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Nveawiah-Yoho, P., Zhou, J., Palmer, M., Sauve, R., Zhou, S., Howe, K. J., Fish, T., & Thannhauser, T. W. (2013). Identification of Proteins for Salt Tolerance Using a Comparative Proteomics Analysis of Tomato Accessions with Contrasting Salt Tolerance, Journal of the American Society for Horticultural Science J. Amer. Soc. Hort. Sci., 138(5), 382-394. Retrieved Jun 16, 2021, from https://journals.ashs.org/jashs/view/journals/jashs/138/5/article-p382.xml

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J. Amer. Soc. Hort. Sci. 138(5):382–394. 2013.

Identification of Proteins for Salt Tolerance Using a Comparative Proteomics Analysis of Tomato Accessions with Contrasting Salt Tolerance

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Additional index words. cellular and metabolic pathways, iTRAQ, protein functions, root development salt-responsive proteins

Abstract. **Tomato (*Solanum lycopersicum*) has a wide variety of genotypes differing in their responses to salinity. This study was performed to identify salt-induced changes in proteomes that are distinguishable among tomatoes with contrasting salt tolerance. Tomato accessions [LA4133 (a salt-tolerant cherry tomato accession) and 'Walter' LA3465 (a salt-susceptible accession)] were subjected to salt treatment (200 mM NaCl) in hydroponic culture. Salt-induced changes in the root proteomes of each tomato accession were identified using the isobaric tags for relative and absolute quantitation (iTRAQ) method. In LA4133, 178 proteins showed significant differences between salt-treated and non-treated control root tissues ($P \leq 0.05$); 169 proteins were induced (1.3- to 5.1-fold) and nine repressed (–1.7- to –1.3-fold). In LA3465, 115 proteins were induced (1.3- to 6.4-fold) and 23 repressed (–2.5- to –1.3-fold). Salt-responsive proteins from the two tomato accessions were involved in the following biological processes: root system development and structural integrity; carbohydrate metabolism; adenosine-5′-triphosphate regeneration and consumption; amino acid metabolism; fatty acid metabolism; signal transduction; cellular detoxification; protein turnover and intracellular trafficking; and molecular activities for regulating gene transcription, protein translation, and post-translational modification. Proteins affecting diverse cellular activities were identified, which include chaperonins and cochaperonins, heat-shock proteins, antioxidant enzymes, and stress proteins. Proteins exhibiting different salt-induced changes between the tolerant and susceptible tomato accessions were identified, and these proteins were divided into two groups: 1) proteins with quantitative differences because they were induced or repressed by salt stress in both accessions but at different fold levels; and 2) proteins showing qualitative differences, where proteins were induced in one vs. repressed or not changed in the other accession. Candidate proteins for tolerance to salt and secondary cellular stresses (such as hypo-osmotic stress and dehydration) were proposed based on findings from the current and previous studies on tomato and by the use of the *Arabidopsis thaliana* protein database. Information provided in this report will be very useful for evaluating and breeding for plant tolerance to salt and/or water deficit stresses.**

Progressive salinization of farmland and diminishing fresh water resources are two major issues affecting sustainability of agricultural crop production. Excess salt (NaCl) content inhibits uptake of essential mineral nutrients and water. Cellular damages under salt stress are attributed to ion (Na^+ and Cl^-) toxicity, intracellular hyperosmotic dehydration, mineral imbalance, and other physiological disorders. To overcome the complex salt stress situation, plants often experience changes at the morphological, cellular, and molecular levels. These include re-adjustment in root structure and plant architecture (Lovelli et al., 2012; Maggio et al., 2007), alteration of the ultrastructure of cell wall and subcellular organelles, and reduction of the cell division and enlargement processes (Petricka et al., 2012). Salt stress induces alteration in the de novo protein biosynthesis and enzymatic activity to increase the production of compatible osmolytes including proline and betaine as well as phytohormones such as abscisic acid (ABA), ethylene, and jasmonic acid (JA) and antioxidant and other protective compounds (Frary et al., 2010; Ma et al., 2006; Panda and Khan, 2009).

When subjected to salt stress, plants, through the changes within cellular and subcellular spaces in the contents of ABA (Ma et al., 2006), H_2O_2 (Avsian-Kretchmer et al., 2004), Ca^{2+} (Mahajan et al., 2008), and other signaling molecules, activate various signaling cascades such as the mitogen-activated protein kinases (MAPK) and protein phosphatases cascades (Luan, 1998; País et al., 2009; Pitzschke et al., 2009), leading to re-adjustment of genome expression and dynamic changes in transcriptomes and proteomes toward development of stress tolerance (Marjanović et al., 2012; Nam et al., 2012; Rasmussen et al., 2013). Ultimately, proteins mediate the adaptation to stress

Received for publication 25 Apr. 2013. Accepted for publication 1 Aug. 2013. This project was supported by the Agriculture and Food Research Initiative competitive grant no. 2010-65114-20405 from the USDA National Institute of Food and Agriculture, NIFA-grant no. 2010-38821-21571, ARS CRIS project 1907-21000-037-00D, and Evans-Allen Research Funds. Statistical analysis using SAS was performed under the supervision of Dr. Dafeng Hui.
Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture.
We thank Drs. Jason de Koff and Nick Gawel and Mr. Timothy Hooper at Tennessee State University for reviewing the manuscript.
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(Lackner et al., 2012). Proteomic analysis, in addition to revealing genes concordantly regulated at transcript and translational levels, is especially important for the identification of stress-responsive proteins (such as the salt tolerance protein eIF5A) for which the encoding genes are not changed at the transcript level (Lan and Schmidt, 2011).

Comparative proteomic analyses are highly effective in the identification of protein changes that are associated with genotypic properties. For instance, it was found that different stress proteomes are expressed in the glycolphyte *Arabidopsis thaliana* than in the halophyte *Thellungiella salsuginea* under salt treatments (Pang et al., 2010). An iTRAQ analysis of root proteomes from drought-susceptible cultivated tomato and tolerant wild tomato (*Solanum chilense*) showed that a large number of proteins was affected by dehydration in the two accessions (Zhou et al., 2013). Those differentially expressed proteins can be used as candidate markers for the selection of tolerance traits.

The extraction and identification of a complete proteome from a tissue sample is still a very challenging task as a result of the complex chemical properties of proteins and their association with other molecules in the cell. The use of protein association network databases (Franceschini et al., 2013) and salt stress protein databases (Zhang et al., 2012) provide information regarding proteins that interact with those identified from experimental studies and their relevance to stress tolerance, which greatly expand the capability of proteomics analysis (Dannenfelser et al., 2012; Franceschini et al., 2013).

Tomato is one of the most widely cultivated vegetable worldwide. It is also among the major crops that have significant impacts on agricultural economy. In the United States, fresh and processed tomatoes account for more than $2 billion in annual farm cash receipts (U.S. Department of Agriculture, 2013). Most tomato cultivars are susceptible to excessive salt, producing low or no yields on soil that becomes saline as a result of long-term application of fertilizers and/or irrigation with contaminated water. Development of tomato cultivars that are tolerant to saline soil has become an imperative task, which can only be achieved through an effective breeding and selection system for elite plants that express all the desirable agronomic traits in addition to stress tolerance.

Cherry tomato (*S. lycopersicum* var. *cerasiforme*) is a genetic admixture between the cultivated tomato and its wild-type accessions (Ranc et al., 2012). The cherry tomato LA4133 was discovered growing in a saline environment near the seashore in Makapuu Beach in Oahu, HI (Tomato Genetics Resource Center, 2001). As a result of natural selection, this tomato accession is highly tolerant of NaCl (Ezin et al., 2010; Nesbitt and Tanksley, 2002). In a screening study for salt-tolerant tomato accessions at Tennessee State University (Nashville), cherry tomato LA4133 and cultivar Walter LA3465 tomato plants were grown for 6 months in a hydroponic culture supplemented with 200 mM NaCl. LA4133 plants produced fruits with fertile seeds, whereas LA3465 only had some vegetative growth, and the former accession developed a larger (measured by root length) root system than the latter accession plants (unpublished data). The observation on these phenotypic differences indicates that LA4133 is more tolerant to excess salt than LA3465.

In this study, the two tomato accessions (LA4133 and LA3465) were subjected to salt treatment, and the salt-induced changes in root proteomes were identified. Proteins showing contrasting differences in the two genotypes were selected. Putative roles of those proteins in conferring salt tolerance and the use of those proteins in developing salt-tolerant tomato cultivars are presented.

Materials and Methods

Plant growth and salt treatment. Seed stocks of two tomato accessions [LA3456 (salt-susceptible) and LA4133 (salt-tolerant)] were obtained from the Tomato Genetics Resource Center at the University of California, Davis. Seeds were propagated at Tennessee State University. For this study, seeds were surface-sterilized by submerging in 25% commercial bleach for 10 min followed by three washes with sterile distilled water. Germinated seeds in seed cubes (Smithers-Oasis, Kent, OH) were transferred into net pots (3.81 cm wide), which were placed in hydroponic tanks filled with half-strength Hoagland's nutrient solution (Hoagland and Aron, 1950). Each hydroponic tank was planted with 22 seedlings with half of the plants from each of the two accessions. Solutions were refreshed every 3 d and constant aeration was provided by submerged pumps.

One-month-old plants bearing two true leaves were subjected to salt treatment. The solution for the three treatment tanks was replaced with half-strength Hoagland's solution supplemented with sufficient NaCl to bring the final concentration to 200 mM. The three control tanks were refreshed with half-strength Hoagland's solution. Greenhouse temperature was 25 °C with no supplemental lighting.

Root samples were collected 2 d after the initiation of salt treatments. To harvest root samples, plants were lifted out of the hydroponic solution, and root segments of 3 cm from root tips were cut from the root system and collected. For each accession, tissues harvested from the same tank were pooled together as one biological sample. Samples were frozen in liquid nitrogen immediately after harvest and stored at –80 °C until used.

Protein extraction and isobaric tags for relative and absolute quantification labeling. Frozen root tissues were ground into a fine powder and resuspended in acetone supplemented with 10% trichloroacetic acid and 1% dithiothreitol (Sigma, St. Louis, MO). After overnight incubation at –20 °C, protein pellets were collected by centrifugation at 10,000 g_n for 10 min at 4 °C and then washed four times in prechilled acetone. Protein pellets were then solubilized in a dissolution buffer (1:10, w/v) consisting of 50 mM triethylammonium bicarbonate (TEAB) and 500 mM urea (Sigma). After incubation on ice for 10 min with vortexing every 2 min, the mixture was centrifuged at 10,000 g_n for 10 min. Proteins in the supernatant were precipitated using the methanol and chloroform method (Wessel and Fugge, 1984). Proteins were dissolved in the same dissolution buffer, and protein contents were determined using a protein assay kit (Bio-Rad, Hercules, CA).

For iTRAQ labeling, 100 µg protein from each sample was denatured in 0.1% (w/v) sodium dodecyl sulfate, reduced with 5 mM [tris (2-carboxyethyl)] phosphine, and oxidized with 10 mM methyl methanethiosulfonate. After overnight trypsin digestion (Promega, Madison, WI) at 37 °C, protein samples were dried down and re-dissolved in 500 mM TEAB buffer. iTRAQ labeling was performed following the manufacturer's instruction (8-plex iTRAQ® labeling kit; AB SCIEX, Foster City, CA). The treated samples were labeled with tags 113, 114, and 115 and the control samples with 116, 117, and 118. Labeled proteins

of the six samples (three control and three treated) from the same tomato accession were combined (multiplexed) and purified through an isotope-coded affinity tags (ICAT) cation exchange cartridge (AB SCIEX).

Chromatography and mass spectrometric analysis. Each sample eluted from the ICAT column was reconstituted in 500 µL 0.1% (v/v) trifluoroacetic acid (TFA). Salts were removed using a solid phase extraction procedure through 1-cm^3, 50-mg cartridges following the manufacturer's instructions (Sep-Pak C_{18}; Waters, Milford, MA). Proteins were eluted in 500 µL 50% (v/v) acetonitrile with 0.1% TFA and dried under vacuum. These protein samples were subjected to high pH first-dimension ultra-performance liquid chromatography (UPLC) separation using an Acquity System (Waters) coupled with a robotic fraction collector (Probot; Dionex, Sunnyvale, CA). One hundred micrograms of the multiplexed sample was injected and fractionated into 48 fractions in a 96-well plate. The 48 fractions were concatenated (Wang et al., 2011) to yield 16 sample pools, which were dried and reconstituted each in 25 µL of 3% (v/v) acetonitrile with 0.1% TFA. These samples were further fractioned using low pH second-dimension reverse phase separation (Yang et al., 2011). Nano-liquid chromatography separation of tryptic peptides was performed with a nano-Acquity system (Waters) equipped with a Symmetry C_{18} 5 µm, 20 mm × 180-µm trapping column and a UPLC BEH C_{18} 1.7 µm, 15 cm × 75-µm analytical column (Waters). Mass spectrometric analysis of tryptic peptides was performed using a high-definition mass spectrometry system (Synapt; Waters). Accurate mass data were obtained by liquid chromatography–mass spectrometry data-dependent acquisition (LC-MS/MS DDA). Instrument settings and data acquisition used the same parameters as described in a previous study (Zhou et al., 2013).

Database search and protein quantification. Mascot Daemon (Version 2.3.2; Matrix Science, Boston, MA) was used to combine .pkl files for the 16 fractions associated with each sample (the multiplexed six labeled protein samples from one accession) and to query them against an ITAG 2.3 tomato protein database [downloaded on 16 Sept. 2011 (Bombarely et al., 2011)]. Furthermore, an exclusion list including the commonly observed peptides of keratin, porcine trypsin, and Con-A was used to avoid accumulating spectra of uninformative ions. Database search criteria were the same as described by Zhou et al. (2013). Briefly, precursor mass tolerance was set to 0.05 Da, whereas fragment tolerance was set to 0.1 Da. One missed tryptic cleavage was allowed. The MS/MS data were searched with S-methylation of cysteine as a fixed modification and the oxidation of methionine residues and the deamidation of asparagine and glutamine as variable modifications. All peptide matches reported herein have an E-value < 0.05. Protein identification required at least one peptide match with an E-value < 0.05. A false discovery rate was calculated by searching the MS/MS data using a reversed decoy database. The protein identification data are presented in Supplemental Table 1.

Theoretically, at least two confidently quantified peptides were required for protein quantification using the peptide data. When comparing the iTRAQ data files from the two tomato accessions, we have found that some proteins contained one peptide in one but two or more in the other accession. To avoid missing information, proteins containing one well-quantified peptide in the six samples in either accession were also analyzed, and information of the number of peptide used for protein quantification is provided in Supplemental Tables 2 and 3.

Analysis and characterization of differential protein expression. For each iTRAQ data file, low signal intensity peptide data (less than 20 signal intensity) and those with missing data in the three biological replicates of the same sample group (control or treated) were removed. Peptides shared among related but distinct proteins or peptides where the spectrum was also matched to a different protein were excluded in quantification. The remaining peptides were included as contributing factors to protein quantification (Boehm et al., 2007). The normalized peak intensities of reporter ions of constituent peptides were $\log_2$ transformed.

To determine the effects of salt treatments on proteome expression in each accession, the quantitative data were subjected to principal component analysis (PCA). To determine the proteome separation between genotypes under treated and non-treated conditions, PCA analysis was performed on peptides that were identified in each of the 12 biological samples from the two accessions (each accession had six samples of three replicates in treated and control groups).

To determine the confidence associated with the quantitative protein changes, the $\log_2$ fold values from all constituent peptides were subjected to *t*-test (general linear model procedure) followed by false discovery rate (FDR) corrections to determine the threshold of statistically significant differences for each protein between salt-treated and control sample groups (Zhou et al., 2013). Statistical analyses were performed using SAS (Version 9.3; SAS Institute, Cary, NC).

Proteins passing the statistical tests ($P \leq 0.05$) were selected, and then the $\log_2$ fold values were back-transformed through antilogarithmic transformation to yield the "fold change" ratio of protein abundance (treated/control). Induced proteins in the salt-treated samples have a fold change greater than 1, and repressed proteins have a fold change less than 1. For ease of comparison, the fold change of repressed proteins is expressed as the negative (–) inverse of the actual fold change. Thus, if a protein's expression was reduced by half after treatment, its fold change would be given as – 2.0-fold, whereas a protein whose expression doubled on treatment would exhibit a fold change of + 2.0-fold. Salt-responsive proteins are selected using the following criteria: passing the statistical tests and with greater than 1.3 (±) -fold change quantified using two and more peptides in either or both accessions.

Determination of protein distribution in the two tomato accessions. The lists of proteins quantified in the two tomato accessions were combined, and proteins were divided into five clusters: Cluster 1, no change, a protein was placed in this group when it was identified as no-change in either accession; Cluster 2, proteins induced in LA3465; Cluster 3, proteins induced in LA4133; Cluster 4, proteins repressed in LA3465; and Cluster 5, proteins repressed in LA4133. The number of proteins in each individual and overlapping clusters was used to describe protein distribution in a Venn diagram.

Determination of the biological functions of tomato salt-responsive proteins and the role in salt tolerance. To determine the biological function of tomato proteins, they were searched using protein names for protein accessions in *A. thaliana* STRING database [Version 9.1 (Franceschini et al., 2013)]. Tomato proteins with no matching names were searched using amino acid sequences retrieved in the annotated tomato genome database (Bombarely et al., 2011). For proteins assigned to multiple accessions in *A. thaliana*, the one annotated to salt or relevant stress factors and/or root development

was selected. The biological processes of the identified proteins were determined using the Gene Ontology (GO) enrichment analysis tool in the database (Franceschini et al., 2013). Proteins are normally annotated to several GO terms because they are in most cases associated with multiple biological processes. In this study, each protein was placed in only one biological process with priority given to root development followed by responses to salt and then to salt-induced secondary stresses (such as hypo-osmotic and water deprivation). Proteins that could not be placed into the GO terms were grouped based on their molecular functions. Roles of tomato proteins in conferring tolerance to salt and/or water deficit stresses were proposed based on the relative changes of selected proteins induced by salt reported in this study and in *S. chilense* (Zhou et al., 2011) and those effected by water deficit in *S. chilense* and 'Walter' (Zhou et al., 2013).

Results and Discussion

Effect of salt treatment on proteome expression in tomato 'Walter' LA3465 and cherry tomato LA4133

PCA of the peptides that were identified in both accessions shows that the two tomato accessions were separated on the second principal component at 2.3 eigenvalue, and treated and control groups from each accession were separated on the third principal component at 0.9 eigenvalue (Fig. 1). These results indicate that the identified proteomes are associated with genotypes under either salt-treated or untreated conditions. The separation of the salt-treated and non-treated control groups was also confirmed from PCA of the quantitative data from each individual accession. In conclusion, the PCA analysis confirmed that the identified proteomes can reflect both the effect of salt treatment as well as genotypic differences between the two tomato accessions.

Then the proteome data from each individual accession was analyzed to determine salt-induced changes (fold change in abundance level from treated to control groups) in each protein and the level of significance of those changes (*t*-test followed by FDR correction and fold change). Proteins passing the statistical tests ($P \leq 0.05$) and having ± 1.3-fold change were listed as significantly changed. Then one compiled file containing all the proteins identified in the two accessions was generated.

The Venn diagram (Fig. 2) represents protein distribution in the two tomato accessions. It can be seen that the majority of the proteins did not exhibit a significant change from salt-treated to non-treated conditions (80% in LA4133, 85% in LA3465). Among the significantly changed proteins, more proteins were induced (95% in LA4133, 83% in LA3465) than repressed (5% in LA4133, 17% in LA3465) in either the salt-tolerant or the susceptible accession. Some proteins had similar responses (either induced or suppressed) to salt treatment in both accessions. More importantly, some proteins were induced in LA4133 but repressed or had no change in LA3465, or vice versa. The protein distribution pattern indicates that both accessions exhibited dynamic changes in protein expression on exposure to salt treatment, and some of those changes are associated with genotypic properties of the two accessions with respect to salt tolerance.

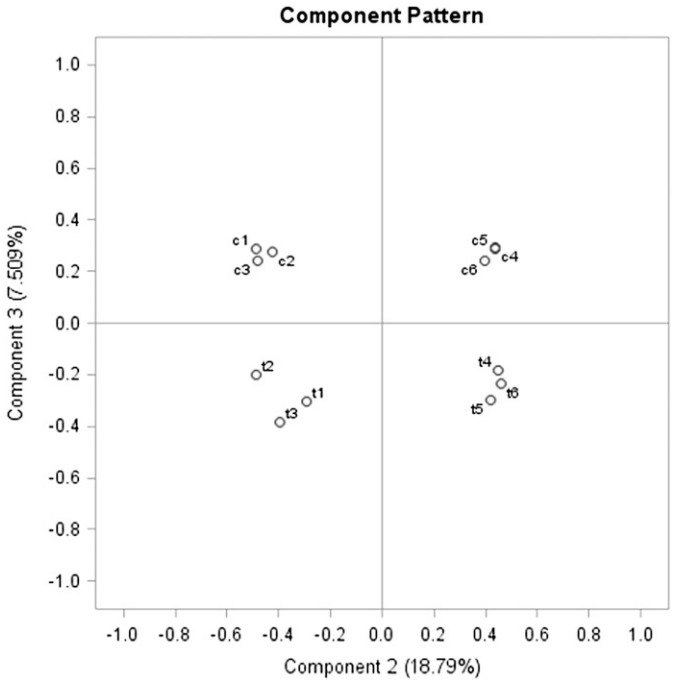

Fig. 1. Principal component analysis of salt-induced root proteomes in salt-tolerant cherry tomato accession LA4133 and salt-susceptible tomato cultivar Walter accession LA3465. Proteomes from salt-treated and control groups of LA4133 (t1, t2, t3 as the treated replicates; c1, c2, c3 as the control replicates) and LA3465 (t4, t5, t6 as the treated replicates; c4, c5, c6 as the control replicates) were identified using the isobaric tags for relative and absolute quantitation (iTRAQ) method. Peptides identified in each of 12 samples were used for the principal component analysis (PCA). The two accessions were separated at the second principal component, and the treated and control groups for each accession were separated at the third principal component.

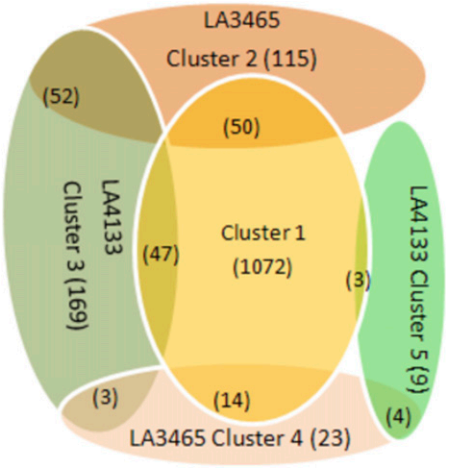

Fig. 2. Venn diagram of protein distribution in the salt-induced root proteomes in tomato accessions with contrasting salt tolerance. Root proteomes in salt-tolerant cherry tomato accession LA4133 and salt-susceptible cultivar Walter accession LA3465 were identified using the isobaric tags for relative and absolute quantitation (iTRAQ) method. Proteins showing significant changes in abundance between salt-treated and control groups [$P \leq 0.05$ in *t* test with false discovery rate (FDR) corrections; > 1.3(±)-fold] were divided into five clusters: Cluster 1 = no change, a protein was placed in this group when it was identified as no change in either accession; Cluster 2 = proteins induced in LA3465; Cluster 3 = proteins induced in LA4133; Cluster 4 = proteins repressed in LA3465; Cluster 5 = proteins repressed in LA4133. The numerical number in the parentheses shows the number of proteins in each individual and overlapping clusters.

Functional categories of salt-responsive proteins

Salt-responsive proteins were classified into 10 groups based on biological and molecular function (Supplemental Table 4). The distribution of the salt-induced proteins were: Group 1, root system development and structural integrity (9%); Group 2, carbohydrate metabolism (16%); Group 3, adenosine-5′-triphosphate (ATP) regeneration and consumption (6%); Group 4, amino acid metabolism (10%); Group 5, fatty acid metabolism (3%); Group 6, proteins affecting diverse cellular activities, which include chaperonins and cochaperonins, heat-shock proteins, antioxidant enzymes, and signal transduction proteins (30%); Group 7, cellular detoxification (3%); Group 8, intracellular trafficking (3%); Group 9, protein turnover and post-translational modification (4%); and Group 10, DNA replication and gene expression (16%) (Fig. 3).

Effect of salt treatment on protein expression affecting root growth and structural integrity

A well-developed root system is essential for growing healthy plants. Excess salt induces a decrease (or arrest) of cell division (in the meristematic zone) and cell elongation and expansion (in the elongation zone) of root tips (West et al., 2004) and suppression of root hair outgrowth in the differentiation zone of roots (Petricka et al., 2012). Therefore, molecular mechanisms that regulate cell cycle relevant to root growth are very important for developing salt-tolerant plants.

In this study several proteins affecting root development were identified (Table 1). The Ran GTPase binding protein, the actin-depolymerizing factor 1 (ADF), and the fructose-bisphosphate aldolase were induced in LA4133 but not changed in LA3465. Earlier studies found that Ran and ADF play key roles in root tip growth by affecting mitotic progress in primordial meristem and cell expansion (Augustine et al., 2011; Kim et al., 2001; Wang et al., 2006), and they also affect root development under salt and osmotic stresses (Franceschini et al., 2013; Huang et al., 2012). Aldolase physically associates with vacuolar H-ATPase in roots and may regulate the vacuolar H-ATPase-mediated control of cell elongation that determines root length in *A. thaliana* (Konishi et al., 2004). The fructose–bisphosphate aldolase was annotated to the root development process in the STRING database (Franceschini et al., 2013). These results indicate that Ran, ADF, and fructose–bisphosphate aldolase play key roles in root growth under salt treatment conditions. The induction of Ran seen here is consistent with that observed during water deficit in *S. chilense* (Zhou et al., 2013); therefore, this protein may also participate in drought tolerance. In addition, the fasciclin-like arabinogalactan protein, which is a cell wall protein required for cell adhesion and communication (Johnson et al., 2003), was also induced in LA4133.

Two proteins, alpha-mannosidase and xylanase inhibitor, were induced in both tomato accessions. The former enzyme is required for glycan maturation, which is necessary for sufficient cell wall formation under salt stress (Liebminger et al., 2009). Activation of xylanase inhibitor prevents cell wall hemicellulose degradation (Durand et al., 2005). An increase in these two proteins may be associated with the protection of cell wall structure integrity and function against salt stress as a universal mechanism in both tolerant and susceptible plants.

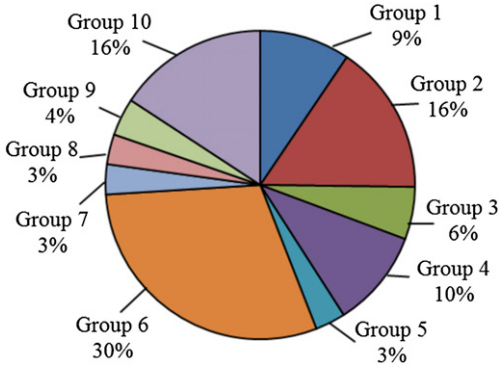

Fig. 3. Functional classification of salt-responsive root proteins in tomato. Root proteomes in salt-tolerant cherry tomato accession LA4133 and salt-susceptible tomato cultivar Walter accession LA3465 were identified using the isobaric tags for relative and absolute quantitation (iTRAQ) method. Proteins showing significant changes in abundance between treated and control groups [$P \leq 0.05$ in t test with false discovery rate (FDR) corrections; > 1.3(±)-fold] from the two tomato accessions were placed into 10 subgroups based on their putative molecular functions in various biological processes: Group 1 = root system development and structural integrity; Group 2 = carbohydrate metabolism; Group 3 = adenosine-5′-triphosphate (ATP) regeneration consumption; Group 4 = amino acid metabolism; Group 5 = fatty acid metabolism; Group 6 = proteins affecting diverse cellular activities; Group 7 = detoxification; Group 8 = intracellular trafficking; Group 9 = protein turnover and post-translational modification; Group 10 = nuclear process and gene expression. The distribution of identified proteins in each group is indicated as a percentage in the total number of salt-responsive proteins.

Effect of salt treatment on protein expression affecting metabolic pathways

Carbohydrate metabolic pathways. Sucrose is the principal carbon source in roots. Two enzymes, sucrose synthase and sucrase, that participate in biochemical reactions hydrolyzing sucrose into xylose (glucose and fructose) were induced by salt treatment. Sucrose synthase seems to increase more in LA3465 than in LA4133 (2.2- vs. 1.4-fold), whereas sucrase (invertase) was induced at an equal level in the two accessions (Table 1).

Sugars converted from sucrose are then metabolized by glycolysis, pentose phosphate, and the anaerobic and aerobic respiratory pathways. From the two accessions, six enzymes were induced under salt treatment, which include phosphoglycerate kinase and glyceraldehyde 3-phosphate dehydrogenase (glycolysis), malate dehydrogenase [tricarboxylic *acid cycle* (TCA)], alcohol dehydrogenase (fermentation), phosphoglucomutase (glycolysis and gluconeogenesis), and uridine triphosphate–glucose 1 phosphate uridylyltransferase (polysaccharide biosynthesis). Five more enzymes in these pathways were induced in LA3465, but not changed in LA4133; they are succinyl-CoA ligase, citrate synthase and malic enzyme (TCA), enolase and pyruvate kinase (glycolysis), and transketolase and 6-phosphogluconate dehydrogenase decarboxylating1 (the pentose pathway). In general, the catabolism of carbohydrates was induced under salt treatment in both tomato accessions, which agrees with results from earlier studies (Forsthoefel et al., 1995; Nam et al., 2012). Despite this commonality, the pentose phosphate pathway and several enzymes in TCA and glycolysis pathways were only induced in LA3465, and the dihydrolipoyl dehydrogenases were induced only in LA4133. These results indicate that there is a difference in the modulation of carbohydrate metabolic pathways when plants with contrasting tolerance are exposed to salt treatment.

ATP regeneration and consumption. The mitochondrial adenosine diphosphate (ADP)/ATP carrier protein for importing ADP into mitochondria and exporting ATP from the organelle

Table 1. The identity of salt-responsive root proteins in salt-tolerant cherry tomato accession LA4133 and salt-susceptible tomato cultivar Walter accession LA3465.[z]

Biological processes	Fold change[y] LA4133	Fold change[y] LA3465	Tomato protein accession[x]
Root system development			
Alpha-mannosidase	1.4[w]	1.3[w]	Solyc06g068860.2.1
Fructose-bisphosphate aldolase[v,u]	1.4[w]	1.1	Solyc05g008600.2.1
Ran GTPase binding protein[u]	1.7[w]	–1.1	Solyc08g062660.2.1
Cell wall and cytoskeleton			
Actin-depolymerizing factor 1	1.7[w]	1.0	Solyc09g010440.2.1
Fasciclin-like arabinogalactan protein[u]	1.4[w]	1.2	Solyc07g053540.1.1
Xylanase inhibitor[u]	1.7[w]	1.7[w]	Solyc01g080010.2.1
Chitinase	1.3[w]	1.2	Solyc10g055820.1.1
Endochitinase[v]	1.3	1.4[w]	Solyc10g055810.1.1
Carbohydrate metabolism			
Sucrase	1.5[w]	1.4	Solyc02g067840.2.1
Sucrose synthase	1.4[w]	2.2[w]	Solyc07g042550.2.1
Phosphoglucomutase[s]	1.6[w]	1.6[w]	Solyc04g045340.2.1
UTP-glucose 1 phosphate uridylyltransferase[u]	1.5[w]	1.6[w]	Solyc11g011960.1.1
Transketolase 1	1.3	1.6[w]	Solyc05g050970.2.1
6-phosphogluconate dehydrogenase decarboxylating[u]	1.3	1.5[w]	Solyc04g005160.1.1
Enolase[u,s]	1.2	1.4[w]	Solyc10g085550.1.1
Pyruvate kinase	1.3	1.5[w]	Solyc04g008740.2.1
Phosphoglycerate kinase[u]	1.4[w]	1.3[w]	Solyc07g066600.2.1
Glyceraldehyde 3-phosphate dehydrogenase[v,u]	1.3[w]	1.4[w]	Solyc05g014470.2.1
Malate dehydrogenase[v,u,s]	1.4[w]	1.4[w]	Solyc07g062650.2.1
Malic enzyme[v,u]	1.1	1.7[w]	Solyc05g050120.2.1
Dihydrolipoyl dehydrogenase[u]	1.3[w]	1.2	Solyc05g053300.2.1
Succinyl-CoA ligase[v]	1.2	1.5[w]	Solyc06g083790.2.1
Citrate synthase	1.2	1.7[w]	Solyc01g073740.2.1
Alcohol dehydrogenase 2[v]	2.1[w]	2.6[w]	Solyc06g059740.2.1
Alcohol dehydrogenase zinc-containing[u]	2.0[w]	1.9[w]	Solyc09g059040.2.1
ATP regeneration and transmembrane ion transport			
Mitochondrial ADP/ATP carrier proteins[u]	1.5[w]	1.8[w]	Solyc11g062130.1.1
Mitochondrial ATP synthase[w]	1.3[w]	–1.1	Solyc00g009020.2.1
ATP synthase[v,v]	1.3[w]	1.5[w]	Solyc12g055800.1.1
ATP synthase subunit alpha	1.1	1.5[w]	Solyc11g039980.1.1
H-ATPase	1.3	1.7[w]	Solyc06g071100.2.1
V-type proton ATPase subunit a[v,u]	1.1	1.5[w]	Solyc01g110120.2.1
Adenosine kinase[u]	1.3	1.6[w]	Solyc10g086190.1.1
Amino acids			
Shikimate hydroxyl-cinnamoyltransferase	1.4	1.8[wr]	Solyc03g117600.2.1
Caffeoyl CoA 3-O-methyltransferase[u]	1.8[w]	1.1	Solyc01g107910.2.1
Alanine aminotransferase[u]	1.5	1.5[w]	Solyc03g123610.2.1
N-acetyl-gamma-glutamyl-phosphate reductase	1.2	1.4[w]	Solyc01g108660.2.1
Asparagine synthetase[u]	1.8[w,r]	1.9[w]	Solyc01g079880.2.1
Aspartate aminotransferase	1.3[w]	1.6[w]	Solyc07g055210.2.1
3-isopropylmalate dehydratase large subunit[u]	1.4	1.6[w]	Solyc07g052350.2.1
3-deoxy-7-phosphoheptulonate synthase[u]	1.4[w]	1.7[w]	Solyc04g074480.2.1
Phosphoserine aminotransferase	1.4	1.6[w]	Solyc02g082830.1.1
Formate dehydrogenase	2.0[w]	1.5[w]	Solyc02g086880.2.1
5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase[v,u,s]	1.4[w]	2.1[w]	Solyc10g081510.1.1
Adenosylhomocysteinase[v,u,s]	1.3[w]	1.5[w]	Solyc09g092380.2.1
O-methyltransferase[v]	2.2[w]	1.7	Solyc03g080180.2.1
Methylenetetrahydrofolate reductase	1.2	1.8[w]	Solyc11g008870.1.1
Fatty acids metabolism			
Acetyl-CoA carboxylase biotin carboxyl carrier protein	1.5[w]	1.2	Solyc01g008330.2.1
3-ketoacyl CoA thiolase 1	1.4	1.3[w]	Solyc09g091470.2.1
Lipase-like	–1.2	2.3[w]	Solyc02g077420.2.1
Patatin[u]	1.9[wr]	–1.4[w]	Solyc08g006860.2.1

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Table 1. Continued.

Biological processes	Fold change[y] LA4133	LA3465	Tomato protein accession[x]
Detoxification			
Aldehyde dehydrogenase	1.5	2.0[w]	Solyc03g114150.2.1
Cyanate hydratase[v]	1.6[w]	1.5[w]	Solyc09g090430.2.1
Polyphenol oxidase[u]	1.1	1.4[w]	Solyc08g074680.2.1
Proteins affecting diverse cellular activities			
HAT family dimerization domain containing protein	NI[t]	2.0[w]	Solyc12g070140.1.1
Chaperonin[v,u]	1.5	1.4[w]	Solyc05g053470.2.1
Chaperone DnaK[v,u]	1.3[w]	1.0	Solyc01g106210.2.1
FK506-binding protein[u,s]	1.5[w]	1.1	Solyc09g057670.2.1
T-complex protein theta subunit[u]	1.4[w]	1.7	Solyc01g088080.2.1
T-complex protein 1 subunit alpha[u]	1.2	1.5[w]	Solyc01g090750.2.1
Heat shock protein C62.5	1.1	1.3[w]	Solyc04g081570.2.1
Heat shock protein 90	1.1	1.7[w]	Solyc12g015880.1.1
Heat shock protein 4[u]	1.4[w]	1.4[w]	Solyc12g043110.1.1
Ubiquitin-fold modifier 1	1.5[w]	1.0	Solyc08g075780.2.1
Dehydrin COR47	1.7[w]	1.5	Solyc04g071610.2.1
Dehydrin[v,u]	1.2	–1.4[w]	Solyc04g082200.2.1
Salt stress root protein (RS1)[v,u]	1.5[w]	1.2	Solyc10g005100.2.1
ASR4[v,u]	5.3[w]	2.6[w]	Solyc04g071620.2.1
Ultraviolet excision repair protein (RAD23)[u]	1.4[w]	1.1	Solyc02g063130.2.1
Elicitor-responsive protein 3	1.4[w]	1.0	Solyc08g080680.2.1
Major allergen Mal d 1[u]	4.9[w]	6.4[wr]	Solyc09g091000.2.1
REF-like stress related protein 1	1.3	1.5[w]	Solyc05g015390.2.1
Ascorbate peroxidase[u]	1.6[w]	1.3[w]	Solyc06g005160.2.1
Ascorbate peroxidase 7[v]	1.5[w]	1.2	Solyc06g060260.2.1
Catalase[u]	2.6[w]	2.5[w]	Solyc12g094620.1.1
Cytoplasmic glutaredoxin thioltransferase	1.8[w]	1.0	Solyc06g005260.2.1
Dehydroascorbate reductase	1.4[w]	1.5[w]	Solyc05g054760.2.1
Glutathione-disulfide reductase	1.4[w]	1.9[w]	Solyc09g091840.2.1
Monodehydroascorbate reductase[v,u]	1.4[w]	1.7[w]	Solyc09g009390.2.1
Peroxidase 1	–1.4[w]	1.8	Solyc00g072400.2.1
Peroxidase 4[u]	1.5[w]	1.4[w]	Solyc04g071890.2.1
Peroxiredoxin[v,u]	1.6[wr]	3.0[w]	Solyc01g007740.2.1
Superoxide dismutase[u,s]	2.4[w]	1.1	Solyc01g067740.2.1
Thioredoxin[v,u]	1.5[w]	1.2	Solyc04g080850.2.1
Ferritin[u]	1.6[w]	NI[t]	Solyc06g050980.2.1
Annexin	1.3[w]	1.2	Solyc04g073990.2.1
Annexin 2[v]	1.8[w]	2.0[w]	Solyc04g055170.2.1
Calmodulin[u]	1.4[w]	–1.4[w]	Solyc01g008950.2.1
Phosphatidylglycerol/phosphatidylinositol transfer protein (PITP)[u]	1.4[w]	1.1	Solyc01g006900.2.1
Mitogen-activated protein kinase kinase phosphatase 1 (MKP1)	1.3[w]	1.0	Solyc03g096540.2.1
Remorin 1[u]	2.4[w]	NI[t]	Solyc03g025850.2.1
GTP-binding protein[u]	1.3	1.4[w]	Solyc02g023970.2.1
Translocation of proteins			
ADP-ribosylation factor	1.1	1.4[w]	Solyc01g008000.2.1
Alpha-soluble NSF attachment protein (SNAP)	1.1	1.6[w]	Solyc05g052310.2.1
Coatomer subunit gamma (COP)	1.5[w]	1.5[w]	Solyc01g109540.2.1
Protein modification and degradation			
Mitochondrial processing peptidase[v,u]	1.3[w]	1.1	Solyc12g008630.1.1
Cathepsin B-like cysteine proteinase[u]	1.3[w]	1.1	Solyc12g088670.1.1
Chymotrypsin inhibitor-2[u]	1.4[w]	1.0	Solyc08g080630.2.1
Beta-hexosaminidase b	1.2	2.9[wr]	Solyc05g054710.2.1
Leucyl aminopeptidase[u]	1.4[w]	1.5[w]	Solyc12g010040.1.1
DNA replication and gene expression			
MFP1 attachment factor 1	2.0[w]	NI[t]	Solyc04g078380.1.1
Glycine-rich RNA-binding protein	1.5[w]	–1.3	Solyc01g109660.2.1

Continued next page

Table 1. Continued.

Biological processes	Fold change[y] LA4133	LA3465	Tomato protein accession[x]
Glycine rich protein-RNA binding protein	1.4	–1.4[w]	Solyc05g053780.2.1
Tudor/nuclease domain-containing protein[v]	1.2	1.5[w]	Solyc03g118020.2.1
Insulin-like growth factor 2 mRNA-binding protein 2	1.4[w]	1.0	Solyc12g095960.1.1
Translation elongation EFTu/EF1A	1.7[w]	1.9[w]	Solyc06g069020.2.1
EF1B	1.3[w]	–1.3	Solyc07g016150.2.1
Elongation factor Tu	1.3[w]	1.0	Solyc09g073000.2.1
Elongation factor EF-2[u]	1.3[w]	1.4[w]	Solyc08g062920.2.1
30S ribosomal protein S5[u]	1.3[w]	1.1	Solyc04g063290.2.1
30S ribosomal protein S19[u]	1.0	–1.7[w]	Solyc02g082000.2.1
60S ribosomal protein L22–2	–1.4	–1.7[wr]	Solyc01g099830.2.1
60S ribosomal protein L35[u]	–1.3	–2.0[wr]	Solyc04g010240.2.1
60S ribosomal protein L6[u]	–1.7	–1.7[w]	Solyc11g012110.1.1
40S ribosomal protein S13	–1.3	–2.5[w]	Solyc01g091220.2.1
40S ribosomal protein S24	–1.4[w]	–1.4	Solyc01g097870.2.1
Histidine triad (HIT) protein[u]	1.5[w]	1.0	Solyc10g081310.1.1

[z]Proteins identified as significantly induced or repressed in either or both tomato accessions by the salt treatment. The relative difference in abundance of each protein, measured by the intensity of its constituent peptides, was compared between treated and control samples within each accession. In every case, the protein from at least one of the two accessions has passed the *t* test [general linear model (GLM)] with false discovery rate (FDR) corrections ($P \leq 0.05$) and with a fold change greater than 1.3-fold (±). Statistical analyses were performed using SAS (Version 9.3; SAS Institute, Cary, NC).

[y]The fold change value for each protein is the ratio of the protein abundance level between treated and control samples within each accession. For example, a value of 2.0 represents a 2-fold increase. whereas –2.0 represents a 2-fold decrease from treated to control conditions.

[x]Protein accession number in the ITAG Protein database (release 2.3 on 26 Apr. 2011; Sol Genomics Network, Boyce Thompson Institute, Ithaca, NY).

[w]Proteins showing significant changes in abundance in treated roots vs. the control condition within the respective accession ($P \leq 0.05$ with 5% FDR correction; > 1.3(±)-fold). Proteins without the symbol had no significant change from treated to control samples.

[v]Protein annotated to the salt response biological process in *Arabidopsis thaliana* String Database [Version 9.0 (Franceschini et al., 2013)].

[u]Protein abundance altered in roots of *Solanum chilense* and/or tomato 'Walter' LA 3465 by dehydration treatment (Zhou et al., 2013).

[t]Proteins not identified in the respective accession.

[s]Protein responded to salt treatment in roots of *S. chilense* (Zhou et al., 2011).

[r]Protein quantified using one peptide.

into cytosol was induced in both accessions. In LA4133, ATP synthases for ATP regeneration were induced. In LA3465, ATPases that use ATP to pump solutes across membranes, for Na^+ sequestration (Barkla et al., 1999) or maintaining ion homeostasis (Tang et al., 2012), were strongly enhanced together with adenosine kinase which converts ATP to ADP (Table 1).

The up-regulation of ATPases in the susceptible tomato accession could create a higher demand for ATPs, which represents a higher-energy consumption cellular metabolism model. This could also explain the greater increase in the sucrolytic and glycolytic enzymes in LA3465. It is well known that photosynthesis is reduced under salt stress, especially in susceptible plants. Eventually, the susceptible plants may succumb to prolonged salt stress as a result of deprivation of carbon sources.

Effect of salt treatment on protein expression affecting amino acid metabolism

Enzymes in the metabolism of aromatic amino acids, free amino acids, methylamine, and branched-chain amino acids (BCAA) were identified (Table 1). The 3-deoxy-7-phosphoheptulonate synthase in the shikimate pathway for the biosynthesis of aromatic amino acids was induced in both accessions. Three enzymes at different steps of phenylpropanoid pathway were identified, shikimate hydroxyl-cinnamoyl transferase was induced in LA3465, and caffeoyl CoA 3-O-methyltransferase (catalyzing the step leading to lignin biosynthesis) and O-methyltransferase were induced in LA4133.

Biosynthesis of methylamines requires adenosylmethionine (SAM) as the methyl donor, which is regenerated through the methyl cycle and SAM (AdoMet) and methionine salvage cycles. In LA4133, two enzymes in the SAM regeneration process, 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase (methioine synthase) and adenosylhomocysteinase, were induced. These enzymes were not changed in LA3465, where methylenetetrahydrofolate reductase was induced instead. These results suggested that the tolerant LA4133 seems to have a more active mechanism for the biosynthesis of methylamine as a compatible osmolyte under salt treatment, which was proposed to be one mechanism underlying genetic difference in salt tolerance in tomato (Manaa et al., 2011).

Enzymes induced in both accessions include asparagine synthetase, which plays a critical role in salt and cold tolerance because it is up-regulated by salt stress, osmotic stress, and ABA (Marroufi-Dguimi et al., 2011; Wang et al., 2005). Formate dehydrogenase was also induced by salt treatment. This enzyme controls the homeostasis of formate and it was also suggested to have some roles in the salt responses regulated by AtMKK1 (a stress response kinase) (Conroy et al., 2013).

Five additional enzymes were induced only in LA3465. In LA3465, alanine aminotransferase in the alanine cycle was induced. The induction of this enzyme may result in lower cellular alanine content as the amino acid is shuttled to make

glucose. In the same tomato accession, phosphoserine aminotransferase, which acts in the biosynthesis pathway of L-glutamate, was induced. Such change could increase cellular glutamic acid content in the treated roots. Induction of these two enzymes could affect free amino acid content. For the biosynthesis of BCAA, 3-isopropylmalate dehydratase in the leucine biosynthesis pathway was induced. Such change in BCAA was found to be linked to salt responses in earlier studies (Nam et al., 2012; Zhou et al., 2009). N-acetyl-gamma-glutamyl-phosphate reductase, which participates in the process of producing urea from ammonia through the ornithine cycle, and amidase hydantoinase/carbamoylase, which is important for allantoin degradation, were also induced by the salt treatment in LA3465. Allantoin is a biomarker of oxidative stress in the human system (Gruber et al., 2009), but not much is known about the relationship between its metabolism and salt or oxidative stress in plants.

Effect of salt treatment on protein expression affecting fatty acid metabolism

Patatin is a phospholipase that catalyzes the cleavage of fatty acids from membrane lipids and also has a role in the removal of oxidized fatty acids from membranes and oxylipin formation against dehydration stress (Yang et al., 2012). This enzyme was induced in LA4133 but repressed in LA3465 (Table 1), and the same enzyme was induced by water deficit in the drought-tolerant *S. chilense* (Zhou et al., 2013). These results suggest a role for patatin in drought and salt responses in tomato.

Lipases catalyze the hydrolysis of triglycerides into free fatty acids, which are degraded into acetyl units through the beta-oxidation process. Lipase was induced in LA3465 but unchanged in LA4133. A peroxisomal enzyme, 3-ketoacyl CoA thiolase catalyzing fatty acid beta-oxidation, was induced in LA3465 (1.3-fold); it was also induced in LA4133 at a comparable fold level (1.4-fold, $P > 0.05$), but in the latter case, it did not pass the FDR test. The acetyl-CoA carboxylase biotin carboxyl carrier protein in the biosynthesis pathway of fatty acids was induced in LA4133 but not changed in LA3465. It seems that the two tomato accessions may use different mechanisms to regulate the turnover of fatty acids in response to salt treatment.

Effect of salt treatment on protein expression affecting cellular detoxification

Four enzymes needed to remove cytotoxic compounds were identified. Cyanate hydratase was induced in both tomato accessions (Table 1). In a study on *A. thaliana*, the homologous gene, *AtCYN,* was induced at the transcriptional level by salt stress (Qian et al., 2011). Together with results from this study, it seems that this gene responds to salt stress at both transcriptional and translational levels. In addition to metabolizing cyanate, the protein may have other functions in stress tolerance.

Two enzymes were only induced in LA3465, which include aldehyde dehydrogenase in detoxifying peroxidic aldehydes, which result from lipid peroxidation, and polyphenol oxidase. Several studies on tomato have shown that an elevated level of polyphenol oxidase (measured by protein content or enzyme activity) reduces plant tolerance to dehydration stress (Thipyapong and Steffens, 1997; Thipyapong et al., 2007; Zhou et al., 2013). An increase in polyphenol oxidase can make plants more susceptible to water and salt stress conditions.

Effects of salt treatment on proteins affecting diverse cellular activities

This group of proteins includes chaperonins, folding proteins, antioxidant enzymes, stress responsive and defense proteins, and proteins in signal transduction pathways. These proteins modulate functions of their target proteins in a wide array of cellular processes.

Chaperones and folding proteins. Chaperone protein DnaK (also known as HSP70, which actively participates in the response to hyperosmotic shock) and FK506-binding protein 2, which functions as an endoplasmic reticulum (ER) chaperone with biological functions of mediating folding of nascent or denatured proteins, were induced in LA4133 but not changed in LA3465 (Table 1). The induction of these proteins in the tolerant tomato accession is similar to those observed in *S. chilense* under dehydration and salt conditions (Zhou et al., 2011, 2013). Conversely, two heat shock proteins, heat shock protein C62.5 and heat shock protein 90, assisting with refolding of denatured proteins (Zuehlke and Johnson, 2010), were induced in LA3465 but not changed in LA4133. It is very likely that when exposed to the same concentration of salt, tomato genotypes with contrasting tolerance are experiencing different levels of intracellular stress, thus requiring different types of chaperonins, and those expressed in the tolerant genotypes may be the proteins responsible for the tolerance mechanism in LA4133.

Stress responsive and defense proteins. Among the eight proteins that are involved in cellular defense against salt, osmotic, and water deficit stress factors, dehydrin is the only one that was repressed in LA3465 but not changed in LA4133 (Table 1). Two proteins, the REF-like stress-related protein 1 and the major allergen Mal d 1, were induced at a higher magnitude in LA3465 (1.5- and 6.4-fold, respectively) than in LA4133 (1.3- and 5.0-fold, respectively). The root salt protein (RS1) and abscisic acid stress ripening protein (ASR4) showed a greater increase in LA4133 (1.5- and 5.3-fold, respectively) than in LA3465 (1.2- to 2.6-fold, respectively). RS1 and ARS4 were also induced by salt in *A. thaliana* (Franceschini et al., 2013; Goldgur et al., 2006) and by water deficit in *S. chilense* (Zhou et al., 2013). These results indicate RS1 and ARS4 are important proteins for salt and drought tolerance in tomato, and these defense reactions are mediated by the ABA signaling pathway (Cakir et al., 2003; Kalifa et al., 2004).

The ultraviolet excision repair protein RAD23, elicitor-responsive protein 3 (a phloem protein for mounting a defense reaction in response to external stimuli), and ubiquitin-fold modifier 1 (UFM1) that participate in preventing ER stress-induced apoptosis in protein secretory cells (Lemaire et al., 2011) were induced in LA4133 but not changed in LA3465. By assisting DNA repair of damages induced by ultraviolet light (Ortolan et al., 2000), RAD23 plays a key role in maintaining genome stability of plants affected by intense light conditions. For tomato LA4133 and *S. chilense*, when growing in their native habitats on the seashore or deserts, plants may experience constant exposure to strong ultraviolet light, which typically coincides with physiological dehydration. Thus, the increase in the protein abundance under salt and dehydration conditions (Zhou et al., 2013) suggests that RAD23 may be a candidate marker protein for tolerance to multiple stresses in tomato.

Antioxidant enzymes. In this study, 12 antioxidant enzymes (including isoforms) for the removal of reactive oxygen species

(ROS) were identified (Table 1). Catalase, glutathione-disulfide reductase, and monodehydroascorbate reductase were induced in both accessions (Table 1). Superoxide dismutase, thioredoxin, and the cytoplasmic glutaredoxin thioltransferase were induced only in LA4133; these enzymes were also induced in *S. chilense* under water deficit treatment (Zhou et al., 2011, 2013). It is conclusive that the salt- and drought-tolerant tomato accessions have antioxidant systems comprised of several more antioxidant enzymes or enzymes expressed at higher levels than the susceptible accessions. These results are consistent with those from an earlier study showing that wild salt-tolerant tomato plants are better protected against ROS, inherently and under salt stress, than the relatively sensitive plants of the cultivated species (Shalata and Tal, 1998).

Ferritin was induced by salt stress in LA4133 and was also induced by dehydration in *S. chilense* (Zhou et al., 2013). However, this protein was not found in root protein samples (controls, salt-treated, or water deficit-treated) from LA3465. Ferritin is the only known protein to concentrate iron to the level required by cells, to store iron in a soluble and biologically available form, to release iron when needed, and to protect the cells against the toxic effects of excess iron (Orino et al., 2001; Wei and Theil, 2000; Xi et al., 2011). In this study, the iron content in salt-treated root tissues of LA4133 was increased by over 32%, and LA3465 roots contained even higher iron content (unpublished data). Technically, the same amount of total protein was used for iTRAQ analysis. Our inability to detect ferritin in LA3465 suggests a lower content of this protein in the whole proteome. Thus, the disparity between iron content and ferretin expression in the susceptible tomato accession and the biological significance of this observation need to be investigated.

Signal transduction. Three important proteins in signal transduction pathways were identified; they are calmodulin (CaM), mitogen-activated protein kinase (MAP)/kinase phosphatase 1 (MKP1), and phosphatidylglycerol/phosphatidylinositol transfer protein (PITP). These proteins were induced in the tolerant LA4133 (Table 1) and *S. chilense* (Zhou et al., 2013), but repressed in the susceptible LA3465, under salt and water deficit treatments. CaM is an important protein in the calcium-mediated signaling pathway to activate cell defense against salt and other stresses (Xu et al., 2011). MKP1 regulates the MAPK signaling cascade by controlling the activity of MAPKs, thus playing a pivotal role in the integration and fine-tuning of plant responses to various environmental challenges (González Besteiro and Ulm, 2013; Osakabe et al., 2013). PITP regulates a wide array of signal transduction processes (Monks et al., 2001). These results indicate that CaM, MKP1, and PITP proteins are important proteins in signal transduction pathways that activate salt and drought tolerance in tomato.

Remorin1 was induced in LA4133 by salt treatment (Table 1) and in *S. chilense* under dehydration (Zhou et al., 2013); however, this protein was not identified in LA3465. Remorins are plant-specific proteins associated with plasma membrane microdomains, called lipid rafts on mature branched plasmodesmata (Raffaele et al., 2009; Tilsner et al., 2011). Those lipid rafts are platforms for various kinds of signaling molecules, and it has been suggested that remorins act as scaffold proteins during early signaling events in defending against pathogenic attack (Jarsch and Ott, 2011). Based on these findings, remorins may play an important role in the signaling process to activate defense reactions in response to abiotic as well as biotic stimuli.

Effect of salt treatment on vesicle proteins for intracellular trafficking

Cytosolic proteins translated on the rough ER are transported to the Golgi by vesicles (transitional vesicles) before targeting to subcellular organelles. The non-clathrin-coated vesicles are covered with coatmer proteins (COP) and are responsible for intracellular trafficking of vesicles produced by ER to the Golgi. Under salt treatment conditions, a COP was equally induced in the two tomato accessions (Table 1).

Two proteins, the alpha-soluble NSF attachment protein mediating intra-Golgi transport of proteins and the ADP-ribosylation factor, which plays a critical role in intracellular trafficking and maintenance of ER morphology (Lee et al., 2002), were induced in LA3465 but not changed in LA4133. These results suggest that the two tomato accessions may use both common and different mechanisms for targeting proteins into the correct subcellular compartments under salt stress condition.

Effect of salt treatment on protein turnover and protein modification

The leucyl aminopeptidase, which regulates protein turnover through the JA signal transduction pathway (Fowler et al., 2009), was induced in both accessions (Table 1). Proteins induced only in LA4133 include cathepsin B-like cysteine proteinase and chymotrypsin inhibitor-2. The lysosomal beta-hexosaminidase b in glycan modification was induced in LA3465 but not changed in LA4133. The differential expression of these proteases could result in different proteome composition in the two tomato accessions, which may affect plant responses to salt treatment. In tomato, we have found that the chymotrypsin inhibitor-2 was consistently induced by salt, drought, and aluminum treatments in tolerant accessions; therefore, this protein might confer tolerance against multiple stress factors.

Effect of salt treatment on gene transcription and protein translation

DNA replicaiton and gene transcription. The MFP1 attachment factor 1 binds double-stranded DNA (Samaniego et al., 2006) and participates in regulation of gene transcription (Meier et al., 1996). It is induced in LA4133 but not changed in LA3465. The glycine-rich RNA-binding protein was induced in LA4133 and repressed in LA3465. This protein is an RNA chaperone and is involved in mRNA alternative splicing during the adaptation process to the environmental stress (Kim et al., 2010). Induction of these two proteins in LA4133 suggests that the tolerant accession may have a more active mechanism to protect and regulate transcript regeneration.

The only protein that was induced in LA3465 is a tudor/nuclease domain-containing protein, which is a member of the RNA-induced silencing complex (Dit Frey et al., 2010). Endogenous RNAi is important in stress tolerance, but the target genes of the RNAi system in tomato need to be identified to determine its role in stress response.

Protein translation. Regulation of the translational machinery is considered to be an important component of cellular stress response (Omidbakhshfard et al., 2012). In the salt-treated tomato roots, several ribosome subunits were repressed in LA3465; only one (the 40S ribosomal protein S24) was repressed in LA4133 (Table 1). The 30S ribosomal protein S5, which plays an important role in translational accuracy

(Vallabhaneni and Farabaugh, 2009), was induced in LA4133. Protein translation effectors showed a more dynamic change. Two elongation factors, EF Tu/EF1A (1.7-fold in LA4133, 1.9-fold in LA4365) and EF2 (1.3-fold in LA4133, 1.4-fold in LA3465) controlling translation fidelity under stress conditions (Fu et al., 2012; Shin et al., 2009), were induced in the two accessions. EF1B, which is required to regenerate EF1A from its inactive form (EF1A-GDP) to its active form (EF1A-GTP) as the rate-limiting step of translation elongation (Andersen and Nyborg, 2001), was induced in LA4133 but repressed in LA3465.

In summary, the efficiency of de novo protein biosynthesis could be reduced more dramatically in LA3465 than in LA4133 as a result of the repression of ribosome subunits under salt treatment in the former accession. Mechanisms to protect the fidelity of protein translation (with a higher abundance in EF Tu/EF1A and EF2) was activated in both tolerant and susceptible tomato accessions, but the tolerant accession may have more strict control on protein translation efficiency as a result of induction in EF1B. Those translation factors provide the candidate for future study of the role of the translation machinery in salt tolerance studies.

Conclusions

This study has identified proteins that are associated with the genotypic differences in salt tolerance in two tomato accessions. Based on the putative functions of those proteins, the corresponding molecular and cellular changes were summarized in Figure 4. The proteome changes in the tolerant LA4133 are comprised of a higher protein expression associated with root growth against salt stress and induced carbohydrate metabolism (but lower than LA3465), which is coupled with ATP regeneration. The amino acid metabolism toward biosynthesis of organic osmolytes was strongly enhanced together with antioxidant enzymes. The two accessions showed different mechanisms in detoxification, fatty acid metabolism, and stress defenses. Chaperonins, signal transduction proteins, protein translation factors, and ribosomes also had differential expression in the two accessions. The salt-induced proteins and information on their responses to salt and dehydration stresses are described in Table 1. It is expected that the findings from this study will help prioritize the use of molecular markers for evaluating and improving traits controlled by the interaction of multiple genes such as tolerance to salt and/or water deficit stress.

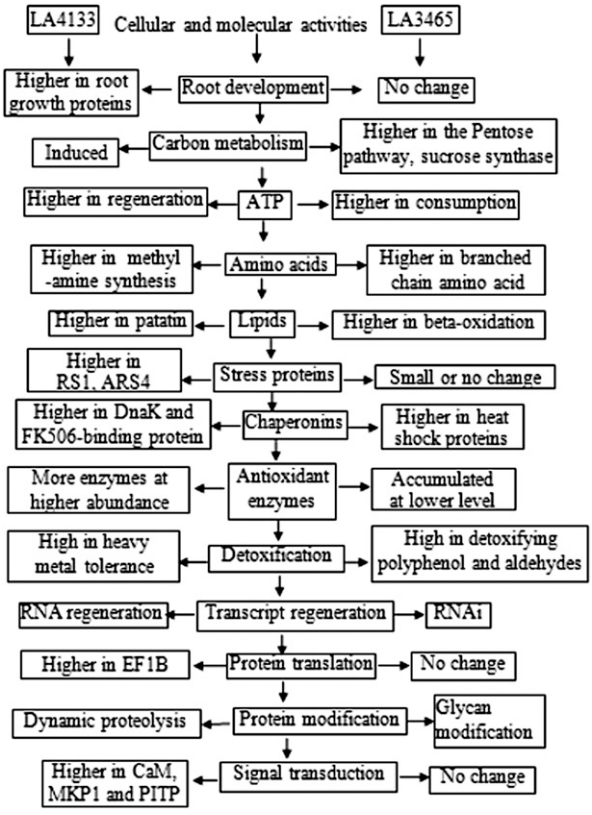

Fig. 4. Differences in molecular and cellular processes between tomato accessions with contrasting salt tolerance. The schematic was developed based on the relative protein changes from salt-treated and non-treated control conditions in salt-tolerant cherry tomato accession LA4133 and salt-susceptible tomato cultivar Walter accession LA3465. Salt-induced proteomes were identified using the isobaric tags for relative and absolute quantitation (iTRAQ) method. The molecular and cellular processes were predicted based on putative functions of the identified proteins.

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Supplemental Table 2. Protein identification information of tomato 'Walter' accession LA3465 using the isobaric tags for relative and absolute quantitation (iTRAQ) analysis.[z]

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc05g008460.2.1	1312	50	48	20	20	56.4	90.94
Solyc04g007550.2.1	1244	46	45	18	18	51.2	90.94
Solyc09g090140.2.1	1125	30	29	10	9	45.2	118.74
Solyc07g052510.2.1	1040	28	26	11	11	45.7	116.39
Solyc09g009020.2.1	939	31	28	16	15	61	90.76
Solyc07g062650.2.1	707	28	27	13	13	63.3	84.63
Solyc03g006700.2.1	592	21	18	8	8	32	107.08
Solyc04g012120.2.1	586	21	20	8	8	45.9	81.95
Solyc10g085550.1.1	583	18	17	10	9	37.6	85.34
Solyc08g080630.2.1	514	12	12	3	3	28.6	86.04
Solyc04g071890.2.1	506	13	13	7	7	35.3	115.46
Solyc06g009020.2.1	483	24	19	8	6	53.1	79.15
Solyc11g005330.1.1	465	17	16	10	10	37.4	93.64
Solyc01g111760.2.1	454	19	14	12	10	40.1	80.36
Solyc10g055670.1.1	449	19	14	12	10	40.1	80.36
Solyc12g099100.1.1	435	13	12	8	8	29.6	116.07
Solyc07g066600.2.1	429	18	17	11	11	42.9	78.39
Solyc01g102310.2.1	417	16	14	15	14	32.9	83.24
Solyc00g072400.2.1	411	15	13	9	9	44.2	86.96
Solyc01g106610.2.1	411	10	8	3	3	38.6	107.72
Solyc11g066060.1.1	410	20	15	13	11	25.8	74.83
Solyc09g010630.2.1	395	19	15	13	12	27.7	74.83
Solyc11g066390.1.1	390	8	8	4	4	39.6	127.94
Solyc05g053300.2.1	389	11	10	7	7	25.8	101.84
Solyc10g055800.1.1	374	12	12	5	5	29.5	87.98
Solyc01g059980.2.1	366	15	14	8	8	42.5	64.83
Solyc05g014470.2.1	363	18	12	9	6	43.5	94.15
Solyc09g082060.2.1	361	13	11	7	6	40.6	80.97
Solyc08g074680.2.1	358	10	9	8	7	6.9	80.74
Solyc02g086880.2.1	353	11	10	7	7	27.3	142.2
Solyc11g067100.1.1	350	13	8	7	6	77	97.11
Solyc10g083570.1.1	344	14	13	9	9	39.4	70.52
Solyc11g010200.1.1	342	13	12	6	5	30.1	78.85
Solyc06g073190.2.1	332	14	12	11	9	47.3	69.52
Solyc10g081510.1.1	329	16	12	11	10	20.7	71.76
Solyc01g105070.2.1	323	7	7	7	7	39.5	104.72
Solyc10g055810.1.1	320	11	11	5	5	31.7	87.98
Solyc09g009260.2.1	317	15	12	9	8	35.2	74.2
Solyc07g051850.2.1	314	8	8	6	6	21.3	85.65
Solyc04g077020.2.1	304	10	9	8	8	29.1	112.29
Solyc09g008280.1.1	300	13	11	7	7	31.5	71.96
Solyc12g010040.1.1	298	9	8	6	6	19.2	77.95
Solyc11g069720.1.1	297	13	9	11	7	22	89.76
Solyc04g074510.2.1	296	12	12	4	4	22.8	79.18
Solyc00g009020.2.1	294	11	10	8	7	33.1	78.46
Solyc07g043320.2.1	292	11	8	10	7	11.3	82.95
Solyc09g009390.2.1	289	16	14	12	10	40	59.44
Solyc09g090980.2.1	288	18	11	8	6	72.5	61.02
Solyc10g086100.1.1	285	9	8	4	3	36.2	80.03
Solyc11g039980.1.1	283	7	7	4	4	38.4	84.79
Solyc02g084790.2.1	282	9	8	7	6	33.4	97.95
Solyc01g100380.2.1	282	11	11	6	6	24.2	82.76
Solyc08g016510.2.1	279	6	6	5	5	36.3	102.65
Solyc06g035970.2.1	278	11	11	7	7	20.6	79.15
Solyc12g088670.1.1	274	10	9	7	6	23.6	99.7
Solyc06g076640.2.1	274	11	11	7	7	20.8	79.15

Continued next page

Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc09g092380.2.1	273	13	11	9	7	32.8	69.76
Solyc02g067460.2.1	273	8	8	5	5	27.2	73.35
Solyc11g010470.1.1	273	9	9	4	4	24.1	79.65
Solyc02g070510.2.1	270	6	6	5	5	36.3	102.65
Solyc08g079930.1.1	269	8	8	7	7	15.7	73.8
Solyc10g076220.1.1	268	11	9	6	6	27.6	87.8
Solyc06g071100.2.1	268	8	7	6	6	11.2	75.05
Solyc08g062920.2.1	267	10	9	9	8	18	83.52
Solyc03g113400.2.1	267	8	7	6	6	10.9	75.05
Solyc04g011510.2.1	263	12	11	7	7	42.5	70.33
Solyc12g005860.1.1	263	9	8	9	8	14.1	82.52
Solyc12g055800.1.1	260	9	9	7	7	19.3	102.19
Solyc12g057110.2.1	257	11	10	6	5	37.4	79.18
Solyc02g063070.2.1	257	11	10	6	5	33.8	87.23
Solyc05g053470.2.1	257	12	12	10	10	26.4	68.33
Solyc04g049450.2.1	255	10	10	7	7	17.9	69.95
Solyc10g055820.1.1	254	9	8	5	5	31.7	87.98
Solyc10g085020.1.1	249	11	11	8	8	23.8	83.77
Solyc07g006650.2.1	247	6	5	4	3	15.6	90.27
Solyc07g053260.2.1	246	9	9	5	5	28.7	73.73
Solyc04g055170.2.1	246	10	10	7	7	23.1	87.85
Solyc10g078550.1.1	244	10	9	9	8	34.5	69.15
Solyc01g099760.2.1	244	10	9	8	7	33.3	68.78
Solyc11g005640.1.1	244	12	11	2	2	14.4	57.28
Solyc04g049330.2.1	243	7	7	4	4	46.8	100.47
Solyc07g042550.2.1	242	12	10	11	10	21.1	79.82
Solyc08g082820.2.1	242	11	9	10	8	21	75.87
Solyc02g080210.2.1	241	10	9	5	4	13.6	55.78
Solyc05g008600.2.1	237	10	8	5	5	23.5	74.77
Solyc03g082920.2.1	236	10	9	9	8	19.6	70.29
Solyc07g045440.1.1	235	9	7	6	5	29.1	71.03
Solyc02g084800.2.1	234	7	6	6	6	34.8	79.88
Solyc04g054980.2.1	234	7	7	4	4	30.3	78.55
Solyc09g007520.2.1	234	6	5	5	5	29	91.52
Solyc02g084780.2.1	232	8	6	7	6	31.6	79.88
Solyc04g081490.2.1	230	11	11	8	8	23.3	83.77
Solyc08g006860.2.1	228	10	8	5	4	19.6	101.75
Solyc09g090990.2.1	227	13	9	8	6	66.9	60.76
Solyc01g103450.2.1	227	7	7	6	6	15.9	66.37
Solyc06g005160.2.1	225	10	6	7	4	53.2	86.87
Solyc11g011960.1.1	225	8	6	7	6	22.2	115.45
Solyc12g095960.1.1	223	9	7	5	4	28.5	109.62
Solyc08g062660.2.1	222	7	6	5	4	35.3	70.54
Solyc03g115990.1.1	222	7	7	7	7	27.2	78.26
Solyc01g101060.2.1	222	11	10	5	5	26	71.45
Solyc06g060290.2.1	222	8	6	5	4	18.7	63.35
Solyc09g073000.2.1	221	10	9	6	5	21.8	70.82
Solyc04g076060.2.1	217	9	9	5	5	30.2	79.65
Solyc01g056940.2.1	215	10	8	3	2	28.2	57.28
Solyc01g111120.2.1	211	9	7	6	4	29.4	55.81
Solyc12g015880.1.1	210	13	9	12	8	24	69.26
Solyc04g073990.2.1	210	10	9	7	7	23.9	59.09
Solyc06g083620.2.1	207	5	5	5	5	20	78.67
Solyc10g086190.1.1	206	7	7	6	6	32.2	81.36
Solyc06g073310.2.1	206	6	6	3	3	25.3	66.18
Solyc10g083970.1.1	204	8	7	5	5	19.7	71.74
Solyc11g072190.1.1	202	8	6	5	5	40.5	83.82

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc11g042930.1.1	202	5	5	3	3	35.5	86.23
Solyc03g019780.2.1	202	7	6	3	3	17.1	63.38
Solyc03g114500.2.1	202	5	4	5	4	17	85.27
Solyc06g071920.2.1	200	6	6	5	5	25.2	97.02
Solyc03g111200.2.1	199	8	8	5	5	23.4	83.11
Solyc05g054580.2.1	198	7	6	4	4	19.9	91.74
Solyc01g091530.2.1	196	6	6	4	4	14.5	73.89
Solyc01g111300.2.1	195	6	4	4	4	36.1	85.91
Solyc06g059740.2.1	194	7	5	7	5	28.1	95.11
Solyc07g044840.2.1	194	7	5	6	4	18.2	83.79
Solyc07g064130.1.1	193	10	8	3	2	8.3	57.28
Solyc12g096700.1.1	192	7	6	4	3	29.4	66.18
Solyc07g052540.2.1	192	5	4	4	3	19.1	127.12
Solyc04g079180.2.1	190	5	5	4	4	24.2	81.91
Solyc07g065120.2.1	189	5	5	5	5	11.8	65.15
Solyc08g080670.1.1	188	9	8	3	3	18.8	54.72
Solyc07g065840.2.1	187	11	9	10	8	19.6	69.26
Solyc07g017780.2.1	187	8	6	7	6	12.6	66.18
Solyc07g020860.2.1	186	8	8	5	5	37	57.82
Solyc08g081530.2.1	186	5	5	5	5	17	94.5
Solyc06g068860.2.1	185	4	4	4	4	5.7	93.96
Solyc10g008140.2.1	184	4	4	4	4	26	88.62
Solyc12g043110.1.1	182	8	8	8	8	14.9	65.67
Solyc12g042650.1.1	179	6	6	4	4	44.7	70.06
Solyc12g056120.1.1	179	5	4	5	4	20.6	85.65
Solyc04g082200.2.1	178	7	6	6	5	30.6	67.19
Solyc10g078620.1.1	178	9	8	4	3	18.1	53.59
Solyc08g079920.1.1	177	5	5	5	5	12.9	62.08
Solyc01g111450.2.1	176	6	4	4	3	21.7	79.19
Solyc08g080680.2.1	175	4	4	2	2	25.5	72.11
Solyc05g046010.2.1	174	9	8	5	5	22.3	66.78
Solyc03g058920.2.1	174	4	4	4	4	14.8	90.32
Solyc06g082630.2.1	174	4	4	3	3	12.1	98.67
Solyc07g052530.2.1	173	5	4	4	3	19.1	127.12
Solyc01g106620.2.1	172	6	6	2	2	21.2	77.26
Solyc00g323130.2.1	170	8	8	5	5	34.8	62.03
Solyc01g009020.2.1	169	3	3	2	2	31.9	75.03
Solyc04g011500.2.1	169	7	6	5	5	22.5	75.59
Solyc07g066610.2.1	169	7	6	5	4	17.4	76.14
Solyc12g094620.1.1	168	6	6	5	5	19.1	51.57
Solyc10g050160.1.1	167	4	4	3	3	19.2	105.11
Solyc06g075180.1.1	165	6	6	4	4	35.5	45.37
Solyc05g046020.2.1	165	9	8	4	4	15.6	66.78
Solyc07g052350.2.1	165	6	6	6	6	8.9	85.21
Solyc10g084050.1.1	164	9	6	9	6	16	89.76
Solyc00g006800.2.1	164	5	5	5	5	15.8	64.86
Solyc01g106210.2.1	163	8	5	7	5	14.5	82.04
Solyc01g100320.2.1	162	9	6	7	4	29.5	46.09
Solyc10g006650.2.1	162	4	3	3	2	24.6	90.39
Solyc05g012480.2.1	161	3	3	2	2	6.8	75.41
Solyc01g008950.2.1	160	5	4	3	3	33.6	67.74
Solyc01g104170.2.1	159	5	5	3	3	19.2	76.03
Solyc10g007290.2.1	158	9	7	8	7	13	67.61
Solyc10g080500.1.1	157	7	6	5	5	22.5	75.59
Solyc09g057670.2.1	155	7	6	4	4	40.3	46.88
Solyc01g089970.2.1	155	6	5	5	4	32.4	69.04
Solyc10g083650.1.1	155	3	3	3	3	25.4	89.25

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc02g082000.2.1	155	4	4	2	2	23.8	62.98
Solyc01g067740.2.1	155	5	5	3	3	23.7	60.31
Solyc04g008740.2.1	155	6	6	6	6	18.8	61.33
Solyc11g069790.1.1	155	6	5	6	5	15.1	78.54
Solyc07g008130.2.1	155	3	3	1	1	11.2	81.1
Solyc06g005940.2.1	154	9	7	7	5	17.2	42.91
Solyc04g077970.2.1	154	4	4	3	3	16.2	80.56
Solyc01g111170.2.1	153	14	10	7	6	50.9	38.26
Solyc03g114150.2.1	152	4	4	4	4	12.1	86.9
Solyc01g005250.2.1	151	2	2	2	2	10.2	102.99
Solyc02g062510.2.1	149	3	2	3	2	13.9	89.24
Solyc04g080850.2.1	148	7	6	4	4	35.8	58.12
Solyc04g005340.2.1	148	7	7	7	7	31.7	52.37
Solyc09g091840.2.1	146	5	5	5	5	15.6	62.13
Solyc11g011380.1.1	145	7	5	6	5	35.3	71.19
Solyc07g042250.2.1	145	7	5	6	5	31.2	78.21
Solyc09g090430.2.1	145	2	2	2	2	26.3	112.32
Solyc01g010760.2.1	145	6	5	5	4	19.9	57.66
Solyc12g010860.1.1	144	3	3	3	3	17.6	92.36
Solyc03g115110.2.1	143	4	4	3	3	16.7	68.89
Solyc01g106260.2.1	143	7	5	7	5	15.4	62.23
Solyc09g090700.1.1	143	3	3	3	3	13	79.72
Solyc12g088720.1.1	143	5	4	5	4	12	63.54
Solyc08g079260.2.1	141	9	7	9	7	20.6	39.54
Solyc09g072700.2.1	140	7	5	5	4	24.5	90.37
Solyc06g074430.2.1	139	6	3	4	2	45.8	80.17
Solyc01g099770.2.1	139	7	6	5	4	36.3	42.09
Solyc10g076240.1.1	139	7	6	6	6	25.2	62.74
Solyc09g007940.2.1	139	4	4	3	3	18.5	81.36
Solyc09g092430.2.1	139	4	2	4	2	14.5	110.89
Solyc02g038690.1.1	137	6	6	1	1	11.2	50.81
Solyc10g005100.2.1	136	6	5	3	3	31.8	49.93
Solyc10g005510.2.1	136	4	3	4	3	16.9	57.79
Solyc04g081570.2.1	136	7	6	7	6	11.5	51.47
Solyc12g009140.1.1	136	3	3	2	2	7.3	62.81
Solyc11g070050.1.1	135	4	4	4	4	42.2	74.16
Solyc07g041310.2.1	135	6	6	5	5	23.8	80.47
Solyc12g014180.1.1	135	5	5	4	4	16.7	75.72
Solyc10g078690.1.1	134	2	2	2	2	22.6	105.8
Solyc01g080010.2.1	134	6	5	5	4	17.8	57.9
Solyc01g110120.2.1	134	4	4	4	4	7.7	67.42
Solyc06g069090.2.1	133	6	5	4	3	35.1	94.58
Solyc01g102380.2.1	133	7	6	2	2	12.5	49.89
Solyc04g014510.2.1	132	8	6	6	4	36	50.4
Solyc05g014980.2.1	132	7	6	4	3	23.6	60.96
Solyc01g005560.2.1	132	6	4	5	4	17.1	62.21
Solyc06g072580.2.1	132	5	4	4	3	14.7	64.95
Solyc02g079500.2.1	132	6	5	3	3	9.3	48.74
Solyc06g005260.2.1	131	4	3	4	3	46.3	74.92
Solyc06g076660.2.1	131	3	3	3	3	23.1	77.23
Solyc10g078150.1.1	131	6	6	3	3	22.2	62.45
Solyc01g090750.2.1	131	3	3	2	2	5.9	69.97
Solyc06g005150.2.1	130	8	4	6	3	43.6	63.85
Solyc02g084920.2.1	128	4	3	4	3	38.1	54.53
Solyc12g014210.1.1	128	2	2	2	2	11.3	77.32
Solyc05g009980.2.1	128	3	3	3	3	8.2	68.86
Solyc05g053810.2.1	127	7	5	5	3	13.4	56.73

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc06g005060.2.1	126	9	7	6	6	20.3	36.13
Solyc07g053280.2.1	126	2	2	2	2	6.2	96.03
Solyc06g083790.2.1	125	7	6	5	5	18.3	48.82
Solyc04g078540.2.1	125	3	3	3	3	10.4	74.06
Solyc01g100370.2.1	124	2	2	2	2	20.5	103.14
Solyc01g107910.2.1	124	2	2	2	2	14.1	105.11
Solyc08g062800.2.1	123	7	5	6	4	19.6	47.18
Solyc09g090520.2.1	123	7	6	6	6	18.3	53.41
Solyc06g060790.1.1	123	2	2	2	2	14.5	94.93
Solyc10g005960.1.1	123	3	3	3	3	12.5	89.88
Solyc07g043420.2.1	122	4	3	4	3	18.4	80.06
Solyc01g028810.2.1	122	7	7	6	6	16	51.35
Solyc05g054090.2.1	121	4	4	4	4	52.1	62.45
Solyc03g111010.2.1	121	8	5	4	3	16.9	47.65
Solyc00g071180.2.1	121	4	4	3	3	15.4	60.79
Solyc02g093230.2.1	121	2	2	2	2	14.9	105.11
Solyc03g097070.2.1	121	3	3	3	3	12.9	95.71
Solyc03g096540.2.1	120	5	4	3	3	22.3	70.89
Solyc07g045240.2.1	120	3	3	3	3	17.2	89.7
Solyc01g107870.2.1	120	5	4	5	4	14	58.75
Solyc01g006300.2.1	120	2	2	2	2	11.1	84.65
Solyc04g005160.1.1	120	4	4	3	3	8.7	58.15
Solyc01g103800.2.1	119	4	4	3	3	32.2	63.34
Solyc06g007610.2.1	119	3	3	2	2	23	65.62
Solyc12g099000.1.1	119	8	7	4	4	20.6	45.13
Solyc04g080570.2.1	118	3	2	3	2	22.3	93.77
Solyc08g079020.2.1	118	2	2	2	2	20.9	85.78
Solyc05g018570.2.1	118	4	4	4	4	15.6	58.49
Solyc08g067020.2.1	117	7	5	4	3	42.3	46.83
Solyc08g008210.2.1	117	5	5	4	4	20.7	55.19
Solyc12g095760.1.1	117	3	3	2	2	5.3	55.72
Solyc11g006070.1.1	116	3	3	2	2	21.6	68.3
Solyc02g092440.2.1	116	3	3	2	2	14.1	66.52
Solyc08g079170.2.1	116	5	3	5	3	11.4	62
Solyc12g056250.1.1	115	4	4	4	4	29.2	55.8
Solyc04g081440.2.1	115	2	2	2	2	6.3	74.44
Solyc01g109660.2.1	114	10	6	5	3	44	39.04
Solyc10g078740.1.1	114	6	6	5	5	17.6	56.61
Solyc09g082780.2.1	114	5	5	3	3	16.7	69.03
Solyc03g112070.2.1	114	3	3	2	2	5.7	64.66
Solyc10g081030.1.1	113	6	6	2	2	15.6	62.45
Solyc02g023970.2.1	113	4	4	4	4	14	57.1
Solyc08g075700.2.1	113	1	1	1	1	11.7	113.13
Solyc11g069000.1.1	113	2	2	2	2	8	98.19
Solyc04g009410.2.1	112	2	2	2	2	15.7	85.72
Solyc09g090600.2.1	112	3	3	2	2	14.8	56.73
Solyc01g044360.2.1	112	1	1	1	1	2.1	111.92
Solyc11g072450.1.1	110	8	8	6	6	38.1	47.96
Solyc10g084400.1.1	110	4	3	3	2	17.9	73.23
Solyc06g069010.2.1	110	5	5	4	4	17.5	59.35
Solyc01g095150.2.1	109	5	4	4	3	29.9	47.14
Solyc06g082120.2.1	109	3	2	2	1	21.3	64.56
Solyc04g080540.2.1	109	1	1	1	1	14.2	109.08
Solyc05g054760.2.1	108	5	5	5	5	31.9	51.06
Solyc02g063130.2.1	108	6	6	4	4	17	45.28
Solyc02g077420.2.1	108	4	4	4	4	15.4	48.01
Solyc03g080180.2.1	108	3	3	3	3	13.7	54.56

Continued next page

Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc08g081190.2.1	108	4	4	2	2	11.9	59.46
Solyc03g123630.2.1	108	5	4	5	4	11.3	44.61
Solyc01g103750.2.1	108	1	1	1	1	5.6	107.83
Solyc01g011000.2.1	107	4	3	4	3	28.3	71.2
Solyc03g097270.2.1	107	3	2	3	2	21.7	65.42
Solyc05g055760.2.1	107	4	3	4	3	20	60.67
Solyc05g056390.2.1	104	5	5	4	4	51.5	40.94
Solyc05g055230.1.1	104	5	5	2	2	26.4	43.93
Solyc09g091470.2.1	104	5	4	5	4	15.7	57.47
Solyc02g080810.2.1	104	2	2	2	2	10.3	69.11
Solyc05g050120.2.1	102	6	6	6	6	17.4	53.6
Solyc06g073370.2.1	102	1	1	1	1	13.2	102.49
Solyc11g062130.1.1	102	3	3	3	3	11.1	74.5
Solyc11g012870.1.1	102	2	2	2	2	9.2	70.34
Solyc01g079940.2.1	102	2	2	2	2	8.8	81.59
Solyc01g087120.2.1	101	6	5	4	3	17.6	45.83
Solyc04g074480.2.1	101	3	3	3	3	9.1	68.39
Solyc02g093900.2.1	101	2	2	1	1	6.3	65.65
Solyc06g007670.2.1	100	4	3	3	2	12	49.72
Solyc02g079510.2.1	100	5	4	3	3	9.4	48.74
Solyc06g050770.2.1	100	3	3	2	2	9	57.92
Solyc12g096520.1.1	100	1	1	1	1	7.5	99.67
Solyc01g109540.2.1	100	4	3	3	2	5.6	66.78
Solyc06g075010.2.1	100	2	2	2	2	4.9	67.18
Solyc09g018750.2.1	99	3	2	3	2	25.9	65.03
Solyc02g068450.2.1	98	3	1	3	1	45.6	96.37
Solyc08g077930.2.1	98	4	4	4	4	20.2	53.25
Solyc01g104110.2.1	98	4	4	4	4	19.6	52.42
Solyc11g069430.1.1	98	3	3	3	3	16.4	66.92
Solyc10g005260.2.1	98	2	2	2	2	7.3	97.46
Solyc01g008000.2.1	97	6	5	6	5	37.8	51.95
Solyc08g015690.2.1	97	6	5	6	5	24.6	41.76
Solyc03g033710.2.1	97	3	2	3	2	13.8	70.4
Solyc04g074230.2.1	97	7	7	2	2	10.9	39.29
Solyc12g008630.1.1	97	2	2	2	2	9.9	84.08
Solyc06g082580.2.1	97	1	1	1	1	7.9	97.36
Solyc07g016150.2.1	96	2	2	2	2	23.7	88.75
Solyc01g006900.2.1	96	4	4	2	2	15.1	65.11
Solyc03g079930.2.1	96	3	3	2	2	15.1	51.81
Solyc09g091180.2.1	96	7	6	5	4	14	40.56
Solyc07g053540.1.1	96	6	5	2	2	10.5	43.21
Solyc02g093340.2.1	96	2	2	2	2	6.9	80.97
Solyc12g056960.1.1	96	2	2	2	2	6.8	77.24
Solyc05g052280.2.1	95	5	4	4	4	18	54.71
Solyc08g080640.1.1	95	4	3	2	1	11.3	59.28
Solyc01g073740.2.1	95	4	4	3	3	9.3	57.67
Solyc02g086460.2.1	95	4	4	4	4	1.5	61.58
Solyc01g107590.2.1	94	4	3	4	3	24.9	49.03
Solyc08g080650.1.1	94	4	3	2	1	17.9	59.28
Solyc03g078290.2.1	94	1	1	1	1	13.2	94.16
Solyc07g006790.2.1	94	3	3	3	3	7.1	60.37
Solyc03g080160.2.1	93	3	2	3	2	21.6	61.87
Solyc08g075830.2.1	93	5	4	3	3	13	52.41
Solyc02g091490.2.1	93	3	3	3	3	11.8	68.37
Solyc06g082870.2.1	93	4	2	3	1	11.6	49.72
Solyc02g083590.2.1	93	2	2	2	2	7.7	64.61
Solyc07g041490.1.1	92	1	1	1	1	7.1	92.47

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc06g050440.2.1	91	7	4	3	3	13.2	42.2
Solyc06g083190.2.1	91	5	3	4	3	9.8	68.63
Solyc09g091070.1.1	90	4	4	4	4	17.8	41.72
Solyc02g082900.2.1	90	1	1	1	1	5.7	89.68
Solyc07g008370.2.1	89	4	4	4	4	18.2	63.79
Solyc02g079060.2.1	89	3	2	2	2	13.5	67.82
Solyc06g060260.2.1	89	4	4	2	2	13	44.39
Solyc01g008330.2.1	89	4	4	4	4	12.1	51.48
Solyc01g005620.2.1	89	2	2	2	2	12.1	71.11
Solyc10g081530.1.1	89	2	2	2	2	5.7	80.25
Solyc03g096550.2.1	88	3	2	3	2	23.5	73.38
Solyc07g008720.2.1	88	3	2	2	2	21.6	76
Solyc05g006520.2.1	87	5	5	5	5	16.9	43.85
Solyc05g056020.2.1	86	2	2	2	2	34.2	76.13
Solyc09g009640.2.1	86	1	1	1	1	18.2	86.27
Solyc08g080660.1.1	86	5	4	2	2	12.8	43.29
Solyc04g011350.2.1	86	1	1	1	1	1.9	85.82
Solyc12g008940.1.1	85	4	2	4	2	13.6	54.45
Solyc09g075450.2.1	85	3	3	3	3	10.1	53.01
Solyc03g096000.2.1	85	2	2	2	2	1.6	72.71
Solyc04g011390.1.1	84	4	4	3	3	29.1	58.68
Solyc07g065110.1.1	84	3	3	2	2	27.9	65.88
Solyc05g012070.2.1	84	5	5	5	5	23.8	55.1
Solyc12g010060.1.1	84	3	3	3	3	22.5	51.58
Solyc06g074780.1.1	84	4	4	1	1	10.5	50.12
Solyc11g011470.1.1	84	4	3	4	3	9.5	47.66
Solyc11g020870.1.1	84	1	1	1	1	5.9	83.62
Solyc04g076880.2.1	84	2	2	2	2	4.8	63.2
Solyc03g119360.2.1	83	4	4	3	3	20.4	55.97
Solyc03g118040.2.1	83	5	4	4	3	11.9	36.49
Solyc09g025240.2.1	83	2	2	2	2	10	65.7
Solyc01g098880.2.1	83	3	2	3	2	9.8	56.22
Solyc01g087850.2.1	83	4	3	4	3	9.2	43.53
Solyc04g082160.2.1	83	2	2	2	2	6.9	65.28
Solyc09g007250.2.1	82	3	3	2	2	6.9	38.91
Solyc03g121070.2.1	82	2	2	2	2	6.8	63.74
Solyc12g042060.1.1	82	3	3	3	3	6.3	43.14
Solyc06g062950.1.1	82	3	3	3	3	5.7	45.76
Solyc01g104950.2.1	82	2	2	2	2	4.1	74.27
Solyc08g077910.2.1	81	1	1	1	1	9.2	80.54
Solyc01g111150.2.1	81	3	3	1	1	5.8	44.99
Solyc05g054710.2.1	81	2	2	1	1	2.5	65.29
Solyc04g080880.2.1	81	1	1	1	1	2.2	80.57
Solyc05g013990.2.1	80	2	2	2	2	8	52.64
Solyc01g088080.2.1	80	2	2	2	2	6.5	57.81
Solyc01g100360.2.1	80	2	2	2	2	6.3	66.18
Solyc06g005670.2.1	80	1	1	1	1	2.2	79.9
Solyc01g088610.2.1	79	2	2	2	2	28.1	61.7
Solyc12g044850.1.1	79	1	1	1	1	14.1	79.45
Solyc07g062610.2.1	79	2	2	2	2	8.7	69.46
Solyc09g061840.2.1	79	2	2	2	2	6.6	50.55
Solyc10g084120.1.1	79	2	2	1	1	6.4	57.96
Solyc09g075940.2.1	79	1	1	1	1	2.7	78.52
Solyc01g099830.2.1	78	2	2	2	2	28.8	57.77
Solyc10g084350.1.1	78	2	2	2	2	13.6	56.15
Solyc02g086730.1.1	78	1	1	1	1	9.5	78.1
Solyc06g065470.2.1	78	3	2	1	1	7.7	46.94

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc06g050590.2.1	78	1	1	1	1	6.2	78.13
Solyc06g007200.2.1	78	1	1	1	1	4.4	77.73
Solyc09g010420.2.1	78	1	1	1	1	4	78.43
Solyc01g099780.2.1	77	4	3	4	3	28.6	35.14
Solyc06g049080.2.1	77	2	2	2	2	14.9	50.92
Solyc07g064800.2.1	77	4	3	3	2	11.5	63.97
Solyc01g104590.2.1	77	3	2	3	2	10.3	53.76
Solyc04g074410.1.1	77	1	1	1	1	6.7	76.67
Solyc07g064240.2.1	77	2	2	1	1	6.4	52.46
Solyc02g088700.2.1	77	2	2	2	2	5.8	51.87
Solyc06g011280.2.1	77	1	1	1	1	4.6	76.71
Solyc12g099570.1.1	76	1	1	1	1	44.4	75.85
Solyc01g099410.2.1	76	2	2	1	1	15.8	67.18
Solyc07g017400.2.1	76	3	3	2	2	9	40.65
Solyc06g063140.2.1	76	2	2	2	2	7.7	50.89
Solyc11g008870.1.1	76	3	3	3	3	7.1	45.36
Solyc05g009600.2.1	76	1	1	1	1	3.2	75.7
Solyc04g082560.2.1	76	1	1	1	1	1.6	75.88
Solyc03g025850.2.1	75	4	3	4	3	25.9	60.63
Solyc10g079830.1.1	75	1	1	1	1	13.1	74.63
Solyc10g074500.1.1	75	3	2	3	2	11.8	60.56
Solyc03g032000.2.1	74	3	3	3	3	19.8	43.61
Solyc11g068430.1.1	74	1	1	1	1	16.1	73.94
Solyc01g008970.2.1	74	3	2	3	2	13.6	46.24
Solyc02g082200.2.1	74	1	1	1	1	10.2	74.05
Solyc03g096460.2.1	74	2	2	1	1	9.8	54.83
Solyc02g078920.2.1	74	1	1	1	1	7.4	73.59
Solyc04g015830.2.1	74	3	2	3	2	5.2	56.33
Solyc10g008010.2.1	73	3	3	3	3	29.8	43.77
Solyc06g007710.2.1	73	2	1	2	1	10.2	66.84
Solyc04g045340.2.1	73	3	3	3	3	9.6	56.29
Solyc08g006850.2.1	73	2	2	2	2	7.4	51.42
Solyc01g097520.2.1	73	1	1	1	1	5.7	72.94
Solyc12g088760.1.1	73	2	2	2	2	4.4	52.44
Solyc09g075150.2.1	72	2	2	2	2	29	57.77
Solyc01g102390.2.1	72	3	2	2	2	13.2	46.06
Solyc10g086010.1.1	72	2	2	2	2	8.3	56.15
Solyc05g012270.2.1	72	2	2	2	2	5.9	68.22
Solyc03g031720.2.1	72	1	1	1	1	5.2	72.35
Solyc11g067230.1.1	72	1	1	1	1	4.4	71.5
Solyc02g077240.2.1	72	1	1	1	1	3.4	71.65
Solyc07g055080.2.1	71	2	2	2	2	17.4	58.88
Solyc02g081700.1.1	71	4	3	3	2	15.7	40.27
Solyc02g088790.2.1	71	3	3	2	2	11.8	51.01
Solyc02g069090.2.1	71	2	2	2	2	11.6	55.1
Solyc01g090120.2.1	71	1	1	1	1	10.1	71.37
Solyc01g112080.2.1	71	2	2	2	2	8.7	47.88
Solyc09g007900.2.1	71	2	2	2	2	5.5	47.72
Solyc08g041710.2.1	71	1	1	1	1	3.6	71.19
Solyc03g045050.2.1	71	1	1	1	1	1.9	70.72
Solyc03g120470.2.1	71	1	1	1	1	1.5	70.73
Solyc01g099900.2.1	70	3	3	3	3	20.3	46.09
Solyc05g015390.2.1	70	2	2	2	2	13	62.34
Solyc02g086740.1.1	70	1	1	1	1	9.7	69.79
Solyc09g089880.2.1	70	1	1	1	1	8.8	70.5
Solyc02g086240.2.1	70	2	2	1	1	7.7	55.78
Solyc05g050970.2.1	70	6	4	5	4	7.5	39.35

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc09g075460.2.1	70	2	2	2	2	6.7	57.64
Solyc06g060760.2.1	70	2	2	1	1	6.4	52.42
Solyc08g079090.2.1	70	2	2	2	2	5.6	61.05
Solyc10g081720.1.1	70	1	1	1	1	3.8	70.44
Solyc01g097300.2.1	69	1	1	1	1	15.6	69.16
Solyc07g005560.2.1	69	1	1	1	1	11.9	68.73
Solyc11g051160.1.1	69	3	3	3	3	9.8	41
Solyc10g083720.1.1	69	2	2	2	2	6.3	48.73
Solyc08g075090.2.1	69	3	3	3	3	5.6	53.65
Solyc11g069400.1.1	69	2	1	2	1	5.2	58.46
Solyc03g111640.2.1	69	1	1	1	1	2.6	69.16
Solyc12g042900.1.1	68	2	2	2	2	14.5	59.2
Solyc05g051510.2.1	68	2	2	2	2	14.4	52.64
Solyc05g056490.2.1	68	2	2	2	2	12.9	46.99
Solyc02g094180.2.1	68	2	2	2	2	10.8	52.59
Solyc04g080590.2.1	68	2	2	2	2	9.8	56.26
Solyc08g014340.2.1	68	4	3	2	2	9.6	33.83
Solyc01g097270.2.1	68	2	2	1	1	8.5	48.11
Solyc02g080630.2.1	68	2	2	2	2	8.2	43.36
Solyc10g006400.2.1	68	2	2	2	2	6.6	51.28
Solyc09g083410.2.1	68	1	1	1	1	3.9	68.5
Solyc07g007210.2.1	68	1	1	1	1	2.3	67.98
Solyc03g083520.2.1	67	4	3	4	3	29.3	37.53
Solyc10g051390.1.1	67	2	2	2	2	22	50.31
Solyc03g097290.2.1	67	2	2	2	2	3.3	53.51
Solyc12g056230.1.1	66	2	2	2	2	13.5	44.53
Solyc01g109940.2.1	66	3	3	3	3	11.8	39.56
Solyc01g080510.2.1	66	2	1	2	1	10.6	60.12
Solyc08g065640.2.1	66	1	1	1	1	10.3	65.78
Solyc10g077030.1.1	66	1	1	1	1	6.8	66.21
Solyc01g109850.2.1	66	2	2	2	2	6.5	47.76
Solyc06g068090.2.1	66	3	1	3	1	6.2	43.64
Solyc06g083300.2.1	66	2	2	2	2	5.5	49.66
Solyc01g080220.2.1	65	2	2	2	2	19.3	58.66
Solyc01g105060.2.1	65	3	2	3	2	17.8	42.08
Solyc04g011400.2.1	65	2	2	2	2	13.1	50.22
Solyc10g005890.2.1	65	3	2	3	2	10.8	52.41
Solyc02g068740.2.1	65	2	2	1	1	10.4	52.64
Solyc10g049890.1.1	65	3	3	3	3	8.2	42.56
Solyc03g123610.2.1	65	3	3	3	3	7.1	36.49
Solyc06g083030.2.1	65	2	1	2	1	6.4	61
Solyc02g067840.2.1	65	1	1	1	1	5.3	64.74
Solyc12g042380.1.1	65	1	1	1	1	4.1	65.35
Solyc06g064940.2.1	65	1	1	1	1	3.3	65.36
Solyc05g053780.2.1	64	3	3	3	3	26.7	36.55
Solyc10g080970.1.1	64	4	3	4	3	21.7	36.66
Solyc09g011660.2.1	64	2	2	2	2	21.3	53.65
Solyc01g097870.2.1	64	2	2	2	2	19.5	48.2
Solyc01g097880.2.1	64	2	2	2	2	15.6	59.39
Solyc10g081180.1.1	64	2	1	2	1	13.2	65.74
Solyc09g090010.2.1	64	1	1	1	1	10.3	64.11
Solyc05g013030.1.1	64	3	2	3	2	9.5	51.06
Solyc03g082580.2.1	64	2	2	2	2	8.8	54.93
Solyc02g063090.2.1	64	2	2	2	2	8.2	52.36
Solyc10g050890.1.1	64	2	2	2	2	4.8	51.69
Solyc12g055830.1.1	63	3	3	3	3	26.8	40.39
Solyc06g073700.2.1	63	1	1	1	1	16.3	62.58

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc01g097460.2.1	63	2	2	2	2	13.3	45.22
Solyc03g005680.2.1	63	5	2	4	2	12.9	37.85
Solyc02g081170.2.1	63	2	2	2	2	11.3	44.74
Solyc06g073280.2.1	63	2	2	2	2	9.5	49.32
Solyc04g079200.2.1	63	2	2	2	2	9	50.38
Solyc05g007940.2.1	63	1	1	1	1	7.6	62.65
Solyc02g082800.2.1	63	2	2	2	2	5.4	40.28
Solyc02g086520.2.1	63	1	1	1	1	2.9	62.51
Solyc10g086510.1.1	62	2	2	2	2	26.9	50.34
Solyc04g072060.2.1	62	1	1	1	1	12.7	61.76
Solyc06g065520.2.1	62	3	3	3	3	7.9	40.12
Solyc02g068640.2.1	62	1	1	1	1	6.5	61.94
Solyc09g075010.2.1	62	2	1	1	1	5.8	56.2
Solyc09g013080.2.1	62	2	1	2	1	3.4	54.68
Solyc01g079540.2.1	61	2	2	2	2	17.6	48.1
Solyc01g104370.2.1	61	1	1	1	1	14.3	61.01
Solyc01g079680.2.1	61	3	3	3	3	9.3	37.09
Solyc06g053460.1.1	61	2	2	2	2	8.9	48.58
Solyc09g066490.2.1	61	1	1	1	1	7.1	61.09
Solyc06g068320.2.1	61	2	2	2	2	5.4	45.81
Solyc04g080960.2.1	61	1	1	1	1	5.2	60.51
Solyc07g008560.2.1	61	2	1	2	1	4.4	49.75
Solyc06g005360.2.1	60	2	2	2	2	23.4	50.88
Solyc02g021400.1.1	60	1	1	1	1	18.5	60.48
Solyc03g120090.1.1	60	2	1	2	1	11.1	51.95
Solyc11g017070.1.1	60	1	1	1	1	9.5	59.64
Solyc01g106080.2.1	60	2	2	2	2	8.6	50.01
Solyc01g106080.2.1	60	2	2	2	2	8.6	33.19
Solyc02g082830.1.1	60	2	2	2	2	7.4	41.11
Solyc05g006750.2.1	60	1	1	1	1	7.4	60.49
Solyc08g081570.2.1	60	1	1	1	1	7	59.6
Solyc08g041870.2.1	60	2	2	2	2	5.8	43.72
Solyc06g074820.2.1	60	1	1	1	1	5.6	60.15
Solyc01g094200.2.1	60	1	1	1	1	2.8	60.42
Solyc11g007200.1.1	59	2	1	2	1	26.5	56.17
Solyc10g081310.1.1	59	2	2	2	2	20.8	49.47
Solyc06g084310.2.1	59	1	1	1	1	17.5	59.16
Solyc06g005810.2.1	59	2	2	2	2	14.4	49.47
Solyc02g078360.2.1	59	2	1	2	1	13.9	48.08
Solyc09g064940.2.1	59	2	2	2	2	11	50.72
Solyc08g068310.2.1	59	2	2	2	2	7.3	42.53
Solyc07g055060.2.1	59	3	3	3	3	5.2	38.03
Solyc07g064880.2.1	58	2	2	2	2	43.4	52.75
Solyc06g008260.2.1	58	2	2	1	1	9	38.8
Solyc12g009590.1.1	58	2	1	2	1	8.8	44.44
Solyc03g044010.2.1	58	1	1	1	1	7.7	57.59
Solyc01g097010.2.1	58	2	2	2	2	7.2	48.6
Solyc10g081120.1.1	58	2	1	2	1	5	56.62
Solyc09g018450.2.1	58	1	1	1	1	1.8	57.69
Solyc04g026100.1.1	57	2	2	2	2	17	53.57
Solyc07g045350.2.1	57	2	2	2	2	13.9	42.22
Solyc01g080280.2.1	57	2	1	2	1	9.7	56.55
Solyc05g018810.2.1	57	3	1	3	1	9.3	36.33
Solyc04g054990.2.1	57	1	1	1	1	9.3	56.65
Solyc04g015620.2.1	57	2	1	2	1	7.8	46.56
Solyc02g082270.2.1	57	1	1	1	1	6.4	57.48
Solyc10g082030.1.1	57	1	1	1	1	6.4	57

Continued next page

Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc10g054280.1.1	57	2	1	1	1	6.1	44.25
Solyc03g118030.2.1	57	2	2	2	2	5.3	46.02
Solyc09g098150.2.1	57	3	3	2	2	5	36.19
Solyc03g118020.2.1	57	3	3	3	3	4.8	46.86
Solyc03g118800.2.1	57	1	1	1	1	4.7	57.26
Solyc08g082280.2.1	57	1	1	1	1	2.7	56.6
Solyc09g014790.2.1	57	1	1	1	1	2.6	56.62
Solyc09g010460.2.1	57	2	2	2	2	2.4	40.9
Solyc01g059880.2.1	56	3	2	3	2	8.4	34.77
Solyc02g085050.2.1	56	1	1	1	1	6.7	56.48
Solyc06g071050.2.1	56	1	1	1	1	5.5	55.67
Solyc02g069790.2.1	56	1	1	1	1	4.6	55.88
Solyc04g007910.2.1	56	1	1	1	1	3.6	56.35
Solyc05g015630.2.1	55	1	1	1	1	15.4	55.2
Solyc01g103370.2.1	55	1	1	1	1	8.4	55.2
Solyc07g066580.2.1	55	1	1	1	1	7	54.63
Solyc02g078540.2.1	55	2	2	1	1	5.2	36.87
Solyc03g120280.1.1	55	1	1	1	1	4.5	55.06
Solyc05g056400.2.1	55	2	2	2	2	3.6	44.66
Solyc05g012080.2.1	54	1	1	1	1	15	53.63
Solyc09g082520.2.1	54	2	2	2	2	12.7	46.41
Solyc04g008810.2.1	54	1	1	1	1	11.7	53.53
Solyc09g059040.2.1	54	2	2	2	2	11.6	48.03
Solyc02g079750.2.1	54	2	2	2	2	10.9	44.55
Solyc01g008550.2.1	54	2	2	2	2	9.7	41.56
Solyc06g076970.2.1	54	1	1	1	1	8.7	54.15
Solyc03g095190.2.1	54	1	1	1	1	8	53.84
Solyc02g078650.2.1	54	2	2	2	2	7	46.17
Solyc08g007420.2.1	54	1	1	1	1	5.8	54.5
Solyc05g056540.2.1	54	2	2	2	2	5.6	44.34
Solyc03g097790.2.1	54	1	1	1	1	5.3	54.38
Solyc02g086830.2.1	54	1	1	1	1	5.3	53.65
Solyc10g007600.2.1	54	2	2	1	1	4.6	39.89
Solyc07g041900.2.1	54	1	1	1	1	4.5	54.37
Solyc01g067750.2.1	54	1	1	1	1	3.5	53.91
Solyc05g056310.2.1	54	1	1	1	1	3.2	54.15
Solyc12g008720.1.1	53	1	1	1	1	20.8	53.17
Solyc02g068150.2.1	53	1	1	1	1	15.4	53.22
Solyc04g071610.2.1	53	3	3	1	1	12.7	39.52
Solyc01g111060.2.1	53	2	1	2	1	9.7	53.42
Solyc12g036790.1.1	53	1	1	1	1	9.1	52.87
Solyc02g067080.2.1	53	2	2	2	2	8.6	40
Solyc01g111710.2.1	53	2	2	2	2	7.4	36.84
Solyc01g102660.2.1	53	1	1	1	1	6.3	52.56
Solyc06g066830.2.1	53	1	1	1	1	6.1	53.02
Solyc03g113220.2.1	53	1	1	1	1	5.6	53.38
Solyc02g021560.2.1	53	1	1	1	1	5.3	52.91
Solyc02g083710.2.1	53	1	1	1	1	4.2	52.88
Solyc10g076510.1.1	53	1	1	1	1	2.7	52.54
Solyc05g052150.2.1	52	1	1	1	1	17.2	52.47
Solyc11g073250.1.1	52	1	1	1	1	15.5	52.46
Solyc03g082600.2.1	52	1	1	1	1	8.4	51.91
Solyc12g096300.1.1	52	2	2	1	1	6	52.04
Solyc08g006040.2.1	52	1	1	1	1	6	51.6
Solyc03g117940.2.1	52	1	1	1	1	5.2	52.41
Solyc02g090210.2.1	52	1	1	1	1	4.6	51.66
Solyc07g055210.2.1	52	1	1	1	1	4.2	51.72

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc01g099150.2.1	52	2	2	2	2	3.5	41.9
Solyc03g097910.2.1	52	1	1	1	1	3.5	51.62
Solyc03g119170.2.1	52	2	2	1	1	3.4	39.36
Solyc08g081320.2.1	52	1	1	1	1	2.1	52.03
Solyc01g049680.2.1	51	2	1	2	1	15.6	51.23
Solyc03g025800.2.1	51	1	1	1	1	14.8	50.7
Solyc09g005500.2.1	51	1	1	1	1	13.2	51.17
Solyc06g065970.1.1	51	1	1	1	1	12.7	50.87
Solyc03g097900.2.1	51	2	2	2	2	11.1	46.41
Solyc03g006680.2.1	51	2	2	2	2	10.6	49.24
Solyc09g090040.2.1	51	1	1	1	1	7	50.87
Solyc07g042570.2.1	51	1	1	1	1	6.8	50.95
Solyc11g011330.1.1	51	1	1	1	1	5.9	51.23
Solyc10g005060.2.1	51	1	1	1	1	4.7	50.9
Solyc12g011160.1.1	51	1	1	1	1	4.2	51.45
Solyc02g079220.2.1	51	1	1	1	1	3.8	51.34
Solyc03g121910.1.1	51	1	1	1	1	3.5	50.79
Solyc11g039830.1.1	51	1	1	1	1	1.9	50.93
Solyc09g010100.2.1	50	3	2	3	2	22.7	32.07
Solyc03g113580.1.1	50	3	2	3	2	18.4	37.81
Solyc01g079610.2.1	50	2	2	2	2	9.3	35.83
Solyc02g068130.2.1	50	1	1	1	1	8.8	49.63
Solyc03g019690.1.1	50	1	1	1	1	7.8	50.21
Solyc08g079830.2.1	50	1	1	1	1	6.4	50.12
Solyc03g113030.2.1	50	1	1	1	1	5.6	50.13
Solyc06g054250.2.1	50	1	1	1	1	5.3	49.86
Solyc10g086150.1.1	50	2	2	1	1	4.5	40.34
Solyc12g096220.1.1	50	3	3	3	3	4.3	35.45
Solyc04g008760.1.1	50	1	1	1	1	4.2	49.72
Solyc03g120720.2.1	50	1	1	1	1	3.2	49.57
Solyc01g008080.2.1	49	2	1	2	1	34.9	37.91
Solyc09g057650.2.1	49	2	2	2	2	13.1	42.98
Solyc07g047800.2.1	49	2	2	2	2	11.3	45.3
Solyc01g022750.2.1	49	1	1	1	1	9.8	49.33
Solyc06g067940.2.1	49	1	1	1	1	8.5	48.64
Solyc08g077900.2.1	49	1	1	1	1	5.1	49.45
Solyc07g062070.2.1	49	1	1	1	1	4.8	48.74
Solyc03g120880.2.1	49	1	1	1	1	3.8	48.59
Solyc01g109350.2.1	49	1	1	1	1	2.8	49.02
Solyc03g113800.2.1	49	1	1	1	1	2.6	48.85
Solyc02g085350.2.1	49	1	1	1	1	2.2	48.83
Solyc00g094530.1.1	48	1	1	1	1	14.7	47.53
Solyc07g008350.2.1	48	2	2	2	2	10.9	40.33
Solyc10g084700.1.1	48	1	1	1	1	7.9	47.62
Solyc02g092730.2.1	48	1	1	1	1	5.5	48.09
Solyc02g082250.2.1	48	1	1	1	1	4.4	48.12
Solyc08g029160.1.1	47	2	1	1	1	15	34.5
Solyc05g026050.2.1	47	2	2	2	2	11.5	36.49
Solyc09g010440.2.1	47	1	1	1	1	11.5	46.78
Solyc10g081440.1.1	47	2	1	2	1	10.8	41.94
Solyc02g088260.2.1	47	2	2	2	2	9.1	43.59
Solyc01g010750.2.1	47	2	2	2	2	8.3	39.64
Solyc11g039840.1.1	47	1	1	1	1	7.2	47.24
Solyc05g053140.2.1	47	2	1	2	1	6.5	40.16
Solyc01g007740.2.1	47	1	1	1	1	6	47.01
Solyc02g021420.2.1	47	2	2	2	2	3	36.58
Solyc07g042520.2.1	47	2	1	2	1	3	39.98

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc09g091000.2.1	46	2	2	2	2	22.6	38.19
Solyc02g071150.2.1	46	2	1	2	1	17.2	46.05
Solyc09g010400.2.1	46	1	1	1	1	15.9	46.07
Solyc06g035870.2.1	46	1	1	1	1	8.3	46.06
Solyc01g106320.2.1	46	1	1	1	1	6.9	45.97
Solyc06g082800.2.1	46	1	1	1	1	5.4	45.86
Solyc08g008530.1.1	46	1	1	1	1	5.1	46.29
Solyc01g088510.2.1	46	1	1	1	1	3.7	46.14
Solyc02g079410.2.1	45	2	1	2	1	13.7	34.33
Solyc01g066840.2.1	45	1	1	1	1	13.4	45.3
Solyc11g066150.1.1	45	2	2	2	2	13	37.13
Solyc02g085040.2.1	45	1	1	1	1	11.1	44.66
Solyc03g062890.2.1	45	1	1	1	1	8.3	44.71
Solyc02g070640.2.1	45	1	1	1	1	7.9	44.58
Solyc03g115760.2.1	45	1	1	1	1	5	44.92
Solyc02g081400.2.1	45	1	1	1	1	4.1	45.45
Solyc10g079500.1.1	45	1	1	1	1	3	45.25
Solyc11g040370.1.1	45	1	1	1	1	2.4	45.45
Solyc01g102700.2.1	45	1	1	1	1	1.9	45.3
Solyc01g091220.2.1	44	3	3	3	3	16.6	32.29
Solyc09g082650.2.1	44	2	2	2	2	11.6	31.96
Solyc02g031740.2.1	44	1	1	1	1	7.1	43.62
Solyc03g116170.2.1	44	1	1	1	1	6.7	44.17
Solyc11g073280.1.1	44	1	1	1	1	6.4	44.25
Solyc01g101240.2.1	44	2	2	2	2	5.3	32.83
Solyc03g123830.2.1	44	2	2	2	2	4.3	36.19
Solyc01g112280.2.1	44	1	1	1	1	2.9	44.37
Solyc08g014000.2.1	44	1	1	1	1	2.1	43.59
Solyc03g114170.2.1	43	1	1	1	1	40	42.88
Solyc05g043430.2.1	43	2	2	2	2	15.5	34.33
Solyc04g071620.2.1	43	2	2	2	2	12.5	34.2
Solyc07g062570.2.1	43	1	1	1	1	9.8	42.97
Solyc03g116590.2.1	43	1	1	1	1	9.7	43.44
Solyc02g078040.2.1	43	1	1	1	1	6.6	42.8
Solyc01g111660.2.1	43	1	1	1	1	6	42.66
Solyc01g105370.2.1	43	1	1	1	1	5.3	42.61
Solyc09g011920.2.1	43	1	1	1	1	5.2	43.32
Solyc03g121580.2.1	43	1	1	1	1	4.3	42.85
Solyc02g090090.2.1	43	1	1	1	1	3.4	43.13
Solyc01g096040.2.1	43	1	1	1	1	3.3	43.24
Solyc07g065680.2.1	43	1	1	1	1	3.1	43.27
Solyc02g092670.1.1	43	1	1	1	1	2.4	43.11
Solyc06g008170.2.1	42	1	1	1	1	12.9	42.14
Solyc05g053670.2.1	42	2	2	2	2	12.1	34.75
Solyc10g007070.2.1	42	2	2	2	2	11.3	37.16
Solyc08g066740.2.1	42	1	1	1	1	10.5	41.71
Solyc06g067960.2.1	42	1	1	1	1	10	42.18
Solyc03g007660.2.1	42	1	1	1	1	8.6	41.86
Solyc02g069100.2.1	42	1	1	1	1	8.2	41.54
Solyc02g068500.2.1	42	1	1	1	1	6.7	41.57
Solyc03g080050.2.1	42	2	2	2	2	6.6	30.48
Solyc07g032250.2.1	42	1	1	1	1	5.6	41.82
Solyc03g007670.2.1	42	1	1	1	1	5.4	41.56
Solyc07g064810.2.1	42	1	1	1	1	2.7	42.11
Solyc01g097990.2.1	41	1	1	1	1	23.1	41.29
Solyc06g073900.2.1	41	1	1	1	1	18.2	41.04
Solyc05g055280.1.1	41	1	1	1	1	15.3	40.59

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc11g012110.1.1	41	2	2	2	2	12.7	38.8
Solyc08g082700.2.1	41	1	1	1	1	6.4	41.44
Solyc01g108860.2.1	41	1	1	1	1	5.4	40.83
Solyc03g111840.2.1	41	1	1	1	1	5.1	41.41
Solyc12g099660.1.1	41	2	2	2	2	4.9	31.74
Solyc09g098280.2.1	41	1	1	1	1	4.1	41.2
Solyc04g081740.2.1	41	1	1	1	1	3.9	41.4
Solyc08g076990.2.1	41	1	1	1	1	3	40.72
Solyc04g072830.2.1	41	2	2	1	1	1	30.11
Solyc03g020010.1.1	40	3	2	3	2	24.9	33.32
Solyc03g020010.1.1	40	3	2	3	2	24.9	29.48
Solyc10g086090.1.1	40	1	1	1	1	14.7	40.41
Solyc08g016420.2.1	40	1	1	1	1	10	39.99
Solyc01g099670.2.1	40	1	1	1	1	8.2	39.85
Solyc03g083610.2.1	40	1	1	1	1	7.2	40.27
Solyc04g008280.2.1	40	1	1	1	1	7.2	40.17
Solyc09g011630.2.1	40	1	1	1	1	6.4	39.8
Solyc01g098550.2.1	40	1	1	1	1	6.1	40.47
Solyc03g007200.1.1	40	1	1	1	1	5.1	40.09
Solyc06g060420.2.1	40	1	1	1	1	4.7	40.37
Solyc12g011270.1.1	40	1	1	1	1	4.6	40.05
Solyc11g011920.1.1	40	2	1	2	1	4.4	39.62
Solyc11g011920.1.1	40	2	1	2	1	4.4	24.86
Solyc02g091970.2.1	40	1	1	1	1	4.2	39.64
Solyc11g006350.1.1	40	1	1	1	1	4	40.2
Solyc05g009030.2.1	40	1	1	1	1	3.7	40.13
Solyc05g018700.2.1	40	1	1	1	1	3.2	40.02
Solyc03g111310.2.1	40	1	1	1	1	3.1	39.5
Solyc03g005730.2.1	40	1	1	1	1	2.8	40.4
Solyc08g075390.2.1	40	1	1	1	1	2.4	39.51
Solyc03g098280.2.1	40	1	1	1	1	1.7	40.11
Solyc01g009100.2.1	39	1	1	1	1	14.3	38.66
Solyc01g098000.2.1	39	1	1	1	1	13.3	39.4
Solyc08g075690.2.1	39	1	1	1	1	13.3	38.9
Solyc09g065830.2.1	39	2	1	2	1	10.2	25.34
Solyc09g065830.2.1	39	2	1	2	1	10.2	32.32
Solyc03g098730.1.1	39	1	1	1	1	7.3	38.6
Solyc02g062540.2.1	39	1	1	1	1	7	38.64
Solyc04g055160.2.1	39	1	1	1	1	5.5	39.18
Solyc03g112650.2.1	39	1	1	1	1	5	38.63
Solyc02g014310.2.1	39	2	2	2	2	3.8	32.42
Solyc12g006980.1.1	39	1	1	1	1	3.6	38.91
Solyc06g075340.2.1	39	1	1	1	1	1.2	39.25
Solyc03g111230.2.1	38	1	1	1	1	14.1	38.21
Solyc03g043960.2.1	38	1	1	1	1	11.4	38.23
Solyc01g066590.2.1	38	1	1	1	1	10.1	38.5
Solyc12g099200.1.1	38	1	1	1	1	9.4	37.73
Solyc01g110390.2.1	38	1	1	1	1	9.2	38.02
Solyc02g088690.2.1	38	1	1	1	1	8.5	37.51
Solyc01g097350.2.1	38	1	1	1	1	8	38.46
Solyc08g082430.2.1	38	2	1	2	1	7.6	29.79
Solyc08g062820.2.1	38	1	1	1	1	7.5	37.58
Solyc09g075670.1.1	38	1	1	1	1	6	38.1
Solyc02g088460.2.1	38	1	1	1	1	5.4	38.29
Solyc01g007910.2.1	38	1	1	1	1	4.5	38.17
Solyc07g043310.2.1	38	2	2	1	1	2.7	31.88
Solyc08g082010.2.1	38	1	1	1	1	1.1	37.85

Continued next page

Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc11g068400.1.1	37	1	1	1	1	15.3	37.46
Solyc07g063680.2.1	37	2	1	2	1	14.9	29.18
Solyc10g008190.2.1	37	1	1	1	1	10.4	36.76
Solyc06g071720.1.1	37	1	1	1	1	10.1	37.48
Solyc09g075810.2.1	37	1	1	1	1	8.7	36.71
Solyc04g071900.2.1	37	3	2	2	1	7.7	30.84
Solyc07g009160.2.1	37	1	1	1	1	6.4	36.66
Solyc04g016360.2.1	37	1	1	1	1	6	37.28
Solyc03g121710.2.1	37	1	1	1	1	5.9	37.06
Solyc08g080940.2.1	37	1	1	1	1	5.4	36.78
Solyc03g121500.2.1	37	1	1	1	1	4.8	37.43
Solyc02g093310.2.1	37	1	1	1	1	4.4	37.05
Solyc03g120450.2.1	37	1	1	1	1	4.1	36.83
Solyc08g029000.2.1	37	2	1	2	1	3.7	30.64
Solyc01g111440.2.1	37	1	1	1	1	3.4	36.57
Solyc04g076090.2.1	37	1	1	1	1	3.2	36.93
Solyc03g117600.2.1	37	1	1	1	1	3	37.42
Solyc01g091190.2.1	37	1	1	1	1	2.7	37.48
Solyc01g008310.2.1	37	1	1	1	1	2.4	36.68
Solyc11g040390.1.1	37	1	1	1	1	2.2	37
Solyc07g053650.2.1	37	1	1	1	1	1.8	37.37
Solyc02g094200.2.1	36	1	1	1	1	23.6	35.88
Solyc03g113730.2.1	36	1	1	1	1	14.4	36.23
Solyc04g010240.2.1	36	1	1	1	1	10.6	35.89
Solyc12g015690.1.1	36	1	1	1	1	10.1	36.22
Solyc01g066860.2.1	36	1	1	1	1	9.7	36.46
Solyc09g005640.2.1	36	1	1	1	1	8.9	36.37
Solyc10g076350.1.1	36	1	1	1	1	8.8	35.89
Solyc12g013900.1.1	36	2	2	2	2	8.2	31.39
Solyc01g079880.2.1	36	1	1	1	1	5.5	35.61
Solyc01g094970.2.1	36	1	1	1	1	3.9	36.27
Solyc12g096190.1.1	36	1	1	1	1	3.9	35.62
Solyc04g079440.2.1	36	1	1	1	1	3.6	35.55
Solyc03g121700.2.1	36	1	1	1	1	3.5	36.36
Solyc06g083730.2.1	36	1	1	1	1	3.5	36.16
Solyc07g047790.2.1	36	1	1	1	1	3.3	35.93
Solyc04g009200.2.1	36	1	1	1	1	2.9	35.8
Solyc03g082940.2.1	36	1	1	1	1	2.9	35.72
Solyc09g007640.2.1	36	1	1	1	1	2.8	36.29
Solyc03g117280.2.1	36	1	1	1	1	2.6	35.7
Solyc01g103480.2.1	36	1	1	1	1	2.3	36.16
Solyc11g068510.1.1	35	1	1	1	1	26.3	35.08
Solyc01g081270.2.1	35	1	1	1	1	6.3	35.18
Solyc11g068540.1.1	35	1	1	1	1	6	34.98
Solyc08g006730.1.1	35	1	1	1	1	5.8	35.46
Solyc03g117810.2.1	35	1	1	1	1	5.3	35.18
Solyc01g073640.2.1	35	1	1	1	1	5	35.42
Solyc02g071330.2.1	35	1	1	1	1	5	35.33
Solyc11g005620.1.1	35	1	1	1	1	4.9	34.8
Solyc04g072560.2.1	35	1	1	1	1	4.7	34.95
Solyc09g082990.2.1	35	1	1	1	1	4.3	35.08
Solyc05g010300.2.1	35	1	1	1	1	4.1	35.08
Solyc01g105810.2.1	35	1	1	1	1	3.1	35.14
Solyc08g065490.2.1	35	1	1	1	1	2.9	34.62
Solyc11g011020.1.1	35	1	1	1	1	2.8	34.88
Solyc01g100390.2.1	35	1	1	1	1	2.1	35.01
Solyc03g113490.2.1	35	1	1	1	1	2	35.22

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc02g068300.2.1	35	1	1	1	1	1.7	34.98
Solyc02g081270.2.1	35	1	1	1	1	1.6	35.14
Solyc02g094440.2.1	34	1	1	1	1	12.5	34.17
Solyc09g005720.2.1	34	1	1	1	1	8.5	34.05
Solyc06g069040.2.1	34	1	1	1	1	6.2	33.7
Solyc06g072220.1.1	34	1	1	1	1	5.7	34.16
Solyc01g096450.2.1	34	2	1	2	1	5.4	26.81
Solyc01g096450.2.1	34	2	1	2	1	5.4	33.58
Solyc02g081140.2.1	34	1	1	1	1	5.3	34.15
Solyc01g105410.2.1	34	1	1	1	1	4.7	34.49
Solyc07g062480.1.1	34	1	1	1	1	4.7	34.04
Solyc12g005200.1.1	34	1	1	1	1	4.2	33.64
Solyc07g017900.2.1	34	1	1	1	1	4.1	33.68
Solyc02g087240.2.1	34	1	1	1	1	3.3	34.21
Solyc04g063280.2.1	34	1	1	1	1	3	34.09
Solyc09g083080.2.1	34	1	1	1	1	2.9	34.46
Solyc08g041890.2.1	34	1	1	1	1	2.3	34.02
Solyc01g104850.2.1	34	1	1	1	1	2.1	34.35
Solyc07g008240.2.1	33	2	1	2	1	15.8	31.85
Solyc11g066130.1.1	33	3	1	3	1	12.7	33.05
Solyc06g075810.2.1	33	1	1	1	1	11.2	33.46
Solyc03g112770.2.1	33	1	1	1	1	10.4	32.59
Solyc03g121330.2.1	33	1	1	1	1	9.1	33.29
Solyc07g026650.2.1	33	1	1	1	1	8	33.2
Solyc09g065270.2.1	33	1	1	1	1	7.5	33.09
Solyc12g096650.1.1	33	1	1	1	1	7	32.88
Solyc09g011570.2.1	33	1	1	1	1	6.7	32.68
Solyc02g032040.1.1	33	1	1	1	1	6.3	33.27
Solyc04g014820.2.1	33	1	1	1	1	6	32.99
Solyc01g058390.2.1	33	1	1	1	1	5.6	33.02
Solyc01g095000.2.1	33	1	1	1	1	5.3	32.53
Solyc02g079210.2.1	33	1	1	1	1	4.8	33.13
Solyc01g087540.2.1	33	1	1	1	1	4.4	33.2
Solyc07g006830.2.1	33	1	1	1	1	2.4	32.71
Solyc04g054470.2.1	33	1	1	1	1	2.3	33.24
Solyc08g079970.1.1	33	1	1	1	1	0.8	32.86
Solyc12g008590.1.1	32	1	1	1	1	36.7	31.8
Solyc04g007760.2.1	32	2	1	2	1	14.4	32.46
Solyc05g052140.2.1	32	1	1	1	1	13.7	32.22
Solyc10g047650.1.1	32	1	1	1	1	10.6	32.29
Solyc03g031600.2.1	32	1	1	1	1	9.2	32.24
Solyc06g060850.2.1	32	1	1	1	1	7.8	32.03
Solyc01g111230.2.1	32	1	1	1	1	6.6	32.06
Solyc04g049710.2.1	32	1	1	1	1	6.4	31.7
Solyc06g069890.2.1	32	1	1	1	1	4.2	31.61
Solyc08g076620.1.1	32	1	1	1	1	4.1	31.97
Solyc10g074590.1.1	32	1	1	1	1	3.8	32.34
Solyc02g093830.2.1	32	1	1	1	1	2.3	31.91
Solyc03g111180.2.1	32	1	1	1	1	2.1	32.45
Solyc01g104680.2.1	31	2	1	2	1	12.2	31.15
Solyc01g067730.2.1	31	1	1	1	1	11	30.57
Solyc01g009990.2.1	31	2	2	2	2	8.9	30.35
Solyc09g010930.2.1	31	1	1	1	1	6.7	31.4
Solyc05g005490.2.1	31	1	1	1	1	5.2	31.32
Solyc07g048090.1.1	31	1	1	1	1	5.2	30.81
Solyc08g067370.1.1	31	1	1	1	1	5.1	31.11
Solyc06g069020.2.1	31	1	1	1	1	4.7	31.41

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Supplemental Table 2. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc04g063290.2.1	31	1	1	1	1	4.6	30.61
Solyc07g064510.2.1	31	1	1	1	1	3.2	30.85
Solyc04g080260.2.1	31	1	1	1	1	3.2	30.53
Solyc09g064370.2.1	31	1	1	1	1	3.1	30.6
Solyc04g076790.2.1	31	1	1	1	1	2.9	31.37
Solyc06g051010.1.1	31	1	1	1	1	2.9	31.21
Solyc04g056590.2.1	31	1	1	1	1	2.7	30.58
Solyc07g063100.2.1	31	1	1	1	1	2.1	30.51
Solyc05g015920.2.1	31	1	1	1	1	1.2	31.2
Solyc06g074640.1.1	31	1	1	1	1	1	30.52
Solyc03g093360.2.1	30	2	1	2	1	9.5	25.26
Solyc07g014730.2.1	30	1	1	1	1	9	29.81
Solyc01g007860.2.1	30	1	1	1	1	8.2	30.46
Solyc02g062240.2.1	30	1	1	1	1	7.6	29.68
Solyc03g007520.2.1	30	1	1	1	1	7.5	30.49
Solyc11g012320.1.1	30	1	1	1	1	6.5	30.04
Solyc06g035920.2.1	30	1	1	1	1	5.9	30.5
Solyc01g090190.2.1	30	1	1	1	1	5.6	30.28
Solyc01g073970.2.1	30	1	1	1	1	5.1	30.14
Solyc08g068690.1.1	30	1	1	1	1	5	30.31
Solyc03g097110.2.1	30	1	1	1	1	4	30.4
Solyc06g066060.2.1	30	1	1	1	1	2.9	30.43
Solyc12g007030.1.1	30	1	1	1	1	2.6	29.53
Solyc02g071560.2.1	30	1	1	1	1	1.7	30.02
Solyc12g039120.1.1	29	2	1	2	1	11.9	29.38
Solyc11g066950.1.1	29	1	1	1	1	11.4	29.09
Solyc02g077880.2.1	29	1	1	1	1	10.6	29.32
Solyc01g108660.2.1	29	2	2	2	2	8.9	31.66
Solyc07g063890.2.1	29	1	1	1	1	4.6	29.26
Solyc01g010540.2.1	29	2	1	1	1	4.6	28.05
Solyc01g090910.2.1	29	1	1	1	1	3.9	29.3
Solyc06g071000.2.1	29	1	1	1	1	2.5	29.03
Solyc02g092580.2.1	28	1	1	1	1	3.6	28.17
Solyc01g102560.2.1	28	1	1	1	1	3.5	28.16
Solyc06g007620.2.1	27	1	1	1	1	8.4	27.15
Solyc04g007750.2.1	27	1	1	1	1	6.1	27.28
Solyc08g007220.2.1	27	1	1	1	1	5.5	27.24
Solyc07g009140.2.1	27	1	1	1	1	3.4	27.31
Solyc05g052690.2.1	27	1	1	1	1	3.2	27.35
Solyc05g053960.2.1	26	2	2	1	1	5.8	24.54
Solyc01g094540.2.1	26	1	1	1	1	4.6	26.41
Solyc03g025340.1.1	23	1	1	1	1	10	23.07
Solyc08g078010.2.1	19	2	1	1	1	8.9	19.44

[z]Information used for the identification of proteins in iTRAQ analysis of tomato root proteomes.
[y]Protein accession number in the ITAG Protein database (Release 2.3 on 26 Apr. 2011; Sol Genomics Network, Boyce Thompson Institute, Ithaca, NY).
[x]Sum of the individual ion scores.
[w]Total number of peptide-spectral matches to a particular protein below the e-value cutoff.
[v]Total number of unique peptide spectral matches to a particular protein below the e-value cutoff.
[u]Total number of peptide spectral matches to a particular protein with a protein score above the identity threshold.
[t]Total number of unique peptide-spectral matches to a particular protein with a protein score above the identity threshold.
[s]Percentage of the total protein sequence represented by the identified peptides.
[r]Highest highest ion score for each identified proteins.

Supplemental Table 3. Protein identification information of cherry tomato accession LA4133 using the isobaric tags for relative and absolute quantitation (iTRAQ) analysis.[z]

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc07g052510.2.1	1686	44	41	13	12	44.2	109.83
Solyc05g008460.2.1	1428	59	52	19	18	52.1	90.58
Solyc04g007550.2.1	1398	61	53	19	18	53	90.58
Solyc09g090140.2.1	945	30	28	9	9	44.6	110.95
Solyc09g009020.2.1	927	34	27	15	13	60.1	95.09
Solyc07g062650.2.1	729	29	26	15	14	76	82.46
Solyc08g080630.2.1	672	26	25	3	3	28.6	80.89
Solyc10g081510.1.1	653	27	24	16	15	32	106.91
Solyc04g012120.2.1	605	23	21	6	6	35.7	87.1
Solyc03g006700.2.1	582	21	17	8	7	32.6	98.55
Solyc01g111760.2.1	571	24	21	12	12	40.9	65.95
Solyc10g085550.1.1	561	21	18	11	10	42.8	95.09
Solyc06g009020.2.1	545	24	22	6	6	42.7	73.41
Solyc10g055670.1.1	532	22	19	12	12	40.9	71.32
Solyc07g066600.2.1	529	26	21	10	9	40.9	74.52
Solyc01g106610.2.1	488	9	8	2	2	30.7	118.17
Solyc11g066390.1.1	442	11	9	4	3	38.7	98.68
Solyc00g071180.2.1	424	14	13	9	8	46.2	86.48
Solyc03g082920.2.1	407	16	16	10	10	24.3	80.37
Solyc03g078400.2.1	385	19	17	8	8	35.3	70.69
Solyc11g010200.1.1	377	14	12	4	4	20.8	79.45
Solyc01g059980.2.1	377	16	15	6	5	27.2	61.92
Solyc09g090980.2.1	377	22	19	9	8	72.5	74.4
Solyc11g067100.1.1	376	12	11	5	5	50.4	93.55
Solyc07g051850.2.1	375	9	9	7	7	23.6	93.61
Solyc08g082820.2.1	372	15	15	9	9	22.4	73.78
Solyc04g074510.2.1	349	12	11	4	4	22.8	75.94
Solyc05g014470.2.1	346	18	15	10	10	46.4	80.82
Solyc09g073000.2.1	337	11	11	6	6	21.8	87.59
Solyc01g105070.2.1	330	6	6	5	5	26.8	103.56
Solyc09g009260.2.1	325	17	13	8	7	33.5	74.66
Solyc12g057110.2.1	317	12	11	5	5	31.1	75.94
Solyc09g092380.2.1	317	16	15	9	9	30.1	66.65
Solyc03g115990.1.1	316	14	14	10	10	33	76.28
Solyc09g082060.2.1	314	9	9	5	5	31.4	72.21
Solyc02g067460.2.1	311	10	10	6	6	30.4	76.72
Solyc12g088670.1.1	310	12	11	7	6	21.2	65.51
Solyc06g073190.2.1	309	11	10	8	8	36	83.73
Solyc11g066060.1.1	309	21	18	12	11	25.9	56.15
Solyc01g100380.2.1	308	13	10	7	6	26.6	71.66
Solyc10g055800.1.1	303	11	11	5	5	29.5	107.25
Solyc06g005160.2.1	299	10	9	6	5	50	72.97
Solyc05g046020.2.1	297	14	12	8	6	30.9	106.58
Solyc04g077020.2.1	297	13	11	10	8	31.8	100.24
Solyc08g062920.2.1	294	12	10	10	8	22.6	117.68
Solyc06g052050.2.1	293	13	13	7	7	18.6	63.91
Solyc10g083570.1.1	292	15	11	7	6	26	74.66
Solyc09g008280.1.1	292	12	11	7	6	28.5	68.95
Solyc11g010470.1.1	281	11	9	5	4	30.5	88.2
Solyc03g111200.2.1	280	9	8	5	4	23.4	91.6
Solyc08g074680.2.1	278	9	8	7	6	6.2	83.97
Solyc12g055800.1.1	277	13	11	11	9	29.7	92.85
Solyc08g080670.1.1	272	14	12	4	4	22.8	58.25
Solyc04g049330.2.1	271	12	11	4	4	46.8	104.59
Solyc00g072400.2.1	270	12	8	7	6	39.5	87.16
Solyc05g053300.2.1	269	7	7	6	6	22.2	111.24

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc05g053470.2.1	267	16	11	12	11	29.5	72.24
Solyc01g102310.2.1	266	10	10	10	10	23.3	70.77
Solyc02g070510.2.1	263	8	8	6	6	39.2	92.74
Solyc00g006800.2.1	263	8	7	7	6	23.6	116.97
Solyc03g098700.1.1	258	7	7	5	5	30.1	71.47
Solyc08g062660.2.1	257	7	6	5	4	35.3	76.89
Solyc12g010040.1.1	256	9	9	8	8	24.4	88.24
Solyc06g060290.2.1	252	13	9	9	6	31.1	50.25
Solyc02g084790.2.1	252	12	12	9	9	40.1	78.78
Solyc12g096700.1.1	251	10	9	5	5	40.2	73.63
Solyc10g078620.1.1	250	12	10	4	4	17.7	59.74
Solyc04g071890.2.1	250	10	7	8	7	36.2	105.44
Solyc07g053260.2.1	249	10	9	5	5	28.7	75.89
Solyc10g076220.1.1	249	7	7	6	6	33.5	83.87
Solyc06g073310.2.1	247	10	9	5	5	40.2	73.63
Solyc07g066610.2.1	246	10	9	5	5	16.8	73.14
Solyc07g045440.1.1	245	8	7	5	5	22.7	61.62
Solyc11g039980.1.1	245	7	6	5	5	44.2	85.9
Solyc11g072190.1.1	243	11	9	8	6	58.6	96.17
Solyc02g084800.2.1	240	10	10	8	8	42.1	77.99
Solyc02g063070.2.1	236	9	8	4	4	25	103.48
Solyc06g071920.2.1	235	7	7	5	5	22.8	79.76
Solyc02g084780.2.1	235	11	11	9	9	35.8	77.99
Solyc05g012480.2.1	233	6	6	3	3	8.4	76.1
Solyc09g009390.2.1	230	12	10	10	8	34.4	63.99
Solyc07g006650.2.1	229	5	5	3	3	13.6	76.42
Solyc01g101060.2.1	229	9	9	4	4	17.3	78.32
Solyc04g055170.2.1	227	7	7	6	6	22.8	83.48
Solyc02g082000.2.1	225	9	8	2	2	23.8	55.51
Solyc08g006860.2.1	225	10	8	6	5	21.9	81.56
Solyc01g067740.2.1	224	8	8	4	4	38.8	71.59
Solyc08g081530.2.1	224	7	7	6	6	19.5	73.86
Solyc02g038690.1.1	218	11	9	2	1	17.9	58.5
Solyc12g014180.1.1	218	7	7	6	6	28.1	82.7
Solyc12g005860.1.1	215	8	8	7	7	11.6	77.78
Solyc07g065840.2.1	215	11	9	9	7	19.2	71.92
Solyc12g099100.1.1	211	6	6	5	5	18.1	92.92
Solyc10g008010.2.1	211	7	7	5	5	42.6	67.87
Solyc01g090750.2.1	208	4	4	3	3	10.3	105.64
Solyc02g080210.2.1	205	12	9	6	5	15.4	46.63
Solyc01g109660.2.1	204	9	9	8	8	73.1	60.76
Solyc10g055810.1.1	203	7	5	5	4	32.9	90.81
Solyc04g049450.2.1	202	9	9	7	7	17.9	71.23
Solyc01g111170.2.1	200	10	8	4	3	39.8	63.44
Solyc00g009020.2.1	199	12	8	8	6	29.8	57.23
Solyc12g094620.1.1	197	9	6	6	5	21.5	46.45
Solyc11g011960.1.1	196	6	5	6	5	19.5	111.66
Solyc03g115110.2.1	195	7	6	6	5	32.1	63.96
Solyc07g043320.2.1	195	10	9	10	9	10.5	55.43
Solyc05g056020.2.1	194	4	4	2	2	34.2	81.78
Solyc11g005640.1.1	194	10	9	2	2	14.4	45.15
Solyc10g083650.1.1	193	4	4	3	3	25.9	93.06
Solyc01g111650.2.1	192	5	5	2	2	21.8	79.09
Solyc01g087120.2.1	192	8	6	4	3	20.5	63.53
Solyc07g052530.2.1	192	6	6	4	4	19.1	108.45
Solyc10g007290.2.1	192	10	7	8	6	15	73.42
Solyc01g100320.2.1	190	8	6	6	4	24.2	53.82

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc06g068860.2.1	189	6	6	6	6	9.9	84.19
Solyc12g095960.1.1	188	7	5	4	3	23.3	106.45
Solyc01g106260.2.1	188	5	5	4	4	10.7	97.26
Solyc08g015690.2.1	188	9	9	8	8	34.1	62.94
Solyc12g015880.1.1	187	9	7	8	6	16.5	69.15
Solyc04g081570.2.1	186	8	5	7	4	13.2	59.95
Solyc07g044840.2.1	186	9	7	6	5	18.2	62.34
Solyc01g099760.2.1	186	10	9	6	6	24.8	61.17
Solyc04g011510.2.1	186	10	9	7	6	39.4	60.88
Solyc03g034180.2.1	184	7	6	3	3	17.8	103.48
Solyc07g042550.2.1	184	11	9	11	9	21.9	64.67
Solyc05g054580.2.1	183	7	7	4	4	19.9	68.65
Solyc08g080680.2.1	182	5	5	2	2	25.5	66.18
Solyc04g077970.2.1	181	4	3	2	1	15.8	93.08
Solyc11g073250.1.1	181	3	3	1	1	15.5	91.38
Solyc04g073990.2.1	181	10	9	8	8	31.5	49.56
Solyc07g043420.2.1	180	7	6	5	5	24	65.75
Solyc10g083970.1.1	179	7	7	4	4	17.2	68.95
Solyc12g042650.1.1	179	6	5	4	4	44.7	93.58
Solyc04g076060.2.1	179	10	8	5	4	30.2	88.2
Solyc06g082630.2.1	177	6	4	4	3	16.2	93.52
Solyc01g111120.2.1	175	7	6	4	3	16.9	58.39
Solyc01g080010.2.1	175	8	6	5	4	17.8	59.8
Solyc10g085020.1.1	175	11	8	8	6	24.2	62.86
Solyc10g080940.1.1	175	11	8	8	6	24.3	59.61
Solyc04g080850.2.1	174	9	6	4	2	35.8	56.28
Solyc12g008630.1.1	174	3	3	3	3	12.9	88.43
Solyc04g081490.2.1	174	11	7	8	5	23.7	62.86
Solyc01g103450.2.1	173	5	5	4	4	11.7	75.46
Solyc07g065120.2.1	173	6	5	5	5	11.8	57.9
Solyc01g102380.2.1	172	7	6	2	2	12.5	54.48
Solyc10g086100.1.1	171	6	5	2	2	33	71.66
Solyc06g035970.2.1	170	11	8	8	6	24.6	59.61
Solyc10g078550.1.1	169	9	9	6	6	25.8	56.17
Solyc03g114500.2.1	167	5	4	4	4	14.3	83.47
Solyc01g107910.2.1	166	4	4	4	4	31.5	98.54
Solyc11g069430.1.1	165	5	5	3	3	16.4	65.88
Solyc10g006650.2.1	164	3	3	2	2	17.2	93.07
Solyc01g009020.2.1	163	3	3	1	1	17.7	80.36
Solyc06g005940.2.1	162	9	9	6	6	17.6	43.8
Solyc08g079930.1.1	161	5	5	4	4	9.7	73.86
Solyc09g007520.2.1	161	4	4	4	4	24.4	83.12
Solyc09g090990.2.1	161	12	6	6	5	47.5	69.47
Solyc10g083720.1.1	159	2	2	2	2	7.6	127.56
Solyc04g082200.2.1	159	8	5	6	4	29.6	85.15
Solyc07g017780.2.1	159	8	6	8	6	13.8	66.51
Solyc04g014510.2.1	159	11	9	6	6	36.8	43.76
Solyc07g065110.1.1	157	7	7	2	2	27.9	65.23
Solyc01g008950.2.1	157	5	5	3	3	33.6	72.99
Solyc10g055820.1.1	155	5	5	4	4	25.8	71.39
Solyc05g008600.2.1	155	9	6	5	4	23.5	51.34
Solyc05g052280.2.1	155	6	6	5	5	28.6	61.13
Solyc11g051160.1.1	153	4	3	4	3	12.7	67.18
Solyc04g074230.2.1	151	9	7	3	3	18.4	73.08
Solyc03g058920.2.1	151	7	6	5	5	17.5	55.86
Solyc05g055230.1.1	150	8	6	2	2	26.4	54.09
Solyc06g075180.1.1	149	7	6	4	4	35.5	67.1

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc06g005150.2.1	147	6	5	4	3	34	52.51
Solyc09g090430.2.1	146	2	2	2	2	26.3	99.1
Solyc01g056940.2.1	146	7	7	2	2	16	45.15
Solyc10g078690.1.1	146	3	3	2	2	22.6	99.16
Solyc06g074980.2.1	146	4	3	4	3	7	90.95
Solyc03g111010.2.1	146	7	6	5	5	21.4	47.02
Solyc10g076240.1.1	145	6	6	5	5	26.2	55.85
Solyc02g068450.2.1	144	3	3	3	3	43.9	93.45
Solyc01g089970.2.1	144	4	4	4	4	26.4	72.97
Solyc02g077420.2.1	144	6	6	6	6	23.9	65.76
Solyc11g069400.1.1	143	3	3	2	2	6.7	64.62
Solyc11g062130.1.1	143	5	4	3	3	11.1	78.2
Solyc12g014210.1.1	142	2	2	2	2	11.3	99.65
Solyc04g071900.2.1	142	5	4	4	4	16.2	65.42
Solyc04g054980.2.1	141	4	3	3	2	25	72.63
Solyc10g050160.1.1	141	5	5	3	3	19.2	98.54
Solyc03g096540.2.1	140	3	3	3	3	27.7	81.69
Solyc08g080650.1.1	140	9	9	5	5	33.7	52.7
Solyc10g086190.1.1	139	5	4	3	3	14.5	63.98
Solyc01g103800.2.1	139	5	5	4	4	44.1	64.49
Solyc06g059740.2.1	137	4	4	4	4	19.3	77.57
Solyc02g081700.1.1	137	5	5	4	4	24.6	95.48
Solyc07g047740.2.1	136	7	7	3	3	13.9	67.83
Solyc06g069090.2.1	135	5	3	4	2	35.1	97.23
Solyc03g112070.2.1	135	4	4	3	3	9.2	66.53
Solyc10g005960.1.1	135	3	3	3	3	13.3	81.1
Solyc12g010860.1.1	134	5	4	4	4	24.9	69.56
Solyc07g055080.2.1	134	5	5	4	4	29.8	65.01
Solyc02g086880.2.1	133	2	2	2	2	9.4	126.1
Solyc11g069000.1.1	133	3	3	3	3	11.8	72.07
Solyc01g099770.2.1	133	6	6	4	4	29.2	45.07
Solyc07g041310.2.1	132	4	4	4	4	18.8	82.71
Solyc10g008140.2.1	131	3	2	3	2	20.8	85.49
Solyc06g083620.2.1	131	4	3	4	3	16.2	70.73
Solyc06g071100.2.1	131	6	4	6	4	10	74.52
Solyc08g079170.2.1	131	5	5	5	5	11.4	63.98
Solyc03g096460.2.1	130	6	5	2	2	14.7	57.22
Solyc01g106620.2.1	129	5	3	2	2	21.2	79.91
Solyc09g007940.2.1	129	5	4	3	3	18.5	63.98
Solyc07g020860.2.1	128	8	6	4	3	36.4	44.12
Solyc06g005060.2.1	128	7	6	4	4	12.5	50.38
Solyc04g011500.2.1	128	8	6	5	5	22.5	50.82
Solyc08g081190.2.1	127	5	5	2	2	11.9	52.07
Solyc12g009140.1.1	127	3	3	2	2	13.4	62.67
Solyc08g061850.2.1	127	4	3	4	3	16.4	82.71
Solyc01g106210.2.1	126	7	7	4	4	8.8	43.09
Solyc07g008720.2.1	125	5	5	4	4	41.4	68.68
Solyc11g069790.1.1	124	6	4	6	4	14.6	74.97
Solyc08g080660.1.1	124	9	7	4	4	22.8	46.47
Solyc01g109940.2.1	124	6	5	4	4	16.1	55.04
Solyc04g079180.2.1	123	5	4	3	3	19.6	65.4
Solyc02g023970.2.1	123	3	3	3	3	14	64.33
Solyc03g113580.1.1	123	5	4	5	4	30	59.06
Solyc06g072580.2.1	123	5	5	4	4	14.7	47.96
Solyc10g080500.1.1	123	8	6	5	5	22.5	50.82
Solyc10g081030.1.1	122	7	6	3	3	23.1	62.71
Solyc11g011380.1.1	122	9	9	6	6	37.3	64.6

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc09g091840.2.1	121	5	4	4	4	13.7	48.18
Solyc05g054480.2.1	121	8	6	5	5	22.5	50.82
Solyc01g011000.2.1	121	7	7	6	6	50.9	76.93
Solyc07g052350.2.1	120	6	6	5	5	8.9	54.95
Solyc01g111300.2.1	119	4	3	3	2	28.3	55.69
Solyc03g113400.2.1	119	5	3	5	3	8.5	74.52
Solyc02g062510.2.1	118	5	5	4	4	16	80.24
Solyc09g091180.2.1	118	12	8	9	8	21.9	46.7
Solyc06g067960.2.1	116	2	2	1	1	10	84.37
Solyc01g079980.2.1	116	4	3	2	2	9.8	60.68
Solyc02g093230.2.1	116	2	2	2	2	14.9	98.54
Solyc01g008000.2.1	115	7	4	5	4	30.6	56.64
Solyc05g053810.2.1	114	4	4	3	3	10.8	51.93
Solyc05g018570.2.1	114	5	4	3	3	11.5	53.61
Solyc01g091530.2.1	114	4	4	4	4	15.5	69.03
Solyc04g011390.1.1	113	6	5	4	3	40.8	74.17
Solyc03g096550.2.1	113	5	5	3	3	23.5	56.35
Solyc05g054760.2.1	113	5	5	5	5	36.7	53.62
Solyc12g043110.1.1	113	5	5	5	5	8.9	62.52
Solyc03g097270.2.1	112	4	4	4	4	25.5	56.09
Solyc01g044360.2.1	111	1	1	1	1	2.1	111.33
Solyc08g075090.2.1	111	4	4	2	2	4.3	55.55
Solyc08g080640.1.1	111	6	6	4	4	25.9	52.7
Solyc03g006580.2.1	110	1	1	1	1	9.9	109.87
Solyc09g005500.2.1	110	3	2	2	1	27.8	64.84
Solyc06g082120.2.1	110	3	3	2	2	16.6	57.74
Solyc01g073740.2.1	110	4	4	3	3	9.3	67.51
Solyc07g045240.2.1	109	2	2	2	2	9.6	91.08
Solyc04g080960.2.1	109	3	3	3	3	16	64.08
Solyc11g007690.1.1	108	1	1	1	1	5.1	107.65
Solyc05g050120.2.1	108	4	2	4	2	12.8	66.73
Solyc01g097460.2.1	108	2	2	2	2	14.3	72.75
Solyc08g067020.2.1	108	7	5	3	2	33.3	44.9
Solyc08g062800.2.1	108	5	4	4	3	15.3	58.86
Solyc03g025800.2.1	107	2	2	1	1	14.8	82.36
Solyc10g084400.1.1	107	4	4	2	2	13.6	32.85
Solyc10g084400.1.1	107	4	4	2	2	13.6	76.11
Solyc01g005560.2.1	107	4	3	4	3	13	62.88
Solyc02g071560.2.1	106	4	3	3	2	6	52.21
Solyc01g111450.2.1	106	5	3	4	3	21.7	44.78
Solyc08g079260.2.1	106	7	6	5	5	14.2	37.5
Solyc10g005510.2.1	105	4	4	4	4	16.9	50.92
Solyc02g088700.2.1	104	2	2	2	2	5.8	82.19
Solyc08g006850.2.1	104	4	4	3	3	10.6	52.7
Solyc01g079540.2.1	104	3	3	3	3	17.6	77.29
Solyc04g080540.2.1	103	1	1	1	1	14.2	102.89
Solyc02g078650.2.1	103	2	2	2	2	5.9	67.04
Solyc03g119360.2.1	103	5	3	4	2	35.1	73.65
Solyc07g053540.1.1	103	7	6	2	2	10.5	43.99
Solyc03g080180.2.1	103	3	3	3	3	13.7	63.41
Solyc06g075010.2.1	103	3	3	3	3	6.5	85.01
Solyc05g006520.2.1	103	4	4	4	4	14.3	47.58
Solyc06g074430.2.1	102	5	4	3	2	34.2	52.94
Solyc06g064940.2.1	102	2	2	2	2	5.9	66.55
Solyc12g056960.1.1	102	2	2	2	2	6.8	80.01
Solyc10g007600.2.1	101	2	2	1	1	4.6	68.53
Solyc04g080570.2.1	101	2	1	2	1	16.5	100.75

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc06g050770.2.1	101	4	4	3	3	15.2	56.28
Solyc06g005260.2.1	101	4	4	4	4	46.3	62.07
Solyc12g009400.1.1	100	1	1	1	1	4.5	100.41
Solyc11g070050.1.1	100	2	2	2	2	22.3	64.24
Solyc08g075830.2.1	99	6	5	3	2	11.2	57.82
Solyc12g096300.1.1	99	2	2	2	2	12.9	65
Solyc12g088760.1.1	98	3	3	3	3	7.1	52.87
Solyc12g043120.1.1	98	5	5	5	5	9.5	45.76
Solyc04g008740.2.1	98	5	5	5	5	15.3	49.14
Solyc10g081310.1.1	97	3	3	3	3	37.7	67.7
Solyc06g072120.2.1	97	4	3	4	3	20.9	58.47
Solyc01g010760.2.1	97	4	4	4	4	19.9	64.14
Solyc06g011280.2.1	96	2	2	1	1	4.6	60.33
Solyc02g065400.2.1	96	1	1	1	1	6.4	95.72
Solyc03g032000.2.1	96	3	2	3	2	19.8	55.06
Solyc01g094200.2.1	96	2	2	2	2	6.2	66.97
Solyc12g056120.1.1	95	4	3	3	2	12.3	73.24
Solyc02g079500.2.1	95	3	3	3	3	10.7	58.44
Solyc04g063290.2.1	95	6	4	5	4	27.9	43.46
Solyc03g121640.2.1	94	1	1	1	1	4	94.4
Solyc06g073370.2.1	94	1	1	1	1	13.2	94.01
Solyc01g099780.2.1	94	4	4	3	3	21.4	45.07
Solyc07g005560.2.1	94	4	3	3	3	33.1	71.24
Solyc08g079020.2.1	93	1	1	1	1	12.6	92.96
Solyc01g104170.2.1	93	3	3	2	2	10.6	55.64
Solyc03g119040.2.1	93	3	3	3	3	14.7	54.34
Solyc09g018590.1.1	92	1	1	1	1	8.8	92.24
Solyc03g025270.2.1	92	1	1	1	1	6.4	92.21
Solyc11g020870.1.1	92	1	1	1	1	5.9	91.61
Solyc10g079890.1.1	91	1	1	1	1	6.2	91.45
Solyc11g011330.1.1	91	3	2	3	2	15.2	69.4
Solyc10g078740.1.1	91	5	3	5	3	20.7	42.38
Solyc06g083190.2.1	90	5	2	5	2	13.8	61.74
Solyc05g046000.2.1	90	5	5	2	2	7.8	61.94
Solyc06g062380.2.1	90	2	2	2	2	15	67.2
Solyc09g057670.2.1	90	7	4	5	3	49	44.23
Solyc01g103480.2.1	90	3	3	3	3	8.5	66.35
Solyc03g025850.2.1	90	4	4	4	4	26.9	49.91
Solyc10g081720.1.1	89	2	2	1	1	3.8	74
Solyc09g018750.2.1	89	4	2	3	2	25.9	54.63
Solyc03g007660.2.1	89	2	2	2	2	19	28.34
Solyc11g012870.1.1	89	3	2	3	2	15.3	51.16
Solyc01g104370.2.1	88	2	2	1	1	14.3	58.98
Solyc05g052690.2.1	88	1	1	1	1	7	88.39
Solyc10g005100.2.1	88	4	2	2	1	10	47.68
Solyc10g078150.1.1	88	4	3	2	1	15.2	62.71
Solyc07g041490.1.1	88	1	1	1	1	7.1	88.02
Solyc02g070570.2.1	88	2	2	2	2	20.7	81.36
Solyc07g064800.2.1	88	3	2	3	2	12	75.34
Solyc02g084920.2.1	88	3	3	3	3	26.5	53.67
Solyc12g010060.1.1	87	3	3	3	3	22.5	59.49
Solyc02g082900.2.1	86	1	1	1	1	5.7	86.49
Solyc09g009640.2.1	86	1	1	1	1	18.2	86.35
Solyc11g068830.1.1	86	2	1	2	1	9.4	85.93
Solyc03g080160.2.1	86	5	5	5	5	35.3	44.97
Solyc07g042250.2.1	85	2	2	1	1	8.7	76.59
Solyc12g096520.1.1	85	1	1	1	1	7.5	84.67

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc02g080810.2.1	85	3	2	3	2	13.5	62.11
Solyc03g118340.2.1	85	2	2	2	2	4.5	63.78
Solyc09g091000.2.1	85	4	4	3	3	30.3	41.75
Solyc03g078290.2.1	84	1	1	1	1	13.2	84.41
Solyc01g099410.2.1	84	3	2	2	1	20.5	81.78
Solyc09g064370.2.1	84	2	1	2	1	10.5	84.03
Solyc05g055770.2.1	84	1	1	1	1	5.1	83.9
Solyc01g109620.2.1	84	2	2	2	2	15.3	60.17
Solyc01g102390.2.1	84	4	3	2	2	13.2	49.83
Solyc08g006040.2.1	84	2	2	2	2	12.9	65
Solyc01g103370.2.1	83	2	2	2	2	17.8	52.69
Solyc02g063130.2.1	83	3	3	2	2	6.3	58.27
Solyc06g068320.2.1	82	1	1	1	1	2.9	82.3
Solyc03g097900.2.1	82	3	3	2	2	11.1	49.9
Solyc10g076510.1.1	82	2	2	2	2	5.3	54.43
Solyc06g050980.2.1	82	4	3	3	2	20.7	51.01
Solyc02g077000.2.1	82	2	2	2	2	7.9	65.76
Solyc02g080630.2.1	82	3	3	3	3	12.9	52.27
Solyc01g006900.2.1	82	4	4	3	3	24.5	56.67
Solyc01g097270.2.1	81	2	2	1	1	8.5	58.97
Solyc10g074690.1.1	81	1	1	1	1	4.4	80.78
Solyc02g086460.2.1	81	2	2	2	2	0.8	58.75
Solyc04g011400.2.1	81	3	3	2	2	9	65.43
Solyc05g055280.1.1	81	2	2	2	2	28.6	61.33
Solyc03g033710.2.1	81	4	4	3	3	10.8	73.09
Solyc01g006290.2.1	80	2	2	1	1	5.5	67.26
Solyc02g077240.2.1	80	1	1	1	1	3.4	79.95
Solyc09g010420.2.1	80	1	1	1	1	4	79.62
Solyc10g006290.2.1	80	2	2	2	2	18.2	51.98
Solyc01g095150.2.1	80	6	4	5	3	39.7	45.49
Solyc04g074480.2.1	80	3	3	3	3	9.1	56.57
Solyc11g072450.1.1	80	6	3	5	3	31	39.92
Solyc12g095760.1.1	80	4	3	4	3	11	52.52
Solyc08g079090.2.1	79	3	3	2	2	5.6	58.11
Solyc04g081440.2.1	79	2	2	2	2	6.3	60.12
Solyc07g016150.2.1	79	3	3	3	3	30.7	53.76
Solyc05g050970.2.1	79	4	3	4	3	7.9	43.37
Solyc07g008130.2.1	78	1	1	1	1	11.2	78.34
Solyc05g012270.2.1	78	1	1	1	1	3.4	77.77
Solyc04g005340.2.1	78	4	4	3	3	12	48.02
Solyc01g107870.2.1	78	4	4	4	4	9.5	38.62
Solyc09g075940.2.1	77	1	1	1	1	2.7	76.91
Solyc08g014130.2.1	77	2	2	2	2	5.9	58.2
Solyc06g005360.2.1	76	2	1	2	1	23.4	76.43
Solyc02g068740.2.1	76	2	2	1	1	10.4	54.94
Solyc03g098710.1.1	76	2	2	2	2	15.2	53.73
Solyc06g050590.2.1	75	2	1	2	1	9.3	67.26
Solyc09g075450.2.1	75	2	2	2	2	8.3	50.39
Solyc09g072700.2.1	75	5	5	2	2	9.3	53.13
Solyc04g009410.2.1	74	1	1	1	1	8.8	74.26
Solyc07g064240.2.1	74	2	2	1	1	6.4	51.48
Solyc01g060470.2.1	74	1	1	1	1	4	73.97
Solyc01g087850.2.1	74	2	2	2	2	4.6	46.35
Solyc04g071610.2.1	74	3	3	2	2	34.5	49.29
Solyc06g060260.2.1	74	3	3	3	3	13.6	45.44
Solyc06g007610.2.1	73	2	2	1	1	13	56.13
Solyc09g064450.2.1	73	1	1	1	1	4.5	72.66

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc12g042900.1.1	73	2	2	1	1	8.7	48.93
Solyc08g078070.2.1	72	1	1	1	1	9.4	72.49
Solyc01g097520.2.1	72	1	1	1	1	5.7	72.46
Solyc06g066830.2.1	72	1	1	1	1	6.1	72.43
Solyc02g067840.2.1	72	1	1	1	1	5.3	72.17
Solyc02g088460.2.1	72	1	1	1	1	5.4	71.99
Solyc03g083390.2.1	72	2	1	2	1	11.3	28.26
Solyc03g083390.2.1	72	2	1	2	1	11.3	60.17
Solyc05g056310.2.1	72	1	1	1	1	3.2	71.81
Solyc05g055760.2.1	72	2	2	2	2	15.7	46.35
Solyc01g104590.2.1	72	2	2	2	2	7.5	50.95
Solyc03g120470.2.1	71	1	1	1	1	1.5	70.74
Solyc02g093900.2.1	71	2	2	2	2	11.2	64.66
Solyc05g009530.2.1	71	2	2	2	2	6.8	60.7
Solyc03g079930.2.1	71	3	3	2	2	16.3	52.15
Solyc10g049890.1.1	71	2	2	2	2	5.4	60.12
Solyc02g079750.2.1	71	4	4	3	3	18.4	36.12
Solyc06g083790.2.1	71	4	4	4	4	12.1	39.67
Solyc09g083410.2.1	70	1	1	1	1	3.9	70.24
Solyc03g005220.2.1	70	1	1	1	1	16.2	70.14
Solyc09g005400.2.1	70	2	2	1	1	9.3	44.91
Solyc06g065520.2.1	70	2	1	2	1	6.1	59.83
Solyc02g094180.2.1	70	2	2	2	2	10.8	55.6
Solyc08g079920.1.1	70	3	2	3	2	7.5	49.5
Solyc08g067100.2.1	69	1	1	1	1	4.2	69.28
Solyc02g086740.1.1	69	1	1	1	1	9.7	68.84
Solyc02g082200.2.1	69	1	1	1	1	10.2	68.75
Solyc01g088700.2.1	69	1	1	1	1	1	68.72
Solyc07g053970.2.1	69	1	1	1	1	2.7	68.54
Solyc05g056390.2.1	69	4	3	2	2	27.8	43.21
Solyc06g007200.2.1	68	1	1	1	1	4.4	68.33
Solyc12g044850.1.1	68	1	1	1	1	14.1	68.18
Solyc01g099830.2.1	68	2	1	2	1	28.8	57.03
Solyc09g010400.2.1	68	2	1	2	1	20.7	68.09
Solyc01g090120.2.1	68	1	1	1	1	10.1	67.84
Solyc07g032250.2.1	68	2	2	1	1	5.6	45.37
Solyc02g085350.2.1	68	2	2	2	2	4.5	46.66
Solyc05g051510.2.1	68	2	2	2	2	14.4	52.61
Solyc06g073700.2.1	67	1	1	1	1	16.3	67.14
Solyc01g079420.2.1	67	1	1	1	1	12.8	66.88
Solyc06g074780.1.1	67	6	5	2	1	16.8	43.53
Solyc07g041900.2.1	67	2	1	1	1	4.5	61.95
Solyc04g078540.2.1	67	4	2	4	2	11.9	43.28
Solyc02g091490.2.1	67	3	2	3	2	9.8	57.83
Solyc04g015830.2.1	67	2	2	2	2	3.3	54.34
Solyc04g076880.2.1	66	1	1	1	1	2.3	66.49
Solyc03g095190.2.1	66	1	1	1	1	8	65.95
Solyc07g047790.2.1	66	2	1	2	1	5.8	59.32
Solyc06g007670.2.1	66	2	2	1	1	4.7	50.42
Solyc03g118040.2.1	66	6	2	5	2	15.2	40.46
Solyc04g007750.2.1	66	4	2	3	2	21.1	51.92
Solyc02g084710.2.1	66	2	2	2	2	21.2	60.08
Solyc10g005890.2.1	66	2	2	2	2	8.4	58.78
Solyc01g073640.2.1	65	4	2	1	1	7.7	32.07
Solyc02g069090.2.1	65	1	1	1	1	6.2	65.43
Solyc09g007250.2.1	65	2	2	1	1	3.9	44.47
Solyc09g018450.2.1	65	1	1	1	1	1.8	65.2

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc02g086730.1.1	65	1	1	1	1	9.5	65.01
Solyc09g075150.2.1	65	2	1	2	1	29	57.03
Solyc03g097070.2.1	65	1	1	1	1	5.3	64.92
Solyc04g074410.1.1	65	1	1	1	1	6.7	64.85
Solyc07g006790.2.1	65	2	1	1	1	3.1	60.07
Solyc10g079830.1.1	65	1	1	1	1	13.1	64.69
Solyc11g067230.1.1	65	1	1	1	1	4.4	64.64
Solyc01g107590.2.1	65	2	2	2	2	12.3	43.54
Solyc11g006070.1.1	64	2	1	2	1	21.6	49.83
Solyc01g008370.2.1	64	2	2	2	2	13.2	49.6
Solyc12g014250.1.1	64	5	3	4	2	7.8	39.2
Solyc06g068090.2.1	64	2	2	2	2	4.3	50.34
Solyc10g086010.1.1	64	2	2	2	2	8.3	50.26
Solyc07g008240.2.1	64	2	2	2	2	17.8	46.23
Solyc09g082520.2.1	64	2	2	2	2	12.7	49.9
Solyc01g109540.2.1	64	3	3	3	3	5.6	42.72
Solyc03g098760.1.1	63	1	1	1	1	9.9	63.47
Solyc09g092430.2.1	63	1	1	1	1	5.1	63.41
Solyc02g065300.1.1	63	1	1	1	1	1.8	63.32
Solyc09g025240.2.1	63	1	1	1	1	6	62.73
Solyc09g064720.2.1	63	1	1	1	1	7.1	62.52
Solyc09g075670.1.1	63	1	1	1	1	6	62.52
Solyc12g088720.1.1	63	3	2	3	2	9	43.52
Solyc09g090700.1.1	63	2	2	2	2	8.8	48.36
Solyc01g111710.2.1	63	3	3	2	2	7.4	47.09
Solyc12g056250.1.1	63	2	2	2	2	11	55.97
Solyc04g082460.2.1	63	2	2	2	2	8.9	46.45
Solyc06g050550.2.1	62	1	1	1	1	3.7	62.3
Solyc04g054990.2.1	62	1	1	1	1	9.3	61.74
Solyc06g050440.2.1	62	4	2	3	2	16.9	41.34
Solyc08g077900.2.1	62	2	2	2	2	12.6	40.64
Solyc04g005160.1.1	62	4	4	3	3	8.7	41.81
Solyc08g082430.2.1	61	3	2	2	1	7.6	42.72
Solyc05g006750.2.1	61	1	1	1	1	7.4	61.31
Solyc02g068640.2.1	61	1	1	1	1	6.5	61.23
Solyc09g090010.2.1	61	1	1	1	1	10.3	61.2
Solyc08g014000.2.1	61	4	2	3	2	5.3	50.85
Solyc03g096000.2.1	61	2	2	2	2	1.6	53.36
Solyc01g098000.2.1	61	2	2	2	2	20.3	44.18
Solyc10g080970.1.1	61	3	2	3	2	14.7	40.73
Solyc05g053940.2.1	61	2	2	2	2	17.2	54.49
Solyc01g028810.2.1	61	4	2	4	2	8.3	55.75
Solyc06g069470.2.1	60	1	1	1	1	4.3	60.44
Solyc01g079940.2.1	60	1	1	1	1	5.1	60.23
Solyc02g021400.1.1	60	2	2	1	1	18.5	47.88
Solyc01g088080.2.1	60	2	2	1	1	3.5	49.11
Solyc01g007740.2.1	60	1	1	1	1	6	59.69
Solyc09g059040.2.1	60	2	1	2	1	11.6	49.15
Solyc06g008260.2.1	60	3	3	2	2	14.9	42.18
Solyc10g007070.2.1	60	2	2	2	2	10.6	49.13
Solyc05g012070.2.1	60	4	3	3	2	14.9	42.67
Solyc07g065490.2.1	60	2	2	2	2	4.4	45.99
Solyc03g083520.2.1	60	3	2	3	2	26.7	43.3
Solyc02g090210.2.1	59	1	1	1	1	4.6	59.35
Solyc02g082250.2.1	59	1	1	1	1	4.4	59.26
Solyc03g123610.2.1	59	1	1	1	1	3.3	59.2
Solyc10g005060.2.1	59	1	1	1	1	4.7	59.09

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc10g079610.1.1	59	1	1	1	1	4.6	59.02
Solyc01g111660.2.1	59	1	1	1	1	6	58.76
Solyc10g082030.1.1	59	1	1	1	1	6.4	58.72
Solyc01g111150.2.1	59	1	1	1	1	5.8	58.67
Solyc01g097870.2.1	59	2	2	2	2	19.5	40.1
Solyc02g085050.2.1	58	1	1	1	1	6.7	58.36
Solyc08g075700.2.1	58	1	1	1	1	11.7	58.21
Solyc02g091970.2.1	58	1	1	1	1	4.2	58.17
Solyc01g088610.2.1	58	1	1	1	1	14.8	57.73
Solyc08g066740.2.1	58	1	1	1	1	10.5	57.59
Solyc08g068310.2.1	58	1	1	1	1	3.8	57.58
Solyc09g011660.2.1	58	2	2	2	2	21.3	45.77
Solyc01g079610.2.1	58	3	3	3	3	14.2	35.94
Solyc07g066580.2.1	57	1	1	1	1	7	57.39
Solyc01g080220.2.1	57	1	1	1	1	8.8	57.28
Solyc04g072000.2.1	57	1	1	1	1	7.6	57.15
Solyc05g018700.2.1	57	1	1	1	1	3.2	57.08
Solyc10g081180.1.1	57	2	1	1	1	9.5	47.95
Solyc06g083030.2.1	57	1	1	1	1	3.8	56.91
Solyc02g068150.2.1	57	1	1	1	1	15.4	56.81
Solyc02g088690.2.1	57	2	2	2	2	15.2	49.59
Solyc11g069150.1.1	57	2	2	2	2	11.8	41.32
Solyc05g054710.2.1	56	2	1	1	1	2.5	48.39
Solyc09g014790.2.1	56	1	1	1	1	2.6	56.46
Solyc04g005350.2.1	56	1	1	1	1	16.8	56.31
Solyc11g066130.1.1	56	3	2	1	1	5.6	31.6
Solyc12g011160.1.1	56	1	1	1	1	4.2	56.16
Solyc09g018790.2.1	56	1	1	1	1	6.3	56.12
Solyc06g083730.2.1	56	1	1	1	1	3.5	56.11
Solyc06g034120.2.1	56	1	1	1	1	4.9	56.04
Solyc02g078040.2.1	56	1	1	1	1	6.6	56.01
Solyc01g081600.2.1	56	1	1	1	1	14.9	55.91
Solyc07g055690.1.1	56	2	1	2	1	6.5	51.21
Solyc02g071150.2.1	56	2	2	1	1	10.9	44.19
Solyc05g052310.2.1	56	2	2	2	2	13.2	42.21
Solyc07g055210.2.1	56	2	2	2	2	7.1	46.99
Solyc07g042570.2.1	56	2	2	2	2	12.4	40.63
Solyc05g013990.2.1	55	1	1	1	1	2.6	55.48
Solyc01g097300.2.1	55	1	1	1	1	15.6	55.26
Solyc03g044010.2.1	55	1	1	1	1	7.7	55.2
Solyc08g007600.1.1	55	1	1	1	1	2.4	55.09
Solyc11g007200.1.1	55	1	1	1	1	15.9	55.08
Solyc04g080880.2.1	55	1	1	1	1	2.2	54.97
Solyc10g008120.2.1	55	1	1	1	1	5.8	54.68
Solyc09g098150.2.1	55	3	2	2	2	5	38.22
Solyc09g010460.2.1	55	2	2	2	2	2.4	41.41
Solyc10g037980.1.1	54	2	2	1	1	11.4	37.43
Solyc06g071050.2.1	54	1	1	1	1	5.5	54.19
Solyc07g008560.2.1	54	2	2	2	2	4.4	43.17
Solyc10g051390.1.1	54	2	2	2	2	25.4	38.78
Solyc09g092530.2.1	53	1	1	1	1	6.1	53.33
Solyc03g019690.1.1	53	1	1	1	1	7.8	53.22
Solyc02g086830.2.1	53	1	1	1	1	5.3	52.77
Solyc01g105060.2.1	53	2	2	2	2	11.6	44.39
Solyc06g051010.1.1	53	2	2	2	2	5.1	39.71
Solyc02g083710.2.1	53	2	2	2	2	11.4	39.4
Solyc10g080710.1.1	52	1	1	1	1	2.6	52.32

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc09g075460.2.1	52	1	1	1	1	3.5	52.16
Solyc11g069270.1.1	52	2	2	2	2	4.5	37.31
Solyc03g123830.2.1	52	2	2	2	2	4	42.49
Solyc04g045340.2.1	52	4	3	4	3	13.7	40.6
Solyc04g008810.2.1	51	1	1	1	1	11.7	51.46
Solyc01g109850.2.1	51	2	1	2	1	6.5	45.8
Solyc04g078380.1.1	51	2	1	2	1	27.6	36.59
Solyc10g077030.1.1	51	1	1	1	1	6.8	51.1
Solyc05g009600.2.1	51	2	1	2	1	5.5	42.76
Solyc06g069570.2.1	51	1	1	1	1	5.2	50.85
Solyc08g041870.2.1	51	1	1	1	1	3	50.65
Solyc01g111060.2.1	51	1	1	1	1	4.9	50.56
Solyc03g121070.2.1	51	2	2	2	2	6.8	46.23
Solyc09g083080.2.1	50	1	1	1	1	2.9	50.42
Solyc04g005030.2.1	50	1	1	1	1	5.2	50.23
Solyc06g008170.2.1	50	1	1	1	1	12.9	50.08
Solyc05g052150.2.1	50	1	1	1	1	17.2	49.81
Solyc11g040390.1.1	50	1	1	1	1	2.2	49.79
Solyc06g007320.2.1	50	1	1	1	1	1.6	49.77
Solyc02g083590.2.1	50	1	1	1	1	4.1	49.75
Solyc03g097790.2.1	50	1	1	1	1	5.3	49.73
Solyc03g118020.2.1	50	3	1	2	1	3.3	47.8
Solyc05g012080.2.1	50	1	1	1	1	15	49.71
Solyc03g111230.2.1	50	1	1	1	1	6.7	49.52
Solyc05g015390.2.1	50	2	2	2	2	13	36.99
Solyc03g097190.2.1	50	2	2	2	2	2.8	34.68
Solyc06g073280.2.1	50	2	2	2	2	6.1	42.75
Solyc09g075010.2.1	49	2	1	1	1	5.8	40.95
Solyc11g008870.1.1	49	2	1	2	1	5.2	36.39
Solyc05g053140.2.1	49	2	1	2	1	6.5	41.86
Solyc06g060760.2.1	49	1	1	1	1	6.4	49.36
Solyc02g084360.2.1	49	1	1	1	1	10.9	49.32
Solyc03g043960.2.1	49	2	1	2	1	19	41.62
Solyc05g052470.2.1	49	3	2	2	1	9.7	37.45
Solyc00g140060.2.1	49	1	1	1	1	8.7	49.14
Solyc08g081780.1.1	49	1	1	1	1	16.9	48.86
Solyc10g081120.1.1	49	1	1	1	1	2.7	48.84
Solyc08g075390.2.1	49	1	1	1	1	2.4	48.63
Solyc01g096450.2.1	49	3	2	2	2	5.6	35.7
Solyc05g018810.2.1	49	2	2	2	2	7.2	39.61
Solyc01g008330.2.1	49	2	2	2	2	7.1	40.42
Solyc07g005600.2.1	48	1	1	1	1	2.3	48.21
Solyc11g039830.1.1	48	1	1	1	1	1.9	48.17
Solyc06g062950.1.1	48	1	1	1	1	1.9	48.09
Solyc01g105370.2.1	48	1	1	1	1	5.3	47.95
Solyc08g075780.2.1	48	2	1	1	1	15.3	44.49
Solyc04g010240.2.1	48	2	2	1	1	10.6	37.68
Solyc02g081170.2.1	48	1	1	1	1	4	47.78
Solyc08g079070.2.1	48	1	1	1	1	4.3	47.74
Solyc05g009980.2.1	48	1	1	1	1	3.2	47.67
Solyc09g083370.2.1	48	1	1	1	1	11.3	47.64
Solyc01g007330.2.1	48	1	1	1	1	4	47.59
Solyc07g064980.2.1	47	1	1	1	1	3.6	47.3
Solyc08g082280.2.1	47	1	1	1	1	2.7	47.2
Solyc01g103750.2.1	47	1	1	1	1	5.6	47.04
Solyc01g005980.2.1	47	1	1	1	1	6	46.85
Solyc12g008940.1.1	47	2	1	2	1	7	39.61

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc12g008370.1.1	47	1	1	1	1	3.6	46.63
Solyc02g082830.1.1	47	2	2	2	2	7.4	36.95
Solyc05g053780.2.1	47	2	2	2	2	16.8	36.34
Solyc02g092440.2.1	47	2	2	2	2	14.1	41.56
Solyc02g077220.2.1	47	2	2	2	2	12.5	36.94
Solyc07g064810.2.1	46	1	1	1	1	2.7	46.49
Solyc06g005810.2.1	46	1	1	1	1	8.3	46.36
Solyc01g110120.2.1	46	1	1	1	1	1.7	46.34
Solyc04g079440.2.1	46	1	1	1	1	4.1	46.32
Solyc08g014340.2.1	46	1	1	1	1	8	46.15
Solyc01g106430.2.1	46	1	1	1	1	6.2	46.12
Solyc01g005250.2.1	46	1	1	1	1	5.2	45.93
Solyc05g054590.2.1	46	2	1	2	1	13.1	38.07
Solyc07g049360.2.1	46	1	1	1	1	15.6	45.88
Solyc01g112080.2.1	46	2	1	2	1	8.7	32.41
Solyc10g079500.1.1	46	1	1	1	1	3	45.69
Solyc04g007120.2.1	46	2	2	2	2	5.9	36.06
Solyc05g056400.2.1	46	5	2	3	2	6.4	35.15
Solyc02g069590.2.1	45	2	1	2	1	14.6	39.6
Solyc11g005620.1.1	45	1	1	1	1	4.9	45.32
Solyc01g087540.2.1	45	1	1	1	1	4.4	45.24
Solyc04g079200.2.1	45	1	1	1	1	4.8	45.2
Solyc10g083120.1.1	45	2	1	1	1	8.2	39.01
Solyc06g083440.2.1	45	1	1	1	1	15.8	44.92
Solyc04g081400.2.1	45	1	1	1	1	3.4	44.9
Solyc04g016360.2.1	45	1	1	1	1	6	44.89
Solyc03g123730.2.1	45	2	1	1	1	3.5	39.84
Solyc03g116170.2.1	45	1	1	1	1	6.7	44.75
Solyc04g082590.2.1	45	1	1	1	1	6.5	44.73
Solyc03g115760.2.1	45	1	1	1	1	5	44.63
Solyc11g068540.1.1	45	1	1	1	1	6	44.52
Solyc01g079680.2.1	45	2	2	2	2	8.4	36.91
Solyc05g009030.2.1	45	2	2	2	2	6.4	38.54
Solyc02g079060.2.1	44	1	1	1	1	6.8	44.34
Solyc04g009550.2.1	44	1	1	1	1	6.7	44.23
Solyc10g086150.1.1	44	1	1	1	1	7.2	44.21
Solyc03g006680.2.1	44	2	1	2	1	11	41.66
Solyc02g094200.2.1	44	1	1	1	1	23.6	44.1
Solyc01g079820.2.1	44	1	1	1	1	6.3	44.03
Solyc10g078540.1.1	44	1	1	1	1	8.2	43.81
Solyc01g022750.2.1	44	1	1	1	1	9.8	43.68
Solyc03g120090.1.1	44	1	1	1	1	6.2	43.63
Solyc08g075690.2.1	44	2	1	2	1	33.3	38.9
Solyc07g008370.2.1	44	2	2	2	2	9.9	36.64
Solyc08g008050.2.1	43	2	2	1	1	4.9	32.9
Solyc01g097880.2.1	43	1	1	1	1	5.9	43.25
Solyc01g099900.2.1	43	1	1	1	1	5.9	43.13
Solyc12g096650.1.1	43	1	1	1	1	7	43.08
Solyc06g054250.2.1	43	1	1	1	1	5.3	42.92
Solyc01g090190.2.1	43	1	1	1	1	5.6	42.8
Solyc12g009960.1.1	43	1	1	1	1	1.9	42.67
Solyc02g071700.2.1	43	1	1	1	1	3.9	42.65
Solyc03g111840.2.1	43	1	1	1	1	5.1	42.6
Solyc11g040370.1.1	43	1	1	1	1	2.4	42.52
Solyc10g050890.1.1	43	3	3	3	3	8.4	38.31
Solyc09g098280.2.1	42	1	1	1	1	4.1	42.39
Solyc08g008210.2.1	42	3	1	3	1	15.8	30.61

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc11g011470.1.1	42	1	1	1	1	3.2	42.2
Solyc01g091220.2.1	42	1	1	1	1	8.6	42.03
Solyc11g039840.1.1	42	2	1	2	1	16.2	42.02
Solyc10g080320.1.1	42	1	1	1	1	3.6	42.01
Solyc02g083270.2.1	42	1	1	1	1	3.5	41.99
Solyc02g082350.2.1	42	1	1	1	1	2.9	41.9
Solyc06g067940.2.1	42	1	1	1	1	8.5	41.8
Solyc08g069040.2.1	42	1	1	1	1	5.1	41.8
Solyc01g097010.2.1	42	1	1	1	1	3.6	41.69
Solyc07g055060.2.1	42	3	1	3	1	4.9	31.97
Solyc08g077930.2.1	42	3	2	3	2	14.4	32.24
Solyc06g009400.2.1	42	3	2	2	2	12.6	33.46
Solyc04g071620.2.1	42	4	3	4	3	16.2	33.81
Solyc02g090090.2.1	41	1	1	1	1	3.4	41.49
Solyc04g082160.2.1	41	1	1	1	1	3.6	41.38
Solyc01g006510.2.1	41	1	1	1	1	4.8	41.29
Solyc09g013080.2.1	41	1	1	1	1	2	41.24
Solyc05g052140.2.1	41	2	1	2	1	24.7	29.07
Solyc01g100030.2.1	41	1	1	1	1	10.1	41.1
Solyc06g072220.1.1	41	1	1	1	1	5.7	41.1
Solyc05g013030.1.1	41	1	1	1	1	3.3	40.95
Solyc06g074820.2.1	41	1	1	1	1	5.6	40.89
Solyc06g007520.2.1	41	1	1	1	1	5.2	40.82
Solyc03g082580.2.1	41	1	1	1	1	4.4	40.64
Solyc06g065970.1.1	41	2	1	1	1	12.7	33.21
Solyc08g076990.2.1	40	1	1	1	1	3	40.38
Solyc03g115360.2.1	40	1	1	1	1	11.9	40.34
Solyc07g006640.2.1	40	1	1	1	1	8.8	40.32
Solyc05g017760.2.1	40	1	1	1	1	4.9	40.31
Solyc04g081740.2.1	40	1	1	1	1	3.9	40.28
Solyc06g083300.2.1	40	1	1	1	1	3.4	40.19
Solyc06g007710.2.1	40	2	1	2	1	10.2	32.55
Solyc01g066840.2.1	40	1	1	1	1	13.4	40.17
Solyc03g083610.2.1	40	1	1	1	1	7.2	40.13
Solyc12g006980.1.1	40	1	1	1	1	3.6	40.09
Solyc02g069790.2.1	40	1	1	1	1	4.6	40
Solyc11g066520.1.1	40	1	1	1	1	4.1	39.94
Solyc09g082650.2.1	40	1	1	1	1	5.8	39.79
Solyc01g008310.2.1	40	1	1	1	1	2.4	39.73
Solyc03g120720.2.1	40	1	1	1	1	3.2	39.73
Solyc12g018990.1.1	40	2	1	2	1	11.8	39.68
Solyc06g066060.2.1	40	2	2	2	2	5.4	31.76
Solyc10g086510.1.1	40	2	2	2	2	29	37.12
Solyc03g082600.2.1	39	1	1	1	1	8.4	39.46
Solyc03g113030.2.1	39	2	1	2	1	10.1	39.42
Solyc02g093630.2.1	39	1	1	1	1	2.6	39.24
Solyc01g007860.2.1	39	1	1	1	1	8.2	39.01
Solyc08g074790.2.1	39	1	1	1	1	6.1	39.01
Solyc02g014310.2.1	39	1	1	1	1	1.9	38.99
Solyc09g091470.2.1	39	1	1	1	1	2.8	38.84
Solyc02g063090.2.1	39	1	1	1	1	3.2	38.81
Solyc05g056490.2.1	39	1	1	1	1	8.6	38.8
Solyc12g042380.1.1	39	1	1	1	1	4.1	38.8
Solyc01g099890.2.1	39	1	1	1	1	11	38.69
Solyc03g121410.2.1	39	1	1	1	1	3.7	38.62
Solyc11g006350.1.1	39	1	1	1	1	4	38.59
Solyc01g110390.2.1	39	3	1	3	1	26.9	35.47

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc03g121330.2.1	38	1	1	1	1	9.1	38.39
Solyc01g066590.2.1	38	1	1	1	1	10.1	38.22
Solyc10g076350.1.1	38	1	1	1	1	8.8	38.06
Solyc12g008720.1.1	38	1	1	1	1	20.8	38.06
Solyc09g083210.2.1	38	1	1	1	1	2.9	37.99
Solyc01g009100.2.1	38	1	1	1	1	14.3	37.88
Solyc04g076790.2.1	38	1	1	1	1	2.9	37.84
Solyc11g072270.1.1	38	2	1	2	1	14.1	33.4
Solyc05g043430.2.1	38	1	1	1	1	10	37.81
Solyc11g007120.1.1	38	1	1	1	1	5.4	37.76
Solyc01g112280.2.1	38	1	1	1	1	2.9	37.72
Solyc02g093310.2.1	38	1	1	1	1	4.4	37.68
Solyc06g060420.2.1	38	1	1	1	1	4.7	37.6
Solyc10g006760.2.1	38	2	1	2	1	10.7	34.58
Solyc02g070310.2.1	38	2	2	2	2	18	34.63
Solyc02g082800.2.1	37	1	1	1	1	2.7	37.45
Solyc01g104950.2.1	37	1	1	1	1	1.5	37.43
Solyc03g114170.2.1	37	1	1	1	1	40	37.41
Solyc10g083290.1.1	37	2	1	2	1	6	31.75
Solyc09g075120.2.1	37	1	1	1	1	11.2	37.28
Solyc01g095000.2.1	37	1	1	1	1	5.3	37.21
Solyc08g067370.1.1	37	1	1	1	1	5.1	37.2
Solyc02g094470.2.1	37	1	1	1	1	3.6	37.16
Solyc02g081400.2.1	37	1	1	1	1	4.1	37.11
Solyc08g082700.2.1	37	1	1	1	1	3.7	37.09
Solyc02g090630.2.1	37	1	1	1	1	7.8	36.81
Solyc12g099570.1.1	37	1	1	1	1	44.4	36.79
Solyc05g055310.2.1	37	1	1	1	1	27.2	36.72
Solyc08g065640.2.1	37	1	1	1	1	10.3	36.69
Solyc07g017900.2.1	37	1	1	1	1	4.1	36.68
Solyc07g017400.2.1	37	1	1	1	1	5	36.6
Solyc12g096190.1.1	36	1	1	1	1	3.9	36.44
Solyc01g110450.2.1	36	1	1	1	1	4.5	36.43
Solyc01g009520.2.1	36	1	1	1	1	6.9	36.33
Solyc06g060790.1.1	36	1	1	1	1	5.9	36.25
Solyc11g012110.1.1	36	1	1	1	1	6.6	36.05
Solyc01g008080.2.1	36	2	1	2	1	29.1	32.14
Solyc04g011350.2.1	36	1	1	1	1	1.9	36.02
Solyc07g065090.1.1	36	1	1	1	1	4.9	35.99
Solyc06g035920.2.1	36	1	1	1	1	5.9	35.96
Solyc09g090520.2.1	36	1	1	1	1	2.3	35.93
Solyc04g076050.2.1	36	1	1	1	1	6.7	35.91
Solyc08g076540.2.1	36	1	1	1	1	11.4	35.75
Solyc02g088790.2.1	36	1	1	1	1	4.3	35.69
Solyc01g096040.2.1	36	1	1	1	1	3.3	35.64
Solyc08g029160.1.1	36	1	1	1	1	15	35.59
Solyc07g008350.2.1	35	1	1	1	1	4	35.49
Solyc02g092730.2.1	35	1	1	1	1	5.5	35.45
Solyc02g070500.1.1	35	1	1	1	1	10.2	35.44
Solyc06g076570.1.1	35	1	1	1	1	11	35.41
Solyc11g017070.1.1	35	1	1	1	1	9.5	35.41
Solyc01g058390.2.1	35	1	1	1	1	5.6	35.23
Solyc09g059620.2.1	35	1	1	1	1	7.1	35.09
Solyc01g008550.2.1	35	1	1	1	1	4.1	35.08
Solyc05g046340.1.1	35	1	1	1	1	5.6	35.08
Solyc08g081250.2.1	35	1	1	1	1	1.7	34.93
Solyc03g098720.2.1	35	2	2	1	1	5.2	32.63

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Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc09g090330.2.1	35	1	1	1	1	6.2	34.75
Solyc03g112650.2.1	35	1	1	1	1	5	34.73
Solyc06g065470.2.1	35	1	1	1	1	7.7	34.73
Solyc04g008760.1.1	35	1	1	1	1	4.2	34.54
Solyc01g009990.2.1	35	1	1	1	1	6	34.52
Solyc09g007640.2.1	34	1	1	1	1	2.8	34.44
Solyc03g114860.2.1	34	1	1	1	1	5.4	34.23
Solyc04g082140.2.1	34	1	1	1	1	3	34.22
Solyc01g067750.2.1	34	1	1	1	1	3.5	34.2
Solyc03g117940.2.1	34	1	1	1	1	5.2	34.15
Solyc10g081240.1.1	34	1	1	1	1	2.6	34.07
Solyc06g076890.1.1	34	1	1	1	1	11.8	34.06
Solyc12g006180.1.1	34	1	1	1	1	3.7	34.06
Solyc11g071610.1.1	34	1	1	1	1	1.3	33.97
Solyc01g100360.2.1	34	1	1	1	1	3.2	33.92
Solyc02g067080.2.1	34	1	1	1	1	5.3	33.92
Solyc02g070640.2.1	34	1	1	1	1	7.9	33.9
Solyc03g082480.2.1	34	1	1	1	1	7	33.89
Solyc08g081320.2.1	34	1	1	1	1	2.1	33.89
Solyc06g084090.2.1	34	1	1	1	1	4.9	33.85
Solyc05g053960.2.1	34	2	2	1	1	5.8	32.83
Solyc06g075340.2.1	34	1	1	1	1	1.2	33.54
Solyc02g070320.2.1	34	2	2	2	2	8.3	32.72
Solyc12g039120.1.1	33	1	1	1	1	11.9	33.26
Solyc06g076660.2.1	33	1	1	1	1	5.7	33.25
Solyc03g007670.2.1	33	1	1	1	1	3.5	33.19
Solyc01g081270.2.1	33	1	1	1	1	6.3	33.07
Solyc10g084120.1.1	33	2	1	2	1	10	33.04
Solyc03g119170.2.1	33	1	1	1	1	3.4	32.86
Solyc12g036790.1.1	33	1	1	1	1	9.1	32.85
Solyc07g042520.2.1	33	1	1	1	1	1.6	32.83
Solyc04g015620.2.1	33	2	1	2	1	7.8	32.77
Solyc07g032100.2.1	33	1	1	1	1	1.5	32.71
Solyc07g009330.2.1	33	1	1	1	1	12.6	32.63
Solyc12g008590.1.1	33	2	1	2	1	50	32.58
Solyc05g054090.2.1	33	1	1	1	1	20.8	32.54
Solyc01g094350.2.1	32	1	1	1	1	2.8	32.42
Solyc09g082990.2.1	32	1	1	1	1	4.3	32.38
Solyc03g097910.2.1	32	2	1	2	1	6.3	31.28
Solyc03g082940.2.1	32	1	1	1	1	2.9	32.31
Solyc01g106080.2.1	32	1	1	1	1	3.2	32.3
Solyc10g007480.2.1	32	1	1	1	1	3.1	32.3
Solyc03g120280.1.1	32	1	1	1	1	4.5	32.29
Solyc06g053460.1.1	32	1	1	1	1	8.9	32.22
Solyc02g091580.2.1	32	1	1	1	1	2.1	32.19
Solyc05g056540.2.1	32	1	1	1	1	2.3	32.19
Solyc06g019170.2.1	32	1	1	1	1	1.5	32.19
Solyc07g043310.2.1	32	1	1	1	1	2.7	32.11
Solyc07g053310.2.1	32	1	1	1	1	5.3	31.84
Solyc05g024410.2.1	32	1	1	1	1	4.9	31.8
Solyc00g323130.2.1	32	1	1	1	1	5.2	31.74
Solyc04g008310.1.1	32	1	1	1	1	2.6	31.65
Solyc01g079880.2.1	32	1	1	1	1	5.5	31.61
Solyc01g008360.2.1	32	1	1	1	1	13.8	31.59
Solyc02g092580.2.1	32	1	1	1	1	5.1	31.54
Solyc11g068430.1.1	31	1	1	1	1	16.1	31.47
Solyc01g010750.2.1	31	1	1	1	1	3.7	31.45

Continued next page

Supplemental Table 3. Continued.

Accession[y]	Protein score[x]	Total matches (no.)[w]	Unique matches (no.)[v]	Total sequences (no.)[u]	Unique sequences (no.)[t]	Protein coverage (%)[s]	Highest peptide score[r]
Solyc11g062440.1.1	31	1	1	1	1	2.1	31.41
Solyc06g075810.2.1	31	1	1	1	1	11.2	31.4
Solyc07g049450.2.1	31	2	1	2	1	6.9	29.59
Solyc07g049450.2.1	31	2	1	2	1	6.9	31.34
Solyc01g104680.2.1	31	1	1	1	1	5.9	31.29
Solyc12g013900.1.1	31	1	1	1	1	2.8	31.28
Solyc01g100390.2.1	31	1	1	1	1	2.1	31.25
Solyc11g011920.1.1	31	1	1	1	1	2.2	31.08
Solyc04g082780.2.1	31	1	1	1	1	5.6	31.07
Solyc07g047800.2.1	31	2	1	2	1	13.2	31.06
Solyc03g117600.2.1	31	1	1	1	1	3	30.93
Solyc03g122310.2.1	31	1	1	1	1	4.7	30.82
Solyc10g074980.1.1	31	1	1	1	1	2.4	30.53
Solyc04g080190.2.1	30	1	1	1	1	6.6	30.45
Solyc04g080590.2.1	30	1	1	1	1	4.1	30.35
Solyc05g053540.2.1	30	1	1	1	1	2.1	30.35
Solyc08g016420.2.1	30	1	1	1	1	10	30.3
Solyc09g007630.2.1	30	1	1	1	1	2.8	30.25
Solyc04g082710.2.1	30	1	1	1	1	3	30.19
Solyc02g076720.2.1	30	1	1	1	1	0.9	30.15
Solyc01g010540.2.1	30	1	1	1	1	4.6	30.1
Solyc01g101240.2.1	30	1	1	1	1	2.8	29.92
Solyc01g008530.2.1	30	1	1	1	1	4.3	29.71
Solyc02g068300.2.1	30	1	1	1	1	1.7	29.56
Solyc04g007030.2.1	30	1	1	1	1	1.1	29.53
Solyc09g089880.2.1	29	1	1	1	1	5.6	29.28
Solyc11g068400.1.1	29	1	1	1	1	15.3	29.12
Solyc05g056160.2.1	29	1	1	1	1	4.8	29.06
Solyc09g010440.2.1	29	1	1	1	1	11.5	28.93
Solyc04g072830.2.1	29	1	1	1	1	1	28.89
Solyc01g099420.1.1	29	1	1	1	1	9.5	28.68
Solyc02g032040.1.1	29	1	1	1	1	6.3	28.68
Solyc05g010300.2.1	28	1	1	1	1	4.1	28.37
Solyc05g056290.2.1	28	1	1	1	1	9.1	28.05
Solyc12g009250.1.1	28	1	1	1	1	14.8	27.63
Solyc10g006560.2.1	27	1	1	1	1	17.4	27.3
Solyc09g007350.2.1	27	1	1	1	1	7.7	26.99
Solyc12g056230.1.1	27	3	1	2	1	11.8	26.84
Solyc02g093830.2.1	26	1	1	1	1	2	26.13
Solyc05g049950.2.1	24	2	1	2	1	7.5	10.28
Solyc05g049950.2.1	24	2	1	2	1	7.5	24.2
Solyc04g007760.2.1	22	2	1	2	1	21.2	29.32
Solyc04g007760.2.1	22	2	1	2	1	21.2	22.42
Solyc01g108660.2.1	22	1	1	1	1	3	21.82
Solyc04g009590.2.1	21	1	1	1	1	11.8	20.66
Solyc03g113800.2.1	20	2	1	2	1	6.5	29.03
Solyc12g099660.1.1	16	1	1	1	1	2.8	16.39

[z]Information used for the identification of proteins in iTRAQ analysis of tomato root proteomes.
[y]Protein accession number in the ITAG Protein database (Release 2.3 on 26 Apr. 2011; Sol Genomics Network, Boyce Thompson Institute, Ithaca, NY).
[x]Sum of the individual ion scores.
[w]Total number of peptide-spectral matches to a particular protein below the e-value cutoff.
[v]Total number of unique peptide spectral matches to a particular protein below the e-value cutoff.
[u]Total number of peptide spectral matches to a particular protein with a protein score above the identity threshold.
[t]Total number of unique peptide-spectral matches to a particular protein with a protein score above the identity threshold.
[s]Percentage of the total protein sequence represented by the identified peptides.
[r]Highest highest ion score for each identified proteins.

Supplemental Table 4. Salt and dehydration responsive proteins in tomato roots.[z]

Protein name	Tomato protein accession[x]	LA4133[y]	LA3465[w]	LA2747[v]	LA1958//LA3465[u]
Root system development and structural integrity					
Ran GTPase binding protein	Solyc08g062660.2.1	1.7[t]	1.1	NI[s]	up/nc[r]
TPR domain containing protein	Solyc02g090090.2.1	1.2	1.3[t]	NI	NI
Alpha-mannosidase	Solyc06g068860.2.1	1.4[t]	1.3[t]	NI	NI
Fructose-bisphosphate aldolase[q]	Solyc05g008600.2.1	1.4[t]	1.1	NI	dn/dn
Actin-depolymerizing factor 1	Solyc09g010440.2.1	1.7[t]	1.0	NI	NI
Fasciclin-like arabinogalactan protein	Solyc07g053540.1.1	1.4[t]	1.2	NI	up/dn
Proline-rich cell wall protein	Solyc03g007520.2.1	NI	1.3[t]	NI	NI
Expansin	Solyc08g077910.2.1	1.2	1.8[t]	NI	NI
Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	Solyc03g117600.2.1	1.4	1.8[t]	NI	NI
Caffeoyl CoA 3-O-methyltransferase	Solyc01g107910.2.1	1.8[t]	1.1	NI	up/nc
Xylanase inhibitor	Solyc01g080010.2.1	1.7[t]	1.7[t]	NI	dn/dn
Carbohydrate metabolism					
Sucrase	Solyc02g067840.2.1	1.5[t]	1.4	NI	NI
Sucrose synthase	Solyc07g042550.2.1	1.4[t]	2.2[t]	NI	dn/up
Phosphoglucomutase	Solyc04g045340.2.1	1.6[t]	1.6[t]	dn	NI
UTP-glucose 1 phosphate uridylyltransferase	Solyc11g011960.1.1	1.5[t]	1.6[t]	NI	dn/nc
Transketolase 1	Solyc05g050970.2.1	1.3	1.6[t]	NI	NI
6-phosphogluconate dehydrogenase[q]	Solyc04g005160.1.1	1.3	1.5[t]	NI	dn/up
Enolase	Solyc10g085550.1.1	1.2	1.4[t]	up	dn/nc
Pyruvate kinase	Solyc04g008740.2.1	1.3	1.5[t]	NI	NI
Phosphoglycerate kinase	Solyc07g066600.2.1	1.4[t]	1.3[t]	NI	up/nc
Glyceraldehyde 3-phosphate dehydrogenase[q]	Solyc05g014470.2.1	1.3[t]	1.4[t]	NI	dn/nc
Malate dehydrogenase[q]	Solyc07g062650.2.1	1.4[t]	1.4[t]	dn	dn/dn
Malic enzyme	Solyc05g050120.2.1	1.1	1.7[t]	up	dn/dn
Dihydrolipoyl dehydrogenase	Solyc05g053300.2.1	1.3[t]	1.2	NI	dn/nc
Succinyl-CoA ligase[q]	Solyc06g083790.2.1	1.2	1.5[t]	NI	NI
Citrate synthase	Solyc01g073740.2.1	1.2	1.7[t]	NI	NI
Alcohol dehydrogenase 2[q]	Solyc06g059740.2.1	2.1[t]	2.6[t]	NI	NI
Alcohol dehydrogenase zinc-containing	Solyc09g059040.2.1	2.0[t]	1.9[t]	NI	dn/nc
Chitinase	Solyc10g055820.1.1	1.3[t]	1.2	NI	NI
Endochitinase[q]	Solyc10g055810.1.1	1.3	1.4[t]	NI	NI
Beta-hexosaminidase b	Solyc05g054710.2.1	1.2	2.9[t]	NI	NI
ATP regeneration and transmembrane ion transport					
Mitochondrial ADP/ATP carrier proteins	Solyc11g062130.1.1	1.5[t]	1.8[t]	NI	dn/nc
Mitochondrial ATP synthase[q]	Solyc00g009020.2.1	1.3[t]	1.1	NI	NI
ATP synthase[q]	Solyc12g55800.1.1	1.3[t]	1.5[t]	up	NI
ATP synthase subunit alpha	Solyc11g039980.1.1	1.1	1.5[t]	NI	NI
H-ATPase	Solyc06g071100.2.1	1.3	1.7[t]	NI	NI
V-type proton ATPase subunit a[q]	Solyc01g110120.2.1	1.1	1.5[t]	NI	up/nc
Adenosine kinase	Solyc10g086190.1.1	1.3	1.6[t]	NI	dn/dn
Amino acid metabolism					
Alanine aminotransferase	Solyc03g123610.2.1	1.5	1.5[t]	NI	dn/nc
N-acetyl-gamma-glutamyl-phosphate reductase	Solyc01g108660.2.1	1.2	1.4[t]	NI	NI
Asparagine synthetase	Solyc01g079880.2.1	1.8[t]	1.9[t]	NI	dn/nc
Aspartate aminotransferase	Solyc07g055210.2.1	1.3[t]	1.6[t]	NI	NI
3-isopropylmalate dehydratase large subunit	Solyc07g052350.2.1	1.4	1.6[t]	NI	dn/dn
Amidase hydantoinase/carbamoylase	Solyc09g083410.2.1	1.3	2.5[t]	NI	NI
3-deoxy-7-phosphoheptulonate synthase	Solyc04g074480.2.1	1.4[t]	1.7[t]	NI	dn/up
Phosphoserine aminotransferase	Solyc02g082830.1.1	1.4	1.6[t]	NI	NI
Formate dehydrogenase	Solyc02g086880.2.1	2.0[t]	1.5[t]	NI	NI
L-threonine 3-dehydrogenase	Solyc01g006510.2.1	1.4[t]	NI	NI	NI
5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase[q]	Solyc10g081510.1.1	1.4[t]	2.1[t]	up	dn/nc
Adenosylhomocysteinase[q]	Solyc09g092380.2.1	1.3[t]	1.5[t]	up	dn/nc
O-methyltransferase[q]	Solyc03g080180.2.1	2.2[t]	1.7	NI	NI

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Supplemental Table 4. Continued.

Protein name	Tomato protein accession[x]	LA4133[y]	LA3465[w]	LA2747[v]	LA1958//LA3465[u]
Methylenetetrahydrofolate reductase	Solyc11g008870.1.1	1.2	1.8[t]	NI	NI
	Fatty acids				
Acetyl-CoA carboxylase biotin carboxyl carrier protein	Solyc01g008330.2.1	1.5[t]	1.2	NI	NI
3-ketoacyl CoA thiolase 1	Solyc09g091470.2.1	1.4	1.3[t]	NI	NI
Lipase-like	Solyc02g077420.2.1	0.9	2.3[t]	NI	NI
Patatin	Solyc08g006860.2.1	1.9[t]	0.7[t]	NI	up/nc
	Detoxification				
Aldehyde dehydrogenase	Solyc03g114150.2.1	1.5	2.0[t]	NI	NI
Cyanate hydratase[q]	Solyc09g090430.2.1	1.6[t]	1.5[t]	NI	NI
Divalent cation tolerance protein CutA	Solyc04g076050.2.1	1.4[t]	NI	NI	NI
Polyphenol oxidase	Solyc08g074680.2.1	1.1	1.4[t]	NI	nc/up
	Proteins affecting diverse cellular activities				
HAT family dimerization domain containing protein	Solyc12g070140.1.1	NI	2.0[t]	NI	NI
Chaperonin[q]	Solyc05g053470.2.1	1.5	1.4[t]	NI	nc/dn
Chaperone DnaK[q]	Solyc01g106210.2.1	1.3[t]	1.0	NI	up/nc
FK506-binding protein 2	Solyc09g057670.2.1	1.5[t]	1.1	up	up/nc
T-complex protein theta subunit	Solyc01g088080.2.1	1.4[t]	1.7	NI	dn/nc
T-complex protein 1 subunit alpha	Solyc01g090750.2.1	1.2	1.5[t]	NI	dn/nc
Heat shock protein C62.5	Solyc04g081570.2.1	1.1	1.3[t]	NI	NI
Heat shock protein 90	Solyc12g015880.1.1	1.1	1.7[t]	NI	NI
Heat shock protein 4	Solyc12g043110.1.1	1.4[t]	1.4[t]	NI	dn/dn
Dehydrin COR47[q]	Solyc04g071610.2.1	1.7[t]	1.5	NI	NI
Dehydrin[q]	Solyc04g082200.2.1	1.2	0.7[t]	NI	up/up
Salt stress root protein RS1[q]	Solyc10g005100.2.1	1.5[t]	1.2	NI	up/nc
ASR4[q]	Solyc04g071620.2.1	5.3[t]	2.6[t]	NI	up/nc
Ultraviolet excision repair protein RAD23	Solyc02g063130.2.1	1.4[t]	1.1	NI	up/nc
Elicitor-responsive protein 3	Solyc08g080680.2.1	1.4[t]	1.0	NI	NI
Major allergen Mal d 1	Solyc09g091000.2.1	4.9[t]	6.4[t]	NI	up/up
REF-like stress related protein 1	Solyc05g015390.2.1	1.3	1.5[t]	NI	NI
Ubiquitin-fold modifier 1	Solyc08g075780.2.1	1.5[t]	1.0	NI	NI
Ascorbate peroxidase	Solyc06g005160.2.1	1.6[t]	1.3[t]	NI	nc/up
Ascorbate peroxidase 7[q]	Solyc06g060260.2.1	1.5[t]	1.2	NI	NI
Catalase	Solyc12g094620.1.1	2.6[t]	2.5[t]	NI	dn/nc
Cytoplasmic glutaredoxin thioltransferase	Solyc06g005260.2.1	1.8[t]	1.0	NI	NI
Dehydroascorbate reductase	Solyc05g054760.2.1	1.4[t]	1.5[t]	NI	NI
Glutathione-disulfide reductase	Solyc09g091840.2.1	1.4[t]	1.9[t]	NI	NI
Monodehydroascorbate reductase[q]	Solyc09g009390.2.1	1.4[t]	1.7[t]	NI	dn/up
Peroxidase 1	Solyc00g072400.2.1	0.7[t]	1.8	NI	NI
Peroxidase 4	Solyc04g071890.2.1	1.5[t]	1.4[t]	NI	up/nc
Peroxiredoxin[q]	Solyc01g007740.2.1	1.6[t]	3.0	NI	up/nc
Superoxide dismutase	Solyc01g067740.2.1	2.4[t]	1.1	up	up/nc
Thioredoxin	Solyc04g080850.2.1	1.5[t]	1.2	up	up/nc
Ferritin	Solyc06g050980.2.1	1.6[t]	NI	NI	up/nc
Annexin[q]	Solyc04g073990.2.1	1.3[t]	1.2	NI	dn/dn
Annexin 2[q]	Solyc04g055170.2.1	1.8[t]	2.0[t]	NI	dn/dn
Calmodulin	Solyc01g008950.2.1	1.4[t]	0.7[t]	NI	up/nc
Receptor like kinase, RLK	Solyc01g102700.2.1	1.7[t]	1.4[t]	NI	NI
Wound/stress protein[q]	Solyc03g096540.2.1	1.3[t]	1.0	NI	up/dn
Histidine triad (HIT) protein	Solyc10g081310.1.1	1.5[t]	1.0	NI	up/nc
ADP-ribosylation factor	Solyc01g008000.2.1	1.1	1.4[t]	NI	NI
GTP-binding protein	Solyc02g023970.2.1	1.3	1.4[t]	NI	dn/nc
Phosphatidylglycerol/phosphatidylinositol transfer protein	Solyc01g006900.2.1	1.4[t]	1.1	NI	up/nc
Remorin 1	Solyc03g025850.2.1	2.4[t]	1.0	NI	up/nc
Coatomer subunit gamma	Solyc01g109540.2.1	1.5[t]	1.5[t]	NI	NI
Alpha-soluble NSF attachment protein	Solyc05g052310.2.1	1.1	1.6[t]	NI	NI

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Supplemental Table 4. Continued.

Protein name	Tomato protein accession[x]	LA4133[y]	LA3465[w]	LA2747[v]	LA1958//LA3465[u]
Translocon-associated protein subunit beta	Solyc02g094440.2.1	1.0	1.3[t]	NI	NI
Mitochondrial import receptor subunit TOM20	Solyc02g068130.2.1	1.5[t]	1.0	NI	NI
Protein turnover and post-translational modification					
Mitochondrial processing peptidase alpha subunit	Solyc12g008630.1.1	1.3[t]	1.1	NI	dn/nc
Cathepsin B-like cysteine proteinase	Solyc12g088670.1.1	1.3[t]	1.1	NI	dn/nc
Protease Do-like (S2 serine-type protease)	Solyc02g086830.2.1	1.5[t]	0.9	NI	NI
Chymotrypsin inhibitor-2	Solyc08g080630.2.1	1.4[t]	1.0	NI	up/nc
Leucyl aminopeptidase	Solyc12g010040.1.1	1.4[t]	1.5[t]	NI	dn/nc
DNA replication and gene expression					
MFP1 attachment factor 1	Solyc04g078380.1.1	2.0[t]	NI	NI	NI
Single-stranded DNA binding protein	Solyc10g086150.1.1	2.0[t]	1.0	NI	NI
Basic leucine zipper and W2 domain protein	Solyc05g055770.2.1	1.8[t]	NI	NI	NI/up
Glycine-rich RNA-binding protein	Solyc01g109660.2.1	1.5[t]	0.8	NI	NI
Tudor/nuclease domain-containing protein	Solyc03g118020.2.1	1.2	1.5[t]	NI	NI
Glycine rich protein-RNA binding protein	Solyc05g053780.2.1	1.4	0.7[t]	NI	NI
Translation elongation EFTu/EF1A	Solyc06g069020.2.1	1.7[t]	1.9[t]	NI	NI
EF1B	Solyc07g016150.2.1	1.3[t]	0.8	NI	NI
Elongation factor Tu	Solyc09g073000.2.1	1.3[t]	1.0	NI	NI
Elongation factor EF-2	Solyc08g062920.2.1	1.3[t]	1.4[t]	NI	dn/dn
Insulin-like growth factor 2 mRNA-binding protein 2	Solyc12g095960.1.1	1.4[t]	1.0	NI	NI
30S ribosomal protein S5	Solyc04g063290.2.1	1.3[t]	1.1	NI	dn/dn
30S ribosomal protein S19	Solyc02g082000.2.1	1.0	0.6[t]	NI	dn/dn
60S ribosomal protein L22-2	Solyc01g099830.2.1	0.7	0.6[t]	NI	NI
60S ribosomal protein L35	Solyc04g010240.2.1	0.8	0.5[t]	NI	up/dn
60S ribosomal protein L6	Solyc11g012110.1.1	0.6	0.6[t]	NI	dn/nc
40S ribosomal protein S13	Solyc01g091220.2.1	0.8	0.4[t]	NI	NI
40S ribosomal protein S24	Solyc01g097870.2.1	0.7[t]	0.7	NI	NI
40S ribosomal protein S7	Solyc06g069090.2.1	1.0	0.7[t]	NI	NI

[z]Proteins identified in the current salt study and their expression previously found in salt and dehydration treatments of different tomato accessions.

[y]Protein accession number in the ITAG Protein database (Release 2.3 on 26 Apr. 2011; Sol Genomics Network, Boyce Thompson Institute, Ithaca, NY).

[x]Fold (treated/control) change in salt treatment of tolerant cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) LA4133 in the current study.

[w]Fold (treated/control) change in salt treatment in susceptible tomato (*S. lycopersicum*) 'Walter' LA3465 in the current study.

[v]Salt treatment of *Solanum chilense (*Zhou et al., 2011).

[u]Dehydration treatment of tolerant *S. chilense* LA1958 and susceptible 'Walter' LA3465 (Zhou et al., 2013).

[t]Protein with significant changes from salt-treated to untreated groups.

[s]NI = not identified in the respective tomato accession.

[r]Protein changes from treated group to non-treated group: up = induced, dn = repressed, nc = no change.

[q]Salt-response protein in *Arabidopsis thaliana* annotated in String Database (Franceschini et al., 2013).