.5151 $\pm$ 3.0595	21.2778 $\pm$ 2.7673
IL 12-3-1	0.0349 $\pm$ 0.0056	0.1091 $\pm$ 0.0084	3.1675 $\pm$ 0.3162	9.8579 $\pm$ 0.9179	14.3630 $\pm$ 3.6009
IL 12-4	0.0562 $\pm$ 0.0056	0.0476 $\pm$ 0.0038	3.1754 $\pm$ 0.1159	14.0492 $\pm$ 0.9712	17.6643 $\pm$ 0.2902
IL 12-4-1	0.0708 $\pm$ 0.0088	0.0802 $\pm$ 0.0178	2.8498 $\pm$ 0.6759	27.6654 $\pm$ 2.9701	21.1578 $\pm$ 3.0132
IL 1-3	0.0633 $\pm$ 0.0056	0.0563 $\pm$ 0.0056	3.6385 $\pm$ 0.2718	21.3382 $\pm$ 2.2180	17.7728 $\pm$ 1.2295
IL 1-4	0.0617 $\pm$ 0.0071	0.0460 $\pm$ 0.0094	3.4285 $\pm$ 0.1216	16.9758 $\pm$ 1.3161	17.4899 $\pm$ 1.4543
IL 1-4-18	0.0443 $\pm$ 0.0078	0.0485 $\pm$ 0.0099	3.7046 $\pm$ 0.5059	17.3843 $\pm$ 1.1269	10.7639 $\pm$ 2.9014
IL 2-1	0.0563 $\pm$ 0.0090	0.3852 $\pm$ 0.0656	3.3759 $\pm$ 0.3841	14.3067 $\pm$ 1.5044	13.1188 $\pm$ 1.6246
IL 2-2	0.0591 $\pm$ 0.0088	0.1682 $\pm$ 0.0243	4.0314 $\pm$ 0.2437	17.4741 $\pm$ 1.1889	8.4657 $\pm$ 2.2120
IL 2-3	0.0589 $\pm$ 0.0078	0.0489 $\pm$ 0.0039	3.8168 $\pm$ 0.3166	22.3876 $\pm$ 3.6051	10.9145 $\pm$ 0.9602
IL 2-4	0.0473 $\pm$ 0.0070	0.0390 $\pm$ 0.0151	3.3480 $\pm$ 0.2149	20.7300 $\pm$ 3.1563	14.7070 $\pm$ 1.0204
IL 2-5	0.0466 $\pm$ 0.0047	0.0647 $\pm$ 0.0094	3.9104 $\pm$ 0.2595	13.7975 $\pm$ 1.5660	16.0273 $\pm$ 1.6603
IL 2-6	0.0555 $\pm$ 0.0100	0.0789 $\pm$ 0.0073	3.3942 $\pm$ 0.1765	20.4034 $\pm$ 1.3088	14.9638 $\pm$ 1.6579
IL 2-6-5	0.0597 $\pm$ 0.0135	0.0476 $\pm$ 0.0080	4.1825 $\pm$ 0.4177	18.1361 $\pm$ 1.7129	8.1182 $\pm$ 1.6603
IL 3-1	0.0342 $\pm$ 0.0024	0.0437 $\pm$ 0.0053	3.8784 $\pm$ 0.3673	19.8569 $\pm$ 1.2136	15.8396 $\pm$ 0.8159
IL 3-2	0.0527 $\pm$ 0.0032	1.8245 $\pm$ 0.2157	3.7290 $\pm$ 0.4984	4.0974 $\pm$ 0.8590	6.2219 $\pm$ 1.3174
IL 3-3	0.0552 $\pm$ 0.0066	0.0318 $\pm$ 0.0041	3.6401 $\pm$ 0.4324	19.5930 $\pm$ 2.8566	10.8054 $\pm$ 0.9416
IL 3-4	0.0371 $\pm$ 0.0040	0.0556 $\pm$ 0.0056	2.8380 $\pm$ 0.1822	18.6772 $\pm$ 1.5909	11.7003 $\pm$ 1.2620
IL 3-5	0.0541 $\pm$ 0.0065	0.0633 $\pm$ 0.0033	4.3588 $\pm$ 0.5466	16.8861 $\pm$ 1.2970	12.6823 $\pm$ 1.1415
IL 4-1-1	0.0477 $\pm$ 0.0043	0.0498 $\pm$ 0.0033	2.3389 $\pm$ 0.1036	18.3254 $\pm$ 0.9840	19.2866 $\pm$ 4.2465
IL 4-2	0.0481 $\pm$ 0.0053	0.0411 $\pm$ 0.0038	3.4271 $\pm$ 0.2855	19.9051 $\pm$ 2.3021	20.8532 $\pm$ 2.1181
IL 4-3	0.0542 $\pm$ 0.0026	0.0750 $\pm$ 0.0099	3.7374 $\pm$ 0.3740	13.2831 $\pm$ 1.2911	17.4428 $\pm$ 2.1635
IL 4-3-2	0.0426 $\pm$ 0.0044	0.0533 $\pm$ 0.0120	3.3112 $\pm$ 0.2839	21.6712 $\pm$ 3.0549	23.9391 $\pm$ 2.0158
IL 4-4	0.0495 $\pm$ 0.0049	0.0725 $\pm$ 0.0096	3.3676 $\pm$ 0.3099	22.4264 $\pm$ 4.3386	16.7273 $\pm$ 2.0050
IL 5-1	0.0696 $\pm$ 0.0101	0.1421 $\pm$ 0.0437	2.9093 $\pm$ 0.4073	22.5565 $\pm$ 1.6584	12.2208 $\pm$ 1.8479
IL 5-3	0.0452 $\pm$ 0.0033	0.0548 $\pm$ 0.0077	4.3885 $\pm$ 0.0690	16.7442 $\pm$ 1.9324	6.2035 $\pm$ 0.8825
IL 5-4	0.0561 $\pm$ 0.0076	0.0511 $\pm$ 0.0077	3.5517 $\pm$ 0.1533	22.4655 $\pm$ 2.4709	18.5830 $\pm$ 2.5839
IL 5-5	0.0378 $\pm$ 0.0028	0.0426 $\pm$ 0.0056	3.1796 $\pm$ 0.4557	19.2338 $\pm$ 1.6077	10.1700 $\pm$ 1.9875
IL 6-1	0.0531 $\pm$ 0.0076	0.0388 $\pm$ 0.0070	4.2006 $\pm$ 0.1802	23.3563 $\pm$ 2.8546	22.7517 $\pm$ 3.7452
IL 6-2	0.0643 $\pm$ 0.0057	0.0585 $\pm$ 0.0058	4.0830 $\pm$ 0.3264	31.1562 $\pm$ 4.3741	21.6343 $\pm$ 2.8758
IL 6-3	0.0658 $\pm$ 0.0057	0.0458 $\pm$ 0.0121	3.5367 $\pm$ 0.3840	24.2950 $\pm$ 2.9183	20.1321 $\pm$ 1.0688
IL 6-4	0.0433 $\pm$ 0.0040	0.0468 $\pm$ 0.0060	3.1365 $\pm$ 0.1392	22.7752 $\pm$ 3.9970	15.5300 $\pm$ 1.6175
IL 7-1	0.0538 $\pm$ 0.0037	0.0490 $\pm$ 0.0085	3.7460 $\pm$ 0.2543	26.3532 $\pm$ 3.5310	20.0605 $\pm$ 2.3897
IL 7-2	0.0385 $\pm$ 0.0061	0.0707 $\pm$ 0.0144	3.8928 $\pm$ 0.1199	20.1934 $\pm$ 2.3590	18.6879 $\pm$ 1.6397
IL 7-3	0.0371 $\pm$ 0.0055	0.0562 $\pm$ 0.0032	3.3545 $\pm$ 0.3751	25.8552 $\pm$ 1.3671	21.8687 $\pm$ 1.7861
IL 7-4	0.0653 $\pm$ 0.0121	0.0440 $\pm$ 0.0076	4.3754 $\pm$ 0.3223	30.5702 $\pm$ 3.6231	23.3717 $\pm$ 1.9898
IL 7-4-1	0.0454 $\pm$ 0.0074	0.0629 $\pm$ 0.0032	4.1895 $\pm$ 0.5156	12.4877 $\pm$ 2.0149	18.0861 $\pm$ 1.3625
IL 7-5	0.0614 $\pm$ 0.0069	0.0373 $\pm$ 0.0063	3.2489 $\pm$ 0.1592	27.6776 $\pm$ 2.5971	21.6183 $\pm$ 1.9094
IL 7-5-5	0.0622 $\pm$ 0.0086	0.0510 $\pm$ 0.0022	3.6923 $\pm$ 0.5226	29.1597 $\pm$ 5.0151	18.8592 $\pm$ 2.2078
IL 8-1	0.0633 $\pm$ 0.0130	0.0640 $\pm$ 0.0136	3.8832 $\pm$ 0.3143	25.5794 $\pm$ 3.4629	15.4581 $\pm$ 1.0776
IL 8-1-1	0.0477 $\pm$ 0.0079	0.0453 $\pm$ 0.0086	3.7098 $\pm$ 0.2800	18.2220 $\pm$ 4.3269	13.6119 $\pm$ 1.7879
IL 8-2	0.0555 $\pm$ 0.0060	0.0521 $\pm$ 0.0068	3.3159 $\pm$ 0.1480	18.0582 $\pm$ 1.5812	23.8680 $\pm$ 1.9677
IL 8-2-1	0.0443 $\pm$ 0.0040	0.0433 $\pm$ 0.0083	3.3511 $\pm$ 0.2030	29.7619 $\pm$ 3.7653	24.5652 $\pm$ 2.0323
IL 8-3	0.0299 $\pm$ 0.0050	0.0530 $\pm$ 0.0087	2.9790 $\pm$ 0.2711	26.9951 $\pm$ 3.3829	23.8288 $\pm$ 1.3801
IL 9-1	0.0622 $\pm$ 0.0030	0.0745 $\pm$ 0.0107	3.9815 $\pm$ 0.2381	19.6247 $\pm$ 1.6397	19.5120 $\pm$ 0.8775
IL 9-1-2	0.0562 $\pm$ 0.0059	0.0441 $\pm$ 0.0093	4.1788 $\pm$ 0.4274	27.6338 $\pm$ 4.1543	18.6980 $\pm$ 1.8893
IL 9-1-3	0.0644 $\pm$ 0.0093	0.5730 $\pm$ 0.1431	4.1882 $\pm$ 0.3472	14.3778 $\pm$ 2.0390	23.3016 $\pm$ 1.0312
IL 9-2	0.0630 $\pm$ 0.0065	0.3831 $\pm$ 0.1451	3.6982 $\pm$ 0.4854	23.2985 $\pm$ 2.9977	17.3982 $\pm$ 2.2305
IL 9-2-5	0.0483 $\pm$ 0.0046	0.0578 $\pm$ 0.0064	3.2668 $\pm$ 0.4519	10.6767 $\pm$ 2.5830	13.2646 $\pm$ 2.4057
IL 9-2-6	0.0707 $\pm$ 0.0022	0.1292 $\pm$ 0.0274	4.0188 $\pm$ 0.2135	17.4226 $\pm$ 1.0265	20.0628 $\pm$ 0.3612
IL 9-3	0.0533 $\pm$ 0.0078	0.0475 $\pm$ 0.0039	4.0478 $\pm$ 0.1138	22.0725 $\pm$ 3.1104	20.0778 $\pm$ 1.4723
IL 9-3-1	0.0444 $\pm$ 0.0033	1.2111 $\pm$ 0.1859	3.3469 $\pm$ 0.3064	14.5808 $\pm$ 0.6066	12.7318 $\pm$ 1.0978
IL 9-3-2	0.0525 $\pm$ 0.0080	0.0379 $\pm$ 0.0070	2.8159 $\pm$ 0.3126	23.1869 $\pm$ 4.5797	18.6348 $\pm$ 2.7530
M82	0.0512 $\pm$ 0.0019	0.0942 $\pm$ 0.0146	3.4712 $\pm$ 0.2547	14.2817 $\pm$ 0.7728	11.2246 $\pm$ 0.6104

IL	Fructose ($\mu\text{mol g}^{-1}\text{FW}$)	Sucrose ($\mu\text{mol g}^{-1}\text{FW}$)	Green fruit FW (g)	Red fruit FW (g)	Stem number (unit)
IL 10-1	2.5010 $\pm$ 0.3206	11.2346 $\pm$ 0.7922	55.3900 $\pm$ 12.5104	45.8450 $\pm$ 7.2530	3.2500 $\pm$ 0.1936
IL 10-1-1	2.3897 $\pm$ 0.2856	7.5317 $\pm$ 0.4227	174.2750 $\pm$ 21.0464	53.7000 $\pm$ 9.1516	2.5000 $\pm$ 0.2236
IL 10-2	2.7225 $\pm$ 0.3220	9.9844 $\pm$ 0.1922	218.6600 $\pm$ 27.2375	123.7700 $\pm$ 2.0066	2.5000 $\pm$ 0.2236
IL 10-2-2	2.2720 $\pm$ 0.5430	12.5402 $\pm$ 1.5432	160.6180 $\pm$ 8.3407	0.0000 $\pm$ 0.0000	2.5000 $\pm$ 0.2236
IL 10-3	3.1565 $\pm$ 0.3768	11.0260 $\pm$ 0.8712	179.7000 $\pm$ 23.2313	0.0000 $\pm$ 0.0000	4.0000 $\pm$ 0.0000
IL 1-1	3.2218 $\pm$ 0.4099	11.4320 $\pm$ 1.0182	244.1750 $\pm$ 30.9156	170.6750 $\pm$ 38.3234	2.2500 $\pm$ 0.1936
IL 11-1	2.6762 $\pm$ 0.2412	10.1621 $\pm$ 1.0022	281.2200 $\pm$ 28.9185	58.1650 $\pm$ 3.5972	2.2500 $\pm$ 0.1936
IL 11-2	3.8104 $\pm$ 0.6532	13.3725 $\pm$ 2.4847	170.6250 $\pm$ 22.1564	187.7000 $\pm$ 25.4187	3.0000 $\pm$ 0.3162
IL 1-1-2	2.7228 $\pm$ 0.2412	11.3127 $\pm$ 1.8020	224.6000 $\pm$ 18.2466	133.4150 $\pm$ 7.5232	2.7500 $\pm$ 0.1936
IL 11-3	2.9254 $\pm$ 0.5634	8.3893 $\pm$ 0.7766	35.3100 $\pm$ 4.5280	0.0000 $\pm$ 0.0000	3.2500 $\pm$ 0.1936
IL 1-1-3	1.5788 $\pm$ 0.1919	9.0566 $\pm$ 0.6091	0.0000 $\pm$ 0.0000	0.0000 $\pm$ 0.0000	2.8000 $\pm$ 0.2000
IL 11-4	1.6858 $\pm$ 0.3417	9.6961 $\pm$ 0.9287	296.7250 $\pm$ 24.8374	133.2050 $\pm$ 13.7229	2.5000 $\pm$ 0.2236
IL 11-4-1	3.2121 $\pm$ 0.4342	13.1209 $\pm$ 0.5640	201.5000 $\pm$ 24.2540	176.7250 $\pm$ 22.8275	3.0000 $\pm$ 0.3162
IL 1-2	2.9641 $\pm$ 0.2967	13.1702 $\pm$ 1.0419	246.5250 $\pm$ 10.9977	184.0500 $\pm$ 24.9842	2.7500 $\pm$ 0.1936
IL 12-1	3.2245 $\pm$ 0.2496	10.4166 $\pm$ 0.4776	264.7750 $\pm$ 13.5314	216.0000 $\pm$ 32.8555	2.9000 $\pm$ 0.1000
IL 12-1-1	2.8196 $\pm$ 0.4659	10.2176 $\pm$ 0.3836	166.7500 $\pm$ 14.2728	48.5250 $\pm$ 10.4611	3.2500 $\pm$ 0.3708
IL 12-2	3.5449 $\pm$ 0.3888	10.6837 $\pm$ 1.5233	186.2250 $\pm$ 31.5059	108.5000 $\pm$ 12.8193	2.5000 $\pm$ 0.2236
IL 12-3	2.7286 $\pm$ 0.3801	10.2206 $\pm$ 1.1539	86.8500 $\pm$ 15.5325	50.6450 $\pm$ 6.4328	1.7500 $\pm$ 0.1936
IL 12-3-1	2.4126 $\pm$ 0.2144	7.1137 $\pm$ 0.2571	201.4000 $\pm$ 19.7120	136.4050 $\pm$ 17.7082	3.2500 $\pm$ 0.1936
IL 12-4	2.6471 $\pm$ 0.2720	8.6131 $\pm$ 0.4448	277.9100 $\pm$ 30.8604	0.0000 $\pm$ 0.0000	2.0000 $\pm$ 0.0000
IL 12-4-1	4.4374 $\pm$ 0.3321	13.6548 $\pm$ 1.1086	299.0750 $\pm$ 29.8522	48.9500 $\pm$ 6.0051	3.0000 $\pm$ 0.0000
IL 1-3	2.3893 $\pm$ 0.1607	12.2374 $\pm$ 0.5362	310.7250 $\pm$ 35.2472	153.0000 $\pm$ 9.9977	3.0000 $\pm$ 0.0000
IL 1-4	1.8627 $\pm$ 0.2165	11.7116 $\pm$ 0.8007	212.5250 $\pm$ 45.8572	80.8200 $\pm$ 10.8288	2.2500 $\pm$ 0.3708
IL 1-4-18	2.3222 $\pm$ 0.3338	10.5088 $\pm$ 1.0556	227.9000 $\pm$ 44.7070	227.4750 $\pm$ 27.7731	2.2500 $\pm$ 0.1936
IL 2-1	2.6050 $\pm$ 0.3154	10.1105 $\pm$ 0.5848	51.8350 $\pm$ 3.5180	122.7750 $\pm$ 10.6394	1.9500 $\pm$ 0.0500
IL 2-2	2.2383 $\pm$ 0.4217	7.4915 $\pm$ 0.6578	154.3700 $\pm$ 15.4588	122.1500 $\pm$ 9.3097	2.7000 $\pm$ 0.2000
IL 2-3	1.9173 $\pm$ 0.2547	10.5246 $\pm$ 0.2175	125.7850 $\pm$ 7.3037	62.2700 $\pm$ 5.0057	2.5000 $\pm$ 0.2236
IL 2-4	3.7476 $\pm$ 0.3949	11.6437 $\pm$ 0.5077	6.2150 $\pm$ 1.0017	0.0000 $\pm$ 0.0000	3.5000 $\pm$ 0.2236
IL 2-5	2.1883 $\pm$ 0.0883	10.0892 $\pm$ 0.7979	39.3050 $\pm$ 4.7901	39.2250 $\pm$ 4.1184	2.7500 $\pm$ 0.1936
IL 2-6	3.0611 $\pm$ 0.3227	8.7858 $\pm$ 0.1924	68.4500 $\pm$ 6.9368	7.4700 $\pm$ 0.3986	3.2500 $\pm$ 0.3708
IL 2-6-5	1.8274 $\pm$ 0.1175	10.3162 $\pm$ 0.9922	175.7000 $\pm$ 19.1384	185.2600 $\pm$ 29.4311	2.2500 $\pm$ 0.1936
IL 3-1	2.1780 $\pm$ 0.2435	12.8836 $\pm$ 0.8096	425.3750 $\pm$ 45.3629	223.9100 $\pm$ 24.0168	3.0000 $\pm$ 0.3162
IL 3-2	2.5491 $\pm$ 0.3341	6.6130 $\pm$ 0.4003	84.5700 $\pm$ 6.7718	59.7300 $\pm$ 6.1437	3.0000 $\pm$ 0.0000
IL 3-3	2.8894 $\pm$ 0.1423	10.9262 $\pm$ 0.7034	0.0000 $\pm$ 0.0000	28.4050 $\pm$ 2.6174	2.2500 $\pm$ 0.1936
IL 3-4	2.7884 $\pm$ 0.2575	10.2128 $\pm$ 0.1456	0.0000 $\pm$ 0.0000	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.3162
IL 3-5	3.2369 $\pm$ 0.4446	11.7157 $\pm$ 1.0724	193.0500 $\pm$ 8.2012	128.0750 $\pm$ 16.8745	3.0000 $\pm$ 0.0000
IL 4-1-1	2.4753 $\pm$ 0.3632	7.5887 $\pm$ 0.2485	0.0000 $\pm$ 0.0000	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.0000
IL 4-2	2.7778 $\pm$ 0.2137	8.5518 $\pm$ 0.5623	275.3000 $\pm$ 28.0175	154.1500 $\pm$ 19.1485	2.7500 $\pm$ 0.1936
IL 4-3	3.2484 $\pm$ 0.3176	8.2192 $\pm$ 0.6834	175.7000 $\pm$ 21.9478	56.2950 $\pm$ 3.8400	3.0000 $\pm$ 0.3162
IL 4-3-2	3.3335 $\pm$ 0.4430	9.1618 $\pm$ 0.8208	216.0450 $\pm$ 31.1439	86.6400 $\pm$ 6.4367	3.2500 $\pm$ 0.3708
IL 4-4	2.9670 $\pm$ 0.0867	11.7795 $\pm$ 0.6872	43.5850 $\pm$ 4.5427	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.3162
IL 5-1	1.9271 $\pm$ 0.2513	8.3729 $\pm$ 0.6286	201.1000 $\pm$ 24.1758	76.7600 $\pm$ 5.7822	2.5000 $\pm$ 0.2236
IL 5-3	2.4183 $\pm$ 0.1792	10.8957 $\pm$ 0.4092	154.3120 $\pm$ 7.4330	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.3162
IL 5-4	1.3669 $\pm$ 0.1729	9.9288 $\pm$ 1.0517	266.9200 $\pm$ 52.7811	0.0000 $\pm$ 0.0000	2.8000 $\pm$ 0.2000
IL 5-5	2.1453 $\pm$ 0.2346	7.8421 $\pm$ 0.4726	161.6750 $\pm$ 10.0421	133.1800 $\pm$ 19.3132	2.5000 $\pm$ 0.2236
IL 6-1	1.0676 $\pm$ 0.2859	10.5221 $\pm$ 0.4587	320.6750 $\pm$ 37.0737	268.9850 $\pm$ 32.3782	2.2500 $\pm$ 0.1936
IL 6-2	2.4458 $\pm$ 0.3803	12.9149 $\pm$ 0.4715	184.4250 $\pm$ 28.9173	255.2750 $\pm$ 22.2530	2.7500 $\pm$ 0.1936
IL 6-3	1.8370 $\pm$ 0.3108	10.1467 $\pm$ 0.5931	5.0950 $\pm$ 1.1981	0.0000 $\pm$ 0.0000	3.2500 $\pm$ 0.1936
IL 6-4	3.3416 $\pm$ 0.5452	11.1645 $\pm$ 1.3479	177.9550 $\pm$ 22.2613	97.3050 $\pm$ 10.1646	2.7500 $\pm$ 0.1936
IL 7-1	3.4378 $\pm$ 0.5297	16.3563 $\pm$ 0.5782	200.0950 $\pm$ 43.9129	234.5000 $\pm$ 27.2390	2.7500 $\pm$ 0.3708
IL 7-2	2.4123 $\pm$ 0.4096	14.6522 $\pm$ 1.2134	3.5900 $\pm$ 0.3894	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.4472
IL 7-3	2.8215 $\pm$ 0.3449	13.8776 $\pm$ 1.5610	146.9000 $\pm$ 12.7553	135.5950 $\pm$ 15.0422	3.7500 $\pm$ 0.1936
IL 7-4	2.1130 $\pm$ 0.2405	12.4046 $\pm$ 0.8176	79.2000 $\pm$ 4.6161	80.5850 $\pm$ 5.2083	1.0000 $\pm$ 0.0000
IL 7-4-1	1.3632 $\pm$ 0.1189	9.3585 $\pm$ 0.5448	216.7250 $\pm$ 14.0708	63.2700 $\pm$ 5.3897	1.9500 $\pm$ 0.0500
IL 7-5	2.4687 $\pm$ 0.2275	13.0214 $\pm$ 0.5981	249.4750 $\pm$ 29.1521	195.5750 $\pm$ 20.2970	2.7500 $\pm$ 0.1936
IL 7-5-5	3.4686 $\pm$ 0.4685	11.8294 $\pm$ 0.8099	259.9250 $\pm$ 15.1216	134.6900 $\pm$ 4.6672	3.0000 $\pm$ 0.0000
IL 8-1	1.8460 $\pm$ 0.1425	11.1701 $\pm$ 0.7495	187.8200 $\pm$ 26.2024	120.9100 $\pm$ 11.8994	1.8000 $\pm$ 0.2000
IL 8-1-1	2.5879 $\pm$ 0.8363	12.4097 $\pm$ 0.6047	49.8350 $\pm$ 5.1702	85.6500 $\pm$ 5.1646	2.5000 $\pm$ 0.2236
IL 8-2	2.5744 $\pm$ 0.3361	10.7949 $\pm$ 1.4760	185.8750 $\pm$ 18.8275	160.6500 $\pm$ 14.1456	2.5000 $\pm$ 0.2236
IL 8-2-1	2.9632 $\pm$ 0.2134	12.8246 $\pm$ 1.3303	61.6450 $\pm$ 7.7380	50.6050 $\pm$ 3.4740	2.7500 $\pm$ 0.1936
IL 8-3	3.0292 $\pm$ 0.2730	9.2277 $\pm$ 0.6161	181.6000 $\pm$ 30.8467	189.5750 $\pm$ 9.6210	2.7500 $\pm$ 0.3708
IL 9-1	1.8480 $\pm$ 0.3798	10.6611 $\pm$ 0.9227	184.5600 $\pm$ 33.9026	48.4500 $\pm$ 3.8218	2.2500 $\pm$ 0.1936
IL 9-1-2	2.2205 $\pm$ 0.0937	12.5463 $\pm$ 1.2968	160.1900 $\pm$ 37.3474	138.9100 $\pm$ 6.4330	2.7500 $\pm$ 0.3708
IL 9-1-3	3.6903 $\pm$ 0.3569	10.3619 $\pm$ 0.4855	195.5000 $\pm$ 21.7955	50.7400 $\pm$ 3.3427	2.7500 $\pm$ 0.1936
IL 9-2	3.0106 $\pm$ 0.2466	8.5943 $\pm$ 1.0081	229.8000 $\pm$ 35.8837	26.9600 $\pm$ 5.0105	2.7500 $\pm$ 0.1936
IL 9-2-5	2.5331 $\pm$ 0.4653	9.2327 $\pm$ 1.5374	170.6750 $\pm$ 21.8058	228.1500 $\pm$ 62.2920	2.2500 $\pm$ 0.1936
IL 9-2-6	2.4241 $\pm$ 0.2555	11.8428 $\pm$ 0.6683	77.3300 $\pm$ 8.4810	156.9800 $\pm$ 10.3476	2.0000 $\pm$ 0.4472
IL 9-3	1.5291 $\pm$ 0.2120	11.7259 $\pm$ 1.0667	168.3750 $\pm$ 29.2778	75.5250 $\pm$ 6.1160	2.5000 $\pm$ 0.2236
IL 9-3-1	3.5396 $\pm$ 0.1655	9.2406 $\pm$ 1.0726	56.1000 $\pm$ 8.5511	0.0000 $\pm$ 0.0000	2.5000 $\pm$ 0.2236
IL 9-3-2	2.3840 $\pm$ 0.3353	11.3853 $\pm$ 1.0150	242.8400 $\pm$ 40.7823	146.6000 $\pm$ 19.4105	2.5000 $\pm$ 0.2236
M82	3.0507 $\pm$ 0.2034	10.3638 $\pm$ 0.5217	187.5860 $\pm$ 7.9228	79.7290 $\pm$ 5.2965	2.8500 $\pm$ 0.0742

IL	Trusses number (unit)	Leaf DW (g)	Stem DW (g)	FBP Ald (nmol g ⁻¹ FW min ⁻¹)	G6PDH (nmol g ⁻¹ FW min ⁻¹)
IL 10-1	2.2500 ± 0.6614	39.5250 ± 2.3046	11.4500 ± 0.7684	7400.0205 ± 935.4806	879.3500 ± 18.4324
IL 10-1-1	4.2500 ± 0.9152	37.6500 ± 1.4699	12.1475 ± 0.5494	13059.7125 ± 899.7042	699.8225 ± 111.7906
IL 10-2	3.7500 ± 1.1124	42.8250 ± 1.2066	18.0750 ± 1.0317	4897.3130 ± 434.7330	819.9950 ± 40.3168
IL 10-2-2	4.0500 ± 0.5268	30.5500 ± 2.6043	8.2000 ± 0.4919	11151.2325 ± 1708.3582	953.6800 ± 77.0344
IL 10-3	4.0000 ± 0.8367	45.3500 ± 4.2372	16.1000 ± 1.0766	15615.1275 ± 604.7213	895.0028 ± 19.6250
IL 1-1	5.7500 ± 0.6614	30.0750 ± 1.7130	10.9250 ± 0.8387	12606.2250 ± 1437.2428	870.2925 ± 62.1661
IL 11-1	6.0500 ± 0.5268	25.7000 ± 1.4960	10.1250 ± 0.7876	9724.7320 ± 524.4027	1096.3108 ± 49.1952
IL 11-2	4.2500 ± 0.4873	34.1500 ± 1.5506	13.1750 ± 0.8511	12528.6350 ± 1022.8990	1075.4700 ± 57.0914
IL 1-1-2	3.5000 ± 0.5477	25.1550 ± 1.9079	9.1175 ± 0.5851	14637.9790 ± 751.4187	1392.2972 ± 150.1347
IL 11-3	4.7500 ± 0.9811	43.5907 ± 3.8789	11.9467 ± 0.9900	10436.8290 ± 393.6775	1066.3610 ± 56.4042
IL 1-1-3	1.6000 ± 0.6000	41.1000 ± 3.9891	13.5500 ± 1.6277	6919.6200 ± 953.6469	548.4725 ± 99.9022
IL 11-4	5.5000 ± 0.3873	32.2500 ± 2.8267	11.2250 ± 0.5589	8732.1910 ± 220.2036	977.9830 ± 18.8345
IL 11-4-1	5.2500 ± 0.7331	42.4000 ± 1.8509	16.1700 ± 0.6785	13464.4355 ± 416.7765	1076.0288 ± 65.0444
IL 1-2	6.4000 ± 0.5099	38.3875 ± 1.1602	13.2850 ± 0.4356	14285.9580 ± 876.5233	915.2228 ± 98.2403
IL 12-1	5.0000 ± 0.9487	25.9650 ± 1.8221	10.2250 ± 0.3836	9939.8600 ± 1165.4857	784.5450 ± 132.6964
IL 12-1-1	4.0500 ± 0.4213	60.9200 ± 1.9683	29.3050 ± 2.3354	9629.6425 ± 743.6473	771.4912 ± 113.5819
IL 12-2	3.7500 ± 0.1936	32.2850 ± 0.6081	12.6150 ± 0.7085	16878.0980 ± 1636.7674	1347.4200 ± 87.9683
IL 12-3	3.2500 ± 0.7331	24.5050 ± 2.5950	7.7525 ± 1.1328	8263.1650 ± 1476.4311	1049.2240 ± 166.9810
IL 12-3-1	5.4000 ± 0.5099	39.1250 ± 3.5311	10.8500 ± 0.6961	11548.9450 ± 890.8035	705.9740 ± 93.4965
IL 12-4	2.4000 ± 0.6782	41.2750 ± 1.1389	9.8225 ± 0.7462	13423.5980 ± 350.2864	1018.6898 ± 25.5931
IL 12-4-1	6.2000 ± 0.4899	44.1000 ± 4.2541	16.8000 ± 1.5281	12511.6213 ± 513.5243	1215.0808 ± 147.5689
IL 1-3	6.5000 ± 0.5000	40.5750 ± 2.7679	14.6250 ± 1.0504	13257.8952 ± 620.6799	1056.2480 ± 111.3150
IL 1-4	3.2500 ± 0.7331	36.8520 ± 3.0089	12.5800 ± 1.2155	12664.4473 ± 393.6095	820.8084 ± 116.7814
IL 1-4-18	4.6500 ± 0.8047	31.6250 ± 1.1770	9.7250 ± 0.6460	6354.2225 ± 739.3394	788.2275 ± 32.5438
IL 2-1	4.4000 ± 0.4000	19.2500 ± 1.9810	7.2250 ± 1.0072	14631.3200 ± 608.0680	802.5260 ± 28.0990
IL 2-2	4.3500 ± 0.5220	43.8750 ± 2.9805	13.2500 ± 1.9785	15562.4700 ± 769.5470	677.2060 ± 47.1249
IL 2-3	3.6000 ± 0.6000	40.9500 ± 0.8953	16.1500 ± 1.3366	15556.2232 ± 626.2239	1285.1624 ± 113.1712
IL 2-4	0.9500 ± 0.0500	62.5250 ± 4.6058	27.5000 ± 1.9867	13997.8512 ± 461.1920	836.3680 ± 43.1293
IL 2-5	3.3500 ± 0.5895	40.0250 ± 3.7516	15.3000 ± 1.5732	7303.6600 ± 882.8719	907.2850 ± 78.1201
IL 2-6	2.9500 ± 0.8231	54.3500 ± 1.6913	20.4500 ± 2.3252	13384.4672 ± 1477.5562	1288.9728 ± 96.4646
IL 2-6-5	4.2500 ± 0.8588	39.5500 ± 2.4579	11.1000 ± 1.0010	12709.3075 ± 860.1706	690.6340 ± 62.7676
IL 3-1	5.8000 ± 0.7348	43.5725 ± 2.9498	16.9225 ± 1.4319	12551.9853 ± 680.3989	950.2228 ± 109.5643
IL 3-2	2.8500 ± 0.3500	38.7000 ± 2.2034	12.5400 ± 1.0012	19064.8573 ± 1536.2879	1171.5972 ± 195.4242
IL 3-3	1.1500 ± 0.2179	14.8000 ± 3.3029	3.9750 ± 0.9254	7302.4073 ± 577.5932	677.3608 ± 163.8678
IL 3-4	0.0500 ± 0.0500	33.0400 ± 0.9899	8.7275 ± 0.5120	12534.9850 ± 904.2514	775.6088 ± 38.8819
IL 3-5	5.5000 ± 0.6708	44.4250 ± 2.2001	15.8625 ± 1.2733	12671.2800 ± 897.9646	856.0190 ± 99.3338
IL 4-1-1	4.8000 ± 0.4899	37.7500 ± 2.1457	11.7200 ± 1.3051	6032.6940 ± 1129.8864	1395.2340 ± 173.9513
IL 4-2	4.7500 ± 0.3708	25.7750 ± 2.1453	9.9750 ± 0.7290	5917.8875 ± 850.9311	769.4040 ± 66.3710
IL 4-3	5.7500 ± 0.7984	39.2875 ± 1.9138	14.7475 ± 0.7257	13725.1975 ± 1299.6339	866.7952 ± 70.0036
IL 4-3-2	5.5500 ± 0.6910	23.4825 ± 2.2869	8.4650 ± 0.6783	12017.5372 ± 626.5761	1261.1468 ± 129.2483
IL 4-4	1.9500 ± 0.3571	50.2500 ± 3.8849	16.2025 ± 1.3905	8497.0833 ± 365.8049	611.4625 ± 97.0719
IL 5-1	4.2500 ± 0.6614	40.1500 ± 3.6653	14.1750 ± 0.6748	12493.6892 ± 954.6011	634.1750 ± 56.5696
IL 5-3	5.6000 ± 0.8124	46.8000 ± 5.1530	17.2250 ± 2.1960	6764.2980 ± 1558.6832	607.6450 ± 35.3020
IL 5-4	5.2000 ± 0.5831	29.3250 ± 2.0053	12.3250 ± 0.5757	11913.8908 ± 2752.8856	1391.9328 ± 187.7216
IL 5-5	5.4000 ± 1.1225	35.9000 ± 2.9036	14.0500 ± 0.9599	6816.1650 ± 528.4435	459.5168 ± 37.6481
IL 6-1	6.0000 ± 0.7071	32.5500 ± 3.6444	14.5750 ± 0.5458	6364.8375 ± 944.0705	914.8072 ± 96.6627
IL 6-2	5.6500 ± 0.5895	34.4500 ± 1.4080	11.9100 ± 1.0274	14442.1250 ± 946.5096	978.9724 ± 109.9095
IL 6-3	1.7000 ± 0.3742	66.2200 ± 3.8131	29.3125 ± 2.2987	13615.6340 ± 649.5667	1454.4700 ± 129.0922
IL 6-4	3.1000 ± 0.6782	38.7500 ± 3.2278	10.7000 ± 1.5547	13415.1275 ± 613.9309	1136.1560 ± 65.9779
IL 7-1	5.0000 ± 0.6325	36.1000 ± 3.5826	13.7925 ± 1.4949	12142.4650 ± 934.0500	913.1615 ± 61.0559
IL 7-2	1.9000 ± 0.4583	47.1533 ± 2.9573	14.5140 ± 1.2562	11767.2380 ± 928.1364	819.4113 ± 79.6858
IL 7-3	4.5000 ± 1.0247	38.6500 ± 1.5312	11.3100 ± 0.5066	8333.1253 ± 634.3919	825.1260 ± 60.5623
IL 7-4	1.4000 ± 0.4000	15.3250 ± 1.4644	3.2250 ± 0.3397	8916.8600 ± 403.6484	1036.3272 ± 65.1123
IL 7-4-1	6.6000 ± 0.4000	26.1250 ± 1.2543	8.0750 ± 0.3527	12401.2050 ± 163.3273	810.3225 ± 83.1314
IL 7-5	5.0000 ± 0.3162	52.6500 ± 4.4721	13.2000 ± 0.7259	6167.4200 ± 1116.5413	693.8925 ± 50.0837
IL 7-5-5	3.5000 ± 0.5000	38.3250 ± 2.9030	12.1500 ± 1.2757	6890.2547 ± 823.1860	814.3300 ± 24.6227
IL 8-1	4.6000 ± 0.2449	23.1750 ± 1.4218	8.6000 ± 0.6075	5653.0400 ± 671.1281	2391.0780 ± 589.1414
IL 8-1-1	4.0500 ± 0.2784	18.6500 ± 1.9459	7.3350 ± 0.3282	6822.0187 ± 643.7205	1193.3116 ± 55.5627
IL 8-2	3.7500 ± 0.1936	35.1500 ± 2.5362	13.8575 ± 1.0736	15579.1275 ± 1903.2672	1502.9968 ± 141.7779
IL 8-2-1	3.4500 ± 0.6344	42.3637 ± 4.2321	9.9223 ± 1.0978	13310.8713 ± 440.3831	1194.8350 ± 71.2840
IL 8-3	4.2500 ± 0.7984	42.5250 ± 2.1616	10.0250 ± 0.4872	6496.1600 ± 605.6155	735.1612 ± 74.9313
IL 9-1	3.5000 ± 0.5000	38.9750 ± 3.0312	13.2450 ± 0.7517	12602.1843 ± 395.1331	689.2780 ± 60.0033
IL 9-1-2	4.3500 ± 0.4153	28.3200 ± 2.6973	7.4500 ± 1.1741	15137.7580 ± 1186.8143	1804.7160 ± 340.9940
IL 9-1-3	5.0000 ± 0.7071	41.1750 ± 3.4261	20.8750 ± 1.9247	8865.3480 ± 899.4151	1062.9216 ± 55.6800
IL 9-2	4.7500 ± 0.4873	45.3750 ± 3.1557	18.2000 ± 1.1866	14888.8775 ± 967.8479	654.1428 ± 118.7297
IL 9-2-5	5.2500 ± 0.3708	30.8300 ± 2.7217	9.9900 ± 0.6755	6457.7525 ± 1349.9774	1273.4688 ± 270.3119
IL 9-2-6	4.2000 ± 0.7348	25.7940 ± 2.1272	6.1420 ± 0.8452	4661.4440 ± 505.9728	1425.6157 ± 120.5001
IL 9-3	2.7500 ± 0.6614	34.1250 ± 3.2632	9.6450 ± 0.7978	11557.8590 ± 550.5550	903.1150 ± 96.5888
IL 9-3-1	2.5000 ± 0.6708	67.2940 ± 0.6131	17.8600 ± 0.4238	4336.1887 ± 134.8608	442.6490 ± 70.1283
IL 9-3-2	4.5000 ± 1.1619	31.2750 ± 2.5234	9.4500 ± 0.7928	3571.4833 ± 419.1927	553.6700 ± 69.2468
M82	4.5900 ± 0.4220	42.1240 ± 1.1670	14.3115 ± 0.4386	15104.6052 ± 275.9219	931.3704 ± 37.4837

IL	PGM (nmol g ⁻¹ FW min ⁻¹)	PGI (nmol g ⁻¹ FW min ⁻¹)	PFK (nmol g ⁻¹ FW min ⁻¹)	Frk (nmol g ⁻¹ FW min ⁻¹)	AGPase (nmol g ⁻¹ FW min ⁻¹)
IL 10-1	721.5524 ± 38.3143	3128.6320 ± 254.3646	2526.9733 ± 439.9353	95.5700 ± 5.0396	148.4950 ± 23.01051
IL 10-1-1	769.8920 ± 23.4673	3247.8340 ± 128.0874	1281.4967 ± 69.2873	337.0290 ± 39.2972	168.8484 ± 18.00220
IL 10-2	853.1800 ± 63.9502	3205.0325 ± 252.1945	2713.4333 ± 412.8236	201.0987 ± 25.8385	177.7200 ± 24.75932
IL 10-2-2	786.0940 ± 82.2493	3449.1240 ± 361.0720	651.4753 ± 76.1949	74.9280 ± 3.9777	212.7400 ± 26.83025
IL 10-3	725.3412 ± 71.7546	2986.5060 ± 320.2209	2363.2025 ± 184.4282	91.0753 ± 1.7278	154.7650 ± 16.22276
IL 1-1	895.6860 ± 18.9278	3641.9640 ± 194.8075	1711.0665 ± 127.9272	168.8645 ± 7.0109	209.2728 ± 31.21813
IL 11-1	701.5146 ± 109.2174	3254.8552 ± 287.4401	1228.9600 ± 92.4532	67.9320 ± 8.9684	177.2960 ± 12.42961
IL 11-2	908.1336 ± 45.2346	3532.6160 ± 269.2170	2014.9450 ± 193.8858	64.5780 ± 9.6727	257.8575 ± 35.80835
IL 1-1-2	1154.2852 ± 67.3431	4383.9140 ± 652.2670	1566.3048 ± 198.5898	174.9740 ± 20.4003	193.5448 ± 29.29644
IL 11-3	782.3223 ± 42.9398	3547.8397 ± 214.4499	1681.2140 ± 99.0107	50.7233 ± 2.7925	109.4000 ± 7.39515
IL 1-1-3	877.8225 ± 25.7785	3107.9150 ± 301.9826	666.8160 ± 77.9754	168.3750 ± 7.4384	341.1350 ± 51.80475
IL 11-4	817.6734 ± 38.1110	3590.6926 ± 239.5887	1669.9996 ± 118.0158	122.9658 ± 10.7088	91.0440 ± 5.50334
IL 11-4-1	918.9068 ± 58.7264	4108.4280 ± 573.1401	1452.2980 ± 103.3879	156.0552 ± 11.3034	245.3560 ± 20.22792
IL 1-2	938.1520 ± 130.8432	3984.3300 ± 185.8523	625.7310 ± 70.3839	200.2300 ± 10.4851	177.8653 ± 21.44383
IL 12-1	803.8540 ± 17.0894	3709.2420 ± 218.1813	2657.6400 ± 327.2302	130.7853 ± 8.7142	181.3100 ± 22.09700
IL 12-1-1	731.8936 ± 43.1105	3261.5540 ± 435.6954	786.6584 ± 80.4333	225.1480 ± 31.6716	229.4156 ± 43.27793
IL 12-2	997.4724 ± 83.1557	3978.8880 ± 325.2966	1910.9690 ± 74.7097	169.5180 ± 17.3197	185.4400 ± 22.84817
IL 12-3	1073.2360 ± 163.3966	4248.4700 ± 459.5715	4446.1725 ± 1080.4821	164.6040 ± 12.7859	199.8800 ± 21.72323
IL 12-3-1	590.2420 ± 34.0830	3260.8420 ± 132.4308	2464.3088 ± 208.7378	114.4000 ± 8.5879	129.0375 ± 10.66760
IL 12-4	778.6220 ± 16.5452	3295.7634 ± 42.4962	2320.9298 ± 166.3543	97.8550 ± 6.7193	182.5650 ± 4.23035
IL 12-4-1	914.5420 ± 75.0848	3827.7140 ± 228.5301	2521.3475 ± 617.8390	128.3625 ± 14.6711	30.99052
IL 1-3	858.7380 ± 40.5248	3805.6600 ± 177.2986	2190.0125 ± 440.7348	173.4925 ± 4.0238	83.8012 ± 8.55231
IL 1-4	777.9932 ± 66.2241	3977.9968 ± 228.0688	1484.0615 ± 147.0032	118.6556 ± 10.1774	142.0564 ± 8.31529
IL 1-4-18	733.2440 ± 59.5219	3037.3540 ± 395.2426	1530.3676 ± 156.8362	80.1425 ± 9.7503	215.9550 ± 21.37234
IL 2-1	845.0400 ± 41.6703	3317.9200 ± 171.9547	1680.8872 ± 188.8928	133.3436 ± 8.6327	178.6520 ± 13.41845
IL 2-2	825.4900 ± 85.3953	3519.1925 ± 171.5321	1489.7031 ± 107.1762	110.7970 ± 7.5943	127.0750 ± 18.99010
IL 2-3	962.9900 ± 28.4737	4406.6820 ± 166.0060	3405.1930 ± 671.1863	137.3100 ± 17.6267	145.3800 ± 15.36289
IL 2-4	767.9140 ± 42.3604	3219.7964 ± 154.2686	1804.9180 ± 98.4803	75.4200 ± 7.6509	245.9353 ± 26.26170
IL 2-5	848.7740 ± 44.2901	4039.7460 ± 232.4771	855.0650 ± 86.9623	149.8450 ± 18.6925	162.9775 ± 15.21738
IL 2-6	757.7632 ± 63.9271	3396.1540 ± 194.8361	1495.6020 ± 112.8211	143.4047 ± 10.5626	144.6836 ± 8.70002
IL 2-6-5	891.2056 ± 69.5439	3239.3784 ± 186.2530	2726.2840 ± 500.1521	84.1075 ± 3.1739	207.2400 ± 14.04157
IL 3-1	712.3660 ± 79.7892	3267.4360 ± 273.0894	1541.5017 ± 164.7031	123.4520 ± 14.6917	157.9000 ± 18.89629
IL 3-2	574.4084 ± 111.6566	4106.9940 ± 461.2616	1772.6583 ± 246.5282	188.4900 ± 31.3443	257.5467 ± 29.69726
IL 3-3	726.8992 ± 75.5304	2982.3368 ± 348.0528	1848.4213 ± 251.2252	156.5425 ± 24.3231	214.0800 ± 29.23646
IL 3-4	736.1560 ± 19.3988	3307.3180 ± 37.6735	1918.5350 ± 297.9028	117.3875 ± 6.9850	134.1775 ± 8.16167
IL 3-5	1162.7540 ± 74.5178	4062.5740 ± 501.2747	901.3453 ± 33.6911	123.4953 ± 9.6782	176.0350 ± 14.37555
IL 4-1-1	974.0770 ± 47.8480	3522.1720 ± 160.7001	2047.4780 ± 304.1021	123.7940 ± 15.2910	202.7220 ± 26.61799
IL 4-2	707.1560 ± 69.3745	3159.6540 ± 340.2896	1912.3800 ± 431.5821	123.2476 ± 9.7948	153.3740 ± 17.91835
IL 4-3	828.2444 ± 47.0608	4032.3520 ± 79.3391	2880.0307 ± 337.2784	152.8050 ± 15.3790	157.2425 ± 8.44879
IL 4-3-2	816.9980 ± 54.2312	3058.6460 ± 209.4196	358.7940 ± 47.0373	63.7870 ± 4.6300	131.7000 ± 17.54585
IL 4-4	721.9860 ± 42.5041	3274.9020 ± 151.2457	1962.8920 ± 327.1187	84.9625 ± 6.9272	162.7784 ± 19.36215
IL 5-1	628.8368 ± 111.2455	3490.7300 ± 320.6071	2686.6950 ± 353.0215	93.7975 ± 11.5232	136.5275 ± 5.86403
IL 5-3	726.9693 ± 58.6953	3808.5440 ± 172.8742	473.3810 ± 39.2617	144.3200 ± 24.7453	118.4894 ± 4.73736
IL 5-4	907.0512 ± 42.2633	4097.9040 ± 472.8232	1342.5227 ± 164.3991	93.8220 ± 11.0803	127.3364 ± 26.30111
IL 5-5	834.6232 ± 61.5146	3532.5320 ± 492.5736	747.2753 ± 99.8497	137.2350 ± 11.1670	151.5350 ± 10.64216
IL 6-1	793.2720 ± 50.1073	3666.7500 ± 356.4409	1244.8650 ± 180.6637	153.0128 ± 13.7759	173.2875 ± 22.65666
IL 6-2	836.8300 ± 38.3912	3677.7880 ± 190.9244	2092.2425 ± 168.7158	133.7275 ± 18.7792	181.6248 ± 31.77241
IL 6-3	950.3160 ± 79.4796	3961.4400 ± 392.1388	3013.4670 ± 122.7886	157.0725 ± 12.1106	101.4650 ± 8.26161
IL 6-4	671.3116 ± 62.9779	2794.2240 ± 161.3039	1498.1620 ± 65.1122	127.0588 ± 9.6308	227.1527 ± 38.24862
IL 7-1	777.4006 ± 70.3395	3476.4798 ± 265.1345	1598.0030 ± 160.0222	117.2378 ± 5.5498	165.2685 ± 10.81098
IL 7-2	871.8050 ± 7.8687	3502.2975 ± 266.8926	1138.1880 ± 107.6121	114.1100 ± 5.8713	178.1075 ± 26.70802
IL 7-3	497.5180 ± 44.6446	2775.5460 ± 125.3811	1404.1307 ± 133.1573	88.5850 ± 10.6867	118.9160 ± 12.16641
IL 7-4	1025.8564 ± 46.2472	3876.9220 ± 207.3904	1189.2040 ± 100.2462	176.8340 ± 28.7507	171.0168 ± 18.14541
IL 7-4-1	807.4440 ± 48.5443	3272.1440 ± 384.2578	1385.2425 ± 302.6980	138.1280 ± 8.7913	152.8800 ± 10.26229
IL 7-5	635.7360 ± 33.0554	2211.5280 ± 345.2532	668.2725 ± 46.7236	132.3720 ± 6.8057	161.8750 ± 8.86241
IL 7-5-5	816.9980 ± 42.4596	3086.4420 ± 281.1763	1846.3905 ± 132.4104	221.2780 ± 29.1102	206.9640 ± 38.59603
IL 8-1	687.3064 ± 90.4714	3862.9940 ± 454.3060	867.5820 ± 79.9956	320.5408 ± 80.6745	172.0850 ± 24.29625
IL 8-1-1	798.9452 ± 53.8607	3554.0320 ± 264.1173	881.1950 ± 49.7669	139.5400 ± 15.3977	63.8300 ± 6.71093
IL 8-2	783.2224 ± 35.6133	3920.1900 ± 225.2745	1029.0560 ± 14.4411	160.5975 ± 4.6300	159.1175 ± 43.40154
IL 8-2-1	678.4120 ± 64.8672	3165.6800 ± 301.7607	2196.3225 ± 301.8111	84.3940 ± 7.0813	172.7488 ± 22.40716
IL 8-3	650.7316 ± 34.2821	2903.3300 ± 166.2182	1094.5803 ± 27.6036	94.2987 ± 6.7577	226.4500 ± 32.94382
IL 9-1	894.9688 ± 34.5613	4172.1874 ± 319.5383	517.3640 ± 15.1921	156.0085 ± 6.5281	137.4435 ± 10.15866
IL 9-1-2	686.8724 ± 58.3209	4088.2280 ± 329.1703	1233.0400 ± 50.9816	145.4100 ± 19.5474	120.0900 ± 14.99662
IL 9-1-3	971.7384 ± 73.4074	5159.1400 ± 212.3671	2561.6387 ± 199.8099	184.3050 ± 26.1349	208.6800 ± 21.01422
IL 9-2	807.9780 ± 49.5265	3612.9400 ± 175.6086	711.0300 ± 58.4948	165.9837 ± 9.5063	143.8525 ± 15.98752
IL 9-2-5	1049.8072 ± 57.5108	3816.4260 ± 198.1747	1254.1320 ± 61.9886	112.8780 ± 6.1690	163.3420 ± 32.34237
IL 9-2-6	863.8040 ± 16.7572	3662.6330 ± 126.1423	3345.7760 ± 313.5178	168.4653 ± 19.8691	239.5210 ± 3.25964
IL 9-3	821.3084 ± 77.4330	3832.7000 ± 174.9579	1912.8785 ± 246.5417	133.7150 ± 25.9685	154.9375 ± 14.89667
IL 9-3-1	624.7220 ± 5.9673	3285.0510 ± 123.4149	1912.8785 ± 246.5417	45.8610 ± 5.1671	240.1830 ± 14.32818
IL 9-3-2	576.3340 ± 34.3289	3044.0780 ± 210.0954	1847.9798 ± 202.9816	45.8610 ± 5.1671	178.9560 ± 28.68867
M82	877.7538 ± 19.0724	3533.8808 ± 197.6896	1997.0609 ± 232.2207	168.8061 ± 7.3763	202.4373 ± 15.35448

IL	GK (nmol g ⁻¹ FW min ⁻¹)	GIDH (nmol g ⁻¹ FW min ⁻¹)
IL 10-1	144.6633 ± 10.9134	134.4980 ± 7.7639
IL 10-1-1	50.0460 ± 3.8019	278.0280 ± 39.3023
IL 10-2	90.4627 ± 8.3059	563.9260 ± 67.8656
IL 10-2-2	59.1870 ± 5.3102	138.2220 ± 6.6822
IL 10-3	65.6940 ± 5.6861	141.7520 ± 9.7551
IL 1-1	232.3200 ± 30.9710	539.0319 ± 66.2303
IL 11-1	58.8810 ± 6.4391	522.8527 ± 24.5294
IL 11-2	70.6160 ± 7.1277	469.3100 ± 52.5777
IL 1-1-2	116.0350 ± 10.4620	567.3456 ± 62.2996
IL 11-3	131.6154 ± 7.4013	583.9260 ± 50.2432
IL 1-1-3	75.1225 ± 6.2010	586.3980 ± 64.4379
IL 11-4	150.9304 ± 8.0043	343.1740 ± 21.2205
IL 11-4-1	100.4316 ± 15.0479	495.8400 ± 67.9836
IL 1-2	65.2896 ± 4.9423	606.5020 ± 57.5622
IL 12-1	157.0447 ± 19.7730	579.1930 ± 105.5850
IL 12-1-1	169.3050 ± 32.7728	442.8693 ± 79.8973
IL 12-2	220.0630 ± 24.7011	313.1540 ± 30.5338
IL 12-3	82.6987 ± 3.0043	230.0630 ± 13.6307
IL 12-3-1	60.5688 ± 9.2220	361.5053 ± 98.0334
IL 12-4	50.3848 ± 4.9875	673.5440 ± 29.3643
IL 12-4-1	66.2675 ± 17.0607	416.4440 ± 17.1383
IL 1-3	59.7960 ± 6.8976	548.0820 ± 18.9439
IL 1-4	70.2296 ± 6.0007	373.0236 ± 51.5980
IL 1-4-18	50.1690 ± 4.9766	345.9050 ± 45.8576
IL 2-1	113.9548 ± 11.3219	353.4170 ± 22.2726
IL 2-2	167.6513 ± 17.0972	68.6500 ± 2.6550
IL 2-3	43.5273 ± 2.9453	340.2820 ± 25.3268
IL 2-4	57.2900 ± 4.4520	358.7120 ± 50.4636
IL 2-5	122.4270 ± 7.2419	479.6896 ± 23.4626
IL 2-6	143.7275 ± 20.7946	269.7024 ± 22.9610
IL 2-6-5	68.9460 ± 11.0905	304.5068 ± 34.3656
IL 3-1	167.4023 ± 6.0481	525.0933 ± 41.1329
IL 3-2	66.2907 ± 3.5935	502.1736 ± 39.4923
IL 3-3	62.7875 ± 8.1430	1641.7980 ± 183.0218
IL 3-4	68.9140 ± 8.8556	452.3460 ± 22.7994
IL 3-5	37.8970 ± 4.8653	565.3240 ± 18.9966
IL 4-1-1	108.8473 ± 4.1799	252.4560 ± 29.0388
IL 4-2	81.7450 ± 5.5519	466.7780 ± 57.9712
IL 4-3	54.8940 ± 4.3937	404.6845 ± 56.2045
IL 4-3-2	61.3340 ± 5.4112	469.2180 ± 37.3311
IL 4-4	69.3080 ± 4.3240	505.1800 ± 44.6270
IL 5-1	100.4267 ± 6.8707	406.7525 ± 26.3764
IL 5-3	49.4880 ± 8.2688	565.3240 ± 18.9966
IL 5-4	70.8475 ± 1.0577	376.1127 ± 22.6435
IL 5-5	55.0933 ± 2.8167	698.7550 ± 71.8027
IL 6-1	155.2075 ± 19.8241	587.3972 ± 81.8904
IL 6-2	70.9375 ± 7.6531	161.9820 ± 13.5089
IL 6-3	96.9153 ± 7.3610	231.3720 ± 10.2027
IL 6-4	144.4400 ± 3.4424	529.1787 ± 27.2733
IL 7-1	122.1720 ± 12.3871	609.1930 ± 82.0709
IL 7-2	66.1020 ± 6.6330	212.2200 ± 26.6008
IL 7-3	54.2780 ± 2.2034	318.2240 ± 30.3265
IL 7-4	73.8380 ± 1.5475	70.1790 ± 2.2306
IL 7-4-1	77.6607 ± 6.9857	156.6520 ± 9.9206
IL 7-5	65.7400 ± 4.1441	132.1900 ± 4.0022
IL 7-5-5	64.4160 ± 2.7338	160.1920 ± 6.9360
IL 8-1	41.3676 ± 8.8859	528.3625 ± 76.2290
IL 8-1-1	107.8950 ± 10.7069	320.5407 ± 39.8658
IL 8-2	141.4525 ± 14.9295	304.9357 ± 27.6936
IL 8-2-1	113.9793 ± 8.6960	166.6040 ± 6.9501
IL 8-3	152.6025 ± 15.1943	264.6860 ± 14.8512
IL 9-1	61.1047 ± 9.6975	232.8207 ± 26.4043
IL 9-1-2	66.8487 ± 4.5322	562.8597 ± 61.9259
IL 9-1-3	140.8836 ± 13.2931	422.3296 ± 68.9360
IL 9-2	110.5630 ± 11.2381	550.4360 ± 40.2263
IL 9-2-5	84.9150 ± 14.9633	561.4150 ± 24.1020
IL 9-2-6	82.8520 ± 8.5156	70.5250 ± 3.0648
IL 9-3	131.2775 ± 21.8753	153.8300 ± 12.9059
IL 9-3-1	135.1360 ± 13.1401	478.7890 ± 55.4107
IL 9-3-2	61.6890 ± 4.5576	291.2070 ± 12.5977
M82	98.2982 ± 5.5630	490.7999 ± 22.5649

Supplemental Table S3: Averages and standard deviation of Leaf (mean $\pm$ SD, n = 5) for each parameter and accessionin of a population of 71 introgression lines (ILs) of *Solanum pennellii* into a genetic background of *Solanum lycopersicum* (M82). Metabolites: aa, Amino acid; NO₃, Nitrate; Starch; Protein; Glucose; Fructose; Sucrose. Harvest data: Green fruit fresh weight; Red fruit fresh weight; Stem number; Truss number; Leaf dry weight; Stem dry weight. Enzymes: FBP Ald, Fructose-bisphosphate aldolase; G6PDH, Glucose-6-phosphate dehydrogenase; PGM, Phosphoglucomutase; PGI, Phosphoglucose Isomerase total; PFK, Phosphofructokinase (ATP); Frk, Fructokinase, AGPase, ADP-glucose pyrophosphorylase; GK, Glucokinase; GLDH, Glutamate DH (NAD).

IL	aa ($\mu\text{mol mg}^{-1}$ FW)	NO ₃ ($\mu\text{mol g}^{-1}$ FW)	Protein (mg mg ⁻¹ FW)	Starch (mmol eq Glucose g ⁻¹ FW)	Glucose ($\mu\text{mol g}^{-1}$ FW)
IL 10-1	0.0838 $\pm$ 0.0039	0.0614 $\pm$ 0.0118	13.2803 $\pm$ 1.1228	67.0172 $\pm$ 6.9150	4.6033 $\pm$ 0.7081
IL 10-1-1	0.0883 $\pm$ 0.0139	0.0389 $\pm$ 0.0047	13.1616 $\pm$ 0.8525	76.4712 $\pm$ 4.2050	5.9729 $\pm$ 0.9235
IL 10-2	0.0868 $\pm$ 0.0123	0.0355 $\pm$ 0.0029	16.9614 $\pm$ 1.2959	70.2942 $\pm$ 5.9864	4.5013 $\pm$ 0.6216
IL 10-2-2	0.1071 $\pm$ 0.0190	0.0454 $\pm$ 0.0071	17.3211 $\pm$ 1.7271	75.7789 $\pm$ 7.3195	4.2376 $\pm$ 0.3937
IL 10-3	0.0756 $\pm$ 0.0068	0.0514 $\pm$ 0.0066	19.5313 $\pm$ 1.4788	74.8683 $\pm$ 3.9211	3.5598 $\pm$ 0.3458
IL 1-1	0.1137 $\pm$ 0.0093	0.0362 $\pm$ 0.0029	19.1215 $\pm$ 1.2648	71.1069 $\pm$ 5.7083	6.1070 $\pm$ 1.0209
IL 11-1	0.1024 $\pm$ 0.0102	0.0350 $\pm$ 0.0045	20.6466 $\pm$ 1.5059	79.7795 $\pm$ 3.7923	4.3548 $\pm$ 0.4232
IL 11-2	0.0832 $\pm$ 0.0090	0.0340 $\pm$ 0.0029	12.1527 $\pm$ 0.8326	91.1689 $\pm$ 1.1074	3.6384 $\pm$ 0.3923
IL 1-1-2	0.0987 $\pm$ 0.0083	0.0522 $\pm$ 0.0077	21.2862 $\pm$ 1.1932	75.7209 $\pm$ 3.8454	3.2285 $\pm$ 0.3947
IL 11-3	0.1060 $\pm$ 0.0128	0.0486 $\pm$ 0.0102	14.9413 $\pm$ 0.8680	66.7614 $\pm$ 9.0430	1.4846 $\pm$ 0.1363
IL 1-1-3	0.1270 $\pm$ 0.0166	0.0531 $\pm$ 0.0137	21.2228 $\pm$ 1.9119	38.3677 $\pm$ 2.4129	2.3257 $\pm$ 0.5181
IL 11-4	0.1082 $\pm$ 0.0085	0.0426 $\pm$ 0.0124	19.2819 $\pm$ 2.3003	76.1766 $\pm$ 5.2662	7.4194 $\pm$ 0.3199
IL 11-4-1	0.0966 $\pm$ 0.0175	0.0477 $\pm$ 0.0088	16.4515 $\pm$ 1.2844	83.6613 $\pm$ 1.9940	4.8385 $\pm$ 0.6444
IL 1-2	0.0986 $\pm$ 0.0116	0.0624 $\pm$ 0.0094	18.3421 $\pm$ 1.7548	78.8941 $\pm$ 6.0100	4.8936 $\pm$ 0.4497
IL 12-1	0.0773 $\pm$ 0.0037	0.0394 $\pm$ 0.0070	16.1386 $\pm$ 0.6364	79.0614 $\pm$ 9.3711	2.9390 $\pm$ 0.4435
IL 12-1-1	0.0870 $\pm$ 0.0115	0.0451 $\pm$ 0.0039	16.7181 $\pm$ 1.7911	79.1415 $\pm$ 3.8220	3.1725 $\pm$ 0.4142
IL 12-2	0.1004 $\pm$ 0.0075	0.0354 $\pm$ 0.0073	19.3036 $\pm$ 1.6451	66.2078 $\pm$ 7.7402	5.2817 $\pm$ 0.8424
IL 12-3	0.1185 $\pm$ 0.0198	0.0292 $\pm$ 0.0058	22.3846 $\pm$ 1.5532	70.9757 $\pm$ 9.3699	6.5549 $\pm$ 0.5186
IL 12-3-1	0.1074 $\pm$ 0.0170	0.0276 $\pm$ 0.0068	20.2876 $\pm$ 2.0457	79.0948 $\pm$ 2.5991	2.5511 $\pm$ 0.2685
IL 12-4	0.0625 $\pm$ 0.0066	0.0374 $\pm$ 0.0032	16.2279 $\pm$ 0.5336	73.0786 $\pm$ 7.1116	4.2050 $\pm$ 0.1662
IL 12-4-1	0.0860 $\pm$ 0.0046	0.0264 $\pm$ 0.0039	17.6502 $\pm$ 1.1057	82.5291 $\pm$ 6.0087	3.9958 $\pm$ 0.6930
IL 1-3	0.1028 $\pm$ 0.0049	0.0519 $\pm$ 0.0080	18.5921 $\pm$ 2.7628	84.9990 $\pm$ 2.0492	3.4171 $\pm$ 0.4148
IL 1-4	0.0924 $\pm$ 0.0027	0.0250 $\pm$ 0.0055	19.5839 $\pm$ 0.7187	82.5099 $\pm$ 4.5985	2.2930 $\pm$ 0.3775
IL 1-4-18	0.1056 $\pm$ 0.0184	0.0276 $\pm$ 0.0059	16.8397 $\pm$ 1.4510	86.4994 $\pm$ 4.0516	3.1377 $\pm$ 0.5330
IL 2-1	0.1192 $\pm$ 0.0126	0.0460 $\pm$ 0.0121	19.0167 $\pm$ 1.5167	84.0441 $\pm$ 3.8367	3.7680 $\pm$ 0.4358
IL 2-2	0.0893 $\pm$ 0.0122	0.0357 $\pm$ 0.0079	18.2438 $\pm$ 1.3566	72.2974 $\pm$ 7.6641	2.7281 $\pm$ 0.4607
IL 2-3	0.0913 $\pm$ 0.0115	0.0539 $\pm$ 0.0099	17.7221 $\pm$ 0.9255	71.4632 $\pm$ 6.6647	5.1708 $\pm$ 0.5234
IL 2-4	0.0945 $\pm$ 0.0124	0.0534 $\pm$ 0.0092	20.8721 $\pm$ 0.8800	78.1178 $\pm$ 2.7351	4.1016 $\pm$ 0.5441
IL 2-5	0.0882 $\pm$ 0.0106	0.0439 $\pm$ 0.0102	17.5021 $\pm$ 1.5613	80.4785 $\pm$ 6.5091	3.4456 $\pm$ 0.7336
IL 2-6	0.1015 $\pm$ 0.0103	0.0282 $\pm$ 0.0088	19.3545 $\pm$ 1.5848	77.6954 $\pm$ 2.9657	2.9358 $\pm$ 1.0864
IL 2-6-5	0.1062 $\pm$ 0.0153	0.0322 $\pm$ 0.0057	17.3545 $\pm$ 0.9644	73.9614 $\pm$ 10.0603	2.7095 $\pm$ 0.1719
IL 3-1	0.0969 $\pm$ 0.0126	0.0204 $\pm$ 0.0041	17.9014 $\pm$ 1.0600	71.3006 $\pm$ 5.4394	3.0254 $\pm$ 0.2195
IL 3-2	0.0995 $\pm$ 0.0125	0.0422 $\pm$ 0.0124	21.4907 $\pm$ 1.3149	38.7794 $\pm$ 4.0033	2.6289 $\pm$ 0.3394
IL 3-3	0.1151 $\pm$ 0.0115	0.0115 $\pm$ 0.0024	18.7857 $\pm$ 1.2873	70.9880 $\pm$ 5.4188	2.3036 $\pm$ 0.2726
IL 3-4	0.0864 $\pm$ 0.0101	0.0491 $\pm$ 0.0051	18.0276 $\pm$ 1.0287	79.3782 $\pm$ 3.1933	2.6706 $\pm$ 0.3608
IL 3-5	0.0893 $\pm$ 0.0149	0.0557 $\pm$ 0.0105	17.0736 $\pm$ 1.8016	81.8107 $\pm$ 4.4208	4.2975 $\pm$ 1.0723
IL 4-1-1	0.0990 $\pm$ 0.0093	0.0311 $\pm$ 0.0040	16.6513 $\pm$ 1.0669	59.5112 $\pm$ 5.8878	3.0712 $\pm$ 0.5883
IL 4-2	0.0908 $\pm$ 0.0073	0.0544 $\pm$ 0.0116	18.5525 $\pm$ 2.1153	75.5113 $\pm$ 5.0704	4.9337 $\pm$ 0.6371
IL 4-3	0.0942 $\pm$ 0.0110	0.0344 $\pm$ 0.0087	16.9016 $\pm$ 1.4076	69.2412 $\pm$ 6.1219	5.4947 $\pm$ 0.7928
IL 4-3-2	0.0874 $\pm$ 0.0052	0.0303 $\pm$ 0.0027	16.3656 $\pm$ 1.5460	84.2445 $\pm$ 4.4836	3.7509 $\pm$ 0.2852
IL 4-4	0.0938 $\pm$ 0.0126	0.0346 $\pm$ 0.0122	19.0307 $\pm$ 1.6878	81.6433 $\pm$ 3.6825	2.1713 $\pm$ 0.3466
IL 5-1	0.0899 $\pm$ 0.0083	0.0533 $\pm$ 0.0086	18.1813 $\pm$ 2.0654	76.9394 $\pm$ 5.6876	2.6050 $\pm$ 0.6323
IL 5-3	0.0965 $\pm$ 0.0060	0.0391 $\pm$ 0.0052	18.6823 $\pm$ 1.4456	74.1325 $\pm$ 3.5346	5.1773 $\pm$ 0.5637
IL 5-4	0.1203 $\pm$ 0.0083	0.0420 $\pm$ 0.0110	17.6971 $\pm$ 1.6334	69.7396 $\pm$ 7.6867	2.9542 $\pm$ 0.3945
IL 5-5	0.0881 $\pm$ 0.0133	0.0435 $\pm$ 0.0077	17.9260 $\pm$ 1.5959	87.3842 $\pm$ 3.2872	2.2475 $\pm$ 0.4100
IL 6-1	0.0950 $\pm$ 0.0102	0.0348 $\pm$ 0.0030	17.4266 $\pm$ 1.4983	86.8290 $\pm$ 3.8530	4.2160 $\pm$ 0.3521
IL 6-2	0.0939 $\pm$ 0.0133	0.0580 $\pm$ 0.0111	19.2754 $\pm$ 1.7882	84.0036 $\pm$ 4.5280	4.3611 $\pm$ 0.4070
IL 6-3	0.1005 $\pm$ 0.0097	0.0526 $\pm$ 0.0033	17.6879 $\pm$ 1.3470	83.9326 $\pm$ 7.2812	3.3603 $\pm$ 0.4220
IL 6-4	0.0969 $\pm$ 0.0133	0.0534 $\pm$ 0.0114	15.5939 $\pm$ 1.6151	76.8612 $\pm$ 2.5060	3.7942 $\pm$ 0.4916
IL 7-1	0.0951 $\pm$ 0.0147	0.0145 $\pm$ 0.0022	15.3918 $\pm$ 1.5139	86.3601 $\pm$ 3.8152	3.6737 $\pm$ 0.3369
IL 7-2	0.1062 $\pm$ 0.0084	0.0319 $\pm$ 0.0041	15.2328 $\pm$ 0.8074	73.3332 $\pm$ 6.2001	2.9472 $\pm$ 0.6546
IL 7-3	0.0722 $\pm$ 0.0064	0.0456 $\pm$ 0.0084	14.5693 $\pm$ 0.8940	86.4295 $\pm$ 1.9764	2.5417 $\pm$ 0.1530
IL 7-4	0.0781 $\pm$ 0.0131	0.0366 $\pm$ 0.0070	15.5598 $\pm$ 1.2253	73.8983 $\pm$ 4.2451	3.5900 $\pm$ 0.4770
IL 7-4-1	0.0926 $\pm$ 0.0110	0.0350 $\pm$ 0.0071	17.1553 $\pm$ 1.9060	74.4704 $\pm$ 4.0270	4.9277 $\pm$ 0.6619
IL 7-5	0.0896 $\pm$ 0.0140	0.0325 $\pm$ 0.0083	15.7648 $\pm$ 1.4879	74.9946 $\pm$ 7.2246	1.9558 $\pm$ 0.2173
IL 7-5-5	0.0956 $\pm$ 0.0142	0.0572 $\pm$ 0.0105	16.7569 $\pm$ 1.6233	72.5007 $\pm$ 8.2010	3.6194 $\pm$ 0.5702
IL 8-1	0.1011 $\pm$ 0.0103	0.0369 $\pm$ 0.0048	18.7630 $\pm$ 1.8873	61.8046 $\pm$ 7.0419	3.8930 $\pm$ 0.4595
IL 8-1-1	0.1124 $\pm$ 0.0144	0.0347 $\pm$ 0.0039	21.3417 $\pm$ 1.5554	88.8579 $\pm$ 1.3063	4.6904 $\pm$ 0.4696
IL 8-2	0.0987 $\pm$ 0.0049	0.0189 $\pm$ 0.0028	17.7880 $\pm$ 0.8008	81.5693 $\pm$ 3.9559	3.2793 $\pm$ 0.3073
IL 8-2-1	0.0923 $\pm$ 0.0148	0.0337 $\pm$ 0.0022	14.4994 $\pm$ 1.2005	85.0055 $\pm$ 4.4946	3.5699 $\pm$ 0.6813
IL 8-3	0.0673 $\pm$ 0.0116	0.0331 $\pm$ 0.0045	12.7374 $\pm$ 0.6596	80.3941 $\pm$ 6.5946	2.7514 $\pm$ 0.3718
IL 9-1	0.0946 $\pm$ 0.0158	0.0310 $\pm$ 0.0048	20.9182 $\pm$ 0.5485	75.0339 $\pm$ 7.9953	4.8039 $\pm$ 0.1082
IL 9-1-2	0.1015 $\pm$ 0.0179	0.0366 $\pm$ 0.0012	17.7177 $\pm$ 1.8852	80.8620 $\pm$ 4.7809	3.5435 $\pm$ 0.3143
IL 9-1-3	0.1585 $\pm$ 0.0188	0.0397 $\pm$ 0.0105	23.5700 $\pm$ 1.9417	56.4693 $\pm$ 6.5486	5.8862 $\pm$ 0.4644
IL 9-2	0.1321 $\pm$ 0.0211	0.0824 $\pm$ 0.0078	18.9423 $\pm$ 3.0154	75.5935 $\pm$ 2.9008	1.9480 $\pm$ 0.3294
IL 9-2-5	0.1407 $\pm$ 0.0126	0.0340 $\pm$ 0.0058	19.2239 $\pm$ 1.4886	53.5713 $\pm$ 11.5460	2.2356 $\pm$ 0.5235
IL 9-2-6	0.1102 $\pm$ 0.0031	0.0259 $\pm$ 0.0015	20.8295 $\pm$ 0.4487	85.2727 $\pm$ 0.8024	3.5255 $\pm$ 0.1742
IL 9-3	0.0981 $\pm$ 0.0100	0.0545 $\pm$ 0.0133	18.8826 $\pm$ 1.8478	83.3132 $\pm$ 4.3525	3.7876 $\pm$ 0.5929
IL 9-3-1	0.0914 $\pm$ 0.0142	0.0670 $\pm$ 0.0101	15.1017 $\pm$ 1.0020	66.9744 $\pm$ 6.5180	1.8988 $\pm$ 0.0909
IL 9-3-2	0.0706 $\pm$ 0.0066	0.0532 $\pm$ 0.0126	15.2216 $\pm$ 1.1472	76.4714 $\pm$ 3.7693	3.1542 $\pm$ 0.6977
M82	0.1079 $\pm$ 0.0040	0.0322 $\pm$ 0.0021	19.4693 $\pm$ 0.7389	71.9640 $\pm$ 2.6797	2.8229 $\pm$ 0.3075

IL	Fructose ($\mu\text{mol g}^{-1}\text{FW}$)	Sucrose ($\mu\text{mol g}^{-1}\text{FW}$)	Green fruit FW (g)	Red fruit FW (g)	Stem number (unit)
IL 10-1	9.4871 $\pm$ 0.2417	4.9091 $\pm$ 0.3153	55.3900 $\pm$ 12.5104	45.8450 $\pm$ 7.2530	3.2500 $\pm$ 0.1936
IL 10-1-1	10.5774 $\pm$ 0.9791	6.2562 $\pm$ 0.5296	174.2750 $\pm$ 21.0464	53.7000 $\pm$ 9.1516	2.5000 $\pm$ 0.2236
IL 10-2	9.6251 $\pm$ 0.8583	5.9476 $\pm$ 0.7623	218.6600 $\pm$ 27.2375	123.7700 $\pm$ 2.0066	2.5000 $\pm$ 0.2236
IL 10-2-2	8.2570 $\pm$ 0.5438	5.1202 $\pm$ 0.6359	160.6180 $\pm$ 8.3407	0.0000 $\pm$ 0.0000	2.5000 $\pm$ 0.2236
IL 10-3	7.4092 $\pm$ 0.6017	5.7240 $\pm$ 0.2159	179.7000 $\pm$ 23.2313	0.0000 $\pm$ 0.0000	4.0000 $\pm$ 0.0000
IL 1-1	9.6820 $\pm$ 0.9606	7.0024 $\pm$ 0.9345	244.1750 $\pm$ 30.9156	170.6750 $\pm$ 38.3234	2.2500 $\pm$ 0.1936
IL 11-1	8.0463 $\pm$ 0.4207	6.3841 $\pm$ 0.2927	281.2200 $\pm$ 28.9185	58.1650 $\pm$ 3.5972	2.2500 $\pm$ 0.1936
IL 11-2	8.4639 $\pm$ 0.3248	7.1377 $\pm$ 0.5685	170.6250 $\pm$ 22.1564	187.7000 $\pm$ 25.4187	3.0000 $\pm$ 0.3162
IL 1-1-2	7.7022 $\pm$ 0.6643	5.7417 $\pm$ 0.6286	224.6000 $\pm$ 18.2466	133.4150 $\pm$ 7.5232	2.7500 $\pm$ 0.1936
IL 11-3	3.2118 $\pm$ 0.2354	5.7295 $\pm$ 0.6681	35.3100 $\pm$ 4.5280	0.0000 $\pm$ 0.0000	3.2500 $\pm$ 0.1936
IL 1-1-3	5.6766 $\pm$ 1.1510	5.8270 $\pm$ 0.6748	0.0000 $\pm$ 0.0000	0.0000 $\pm$ 0.0000	2.8000 $\pm$ 0.2000
IL 11-4	12.3302 $\pm$ 0.2065	8.7350 $\pm$ 1.2052	296.7250 $\pm$ 24.8374	133.2050 $\pm$ 13.7229	2.5000 $\pm$ 0.2236
IL 11-4-1	7.2189 $\pm$ 0.9875	6.1001 $\pm$ 0.7213	201.5000 $\pm$ 24.2540	176.7250 $\pm$ 22.8275	3.0000 $\pm$ 0.3162
IL 1-2	10.0461 $\pm$ 0.6019	6.2307 $\pm$ 0.7113	246.5250 $\pm$ 10.9977	184.0500 $\pm$ 24.9842	2.7500 $\pm$ 0.1936
IL 12-1	9.1281 $\pm$ 0.5630	6.5051 $\pm$ 0.8415	264.7750 $\pm$ 13.5314	216.0000 $\pm$ 32.8555	2.9000 $\pm$ 0.1000
IL 12-1-1	7.7341 $\pm$ 0.5578	6.1950 $\pm$ 0.2240	166.7500 $\pm$ 14.2728	48.5250 $\pm$ 10.4611	3.2500 $\pm$ 0.3708
IL 12-2	8.9019 $\pm$ 0.5737	6.6098 $\pm$ 0.6198	186.2250 $\pm$ 31.5059	108.5000 $\pm$ 12.8193	2.5000 $\pm$ 0.2236
IL 12-3	11.8095 $\pm$ 0.9692	6.6392 $\pm$ 0.6003	86.8500 $\pm$ 15.5325	50.6450 $\pm$ 6.4328	1.7500 $\pm$ 0.1936
IL 12-3-1	5.7404 $\pm$ 0.6126	6.8523 $\pm$ 0.6443	201.4000 $\pm$ 19.7120	136.4050 $\pm$ 17.7082	3.2500 $\pm$ 0.1936
IL 12-4	7.8266 $\pm$ 0.2787	4.5467 $\pm$ 0.5157	277.9100 $\pm$ 30.8604	0.0000 $\pm$ 0.0000	2.0000 $\pm$ 0.0000
IL 12-4-1	8.9595 $\pm$ 0.8189	5.8745 $\pm$ 0.6042	299.0750 $\pm$ 29.8522	48.9500 $\pm$ 6.0051	3.0000 $\pm$ 0.0000
IL 1-3	7.6728 $\pm$ 0.4635	6.3480 $\pm$ 0.4058	310.7250 $\pm$ 35.2472	153.0000 $\pm$ 9.9977	3.0000 $\pm$ 0.0000
IL 1-4	5.8224 $\pm$ 0.5861	6.3958 $\pm$ 0.2901	212.5250 $\pm$ 45.8572	80.8200 $\pm$ 10.8288	2.2500 $\pm$ 0.3708
IL 1-4-18	7.1962 $\pm$ 0.6188	6.8384 $\pm$ 0.3429	227.9000 $\pm$ 44.7070	227.4750 $\pm$ 27.7731	2.2500 $\pm$ 0.1936
IL 2-1	7.1291 $\pm$ 0.3498	6.3131 $\pm$ 0.4826	51.8350 $\pm$ 3.5180	122.7750 $\pm$ 10.6394	1.9500 $\pm$ 0.0500
IL 2-2	5.8302 $\pm$ 0.5654	5.6496 $\pm$ 0.7378	154.3700 $\pm$ 15.4588	122.1500 $\pm$ 9.3097	2.7000 $\pm$ 0.2000
IL 2-3	10.2968 $\pm$ 0.2633	6.2616 $\pm$ 0.4845	125.7850 $\pm$ 7.3037	62.2700 $\pm$ 5.0057	2.5000 $\pm$ 0.2236
IL 2-4	8.9128 $\pm$ 0.4342	6.7140 $\pm$ 0.6300	6.2150 $\pm$ 1.0017	0.0000 $\pm$ 0.0000	3.5000 $\pm$ 0.2236
IL 2-5	5.7217 $\pm$ 0.5116	5.4032 $\pm$ 0.3761	39.3050 $\pm$ 4.7901	39.2250 $\pm$ 4.1184	2.7500 $\pm$ 0.1936
IL 2-6	4.3972 $\pm$ 0.7506	5.4021 $\pm$ 0.1773	68.4500 $\pm$ 6.9368	7.4700 $\pm$ 0.3986	3.2500 $\pm$ 0.3708
IL 2-6-5	6.4532 $\pm$ 0.6046	5.7080 $\pm$ 0.5170	241.1500 $\pm$ 19.1384	185.2600 $\pm$ 29.4311	2.2500 $\pm$ 0.1936
IL 3-1	6.0709 $\pm$ 0.6158	6.7976 $\pm$ 0.5473	425.3750 $\pm$ 45.3629	223.9100 $\pm$ 24.0168	3.0000 $\pm$ 0.3162
IL 3-2	5.6399 $\pm$ 0.2647	4.5114 $\pm$ 0.4087	84.5700 $\pm$ 6.7718	59.7300 $\pm$ 6.1437	3.0000 $\pm$ 0.0000
IL 3-3	6.1741 $\pm$ 0.4158	5.5804 $\pm$ 0.3983	0.0000 $\pm$ 0.0000	28.4050 $\pm$ 2.6174	2.2500 $\pm$ 0.1936
IL 3-4	6.5774 $\pm$ 0.6079	6.9329 $\pm$ 0.2126	0.0000 $\pm$ 0.0000	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.3162
IL 3-5	5.9868 $\pm$ 0.5140	6.5530 $\pm$ 0.4133	193.0500 $\pm$ 8.2012	128.0750 $\pm$ 16.8745	3.0000 $\pm$ 0.0000
IL 4-1-1	6.7453 $\pm$ 0.5723	4.5679 $\pm$ 0.3243	0.0000 $\pm$ 0.0000	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.0000
IL 4-2	9.9892 $\pm$ 1.0667	4.9993 $\pm$ 0.4997	275.3000 $\pm$ 28.0175	154.1500 $\pm$ 19.1485	2.7500 $\pm$ 0.1936
IL 4-3	10.6504 $\pm$ 1.1575	4.9408 $\pm$ 0.7027	175.7000 $\pm$ 21.9478	56.2950 $\pm$ 3.8400	3.0000 $\pm$ 0.3162
IL 4-3-2	8.2755 $\pm$ 0.4593	5.9127 $\pm$ 0.3320	216.0450 $\pm$ 31.1439	86.6400 $\pm$ 6.4367	3.2500 $\pm$ 0.3708
IL 4-4	5.5194 $\pm$ 0.2770	6.3630 $\pm$ 0.3005	43.5850 $\pm$ 4.5427	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.3162
IL 5-1	5.9886 $\pm$ 0.3111	7.1012 $\pm$ 0.6480	201.1000 $\pm$ 24.1758	76.7600 $\pm$ 5.7822	2.5000 $\pm$ 0.2236
IL 5-3	6.7092 $\pm$ 1.1760	5.6499 $\pm$ 0.5836	154.3120 $\pm$ 7.4330	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.3162
IL 5-4	7.4308 $\pm$ 0.6170	7.4910 $\pm$ 0.5203	266.9200 $\pm$ 52.7811	0.0000 $\pm$ 0.0000	2.8000 $\pm$ 0.2000
IL 5-5	5.6458 $\pm$ 0.7506	6.8522 $\pm$ 0.6061	161.6750 $\pm$ 10.0421	133.1800 $\pm$ 19.3132	2.5000 $\pm$ 0.2236
IL 6-1	9.1730 $\pm$ 0.2847	6.7089 $\pm$ 0.3772	320.6750 $\pm$ 37.0737	268.9850 $\pm$ 32.3782	2.2500 $\pm$ 0.1936
IL 6-2	9.4747 $\pm$ 0.8805	6.0529 $\pm$ 0.5600	184.4250 $\pm$ 28.9173	255.2750 $\pm$ 22.2530	2.7500 $\pm$ 0.1936
IL 6-3	6.4984 $\pm$ 0.7598	5.6625 $\pm$ 0.7182	5.0950 $\pm$ 1.1981	0.0000 $\pm$ 0.0000	3.2500 $\pm$ 0.1936
IL 6-4	7.6528 $\pm$ 0.2962	6.1925 $\pm$ 0.6664	177.9550 $\pm$ 22.2613	97.3050 $\pm$ 10.1646	2.7500 $\pm$ 0.1936
IL 7-1	8.7150 $\pm$ 0.1438	6.2585 $\pm$ 0.7018	200.0950 $\pm$ 43.9129	234.5000 $\pm$ 27.2390	2.7500 $\pm$ 0.3708
IL 7-2	7.1139 $\pm$ 0.7740	6.2236 $\pm$ 0.2293	3.5900 $\pm$ 0.3894	0.0000 $\pm$ 0.0000	3.0000 $\pm$ 0.4472
IL 7-3	6.7296 $\pm$ 0.5597	7.6009 $\pm$ 0.6632	146.9000 $\pm$ 12.7553	135.5950 $\pm$ 15.0422	3.7500 $\pm$ 0.1936
IL 7-4	7.1395 $\pm$ 0.6123	6.2433 $\pm$ 0.3605	79.2000 $\pm$ 4.6161	80.5850 $\pm$ 5.2083	1.0000 $\pm$ 0.0000
IL 7-4-1	9.2812 $\pm$ 0.6653	7.1704 $\pm$ 0.8108	216.7250 $\pm$ 14.0708	63.2700 $\pm$ 5.3897	1.9500 $\pm$ 0.0500
IL 7-5	5.9691 $\pm$ 0.7643	6.8113 $\pm$ 0.9834	249.4750 $\pm$ 29.1521	195.5750 $\pm$ 20.2970	2.7500 $\pm$ 0.1936
IL 7-5-5	7.6961 $\pm$ 0.5706	7.2585 $\pm$ 0.8005	259.9250 $\pm$ 15.1216	134.6900 $\pm$ 4.6672	3.0000 $\pm$ 0.0000
IL 8-1	8.9382 $\pm$ 0.3403	6.4566 $\pm$ 0.5081	187.8200 $\pm$ 26.2024	120.9100 $\pm$ 11.8994	1.8000 $\pm$ 0.2000
IL 8-1-1	11.4111 $\pm$ 0.2069	6.7245 $\pm$ 0.5672	49.8350 $\pm$ 5.1702	85.6500 $\pm$ 5.1646	2.5000 $\pm$ 0.2236
IL 8-2	7.9065 $\pm$ 0.5567	6.5397 $\pm$ 0.2329	185.8750 $\pm$ 18.8275	160.6500 $\pm$ 14.1456	2.5000 $\pm$ 0.2236
IL 8-2-1	8.3622 $\pm$ 0.8081	7.8060 $\pm$ 0.3564	61.6450 $\pm$ 7.7380	50.6050 $\pm$ 3.4740	2.7500 $\pm$ 0.1936
IL 8-3	4.0624 $\pm$ 1.0852	5.9097 $\pm$ 0.7047	181.6000 $\pm$ 30.8467	189.5750 $\pm$ 9.6210	2.7500 $\pm$ 0.3708
IL 9-1	10.2414 $\pm$ 0.8948	7.4198 $\pm$ 0.9621	184.5600 $\pm$ 33.9026	48.4500 $\pm$ 3.8218	2.2500 $\pm$ 0.1936
IL 9-1-2	8.0753 $\pm$ 0.6811	8.2969 $\pm$ 1.0059	160.1900 $\pm$ 37.3474	138.9100 $\pm$ 6.4330	2.7500 $\pm$ 0.3708
IL 9-1-3	12.4561 $\pm$ 0.7588	7.0992 $\pm$ 0.6723	195.5000 $\pm$ 21.7955	50.7400 $\pm$ 3.3427	2.7500 $\pm$ 0.1936
IL 9-2	3.5734 $\pm$ 0.4815	5.5543 $\pm$ 0.4222	229.8000 $\pm$ 35.8837	26.9600 $\pm$ 5.0105	2.7500 $\pm$ 0.1936
IL 9-2-5	7.5794 $\pm$ 1.0310	6.0201 $\pm$ 0.7121	170.6750 $\pm$ 21.8058	228.1500 $\pm$ 62.2920	2.2500 $\pm$ 0.1936
IL 9-2-6	9.0646 $\pm$ 0.3315	6.8780 $\pm$ 0.1509	77.3300 $\pm$ 8.4810	156.9800 $\pm$ 10.3476	2.0000 $\pm$ 0.4472
IL 9-3	7.3477 $\pm$ 0.6601	6.8913 $\pm$ 0.2817	168.3750 $\pm$ 29.2778	75.5250 $\pm$ 6.1160	2.5000 $\pm$ 0.2236
IL 9-3-1	5.0774 $\pm$ 0.4554	4.4176 $\pm$ 0.4034	56.1000 $\pm$ 8.5511	0.0000 $\pm$ 0.0000	2.5000 $\pm$ 0.2236
IL 9-3-2	5.9398 $\pm$ 0.7645	4.9954 $\pm$ 0.5219	242.8400 $\pm$ 40.7823	146.6000 $\pm$ 19.4105	2.5000 $\pm$ 0.2236
M82	6.6491 $\pm$ 0.4012	6.0612 $\pm$ 0.2238	187.5860 $\pm$ 7.9228	79.7290 $\pm$ 5.2965	2.8500 $\pm$ 0.0742

IL	Trusses number (unit)	Leaf DW (g)	Stem DW (g)	FBP Ald (nmol g ⁻¹ FW min ⁻¹)	G6PDH (nmol g ⁻¹ FW min ⁻¹)
IL 10-1	2.2500 ± 0.6614	39.5250 ± 2.3046	11.4500 ± 0.7684	5729.5000 ± 485.7729	368.7520 ± 50.4356
IL 10-1-1	4.2500 ± 0.9152	37.6500 ± 1.4699	12.1475 ± 0.5494	4359.9860 ± 433.6933	309.3400 ± 18.8544
IL 10-2	3.7500 ± 1.1124	42.8250 ± 1.2066	18.0750 ± 1.0317	4383.7500 ± 596.7611	258.5980 ± 53.1117
IL 10-2-2	4.0500 ± 0.5268	30.5500 ± 2.6043	8.2000 ± 0.4919	4284.7520 ± 725.2172	324.1520 ± 34.8514
IL 10-3	4.0000 ± 0.8367	45.3500 ± 4.2372	16.1000 ± 1.0766	5284.5260 ± 966.1970	260.9060 ± 53.9540
IL 1-1	5.7500 ± 0.6614	30.0750 ± 1.7130	10.9250 ± 0.8387	4315.6460 ± 395.1980	380.5920 ± 70.4077
IL 11-1	6.0500 ± 0.5268	25.7000 ± 1.4960	10.1250 ± 0.7876	7656.9100 ± 1285.8540	294.3640 ± 63.4202
IL 11-2	4.2500 ± 0.4873	34.1500 ± 1.5506	13.1750 ± 0.8511	4685.8700 ± 509.5822	243.6180 ± 46.0132
IL 1-1-2	3.5000 ± 0.5477	25.1550 ± 1.9079	9.1175 ± 0.5851	4571.9450 ± 1122.8974	498.0260 ± 63.0417
IL 11-3	4.7500 ± 0.9811	43.5907 ± 3.8789	11.9467 ± 0.9900	4455.9833 ± 905.9128	402.9620 ± 34.1864
IL 1-1-3	1.6000 ± 0.6000	41.1000 ± 3.9891	13.5500 ± 1.6277	5172.8560 ± 1344.8386	423.9820 ± 85.6541
IL 11-4	5.5000 ± 0.3873	32.2500 ± 2.8267	11.2250 ± 0.5589	3791.1140 ± 949.3717	275.3460 ± 43.0538
IL 11-4-1	5.2500 ± 0.7331	42.4000 ± 1.8509	16.1700 ± 0.6785	5970.7840 ± 1070.9346	326.2410 ± 64.9592
IL 1-2	6.4000 ± 0.5099	38.3875 ± 1.1602	13.2850 ± 0.4356	4001.3125 ± 470.1804	326.8600 ± 62.4919
IL 12-1	5.0000 ± 0.9487	25.9650 ± 1.8221	10.2250 ± 0.3836	4123.2440 ± 540.8631	286.6810 ± 46.9121
IL 12-1-1	4.0500 ± 0.4213	60.9200 ± 1.9683	29.3050 ± 2.3354	3776.5880 ± 808.4094	361.8300 ± 31.4670
IL 12-2	3.7500 ± 0.1936	32.2850 ± 0.6081	12.6150 ± 0.7085	5464.1280 ± 1298.1189	489.5660 ± 94.4705
IL 12-3	3.2500 ± 0.7331	24.5050 ± 2.5950	7.7525 ± 1.1328	6913.0020 ± 1025.8129	566.6760 ± 93.4135
IL 12-3-1	5.4000 ± 0.5099	39.1250 ± 3.5311	10.8500 ± 0.6961	8555.0920 ± 2163.6342	316.9160 ± 60.9791
IL 12-4	2.4000 ± 0.6782	41.2750 ± 1.1389	9.8225 ± 0.7462	5936.8850 ± 364.4500	291.9000 ± 9.4675
IL 12-4-1	6.2000 ± 0.4899	44.1000 ± 4.2541	16.8000 ± 1.5281	5768.9020 ± 541.4110	346.5220 ± 19.7730
IL 1-3	6.5000 ± 0.5000	40.5750 ± 2.7679	14.6250 ± 1.0504	4810.2000 ± 660.0131	289.6620 ± 43.2549
IL 1-4	3.2500 ± 0.7331	36.8520 ± 3.0089	12.5800 ± 1.2155	3790.5800 ± 885.3118	299.6900 ± 22.1982
IL 1-4-18	4.6500 ± 0.8047	31.6250 ± 1.1770	9.7250 ± 0.6460	5008.5420 ± 1285.8318	414.2760 ± 126.5314
IL 2-1	4.4000 ± 0.4000	19.2500 ± 1.9810	7.2250 ± 1.0072	7428.3480 ± 1834.7118	411.5840 ± 131.8200
IL 2-2	4.3500 ± 0.5220	43.8750 ± 2.9805	13.2500 ± 1.9785	4140.2225 ± 1001.8671	336.6295 ± 68.2066
IL 2-3	3.6000 ± 0.6000	40.9500 ± 0.8953	16.1500 ± 1.3366	11792.4600 ± 2480.3262	423.1920 ± 90.3560
IL 2-4	0.9500 ± 0.0500	62.5250 ± 4.6058	27.5000 ± 1.9867	9327.1875 ± 886.3072	261.0900 ± 6.1882
IL 2-5	3.3500 ± 0.5895	40.0250 ± 3.7516	15.3000 ± 1.5732	4555.3320 ± 938.2005	244.7665 ± 25.6140
IL 2-6	2.9500 ± 0.8231	54.3500 ± 1.6913	20.4500 ± 2.3252	6254.1900 ± 1756.6761	528.1920 ± 98.1720
IL 2-6-5	4.2500 ± 0.8588	39.5500 ± 2.4579	11.1000 ± 1.0010	7092.1840 ± 682.9371	258.6280 ± 50.8014
IL 3-1	5.8000 ± 0.7348	43.5725 ± 2.9498	16.9225 ± 1.4319	4870.9000 ± 1025.3642	417.7290 ± 50.5167
IL 3-2	2.8500 ± 0.3500	38.7000 ± 2.2034	12.5400 ± 1.0012	8544.5220 ± 1523.1033	375.3580 ± 119.7292
IL 3-3	1.1500 ± 0.2179	14.8000 ± 3.3029	3.9750 ± 0.9254	6566.9970 ± 921.4491	470.2280 ± 80.5915
IL 3-4	0.0500 ± 0.0500	33.0400 ± 0.9899	8.7275 ± 0.5120	4659.3780 ± 646.4245	181.3580 ± 9.8901
IL 3-5	5.5000 ± 0.6708	44.4250 ± 2.2001	15.8625 ± 1.2733	3165.4680 ± 610.8220	335.8340 ± 66.2349
IL 4-1-1	4.8000 ± 0.4899	37.7500 ± 2.1457	11.7200 ± 1.3051	3746.1850 ± 83.0185	406.6500 ± 37.7672
IL 4-2	4.7500 ± 0.3708	25.7750 ± 2.1453	9.9750 ± 0.7290	5406.6140 ± 186.8599	389.2620 ± 46.9635
IL 4-3	5.7500 ± 0.7984	39.2875 ± 1.9138	14.7475 ± 0.7257	6818.1260 ± 1255.0056	355.8480 ± 44.2785
IL 4-3-2	5.5500 ± 0.6910	23.4825 ± 2.2869	8.4650 ± 0.6783	4477.7168 ± 725.2179	444.1625 ± 78.4043
IL 4-4	1.9500 ± 0.3571	50.2500 ± 3.8849	16.2025 ± 1.3905	5536.4020 ± 891.2433	308.4720 ± 43.8743
IL 5-1	4.2500 ± 0.6614	40.1500 ± 3.6653	14.1750 ± 0.6748	4673.6140 ± 338.7812	338.8520 ± 70.5121
IL 5-3	5.6000 ± 0.8124	46.8000 ± 5.1530	17.2250 ± 2.1960	5108.7420 ± 1435.4075	453.4952 ± 78.6985
IL 5-4	5.2000 ± 0.5831	29.3250 ± 2.0053	12.3250 ± 0.5757	4516.5940 ± 1561.3803	394.2580 ± 83.8486
IL 5-5	5.4000 ± 1.1225	35.9000 ± 2.9036	14.0500 ± 0.9599	4368.2410 ± 811.9675	388.0620 ± 97.5580
IL 6-1	6.0000 ± 0.7071	32.5500 ± 3.6444	14.5750 ± 0.5458	5062.9000 ± 1132.8790	256.4200 ± 10.6218
IL 6-2	5.6500 ± 0.5895	34.4500 ± 1.4080	11.9100 ± 1.0274	5059.9380 ± 805.5320	363.7340 ± 40.1831
IL 6-3	1.7000 ± 0.3742	66.2200 ± 3.8131	29.3125 ± 2.2987	5546.7600 ± 1099.9946	244.4900 ± 35.2777
IL 6-4	3.1000 ± 0.6782	38.7500 ± 3.2278	10.7000 ± 1.5547	4500.3200 ± 495.8593	213.5520 ± 41.4743
IL 7-1	5.0000 ± 0.6325	36.1000 ± 3.5826	13.7925 ± 1.4949	4084.9860 ± 786.2251	318.7780 ± 27.0202
IL 7-2	1.9000 ± 0.4583	47.1533 ± 2.9573	14.5140 ± 1.2562	5421.5550 ± 265.6937	459.4525 ± 36.3702
IL 7-3	4.5000 ± 1.0247	38.6500 ± 1.5312	11.3100 ± 0.5066	4318.7660 ± 842.7635	312.3320 ± 61.9063
IL 7-4	1.4000 ± 0.4000	15.3250 ± 1.4644	3.2250 ± 0.3397	6134.7120 ± 1679.0142	360.1780 ± 47.3819
IL 7-4-1	6.6000 ± 0.4000	26.1250 ± 1.2543	8.0750 ± 0.3527	6662.7575 ± 1519.0869	332.1100 ± 54.3202
IL 7-5	5.0000 ± 0.3162	52.6500 ± 4.4721	13.2000 ± 0.7259	4765.8160 ± 1089.6762	264.6800 ± 16.4415
IL 7-5-5	3.5000 ± 0.5000	38.3250 ± 2.9030	12.1500 ± 1.2757	5227.2360 ± 908.8675	276.8920 ± 17.2877
IL 8-1	4.6000 ± 0.2449	23.1750 ± 1.4218	8.6000 ± 0.6075	5294.8590 ± 846.5966	316.8596 ± 29.8722
IL 8-1-1	4.0500 ± 0.2784	18.6500 ± 1.9459	7.3350 ± 0.3282	6390.8460 ± 2273.7394	219.9380 ± 33.8668
IL 8-2	3.7500 ± 0.1936	35.1500 ± 2.5362	13.8575 ± 1.0736	2968.9140 ± 590.2042	326.1980 ± 76.4207
IL 8-2-1	3.4500 ± 0.6344	42.3637 ± 4.2321	9.9223 ± 1.0978	3088.5760 ± 837.7458	252.1340 ± 26.4308
IL 8-3	4.2500 ± 0.7984	42.5250 ± 2.1616	10.0250 ± 0.4872	5268.9360 ± 1068.2249	291.6120 ± 45.4601
IL 9-1	3.5000 ± 0.5000	38.9750 ± 3.0312	13.2450 ± 0.7517	6119.3018 ± 1628.7184	323.7370 ± 85.2207
IL 9-1-2	4.3500 ± 0.4153	28.3200 ± 2.6973	7.4500 ± 1.1741	4927.4660 ± 1112.8902	261.6480 ± 55.1684
IL 9-1-3	5.0000 ± 0.7071	41.1750 ± 3.4261	20.8750 ± 1.9247	8491.4480 ± 1430.3890	410.4420 ± 47.7118
IL 9-2	4.7500 ± 0.4873	45.3750 ± 3.1557	18.2000 ± 1.1866	5533.3960 ± 952.2978	550.4880 ± 101.6662
IL 9-2-5	5.2500 ± 0.3708	30.8300 ± 2.7217	9.9900 ± 0.6755	6261.4640 ± 1209.7147	293.3720 ± 44.3186
IL 9-2-6	4.2000 ± 0.7348	25.7940 ± 2.1272	6.1420 ± 0.8452	6700.2500 ± 1575.9628	322.1050 ± 19.6796
IL 9-3	2.7500 ± 0.6614	34.1250 ± 3.2632	9.6450 ± 0.7978	4916.5730 ± 465.6981	407.5180 ± 82.6650
IL 9-3-1	2.5000 ± 0.6708	67.2940 ± 0.6131	17.8600 ± 0.4238	3761.2250 ± 951.1182	274.7600 ± 31.2692
IL 9-3-2	4.5000 ± 1.1619	31.2750 ± 2.5234	9.4500 ± 0.7928	5403.6300 ± 1378.4637	214.0200 ± 51.9749
M82	4.5900 ± 0.4220	42.1240 ± 1.1670	14.3115 ± 0.4386	4764.9924 ± 377.0951	397.2898 ± 40.5071

IL	PGM (nmol g ⁻¹ FW min ⁻¹)	PGI (nmol g ⁻¹ FW min ⁻¹)	PFK (nmol g ⁻¹ FW min ⁻¹)	Frk (nmol g ⁻¹ FW min ⁻¹)	AGPase (nmol g ⁻¹ FW min ⁻¹)
IL 10-1	1159.5920 ± 78.8775	885.6800 ± 61.6626	164.9300 ± 12.5221	124.6340 ± 12.2418	430.6220 ± 33.60307
IL 10-1-1	1091.0560 ± 95.0715	936.2480 ± 63.8046	168.1620 ± 23.9822	141.6200 ± 18.8217	399.9920 ± 29.13671
IL 10-2	1222.9900 ± 79.9505	1087.1400 ± 75.9188	165.8840 ± 10.6242	136.2380 ± 4.4801	388.7980 ± 54.30689
IL 10-2-2	1212.8520 ± 129.7516	1160.8080 ± 76.8811	192.6560 ± 35.2227	110.9580 ± 13.1195	256.9980 ± 56.17241
IL 10-3	1121.7600 ± 60.0356	998.1860 ± 140.3904	208.6380 ± 45.6649	103.7240 ± 22.7135	374.5760 ± 65.11787
IL 1-1	1231.0580 ± 82.1481	1111.1460 ± 60.8058	224.6140 ± 68.0584	154.3560 ± 8.6698	449.7400 ± 50.52521
IL 11-1	1589.6440 ± 213.8252	1560.3280 ± 275.8366	163.5900 ± 21.3151	176.6440 ± 23.7163	385.7980 ± 73.12602
IL 11-2	1185.9400 ± 103.5962	937.8460 ± 117.6151	141.1340 ± 10.6913	140.2400 ± 14.7903	381.4180 ± 64.16405
IL 1-1-2	1462.1420 ± 132.7960	1407.3680 ± 188.4421	201.9260 ± 28.8490	253.9380 ± 52.2773	389.4600 ± 34.65258
IL 11-3	1485.2413 ± 68.0698	1145.3653 ± 39.7844	137.0233 ± 9.0508	122.5613 ± 2.0654	223.1813 ± 41.66064
IL 1-1-3	1392.1660 ± 39.4267	1268.6220 ± 66.0953	240.0800 ± 44.3139	96.9560 ± 8.3615	424.7120 ± 35.36964
IL 11-4	1259.4460 ± 73.2908	1173.1120 ± 73.1855	194.4940 ± 9.7413	135.0680 ± 17.4210	368.3160 ± 23.99500
IL 11-4-1	1100.8630 ± 97.1079	1020.0740 ± 55.5425	249.2580 ± 17.9641	156.5280 ± 11.5508	356.4360 ± 62.26838
IL 1-2	1089.8545 ± 113.3555	1109.2780 ± 77.5776	168.0425 ± 9.2480	122.2750 ± 12.5022	480.6425 ± 82.28925
IL 12-1	1044.3180 ± 68.7588	981.5780 ± 45.9111	160.1960 ± 35.3930	126.8140 ± 16.6337	338.1770 ± 32.62015
IL 12-1-1	1227.8720 ± 60.3404	1200.4240 ± 104.5451	69.5900 ± 9.0715	181.9160 ± 19.2806	439.4080 ± 26.60265
IL 12-2	1526.4400 ± 191.4771	1513.5700 ± 160.7324	210.4420 ± 23.8831	146.7480 ± 20.0908	455.7000 ± 80.54457
IL 12-3	1744.4300 ± 229.2250	1766.0620 ± 225.2075	223.9120 ± 26.1890	159.2500 ± 15.6601	611.2380 ± 36.24726
IL 12-3-1	1426.2100 ± 81.6051	1196.3740 ± 149.0576	131.7420 ± 21.9112	125.5440 ± 21.0629	466.8540 ± 63.92014
IL 12-4	1102.9500 ± 4.5705	772.3600 ± 27.6289	171.7350 ± 6.6031	133.4050 ± 3.1685	440.4200 ± 15.54514
IL 12-4-1	1225.4880 ± 62.4760	1205.1520 ± 45.4299	255.7700 ± 33.8443	153.9700 ± 13.9362	515.8620 ± 73.3411
IL 1-3	1276.0420 ± 50.8304	1159.2280 ± 154.0975	185.7380 ± 41.1355	119.3260 ± 22.6164	405.4460 ± 37.49595
IL 1-4	1475.3980 ± 80.2250	1068.4870 ± 79.7196	121.7510 ± 27.5457	151.9650 ± 28.3982	325.6420 ± 59.68727
IL 1-4-18	1290.0960 ± 15.5181	1151.3040 ± 154.4022	238.8820 ± 72.8278	172.8180 ± 7.8814	368.5480 ± 47.14806
IL 2-1	1379.5340 ± 111.3223	1195.7420 ± 178.1124	247.5560 ± 59.8170	154.6720 ± 30.3944	444.1940 ± 49.04118
IL 2-2	1029.8875 ± 175.4071	1311.3595 ± 109.3129	130.2600 ± 33.8939	168.8325 ± 23.3732	499.3500 ± 24.10180
IL 2-3	1348.1320 ± 60.4889	1181.9700 ± 88.5816	278.3020 ± 63.0117	160.9180 ± 20.3934	512.6460 ± 37.74785
IL 2-4	1382.8525 ± 148.5730	1327.1025 ± 197.0199	251.4075 ± 42.4516	113.9810 ± 11.2528	246.9700 ± 36.86117
IL 2-5	1438.8050 ± 146.1880	1158.9090 ± 54.1658	83.8075 ± 12.1774	127.5250 ± 9.4039	567.5200 ± 96.34144
IL 2-6	1315.8380 ± 73.0495	1120.0500 ± 124.1704	235.5080 ± 38.8316	112.9240 ± 5.0586	413.7800 ± 99.12058
IL 2-6-5	1268.1700 ± 127.7890	1025.2440 ± 73.0404	234.7060 ± 61.9011	100.0600 ± 19.2873	430.0000 ± 55.08087
IL 3-1	1081.3155 ± 23.6852	987.1475 ± 55.1970	139.2800 ± 5.1068	155.1600 ± 5.2695	447.7300 ± 8.19973
IL 3-2	1432.5920 ± 175.9557	1418.0100 ± 162.8079	235.0200 ± 49.2769	122.7920 ± 25.3364	465.5240 ± 73.18830
IL 3-3	1372.2460 ± 41.9799	1127.9160 ± 47.2967	204.8830 ± 22.6494	120.8060 ± 7.9276	482.4710 ± 61.00498
IL 3-4	805.2800 ± 34.2686	997.8420 ± 86.6826	96.8660 ± 24.6126	79.8060 ± 14.5700	401.3420 ± 38.18368
IL 3-5	1284.5660 ± 83.6659	1258.0480 ± 53.6152	138.2200 ± 12.6257	172.8360 ± 20.1158	465.5400 ± 31.09689
IL 4-1-1	1163.4450 ± 92.9033	846.2050 ± 153.2758	183.5650 ± 10.1808	167.7700 ± 21.5065	445.8800 ± 83.60211
IL 4-2	1273.2920 ± 46.7000	906.2660 ± 104.5868	175.9020 ± 44.2370	78.1100 ± 16.6721	406.9160 ± 40.11733
IL 4-3	1397.3520 ± 74.5462	1199.0020 ± 169.2674	221.2940 ± 33.8672	154.5480 ± 26.8513	469.9140 ± 77.18039
IL 4-3-2	1089.0886 ± 68.9471	759.1328 ± 63.7554	194.6130 ± 8.3266	127.7078 ± 29.9245	379.9880 ± 46.71791
IL 4-4	776.5900 ± 100.3676	884.3420 ± 45.5131	164.3740 ± 33.3039	89.3840 ± 11.4248	375.5780 ± 34.67643
IL 5-1	1172.2680 ± 193.9871	1278.6680 ± 172.9014	253.5360 ± 64.8932	117.4000 ± 32.1035	310.2060 ± 59.77024
IL 5-3	1312.8084 ± 99.9193	1207.9866 ± 135.5225	276.7662 ± 57.2959	159.5612 ± 13.1418	479.7432 ± 50.59784
IL 5-4	1230.0900 ± 130.5694	961.7360 ± 21.6463	142.1380 ± 27.2360	84.2560 ± 17.3590	336.3040 ± 44.77577
IL 5-5	1294.6290 ± 58.4846	1108.9400 ± 59.0050	130.3080 ± 18.2381	148.2960 ± 6.3277	478.4300 ± 37.79189
IL 6-1	1282.7460 ± 110.5678	1268.7840 ± 174.4605	135.8780 ± 30.3294	147.0640 ± 14.6970	417.6380 ± 38.96379
IL 6-2	1211.6320 ± 37.2065	1089.2420 ± 73.1140	189.5880 ± 14.5972	154.3080 ± 19.3628	352.4380 ± 47.98234
IL 6-3	1180.6420 ± 125.9620	1133.2280 ± 21.8585	168.6700 ± 14.6154	91.8680 ± 4.1450	379.8840 ± 36.07275
IL 6-4	932.6880 ± 32.9053	881.9800 ± 52.0092	159.8200 ± 20.5035	156.2960 ± 20.4296	426.6680 ± 81.60195
IL 7-1	1043.8160 ± 35.7598	873.5320 ± 62.0139	162.5300 ± 28.7601	118.0360 ± 7.6032	367.9720 ± 45.13876
IL 7-2	1189.2950 ± 43.9327	978.4650 ± 23.6566	183.1225 ± 12.0254	111.8170 ± 13.0579	417.1950 ± 50.82348
IL 7-3	1059.6800 ± 95.6903	1018.4780 ± 36.2169	153.3640 ± 7.3202	126.9140 ± 13.2136	366.1540 ± 23.88960
IL 7-4	1318.8660 ± 97.8282	1239.0200 ± 101.3028	202.7360 ± 57.9776	163.8000 ± 20.2834	419.1800 ± 66.84324
IL 7-4-1	1426.8500 ± 108.0291	1184.2575 ± 55.6329	224.0025 ± 38.9077	149.2050 ± 21.4103	468.4175 ± 49.35189
IL 7-5	1295.5620 ± 97.5603	1060.6200 ± 139.5847	210.6080 ± 40.6531	125.3820 ± 8.6584	287.1700 ± 82.94342
IL 7-5-5	1018.4920 ± 73.1923	912.9100 ± 121.7094	235.2100 ± 20.1609	119.6040 ± 21.7549	357.3460 ± 29.84780
IL 8-1	1273.1288 ± 107.3720	1562.8620 ± 185.4634	148.5132 ± 12.5615	151.9520 ± 11.7259	462.8674 ± 29.01908
IL 8-1-1	1007.9160 ± 89.1602	805.3620 ± 47.8098	189.0420 ± 84.7840	127.1200 ± 18.8271	363.8300 ± 37.70622
IL 8-2	1109.3680 ± 35.8327	988.8720 ± 66.1884	101.8700 ± 25.1857	144.1180 ± 8.5651	433.5360 ± 32.52917
IL 8-2-1	1000.5240 ± 113.5408	718.1200 ± 90.6023	124.7620 ± 21.1054	149.5020 ± 6.2142	432.7240 ± 63.54964
IL 8-3	1021.3760 ± 29.9667	795.7900 ± 82.9889	131.4180 ± 30.1832	100.1600 ± 15.7297	389.8800 ± 57.99869
IL 9-1	1280.2266 ± 101.9982	1200.2886 ± 59.8379	186.2540 ± 45.2665	159.6552 ± 15.0513	455.0322 ± 26.64703
IL 9-1-2	1197.5280 ± 74.0778	1047.9240 ± 111.6028	169.3400 ± 15.6617	158.2220 ± 30.0938	389.4400 ± 38.30723
IL 9-1-3	1694.1760 ± 104.4323	1587.9560 ± 141.9829	267.1560 ± 57.4447	172.1420 ± 7.6996	499.2960 ± 61.69896
IL 9-2	1378.7960 ± 81.5554	1146.4980 ± 77.8113	255.0280 ± 61.1646	167.7080 ± 16.9138	419.0400 ± 28.26069
IL 9-2-5	1507.1200 ± 175.8063	992.6360 ± 99.8224	242.1800 ± 47.7232	90.7860 ± 16.0534	482.4640 ± 77.13322
IL 9-2-6	1407.1200 ± 54.1218	677.9600 ± 15.1203	278.4150 ± 44.3211	79.2250 ± 18.9686	461.3050 ± 15.31930
IL 9-3	1345.4490 ± 125.1664	1168.9790 ± 137.9123	105.6030 ± 8.7044	138.2590 ± 21.9236	468.6170 ± 41.76035
IL 9-3-1	1058.6100 ± 110.0727	1070.3750 ± 36.6156	174.0500 ± 53.8043	129.8000 ± 13.7921	217.1750 ± 19.54100
IL 9-3-2	1052.8800 ± 93.0661	1002.1700 ± 27.7829	255.8700 ± 48.2491	104.7600 ± 7.8899	326.3200 ± 51.08317
M82	1201.5822 ± 34.5134	1199.4641 ± 57.7308	206.0414 ± 19.6542	148.9035 ± 12.3608	412.8416 ± 21.73640

IL	GK (nmol g ⁻¹ FW min ⁻¹)	GIDH (nmol g ⁻¹ FW min ⁻¹)
IL 10-1	78.3880 ± 5.9612	310.2260 ± 43.6743
IL 10-1-1	72.0760 ± 8.3664	227.9480 ± 13.5545
IL 10-2	50.1000 ± 9.7117	280.9800 ± 4.9933
IL 10-2-2	87.9800 ± 15.2228	207.5220 ± 23.0880
IL 10-3	78.5500 ± 13.0586	290.6980 ± 14.9000
IL 1-1	100.4960 ± 9.8972	202.4420 ± 23.0723
IL 11-1	120.9640 ± 15.5341	357.5480 ± 21.5990
IL 11-2	96.4540 ± 6.2580	321.5060 ± 25.5046
IL 1-1-2	150.6140 ± 13.2748	303.0020 ± 51.5368
IL 11-3	76.5493 ± 11.1651	448.8050 ± 31.5215
IL 1-1-3	80.3800 ± 6.0338	248.3480 ± 35.0444
IL 11-4	118.3160 ± 13.1108	197.2520 ± 33.6287
IL 11-4-1	96.2880 ± 12.9497	259.4410 ± 32.3857
IL 1-2	112.9085 ± 9.7298	202.7275 ± 18.9404
IL 12-1	77.4360 ± 9.6650	230.7380 ± 27.9953
IL 12-1-1	121.6180 ± 10.5348	251.7980 ± 30.5019
IL 12-2	148.6180 ± 6.5246	238.3700 ± 13.6015
IL 12-3	127.8300 ± 15.9833	276.7960 ± 27.0489
IL 12-3-1	111.2980 ± 12.8310	227.8100 ± 22.1326
IL 12-4	83.8450 ± 10.7354	124.3650 ± 37.7202
IL 12-4-1	116.4540 ± 6.5482	259.8520 ± 26.4873
IL 1-3	100.3540 ± 16.5231	232.5640 ± 40.0401
IL 1-4	109.8380 ± 11.4479	260.0150 ± 36.2416
IL 1-4-18	40.8860 ± 16.4828	246.8780 ± 27.4904
IL 2-1	109.6280 ± 18.4933	241.6500 ± 10.4194
IL 2-2	103.1475 ± 12.8626	287.3275 ± 23.9920
IL 2-3	124.5920 ± 14.3758	258.3900 ± 16.9127
IL 2-4	91.2400 ± 14.2535	340.9770 ± 13.1872
IL 2-5	88.3700 ± 11.9879	264.4425 ± 44.4930
IL 2-6	93.0540 ± 9.3735	244.7620 ± 39.4419
IL 2-6-5	36.5380 ± 13.3324	281.5030 ± 4.6021
IL 3-1	89.5730 ± 7.4153	248.6175 ± 45.3712
IL 3-2	114.2280 ± 12.6066	247.3360 ± 44.2357
IL 3-3	117.6960 ± 18.2143	205.0220 ± 17.7827
IL 3-4	79.3380 ± 11.7489	238.8700 ± 18.1907
IL 3-5	114.1980 ± 16.1669	217.4600 ± 54.6795
IL 4-1-1	119.8300 ± 13.1704	191.2940 ± 0.3040
IL 4-2	86.8200 ± 8.4722	259.8520 ± 1.9954
IL 4-3	81.0620 ± 6.6173	238.4560 ± 34.7623
IL 4-3-2	63.2468 ± 6.1817	256.2067 ± 19.4216
IL 4-4	83.7380 ± 5.4204	267.4420 ± 36.3917
IL 5-1	86.7710 ± 22.1191	222.8120 ± 37.9604
IL 5-3	121.5736 ± 9.2226	338.3524 ± 5.6212
IL 5-4	65.5500 ± 13.4954	184.7400 ± 20.3672
IL 5-5	96.7580 ± 6.8756	381.0440 ± 52.7502
IL 6-1	78.8780 ± 7.4393	263.5400 ± 41.3114
IL 6-2	94.3100 ± 3.9202	281.9120 ± 20.4411
IL 6-3	81.9580 ± 10.6389	193.2420 ± 33.3971
IL 6-4	79.4000 ± 12.8694	201.3500 ± 27.6389
IL 7-1	88.2880 ± 8.0499	205.0860 ± 29.1469
IL 7-2	146.3725 ± 23.8577	316.9240 ± 10.6491
IL 7-3	95.2200 ± 3.8672	342.2360 ± 23.7513
IL 7-4	120.0880 ± 6.4483	381.8180 ± 18.7748
IL 7-4-1	123.7050 ± 10.0372	286.7367 ± 18.4191
IL 7-5	74.9400 ± 9.4101	178.9780 ± 40.4790
IL 7-5-5	70.2720 ± 10.8627	239.1480 ± 24.8116
IL 8-1	106.4158 ± 7.1645	311.9780 ± 41.9299
IL 8-1-1	86.9080 ± 8.7289	249.2520 ± 27.9420
IL 8-2	83.4400 ± 13.4876	230.2240 ± 25.1733
IL 8-2-1	85.4080 ± 16.0262	316.9400 ± 9.5021
IL 8-3	66.2080 ± 11.9507	230.9740 ± 36.0006
IL 9-1	111.2092 ± 8.7363	241.3418 ± 23.9906
IL 9-1-2	70.0820 ± 12.8608	289.5660 ± 34.7211
IL 9-1-3	143.8560 ± 13.2197	254.4080 ± 12.2799
IL 9-2	90.2260 ± 21.1530	273.6420 ± 62.0886
IL 9-2-5	102.8420 ± 7.1280	258.5220 ± 47.3688
IL 9-2-6	117.9550 ± 8.9510	146.4060 ± 4.0440
IL 9-3	110.3680 ± 10.0411	230.6000 ± 33.0638
IL 9-3-1	73.6650 ± 2.2964	171.9750 ± 26.3431
IL 9-3-2	72.2100 ± 13.6482	267.3660 ± 17.9957
M82	92.4663 ± 4.3756	232.1227 ± 17.8865

Supplemental Table S4: The BINs map to significant changes in the three organ; stem, petiole and leaf of a population of 71 introgression lines (ILs) of *Solanum pennellii* into a genetic background of *Solanum lycopersicum* (M82). The table summarizes the genomic regions retrieved by the corresponding markers to overlap between the introgressed regions of the ILs with the same phenotype in order to map the identified QTL to smaller intervals, termed BINs. Metabolites: aa, Amino acid; NO₃, Nitrate; Starch; Protein; Gluc, Glucose; Fruc, Fructose; Sucr, Sucrose. Harvest data: GF FW, Green fruit fresh weight; RD FW, Red fruit fresh weight; Stem Num, Stem number; Truss Num, Truss number; Leaf DW, Leaf dry weight; Stem DW, Stem dry weight. Enzymes: FBP Ald, Fructose-bisphosphate aldolase; G6PDH, Glucose-6-phosphate dehydrogenase; PGM, Phosphoglucumutase; PGI, Phosphoglucose Isomerase total; PFK, Phosphofructokinase (ATP); Frk, Fructokinase, AGPase, ADP-glucose pyrophosphorylase; GK, Glucokinase; GIDH, Glutamate DH (NAD). Traits indicate a positive (red) or negative (green) significant changes as compared to M82 as identified by Dunnett's test.

STEM BINs				PETIOLE BINs				LEAF BINs			
CHROMOSOMAL REGION		MARKERS ⁽¹⁾		CHROMOSOMAL REGION		MARKERS ⁽¹⁾		CHROMOSOMAL REGION		MARKERS ⁽¹⁾	
QTL	BINs	North	South	QTL	BINs	North	South	QTL	BINs	North	South
FBP Ald	4H	TG155	CT173	AGPase	11F	TG36	TG26	FBP Ald	2G	TG554	TG493
Fruc	8AB	TG176	CT228	FBP Ald	7B	CT211B	TG61	Fruc	1D	CD15	TG460
Fruc	9D	CT143	CT32	FBP Ald	7E	CT158	TG572	Fruc	9B	GP39	CT143
Fruc	10E	TG408	CP49	FBP Ald	8AB	TG176	CT228	Fruc	10A	TG230	TG540
Fruc	12B	CT19A	CT79	FBP Ald	10C	TG280	PGAL	Fruc	10C	TG280	PGAL
GK	1A	CT233	TG24	FBP Ald	11F	TG36	TG26	Gluc	1D	CD15	TG460
GK	12D	CT79	TG288	FBP Ald	12A	TG180	TG68	Gluc	4E	TG182	TG75A
GIDH	2C	CT106A	CT140	FBP Ald	9J	GP129	CT112A	Gluc	9B	GP39	CT143
GIDH	3B	TG585	TG130	Frk	4H	TG155	CT173	Gluc	11H	TG26	TG393
GIDH	3H	TG377	TG411	GK	12A	TG180	TG68	Gluc	12DE	CT79	TG288
GIDH	4D	CT175	CT157	GIDH	6E	TG292	TG548	GF FW	1H	TG237	TG17
GIDH	6G	PC5	TG221	GIDH	7B	CT211B	TG61	GF FW	2I	TG493	CT232
PGI	1A	CT233	TG24	GIDH	9H	TG551	TG348	GF FW	2H	TG494	TG493
PGM	1A	CT233	TG24	GIDH	10A	TG230	TG540	GF FW	2K	TG492	TG141A
PGM	5H	CT80A	CD74A	Gluc	4E	TG182	TG75A	GF FW	3F	TG129	TG377
PGM	9D	CT143	CT32	Gluc	6B	TG590	TG25	GF FW	7D	TG61	TG143
PGM	9G	CT20B	TG404	Gluc	6E	TG292	TG548	GF FW	7E	CT158	TG572
Starch	11D	CP58A	TG562	Gluc	7C	TG272A	CD5A	Leaf DW	4E	TG182	TG75A
Starch	12A	TG180	TG68	Gluc	7E	CT158	TG572	Leaf DW	7D	TG61	TG143
GF FW	1H	TG237	TG17	Gluc	8D	CT228	CT69	Leaf DW	8AB	TG176	CT228
GF FW	2I	TG493	CT232	Gluc	8F	TG330	CT28A	RF FW	1D	CD15	TG460
GF FW	2H	TG494	TG493	Gluc	10A	TG230	TG540	RF FW	1F	CT191	TG326
GF FW	2K	TG492	TG141A	Gluc	11B	TG651	CP58A	RF FW	5F	TG23	TG60
GF FW	3D	CP116A	TG129	Gluc	11H	TG26	TG393	RF FW	6B	TG590	TG25
GF FW	3F	TG129	TG377	Gluc	12A	TG180	TG68	RF FW	8F	TG330	CT28A
GF FW	7E	CT158	TG572	NO ₃	1A	CT233	TG24	Stem DW	3F	TG129	TG377
Leaf DW	4E	TG182	TG75A	NO ₃	9D	CT143	CT32	Stem DW	7D	TG61	TG143
Leaf DW	7D	TG61	TG143	PFK	1B	TG301	CD15	Stem DW	8AB	TG176	CT228
Leaf DW	8AB	TG176	CT228	PFK	8AB	TG176	CT228	Stem DW	9H	TG551	TG348
RF FW	1D	CD15	TG71	Starch	6E	TG292	TG548	Stem DW	9J	GP129	CT112A
RF FW	1F	CT191	TG326	Starch	7B	CT211B	TG61	Truss Num	3F	TG129	TG377
RF FW	5F	TG23	TG60	Starch	7E	CT158	TG572	Truss Num	7E	CT158	TG572
RF FW	6B	TG590	TG25	Sucr	7F	CT84	TG199				
RF FW	8F	TG330	CT28A	Sucr	7H	TG199	TG499				
Stem DW	3F	TG129	TG377	GF FW	1H	TG237	TG17				
Stem DW	7D	TG61	TG143	GF FW	2I	TG493	CT232				
Stem DW	8AB	TG176	CT228	GF FW	2H	TG494	TG493				
Stem DW	9H	TG551	TG348	GF FW	2K	TG492	TG141A				
Stem DW	9J	GP129	CT112A	GF FW	3F	TG129	TG377				
Truss Num	3F	TG129	TG377	GF FW	7D	TG61	TG143				
Truss Num	7E	CT158	TG572	GF FW	7E	CT158	TG572				
				Leaf DW	4E	TG182	TG75A				
				Leaf DW	7D	TG61	TG143				
				Leaf DW	8AB	TG176	CT228				
				RF FW	1D	CD15	TG460				
				RF FW	1F	CT191	TG326				
				RF FW	5F	TG23	TG60				
				RF FW	6B	TG590	TG25				
				RF FW	8F	TG330	CT28A				
				Stem DW	3F	TG129	TG377				
				Stem DW	7D	TG61	TG143				
				Stem DW	8AB	TG176	CT228				
				Stem DW	9H	TG551	TG348				
				Stem DW	9J	GP129	CT112A				
				Truss Num	3F	TG129	TG377				
				Truss Num	7E	CT158	TG572				

(1)Marker codes are those assigned in Sol Genomics Network

CHAPTER 3

Exploiting Natural Variation to Discover Candidate Genes Involved in Photosynthesis- Related Traits

Exploiting Natural Variation to Discover Candidate Genes Involved in Photosynthesis-Related Traits

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Running Head: Identification of new players on photosynthesis

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Abstract

Naturally occurring genetic variation in plants can be very useful to dissect the complex regulation of primary metabolism as well as of physiological traits such as photosynthesis. The physiological and genetic mechanisms underlying natural variation in closely related species or accessions may provide important information that can be used to improve crop yield. In this chapter we describe the use of a population of introgression lines (ILs), with the *Solanum pennellii* IL population as a study case, as a tool for the identification of genomic regions involved in the control of photosynthetic efficiency.

Key words: introgression lines population; fluorescence; natural variation; photorespiration; photosynthesis.

INTRODUCTION

Natural genetic variation in plant photosynthesis exists among and within species (Hikosaka 2010; Lawson, Kramer, and Raines 2012) and it can be used as a tool to identify genetic determinants which can be exploited for further improvement of crop yields (Flood, Harbinson, and Aarts 2011; Lawson et al. 2012; Nunes-nesi et al. 2016). In spite of the growing number of studies, the genetic factors responsible for the variation in photosynthesis and related parameters, such as photorespiration and respiration, still remain largely unknown (Flood et al. 2011; Nunes-nesi et al. 2016). The identification of genes encoding auxiliary factors or modifiers of photosynthesis is expected to provide further insight into the regulation of crop yield and thus providing immediate information with practical value. Furthermore, such factors have been identified in previous mutant screenings due to potential redundancy and numerous genes involved with small effects on the observed phenotypes (Flood et al. 2011).

Quantitative Trait Locus (QTL) mapping is a powerful technique for dissecting the genetic basis of phenotypic differences between species and cultivars (Collard et al. 2005; Nunes-nesi et al. 2016; Tanksley 1997). The creation of populations of introgression lines (ILs), whereby the genome of a species is broken down in discrete, overlapping chromosomal segments, boosted significant progress in QTL mapping in both monocots (Jena, Kochert, and Khush 1992; Li et al. 2005; Tian et al. 2006) and eudicots (Canady, Meglic, and Chetelat 2005; Do et al. 2010; Eshed and Zamir 1994). A particularly useful collection of lines is the *Solanum pennellii* introgression population in which defined genomic segments of the *S. pennellii* genome replaced homologous

regions in the tomato (*S. lycopersicum* cv M82) genomic background (Figure 1). Originally mapped by RFLP (Eshed and Zamir 1994), and more recently thoroughly resequencing (Chitwood et al. 2013), the *S. pennellii* IL population is very useful for identifying QTLs, given that any phenotypic difference between an IL and the recurrent parental line is attributed solely to donor parent genes within the introgressed chromosomal segment (Fulop et al. 2016). An added advantage is the existence of overlapping segments of *S. pennellii* genome in different ILs, which allows fine-mapping of candidate genes. Thus, the assessment of ILs represents a powerful tool for identifying and understanding the genetic determinants involved in quantitative traits linked to processes such as photosynthesis, photorespiration, and underlying traits.

For QTL mapping of photosynthesis related traits, a detailed characterization of the experimental material is a critical requirement for a meaningful analysis by bioinformatics tools and for publication needs. While information directly related to the experimental approach (e.g. the day length and the species in a diurnal cycle experiment) is often recorded in a standardised way along with the results in spreadsheet formats, other relevant information (e.g. air temperature, light intensity, plant age at sampling) is frequently left out. It should also be mentioned that chlorophyll fluorescence and gas exchange measurements performed on the same fully expanded source leaves is extremely important for an accurate and full understanding of the responses of the photosynthetic apparatus (Gu et al. 2012, 2014).

In this chapter we describe the use of an IL population in tomato as a powerful tool to identify genetic factors involved in the regulation of photosynthetic related parameters as well as photorespiration.

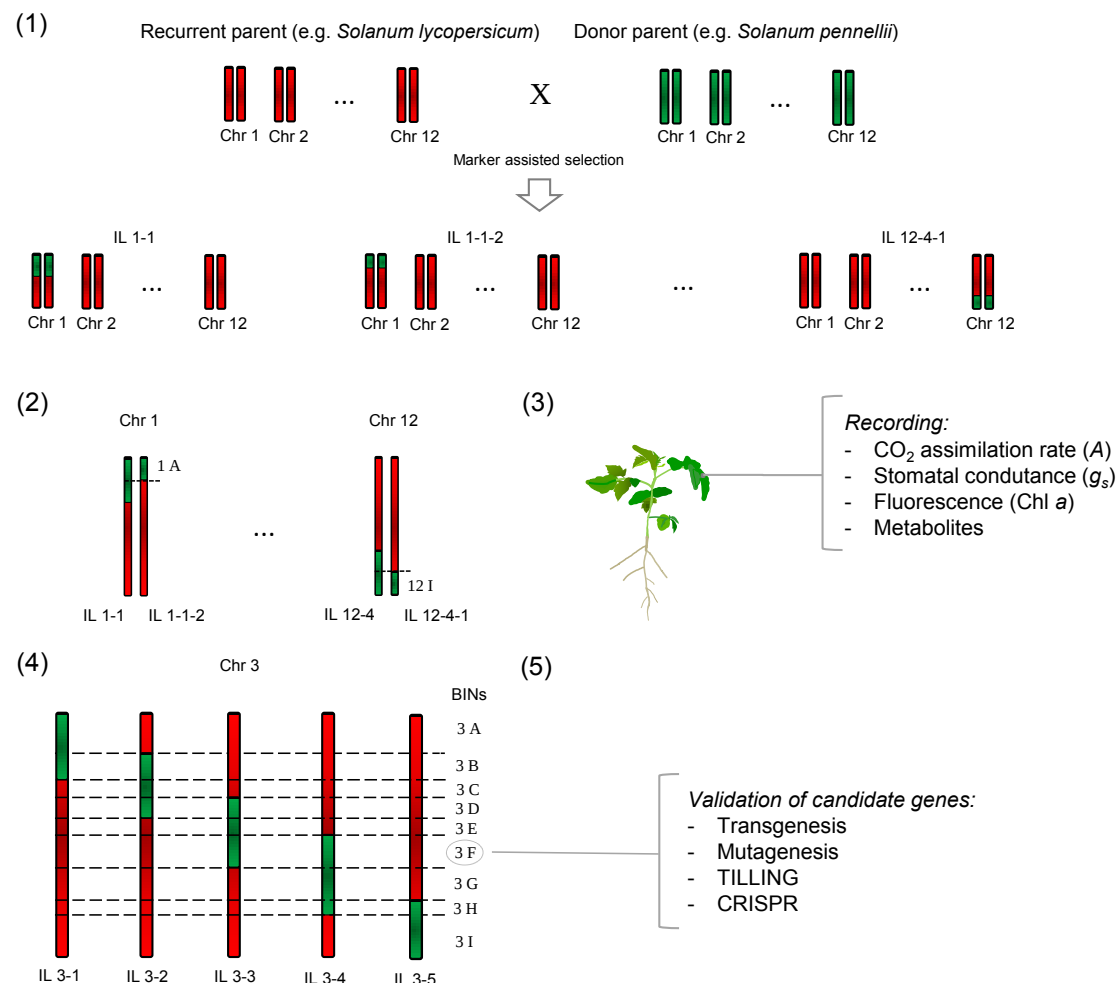


Figure 1. Schematic representation of a pipeline designed to detect genomic regions and identify candidate genes controlling photosynthesis-related traits. (1) Cultivation of an IL population covering the entire genome (2) enables mapping traits to specific bins. The IL population was previously produced through controlled introgression and marker-assisted selection generating a set of recurrent parent lines with single introgressed segments ((Eshed and Zamir 1995)). (3) Evaluation of gas exchange, fluorescence (Chl *a*), metabolites ((Obata et al. 2016)) and other methods ((Busch 2013)) should be carried out at least two times or more in the whole population. (4) ILs showing significant differences in the trait of interest (ILs 3-3 and IL 3-4, in the example), indicating genomic regions (chromosome position using the bin mapping method) with significant variation in the parameter evaluated relative to recurrent parent. Precise genome localization is possible by the existence of overlapping introgressed regions (bin 3F, in the example). (5) The identification of genes potentially related to trait of interest then requires creating a list of the genes between the flanking markers delimiting the bin. Subsequently sequence analysis can be performed using the NCBI protein database and the Blast algorithm (Blastx, Blast2GO and Blastp) – this survey results in a catalogue of candidate genes with sequence homology to previously characterized expressed sequences. The validation of candidate genes can be carried out by transgenesis, mutagenesis, TILLING and CRISPR. Allele comparison is finally performed through identification of nucleotide and amino-acid polymorphisms.

MATERIALS

1. The *S. pennellii* population of ILs is composed of 76 distinct lines which are distributed by The C.M. Rick Tomato Genetics Resource Center, University of California Davis (<http://tgrc.ucdavis.edu/>).
2. Facility to grow many plants simultaneously, under the assay conditions, is necessary in order to perform gas-exchange and chlorophyll *a* analysis of whole IL population.
3. Portable system for measurement of photosynthesis and chlorophyll fluorescence parameters.
4. Gas chromatography mass spectrometry (GC-MS) systems are recommended as analytical tools to measure primary metabolites related to primary carbon metabolism.
5. Authentic standards for photorespiratory intermediates and other metabolites for determination of absolute values of each.
6. Reference library mass spectra and retention indices can be obtained, for instance, from the Golm Metabolome Database (<http://gmd.mpimp-golm.mpg.de>) (Kopka et al. 2005).

METHODS

Plant materials

Solanum pennellii ILs population composed of 76 ILs containing a defined genomic segment of the *S. pennellii* (LA0716) genome replacing homologous regions in a tomato (*S. lycopersicum* cv. M82) background (Chitwood et al. 2013; Eshed and Zamir 1994). This IL population is a set of nearly isogenic lines developed through a succession of backcrosses, where each line carries a single genetically defined chromosome segment from a

divergent genome (Zamir 2001). The IL map is linked to the high-resolution F2 map composed of 1500 markers achieved by probing all of the specific chromosome lines with the RFLP markers from the framework F2 map. A total of 614 markers were probed and the ends of the introgressions were mapped with the resolution of the F2 map (Eshed et al. 1992). In addition, a set of 285 smaller sublines with marker-defined introgressions smaller than the original set of the 37 largest ILs of the initial population and large quantities of F2 seeds derived from selfing of the hybrids of the ILs with M82 were recently generated (Alseekh et al. 2013). Thus, it is expected that this new population will speed up the discovery of genes underlying traits of interest.

Growth conditions

1. Seeds are germinated in peat and subsequently rooted plantlets are acclimatized and transferred to 1 L pots containing 8 g of commercial substrate supplemented with chemical fertilizer (N: 4; P₂O₅: 14; K₂O: 8).
2. The population is grown in a randomized block design for minimizing the effect of variability when it is associated with discrete units (e.g. location, operator, plant, batch, time). The usual case is to randomize one plant of the 76 ILs and at least one M82 control plant within each block.
3. Environmental conditions within the glasshouse can be semi-controlled: natural light with temperature maintained within the range of 15 °C (night) to 25 °C (day) and relative humidity of 45-50%.

Photosynthesis and chlorophyll fluorescence measurements

1. Measurement of photosynthesis via CO₂ uptake is carried out with an Infra-Red Gas Analyser (IRGA). The IRGA compares the CO₂ concentration in gas passing through a chamber containing a leaf/plant and the concentration of CO₂ leaving the chamber.
2. Since maximal photosynthetic rate is observed in the morning, gas-exchange and fluorescence measurements are performed at the beginning of the day. Thus, CO₂ assimilation rate (A), stomatal conductance (g_s), internal CO₂ concentration (C_i) and transpiration (E) are measured between one and six hours after dawn.
3. The measurements are performed on the second terminal leaflet of the third fully expanded leaf from the apex of four week-old non-flowering plants. The IRGA is set to an external CO₂ concentration of 400 $\mu\text{mol mol}^{-1}$ air and flow rate of 300 $\mu\text{mol s}^{-1}$. The air temperature and VPD of 25 °C and 1.2 kPa, respectively, and artificial saturating light of 1300 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ with 10% blue light in order to maximize stomatal opening.
4. Chlorophyll *a* fluorescence parameters are determined simultaneously with gas exchange measurements using an open-flow infrared gas exchange analyzer system equipped with an integrated fluorescence chamber.
5. For analytical methods used for generation of dataset the chlorophyll fluorescence parameters are measured in the same leaf used for gas-exchange analysis. After one hour of dark adaptation, the leaf should be illuminated with weak modulated measuring beams (0.03 $\mu\text{mol m}^{-2}$

s⁻¹) to obtain the initial fluorescence (F_0). Subsequently, saturating white light pulses of 8,000 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ is applied for 0.8 s to ensure maximum fluorescence emissions (F_m).

6. In light-adapted leaves, the steady-state fluorescence yield (F_s) is obtained following a saturating white light pulse (8,000 $\mu\text{mol m}^{-2} \text{s}^{-1}$, 0.8 s) which is applied to achieve the light-adapted maximum fluorescence (F_m'). Thereafter, actinic light is turned off and far-red illumination is applied (2 $\mu\text{mol m}^{-2} \text{s}^{-1}$) to measure the light-adapted initial fluorescence (F_0') (Aucique-Perez et al. 2014).
7. The chlorophyll fluorescence dataset obtained is used to determine the actual quantum yield of PSII [1], the coefficients of photochemical quenching [2] and non-photochemical quenching [3], and the electron transport rate [4]; where PPFD is photosynthetic photon flux density; α is leaf absorptance and β reflects the partitioning of absorbed quanta between PSII and PSI, and the product $\alpha.\beta$ is adopted as described in the literature for tomato as equal to 0.43 (Aucique-Perez et al. 2014; Maxwell and Johnson 2000).

$$\delta PSII = (F_m' - F_s) / F_m' \quad [1]$$

$$qP = (F_m' - F_s) / (F_m' - F_0') \quad [2]$$

$$NPQ = (F_m - F_m') / F_m' \quad [3]$$

$$ETR = \delta PSII . \alpha . \beta . PPFD \quad [4]$$

Estimation of photorespiration

There is a growing demand for protocols allowing rapid screening of photorespiration that provide high-resolution information regarding a plant's physiological status which is often in relation to plant-based growth/developmental parameters and yield or stress; (Furbank et al. 2009; Montes, Melchinger, and Reif 2007) and where a high number of measurements need to be carried out in a short period of time. Determination of photosynthetic and chlorophyll *a* fluorescence parameters is an efficient tool to derive values of photorespiration (Valentini et al. 1995). From this relationship, it is possible to estimate the rate of total electron flow through PSII by means of *in vivo* coupled measurements of those parameters on intact leaves, to partition the electron flow between assimilative and non-assimilative processes, and to derive values of photorespiration (Peterson 1990; Valentini et al. 1995).

1. To estimate the photorespiration (Pr), as previously described by (Valentini et al. 1995), the electron transport rate (ETR) should be calculated on the basis of equation [5].
2. Once ETR is known, it is possible to estimate photorespiration according to equation [6]. Dark respiration (R_d) can be measured using the same gas exchange system as described above after at least one hour in the dark period and after that divided by two ($R_d/2$) to estimate the mitochondrial respiration rate in the light (R_L) (Niinemets and Sack 2006; Niinemets et al. 2005, 2009).

$$ETR = \delta PSII \cdot \alpha \cdot \beta \cdot PPFD \quad [5]$$

$$Pr = 1/12(ETR - 4(A + R_L)) \quad [6]$$

Quantification of intermediate metabolites of photorespiration

The integration of molecular and genetic approaches with biochemical ones, such as metabolite profiling, is now driving rapid advances in knowledge of the key metabolic roles and connections of the enzymes and genes of the photorespiratory pathway (Fernie et al. 2013). For photorespiratory metabolism, eight intermediates, *glutamate*, *glutamine*, *glycine*, *serine*, *glycerate*, *2-oxoglutarate*, *GABA* and *glycolate*, have been reported on the interplay between photorespiration and other metabolic pathways (Obata et al. 2016).

These targeted metabolites can be determined using an established gas chromatography–mass spectrometry (GC-MS)-based protocol as described previously (Osorio et al. 2012). For this analysis, approximately 25 mg of leaf samples are collected in the middle of the light period and stored at -80°C . Chromatograms and mass spectra can be evaluated using computational tools, such as Chroma TOF[®] 4.2 (Leco, St Joseph, MI) and TagFinder 4.0 (Luedemann et al. 2012). Metabolites are manually identified using TagFinder by comparing to the reference library mass spectra and retention indices in the Golm Metabolome Database (Kopka et al. 2005). Quantities of metabolites are expressed as relative intensity, based on peak integration, and relative to the internal standard. Metabolite profiling data should be reported following recent recommendations (Fernie et al. 2011).

Genomic localization and analyses of the identified QTL

The *S. pennellii* ILs have been extensively phenotyped for numerous traits, such as morphology, yield, fruit quality, fruit primary and secondary metabolites for identification of QTL (Schauer et al. 2008). These chromosomal locations of putative QTLs are determined first by analysis of variance (ANOVA). Thereafter, QTLs localization is determined using Dunnett's

test to compare statistically each IL with the control M82. Thus, ILs that displayed the same changes following different experiments can be considered as true QTL and used for further investigations. Once the QTLs are identified, bin mapping can be a qualitative endeavor. The criteria to select the QTL-associated bins for further comparative genomic analyses can be: (i) regions covered by at least one IL displaying the same phenotype in at least two independent experiments (Figure 2A) and (ii) selection of regions spanned by more than two ILs (overlapping region), which showed the same phenotype in at least two independent experiments (Figure 2B). Following screening of the IL population for photosynthesis-related parameters in which chromosome regions are identified as containing the genetic determinants responsible for a specific phenotype, subsequent genomic analyses (described below) are necessary to further resolve the gene or genes involved in the determination of the trait of interest.

Identification of candidate genes for photorespiration

The candidate gene approach, which consists of looking for genes segregating around a locus putatively responsible for the variation of a trait, has been proposed as a way to start QTL characterization (Etienne et al. 2002; Pflieger, Lefebvre, and Causse 2001). Once the bin (defined genomic region between two known genetic markers) is identified, sequences of the selected region can be retrieved from both the M82 and *S. pennellii* genomes (Bolger et al. 2014) by probing the flanking markers (according to the IL genetic map deposited in the Sol Genomics Network website – *solgenomics.net*) in both genome sequences to identify polymorphisms between the parental lines. Thus, all the polymorphisms in the region of interest are evaluated in more detail to select the most likely gene(s) affecting the analyzed trait and bioinformatically

predict the potential functional effects of each identified polymorphism (Ahsan et al. 2013).

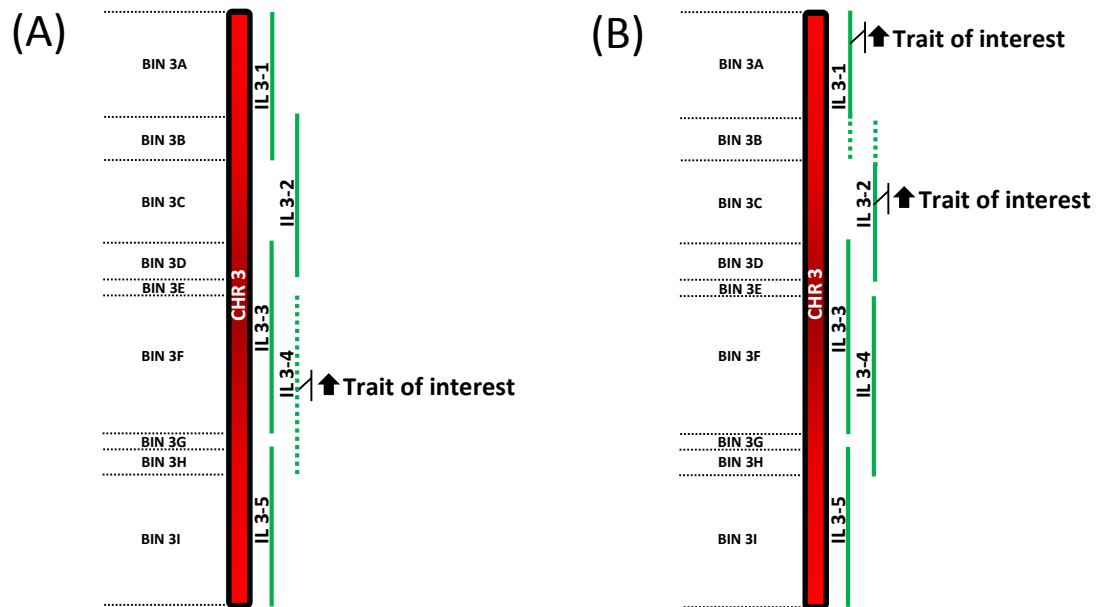


Figure 2. A random hypothetical example of putative QTLs detected in chromosome 3 of the population of 76 introgression lines (ILs) of *Solanum pennellii* (green lines) into a genetic background of *Solanum lycopersicum* (M82). Composite interval mapping was implemented using IL cartographer from www.sqn.cornell.edu. Black arrows indicate changes (can be positive or negative) relative to the trait of interest in independent experiments and dashed lines represent the chromosome fragments to putative QTLs. Candidate QTL in the region covered by one IL displaying the same phenotype in at least two independent experiments (A). Candidate QTL in an overlapping region (dashed line) between two ILs that show the same phenotype in two different experiments (B).

One approach to reduce the number of candidate genes is to conduct further experiments using larger numbers of segregating progeny to reduce the size of the QTL-containing interval. Then, classical methods such as positional cloning (Chen et al. 2012), insertional mutagenesis (Ikeda et al. 2013) and reverse genetics (TILLING, CRISPR) should be used to identify the relevant genes. A complementary approach would be to use the bioinformatics tools and genome and 'Omics' information to assign genes in the QTL interval to bins of higher probability than other candidates (Schauer et al. 2006).

NOTES

1. In the same way as for the *Solanum pennellii* ILs population, the power of the approach for QTL detection in germplasm development and extraction of valuable and novel alleles from exotic germplasm, can be realized in other model systems, including major food and biofuel crops such as pepper, rice, barley, wheat, maize, soybean and Arabidopsis.
2. High variability is observed due to changes in environmental conditions. Therefore, it is highly recommended to repeat the experiment and analysis in two or more independent experiments and select the ILs with conserved changes.
3. The majority of research on natural genetic variation on ILs population must be carried under controlled conditions in order to only establish the plant genetic effect (G) in the phenotypic trait. However, because of the strong effect of G x E (environment) on QTL mapping, evaluations of genotypes under field conditions is essential to gain

further insight into the extent of G x E into its underlying genetic causes.

4. Grow more than four M82 control plant per block. In case of photosynthesis and chlorophyll fluorescence parameters, it is important to collect data set along the day due to slight fluctuations in environmental conditions.
5. High density of plants can cause competition between plants per light, affecting the photosynthetic performance. In the case of 4 weeks, old tomato plants 30 cm between plants and 35 cm between rows is recommended.
6. The identification of the loci and specific alleles underlying variation in quantitative traits is an important goal for dissecting complex traits. Despite major advancements in genomics technology, moving from QTL to causal alleles remains a major challenge in genetics research. Then, the use of sub ILs to reduce the genomic regions and reduce the number of candidate genes are the ideal raw material for QTL validation, refinement of QTL location and, ultimately, gene discovery.

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OVERALL CONCLUSION

- Through analyses on the transposable elements (TEs) and expression levels of the previous published RNA-seq data, we identified promising candidate genes that might be involved in the regulation of photosynthesis, primary metabolism and plant growth, and provide new avenues for crop improvement.
- The Integrated view of metabolite with enzyme activity reveals a very high frequency of positive correlations between enzyme activities, a moderate frequency of correlations between related metabolites, and remarkably few correlations between enzyme activities and metabolite levels.
- An extensive analysis of QTLs controlling correlations between enzyme activities and metabolites levels in three different organs of the IL population of *S. pennellii* has been presented. Possible candidate genes for different QTLs will be proposed and further work is going to be carried out in order to validate them and to find new candidate genes for remaining QTLs.
- The current study is, to our knowledge, the largest study in the natural genetic variation the integrate physiological parameters, growth parameters, metabolic levels and enzyme activity, to date. Here, we provide an invaluable genetic resource to understanding of the physiological and biochemical mechanisms involved in the regulation of primary metabolism in tomato plants