SYSTEMIN AND PROSYSTEMIN: NOVEL BENEFITS FOR SUSTAINABLE PROTECTION OF TOMATO CROP

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per sempre indelebile

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Riassunto

La crescente richiesta di soddisfare il fabbisogno alimentare della popolazione mondiale in continuo aumento pone l'urgenza di incrementare le rese produttive agricole, salvaguardando i raccolti dai principali agenti di danno di natura biotica e abiotica (Seddon et al., 2021). In aggiunta, gli attuali cambiamenti climatici esacerbano gli effetti avversi che tali condizioni di stress hanno sulle colture agrarie (Corwin, 2021). Negli scorsi decenni per il contenimento degli organismi dannosi è stato effettuato un ampio utilizzo di sostanze chimiche quali pesticidi ed erbicidi (Guo et al., 2021). Il rischio connesso con l'uso continuativo di tali sostanze include il bioaccumulo di tossine negli alimenti, effetti indesiderati nei confronti di organismi utili, problemi di farmaco resistenza e la contaminazione dell'aria e dell'acqua con conseguenti rischi per la salute umana e per l'ambiente (Rincón et al., 2020). Tali aspetti indesiderati rendono necessaria un'inversione di rotta delle pratiche agricole in termini di sostenibilità ambientale. L'interesse della comunità scientifica nel settore della scoperta e dello sviluppo di soluzioni alternative e a basso impatto ambientale per il contenimento degli organismi nocivi in agricoltura è quindi in continua crescita. In questo contesto, l'induzione delle resistenze endogene delle piante è un utile approccio. Essa consiste nello stimolare l'attivazione di meccanismi di difesa nelle piante mediante elicitori, molecole di sintesi o naturali che mimano l'attacco di un patogeno o uno stato di stress (Iriti and Vitalini, 2020). Tra gli elicitori di origine vegetali figura una famiglia di ormoni peptidici, chiamati sistemine, che sono coinvolti nell'attivazione dei geni di difesa in risposta a ferita prodotta da insetti erbivori o da danno meccanico (Ryan and Pearce, 2003). La Sistemina (Sys) di pomodoro, di lunghezza pari a 18 amminoacidi, è stato il primo peptide ad azione ormale indentificato in pianta (Pearce et al., 1991). Tale peptide è localizzato all'estremità carbossi-terminale di un pro-ormone di 200 aminoacidi chiamato Prosistemina (ProSys). L'interazione Sys-recettore di membrana SYR1 (SYS receptor 1) induce l'attivazione di una complessa cascata di segnali intracellulari che tramite la depolarizzazione della membrana plasmatica, l'incremento della concentrazione intracellulare del calcio, l'attivazione di MAP chinasi portano all'induzione del pathway degli octadecanoidi (Wang et al., 2018; Zhang et al., 2020). I prodotti principali di questo processo sono l'acido Jasmonico (JA) e suoi derivati responsabili dell'induzione di geni precoci e tardivi della risposta al danno.

La somministrazione esogena del peptide su foglie di piante di pomodoro attiva geni associati alla difesa, rendendo le piante resistenti a larve del lepidottero *Spodoptera littoralis* ed al fungo fitopatogeno *Botrytis cinerea* e modifica qualitativamente e quantitativamente la miscela di volati emessi dalla pianta aumentando l'attrattività dei nemici naturali degli insetti (Coppola et al., 2019a). Risultati simili sono stati ottenuti su piante di vite (Vitis vinifera L.) e melanzana (Solanum melongena L.) che non presentano nel loro genoma il gene ProSys ma che hanno ortologhi di SYR1 (Molisso et al., 2020). È stato recentemente dimostrato che una strategia utile per potenziare l'efficacia degli induttori di resistenza è quella di combinarli tra loro (Tsoulnara and Port, 2016; Abd-El-Khair et al., 2019). Attualmente, prodotti a base di microorganismi benefici appartenenti al genere *Trichoderma*, sono tra i principali bioformulati impiegati

in agricoltura e presenti in commercio (Woo et al., 2014). Sfortunatamente il loro effetto protettivo è fortemente influenzato dalle condizioni ambientali rendendo così l'utilizzo esclusivo di tali microrganismi non sufficiente per la protezione delle colture. Partendo dalla considerazione che sia la Sys che il *Trichoderma* attivano il pathway dell'JA, un hub centrale nelle risposte di difesa contro insetti e funghi, abbiamo ipotizzano che il loro utilizzo combinato potesse risultare in un effetto protettivo potenziato contro gli agenti di danno. È stato inizialmente verificato che la Sys non avesse alcune effetto inibitorio diretto sulla crescita del fungo benefico, prerequisito essenziale per tale tipo di sperimentazione (capitolo 1). Successivamente, è stato dimostrato che piante di pomodoro nate da seme confettato con spore di *Trichoderma afroharzianum* (ceppo T22) e trattate mediante applicazione fogliare del peptide Sys, risultavano protette dall'attacco del fungo terricolo *Fusarium Oxysporum*, agente patogeno di una delle malattie del suolo più comuni in tale coltura (Lecomte et al., 2016). Inoltre, il singolo trattamento non conferiva protezione alla pianta. La combinazione è risultata efficace anche contro la Tignola del pomodoro (*Tuta absoluta*), insetto fillominatore che scava mine, dapprima all'interno delle foglie, poi nel fusto e infine nelle bacche a qualsiasi stadio di maturazione, causando ingenti danni alla produzione agricola (Agbessenou et al., 2020). L'incremento della capacità difensiva della pianta oggetto del doppio trattamento è stato associato ad una più efficiente attivazione del pathway dell'JA rispetto a quanto accade nelle piante sottoposte ai due singoli trattamenti. Questo risultato è stato confermato monitorando il livello di espressione di geni chiave di tale pathway e la produzione di JA e metaboliti ad esso associati mediante analisi metabolomica targeted. Tali risultati hanno confermato che lo spettro di efficacia della Sys può essere esteso a nuovi patogeni mediante la combinazione con altri induttori di resistenza quali microrganismi benefici.

È noto che l'JA è coinvolto anche nell'aumento della tolleranza delle piante a fattori di stress abiotici quali salinità e siccità (Orsini et al., 2010; Zhang et al., 2020). A tal proposito abbiamo dimostrato che piante irrigate con una soluzione contenente Sys ad una concentrazione finale di 100pM mostrano tolleranza allo stress da NaCl (capitolo 1). Tale fenotipo è stato associato all'incremento dei trascritti di geni codificanti trasportatori di ioni quali *Salt Overly Sensitive1, Sodium-hydrogen antiporters 1* e *High-Affinity Potassium Transporter 1*. Questo suggerisce che le piante trattate hanno una maggiore capacità di regolare il livello di sodio nel citosol, aspetto essenziale per la tolleranza delle piante al sale. Inoltre, le piante mostrano l'incremento di trascritti dei geni *superossido dismutasi*, e *ascorbato perossidasi*, coinvolti nell'eliminazione delle specie reattive dell'ossigeno proteggendo la pianta dal danno ossidativo che si verifica a seguito di uno stress. Le stesse piante mostrano anche un incremento dei trascritti codificanti per l'*Inibitore di proteasi II*. Gli inibitori di proteasi svolgono un ruolo chiave per bilanciamento dello stress osmotico oltre che per la tolleranza a diversi fattori di stress biotico. La Sys sembra quindi essere un importante elemento del crosstalk nelle risposte della pianta a stress abiotici e biotici.

È stato dimostrato che lo stato di maggiore capacità difensiva della pianta può essere mantenuto per lunghi periodi fino ad essere trasmesso alle generazioni successive (Hilker and Schmülling, 2019; Bhadouriya et al., 2021). Qui è stato provato che il trattamento con la Sys induce una memoria a lungo termine dato che la progenie F_1 di piante trattate è resistente all'attacco del fungo necrotrofo *B. cinerea* (capitolo 2). Dati trascrittomici ottenuti da piante parentali, 24h dopo l'applicazione di Sys, mostrano un overlap di 768 geni differenzialmente espressi con quelli della loro progenie, suggerendo che il trattamento con il peptide produce un segnale che è trasmesso da una generazione all'altra. È noto, che tale tipo di memoria a lungo termine può essere programmata epigeneticamente (Mladenov et al., 2021). Per epigenetica si intendono modificazioni ereditabili che inducono variazioni dell'espressione genica senza però alterare la sequenza del DNA e che avvengono mediante diversi meccanismi che includono la metilazione del DNA, la modifica degli istoni e l'azione degli RNA non codificanti (Thiebaut et al., 2019). La metilazione del DNA consiste nell'aggiunta di un gruppo metile in punti specifici del DNA, generalmente bloccando l'espressione del gene impedendo la trascrizione del DNA. Il processo opposto, la demetilazione, in genere, porta all'espressione del gene. Per modificazione degli istoni ci si riferisce invece, all'aggiunta di gruppi chimici agli istoni. A seconda del tipo (i.e acetilazione, metilazione e forsforilazione) e del sito di modifica c'è una variazione nella struttura della cromatina, che la rende più o meno accessibile all'RNA polimerasi e quindi alla trascrizione (Crespo-Salvador et al., 2020). Lo studio dei dati trascrittomici prodotti ha evidenziato la regolazione di diversi geni coinvolti in tali tipi di modifiche (i.e DNA metiltrasferasi, DNA demetilasi, metiltransferasi istonica specifiche per la lisina). Questo ci ha indotto a ricercare possibili modiche istoniche presenti nella regione del promotore di geni di difesa overespressi in entrambe le generazioni. Mediante immunoprecipitazione della cromatina (chip) effettuata utilizzando anticorpi che riconoscono specifiche modifiche chimiche a carico degli istoni, in questo caso la trimetilazione della lisina in posizione 4 sull'istone H3, e successiva amplificazione per RT-PCR è stato possibile osservare che il promotore del gene di difesa *PAL* (fenilalanina ammonio liasi) contiene questa modifica istonica. Essa è considerata un marcatore epigenetico coinvolto nell'attivazione della trascrizione dei geni. Nessuna variazione del livello di metilazione del DNA è stata evidenziata nei geni analizzati. A nostra conoscenza, questa è la prima evidenza che il trattamento di piante di pomodoro con Sys induce risposte di difese intergenerazionali. Ulteriori analisi saranno necessarie per chiarire i segnali molecolari che vengono trasmessi alla progenie delle piante trattate.

Per lungo tempo l'attività biologica della ProSys è stata attribuita essenzialmente al peptide Sys. Tuttavia, recenti ricerche bioinformatiche e spettroscopiche hanno mostrato che ProSys è una proteina intrinsecamente disordinata (IDP) cioè priva di una struttura tridimensionale stabile o ordinata (Buonanno et al., 2018). Questa peculiare flessibilità delle IDP permette loro di assumere un ampio spettro di strutture a seguito di interazione con partner molecolari diversi. Le IDP svolgono un ruolo centrale nella regolazione delle vie di trasduzione di vari segnali, in eventi di *signaling,* di risposta a stress, di regolazione del ciclo cellulare (Wright and Dyson, 2015; Uversky, 2019). La molteplicità strutturale di tali proteine suggerisce che la ProSys possa avere un ruolo biologico ben più importante del solo rilascio del peptide Sys. Essa, infatti, legandosi a partner molecolari diversi a seconda delle condizioni

ambientali potrebbe, di volta in volta, innescare l'attivazione di geni e segnali coinvolti nella protezione della pianta contro diversi agenti di stress. Inoltre, è stato recentemente dimostrato che l'espressione in pomodoro del gene ProSys modificato, nel quale è stata rimossa la regione codificante per Sys rende le piante resistenti a funghi e insetti e induce la via di trasduzione del segnale mediata dagli oligogalatturonidi, frammenti di pectina che si originano dalla parete cellulare a seguito di ferita e che attivano l'immunità innata della pianta (Molisso et al., 2022b). Inoltre, piante trattate con ProSys (1-178), il precursore privo della sequenza Sys, sono resistenti all'attacco di diversi agenti dello stress biotico. Questi dati dimostrano che la regione N terminale di ProSys è biologicamente attiva. A tal proposito, due frammenti proteici localizzati in questa regione del precursore e aventi le caratteristiche di IDP, sono stati prodotti per via ricombinante (Molisso et al., 2022a) e qui saggiati su piante di pomodoro per verificarne la loro attività biologica (capitolo 3). Questi peptidi, denominati P1-70 e P1-120 perché contenenti rispettivamente i primi 70 e 120 amminoacidi della ProSys sono biologicamente attivi a concentrazioni femtomolari, quindi ormonali. Le piante trattate con P1-70 e P1-120 sono resistenti all'attacco dell'insetto masticatore *Spodoptera littoralis* e dall'infezione del fungo *B. cinerea*. Il fenotipo resistente è associato ad un incremento dei trascritti di geni legati alla difesa. Inoltre, P1-70 e P1-120 hanno mostrato un'attivazione diversa dei geni in esame. Questo può essere collegato anche alle loro diverse performance contro i patogeni testati. P1-70 è più efficace contro insetto mentre P1-120 contro fungo. Ulteriori esperimenti hanno provato che entrambi i frammenti non hanno alcuno effetto tossico diretto sui patogeni testati, confermando che l'effetto protettivo è dovuto alla percezione del frammento proteico da parte della pianta e alla successiva stimolazione delle sue difese endogene. Inoltre, sono stati effettuati test di tossicità sia su cellule umane che su microalghe, che hanno dimostrato che P1-70 e P1-120 non sono tossici per gli organismi non-target. Entrambi i frammenti sono stati brevettati in Italia ed è in corso l'estensione internazionale del brevetto.

Nell'ottica di un'agricoltura più sostenibile, l'utilizzo di peptidi e proteine vegetali in grado di stimolare le difese endogene della pianta rappresenta un valido strumento biotecnologico che punta alla riduzione dell'utilizzo dei pesticidi in campo, preservando allo stesso tempo la qualità e quantità dei raccolti anche in condizioni ambientali sfavorevoli. Qui, è stato dimostrato che il peptide Sys può essere utilizzato in combinazione con altri organismi che fungono da induttori di resistenza per la pianta, quali il fungo benefico *T. harzianum* T22. L'efficacia della Sys risulta rafforzata ed ampliata a nuovi patogeni. Inoltre, l'irrigazione di piante di pomodoro con una soluzione con Sys conferisce difesa anche a fattori di stress abiotici quali lo stress salino. L'effetto protettivo della Sys può essere trasferito anche alla progenie delle piante trattate. La produzione di semi aventi un'aumentata resistenza ai patogeni grazie a trattamenti sulle generazioni parentali è un aspetto innovativo che può presentare numerosi vantaggi per l'agricoltura. Infine, nuovi frammenti proteici derivanti dalla ProSys sono risultati attivi contro vari agenti di danno. È evidente, dunque, che dallo studio approfondito delle risposte fenotipiche e molecolari che le piante usano per contrastare i danni imposti da vari agenti di stress e dalla identificazione dei geni con ruolo chiave nelle difese, scaturiscono importanti conoscenze che possono condurre alla definizione di nuove biotecnologie per la difesa sostenibile delle colture agrarie.

Summary

The variations in global climate have increased the attention of researchers worldwide, as these changes negatively affect agriculture by reducing crop productivity and food security. Climate change is a dynamic, complex system of alterations of environmental conditions that affect abiotic and biotic components of the world. It results in alteration in environmental conditions such as intensity of rainfall, soil salt concentration and temperature that lead to rise in new pests, weeds and pathogens. To overcome the impact of abiotic stressors, many strategies could be considered to support plant growth including the use of chemical induction of endogenous defense. Recent research suggests that chemical induction is a promising field in crop stress management because plants can be prepared (or primed) by chemical agents to increase their tolerance to various environmental stresses. To overcome pesticide drawbacks, growing interest has arisen in plant biotechnology towards the study of new molecules able to prevent, reduce or eradicate plant pests. In the current scenario, plant resistance inducers, acting by stimulating plant defense mechanisms, are seen as an eco-friendly and promising option to conventional pesticides, and their implementation in integrated pest management strategy is strongly encouraged. The tomato peptide Systemin (Sys) proved to be a very effective activator of plant defense in tomato, grapevine, and eggplant. It is an octadecapeptide proteolytically released, upon wounding and herbivore attack, from its precursor Prosystemin (ProSys). The interaction of Sys with its receptor activates the octadecanoid pathway and the production of Jasmonic Acid (JA), its derivatives and other molecules able to interfere with the colonization of fungal pathogens (e.g., the necrotrophic fungus *Botrytis cinerea*) or the growth and survival of insect pests (e.g., the noctuid moth *Spodoptera littoralis*). A novel approach to increase plant disease control is to combine different resistance inducers (e.g., chemical and/or biological). In chapter 1, we show that plant treatment with *Trichoderma afroharzianum* T22, one of the most widely used plant beneficial fungi in agriculture, and Sys confers protection against the fungal pathogen *Fusarium oxysporum,* and the insect pest *Tuta absoluta.* The observed defensive response was associated with an increase of JA and the expression of related genes and metabolites, and a decrease of Salicylic acid and its metabolites. Since plant responses to biotic and abiotic stress agents have some overlapping component, we investigated a possible role of Sys in plant protection from salt stress. We report that a soil drench of Sys solution increases salt stress tolerance by the upregulation of sodium transporters, and the enhancement of the cellular antioxidant power. Several evidences reported that the state of induced defense can be maintained through generations. In chapter 2, we show that Sys treatment induces a long-term stress memory since the progeny of treated plants showed reduced *B. cinerea* damages when attacked. Transcriptomic data of parental plants 24h post Sys treatments revealed an overlap of 768 differentially expressed genes (DEGs) with those of their progeny suggesting that Sys treatment induces a signal that is transmitted to progeny. Since stress memory can be programmed epigenetically, we investigated the epigenetic regulation of a subset of defense related DEGs common to both transcriptomic datasets, showing that the promoter region of PAL gene was enriched with an increased level of tri-methylation of lysine 4 on histone H3, a chromatin mark generally associated with gene activation. Sys was traditionally considered as the main actor of tomato resistance. Recent evidences suggest that ProSys is not only the precursor of Sys peptide but likely contribute itself to defense responses. Two different ProSys fragments, not including Sys, were used in bioassays to evaluate their biological activity. In chapter 3, we proved that both fragments were active at femtomolar concentration, being able to modulate the expression of defense-related genes and protect tomato plants against noctuid moth and a necrotrophic fungal pathogen. Interestingly, the biological activity of the two fragments is not overlapping for both and for Sys and does not show any toxicity on non-target organisms. The identification of these novel protein fragments may lead to a better understanding of ProSys defense mechanism. In addition, they represent novel tools to enhance plant stress resilience reducing the use of agrochemicals.

Chapter 1

Systemin supply alone or in combination with *Trichoderma afroharzianum* T22 improves tomato protection against biotic and abiotic stresses

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Abstract

Due to global warming, crops encounter an increased number of biotic and abiotic stressors, which severely impair their growth and production performance. In the present context of sustainable agriculture and growing demand for healthy food, plant resistance inducers acting by stimulating plant defense mechanisms, are seen as an eco-friendly and promising option to conventional pesticides, and their implementation in integrated pest management strategy is strongly encouraged. Systemin is a tomato peptide able to enhance plant response against a wide range of stress agents. A novel approach to increase plant disease control is to combine different resistance inducers (e.g., chemical and/or biological). *Trichoderma* spp. are among the most widely used plant beneficial fungi in agriculture.

Here, we show that plant treatment with *Trichoderma afroharzianum* (strain T22) and Systemin confers protection against the fungal pathogens *Fusarium oxysporum,* and the insect pest *Tuta absoluta.* The observed defensive response was associated with an increase of Jasmonic Acid and the expression of related genes and metabolites, and a decrease of Salicylic acid and its metabolites. Since plant responses to biotic and abiotic stress agents have some overlapping component, here we investigated a possible role of Systemin in plant protection from salt stress. We report that a soil drench of Systemin solution increases tomato salt stress tolerance by the upregulation of the main sodium transporters, the enhancement of the cellular antioxidant power, and the balance of the protease activity induced by salt stress. These results suggest that Systemin may represent an important component of the crosstalk between biotic and abiotic stress responses in plants. The peptide could fulfill an important and much coveted task that is the protection of crop from biotic and abiotic stresses.

1.1 Introduction

Due to the rapidly climate changing and global warming there is an urgent need to discover and develop new and more sustainable strategies of crop protection that meet the present and future needs of a growing world population (Seddon et al., 2021). Agriculture is directly linked to climate change. Changes in precipitation patterns, atmospheric CO_2 concentration, and alteration of global temperature, resulted in rising sea level, salinity alterations in arable land, crop yield and plant diversity modification (Corwin, 2021). Overall, these events impact the agricultural productivity. Hence, it is pivotal to find new strategies to increase plant tolerance to stress exposure for ensuring food safety and security.

Tomato (*Solanum lycopersicum* L.) is the second most important vegetable crop after potato (*Solanum tuberosum* L.), with cultivation covering 4.85 million ha and annual fruit production amount to 182.3 million tons (FAOStat, 2019). Large amounts of pesticides are needed to protect the crop from pathogens and pests (Rincón et al., 2020; Guo et al., 2021) with well-known undesirable effects on the environment (pollution, soil depletion, biodiversity loss) and human health (Rincón et al., 2020). Public concerns encouraged the research for alternative strategies of plant protection that are effective, reliable, and sustainable (Iriti and Vitalini, 2020). Research on plant-insect and plant-microbe interactions, both beneficial and pathogenic, is crucial to gain a better understanding of these intricate relationships from which it is possible to derive knowledge and tools for the development of new crop protection strategies. Plants detect pathogen attack through the perception non-self-molecules belonging to conserved microbial signatures, named microbe-associated molecular patterns (MAMPs). MAMPs consist of microbial structural components like bacterial lipopolysaccharide, flagellin, lipoproteins, peptidoglycans, fungal chitin and also secreted toxins or enzymes such as fungal xylanase or endopolygalacturonase (Savatin et al., 2014). In the presence of these molecules, plants activate innate immune responses and display enhanced resistance to a broad spectrum of microbial pathogens. In addition to pathogen attack, the relocation of endogenous molecules as a result of tissue or cellular damage, is perceived as a danger signal that also leads to the induction of innate immune responses. Recently, it was proposed by Gust (Gust et al., 2017) that host-derived elicitors can be divided into two categories: Damage-Associated Molecular Patterns (DAMPs) and phytocytokines. DAMPs are primary endogenous danger signals and include host molecules such as cell wall- derived fragments that are passively released after cell damage and disruption. Phytocytokines are secondary endogenous danger signals, more specifically small peptides secreted after damage perception to bind cell membrane receptors and amplify the immune response. They include three peptide families discovered by Ryan and his group during their studies to identify the Systemin (Sys) peptide (Ryan et al., 2002). The perception of non-self and endogenous molecules triggers a complex cascade of signaling events, partially overlapping, involving ion fluxes such as Ca^{2+} influx, the production of reactive oxygen species (ROS) and nitric oxide (NO), and the activation of mitogen-activated protein kinases (MAPKs). These early events induce a transcriptional reprogramming of primary and secondary metabolisms such as the induction defense-related genes antimicrobial compounds, proteins involved in the hypersensitive response (HR) (Hückelhoven, 2007). Overall, these defense reactions are finely regulated by phytohormones to finally inhibit or delay pathogen infection, thus ensuring a basal plant resistance to pathogens. The activation of plant immunity led to the development of induced resistance (IR) a plant strategy to counteract pests (Wiesel et al., 2014).

Plant resistance inducers (PRIs), also known as elicitors, can be purified MAMPs, DAMPs, peptides, biological organisms, natural extracts, DNA and volatile organic compounds (VOCs), (Walters and Fountaine, 2009). Several active substances are registered as elicitors in the European Union (Iriti and Vitalini, 2020). These products are innovative tools in crop protection that are not directly toxic for the pathogens but affect the plant host immune system (Sandroni et al., 2020). The tomato peptide Sys proved to be a very effective elicitor of plant defense in tomato, grapevine, and eggplant (Coppola et al., 2019a; Molisso et al., 2020). Sys was the first peptide signal discovered in plants (Pearce et al. 1991). It is an octadecapeptide proteolytically released, upon wounding and herbivore attack, from the carboxy terminus of its 200 amino-acid precursor Prosystemin (ProSys) (Ryan and Pearce 2003). The interaction of Sys with its receptor actives the octadecanoid pathway and the production of Jasmonic Acid (JA) and its derivatives (JAs) (Pearce et al. 1991). Recently, it was demonstrated that exogenous supply of Sys by spray or hydroponics induces an array of defense-related responses leading to the final accumulation of proteinase inhibitors (PIs) and other molecules able to interfere with the colonization of fungal pathogens (e.g., the necrotrophic fungi *Botrytis cinerea*) or the growth and survival of insect pests (e.g., the noctuid moth *Spodoptera littoralis*) (Coppola et al. 2019a; Molisso et al. 2021). In addition, Sys-treated plants proved to be more attractive for pest natural enemies because of the modified blend of volatile compounds (VOCs) emitted, which is known to be used by predators and parasitoids of phytophagous insects to locate their preys and hosts (Coppola et al., 2019a). The observed plant phenotypes were correlated with a modified gene expression pattern, with an increased expression of early and late genes of the octadecanoid pathway.

The control of plant disease and pest , can be improved by combining PRIs with biocontrol agents, e.g., living microorganisms, which are able to control pest-induced damage on plants either through stimulation of plant defense or by limiting plant pathogen populations through mycoparasitism, competition, and antibiosis (Tucci et al., 2011; Battaglia et al., 2013; Coppola et al., 2019b). For example, previous studies suggested that Sys might play an important role in the modulation of local and/or systemic resistance responses triggered in mycorrhizal tomato plants infected with several fungal and oomycete pathogens and in the mycorrhizal colonization process itself (de la Noval et al., 2007). Arbuscular mycorrhizal fungi (AMF), are obligate biotrophs of plants, exchanging carbon provided by the plants for mineral nutrients extracted by them from the soil. The AMF symbiosis is known to enhance the plant’s ability to overcome biotic and abiotic stresses (Kumar and Verma, 2018; Evelin et al., 2019). Other plant beneficial fungi belong to *Trichoderma* genus one of the most widespread soil microbes used in agriculture and a major component of commercially available biological products (e.g., biopesticides, biostimulants, biofertilizers) (Woo et al., 2014). It is well known that plant protection mediated by *Trichoderma* spp. can be deeply influenced by environmental conditions and ecological fitness of biocontrol agents hence being poorly predictable a priori (Lecomte et al., 2016; Malik et al., 2018). Consequently, the sole use of plant beneficial microorganism may not be always sufficient to fully protect plants against stresses. To overcome such limitations, novel approaches to increase plant resistance may focus on the combined application of different resistance inducers (e.g., chemical and/or biological) (Zehra et al., 2017; Abd-El-Khair et al., 2019). As both *Trichoderma* and Sys activate the JA pathway, a key hub for plant defense and resistance towards insects and fungi, we hypothesized that their combined treatment on plants could lead to in an increased disease and pest control effect. Furthermore, considering that the endophytic root colonization by the beneficial fungus is limited by Salicylic Acid (SA) pathway, while JA triggered defenses have positive effect on it, (Martínez-Medina et al., 2017), Sys application on the plant could trigger a more efficient root colonization of T22 due to the negative crosstalk between the JA- and the SA-regulated pathways (Pieterse et al., 2012). Here we show that their combination confers protection to tomato plants towards the hemibiotrophic *Fusarium oxysporum* fungal pathogens, and the insect pest *Tuta absoluta*. Since the activation of JA pathway increase plant tolerance to different abiotic stresses such as drought and salinity (de la Noval et al., 2007; Orsini et al., 2010; Pastor et al., 2018; Zhang et al., 2020) we also hypothesized that exogeneous Sys application, could reduce salt damages in tomato plants. Here we show that soil drench application of Sys enhanced biomass accumulation in tomato plants exposed to salt stress by potentiating ion homeostasis, oxidative stress protection, and protein stability.

1.2 Results

1.2.1 Systemin peptide did not directly affect Trichoderma afroharzianum T22 growth

To assess if the Sys had a direct antimicrobial effect on *T. afroharzianum T22*, an *in vitro* assay was carried out to measure fungal growth in presence or absence of different concentrations of the peptide (**Figure 1**). Switch was used as a growth inhibitory positive control. Sys treatment did not impact on T22 proving that Sys does not have inhibitory effect on *Trichoderma* growth.

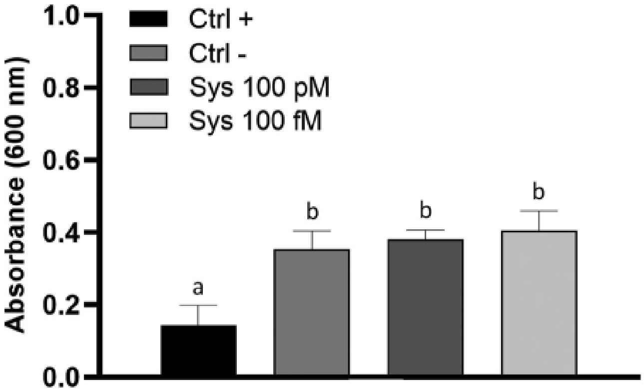

Fig 1. **Effect of Sys on *T. afroharzianum* T22.** Fungal growth in absence (Ctrl −) or presence of Sys (100 fM/pM) was evaluated 24 h after fungal inoculation by assessing changes in optical density (OD600). Switch (200 µg/ml) was used as a positive control (Ctrl +). Different letters indicate statistically significant differences (One-Way ANOVA, P < 0.05). Error bars indicate standard error (n = 5).

1.2.2 Systemin and *Trichoderma afroharzianum* T22 combined application decrease *Fusarium oxysporum* disease symptoms

To assess if treatments with Sys and/or *T. afroharzianum* T22 were able to control *F. oxysporum* wilt disease on tomato plants, roots of two-week-old seedlings were left uninoculated, inoculated with the *Fol* wt strain or with the *Fol fmk1*Δ avirulent mutant strain. The survival of treated versus untreated plants was recorded over time. Unsurprisingly, in all experiments and regardless of the treatment used (PBS control, Sys *or* T22), uninoculated or *fmk1*Δ inoculated plants showed neither wilting symptoms nor mortality throughout the whole testing process (**Fig. 2 A, B, C and D**).

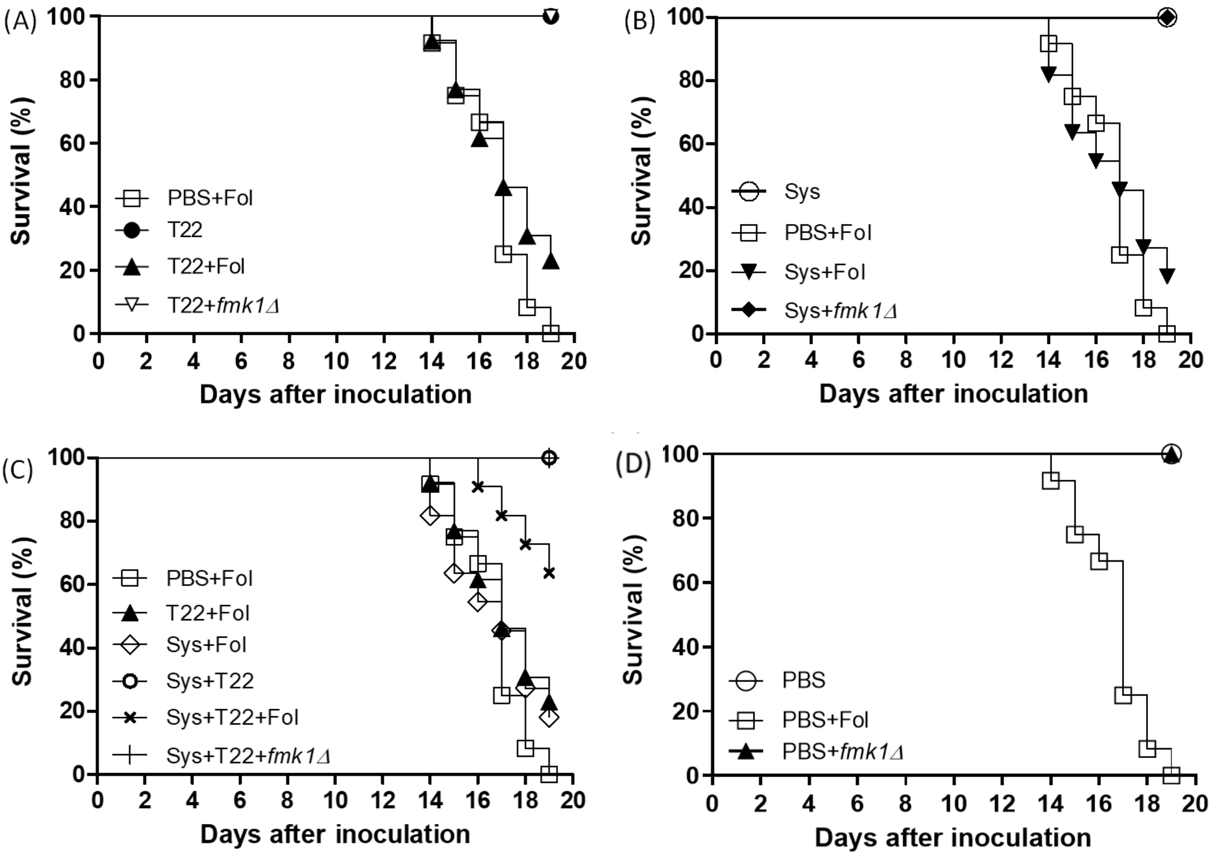

Fig 2. ***T. afroharzianum* and Sys additively reduce *F. oxyporum* virulence on tomato plants**. Kaplan–Meier plots showing survival of tomato control plants treated with PBS (A, B, C and D), *T. afroharzianum* (A), Sys (B), or both (C), and not inoculated or inoculated by dipping roots into a suspension of 5 × 10^6 conidia/ml of the indicated Fol strains. Experiments were performed at least three times with similar results. Percentage survival of tomato plants was plotted for 20 days. Data shown are from one representative experiment.

In contrast, plants germinated from Ctrl seeds and inoculated with the *Fol* wt strain showed progressive wilting symptoms and died after 19 days post inoculation (DPI) (**Fig.1 D**). Plants treatment with Sys or seed coated with *T. afroharzianum* T22 only partially, though not significantly, decreased *Fol*-mediated wilting and death of plants (**Fig. 2 A, B**) (T22+Fol, Log-Rank test, $\chi2$ = 1.588, df = 1; P = 0,2077; Sys+ Fol, Log-Rank test, $\chi2$ = 0.771, df = 1, P = 0,3797). Notable, combined treatment of tomato plants with both Sys and *T. afroharzianum* T22 proved a stronger and significant decrease of plant mortality (Sys+T22+Fol, Log-Rank test, $\chi2$ = 12.28, df = 1, P= 0,0005) as only 40% of these plants had died after 19 DPI, contrarily to those derived from Ctrl seeds where 100% mortality was observed (**Fig. 2 C**).

1.2.3 Systemin exogenous supply and *Trichoderma afroharzianum* T22 colonization modifies *Tuta absoluta* infestation

The tested treatments affected the number of *T. absoluta* eggs laid per plant (**Fig. 3 A**, ANOVA, df=3, F=10.03, P<0.001) which resulted reduced by Sys and raised by T22 colonization.

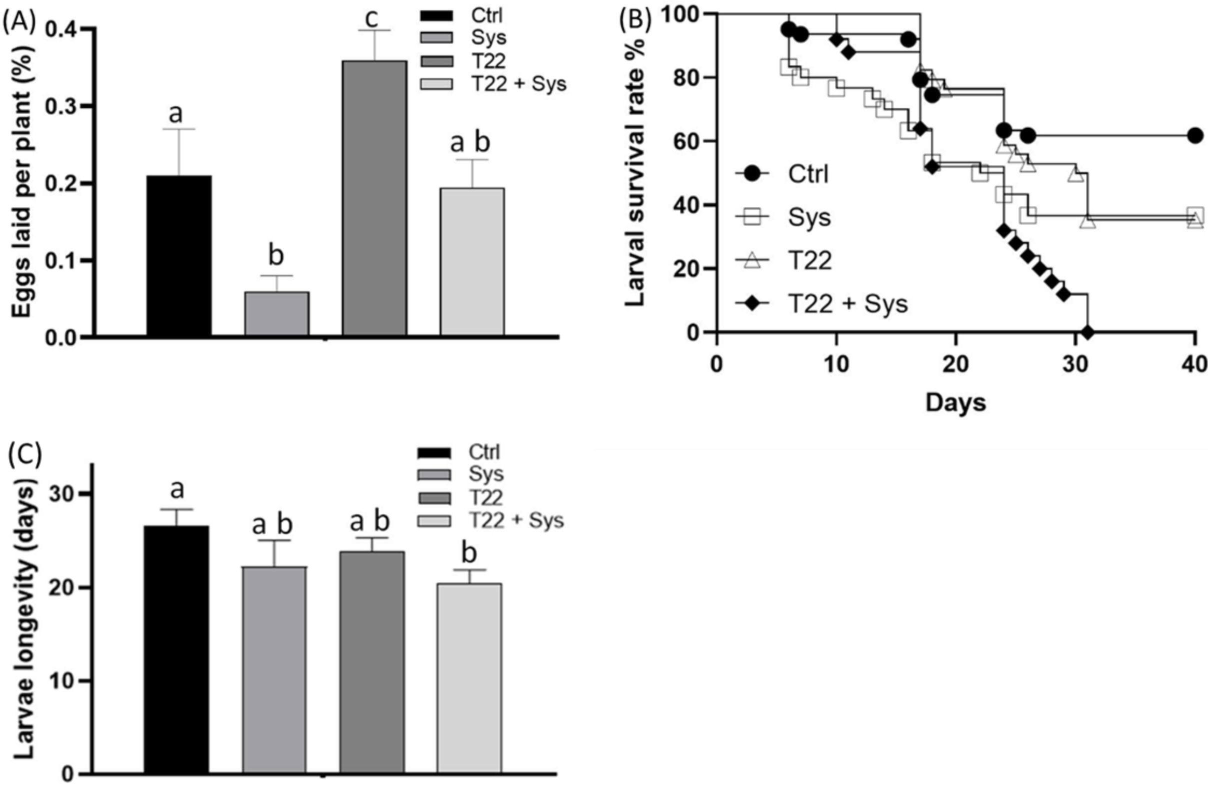

Fig. 3. ***T. absoluta* assays**. (A) Eggs laid per plant by *T. absoluta* adults and (B) larvae survival curves on tomato plants treated with Sys and *T. afroharzianum* T22, their combinations and relative control. (C) Larvae longevity reared on tomato plants treated as above described.

Larvae survival curves, from eggs to pupation, showed a significant effects of *T. afroharzianum* inoculation and Sys treatment on *T. absoluta* when used alone or in combination (**Fig. 3 B**, Log-Rank test, χ2 = 21.6, df = 3, P < 0.001). Survival rates were significantly lower for larvae fed on T22-treated leaves (Log-Rank test, χ2 = 7, df = 1, P = 0.008) and for larvae fed on Sys-treated leaves (Log-Rank test, χ2 = 18, df = 1, P < 0.001), in respect to control plants (**Fig. 3 C**). An additive effect was registered for combined T22-Sys treatment (Pairwise log-Rank test T22 vs T22+Sys χ2 =10.64 df = 3, P = 0.014). Similarly, larval longevity was reduced by the combined application of T22 and Sys while no significant effect was recorded when the treatments were applied alone (**Fig. 3 B**) Welch ANOVA, $F_{3,146}$=2.708, P =0.047).

1.2.4 Defense-related genes are up-regulated in Systemin and *Trichoderma afroharzianum* T22 treated plants

The induction of defense related genes in *T.afroharzianum* T22 and Sys treated plants was monitored by qRT-PCR. A significant increase of *Allene Oxide Synthase* (*AOS), Wound-induced Proteinase Inhibitor I* (*Pin I*), *Threonine deaminase* (*TD*), and *Leucine aminopeptidase A* (*LapA*), but not of *Lipoxygenase D* (*LoxD)*, transcripts was recorded after Sys or T22 application. All gene transcripts, including those of the *LoxD* gene, were significantly more expressed in plants simultaneously treated with Sys and T22 compared to those treated with Sys or T22 alone (**Fig. 4**).

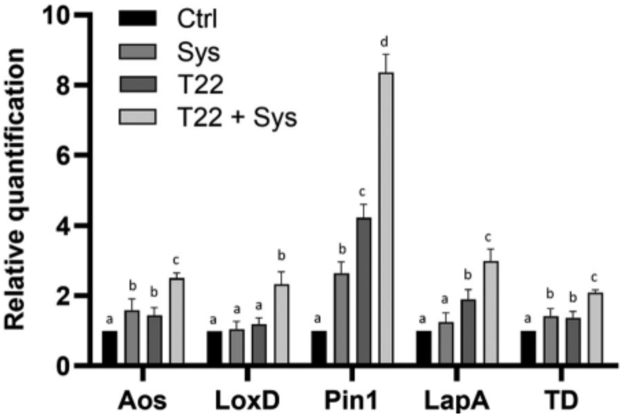

Fig. 4. Level of defense-related genes expression in tomato plants grown from uncoated (Ctrl) or *T. afroharzianum* -coated seeds (T22) and treated or not with 100 fM Sys. Transcript levels of the following genes were analyzed: *AOS*, *LoxD*, *Pin I*, *TD*, and *LapA*. Quantities of transcripts are relative to the calibrator Ctrl condition. Different letters indicate statistically significant differences (One-Way ANOVA, $P < 0.05$). Error bars indicate standard error (n = 3)

1.2.5 Systemin exogenous supply and *Trichoderma afroharzianum* T22 colonization alter the production of JA, SA and related metabolites

Moreover, Sys treated plants showed higher levels in 12-OPDA in respect to controls, while another intermediate, 12,13(S)-EOT, increased in T22+Sys plants. Furthermore, JA over-accumulated in plants treated with Sys and T22, alone or in combination, with a maximum fold of 1.74 in T22+Sys samples. Production of Tuberonic acid-glucoside, involved in JA metabolization, was higher in single (Sys or T22) treatments, and unaltered in T22+Sys plants Finally, MeJA resulted over-accumulated in plants treated with both Sys and T22 (1,94-fold higher than Ctrl) (**Fig. 5**).

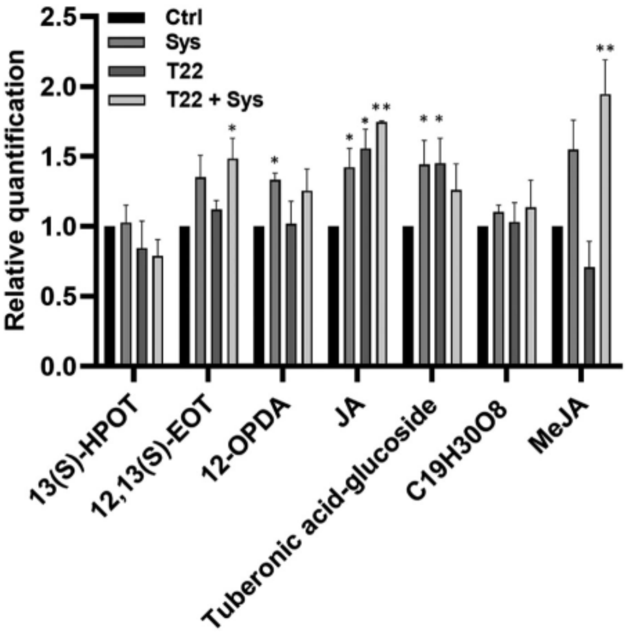

Fig 5. Semi-polar metabolites level in the JA pathway. Metabolites were relatively quantified as fold internal standard level, normalized on the control (Ctrl; for more details, see materials and methods). Data represents the average of three independent biological replicates, and a student's t-test was used to identify metabolites whose abundance significantly changed with respect to the Ctrl condition (*P < 0.05; **P < 0.01).

Sys treatment significantly decreased the amounts of Chorismic acid, Prephenic acid, SA and its glycosylated form while T22 increased Chorismic acid and reduced Prephenic acid and SA. The combined treatment increased Chorismic acid (even if it was less than what reached by T22 treatment) and DL-Phenylalanine while decreased Prephenic acid and SA (**Fig. 6**).

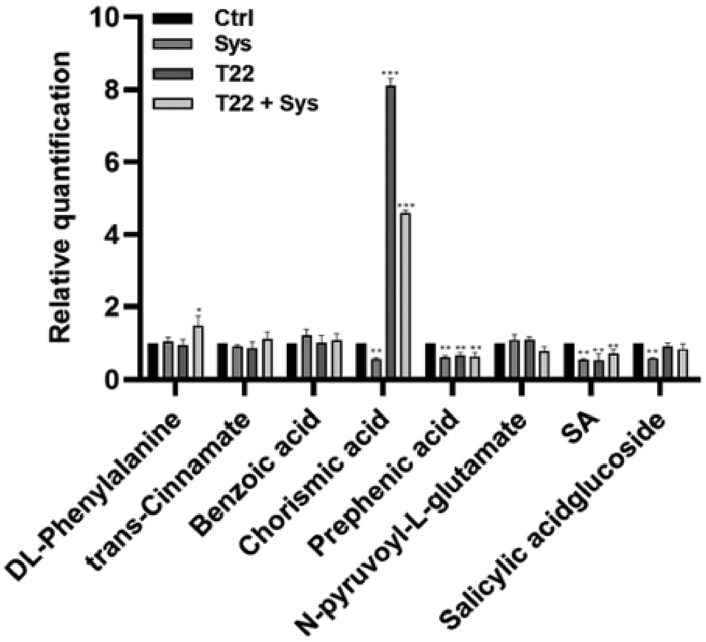

Fig. 6. Targeted LC-HESI (-)-HRMS analysis of semi-polar metabolites in the SA pathway. Metabolites were relatively quantified as fold internal standard level, normalized on the control (Ctrl; for more details, see materials and methods). Data represents the average of three independent biological replicates, and a student's t-test was used to identify metabolites whose abundance significantly changed with respect to the Ctrl condition. (*$P < 0.05$; **$P < 0.01$)

1.2.6. Systemin exogenous supply improved biomass accumulation under salt stress conditions

To evaluate the potential of Sys for improving plant growth and salt tolerance, tomato plants were treated at transplant with a solution of Sys (100 pM) and then exposed to two different concentrations of NaCl. In mock treated plants, the exposure to 100 mM NaCl (NC_1; NC=NaCl) induced significant decreases in leaf area (− 24.4%) and shoot dry weight (DW) (− 22.8%) compared to non-salinized mock plants. Similarly, the highest concentration of NaCl (150 mM NC_2) induced significant reduction in leaf area (− 32.4%) and shoot DW (− 41.2%). (**Fig. 7 A, B**).

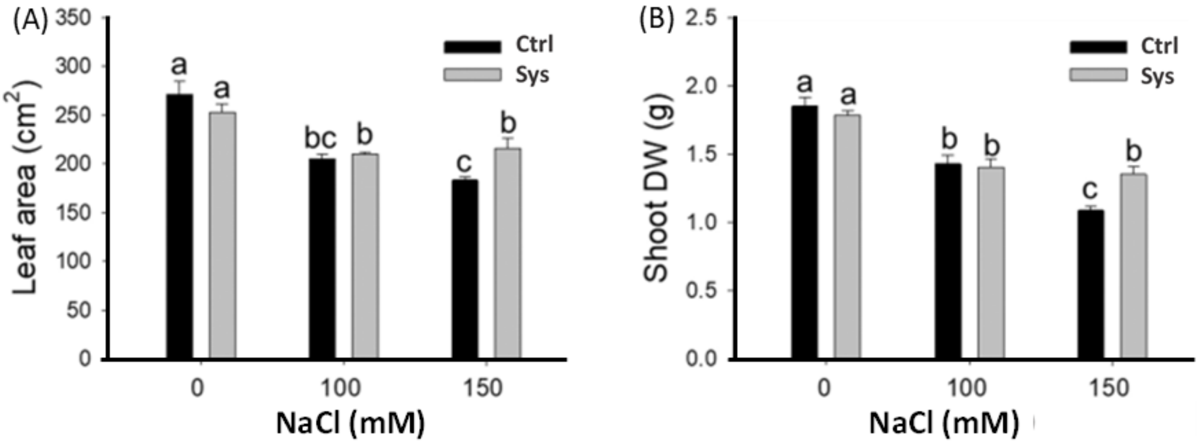

Fig. 7. Biometric parameters of tomato plants treated or not with 100 pM Sys and grown under 0,100 or 150 mM NaCl. A) Leaf area and B) shoot DW. The values are mean ± standard error (n = 8). Different letters indicate significant differences according to Tuckey's post-hoc test ($p < 0.05$).

The treatment with Sys did not significantly affect these parameters under control growth condition (NC_0) and 100 mM NaCl (NC_1) compared to the mock-treated plants. In contrast, under NC_2 conditions, the treatment with Sys improved the total leaf area (+17.9%) and shoot DW (+24.3%) compared to mock-treated plants (**Fig. 1 A, B**).

1.2.7. Systemin application alleviates stomatal conductance and relative water content reduction under salt stress

Stomatal conductance (gs) was severely affected by salt stress in both mock-treated and Sys treated plants. Sys treatment did not affect gs under control condition (NC_0). In mock-treated plants, this parameter was reduced for NC_1 (− 79.5%) and for NC_2 (− 78.2%) compared to the control (NC_0). Plants treated with Sys peptide showed milder yet significant reduction of gs for NC_1 (65.9%) and for NC_2 (− 60.9%) (**Fig. 8 A**) compared to the control (NC_0).

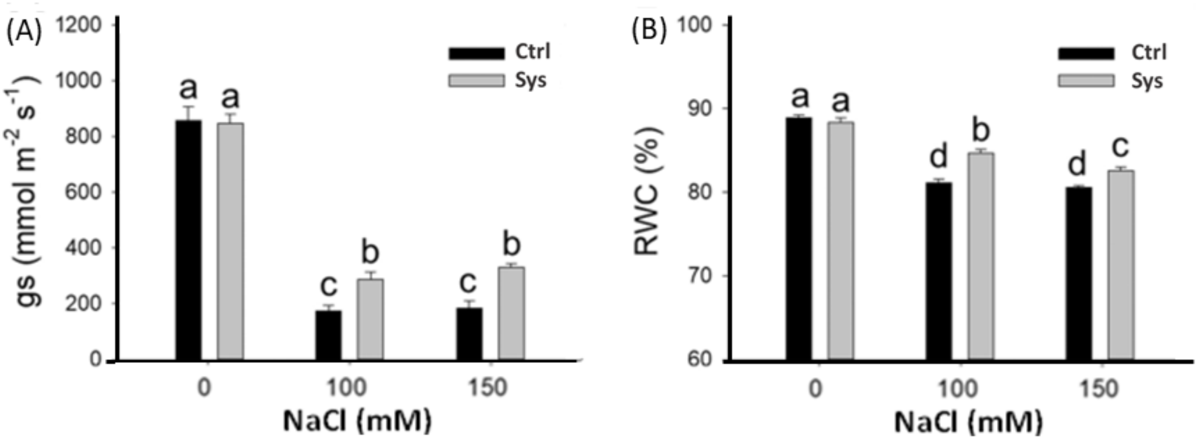

Fig. 8. Physiological response of tomato plants treated or not with 100 pM Sys and grown under 0,100 or 150 mM NaCl. A) Gs and B) RWC. The values are mean ± standard error (n = 8. Different letters indicate significant differences according to Tuckey's post-hoc test ($p < 0.05$)

The leaf relative water content (RWC) was not affected by Sys treatment under control condition (NC_0) (**Fig. 8 B**). However, at NC_1 and NC_2 mock-treated plants showed a lower RWC compared to the control (− 8.7% and − 9.4%, respectively) while in Sys treated ones this parameter was reduced only by − 4% at NC_1 and − 6.5% at NC_2 compared to control conditions (**Fig. 8 B**).

1.2.8. Expression analysis of stress related genes and evaluation of proline content in Systemin treated plant under salt stress

The effective salinity adaptation of tomato plants involved a possible relevance for the level of expression of some key defense-related genes. To further examine this issue, we looked at three main categories of genes: ion transporters, genes involved in antioxidant response systems, and Sys/JA-related defense genes. Transcript accumulation of selected genes was analyzed eight days after salt treatment (8 DAT) by means of qRT-PCR. Notably, in absence of salinity, *Salt Overly Sensitive 1* (*SOS1)* was significantly upregulated by 1.6 -fold change in Sys treated plants compared to mock ones (**Fig. 9 A**).

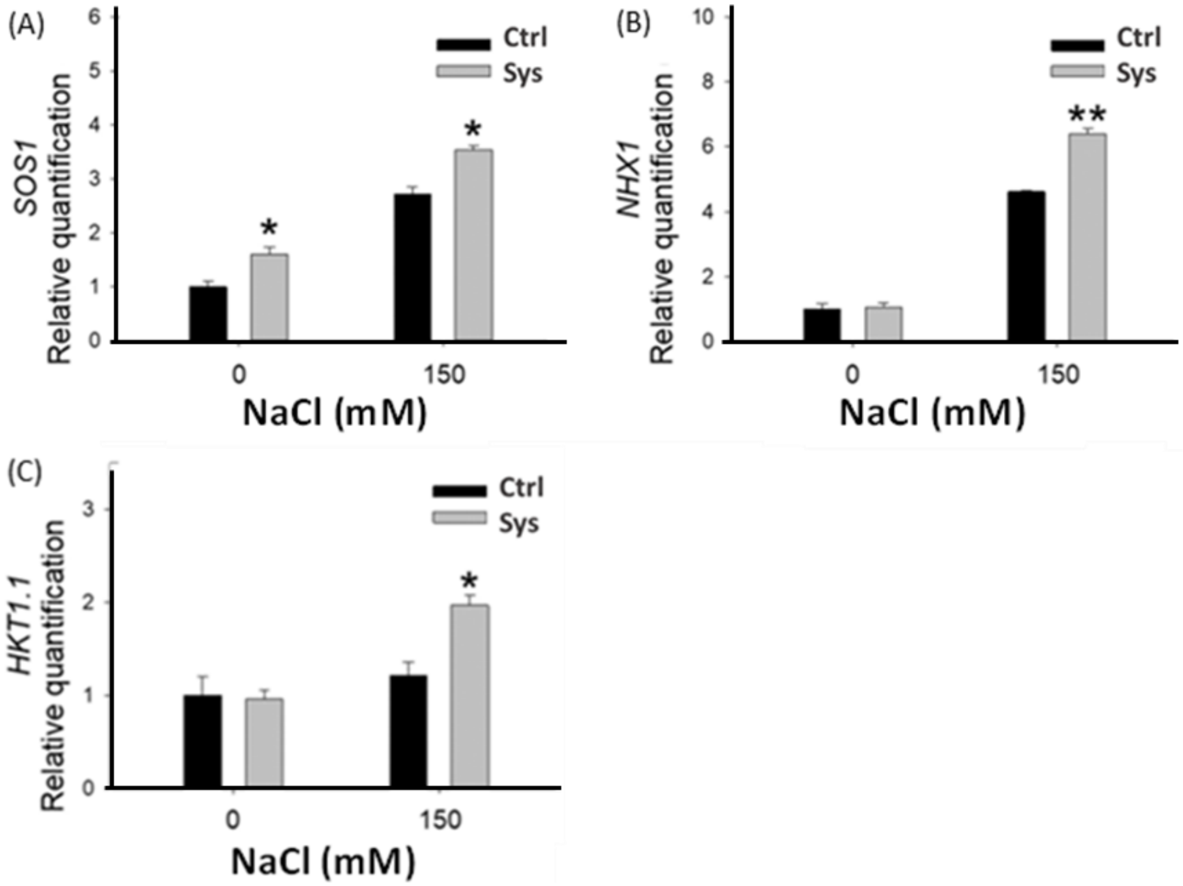

Fig. 9. Relative quantification of ion transporters gene expression in tomato plants treated or not with 100 pM Sys and grown under 0,100 or 150 mM NaCl. A) SOS1; B) NHX1; and C) HKT1.1. The values are mean ± standard error (n = 4). Quantities are relative to the calibrator represented by mock treated plants within each salinity level. Statistical analysis was performed with Student's t-test (* $p < 0.05$; ** $p < 0.01$)

About *Sodium-hydrogen antiporters 1* (*NHX1*) and *High-Affinity Potassium Transporter 1* (*HKT1.1*) genes, the expression level was not changed by Sys treatment under control conditions (**Fig. 9 B, C**). In contrast, when salinity stress was imposed, we observed increased expression of all these genes in all tested plants. A significant increase of SOS1, NHX1 and HKT1.1 transcript was found in Sys-treated plants compared to control ones for NC$_2$ treatment by 1.4-, 1.5- and 1.6- fold, respectively (**Fig. 9 A, B, C**). Salt stress strongly induced the accumulation of proline in leaves of untreated and Sys-treated plants by 4.3- and 6.4-fold changes respectively (**Fig. 10**).

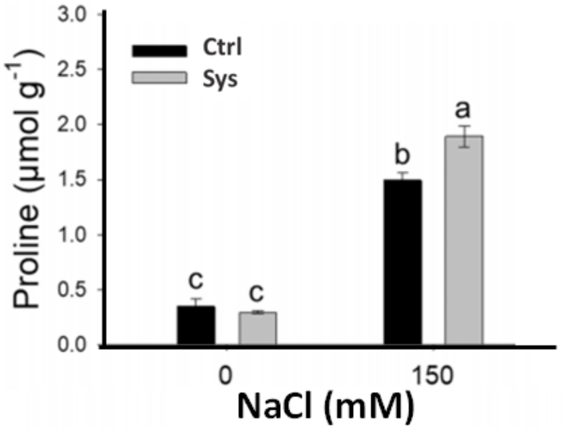

Fig. 10. Proline accumulation of tomato plants treated or not with 100 pM Sys and grown under 0,100 or 150 mM NaCl. The values are mean ± standard error (n = 4). Different letters indicate significant differences according to Tukey post-hoc test ($p < 0.05$)

Notable, the accumulation was significantly higher in Sys-treated plants, + 26.2% compared to untreated plants, under salt stress, (**Fig. 10**). We also monitored genes associated with the enzymatic antioxidant system whose function is to protect cells from damages by scavenging excessive ROS. In particular, the expression level of Copper-zinc superoxide dismutase (SOD1), was significantly upregulated by Sys treatment under control and salt stress conditions compared to the mock-treated plants (1.8- and 1.6- fold, respectively) (**Fig. 11 A**).

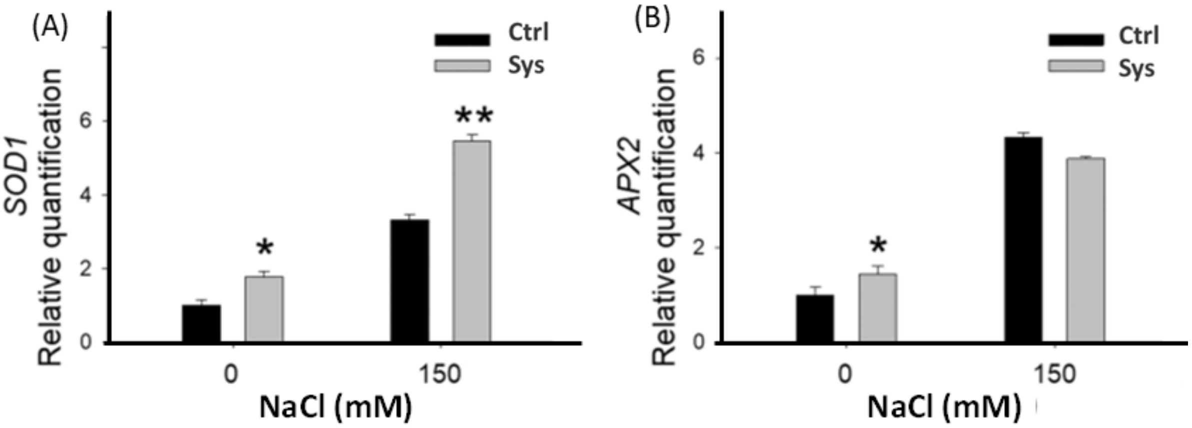

Fig. 11. Relative quantification of antioxidant machinery-related genes induced in tomato plants treated or not with 100 pM Sys and grown under 0,100 or 150 mM NaCl. Genes under investigation were: APX2 and SOD1. The values are mean ± standard error (n = 4). Quantities are relative to the calibrator represented by mock treated plants. Statistical analysis was performed with Student's t-test (* $p < 0.05$; ** $p < 0.01$)

Otherwise, the expression profile of the cytosolic ascorbate peroxidase 2 (APX2) was significantly upregulated by Sys treatment under NC_0 (1.6- fold higher than control), while under NC_2 no significant transcript change was observed when compared to the mock-treated plants (**Fig. 11 B**). Moreover, we examined the expression profile of

Allene Oxidase Sintase (AOS) and Pin II. Under NC_0 condition, Sys treatment did not significantly alter AOS expression (**Fig. 12 A**), while it increased Pin II expression by 2.6 -fold change, compared to mock-treated plants (**Fig. 12 B)**.

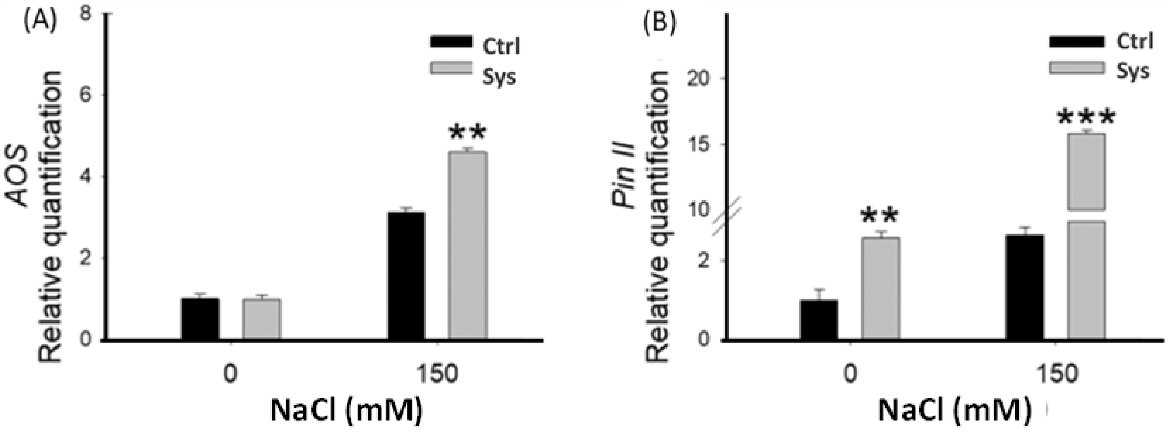

Fig. 12. Relative quantification of key defense-related genes induced in tomato plants treated or not with 100 pM Sys and grown under 0,100 or 150 mM NaCl. A) AOS and B) Pin II. The values are mean ± standard error. (n = 4). Quantities are relative to the calibrator represented by mock treated plants. Statistical analysis was performed with Student's t-test (** $p < 0.01$; *** $p < 0.001$)

In presence of salinity, Sys treatment induced an increase of expression of AOS and Pin II (4.5-fold and 15.9-fold increase respectively) compared to mock-treated plants (**Fig. 12 A, B**).

1.3 Discussion

To promote more sustainable agricultural systems, EU Directive 2009/128/EC established several key principles to reduce pesticide use, fostering the adoption of prevention measures, nonchemical control methods, and chemical compounds with lower environmental impacts. The European Green Deal aims to reduce the use of chemical pesticides by half by 2030. PRIs use in agriculture is very promising as it might be able to reduce the number and amount of pesticide treatments However, some important aspects should be considered. PRIs efficacy may be modulated by environmental conditions or limited by plant species reactions upon their perception. For example, although it was previously demonstrated that the exogenous supply of the Sys peptide to plants increased their resistance against insect pests and pathogenic fungi (Coppola et al., 2017; Coppola et al., 2019a; Molisso et al., 2020), we observed that Sys application was not able to control *F. oxysporum* wilt disease on tomato plant. Fusarium wilt caused by the soil-borne fungus *F. oxysporum* is one of the most devastating diseases of tomato (Hasan et al., 2020). The infection produces huge losses, particularly on susceptible varieties of tomato and when air temperatures is high. The classical strategies based on fungicides and resistant varieties have largely been ineffective in controlling the disease because of soil-borne nature and occurrence of new race of the pathogen (Mandal et al., 2009; Lamichhane et al., 2017).. In our experiments we tried to control this disease by combining Sys application with the beneficial microorganism *T. afroharzianum* T22 which resulted in a significant decrease of Fol-mediated wilting and death of infected plants. Indeed*,* an emerging approaches to increase the effectiveness of PRIs is to combine different types of them (e.g., chemical and/or biological) (Zehra et al., 2017; Zhou et al., 2021).

An important prerequisite to carry out combined plant treatments with beneficial microorganisms and natural-derived compounds is the absence of both direct or indirect antagonistic effects between the two treatments. Importantly, in our experiments, Sys addition to T22 fungal cultures did not show any growth inhibitory effect. Trichoderma and Sys ability to suppress different biotic threats resides in their propensity to enhance plant defense responses through the modulation of different signaling pathways, including those of JA, ET, and SA (Shoresh et al., 2005; Martínez-Medina et al., 2017; Yuan et al., 2019). The expression analysis of JA-associated genes in T22 and in Sys treated plants revealed an up-regulation of *AOS*, an early defense-related gene, active in the octadecanoid signaling pathway that leads to JA biosynthesis, and of *Pin I* and *TD*, two late defense-related genes responsive to JA. It is well explained that JA stimulates a cascade of defense responses that are spatially (local and systemic) and temporally (early and late) regulated in tomatoes (Ryan, 2000). The early and late wounding-responsive genes are regulated by distinct mechanisms. Local wounding leads to the processing of ProSys followed by Sys binding to SYR1, a membrane located receptor (Wang et al., 2018), and the subsequent activation of genes involved in JA biosynthesis. The boost of endogenous JA levels leads to the activation of late JA responsive genes that play a direct role in defense. Late defense genes include *PIs*, *TD*, and *LapA* (Howe, 2004). Tomato *LapA* is important in preventing herbivory induced damage and controlling insect growth (Walling, 2000), while *Pin I* stimuluses the formation of highly stable complexes with insect digestive proteases resulting in decreased digestion of dietary protein, depletion of essential amino acids, and, thus, reducing rates of insect growth and development (Kim et al., 2009). Furthermore, PIs in general and, Pin I in particular, efficiently target microbial secreted proteases thus inhibiting a variety of plant pathogens including bacteria and fungi through suppression of cell growth (Hermosa et al., 2006; Turra and Lorito, 2011; Turrà et al., 2020). *TD* is a gene involved in the resistance against chewing insects. Remarkably, *TD* activity in the insect's midgut correlates with reduced levels of free threonine, which is a dietary requirement for phytophagous insects (Chen et al., 2007). We observed that the combination of the two treatments (Sys and T22) results in higher levels of transcripts related to the activation of the previously mentioned genes, and of *LoxD*, a gene that also contributes to JA biosynthesis consequently, enhancing resistance against insect herbivores (Yan et al., 2013b; Thakur and Udayashankar, 2019).

Metabolite data, obtained by LC-HRMS analyses, partly paralleled transcript profiles: single and double treatments were characterized by higher levels in JA, the end-product of the octadecanoic pathway involved in a series of physiological plant responses (Yang et al., 2019), in respect to control. The magnitude of alteration was stronger in T22 + Sys plants compared to single treatments. A significant increase of MeJA, the JA volatile methyl ester, was also registered in plants simultaneously treated with both Sys and T22. Tuberonic acid-glucoside, a metabolite produced in the frame of JA catabolism, so-called by virtue of its capacity to induce tuber formation in potato (S. tuberosum), also increased in Sys and T22 but not in the double-treated plants. Its synthesis looks to be part of a general mechanism aimed at turning on and switching off JA levels and functions (Miersch et al., 2008): thus, in this context, the higher JA content in T22 + Sys plants could reflect either the increased upstream metabolic flux, as highlighted at the gene expression level, or the reduced catabolism in the double compared to the single treatments. Additional increases in JA intermediates were found in Sys and T22 + Sys samples, although this appears to be more related to stochastic events rather than to a solid tendency. As expected, metabolite data showed an impact of Sys and T22 plant treatment on SA pathway increasing phenylaniline and chorismic acid but decreasing SA. Since chorismate is a branch-point metabolite for SA and phenylalanine biosynthesis, it appears that the combined treatment 'pushed' the pathway's flow in the direction of phenylaniline production that should lead to phenylpropanoid biosynthesis, a class of compounds known to be produced by the plant under biotic stress. In addition, the reduction of SA should be connected to a faster and more intense T22 colonization since endophytic root expansion of the beneficial fungus is limited by SA pathway. Previous work has shown that endophytic colonization of Arabidopsis thaliana roots by *T. harzianum* is strictly dependent on the relative abundance of the two antagonistic plant hormones JA and SA. Indeed, exogenous application of SA reduces Trichoderma root colonization, while induction of the JA pathway or impairment of the SA one promotes it (Alonso-Ramírez et al., 2014; Martínez-Aguilar et al., 2016). In line with this, Sys treatment likely results in enhanced colonization of plant roots by Trichoderma which in turn contributes together with Sys to boost plant immunity and broad-spectrum resistance against both foliar and root fungal pathogens. The central role of JA in Trichoderma colonized plants in modulating defense responses has been demonstrated and confirmed through several mutant studies. For example, plants, of the JA-deficient defenseless1 (def1) mutant, were susceptible to disease development even after Trichoderma treatment, demonstrating that JA pathway is required for plant resistance in pathogen-challenged conditions (Martínez-Medina et al., 2013). It has also been shown that JA plays a protective role against Fusarium wilt disease in tomato (Hernández-Aparicio et al., 2021). In addition, recent evidences shown that JA is involved in *Trichoderma virens*-mediated resistance against *F. oxysporum* in tomato plants. In this context, the activation of the JA signaling pathway in Sys+T22 treated plants nicely correlates with *F. oxysporum* induced mortality. JA is also a key player in plant defense response against insect pests (War et al., 2012). Exogenous supply of JA and MeJA through soil drenching or foliar sprays increases resistance against several insects in numerous agricultural crops under greenhouse and field conditions (Haas et al., 2018; Nouri-Ganbalani et al., 2018; Stella de Freitas et al., 2019). Strapasson (Strapasson et al., 2014) found that the treatment of tomato seeds with MeJA- significantly decreased the pupal weight of *T. absoluta*. Our findings showed for the first time that Sys strongly reduces the survival rate of larvae of *T. absoluta* and corroborate previous findings showing that Trichoderma endophytic colonization negatively affects *T. absoluta* fitness through significant reduction of larval survival (Agbessenou et al., 2020). Furthermore, our study highlighted the usefulness of combined treatments to enhance plant resistance to *T. absoluta*. Previous works had shown a synergistic effect of different treatments on its fitness. For example, the combination of *Beauveria bassiana* and *Bacillus thuringiensis* strongly reduced *T. absoluta* larvae survival (Tsoulnara and Port, 2016). Yet, the usefulness of co-expression of different PIs to enhance plant resistance to *T. absoluta* has been highlighted (Hamza et al., 2018). Nonetheless, this is the first study to evaluate the impact of combined peptide treatment and endophytic colonization. Apparently, the combined application of Sys and T22 did not alter the oviposition behavior of *T. absoluta* with respect to the single powerful treatment with Sys. This result could have many explanations. For example, *T. absoluta* develops many overlapping generations/year, therefore mated females frequently oviposit on highly infested plants that are highly activated as Sys treatment. The combined treatment showed an additive effect on larval longevity/survival of *T. absoluta* in respect to the single treatments and this could correlate to the larger accumulation of JA-derived metabolites. Other than the protection against these biotic stress agents, high JA-derived metabolites levels were shown to increase plant tolerance to different abiotic stresses such as drought and salinity (de la Noval et al., 2007; Orsini et al., 2010; Pastor et al., 2018; Zhang et al., 2020).

Soil salinity is one of the major and widespread challenges in the recent era that hinders global food security and environmental sustainability (Mukhopadhyay et al., 2021). Aggravating the situation, the harmful impacts of climate change accelerate the development of soil salinity, potentially spreading the problem soon to currently unaffected regions. Soil salinity is considered a dominant cause of detrimental effects on soil physicochemical and biological properties and the consequent loss of crop yield (Rajput et al., 2015; Ma et al., 2020; Alzahrani et al., 2021). Thus, it is essential to find new strategies to increase plant tolerance to salt stress to reduce its negative impact on crop productivity (Giorio et al., 2020). Here, tomato plants treated with Sys showed higher tolerance to salt stress, evidenced by higher biomass accumulation, improved stomatal functionality, and enhanced water status. These results confirm previous findings in which transgenic tomato plants constitutively accumulating ProSys showed higher stomatal conductance and unchanged leaf water potential under salt stress compared to wild type (Orsini et al., 2010). In addition, here, has been demonstrated that exogenous applications of Sys at pM concentration triggered specific salt stress adaptation mechanisms, which are essential to deal with high salt concentrations in the root zone. Analysis of transcript expression shows that SOS1, a proton pump responsible for excluding sodium excess from the cytosol, NHX1, a vacuolar pump needed to compartmentalize sodium into the vacuole, and HKT1.1, a sodium/potassium transporter associated with ion fluxes in the xylem, are significantly upregulated by Sys under salt stress. This indicates that Sys-treated plants showed an enhanced ability to regulate the level of sodium in the cytosol. The exclusion and compartmentalization of sodium excess via SOS1, NHX and HKT is a central component of plants tolerance to salt stress (Ali and Baek, 2020). Moreover, plants treated with Sys showed a significant increase of proline content under salt stress compared to untreated plants. Proline is a well-known plant stress molecule acting as signal (Ruggiero et al., 2004) and compatible solute under salinity and drought (Meena et al., 2019). Under salt stress, proline normally compensates the osmotic imbalance generated by Na+ extrusion and/or compartmentalization at cellular level (Shabala et al., 2010; Bartha et al., 2015; Ma et al., 2020). High proline levels in Sys treated plants was consistent with an enhanced extrusion of Na+ as indicated by the upregulation of *SOS1*, *NHX* and *HKT* transcript expression. The effective role of proline in controlling cellular/tissue water homeostasis was confirmed by the higher stomatal conductance and relative water content found in Sys treated plants. These results indicate that Sys can induce ion and water homeostasis regulation in plant leaves, which contributed to ameliorate the physiological state of the plant and overall growth performances under salt stress. The higher activity of SOS1 triggered by Sys in absence of salt stress is of interest since it calls back some earlier thoughts on the origin of salt stress responses in plants. Cheesman (Cheeseman, 2015) hypothesized that the ability to reduce the sodium content in plant tissues, via exclusion mechanisms at root level, was at the base of plant resistance to herbivores feeding. Herbivores, including insects (Xiao et al., 2010) and mammals (Batzli, 1986; Dudley et al., 2012), need sodium and, therefore, prefer plants with high level of cellular sodium compared to sodium excluder plants. Animal sodium deficiencies induce lower survival, reduced growth and slower flight speed in *Helicoverpa armigera* (Hübner) (Xiao et al., 2010). The frequent salt licking of different herbivores is clear evidence of the importance of an adequate sodium supply in their diet, which is not only met by feeding on plants (Dudley et al., 2012). The selective pressure exerted by herbivores certainly favored sodium-excluder plants over sodium-accumulators, which represents a highly conserved mechanism in plant evolution potentially explaining the vast majority of glycophytes over halophytes in the plant kingdom (Cheeseman, 2015).

Our results are in line with Cheeseman (2015) intuition: the exogenous treatment with Sys is a signal of the occurrence of an attack from an herbivore, which initiates the JA pathway to activate the plant immune system, but also SOS1, a sodium pump able to exclude sodium from the cell, which reduces the leaf palatability for herbivores. These results can open interesting scenarios, since it is possible that engineering plants for lower cellular sodium concentration could improve their tolerance to herbivores feeding, further confirming the complexity of the ecological crosstalk among plants and the other biotic and abiotic actors of the environment. Systemin boosts the antioxidant machinery in tomato leaves ROS production is a side-effect of salt stress which impairs cell functioning due to damages on membranes, proteins, and enzymes (Qi et al., 2018; Liu et al., 2021).Plants activate a series of molecular intermediates to detoxify ROS excess and reduce the detrimental effects on sensitive cellular components (Gill and Tuteja, 2010). The first step of the ROS detoxification system is the conversion of toxic O2-· radicals into hydrogen peroxide carried out by SOD (Wang et al., 2016). Hydrogen peroxide is then converted to water via APX and catalase (CAT), which represent the central antioxidant components in plants. Our results show that, under unstressed conditions, SOD1 and APX2 are upregulated in Sys-treated plants compared to untreated plants indicating that the exogenous treatment with Sys triggers the antioxidant machinery in absence of stress, possibly enhancing and/or anticipating the protection of cellular components to oxidative stress. In addition, the increased H2O2 levels associated to SOD activity could indirectly serve as a priming signal able to 'alert' plants of ongoing, oncoming, or prolonged stress (Mauch-Mani et al., 2017). ROS are produced under different stresses and actively contribute to the impairment of plant functioning and development (Qi et al., 2018). A balanced redox status in plant leaves has been previously correlated with stress tolerance in plants, since it reflects an efficient control of negative effects of ROS on cell membranes (Gill and Tuteja, 2010). Sys is known to increase ROS and ethylene production in plants, triggering antioxidant responses (Tcherkez and Limami, 2019). This would explain the higher SOD1 and APX2 relative expression under control conditions. This priming effect on the antioxidant system made plants more prone to effectively react to the subsequent salt stress, a mechanism previously shown to be effective in enhancing plants tolerance to salt stress (Omidbakhshfard et al., 2020; Rasul et al., 2021). The exogenous treatment with Sys potentiated the protection of cellular components against ROS, possibly contributing to the higher tolerance to salt stress in Sys- treated plants. Considering the direct effect of ROS on stomatal movements (Qi et al., 2018), it is possible that Sys activation of the antioxidant machinery improved stomatal conductance under salt stress, which allowed plants to maintain higher growth rates. A possible shared mechanisms of tolerance between biotic and salt stress is the increase of PIs, which was found in Sys treated plants. The involvement of PIs into plant tolerance to different abiotic stresses, such as drought and salinity has been reported in published literature (Li et al., 2015; Islam et al., 2017). PIs are necessary to regulate the baseline protease activity for cellular homeostasis, a crucial process for plant growth and survival (Fan et al., 2019). However, different stresses, including salinity, are known to induce protease activity, which impairs protein functioning and the whole plant fitness (Parida et al., 2004). Tobacco plants constitutively expressing PIs-related genes showed tolerance to multiple stresses, including herbivore feeding, osmotic stress and alkalinity of the media (Srinivasan and Kirti, 2012). Balancing the stress-induced protease activity is a central mechanism that plants use to maintain efficient protein and enzyme functioning under stress. Our results indicate that Sys induction of *Pin II* can represent a beneficial mechanism for plants to cope with salt stress, suggesting that the constitutively upregulation of PIs in plant leaves could have contributed to their higher growth performances under salt stress. Moreover, it confirms PIs as central molecular target for salt stress tolerance, identifying Sys as a potent inducer of this effective tolerance mechanism (Srinivasan and Kirti, 2012). From the outcome of our investigation, it is possible to conclude that Sys treatment increased tomato resistance against multiple stressors and provided evidence of a crosstalk between the mechanisms of tolerance to biotic and abiotic stresses in plants mediated by Sys. In addition, this resistance phenotype can be reinforced and extended to new pathogens and pest thanks to the combined use of Sys with the beneficial microorganisms *T. afroharzianoum*. From an applied perspective these data promote the use of combination of plant beneficial microorganisms and plant endogenous defense elicitor to protect crop from multiple stresses an important goal for future agri-food production.

1.4 Material and methods

1.4.1 *Tuta absoluta* rearing and preparation of *Trichoderma afroharzianum* t22 and *Fusarium oxysporum* cultures

Fungal cultures were obtained from the collection available at the department of agricultural sciences of the University of Naples Federico II. *T. afroharzianum (*formerly-*T. harzianum)* strain T22 (T22), was isolated from the commercial product Trianum-P (Koppert Biological Systems, Rotterdam, the Netherlands), cultured on potato dextrose agar (PDA; HiMedia) and grown at 25°C until complete sporulation. Conidia were collected in sterile distilled water by scraping the surface of sporulating fungal cultures and recovering the spores by centrifugation at 2,700 g for 10 min. Conidia concentration was adjusted to 10^7 spores/mL for subsequent bioassays.

F. oxysporum f.sp. *lycopersici* (*Fol*) race 2 isolate 4287, and the *Fol* knockout mutant *fmk1*Δ were grown in potato dextrose broth (PDB) at 28°C with orbital shaking at 170 rpm. Phleomycin (5.5µg /ml) was added to the culture medium when required. Fresh conidia were separated from the mycelium by filtering 5 day-old cultures through a nylon filter membrane (mesh size 10 µm) and collected after centrifugation at 2,700 g for 10 min. Storage of the obtained conidia was performed as previously described (Di Pietro et al., 2001).

The original strain of *T. absoluta* was collected in 2019 in tomato greenhouses located in Battipaglia (Salerno, Italy) (Gontijo et al., 2019). The insect was continuously reared at the National Research Council, Institute for Sustainable Plant Protection (CNR-IPSP, Portici), inside aerated cages (Vermandel ®, The Netherlands) at 22± 5%°C, 65± 5% relative humidity (RH) and 16L:8D photoperiod.

1.4.2 Systemin peptide synthesis

The Sys peptide synthesis, and purification was obtained as previously described (Coppola et al., 2019a).Briefly, Sys was produced by solid phase synthesis following standard protocols (Romanelli et al., 2011). Purification of the peptide was carried out by Reversed-Phase High-Performance Liquid Chromatography (RP-HPLC) on a semipreparative column (Jupiter 10 µ, Proteo 90 Å, 250 × 10 mm) using a gradient of acetonitrile (0.1% TFA) in water (0.1% TFA) from 5 to 50% in 30 min at 5 mL/min. Sys was characterized by mass spectrometry (LC-MS ESI-TOF 6230 Agilent Technologies, Milan, Italy). Sequences and mass spectrometry data follow. Sys sequence: AVQSKPPSKRDPPKMQTD. Mass calculated (Da): 2009.3 Mass spectrum fragmentation data (Da): 670.94 [M + 3 H]3+; 1005.60 [M + 2 H]2+. Analysis of the HPLC (Shimadzu LC-8A, equipped with a SPD-M10 AV) profiles and of the mass spectra collected indicates the peptide stability in all the tested conditions.

1.4.3 *In Vitro* Systemin-Trichoderma compatibility assay

To assess if Sys had a direct antimicrobial effect on *T. afroharzianum T22*, an *in vitro* assay was carried out to measure fungal growth in presence or absence of Sys 100fM or pM concentrations. Antifungal assays were conducted as previously described (Pastor-Fernández et al., 2020). Wells of a sterile 12-well plate were filled with 1 ml of half-strength potato dextrose broth (PDB 1/2) medium containing Sys, at a final concentration of 100 pM or 100 fM except for the negative control wells. The positive control was filled with 200 µg/ml Switch® fungicide (Syngenta, 37.5% w/w cyprodinil and 25% w/w fludioxonil). Conidia of *T. afroharzianum* T22 were then added to each well to reach a final concentration of 10^4 conidia/ml. Each plate was then placed in a shaker and incubated for 24 hours at 25 ± 1°C. End-point fungal growth was assessed by measuring the medium turbidity at a wavelength of 600 nm (OD_{600}) on BioPhotometer Spectrophotometer UV/VIS (Eppendorf, Hamburg, Germany).

1.4.4 Tomato seed treatment and plant growth

Seeds of *Solanum lycopersicum* cultivar "San Marzano Nano" were surface sterilized with 2% sodium hypochlorite for 10 min, then fully rinsed in sterile distilled water. For the seed treatments, washed tomato seeds were either coated by immersion in a fresh spore suspension (final concentration of 10^7 conidia/mL) of *T. afroharzianum* T22, or treated with water (Ctrl), stirred frequently to uniformly cover the seed surface, left to air dry for 24 h and stored at 4°C until use. Seeds were germinated on Whatman® sterile filter paper (Sigma-Aldrich, Darmstadt, Germany), moistened with sterile distilled water and placed in a growth chamber at 24 ± 1°C and 60 ± 5% RH in the dark. At the emergence of the cotyledons, germinated seedlings were individually transplanted into pots containing sterile commercial soil (Universal Potting Soil, Floragard, Oldenburg, Germany) and kept in a growth chamber at 26 ± 1°C and 60 ± 5% RH., 18L:6D- photoperiod by lamps of 5,000 lux. After 2 weeks, tomato seedlings were transplanted into 10-cm diameter plastic pots containing sterilized soil and grown for 2 weeks under the same environmental conditions. For *F. oxysporum* assay, seeds were planted on wet vermiculite in plastic trays and incubated in plant growth chambers for two weeks at 26 ± 1°C and 60 ± 5% RH.

The experimental design for salt stress assay, consisted of a combination of two treatments: mock-treated plants, Sys-treated plants, and three concentrations of salt stress (NC_0: 0 mM; NC_1:100 mM and NC_2:150 mM NaCl). Plants were arranged in a completely randomized design with eight replicates. Briefly, after 7 days from the transplanting, the plants were irrigated with 120 mL of 100 pM Sys peptide in PBS buffer 0.1X (phosphate buffer saline, 1 mM phosphates, 14 mM NaCl, 0.27 mM KCl, pH 7.4, Sigma-Aldrich, Milan, Italy) or 120 mL of PBS 0.1X (mock treatment control). Salt stress was initiated one DAT by adding 100 mL of water (NC_0, as control) or 100 mL of 100 mM(NC_1) and 150 mM L-1 (NC_2) NaCl solution. The irrigation was provided every two days. Leaf samples from control and treated plants were harvested 8 DAT and used for the gene expression analysis.

1.4.5 *In vivo Fusarium oxysporum* infection assays

Two weeks-old plants (Ctrl and T22 seed-treated), treated with Sys or PBS buffer 1X dissolved in 5 ml of *distilled water (*final Sys concentration 100 fM)*,* were tested for resistance to *F. oxysporum.* Twenty four hours after Sys application *Fol* infection was performed by dipping tomato roots in a microconidia suspension ($5x10^{6}$ conidia/ml) from *Fol* wt or *fmk1Δ* strains (Di Pietro and Roncero, 1998). Tomato seedlings were planted into minipots containing vermiculite and maintained in a growth chamber (28 °C; 14L:10D photoperiod). Plant infection was recorded daily up to 20 days and percentage of plant survival calculated by the Kaplan–Meier method (López-Berges, 2012). Fifteen plants per treatment were used and each experiment was repeated in three independent occasions.

1.4.6 *In vivo Tuta absoluta* assays

To evaluate the possible induction of repellency linked to the alteration of the profile of volatile organic compounds released, a choice test was performed using a random block experimental design. Three 4-weeks old plants (Ctrl and T22) were treated with 100 fM Sys or PBS by foliar spotting. After 6 hours, plants were placed into a single mesh cage (60x60x180 cm; Vermandel, The Netherlands) at a distance of 20 cm from each other. Three to 5 days old mated females of *T. absoluta* were released into the cage keeping a 1:1 ratio between them and the plants. After 2 days (oviposition period), females were removed from the cage by an insect aspirator and the eggs laid were counted. The test was replicated four times totalling twelve females/plant tested. To evaluate antibiosis/antixenosis, a no-choice test was performed by feeding *T. absoluta* larvae with detached leaves from each treatment and relative control. Fully expanded leaves to be used in the test were cut from plants treated as described before and immediately placed through the petiole in a 5-mL tube capped by cotton wick, sealed by parafilm tape and filled with tap water. Larvae to be used in the test came from tomato plants exposed for 24 h to hundreds of *T. absoluta* adults in a mesh cage. Tomato leaves with eggs were transferred into aerated cages and a single hatched larva was gently transferred onto a detached leaf by a soft brush and kept into a plastic box (Duchefa, The Netherlands) constituting the experimental unit. Thirty larvae were tested for each treatment. Leaves were examined daily to check the larval longevity and survival and to record the time to pupation.

1.4.7 Gene expression analysis

Expression levels of defense-related genes were quantified by RT-PCR. Fully expanded leaves from 4 weeks old plants (Ctrl or T22) were collected 6 hours after Sys treatment and immediately frozen in liquid nitrogen. For salt stress assay, at eight DAT, leaves of tomato plants, treated or not with 100 pM Sys peptide, under NC_0, NC_1 and NC_2 conditions, were harvested and immediately frozen at − 80 ◦C. Since the effects of Sys peptide application on biomass accumulation, stomatal conductance, and RWC at the end of the experiment were maximized at NC_2, gene relative expression analysis and proline quantification were performed only on this level of salt stress imposed.

Total RNA extraction, first strand cDNA synthesis and RT-PCR were performed according to standard procedures, as reported elsewhere (Corrado et al., 2012). RT-PCR was performed using Rotor Gene 6000 (Corbett Research; Sydney, Australia). For each sample, two technical replicates from each of the three biological replicates were used for gene expression analysis. The housekeeping gene EF-1α was used as endogenous reference gene for the normalization of the expression level of target genes (Müller et al., 2015). Relative quantification of gene expression was carried out using the $2^{-\Delta\Delta Ct}$ method and referred to the mock-treated control (seeds treated with PBS 1X) (relative quantification, RQ = 1). Primers and their main features are reported in **Table 1.**

Tab. 1. List of Primers used for qPCR analysis.

Gene name	Primer	Sequence (5'-3')	Name/Gene symbol	Accession number
AOS	Fw	GATCGGTTCGTCGGAGAAGAA	*Allene Oxide Synthase 2*	Solyc11g069800
	Rv	GCGCACTGTTTATTCCCCACT		
APX2	Fw	ATGGTAGCTGGAGGAGACC	*Ascorbate Peroxidase*	Solyc06g005150
	Rv	TTGAGGGAGCATGGACCAAC		
EF-1α	Fw	CTCCATTGGGTCGTTTTGCT	*Elongation Factor 1 Alpha*	Solyc06g005060
	Rv	GGTCACCTTGGCACCAGTTG		
HKT1.1	Fw	TCTAGCCCAAGAAACTCAAAT	*High-Affinity Potassium Transporter 1*	Solyc07g014680
	Rv	CTAATGTTACAACTCCAAGGAATT		
LapA	Fw	ATCTCAGGTTTCCTGGTGGAAGGA	*Leucine Aminopeptidase A*	Solyc12g010030
	Rv	AGTTGCTATGGCAGAGGCAGAG		
LoxD	Fw	TTCATGGCCGTGGTTGACA	*Lipoxygenase D*	Solyc03g122340
	Rv	AACAATCTCTGCATCTCCGG		
NHX1	Fw	CACGATATGGTGGGCTGGTT	*Sodium-Hydrogen Antiporters 1*	Solyc06g008820
	Rv	GGGTGTGGCCAAATCTCGTA		
Pin I	Fw	GAAACTCTCATGGCACGAAAAG	*Wound-Induced Proteinase Inhibitor 2*	Solyc09g084470
	Rv	CACCAATAAGTTCTGGCCACAT		
Pin II	Fw	CCAAAAAGGCCAAATGCTTG	*Wound-Induced Proteinase Inhibitor 2*	Solyc09g084450
	Rv	TGTGCAACACGTGGTACATCC		
SOD1	Fw	AGCGGTGGTGTCTGTCTTAG	*Copper-Zinc Superoxide Dismutase*	Solyc01g067740
	Rv	ACCCCAATTCAAAAGGCGTC		
SOS1	Fw	TCGAGTGATGATTCTGGTGG	*Salt Overly Sensitive 1*	Solyc01g005020
	Rv	ATCACAGTGTGGAAAGGCT		
TD	Fw	TTAGACGCTTTCTCCCCTCGT	*Threonine Deaminase*	Solyc09g008670
	Rv	GCTTGAGGAACTTGGAATCCC		

1.4.8 LC-HESI(-)-HRMS of Jasmonic Acid and Salicylic Acid and related metabolites

By using LC-HESI(-)-HRMS analysis, the levels of JA, its glycosylated (tuberonic acid-glucoside) and methylated form (MeJA) as well as three of its intermediates (13(S)-HPOT, 12,13(S)-EOT and 12-OPDA) were measured in control plants or in plants treated with Sys, T22 or both. Detection and quantification of JA and JA-related metabolites was performed as previously reported with slight modifications (Liu et al., 2010; Van Meulebroek et al., 2012; Grosso et al., 2018). Briefly, 100 mg frozen leaf samples of 4 weeks old plants (Ctrl or T22) were collected 6 hours after Sys treatment and homogenized with 1ml cold extraction buffer (methanol, ultrapure water and formic acid (75:20:5, v/v/v) spiked with 10 µg ml-1 formononetin as internal standard), vortexed continuously at -20°C o.n. Following centrifugation at 15,000 g for 20’ at 4°C, 500 ml were transferred to 30 kDa Amicon® Ultra centrifugal filter unit (Merck Millipore Corporation, Massachusetts, USA), and centrifuged for 15’ at 15,000 g and 4 ◦C. Finally, extracts were evaporated by speedvac until a final volume of 50 µl was reached, and then transferred to the LC vials. LC-HESI(-)-HRMS analyses were carried out using a Dionex high performance liquid chromatography-diode-array detector (LC-DAD) coupled to high resolution mass spectrometry equipped with a heated electrospray source operating in negative ione mode (ESI(-)HRSMS) (Thermo Fisher Scientific, Waltham, MA, USA). LC analysis was performed as reported before (Liu et al., 2010; Van Meulebroek et al., 2012; Grosso et al., 2018), whereas mass spectrometry analysis was performed using a quadrupole-Orbitrap Q-exactive system (Thermo Fisher scientific, USA), using a single ion monitoring (SIM) method. More in detail, metabolite ionization was carried out using the following parameters: nitrogen was used as sheath and auxiliary gas (40 and 15 units, respectively); capillary and vaporizer temperatures set at 300˚C and 280˚C, respectively, discharge current at 3.5 KV, probe heater temperature at 360 ˚C, S-lens RF level at 50 V. The acquisition was carried out in the 110/1600 m/z scan range, according to the following parameters: resolution 70,000, microscan 1, AGC target 1e6, and maximum injection time 50. Data were analyzed using the Xcalibur 3.1 software (ThermoFisher scientific, USA). Metabolites were identified based on their accurate monoisotopic and adduct masses (m/z) and MS fragmentation, using both in house database and public sources (i.e. KEGG, MetaCyc, ChemSpider, PubChem, Metlin, Phenol-Explorer), as well by comparing chromatographic and spectral properties with authentic standards, when available. Relative abundances of the metabolites studied were calculated using the Xcalibur 3.1 software (Thermo Fisher scientific, USA). JA, and JA-related metabolites were quantified in a relative way by normalization on the internal standard amounts. Data are presented as means and standard deviations of three independent biological replicates.

1.4.9. Growth and water relation analyses

Destructive harvest and biometrics were taken at 15 DAT to measure shoot biomass and leaf area. Eight biological replicates were used for each treatment tested.

The whole plant was then dried at 60 ◦C to constant weight for shoot dry weight determination. To measure leaf area, leaves were separated from the stem and arranged on a white panel and one overhead photo for each plant was taken. Leaf area was measured using ImageJ v1.52a (U.S. National Institutes of Health, Bethesda, MD, USA) (Cirillo et al., 2021).To measure RWC, a leaf sample was harvested and promptly weighted to determine its FW. The sample was then transferred in deionized water. After 24 h the sample was superficially dried with a paper towel and weighted for saturated weight (SW). The leaf samples were then dried for one week at 60 ◦C and weighted for the determination of shoot dry weight (DW). RWC was calculated as: [(FW-DW)/(SW-DW) x 100]. Moreover, stomatal conductance (gs, mM H2O m− 2 s− 1) was measured at 15 DAT with a portable porometer AP4 (Delta-T Devices Ltd, Cambridge, UK). Measurements were performed from 10 am to 2 pm on a fully expanded leaf per plant.

1.4.10 Proline quantification

The quantification of the proline content was carried out by using a ninhydrin based colorimetric assay on two technical replicates for each of the eight biological repetition (Claussen, 2005). Proline concentration was expressed in µmol g-1 FW after comparison with a standard curve.

1.4.11 Statistical analysis

F. oxysporum and tomato plants infested by *T. absoluta* larvae were analyzed using the Kaplan–Meier method and compared among groups using the log-rank test. One-Way ANOVA test, followed by Tukey’s post-hoc multiple comparison test ($P < 0.05$), were used to evaluate: differences in relative transcripts abundance, the effect of Sys on T22 growth, and in *T. absoluta* oviposition rate. Welch’s ANOVA test followed by Dunnett’s test was used to evaluate differences *T. absoluta* larval longevity. Student’s t-test was used to identify metabolites whose abundance significantly changed with respect to the control condition. Biometric measurements were statistically analyzed by using a twoway ANOVA procedure with Duncan’s multiple comparisons test. Gene expression analysis for salt stress experiment was analyzed with the Student’s t-test or Tuckey’s post-hoc test ($p< 0.05$).

Chapter 2

LONG-LASTING INDUCED DEFENSES FOLLOWING SYSTEMIN TREATMENTS OF TOMATO PLANTS

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Abstract

Upon perception of specific stimuli, plants can develop a state of enhanced defensive capacity against pathogens and pests, resulting in a phenotype called 'induced resistance'. In many cases, this state of enhanced defense can be maintained for long periods, extending for the lifetime of the plant and in some instances, it may even perdure into the following generation. One of the best-studied peptides in plants acting as a resistance inducer is Systemin. Systemin is a hormone peptide, playing a central role in the activation of plant endogenous defenses. The exogenous application of Systemin to tomato plants enhances defense barriers against a wide range of stress agents. Nonetheless, the involvement of this small peptide in long-lasting induced defenses has been scarcely explored. Here, we show that Systemin treatment induce a kind of stress memory as the progeny of treated plants reduces the damages of the necrotrophic fungus *Botrytis cinerea*. Transcriptomic data of parental plants 24h post Systemin treatments revealed an overlap of 768 differentially expressed genes with those of their progeny suggesting that Systemin treatment induces a signal that is transmitted to progeny. Since stress memory can be programmed epigenetically, we investigated the epigenetic regulation of a subset of defense related differentially expressed genes common to both transcriptomic datasets. We demonstrated that Systemin treatment modified histones associated to the promoter region of PAL gene. These results indicate that Systemin treatment promotes an intergenerational defense signaling, possibly acting at epigenetic level, that possibly influence gene transcription. From a practical point of view, these findings may pave the way to the generation of seeds with enhanced resistance to pathogens through parental treatments.

2.1 Introduction

Biotic and abiotic stresses are unavoidable elements of any ecosystem; all living organisms thrive to keep away from them. Plants, being sessile organisms, may seldom move away from stressors and have thus evolved alternative strategies of adaptation for survival (Gimenez et al., 2018). Recent studies suggest that plants are able to remember past environmental events (Hilker and Schmülling, 2019). Memory formation in both animals and plants helps perceive the stimulus, storing the experiences, and interpreting information to gain adaptive skills which, in turn, enhance survival under stressful conditions. In plants, stress memories may be retained just shortly, for a brief part of the organism's life cycle, but they may persist for long as well, being even transmitted to the offspring, grand progeny, and subsequent generations (Bhadouriya et al., 2021). Short-term stress memory, that persists for only one generation of an organism, is known as somatic stress memory. This kind of memory may be mitotically heritable but will not be transmitted to further generations. A memory effect inherited only by the first stress-free generation (F_1) is called intergenerational memory. Finally, when memory is maintained for at least two stress-free generations (F_2), the term 'transgenerational memory' is used (Lämke and Bäurle, 2017) Environment-induced inter/transgenerational effects have been reported in several studies performed using different biotic and abiotic environmental treatments. For instance, the existence of an intergenerational stress memory was observed in *Arabidopsis thaliana*: the offspring of plants that had been exposed to repeated hyperosmotic stresses showed enhanced tolerance to environmental challenges during their vegetative stage. However, after a single stress-free generation, this memory was quickly lost (Wibowo et al., 2016). Rasmann et al. (2012) have demonstrated that *A. thaliana* or tomato plants (*Solanum lycopersicum*) that were wounded or pre-treated with Methyl Jasmonate (MeJA) were able to transfer to their offspring an enhanced resistance against caterpillars, which grew smaller when alimented with the progeny of treated and stressed plants (Rasmann et al., 2012). Moreover, progeny of *A. thaliana* plants that had been either treated with β-aminobutyric acid (BABA) or inoculated with *Pseudomonas syringae* showed higher resistance against *P. syringae* and *Hyaloperonospora arabidopsidis*, as well as increased expression of defense-related genes (Slaughter et al., 2012).

Chromatin structure regulates the accessibility of genes for the transcriptional machinery and it is thus an essential part of the regulatory mechanism controlling gene expression during stress responses and development (Avramova, 2015; Venkatesh and Workman, 2015). Essentially, the positioning and spacing of nucleosomes affects both the overall packaging and the accessibility of individual regulatory elements. Modifying DNA accessibility through epigenetic modifications that may be transmitted between generations represents a way for maintaining environmentally induced gene expression even after the removal of the initial stressing stimulus (Mladenov et al., 2021). Common epigenetic changes involve DNA methylation, histone post-translational modifications (e.g., acetylation, methylation, phosphorylation, and ubiquitination) and small RNA-based regulatory mechanisms, as well as deeper alterations in chromatin topology (Thiebaut et al., 2019). Different histone modifications may play different biological roles, depending on the site where they happen and the number and chemical structure of added groups. Histone acetylation typically activates gene expression by relaxing the chromatin, whereas histone deacetylation causes transcriptional repression (Gräff and Tsai, 2013). Histone methylation may either activate or repress transcription depending on its target. For example, in *Arabidopsis* and tomato genes responding to *Botrytis cinerea* infection, trimethylation of H3K27 (H3K27me3) is associated with the repression of transcription of nearby genes, and may be considered as a repressive mark while, trimethylation of H3K4 (H3me3K4) is associated with the activation of transcription of closely located genes (Crespo-Salvador et al., 2020). It is well known that cells have the potential to retain some of these epigenetic changes even after several mitosis or meiosis; therefore, these changes may be inherited through generations (Campos et al., 2014). The epigenetic marks described above (and many others) constitute a “code language” that can deeply influence the phenotype of the progeny, a phenomenon known as epigenetic memory (Joseph and Shah, 2022). Examples of transgenerational effects include histone H3 lysine acetylation or DNA hypomethylation in genes linked to Salicylic acid (SA) defense responses (Luna et al., 2012).

Sys is a hormone peptide able to enhance plant responses against a wide range of stress agents, including wound, phytopathogenic fungi, phytophagous and sucking insects by its exogenous supply (Constabel et al., 1995; Corrado et al., 2007; Coppola et al., 2017; Coppola et al., 2019a; Molisso et al., 2020). In addition, exogenous treatment with Sys enhances salt stress tolerance in tomato plants (Cirillo et al., 2022). Nonetheless, the involvement of this small peptide in long-lasting stress memory has been scarcely investigated. Here, we show that Sys treatment results in long-lasting resistance since progeny of Sys-treated plants (S_1; S=Sys) counteracts plant colonization by the necrotrophic fungus *B. cinerea* compared to progeny of control plants (C_1; C= Ctrl). Then, we used RNA-seq expression profiling to evaluate how leaf gene expression is affected in S_1 plants. Transcriptomic data analysis of parental (S_0), 24 hours after Sys exogenous supply, and S_1 lines revealed an overlap of differentially expressed genes (DEGs) between the two. Enriched Gene Ontology terms of DEGs highlighted an association with defense responses and metabolic processes. Then, we investigated epigenetic regulation of a set of defense related DEGs common to both transcriptomic datasets by analyzing epigenetic marks such as specific histone modifications (H3me3K4) and DNA methylation. We proved that Sys treatment induced the modification of the histones associated to the promoter region of defense genes.

2.2 Results

2.2.1 Resistance to *Botrytis cinerea* in F_1 progeny of Systemin treated plants

In order to evaluate whether Sys treatment could produce resistant offspring in tomato plants, basal levels of resistance against the necrotrophic fungus *B. cinerea* were assessed in control (C_1) and Sys-treated (S_1) progeny lines.

S_1 plants showed significant reduction in *B. cinerea* lesion formation compared with naïve progeny already visible 1 day post inoculum (DPI), (p = 0.02), as shown in **Fig. 1**. This difference furtherly increased 3 DPI, resulting in lesion size reduction of 27,2%, 26,7%, and 22,5%, respectively 3-5-7 DPIs.

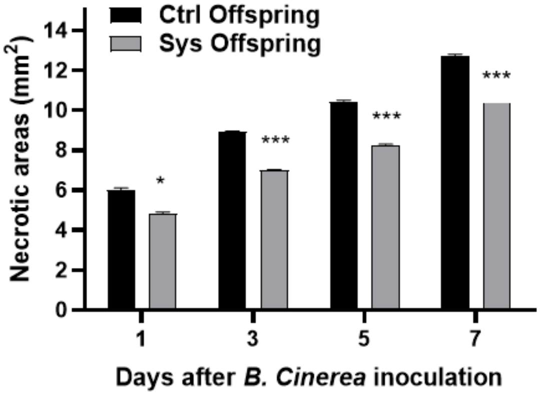

Fig 1. *Botrytis cinerea* necrosis area assay. Response to *B. cinerea* on leaves from the offspring of Sys-treated and control plants. The graph displays the average (± s. e.) lesion size at 1-3-5-7 DP1. Asterisks indicate data statistical significance (Student's t-test; * *P* <0.05, *** *P* <0.001). Error bars indicate standard error.

2.2.2 Effects of direct Systemin exposure on gene expression of treated plants

RNA-seq expression profiling was used to evaluate how leaf gene expression is affected by Sys treatment. Sys treated plants showed a strong modification of the transcriptomic profile; a total of 4.308 differentially expressed genes (DEGs) were found, of which 1975 were up-regulated and 2333 were down-regulated (**fig. 2 A**). listed **Tab. 1** in appendix list all differentially expressed transcripts identified. The classification of DEGs, based on the ontological domain "biological process", is shown in **fig.2 B**. The principal categories directly correlated with defense modifies, in Sys treated plants, are represented by "response to stress" "response to stimulus" "response to chemical". Several GO terms related to lipid, carboxylic and oxoacid acid metabolism were enriched.

Fig 2. Transcriptomic data on parental (24h after Sys treatments) lines. General overview of the transcriptomic rearrangement of tomato plants imposed by Sys treatments compared to control plants. (**A**) Main Gene Ontology "Biological Process" terms associated with up-regulated (red bars) and down-regulated (green bars) genes (**B**).

Several genes involved in early signals of defense responses against environmental cues as, for example, *Leucine-rich repeat protein kinase*, *Serine/threonine-protein kinase*, *Glutathione S-transferase*, and others (listed in **tab. 1** in appendix) were up-regulated. Similarly, the up-regulation of genes coding for transcription factors (TF), such as *bHLH, WRKY, MYB,* and *bZIP TF,* was registered. These genes are likely implicated in the regulation of plant defense response (Conrath et al., 2015). As expected, the up-regulation of genes associated with JA pathways (e.g., *metallocarboxypeptidase inhibitor*, *protease inhibitor 1*, *Kunitz-like protease inhibitor*) were also observed.

2.2.3 RNA-seq expression profiling in the 1st generation progeny of Systemin treated plants

RNA-seq expression profiling was performed to evaluate how leaf gene expression is affected in the F_1 obtained by self-fertilization of Sys treated plants. These plants revealed a strong modification of the transcriptomic profile compared to control plants, up-regulating 2095 and down-regulating 992 transcripts (**fig 3 A.**) (listed in **tab. 2** in appendix). Several functional categories of DEGs were connected to plant reaction to stress, for example, “response to stimuli”, “response to chemical” and “response to stress” plus some metabolic processes.

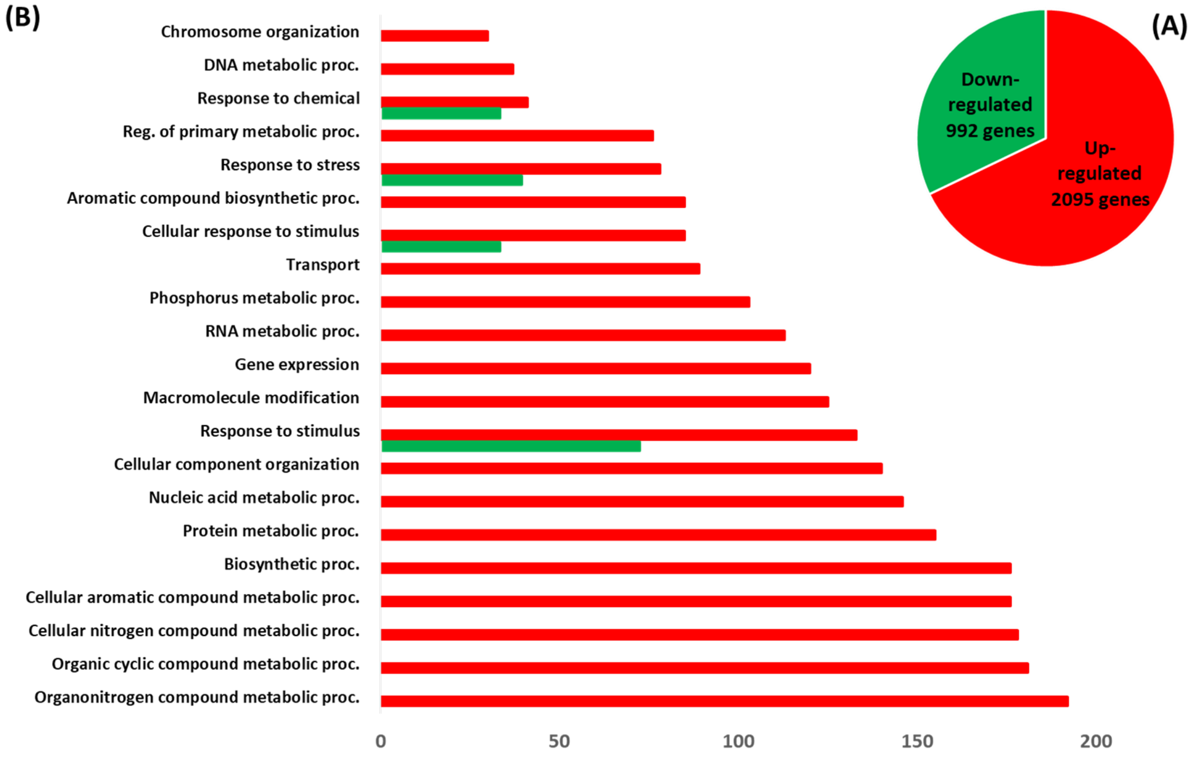

Fig 3. Transcriptomic data on progeny lines. General overview of the transcriptomic rearrangement in the progeny of Sys treated plants compared to control plants. (**A**) Main Gene Ontology “Biological Process” terms associated with up-regulated (red bars) and down-regulated (green bars) genes (**B**).

Among the overexpressed genes several were related to epigenetic control of gene expression; twelve *histone-lysine N-methyltransferases*, two *Lysine-specific histone demethylase*, one *histone acetyltransferase*, along with five genes coding for the histones H1, H3 and H4. ATP-dependent chromatin remodelers were also up-regulated (specifically *ATP-dependent helicase BRM*, *remodeling complex protein SYD*, *ATP-dependent DNA helicase DDM1*, *chromatin-remodeling factor*). In addition, also gene involved in the DNA methylation and demethylation machineries (i.e., *SIZ1*, *cytosine-5 DNA methyltransferase3L*, *DNA demethylase 1*, *DNA demethylase 3*) were up-regulated.

2.2.4 Transcriptomic data overlap between parental and progeny lines

Transcriptomic data on parental and progeny lines revealed an overlap of 768 DEGs of the parents 24h after Sys treatment with those of their progeny (**Fig.4 A**). Gene Ontology "Biological Process" terms associated to the 768 overlapping genes were manly related to defense response (e.g., "response to stress" "response to stimulus" "response to chemical" and different metabolic processes (**Fig. 4 B**).

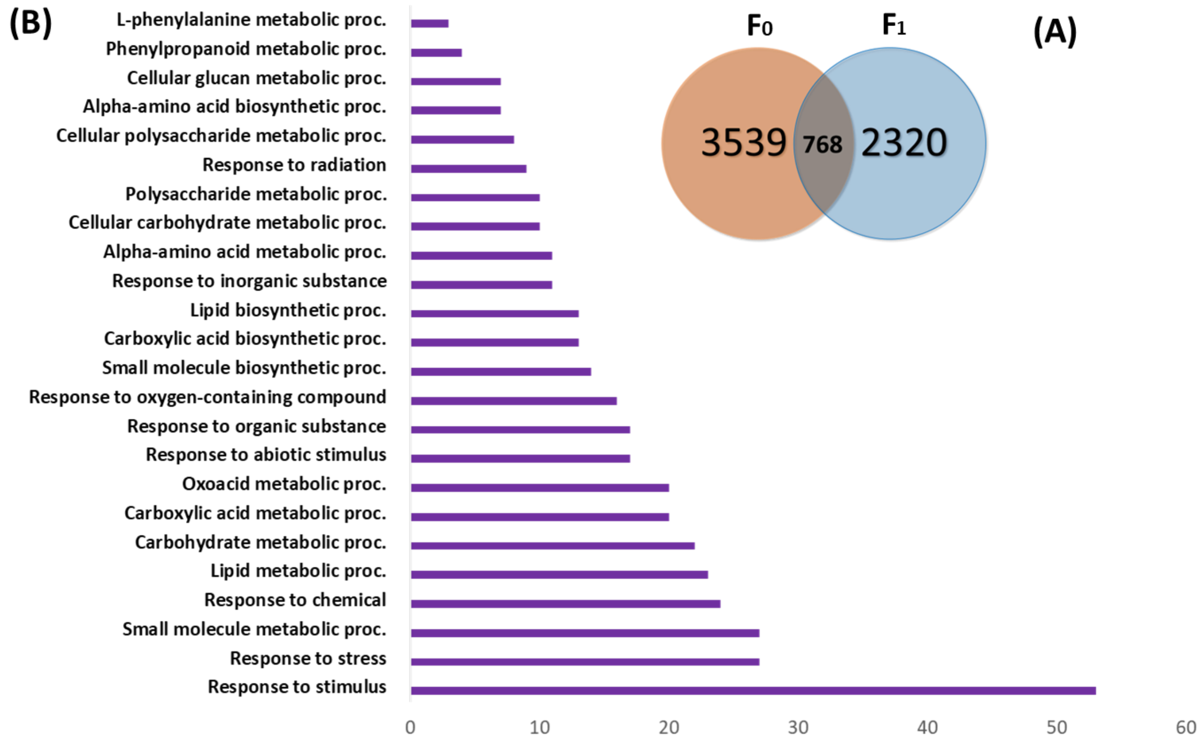

Fig 4. Transcriptomic data on parental (24h after Sys treatments) and progeny lines. DEGs overlapping between parental (F0) and progeny lines (F1) (**A**). Gene Ontology "Biological Process" terms associated to the 768 overlapping genes (**B**).

Among the up-regulated genes included in these categories some are involved in plant resistance against necrotrophic fungal pathogens, as, for example, *proteinase inhibitor I* (*Pin1*), *terpene synthase* (*TS*), *subtilisin-like proteases* (*Subt*) and *Phenylalanine* ammonia *lyase* (*PAL*).

2.2.5. Histone H3 post-translational modifications at defense gene promoters

Post-translational modifications at the N-terminal tail of histone H3 can influence defense-related gene expression (Ramos-Cruz et al., 2021). Because these chromatin modifications can have long-lasting impacts on plant gene expression (Vaillant and Paszkowski, 2007), we investigated whether the upregulation of selected defense genes common to both parental and progeny line was associated with changes in chromatin structure at the promoter regions of these genes. For this purpose, chromatin immunoprecipitation (ChIP) analysis of *PAL*, *PIN1*, *SUBT*, and *TS* genes promoters was performed, using antibodies against triple-methylated H3 at Lys-4 (H3me3K4). *PAL* promoter of S_0 parental plants, 24h after Sys treatment, was associated with increased levels of H3me3K4 compared to C_0 control plants (**fig. 5**); this was assessed using different primer pairs against separate regions of the promoter (indicated as “A” and “B”). By contrast, *PIN1, SUBT* and *TS* promoters did not show significantly increased levels of H3me3K4. As expected, H3me3K4 levels were not altered at the housekeeping genes *EF* (elongation factor) promotor.

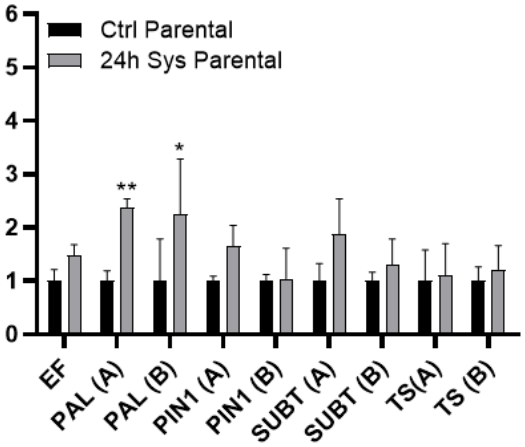

Fig. 5. Quantification by RT-PCR of DNA fragments corresponding to two different promoter regions of selected genes, after ChIP performed with H3me3K4 antibody. Data represent average fold change values (n = 3) in parental plants (24h after Sys treatment) compared to control ones. Asterisks indicate data statistical significance (Student’s t-test; * $P < 0.05$, ** $P < 0.01$). Error bars indicate standard error.

Subsequently, the H3K4 modification was evaluated in progeny lines of both Sys-treated and control plants. Again, a significant enrichment of H3me3K4 was highlighted at *PAL* promoter of S_1 plants (**fig. 6**). Likewise, promoters of *PIN1*, *SUBT* and *TS* in S_1 plants were not enriched with H3me3K4, as observed in the parental lines (**fig.6**).

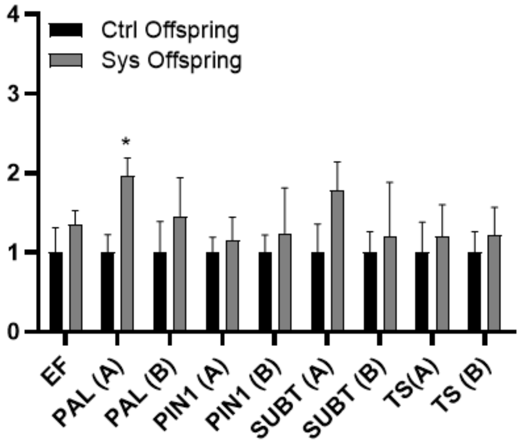

Fig. 6. Quantification by RT-PCR of DNA fragments corresponding to two different promoter regions of selected genes, after ChIP performed with an antibody against H3me3K4. Data represent average fold change values (n = 3) in the progeny of Sys treated plants compared to naïve progeny. Asterisks indicate data statistical significance (Student's t-test; * P <0.05). Error bars indicate standard error.

2.2.6 DNA methylation changes at defense gene promoters

DNA demethylation at the promoter region is believed to play an important role in activating gene transcription (Harris et al., 2018). Thus, we decided to perform DNA-methylation-sensitive restriction-endonuclease digestion followed by PCR (Chop–PCR). The restriction enzyme McrBC digests (chops) DNA fragments bearing two or more purine-methyl motifs thereby preventing subsequent amplification of the template by PCR. This assay gave us the opportunity to investigate DNA methylation changes in the promotor region of selected upregulated defense gene common to both parental and progeny lines. DNA methylation status of *PAL, PIN1, SUBT* and *TS* promotor region was not altered by Sys treatment compared to control plants (**fig. 7**)

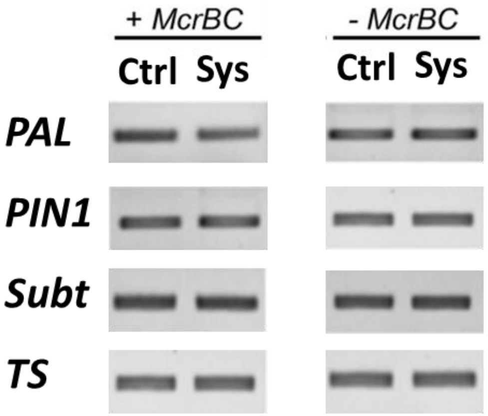

Fig.7. DNA methylation analysis at defense gene promoters determined by McrBC digestion. Chop–PCR analysis of PAL, PIN1, SUBT and TS promotor region in leaves of plants after 24h Sys treatment and control plants. Undigested genomic DNA was used as control. One out of three biological replicates per sample is shown.

DNA methylation was furtherly tested in the progeny of Sys-treated and control plants. *PAL, PIN1, SUBT* and *TS* promoters did not show altered methylation levels in S_1 individuals. These results confirmed a stable methylation level between generations at the promoter region of the tested genes (**fig. 8**).

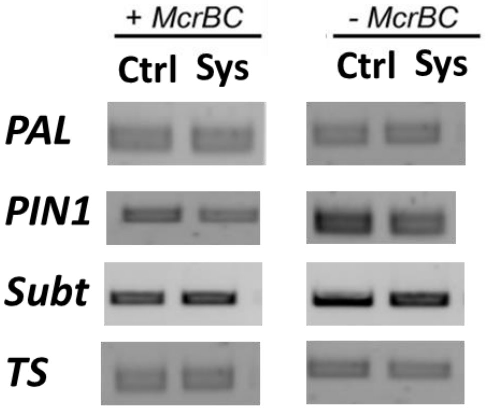

Fig. 8. DNA methylation analysis at defense gene promoters determined by McrBC digestion. Chop–PCR analysis of PAL, PIN1, SUBT and TS promotor region in leaves of the progeny of plants treated with Sys and control ones. Undigested genomic DNA was used as a control. One of the three biological replicates per sample is shown.

2.3 Discussion

Resistance inducers (RIs), also known as plant activators, are a class of compounds that activate plant defenses against different kinds of stress (De Kesel et al., 2021). The enhanced-defense state is induced by several natural or synthetic compounds, including JA, MeJA, SA, benzothiadiazole, or BABA (Yassin et al., 2021; Ren et al., 2022). Interestingly, several reports demonstrated that induced resistance in plants can be transmitted to the offspring, (Lämke and Bäurle, 2017).

Of particular interest is the use of natural compounds able to induce plant immunity that is now becoming commercially attractive, being more ecologically sustainable and ethically approvable in respect to commonly used chemical pesticides (Bektas and Eulgem, 2015). One of the best studied peptides acting as resistance inducers in plants is the tomato Sys (Pastor-Fernández et al., 2022) a peptide playing a central role in the activation of plant endogenous defenses (Coppola et al., 2015). Exogenous application of Sys to tomato plants enhances their defense barriers against a wide range of stress agents (Coppola et al., 2017; Coppola et al., 2019a; Molisso et al., 2020; Cirillo et al., 2022). Here we demonstrated that Sys-induced resistance is transmitted from parents to their progenies. Plant (F_1) grown from seeds of plants previously treated with Sys showed an important reduction of *B. cinerea* disease severity. Seven days after fungal inoculum, the necrotic area was 22% lower in S_1 plants, compared to naïve plants. Therefore, these data showed that the offspring of Sys treated plants, over one stress-free generation, maintained an enhanced resistance to *B. cinerea*. This state of intergenerational resistance to pathogens encouraged us to investigate whether this phenotype was related to a transcriptional memory of gene expression.

Our study provides clear evidence that parental exposure to Sys impact on the molecular phenotypes of the progeny. Transcriptomic data from parental and progeny lines revealed a significant degree of overlap ($\simeq$ 750) of DEGs between parents 24h after Sys treatment and their progeny. As far as defense induction is concerned, very few transcriptome-wide studies have been performed and their outputs are often contradictory, likely depending on the plant species used in the study. It has been described no effect of the parental's environment on the offspring (Molinier et al., 2006) or a widespread effect (Colicchio et al., 2015) as also reported in the present study. In addition, our results are in accordance with the transcriptional memory classified into type I, in which gene activation is persistent in time, in contrast with type II, in which an initial stress-induced transcription is followed by a transcription decay (Lämke and Bäurle, 2017).

The GO classification of reported DEGs, is consistent with the treatment-induced effect, as both transcriptomics data of parental and progeny lines converge on defense-related response enrichment. Specifically, key genes involved in defense response were up regulated in both transcriptomic data. Among them, *Pin1* is known to reduce fungal infections by targeting microbial secreted proteases thus inhibiting cell growth (Hermosa et al., 2006; Turra and Lorito, 2011; Turrà et al., 2020). PAL is the key enzyme of the phenylpropanoid pathway and associated with the enhancement of physical barriers in plant against the attack by pathogens (Li et al., 2017). *Subt* is involved in plant defense responses against the most diverse pathogens (Figueiredo et al., 2018). *TS* is involved in the terpene biosynthesis pathway playing a key role in response to *B. cinerea* infection (Zhang et al., 2022). All together these data explain the better performance of S_1 plants against fungus, as observed in our bioassays, suggesting that SYS treatment is able to induce an intergenerational memory that it would be interesting to evaluate it also trangenerationally.

A research field that is recently gaining relevance is the study of epigenetic mechanisms allowing plants to keep track of past exposure to environmental challenges, and to transmit these memories to future generations (Lämke and Bäurle, 2017). Different pieces of evidence demonstrate that, in presence of a stress that triggers transcriptional changes, epigenetic modifications will be added or removed to/from key stress-response genes to create a stable chromatin environment that will last even when the stressor is removed (Lloyd and Lister, 2022). On a biological point of view, this environmentally-triggered epigenetic memory is very intriguing as it may contribute to plant phenotypic plasticity in the event of a new stress, playing a very important role in stress adaptation (Mozgova et al., 2019).

In order to find a functional correlation between the observed transcriptional memory linked to improved resistance against *B. cinerea* and epigenetic modifications, we examined the gene methylation and demethylation status in S_0 and S_1 tomato plants. Indeed, cytosine methylation is a highly conserved epigenetic mechanism that influences the expression of a gene without altering its sequence. It happens primarily at CpG dinucleotides, which are normally clustered together in genome regions known as “CpG islands”; in turns, CpG islands tend to be enriched in the promoter region of genes (Scheid et al., 2021). DNA methylation marks usually silence gene expression by forming densely compact chromatin; these marks are environmentally sensitive and heritable over multiple (i.e., ≥8) generations (Gent et al., 2013; Stassen et al., 2018). The DNA methylation status is maintained not only by DNA methyltransferases but also by several DNA demethylases, such as ROS1 (repressor of silencing 1), DME (Demeter), DML2 (Demeter-like 2) and DML3 (Zhang et al., 2018). Increasing evidence showed a role of the DNA methylation and demethylation machineries in controlling plant defenses. As an example, plants trigger changes in DNA methylation upon pathogen attack (López Sánchez et al., 2016). Active DNA demethylation has been observed in response to infections by *Pseudomonas syringae* or application of pathogen-associated molecular patterns (PAMPs) as flagellin (Yu et al., 2013). This demethylation seems to be a consequence of the active removal of methyl groups from cytosines by ROS1. SUMO E3 ligase SIZ1 is a key regulator of DNA demethylation: it physically interacts with ROS1 mediating the SUMOylation of ROS1. Accordingly, SUMOylation of ROS1 is reduced in *siz1* mutant plants (Kong et al., 2020). Protein levels of ROS1 are significantly reduced in *siz1* mutant plants, whereas an increased level of *ROS1* transcript compared to wild-type individuals is observed. These observations suggest that SIZ1-mediated SUMOylation of ROS1, promotes its stability and positively regulates active DNA demethylation.

Our transcriptomic data revealed the up-regulation of several genes related to the DNA methylation and demethylation machineries (i.e., *SIZ1*, *cytosine-5 DNA methyltransferase3L*, *DNA demethylase 1*, *DNA demethylase 3*) in the progeny of Sys-treated plants. This evidence has brought us to investigate the methylation status of promoter regions of genes as *PAL*, *PIN1*, *SUBT* and *TS* in parental and progeny lines to understand whether the differences in gene expression of our samples could depend on the modifications of DNA methylation. The results of our methylation-sensitive PCR analysis clearly showed that the methylation status of the CpG islands considered was unaltered between all tested conditions. These results indicate that, in our experimental conditions, Sys treatment did not drive changes in DNA methylation at the selected defense gene promoters.

It is widely established that, in addition to DNA methylation, histone post-translational modifications are deeply involved in the regulation of gene expression. Likewise, it is known that these modifications can account for long-lasting changes in gene expression, which may represent a mechanism for inter/trans-generational inheritance of enhanced defense (Pastor et al., 2013). Histone methylation in chromatin has been associated with activation as well as repression of genes, depending on the site where it occurs and the number of methyl groups that are attached to the protein. The major correlation between histone methylation and gene activity was reported for the H3me3K4 on promoters of active genes (Ruthenburg et al., 2007). Therefore, we looked for this histone modification on the promoters of *PAL*, *PIN1*, *SUBT* and TS genes to investigate a possible correlation between it and the transcript abundance of both in parental and offspring lines. According to our hypothesis, Sys threated plants and their progenies shared a significant enrichment of H3me3K4 in the promoter region of *PAL* gene, which was also actively transcribed in the same plants. In addition, transcriptomic data of progeny lines revealed an upregulation of several genes involved in histone post translational modification. This result led to the hypothesis that H3me3K4 could be involved in long-lasting induction of *PAL* expression. This finding agrees with previous works in which induction treatments using stress related phytohormones or hormone analogs were reported to provoke changes in histone methylation at the promoter of some hormone responsive genes (Jaskiewicz et al., 2011; Bertini et al., 2018). For instance, studies conducted on *Arabidopsis* plants demonstrated that BTH stress memory on the WRKY29 and WRKY6 promoters is associated with increased trimethylation of H3K4 (Jaskiewicz et al., 2011).Our understanding of long-lasting stress memory in plants upon Sys treatment remains fragmentary. A more extensive analysis of different histone modifications would allow a better comprehension of Sys long lasting stress memory. In addition, other mechanisms must be considered that could contribute to this memory: as an example, metabolites or proteins deposited inside the seed or the embryo could explain some intergenerational inheritance (Lämke and Bäurle, 2017). Nevertheless, here we report for the first time the ability of Sys to induce an intergenerational memory able to protect tomato plants against *B. cinerea* colonization, likely associated with the H3me3K4 modification of *PAL* promoter.

In conclusion, this research demonstrates that plant treatment with Sys can activate long-lasting defense effects that are visible in the offspring individuals both at a transcriptomic and phenotypic level. Our results also provide a starting point for further experiments aimed to unravel the mechanisms mediating inter- or transgenerational stress memory in plants. The opportunity to produce resistant plant phenotypes not using genetic transformation might promote innovative and acceptable approaches which could have important implications in agricultures since boosting plants' natural immune system has been suggested as the safest approach to improve crop yields while minimizing environmental impacts and health threats (Quintana-Rodriguez et al., 2018).

2.4 Material and methods

2.4.1 Plant material and experimental treatments

Tomato seeds (*S. lycopersicum* L. cultivar "Dwarf San Marzano") were surface sterilized with 70% ethanol for 2 minutes, rinsed, washed with 2% sodium hypochlorite for 10 minutes and rinsed five times with sterile distilled water. Seeds were germinated in Petri dishes on wet sterile paper and placed in a growth chamber at 24 ± 1°C and 60 ± 5% of relative humidity (RH) in darkness. Upon roots emergence, plantlets were transferred to a polystyrene plateau with barren substrate S-type (Floragard, Oldenburg, Germany) in a growth chamber at 26 ± 1°C and 60 ± 5% RH, with a 18:6 hour light/dark photoperiod, at a brightness of 5,000 lux. After 2 weeks, plants were transferred to sterile soil mixture in 9 cm diameter pots and grown upon the same growth conditions. Fully expanded leaves of tomato plants were treated by foliar spotting with 100 fM Sys (S_0), and PBS 0,1X (C_0) for mock condition, at two time points (4 and 8 weeks-old plants).

To assess durability of Sys induced defense in the next generation, 10 individuals from C_1 and S_1 were allowed to set seed under stress-free conditions, providing C_1 and S_1 progeny lines, respectively. These seeds were sowed, and the progeny plants grown under identical, nonstress conditions, of parental plants.

2.4.2 Botrytis cinerea bioassay

B. cinerea spores were cultivated on MEP (Mannitol Egg yolk Polymyxin) solid medium at 22°C. Spores were collected by washing agar surface with sterile distilled water containing 0.1% Tween 20, filtered through sterile Kimwipes (Kimberly-Clark Dallas, Texas, USA), to eliminate fragments of hyphae, and corrected to a concentration of 1×10^6 conidia/ml. Four-weeks old plants of C_1 and S_1 lines were tested for resistance against *B. cinerea* by applying 10 µl aliquots of *B. cinerea* spore suspension on leaves. The assay was carried out using 5 leaves from 5 different plants for each thesis. Detached leaves were placed on sponges soaked in sterile water and incubated in a growth chamber at 23°C, under 16:8-hour light/dark photoperiod and 90% ± 5% RH. The size of the lesions was measured at 1, 3, 5 and 7 days after infection using a digital caliper.

2.4.3 RNA-seq expression analysis

Fully expanded leaves of tomato plants for each treatment were used for total RNA extraction. Each of the 3 biological replicates was obtained as pools of 2 independent plant. Leaf samples were taken from parental (C_0, S_0) (24h after Sys treatment) and progeny (C_1, S_1) lines. Total RNA was extracted using the Plant RNeasy mini kit (Qiagen) according to manufacturer's protocol. Samples were analyzed with a 2,100 Bioanalyzer system (Agilent Technologies) for size, quantification, and quality control of RNA. Only samples with a 260/280 nm absorbance >1.8 and a 260/230 nm absorbance >2 were selected for sequencing. Total RNA (8 µg) of each sample was used for library preparation and sequencing by an external sequencing service. A paired-end sequencing (2 × 30 million of reads) on Illumina HiSeq 2,500 platform was chosen. RNA-Seq raw sequences were cleaned using Trim Galore package (http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/). Low-quality bases were trimmed from the sequences and the adapter sequences were removed by Cutadapt (Martin, 2011); default parameters for the pair-end sequences were used. The cleaned sequences were then mapped on the tomato genome (version 4.0) using Bowtie version 2.1.0 (Langmead and Salzberg, 2012) and Tophat version 2.0.8 (Kim et al., 2013). Quantification of the reads abundance per each gene (exon level) available from iTAG (International Tomato *Annotation* Group) gene annotation (version 4.0) was done using AIR (https://transcriptomics.sequentiabiotech.com/). To identify the set of DEGs between the different experimental conditions, Negative Binomial test and Generalized Linear Model (GLM) were used, as implemented in EdgeR package (Robinson et al., 2010), with a false discovery rate (FDR) < 0.05. All DEGs are listed in **tab.** 1 and 2 in appendix

2.4.4 Gene ontology and pathway enrichment

Gene ontology (GO) analysis was performed utilizing ShinyGo (Ge et al., 2020), using all DEGs taken together and DEGs up- or down-regulated, separately. Terms belonging to the three main ontological groups (i.e., Biological processes, BP; Molecular function, MF; and Cellular component, CC) were considered as significantly enriched when the corrected p-value and FDR were both ≤ 0.05 according to the Benjamini–Hochberg method (Haynes, 2013).

2.4.5 Chromatin immunoprecipitation assay

All assays were performed according to the manufacturer's protocol (EpiQuik Plant ChIP kit; Epigentek) using leaves from 4-week-old plants: leaf samples from parental (C_0,S_0) (24h after Sys treatment) and progeny (C_1, S_1) lines. Three biological replicates were used for each thesis tested. Chromatin samples were immunoprecipitated using antibodies against trimethyl-H3K27 (ab8580, Abcam). Specific DNA regions abundance in chromatin extracts was determined by quantitative PCR from two independent precipitation reactions using an ABI PRISM 7900 HT sequence detection system (Applied Biosystems). Reactions were achieved in a final volume of 25 µL with Jump Start SYBR Green (Sigma-S4438).). Results were normalized to initial DNA amounts in the input control, as described (Haring et al., 2007), and calibrated to control samples. Primers and their main features are reported in **Tab. 1.**

Tab. 1. List of Primers used for Real-time PCR analysis.

Gene name	Primer	Sequence (5’-3’)	Name/Gene symbol	Accession number
PAL (A)	Fw Rv	AAGCACCAAACCTTTTGCCA TATATGGACAGCGTGGGGGA	*Phenylalanine ammonia lyase*	Solyc10g086180
PAL (B)	Fw Rv	AGTTTCTCGTCTTGACACCCC GGCAAAAGGTTTGGTGCTT	*Phenylalanine ammonia lyase*	Solyc10g086180
PIN 1 (A)	Fw Rv	CACAGTCTCCCCTCACTTCTTG TGTAGTGAGGTGCTAGTGGTGT	*Wound-Induced Proteinase Inhibitor 1*	Solyc09g084460
PIN 1 (B)	Fw Rv	TCAATTTTCACAGTCTCCCCTC ATTGTAGTGAGGTGCTAGTGGT	*Wound-Induced Proteinase Inhibitor 1*	Solyc09g084460
SUBT (A)	Fw Rv	GGTGGCTCCGCCTTTGATAA GTAAGTTGTGGTGGGACGGA	*Subtilisin-like protease*	Solyc08g007680
SUBT (B)	Fw Rv	TTATTGGTGTTTGGTGTTCCCTTT TCTGACTCTGCCTCTGAGCTTT	*Subtilisin-like protease*	Solyc08g007680
TS (A)	Fw Rv	TTGCTACCTAGTCCCTATTTTCACC ACGAACCTTATCCAACAACCCAA	*Terpene synthase*	Solyc01g105890
TS (B)	Fw Rv	AGATCATTGCTACCTAGTCCCT ACGAACCTTATCCAACAACCCA	*Terpene synthase*	Solyc01g105890

2.4.6 DNA methylation assay

DNA methylation status was analyzed by Chop-PCR. Genomic DNA was extracted from leaves of 4-weeks old plants from parental (C_0, S_0) (24h after Sys treatment) and progeny (C_1, S_1) lines, using the DNeasy Plant Mini Kit (Qiagen). Three biological replicates were used for each thesis tested. For Chop-PCR, genomic DNA (500 ng) was digested overnight with the methylated DNA digesting enzyme McrBC. According to the manufacturer’s instructions, McrBC (New England Biolabs, M0272L) cuts (chop) approximately 30 base pairs from the methylated cytosine distributed over several base pairs. Unmethylated DNA is not cleaved by McrBC. Digested DNA was used for the amplification of PAL, PIN1, SUBT, and TS promoters using *Taq* DNA Polymerase (New England Biolabs) and the primers listed **Tab. 2**. PCR was performed as follows: an initial denaturation step of 2 min at 95°C, followed by 25 cycles of 30 sec denaturation at 95°C, 30 sec annealing at 57°C and 1 min elongation at 68°C. PCR products were then used for agarose gel electrophoresis. Undigested genomic DNA was amplified as an internal control.

Tab. 2. List of Primers used for PCR analysis.

Gene name	Primer	Sequence (5’-3’)	Name/Gene symbol	Accession number
PAL (A)	Fw Rv	TTCTCGTCTTGACACCCCAC GGGGGCTTGAATGGGTGTAAT	*Phenylalanine ammonia lyase*	Solyc10g086180
PAL (B)	Fw Rv	ACAAAATACAAAGATGTTAAAGCGG GGAGGGGGACGAGAGATTTG	*Phenylalanine ammonia lyase*	Solyc10g086180
PIN 1 (A)	Fw Rv	AGCTAATTGTGCTTTCCGTCTC TGTAGTGAGGTGCTAGTGGTGT	*Wound-Induced Proteinase Inhibitor 1*	Solyc09g084460
PIN 1 (B)	Fw Rv	TGGGGCTTTGATTCGTACTC TTGCTCCCAAGTATTCTGCCT	*Wound-Induced Proteinase Inhibitor 1*	Solyc09g084460
SUBT (A)	Fw Rv	GCATGGCTTGCAAGTAGTATGA TGTGTGGGAGAAAGTGAAGTATCA	*Subtilisin-like protease*	Solyc08g007680
SUBT (B)	Fw Rv	CGTCCCACCACAACTTACGA ACACCACCTAATGATGGGAACT	*Subtilisin-like protease*	Solyc08g007680
TS (A)	Fw Rv	GAATTTGAGTCATGGAGTTACTT CGGAGCCACAGTGAAGGG	*Terpene synthase*	Solyc01g105890
TS (B)	Fw Rv	ATGGTGAGGGTGTGTGTCTC ATATTTCAACGCTTCCTTGCG	*Terpene synthase*	Solyc01g105890

2.4.7 Statistical analysis

Student’s t-test was used to identify differences in necrosis diameter development experimental samples and controls. Moreover, the chromatin immunoprecipitated with antibodies was compared by Student’s t-test between experimental samples and controls. Error bars referring to standard error were displayed.

Chapter 3

Non only Systemin: Prosystemin harbors protein fragments able to protect tomato plants

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Abstract

Systemin was usually considered as the main actor of tomato resistance to a wide range of biotic/abiotic stress, as suggested by the increased production of Proteinase Inhibitors upon its application on wounded or intact stems and leaves. Recent evidences suggest that Prosystemin is not only the precursor of Systemin peptide but likely contribute itself to defense responses. A detailed characterization of this pro-hormone proved that it is a member of the Intrinsically Disordered Proteins family. These proteins play a central role in regulating the transduction pathways of several signals, including the “defense signal”. Moreover, their disordered structure promotes the binding of different molecular partners and the possible activation of multiple stress-related pathways. These observations, combined with recent findings demonstrating that Prosystemin even when deprived of Systemin is biologically active, encouraged us to investigate the putative biological role of the precursor N-terminal protein sequence.

Two different Prosystemin fragments, not including Sys, were designed, recombinantly produced and used in bioassays to evaluate their biological activity. Both fragments were active at femtomolar concentration, being able to modulate the expression of defense-related genes and protect tomato plants against noctuid moth and a necrotrophic fungal pathogen. Interestingly, the biological activity of the two fragments is not overlapping for both and for Sys and does not show any toxicity on non-target organisms tested.

3.1 Introduction

All multicellular organisms have developed mechanisms to perceive and respond to extracellular stimuli (Sharifi and Ryu, 2021). These include endogenous hormones and cues from pathogens, symbiotic organisms, and environment. In animals, intercellular communications are mainly mediated by peptides because of their great variety in sequence, length, and posttranslational modifications (Fiers et al., 2007). The first peptide hormone, insulin, was detected in animals in 1921 (Vecchio et al., 2018). In plants, due to the early discovery of nonpeptidic hormones (auxins, cytokinins, gibberellins, ethylene, etc), peptide hormones remained in the shadow for a long time. However, the first plant peptide hormone, Sys, was detected in 1991 as a part of the stress response in tomato (Pearce et al., 1991).The discovery of this peptide inspired plant biologists to search for other signal peptides. Therefore, over the last two decades, plant peptides not only have been studied as actors of defense responses, but they have also emerged as a distinct class of hormones (Segonzac and Monaghan, 2019), as they are able to act both locally and systemically at extremely low concentration (Davies, 2010). Most peptides identified up to now derived from a longer precursor similarly to Sys that, as mentioned previously, is released from a 200-amino-acid precursor protein ProSys upon proteolytic cleavage mediated by phytaspase.(Beloshistov et al., 2018). ProSys is known to accumulate in tomato cells in response to wounding, insect herbivory or exogenous treatment with methyl jasmonate (MeJA). ProSys genes were identified in a limited number of *Solanaceae* species including tomato, potato, bell pepper and nightshade, and the Sys primary structure was found to be well conserved (Constabel et al., 1998). Evidence gathered via the production of transgenic tomato plants showing either constitutive expression of ProSys gene, or knockdown by anti-sense silencing, clearly demonstrated the role of ProSys in orchestrating resistance against a wide range of stress agents. Indeed, constitutive production of ProSys resulted not only in increased plant resistance against chewing insect herbivores, phytopathogenic fungi and viruses; on top of that, ProSys heightened emissions of volatile organic compounds promoting indirect defense responses through the attraction of parasitoid wasps (McGuRL et al., 1994; Coppola et al., 2015; Corrado et al., 2016; Bubici et al., 2017). Moreover, these transgenic plants were found to have increased tolerance to moderate salt stress (Orsini et al., 2010). The Sys peptide is traditionally considered the main player of tomato disease resistance, meaning that a single peptide is involved in the regulation and response to a broad spectrum of stress agents. The mechanism underpinning such an extensive plant protection effect has not been clearly identified yet; it could be related to the structural features of the ProSys protein itself, which was demonstrated to be an Intrinsically Disordered Protein (IDP) having no stable or ordered three-dimensional structure (Buonanno et al., 2018). The IDP structural flexibility allows them to assume a wide spectrum of conformations which, according to specific conditions, induce their transient and specific interactions with multiple molecular partners (Uversky et al., 2013; Wright and Dyson, 2015).The binding promiscuity of IDPs allows them to regulate many signal transduction pathways, thus integrating multiple environmental stimuli (Kragelund et al., 2012). An interesting example is given by DELLA proteins, a subfamily of the GRAS protein family, which act as key regulators of gibberellin, Jasmonate, and light signaling (Sun et al., 2012). DELLAs modulate diverse signaling processes through dynamic interactions of their intrinsically disordered regions (IDRs) with hormone receptors and light-responsive transcription factors (Sun et al., 2013; Fan et al., 2021). Likewise, the ProSys IDRs could interact with different partners activating simultaneous defense signals. This hypothesis is supported by data showing that tobacco transgenic plants constitutively expressing the truncated ProSys (lacking the exon encoding Sys) have significant alterations in their proteomic profile and perform better against *Botrytis cinerea* infection (Corrado et al., 2016). Recent experiments with transgenic tomato plants overexpressing the truncated ProSys, and tomato plants treated with recombinant truncated ProSys provide further direct evidence in support of the multifunctional role of ProSys (Molisso et al., 2022b). In both cases, a clear modulation of the expression of genes, linked with defense responses, was observed, which resulted in enhanced protection against the lepidopteran pest *Spodoptera littoralis* and the fungus *B. cinerea*.

To better investigate the putative biological role of the precursor N-terminal region, two different recombinant ProSys fragments, namely PS1-70 and PS 1-120 previously design and produced recombinantly, were here analyzed fo their biological activity. Our results show that both fragments, which maintained the intrinsic disordered structure of the precursor, induce defense-related genes in tomato plants, conferring protection against necrotrophic fungi and noctuid moths at femtomolar concentration.

Interestingly, biological activity of each of the two N-terminal fragments and of Sys is similar but not quite the same. PS1-70 and PS1-120 did not show any direct toxicity on experimental non-targets organisms tested: the photosynthetic microorganism *Chlamydomonas reinhardtii* and a human keratinocyte (HaCaT) cell line. Taken together, these results confirm our hypothesis that ProSys is not only a mere scaffold of Sys but a regulatory multi-subunit complex containing multiple biologically active sequences, potentiating the effects of the well-known Sys peptide.

3.2 RESULTS

3.2.1 Prosystemin fragments application enhances the expression of plant defense-related genes

In order to evaluate if tomato plants were able to sense ProSys fragments when externally applied, different peptide delivery systems have been tested to evaluate their efficacy.

To explore the effect of exogenous peptide supply at a molecular level, qPCR has been performed to monitor the expression profile of defense-related genes 6 and 24 hours after ProSys fragments treatment and compared with Sys treated plants. The first system tested is based on peptide supply through hydroponic cultures. The expression of *AOS* gene was not significantly induced neither 6 nor 24 hours after the application of any of these peptides. Conversely, a consistent over-expression of *Pin I* and *Pin II* was observed at 6 hours and 24 hours, respectively, after the application of Sys and PS1-70. These results suggest that the hydroponic supply of the experimental peptides enhances a faster response in Sys treated plants compared to PS1-70 **(Fig. 1).**

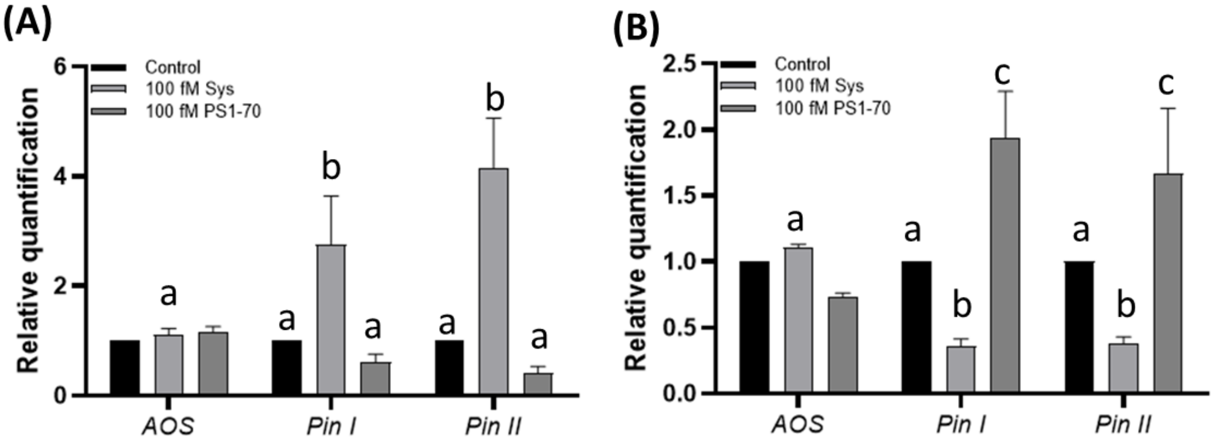

Fig. 1. Gene expression analysis in tomato plants grown in hydroponic solution containing 100 fM Sys or PS1-70. Relative quantification of early and late defense genes induced at 6 (A) and 24 (B) HPT (hours post treatment) with 100 fM of Sys or PS1-70. Quantities are shown relative to the calibrator control condition, set as 1 (mock-treated plants). Letters indicate different statistical groups (One-Way ANOVA, P<0.05). Error bars indicate standard error.

The second system tested is based on peptide supply by soil irrigation. The expression of *AOS* gene showed a significant induction at 6 hours after application of both peptides, followed by a reduction at 24 hours. The expression of *Pin I* and *Pin II* showed a significant increase at both 6 and 24 hours after Sys treatment but only at 24 hours after PS1-70 exogenous supply **(Fig. 2).** These results were quite similar to those obtained from the 1st delivery system tested.

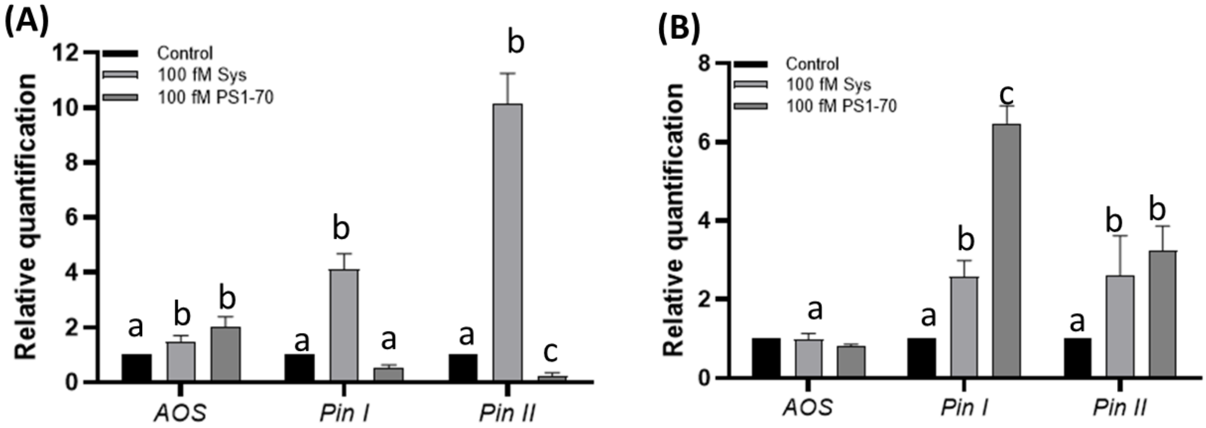

Fig. 2. Gene expression analysis in tomato plants grown irrigated with 100 fM Sys or PS1-70. Relative quantification of early and late defense genes induced at 6 (A) and 24 (B) HPT with 100 fM of Sys and PS1-70. Quantities are shown relative to the calibrator control condition, set as 1 (mock-treated plants). Letters indicate different statistical groups (One-Way ANOVA, P<0.05). Error bars indicate standard error.

The third delivery system tested consists of plant treatment by foliar spotting. All the experimental peptides induced a stronger over-expression of the selected genes already 6 hours post treatment (HPT) (**Fig. 3**) These results indicated that the most effective peptide delivery system in inducing tomato endogenous defense was the foliar spotting. Therefore, we decided to use this peptide supply system for all the following experiments.

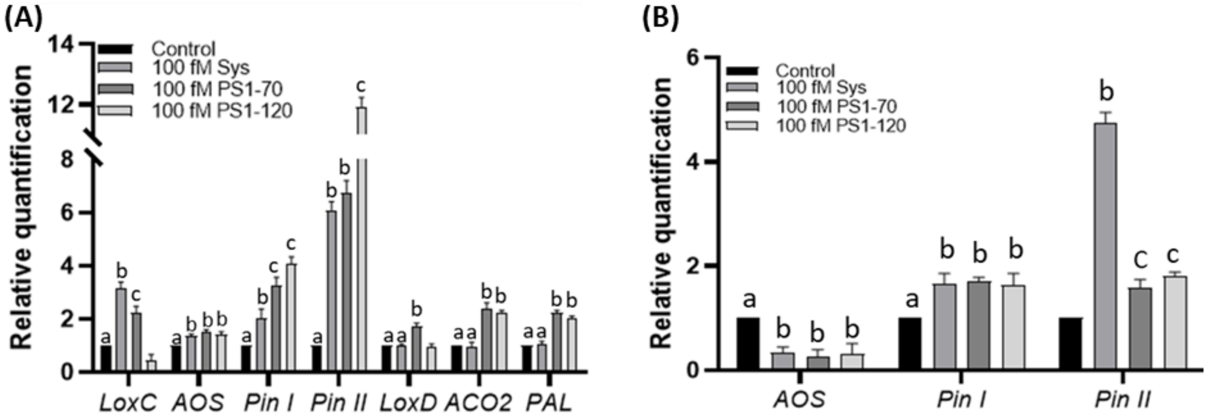

Fig. 3. Gene expression analysis in tomato plants grown in soil and treated with 100 fM Sys, PS1-70 or PS1-120 by foliar spotting. Relative quantification of early and late defense genes induced at 6 (A) and 24 (B) HPT with 100 fM of Sys and PS1-70. Quantities are shown relative to the calibrator control condition, set as 1 (mock-treated plants). Letters indicate different statistical groups (One-Way ANOVA, $P<0.05$). Error bars indicate standard error.

In addition, some significant differences were observed 6 HPT in the level of transcripts encoding LoxC (*Lipoxygenase C)*, Pin I and Pin II proteins, and the expression of different genes was differently induced by the experimental peptides. While *AOS* is similarly induced by the three peptides, *LoxD* transcription appears to be induced uniquely by PS1-70 and *ACO2 (1-aminocyclopropane-1-carboxylate oxidase)* and *PAL* by PS1-70 and PS1-120, but not by Sys peptide.

3.2.2 Impact of PS1-70 and PS1-120 on pathogens and pests

S. littoralis larvae fed with leaves treated with Sys, PS1-70 and PS1-120 were severely impaired in their growth [Log-rank (Mantel-Cox) test: $\chi^2= 110.8$, dF = 3, $P < 0.0001$)]. PS1-70 treated leaves produce a significantly stronger negative effect than leaves treated with Sys (Log-rank test: $\chi^2 = 9.593$, df = 1, $P < 0.002$) or with PS1-120 (Log-rank test: $\chi^2 = 13.18$, df = 1, $P = 0.0003$), which did not differ between them (Log-rank test: $\chi^2 = 144$, df = 1, $P = 0.7356$) (**Fig. 4**).

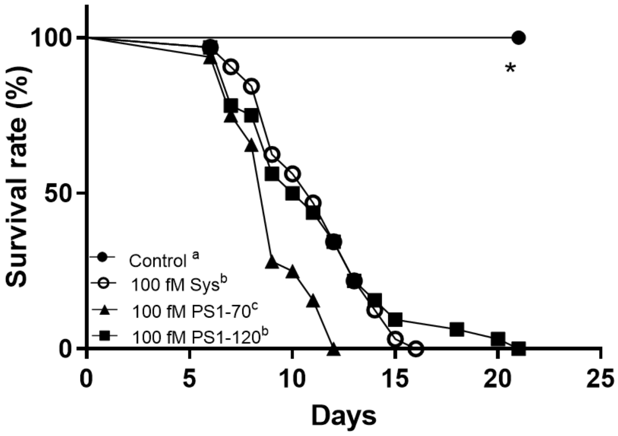

Fig. 4. Effect of 100 fM Sys, PS1-70 and PS1-120 on *S. littoralis* larvae. Survival rate of *S. littoralis* larvae fed with experimental peptide-treated leaves. Different letters denote significant differences in the survival curve (Log-Rank test, $P < 0.0001$).

Moreover, both topical and oral direct applications of PS1-70, PS1-120 and Sys, at different concentrations, showed no larvicidal effect on 4th larval instar of *S. littoralis*; all experimental larvae exhibited similar developmental patterns (**Tab. 1-2**).

Tab. 1. Evaluation of the larvicidal effect of the direct delivery (oral ingestion) of ProSys fragments at different concentrations on *S. littoralis* larvae.

Oral ingestion	**4th instar**	**pupal stage**	**% survival**
Control	16	15	93,75
100 fM Sys	16	16	100
100 pM Sys	16	15	93,75
100 nM Sys	16	16	100
100 fM PS1-70	16	16	100
100 fM PS1-70	16	15	93,75
100 nM PS1-70	16	15	93,75
100 fM PS1-120	16	16	100
100 pM PS1-120	16	16	100
100 nM PS1-120	16	15	93,75

Tab. 2. Evaluation of the larvicidal effect of the direct delivery (topical application) of ProSys fragments at different concentrations on *S. littoralis* larvae.

Topical application	**4th instar**	**pupal stage**	**% survival**
Control	16	15	93,75
100 fM Sys	16	16	100
100 pM Sys	16	16	100
100 nM Sys	16	16	100
100 fM PS1-70	16	15	93,75
100 fM PS1-70	16	16	100
100 nM PS1-70	16	15	93,75
100 fM PS1-120	16	15	93,75
100 pM PS1-120	16	16	100
100 nM PS1-120	16	16	100

Leaves treatment with Sys, PS1-70 and PS1-120 caused a strong reduction of *B. cinerea* colonization with a consequent reduction of necrosis areas already visible 1 DPI (days post inoculum). This difference increased over time; after 5 DPI, leaves treated with PS1-120 showed the strongest reduction of disease severity compared to the other tested peptides (**Fig 5**).

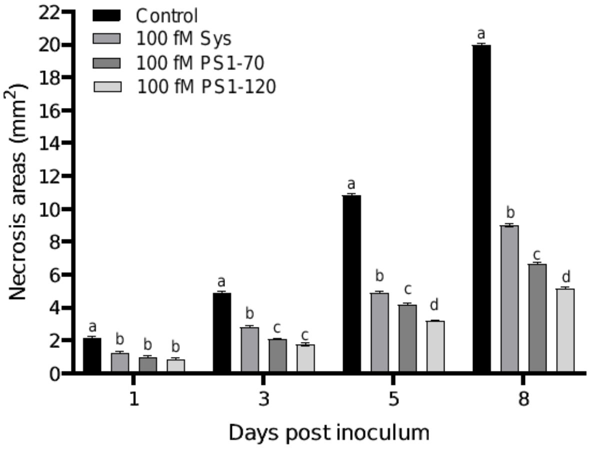

Fig. 5. Treatment with ProSys fragments and Sys peptide reduces *B. cinerea* virulence on tomato plants. Response to *B. cinerea* infection in leaves from mock-treated and Sys, PS1-70 and PS1-120 treated plants. Graphs display mean necrosis area size at 1, 3, 5 and 8 DP1. Letters indicate different statistical groups (One-Way ANOVA, P<0.05). Error bars indicate standard error.

In order to evaluate whether the reduction of *B. cinerea* necrosis area was due to a direct antimicrobial effect of fragments on the fungus, an *in vitro* assay was carried out to measure fungal growth in presence or absence of the peptides. No impact of the tested fragments on fungus vitality was observed as shown in **Fig. 6**.

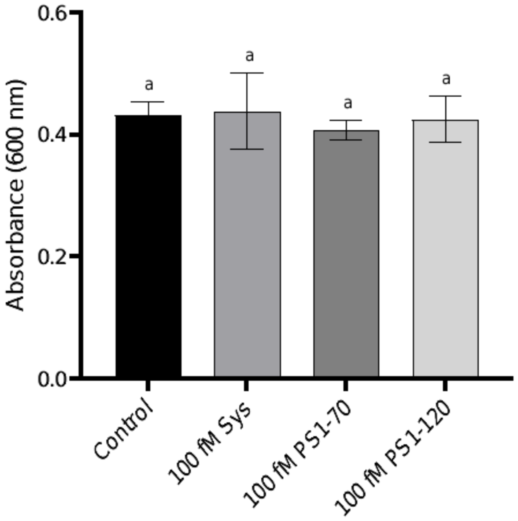

Fig. 6. Effect of Sys and ProSys fragments on *B. cinerea* vitality. Spores of *B. cinerea* were added to wells filled with 1 ml of PDB1/2 medium containing the peptides at a final concentration of 100 fM, except for the broth sterility control wells. Fungal growth was assessed 24 hours after pathogen inoculation evaluating the OD_{600} of the medium. Different letters indicate statistically significant differences (One-Way ANOVA, $P < 0.05$). Error bars indicate standard error.

3.2.3 Impact of Prosystemin fragments on microorganism and mammalian cells

In order to verify if ProSys fragments exert a cytotoxic effect on photosynthetic microorganisms or human cells, cell viability and growth of microalgae were explored when exposed to the tested peptide. *C. reinhardtii* cells incubated with different concentrations of Sys, PS1-70 and PS1-120 showed a similar grown rate as untreated control, at every considered time point. (**Fig. 7**).

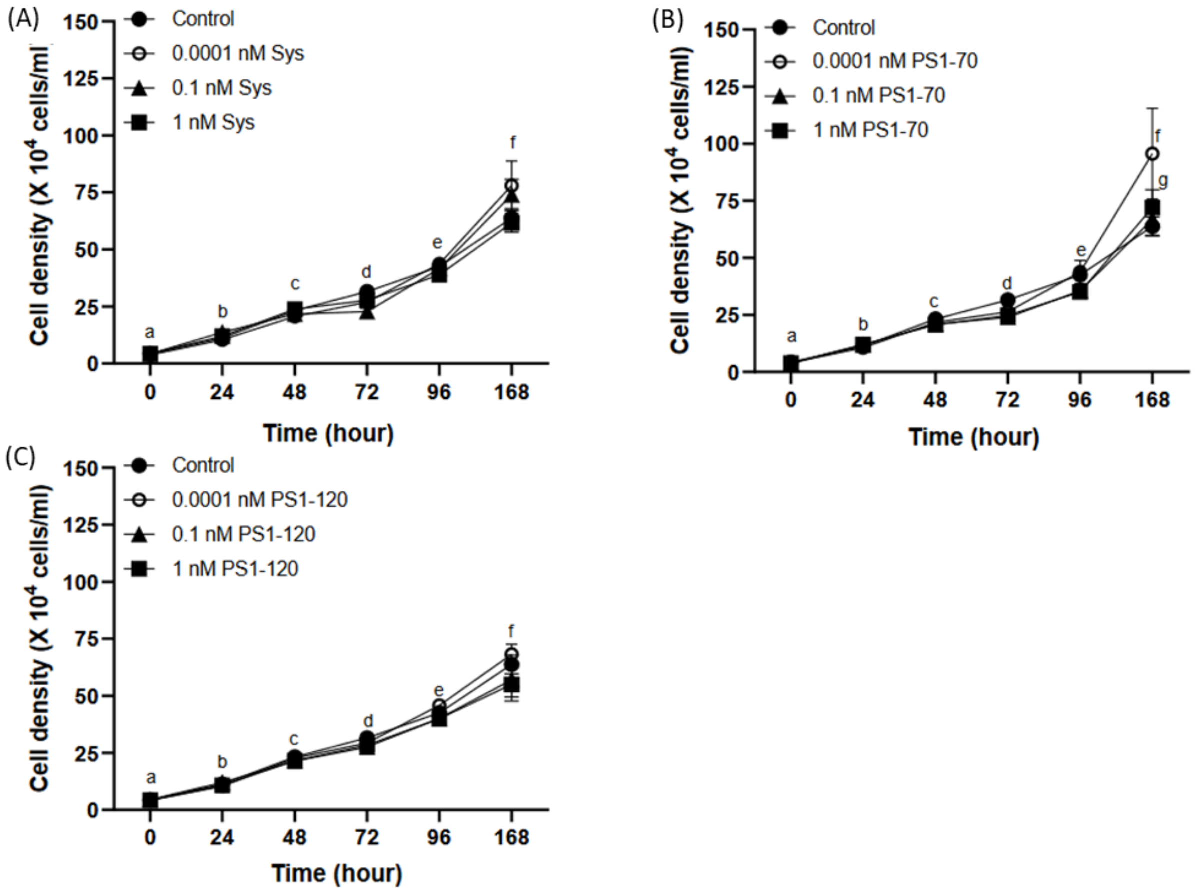

Fig.7. Growth curves of microalgae *C. reinhardtii* treated with different concentrations of peptides. (**A**) Sys, (**B**) PS1-70, and (**C**) PS1-120. (One way ANOVA, P< 0.05, not significant). Error bars indicate standard deviation.

Therefore, no toxic effect of PS1-70 and PS1-120 was observed on microalgae, even at the highest concentration tested (1nM) which was much higher than that inducing the observed biological effects.

Likewise, to previous experiments, proliferation and morphology of human keratinocytes (HaCaT) upon treatment were assayed exposing the cells at high concentrations (100 nM) of each peptide for 24 hours. Cell viability, evaluated by absorbance of CCK-8 assay, was ≈100% (97.9% for PS1-70 and 100% for PS1-120) (**Fig. 8 A)**. This result is in accordance with that obtained by manual cell count (94% for PS1-70 and 95% for PS1-120). Overall, these results clearly indicate that all the experimental peptides did not exert any cytotoxic effects against mammalian cells, even using concentrations much higher than those used for plant treatments. Furthermore, possible variations of cell morphology in treated HaCaT cells were analysed by phase-contrast microscopy. As shown in the micrographs reported in **Fig.8 B**, both peptides did not induce any morphological change in the experimental cells.

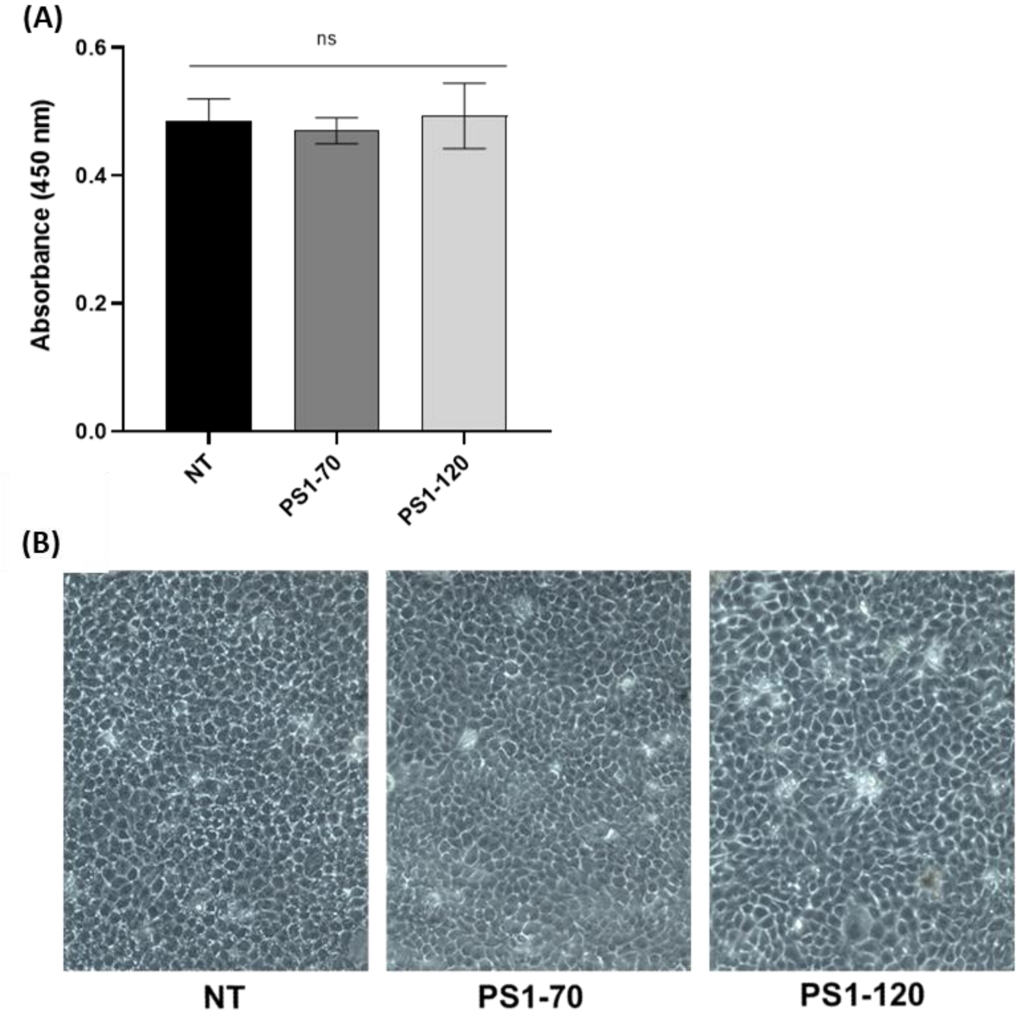

Fig.8. Cell viability and morphology of HaCaT cells incubated with PS1-70 or PS1-120. **(A)** Cell viability of HaCaT cells incubated at 37°C for 24 hours in the absence (NT) or presence of 100 nM PS1-70 or PS1-120, was evaluated by CCK-8 assay. (**B)** Phase-contrast microscopy images of HaCaT cells, either untreated (NT) or treated with 100 nM of PS1-70 or PS1-120 at 37°C for 24 hours. Representative microscope images of three independent experiments performed in triplicate were shown. Bars are presented as mean (Student's t-test, $P< 0.05$). Error bars indicate standard deviation.

3.2.4 Lipid peroxidation status and H_2O_2 content in tomato leaves after ProSys fragments application

The redox state of treated leaves 1, 6 and 24 HPT, was then investigated. H_2O_2 content in Sys treated leaves was significantly higher than in untreated control at every time point, achieving its maximum after 6 HPT [Tukey test, $F (3.23) = 63.36$; $P < 0.0001$]. A different profile was observed for H_2O_2 content in PS1-70 and PS1-120 treated leaves: the former led to a significant increase of the ROS species only 6 HPT, while the latter did not impact H_2O_2 content at all (**Fig. 9 A)**. This is consistent with the lipid peroxidation value, determined by malondealdehyde (MDA) content, a significant increase of which was observed in Sys and PS1-70 treated plants 6 HPT compared to controls. A further increase of this value occurred at 24 HPT in Sys treated leaves (**Fig. 9 B**). Conversely, no differences between PS1-120 treated plants and controls was found (**Fig. 9 B**).

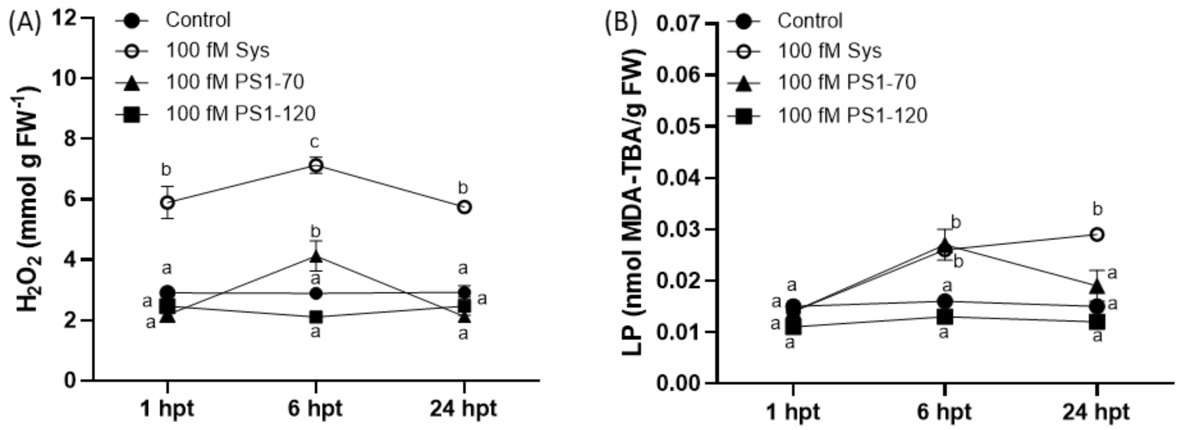

Fig. 9. H_2O_2 and MDA content in tomato leaves treated with 100 fM Sys or ProSys fragments. H_2O_2 (A) and MDA (B) contents were measured in control (PBS1X) and in 100 fM Sys, PS1-70 or PS1-120 treated leaves at 1, 6, and 24 HPT. Different letters indicate statistically significant differences (One-Way ANOVA, $P< 0.05$). Error bars indicate standard error.

3.3 Discussion .

Plants have evolved different families of peptide signals involved in defense responses against insects and pathogens (Hu et al., 2018).. These molecules, active at very low concentrations (Roy et al., 2018), trigger a huge range of defense responses upon cell damage by pests and pathogens through signaling cascades that trigger the transcription of defense-related genes. Over the last decade, several plant endogenous peptides have been identified as regulators of immune response to herbivory and/or microbial infection. Understanding their role in plant defense mechanisms is an important pre-requisite for their possible use in crop defense strategies (Gust et al., 2017; Hu et al., 2018). Elicitor peptides are typically released from large precursor proteins (Yamaguchi and Huffaker, 2011). Being able to trigger plant immunity, these molecules may become interesting players in pest management, offering new opportunities for pest control and contributing to agro-food safety (Delaunois et al., 2014). Despite Sys has been considered for long time the major player on tomato defense responses (McGuRL et al., 1994; Howe and Ryan, 1999; Ryan, 2000; Coppola et al., 2015; Corrado et al., 2016), recent findings evidenced that ProSys is an intrinsically disordered protein (IDR) (Buonanno et al., 2018). IDRs allow proteins to bind multiple molecular partners having often different functional effects suggesting that, besides Sys, other ProSys regions could play a role in defense responses (Wright and Dyson, 2015). These observations were corroborated by recent findings which demonstrate that transgenic tomato plants expressing a truncated form of ProSys lacking the Sys fragment are resistant against pests likely as a consequence of the induced expression of defense-related genes and proteins (Molisso et al., 2022b). These results prompted to investigate more closely the structural and biological activity of some regions of the precursor devoid of the Sys peptide. To this aim two ProSys recombinant fragments, namely PS1-70 and PS1-120, have been designed and produced as reported by (Molisso et al., 2022b) and tested here for their capability to induce tomato endogenous defense at femtomolar concentration.

Interestingly, PS1-70 and PS1-120, like Sys, behave as phytohormone molecules able to confer protection against pests at an extremely low concentration (100 fM). The best performance of tomato plants against *S. littoralis* larvae was observed after the treatment with PS1-70, which induced 100% mortality of the insect larvae 13 days after the treatment. On the contrary, PS1-120 proved more effective in reducing *B. cinerea* produced necrotic area, compared with both Sys peptide and the PS1-70 fragment. *In vitro* bioassays showed that the tested peptides do not exert any direct antifungal or larvicidal activity, confirming that they protect the plant through the promotion of the plant immune system.

The exogenous supply of the tested peptide by foliar spotting, soil drenching or hydroponic culture also display a difference in the perception of the tested peptides. Further investigations are necessary to clarify this aspect. Moreover, PS1-70 and PS1-120 induce, by foliar spotting, the expression of genes associated with the octadecanoid signaling pathway (*Lox C,* and *AOS*), that is known to play a central role in plant defense against a wide range of biotic stressors (Thakur and Udayashankar, 2019; Zeng et al., 2021), and of JA responsive genes (*Pin I* and *Pin II*). Proteinase inhibitors (PIs) act against insect pests by binding to the active site of the digestive proteases, blocking their proteolytic activity and leading to a decreased or fully disrupted dietary-protein digestion (Napoleão et al., 2019). This action reduces the essential amino acids in the insect intestine, which are required for insect growth and adult survival as well as for the growth and development of the larvae (Cotabarren et al., 2020). In addition, PIs are involved in programmed cell death, and other actions related to plant protection against pests and pathogens (Clemente et al., 2019). Intriguingly, PS1-70 induces the expression of *LoxD*: when overexpressed in tomato plants, this gene improves JA biosynthesis and increases the expression of wound-responsive genes, consequently enhancing resistance against insect herbivores (Song et al., 2013; Yan et al., 2013a). These observations nicely correlate with the effective protection against the herbivorous pest triggered by PS1-70. Moreover, PS1-70 and PS1-120 induced the expression of *ACO*, a gene associated with ethylene production (Houben and Van de Poel, 2019), an important regulator of plant responses against biotic and abiotic stress agents, and of *Pal*, a gene encoding a key enzyme of plant metabolism leading to changes in lignin contents and thickness of cell walls, involved in plant defense responses against parasites (Lee et al., 2019).

Upon stress conditions, homeostasis of intracellular redox state is impaired, with the consequent increase of ROS and cell damage through lipid peroxidation (Huang et al., 2019). Oxidative parameters analysis showed an additional difference in terms of ROS generation among PS1-70, PS1-120 and Sys. Taken together, these results indicate that PS1-70, PS1-120 and Sys all confer protection to treated plants, but to a different extent, which partly accounts for the diversity of functional responses observed.

Importantly, Sys, PS1-70 and PS1-120 did not show any toxic activity on microalgae and on human HaCaT cells, suggesting a null effect at a moderate dosage on non-target organisms. HaCaT cell lines are among the most common type of cell lines used to assess the effect of toxins and other metabolites at morphological and molecular level in humans (Arunkumar et al., 2020). Peptides that meet the requirements of high efficiency and safety are very beneficial to plant protection in eco-agriculture.

Summing up, these results indicate that ProSys fragments interact with different receptors to produce several different signals which, in turn, control complementary and synergistic defense pathways (Zhang et al., 2020). Recent evidences gathered via the study of ProSys-protein network showed that ProSys is involved in a far greater number of interactions likely due to its ID structure (Natale et al., 2023). This appears to be a common strategy of response to stress agents allowing a faster and more effective response against stress through the induction of an alert state in the entire organism (Olsson et al., 2019; Stührwohldt and Schaller, 2019). The evidence for a plant prohormone, from which can be generated multiple polypeptides with independent biologically activities, is still novel, though there are several examples in both animals and yeast.

Two peptides, named hydroxyproline-rich systemin I and II (HypSys I and II), were first found to associate with wounding and enhance herbivore resistance in tobacco (Ren and Lu, 2006). These two endogenous HypSys are 18-amino-acid peptides both released from a 165 amino acid precursor protein. This was the first example of production in plants of multiple bioactive peptides derived from a single precursor protein. A similar gene was described in tomato witch encodes a polypeptide of 145 amino acids from which three different small defense signaling glycopeptides are released (Ryan and Pearce, 2003). Numerous other examples were lately reported (Chen et al., 2020), evidencing the very important biological role played by plant peptides and protein fragments in physiological responses, which have been underestimated for many years.

From the outcome of our investigation, it is possible to conclude that the identification of these novel peptides has the potential not only to advance plant stress biology, but also to sustainably improve crop productivity developing alternative ways to enhanced stress tolerance or resistance and minimizing the use of agrochemicals. The ProSys fragments tested are effective for stimulating tomato immunity against chewing insect pests as well as fungal pathogens. A potential limitation of PS1-70 and PS1-120 in agricultural application may be its reduced stability in agro-environments. However, novel materials are nowadays available to protect peptide and other compounds in different environment such nanomaterials (Xi et al., 2022). Moreover, plant watering with peptides solution, both in soilless and in-soil cultivation systems, as well as foliar spray could represent an efficient and easily exploitable peptide delivery system for tomato crop protection considering also that a very small amount of the tested peptides is sufficient to control pathogens, and insects.

3.4 Material and methods

3.4.1 Plant materials and growth conditions

Seeds of *Solanum lycopersicum* L. cultivar “Dwarf San Marzano Nano” were surface sterilized by soaking in 70% ethanol for 2 min, rinsed, washed with 2% sodium hypochlorite for 10 min and then washed at least five times with sterile water. Seeds were then germinated in Petri dishes Whatman® sterile filter paper (Sigma-Aldrich, Darmstadt, Germany), kept in the dark for 3 days in a growth chamber at 24 ± 1 C and 60% of relative humidity (RH). At the emergence of the cotyledons, germinated seedlings were individually transplanted into polystyrene pots containing sterile commercial soil (Universal Potting Soil, Floragard, Oldenburg, Germany) and kept in a growth chamber at 26 ± 1°C and 60 ± 5% RH, 18L:6D- photoperiod by lamps of 5,000 lux. After 2 weeks, the plants were transferred into 9 cm diameter pots filled with a sterile soil mixture using the same growth conditions.

3.4.2 Plant Treatments

Four-week-old plants, grown in pots filled with sterile soil, were irrigated with 100 ml distilled water enriched with Sys or PS 1-70 to a final concentration of 100 fM. Control plants were similarly treated with PBS buffer 0,1X (phosphate buffer saline, 1 mmol L -1 phosphates, 14 mmol L -1 NaCl, 0.27 mmol L -1 KCl, pH 7.4, Sigma-Aldrich, Milan, Italy). Leaf samples were collected 6 and 24 HPT for gene expression analysis.

For hydroponics system, tomato seeds at 2-cotyledon stage (5 days after sowing), were transferred into a hydroponic system, and grown for 4 weeks in a 5 L solution, containing $Mg(NO_3)_2 \cdot 6H_2O$ (384.0 mg/L), $Ca(NO_3)_2 \cdot 4H_2O$ (812.9 mg/L), KNO_3 (101.5 mg/L), K_2SO_4 (319.3 mg/L), KH_2PO_4 (204.8 mg/L), Hydromix (14.0 mg/L), and the experimental peptides to a final concentration of 100 fM. Leaf samples were collected 6 and 24 HPT for gene expression analysis.

For the foliar spotting system, healthy and fully expanded leaves of four-week-old plants were treated with 100 fM purified recombinant fragments. In particular, 15 spots of 2 ml of the tested peptides were gently placed on the adaxial surface of the leaves. A similar treatment was done with Sys obtained as previously described (Coppola et al., 2019a), , while a mock treatment with PBS buffer 0.1X was used as control. Leaf samples were collected 6 and 24 HPT for bioassays and molecular analyses, unless otherwise indicated.

3.4.3 Gene Expression Analysis

Total RNA extraction, first strand cDNA synthesis and RT-PCR were performed according to standard procedures, as reported elsewhere (Corrado et al., 2012) RT-PCR was performed using Rotor Gene 6000 (Corbett Research; Sydney, Australia). For each sample, two technical replicates from each of the three biological replicates were used for gene expression analysis. The housekeeping gene EF-1α was used as endogenous reference gene for the normalization of the expression level of target genes (Müller et al., 2015). The selected genes for the analysis were: *AOS* (Solyc11g069800), *LoxC;* (Solyc01g006540), *LoxD;* (Solyc03g122340), *ACO2* (Solyc12g005940), *Pin I* (Solyc09g084470) and *Pin II* (Solyc09g084450), *PAL (*Solyc09g007910). Relative quantification of gene expression was carried out using the $2^{-\Delta\Delta Ct}$ method and referred to the mock-treated control (relative quantification, RQ = 1). Primers used and their main features are reported in **Tab 3.**

Tab.3. List of Primers used for qPCR analysis.

Gene name	Primer	Sequence (5'-3')	Name/Gene symbol	Accession number
ACO	Fw	AACTCCTCAAAGACGGTGA	*1-aminocyclopropane-1-carboxylate oxidase*	Solyc12g005940
	Rv	TCCCGTTCGTGATTACCTCG		
AOS	Fw	GATCGGTTCGTCGGAGAAGAA	*Allene oxide synthase 2*	Solyc11g069800
	Rv	GCGCACTGTTTATTCCCCACT		
EF-1α	Fw	CTCCATTGGGTCGTTTTGCT	*elongation Factor 1 alpha*	Solyc06g005060
	Rv	GGTCACCTTGGCACCAGTTG		
LoxC	Fw	TTGCCTATGGTGCTGAATGGA	*LipoxygenaseC*	Solyc01g006540
	Rv	CAAGCCATGTGGTTCATTTGG		
LoxD	Fw	TTCATGGCCGTGGTTGACA	*LipoxygenaseD*	Solyc03g122340
	Rv	AACAATCTCTGCATCTCCGG		
Pal	Fw	CCACATTCAGCAACAAGGGC	*Phenylalanine ammonia lyase*	Solyc09g007910
	Rv	ACACGGGGTAATGTTGCTGT		
Pin I	Fw	GAAACTCTCATGGCACGAAAAG	*Wound-induced proteinase inhibitor 2*	Solyc09g084470
	Rv	CACCAATAAGTTCTGGCCACAT		
Pin II	Fw	CCAAAAAGGCCAAATGCTTG	*Wound-induced proteinase inhibitor 2*	Solyc09g084450
	Rv	TGTGCAACACGTGGTACATCC		

3.4.4 Assays

3.4.4.1 *In vivo Spodoptera littoralis* feeding bioassay

S. littoralis larvae (*Lepidoptera*, *Noctuidae*) were reared on artificial diet (41.4g/l wheat germ, 59.2g/l brewer's yeast, 165g/l corn meal, 5.9g/l ascorbic acid, 1.53g/l benzoic acid, 1.8g/l methyl 4-hydroxybenzoate and 29.6g/l agar),) at 25 ± 1C and 70 ± 5% RH, 18L:6D- photoperiod until they attained the 2nd instar as previously described (Di Lelio et al., 2014). Then, newly molted 3rd instar larvae were selected, weighted, and singly isolated in 4-wells plastic rearing trays (RT32W, Frontier Agricultural Sciences, Pitman, NJ, United States). In each well, 3 ml of 1.5% agar-agar (w/v) were dispensed and closed by perforated plastic lids (RTCV4, Frontier Agricultural Sciences; Newark, Germany). For each treatment, 32 larvae were fed with leaf disks of tomato plant. The experimental larvae were maintained at the rearing condition described above. Larvae mortality was daily checked until pupation.

3.4.4.2 *In vivo Spodoptera littoralis* larvicidal assays

The toxicity assays were carried out on 4th instars *S. littoralis* larvae, following oral ingestion or topical exposure, as reported elsewhere (Pavela, 2010), using a range of three experimental doses (100 nM/pM/fM). 16 *S. littoralis* larvae were treated for each dose. Briefly, for oral ingestion larvae were anesthetized on ice and 1 ml of the solution containing the ProSys fragments was poured into the foregut lumen larvae with a Hamilton Microliter syringe (1701RNR 10 ll, gauge 26s, length 55 mm, needle 3). For topical application, sedated larvae were treated on the neck membrane with 1 ml of the tested solution, using a Gilson pipette P10 (PIPETMAN classic P10). Control larvae were identically treated with PBS 1X buffer. Then, larvae were singly separated into polystyrene rearing trays, provided with artificial diet and kept at the rearing conditions reported above. Larval mortality was recorded until pupation, which took place into plastic boxes containing vermiculite (25 cm × 10 cm × 15 cm).

3.4.4.3 *In vivo Botrytis cinerea* infection assay

Fungal cultures were obtained from the collection available at the Department of Agricultural Sciences of the University of Naples Federico II. *B. cinerea* was grown on MEP (Malt extract with peptone) solid medium at 22°C. Conidia were collected by washing the agar surface with sterile distilled water containing 0.1% Tween 20, filtered, and adjusted to a concentration of 1×10^6 conidia /ml with sterile distilled water. Tomato leaves 6 HPT with 100 fM ProSys fragments or Sys peptide were tested for resistance to *B. cinerea.* Briefly, 10 µl drops of spore suspension (1×10^6 conidia/ml) were put on tomato leaves, using 10 different inoculation points per detached leaf from 5 different plants for each individual treatment. Detached leaves were put on sponges soaked in sterile water and incubated in a growth chamber at 23°C, under 16L:8D photoperiod and 90% ± 5% RH. Disease severity was quantified measuring the development of necrotic leaf areas caused by the fungal pathogen attack, at 1, 3, 5, and 8 DPI using a digital caliper (Neiko 01407A; Neiko Tools, Taiwan, China) .

3.4.4.4 *In vitro Botrytis cinerea* antifungal assay

Antifungal assay was conducted as previously described (Pastor-Fernández et al., 2020). Wells of a sterile 12-well plate were filled with 1 ml of half-strength potato dextrose broth (PDB 1/2) medium containing ProSys fragments, at a final concentration of 100 fM except for the control wells which contained no peptides. Conidia of *B. cinerea* were then added to each well to reach a final concentration of 10^4 conidia/ml. Each plate was then placed in a shaker and incubated for 24 hours at 25 ± 1°C. End-point fungal growth was assessed by measuring the medium turbidity at a wavelength of 600 nm (OD_{600}) on a BioPhotometer Spectrophotometer UV/VIS (Eppendorf, Hamburg, Germany).

3.4.5 H_2O_2 and lipid peroxidation quantification

Quantification of H_2O_2 content was carried out using a colorimetric method, as reported elsewhere (Sergiev et al., 1997). Briefly, 100 mg of frozen powder from tomato leaves of three biological replicates per treatment were extracted with 1 ml of icecold 0.1%

trichloroacetic acid (TCA); the mixture was then incubated for 15 min on ice and then centrifuged at 10,000 rpm for 15 min at 4C. Subsequently, 500 µl phosphate buffer (pH 7.0) and 1 ml of potassium iodide 1 M were added to 500 µl of the supernatant. The mixture was then incubated in the dark for 40 min and absorbance was measured at 525 nm, using a Nano Photometer TM (Implen, Munich, Germany).

Three separate biological replicates for each sample and three technical assays for each biological replicate were measured. Concentration was expressed in mmol−1g FW (Fresh Weight). For the determination of MDA 200 mg of leaf sample was ground after adding 1 ml of ice cold 0.1% trichloroacetic acid (TCA).

The samples were incubated for 15 min on ice and centrifuged at 10,000 rpm for 10 min at 4C. Subsequently, 250 µl of the supernatant was mixed with 1,250 µl reaction solution (TCA 20% C 2-thiobarbituric acid (TBA) 0.5%), water-bathed for 30 min at 95C and measured at 532 and 600 nm using a Nano Photometer TM (Implen, Munich, Germany). Three separated biological replicates for each sample and three technical assays for each biological replicate were measured. Concentration was expressed as quantity of MDA-TBA complex (Zhang and Kirkham, 1996).

3.4.6 Toxicity bioassays of protein fragments on microalgae

Cultures of *Chlamydomonas reinhardtii* were axenically grown under phototrophic conditions in a mineral nutrient solution (MNS) at 24 ± 1 °C, with a rotatory agitation at 100 rpm with a 18L:6D, at 100 E m^{-2} s^{-1} (Bischoff, 1963; Chiaiese et al., 2011). The cultures were weekly maintained by inoculation of 500 µl of culture in 50 ml of MNS medium.

The growth inhibition assay was assessed following (Klemm, 1994) procedures with some modification. A replicated design was applied by exposing microalgae at three different concentrations (0.0001, 0.1 and 1 nM) of ProSys fragments and Sys peptide in 24 well plate and incubated for 7 days. Microalgae incubated in the growth medium without peptides were used as control. Cell density was determined every 24 h by direct counting under a Leica DMR optical microscope (Leica Imaging Systems, Cambridge, United Kingdom). Growth rates (m) were calculated using the following equations:

$$\mu = \frac{lnN_2 - lnN_1}{t_2 - t_1}$$

where N_2 and N_1 are the cell density at times t_2 and t_1;

Data were expressed as means and standard deviation for three replicate cultures.

3.4.7 Toxicity Bioassays of Protein Fragments on Human Keratinocyte

The human keratinocyte (HaCaT) cell line was obtained from the American type culture collection (CRC 1424; Virginia, MD, USA). HaCaT cells were incubated in Dulbecco's modified eagle's medium containing 10% heat-inactivated fetal calf serum, 1,000 U/ml penicillin and 100 mg/ml streptomycin at 37°C in a humidified atmosphere incubator containing 5% CO_2.To evaluate cell viability, cell counting Kit-8 (CCK-8 assay, ab228554; Abcam, Cambridge, MA, USA) assay and manual cell count were performed.

The CCK-8 is a sensitive colorimetric assay for quantisation of viable cells in proliferation and cytotoxicity assays. All experiments were performed in cells by using the protocols recommended by the manufacturer. In brief, 70% confluent cultured flasks, containing $5x10^3$ cells/100µl, were plated at 2×10^4/ml per well into 24-well plates and incubated overnight at 37°C to *l* to adhere to the *bottom* of *wells*. Then, cells were washed with PBS and exposed to PS-70 or PS1-120 fragments. Specifically, the ProSys fragments were suspended in DMEM medium and added to the cells at a final concentration of 100nM. Non-treated cells were included as negative controls. After 24 hours of incubation, Kit-8 reagent was added to each well, and the plate was further incubated at 37°C for 3 hours.

The absorbance at 450 nm was then recorded by a microplate reader. The cell viability was determined as follows: cell viability (%)=[($OD_{experiment}$ OD_{blank})/($OD_{negative}$ control OD_{blank})] x 100%, where $OD_{experiment}$ is the absorbance of a well with a treated cell and CCK-8; OD_{blank} is the absorbance of a well with medium and CCK-8 but without cells; and $OD_{negative}$ control is the absorbance of a well with untreated cells and CCK-8. For manual counts, 50 µl of sample was mixed with 50 µl of 0.4% trypan blue by gently pipetting, and 20 µl of the mix were then loaded into each chamber of the hemocytometer. Counts were performed in triplicate by one analyst under a 20× objective according to the standard methodology.

Afterwards cells, untreated or treated with each fragment, were washed, fixed with 4% paraformaldehyde and visualised by phase-contrast microscopy, using a DMI6000B inverted fully automated microscope equipped with DFC 420 RGB camera (Leica Microsystems, Wetzelar, Germany). Leica LAS V5.4 software was used for image acquisition and elaboration (contrast/gamma adjusting). All analyses were performed in triplicate on three independent *in vitro* experiments.

3.4.8 Statistical analysis

One-Way ANOVA test, followed by Tukey's post-hoc multiple comparison test ($P< 0.05$), was used to evaluate the effect of ProSys fragments on *B. cinerea* growth and infection, the differences in relative quantities of transcripts abundance, and the quantification of the amount of H_2O_2 and MDA levels. Differences in *S. littoralis* larvae survival rate was compared by using Kaplan-Meier and log-rank analysis.

For the evaluation of ProSys fragments effect on microalgal growth, statistical analysis was performed by One-Way ANOVA coupled with Dunnet test. For HaCaT cell viability assay, OD450 values were compared by using Student's t test (*p*<0.05). Data were analyzed using GraphPad Prism version 6.01 (GraphPad software; San Diego, California, USA).

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Stage

Sixth months stage (06/01/2022- 30/06/2022) at the School of Biosciences University of Birmingham, Birmingham (UK): group of: Dr Estrella Luna-Diez to perform study of epigenetic modification (DNA methylation and histone post-translational modifications) by chromatin immunoprecipitation (ChIP) and Chop–PCR analysis”

Publications

Paper: **Aprile, A. M**., Coppola, M., Turrà, D., Vitale, S., Cascone, P., Diretto, G.,… & Rao, R. (2022). Combination of the Systemin peptide with the beneficial fungus Trichoderma afroharzianum T22 improves plant defense responses against pests and diseases. Journal of Plant Interactions, 17(1), 569-579. doi.org/10.1080/17429145.2022.2072528

Paper: Cirillo, V., Molisso, D., **Aprile, A. M**., Maggio, A., & Rao, R. (2022). Systemin peptide application improves tomato salt stress tolerance and reveals common adaptation mechanisms to biotic and abiotic stress in plants. Environmental and Experimental Botany, 199, 104865. doi.org/10.1016/j.envexpbot.2022.104865

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Paper: Molisso, D., Coppola, M., **Aprile, A. M**., Avitabile, C., Natale, R., Romanelli, A.,… & Rao, R. (2020). Colonization of Solanum melongena and Vitis vinifera plants by Botrytis cinerea is strongly reduced by the exogenous application of tomato systemin. Journal of Fungi, 7(1), 15. doi.org/10.3390/jof7010015

Book: **Aprile, A. M**., Molisso D., Coppola M., Corrado G., Rao R. Chapter 6th. Le risposte delle piante agli stress biotici: dai geni alle biotecnologie recenti progressi nella genetica agraria. Idelson Gnocchi

Poster: **Aprile A. M**., Coppola M., Turrà D., Vitale S., Cascone P., Di Lelio I., Diretto G., Fiore A., Castaldi V., Guerrieri E., Pennacchio F., Woo S.L., Rao R. Enhancing Tomato Endogenous Defenses By The Combined Application Of The Systemin Peptide And The Beneficial Fungus *Trichoderma Afroharzianum*. *Proceedings Of IOBC-WPRS PR-IR, “Priming the Future for Healthy Plants” CONFERENCE.: SHEFFIELD, UK.* 4/7 April, 2022

Poster: **Aprile A. M**., Coppola M., Catoni M., Luna E., Rao R. Systemin Treated Tomato Plants Transmit To The Progeny An Epigenetic Defense Signal. *Proceedings Of The LXV Siga Annual Congress Piacenza,* 6/9 September, 2022. ISBN: 978-88-944843-3-5.

Poster: Castaldi V., Molisso D., Langella E., Buonanno M., Di Lelio I., **Aprile A. M.**, Criscuolo M., Monti S. M., Pennacchio F., Rao R. Prosystemin Peptides As Novel Tools For Sustainable Tomato Crop Protection. *Proceedings Of The LXV Siga Annual Congress Piacenza,* 6/9 September, 2022. ISBN: 978-88-944843-3-5.

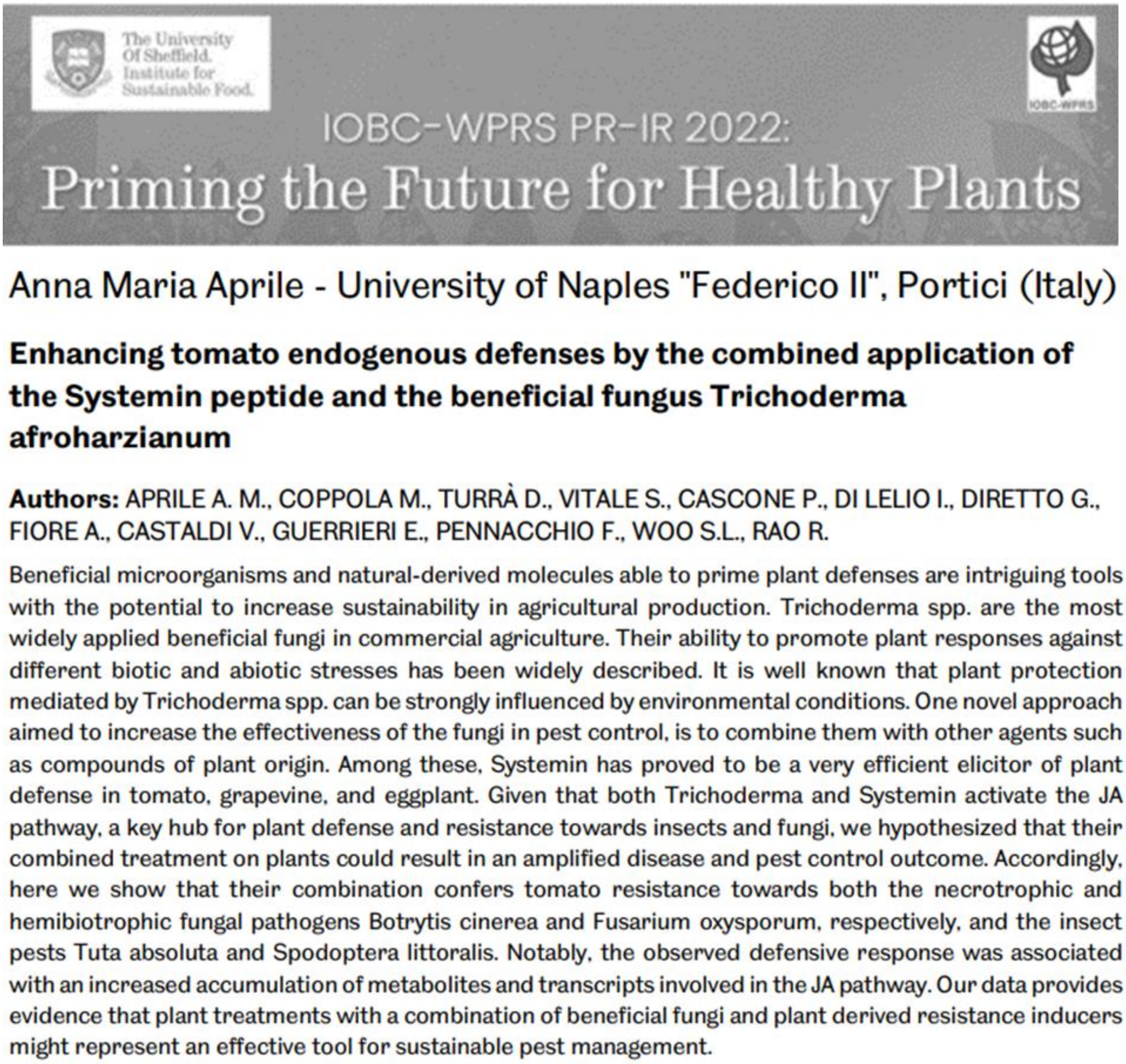
Poster: Magliulo R., Cirillo V., Molisso D., Monti S. M., Langella E., Buonanno M., **Aprile A. M**., Criscuolo M. C., Castaldi V., Maggio A., Rao R. Novel Protein Fragments For Tomato Resilience To Salt Stress. *Proceedings Of The LXV Siga Annual Congress Piacenza,* 6/9 September, 2022. ISBN: 978-88-944843-3-5.

Poster: **Aprile, A.M**., Coppola, M., Diretto, G., Molisso, D., Di Lelio, I., Sinno, M., Woo, S.L., Pennacchio, F., Rao, R. The Combined Application Of The *Trichoderma Harzianum* Bioagent And The Systemin Peptide On Tomato Plants Is A Very Efficient Strategy For Pest Control. *Proceedings Of The LXIV Annual Congress Online.* 14th-16th September 2021.

Poster: Molisso, D., Cirillo, V., **Aprile, A.M.,** Lentini, M., Esposito, M., Chiaiese, P., Maggio, A., Rao, R. Tomato Systemin: A Valid Weapon Against Biotic And Abiotic Stress Agents. *Proceedings Of The LXIV Annual Congress Online.* 14th-16th September 2021.

Poster: **Aprile, A.M**., Molisso, D., Coppola, M., Chiaiese, P., Rao, R. The Tomato Peptide Sytemin Elicits Defense Responses In *Solanum Melongena* And *Vitis Vinifera* Conferring Protection Against *Botrytis Cinerea*. *Proceedings Of The SIGA-SEI-SIBV-SIPAV Web Workshop "Young Scientists For Plant Health".* 16th December 2020. ISBN 978-88-944843-1-1.

Poster: **Aprile A.M**.*, Coppola M.*, Woo S.L.**, Digilio M.C.*, Rao R.*. Tomato Plants Treated With *Trichoderma Atroviride* P1 Reprogramme The Transcriptome Priming Defense Responses Against Aphids. Proceedings of the SIGA Young Web Meeting 7 July, 2020 ISBN 978-88-944843-0-4



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IOBC-WPRS PR-IR 2022:

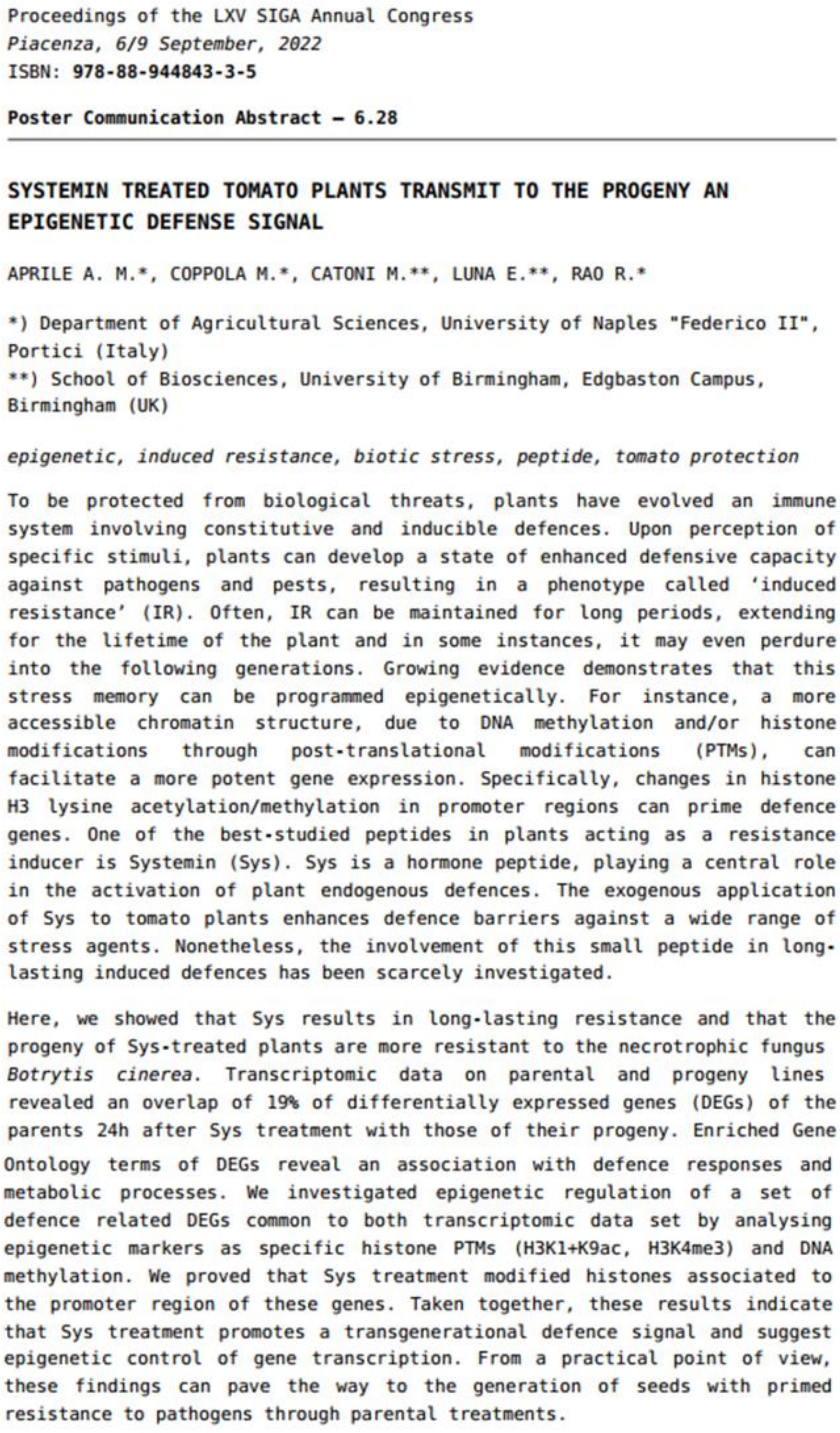
Priming the Future for Healthy Plants

Anna Maria Aprile - University of Naples "Federico II", Portici (Italy)

Enhancing tomato endogenous defenses by the combined application of the Systemin peptide and the beneficial fungus Trichoderma afroharzianum

Authors: APRILE A. M., COPPOLA M., TURRÀ D., VITALE S., CASCONE P., DI LELIO I., DIRETTO G., FIORE A., CASTALDI V., GUERRIERI E., PENNACCHIO F., WOO S.L., RAO R.

Beneficial microorganisms and natural-derived molecules able to prime plant defenses are intriguing tools with the potential to increase sustainability in agricultural production. Trichoderma spp. are the most widely applied beneficial fungi in commercial agriculture. Their ability to promote plant responses against different biotic and abiotic stresses has been widely described. It is well known that plant protection mediated by Trichoderma spp. can be strongly influenced by environmental conditions. One novel approach aimed to increase the effectiveness of the fungi in pest control, is to combine them with other agents such as compounds of plant origin. Among these, Systemin has proved to be a very efficient elicitor of plant defense in tomato, grapevine, and eggplant. Given that both Trichoderma and Systemin activate the JA pathway, a key hub for plant defense and resistance towards insects and fungi, we hypothesized that their combined treatment on plants could result in an amplified disease and pest control outcome. Accordingly, here we show that their combination confers tomato resistance towards both the necrotrophic and hemibiotrophic fungal pathogens Botrytis cinerea and Fusarium oxysporum, respectively, and the insect pests Tuta absoluta and Spodoptera littoralis. Notably, the observed defensive response was associated with an increased accumulation of metabolites and transcripts involved in the JA pathway. Our data provides evidence that plant treatments with a combination of beneficial fungi and plant derived resistance inducers might represent an effective tool for sustainable pest management.



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Poster Communication Abstract – 6.28

SYSTEMIN TREATED TOMATO PLANTS TRANSMIT TO THE PROGENY AN EPIGENETIC DEFENSE SIGNAL

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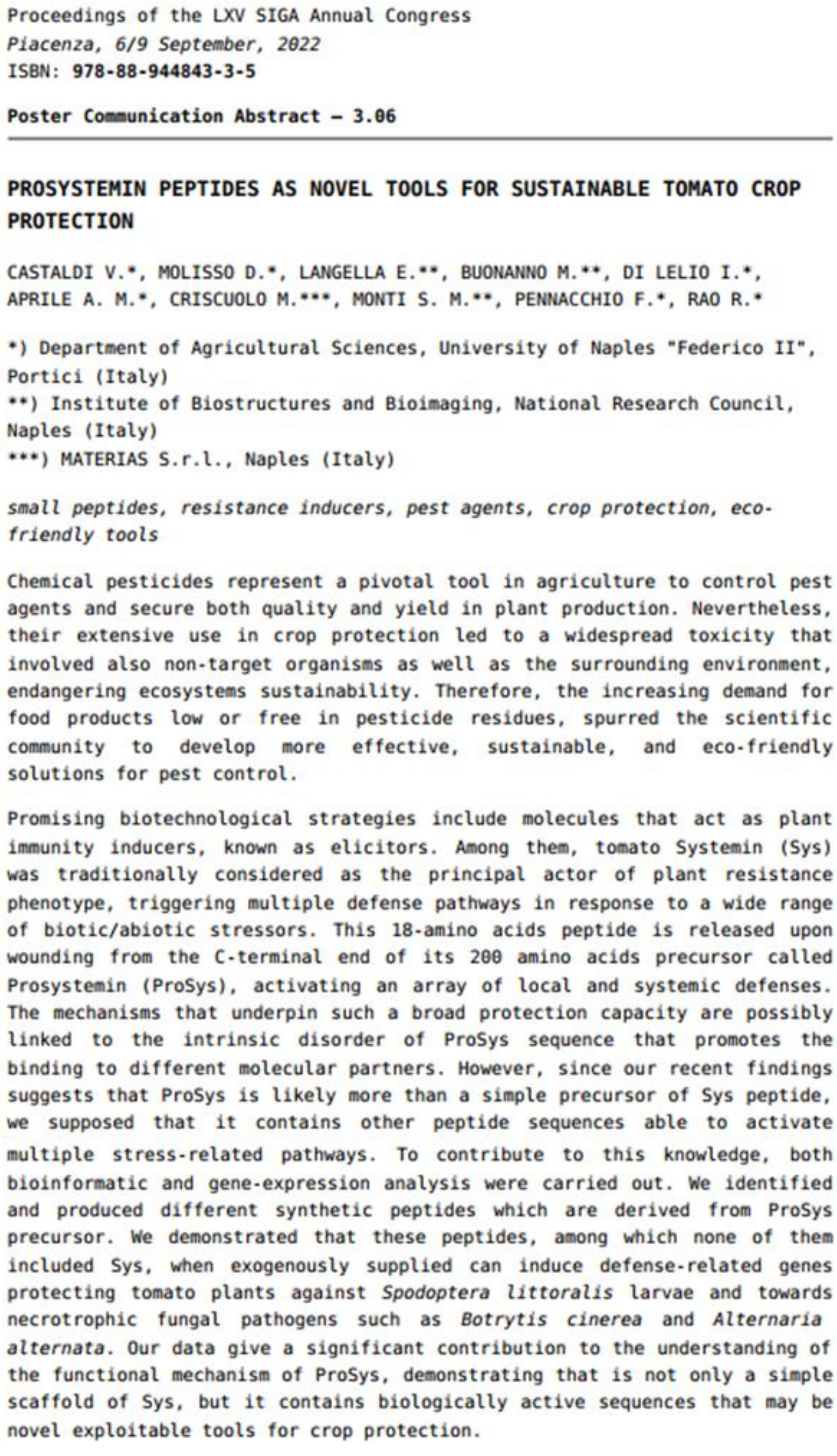
epigenetic, induced resistance, biotic stress, peptide, tomato protection

To be protected from biological threats, plants have evolved an immune system involving constitutive and inducible defences. Upon perception of specific stimuli, plants can develop a state of enhanced defensive capacity against pathogens and pests, resulting in a phenotype called ‘induced resistance’ (IR). Often, IR can be maintained for long periods, extending for the lifetime of the plant and in some instances, it may even perdure into the following generations. Growing evidence demonstrates that this stress memory can be programmed epigenetically. For instance, a more accessible chromatin structure, due to DNA methylation and/or histone modifications through post-translational modifications (PTMs), can facilitate a more potent gene expression. Specifically, changes in histone H3 lysine acetylation/methylation in promoter regions can prime defence genes. One of the best-studied peptides in plants acting as a resistance inducer is Systemin (Sys). Sys is a hormone peptide, playing a central role in the activation of plant endogenous defences. The exogenous application of Sys to tomato plants enhances defence barriers against a wide range of stress agents. Nonetheless, the involvement of this small peptide in long-lasting induced defences has been scarcely investigated.

Here, we showed that Sys results in long-lasting resistance and that the progeny of Sys-treated plants are more resistant to the necrotrophic fungus *Botrytis cinerea*. Transcriptomic data on parental and progeny lines revealed an overlap of 19% of differentially expressed genes (DEGs) of the parents 24h after Sys treatment with those of their progeny. Enriched Gene Ontology terms of DEGs reveal an association with defence responses and metabolic processes. We investigated epigenetic regulation of a set of defence related DEGs common to both transcriptomic data set by analysing epigenetic markers as specific histone PTMs (H3K1+K9ac, H3K4me3) and DNA methylation. We proved that Sys treatment modified histones associated to the promoter region of these genes. Taken together, these results indicate that Sys treatment promotes a transgenerational defence signal and suggest epigenetic control of gene transcription. From a practical point of view, these findings can pave the way to the generation of seeds with primed resistance to pathogens through parental treatments.



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Poster Communication Abstract – 3.06

PROSYSTEMIN PEPTIDES AS NOVEL TOOLS FOR SUSTAINABLE TOMATO CROP PROTECTION

CASTALDI V.*, MOLISSO D.*, LANGELLA E.**, BUONANNO M.**, DI LELIO I.*, APRILE A. M.*, CRISCUOLO M.***, MONTI S. M.**, PENNACCHIO F.*, RAO R.*

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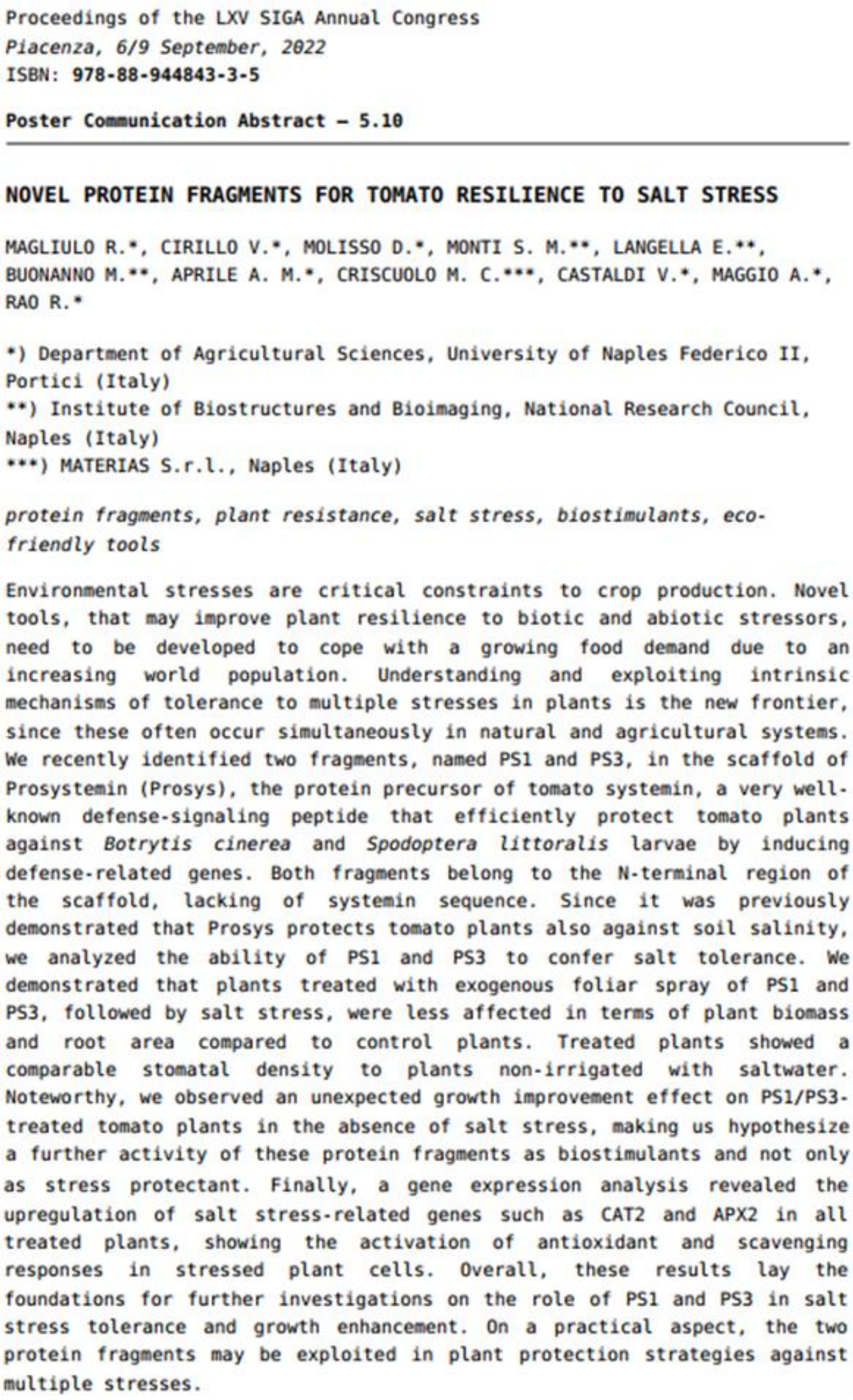
small peptides, resistance inducers, pest agents, crop protection, eco-friendly tools

Chemical pesticides represent a pivotal tool in agriculture to control pest agents and secure both quality and yield in plant production. Nevertheless, their extensive use in crop protection led to a widespread toxicity that involved also non-target organisms as well as the surrounding environment, endangering ecosystems sustainability. Therefore, the increasing demand for food products low or free in pesticide residues, spurred the scientific community to develop more effective, sustainable, and eco-friendly solutions for pest control.

Promising biotechnological strategies include molecules that act as plant immunity inducers, known as elicitors. Among them, tomato Systemin (Sys) was traditionally considered as the principal actor of plant resistance phenotype, triggering multiple defense pathways in response to a wide range of biotic/abiotic stressors. This 18-amino acids peptide is released upon wounding from the C-terminal end of its 200 amino acids precursor called Prosystemin (ProSys), activating an array of local and systemic defenses. The mechanisms that underpin such a broad protection capacity are possibly linked to the intrinsic disorder of ProSys sequence that promotes the binding to different molecular partners. However, since our recent findings suggests that ProSys is likely more than a simple precursor of Sys peptide, we supposed that it contains other peptide sequences able to activate multiple stress-related pathways. To contribute to this knowledge, both bioinformatic and gene-expression analysis were carried out. We identified and produced different synthetic peptides which are derived from ProSys precursor. We demonstrated that these peptides, among which none of them included Sys, when exogenously supplied can induce defense-related genes protecting tomato plants against *Spodoptera littoralis* larvae and towards necrotrophic fungal pathogens such as *Botrytis cinerea* and *Alternaria alternata*. Our data give a significant contribution to the understanding of the functional mechanism of ProSys, demonstrating that is not only a simple scaffold of Sys, but it contains biologically active sequences that may be novel exploitable tools for crop protection.



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Poster Communication Abstract – 5.10

NOVEL PROTEIN FRAGMENTS FOR TOMATO RESILIENCE TO SALT STRESS

MAGLIULO R.*, CIRILLO V.*, MOLISSO D.*, MONTI S. M.**, LANGELLA E.**, BUONANNO M.**, APRILE A. M.*, CRISCUOLO M. C.***, CASTALDI V.*, MAGGIO A.*, RAO R.*

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protein fragments, plant resistance, salt stress, biostimulants, eco-friendly tools

Environmental stresses are critical constraints to crop production. Novel tools, that may improve plant resilience to biotic and abiotic stressors, need to be developed to cope with a growing food demand due to an increasing world population. Understanding and exploiting intrinsic mechanisms of tolerance to multiple stresses in plants is the new frontier, since these often occur simultaneously in natural and agricultural systems. We recently identified two fragments, named PS1 and PS3, in the scaffold of Prosystemin (Prosys), the protein precursor of tomato systemin, a very well-known defense-signaling peptide that efficiently protect tomato plants against *Botrytis cinerea* and *Spodoptera littoralis* larvae by inducing defense-related genes. Both fragments belong to the N-terminal region of the scaffold, lacking of systemin sequence. Since it was previously demonstrated that Prosys protects tomato plants also against soil salinity, we analyzed the ability of PS1 and PS3 to confer salt tolerance. We demonstrated that plants treated with exogenous foliar spray of PS1 and PS3, followed by salt stress, were less affected in terms of plant biomass and root area compared to control plants. Treated plants showed a comparable stomatal density to plants non-irrigated with saltwater. Noteworthy, we observed an unexpected growth improvement effect on PS1/PS3-treated tomato plants in the absence of salt stress, making us hypothesize a further activity of these protein fragments as biostimulants and not only as stress protectant. Finally, a gene expression analysis revealed the upregulation of salt stress-related genes such as CAT2 and APX2 in all treated plants, showing the activation of antioxidant and scavenging responses in stressed plant cells. Overall, these results lay the foundations for further investigations on the role of PS1 and PS3 in salt stress tolerance and growth enhancement. On a practical aspect, the two protein fragments may be exploited in plant protection strategies against multiple stresses.

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Poster Communication Abstract – 4.29

THE COMBINED APPLICATION OF THE TRICHODERMA HARZIANUM BIOAGENT AND THE SYSTEMIN PEPTIDE ON TOMATO PLANTS IS A VERY EFFICIENT STRATEGY FOR PEST CONTROL

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bioagents, resistance inducers, gene expression analysis, bioassays, crop protection

In the current scenario, the plant protection provided by induction of systemic resistance is an efficient and simple strategy for pest and disease management programs. The resistance of plants to pathogens can be enhanced by the application of natural bioactive compounds and biological agents. The latter ones can induce resistance against various diseases caused by many pathogens. *Trichoderma* spp. are the most widely applied beneficial fungi in commercial agriculture. Their ability to promote plant responses against different biotic and abiotic stresses has been widely described. However, one novel approach aimed to increase the effectiveness of the fungi in pest control, is to combine them with other agents such as metabolites of plant origin. Among these systemin, the first bioactive peptide hormone identified in plants, is very efficient in tomato, grapevine, and eggplant protection. The modulation of defenses triggered by systemin in tomato plants in response to insect and pathogen attack include the production of the plant hormone jasmonic acid and its derivatives, with the final synthesis of compounds interfering with fungal colonization and larval survival; while the induction of resistance by *Trichoderma* spp. is due to the rise in the amounts of defensive metabolites as well as enzymes. Although, the biological role of these two resistance inducers is well established, little is known about their combined effect on the promotion of plant endogenous defenses. To fill this research gap, the objective of this study was to explore the impact of *Trichoderma harzianum* (strain T22) colonization and systemin treatment on the induction of defense responses in tomato plants (cultivar San Marzano nano). We found that the joint application of Trichoderma and systemin proved more efficient in controlling the noctuid moth *Spodoptera littoralis* and the fungal pathogen *Botrytis cinerea* rather than the single agent alone. The targeted metabolome analysis revealed a wide metabolome alteration in plants treated with the combined application showing an increased accumulation of metabolites involved in ethylene, jasmonate and salicylic acid signaling pathways. These results were corroborated by gene expression analysis, in which Trichoderma-systemin treated plants showed the over-expression of transcripts coding for several defense genes involved in these defense pathways.

Summarizing, our data indicate that the combined usage of different resistance inducers is an interesting strategy for crop protection against several invaders.

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Poster Communication Abstract – 5.13

TOMATO SYSTEMIN: A VALID WEAPON AGAINST BIOTIC AND ABIOTIC STRESS AGENTS

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systemin, soil drench, salt stress, defense responses, plant growth

Plant signaling peptides trigger several signal transductions of external and internal stimuli that lead to the production of hormones and to the successive activation of genes modulating many physiological events including defense. Some of these peptides have been defined as plant resistance activators or elicitors that lead to improved protection of the plant’s own defense. One of the best characterized signaling peptide is systemin (Sys), an octadecapeptide synthesized as a part of a larger precursor protein, prosystemin (ProSys). Sys was isolated from tomato leaves and proved to be able to activate the octadecanoid pathway, which leads to the production of the plant hormone jasmonic acid (JA) and its derivatives, which are powerful activators of plant defense genes. Transgenic plants constitutively expressing ProSys have shown a wide transcriptome reprogramming which reflected in novel phenotypes resistant to different pests and tolerant to moderate salt stress. It is well known that JA and its derivatives provide a direct way of alleviating the biotic and abiotic stresses activating the plant’s defense mechanisms, which also involve antioxidative enzymes and other defensive compounds. Recently, by combining gene expression studies and bioassay with different pests, we demonstrated that the exogenous application of the Sys peptide to tomato plants enhances both direct and indirect defense barriers. Nonetheless, the ability of the exogenous supply of Sys peptide to reduce salt stress damages was not investigated. To contribute to this knowledge, we evaluated the effect of a single application of the peptide via soil drench, on the expression of abiotic stress-related genes, on plant growth characteristics and on metabolic parameters of tomato plants exposed to two concentrations of NaCl (100 and 150 mM). Our results indicate that the delivery of this peptide alleviated the negative effect of salinity on plant growth, as indicated by the higher shoot biomass evidenced in treated plants under 150 mM NaCl. This was correlated with higher leaf proline content and the upregulation of key salt stress related genes. It was also observed that under nonstress condition, Sys did not alter plant growth in terms of shoot fresh weight or leaf area but promoted a significant increase of root area. The present study indicates that Sys peptide can increase the resistance of tomato plants to salt stress, likely triggering plant defense responses. Our results may give new insights in the cross-talk between plant responses to biotic and abiotic stresses, understanding of which represents an important contribution for crop protection.

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Poster Communication Abstract – PH.15

THE TOMATO PEPTIDE SYSTEMIN ELICITS DEFENSE RESPONSES IN *SOLANUM MELONGENA* AND *VITIS VINIFERA* CONFERRING PROTECTION AGAINST *BOTRYTIS CINEREA*

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defense gene, crop protection, pests, Solanum lycopersicum, genetics

The well known problems of toxicity and environmental pollution due to the use of pesticides have led to the urgent need to develop more sustainable tools for pest control. The growing knowledge of plant signaling pathways has encouraged the possibility of using elicitors of plant defense responses as an effective new bio-based strategy for crop protection. Systemin is an 18-amino acid peptide of tomato plants known as endogenous amplifier of innate immunity. Upon pest attack, systemin interacts with a leucine-rich repeat receptor kinase, the systemin receptor SYR, triggering local and systemic defense responses. Its exogenous supply confers protection against a broad spectrum of biotic/abiotic threats by inducing the transcription of defense-related genes. However, little is known about systemin sensing in heterologous plants despite it has been recently shown that ortholog of SYR are present in several plant species, including eggplant and grapevine plant. In the present study we demonstrated that the tomato peptide is perceived by the taxonomically close species Solanum melongena and in the more distant species Vitis vinifera and conferred protection against the necrotrophic fungus Botrytis cinerea. The observed disease tolerance is associated with the increase of total soluble phenolic content, the activation of antioxidant enzymes and the up-regulation of defence related genes in peptide-treated plants. In vitro bioassays showed that systemin does not have a direct antimicrobial effect, indicating that it protects these two important crops through the activation of their immune systems. In conclusion, tomato systemin induces resistance against B. cinerea indicating that the two species perceive the non-self-peptide and activate the defence and the antioxidant machineries. These results open novel perspective in the use of plant peptides in crop protection. From an applied perspective, the exogenous delivery of plant signaling peptides may offer a useful contribution for the reduction of chemical pesticide in field.

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Abstract – SY02

TOMATO PLANTS TREATED WITH *TRICHODERMA ATROVIRIDE* P1 REPROGRAMME THE TRANSCRIPTOME PRIMING DEFENSE RESPONSES AGAINST APHIDS

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Plants colonized by *Trichoderma* spp. have often shown multiple beneficial effects. Although several reports have addressed the role of these fungi on the promotion of plant defense responses against pathogen attacks, little is known about their ability to induce of barriers active against insects. In order to shed light on this important issue, we studied the impact of Trichoderma atroviride P1(P1) colonization on tomato plant defense responses against the aphid Macrosiphum euphorbiae. Transcriptomic analyses of the tomato cultivar "San Marzano nano" were conducted by comparing Trichoderma treated and untreated plants. Plants treated with P1 showed a wide transcriptome reprogramming, which included the up-regulation of a large group of defense-related genes. Both genes involved in early signals and genes related to the plant oxidative defense, known for their effect on aphid survival, were up-regulated like families of genes encoding for transcription factors (i.e. ERF, WRKY, MYB, and bZIP). These results indicate that treated plants 'prepare' themselves for future biotic pest attacks in order to mount a more rapid and effective defense responses against invaders. Indeed, M. euphorbiae showed a significantly reduced survival rate when reared on P1-treated plants in respect to control. In conclusion, our data suggest a wide and articulated contribution of T. atroviridae P1 to the promotion of tomato endogenous defenses against phloem-feeders by triggering a 'defense priming' status.

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Combination of the Systemin peptide with the beneficial fungus *Trichoderma afroharzianum* T22 improves plant defense responses against pests and diseases

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ABSTRACT
Trichoderma spp. are among the most widely used plant beneficial fungi in agriculture. Its interaction with the plant triggers resistance responses by the activation of Induced Systemic Resistance mediated by Jasmonic acid and Ethylene and/or Systemic Acquired Resistance, which involves Salicylic acid, with the consequent control of a wide range of plant parasites. However, the benefit they can confer to plants may be reduced or nullified by environmental conditions or fungal ecological fitness. A novel approach to enhance their effectiveness in plant defense is to combine them with bioactive molecules including plant-derived compounds. Here, we show that plant treatment with *Trichoderma afroharzianum* (strain T22) and Systemin, a tomato peptide active in triggering plant defense, confers protection against the fungal pathogens *Fusarium oxysporum*, *Botrytis cinerea* and the insect pest *Tuta absoluta*. The observed defensive response was associated with an increase of Jasmonic acid and related metabolites and a decrease of Salicylic acid.

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Tomato protection; bioactive molecules; plant induced defense; *Tuta absoluta*; *Fusarium oxysporum*; *Botrytis cinerea*

1. Introduction

Tomato (*Solanum lycopersicum* L.) is the second most important economic crop in the world after potato (*Solanum tuberosum* L.), with cultivation covering 4.85 million ha and fruit production totaling about 182.3 million tons every year (FAOSTAT 2019). In pre-Covid-19 pandemic era, global tomato market income amounted to $190.4 billion (Research and Markets 2020). Regardless of the type of cultivation or the plant life-cycle, increasing amounts of pesticides are required to protect tomato plants from pathogens and pests worldwide (Almeida et al. 2019; Savary et al. 2019; Abbas et al. 2020) with well-known undesirable effects on the environment (pollution, soil depletion, biodiversity loss) and human health (Rani et al. 2021). Public concerns prompted the research for alternative strategies of plant protection that are effective, reliable, and sustainable (Iriti and Vitalini 2020). In this context, biological control of plant diseases through the application of bioagents is a highly promising approach (Vinale et al. 2008). Among biological control agents (BCA), beneficial fungi belonging to *Trichoderma* spp. represent the most widespread soil microbes used in agriculture and a major constituent of commercially available biological products (i.e. biopesticides, biostimulants, biofertilizers) (Woo et al. 2014). Different *Trichoderma* species/strains and their metabolites act against plant pathogens through several mechanisms, including direct antagonism of disease agents (mycoparasitism) (Poveda 2021), antibiotic-mediated suppression, secretion of lytic enzymes and other byproducts, competition for nutrients (Al-Ani 2018). Additionally, *Trichoderma* root colonization induces a state of alert (defense priming) in plants leading to a faster and stronger defense response against future pathogen attacks, this is achieved by reducing the effector-triggered susceptibility (ETS) and concurrently enhancing the effector-triggered immunity (ETI) (Hermosa et al. 2012; Martinez-Medina et al. 2017). Within this scenario, the use of inducers of plant endogenous defenses is considered one of the most promising approaches for the promotion of sustainable agricultural practices that may reduce synthetic chemical inputs (Burketova et al. 2015).

A pioneering study showed that plant root colonization by *T. afroharzianum* is associated with a reduction of the symptoms produced by the necrotrophic fungus *Botrytis cinerea* as a consequence of systemic defense responses elicitation (De Meyer et al. 1998). More recent studies demonstrated that different *Trichoderma* species can control several diseases deriving from bacterial, oomycete, fungal, or nematode infections (Poveda et al. 2020; Sood et al. 2020). Other studies showed that *Trichoderma* interaction with plants is able to induce a set of defense-related genes associated with the Jasmonic acid (JA) and Ethylene (ET)

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pathways which may explain at molecular level the observed broad spectrum biocontrol activity of this fungus (Shoresh et al. 2005; Korolev et al. 2008). Notably, *Trichoderma* spp. do not only protect against parasitic microorganisms or nematodes but also against different insect pests (Muvea et al. 2014; Contreras-Cornejo et al. 2018). Indeed, it was previously demonstrated (Coppola et al. 2019a) that *Trichoderma atroviride* induced defenses are effective against two tomato pests with distinct eating habits: the piercing–sucking aphid *Macrosiphum euphorbiae* and the chewing noctuid moth *Spodoptera littoralis*. Moreover, plant colonization by the fungus activated indirect defenses via the production of volatile organic compounds (VOCs) that attracted the pest parasitoid *Aphidius ervi*.

It is well known that plant protection mediated by *Trichoderma* spp. can be deeply influenced by environmental conditions and ecological fitness of biocontrol agents hence being poorly predictable *a priori* (Howell 2003; Alabouvette et al. 2009; Lecomte et al. 2016; Malik et al. 2018). Consequently, the sole use of plant beneficial microorganism may not be always sufficient to fully protect plants against biotic stresses. To overcome such limitations, new approaches to increase plant resistance may focus on the combined application of different resistance inducers (*i.e.* chemical and/or biological) (Zehra et al. 2017; Zhou et al. 2021).

Among plants-derived molecules, the tomato peptide Systemin (Sys) has proved to be a very efficient elicitor of plant defense in tomato, grapevine, and eggplant (Coppola et al. 2019c; Molisso et al. 2021). Sys was the first peptide signal to be discovered in plants (Pearce et al. 1991). It is an octadecapeptide proteolytically released, upon wounding and herbivore attack, from the carboxy terminus of its 200 amino-acid precursor ProSystemin (ProSys) (Ryan and Pearce 2003). In plants, the autocrine interaction of Sys with its receptor is followed by the activation of the octadecanoid pathway and the production of JA and its derivatives (JAs) (Pearce et al. 1991). The role of Sys in the defense response against wounding or herbivory was evaluated in several studies exploiting transgenic plants overexpressing or downregulating ProSys. Its overexpression increased not only the resistance of plants against lepidopteran larvae, fungi, and aphids, but also the tolerance to salt stress (Mcgurl et al. 1994; Orsini et al. 2010; Coppola et al. 2015), while its downregulation strongly increased plant susceptibility to herbivores (Orozco-Cardenas et al. 1993).

Recently, it was demonstrated that exogenous supply of Sys induces an array of defense-related responses leading to the final accumulation of proteinase inhibitors (PIs) and other molecules able to interfere with the colonization of fungal pathogens or the growth and survival of herbivores (Coppola et al. 2019c; Molisso et al. 2021). Also, Sys-treated plants proved to be more attractive for pest natural enemies as a consequence of the modified blend of volatile compounds emitted, which is known to be used by predators and parasitoids of phytophagous insects to locate their preys and hosts.

Given that both *Trichoderma* and Sys activate the JA pathway, a key hub for plant defense and resistance towards insects and fungi, we hypothesized that their combined treatment on plants could result in an amplified disease and pest control outcome. In addition, considering that the endophytic root colonization by the beneficial fungus is limited by Salicylic Acid (SA) pathway, while JA triggered defenses have positive effect on it, (Alonso-Ramirez et al. 2014; Martinez-Medina et al. 2017) Sys application on the plant could define a more efficient root colonization of T22 due to the negative crosstalk between the JA- and the SA-regulated pathways (Pieterse et al. 2012).

Accordingly, here we show that their combination confers resistance to tomato plants towards both the necrotrophic *B. cinerea* and hemibiotrophic *Fusarium oxysporum* fungal pathogens, and the insect pest *Tuta absoluta*. Our data provides evidence that plant treatments in a combination of beneficial fungi and plant-derived resistance inducers might represent an effective tool for sustainable pest management.

2. Materials and methods

2.1. Preparation of fungal cultures and inoculum and insects rearing

Fungal cultures were obtained from the collection available at the Department of Agricultural Sciences of the University of Naples Federico II. *T. afroharzianum* (formerly-*T. harzianum*) strain T22 (T22), was isolated from the commercial product Trianum-P (Koppert Biological Systems, Rotterdam, the Netherlands), cultured on potato dextrose agar (PDA; HiMedia) and grown at 25°C until complete sporulation. Conidia were collected in sterile distilled water by scraping the surface of sporulating fungal cultures and recovering the spores by centrifugation at 2700 g for 10 min. Conidia concentration was adjusted to 10^7 spores/ml for subsequent bioassays.

F. oxysporum f.sp. *lycopersici* (*Fol*) race 2 isolate 4287, and the *Fol* knockout mutant *fmk1Δ* were grown in potato dextrose broth (PDB) at 28°C with orbital shaking at 170 rpm. Phleomycin (5.5 µg/ml) was added to the culture medium when required. Fresh conidia were separated from the mycelium by filtering 5 d-old cultures through a nylon filter membrane (mesh size 10 µm) and collected after centrifugation at 2700 g for 10 min. Storage of the obtained conidia was performed as previously described (Di Pietro et al. 2001).

B. cinerea was grown on MEP (Malt extract with peptone) solid medium at 22°C. Conidia were collected by washing the agar surface with sterile distilled water containing 0.1% Tween 20, filtered, and adjusted to a concentration of 1×10^6 conidia/ml with sterile distilled water.

The original strain of *T. absoluta* was collected in 2019 in tomato greenhouses located in Battipaglia (Salerno, Italy) (Gontijo et al. 2019). The insect was continuously reared at the National Research Council, Institute for Sustainable Plant Protection (CNR-IPSP, Portici), inside aerated cages (Vermandelˆ, The Netherlands) at 22 ± 5%°C, 65 ± 5% relative humidity (RH) and 16L:8D photoperiod.

2.2. Peptide synthesis

The Sys peptide synthesis and purification were obtained as previously described (Coppola et al. 2019c). In brief, Sys was obtained by solid phase synthesis following standard protocols (Romanelli et al. 2011). Purification of the peptide was carried out by RP-HPLC on a semipreparative column (Jupiter 10 µ, Proteo 90 Å, 250 × 10 mm) using a gradient of acetonitrile (0.1% TFA) in water (0.1% TFA) from 5 to 50% in 30 min at 5 ml/min. Sys was characterized by mass spectrometry (LC-MS ESI-TOF 6230 Agilent Technologies, Milan, Italy). Sequences and mass spectrometry data follow. Sys sequence: AVQSKPPSKRDPPKMQTD. Mass calculated (Da): 2009.3 Mass spectrum fragmentation data (Da): 670.94

[M + 3 H]3+; 1005.60 [M + 2 H]2+. Analysis of the HPLC (Shimadzu LC-8A, equipped with a SPD-M10 AV) profiles and of the mass spectra collected indicates the peptide stability in all the tested conditions.

2.3. In Vitro *Trichoderma-Sys compatibility assay*

To assess if Sys had a direct antimicrobial effect on *T. afroharzianum T22*, an *in vitro* assay was carried out to measure fungal growth in the presence or absence of different concentrations of the peptide. Antifungal assay was conducted as previously described (Pastor-Fernández et al. 2020). Wells of a sterile 12-well plate were filled with 1 ml of half-strength potato dextrose broth (PDB 1/2) medium containing Sys, at a final concentration of 100 pM or 100 fM except for the negative control wells. The positive control was filled with 200 µg/ml Switch® fungicide (Syngenta, 37.5% w/w cyprodinil and 25% w/w fludioxonil). Conidia of *T. afroharzianum* T22 were then added to each well to reach a final concentration of 10^4 conidia/ml. Each plate was then placed in a shaker and incubated for 24 h at 25 ± 1°C. End-point fungal growth was assessed by measuring the medium turbidity at a wavelength of 600 nm (OD_{600}) on BioPhotometer Spectrophotometer UV/VIS (Eppendorf, Hamburg, Germany).

2.4. Seed treatment and plant growth

Seeds of *S. lyccpersicum* cultivar 'San Marzano Nano' were surface sterilized with 2% sodium hypochlorite for 10 min, then fully rinsed in sterile distilled water. For the seed treatments, washed tomato seeds were either coated by immersion in a fresh spore suspension (final concentration of 10^7 conidia/mL) of *T. afroharzianum* T22, or treated with water (Ctrl), stirred frequently to uniformly cover the seed surface, left to air dry for 24 h and stored at 4°C until use. Seeds were germinated on Whatman® sterile filter paper (Sigma-Aldrich, Darmstadt, Germany), moistened with sterile distilled water, and placed in a growth chamber at 24 ± 1° C and 60 ± 5% RH in the dark. At the emergence of the cotyledons, germinated seedlings were individually transplanted into pots containing sterile commercial soil (Universal Potting Soil, Floragard, Oldenburg, Germany) and kept in a growth chamber at 26 ± 1°C and 60 ± 5% RH., 18L:6D-photoperiod by lamps of 5000 lux. After 2 weeks, tomato seedlings were transplanted into 10-cm diameter plastic pots containing sterilized soil and grown for 2 weeks under the same environmental conditions. For *F. oxysporum* assay, seeds were planted on wet vermiculite in plastic trays and incubated in plant growth chambers for two weeks at 26 ± 1°C and 60 ± 5% RH.

2.5. In vivo F. oxysporum *infection assays*

Two weeks-old plants (Ctrl and T22 seed-treated), treated with Sys or PBS buffer 1X dissolved in 5 ml of *distilled water* (final Sys concentration 100 fM), were tested for resistance to *F. oxysporum*. Twenty-four hours after Sys application *Fol* infection was performed by dipping tomato roots in a microconidia suspension (5×10^6 conidia/ml) from *Fol* wt or *fmk1Δ* strains (Di Pietro and Roncero 1998). Tomato seedlings were planted into minipots containing vermiculite and maintained in a growth chamber (28°C; 14L:10D photoperiod). Plant infection was recorded daily for up to 20 days and percentage of plant survival was calculated by the Kaplan–Meier method (López-Berges et al. 2012). Fifteen plants per treatment were used and each experiment was repeated on three independent occasions.

2.6. In vivo B. cinerea *infection assays*

The application of Sys and *T. afroharzianum* was tested either alone or in combination to evaluate the effects of each treatment on *B. cinerea* leaf colonization. Fully expanded leaves from four-week-old plants (Ctrl and T22) were treated with 15 spots of 2 µl of 100 fM Sys or PBS; spots were produced on the abaxial surface using a pipette. Leaves were tested for resistance to *B. cinerea* after 6 h by applying 10 µl drops of *B. cinerea* spores (1×10^6 conidia/ml) between tomato leaf veins, using 8 different inoculation points per leaf from 5 different plants for each individual treatment. Detached leaves were placed on sponges soaked in sterile water and incubated in a growth chamber at 23°C, under 16L:8D photoperiod and 90% ± 5% RH. Disease severity was quantified by measuring the development of necrotic leaf areas caused by the fungal pathogen over time at different days post inoculums (DPI) using a digital caliper (Neiko 01407A; Neiko Tools, Taiwan, China).

2.7. In vivo T. absoluta *assays*

To evaluate the possible induction of repellency linked to the alteration of the profile of volatile organic compounds released by tomato plants, a choice test was performed using a random block experimental design. Three 4-weeks old plants (Ctrl and T22) were treated with 100 fM Sys or PBS by foliar spotting. After 6 h, plants were placed into a single mesh cage (60 × 60 × 180 cm; Vermandel, The Netherlands) at a distance of 20 cm from each other. Three to 5 days old mated females of *T. absoluta* were released into the cage keeping a 1:1 ratio between them and the plants. After 2 days (oviposition period), females were removed from the cage by an insect aspirator and the eggs laid were counted. The test was replicated four times totaling 12 females/plant tested. To evaluate antibiosis/antixenosis, a no-choice test was performed by feeding *T. absoluta* larvae with detached leaves from each treatment and relative control. Fully expanded leaves to be used in the test were cut from plants treated as described before and immediately placed through the petiole in a 5-mL tube capped by a cotton wick, sealed by parafilm tape, and filled with tap water. Larvae to be used in the test came from tomato plants exposed for 24 h to hundreds of *T. absoluta* adults in a mesh cage. Tomato leaves with eggs were transferred into aerated cages and a single hatched larva was gently transferred onto a detached leaf by a soft brush and kept in a plastic box (Duchefa, The Netherlands) constituting the experimental unit. Thirty larvae were tested for each treatment. Leaves were examined daily to check the larval longevity and survival and to record the time to pupation.

2.8. Gene expression analysis

Expression levels of defense-related genes in control and *T. afroharzianum* – and/or Sys-treated tomato plants were quantified by real-time PCR (RT–PCR). The selected genes were: *Allene Oxide Synthase* (*AOS;* Solyc11g069800), *Lipoxygenase D* (*LoxD*; Solyc03g122340), *Wound-induced Proteinase Inhinbitor I* (*Pin I*; Solyc09g084470), *Threonine deaminase* (*TD*; Solyc09g008670), and *Leucine aminopeptidase* (*LapA*; *Solyc12g010030*). Fully expanded leaves from 4 weeks old plants (Ctrl or T22) were collected 6 h after Sys treatment and immediately frozen in liquid nitrogen. Total RNA extraction, first strand cDNA synthesis and RT–PCR were performed according to standard procedures, as reported elsewhere (Corrado et al. 2012). RT–PCR was performed using Rotor Gene 6000 (Corbett Research; Sydney, Australia). For each sample, two technical replicates from each biological replicate were used for gene expression analysis. The housekeeping gene EF-1α was used as endogenous reference gene for the normalization of the expression level of target genes (Müller et al. 2015). Relative quantification of gene expression was carried out using the $2^{-\Delta\Delta Ct}$ method and referred to the mock-treated control (relative quantification, RQ = 1). Primers and their main features are reported in Additional file 2: Table S1.

2.9. LC-HESI(-)-HRMS of JA/SA and JA/SA-related metabolites

By using LC-HESI(-)-HRMS analysis, the levels of JA, its glycosylated (tuberonic acid-glucoside) and methylated form (MeJA) as well as three of its intermediates (13(S)-HPOT, 12,13(S)-EOT and 12-OPDA), the levels of SA, its glycosylated form (Salicylic acid glucoside) together with five of its intermediates (DL-Phenylalanine, trans-Cinnamate, Benzoic acid, Chorismic acid, and Prephenic acid) were measured in control plants or in plants treated with Sys, T22 or both. Detection and quantification of JA/SA and JA/SA-related metabolites were performed as previously reported with slight modifications (Liu et al. 2010; Van Meulebroek et al. 2012; Grosso et al. 2018). Briefly, 100 mg frozen leaf samples of 4 weeks old plants (Ctrl or T22) were collected 6 h after Sys treatment and homogenized with 1 ml cold extraction buffer (methanol, ultrapure water, and formic acid (75:20:5, v/v/v) spiked with 10 μg ml^{-1} formononetin as internal standard), vortexed continuously at −20°C o.n. Following centrifugation at 15,000 g for 20′ at 4°C, 500 ml were transferred to 30 kDa Amicon$^{®}$ Ultra centrifugal filter unit (Merck Millipore Corporation, MA, USA), and centrifuged for 15′ at 15,000 g and 4°C. Finally, extracts were evaporated by speedvac until a final volume of 50 μl was reached, and then transferred to the LC vials. LC-HESI(-)-HRMS analyses were carried out using a Dionex high performance liquid chromatography-diode-array detector (LC-DAD) coupled to high-resolution mass spectrometry equipped with a heated electrospray source operating in negative ione mode (ESI(-)HRSMS) (Thermo Fisher Scientific, Waltham, MA, USA). LC analysis was performed as reported before (Liu et al. 2010; Van Meulebroek et al. 2012; Grosso et al. 2018), whereas mass spectrometry analysis was performed using a quadrupole-Orbitrap Q-exactive system (Thermo Fisher Scientific, USA), using a single ion monitoring (SIM) method. More in detail, metabolite ionization was carried out using the following parameters: nitrogen was used as sheath and auxiliary gas (40 and 15 units, respectively); capillary and vaporizer temperatures were set at 300̊C and 280°C, respectively, discharge current at 3.5 KV, probe heater temperature at 360°C, S-lens RF level at 50 V. The acquisition was carried out in the 110/1600 m/z scan range, according to the following parameters: resolution 70,000, microscan 1, AGC target 1e6, and maximum injection time 50. Data were analyzed using the Xcalibur 3.1 software (ThermoFisher Scientific, USA). Metabolites were identified based on their accurate monoisotopic and adduct masses (m/z) and MS fragmentation, using both in house database and public sources (i.e. KEGG, MetaCyc, ChemSpider, PubChem, Metlin, Phenol-Explorer), as well by comparing chromatographic and spectral properties with authentic standards, when available. Relative abundances of the metabolites studied were calculated using the Xcalibur 3.1 software (Thermo Fisher Scientific, USA). JA/SA, and JA/SA-related metabolites were quantified in a relative way by normalization on the internal standard amounts. Data are presented as means and standard deviations of three independent biological replicates.

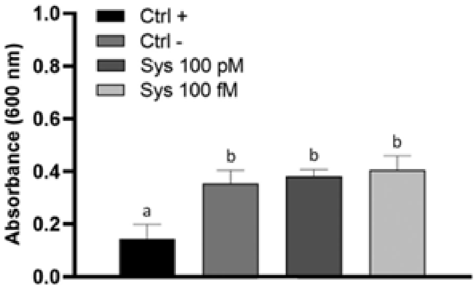

Figure 1. Effect of Sys on *T. afroharzianum* T22. Fungal growth in absence (Ctrl −) or presence of Sys (100 pM and 100 fM) was evalueted 24 h after fungal inoculation by assessing changes in optical density (OD$_{600}$). Switch (200 μg/ml) was used as a positive control (Ctrl +). Different letters indicate statistically significant differences (One-Way ANOVA, $P < 0.05$). Error bars indicate standard error ($n = 5$).

2.10. Statistical analysis

Differences in the survival rate of tomato plants infected by *F. oxysporum* and tomato plants infested by *T. absoluta* larvae were analyzed using the Kaplan–Meier method and compared among groups using the log-rank test. One-Way ANOVA test, followed by Tukey's *post-hoc* multiple comparison test ($P < 0.05$), were used to evaluate: differences in relative transcripts abundance, in necrosis diameter development, the effect of Sys on T22 growth, and in *T. absoluta* oviposition rate. Welch's ANOVA test followed by Dunnett's T3 test was used to evaluate differences *T. absoluta* larval longevity. Student's *t*-test was used to identify metabolites whose abundance significantly changed with respect to the control condition.

3. Results

3.1. Sys peptide did not directly impact T. afroharzianum *T22 growth*

Sys treatment did not impact T22 proving that Sys does not have inhibitory effect on fungal growth (Figure 1).

3.2. Sys and T. afroharzianum *T22 reduce* F. oxysporum *infection*

To evaluate if treatments with Sys and/or *T. afroharzianum* T22 were able to control *F. oxysporum* wilt disease on tomato

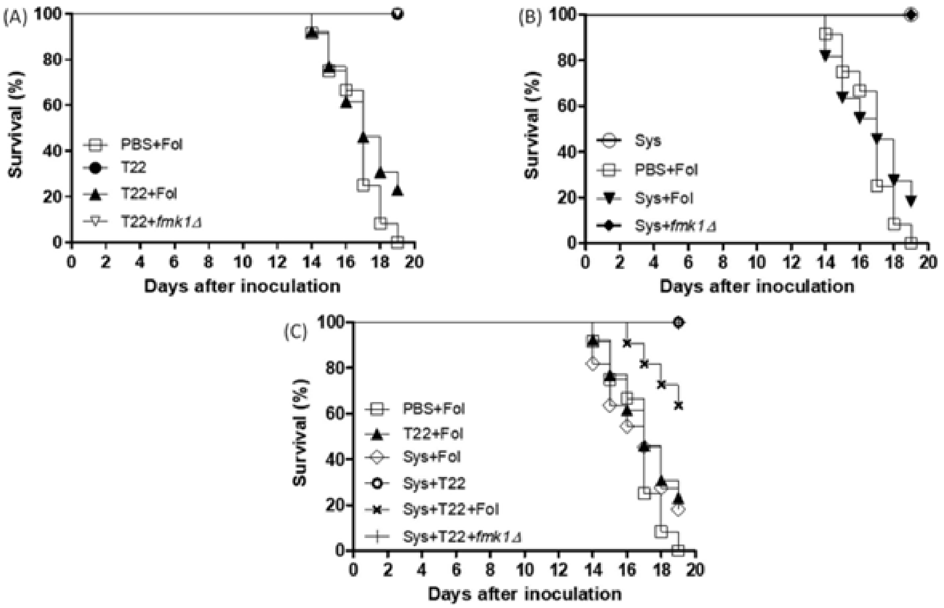

Figure 2. *T. afroharzianum* and Sys additively reduce *F. oxyporum* virulence on tomato plants. Kaplan–Meier plots showing survival of tomato plants treated with PBS (A, B, C), *T. afroharzianum* (A), Sys (B), or both (C), and not inoculated or inoculated by dipping roots into a suspension of 5 × 10^6 conidia/ml of the indicated *Fol* strains. Experiments were performed at least three times with similar results. Percentage survival of tomato plants was plotted for 20 days. Data shown are from one representative experiment.

plants, roots of two-week-old seedlings were left uninoculated, inoculated with the *Fol* wt strain or with the *Fol fmk1Δ* avirulent mutant strain and survival of treated versus untreated plants was recorded over time. As expected, in all experiments and regardless of the applied treatment (PBS control, Sys, or T22), uninoculated or *fmk1Δ* inoculated plants displayed neither wilting symptoms nor mortality throughout the whole evaluation process (Additional file 1: Figure S1).

On the contrary, most tomato plants germinated from Ctrl seeds and inoculated with the *Fol* wt strain showed progressive wilting symptoms and died after 19 days post inoculation (Additional file 1: Figure S1). Plants treatment with Sys or seed coated with *T. afroharzianum* T22 only partially, though not significantly, decreased *Fol*-mediated wilting and death of plants (Figure 2(A,B)) (T22 + Fol, Log-Rank test, $\chi^2 = 1.588$, df = 1; $P = 0{,}2077$; Sys+ Fol, Log-Rank test, $\chi^2 = 0.771$, df = 1, $P = 0{,}3797$). Noteworthy, combined treatment of tomato plants with both Sys and *T. afroharzianum* T22 showed a stronger and significant reduction in plant mortality (Sys + T22 + Fol, Log-Rank test, $\chi^2 = 12.28$, df = 1, $P = 0{,}0005$) as only 40% of these plants had died after 19 DPI, contrarily to those derived from Ctrl seeds where 100% mortality was observed (Figure 2(C)).

3.3. *Sys and* T. afroharzianum *reduce* B. cinearea *infection*

Plants treated with Sys alone or in combination with T22 showed a significant reduction of foliar damage already one day after *B. cinerea* inoculation. Conversely, T22 alone treated plants exhibited significant differences in disease severity only after 5 days post inoculation when compared to control plants. A further decrease in necrotic leaf area development could be observed 7 DPI in plants concomitantly treated with both Sys and T22, with about 63% reduction in disease severity compared to the control. Disease severity in these plants was significantly lower than the one observed in plants where each treatment was applied separately (−52% for Sys treatment and −40% for T22) (Figure 3).

3.4. *Sys exogenous supply and* T. afroharzianum *colonization alters* T. absoluta *infestation*

The number of eggs laid per plant was influenced by treatments (Figure 4(A), ANOVA, df = 3, F = 10.03, $P < 0.001$), resulting lowered by Sys and raised by T22 colonization. The combined application of T22 and Sys did not affect this parameter. Larvae survival curves revealed significant antibiotic effects of *T. afroharzianum* inoculation and Sys

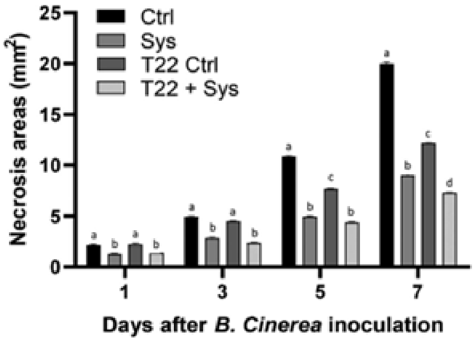

Figure 3. *T. afroharzianum* and Sys reduce *B. cinerea* virulence on tomato plants. Necrotic areas observed on *B. cinerea* inoculated leaves from tomato plants germinated from uncoated (Ctrl) or *T. afroharzianum* -coated seeds and treated or not with 100 fM Sys. The graph displays the average area of necrotic lesions formed 1, 3, 5, and 7 DPI. Letters indicate different statistical groups (One-Way ANOVA, $P < 0.05$). Error bars indicate standard error ($n = 90$).

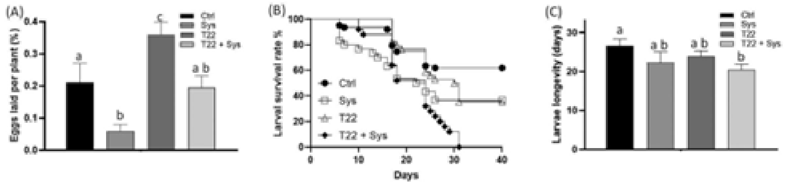

Figure 4. *T. absoluta* assays. (A) Eggs laid per plant by T. absoluta adults and (B) larvae survival curves on tomato plants treated with Sys and *T. afroharzianum* T22, their combinations and relative control. (C) Larvae longevity reared on the tomato plants treated as above described.

treatment on *T. absoluta* development when used alone or in combination (Figure 4(B), Log-Rank test, $\chi^2 = 21.6$, df = 3, $P < 0.001$). Survival rates, from eggs to pupation, were significantly lower for larvae fed on T22-treated leaves (Log-Rank test, $\chi^2 = 7$, df = 1, $P = 0.008$) and for larvae fed on Sys-treated leaves (Log-Rank test, $\chi^2 = 18$, df = 1, $P < 0.001$), in respect to control plants (Figure 4(B)). An additive effect was recoded for combined T22-Sys treatment (Pairwise log-Rank test T22 vs T22 + Sys $\chi^2 = 10.64$, df = 3, $P = 0.014$). Similarly, larval longevity was lowered by the combined application of T22 and Sys while no significant effect was recorded when the treatments were tested alone (Figure 4(C), Welch ANOVA, $F_{3,146} = 2.708$, $P = 0.047$).

3.5. Sys and T. afroharzianum *enhance the expression of plant defense-related genes*

A significant increase of *AOS, Pin I, LapA,* and *TD,* but not of *LoxD,* transcripts were recorded after Sys or T22 application). All gene transcripts, including those of the *LoxD* gene, were significantly more expressed in plants simultaneously treated with Sys and T22 compared to those treated with Sys or T22 alone (Figure 5).

3.6. Sys exogenous supply and T. afroharzianum *colonization modify the accumulation of JA, SA, and related metabolites*

JA over-accumulated in plants treated with Sys and T22, alone or in combination, with a maximum fold of 1.74 in T22 + Sys samples in addition, Sys treated plants also displayed higher levels in 12-OPDA in respect to controls, while another intermediate, 12,13(S)-EOT, increased in T22 + Sys plants. Accumulation of tuberonic acid-glucoside, involved in JA metabolization, was higher in single (Sys and T22) treatments, and unaltered in T22 + Sys plants Finally, MeJA resulted over-accumulated in plants treated with both Sys and T22 (1,94 fold higher than Ctrl (Figure 6). Sys treatment significantly reduced the amounts of Chorismic acid, Prephenic acid, SA, and its glycosylated form while T22 increased Chorismic acid and decreased Prephenic acid and SA. The combined treatment increased chorismic acid (although to a lesser amount than the value reached by T22 treatment) and DL-Phenylalanine while decreasing Prephenic acid and SA (Figure 7).

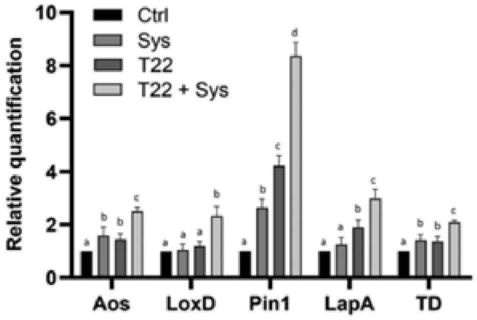

Figure 5. Level of defense-related genes expression in tomato plants grown from uncoated (Ctrl) or *T. afroharzianum* -coated seeds (T22) and treated or not with 100 fM Sys. Transcript levels of the following genes were analyzed: *Allene Oxide Synthase* (*AOS*), *LipoxygenaseD* (*LoxD*), *Wound-induced Proteinase inhibitor I* (*Pin I*), *Threonine deaminase* (*TD*), and *Leucine aminopeptidase A* (*LapA*). Quantities of transcripts are relative to the calibrator Ctrl condition. Different letters indicate statistically significant differences (One-Way ANOVA, $P < 0.05$). Error bars indicate standard error ($n = 3$).

4. Discussion

The discovery of novel strategies for pathogen or pest control able to reduce the use of chemical pesticides represents an important challenge in modern agriculture. Beneficial microorganisms and natural-derived molecules with the potential to prime plant defenses are intriguing tools for the development of new generation biopesticides which could increase the sustainability of agricultural production. Some soil-dwelling fungi belonging to the genus *Trichoderma* have a profound impact on plant growth and protection limiting plant pathogen populations through mycoparasitism, competition, and antibiosis (Harman et al. 2004; Verma et al. 2007; Yuan et al. 2019). In addition to pathogen control, root colonization by *Trichoderma* spp. limits pest-induced damage on plants either through stimulation of plant defense or by attracting natural enemies of insect pests (Tucci et al. 2011; Battaglia et al. 2013; Coppola et al. 2019b). Despite the efficacy of these fungal species in promoting plant growth and resistance against biotic threats, their potential can be limited in certain ecological contexts where their fitness is low (Di Lelio et al. 2021). To overcome this limitation, a combination of *Trichoderma* and other natural-derived elicitors of plant's endogenous defense may represent an effective strategy to boost *Trichoderma* biocontrol activity both in fungal-friendly or harsh environments. A feasible strategy is represented by the combined use of these root symbionts with natural-derived compounds, including plant-derived signaling molecules (Isman 2006), semiochemicals (Witzgall et al. 2010), and interfering RNAs (Zhu et al. 2011; Koch et al. 2016) to attain satisfactory levels of plant protection. Natural molecules able to trigger plant immunity, such as Damage Associated Molecular Partners (DAMPs), are interesting players in pathogen and pest management. One of these is Sys, which acts as an elicitor of immune responses in tomato plants following insect or mechanical damage

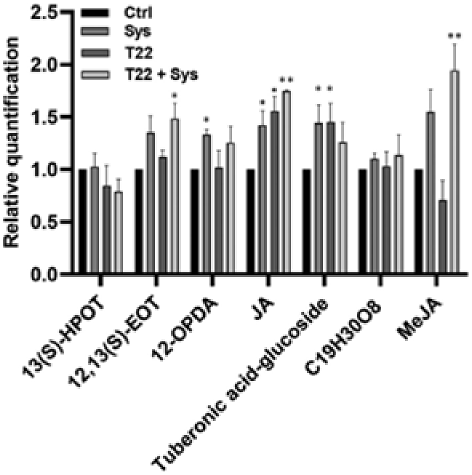

Figure 6. Targeted LC-HESI (-)-HRMS analysis of semi-polar metabolites in the JA pathway. Metabolites were relatively quantified as fold internal standard level, normalized on the control (Ctrl; for more details, see materials and methods). Data represents the average of three independent biological replicates, and a student's t-test was used to identify metabolites whose abundance significantly changed with respect to the Ctrl condition. (*$P \leq 0.05$; **$P \leq 0.01$).

(Ryan 2000; Ryan and Pearce 2003). Our group (Coppola et al. 2019c; Molisso et al. 2021) demonstrated that the exogenous supply of the peptide to intact plants enhanced their resistance against the noctuid moth *S. littoralis* and the fungal pathogen *B. cinerea*. These results are likely linked to the induction of plant's defense-related genes through the accumulation of active compounds.

An important prerequisite to carry out combined plant treatments with *Trichoderma* and natural-derived compounds is the absence of either direct or indirect antagonistic effects between the two treatments. Importantly, in our experiments, Sys addition to T22 fungal cultures did not show any growth inhibitory effect.

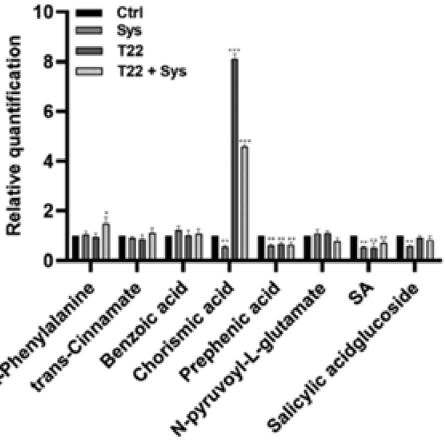

Figure 7. Targeted LC-HESI (-)-HRMS analysis of semi-polar metabolites in the SA pathway. Metabolites were relatively quantified as fold internal standard level, normalized on the control (Ctrl; for more details, see materials and methods). Data represents the average of three independent biological replicates, and a student's t-test was used to identify metabolites whose abundance significantly changed with respect to the Ctrl condition (*$P \leq 0.05$; **$P \leq 0.01$, *** $P \leq 0.001$).

Trichoderma and Sys ability to suppress different biotic threats resides in their propensity to prime plant defense responses through the modulation of different signaling pathways, including those of JA, ET, and SA (Shoresh et al. 2005; Martinez-Medina et al. 2017; Yuan et al. 2019). Priming is an intrinsic part of induced resistance during which the plant 'projects' a defense strategy against the potential invader while preparing its defensive approach for a faster and/or stronger reaction to future challenges (Mauch-Mani et al. 2017). The analysis of the expression of JA-associated genes in T22 and in Sys treated plants showed an up-regulation of *Aos*, an early defense-related gene, active in the octadecanoid signaling pathway that leads to JA biosynthesis, and of *Pin I* and *TD*, two late defense-related genes responsive to JA. It is well described that JA activates a cascade of defense responses that are temporally (early and late) and spatially (local and systemic) regulated in tomatoes (Ryan 2000). The early and late wounding-response genes are regulated by distinct mechanisms. Local wounding leads to the processing of ProSys followed by Sys binding to SYR1, a membrane located receptor (Wang et al. 2018), and the subsequent activation of genes involved in JA biosynthesis. The increase of endogenous JA levels leads to the activation of late JA responsive genes that play a direct role in defense. Late defense genes include *PIs*, *TD*, and *LapA* (Howe 2004). Tomato *LapA* is important in deterring herbivory-induced damage and controlling insect growth (Fowler et al. 2009), while *Pin I* prompts the formation of highly stable complexes with insect digestive proteases resulting in decreased digestion of dietary protein, depletion of essential amino acids, and, consequently, reduced rates of insect growth and development (Lorito et al. 1994). Furthermore, PIs in general and Pin I efficiently target microbial secreted proteases thus inhibiting a variety of plant pathogens including bacteria and fungi through suppression of cell growth (Hermosa et al. 2006; Turra and Lorito 2011; Turrà et al. 2020). *TD* is a gene involved in the resistance against chewing insects. Remarkably, TD activity in the insect's midgut correlates with reduced levels of free threonine, which is a dietary requirement for phytophagous insects (Chen et al. 2007). We observed that the combination of the two treatments (Sys and T22) results in higher levels of transcripts related to the activation of the aforementioned genes, and of *LoxD*, a gene that also contributes to JA biosynthesis consequently, enhancing resistance against insect herbivores (Yan et al. 2013; Thakur and Udayashankar 2019).

Metabolite data, obtained by LC-HRMS analyses, partly paralleled transcript profiles: single and double treatments were characterized by higher levels in JA, the end-product of the octadecanoic pathway involved in a series of physiological plant responses, in respect to control (Yang et al. 2019); the magnitude of alteration was stronger in T22 + Sys plants compared to single treatments. A significant increase of MeJA, the JA volatile methyl ester, was also registered in plants simultaneously treated with both Sys and T22. Tuberonic acid-glucoside, a metabolite produced in the frame of JA catabolism, so-called by virtue of its capacity to induce tuber formation in potato (*S. tuberosum*), also increased in Sys and T22 but not in the double-treated plants. Its synthesis looks to be part of a general mechanism aimed at turning on and switching off JA levels and functions (Miersch et al. 2008): thus, in this context, the higher JA content in T22 + Sys plants could reflect either the increased upstream metabolic flux, as highlighted at the gene expression level, or the reduced catabolism in the double compared to the single treatments. Additional increases in JA intermediates were found in Sys and T22 + Sys samples, although this appears to be more related to stochastic events rather than to a solid tendency. As expected, metabolite data showed an impact of Sys and T22 plant treatment on SA pathway increasing phenylaniline and chorismic acid but decreasing SA. Since chorismate is a branch-point metabolite for SA and phenylalanine biosynthesis, it appears that the combined treatment 'pushed' the pathway's flow in the direction of phenylaniline production that should lead to phenylpropanoid biosynthesis, a class of compounds known to be produced by the plant under biotic stress. In addition, the reduction of SA should be connected to a faster and more intense T22 colonization since endophytic root expansion of the beneficial fungus is limited by SA pathway. Previous work has shown that endophytic colonization of *Arabidopsis thaliana* roots by *T. harzianum* is strictly dependent on the relative abundance of the two antagonistic plant hormones JA and SA. Indeed, exogenous application of SA reduces *Trichoderma* root colonization, while induction of the JA pathway or impairment of the SA one promotes it (Alonso-Ramirez et al. 2014; Martinez-Medina et al. 2017). In line with this, Sys treatment likely results in enhanced colonization of plant roots by *Trichoderma* which in turn contributes together with Sys to boost plant immunity and broad-spectrum resistance against both foliar and root fungal pathogens. The central role of JA in *Trichoderma* colonized plants in modulating defense responses has been demonstrated and confirmed through several mutant studies. For example, plants, of the JA-deficient defenseless1 (def1) mutant, were susceptible to disease development even after *Trichoderma* treatment, demonstrating that JA pathway is required for plant resistance in pathogen-challenged conditions (Martinez-Medina et al. 2013). It has also been shown that JA plays key role during plant defense against necrotrophic fungal pathogens, such as *B. cinerea* and *Alternaria brassicicola*. The mutation of COI1, a receptor involved in JA signaling, makes plants more susceptible to *B. cinerea* (An et al. 2019). Other results showed the protective role of JA against *Fusarium* wilt disease in tomato (Hernández-Aparicio et al. 2021). In addition, recent evidences shown that JA is involved in *Trichoderma virens*-mediated resistance against *F. oxysporum* in tomato plants. In this context, the activation of the JA signaling pathway in Sys + T22 treated plants nicely correlates with the reduction of *B. cinerea* disease severity and *F. oxysporum* induced mortality. JA is also a crucial player in plant defense response against insect pests (War et al. 2012). Exogenous supply of JA and MeJA through soil drenching or foliar sprays increases resistance against a broad spectrum of insects in numerous agricultural crops under greenhouse and field conditions (Haas et al. 2018; Nouri-Ganbalani et al. 2018; Stella de Freitas et al. 2019). Strapasson (2014) found that the treatment of tomato seeds with MeJA- significantly decreased the pupal weight of *T. absoluta*. Our findings showed for the first time that Sys strongly reduces the survival rate of larvae of *T. absoluta*, and corroborate previous findings showing that *Trichoderma* endophytic colonization negatively affects *T. absoluta* fitness through significant reduction of larval survival (Agbessenou et al. 2020). Furthermore, our study highlighted the usefulness of combined treatments to enhance plant resistance to *T. absoluta*. Previous works had shown a synergistic effect of different treatments on its fitness. For example, the combination of *Beauveria bassiana* and *Bacillus thuringiensis* strongly reduced *T. absoluta* larvae survival (Tsoulnara and Port 2016). Yet, the usefulness of co-expression of different PIs to enhance plant resistance to *T. absoluta* has been highlighted (Hamza et al. 2018). Nonetheless, this is the first study to evaluate the impact of combined peptide treatment and endophytic colonization.

Apparently, the combined application of Sys and T22 did not alter the oviposition behavior of *T. absoluta* with respect to the single powerful treatment with Sys. This result could have many explanations. For example, *T. absoluta* develops many overlapping generations/year, therefore mated females frequently oviposit on highly infested plants that are highly activated as Sys treatment. The combined treatment showed an additive effect on larval longevity/survival of *T. absoluta* in respect to the single treatments and this could correlate to the larger accumulation of JA-derived metabolites. It will be now interesting to test the effect of the combined treatments on the natural antagonists of *T. absoluta*, known to exploit plant VOCs to locate their victim (Lins et al. 2014; Gontijo et al. 2019).

In conclusion, the combined application of *Trichoderma* and Sys on tomato plants increases the level of JA while decreasing the amount of SA, thus promoting a defense priming state and likely enhancing T22 plant colonization. Altogether, these events result in a boost of plant immunity. Since JA and its derivatives trigger VOCs emission (Tamogami et al. 2012), the increased levels of JA produced in treated plants may amplify the attractiveness of natural enemies of pests, thus promoting indirect defenses of treated plants that could be protected also against other agents or biotic stresses.

Disclosure statement

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Author contributions

AMA performed bioassays, gene expression studies; MC; supervised and participate to the experimental work; DT, SV designed and carried out experiments with *F. oxysporum*, PC, EG designed and carried out *T. absoluta* bioassays; AF, GD, performed metabolomic analysis; CA, AR synthetized and purified Sys; VC contributed to gene expression analyses; SW supervised experimental work and revised the manuscript; RR conceived and supervised the work and wrote the manuscript. All the authors contributed to manuscript writing.

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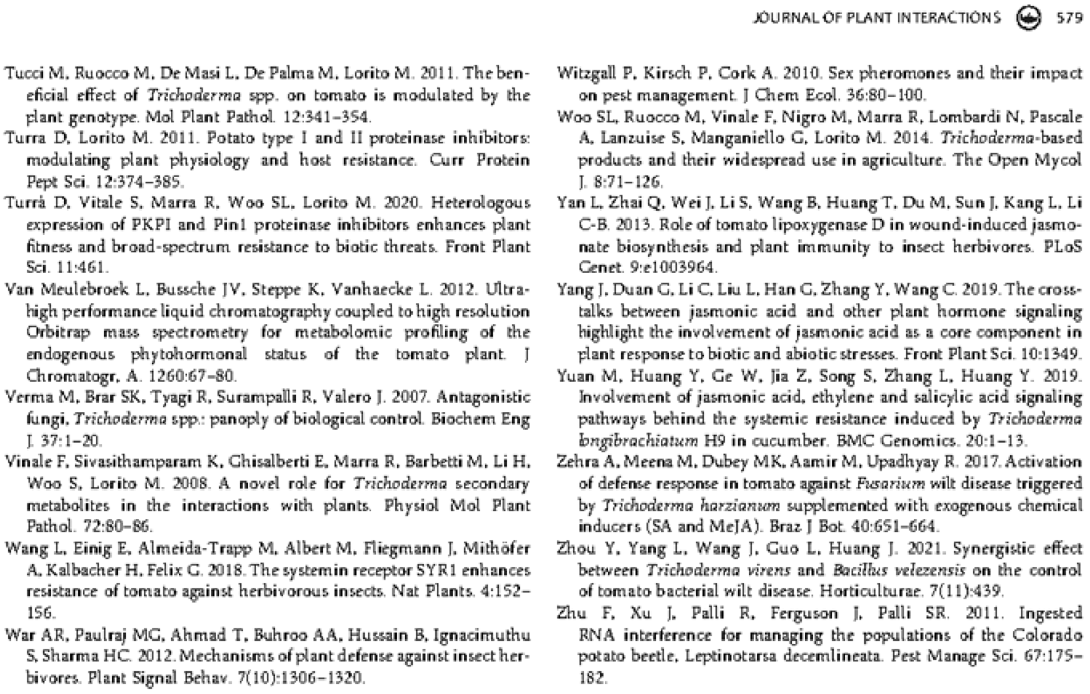

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Systemin peptide application improves tomato salt stress tolerance and reveals common adaptation mechanisms to biotic and abiotic stress in plants

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ABSTRACT

Plants are continuously challenged by several environmental stresses that impair their growth and production performances. Stresses encountered by plants can be caused by biotic agents (*e.g.*, herbivores, parasitic microorganisms, weeds) and abiotic factors (*e.g.*, cold, drought, soil and water salinity). Despite these differences, plants respond to biotic and abiotic stresses with shared adaptive mechanisms resulting in complex and interlinked cross-talks. Systemin is a hormone peptide, playing a central role in the regulation of plant response against a wide range of stress agents, including wound, phytopathogenic fungi and phytophagous and sucking insects. It has also been shown that upregulation of prosystemin, the precursor protein of systemin, enhanced the tolerance of tomato plants to salt stress, indicating that systemin induced molecular adaptations to biotic stress can also be beneficial to plants exposed to salt stress. Considering that systemin is a small peptide that can be sensed by plants both as soil drench and foliar applications, we hypothesized that exogenous applications of systemin may increase salt stress tolerance in tomato plants through the activation of multiple adaptation mechanisms. Here we report that a soil drench picomolar solution of systemin increases tomato salt stress tolerance by i) activating of *SOS1*, *NHX* and *HKT* Na^+ transporters in leaves ii) enhancing the cellular antioxidant power, and iii) balancing the protease activity induced by salt stress. Activation of these responses upon exogeneous application of systemin was highly correlated to an improved tomato growth under salt stress, suggesting that systemin may represent an important component of the crosstalk between biotic and abiotic stress responses in plants.

1. Introduction

In nature, plants are continuously exposed to a wide range of biotic and abiotic stresses caused by living organisms (e.g., bacteria, fungi, nematodes, weeds) and physicochemical factors (e.g., salinity, waterlogging, drought). Exposure of plants to these stressors causes a disruption in the metabolism that adversely affects their growth, development and productivity (Verma et al., 2020; Waqas et al., 2019). The selective pressure of the environment induced the evolution of sophisticated defense network, also called innate immune system, allowing plants to survive against specific and combined biotic/abiotic stresses (Nejat and Mantri, 2017).

Plant responses to biotic and abiotic stresses share several common features, that results in complex and interlinked cross-talks at molecular and cellular level (Ali and Baek, 2020). This can be due to the innate immobility of plants that requires fast molecular communication and non-specific responses to environmental stimuli, which often are a combination of biotic and abiotic stresses (Ali et al., 2019; Kim et al., 2014; Kissoudis et al., 2014; Mittler and Blumwald, 2010; Muchate et al., 2016; Nikalje and Suprasanna, 2018; Suprasanna and Ghag, 2019). Understanding the molecular and physiological basis of multiple stress responses in plants is therefore pivotal to properly approach future plant management in a climate change scenario.

The crosstalk between biotic and abiotic stresses in plants has been well discussed in the literature. Capiati et al. (2006) showed that plants wounded by herbivores had higher tolerance to salt stress; moreover, salt stress induces an increase of pathogen related proteins (PRs) that makes plants more tolerant to insect attacks (Dombrowski, 2003). Hao et al. (2021) observed that *Vitis vinifera* (L.) plants infected by the *Grapevine leafroll-associated virus-3* (GLRaV-3) cultivated under salt

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stress conditions were more tolerant to high salinity than the healthy ones. Similarly, salt-stressed tomato and barley plants showed higher tolerance against the powdery mildew (*Botrytis cinerea* Pers.) (Achuo et al., 2006; Romero-Puertas et al., 2021; Wiese et al., 2004). Orsini et al. (2010) also demonstrated that tomato plants overexpressing prosystemin (ProSys) protein, a key component of the wound-induced signaling pathway, had an increased salt stress tolerance in tomato, suggesting that a constitutive activation of wound responses is advantageous in saline environment. ProSys is a pro-hormone of 200 aminoacidic residues which releases, upon proteolytic cleavage, a bioactive peptide hormone of 18 amino acids called systemin (Sys) involved in the activation of defense genes in tomato in response to wound and herbivory attacks (Beloshistov et al., 2018; Coppola et al., 2015; Corrado et al., 2007; Degenhardt et al., 2010; Ryan, 2000; Schilmiller and Howe, 2005). Insect attacks or severe wounding induce the upregulation of ProSys mRNA as compared to unwounded tomato leaves (Lee and Howe, 2003; Li et al., 2002; McGurl et al., 1992). The encoded protein is processed to release Sys peptide, which binds a leucine rich repeat receptor like-kinase (LRR-RLK), SYR1, triggering a complex intracellular signaling pathway that leads to the generation of early cellular responses such as depolarization of the plasma membrane, apoplastic alkalization, opening of ion channels with the consequent increase of cytosolic calcium, generation of ethylene (ET) and reactive oxygen species (ROS), and an extensively alteration of phosphorylation protein patterns (Ahmad et al., 2019; Felix and Boller, 1995; Moyen et al., 1998; Schaller and Oecking, 1999; Zenda et al., 2018). The concurrent activation of a mitogen-activated protein kinase (*MAPKs*), calmodulin, and a phospholipase A2 (*PLA2*), and the release of linolenic acid from membrane phospholipids altogether promote the induction of the octadecanoid pathway and the downstream biosynthesis of 12-oxophytodienoic acid (OPDA) and jasmonic acid (JA). This cascade leads to the subsequent activation of wound responses through the induction of several defense genes/proteins, such as proteinase inhibitors (PIs) (McGurl et al., 1992; Pearce et al., 1990). The role of proteinase inhibitors in plant response to biotic stresses is well characterized (Hamza et al., 2018) and has been reported for different plant-parasitic organisms (Fan et al., 2020). Different orders of insects (Diptera, Coleoptera, Lepidoptera) use serine and cysteine proteinases to degrade proteins in the ingested food (Habib and Fazili, 2007; Hamza et al., 2018). Similarly, several phytopathogenic fungi produce extracellular proteinases for plant tissue colonization (Kim et al., 2009). Nematodes feeding on tomato plants also induce the upregulation of PIs at the early stages of infection, suggesting an important role of proteases for successful nematodes colonization of plants (Bozbuga, 2021).

Other than the protection against these biotic stress agents, high PIs levels were shown to increase plant tolerance to different abiotic stresses such as drought and salinity (Coppola et al., 2010; De La Noval et al., 2007; Orsini et al., 2010; Pastor et al., 2018; Zhang et al., 2020). Recently, by combining gene expression analyses and bioassays with different pests, it was demonstrated that the exogenous application of Sys peptide to tomato plants enhances both direct and indirect defense barriers (Coppola et al., 2019). Nonetheless, the involvement of the exogenous supply of this small peptide in salt stress tolerance has been scarcely investigated.

Based on this evidence, we hypothesized that exogeneous Sys application, which has been reported to be sensed by plants when applied as soil drench (Molisso et al., 2021), could help counteracting salt stress in tomato by triggering multiple plant defense-response. Here we demonstrate that soil drench application of Sys enhanced biomass accumulation in tomato plants exposed to salt stress by potentiating ion homeostasis, oxidative stress protection, and protein stability.

2. Materials and methods

2.1. Plant material and growth conditions

Tomato seeds (*Solanum lycopersicum* L. cultivar "Dwarf San Marzano") were surface sterilized with 70% ethanol for 2 min, rinsed, washed with 2% sodium hypochlorite for 10 min and rinsed at least five times with sterile distilled water. Seeds were then germinated in petri dishes on wet sterile paper and kept in the dark for 3 days in a growth chamber at 24 ± 1 °C and 60 ± 5% of relative humidity (RH). Upon roots emergence, plantlets were transferred to a polystyrene tray with barren sterile S-type substrate (FloraGard; Oldenburg, Germany) in a growth chamber at 26 ± 1 °C and 60 ± % RH with 18:6 h light/dark photoperiod. After two weeks, plants were transplanted into plastic pots filled with S-type substrate (FloraGard; Oldenburg, Germany) with the same growth conditions. The synthesis, purification and stability of the Sys peptide have been previously described (Molisso et al., 2021). Briefly, the purification of the Sys peptide was carried out by Reversed-Phase High-Performance Liquid Chromatography (RP-HPLC) (Shimadzu LC-8A, equipped with a SPD-M10 AV) on a semipreparative column (Jupiter 10μProteo 90 A, 250 × 10.0 mm, Phenomenex, Torrance, CA, USA) using a gradient of acetonitrile (0.1% TFA) in water (0.1% TFA) from 5% to 50% in 30 min at 5 mL/min. Peptides characterization was subsequently performed by mass spectrometry (LC-MS ESI-TOF 6230 Agilent Technologies, Milan, Italy). The sequence of the Sys peptide sequence was the following: AVQSKPPSKRDPPKMQTD, with a mass of 670.94 $[M + 3H]^{3+}$; 1005.60 $[M + 2H]^{2+}$.

Finally, Sys peptide stability was tested by HPLC analysis (Shimadzu LC-8A, equipped with a SPD-M10 AV) and stock solutions prepared as previously reported (Coppola et al., 2019).

The experimental design consisted of a combination of two treatments: mock-treated plants, Sys-treated plants, and three concentrations of salt stress (S0: 0 mmol L^{-1}; S1:100 mmol L^{-1} and S2:150 mmol L^{-1} NaCl). Plants were arranged in a completely randomized design with eight replicates. Briefly, after 7 days from the transplanting, the plants were irrigated with 120 mL of 100 pmol L^{-1} Sys peptide in PBS buffer 0.1X (phosphate buffer saline, 1 mmol L^{-1} phosphates, 14 mmol L^{-1} NaCl, 0.27 mmol L^{-1} KCl, pH 7.4, Sigma-Aldrich, Milan, Italy) or 120 mL of PBS 0.1X (mock treatment control). Salt stress was initiated one day after treatment (DAT) by adding 100 mL of water (S0, as control) or 100 mL of 100 mmol L^{-1} (S1) and 150 mmol L^{-1} (S2) NaCl solution. The irrigation was provided every two days. Leaf samples from control and treated plants were harvested 8 DAT and used for the gene expression analysis.

2.2. Growth and water relation analyses

Destructive harvest and biometrics were taken at 15 DAT to measure shoot biomass and leaf area. The whole plant was then dried at 60 °C to constant weight for shoot dry weight determination. To measure leaf area, leaves were separated from the stem and arranged on a white panel and one overhead photo for each plant was taken. Leaf area was measured using ImageJ v1.52a (U.S. National Institutes of Health, Bethesda, MD, USA) (Cirillo et al., 2021). To measure relative water content (RWC), a leaf sample was harvested and promptly weighted to determine its fresh weight (FW). The sample was then transferred in deionized water. After 24 h the sample was superficially dried with a paper towel and weighted for saturated weight (SW). The leaf samples were then dried for one week at 60 °C and weighted for the determination of shoot dry weight (DW). RWC was calculated as: [(FW-DW)/(SW-DW) x 100]. Moreover, stomatal conductance (gs, mmol H_2O m^{-2} s^{-1}) was measured at 15 DAT with a portable porometer AP4 (Delta-T Devices Ltd, Cambridge, UK). Measurements were performed from 10 am to 2 pm on a fully expanded leaf per plant.

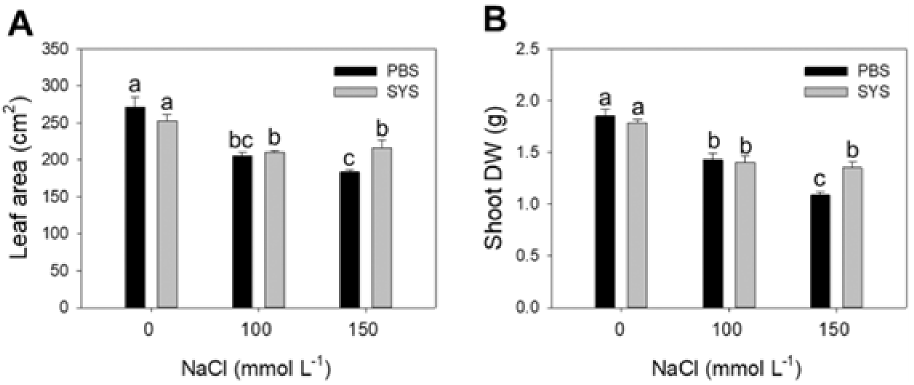

Fig. 1. Biometric parameters of tomato plants treated or not with 100 pmol L^{-1} Sys and grown under 0 mmol L^{-1}, 100 mmol L^{-1} and 150 mmol L^{-1} NaCl. A) Leaf area and B) shoot dry weight (DW). The values are mean ± standard error (n = 8). Different letters indicate significant differences according to Tuckey's post-hoc test ($p < 0.05$).

2.3. *Molecular analysis*

At 8 DAT, leaves of tomato plants, treated or not with 100 pmol L^{-1} Sys peptide, under S0, S1 and S2 conditions, were harvested and immediately frozen at − 80 °C. Since the effects of Sys peptide application on biomass accumulation, stomatal conductance, and RWC at the end of the experiment were maximized at S2, gene relative expression analysis and proline quantification were performed only on this level of salt stress imposed. Leaves from the same treatment were mixed and four replicates per bulk were analyzed. Total RNA extraction, single-strand cDNA synthesis and Real Time RT-PCRs were performed according to standard procedures, as already described elsewhere (Corrado et al., 2007). Gene expression analysis was carried out using two technical replicates for each biological replicates. Relative quantification of gene expression was carried out using the comparative method, $2^{-\Delta\Delta Ct}$ (Livak and Schmittgen, 2001). The housekeeping gene EF-1α was used as endogenous reference gene to normalize the expression level of the target genes and calculate the relative transcript levels (Marum et al., 2012; Müller et al., 2015). Primers of the gene under investigation are reported in Table S1.

2.4. *Proline quantification*

The quantification of the proline content was carried out by using a ninhydrin based colorimetric assay on two technical replicates for each biological repetition (Claussen, 2005). Proline concentration was expressed in μmol g^{-1} FW after comparison with a standard curve.

2.5. *Statistical analysis*

Biometric measurements were statistically analysed by using a two-way ANOVA procedure with Duncan's multiple comparisons test. Differences of $p < 0.05$ were considered significant. ANOVA was performed by using SPSS (Statistical Package for Social Sciences) Package 6, version 23. Gene expression analysis was analyzed with the Student's *t*-test or Tuckey's post-hoc test ($p < 0.05$). Cluster heatmap was produced with ClustVis tool (http://biit.cs.ut.ee/clustvis/) using Euclidean distance as the similarity measure and Ward as linkage rule (Metsalu and Vilo, 2015).

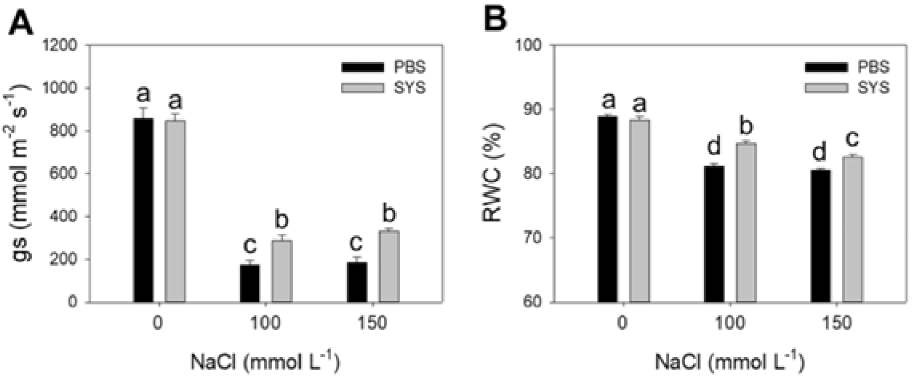

Fig. 2. Physiological response of tomato plants treated or not with 100 pmol L^{-1} Sys and grown under 0 mmol L^{-1}, 100 mmol L^{-1} and 150 mmol L^{-1} NaCl. A) Stomatal conductance (gs) and B) relative water content (RWC). The values are mean ± standard error (n = 8. Different letters indicate significant differences according to Tuckey's post-hoc test ($p < 0.05$).

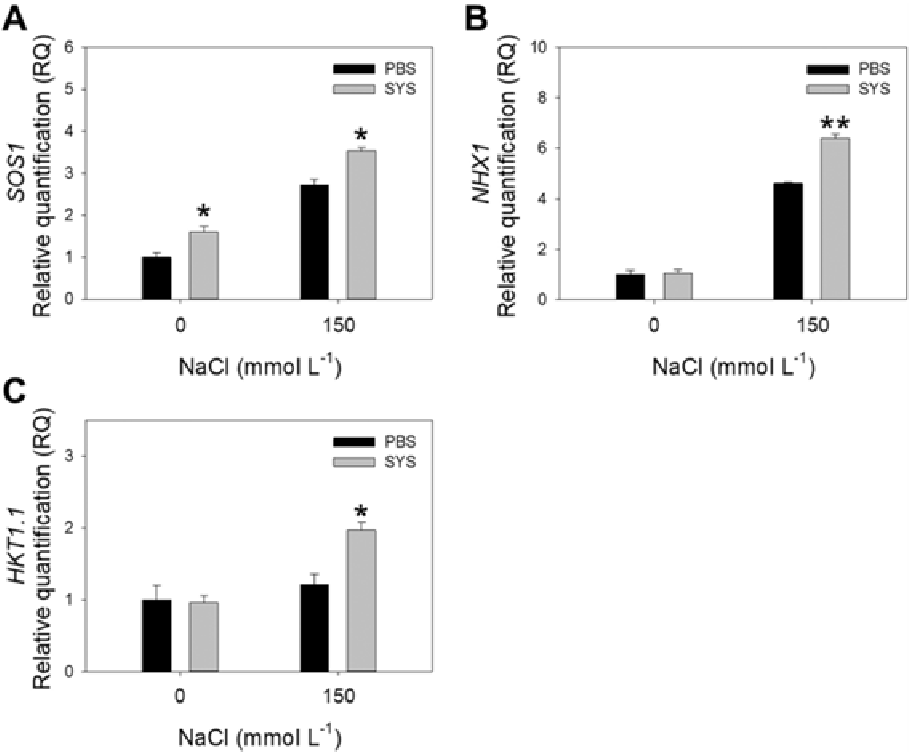

Fig. 3. Relative quantification of ion transporters gene expression in tomato plants treated or not with 100 pmol L^{-1} Sys and grown under 0 mmol L^{-1} and 150 mmol L^{-1} NaCl. A) *SOS1* (Salt Overly Sensitive 1); B) *NHX1* (Sodium-hydrogen antiporters 1; and C) *HKT1.1* (High-Affinity Potassium Transporter 1). The values are mean ± standard error (n = 4). Quantities are relative to the calibrator represented by mock treated plants within each salinity level. Statistical analysis was performed with Student's t-test (* $p < 0.05$; ** $p < 0.01$).

3. Results

3.1. *Biomass accumulation*

To assess the potential of exogenous applications of Sys for improving plant growth and salt tolerance, we conducted an experiment on tomato plants treated at transplant with a solution of 100 pmol L^{-1} Sys and then exposed to two different concentrations of NaCl. In mock-treated plants, the exposure to 100 mmol L^{-1} NaCl (S1) induced significant reductions in leaf area and shoot dry weight (DW) (−24.4% and −22.8%, respectively) compared to non-salinized control plants. Similarly, the highest concentration of NaCl (150 mmol L^{-1}, S2) induced − 32.4% leaf area and − 41.2% shoot DW reductions. (Fig. 1A, B). The treatment with Sys did not significantly affect these parameters under control growth condition (S0) and 100 mmol L^{-1} NaCl (S1) showing not significant differences compared to the mock-treated plants. On the contrary, under S2 conditions, the treatment with Sys increased the total leaf area (+17.9%) and shoot DW (+24.3%) compared to mock-treated plants (Fig. 1A, B).

3.2. *Stomatal conductance and relative water content (RWC)*

Stomatal conductance (*gs*) was severely affected by salt stress in both mock-treated and Sys treated plants. Sys treatment did not affect gs under control condition (S0). In mock-treated plants, this parameter was reduced by − 79.5% for S1 and − 78.2% for S2 compared to the control (S0). Plants treated with Sys peptide showed milder yet significant reduction of *gs*, with − 65.9% for S1 and − 60.9% for S2 (Fig. 2A) compared to the control (S0).

The leaf relative water content (RWC) was not affected by Sys treatment under control condition (S0) (Fig. 2B). However, at S1 and S2 mock-treated plants showed a lower relative water content (RWC) compared to the control (−8.7% and −9.4%, respectively) while in Sys treated ones this parameter was reduced only by − 4% at S1 and − 6.5% at S2 compared to control conditions (Fig. 2B).

3.3. *Gene expression analysis and proline content*

The successful adaptation of tomato plants to salinity suggested a potential role of the expression level of some key defence-related genes. To better investigate this point, we looked at three main categories of genes: ion transporters, genes involved in antioxidant response systems, and Sys/JA-related defence genes. Transcript accumulation of target genes was analyzed eight days after salt treatment (8 DAT) by means of qRT-PCR. Notably, in absence of salinity, *SOS1* was significantly upregulated by 1.6 -fold change in Sys treated plants compared to mock ones (Fig. 3A). Regarding *NHX1* and *HKT1.1*, the expression level was not changed by Sys treatment under control conditions (Fig. 3B-C). In contrast, when salinity stress was imposed, we observed increased expression of all these genes in all tested plants. We found a significant increase of *SOS1*, *NHX1* and *HKT1.1* transcript in Sys-treated plants compared to control ones for S2 treatment by 1.4-, 1.5- and 1.6- fold, respectively (Fig. 3A, B, C).

Salt stress strongly induced the accumulation of proline in leaves of

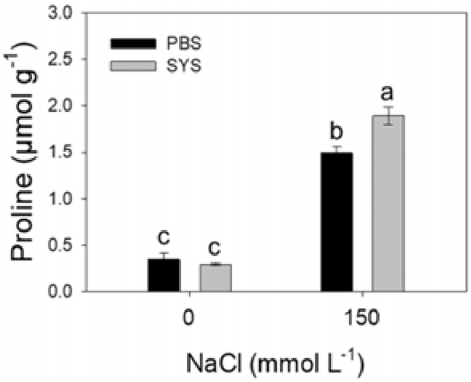

Fig. 4. Proline accumulation of tomato plants treated or not with 100 pmol L^{-1} Sys and grown under 0 mmol L^{-1} and 150 mmol L^{-1} NaCl. The values are mean ± standard error (n = 4). Different letters indicate significant differences according to Tukey post-hoc test ($p < 0.05$).

untreated and Sys-treated plants by 4.3- and 6.4-fold changes respectively (Fig. 4). Noteworthy, under salt stress, the accumulation was significantly higher in Sys-treated plants, + 26.2% compared to untreated plants (Fig. 4).

We also monitored genes associated with the enzymatic antioxidant system whose function is to protect cells from damages by scavenging excessive reactive oxygen species (ROS). In particular, the expression level of superoxide dismutase (*SOD1*), was significantly upregulated by Sys treatment under control and salt stress conditions compared to the mock-treated plants (1.8- and 1.6- fold, respectively) (Fig. 5A).

Differently the expression profile of the cytosolic ascorbate peroxidase (*APX2*) was significantly upregulated by systemin treatment under S0 (1.6- fold higher than control), while under S2 no significant transcript change was observed when compared to the mock-treated plants (Fig. 5B).

Moreover, we examined the expression profile of *AOS* and *Pin II*, key defense-related genes known to be induced by Sys peptide (Coppola et al., 2019; Zhang et al., 2020). Under S0 condition Sys treatment did not significantly alter *AOS* expression (Fig. 6A), while it increased *Pin II* expression by 2.6 -fold change, compared to mock-treated plants. In presence of salinity, systemin treatment induced an increase of expression of *AOS* and *Pin II* (1.5-fold and 5.9-fold increase respectively) compared to mock-treated plants (Fig. 6A, B).

3.4. *Heatmap cluster analysis*

The heatmap in Fig. 7 clearly summarizes the results presented in this study. Under control conditions (S0), Sys treatment did not alter the biometrics, physiological parameters, and leaf proline content compared with the untreated plants (PBS). On the contrary, Sys treated plants showed the upregulation of genes correlated with sodium homeostasis (*SOS1*), antioxidant machinery (*SOD1* and *APX2*), and with defense (*Pin II*). Moreover, the heatmap shows that the negative effect of salinity on biometrics (leaf area and shoot DW) and physiological parameters (RWC and gs) are milder in Sys treated plants compared to the ones reported for control plants (PBS). Under salt stress, genes correlated with sodium transporters (*SOS1*, *NHX1* and *HKT1.1*), antioxidant machinery (*SOD1*), and defense (*AOS* and *Pin II*) were highly upregulated in Sys treated plants compared to untreated ones, as well as the leaf proline content. The clustering on columns indicate that salinity is the main factor affecting the differences between treatments. However, the differences induced by Sys treatment are higher under salt stress (S2) compared to control condition (S0), as indicated by the higher clustering point of the former compared with the latter. Finally, the variables are divided in two main clusters that clearly separate the responses on biometrics and physiological parameters (in the top of the heatmap) from the molecular responses (at the bottom of the heatmap).

4. Discussion

4.1. *Systemin as stress protectant under climate change*

Soil salinity is an expanding phenomenon worldwide, due to climate change and the misuse of coastal agricultural lands (Di Stasio et al., 2020). It has been estimated that soil salinity currently affects 20% and 33% of cultivated and irrigated agricultural lands respectively (Shrivastava and Kumar, 2015) and it has been expected that it will increase at a faster rate than now by 2050 (Cirillo et al., 2018; Di Stasio et al., 2020; Rajput et al., 2015). Soil salinity is considered a dominant cause of detrimental effects on soil physicochemical and biological properties and the consequent loss of crop yield (Alzahrani et al., 2021; Ma et al., 2020; Rajput et al., 2015). For this reason, it is pivotal to find new strategies to increase plant tolerance to salt stress to reduce its negative impact on crop productivity (Giorio et al., 2020; Mishra and Tanna,

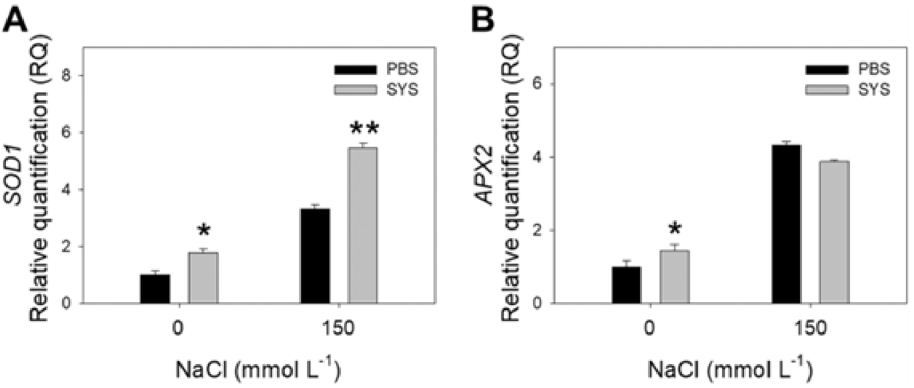

Fig. 5. Relative quantification of antioxidant machinery-related genes induced in tomato plants treated or not with 100 pmol L^{-1} Sys and grown under 0 mmol L^{-1} and 150 mmol L^{-1} NaCl. Genes under investigation were: *APX2* (Ascorbate Peroxidase 2) and *SOD1* (Copper-zinc superoxide dismutase). The values are mean ± standard error (n = 4). Quantities are relative to the calibrator represented by mock treated plants. Statistical analysis was performed with Student's t-test (* $p < 0.05$; ** $p < 0.01$).

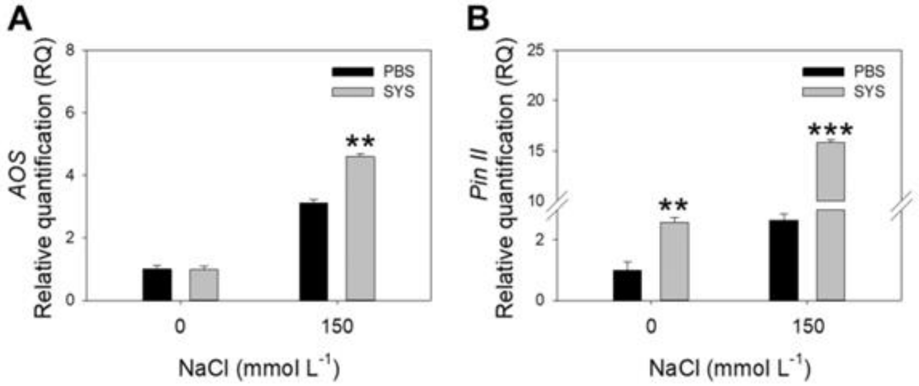

Fig. 6. Relative quantification of key defense-related genes induced in tomato plants treated or not with 100 pmol L^{-1} Sys and grown under 0 mmol L^{-1} and 150 mmol L^{-1} NaCl. A) *AOS* (Allene Oxidase Sintase) and B) *Pin II* (Proteinase Inhibitor I). The values are mean ± standard error. (n = 4). Quantities are relative to the calibrator represented by mock treated plants. Statistical analysis was performed with Student's t-test (** $p < 0.01$; *** $p < 0.001$).

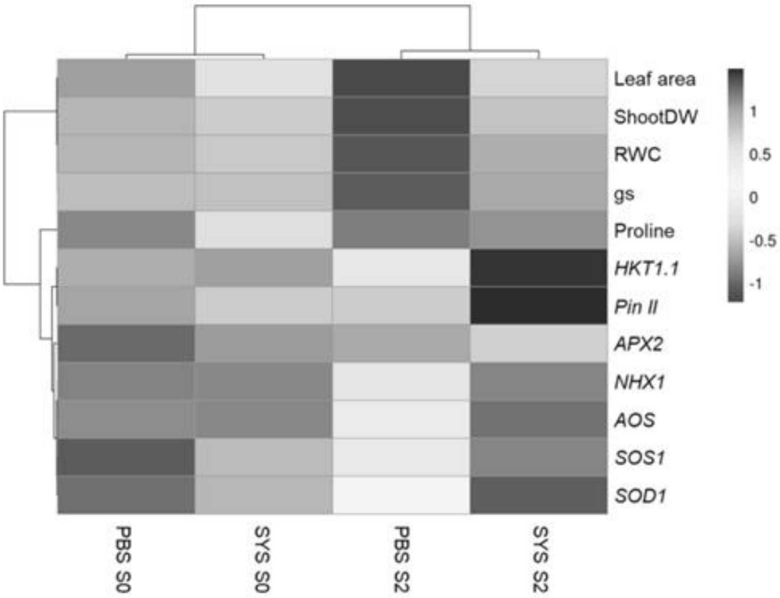

Fig. 7. Cluster heatmap showing the relations between the parameters evaluated in the study. Tomato plants were treated or not with 100 pmol L^{-1} Sys and grown under 0 and 150 mmol L^{-1} NaCl (S0 and S2, respectively). Dendrograms were built on the heatmap with Euclidean similarity and Ward linkage rule.

2017; Silletti et al., 2021). It is acknowledged that the basis of salt stress tolerance involves different molecular pathways, with a high level of crosstalk that affect plant performances (Lamaoui et al., 2018). In this experiment, tomato plants treated with Sys showed higher tolerance to salt stress, evidenced by higher biomass accumulation (Fig. 1A, B), improved stomatal functionality (Fig. 2A), and enhanced water status (Fig. 2B). These results confirm previous findings in which tomato plants constitutively accumulating Sys showed higher stomatal conductance and unchanged leaf water potential under salt stress compared to wild type (Orsini et al., 2010). Similarly, Capiati et al. (2006) showed that exogenous applications of Sys on tomato plants improved their leaf relative water content compared to untreated plants under salt stress. These results were correlated with the activation of multiple mechanisms of salt stress tolerance in plants.

4.2. Systemin triggers sodium-transporters activity in tomato

Systemin is a hormone peptide, playing a central role in the regulation of plant response against a wide range of stress agents, including wound, phytopathogenic fungi and phytophagous and sucking insects (Coppola et al., 2015; Schilmiller and Howe, 2005). Sys mediated overlapping responses to biotic and abiotic stresses have been previously documented (Capiati et al., 2006; Orsini et al., 2010). However, here we demonstrate that exogenous applications of a picomolar solution of Sys activated specific salt stress adaptation mechanisms, which are essential to cope with high salt concentrations in the root zone. Analysis of transcript expression shows that *SOS1*, a proton pump responsible for excluding sodium excess from the cytosol, *NHX1*, a vacuolar pump needed to compartmentalize sodium into the vacuole, and *HKT1.1*, a sodium/potassium transporter associated with ion fluxes in the xylem, are significantly upregulated by Sys under salt stress (Fig. 3). This indicates that Sys-treated plants showed an enhanced ability to regulate the level of sodium in the cytosol. The exclusion and compartmentalization of sodium excess via *SOS1* , *NHX* and *HKT* is a central component of plants tolerance to salt stress (Ali et al., 2021; Zhang et al., 2021). Moreover, plants treated with Sys showed a significant increase of proline content under salt stress compared to untreated plants (Fig. 4). Proline is a well-known plant stress molecule acting as signal (Ruggiero et al., 2004) and compatible solute under salinity and drought (Meena et al., 2019). Under salt stress, proline normally compensates the osmotic imbalance generated by Na^+ extrusion and/or compartmentalization at cellular level (Bartha et al., 2015; Ma et al., 2020; Shabala et al., 2010). High proline levels in Sys treated plants was consistent with an enhanced extrusion of Na^+ as indicated by the upregulation of *SOS1*, *NHX* and *HKT* transcript expression (Fig. 3A and Fig. 4). The effective role of proline in controlling cellular/tissue water homeostasis was confirmed by the higher stomatal conductance (Fig. 2A) and relative water content found in Sys treated plants (Fig. 2B).

These results indicate that Sys can simultaneously regulate ion and water homeostasis in plant leaves, which contributed to ameliorate the physiological state of the plant and overall growth performances under salt stress. The higher activity of *SOS1* triggered by Sys in absence of salt stress is of interest since it calls back some earlier thoughts on the origin of salt stress responses in plants. Cheesman et al. (2015) hypothesized that the ability to reduce the sodium content in plant tissues, via exclusion mechanisms at root level, was at the base of plant resistance to herbivores feeding. Herbivores, including insects (Xiao et al., 2010) and mammals (Batzli, 1986; Dudley et al., 2012), need sodium and, therefore, prefer plants with high level of cellular sodium compared to sodium excluder plants. Animal sodium deficiencies induce lower survival, reduced growth and slower flight speed in *Helicoverpa armigera* (Hübner) (Xiao et al., 2010). The frequent salt licking of different herbivores is a clear evidence of the importance of an adequate sodium supply in their diet, which is not only met by feeding on plants (Dudley et al., 2012). The selective pressure exerted by herbivores certainly favored sodium-excluder plants over sodium-accumulators, which represents a highly conserved mechanism in plant evolution potentially explaining the vast majority of glycophytes over halophytes in the plant kingdom (Cheeseman, 2015). Our results are in line with Cheeseman (2015) intuition: the exogenous treatment with Sys is a signal of the occurrence of an attack from an herbivore, which initiates the jasmonate pathway to activate the plant immune system, but also *SOS1*, a sodium pump able to exclude sodium from the cell, which reduces the leaf palatability for herbivores. These results can open interesting scenarios, since it is possible that engineering plants for lower cellular sodium concentration could improve their tolerance to herbivores feeding, further confirming the complexity of the ecological crosstalk among plants and the other biotic and abiotic actors of the environment.

4.3. *Systemin boosts the antioxidant machinery in tomato leaves*

ROS production is a side-effect of salt stress which impairs cell functioning due to damages on membranes, proteins, and enzymes (Liu et al., 2021; Qi et al., 2018). Plants activate a series of molecular intermediates to detoxify ROS excess and reduce the detrimental effects on sensitive cellular components (Gill and Tuteja, 2010). The first step of the ROS detoxification system is the conversion of toxic $O_2^{\cdot-}$ radicals into hydrogen peroxide carried out by superoxide dismutase (*SOD*) (Wang et al., 2016). Hydrogen peroxide is then converted to water via ascorbate peroxidase (*APX*) and catalase (*CAT*), which represent the central antioxidant components in plants. Our results show that, under unstressed conditions, *SOD1* and *APX2* are upregulated in Sys-treated plants compared to untreated plants (Fig. 5), indicating that the exogenous treatment with Sys triggers the antioxidant machinery in absence of stress, possibly enhancing and/or anticipating the protection of cellular components to oxidative stress. In addition, the increased H_2O_2 levels associated to *SOD* activity could indirectly serve as a priming signal able to 'alert' plants of ongoing, oncoming or prolonged stress (Mauch-Mani et al., 2017). ROS are produced under different stresses and actively contribute to the impairment of plant functioning and development (Qi et al., 2018). A balanced redox status in plant leaves has been previously correlated with stress tolerance in plants, since it reflects an efficient control of negative effects of ROS on cell membranes (Gill and Tuteja, 2010).

Sys is known to increase ROS and ethylene production in plants, triggering antioxidant responses (Tcherkez and Limami, 2019). This would explain the higher *SOD1* and *APX2* relative expression under control conditions (Fig. 5). This *priming* effect on the antioxidant system made plants more prone to effectively react to the subsequent salt stress, a mechanism previously shown to be effective in enhancing plants tolerance to salt stress (Omidbakhshfard et al., 2020; Rasul et al., 2021). The exogenous treatment with Sys potentiated the protection of cellular components against ROS, possibly contributing to the higher tolerance to salt stress in Sys- treated plants. Considering the direct effect of ROS on stomatal movements (Qi et al., 2018), it is possible that Sys activation of the antioxidant machinery improved stomatal conductance under salt stress, which allowed plants to maintain higher growth rates.

4.4. *Systemin inhibits protein degradation under salt stress*

A possible shared mechanisms of tolerance between biotic and salt stress is the increase of proteinase inhibitor (PIs), which was found in Sys treated plants. Sys-induced upregulation of PIs in plant tissues is mediated by jasmonate and it may represent an effective mechanism to counteract herbivore feeding, since PIs inhibit proteases produced by pests for leaf digestion and/or tissue penetration (Kim et al., 2009). The involvement of PIs into plant tolerance to different abiotic stresses, such as drought and salinity has been reported in published literature (Islam et al., 2017; Li et al., 2015). PIs are necessary to regulate the baseline protease activity for cellular homeostasis, a crucial process for plant growth and survival (Fan et al., 2020). However, different stresses, including salinity, are known to induce protease activity, , which impairs protein functioning and the whole plant fitness (Parida et al., 2004). Tobacco plants constitutively expressing PIs-related genes showed tolerance to multiple stresses, including herbivore feeding, osmotic stress and alkalinity of the media (Srinivasan et al., 2009). Balancing the stress-induced protease activity is a central mechanism that plants use to maintain efficient protein and enzyme functioning under stress.

Our results indicate that Sys induction of *Pin II* (Fig. 6) can represent a beneficial mechanism for plants to cope with salt stress, suggesting that the constitutively upregulation of PIs in plant leaves could have contributed to their higher growth performances under salt stress. Moreover, it confirms PIs as central molecular target for salt stress tolerance, identifying Sys as a potent inducer of this effective tolerance mechanism (Srinivasan and Kirti, 2012).

5. Conclusions

From the outcome of our investigation it is possible to conclude that the enhanced response of tomato plants to salt stress as induced by exogenous treatment with Sys was mediated by i) a higher ability to exclude and compartmentalize sodium excesses in plant leaves, as indicated by the upregulation of the main sodium transporters in plants (*SOS1* , *NHX1* and *HKT1.1*); ii) an improved redox status, which reduced the oxidative damages to membranes, as indicated by the combined upregulation of *SOD1* and *APX2*; iii) enhanced protein stability and functioning, as a consequence of upregulation of PIs (Fig. 8). The

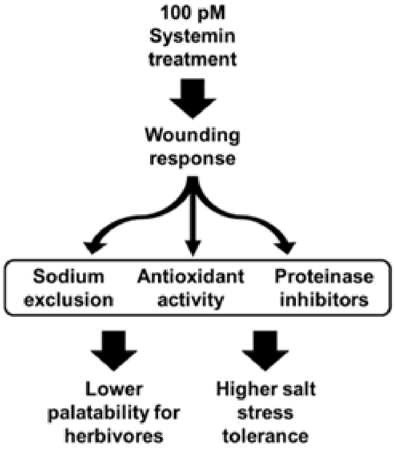

Fig. 8. Graphical representation explaining the effects of systemin treatment on tomato plants. Systemin triggers wounding responses in plants, thus inducing the activation of different mechanisms of adaptation such as sodium exclusion, increased antioxidant activity, and enhanced proteinase inhibitor synthesis. The same mechanisms of adaptation are known to be part of plant responses to salt stress, conferring tolerance thanks to i) improved cellular osmotic balance, ii) reduced ROS damages, and iii) improved protein functionality and stability. These results indicate the existence of a tight crosstalk between abiotic and biotic stress responses.

multiple activity mediated by Sys treatment increased plant growth and its physiological state and provided evidence of a crosstalk between the mechanisms of tolerance to biotic and abiotic stresses in plants. Overall Sys can be identified as a peptide able to enhance plant responses to multiple stresses via shared tolerance mechanisms. From an applied perspective these data provide a scientific basis to isolate and/or design effective biomolecules for crop protection against both biotic and abiotic stresses, which represents one of the main goals for the future food production.

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CRediT authorship contribution statement

Cirillo Valerio: Investigation, Methodology, Data curation, Visualization, Writing – original draft, Writing – review & editing. **Molisso Donata:** Investigation, Methodology, Writing – original draft, Writing – review & editing. **Aprile Anna Maria:** Investigation, Methodology. **Maggio Albino:** Conceptualization, Supervision Writing – review & editing, Funding acquisition. **Rao Rosa:** Conceptualization, Supervision, Writing – review & editing, Funding acquisition.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.envexpbot.2022.104865.

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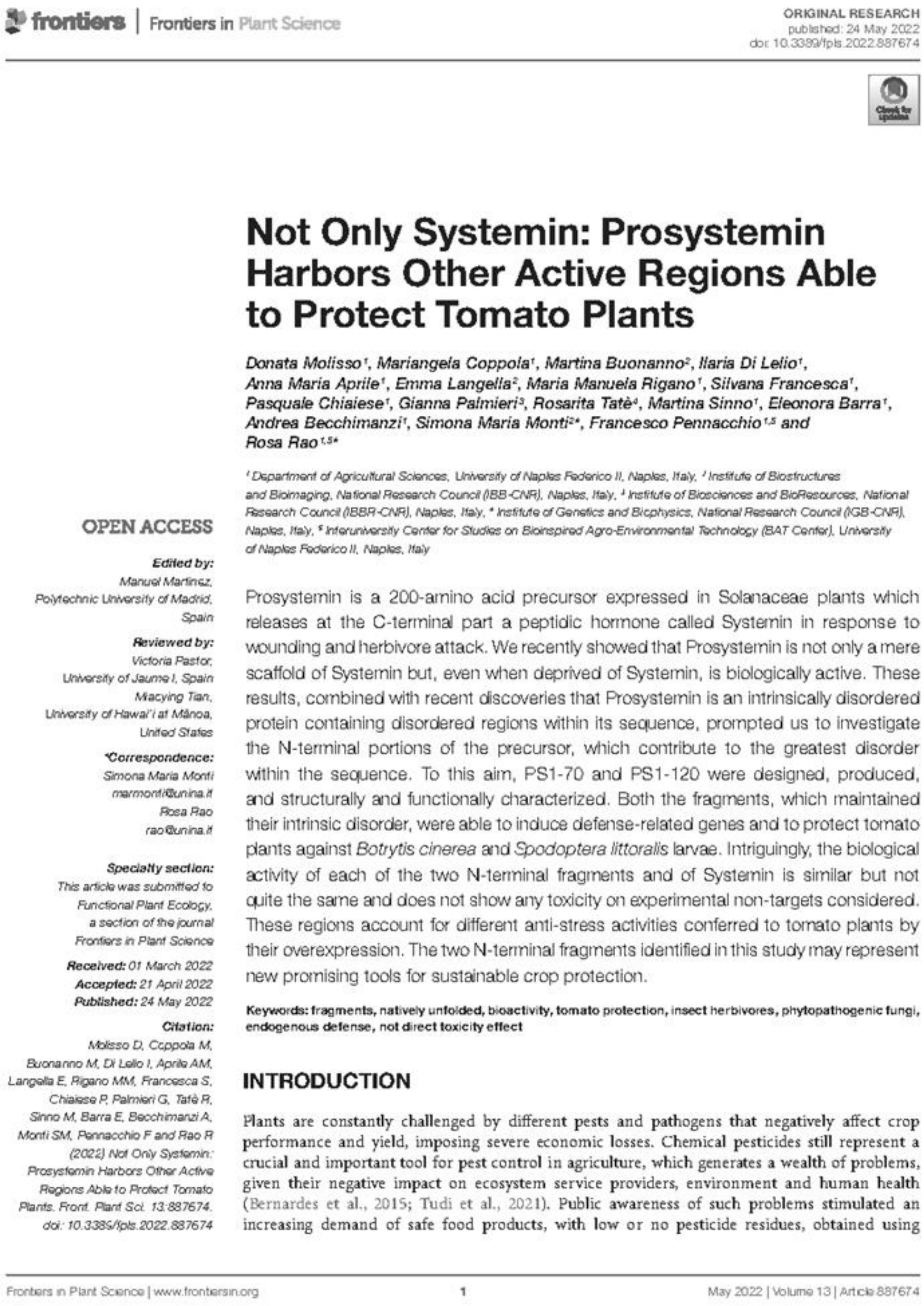

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Not Only Systemin: Prosystemin Harbors Other Active Regions Able to Protect Tomato Plants

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Prosystemin is a 200-amino acid precursor expressed in Solanaceae plants which releases at the C-terminal part a peptidic hormone called Systemin in response to wounding and herbivore attack. We recently showed that Prosystemin is not only a mere scaffold of Systemin but, even when deprived of Systemin, is biologically active. These results, combined with recent discoveries that Prosystemin is an intrinsically disordered protein containing disordered regions within its sequence, prompted us to investigate the N-terminal portions of the precursor, which contribute to the greatest disorder within the sequence. To this aim, PS1-70 and PS1-120 were designed, produced, and structurally and functionally characterized. Both the fragments, which maintained their intrinsic disorder, were able to induce defense-related genes and to protect tomato plants against *Botrytis cinerea* and *Spodoptera littoralis* larvae. Intriguingly, the biological activity of each of the two N-terminal fragments and of Systemin is similar but not quite the same and does not show any toxicity on experimental non-targets considered. These regions account for different anti-stress activities conferred to tomato plants by their overexpression. The two N-terminal fragments identified in this study may represent new promising tools for sustainable crop protection.

Keywords: fragments, natively unfolded, bioactivity, tomato protection, insect herbivores, phytopathogenic fungi, endogenous defense, not direct toxicity effect

INTRODUCTION

Plants are constantly challenged by different pests and pathogens that negatively affect crop performance and yield, imposing severe economic losses. Chemical pesticides still represent a crucial and important tool for pest control in agriculture, which generates a wealth of problems, given their negative impact on ecosystem service providers, environment and human health (Bernardes et al., 2015; Tudi et al., 2021). Public awareness of such problems stimulated an increasing demand of safe food products, with low or no pesticide residues, obtained using ecologically sustainable production management (Zikankuba et al., 2019; Gomes et al., 2020). To further promote this process, and, more generally, a one-health vision underlying a sustainable management strategy of our planet, the United Nations declared 2020 as the International Year of Plant Health[1].

Considerable efforts are currently being devoted to the development of new tools and strategies for sustainable pest control. A special attention has been given to the use of natural antagonism and of regulating molecules and genes that mediate pest suppression mechanisms shaped by long-term co-evolutionary processes, driven by the continuous contrast between immune defense barriers and virulence strategies (Gupta and Dikshit, 2010; Pennacchio et al., 2012; Coppola et al., 2019; Hay et al., 2020; Basaid et al., 2021). This approach represents a further development of biological control which goes beyond the organism level and exploits all types of natural antagonism.

In this context, a wealth of information on plant-pest/pathogen interactions is becoming increasingly available, offering new opportunities for plant protection. The first line of inducible plant defense is triggered by the detection of non-self molecules which are called pathogen/herbivore-associated molecular patterns (PAMPs, HAMPs). PAMPs and HAMPs activate the so-called pattern-triggered immunity (PTI) (Bigeard et al., 2015; Abdul Malik et al., 2020). Plant perception of these highly conserved molecules is mediated by plasma membrane-localized pattern recognition receptors (PRRs), that initiate the PRRs-mediated immune responses triggering a complex cascade of signaling events including depolarization of cellular membrane, rapid transient fluctuations in the concentration of intracellular calcium ions, production of reactive oxygen species (ROS), activation of mitogen-activated protein kinases (MAPKs) and extensive transcriptomic and metabolomic reprogramming (Bigeard et al., 2015; Trapet et al., 2015). The amplification of immune signals rapidly after the PAMPs/HAMPs perception is a key-event to efficiently counteract pest invasion and it is mediated by plant sensitivity to some host derived molecules, named damage-associated molecular patterns (DAMPs), and partially overlapping PTI signaling components (Lotze et al., 2007; Boller and Felix, 2009). DAMPs include mainly cell wall protein or polysaccharide fragments, peptides, amino acids, and nucleotides (Boller and Felix, 2009; Henry et al., 2012; Thakur and Sohal, 2013) released from the damaged tissues following pest invasion. Exogenous treatment of plants with DAMPs activates a wide range of defense responses, including the production of ROS and the expression of defense-related genes (Hou et al., 2019). A well characterized class of plant DAMPs are peptides released from precursor proteins (Choi and Klessig, 2016). These include a family of small defense-related peptide hormones called systemins, that are released from larger precursors by plants of *Solanaceae* family in response to wounding and herbivore attack (Pearce et al., 1991; Ryan and Pearce, 2003).

Tomato Systemin (Sys) is a small peptide consisting of 18 residues released from the C-terminal region of a 200 amino acid precursor protein called Prosystemin (ProSys) (Beloshistov et al., 2018). *ProSys* gene is transcribed at very low level in unchallenged plants, while its expression greatly increases in response to mechanical wounding or insect herbivore attack (McGurl et al., 1994; Ryan, 2000). The role of ProSys in plant defense against wounding and biotic damages was clearly demonstrated through the analysis of transgenic tomato plants expressing the *ProSys* gene. Indeed, the constitutive production of ProSys resulted in an increased plant resistance to several biotic stress agents due to a wide transcriptomic reprogramming that included the up-regulation of an array of defense-related genes involved in both direct and indirect defenses (McGurl et al., 1994; Ryan, 2000; Diaz et al., 2002; Corrado et al., 2007; Degenhardt et al., 2010; El Oirdi et al., 2011; Coppola et al., 2015). In addition, it was observed that transgenic plants tolerate moderate salinity stress (Orsini et al., 2010), virus spread (Bubici et al., 2017) and, more recent evidence indicate a reduction of nematode colonization (Martínez-Medina et al., 2021).

The mechanisms that underpin the wide array of activated defense barriers are not fully understood and appear to be in part linked to the structure of the protein precursor. A detailed biophysical and biochemical characterization of ProSys revealed that the precursor is a member of the Intrinsically Disordered Protein (IDP) family (Buonanno et al., 2018), containing Intrinsically Disordered Regions (IDRs) within its sequence. IDPs are highly flexible proteins lacking a stable or ordered three-dimensional structure. It has been demonstrated that IDPs have crucial roles in cellular processes by conferring functional advantages in stress response, signaling and regulation (Sun et al., 2013; Uversky, 2013). The structural flexibility allows them to assume alternative conformations which, according to specific conditions, prompt their transient, but specific, interactions with multiple molecular partners (Uversky, 2013; Wright and Dyson, 2015; Covarrubias et al., 2017). It is then possible that different regions of the precursor interact with different partners activating concurrent defense signals. Consistent with this, we previously demonstrated that the expression in tobacco plants of a truncated ProSys gene, lacking the exon encoding Sys, altered the proteomic profile and increased plant resistance against *Botrytis cinerea* (Corrado et al., 2016). Recently, effects on tomato defense of either transgenic tomato plants expressing a truncated ProSys gene or tomato plants treated with recombinant truncated Prosys$_{(1-178)}$ (devoided of Sys sequence) were investigated (Molisso et al., 2022). In both cases it was observed a clear modulation of the expression of genes linked with defense responses which resulted in protection against the lepidopteran pest *Spodoptera littoralis* and the fungus *Botrytis cinerea*. In order to further identify the regions of ProSys scaffold which confer biological activity, we designed and produced two different recombinant ProSys fragments starting from the N-terminal part of the protein, namely PS1-70 and PS 1-120, which contributed to the greatest content of disorder. These two fragments were structurally and functionally characterized. We demonstrated that both fragments, which maintained the intrinsic disorder of the precursor, induce defense-related genes and protect tomato plants against *Botrytis cinerea* and *Spodoptera littoralis* larvae. Intriguingly, the biological activity of each of the two fragments and of Sys was similar but not quite the same with each

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[1] https://www.fao.org/plant-health-2020/about/en/

other and with the Sys peptide used as comparison. We also monitored the direct toxic effect of these two fragments against two different cellular cultures: a photosynthetic microorganism *Chlamydomonas reinhardtii* and a human keratinocyte HaCaT cells line. As expected PS1-70 and PS1-120 did not show any toxicity on experimental non-targets considered making them novel and interesting tools to be used for crop protection. Taken together, our results confirm previous hypothesis that ProSys is not only a mere scaffold of Sys but contains multiple biologically active sequences, different from the well-known Sys peptide, which have been here identified and characterized.

MATERIALS AND METHODS

Plant Material and Growth Condition

Tomato seeds (*Solanum lycopersicum* L. cultivar "Dwarf San Marzano") were surface sterilized with 70% ethanol for 2 min, rinsed, washed with 2% sodium hypochlorite for 10 min and rinsed five times with sterile distilled water. Seeds were germinated in Petri dishes on wet sterile paper and placed in a growth chamber at 24 ± 1°C and 60 ± 5% of relative humidity (RH) in darkness. Upon roots emergence, plantlets were transferred to a polystyrene plateau with barren substrate S-type (Floragard, Oldenburg, Germany) in a growth chamber at 26 ± 1°C and 60 ± 5% RH, with 18:6 h light/dark photoperiod, at a brightness of 5,000 lux. After 2 weeks, plants were transferred to sterile soil mixture in pots of diameter of 9 cm and grown using the same growth conditions.

Molecular Cloning, Expression, and Purification of ProSys Fragments

Two DNA fragments, PS1-70 and PS1-120, were amplified from the full-length ProSys cDNA, using the primers reported in **Supplementary Table 1** and as described by Buonanno et al. (2018); PCR-fragments were cloned in pETM11 vector (a kind gift from EMBL, Heidelberg) using *Nco*I- *Xho*I restriction sites. The generated plasmids were checked by appropriate digestion with restriction enzymes and nucleotide sequencing. Optimized expression of the recombinant ProSys fragments was obtained in *E. coli* BL21(DE3) cells in different selective media: LB (Luria-Bertani) for PS1-70 and 2-YT (Yeast extract-Tryptone) for PS1-120. Large-scale production was carried out inducing with 2 mM IPTG (Isopropyl β-D-1-thiogalactopyranoside) for 16 h at 22°C. Cells were harvested by centrifugation (20 min at 6,000 *g* at 4°C) and resuspended in lysis buffer [20 mM Tris–HCl, 20 mM imidazole, 50 mM NaCl, 1 mM dithiothreitol (DTT), pH 8.0] in presence of 0.1 mM phenylmethanesulfonylfluoride (PMSF), 5 μg/ml DNaseI, 0.1 mg/ml lysozyme and 1X protease inhibitors (Sigma-Aldrich, Milan, Italy). Cells were disrupted by sonication on ice and after centrifugation (30 min at 30,000 *g* at 4°C) the supernatant of each ProSys fragment was purified by an ÄKTA FPLC, on a 1 ml HisTrap FF column (GE Healthcare, Milan, Italy), according to manufacturer's instruction (GE Healthcare Milan, Italy). After elution, ProSys fragments were dialyzed in 20 mM Tris–HCl, 50 mM NaCl, 100 mM PMSF, 1 mM DTT, pH 8.0 and purified by size exclusion chromatography (SEC) on a Superdex 75 10/300 HP (GE Healthcare Milan, Italy), in PBS 1X (Phosphate buffer saline, 10 mM phosphates, 140 mM NaCl, 2.7 mM KCl, pH 7.4, Sigma-Aldrich St. Louis, MO, United States), 100 μM PMSF, 1 mM DTT pH 8.0. Calibration was carried out using the following standards (Sigma Aldrich, St. Louis, MO, United States): horse cytochrome c (Cit c, 12.4 kDa), chicken ovalbumin (Ova, 45 kDa), bovine serum albumin (BSA 66 kDa), carbonic anhydrase from bovine erythrocytes (CA, 29 kDa), recombinant carbonic anhydrase XIV (CA XIV, 37 kDa, homemade) and the full-length Prosystemin (ProSys, 26 kDa, homemade). The purity level of the recombinant fragments was assessed by SDS-PAGE on a 15% gel using Biorad Precision Plus Protein All Blue Standards (10–250 kDa) as molecular mass marker. LC-ESI-MS analysis of the protein, performed as previously described (Buonanno et al., 2018; Langella et al., 2018) confirmed their identities.

Light-Scattering Analysis

Light scattering analysis of PS1-70 and PS1-120 was performed as previously described in Alterio et al. (2019) by combining SEC with MALS-QELS (MultiAngle Ligh Scattering-Quasi-Elastic Light Scattering) detectors equipment. Experiments were run at 0.5 ml/min PBS 1X, 100 μM PMSF, 1 mM DTT, pH 8.0 on a Biosep-SEC-s2000 column (Phenomenex, Torrance, CA, United States) linked to an ÄKTA FPLC coupled to a light scattering detector (mini-DAWN TREO, Wyatt Technology) and to a refractive index detector (Shodex RI-101). All data collected were processed using the ASTRA 5.3.4.14 software (Wyatt Technologies Corporation).

Circular Dichroism Spectroscopy

Measurements were performed on a Jasco J-715 (Easton, MD, United States) spectropolarimeter equipped with a Peltier temperature control system (Model PTC-423-S), using a Hellma quartz cell of 0.1-cm-path length in the far-UV from 190 to 260 nm (20 nm/min scan speed). Circular dichroism (CD) spectra, collected as previously described (D'Agostino et al., 2019) were signal averaged over at least three scans, and the baseline was corrected by subtracting the buffer spectrum. Spectra were recorded at 20°C in 10 mM sodium phosphate buffer pH 7.4 at fragments concentrations for PS1-70 and PS1-120 of 4.4 and 3.5 μM, respectively. The same parameters were applied for measurements in the temperature range of 10–80°C. Spectra were collected every 10°C. Molar ellipticity values, recorded at 222 nm for both experiments were plotted as function of the temperature using GraphPad Prism version 6.01 (GraphPad software; San Diego, California, United States).

Titration with increasing concentration of trifluoroethanol (from 0% up to 25%TFE), measurements were performed at 20°C for fragment concentration of 5.15 and 3.5 μM, for PS1-70 and PS1-120, respectively. DICHROWEB[2] (Whitmore and Wallace, 2004) was used to analyze data. CDSSTR was used as a deconvolution method (Whitmore and Wallace, 2008) to evaluate the percentage of α-helical content of the ProSys fragments.

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[2] http://dichroweb.cryst.bbk.ac.uk/html/home.shtml

Sequence Analysis

The primary sequence of PS1-70 and PS1-120 was analyzed using Composition Profiler tool[3] (Vacic et al., 2007). The query samples were compared with the reference value of the average amino acid frequencies of the Swiss-Prot database[4] (Vacic et al., 2007). Composition analysis was carried out using the relation (CPX −CSX)/CSX, where CPX means the content of an amino acid X within the protein of interest, whereas CSX is the typical composition of X in Swiss-Prot proteins. In the final output, the less abundant amino acids are represented with negative values, whereas those more abundant with positive values.

Plant Treatments and Gene Expression Analysis

Healthy and fully expanded leaves of four-week-old plants were treated with 100 fM purified recombinant fragments. In particular, 15 spots of 2 µl of 100 fM PS1-70 or PS1-120 were gently placed on the adaxial surface of the intact leaves. A similar treatment was done with Sys obtained as previously described (Coppola et al., 2019), while a mock treatment with PBS was used as control. Leaf samples were collected 6 hpt for bioassays and molecular analyses, unless otherwise indicated.

Bioassays

Spodoptera littoralis Bioassay

Spodoptera littoralis larvae (Lepidoptera, Noctuidae) were reared on artificial diet at 25 ± 1°C and 70 ± 5% RH, with 16:8 h light-dark photoperiod as previously described (Di Lelio et al., 2014). Newborn larvae were allowed to grow on this artificial diet until they attained the 2nd instar. Then, newly molted 3rd instar larvae were selected, weighted and singly isolated in 4-wells plastic rearing trays (RT32W, Frontier Agricultural Sciences, Pitman, NJ, United States). In each well, 3 ml of 1.5% agar-agar (w/v) were dispensed, in order to keep tomato leaves turgid, in a moist environment, and the rearing wells were closed with perforated plastic lids (RTCV4, Frontier Agricultural Sciences, Pitman, NJ, United State). In order to select the most appropriate concentration of Sys, PS1-70 and PS1-120 on the survival rate of larvae alimented with treated leaves we compared 100 pM and 100 fM concentrations in a preliminary assay. For each treatment, 32 larvae were fed with leaf disks of tomato plant. The experimental larvae were maintained at the rearing condition described above. Larvae were weighted every 2 days and mortality was daily checked until pupation.

Larval Toxicity Assay

The larvicidal assays were carried out on 4th instars, following topical exposure or oral ingestion, as reported elsewhere (Pavela, 2010), using a range of three experimental doses (100 nM, 100 pM and 100 fM); for each dose, 16 *S. littoralis* larvae were treated. Briefly, for topical application the larvae were anesthetized on ice an directly treated with the solution containing the ProSys fragments through the direct application of 1 µl of the solution containing the ProSys fragments on the neck membrane, using a Gilson pipette P10 (PIPETMAN classic P10), while for oral ingestion 1 µl of experimental solutions was poured into the foregut lumen of the anesthetized larvae by means of a Hamilton Microliter syringe (1701RNR 10 ll, gauge 26s, length 55 mm, needle 3). Control larvae were identically treated with PBS 1X buffer.

After the treatments, the larvae were singly separated into polystyrene rearing trays, provided with food and kept at the rearing conditions reported above. Larval mortality was recorded until pupation, which took place into plastic boxes containing vermiculite (25 cm × 10 cm × 15 cm).

Botrytis cinerea Bioassay

Botrytis cinerea spores were cultivated on MEP (Mannitol Egg yolk Polymyxin) solid medium at 22°C. Spores were collected by washing the agar surface with sterile distilled water containing 0.1% Tween 20, filtered through sterile Kimwipes (Kimberly-Clark Dallas, Texas, United States), to remove fragments of hyphae, and adjusted to a concentration of 1×10^6 conidia/ml. Ten µl drops of spore suspension were put on tomato leaves, 6 hpt with 100 fM ProSys fragments, using 10 different inoculation points per detached leaf. The assay was carried out using for each compound leaves from 5 different plants. Detached leaves were placed on sponges soaked in sterile water and incubated in a growth chamber at 23°C, under 16:8 h light/dark photoperiod and 90% ± 5% RH. The size of the lesions was measured at 1, 3, 5, and 8 days after infection using a digital caliper.

In vitro Antifungal Assay

The antifungal assay was carried out as already reported (Pastor-Fernández et al., 2020; Molisso et al., 2021). A sterile 12-well plate was filled with potato dextrose broth (PDB 1/2) medium, containing ProSys fragments at the final concentration of 100 fM. A solution with *B. cinerea* spores was added to each well, in order to reach a final concentration of 10^4 spores/ml, then the plate was placed in a shaker and incubated for 24 h at 25 ± 1°C. To assess the fungal growth, the value of optical density (OD) at a wavelength of 600 nm (OD_{600}) was measured in triplicate on a BioPhotometer Spectrophotometer UV/VIS (Eppendorf, Hamburg, Germany).

Gene Expression Analysis

Total RNA extraction, synthesis of the first strand cDNA and Real Time-PCRs (RT-PCR) were carried out according to standard procedure, as already published (Corrado et al., 2012). RT-PCR was performed using Rotor Gene 6000 (Corbett Research; Sydney, Australia). Gene expression analysis was carried out using two technical replicates for each of the three biological replicates per samples. The housekeeping *EF-1α* gene was the endogenous reference gene used for the normalization of the expression levels of the target genes (Marum et al., 2012; Müller et al., 2015). Relative quantification of gene expression was carried out using the $2^{-\Delta\Delta Ct}$ method (Livak and Schmittgen, 2001). Primers and their main features are described in **Supplementary Table 2**.

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[3] http://www.cprofiler.org/

[4] http://us.expasy.org/sprot

Hydrogen Peroxide and Malondialdehyde Determination

Quantification of H_2O_2 content was carried out by using a colorimetric method (Sergiev et al., 1997). Briefly, 0.1 g of frozen powder from tomato leaves were extracted with 1 ml of ice-cold 0.1% trichloroacetic acid (TCA) and the mixture was then incubated for 15 min on ice and centrifuged at 10,000 rpm for 15 min at 4°C. Subsequently, 500 μl phosphate buffer (pH 7.0) and 1 ml of potassium iodide 1 M were added to 500 μl of supernatant. The mixture was then incubated in the dark for 40 min and measured at 525 nm, using a Nano Photometer TM (Implen, Munich, Germany). Three separate biological replicates for each sample and three technical assays for each biological replicate were measured. The concentration was expressed in $mmol^{-1}$g FW (Fresh Weight).

The malondialdehyde (MDA) levels in leaf tissues indicate the levels of membrane lipid peroxidation. For the determination of MDA, 0.2 g of leaf sample was ground after adding 1 ml of ice cold 0.1% trichloroacetic acid (TCA). The samples were incubated for 15 min on ice and centrifuged at 10,000 rpm for 10 min at 4°C. Subsequently, 250 μl of the supernatant was mixed with 1,250 μl reaction solution (TCA 20% + 2-thiobarbituric acid (TBA) 0.5%), water-bathed for 30 min at 95°C and measured at 532 and 600 nm using a Nano Photometer TM (Implen, Munich, Germany). Three separated biological replicates for each sample and three technical assays for each biological replicate were measured. The concentration was expressed as quantity of MDA-TBA complex (Zhang and Kirkham, 1996).

Toxicity Bioassays of Protein Fragments on Microalgae and on Human Keratinocyte

Cultures of *Chlamydomonas reinhardtii* were axenically grown under phototrophic conditions, in a mineral nutrient solution (MNS) at 24 ± 1°C, with a rotatory agitation at 100 rpm with a 16:8 h light/dark photoperiod, at 100 E m^{-2} s^{-1} (Bischoff, 1963; Chiaiese et al., 2011). The cultures were weekly maintained by inoculation of 500 μl of culture in 50 ml of MNS medium.

The growth inhibition assay was assessed following (Lewis, 1994) and (OECD, 2011) procedures with some modification. A replicated design was applied by exposing microalgae at three different concentrations of ProSys fragments; 0.0001, 0.1 and 1 nM in 24 well plate and incubated for 7 days. Microalgae incubated in the growth medium without ProSys fragments were used as control. Cell density was determined every 24 h by direct counting under a Leica DMR optical microscope (Leica Imaging Systems, Cambridge, United Kingdom).

The growth rates (μ) and percentages of growth inhibition (%I) at 96 h were calculated using the following equations:

$$\mu = \frac{lnN_2 - lnN_1}{t_2 - t_1}$$

where N_2 and N_1 are the cell density at times t_2 and t_1

$$\%I = \frac{\mu_c - \mu_i}{\mu_c}$$

where c is the specific growth rate in the control group and μ_i is the specific growth rate in each treatment. The data were expressed as means and standard deviation for three replicate cultures.

Cell Culture and Maintenance

The human keratinocyte HaCaT cells line was obtained from the American type culture collection (CRC 1424; Virginia, MD, United States). HaCaT cells were incubated in Dulbecco's modified eagle's medium containing 10% heat-inactivated fetal calf serum, 1,000 U/ml penicillin and 100 mg/ml streptomycin at 37°C in a humidified atmosphere incubator containing 5% CO_2.

Cell Viability and Morphology Studies

To assess cell viability, cell counting Kit-8 (CCK-8 assay, ab228554; Abcam, Cambridge, MA, United States) assay and manual cell count were performed. The CCK-8 was a sensitive colorimetric assay for quantization of viable cell number in proliferation and cytotoxicity assays. The experiments were performed in cells by using the protocols recommended by the manufacturer. In brief, 70% confluent cultured flasks, containing 5 × 10^3 cells/100 μl, were plated at 2 × 10^4/ml per well into 24-well and the plates were incubated overnight at 37°C to allow cells to adhere to the bottom of wells. Then, cells were washed with PBS and exposed to PS-70 or PS1-120 fragments. Specifically, the ProSys fragments were suspended in DMEM medium and added to the cells at a final concentration of 100 nM. Non-treated cells were included as negative controls. After 24 h of incubation, Kit-8 reagent was added to each well, and the plate was further incubated at 37°C for 3 h. The absorbance at 450 nm was then recorded by a microplate reader. The cell viability was determined as follows: cell viability (%) = $[(OD_{experiment} - OD_{blank})/(OD_{negative\ control} - OD_{blank})] \times 100\%$, where $OD_{experiment}$ is the absorbance of a well with a treated cell and CCK-8; OD_{blank} is the absorbance of a well with medium and CCK-8 but without cells; and $OD_{negative}$ control is the absorbance of a well with untreated cells and CCK-8. For manual counts 50 μl of sample was mixed with 50 μl of 0.4% trypan blue by gently pipetting, and then 20 μl of the mix were loaded into each chamber of the hemocytometer. Counts were performed in triplicate by one analyst under a 20 × objective according to the standard methodology.

Afterward, the cells, untreated or treated with each fragment, were washed, fixed with paraformaldeide 4% and visualized by phase-contrast microscopy, using the DMI6000B inverted fully automated microscope with DFC 420 RGB camera (Leica Microsystems, Wetzlar, Germany). Leica LAS V5.4 software was utilized for image acquisition/elaboration (contrast/gamma adjusting). All analyses were performed in triplicate on three independent *in vitro* experiments.

Statistical Analysis

Differences in survival rate were compared by using Kaplan–Meier and log-rank analysis.

One-Way ANOVA test, followed by the Tukey's *post hoc* multiple comparison test ($P < 0.05$), was used to evaluate: the differences in larval weights and in necrosis diameter development, the effect of ProSys fragments on *B. cinerea* growth and infection, the differences in relative quantities of transcripts abundance, and the quantification of the amount of H_2O_2 and MDA levels. For the evaluation of ProSys fragments effect on microalgal growth, the statistical analysis was performed by One Way ANOVA coupled with Dunnet test. HaCaT cell viability assay was performed in triplicate on three independent sets of experiments. OD_{450} values were compared by using Student's *t*-test ($P < 0.05$). Data were analyzed using GraphPad Prism version 6.01 (GraphPad software; San Diego, California, United States).

RESULTS

Design, Production, and Characterization of PS1-70 and PS1-120 Fragments

Based on the structural characterization of ProSys (Buonanno et al., 2018), we produced two fragments designed from the N-terminal part of the protein (**Figure 1A**), hereafter referred as PS1-70 and PS1-120, which were expressed and purified. PS1-70 and PS1-120 were designed based on our previous bioinformatic analyses carried out on the full-length ProSys protein by means of structure and disorder predictions (Buonanno et al., 2018). According to this data, ProSys was defined as an IDP, being characterized by the presence of both structured and long disordered regions. In details, PS1-70, which encompasses the first 70 residues starting from the N-terminal portion of the precursor, was predicted to be the most disordered fragment; on the contrary, PS1-120 which included 50 more residues encompassing the central part of the protein, was predicted to contain some secondary structure elements (**Figure 1A**). The rationale behind the design of the two constructs aimed to disclose potential structure-function relationships for these protein regions, which did not contain Sys peptide to avoid any overlapping biological effect with confounding effects.

Highly purified PS1-70 and PS1-120 were obtained following a two-step procedure with a final yield of about 2 mg/l of growth medium. The identity of the purified fragments (inclusive of the His-tag) was confirmed by LC-ESI-MS (**Figures 1B,C**). Similarly to ProSys, the recombinant fragments eluted from the SEC column with an anomalous retention volume, indicative of an apparent molecular mass (MM_{app}) of 28.4 and 48.0 kDa, respectively, as estimated by the calibration curve (**Supplementary Figure 1**). Light scattering experiments confirmed that PS1-70 and PS1-120 are present in solution as monomers of about 9.36 ± 0.60 and 19.98 ± 1.50 g/mol, respectively, in full agreement with the MM_{theo} (**Supplementary Figure 2**) and with the solution behavior of ProSys. Indeed, the high presence of disorder-promoting residues, compared to the order-promoting ones (**Supplementary Figure 3**; Dunker et al., 2001; Radivojac et al., 2007; Midic and Obradovic, 2012; Uversky et al., 2013), conferred disordered features to PS1-70 and PS1-120.

Conformational Features of PS1-70 and PS1-120 and Temperature Effects

The secondary structure of PS1-70 and PS1-120 was investigated by means of far-UV CD spectroscopy which measures the

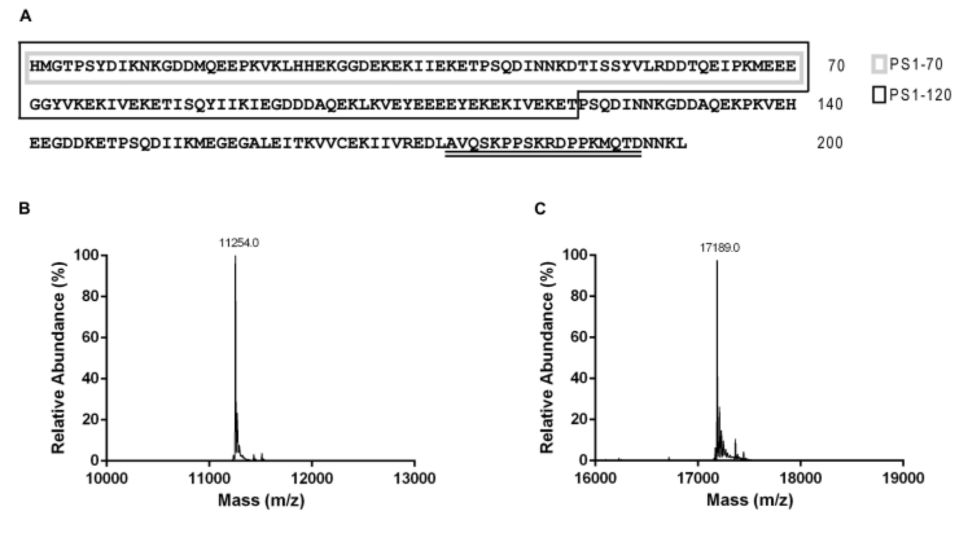

FIGURE 1 | Primary sequences of ProSys and its fragments PS1-70 and PS1-120 and LC-ESI-MS analysis of the two fragments. **(A)** ProSys primary sequence: PS1-70 and PS1-120 sequences are indicated by a gray and a black box, respectively; Systemin sequence is double underlined. Deconvoluted mass spectrum of purified **(B)** PS1-70 and **(C)** PS1-120.

differential absorption of left- and right-circularly polarized light by chiral molecules. At these wavelengths the peptide bond contributions dominate, and the secondary structure give rise to a characteristic shape and magnitude of CD spectrum (Sreerama and Woody, 2004). In particular, a CD spectrum with a low ellipticity at 190 nm and a large negative ellipticity at 198 nm (**Figures 2A,B**) is typical of disordered proteins, confirming that, in agreement with previous investigations (Buonanno et al., 2018), also these two fragments have largely disordered conformation. The propensity of PS1-70 and PS1-120 to fold in water/trifluoroethanol (TFE) mixtures was evaluated, recording CD spectra at increased concentration of the co-solvent. The fragments behaved differently in presence of TFE. PS1-70 showed small differences in the CD spectra (**Figure 2C**), whereas PS1-120 displayed an increased α-helical content, as indicated by the positive maximum at near 190 nm and negative minima at 208 and 222 nm (**Figure 2D**).

Finally, PS1-70 and PS1-120 underwent modest temperature-induced changes, as already observed for the precursor. In fact, as the temperature increased to 80°C, only a small gain in secondary structures was observed (**Supplementary Figure 4**).

Impact of PS1-70 and PS1-120 on Pests

The results of the preliminary assay indicated that the most effective concentration of Sys, PS1-70 and PS1-120 in reducing larvae survival rate was the lowest (100 fM) (**Supplementary Figure 5**). Consequently, we used this concentration for all the other experiments. **Supplementary Table 3** and **Figure 3** showed the results observed for larvae fed with leaves treated with 100 fM Sys, PS1-70 and PS1-120: a very strong reduction of their weight and survival rates was registered in comparison with controls. The three experimental protein fragments showed a significant impact on larval survival [Log-rank (Mantel-Cox) test: $\chi^2 = 110.8$, dF = 3, $P < 0.0001$)], with PS1-70 treated leaf disks exerting a significantly stronger negative effect than leaves treated with Sys (Log-rank test: $\chi^2 = 9.593$, df = 1, $P < 0.002$) or with PS1-120 (Log-rank test: $\chi^2 = 13.18$, df = 1, $P = 0.0003$), which

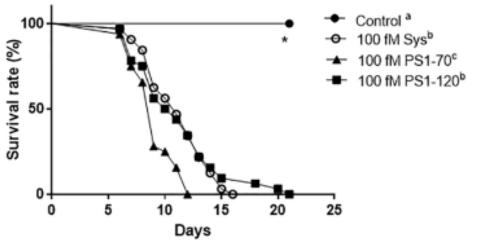

FIGURE 3 | Effect of 100 fM Sys, PS1-70 and PS1-120 on *S. littoralis* larvae. Survival rate of experimental *S. littoralis* larvae. Different letters denote significant differences in the survival curve (Log-Rank test, $P < 0.0001$).

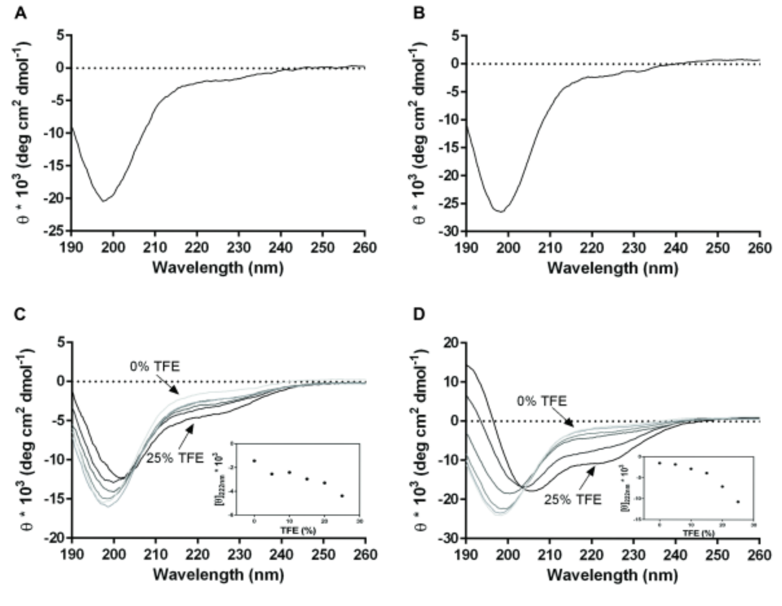

FIGURE 2 | CD spectra of PS1-70 and PS1-120 and TFE titration. Far-UV CD spectra of **(A)** PS1-70 and **(B)** PS1-120. CD spectra overlapping of **(C)** PS1-70 and **(D)** PS1-120 recorded at increasing concentrations of TFE (0, 5, 10, 15 20, and 25%). Changes in molar ellipticity at 222 nm, as a function of TFE percentage are shown in the inset for both fragments. Spectra were acquired at 20°C in 10 mM phosphate buffer, pH 7.4.

did not differ between them (Log-rank test: $\chi^2 = 144$, df = 1, $P = 0.7356$) (**Figure 3**).

No direct toxicity effect of PS1-70, PS1-120 and Sys on 4th larval instar of *S. littoralis* was observed as indicated in **Supplementary Table 4**. Both topical and oral applications, at different concentrations, had no larvicidal effect; all experimental larvae exhibited similar developmental patterns.

Similarly, PS1-70 and PS1-120 were compared to Sys for the ability to control *B. cinerea* leaf colonization. Leaves treated with Sys, PS1-70 and PS1-120 showed a strong reduction of the leaf damages produced by the fungus already 1 day post-inoculum, and this difference increased over time, as shown in **Figures 4A,B**

In order to evaluate whether the reduction of *B. cinerea* necrosis area was due to a direct effect of fragments on the fungus, an *in vitro* assay was carried out. No impact of the tested fragments on fungus vitality was observed as shown in **Supplementary Figure 6**.

Hydrogen Peroxide and Lipid Peroxidation Content in Tomato Leaves After ProSys Fragments Application

We further investigated the effect of Sys, PS1-70 and PS1-120 fragments treatments on oxidative status in tomato plants after 1, 6, and 24 hours post treatment (hpt). As observed in **Figure 5A**, H_2O_2 content in Sys treated leaves was significantly higher than in untreated control at every time point, reaching its maximum level after 6 hpt [Tukey test, $F(3.23) = 63.36$; $P < 0.0001$]. Conversely, a different profile was observed for H_2O_2 content in PS1-70 and PS1-120 treated leaves. The former produced a significant increase of the ROS species only 6 hpt, while the latter did not affect H_2O_2 content. Coherently with these observed values, lipid peroxidation, determined by MDA content, showed no differences between PS1-120 treated plants and control, while a significant increase of MDA was observed in Sys and PS1-70 treated plants 6 hpt compared to controls (**Figure 5B**). In addition, in Sys treated leaves the lipid peroxidation showed a further increase at 24 hpt (**Figure 5B**).

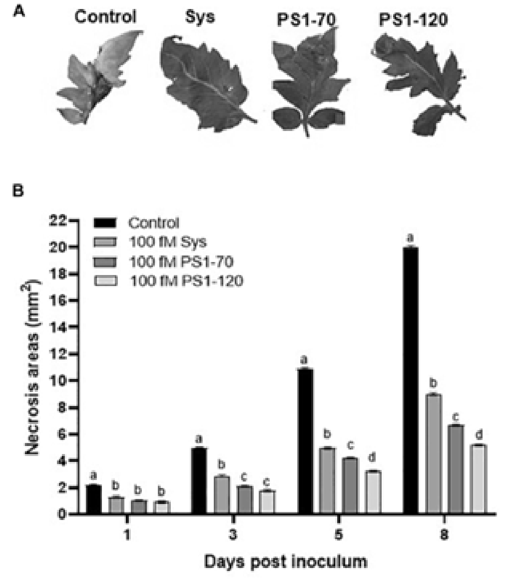

FIGURE 4 | Enhanced resistance to *B. cinerea* by plants treated with ProSys fragments and Sys peptide. Response to *B. cinerea* infection in leaves from mock-treated (Control) and Sys, PS1-70 and PS1-120 treated plants. **(A)** Pictures show necrosis symptoms on detached tomato leaves 8 days after fungus inoculation. **(B)** The graphs display the mean of the lesion size at 1, 3, 5, and 8 days post-inoculum. Letters indicate different statistical groups (One-Way ANOVA, $P < 0.05$). Error bars indicate standard error.

Induction of the Expression of Plant Defense-Related Genes After ProSys Fragments Application

The evaluation of the perception and the effect of the exogenous supply of Sys, PS1-70 and PS1-120 on the expression of defense genes was performed quantifying the transcripts of selected defense-related genes (listed in **Supplementary Table 2**) by qPCR, 6 h after peptide delivery on healthy leaves *Allene Oxide Synthase* (*AOS*; Solyc11g069800), *Lipoxygenase C* (*LoxC*; Solyc01g006540), *Lipoxygenase D* (*LoxD*; Solyc03g122340), *1-aminocyclopropane-1-carboxylate oxidase* (*ACO2*; Solyc12g005940), *Wound-induced Proteinase Inhibitor I* and *II*, (*Pin I* and *Pin II*; Solyc09g084470 and Solyc03g020060), *Phenylalanine ammonia-lyase* (*PAL*; Solyc09g007910) were considered for the expression analyses.

All the experimental peptides induced the expression of the selected genes as shown in **Figure 6**. Interestingly, some remarkable differences were observed in the level of transcripts encoding LoxC, Pin I and Pin II proteins. However, the expression of different genes was differently induced by the experimental peptides. AOS is similarly induced by the three peptides, LoxD transcription appears to be induced uniquely by PS1-70, while the transcription of ACO2 and PAL by PS1-70 and PS1-120, but not by Sys peptide.

Effects of ProSys Fragments on Microorganism and Mammalian Cells

To evaluate if ProSys fragments under investigation have a cytotoxic effect on photosynthetic microorganism and human cells, we investigated cell viability and growth of fragment-treated microalgae and the proliferation and morphology of fragment-treated human keratinocytes (HaCaT).

Exposure of the microalgal cells to different concentration of ProSys fragments did not affect their viability. Growth curves of *Chlamydomonas* cells exposed at different concentrations of Sys, PS1-70 and PS1-120 were comparable to that of control cells, across the whole duration of the experiment (**Supplementary Figure 7**). Similarly, all experimental treatments did not inhibit growth of algae (**Supplementary Table 5**). Therefore, these results indicate that neither Sys nor the

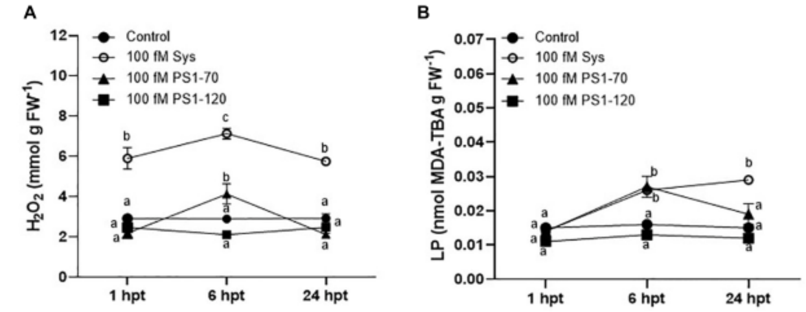

FIGURE 5 | H_2O_2 and MDA content in tomato leaves treated with 100 fM ProSys fragments. H_2O_2. **(A)** and MDA, **(B)** contents were measured in control (PBS1X) and in treated leaves at 1, 6, and 24 hpt with 100 fM Sys, PS1-70 and PS1-120. Different letters indicate statistically significant differences (One-Way ANOVA, $P < 0.05$). Error bars indicate standard error.

N-terminal fragments 1-70 and 1-120 of ProSys have toxicity effect on microalgae. Finally, even using peptide concentrations much higher than those used for plant treatments, toxicity was not observed.

The potential of PS1-70 or PS1-120 to affect mammalian cell proliferation and morphology was evaluated on human keratinocytes (HaCaT) cell line, exposing the cells at high concentrations (100 nM) of each peptide for 24 h. The cell line viability was assessed by cell viability Kit-8 assay and manual cell count, while the cell morphology was evaluated by phase-contrast microscopy. As reported in **Figure 7A**, following the treatment of HaCaT cells with 100 nM of each fragments for 24 h, the cell viability determined on the basis of absorbance of CCK-8 assay was about 100% (97.9% for PS1-70 and 100% for PS1-120), as also confirmed by the results obtained by manual cell count (94% for PS1-70 and 95% for PS1-120). These findings clearly revealed that PS1-70 and PS1-120 did not exert any cytotoxic effects against the mammalian cells used, even at the highest concentration tested (100 nM), which was much higher than that inducing the observed biological effects. In addition, to evidence possible alterations of cell morphology caused by treatments with ProSys fragments, HaCaT cell line was also visualized and analyzed by phase-contrast microscopy after 24 h exposure to 100 nM of PS1-70 or PS1-120. As shown in the micrographs reported in **Figure 7B**, both fragments did not induce any morphological change in the experimental cells.

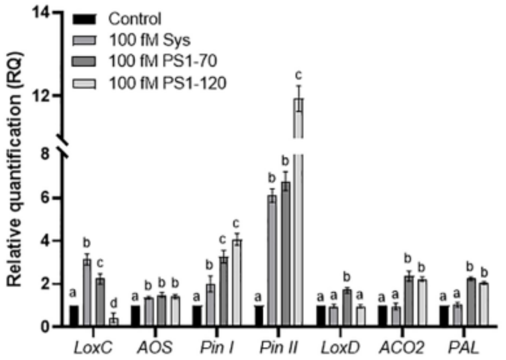

FIGURE 6 | Expression analysis of defense related genes by RT-PCR. Relative quantification of early and late defense genes induced at 6 h post treatment with 100 fM of Sys, PS1-70 and PS1-120. Quantities are shown relative to the calibrator control condition, set as 1 (mock-treated plants). Letters indicate different statistical groups (One-Way ANOVA, $P < 0.05$). Error bars indicate standard error.

DISCUSSION

The development of sustainable plant protection strategies is currently being pursued through a wealth of bioinspired approaches, based on the use of natural antagonists or of molecules/genes that modulate their interactions with target pests and pathogens, trying to control them by mimicking natural mechanisms of pest suppression (Pennacchio et al., 2012). Indeed, in addition to the use of living organisms, it is possible to use nature-based substances, such as, for example, plant-derived molecules (Isman, 2006), semiochemicals (Bruce et al., 2005; Witzgall et al., 2010), protein applications (Thakur and Sohal, 2013), and RNA interference (Zhu et al., 2011; Koch et al., 2016). The International Biocontrol Manufacturers' Association (IBMA) promotes the broader term *bioprotection*, which includes the use of both biocontrol agents and non-living plant protection tools originated from nature (Stenberg et al., 2021). The growing knowledge on the functional basis of biological control allows to include in this definition also the use of molecules/genes deriving from natural antagonists, which can reproduce the lethal syndrome they induce in the target pests used as hosts (Bale et al., 2008; Pennacchio et al., 2012; Mahmood et al., 2016). Indeed, many bioactive molecules that regulate

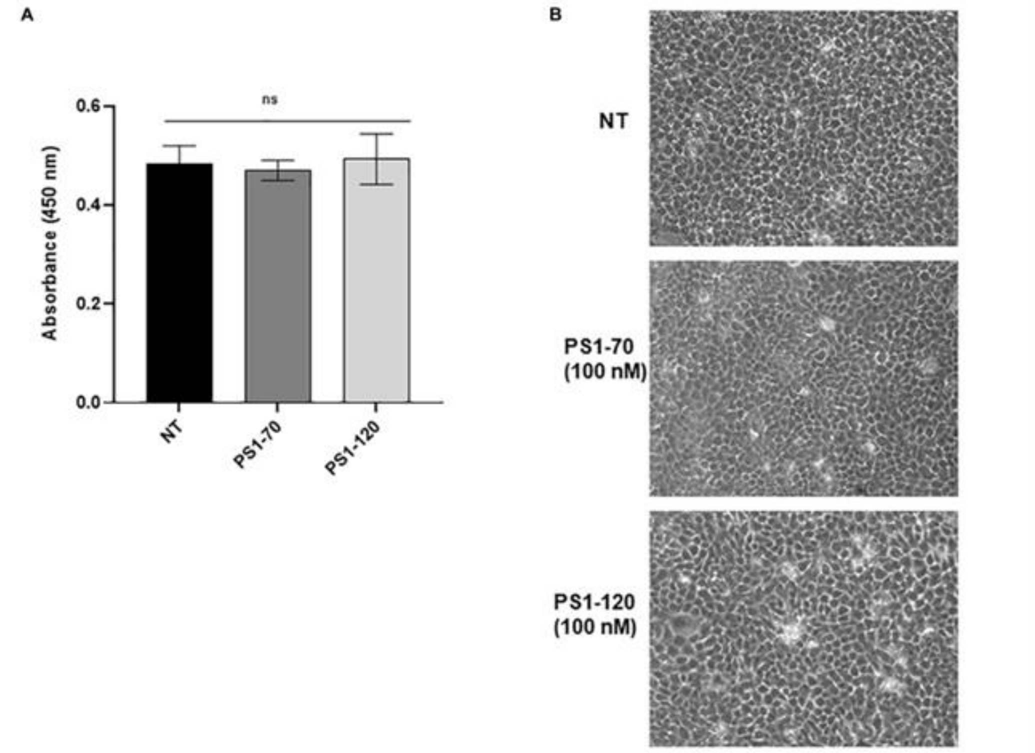

FIGURE 7 | Cell viability and morphology of human keratinocyte cells (HaCaT cells) treated with PS1-70 or PS1-120. **(A)** Cell viability of HaCaT, incubated at 37°C for 24 h in the absence (NT) or presence of PS1-70 or PS1-120 at 100 nM, was evaluated by CCK-8 assay. **(B)** Phase-contrast microscopy images of HaCaT cells not treated (NT) or treated with 100 nM of PS1-70 or PS1-120 at 37°C for 24 h. The microscope images were representative of three independent experiments performed in triplicate. Bars are presented as mean (Student's *t*-test, $P < 0.05$). Error bars indicate standard deviation.

insect antagonistic interactions have already been isolated and characterized from plants and microorganisms (bacteria, fungi and viruses), to obtain insecticides of natural origins (Kachhawa, 2017), and many other untapped sources are available in nature.

This strategy can be applied to all kind of antagonistic associations existing in nature, including those among plants and their biotic stress agents. Natural molecules able to trigger plant immunity, such as DAMPs, may be interesting players in pest management, to activate defense responses; therefore, the discovery of novel DAMP-molecules may offer new opportunities for pest control, contributing to agro-food safety (Delaunois et al., 2014).

Here we describe the biological activity of two N-terminal fragments of ProSys, consisting of the first 70 and 120 amino acid residues, which, when exogenously supplied to tomato plants, protect them against *S. littoralis* larvae and *B. cinerea* infection.

SEC and LS investigations of PS1-70 and PS1-120, revealed the lack of a globular structure and a monomeric state in solution, in agreement with their disordered features, supported by CD and sequence analysis. As expected, the structural features of PS1-70 and PS1-120 strongly resemble those of the precursor (Radivojac et al., 2007; Midic and Obradovic, 2012; Buonanno et al., 2018; Uversky, 2019). When titrating with TFE, CD spectra showed that PS1-120 gained a more ordered three-dimensional structure compared with PS1-70, which retained most of its disordered conformation (**Figures 2C,D**). It is tempting to speculate that the conformational differences between the two fragments could promote a different recognition mechanism carried out by the same or by different partners (Uversky, 2019; Wang and Wang, 2019). However, this aspect deserves further investigations. In any case, the observed differences between PS1-70 and PS1-120, may well be dependent from their structures as PS1-70 encompasses the N-terminal region, which was predicted to be highly disordered, whereas PS1-120 also includes the central region 71-120, which was predicted to gain some secondary structure content.

Notably, PS1-70 and PS1-120, like Sys, possibly behave as hormone molecules being able to act at extremely low concentration, conferring to the treated plants different levels of protection against *S. littoralis* larvae and *B. cinerea*. The best performance of tomato plants against *S. littoralis* larvae was observed after the treatment with PS1-70, which induced 100% mortality 13 days after the treatment. Conversely, PS1-120 was more effective in reducing *B. cinerea* colonization, compared with Sys peptide and the PS1-70 fragment. The observed plant defense responses are mediated by PS1-70 and PS1-120 that, similarly to Sys (Coppola et al., 2019), likely penetrate the cell wall, by unknown mechanisms, and trigger the expression of defense-related genes. However, these protein fragments may contain shorter bioactive peptide sequences that are worth further research efforts.

The absence of direct effects of the investigated fragments on *S. littoralis* larvae and *B. cinerea* further demonstrates that plant protection is due to the induction of endogenous defenses, which is coupled with a high level of safety toward the non-target organisms considered.

We propose that both PS1-70 and PS1-120 can act as resistance inducer molecules, that enhance plant defense barriers upon challenge (Mauch-Mani et al., 2017). Indeed, PS1-70 and PS1-120 induce the expression of genes associated with the octadecanoid signaling pathway (*Lox C*, and *AOS*), that is known to play an important role in plant defense against a variety of insects and fungal pathogens (Thakur and Udayashankar, 2019; Viswanath et al., 2020; Zeng et al., 2021), and of jasmonic acid (JA) responsive genes (*Pin I* and *Pin II*), known to reduce larval nutrient digestion and, consequently, their growth and survival, as well as *B. cinerea* development, both *in vitro* and *in vivo* (Lorito et al., 1994; Hermosa et al., 2006). Intriguingly, PS1-70 induces the expression of *LoxD*, a gene that, when overexpressed in tomato plants, boosts JA biosynthesis, increasing the expression of wound-responsive genes and, consequently, enhancing resistance against insect herbivores (Yan et al., 2013). These observations nicely correlate with the efficient protection against the herbivorous pest triggered by PS1-70. In addition, PS1-70 and PS1-120 induced the expression of *ACO*, a gene associated with ethylene production (Houben and Van de Poel, 2019), an important regulator of plant responses to biotic and abiotic stress agents (Van de Poel et al., 2016), and of *Pal*, a gene encoding a key-enzyme of plant metabolism leading to changes in lignin contents and thickness of cell walls, involved in plant defense responses against parasites (Tonnessen et al., 2015; Chen et al., 2017).

Upon stress conditions, homeostasis of intracellular oxidation-reduction is impaired, with the consequent increase of ROS that damage the cells through lipid peroxidation (Huang et al., 2019). By measuring the malondialdehyde (MDA), which is the result of lipid peroxidation, the amount of plant cell stress can be measured (Grotto et al., 2009). Oxidative parameters showed an additional difference in terms of ROS generation among PS1-70, PS1-120 and Sys. Taken together, these results indicate that PS1-70, PS1-120 and Sys all confer protection to treated plants, but to a different extent, which partly accounts for the diversity of functional responses observed.

Importantly, Sys, PS1-70 and PS1-120 did not show toxic activity on microalgae and on HaCaT cells, making them suitable for crop protection.

Collectively, these results indicate that ProSys fragments act as multiple signals which may interact with different receptors controlling complementary and synergistic defense pathways (Zhang et al., 2020). This appears to be a widespread strategy of response to stress agents, which is able to rapidly produce multiple signals alerting the whole organism, to allow a more effective and rapid response against stress (Olsson et al., 2019; Stührwohldt and Schaller, 2019). The Hydroxyproline-rich systemins (HypSys) were the first example of production in plants of multiple bioactive peptides from a single precursor protein (Pearce et al., 2001; Pearce and Ryan, 2003). A similar gene, *SlpreproHypSys* was also described in tomato; the gene encodes a polypeptide of 145 amino acids from which three different small defense signaling glycopeptides are released (Ryan and Pearce, 2003). Several other examples were lately reported (Chen et al., 2020), evidencing the very important biological role played by plant peptides and protein fragments in physiological responses, which have been underestimated for many years.

Although ProSys was discovered several decades ago (McGurl et al., 1992), and many observations proved its important role in tomato protection, our results show for the first time that this protein contains multiple fragments with biological activity, likely accounting for the different "anti stress" activities conferred to tomato plants by its overexpression. The two ProSys fragments identified in this study represent new promising tools for sustainable crop protection. Any shorter bioactive sequence deriving from them is currently being investigated by us, to identify new plant protection products and biostimulants that will contribute to the important goal of reducing the use of synthetic pesticides in agriculture.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

AUTHOR CONTRIBUTIONS

DM produced and structurally characterized ProSys fragments, performed the bioassays, and contributed to manuscript writing. MC participated to the experimental work and contributed to the manuscript writing. EL conceived the fragments and contributed to the manuscript writing. MB characterized the ProSys fragment and revised the manuscript. IDL, EB, and AB carried out the insect bioassays. AA performed the gene expression studies and insect and fungi assays. SMM supervised the biochemical work, conceived the work, and contributed to the manuscript writing. MR and SF performed the biochemical assays and manuscript revisions. PC carried out the microalgal assay. GP and RT performed the human cell assays. MS carried out the fungi bioassays. FP contributed to the insect work, supervision, and manuscript revision. RR conceived and supervised the work and wrote the manuscript. All authors contributed to the article and approved the submitted version.

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SUPPLEMENTARY MATERIAL

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Colonization of *Solanum melongena* and *Vitis vinifera* Plants by *Botrytis cinerea* Is Strongly Reduced by the Exogenous Application of Tomato Systemin

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Abstract: Plant defense peptides are able to control immune barriers and represent a potential novel resource for crop protection. One of the best-characterized plant peptides is tomato Systemin (Sys) an octadecapeptide synthesized as part of a larger precursor protein. Upon pest attack, Sys interacts with a leucine-rich repeat receptor kinase, systemin receptor SYR, activating a complex intracellular signaling pathway that leads to the wound response. Here, we demonstrated, for the first time, that the direct delivery of the peptide to *Solanum melongena* and *Vitis vinifera* plants protects from the agent of Grey mould (*Botrytis cinerea*). The observed disease tolerance is associated with the increase of total soluble phenolic content, the activation of antioxidant enzymes, and the up-regulation of defense-related genes in plants treated with the peptide. Our results suggest that in treated plants, the biotic defense system is triggered by the Sys signaling pathway as a consequence of Sys interaction with a SYR-like receptor recently found in several plant species, including those under investigation. We propose that this biotechnological use of Sys, promoting defense responses against invaders, represents a useful tool to integrate into pest management programs for the development of novel strategies of crop protection.

Keywords: crop protection; signaling peptide; plant defense; foliar application; hydroponics; antioxidant activity

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1. Introduction

The success of modern agriculture relies in part on discovery and adoption of pesticides for pest control [1]. However, the onset of different concerns on the impact of pesticides on the environment, biodiversity, as well as on human health, pressed the introduction of more stringent pesticide registration procedures. Furthermore, the tendency in European Union policy is to encourage the development of eco-friendly and sustainable control strategies to protect crops reducing chemical inputs [2]. One of the main challenges facing the agricultural sector is to reduce the negative impact on soil, water, and the atmosphere.

Sustainable strategies for pest control have been applied to agricultural practices, such as biological control. This approach includes the use of beneficial microorganisms or bioactive compounds that bio-stimulate plant performance against pathogens by competing or by directly antagonizing them [3–6]. Some other alternative control strategies of plant diseases are based on the use of plant resistance inducers (PRIs, also called elicitors or plant defense/resistance activators), which offer the prospect of durable, broad-spectrum disease control [7]. PRIs can be chemical compounds [8] as well as biological stimulators [9] able to activate and/or prime plant defense responses by their exogenous application [10]. Depending on their nature, they either mimic plant downstream signaling molecules, such as phytohormone or derivates, or act as non-self molecules, classified as microbe/pathogen/herbivore-associated molecular patterns (MAMPs/PAMPs/HAMPs), or signals from damaged cells, generally referred to danger- or damage-associated molecular patterns (DAMPs) [11–14] or phytocytochines [15]. PRIs are recognized by plasma-membrane localized pattern recognition receptors (PRRs) to initiate signal transduction pathway [7]. One of the best characterized DAMP is systemin (Sys), an octadecapeptide synthesized as a part of a larger precursor protein, prosystemin (ProSys) [16,17]. Sys was isolated from tomato leaves and proved to be able to activate the octadecanoid pathway, which leads to the production of the plant hormone jasmonic acid (JA) and its derivatives, powerful activators of plant defense genes [18,19]. Transgenic tomato plants constitutively expressing *ProSys* proved to be resistant to insect herbivores and phytopathogenic fungi [20–22] and tolerant to moderate salt stress [23]. Homologs of the tomato *ProSys* gene have been identified only in some economically important species of Solanoideae subfamily, but other genetically distinct families of plant defense signal peptides have been described in several species [24–30].

Upon either pests or other environmental challenges cues, Sys interacts with a leucine-rich repeat receptor like-kinase (LRR-RLK), RLK SYSTEMIN RECEPTOR 1 (SYR1) and with lower affinity its homologous SYR2, triggering a complex intracellular signaling pathway that leads to the generation of early and late defense responses [31]. It was recently observed that although both SYR1 and SYR2 receptors are restricted to the species of Solanoideae subfamily (e.g., tomato, potato, eggplant, and pepper), other SYR-like genes are present in other plants species, including *Vitis vinifera* [31].

Sys perception at the cellular surface induces depolarization of the plasma membrane, mitogen-activated protein kinases (MAPKs), the opening of ion channels, with the consequent increase of intracellular Ca^{2+} concentration, and accumulation of reactive oxygen species (ROS) [32].

Since ROS participate in signaling events, they are highly reactive but also toxic to the cells. To control the level of ROS and protect cells under stress conditions, plants have developed a sophisticated ROS scavenging system that includes the activity of several enzymes such as catalase (CAT) and ascorbate peroxidase (APX) as well as non-enzymatic low molecular compounds such as phenolics compounds [33–36].

Eggplants (*Solanum melongena* L.) and grapevine (*Vitis vinifera* L.) are particularly susceptible to important fungal pathogens, among them *Botrytis cinerea*, the agent causing grey mold which diminish yield and depreciate quality throughout their entire biological cycle [37,38]. Phytochemicals are commonly used to prevent and reduce the damages of this pathogen infection, but pathogen strains with pesticide-resistance have been reported [39,40]. In an effort to protect crops from such a dangerous enemy and yet reduce the impact of chemicals on the environment, considerable interest has been focused on the identification of novel biotechnological tools that use elicitors to strengthen the endogenous defenses of plants. In this work, we demonstrated that the direct delivery of Sys to *Vitis vinifera* and *Solanum melongena* plants strongly reduces *B. cinerea* plant colonization.

2. Materials and Methods

2.1. *Peptides*

Two different purified peptides were assayed: Systemin (Sys) and its scrambled form (Scp) that does not activate the plant defense response in tomato. Peptides synthesis, purification, and stability are reported elsewhere [41].

2.2. *Plant Materials and Growth Conditions*

The eggplant variety used was "Violetta Lunga". For this crop, two different growth systems were carried out: In soil and in hydroponic culture.

Seeds were germinated in Petri dishes on wet sterile paper and kept in the dark for three days in a growth chamber at 24 ± 1 °C and 60% relative humidity (RH). Upon roots emergence, for soil culture, eighteen plantlets were transferred to a polystyrene plateau with inert substrate S-type (Floragard, Oldenburg, Germany) in a growth chamber at 26 ± 1 °C and 60% RH with a photoperiod of 18/6 h light/dark. After two weeks, plants were transplanted in pots of 9 cm diameter with sterile soil mixture using the same growth conditions. For hydroponic culture, eighteen plantlets of 2 cm were transferred to hydroponic system and divided into three different plastic containers (5 L) supplemented with $Mg(NO_3)_2 \cdot 6H_2O$ (384 mg/L), $Ca(NO_3)_2 \cdot 4H_2O$ (812.9 mg/L), KNO_3 (101.5 mg/L), K_2SO_4 (319.3 mg/L), KH_2PO_4 (204.8 mg/L), Hydromix (14.0 mg/L). Four weeks-old plants were used for biological and molecular investigations unless otherwise indicated.

Grapevine, cultivar "Cabernet Sauvignon" cuttings (rootstock genotype 101.14 CL. 759), were grown in a greenhouse in pots of 20 cm diameter until they developed six to eight leaves. The second and third youngest adult leaves from each cutting were used for biological and molecular investigations.

2.3. *Plant Treatments with Peptides and Botrytis cinerea Assay*

Intact leaves of eggplant and grapevine plants grown in soil were treated with 100 pM of Sys or Scp peptides in PBS buffer (phosphate buffer saline, 10 mM phosphates, 140 mM NaCl, 2.7 mM KCl, pH 7.4, Sigma-Aldrich, Milan, Italy) while to eggplants growing in hydroponics, peptides were added into a nutrient solution at the same final concentration. Control plants were similarly treated with PBS buffer.

Four weeks-old plants, leaf-treated or grown in hydroponics enriched with the Sys or Scp, were tested for resistance to the necrotrophic airborne pathogen, *B. cinerea*, as already reported [42]. The assay used five leaves per treatment from three different plants per each thesis. Control and treated leaves were placed on sponges soaked in sterile water and incubated in a growth chamber at 23 ± 1 °C under 16/8 h light/dark photoperiod and 90% RH as also described by [43,44].

Necrosis areas were measured at 1, 3, 5, and 7 days post inoculum (pi) with a digital caliber (Neiko 01407A, Neiko Tools, Taiwan, China).

2.4. *In Vitro Antifungal Assay*

The antifungal assay was carried out as already reported [45]. Briefly, a sterile 12-well plate was filled with potato dextrose broth (PDB 1/2) medium containing Sys and Scp peptides at the final concentration of 100 pM. A solution with *B. cinerea* spores was added to each well in order to reach a final concentration of 10^4 spores/mL in each well, the plate was placed in a shaker and incubated for 24 h at 25 ± 1 °C. To assess the fungal growth, the value of optical density (OD) at a wavelength of 600 nm was measured in triplicate on a BioPhotometer Spectrophotometer UV/VIS (Eppendorf, Hamburg, Germany).

2.5. *Gene Expression Analyses*

Total RNA extraction, single-strand cDNA synthesis, and quantitative reverse transcription (RT)-PCR were performed as already reported [46]. Expression analysis of selected defense-related genes was monitored 3 h and 6 h after Sys foliar and hydroponic application, respectively. Gene expression analysis was carried out using two technical replicates for each of the three biological replicates. Relative quantification of gene expression was carried out using the comparative method with the $2^{-\Delta\Delta Ct}$ formula [47] where ΔCt = Ct target gene—Ct endogenous control and $\Delta\Delta Ct$ = ΔCt sample—ΔCt calibrator. The housekeeping *APRT* (*adenine phosphoribosyl transferase*) and the *EF-1α* (*elongation factor-1α*) genes were the endogenous reference genes, respectively, for eggplant and grapevine plants, used for the normalization of the expression levels of the target genes. Primers and related genes under investigation are listed in Table S1.

2.6. Biochemical Analyses

Total phenolic content (TPC) and antioxidant enzyme activities were assessed spectrophotometrically in treated leaves of eggplant and grapevine plants collected at various time intervals: 1, 3, 6, and 24 h after peptides treatment using three technical replicates for each of the three biological replicates. Untreated leaves were used as control.

For the extraction of total soluble proteins, frozen leaf sample (0.1 g) was ground with 1 mL ice-cold 50 mM $KHPO_4$ (pH 7.8) containing 0.1 mM EDTA. Homogenates were centrifuged at 14,000 rpm for 20 min at 4 °C.

Protein concentration was measured by the Bradford method using bovine serum albumin as a standard protein [48]. TPC was evaluated by using Folin–Ciocalteu colorimetric method as described before [49].

The catalase (CAT) activity was measured following the previously described protocols [50,51], monitoring the decrease in absorbance at 240 nm. Ascorbate peroxidase (APX) activity was analyzed by measuring the decrease in absorbance at 290 nm monitored according to the method previously described [52].

2.7. Statistical Analyses

For the evaluation of Sys effect on *B. cinerea* growth and infection, necrosis area differences between controls and Sys-treated or Scp-treated sample were compared and analyzed by one-way Analysis Of Variance (ANOVA) coupled with Tukey–Kramer Honestly Significant Difference (HSD) test. Differences in relative quantities of defense transcripts were analyzed by comparing ΔCt values for all the replicates of tests and controls using a two-tailed Student's t-test. Moreover, the quantification of the amount of total phenolic content and the evaluation of the activities of antioxidant enzymes were analyzed by one-way ANOVA coupled with Tukey–Kramer multiple comparisons test. Error bars referring to standard error have been displayed.

3. Results

3.1. Systemin Exogenous Supply Reduces *B. cinerea* Colonization of Eggplant and Grapevine Leaves

The performance of Sys-treated eggplants and grapevine against *B. cinerea* was evaluated at 1, 3, 5, and 7 days post inoculum (pi). The assay was carried out using detached leaves harvested 6 h after peptides, Sys or Scp, application to intact plants [41,42]. Disease severity was quantified by measuring the necrotic leaf areas caused by fungal colonization. In eggplants, as shown in Figure 1, Sys significantly reduced the lesions since five days pi (Figure 1A), whereas in leaves deriving from hydroponic cultures, a reduction of the lesions was evident already 24 h pi (Figure 1B). No differences were observed for eggplants treated with buffer and Scp-peptide. Similarly, grapevine Sys-treated leaves displayed a marked reduction of *B. cinerea* induced lesions after seven days pi compared with the control ones (Figure 1C). Likewise to the previous experiment, no effect was detected in Scp or buffer treated leaves. These results demonstrate that the exogenous supply of Sys peptide to healthy plants reduced disease severity.

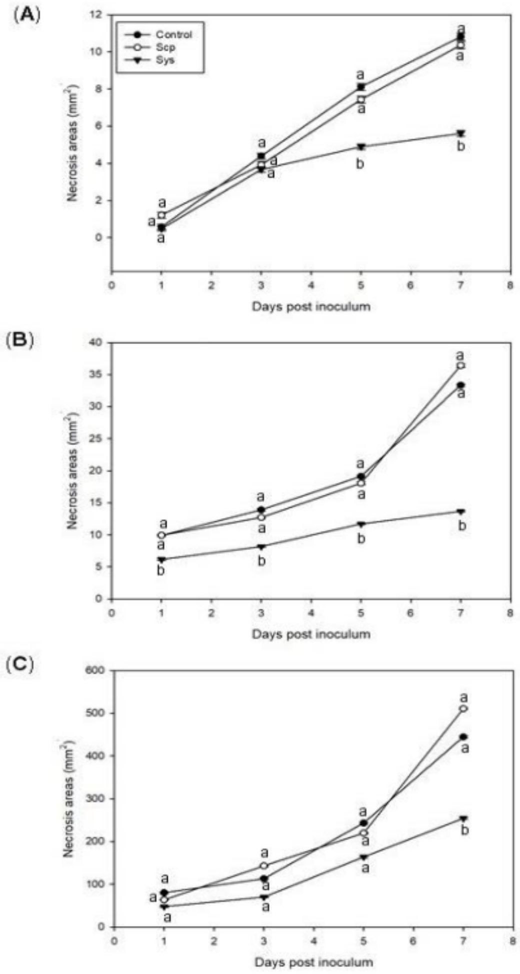

Figure 1. *Botrytis cinerea* necrosis area assay. Sys was applied to eggplant leaves (**A**) or added to hydroponic solution (**B**), while for the grapevine plants, only leaves were treated (**C**). Response to *B. cinerea* infection on leaves from plants treated with 100 pM Sys or Scp or Control (PBS 1X). The graph displays the average (±S. E., standard error) of the lesion size at 1, 3, 5, and 7 days post-inoculation. Letters indicate statistically significant differences (one-way Analysis of Variance, ANOVA, Tukey–Kramer Honestly Significant Differences (HSD) test with $p < 0.05$). Error bars indicate standard error.

Moreover, in order to evaluate whether the reduction of *B. cinerea* necrosis area was due to a direct antimicrobial effect of the Sys peptide on the fungus, an in vitro assay to measure fungal growth in the presence of Sys and Scp peptides was carried out.

As shown in Figure 2, Sys peptide did not directly impact fungus vitality. The growth of *B. cinerea*, monitored by measuring the absorbance at 600 nm, was similar in all three treatments. This result indicates that the observed reduction of *B. cinerea* plant colonization is determined by the induction of plant endogenous defenses upon Sys treatment.

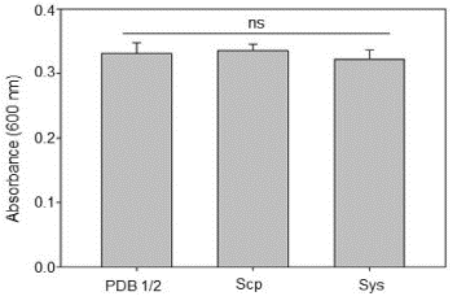

Figure 2. In vitro antifungal vitality assay. Each 12-well sterile plate was filled with 1 mL of PDB 1/2 medium containing the peptides at the final concentration of 100 pM, except for the broth sterility control wells. Thereafter, spores of *B. cinerea* were added to each well, and fungal growth was assessed 24 h after pathogen inoculation by evaluating the optical density (OD) of the medium at 600 nm. Letters indicate statistically significant differences (one-way ANOVA, Tukey–Kramer Honestly Significant Differences (HSD) test with $p < 0.05$; ns, not significant). Error bars indicate standard error.

3.2. Systemin Exogenous Supply Activated the Expression of S. melongena and V. vinifera Defense-Related Genes

In order to verify the ability of Sys-treatments to induce the expression of defense-related genes, we performed a qRT-PCR of selected genes for the two plant species. The genes analyzed were: *Allene Oxide Synthase* (*AOS*), *Wound-induced proteinase inhinbitor I* and *II* (*Pin I* and *Pin II*), *Pathogenesis-related protein 4* (*PR4*), *Dihydroflavonol 4-reductase* (*DFR*) and *Polyphenol oxidase* (*PPO*) for eggplants, the *basic-helix-loop-helix* (*bHLH*) *transcription factor* (*TF*) (*MYC2*), *AOS*, *Pin I*, *Pin II*, *PR4*, *Phenylalanine ammonia-lyase* (*PAL*) and *Flavonol synthase 5* (*FLS5*) for grapevine plants. The expression of the target genes was analyzed at two time intervals after treatment. Relative quantification of treated samples was referred to the mock-treated control (relative quantification, RQ = 1).

As shown in Figure 3A, in eggplants, a strong increase of *AOS* transcript was recorded 3 h after Sys application followed by a reduction of the transcript after 6 h from peptide application. Conversely, the expression profile of *Pin I* and *II* showed a gradual increase in their transcripts that reached the highest expression level 6 h after Sys treatment. Moreover, *PR4*, *DRF*, and *PPO* transcripts resulted significantly up-regulated (Figure 3A). We also monitored the expression of the same genes in leaves of eggplants grown in hydroponics enriched with the peptide. As shown in Figure 3B, *Pin I*, *Pin II*, and *PR4*, transcripts resulted significantly up-regulated after 6 h and no significant variation in transcript level was recorded for the other three genes.

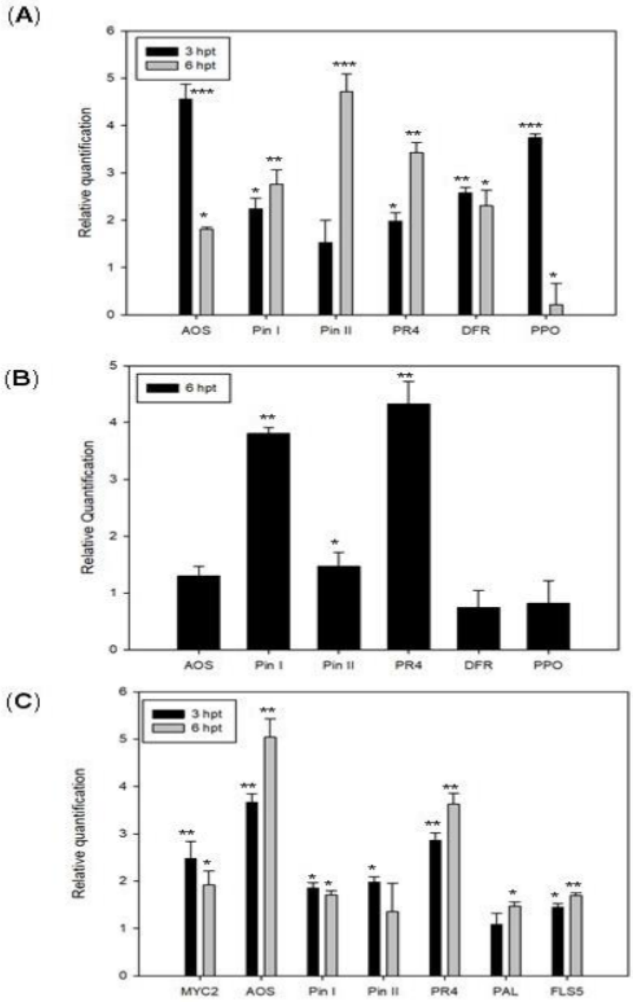

Figure 3. Expression analysis of defense-related genes following Sys treatments (100 pM) on eggplants and grapevine plants. Relative gene expression of defense-related genes by qRT-PCR in eggplants-treated leaves (**A**), in leaves of eggplants grown in a hydroponic system (**B**) and in grapevine-treated leaves (**C**). Quantities are relative to the calibrator control condition, mock-treated plants. Asterisks indicate data statistical significance (Student's *t*-test, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$). Error bars indicate standard error.

Figure 3C shows the results of the gene expression analyses in treated leaves of grapevine plants. All the target transcripts resulted significantly up-regulated. Taken together, the results demonstrate that Sys, under two different delivery systems, is able to induce the transcription of defense-related genes in both plant species.

3.3. Systemin Increases the Production of Total Soluble Phenolic Content and Antioxidant Capacity in Treated Eggplant and Grapevine

We quantified the amount of total phenolic content (TPC) and analyzed the activities of some key antioxidant enzymes that are responsible for rapid scavenging of ROS. Sys induced in treated plants a rapid antioxidant response, the TPC pool increased significantly by about 70% in eggplants (Figure 4A) 3 h after Sys application while the response of grapevine plants was more rapid with the increase of TPC after 1 h of roughly 16%. In addition, the TPC content in the treated plant species reached the highest content 3 h after Sys treatment (Figure 4, Table S2). On the contrary, as expected, the application of Scp peptide to the plants did not induce any TPC content variation (Figure 4, Table S2).

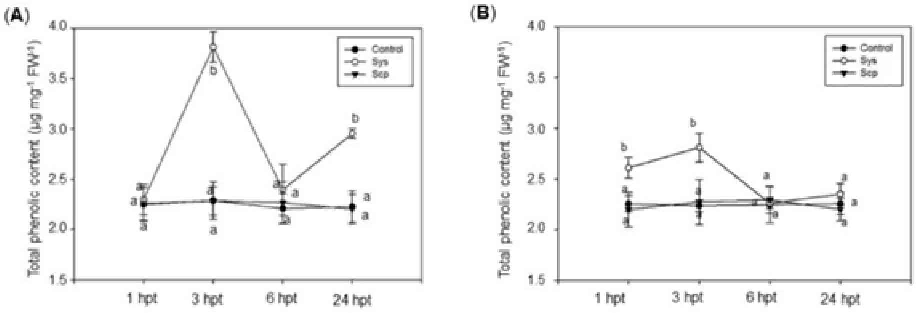

Figure 4. Total phenolic content (TPC) in eggplant (**A**) and grapevine (**B**) leaves treated with Sys. TPC was measured in control (PBS1X) and in treated leaves at 1, 3, 6, and 24 h after 100 pM Scp or Sys application. Letters indicate statistically significant differences (one-way ANOVA, Tukey test with $p < 0.05$). Error bars indicate standard error.

In addition to the investigation on the non-enzymatic components that regulate redox status, we monitored two enzymes that are included in the other arm of the antioxidant defense machinery. A significant increase in the activities of CAT and APX enzymes was observed in eggplant-treated leaves, respectively, of about four times and 100 times higher than control, 1 h and 6 h following Sys application, respectively (Figure 5A,B, Table S3). A different profile of CAT activity was observed in grapevine-treated leaves, which showed a steady increase after 3 h up to 40 times higher the control value 24 h post-treatment (Figure 6A, Table S4). In the same species, a significant increase in APX, about 11 times control value, was observed 24 h post-treatment (Figure 6B, Table S4). No significant variation in the activity of those enzymes was registered in leaves treated with Scp (Figures 5 and 6, Tables S3 and S4).

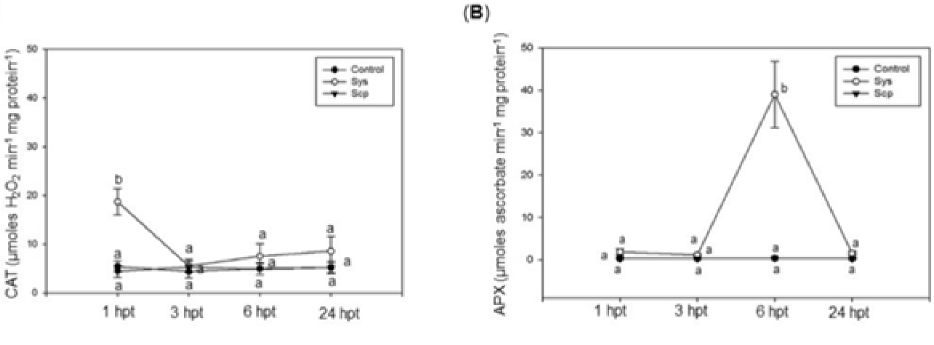

Figure 5. Catalase (CAT) (**A**) and ascorbate peroxidase (APX) (**B**) activity at various time intervals in eggplant leaves treated with Sys. CAT and APX activity was assessed in control leaves (PBS1X) and in treated leaves at 1, 3, 6, and 24 h after 100 pM Sys and Scp application. Letters indicate statistically significant differences (one-way ANOVA, Tukey test with $p < 0.05$). Error bars indicate standard error.

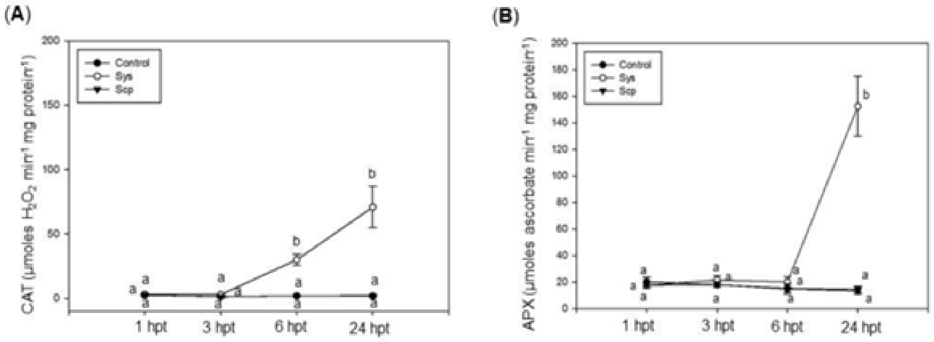

Figure 6. Catalase (CAT) (**A**) and ascorbate peroxidase (APX) (**B**) activity at various time intervals and grapevine leaves treated with Sys. CAT and APX activity was assessed in control leaves (PBS1X) and in treated leaves at 1, 3, 6, and 24 h after 100 pM Sys and Scp application. Letters indicate statistically significant differences (one-way ANOVA, Tukey test with $p < 0.05$). Error bars indicate standard error.

4. Discussion

The development of safe and sustainable crop protection strategies is a challenging goal facing our society. This is increasingly pursued through bio-inspired research efforts, aiming to mimic natural mechanisms of pest suppression by exploiting biotechnological applications of biomolecules active in plant defense [53]. A promising control strategy is based on the application of elicitors to the plant that stimulate and/or potentiate plant defense responses affecting the fitness and behavior of herbivores and pathogens [42,54].

Among pathogenic plant agents, the necrotrophic fungus *B. cinerea* is a very dangerous fungus that infects many economically important crops, such as grapevine, strawberry, tomato, and eggplant. Grapevine is one of the major fruit crops in the world based on hectares cultivated with this crop and its economic value [55]. The species is particularly sensitive to various pathogenic fungi, including *B. cinerea* that causes significant losses in terms of production and quality. This pathogen is controlled by fungicide treatments, but pathogen strains with fungicide resistance have been reported [39]. Eggplant is one of the most important vegetable crops, especially for the Mediterranean basin, after potato (*Solanum tuberosum*) and tomato (*Solanum lycopersicum*) [56]. The plants are very susceptible to important fungal pathogens, including *B. cinerea*, throughout their entire biological cycle and the fungal control has been adversely affected by the development of fungicide resistance [40]. Therefore, the identification of novel biotechnological tools able to protect these crops from such a dangerous enemy is of great importance.

In this paper, we investigated the ability of tomato Sys to protect *S. melongena* and *V. vinifera* plants from *B. cinerea*, demonstrating, for the first time, that the exogenous supply of the peptide to intact healthy plants severely counteracted fungal growth. This is likely the consequence of the induction of plants defense-related genes that promote the accumulation of compounds active in plant defense [10,57]. Consequently, Sys-treated plants respond more effectively than controls when exposed to biotic stress. Both peptide delivery systems (leaf application or hydroponics uptake) proved to be very effective in conferring measurable protection against the necrotrophic fungus. The absence of inhibition of mycelium growth in the presence of Sys fully excluded that the peptide has a direct effect on the fungus. Therefore, the observed reduction of plant colonization is likely the consequence of the activation of plant endogenous defenses following Sys treatment. As a matter of fact, we observed the induction of a set of defense-related genes. *AOS*, a gene of the octadecanoid pathways, leads to the biosynthesis of JA that subsequently activate the late defense genes *PPO*, *Pin I*, and *Pin II*. Tomato *PPO* is induced by Sys and jasmonate, and it is involved in defense against pests [58,59]. In addition, *PPO* and *pro-*

tease inhibitors (*PIs*) are up-regulated by tobacco Sys as well as by the endogenous supply of a JA derived compound, the methyl jasmonate (MeJA) [60,61]. It has been demonstrated that PIs are very effective against *B. cinerea* both in vitro and in vivo: PIs isolated from young cabbage leaves were able to inhibit *B. cinerea* spore germination and germ tube elongation in vitro [62], whereas a strong inhibitory activity of a PIs mixture purified from tuber sprouts was observed against *B. cinerea* spore germination, germ tube elongation, and necrotic symptom development in vivo [63]. We also observed that the exogenous supply of Sys, under two different delivery systems, is able to induce the transcription of *PR4* genes in the two species. Pathogenesis-related proteins are a group of proteins involved in higher-plant responses to biotic stresses, whose expression is triggered by several pathogens, including fungi, bacteria, and viruses [64]. Many in vitro studies revealed that over-expression in various crops of *PR* genes (*PR2, PR3, PR4, PR5, PR12*), alone or in combination, leads to enhanced disease resistance against biotrophic and necrotrophic fungal phytopathogens [65]. Therefore, the disease reduction observed in our experimental plants is likely due, at least in part, to the increased level of protease inhibitors, polyphenol oxidase and PR4. Sys-treated eggplants showed an increased level of *DFR* transcript. *DFR*, together with *FAL, CHS, CHI* represents an essential component of the anthocyanin biosynthetic pathway. Developmental stages, diverse stresses, such as drought, temperature, wounding, and pathogen attack, are known to regulate anthocyanin biosynthesis. Previous studies showed that MeJA significantly induces anthocyanin accumulation through the up-regulation of genes encoding for anthocyanin biosynthetic enzymes, such as *DFR, LOX,* and *UF3GT* [66,67]. Sys-treated eggplants likely increase the MeJA production that may modulate the anthocyanin biosynthetic pathway [68].

Moreover, in grapevine, we observed that Sys application activated the phenylpropanoid pathway, as shown by the increased level of *FAL* transcript, and the induction of *MYC2* and *FLS5* genes. FAL, the first enzyme of the phenylpropanoid pathway, is involved in the biosynthesis of secondary metabolites, especially the production of phytoalexins and salicylic acid (SA) which were proposed to reduce the incidence of plant disease through antifungal activity and to stimulate plant defense responses, respectively [69,70]. It has also been shown that priming of *FAL1* is associated with responses to pathogen infection and wounding [71]. Interestingly, it was recently demonstrated that the exogenous application of MeJA in grapevine raises *FAL* gene expression and the consequent accumulation of several bioactive compounds (e.g., total phenolic and anthocyanin concentration) [72,73]. Therefore, in grapevine like in eggplant, Sys may induce an increase of MeJA that likely contribute to the accumulation of defense compounds. In addition, the up-regulation of *MYC2*, in Sys-treated grapevine plants, linked to the observed disease reduction, confirmed that this transcription factor is required for JA-mediated defense responses against the necrotrophic fungus *B. cinerea* [74].

Flavonols are the most abundant component of flavonoids, important secondary metabolites with a myriad of functions, including plant defense following pathogen attack, thanks to their antioxidant properties [75]. The increased level of *FLS5* transcripts registered in Sys-treated grapevine plants may favor the accumulation of these compounds that reduce disease severity following fungal infection.

Taken together, the most likely explanation of these results is the ability of Sys to bind SYR-like receptors or closely related genes recently identified in eggplants and grapevine plants, besides other plant species [31]. Following Sys-SYR interaction, the initiated signaling pathway leads to the systemic defense responses by the induction of JA synthesis that triggers the plant defense machine able to reduce the growth of with *B cinerea*.

It was previously shown that in tomato Sys causes very rapid changes in cellular redox homeostasis with the generation of excessive ROS [76,77], which may damage cell organelles. Since our data show that Sys is perceived by both eggplants and grapevine plants, in Sys treated plants, ROS likely increased and the plants reacted by activating the antioxidant defense machinery that boosted the TPC and the activity of CAT and APX enzymes, two key actors of the enzymatic H_2O_2 scavenging mechanism in plants [78].

Generally, in plants, the metabolism of H_2O_2 is controlled by several antioxidant scavenging enzymes, such as SOD, APX, and CAT [79,80]. The increased level of CAT and APX activities observed in treated plants of both species is likely functionally related to the cell requirement of a reduction of redox potential caused by Sys treatment. Similarly, the increased level of phenolic compounds may be linked to this function. In fact, they participate as antioxidants in the prevention of the plant from suffering molecular damage caused by microorganisms, insects, and herbivores [81]. In addition, it is worth noting that phenolic compounds play an important role in plant disease resistance responses representing an early defense plant reply to several biotic stresses [82]. As they are toxic to pathogens, their accumulation at the infection site can restrict pathogen development and the successive plant colonization or contrast infections by increasing the mechanical strength of the host cell wall [83]. Jasmonates (JAs), or their derivates, enhance the accumulation of phenolic compounds in different plant species contributing to the resistance against *B. cinerea* [84,85] and have a pivotal role in the reduction of H_2O_2 level by the enhancement of antioxidant enzymes activity in plant cells [86,87]. Sys-treated plants likely increase the JAs production that may modulate the activity of CAT and APX antioxidant enzymes in both plant species. Previous studies showed that the application of MeJA to in vitro cultures induced not only the expression of defense-related genes but also the antioxidant enzyme activity and the over-production of secondary metabolites [86]. Our results demonstrate the increase of both phenolic content and the antioxidative activity of CAT and APX enzymes likely determined by the activation of the JA pathways triggered by Sys treatment. In our experimental conditions, the increased level of TPC likely contributed to the observed reduction of damages on Sys treated leaves [84,88].

In conclusion, tomato systemin induces resistance against *B. cinerea*, indicating that the two species perceive the non-self-peptide and activate the defense and the antioxidant machineries. These results open a novel perspective on the use of plant peptides in crop protection. From an applied perspective, the exogenous delivery of plant signaling peptides integrated into pest management programs may offer a useful contribution to the reduction of chemical pesticide both in greenhouses and in the field.

Supplementary Materials: The following are available online at https://www.mdpi.com/2309-608X/7/1/15/s1. Table S1: Oligonucleotide sequence, gene symbol, accession number and plant species; Table S2: Effect of systemin peptide on total phenolic content at different times of leaf treatment in eggplant and grapevine plants; Table S3: Effect of systemin peptide on catalase (CAT) and ascorbate peroxidase (APX) activity at different times in eggplant treated leaves; Table S4: Effect of systemin peptide on catalase (CAT) and ascorbate peroxidase (APX) activity at different times in grapevine treated leaves.

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Ethical Statement: The plant species and variety used in this experiment is a widely cultivated variety and we have followed all proper ethical standard. All of the reagent and fertilizers used are properly recommended by the authority.

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Tab. 1. List of differentially expressed genes identified in parental lines

Gene ID	logFC	P-value	FDR	Gene description
Solyc02g063000.4	10,87	4,02E-168	1,29E-164	Glycosyltransferase
Solyc01g091870.3	10,15	3,35E-106	1,95E-103	SPX domain-containing protein
Solyc10g084430.2	9,22	8,61E-100	4,59E-97	RING/U-box superfamily protein
Solyc03g025710.3	9,01	2,53E-162	6,06E-159	Acyl-CoA N-acyltransferase (NAT) superfamily protein
Solyc05g052950.4	8,83	1,29E-98	6,70E-96	Regulator of chromosome condensation (RCC1) family protein
Solyc02g079490.3	8,82	5,79E-138	6,95E-135	HXXXD-type acyl-transferase family protein
Solyc10g005080.3	8,69	3,94E-182	2,52E-178	Late elongated hypocotyl
Solyc10g084370.3	8,48	8,40E-149	1,47E-145	Homeodomain-like superfamily protein
Solyc10g079620.2	8,18	1,36E-171	5,22E-168	haloacid dehalogenase-like hydrolase domain-containing protein 3
Solyc09g011080.3	8,06	6,65E-138	7,51E-135	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic
Solyc07g064410.1	7,91	1,56E-106	9,35E-104	Fatty acid desaturase 4, chloroplastic
Solyc07g042400.2	7,54	6,21E-67	1,11E-64	Unknown protein
Solyc03g098320.4	7,44	2,27E-166	6,21E-163	Protein REVEILLE 1
Solyc04g080040.3	7,29	3,35E-54	3,95E-52	Auxilin-related protein 2
Solyc02g081550.3	7,28	7,05E-37	4,50E-35	LeftsH6FtsH protease
Solyc10g085870.1	7,22	2,67E-73	5,89E-71	Glycosyltransferase
Solyc06g009490.3	7,22	3,28E-14	5,83E-13	Pentatricopeptide repeat
Solyc01g060375.1	7,12	9,53E-10	1,07E-08	Unknown protein
Solyc09g011160.4	7,09	3,18E-91	1,22E-88	Regulator of chromosome condensation (RCC1) family protein
Solyc10g011680.4	7,06	1,14E-13	1,92E-12	Unknown protein
Solyc07g055560.4	7,05	1,43E-76	3,49E-74	Cytochrome
Solyc09g010530.3	7,03	2,48E-112	1,70E-109	Cation/H(+) antiporter 20
Solyc09g092490.3	6,98	5,13E-140	6,57E-137	Glycosyltransferase
Solyc10g085230.2	6,92	9,01E-40	6,34E-38	ripening-related mRNA 1b
Solyc05g055460.1	6,90	7,06E-45	6,22E-43	Unknown protein
Solyc01g107460.2	6,87	4,41E-179	2,11E-175	Neuronal PAS domain protein
Solyc02g084420.3	6,86	5,87E-63	9,24E-61	Zinc finger, B-box
Solyc03g098720.3	6,79	1,28E-11	1,73E-10	Kunitz trypsin inhibitor
Solyc03g098710.1	6,78	2,97E-07	2,34E-06	Kunitz-like protease inhibitor
Solyc02g084430.3	6,78	5,48E-59	7,74E-57	B-box zinc finger protein 19
Solyc12g006050.2	6,69	1,14E-94	5,08E-92	Protein NRT1/ PTR FAMILY 6.4
Solyc06g066700.1	6,60	1,02E-85	3,26E-83	serine-rich protein-like protein
Solyc06g009420.4	6,58	1,39E-18	3,55E-17	Unknown protein
Solyc06g066530.1	6,58	1,62E-41	1,21E-39	DUF1677 domain-containing protein
Solyc05g051580.3	6,49	5,94E-18	1,45E-16	Phototropic-responsive NPH3 family protein
Solyc05g015800.3	6,41	7,02E-37	4,49E-35	Alcohol acyl transferase
Solyc06g063280.1	6,39	7,10E-17	1,58E-15	Zinc finger protein
Solyc02g067230.3	6,32	6,54E-57	8,59E-55	Dof zinc finger protein3
Solyc03g025720.3	6,31	7,48E-78	1,84E-75	Oxalate--CoA ligase
Solyc08g082590.3	6,12	6,40E-135	6,82E-132	Glutaredoxin
Solyc12g038430.3	6,10	1,41E-04	7,10E-04	Transposase, Ptta/En/Spm, plant
Solyc01g099560.3	6,07	9,52E-41	6,97E-39	(+)-neomenthol dehydrogenase-like
Solyc03g120920.1	5,98	1,19E-63	1,92E-61	DUF1677 domain-containing protein
Solyc11g012360.2	5,96	8,06E-58	1,10E-55	Tonoplast dicarboxylate transporter
Solyc11g011340.2	5,89	3,07E-42	2,35E-40	cultivar Rio Grande ELI3
Solyc10g078360.3	5,88	7,99E-05	4,23E-04	NAD(P)-binding Rossmann-fold superfamily protein
Solyc11g006290.2	5,86	1,16E-48	1,15E-46	3-oxo-5-alpha-steroid 4-dehydrogenase
Solyc02g093720.3	5,81	7,77E-40	5,48E-38	TPX2 (Targeting protein for Xklp2) protein family
Solyc09g075470.2	5,80	2,59E-81	6,81E-79	DnaJ-like protein subfamily B member 6
Solyc11g006300.2	5,75	1,09E-67	2,08E-65	3-oxo-5-alpha-steroid 4-dehydrogenase
Solyc12g005310.2	5,72	5,15E-43	4,08E-41	Auxin-responsive GH3 family protein
Solyc05g012230.4	5,71	1,52E-108	9,72E-106	hypothetical protein
Solyc06g064550.3	5,70	4,45E-49	4,52E-47	Aspartokinase-homoserine dehydrogenase
Solyc05g007880.4	5,63	1,78E-78	4,49E-76	cyclic dof factor 2-like
Solyc09g082550.3	5,60	2,22E-76	5,33E-74	Sulfate transporter
Solyc02g092110.3	5,53	1,36E-92	5,67E-90	Phytosulfokines 3
Solyc04g008230.3	5,53	1,01E-18	2,61E-17	Pectin lyase-like superfamily protein
Solyc09g007770.3	5,49	2,74E-13	4,45E-12	plasma membrane intrinsic protein 2.1
Solyc03g097580.4	5,45	8,04E-61	1,20E-58	Bidirectional sugar transporter SWEET
Solyc10g007110.3	5,43	5,39E-98	2,72E-95	Tyrosine aminotransferase
Solyc05g007000.4	5,41	9,04E-27	3,69E-25	Major facilitator superfamily protein
Solyc05g051850.3	5,40	2,58E-134	2,61E-131	putative myo-inositol-1-phosphatase
Solyc07g063120.4	5,34	3,06E-85	9,48E-83	Protein SPA1-RELATED 3
Solyc07g005370.4	5,32	1,07E-58	1,50E-56	Bet v I domain
Solyc06g064610.1	5,28	8,19E-46	7,42E-44	hypothetical protein
Solyc02g089540.3	5,27	1,17E-86	3,86E-84	CONSTANS 1
Solyc05g054750.3	5,26	9,50E-22	2,93E-20	Plant protein 1589 of Uncharacterized protein function
Solyc03g116270.3	5,25	7,20E-44	6,00E-42	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc08g075210.2	5,24	4,04E-37	2,60E-35	HXXXD-type acyl-transferase family protein
Solyc05g011890.1	5,18	4,56E-79	1,18E-76	Sulfotransferase
Solyc01g102610.3	5,17	4,55E-127	3,97E-124	Ferric reduction oxidase 6
Solyc06g036260.3	5,16	3,38E-124	2,82E-121	beta-carotene hydroxylase-1
Solyc03g120020.4	5,16	2,96E-51	3,28E-49	HCO3-transporter family
Solyc11g042630.3	5,14	3,15E-56	4,03E-54	DUF506 domain-containing protein
Solyc03g007370.3	5,13	1,36E-22	4,43E-21	Sigma factor
Solyc03g116730.4	5,11	1,06E-78	2,72E-76	Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplastic
Solyc10g083170.2	5,10	1,08E-31	5,60E-30	NAD(P)-binding Rossmann-fold superfamily protein
Solyc02g086650.3	5,09	3,93E-44	3,35E-42	Phosphoenolpyruvate/phosphate translocator 2, chloroplastic
Solyc02g072540.3	5,09	4,71E-71	9,69E-69	Non-specific serine/threonine protein kinase
Solyc07g047850.3	5,07	1,28E-121	9,67E-119	Chlorophyll a-b binding protein, chloroplastic
Solyc05g050750.1	5,07	1,09E-35	6,71E-34	Calmodulin-like protein 5
Solyc07g005390.3	5,06	2,44E-95	1,14E-92	Aldehyde dehydrogenase 11A3
Solyc07g053140.3	5,06	2,39E-88	8,05E-86	Zinc finger protein/CONSTANS-like protein
Solyc01g066910.3	5,03	1,59E-13	2,64E-12	Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain containing protein
Solyc07g043130.3	5,02	2,33E-74	5,32E-72	Phototropic-responsive NPH3 family protein
Solyc12g094440.2	5,01	8,20E-35	4,84E-33	High mobility group B protein 9
Solyc05g014280.4	5,00	3,46E-16	7,27E-15	small heat shock protein 1
Solyc12g006140.2	4,97	1,83E-96	8,78E-94	Cab-5 gene encoding chlorophyll a/b-binding protein
Solyc10g086720.2	4,96	7,87E-51	8,44E-49	Fructose-1,6-bisphosphatase
Solyc01g095530.2	4,96	4,74E-71	9,69E-69	hypothetical protein
Solyc10g084120.2	4,94	2,39E-13	3,91E-12	plasma membrane intrinsic protein 2.5
Solyc03g096760.1	4,94	1,46E-20	4,23E-19	Protein RESPONSE TO LOW SULFUR 2
Solyc05g054850.1	4,90	4,91E-08	4,35E-07	membrane-associated kinase regulator
Solyc09g082690.3	4,87	6,67E-41	4,91E-39	superoxide dismutase
Solyc08g083190.3	4,82	3,31E-56	4,21E-54	Alpha/beta-Hydrolases superfamily protein
Solyc09g008750.1	4,82	3,38E-10	3,97E-09	VQ motif-containing protein 29
Solyc01g110370.4	4,74	1,56E-68	3,05E-66	Zinc finger, B-box
Solyc09g007760.4	4,72	3,60E-22	1,13E-20	plasma membrane intrinsic protein 2.10
Solyc10g054820.2	4,68	9,67E-74	2,16E-71	X-intrinsic protein 1.2
Solyc12g005750.1	4,68	3,92E-10	4,58E-09	B-box zinc finger protein 32
Solyc11g066140.2	4,68	1,21E-17	2,86E-16	Para-hydroxybenzoic acid efflux pump subunit AaeB/fusaric acid resistance protein
Solyc02g072560.1	4,58	4,40E-16	9,17E-15	Delay of germination 1
Solyc04g015750.3	4,56	1,32E-21	4,05E-20	CobN/magnesium chelatase
Solyc07g064870.3	4,54	2,42E-23	8,33E-22	Endoglucanase
Solyc10g008160.3	4,54	4,35E-43	3,46E-41	uniform ripening
Solyc09g091960.3	4,50	6,13E-42	4,63E-40	High mobility group B protein 15
Solyc09g084460.3	4,50	3,25E-09	3,40E-08	Protease inhibitor I
Solyc05g025890.3	4,50	5,94E-72	1,24E-69	Acyl-CoA N-acyltransferases (NAT) superfamily protein
Solyc02g084990.3	4,50	7,48E-56	9,33E-54	Mannan endo-1,4-beta-mannosidase
Solyc09g089730.3	4,48	1,92E-107	1,19E-104	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein

Solyc05g056470.1	4,45	7,44E-30	3,54E-28	ABC transporter G family member 5
Solyc01g079150.4	4,45	4,93E-44	4,17E-42	HCO3-transporter family
Solyc06g036290.3	4,44	1,81E-18	4,57E-17	heat shock protein 90
Solyc04g010285.1	4,42	1,00E-17	2,40E-16	Plant protein 1589 of Uncharacterized protein function
Solyc06g065970.1	4,42	2,83E-65	4,85E-63	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc03g116630.3	4,42	9,26E-57	1,21E-54	cytochrome P450 family protein
Solyc10g054720.1	4,38	4,52E-16	9,40E-15	Small auxin up-regulated RNA78
Solyc06g083560.3	4,35	4,00E-09	4,12E-08	hypothetical protein
Solyc01g105450.4	4,33	4,43E-46	4,07E-44	ABC transporter G family member 11
Solyc08g083320.4	4,33	1,60E-56	2,06E-54	Starch synthase, chloroplastic/amyloplastic
Solyc10g084230.2	4,30	3,28E-67	5,95E-65	hypothetical protein (DUF1685)
Solyc02g072550.1	4,29	2,26E-12	3,34E-11	Delay of germination 1
Solyc02g089610.2	4,29	3,30E-101	1,87E-98	S-adenosylmethionine decarboxylase 2
Solyc03g096660.2	4,28	3,51E-13	5,64E-12	NAD(P)-binding Rossmann-fold superfamily protein
Solyc06g083800.4	4,28	9,71E-22	2,99E-20	CRIB domain-containing protein RIC6
Solyc07g007260.4	4,27	2,13E-34	1,23E-32	Metallocarboxypeptidase inhibitor
Solyc07g052490.4	4,27	4,56E-15	8,63E-14	MYB-like transcription factor ETC1
Solyc04g050440.3	4,26	5,98E-60	8,64E-58	ammonium transporter
Solyc07g063560.4	4,25	5,07E-10	5,87E-09	Cotton fiber (DUF761)
Solyc02g070980.1	4,25	9,80E-52	1,10E-49	Chlorophyll a-b binding protein, chloroplastic
Solyc07g006670.1	4,25	3,45E-22	1,08E-20	HXXXD-type acyl-transferase family protein
Solyc09g065660.4	4,24	4,82E-44	4,09E-42	Heat shock transcription factor
Solyc09g083090.4	4,24	7,45E-56	9,33E-54	Non-specific serine/threonine protein kinase
Solyc06g062460.3	4,23	3,29E-21	9,88E-20	bHLH transcription factor136
Solyc01g095030.3	4,22	2,42E-82	6,64E-80	Altered Response to Salt Stress 1
Solyc04g072700.4	4,21	2,99E-28	1,31E-26	Heavy metal-associated isoprenylated plant protein
Solyc02g070970.1	4,20	7,11E-28	3,04E-26	Chlorophyll a-b binding protein, chloroplastic
Solyc05g008240.2	4,20	7,47E-24	2,64E-22	myb-related protein Hv1
Solyc05g005870.3	4,20	7,13E-20	1,98E-18	WAT1-related protein
Solyc02g071000.1	4,18	1,02E-31	5,30E-30	Chlorophyll a-b binding protein, chloroplastic
Solyc11g066100.2	4,17	5,62E-26	2,16E-24	Heat shock protein 70
Solyc01g080870.3	4,15	5,78E-45	5,12E-43	Protein NRT1/ PTR FAMILY 7.3
Solyc02g150147.1	4,15	8,45E-76	1,98E-73	S-adenosylmethionine decarboxylase
Solyc02g070940.1	4,13	4,68E-93	2,00E-90	Chlorophyll a-b binding protein, chloroplastic
Solyc11g044250.3	4,11	8,14E-53	9,30E-51	K(+) efflux antiporter 3, chloroplastic
Solyc10g085030.1	4,09	2,38E-55	2,95E-53	Heme-binding-like protein
Solyc11g007540.2	4,08	1,95E-43	1,60E-41	Cytochrome P450
Solyc09g091965.1	4,08	1,45E-15	2,87E-14	Unknown protein
Solyc08g007130.4	4,07	2,28E-51	2,54E-49	Beta-amylase
Solyc06g062540.3	4,04	3,78E-08	3,40E-07	phosphatase (psi14C gene)
Solyc05g024260.3	4,03	3,91E-53	4,49E-51	Bidirectional sugar transporter SWEET
Solyc07g056240.3	4,01	4,17E-58	5,76E-56	myosin-G heavy chain-like protein
Solyc11g011500.2	4,01	3,58E-14	6,35E-13	Potassium channel SKOR
Solyc07g040680.3	4,00	6,33E-18	1,54E-16	Heat shock transcription factor
Solyc02g090350.4	3,98	1,04E-42	8,08E-41	Geraniol 8-hydroxylase
Solyc03g116280.3	3,97	6,17E-55	7,54E-53	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc03g114350.1	3,97	3,23E-68	6,20E-66	DUF1645 family protein
Solyc10g085830.2	3,97	5,89E-84	1,71E-81	O-methyltransferase, putative
Solyc01g094700.4	3,97	3,34E-83	9,56E-81	Glycerol-3-phosphate acyltransferase, expressed
Solyc04g054190.3	3,93	1,13E-23	3,93E-22	Protein kinase superfamily protein
Solyc11g013810.3	3,92	2,20E-35	1,32E-33	Nitrate reductase
Solyc09g090570.2	3,92	8,67E-54	1,01E-51	Proton gradient regulation 5
Solyc03g098010.3	3,92	1,19E-45	1,07E-43	phosphate starvation inducible gene TPSI1
Solyc10g086580.2	3,92	1,19E-50	1,27E-48	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic
Solyc02g071010.1	3,90	2,61E-69	5,17E-67	Chlorophyll a-b binding protein, chloroplastic
Solyc01g096620.4	3,90	4,56E-58	6,25E-56	Cilia-and flagella-associated protein 20
Solyc07g032490.3	3,89	1,11E-56	1,44E-54	Major facilitator superfamily protein
Solyc01g087270.3	3,87	5,32E-44	4,46E-42	Carotenoid cleavage dioxygenase 1
Solyc08g080640.2	3,86	3,23E-13	5,21E-12	NP24 protein precursor
Solyc01g105120.4	3,86	8,79E-47	8,27E-45	protein LNK1
Solyc12g087840.1	3,85	5,26E-23	1,77E-21	RING/U-box superfamily protein
Solyc06g073180.3	3,84	8,31E-71	1,68E-68	CONSTANS interacting protein 1
Solyc06g005910.4	3,84	2,29E-54	2,72E-52	Tubulin beta chain
Solyc01g087150.3	3,84	2,85E-20	8,09E-19	Protein DETOXIFICATION
Solyc03g112010.4	3,84	5,09E-44	4,29E-42	Cytochrome P450 71A6
Solyc04g054740.3	3,81	1,89E-54	2,25E-52	myo-inositol-1-phosphate synthase
Solyc01g068560.3	3,81	8,87E-63	1,38E-60	protein LNK2 isoform X1
Solyc02g077130.2	3,80	2,14E-20	6,14E-19	GDSL esterase/lipase
Solyc00g500065.1	3,80	2,99E-03	1,09E-02	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic
Solyc04g064670.3	3,79	3,02E-60	4,43E-58	Photosystem II reaction center PsbP family protein
Solyc08g076150.4	3,79	1,02E-44	8,93E-43	Pentatricopeptide repeat-containing protein
Solyc01g058720.4	3,79	9,36E-27	3,82E-25	Calcium-binding EF-hand
Solyc07g019460.3	3,78	1,01E-69	2,02E-67	NADPH--cytochrome P450 reductase
Solyc06g073320.3	3,77	2,48E-94	1,08E-91	GDP-L-galactose phosphorylase 1
Solyc03g119540.3	3,77	5,30E-20	1,48E-18	Zinc finger protein
Solyc09g008360.2	3,76	1,29E-03	5,18E-03	Heparan-alpha-glucosaminide N-acetyltransferase-like protein (DUF1624)
Solyc02g085490.2	3,76	3,25E-11	4,23E-10	DUF620 domain-containing protein
Solyc10g081560.3	3,75	2,88E-33	1,61E-31	NAD(P)-binding Rossmann-fold superfamily protein
Solyc12g095750.2	3,75	2,32E-41	1,72E-39	Auxin efflux carrier
Solyc01g096630.3	3,75	4,04E-57	5,45E-55	Cilia-and flagella-associated protein 20
Solyc12g094690.1	3,74	1,60E-21	4,86E-20	RING/U-box superfamily protein
Solyc04g008330.1	3,74	2,61E-35	1,56E-33	Glycosyltransferase
Solyc00g500063.1	3,73	1,86E-07	1,51E-06	Ribulose bisphosphate carboxylase large chain
Solyc06g049050.3	3,73	2,04E-45	1,83E-43	expansin 2
Solyc01g094210.2	3,72	3,85E-47	3,70E-45	NAD(P)-binding Rossmann-fold superfamily protein
Solyc12g014580.2	3,71	1,22E-08	1,18E-07	Major pollen allergen Ole e 6
Solyc09g010940.4	3,71	2,88E-74	6,51E-72	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Solyc08g066420.1	3,71	5,70E-30	2,73E-28	Polyketide cyclase/dehydrase and lipid transport superfamily protein
Solyc10g052550.1	3,70	1,50E-07	1,24E-06	Small auxin up-regulated RNA74
Solyc08g067540.1	3,69	6,97E-40	4,94E-38	Non-specific lipid-transfer protein
Solyc10g083940.1	3,69	2,24E-32	1,22E-30	Major facilitator superfamily
Solyc03g006620.3	3,69	3,65E-51	4,01E-49	Cotton fiber (DUF761)
Solyc06g069730.3	3,69	9,37E-25	3,43E-23	Chlorophyll a-b binding protein, chloroplastic
Solyc10g078410.2	3,67	2,86E-31	1,46E-29	F-box protein
Solyc10g008660.2	3,67	5,74E-36	3,55E-34	Anthocyanidin 3-O-glucoside-6''-O-malonyltransferase
Solyc06g051940.4	3,66	2,84E-11	3,73E-10	Protein phosphatase 2C
Solyc06g035530.3	3,65	2,01E-05	1,20E-04	gibberellin 20-oxidase-2
Solyc08g006160.4	3,64	7,99E-75	1,85E-72	Plastid-lipid associated protein PAP / fibrillin family protein
Solyc04g071150.3	3,61	3,29E-08	2,99E-07	Cytochrome P450
Solyc02g069490.4	3,60	5,47E-15	1,03E-13	Delta(24)-sterol reductase
Solyc05g053210.4	3,60	2,37E-59	3,39E-57	Non-specific serine/threonine protein kinase
Solyc11g065830.2	3,60	1,38E-35	8,36E-34	Dicarboxylate transporter 1, chloroplastic
Solyc09g082630.3	3,59	6,28E-82	1,67E-79	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase
Solyc08g082890.3	3,59	2,34E-10	2,80E-09	R2R3MYB transcription factor 9
Solyc09g089620.1	3,59	1,07E-06	7,76E-06	AT-hook motif nuclear-localized protein
Solyc03g097370.4	3,58	7,68E-28	3,27E-26	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc07g043390.4	3,58	1,94E-13	3,21E-12	Cellulose synthase
Solyc03g115230.3	3,57	7,29E-17	1,62E-15	Solanum lycopersicum heat shock protein
Solyc03g121240.1	3,56	9,25E-19	2,38E-17	Transcription factor HEC2
Solyc03g111950.3	3,55	2,38E-18	5,95E-17	Cytochrome P450 71A6
Solyc01g095960.4	3,55	2,75E-07	2,18E-06	O-acyltransferase WSD1-like
Solyc04g052990.1	3,54	1,28E-08	1,23E-07	Auxin-responsive protein SAUR65
Solyc01g110660.4	3,54	1,12E-22	3,68E-21	Auxin-responsive protein SAUR21
Solyc01g110940.3	3,54	4,57E-30	2,22E-28	Auxin-responsive protein SAUR20
Solyc08g075540.5.1	3,53	4,25E-57	5,70E-55	alternative oxidase
Solyc06g005750.3	3,53	1,86E-48	1,83E-46	Methylsterol monooxygenase 2-1

Solyc07g005510.3	3,52	1,80E-53	2,09E-51	Omega-6 fatty acid desaturase, chloroplastic
Solyc11g069650.2	3,52	1,96E-05	1,17E-04	Unknown protein
Solyc04g016230.4	3,51	2,38E-30	1,18E-28	Glycosyltransferase
Solyc02g070920.3	3,51	1,14E-19	3,13E-18	Unknown protein
Solyc07g052150.4	3,51	4,88E-06	3,21E-05	Sesquiterpene synthase
Solyc03g117600.3	3,50	1,80E-31	9,30E-30	Transferase
Solyc03g123540.3	3,50	6,25E-19	1,63E-17	17.4 kDa class III heat shock protein
Solyc06g061027.1	3,49	7,10E-16	1,46E-14	Cytochrome P450
Solyc09g010570.1	3,48	1,47E-14	2,70E-13	Para-hydroxybenzoic acid efflux pump subunit AaeB/fusaric acid resistance protein
Solyc12g039080.3	3,48	7,06E-06	4,53E-05	Leucine-rich repeat protein kinase family protein
Solyc03g096650.2	3,48	1,28E-08	1,23E-07	Tropinone reductase-like protein
Solyc09g005610.4	3,47	1,11E-15	2,23E-14	Transcription factor
Solyc09g011130.1	3,47	1,98E-11	2,63E-10	NAD(P)-binding Rossmann-fold superfamily protein
Solyc03g116910.3	3,47	1,32E-44	1,15E-42	cinnamoyl-CoA reductase 2
Solyc12g011450.2	3,47	2,12E-49	2,18E-47	Chlorophyll a-b binding protein, chloroplastic
Solyc05g051200.1	3,46	1,38E-20	4,01E-19	ethylene-responsive factor 1
Solyc02g067790.4	3,46	1,16E-19	3,17E-18	High affinity nitrate transporter 2.7
Solyc07g043420.3	3,46	3,33E-26	1,31E-24	2-oxoglutarate-dependent dioxygenase 2
Solyc07g008240.3	3,46	2,01E-09	2,17E-08	Non-symbiotic hemoglobin like
Solyc10g009270.3	3,45	1,34E-08	1,28E-07	bHLH transcription factor154
Solyc08g077170.3	3,45	1,85E-28	8,26E-27	Protein NRT1/ PTR FAMILY 7.3
Solyc07g047940.4	3,44	3,60E-24	1,28E-22	Zinc finger transcription factor 49
Solyc11g011740.1	3,43	2,11E-08	1,98E-07	Ethylene-responsive transcription factor
Solyc08g078670.2	3,43	3,10E-29	1,43E-27	Eukaryotic aspartyl protease family protein
Solyc05g053760.4	3,41	9,95E-47	9,31E-45	Chaperone protein DnaJ
Solyc11g012850.2	3,41	2,82E-37	1,83E-35	Chlorophyllide a oxygenase, chloroplastic
Solyc06g076020.3	3,41	1,91E-14	3,46E-13	heat shock protein 70 kD
Solyc10g005030.4	3,41	5,25E-18	1,28E-16	Two-component response regulator-like APRR5
Solyc10g079210.2	3,41	5,40E-19	1,41E-17	Glycosyltransferase-like KOBITO 1
Solyc05g053120.1	3,40	7,10E-16	1,46E-14	Glycosyltransferase
Solyc12g013840.3	3,39	1,03E-24	3,78E-23	Protein SPA1-RELATED 3
Solyc01g090965.1	3,38	2,31E-43	1,87E-41	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc05g050240.3	3,38	3,49E-22	1,10E-20	Plastid division protein PDV1
Solyc03g116290.3	3,36	3,65E-10	4,27E-09	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc01g097770.4	3,36	1,33E-10	1,63E-09	phototropin 2
Solyc01g009080.4	3,35	1,66E-44	1,43E-42	Zeaxanthin epoxidase, chloroplastic
Solyc05g053400.3	3,34	2,94E-21	8,88E-20	Glycosyltransferase
Solyc09g092480.1	3,34	5,53E-38	3,71E-36	Glycosyltransferase
Solyc10g077040.2	3,33	1,01E-63	1,65E-61	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic
Solyc02g086350.3	3,32	8,38E-12	1,16E-10	Protein PLASTID MOVEMENT IMPAIRED 2
Solyc01g110360.3	3,31	1,12E-49	1,17E-47	Fructose-bisphosphate aldolase
Solyc09g061715.1	3,31	7,46E-08	6,40E-07	hypothetical protein
Solyc02g080640.4	3,30	1,55E-31	8,02E-30	adenylyl-sulfate reductase
Solyc01g105387.1	3,29	2,41E-07	1,93E-06	ABC transporter G family member 11
Solyc12g040640.2	3,28	4,73E-17	1,07E-15	Beta-glucosidase
Solyc09g009420.1	3,28	6,78E-31	3,42E-29	hypothetical protein
Solyc08g062340.3	3,28	9,28E-14	1,58E-12	17.9 kDa class II heat shock protein
Solyc07g055550.2	3,28	2,38E-08	2,22E-07	Cytochrome
Solyc10g083690.3	3,26	6,58E-19	1,71E-17	Cytochrome P450
Solyc07g039310.1	3,26	2,78E-32	1,50E-30	lysine-specific histone demethylase 1 homolog 1
Solyc04g077500.4	3,25	1,48E-67	2,76E-65	transmembrane protein
Solyc02g082760.3	3,25	7,18E-67	1,28E-64	ethylene-responsive catalase
Solyc07g065160.4	3,25	1,93E-27	8,14E-26	Pirin-like protein
Solyc09g092500.1	3,25	4,14E-43	3,33E-41	UDP-glycosyltransferase 75C1
Solyc07g006700.1	3,23	3,99E-15	7,62E-14	Pathogenesis-related protein PR-1
Solyc12g096770.1	3,23	7,99E-31	4,02E-29	HXXXD-type acyl-transferase family protein
Solyc02g092700.3	3,23	4,72E-64	7,80E-62	DUF1230 family protein (DUF1230)
Solyc07g007250.4	3,21	1,25E-10	1,53E-09	Metallocarboxypeptidase inhibitor
Solyc08g062437.1	3,21	3,42E-09	3,56E-08	17.9 kDa class II heat shock protein
Solyc04g011440.4	3,21	1,46E-19	3,95E-18	ethylene-responsive heat shock protein cognate 70
Solyc02g065610.3	3,20	1,10E-26	4,44E-25	Protein trichome birefringence-like 21
Solyc12g015630.2	3,19	3,69E-36	2,30E-34	transmembrane protein
Solyc09g008970.1	3,19	1,39E-06	9,90E-06	plant/protein
Solyc01g102280.3	3,19	9,07E-16	1,84E-14	Unknown protein
Solyc07g042500.4	3,18	5,80E-19	1,52E-17	alpha/beta-Hydrolases superfamily protein
Solyc03g111993.1	3,18	6,38E-15	1,20E-13	Cytochrome P450
Solyc09g011140.4	3,18	1,25E-58	1,74E-56	NAD(P)-binding Rossmann-fold superfamily protein
Solyc05g010630.4	3,18	1,06E-09	1,19E-08	RING-type E3 ubiquitin transferase
Solyc11g005190.3	3,17	1,98E-23	6,85E-22	WD40 repeat
Solyc09g007910.4	3,16	2,02E-28	8,98E-27	Phenylalanine ammonia-lyase
Solyc04g040160.4	3,16	3,25E-44	2,78E-42	Protochlorophyllide-dependent translocon component 52, chloroplastic
Solyc01g087260.4	3,15	3,78E-28	1,64E-26	carotenoid cleavage dioxygenase 1B
Solyc01g110570.3	3,15	4,37E-29	2,00E-27	Small auxin up-regulated RNA4
Solyc04g015030.4	3,14	3,00E-19	7,94E-18	Heavy metal-associated isoprenylated plant protein
Solyc12g039100.2	3,14	9,02E-07	6,61E-06	ACT domain-containing protein
Solyc10g078580.1	3,14	2,42E-28	1,07E-26	arabinogalactan protein 14
Solyc02g071030.2	3,14	4,07E-61	6,15E-59	Chlorophyll a-b binding protein, chloroplastic
Solyc09g007920.4	3,13	6,44E-18	1,56E-16	Phenylalanine ammonia-lyase
Solyc12g088190.2	3,12	7,20E-28	3,08E-26	Amino acid permease
Solyc02g086180.4	3,12	1,01E-25	3,87E-24	Delta(7)-sterol-C5(6)-desaturase
Solyc07g042630.4	3,11	1,48E-26	5,96E-25	Terpene cyclase/mutase family member
Solyc05g005480.2	3,11	4,47E-60	6,49E-58	Quinone oxidoreductase-like protein
Solyc01g006790.3	3,09	2,77E-25	1,04E-23	hypothetical protein
Solyc03g082610.1	3,08	4,17E-40	2,98E-38	Senescence regulator S40
Solyc01g095240.3	3,07	4,50E-21	1,35E-19	Calcium-transporting ATPase 2, endoplasmic reticulum-type
Solyc07g061990.3	3,06	3,68E-64	6,19E-62	Solanesyl diphosphate synthase
Solyc06g060340.3	3,06	7,75E-28	3,30E-26	Photosystem II 22 kDa protein, chloroplastic
Solyc08g014440.4	3,06	6,13E-39	4,22E-37	BTB/POZ and TAZ domain-containing protein 3
Solyc05g013380.3	3,05	3,56E-50	3,71E-48	Alanine aminotransferase 2
Solyc00g500066.1	3,05	6,99E-03	2,26E-02	Photosystem I assembly protein Ycf4
Solyc09g008760.1	3,04	8,61E-06	5,43E-05	VQ motif-containing protein 29
Solyc03g111997.1	3,03	2,30E-17	5,33E-16	Cytochrome P450
Solyc06g060830.3	3,02	1,05E-43	8,69E-42	Homeobox-leucine zipper protein HAT2
Solyc01g067660.3	3,02	7,11E-46	6,47E-44	1,4-alpha-glucan-maltohydrolase
Solyc03g117870.3	3,02	2,51E-52	2,83E-50	4-coumarate:CoA ligase
Solyc09g008780.4	3,02	1,31E-38	8,92E-37	Sulfite exporter TauE/SafE family protein
Solyc06g060310.3	3,01	1,65E-39	1,15E-37	Chlorophyllide a oxygenase, chloroplastic
Solyc05g049990.4	3,01	7,83E-30	3,70E-28	Heavy metal-associated isoprenylated plant protein
Solyc06g053260.1	3,01	5,23E-28	2,26E-26	Auxin-responsive protein SAUR32
Solyc12g006805.1	3,01	6,50E-57	8,59E-55	SOUL heme-binding family protein
Solyc10g079200.2	3,00	1,88E-42	1,44E-40	Mitochondrial carnitine/acylcarnitine carrier-like protein
Solyc08g080540.3	3,00	2,90E-37	1,88E-35	Heat stress transcription factor B-2b
Solyc06g068970.3	3,00	3,15E-28	1,38E-26	3-oxo-5-alpha-steroid 4-dehydrogenase (DUF1295)
Solyc02g086452.1	3,00	2,21E-09	2,38E-08	titin isoform X3
Solyc03g115900.4	3,00	8,35E-39	5,72E-37	Chlorophyll a-b binding protein, chloroplastic
Solyc12g011280.2	2,99	8,93E-55	1,09E-52	Chlorophyll a-b binding protein, chloroplastic
Solyc02g086820.3	2,98	3,22E-07	2,53E-06	chloroplast carbonic anhydrase
Solyc03g116770.3	2,98	3,93E-07	3,04E-06	seed dormancy control protein
Solyc02g084440.4	2,98	1,22E-60	1,81E-58	Fructose-bisphosphate aldolase
Solyc12g042120.3	2,97	4,88E-08	4,32E-07	transmembrane protein
Solyc02g071380.2	2,97	2,56E-48	2,50E-46	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc04g080620.3	2,97	1,94E-09	2,10E-08	Mannan endo-1,4-beta-mannosidase 1
Solyc01g066980.3	2,97	2,31E-08	2,16E-07	Flowering-promoting factor 1
Solyc06g053620.4	2,97	1,37E-32	7,55E-31	phosphoenolpyruvate carboxylase kinase 2
Solyc02g089120.4	2,96	1,18E-46	1,10E-44	COBRA-like protein
Solyc08g080650.3	2,96	4,95E-10	5,73E-09	PATHOGENESIS RELATED PROTEIN P23

Solyc08g081690.3	2,95	2,13E-30	1,05E-28	NADPH oxidase
Solyc04g080820.2	2,95	1,55E-15	3,07E-14	cytokinin oxidase4
Solyc01g109120.3	2,94	9,94E-10	1,12E-08	Transducin/WD40 repeat-like superfamily protein
Solyc09g091030.3	2,94	2,10E-52	2,38E-50	Beta-amylase
Solyc11g010380.2	2,93	3,82E-22	1,20E-20	Protein DETOXIFICATION
Solyc04g009050.4	2,93	1,99E-20	5,72E-19	agglutinin-like protein
Solyc12g094570.1	2,92	1,50E-19	4,05E-18	inactive purple acid phosphatase-like protein
Solyc09g009010.4	2,92	2,98E-29	1,38E-27	Glucomannan 4-beta-mannosyltransferase 2
Solyc10g052530.1	2,92	1,57E-12	2,36E-11	Small auxin up-regulated RNA72
Solyc11g011440.1	2,91	6,94E-26	2,67E-24	aspartic proteinase PCS1-like
Solyc01g079160.4	2,90	2,87E-09	3,02E-08	GDSL esterase/lipase
Solyc01g102960.3	2,90	1,08E-08	1,05E-07	22.0 kDa class IV heat shock protein
Solyc08g075790.4	2,90	2,11E-27	8,86E-26	Vacuolar protein sorting-associated protein 62
Solyc09g089930.3	2,90	2,56E-08	2,36E-07	ethylene responsive factor E.2
Solyc03g093140.3	2,90	4,07E-47	3,88E-45	Glycerol-3-phosphate transporter 1-like protein
Solyc12g056600.3	2,90	6,14E-15	1,15E-13	NAD(P)-binding Rossmann-fold superfamily protein
Solyc01g058250.2	2,89	4,00E-04	1,81E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc04g079420.3	2,89	3,39E-25	1,26E-23	Disease resistance protein (CC-NBS-LRR class) family
Solyc10g085880.1	2,89	5,80E-30	2,78E-28	UDP-glycosyltransferase 73C4
Solyc11g010560.3	2,89	3,14E-09	3,30E-08	Kinesin
Solyc01g091320.3	2,89	7,79E-17	1,72E-15	Methylsterol monooxygenase 1-2
Solyc03g031860.3	2,89	3,45E-50	3,64E-48	Phytoene synthase 1,Pfam:PF00494
Solyc04g051420.3	2,89	1,72E-05	1,03E-04	Unknown protein
Solyc01g006290.4	2,88	2,07E-22	6,64E-21	Peroxidase
Solyc06g071750.3	2,88	1,78E-20	5,11E-19	Octicosapeptide/Phox/Bem1p
Solyc06g074200.4	2,88	1,53E-35	9,26E-34	Photosystem I subunit O
Solyc08g078700.2	2,88	1,62E-18	4,12E-17	mitochondrial small heat shock protein
Solyc06g065380.4	2,88	1,07E-13	1,81E-12	Calcium-dependent protein kinase
Solyc06g075550.3	2,87	3,89E-30	1,89E-28	Receptor-like cytoplasmic protein kinase 1
Solyc10g054870.3	2,86	2,89E-24	1,03E-22	Triosephosphate isomerase
Solyc06g061023.1	2,86	1,29E-05	7,94E-05	Cytochrome
Solyc01g095570.3	2,86	7,75E-30	3,67E-28	Mitochondrial carrier protein
Solyc02g037550.3	2,86	2,11E-21	6,39E-20	Auxin efflux carrier
Solyc09g007150.3	2,85	6,08E-31	3,08E-29	Glutathione S-transferase
Solyc01g109500.4	2,85	3,03E-16	6,40E-15	BURP domain-containing protein
Solyc03g026370.1	2,85	4,10E-09	4,22E-08	Peptidoglycan-binding LysM domain-containing protein
Solyc09g014350.3	2,85	1,32E-24	4,78E-23	Glycerol-3-phosphate acyltransferase, expressed
Solyc04g005610.3	2,85	9,17E-19	2,37E-17	NAC domain-containing protein 2
Solyc04g005100.3	2,85	8,83E-19	2,28E-17	transcription factor MYB1R1-like
Solyc02g020910.4	2,84	3,05E-08	2,78E-07	Unknown protein
Solyc01g098130.2	2,84	3,32E-05	1,90E-04	Unknown protein
Solyc09g065780.3	2,83	4,88E-32	2,58E-30	3-ketoacyl-CoA synthase
Solyc01g107910.4	2,83	2,54E-37	1,65E-35	caffeoyl-CoA O-methyltransferase
Solyc03g117050.4	2,82	2,98E-27	1,25E-25	NOD26-like intrinsic protein 6.1
Solyc03g005780.3	2,82	2,17E-49	2,23E-47	Chlorophyll a-b binding protein, chloroplastic
Solyc01g094910.3	2,82	1,33E-25	5,04E-24	ferric-chelate reductase
Solyc04g077440.4	2,82	1,24E-27	5,22E-26	Squalene epoxidase
Solyc02g069860.4	2,81	6,90E-23	2,30E-21	Nuclear transcription factor Y subunit A-7
Solyc03g007890.3	2,81	2,66E-28	1,17E-26	class 2 small heat shock protein Le-HSP17.6
Solyc09g091580.3	2,81	2,60E-50	2,75E-48	Protein kinase domain
Solyc10g009150.3	2,81	6,26E-22	1,94E-20	Organ specific protein
Solyc12g042090.1	2,81	2,00E-17	4,67E-16	Unknown protein
Solyc03g078780.3	2,80	1,56E-20	4,51E-19	UDP-glycosyltransferase 76C4-like
Solyc12g005660.2	2,80	1,00E-19	2,76E-18	Zinc finger protein/CONSTANS-like protein
Solyc06g073290.1	2,79	4,31E-43	3,44E-41	Tetrapyrrole-binding protein, chloroplastic
Solyc07g032380.4	2,79	4,42E-34	2,55E-32	Pentatricopeptide repeat-containing protein
Solyc12g014530.3	2,78	6,83E-21	2,03E-19	L-aspartate oxidase
Solyc01g014320.4	2,77	4,66E-25	1,74E-23	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc01g095720.3	2,75	7,90E-10	8,96E-09	Alpha/beta-Hydrolases superfamily protein
Solyc10g075160.1	2,75	4,06E-19	1,07E-17	Ferredoxin
Solyc07g045140.4	2,75	3,90E-13	6,23E-12	transmembrane protein
Solyc05g012030.1	2,75	7,46E-07	5,54E-06	protein BIG GRAIN 1-like E
Solyc02g070950.1	2,75	1,42E-32	7,81E-31	Chlorophyll a-b binding protein, chloroplastic
Solyc07g007200.4	2,73	2,20E-28	9,72E-27	RING/U-box superfamily protein
Solyc08g082010.3	2,73	3,26E-05	1,86E-04	Myosin heavy chain-related protein
Solyc03g111690.4	2,73	2,54E-40	1,83E-38	Pectate lyase
Solyc04g071340.5	2,73	1,88E-13	3,12E-12	Fructose-1,6-bisphosphatase
Solyc03g114450.3	2,72	9,95E-43	7,79E-41	Calcium sensing receptor, chloroplastic
Solyc02g072260.4	2,72	6,81E-18	1,65E-16	Rho termination factor
Solyc11g073120.2	2,72	7,16E-34	4,08E-32	R2R3MYB transcription factor 58
Solyc06g060640.1	2,72	3,69E-41	2,73E-39	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc05g008070.4	2,72	3,60E-14	6,38E-13	Disease resistance protein
Solyc08g075470.3	2,72	1,52E-32	8,33E-31	WAT1-related protein
Solyc04g008570.4	2,72	9,78E-31	4,91E-29	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc02g063355.1	2,71	2,63E-23	9,03E-22	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc03g046440.3	2,71	5,96E-09	5,98E-08	Basic leucine zipper 43
Solyc01g098820.3	2,71	2,14E-07	1,73E-06	Phototropic-responsive NPH3 family protein
Solyc10g085040.1	2,71	1,14E-29	5,39E-28	Heme-binding-like protein
Solyc04g005090.4	2,70	5,24E-31	2,67E-29	Cofactor assembly of complex C
Solyc00g021640.2	2,70	6,31E-03	2,07E-02	Ribosomal protein S4
Solyc02g086454.1	2,70	2,37E-07	1,90E-06	titin isoform X6
Solyc05g005540.4	2,70	2,59E-09	2,74E-08	Polygalacturonase-1 non-catalytic subunit beta
Solyc02g084400.4	2,69	6,60E-28	2,84E-26	Protein kinase superfamily protein
Solyc07g008210.4	2,69	9,18E-29	4,14E-27	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc02g070990.1	2,69	2,14E-12	3,18E-11	Chlorophyll a-b binding protein, chloroplastic
Solyc11g072110.2	2,68	2,92E-30	1,44E-28	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc03g006780.2	2,68	8,62E-11	1,08E-09	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc09g007900.4	2,68	3,55E-10	4,17E-09	Phenylalanine ammonia-lyase
Solyc12g008530.2	2,68	1,48E-12	2,23E-11	Pectinesterase
Solyc05g053890.3	2,68	2,12E-22	6,78E-21	Glycosyltransferase
Solyc05g007950.4	2,68	6,95E-05	3,72E-04	LERNALE L.esculentum ribonuclease le
Solyc01g096410.4	2,67	1,37E-07	1,14E-06	Phosphatidylinositol 4-phosphate 5-kinase
Solyc06g063190.3	2,67	2,46E-14	4,43E-13	glutamate receptor-like 2.3
Solyc05g009500.3	2,66	8,38E-23	2,78E-21	Protein NRT1/ PTR FAMILY 3.1
Solyc06g073260.3	2,66	2,27E-37	1,50E-35	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic
Solyc08g078840.3	2,66	1,30E-15	2,60E-14	Root meristem growth factor 6
Solyc04g081290.3	2,66	2,13E-34	1,23E-32	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc07g051820.3	2,64	1,17E-37	7,82E-36	Cellulose synthase
Solyc08g005100.3	2,64	4,63E-26	1,80E-24	PLATZ transcription factor family protein
Solyc01g090340.3	2,64	1,55E-16	3,32E-15	Ethylene-responsive transcription factor 2
Solyc12g094580.3	2,63	1,69E-14	3,08E-13	inactive purple acid phosphatase-like protein
Solyc08g016080.3	2,63	2,22E-12	3,28E-11	High chlorophyll fluorescence phenotype 173
Solyc02g077140.3	2,63	9,27E-19	2,39E-17	Phospholipase A1-II 1
Solyc04g072740.3	2,62	9,78E-36	6,01E-34	Sulfate transporter 2.1
Solyc01g091260.3	2,62	6,64E-11	8,43E-10	myeloid leukemia factor
Solyc01g105050.3	2,62	2,31E-37	1,52E-35	Chlorophyll a-b binding protein, chloroplastic
Solyc04g009960.3	2,62	2,45E-44	2,11E-42	Threonine aldolase
Solyc06g069600.3	2,61	1,09E-08	1,06E-07	bHLH transcription factor 047
Solyc11g066660.3	2,61	7,02E-14	1,21E-12	Magnesium transporter MRS2-A, chloroplastic
Solyc07g007560.3	2,61	2,58E-25	9,73E-24	Phosphate transporter 45
Solyc10g084380.1	2,61	2,62E-06	1,80E-05	WRKY transcription factor 44
Solyc02g082737.1	2,60	4,34E-08	3,87E-07	Unknown protein
Solyc02g092580.3	2,59	6,32E-11	8,03E-10	Peroxidase
Solyc08g067530.1	2,59	5,18E-25	1,92E-23	Non-specific lipid-transfer protein
Solyc09g059240.3	2,59	1,12E-38	7,65E-37	Cytochrome P450
Solyc12g042910.2	2,59	1,41E-21	4,32E-20	DNA photolyase

Solyc04g011870.1	2,59	2,98E-04	1,39E-03	Glutaredoxin
Solyc06g036110.1	2,58	2,05E-15	4,02E-14	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc10g079610.2	2,58	2,07E-29	9,69E-28	Strictosidine synthase family protein
Solyc02g086456.1	2,57	1,64E-05	9,91E-05	titin isoform X6
Solyc02g062340.3	2,57	6,28E-32	3,29E-30	Fructose-bisphosphate aldolase
Solyc09g065570.4	2,57	3,20E-10	3,77E-09	Serine/threonine-protein kinase Nek2
Solyc01g010000.3	2,57	2,07E-34	1,21E-32	ACT domain-containing protein
Solyc08g013670.3	2,57	4,69E-32	2,49E-30	Photosystem I reaction center subunit N, chloroplastic
Solyc01g008850.3	2,57	1,68E-28	7,53E-27	Non-specific serine/threonine protein kinase
Solyc09g011490.3	2,57	2,52E-25	9,51E-24	Glutathione S-transferase
Solyc03g115980.1	2,57	8,04E-25	2,95E-23	Geranylgeranyl diphosphate reductase, chloroplastic
Solyc09g075210.3	2,56	1,16E-29	5,47E-28	Late embryogenesis abundant protein Lea5
Solyc11g066670.1	2,56	6,52E-17	1,46E-15	Glycosyltransferase
Solyc08g008480.4	2,56	2,74E-13	4,45E-12	R2R3MYB transcription factor 4
Solyc03g019790.3	2,56	2,35E-32	1,28E-30	alpha-galactosidase
Solyc01g105880.4	2,55	1,05E-04	5,42E-04	Monoterpenoid synthase 2
Solyc10g044700.2	2,55	9,01E-05	4,72E-04	Calcium-binding EF-hand
Solyc08g065220.3	2,54	4,01E-20	1,13E-18	glycine decarboxylase p-protein
Solyc04g040190.1	2,54	1,40E-33	7,93E-32	lycopene beta-cyclase,Pfam:PF05834
Solyc02g062610.3	2,54	7,87E-43	6,19E-41	Alpha/beta-Hydrolases superfamily protein
Solyc07g006230.1	2,53	1,05E-22	3,47E-21	Unknown protein
Solyc04g082480.3	2,53	7,08E-18	1,71E-16	Plant regulator RWP-RK family protein, putative
Solyc01g108630.3	2,53	1,75E-11	2,34E-10	nii1 nitrite reductase
Solyc02g082100.4	2,53	3,34E-08	3,03E-07	RING/U-box superfamily protein
Solyc05g056300.4	2,52	1,02E-42	7,93E-41	Thioredoxin F-type, chloroplastic
Solyc01g005590.2	2,51	1,29E-24	4,69E-23	Unknown protein
Solyc04g064630.3	2,51	6,03E-11	7,69E-10	Bidirectional sugar transporter SWEET
Solyc07g045160.3	2,50	4,71E-33	2,61E-31	ATP-dependent 6-phosphofructokinase
Solyc11g022590.1	2,50	2,29E-08	2,14E-07	trypsin inhibitor-like protein precursor
Solyc07g025140.4	2,49	8,88E-12	1,23E-10	Transducin/WD40 repeat-like superfamily protein
Solyc10g086390.2	2,49	3,05E-20	8,63E-19	Short-chain dehydrogenase TIC 32, chloroplastic
Solyc04g080380.3	2,49	4,77E-17	1,08E-15	Leucine carboxyl methyltransferase
Solyc06g075090.4	2,49	3,69E-20	1,04E-18	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc10g007750.1	2,49	1,24E-07	1,04E-06	Plant basic secretory protein (BSP) family protein
Solyc08g013740.4	2,48	1,34E-11	1,81E-10	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc02g081180.2	2,48	3,06E-05	1,76E-04	RING/U-box superfamily protein
Solyc01g087710.2	2,48	3,08E-26	1,21E-24	UPF0114 domain-containing protein
Solyc08g081220.1	2,47	2,46E-24	8,80E-23	Cytochrome P450
Solyc02g081170.4	2,47	1,07E-37	7,18E-36	plastid lipid associated protein CHRC
Solyc12g010550.1	2,47	1,22E-08	1,17E-07	counting factor 45-1-like
Solyc10g055680.1	2,47	4,13E-22	1,29E-20	Methyltransferase
Solyc01g105030.3	2,46	6,78E-43	5,36E-41	Chlorophyll a-b binding protein, chloroplastic
Solyc06g060620.4	2,46	4,92E-09	5,01E-08	Protein NRT1/ PTR FAMILY 6.3
Solyc08g074960.3	2,46	4,12E-20	1,15E-18	Major facilitator superfamily protein
Solyc01g107890.3	2,46	1,78E-05	1,07E-04	Filament-like plant protein 7
Solyc07g063600.3	2,45	4,66E-42	3,55E-40	Chlorophyll a-b binding protein, chloroplastic
Solyc05g052670.1	2,45	1,17E-04	5,95E-04	HXXXD-type acyl-transferase family protein
Solyc02g088530.1	2,44	5,38E-07	4,08E-06	Unknown protein
Solyc08g079180.3	2,44	3,16E-08	2,88E-07	Elongation factor G
Solyc06g066650.4	2,44	4,04E-16	8,45E-15	Rop guanine nucleotide exchange factor 12
Solyc01g103100.3	2,43	4,15E-29	1,92E-27	NAD(P)-binding Rossmann-fold superfamily protein
Solyc05g052275.1	2,43	5,51E-13	8,65E-12	Unknown protein
Solyc04g008370.3	2,43	1,38E-10	1,68E-09	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc11g044520.1	2,43	9,78E-05	5,09E-04	Unknown protein
Solyc06g074090.3	2,43	1,41E-22	4,58E-21	7-dehydrocholesterol reductase
Solyc02g093545.1	2,43	2,77E-10	3,28E-09	CytochromeB1
Solyc03g123390.4	2,43	2,49E-13	4,06E-12	Alpha/beta-Hydrolases superfamily protein
Solyc06g060880.4	2,42	3,49E-20	9,85E-19	FAD/NAD(P)-binding oxidoreductase family protein
Solyc12g006020.1	2,42	6,45E-27	2,66E-25	Receptor protein kinase, putative
Solyc09g061860.4	2,42	2,12E-17	4,92E-16	Sterol 3-beta-glucosyltransferase
Solyc03g111550.4	2,42	2,92E-18	7,26E-17	GDSL esterase/lipase
Solyc04g079050.3	2,41	4,22E-32	2,25E-30	UDP-glycosyltransferase 79B2
Solyc07g051860.1	2,41	1,65E-06	1,17E-05	MAP kinase kinase kinase 50
Solyc01g106820.3	2,41	5,48E-30	2,63E-28	Ethylene-dependent gravitropism-deficient and yellow-green-like 3
Solyc01g150148.1	2,40	2,75E-07	2,18E-06	Unknown protein
Solyc08g081190.3	2,40	6,74E-27	2,78E-25	plasma membrane intrinsic protein 1.5
Solyc01g108210.4	2,40	1,46E-13	2,44E-12	Cytochrome P450
Solyc04g005620.3	2,40	7,38E-07	5,48E-06	Casparian strip membrane protein 1
Solyc06g053840.3	2,39	1,87E-37	1,24E-35	auxin-regulated IAA4
Solyc01g112190.3	2,39	1,32E-11	1,79E-10	Plant regulator RWP-RK family protein, putative
Solyc01g079260.4	2,39	7,82E-18	1,88E-16	WRKY transcription factor 23
Solyc05g008080.3	2,39	4,53E-08	4,03E-07	NOD26-like intrinsic protein 4.2
Solyc05g043330.3	2,38	3,14E-10	3,71E-09	GDSL esterase/lipase
Solyc03g034400.3	2,38	1,11E-22	3,65E-21	Protein DETOXIFICATION
Solyc01g006720.4	2,37	9,06E-32	4,74E-30	ABC transporter G family member 27
Solyc01g103990.3	2,37	9,54E-10	1,07E-08	T-complex protein 11
Solyc01g096320.3	2,37	1,06E-19	2,91E-18	Homeobox-leucine zipper protein HOX6
Solyc02g092720.1	2,36	5,22E-13	8,21E-12	hypothetical protein
Solyc02g071320.4	2,36	8,63E-15	1,61E-13	Unknown protein
Solyc08g029000.3	2,36	7,18E-06	4,59E-05	Lipoxygenase
Solyc10g006330.3	2,36	2,40E-10	2,87E-09	protein PLASTID MOVEMENT IMPAIRED 1
Solyc07g054810.1	2,36	6,53E-11	8,29E-10	Unknown protein
Solyc12g099930.2	2,36	4,76E-28	2,06E-26	Serine--glyoxylate aminotransferase
Solyc04g009440.3	2,36	1,32E-08	1,26E-07	NAC domain protein AY498713
Solyc11g012660.2	2,36	5,14E-04	2,28E-03	Microtubule-associated protein 70
Solyc10g085280.1	2,36	5,89E-08	5,14E-07	UDP-glycosyltransferase 76E1
Solyc11g010930.2	2,35	7,38E-12	1,03E-10	HVA22-like protein
Solyc12g057020.2	2,35	2,00E-05	1,19E-04	Carbohydrate esterase, putative (DUF303)
Solyc12g042600.2	2,35	3,74E-11	4,83E-10	Glycosyltransferase
Solyc01g067120.4	2,35	1,07E-15	2,16E-14	cullin-1-like
Solyc04g053000.1	2,35	1,75E-06	1,23E-05	Auxin-responsive protein SAUR24
Solyc03g119700.3	2,35	1,64E-40	1,19E-38	ATP-dependent Clp protease adapter protein ClpS
Solyc01g006430.3	2,35	9,74E-27	3,96E-25	Fatty acid desaturase
Solyc01g093965.2	2,35	1,50E-14	2,74E-13	MADS-box transcription factor
Solyc10g006860.4	2,35	5,86E-10	6,73E-09	NAD(P)-binding Rossmann-fold superfamily protein
Solyc12g042110.3	2,34	1,41E-15	2,81E-14	replication protein A 70 kDa DNA-binding subunit B-like isoform X1
Solyc08g081700.1	2,34	1,08E-10	1,34E-09	late embryogenesis abundant protein At1g64065-like
Solyc08g016310.3	2,34	5,33E-27	2,20E-25	LOW QUALITY PROTEIN: LRR receptor-like serine/threonine-protein kinase GSO1
Solyc04g076870.4	2,34	1,24E-22	4,04E-21	Glutamyl-tRNA reductase
Solyc09g065560.3	2,34	1,04E-20	3,05E-19	Sulfate transporter
Solyc05g010640.3	2,33	3,74E-06	2,51E-05	RING-type E3 ubiquitin transferase
Solyc11g008250.2	2,33	2,89E-12	4,20E-11	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc10g086430.3	2,33	3,97E-07	3,07E-06	WD40 repeat
Solyc02g061990.3	2,33	1,06E-13	1,79E-12	BZIP transcription factor FD
Solyc10g085820.2	2,32	2,11E-23	7,27E-22	dnaJ homolog subfamily C member 28
Solyc04g005070.3	2,32	3,17E-11	4,13E-10	Major facilitator superfamily protein
Solyc04g078970.3	2,32	9,92E-06	6,21E-05	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1
Solyc10g086180.2	2,32	2,18E-16	4,64E-15	Phenylalanine ammonia-lyase
Solyc02g091920.3	2,31	3,26E-30	1,59E-28	xyloglucan endotransglucosylase-hydrolase 7
Solyc11g011710.1	2,31	3,15E-04	1,46E-03	Small auxin up-regulated RNA95
Solyc06g063370.3	2,31	4,32E-35	2,56E-33	Chlorophyll a-b binding protein, chloroplastic
Solyc10g052540.1	2,31	2,40E-12	3,53E-11	Small auxin up-regulated RNA73
Solyc05g051425.2	2,31	4,09E-14	7,17E-13	Dihydrofolate reductase-like protein
Solyc11g030730.2	2,30	5,79E-07	4,36E-06	Cytochrome P450
Solyc06g069370.4	2,30	2,35E-12	3,46E-11	bHLH transcription factor 046
Solyc01g107590.3	2,30	2,96E-30	1,45E-28	Cinnamyl alcohol dehydrogenase

Solyc02g014460.4	2,29	2,43E-24	8,73E-23	DNA damage-binding protein CMR1
Solyc02g150140.1	2,29	1,09E-14	2,02E-13	Unknown protein
Solyc11g069960.2	2,29	8,38E-18	2,02E-16	RLK-1
Solyc01g081480.3	2,29	8,02E-23	2,66E-21	GPI inositol-deacylase PGAP1-like protein
Solyc04g049360.3	2,29	6,71E-22	2,08E-20	aminodeoxychorismate synthase/glutamine amidotransferase
Solyc02g072220.1	2,29	6,70E-04	2,88E-03	DUF1685 family protein
Solyc02g068615.1	2,28	3,75E-08	3,38E-07	Ankyrin repeat
Solyc04g007530.3	2,28	5,58E-25	2,07E-23	Protein DETOXIFICATION
Solyc04g051800.3	2,28	1,46E-12	2,20E-11	ABC transporter-like
Solyc12g044600.3	2,27	1,52E-33	8,57E-32	NADP-malic enzyme
Solyc12g044330.2	2,27	3,54E-18	8,74E-17	tonoplast intrinsic protein 2.1
Solyc01g087810.2	2,27	7,25E-08	6,22E-07	Subtilisin-like protease
Solyc09g009830.3	2,26	4,25E-29	1,95E-27	Alpha carbonic anhydrase
Solyc02g082260.3	2,26	1,09E-18	2,81E-17	3-hydroxy-3-methylglutaryl CoA reductase
Solyc06g076400.3	2,26	4,67E-30	2,26E-28	Protein phosphatase 2C
Solyc02g093290.3	2,26	8,86E-27	3,62E-25	Nicotinate phosphoribosyltransferase
Solyc03g059260.4	2,26	7,50E-18	1,81E-16	Carboxyl-terminal-processing protease
Solyc05g053410.4	2,26	9,00E-17	1,97E-15	phytochrome B2
Solyc03g096290.3	2,26	1,80E-07	1,47E-06	plasma membrane intrinsic protein 1.7
Solyc08g080630.4	2,25	7,23E-03	2,32E-02	Ethylene-responsive proteinase inhibitor 1
Solyc07g049530.3	2,25	4,87E-26	1,88E-24	1-aminocyclopropane-1-carboxylate oxidase 1
Solyc07g052620.1	2,25	4,18E-05	2,34E-04	B-box zinc finger protein 32
Solyc01g097340.3	2,25	1,01E-21	3,12E-20	GDP-mannose-3',5'-epimerase
Solyc07g006630.4	2,24	1,79E-17	4,21E-16	Zinc finger protein CONSTANS-like 5-like
Solyc01g099910.4	2,24	2,87E-16	6,07E-15	Alpha/beta-Hydrolases superfamily protein
Solyc09g007470.2	2,23	5,56E-14	9,68E-13	Protamine P1 family protein
Solyc07g063710.2	2,23	9,56E-03	2,94E-02	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc01g080460.3	2,23	6,83E-08	5,89E-07	Pyruvate, phosphate dikinase
Solyc05g052270.3	2,23	7,44E-11	9,38E-10	Non-specific serine/threonine protein kinase
Solyc11g066060.3	2,23	1,88E-18	4,74E-17	70 kDa heat shock protein
Solyc02g091080.2	2,22	2,80E-11	3,67E-10	Protein DETOXIFICATION
Solyc11g042820.2	2,22	3,60E-11	4,66E-10	Major facilitator superfamily protein
Solyc05g008920.3	2,22	4,48E-28	1,95E-26	DUF789 domain-containing protein
Solyc10g054440.3	2,22	9,88E-14	1,68E-12	arginine decarboxylase 1
Solyc06g081980.1	2,22	1,38E-22	4,49E-21	Pyridoxal 5'-phosphate synthase pdxS subunit
Solyc07g055260.3	2,22	3,89E-32	2,08E-30	Chaperone protein dnaJ
Solyc04g080270.4	2,21	7,70E-03	2,45E-02	hypothetical protein
Solyc06g053830.3	2,21	1,11E-16	2,40E-15	auxin-regulated IAA7
Solyc01g111630.3	2,21	7,80E-27	3,21E-25	glycerate dehydrogenase
Solyc01g005730.3	2,20	7,24E-21	2,14E-19	NL0C
Solyc10g076550.1	2,20	5,20E-10	6,01E-09	Wall-associated receptor kinase 1
Solyc04g080300.4	2,20	8,63E-26	3,31E-24	Erythronate-4-phosphate dehydrogenase family protein
Solyc11g068530.1	2,20	5,58E-18	1,36E-16	The fantastic four family
Solyc07g065060.1	2,20	2,25E-10	2,70E-09	MBOAT (Membrane bound O-acyl transferase) family protein
Solyc01g150101.1	2,19	1,75E-15	3,44E-14	Basic helix-loop-helix (BHLH) DNA-binding superfamily protein
Solyc03g112150.1	2,19	5,19E-30	2,50E-28	Elongation factor Tu
Solyc05g013510.4	2,18	4,47E-31	2,28E-29	Phosphate transporter
Solyc01g014140.3	2,18	2,72E-13	4,43E-12	receptor-like protein 12
Solyc01g110720.2	2,18	1,83E-04	8,97E-04	Auxin-responsive protein SAUR21
Solyc01g105920.3	2,18	2,06E-13	3,39E-12	Beta myrcene/limonene synthase
Solyc10g006230.3	2,18	1,17E-23	4,06E-22	Chlorophyll a-b binding protein, chloroplastic
Solyc01g110520.3	2,18	1,84E-28	8,23E-27	Amidophosphoribosyltransferase
Solyc07g052440.3	2,18	8,16E-04	3,44E-03	transmembrane protein 97-like
Solyc03g118840.3	2,18	5,10E-23	1,72E-21	RING/U-box superfamily protein
Solyc03g113280.3	2,18	1,81E-26	7,22E-25	Integral membrane HPP family protein
Solyc04g007290.4	2,18	5,85E-09	5,89E-08	DUF639 domain-containing protein
Solyc01g110960.4	2,18	2,50E-03	9,29E-03	Prefoldin chaperone subunit family protein
Solyc05g041200.4	2,17	4,20E-29	1,93E-27	4-hydroxyphenylpyruvate dioxygenase
Solyc03g007130.4	2,17	1,26E-04	6,37E-04	65-kDa microtubule-associated protein 3
Solyc06g071920.4	2,17	1,96E-35	1,18E-33	Glyceraldehyde-3-phosphate dehydrogenase
Solyc01g005720.3	2,17	7,36E-17	1,63E-15	NL0D
Solyc07g006710.2	2,17	4,87E-10	5,64E-09	Pathogenesis-related protein PR-1
Solyc09g089720.3	2,17	1,63E-13	2,71E-12	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc12g008380.1	2,16	6,99E-11	8,81E-10	Avr9/Cf-9 rapidly elicited protein
Solyc03g097030.3	2,16	5,63E-24	1,99E-22	4-coumarate:CoA ligase
Solyc04g014510.3	2,16	4,64E-20	1,30E-18	glutamine synthase
Solyc05g055790.4	2,16	4,66E-27	1,93E-25	Protein phosphatase 2C family protein
Solyc03g078783.1	2,16	7,02E-05	3,76E-04	Unknown protein
Solyc09g083390.3	2,16	1,32E-11	1,79E-10	zinc knuckle (CCHC-type) family protein
Solyc01g104740.3	2,16	6,96E-15	1,30E-13	Multiprotein-bridging factor 1c
Solyc08g077880.3	2,15	2,16E-22	6,87E-21	Chlorophyll A-B binding protein
Solyc05g015640.3	2,14	7,96E-13	1,23E-11	transmembrane protein
Solyc04g082630.3	2,14	6,82E-29	3,09E-27	Glyceraldehyde-3-phosphate dehydrogenase
Solyc04g074640.4	2,14	4,01E-10	4,68E-09	Ascorbate peroxidase
Solyc12g056940.2	2,13	5,63E-07	4,25E-06	Acetyl CoA carboxylase
Solyc12g015880.2	2,13	2,76E-09	2,92E-08	Heat shock protein 90-1
Solyc07g053180.3	2,13	1,30E-19	3,53E-18	Outer arm dynein light chain 1 protein
Solyc02g078400.3	2,13	1,13E-20	3,30E-19	Allantoinase
Solyc01g087450.3	2,13	4,26E-08	3,81E-07	Arm repeat superfamily protein
Solyc10g083860.3	2,13	8,44E-13	1,30E-11	Glycosyltransferase
Solyc07g043460.3	2,13	2,86E-12	4,18E-11	Cytochrome P450
Solyc06g011350.3	2,12	2,24E-10	2,69E-09	plasma membrane intrinsic protein 2.4
Solyc10g076540.1	2,12	6,84E-09	6,83E-08	Wall-associated receptor kinase-like 9
Solyc07g065080.4	2,12	2,34E-15	4,53E-14	Fimbrin-3
Solyc01g096660.3	2,12	3,88E-32	2,08E-30	proline-rich family protein
Solyc01g100910.3	2,11	6,41E-14	1,11E-12	WAT1-related protein
Solyc03g093180.1	2,11	1,14E-14	2,11E-13	Peroxisomal membrane protein 11-4
Solyc12g007010.2	2,11	7,10E-25	2,61E-23	Iron-sulfur cluster carrier protein
Solyc01g106620.2	2,11	2,33E-09	2,49E-08	pathogenesis-related protein 1-like
Solyc10g083360.2	2,11	2,15E-26	8,50E-25	Calmodulin-binding family protein, putative, expressed
Solyc02g071930.2	2,11	1,20E-03	4,86E-03	Ctd small phosphatase-like protein
Solyc04g078950.1	2,10	3,25E-04	1,50E-03	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1
Solyc01g110440.5.1	2,10	2,45E-19	6,52E-18	arginine decarboxylase
Solyc08g077180.3	2,10	1,90E-22	6,13E-21	Pyruvate kinase
Solyc04g081260.3	2,09	2,92E-05	1,69E-04	filament-like plant protein 4
Solyc02g078750.3	2,09	9,18E-07	6,71E-06	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc04g072160.3	2,09	7,27E-13	1,13E-11	ripening regulated protein DDTFR8
Solyc01g086940.2	2,09	3,56E-08	3,21E-07	Zinc finger CCCH domain-containing protein
Solyc04g082120.3	2,09	5,22E-06	3,42E-05	Prolyl oligopeptidase
Solyc10g078240.2	2,09	8,18E-25	3,00E-23	Cytochrome P450
Solyc04g057930.4	2,09	9,83E-31	4,93E-29	Pkinase domain-containing protein/Usp domain-containing protein
Solyc09g018280.1	2,09	6,69E-14	1,16E-12	Non-specific serine/threonine protein kinase
Solyc04g053010.1	2,09	4,50E-06	2,98E-05	Auxin-responsive protein SAUR65
Solyc02g085940.4	2,09	1,44E-08	1,38E-07	Ribulose bisphosphate carboxylase small chain
Solyc02g061760.4	2,08	2,96E-21	8,91E-20	Protein DETOXIFICATION
Solyc07g062520.3	2,08	1,26E-10	1,54E-09	Cytochrome
Solyc09g072990.3	2,08	3,00E-17	6,87E-16	hypothetical protein
Solyc06g054010.3	2,08	9,23E-17	2,02E-15	inositol-1,4,5-triphosphate-5-phosphatase 3
Solyc08g005930.1	2,08	3,62E-16	7,60E-15	F-box/kelch-repeat protein SKIP25
Solyc03g006640.3	2,08	1,18E-20	3,44E-19	F-box family protein
Solyc08g067030.3	2,08	1,86E-21	5,66E-20	DUF642 domain-containing protein
Solyc01g095070.4	2,08	8,62E-21	2,55E-19	Heavy metal-associated isoprenylated plant protein
Solyc02g031950.3	2,08	6,54E-04	2,82E-03	pathogenesis-related family protein
Solyc01g094140.3	2,08	8,45E-11	1,06E-09	Cytochrome P450
Solyc02g089930.4	2,08	8,63E-27	3,54E-25	Protein DA1
Solyc02g062580.3	2,08	1,68E-11	2,25E-10	Lipid phosphate phosphatase epsilon 2, chloroplastic

Solyc11g008540.3	2,08	1,66E-08	1,58E-07	Dicer-like 2b
Solyc05g014190.4	2,08	1,56E-24	5,63E-23	CAAX amino terminal protease family protein
Solyc03g097230.1	2,07	8,74E-08	7,45E-07	AIG2-like (Avirulence induced gene) family protein
Solyc07g056708.1	2,07	1,44E-03	5,68E-03	DUF239 domain-containing protein/DUF4409 domain-containing protein
Solyc11g065000.2	2,07	2,71E-20	7,73E-19	F-box protein
Solyc06g084170.3	2,07	2,89E-06	1,97E-05	Unknown protein
Solyc05g046020.3	2,07	1,19E-05	7,35E-05	Peroxidase
Solyc02g070890.3	2,07	8,73E-08	7,45E-07	Flagellin Sensing 2
Solyc11g010850.2	2,06	5,58E-13	8,74E-12	1-deoxy-d-xylulose-5-phosphate synthase 1
Solyc02g086458.1	2,06	4,43E-04	1,99E-03	titin isoform X2
Solyc08g007970.3	2,06	1,27E-03	5,10E-03	Myosin heavy chain-related protein
Solyc08g075020.3	2,06	4,19E-26	1,63E-24	Pectin acetylesterase
Solyc12g096870.1	2,06	2,47E-19	6,58E-18	Glycosyltransferase
Solyc03g044793.1	2,05	2,49E-05	1,46E-04	Unknown protein
Solyc02g091890.3	2,05	9,39E-04	3,91E-03	myb-like protein X
Solyc04g009030.3	2,05	1,92E-26	7,63E-25	Glyceraldehyde-3-phosphate dehydrogenase
Solyc06g009120.3	2,05	1,93E-22	6,22E-21	LYR motif protein
Solyc04g011500.3	2,05	1,03E-25	3,95E-24	Actin
Solyc12g096020.3	2,04	2,10E-28	9,29E-27	Protein phosphatase 2c
Solyc12g088230.3	2,04	2,32E-24	8,35E-23	mitochondrial malate dehydrogenase
Solyc01g106470.3	2,04	7,23E-19	1,87E-17	Tunicamycin induced protein
Solyc02g082450.3	2,04	2,95E-11	3,86E-10	Auxin efflux carrier
Solyc04g079700.3	2,04	8,57E-16	1,74E-14	Transducin/WD40 repeat-like superfamily protein
Solyc02g071860.4	2,04	3,65E-08	3,29E-07	LRR_1 domain-containing protein/Pkinase_Tyr domain-containing protein/Malectin domain-containing protein
Solyc02g085750.4	2,03	2,02E-05	1,20E-04	Mental retardation GTPase activating protein
Solyc02g067120.4	2,03	7,78E-24	2,74E-22	hypothetical protein (DUF1997)
Solyc10g086200.1	2,02	1,83E-04	8,97E-04	SAUR-like auxin-responsive protein family
Solyc04g082290.4	2,02	5,72E-15	1,08E-13	inactive purple acid phosphatase-like protein
Solyc03g080100.4	2,02	1,49E-06	1,05E-05	Heavy metal-associated isoprenylated plant protein
Solyc09g090930.3	2,02	2,27E-24	8,18E-23	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc06g075440.3	2,01	2,00E-05	1,19E-04	protein NRT1/ PTR FAMILY 2.7-like
Solyc12g006000.1	2,01	1,55E-09	1,70E-08	Clathrin coat assembly protein
Solyc07g064420.3	2,01	3,58E-23	1,21E-21	inositol-1%2C4%2C5-trisphosphate 5-phosphatase
Solyc03g116260.3	2,01	1,12E-08	1,08E-07	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc10g083460.1	2,01	6,53E-10	7,46E-09	Zinc finger A20 and AN1 domain-containing stress-associated protein
Solyc02g070490.4	2,01	4,13E-26	1,61E-24	Alpha/beta-Hydrolases superfamily protein
Solyc04g063240.3	2,00	6,64E-23	2,21E-21	Protein STAY-GREEN, chloroplastic
Solyc03g044797.1	2,00	4,77E-03	1,63E-02	Retrovirus-related Pol polyprotein from transposon TNT 1-94
Solyc02g081330.4	2,00	2,83E-18	7,05E-17	phytoene synthase 2,Pfam:PF00494
Solyc00g500064.1	2,00	2,64E-05	1,54E-04	Ycf15
Solyc08g067330.1	2,00	7,33E-07	5,46E-06	Chlorophyll a-b binding protein, chloroplastic
Solyc07g065980.3	1,99	4,49E-15	8,51E-14	alkaline alpha-galactosidase seed imbibition protein
Solyc06g150137.1	1,99	5,11E-12	7,24E-11	Cytochrome P450
Solyc05g015840.3	1,99	1,42E-10	1,73E-09	Squamosa promoter binding protein 13
Solyc01g110670.3	1,99	5,25E-09	5,33E-08	Auxin-responsive protein SAUR21
Solyc03g082945.1	1,99	2,09E-04	1,01E-03	protein PSY2-like
Solyc02g068070.4	1,99	4,15E-05	2,33E-04	Lipase
Solyc12g014590.3	1,99	1,12E-06	8,08E-06	Pirin-like protein
Solyc09g082820.3	1,99	2,86E-14	5,11E-13	Unknown protein
Solyc08g065190.3	1,99	2,41E-12	3,55E-11	Fe(2+) transport protein 3, chloroplastic
Solyc04g049380.4	1,99	3,09E-18	7,65E-17	Protein kinase superfamily protein
Solyc01g008110.4	1,98	1,16E-26	4,67E-25	Cytochrome P450
Solyc10g084440.3	1,98	3,99E-15	7,62E-14	Dirigent protein 17
Solyc01g108600.3	1,98	3,16E-11	4,12E-10	Presequence protease chloroplastic/mitochondrial-like
Solyc09g011010.3	1,98	9,33E-13	1,43E-11	High-light-induced protein, chloroplastic
Solyc07g054060.3	1,98	1,41E-17	3,33E-16	hypothetical protein
Solyc02g084390.3	1,97	1,19E-03	4,81E-03	Kinesin-like protein
Solyc02g077920.4	1,97	1,18E-12	1,80E-11	Colorless non-ripening
Solyc06g008620.1	1,97	3,91E-14	6,87E-13	TolB protein-related protein
Solyc06g059810.1	1,97	1,02E-07	8,63E-07	F-box protein
Solyc04g052970.3	1,97	1,52E-04	7,60E-04	Auxin-responsive protein SAUR24
Solyc12g009190.2	1,96	4,34E-05	2,42E-04	pollen receptor-like kinase 3
Solyc06g074800.1	1,96	2,91E-14	5,18E-13	Zinc finger protein
Solyc02g079740.1	1,96	3,01E-18	7,47E-17	RING-type E3 ubiquitin transferase
Solyc06g076670.3	1,96	1,11E-17	2,64E-16	RNA-binding (RRM/RBD/RNP motifs) family protein
Solyc07g063770.3	1,96	2,88E-11	3,77E-10	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc01g105290.3	1,96	4,33E-18	1,06E-16	BTB/POZ domain protein
Solyc01g110710.3	1,96	2,85E-06	1,94E-05	Small auxin up-regulated RNA10
Solyc03g083960.3	1,96	9,74E-28	4,13E-26	Trehalose 6-phosphate phosphatase
Solyc06g072830.4	1,95	1,01E-03	4,19E-03	cell division cycle 20.2, cofactor of APC complex-like
Solyc05g021580.3	1,95	9,23E-04	3,85E-03	Serine/threonine-protein kinase TOR
Solyc04g074270.3	1,95	4,39E-15	8,34E-14	Outer arm dynein light chain 1
Solyc05g009930.3	1,95	3,24E-07	2,54E-06	Protein CHUP1, chloroplastic
Solyc11g071830.2	1,94	1,65E-08	1,56E-07	DnaJ protein like
Solyc10g007600.3	1,94	2,49E-18	6,23E-17	glycolate oxidase
Solyc05g050980.3	1,94	1,12E-15	2,25E-14	3-phosphoshikimate 1-carboxyvinyltransferase
Solyc01g111000.4	1,94	7,13E-08	6,13E-07	Auxin-responsive protein SAUR20
Solyc02g093980.3	1,94	2,11E-12	3,14E-11	Nucleolar-like protein
Solyc10g076180.1	1,94	1,32E-05	8,12E-05	ovate family protein 20
Solyc02g080160.4	1,94	2,95E-08	2,69E-07	Xyloglucan endotransglucosylase/hydrolase
Solyc09g014400.3	1,94	1,43E-08	1,37E-07	Phosphoglucan, water dikinase, chloroplastic
Solyc07g043170.4	1,94	7,12E-05	3,81E-04	Glycosyltransferase
Solyc04g082430.3	1,94	7,33E-06	4,68E-05	cyclinB2_4
Solyc01g105890.3	1,93	1,50E-10	1,83E-09	Monoterpene synthase 1
Solyc02g085145.1	1,93	1,23E-11	1,66E-10	Transcription factor RADIALIS
Solyc10g085500.2	1,93	2,89E-14	5,15E-13	Cytochrome P450
Solyc07g063970.3	1,93	1,10E-10	1,37E-09	C2H2 zinc finger protein
Solyc01g103920.3	1,93	1,07E-03	4,39E-03	Ferredoxin
Solyc03g117610.2	1,93	1,03E-09	1,15E-08	Unknown protein
Solyc04g078420.1	1,93	1,34E-20	3,89E-19	R2R3MYB transcription factor 70
Solyc06g071830.2	1,93	2,30E-07	1,84E-06	BTB/POZ and TAZ domain-containing protein 2
Solyc05g010060.4	1,93	4,93E-05	2,72E-04	Phosphate transporter PHO1-3
Solyc03g097380.4	1,93	7,03E-06	4,51E-05	Heavy metal-associated isoprenylated plant protein
Solyc11g042640.2	1,92	1,50E-28	6,75E-27	Rieske (2Fe-2S) domain-containing protein
Solyc06g034290.3	1,92	8,10E-17	1,79E-15	Glycerol-3-phosphate transporter 1-like protein
Solyc06g051930.3	1,92	3,05E-09	3,21E-08	Pyruvate kinase
Solyc07g006030.4	1,92	4,12E-04	1,86E-03	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc03g094177.1	1,92	9,09E-03	2,82E-02	Transcriptional coactivator/pterin dehydratase
Solyc01g099150.5.1	1,92	3,73E-03	1,32E-02	Lipoxygenase
Solyc09g010910.3	1,92	1,86E-03	7,12E-03	Unknown protein
Solyc09g089610.3	1,92	1,19E-09	1,32E-08	ethylene receptor-like protein (ETR6)
Solyc06g084770.2	1,92	4,86E-16	1,01E-14	cytochrome P450 CYP72A219
Solyc09g011810.3	1,92	3,30E-10	3,88E-09	Fructose-1,6-bisphosphatase
Solyc10g044520.3	1,91	1,84E-22	5,96E-21	Ferredoxin
Solyc05g053600.3	1,91	3,96E-07	3,06E-06	Pleiotropic drug resistance protein
Solyc09g065240.3	1,91	2,22E-04	1,07E-03	Patatin
Solyc11g011170.2	1,91	2,18E-24	7,89E-23	Senescence-associated family protein
Solyc12g056800.2	1,91	2,14E-19	5,75E-18	Oxidoreductase
Solyc03g095860.3	1,91	1,42E-13	2,36E-12	Ankyrin repeat-containing protein
Solyc08g076220.3	1,91	3,65E-14	6,45E-13	Phosphoribulokinase
Solyc01g090440.2	1,91	5,25E-07	4,00E-06	cotton fiber protein
Solyc10g085140.2	1,90	1,36E-09	1,50E-08	Alkyl transferase
Solyc07g043500.1	1,90	8,81E-11	1,10E-09	Glycosyltransferase
Solyc03g110940.3	1,90	1,99E-11	2,64E-10	Protein kinase superfamily protein
Solyc04g053020.2	1,90	1,19E-05	7,37E-05	Auxin-responsive protein SAUR65

Solyc05g053330.3	1,90	7,42E-04	3,16E-03	Transcription factor
Solyc02g082490.4	1,89	4,20E-11	5,41E-10	Protein phosphatase 2C family protein
Solyc10g045240.2	1,89	2,60E-17	6,01E-16	Beta-glucosidase
Solyc10g009230.1	1,89	1,38E-11	1,86E-10	death domain associated protein
Solyc07g049300.3	1,88	5,82E-10	6,69E-09	Endoglucanase
Solyc04g052980.1	1,88	1,09E-03	4,45E-03	Auxin-responsive protein SAUR65
Solyc10g009340.1	1,88	2,76E-17	6,34E-16	Calcium-binding protein KIC
Solyc02g086440.4	1,88	5,45E-18	1,33E-16	F-box/LRR-repeat protein 3
Solyc09g063010.4	1,88	6,83E-11	8,65E-10	bHLH transcription factor 058
Solyc04g079780.4	1,88	9,99E-05	5,18E-04	RBR-type E3 ubiquitin transferase
Solyc01g110290.3	1,87	3,08E-19	8,14E-18	Squalene synthase
Solyc01g110340.4	1,87	2,75E-13	4,45E-12	Endoglucanase
Solyc08g067250.4	1,87	1,12E-08	1,08E-07	DNA cross-link repair protein SNM1
Solyc01g102450.3	1,87	2,35E-04	1,13E-03	organic solute transporter ostalpha protein (DUF300)
Solyc04g016220.4	1,87	5,63E-15	1,06E-13	Glycosyltransferase
Solyc09g097910.4	1,87	4,90E-22	1,53E-20	30S ribosomal protein s1-like
Solyc03g096900.4	1,87	9,54E-12	1,31E-10	GTP pyrophosphokinase
Solyc07g022830.3	1,87	7,16E-09	7,12E-08	EXS
Solyc11g045460.3	1,87	6,13E-09	6,14E-08	Alpha/beta-Hydrolases superfamily protein
Solyc12g088400.1	1,87	9,62E-06	6,02E-05	Zinc-finger protein
Solyc11g011720.1	1,87	9,97E-05	5,18E-04	Auxin-responsive protein SAUR24
Solyc08g079750.3	1,87	2,33E-22	7,38E-21	1-aminocyclopropane-1-carboxylate synthase
Solyc06g072430.3	1,86	2,40E-07	1,92E-06	BAG family molecular chaperone regulator 5, mitochondrial
Solyc04g077690.3	1,86	3,71E-06	2,48E-05	hypothetical protein
Solyc10g084400.2	1,86	4,70E-15	8,90E-14	Glutathione S-transferase
Solyc03g095810.3	1,86	1,67E-06	1,18E-05	Protein trichome birefringence-like 32
Solyc06g005070.3	1,86	1,19E-18	3,05E-17	Major facilitator superfamily protein
Solyc05g006550.4	1,86	4,91E-06	3,23E-05	Microtubule-associated protein TORTIFOLIA1
Solyc10g084170.1	1,86	3,23E-07	2,54E-06	Bag family molecular chaperone regulator mitochondrial-like
Solyc07g041920.4	1,86	1,50E-06	1,06E-05	Cysteine protease
Solyc03g007290.4	1,86	1,40E-06	9,98E-06	Trehalose 6-phosphate phosphatase
Solyc08g007680.1	1,86	3,24E-12	4,70E-11	Subtilisin-like protease
Solyc09g075550.3	1,86	2,72E-04	1,28E-03	Cellulose synthase
Solyc03g121170.3	1,86	1,07E-16	2,33E-15	GDSL esterase/lipase
Solyc03g006250.2	1,86	2,41E-09	2,57E-08	GDSL esterase/lipase
Solyc03g033330.3	1,85	6,28E-13	9,79E-12	RING/U-box superfamily protein
Solyc04g049390.3	1,85	9,53E-17	2,08E-15	Protein kinase superfamily protein
Solyc02g090890.4	1,85	4,95E-21	1,48E-19	zeaxanthin epoxidase
Solyc05g051710.4	1,85	2,08E-09	2,25E-08	sorbin/SH3 domain protein
Solyc03g119640.4	1,85	1,13E-07	9,48E-07	Aluminum-activated malate transporter-like
Solyc05g056050.3	1,85	5,12E-23	1,72E-21	Chlorophyll a-b binding protein, chloroplastic
Solyc10g044840.2	1,85	2,73E-16	5,79E-15	YacP-like NYN domain protein
Solyc03g098020.4	1,85	1,29E-21	3,97E-20	Alpha/beta-Hydrolases superfamily protein
Solyc07g049550.3	1,85	4,70E-14	8,23E-13	1-aminocyclopropane-1-carboxylate oxidase 2
Solyc07g042470.3	1,85	1,57E-05	9,50E-05	Small auxin up-regulated RNA64
Solyc03g063560.3	1,84	4,22E-07	3,25E-06	Glutamate synthase
Solyc03g098300.1	1,84	3,17E-03	1,15E-02	Ornithine decarboxylase
Solyc03g121600.4	1,84	7,71E-08	6,60E-07	Glucose-methanol-choline (GMC) oxidoreductase family protein
Solyc08g014000.3	1,84	1,51E-03	5,92E-03	lipoxygenase A
Solyc03g098000.3	1,84	4,13E-24	1,47E-22	Alanine-tRNA ligase, putative (DUF760)
Solyc01g110680.4	1,84	4,88E-04	2,17E-03	Small auxin up-regulated RNA12
Solyc04g016430.3	1,83	4,46E-10	5,18E-09	Cytokinin dehydrogenase 1
Solyc08g079900.3	1,83	2,20E-07	1,77E-06	Subtilisin-like protease
Solyc04g053030.1	1,83	1,77E-05	1,07E-04	Auxin-responsive protein SAUR65
Solyc12g006470.2	1,83	1,54E-15	3,06E-14	viroid RNA-binding protein
Solyc01g079170.3	1,83	7,36E-03	2,36E-02	Hexosyltransferase
Solyc03g082470.4	1,83	1,15E-09	1,28E-08	systemin receptor 1
Solyc08g007540.3	1,83	1,29E-06	9,26E-06	ACT domain-containing protein
Solyc03g114090.1	1,82	4,36E-07	3,35E-06	RING/U-box superfamily protein
Solyc12g055980.1	1,82	1,01E-09	1,13E-08	Endoglucanase
Solyc05g052240.3	1,82	3,06E-13	4,95E-12	Chalcone-flavonone isomerase family protein
Solyc04g082250.3	1,82	4,92E-27	2,04E-25	FtsH-like protein precursor
Solyc05g005980.4	1,82	1,08E-08	1,05E-07	protein NRT1/ PTR FAMILY 1.2-like
Solyc03g116740.3	1,82	2,81E-12	4,11E-11	Phosphatidylcholine:diacylglycerol cholinephosphotransferase 1
Solyc01g099010.3	1,82	9,47E-10	1,07E-08	GDSL esterase/lipase At5g03980-like
Solyc09g007710.3	1,81	4,07E-05	2,29E-04	Disease resistance protein (TIR-NBS-LRR class)
Solyc04g070980.4	1,81	8,96E-18	2,15E-16	cycloartenol synthase 1
Solyc01g079410.3	1,81	3,87E-14	6,82E-13	Calcium-dependent phosphotriesterase superfamily protein
Solyc06g062550.4	1,81	1,40E-04	7,02E-04	LES459817 putative phosphatase 14A
Solyc11g010130.3	1,81	7,03E-18	1,70E-16	Protein kinase
Solyc01g005870.3	1,81	7,26E-16	1,49E-14	Cf-like protein
Solyc12g096550.2	1,81	9,65E-18	2,32E-16	Pheophorbide a oxygenase
Solyc04g081870.4	1,81	5,10E-08	4,51E-07	Expansin A11
Solyc01g094750.4	1,81	4,66E-08	4,14E-07	Cytochrome P450
Solyc05g055740.4	1,80	1,11E-12	1,69E-11	Tyrosine phosphatase family protein
Solyc09g010650.1	1,80	2,87E-05	1,66E-04	RING/U-box superfamily protein
Solyc06g060560.3	1,80	2,62E-13	4,28E-12	hypothetical protein
Solyc03g113920.4	1,80	2,69E-17	6,21E-16	Calmodulin binding protein
Solyc12g040700.1	1,80	1,16E-03	4,70E-03	Sucrose synthase
Solyc01g008690.3	1,80	3,77E-05	2,13E-04	GDP-mannose transporter
Solyc07g006870.4	1,80	2,93E-05	1,70E-04	Xyloglucan endotransglucosylase/hydrolase
Solyc09g074630.3	1,80	7,16E-06	4,58E-05	BTB domain-containing protein/NPH3 domain-containing protein
Solyc07g043320.3	1,80	1,39E-03	5,50E-03	myosin heavy chain%2C embryonic smooth protein
Solyc05g006650.3	1,79	2,71E-23	9,26E-22	bHLH transcription factor 036
Solyc01g087080.4	1,79	2,72E-03	1,00E-02	interferon-activable protein
Solyc08g006990.3	1,79	9,21E-09	9,05E-08	Aluminum activated malate transporter family protein
Solyc08g006470.4	1,79	3,65E-05	2,07E-04	Zinc finger protein
Solyc12g009930.3	1,79	1,99E-08	1,87E-07	Glycosyltransferase
Solyc06g068650.4	1,79	5,66E-16	1,17E-14	4-coumarate:CoA ligase
Solyc05g041430.3	1,79	1,41E-15	2,80E-14	PTB domain engulfment adapter
Solyc01g059870.4	1,78	6,66E-12	9,34E-11	phytochrome B1
Solyc01g014105.1	1,78	5,94E-16	1,22E-14	IRK-interacting protein
Solyc01g080280.3	1,78	2,72E-19	7,23E-18	chloroplast glutamine synthetase
Solyc06g065960.1	1,78	8,79E-05	4,62E-04	Agamous-like MADS-box protein AGL61
Solyc02g078800.4	1,78	1,08E-09	1,20E-08	Katanin p80 WD40 repeat-containing subunit B1
Solyc12g010130.1	1,78	3,28E-17	7,49E-16	Non-specific serine/threonine protein kinase
Solyc02g069260.3	1,78	2,01E-17	4,69E-16	Argonaute2a
Solyc02g090100.1	1,78	7,85E-24	2,76E-22	homolog of Synechocystis YCF37
Solyc04g008260.3	1,77	3,33E-10	3,92E-09	Purple acid phosphatase
Solyc02g150126.1	1,77	2,28E-04	1,09E-03	Unknown protein
Solyc03g082510.1	1,77	8,17E-11	1,03E-09	Small auxin up-regulated RNA35
Solyc03g065200.4	1,77	2,67E-04	1,26E-03	Protein ENHANCED DISEASE RESISTANCE 2-like
Solyc12g013620.2	1,77	1,52E-17	3,58E-16	jasmonic acid 2
Solyc01g086950.4	1,77	2,46E-06	1,69E-05	Zinc finger CCCH domain-containing protein
Solyc01g105020.3	1,77	6,13E-05	3,32E-04	Protein phosphatase 2C (PP2C)-like domain
Solyc03g112590.4	1,76	1,27E-04	6,45E-04	Cell division cycle protein 48-like protein
Solyc12g044280.2	1,76	2,90E-14	5,17E-13	Photosystem I reaction center subunit VI, chloroplastic
Solyc02g091560.3	1,76	1,52E-11	2,04E-10	Serine hydroxymethyltransferase
Solyc08g075120.3	1,76	2,41E-14	4,34E-13	Rop guanine nucleotide exchange factor 14
Solyc11g006040.2	1,76	3,56E-18	8,79E-17	Receptor protein kinase
Solyc12g038343.1	1,76	4,84E-03	1,65E-02	Unknown protein
Solyc01g087750.4	1,76	9,05E-12	1,25E-10	protein RETICULATA-RELATED 4, chloroplastic-like
Solyc12g100010.1	1,76	6,97E-11	8,80E-10	receptor-like protein 12
Solyc01g079790.4	1,75	3,17E-06	2,14E-05	ADP-glucose pyrophosphorylase large subunit 3
Solyc12g150101.1	1,75	2,35E-11	3,11E-10	Photosystem II reaction center X protein
Solyc07g063720.1	1,75	1,17E-03	4,75E-03	G-type lectin S-receptor-like serine/threonine-protein kinase

Solyc09g061250.4	1,75	4,06E-11	5,23E-10	BTB/POZ domain-containing protein
Solyc03g111970.4	1,75	1,70E-15	3,33E-14	Cytochrome P450 71A6
Solyc11g065070.2	1,75	4,20E-19	1,11E-17	Hydroxymethylglutaryl-CoA lyase, mitochondrial
Solyc01g110770.2	1,75	1,19E-03	4,81E-03	Small auxin up-regulated RNA11
Solyc07g020790.4	1,75	8,17E-13	1,26E-11	plastidic glucose translocator 3
Solyc10g083300.2	1,74	3,57E-08	3,22E-07	invertase 8
Solyc04g072050.4	1,74	2,85E-11	3,74E-10	transmembrane protein
Solyc11g072080.1	1,74	2,08E-06	1,44E-05	F-box/kelch-repeat protein
Solyc11g008900.2	1,74	3,85E-15	7,37E-14	Zinc finger transcription factor 65
Solyc01g099020.3	1,74	2,71E-22	8,56E-21	GDSL esterase/lipase
Solyc08g080170.3	1,74	3,18E-14	5,66E-13	3-hydroxy-3-methylglutaryl coenzyme A synthase
Solyc01g102300.3	1,74	8,74E-11	1,10E-09	bHLH transcription factor 006
Solyc05g053850.3	1,74	2,37E-09	2,53E-08	Protein FLOWERING LOCUS T
Solyc03g114950.2	1,74	1,57E-11	2,11E-10	ABC transporter B family member 27
Solyc12g006760.1	1,74	2,40E-03	8,95E-03	Unknown protein
Solyc12g088460.3	1,74	3,54E-09	3,67E-08	Cytochrome P450
Solyc12g055970.3	1,73	1,18E-13	1,99E-12	Endoglucanase
Solyc12g088760.1	1,73	8,17E-12	1,13E-10	Subtilisin-like protease preproenzyme
Solyc01g110730.4	1,73	3,75E-04	1,71E-03	Auxin-responsive protein SAUR20
Solyc02g067180.3	1,73	3,92E-17	8,89E-16	cystathionine gamma synthase
Solyc12g005760.2	1,73	6,12E-16	1,26E-14	Peroxisome biogenesis protein 22
Solyc07g053700.4	1,73	1,99E-03	7,58E-03	Reticulon-like protein
Solyc06g019170.3	1,73	6,84E-12	9,58E-11	Delta-1-pyrroline-5-carboxylate synthase
Solyc06g068550.4	1,73	8,14E-05	4,31E-04	Eukaryotic aspartyl protease family protein
Solyc03g007430.3	1,72	2,61E-17	6,04E-16	Mitochondrial carrier protein MTM1
Solyc10g009210.4	1,72	4,73E-12	6,73E-11	Calmodulin binding protein-like
Solyc02g020880.2	1,72	5,63E-08	4,93E-07	Unknown protein
Solyc01g005710.2	1,72	2,62E-06	1,79E-05	Hcr9-Avr9-hir2
Solyc07g065340.1	1,72	4,52E-12	6,47E-11	Serine acetyltransferase
Solyc03g006610.3	1,72	1,08E-06	7,80E-06	Arf GTPase activating protein
Solyc06g083660.4	1,72	3,22E-08	2,93E-07	Methyl-coenzyme M reductase II subunit gamma, putative (DUF3741)
Solyc09g008670.3	1,72	8,44E-05	4,45E-04	threonine deaminase
Solyc06g052010.2	1,72	2,72E-05	1,58E-04	SUN-like protein 16
Solyc02g087430.4	1,72	1,32E-05	8,07E-05	inositol-1,4,5-triphosphate-5-phosphatase 4
Solyc04g040120.1	1,72	4,32E-03	1,49E-02	Fatty acid desaturase
Solyc01g099880.4	1,72	9,08E-08	7,73E-07	Bidirectional sugar transporter SWEET
Solyc04g081300.4	1,71	1,92E-13	3,18E-12	Endoglucanase
Solyc08g068520.3	1,71	1,75E-03	6,76E-03	F-box protein
Solyc09g091550.3	1,71	5,67E-16	1,17E-14	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc02g092150.3	1,71	6,94E-14	1,20E-12	ACT domain-containing protein
Solyc09g005260.4	1,71	3,38E-12	4,90E-11	Vacuolar cation/proton exchanger
Solyc01g008780.3	1,71	8,98E-21	2,65E-19	Phospholipase A2 family protein
Solyc02g005180.3	1,71	1,17E-16	2,54E-15	Sugar facilitator protein 2
Solyc10g008020.3	1,71	1,53E-10	1,86E-09	S-adenosyl-L-methionine-dependent methyltransferase
Solyc12g096570.1	1,71	4,40E-04	1,98E-03	auxin-regulated gene involved in organ size
Solyc05g056170.3	1,71	3,14E-08	2,86E-07	Phenylalanine ammonia-lyase
Solyc04g077140.3	1,71	1,08E-15	2,18E-14	DUF1005 domain-containing protein
Solyc12g006505.1	1,70	1,69E-07	1,39E-06	Terpene cyclase/mutase family member
Solyc01g058350.1	1,70	5,03E-04	2,23E-03	Unknown protein
Solyc07g040950.3	1,70	3,04E-20	8,62E-19	Lactoylglutathione lyase / glyoxalase I family protein
Solyc11g010470.2	1,70	6,00E-22	1,86E-20	14-3-3 protein
Solyc03g007775.2	1,70	1,59E-06	1,12E-05	membrane-associated kinase regulator
Solyc02g071470.4	1,70	1,29E-04	6,52E-04	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc09g014520.3	1,70	1,11E-19	3,05E-18	Chlorophyll a-b binding protein, chloroplastic
Solyc08g068390.3	1,70	5,23E-11	6,70E-10	Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a
Solyc05g008230.3	1,69	2,51E-08	2,32E-07	RING-type E3 ubiquitin transferase
Solyc10g078530.2	1,69	6,14E-15	1,15E-13	Patatin
Solyc01g066870.3	1,69	6,83E-17	1,52E-15	Protein phosphatase 2C
Solyc03g013240.4	1,69	6,64E-17	1,48E-15	lysine-tRNA ligase
Solyc10g052470.1	1,69	1,99E-06	1,39E-05	Protein RADIALIS-like 6
Solyc05g150117.1	1,69	1,73E-07	1,41E-06	Unknown protein
Solyc07g066610.3	1,69	1,74E-20	5,01E-19	Phosphoglycerate kinase
Solyc07g045420.4	1,68	3,76E-13	6,02E-12	Protein kinase superfamily protein
Solyc09g007480.3	1,68	5,34E-09	5,40E-08	transmembrane protein
Solyc04g018055.1	1,68	2,73E-04	1,28E-03	Glyceraldehyde-3-phosphate dehydrogenase
Solyc06g009020.2	1,68	6,29E-13	9,80E-12	Glutathione S-transferase
Solyc07g053615.1	1,68	1,76E-15	3,44E-14	DnaJ like protein
Solyc03g078770.3	1,68	5,18E-04	2,29E-03	Glycosyltransferase
Solyc05g053080.2	1,68	8,78E-03	2,74E-02	Unknown protein
Solyc12g098600.1	1,68	1,97E-16	4,21E-15	Glycosyltransferase
Solyc08g068780.3	1,68	2,58E-06	1,77E-05	N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase THT7-8
Solyc12g044630.2	1,68	2,92E-06	1,98E-05	Profilin
Solyc02g080570.3	1,67	1,02E-04	5,28E-04	Soluble starch synthase
Solyc02g020940.3	1,67	5,21E-18	1,27E-16	Glyceraldehyde-3-phosphate dehydrogenase
Solyc02g078240.4	1,67	4,16E-10	4,85E-09	Phosphoglycerate mutase
Solyc08g006790.4	1,67	3,51E-05	2,00E-04	Early nodulin-like protein 3
Solyc04g005660.4	1,67	3,02E-04	1,41E-03	transcription factor PRE6-like
Solyc02g080810.3	1,67	7,60E-20	2,10E-18	Aminomethyltransferase
Solyc03g005730.4	1,67	5,04E-16	1,05E-14	3-isopropylmalate dehydratase large subunit
Solyc02g093525.1	1,67	3,93E-13	6,27E-12	hypothetical protein
Solyc07g054690.1	1,67	4,97E-04	2,21E-03	hypothetical protein
Solyc03g121960.3	1,67	9,39E-14	1,60E-12	Phospholipid:diacylglycerol acyltransferase
Solyc06g062600.3	1,67	6,50E-07	4,87E-06	Glucose-methanol-choline (GMC) oxidoreductase family protein
Solyc12g005980.2	1,67	4,30E-07	3,31E-06	WLM domain-containing protein/PUB domain-containing protein
Solyc02g078660.4	1,66	5,47E-07	4,14E-06	Hydroxyproline-rich glycoprotein family protein
Solyc11g042460.2	1,66	4,24E-06	2,82E-05	Non-lysosomal glucosylceramidase
Solyc12g042920.2	1,66	3,42E-19	9,05E-18	Cytochrome c1
Solyc03g098460.3	1,66	3,99E-09	4,11E-08	NAD(P)-binding Rossmann-fold superfamily protein
Solyc06g011380.2	1,66	8,35E-04	3,51E-03	Chaperone protein ClpB
Solyc12g008350.3	1,66	1,03E-05	6,42E-05	dehydration responsive element binding protein 2
Solyc08g081390.4	1,66	9,17E-07	6,71E-06	Phosphoglycerate mutase-like protein AT74
Solyc07g049290.3	1,66	3,23E-12	4,69E-11	Protein NRT1/ PTR FAMILY 6.4
Solyc01g056690.4	1,66	8,99E-15	1,67E-13	Protein kinase and PP2C-like domain-containing protein
Solyc06g060510.2	1,66	2,42E-03	9,04E-03	DUF1191 domain-containing protein
Solyc01g098120.2	1,66	2,89E-04	1,35E-03	Unknown protein
Solyc10g086730.2	1,66	6,47E-07	4,85E-06	Fructose-1,6-bisphosphatase
Solyc08g067320.3	1,66	9,74E-07	7,10E-06	Chlorophyll a-b binding protein, chloroplastic
Solyc02g085950.4	1,65	6,90E-11	8,73E-10	cell wall protein X77373
Solyc09g015080.3	1,65	6,03E-14	1,05E-12	Patellin-6
Solyc08g080280.3	1,65	1,10E-04	5,66E-04	hypothetical protein
Solyc03g044330.1	1,65	8,11E-19	2,10E-17	Acetolactate synthase
Solyc03g007030.3	1,65	7,52E-12	1,05E-10	CDGSH iron-sulfur domain-containing protein NEET
Solyc10g080730.3	1,65	3,30E-12	4,79E-11	Thioredoxin-like 1-1, chloroplastic
Solyc12g005400.3	1,65	1,14E-11	1,56E-10	cyclic nucleotide-gated ion channel 4
Solyc09g010360.3	1,65	2,52E-12	3,70E-11	WAT1-related protein
Solyc06g007440.4	1,65	7,13E-10	8,11E-09	Non-specific serine/threonine protein kinase
Solyc06g082530.3	1,65	4,82E-04	2,15E-03	Scarecrow-like protein 9
Solyc08g008630.4	1,65	4,22E-12	6,06E-11	beta-carotene isomerase D27, chloroplastic
Solyc02g090400.4	1,65	7,13E-03	2,29E-02	Myb family transcription factor
Solyc08g067960.3	1,65	1,77E-10	2,14E-09	CHY-type/CTCHY-type/RING-type Zinc finger protein
Solyc08g076290.3	1,65	2,10E-15	4,10E-14	Plastidal glycolate/glycerate translocator 1, chloroplastic
Solyc03g123680.1	1,65	7,27E-03	2,33E-02	RING/U-box superfamily protein
Solyc11g010250.1	1,65	1,37E-03	5,45E-03	Avr9/Cf-9 rapidly elicited protein 75
Solyc03g080060.1	1,65	2,55E-15	4,94E-14	L-type lectin-domain containing receptor kinase VIII.2-like
Solyc03g082620.4	1,65	3,23E-15	6,23E-14	Metal-nicotianamine transporter YSL1
Solyc02g079640.3	1,64	2,27E-04	1,09E-03	G-type lectin S-receptor-like serine/threonine-protein kinase

Solyc12g006520.2	1,64	2,79E-14	5,00E-13	Terpene cyclase/mutase family member
Solyc06g050170.4	1,64	3,47E-15	6,66E-14	Potassium transporter
Solyc04g009520.3	1,64	9,43E-07	6,88E-06	Nuclear transcription factor Y subunit B
Solyc01g058260.4	1,64	1,87E-17	4,37E-16	Nuclear poly(A) polymerase 3
Solyc11g044450.3	1,64	1,44E-13	2,41E-12	DnaJ protein
Solyc07g042900.4	1,64	3,56E-17	8,08E-16	Organic cation/carnitine transporter 7
Solyc04g071480.1	1,64	8,80E-16	1,79E-14	Plant/F1M20-13 protein
Solyc09g019970.3	1,63	9,44E-08	8,02E-07	Ubiquitin carboxyl-terminal hydrolase
Solyc10g008665.1	1,63	2,46E-04	1,17E-03	HXXXD-type acyl-transferase family protein
Solyc07g052040.3	1,63	1,28E-02	3,74E-02	Tubulin beta chain
Solyc07g055060.3	1,63	3,36E-13	5,41E-12	Phosphoenolpyruvate carboxylase
Solyc06g059800.3	1,63	2,19E-08	2,04E-07	ACT domain-containing protein ACR3
Solyc06g074710.1	1,63	1,24E-02	3,66E-02	Transferase
Solyc07g043590.3	1,63	4,76E-19	1,25E-17	Polyamine oxidase 3
Solyc01g090180.4	1,63	2,40E-07	1,92E-06	4,5-DOPA dioxygenase extradiol
Solyc05g005150.1	1,62	2,09E-07	1,68E-06	F-box/Kelch repeat-containing F-box family protein
Solyc04g076010.3	1,62	9,23E-09	9,07E-08	zinc ion-binding protein
Solyc06g060060.4	1,62	1,38E-06	9,83E-06	NAD kinase
Solyc06g074530.1	1,62	4,63E-05	2,57E-04	Arogenate dehydratase
Solyc04g072035.1	1,62	6,34E-06	4,10E-05	Inositol polyphosphate 5-phosphatase I
Solyc06g051400.3	1,62	1,18E-15	2,37E-14	omega-3 fatty acid desaturase
Solyc03g114340.3	1,62	6,23E-16	1,28E-14	1-deoxy-D-xylulose-5-phosphate reductoisomerase
Solyc01g109780.3	1,62	5,23E-09	5,31E-08	F-box family protein
Solyc06g084140.4	1,62	4,09E-13	6,51E-12	Sulfate transporter
Solyc12g010980.3	1,62	4,72E-04	2,11E-03	HXXXD-type acyl-transferase family protein
Solyc07g052610.3	1,61	3,96E-10	4,62E-09	cyclinU1_1
Solyc03g095870.3	1,61	3,62E-03	1,28E-02	Eukaryotic translation initiation factor 2 subunit alpha
Solyc06g076790.1	1,61	4,22E-13	6,71E-12	Thylakoid soluble phosphoprotein TSP9
Solyc09g018010.3	1,61	8,01E-14	1,38E-12	Non-specific lipid-transfer protein
Solyc09g075020.3	1,61	1,71E-11	2,28E-10	ABC transporter C family member 4
Solyc04g011880.1	1,61	2,07E-06	1,44E-05	Monothiol glutaredoxin-S1
Solyc03g098630.4	1,61	7,37E-04	3,14E-03	DUF789 domain-containing protein
Solyc06g082410.1	1,61	4,62E-05	2,56E-04	Major facilitator superfamily protein
Solyc06g084760.3	1,61	1,59E-03	6,23E-03	Cytochrome P450
Solyc06g069760.3	1,61	5,24E-17	1,18E-15	Dof zinc finger protein
Solyc12g010870.3	1,60	2,88E-19	7,65E-18	ATP synthase protein I-related protein
Solyc12g099360.2	1,60	1,18E-06	8,50E-06	AMP-dependent synthetase/ligase
Solyc02g080440.3	1,60	8,46E-12	1,17E-10	Fe-S cluster assembly protein SufB
Solyc08g066050.3	1,60	3,62E-03	1,29E-02	Protein kinase domain
Solyc06g008590.3	1,60	2,24E-16	4,76E-15	auxin-regulated IAA17
Solyc01g005520.4	1,60	1,16E-14	2,13E-13	Protein LOW PSII ACCUMULATION 1, chloroplastic
Solyc07g019670.4	1,60	1,10E-11	1,50E-10	Peroxisomal fatty acid beta-oxidation multifunctional protein
Solyc05g005000.4	1,60	2,10E-12	3,13E-11	Alpha/beta-Hydrolases superfamily protein
Solyc03g025320.4	1,59	1,94E-19	5,21E-18	HXXXD-type acyl-transferase family protein
Solyc09g090360.3	1,59	3,43E-15	6,60E-14	phosphate transporter PHO1-like
Solyc08g006930.3	1,59	9,99E-13	1,53E-11	photosystem I reaction center subunit psaK, chloroplastic
Solyc10g006970.3	1,59	1,72E-18	4,36E-17	Thioredoxin
Solyc07g008570.3	1,59	1,26E-03	5,07E-03	Purple acid phosphatase
Solyc05g042155.1	1,59	4,36E-04	1,96E-03	Transposon protein
Solyc07g041000.4	1,59	2,30E-03	8,63E-03	Cleavage and polyadenylation specificity factor subunit 5-like protein
Solyc10g081910.2	1,58	1,65E-18	4,18E-17	Receptor-like kinase
Solyc01g103030.3	1,58	1,06E-12	1,62E-11	Major facilitator superfamily protein
Solyc10g086410.3	1,58	2,56E-11	3,38E-10	LEHSC270 hsc-2heat shock protein cognate 70
Solyc04g077590.4	1,58	3,87E-14	6,82E-13	Protein PHLOEM PROTEIN 2-LIKE A10
Solyc07g049560.3	1,58	1,95E-08	1,84E-07	Protein-tyrosine phosphatase
Solyc11g010780.1	1,58	4,80E-05	2,65E-04	UDP-glycosyltransferase 91A1
Solyc04g007110.4	1,58	9,69E-16	1,96E-14	transmembrane protein
Solyc05g013680.3	1,58	2,87E-08	2,63E-07	Gdsl esterase/lipase
Solyc01g079400.3	1,58	6,86E-12	9,61E-11	Protein trichome birefringence-like 6
Solyc12g088250.2	1,58	1,21E-13	2,02E-12	Serine carboxypeptidase
Solyc06g068230.4	1,58	1,26E-03	5,05E-03	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc09g065800.4	1,58	3,19E-03	1,15E-02	3-ketoacyl-CoA synthase
Solyc07g043490.1	1,58	2,48E-09	2,65E-08	Glycosyltransferase
Solyc04g072034.1	1,58	2,55E-08	2,35E-07	NAD(P)-binding Rossmann-fold superfamily protein
Solyc07g009410.4	1,58	7,84E-03	2,49E-02	F-box/kelch-repeat protein
Solyc01g101130.3	1,58	1,84E-05	1,10E-04	Myosin heavy chain, cardiac protein
Solyc03g006880.3	1,58	1,07E-08	1,04E-07	gibberellin 20-oxidase-1
Solyc02g070770.3	1,57	2,39E-18	5,99E-17	NAD(P)-binding Rossmann-fold superfamily protein
Solyc05g017793.1	1,57	3,48E-03	1,24E-02	Unknown protein
Solyc07g065420.1	1,57	1,40E-04	7,06E-04	Protein MIZU-KUSSEI 1
Solyc05g025870.4	1,57	1,46E-05	8,91E-05	mast cell carboxypeptidase A
Solyc12g049550.2	1,57	7,61E-09	7,55E-08	GDSL esterase/lipase 5-like
Solyc10g081510.2	1,57	5,04E-13	7,95E-12	ethylene-responsive methionine synthase
Solyc06g075650.3	1,57	4,52E-03	1,56E-02	tonoplast intrinsic protein 1.2
Solyc04g007950.4	1,57	3,52E-12	5,08E-11	Cysteine-rich repeat secretory protein 60
Solyc01g098500.3	1,57	8,72E-20	2,41E-18	Sugar facilitator protein 5
Solyc03g095610.4	1,57	2,82E-05	1,64E-04	DUF3133 domain-containing protein
Solyc03g095970.3	1,57	4,28E-04	1,93E-03	Short-chain dehydrogenase reductase 4
Solyc02g078480.3	1,57	2,51E-12	3,68E-11	CBS domain-containing protein
Solyc01g014373.1	1,56	2,71E-13	4,41E-12	IRK-interacting protein
Solyc04g053130.4	1,56	5,47E-12	7,73E-11	Stress enhanced protein 2, chloroplastic
Solyc09g065900.3	1,56	1,32E-18	3,37E-17	Glutathione reductase
Solyc03g013305.1	1,56	1,45E-02	4,17E-02	Transposon-like protein
Solyc06g083480.4	1,56	4,56E-03	1,57E-02	NAD(P)-binding Rossmann-fold superfamily protein
Solyc06g066640.3	1,56	5,49E-13	8,62E-12	Photosystem I reaction center subunit VI, chloroplastic
Solyc11g067080.3	1,56	1,12E-12	1,72E-11	Serine/threonine-protein kinase D6PKL2
Solyc03g097820.2	1,56	3,16E-10	3,72E-09	bHLH transcription factor 022
Solyc07g054130.2	1,56	1,36E-03	5,41E-03	Unknown protein
Solyc03g117270.1	1,56	1,69E-09	1,84E-08	F-box family protein
Solyc04g076980.3	1,56	7,79E-09	7,71E-08	Receptor-like protein kinase
Solyc07g007020.3	1,56	6,81E-05	3,65E-04	Protein kinase
Solyc10g082064.1	1,56	2,52E-12	3,69E-11	furry
Solyc06g008180.3	1,55	5,18E-03	1,75E-02	Unknown protein
Solyc05g054930.3	1,55	1,59E-05	9,61E-05	CAP-gly domain linker
Solyc06g065040.4	1,55	8,60E-14	1,47E-12	bHLH transcription factor 086
Solyc04g017750.4	1,55	7,91E-03	2,51E-02	Plant calmodulin-binding-like protein
Solyc02g080780.3	1,55	3,94E-17	8,93E-16	orotidine 5'-phosphate decarboxylase
Solyc07g009150.3	1,55	8,95E-07	6,57E-06	Protein kinase superfamily protein
Solyc05g054315.1	1,55	1,56E-14	2,85E-13	Epoxide hydrolase
Solyc10g006150.3	1,55	3,27E-07	2,56E-06	DUF761 domain-containing protein/DUF4408 domain-containing protein
Solyc09g025270.3	1,55	2,73E-09	2,89E-08	RING-type E3 ubiquitin transferase
Solyc02g081730.3	1,55	3,29E-09	3,43E-08	3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 1
Solyc10g009570.3	1,55	8,40E-12	1,16E-10	Rhodanese-like domain-containing protein 4, chloroplastic
Solyc10g044680.2	1,54	3,89E-03	1,37E-02	R2R3MYB transcription factor 55
Solyc05g007980.3	1,54	9,63E-11	1,20E-09	Sulfate transporter
Solyc12g049380.3	1,54	3,79E-03	1,33E-02	hypothetical protein
Solyc03g113990.3	1,54	2,42E-15	4,68E-14	Thiol-disulfide oxidoreductase DCC
Solyc09g059650.4	1,54	2,43E-05	1,43E-04	Unknown protein
Solyc05g008580.3	1,54	1,97E-11	2,62E-10	CDP-diacylglycerol--serine O-phosphatidyltransferase 1
Solyc03g112060.3	1,54	9,46E-12	1,30E-10	Quinolinate synthase, chloroplastic
Solyc02g087960.3	1,54	7,57E-05	4,03E-04	R2R3MYB transcription factor 94
Solyc12g043110.2	1,54	5,81E-10	6,68E-09	LETSW12
Solyc11g013180.2	1,54	2,26E-11	2,99E-10	Phosphatidylinositol 4-phosphate 5-kinase
Solyc06g074670.4	1,54	2,46E-12	3,61E-11	UDP-apiose/UDP-xylose synthase
Solyc09g098130.3	1,54	1,18E-06	8,49E-06	Spotted wilt resistance-5
Solyc03g116590.3	1,54	2,84E-14	5,07E-13	Embryo-specific protein

Solyc10g081570.3	1,54	5,43E-03	1,82E-02	Marmande
Solyc02g084650.3	1,53	2,64E-11	3,48E-10	UPF0651 protein, mitochondrial
Solyc04g054890.3	1,53	8,38E-08	7,15E-07	Acyl-coenzyme A oxidase
Solyc04g009130.4	1,53	4,11E-04	1,85E-03	Disease resistance protein
Solyc08g077380.4	1,53	6,37E-08	5,52E-07	Purine permease
Solyc07g049610.1	1,53	3,51E-06	2,35E-05	Xyloglucan galactosyltransferase KATAMARI1
Solyc06g072710.3	1,53	9,94E-07	7,23E-06	RNA polymerase sigma factor sigA
Solyc08g080200.4	1,53	2,03E-18	5,11E-17	SPX domain-containing protein
Solyc02g085000.3	1,53	6,87E-10	7,83E-09	netrin receptor DCC
Solyc11g069270.2	1,53	6,68E-07	5,00E-06	beta-galactosidase 5
Solyc10g007690.3	1,53	5,14E-19	1,35E-17	Chlorophyll a-b binding protein, chloroplastic
Solyc06g083410.4	1,53	6,40E-07	4,80E-06	protein XRI1
Solyc07g056540.3	1,52	6,48E-14	1,12E-12	glycolate oxidase X92888
Solyc02g065590.3	1,52	1,28E-11	1,74E-10	Alpha/Beta hydrolase fold protein
Solyc09g061890.3	1,52	6,16E-05	3,34E-04	Pectate lyase
Solyc01g060180.4	1,52	3,06E-17	6,99E-16	AMP-dependent synthetase/ligase
Solyc08g078760.1	1,52	6,11E-04	2,65E-03	transmembrane protein
Solyc06g005710.3	1,52	1,04E-04	5,37E-04	Protein TIC 62, chloroplastic
Solyc01g102440.3	1,51	3,05E-03	1,11E-02	organic solute transporter ostalpha protein (DUF300)
Solyc08g080050.4	1,51	2,74E-17	6,31E-16	PGR5-like protein 1A, chloroplastic
Solyc10g084650.3	1,51	5,56E-04	2,44E-03	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein
Solyc09g074450.1	1,51	6,70E-09	6,69E-08	Classical arabinogalactan protein 26
Solyc07g008840.3	1,51	1,80E-14	3,26E-13	Rab-GTPase-TBC domain
Solyc08g080040.4	1,51	3,10E-04	1,44E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc01g096880.4	1,51	9,32E-11	1,16E-09	Major facilitator superfamily protein
Solyc08g016587.1	1,51	5,45E-03	1,82E-02	Unknown protein
Solyc10g049870.1	1,51	1,16E-03	4,73E-03	Zinc finger protein
Solyc03g115540.2	1,50	1,65E-07	1,35E-06	bHLH transcription factor 024
Solyc02g090260.3	1,50	4,67E-05	2,59E-04	golgin
Solyc03g059180.4	1,50	2,63E-14	4,72E-13	Calcium sensing receptor, chloroplastic
Solyc04g007960.4	1,50	9,31E-06	5,85E-05	Caleosin
Solyc01g108540.3	1,50	4,09E-11	5,27E-10	Alpha/beta-Hydrolases superfamily protein
Solyc09g066140.3	1,50	4,30E-03	1,49E-02	myosin-binding protein 1-like
Solyc01g008220.3	1,50	1,47E-04	7,35E-04	UPF0664 stress-induced protein C29B12.11c
Solyc02g093360.3	1,50	4,24E-09	4,36E-08	Stpk1 protein kinase
Solyc08g066310.3	1,50	1,23E-06	8,81E-06	Receptor-like protein kinase
Solyc11g011630.3	1,50	9,93E-05	5,16E-04	Auxin-responsive protein SAUR65
Solyc12g006530.2	1,50	3,43E-09	3,57E-08	Terpene cyclase/mutase family member
Solyc12g007100.2	1,50	1,96E-14	3,54E-13	AAA-type ATPase family protein / ankyrin repeat family protein
Solyc01g028803.1	1,50	2,52E-07	2,01E-06	Cytochrome P450
Solyc03g058430.3	1,50	4,71E-10	5,46E-09	Fatty acid desaturase
Solyc08g074682.1	1,50	2,24E-04	1,07E-03	Polyphenol oxidase
Solyc07g066620.3	1,50	1,14E-13	1,92E-12	ATP-dependent zinc metalloprotease
Solyc04g016040.1	1,49	1,75E-03	6,77E-03	Unknown protein
Solyc07g044860.3	1,49	5,85E-12	8,25E-11	psbXphotosystem II 23 kDa protein
Solyc05g010030.4	1,49	3,38E-07	2,64E-06	Unknown protein
Solyc10g081260.2	1,49	8,16E-12	1,13E-10	Protein DETOXIFICATION
Solyc01g095430.3	1,49	8,34E-11	1,05E-09	Protein CURVATURE THYLAKOID 1A, chloroplastic
Solyc08g076400.3	1,49	9,51E-08	8,06E-07	Homeodomain-like superfamily protein
Solyc04g080920.3	1,49	1,87E-07	1,52E-06	Purple acid phosphatase
Solyc05g150130.1	1,49	3,75E-03	1,32E-02	Alcohol dehydrogenase
Solyc01g074030.3	1,49	4,64E-16	9,65E-15	Beta-glucosidase
Solyc05g007210.2	1,48	1,05E-03	4,32E-03	Transcription factor PRE4
Solyc08g078030.4	1,48	1,62E-04	8,01E-04	Transferase domain-containing protein
Solyc11g007270.3	1,48	1,01E-09	1,13E-08	Alkaline/neutral invertase
Solyc11g009080.2	1,48	4,69E-16	9,75E-15	DAHP synthase 1 precursor
Solyc01g091530.4	1,48	8,78E-14	1,50E-12	Fasciclin-like arabinogalactan protein
Solyc11g068515.1	1,48	2,19E-09	2,36E-08	Unknown protein
Solyc06g011370.4	1,48	8,88E-03	2,77E-02	Chaperone protein ClpB
Solyc11g008905.1	1,48	3,64E-03	1,29E-02	Unknown protein
Solyc02g076680.3	1,48	3,09E-08	2,82E-07	DUF688 domain-containing protein
Solyc03g006970.1	1,48	6,51E-09	6,51E-08	serine protease SBT2
Solyc10g080550.2	1,47	8,23E-06	5,21E-05	Protein trichome birefringence
Solyc08g076450.3	1,47	5,27E-17	1,18E-15	NAD(P)-binding Rossmann-fold superfamily protein
Solyc02g084640.4	1,47	6,65E-08	5,75E-07	Aldehyde dehydrogenase
Solyc06g076410.4	1,47	1,28E-12	1,95E-11	Methylsterol monooxygenase 2-1
Solyc03g121870.3	1,47	2,45E-06	1,69E-05	Methyltransferase-like protein
Solyc12g005690.1	1,47	1,98E-03	7,56E-03	transmembrane protein
Solyc08g016220.1	1,47	4,91E-09	5,00E-08	Receptor like protein
Solyc10g086170.1	1,47	2,47E-12	3,63E-11	Amidase 1
Solyc05g050830.3	1,47	1,17E-08	1,13E-07	Ethylene-responsive transcription factor
Solyc05g005160.3	1,47	1,86E-08	1,76E-07	ATP-citrate synthase
Solyc09g065430.4	1,46	8,95E-03	2,79E-02	Lipid transfer protein
Solyc07g053130.4	1,46	1,85E-07	1,50E-06	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc09g061310.3	1,46	8,25E-12	1,14E-10	PPPDE putative thiol peptidase family protein
Solyc06g075600.3	1,46	4,35E-03	1,50E-02	Ankyrin repeat-containing protein
Solyc04g077920.3	1,46	2,19E-13	3,59E-12	Interferon-related developmental regulator family protein / IFRD protein family
Solyc01g110590.4	1,46	2,66E-06	1,82E-05	Small auxin up-regulated RNA6
Solyc01g102850.3	1,46	1,49E-04	7,45E-04	Disease resistance protein (TIR-NBS-LRR class) family
Solyc05g018130.3	1,46	5,31E-13	8,35E-12	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc07g052320.3	1,46	1,01E-06	7,33E-06	Hexosyltransferase
Solyc09g011240.3	1,46	1,56E-13	2,60E-12	NAD(P)-linked oxidoreductase superfamily protein
Solyc12g098910.2	1,46	3,17E-06	2,14E-05	Non-specific serine/threonine protein kinase
Solyc03g025390.3	1,46	2,61E-09	2,77E-08	Short-chain dehydrogenase TIC 32, chloroplastic
Solyc08g081030.1	1,46	1,33E-17	3,14E-16	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Solyc01g106790.3	1,46	1,24E-12	1,88E-11	Tubulin alpha-6 chain, putative
Solyc08g081810.3	1,46	1,20E-10	1,48E-09	Cation/H(+) antiporter 17
Solyc02g094120.3	1,46	4,95E-07	3,77E-06	sulfite oxidase
Solyc09g098590.4	1,46	2,74E-10	3,24E-09	Sucrose synthase
Solyc01g073710.2	1,46	6,01E-10	6,89E-09	Calcium-binding EF-hand family protein
Solyc05g050550.4	1,46	5,42E-10	6,25E-09	hypothetical protein
Solyc03g111110.1	1,45	4,85E-07	3,71E-06	Unknown protein
Solyc10g083380.2	1,45	7,08E-06	4,54E-05	Basic-leucine zipper (BZIP) transcription factor family protein
Solyc12g036310.1	1,45	1,19E-02	3,53E-02	Unknown protein
Solyc01g007800.3	1,45	4,25E-04	1,91E-03	ovate family protein 2
Solyc01g100750.2	1,45	9,79E-05	5,09E-04	DUF538 domain-containing protein
Solyc11g071780.1	1,45	7,51E-07	5,57E-06	Unknown protein
Solyc11g006470.2	1,45	6,04E-06	3,92E-05	Core-2 i-branching beta-n-acetylglucosaminyltransferase family protein
Solyc03g034170.4	1,45	2,43E-13	3,96E-12	acclimation of photosynthesis to environment
Solyc07g065900.3	1,45	9,58E-08	8,12E-07	Fructose-bisphosphate aldolase
Solyc01g100770.2	1,45	1,22E-10	1,51E-09	DUF538 domain-containing protein
Solyc06g009510.1	1,45	4,60E-06	3,04E-05	transcription factor UPBEAT1
Solyc12g042470.2	1,45	2,91E-11	3,81E-10	Non-functional NADPH-dependent codeinone reductase 2
Solyc04g079030.2	1,45	3,56E-04	1,63E-03	Glycosyltransferase
Solyc01g095980.3	1,45	1,15E-08	1,11E-07	Acid phosphatase/vanadium-dependent haloperoxidase-related protein
Solyc09g064380.3	1,45	2,78E-11	3,66E-10	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc06g072740.1	1,45	6,06E-04	2,63E-03	Inositol-tetrakisphosphate 1-kinase
Solyc01g110280.3	1,45	1,11E-13	1,88E-12	Protein DETOXIFICATION
Solyc10g081900.3	1,44	7,69E-10	8,73E-09	Digalactosyldiacylglycerol synthase 1, chloroplastic
Solyc09g065550.4	1,44	1,63E-02	4,61E-02	Kinase interacting (KIP1-like) family protein
Solyc07g066150.1	1,44	1,61E-15	3,18E-14	Photosystem I reaction center subunit V, chloroplastic
Solyc09g091970.4	1,44	2,21E-14	3,98E-13	Epimerase family protein SDR39U1-like protein, chloroplastic
Solyc02g087880.3	1,44	4,38E-04	1,97E-03	Tubulin alpha chain
Solyc08g082250.3	1,44	6,43E-10	7,34E-09	endo-beta-1,4-D-glucanase (Cel8)
Solyc08g079170.3	1,44	4,15E-05	2,33E-04	Hsp70-Hsp90 organizing protein 1
Solyc11g056680.1	1,44	8,95E-09	8,80E-08	Leucine-rich repeat receptor-like protein

Solyc12g094640.3	1,44	9,46E-08	8,03E-07	Glyceraldehyde-3-phosphate dehydrogenase
Solyc02g065700.3	1,44	1,96E-10	2,36E-09	Alpha/beta-Hydrolases superfamily protein
Solyc01g094360.3	1,43	8,36E-04	3,51E-03	MYB transcription factor
Solyc01g065690.3	1,43	1,81E-08	1,71E-07	Heavy metal-associated isoprenylated plant protein
Solyc03g083320.4	1,43	1,93E-03	7,38E-03	calcium sensor calcineurin B
Solyc11g006230.3	1,43	5,25E-09	5,33E-08	GRF1-interacting factor 1
Solyc06g053910.4	1,43	1,24E-12	1,88E-11	DUF506 domain-containing protein
Solyc01g067010.3	1,43	2,68E-07	2,13E-06	F-box protein
Solyc03g083060.3	1,43	1,15E-02	3,42E-02	Ribonuclease P protein subunit P38-like protein
Solyc10g086280.2	1,43	5,28E-05	2,89E-04	heavy metal-associated isoprenylated plant protein 3-like
Solyc02g087780.3	1,43	3,21E-08	2,92E-07	Aldose 1-epimerase
Solyc02g068380.3	1,43	1,60E-15	3,16E-14	Allantoate deiminase/N-carbamoyl-L-amino-acid hydrolase
Solyc07g056350.3	1,43	2,38E-12	3,51E-11	mitogen-activated protein kinase 12
Solyc05g052600.4	1,43	7,32E-15	1,37E-13	Sedoheptulose-1,7-bisphosphatase, chloroplastic
Solyc03g034220.3	1,43	1,02E-10	1,27E-09	Tomato RuBP carboxylase small subunit
Solyc09g065850.4	1,43	1,49E-07	1,23E-06	auxin-regulated IAA3
Solyc03g116570.3	1,43	2,86E-10	3,39E-09	Thiol-disulfide oxidoreductase DCC family protein
Solyc10g080080.3	1,43	1,53E-16	3,29E-15	Thioredoxin reductase
Solyc01g100920.3	1,43	2,96E-04	1,38E-03	WAT1-related protein
Solyc12g010200.2	1,43	1,03E-02	3,12E-02	Hexosyltransferase
Solyc01g010640.3	1,43	3,40E-10	3,99E-09	NAD(P)-linked oxidoreductase superfamily protein
Solyc04g063390.2	1,43	5,96E-05	3,24E-04	Chaperone protein dnaJ 10
Solyc09g089680.4	1,43	1,36E-05	8,33E-05	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc04g072760.3	1,43	1,30E-06	9,28E-06	Sulfate transporter
Solyc03g095600.1	1,42	1,62E-04	8,00E-04	KIP1-like
Solyc01g066740.3	1,42	1,03E-02	3,13E-02	Transducin/WD40 repeat-like superfamily protein
Solyc07g008205.1	1,42	7,50E-05	4,00E-04	EPIDERMAL PATTERNING FACTOR-like protein 8
Solyc06g083230.3	1,42	1,29E-14	2,36E-13	GTP cyclohydrolase 1
Solyc02g084720.3	1,42	4,37E-06	2,90E-05	beta-galactosidase 6
Solyc02g084740.4	1,42	1,29E-12	1,95E-11	Cytochrome P450
Solyc06g065990.1	1,42	2,08E-16	4,42E-15	ATP synthase subunit b', chloroplastic
Solyc12g009650.2	1,42	5,49E-08	4,82E-07	Sl proline-rich protein
Solyc03g120380.3	1,42	5,36E-08	4,71E-07	auxin-regulated IAA19
Solyc01g105350.3	1,42	4,47E-06	2,96E-05	Glycosyltransferase
Solyc08g076480.3	1,41	6,74E-15	1,26E-13	Plastid lipid-associated protein chloroplastic-like
Solyc10g044470.3	1,41	1,11E-13	1,87E-12	Chloride channel protein
Solyc03g080180.4	1,41	2,90E-09	3,06E-08	O-methyltransferase, putative
Solyc04g074350.3	1,41	3,03E-11	3,96E-10	Glycosyltransferase
Solyc02g069510.1	1,41	1,03E-04	5,31E-04	Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 6
Solyc07g063430.3	1,41	9,30E-17	2,03E-15	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein
Solyc01g112260.4	1,41	1,02E-10	1,27E-09	hypothetical protein
Solyc01g090800.3	1,41	2,68E-07	2,12E-06	cyclinU2_1
Solyc05g015390.3	1,41	1,68E-15	3,29E-14	REF/SRPP-like protein
Solyc05g013810.4	1,41	1,09E-11	1,48E-10	Cellulase (Glycosyl hydrolase family 5) protein
Solyc07g006680.1	1,41	7,29E-08	6,26E-07	HXXXD-type acyl-transferase family protein
Solyc11g009020.2	1,40	2,03E-10	2,45E-09	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Solyc08g082400.1	1,40	2,71E-13	4,41E-12	Chlororespiratory reduction31
Solyc10g080900.3	1,40	8,67E-09	8,54E-08	ripening related X72730
Solyc01g098570.2	1,40	2,41E-08	2,24E-07	FANTASTIC four-like protein (DUF3049)
Solyc02g086670.4	1,40	3,95E-14	6,94E-13	Shaggy-related protein kinase gamma
Solyc09g091880.4	1,40	2,63E-08	2,42E-07	Myb family transcription factor APL
Solyc03g083650.4	1,40	2,24E-07	1,80E-06	Glycosyltransferase
Solyc06g082470.3	1,40	3,55E-04	1,63E-03	MAP kinase kinase kinase 42
Solyc05g014000.4	1,40	2,41E-10	2,88E-09	Pectate lyase
Solyc12g007020.2	1,40	5,93E-03	1,96E-02	DUF936 domain-containing protein
Solyc01g008150.1	1,40	1,30E-03	5,21E-03	Unknown protein
Solyc12g006370.3	1,40	1,14E-12	1,74E-11	Polyamine oxidase-like protein
Solyc12g010380.3	1,40	2,91E-06	1,98E-05	Adenylate kinase
Solyc04g080790.3	1,39	3,27E-07	2,56E-06	BEL1-like homeodomain protein 7
Solyc09g015000.4	1,39	3,93E-06	2,62E-05	Class I heat shock protein
Solyc03g117850.4	1,39	3,71E-14	6,55E-13	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic
Solyc02g065400.3	1,39	5,02E-12	7,12E-11	33kDa precursor protein of oxygen-evolving complex
Solyc01g107470.4	1,39	2,56E-09	2,72E-08	Unknown protein
Solyc04g014500.3	1,39	8,23E-08	7,03E-07	Nudix hydrolase 4
Solyc03g111610.3	1,39	5,65E-10	6,49E-09	Haloacid dehalogenase-like hydrolase domain-containing protein
Solyc04g014600.3	1,39	6,13E-06	3,97E-05	Adenine nucleotide alpha hydrolases-like superfamily protein
Solyc11g005340.3	1,39	6,01E-05	3,26E-04	Plastid-lipid associated protein PAP / fibrillin family protein
Solyc06g069880.1	1,39	2,89E-06	1,97E-05	protein PHYTOCHROME KINASE SUBSTRATE 3-like
Solyc05g053620.3	1,39	5,05E-03	1,71E-02	F-box protein PP2-B11-like
Solyc11g010960.2	1,39	1,17E-11	1,59E-10	Alcohol dehydrogenase
Solyc10g078930.2	1,39	3,75E-10	4,38E-09	Activator of 90 kDa heat shock protein ATPase-like protein 1
Solyc08g076880.3	1,39	1,19E-10	1,48E-09	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial
Solyc08g066180.3	1,38	2,17E-12	3,22E-11	Haloacid dehalogenase-like hydrolase family protein
Solyc01g100020.4	1,38	7,87E-03	2,50E-02	Phospholipase
Solyc09g065020.4	1,38	7,08E-12	9,90E-11	F-box protein
Solyc05g007470.4	1,38	2,79E-03	1,02E-02	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc01g106340.3	1,38	6,06E-05	3,28E-04	Glutamyl-tRNA(Gln) amidotransferase subunit A
Solyc03g123560.3	1,38	2,10E-11	2,78E-10	Chaperone protein DnaJ
Solyc06g007190.4	1,38	4,69E-04	2,09E-03	Protein phosphatase 2C
Solyc11g012000.2	1,38	2,44E-07	1,95E-06	Transmembrane protein, putative (DUF3537)
Solyc07g066310.3	1,38	9,35E-15	1,74E-13	Photosystem II 10 kDa polypeptide, chloroplastic
Solyc05g005290.4	1,38	3,39E-06	2,28E-05	Poly [ADP-ribose] polymerase
Solyc04g081320.4	1,38	2,34E-08	2,18E-07	Protein disulfide-isomerase LQY1, chloroplastic
Solyc08g075080.3	1,38	2,09E-03	7,91E-03	RING/U-box superfamily protein
Solyc06g035960.3	1,37	5,19E-08	4,57E-07	Oxalate--CoA ligase
Solyc09g064480.1	1,37	1,86E-09	2,02E-08	Xyloglucan galactosyltransferase KATAMARI1
Solyc12g040790.2	1,37	5,70E-09	5,74E-08	Phosphoethanolamine N-methyltransferase
Solyc10g005200.3	1,37	1,18E-10	1,46E-09	galactan beta-1,4-galactosyltransferase GALS3
Solyc05g050770.4	1,37	6,02E-09	6,04E-08	Serine carboxypeptidase
Solyc08g079770.3	1,37	3,67E-07	2,86E-06	Guard cell S-type anion channel SLAC1
Solyc01g005120.3	1,37	6,12E-07	4,60E-06	Xyloglucan endotransglucosylase/hydrolase
Solyc12g010840.2	1,37	2,60E-13	4,24E-12	Ketol-acid reductoisomerase
Solyc10g006740.4	1,37	2,86E-03	1,05E-02	Calcium-binding protein PBP1
Solyc01g100120.4	1,37	1,01E-04	5,22E-04	Kinesin-like protein
Solyc11g006150.1	1,37	5,17E-03	1,75E-02	Ethylene receptor
Solyc11g071870.2	1,36	5,89E-09	5,92E-08	Ubiquitin-conjugating enzyme
Solyc09g007830.3	1,36	8,45E-10	9,56E-09	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc07g006370.1	1,36	2,70E-03	9,93E-03	cation/calcium exchanger 1
Solyc04g057940.4	1,36	5,48E-03	1,83E-02	RING-type E3 ubiquitin transferase
Solyc06g066000.3	1,36	2,94E-16	6,22E-15	ATP synthase subunit b', chloroplastic
Solyc03g119220.3	1,36	9,49E-03	2,93E-02	Kinesin-like protein
Solyc04g083010.4	1,36	9,92E-16	2,01E-14	Protein kinase superfamily protein
Solyc09g005840.2	1,36	4,54E-03	1,56E-02	Exocyst subunit Exo70 family protein
Solyc02g092740.1	1,36	1,04E-03	4,27E-03	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial
Solyc06g067860.3	1,36	1,07E-03	4,41E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc01g103350.3	1,36	1,51E-07	1,24E-06	Cyclin-dependent kinase C-2
Solyc01g100610.3	1,36	4,05E-13	6,45E-12	Solute carrier family 40 protein
Solyc04g079960.1	1,35	2,35E-06	1,62E-05	geranylgeranyl pyrophosphate synthase 2
Solyc05g015780.1	1,35	3,59E-09	3,71E-08	Unknown protein
Solyc12g088390.1	1,35	1,12E-02	3,37E-02	Zinc-finger protein
Solyc07g006890.1	1,35	1,44E-09	1,58E-08	Cytochrome P450
Solyc01g087190.4	1,35	1,25E-12	1,90E-11	Chaperonin-like RbcX
Solyc06g036640.4	1,35	1,96E-09	2,13E-08	alpha-(1%2C6)-fucosyltransferase
Solyc05g005960.3	1,35	1,87E-07	1,52E-06	Protein NRT1/ PTR FAMILY 1.2
Solyc01g108670.4	1,35	1,78E-02	4,97E-02	Kinesin
Solyc09g014525.1	1,35	1,96E-07	1,59E-06	MLP-like protein 43

Solyc12g039070.2	1,35	3,37E-03	1,21E-02	Strictosidine synthase family protein
Solyc04g076990.3	1,35	3,76E-05	2,13E-04	Receptor-like protein kinase
Solyc11g069670.2	1,35	1,13E-02	3,38E-02	CC-NBS-LRR type resistance-like protein
Solyc10g085120.3	1,35	1,09E-04	5,58E-04	Leucine-rich receptor-like kinase family protein
Solyc11g040340.3	1,35	2,76E-06	1,88E-05	LEE14BDGL L.esculentum endo-1,4-beta-D-glucanase
Solyc02g080600.1	1,35	5,40E-09	5,45E-08	Unknown protein
Solyc02g093220.3	1,35	1,14E-10	1,42E-09	F-box protein
Solyc12g006380.2	1,35	7,12E-05	3,81E-04	2-oxoglutarate-dependent dioxygenase
Solyc05g009080.4	1,35	3,13E-04	1,45E-03	Cyclase/dehydrase family protein
Solyc01g091050.4	1,35	1,04E-03	4,28E-03	Pectinesterase
Solyc02g089800.3	1,35	1,17E-02	3,47E-02	Nuclear matrix constituent-like protein 1
Solyc10g079755.1	1,35	6,33E-11	8,04E-10	Calcium-dependent protein kinase
Solyc08g082790.3	1,34	2,59E-08	2,38E-07	Unknown protein
Solyc07g026873.1	1,34	1,64E-03	6,40E-03	Heavy metal-associated isoprenylated plant protein 26
Solyc06g073450.4	1,34	1,33E-13	2,22E-12	hypothetical protein (DUF1685)
Solyc12g042530.2	1,34	2,80E-05	1,63E-04	Phosphatidylinositol-glycan biosynthesis class F protein
Solyc06g082980.3	1,34	1,58E-13	2,63E-12	Emopamil-binding
Solyc02g078620.1	1,34	5,09E-06	3,34E-05	Dof zinc finger protein DOF5.3
Solyc06g067980.3	1,34	1,42E-02	4,11E-02	repressed By RIM101 protein 1
Solyc05g009120.3	1,34	6,67E-03	2,17E-02	Core-2 i-branching beta-n-acetylglucosaminyltransferase family protein
Solyc06g068220.3	1,34	5,45E-14	9,51E-13	Alpha/beta-Hydrolases superfamily protein
Solyc11g068810.2	1,34	7,28E-09	7,23E-08	aspartyl/glutamyl-tRNA (Asn/Gln) amidotransferase subunit B
Solyc03g006500.3	1,34	3,77E-05	2,13E-04	Protein kinase domain
Solyc08g081040.3	1,34	7,22E-04	3,08E-03	RNAse P, Rpr2/Rpp21 subunit
Solyc11g066860.2	1,34	1,65E-06	1,17E-05	hypothetical protein
Solyc02g079360.3	1,34	1,06E-08	1,04E-07	Phox/Bem1p
Solyc10g080500.2	1,34	4,06E-14	7,13E-13	Actin
Solyc10g085610.2	1,33	2,20E-04	1,06E-03	Calmodulin-binding family protein, putative, expressed
Solyc01g008250.3	1,33	5,38E-08	4,72E-07	Thioredoxin
Solyc01g111040.4	1,33	1,40E-06	9,96E-06	Calcium-binding EF-hand family protein
Solyc10g005480.3	1,33	2,67E-06	1,82E-05	F-box family protein
Solyc03g122310.4	1,33	2,45E-10	2,93E-09	Aldehyde dehydrogenase
Solyc09g074470.3	1,33	1,40E-02	4,06E-02	Kinase interacting (KIP1-like) protein
Solyc04g082920.4	1,33	4,93E-13	7,78E-12	Retrovirus-related Pol polyprotein from transposon TNT 1-94
Solyc08g005630.3	1,33	2,40E-03	8,97E-03	Long-chain-alcohol oxidase
Solyc02g090960.1	1,33	3,67E-03	1,30E-02	Protein RALF-like 34
Solyc10g085850.1	1,33	4,84E-05	2,67E-04	TPSI1 protein
Solyc03g117070.1	1,33	1,51E-02	4,32E-02	Zinc finger protein 4
Solyc01g103750.4	1,32	1,39E-11	1,87E-10	ATP phosphoribosyltransferase
Solyc06g050710.4	1,32	1,64E-07	1,34E-06	Heavy metal transport/detoxification superfamily protein
Solyc01g107780.4	1,32	5,98E-04	2,60E-03	Glycosyltransferase
Solyc08g077780.3	1,32	6,16E-11	7,86E-10	Protein kinase
Solyc10g008510.3	1,32	3,80E-05	2,15E-04	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc02g079430.4	1,32	1,26E-05	7,74E-05	Zinc finger protein CONSTANS-LIKE 13
Solyc11g069590.2	1,32	3,95E-09	4,07E-08	Receptor-like serine/threonine-protein kinase NCRK
Solyc07g064720.3	1,32	3,08E-04	1,43E-03	Gdsl esterase/lipase
Solyc09g074610.3	1,32	1,10E-09	1,23E-08	Chaperone protein DnaJ
Solyc04g074850.3	1,31	5,69E-09	5,74E-08	ripening regulated protein DDTFR18
Solyc11g012240.1	1,31	1,70E-03	6,58E-03	MBOAT (Membrane bound O-acyl transferase) family protein
Solyc02g090510.3	1,31	3,66E-07	2,85E-06	CDPK-related protein kinase
Solyc10g008540.3	1,31	1,68E-04	8,28E-04	multidrug resistance protein
Solyc06g076630.3	1,31	1,68E-09	1,84E-08	Peroxidase
Solyc03g113690.1	1,31	1,20E-05	7,42E-05	ABC transporter G family member 23
Solyc01g108000.3	1,31	5,74E-03	1,91E-02	Protein kinase domain
Solyc05g052350.3	1,31	4,87E-07	3,72E-06	Leucine-rich repeat receptor-like protein kinase
Solyc02g094400.4	1,31	5,48E-11	7,01E-10	Glycerophosphodiester phosphodiesterase GDPD2
Solyc05g018630.1	1,31	7,02E-10	7,99E-09	Regulator of chromosome condensation (RCC1) family protein
Solyc07g062500.3	1,31	2,99E-07	2,35E-06	Cytochrome
Solyc06g150136.1	1,31	1,35E-02	3,94E-02	RING/U-box superfamily protein
Solyc11g071720.2	1,31	6,06E-06	3,93E-05	Alpha/beta-Hydrolases superfamily protein
Solyc04g009020.4	1,31	2,27E-05	1,34E-04	High chlorophyll fluorescent 107
Solyc01g060140.4	1,31	2,04E-05	1,21E-04	Calmodulin-binding transcription activator 5
Solyc07g017800.4	1,31	4,49E-07	3,45E-06	Unknown protein
Solyc06g060170.3	1,31	2,16E-07	1,73E-06	Pectin lyase-like superfamily protein
Solyc08g081160.3	1,31	4,93E-03	1,67E-02	DUF3741 domain-containing protein/DUF4378 domain-containing protein
Solyc01g095090.3	1,31	3,33E-04	1,54E-03	RING/U-box superfamily protein
Solyc07g053030.4	1,31	2,38E-03	8,90E-03	Auxin-responsive GH3 family protein
Solyc08g079650.3	1,31	2,01E-07	1,63E-06	ACT domain-containing protein
Solyc01g104020.2	1,31	8,35E-07	6,16E-06	Embryo-specific protein
Solyc12g005950.2	1,31	4,18E-06	2,78E-05	COP1 homolog
Solyc02g090900.3	1,31	4,53E-08	4,03E-07	Remorin
Solyc02g088830.4	1,30	3,33E-03	1,19E-02	hydroxyproline-rich glycoprotein family protein
Solyc07g055320.4	1,30	1,50E-09	1,65E-08	ATP-dependent zinc metalloprotease ftsh chloroplastic-like
Solyc06g072700.3	1,30	1,50E-06	1,07E-05	Heavy metal-associated isoprenylated plant protein
Solyc03g058190.3	1,30	3,17E-09	3,32E-08	GTP-binding protein TypA
Solyc05g042010.1	1,30	5,15E-03	1,74E-02	Heavy metal-associated isoprenylated plant protein 26
Solyc06g007340.3	1,30	1,20E-09	1,34E-08	gamma-interferon-inducible lysosomal thiol reductase-like
Solyc10g083370.1	1,30	1,20E-03	4,86E-03	Unknown protein
Solyc03g113350.3	1,30	4,38E-04	1,97E-03	Zinc finger protein
Solyc03g005770.3	1,30	9,01E-11	1,13E-09	Chlorophyll a-b binding protein, chloroplastic
Solyc11g066830.2	1,30	5,00E-04	2,22E-03	Zinc finger transcription factor 68
Solyc06g082590.1	1,30	1,91E-05	1,14E-04	DNA-binding protein Pti6
Solyc06g073110.3	1,30	3,13E-08	2,85E-07	mRNA, clone: RTFL01-36-E19
Solyc01g087590.3	1,30	1,73E-03	6,72E-03	Polyamine oxidase
Solyc11g066680.1	1,30	1,05E-07	8,88E-07	Glycosyltransferase
Solyc01g005620.3	1,30	3,19E-11	4,16E-10	oxoglutarate/malate translocator
Solyc05g005140.4	1,30	1,41E-08	1,35E-07	Protein NSP-INTERACTING KINASE 3
Solyc09g092640.3	1,30	3,46E-07	2,70E-06	Cytochrome
Solyc02g067350.3	1,30	7,98E-05	4,23E-04	DUF1666 domain-containing protein
Solyc01g073680.4	1,30	1,11E-06	8,00E-06	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc03g119340.3	1,29	6,77E-08	5,84E-07	Cysteine-rich receptor-like protein kinase 8
Solyc03g005760.1	1,29	1,61E-13	2,68E-12	Chlorophyll a-b binding protein, chloroplastic
Solyc01g066710.4	1,29	6,33E-03	2,07E-02	UDP-glucuronic acid decarboxylase 4
Solyc03g059170.2	1,29	1,31E-08	1,26E-07	Rhodanese/cell cycle control phosphatase superfamily protein
Solyc04g082500.4	1,29	3,27E-03	1,18E-02	Protein kinase APK1B, chloroplastic
Solyc12g006060.2	1,29	8,33E-05	4,40E-04	SAWADEE domain-containing protein
Solyc12g098920.2	1,29	1,31E-08	1,25E-07	Guanosine-3'5'-bis(Diphosphate) 3'-pyrophosphohydrolase
Solyc06g065200.4	1,29	1,58E-07	1,30E-06	beta-mannosyltransferase-like protein
Solyc02g065230.3	1,29	2,23E-04	1,07E-03	Cytochrome P450
Solyc02g082690.3	1,29	1,33E-05	8,16E-05	Transducin/WD40 repeat-like superfamily protein
Solyc01g103450.3	1,29	5,75E-14	1,00E-12	70 kDa heat shock protein
Solyc01g090790.4	1,29	1,86E-13	3,08E-12	bHLH transcription factor
Solyc01g091270.3	1,29	1,49E-03	5,87E-03	myeloid leukemia factor
Solyc11g064960.2	1,29	5,32E-03	1,79E-02	Vacuolar iron transporter-like protein 3
Solyc02g068610.2	1,28	5,41E-03	1,81E-02	Ankyrin repeat-containing protein
Solyc05g050230.4	1,28	1,86E-07	1,51E-06	Ubiquitin-conjugating enzyme
Solyc07g009130.4	1,28	8,39E-03	2,63E-02	Cadmium/zinc-transporting ATPase HMA2
Solyc10g008520.3	1,28	9,47E-13	1,45E-11	Auxin-responsive GH3 family protein
Solyc03g005570.3	1,28	1,39E-04	6,98E-04	Myb-related transcription factor LBM2
Solyc02g070760.4	1,28	9,27E-10	1,05E-08	NAD(P)-binding Rossmann-fold superfamily protein
Solyc08g075450.3	1,28	3,99E-10	4,65E-09	WAT1-related protein
Solyc08g079590.3	1,28	3,78E-06	2,53E-05	PPR containing protein
Solyc11g065990.2	1,28	4,56E-03	1,57E-02	Actin
Solyc01g088050.3	1,28	1,15E-10	1,43E-09	Serine/threonine-protein kinase-like protein
Solyc04g014810.3	1,28	3,43E-09	3,57E-08	RING-type E3 ubiquitin transferase
Solyc12g100120.2	1,28	3,37E-08	3,05E-07	Proline-tRNA ligase (DUF1680)

Solyc08g082280.4	1,28	1,81E-09	1,97E-08	Long chain acyl-CoA synthetase 2
Solyc02g077950.3	1,27	2,68E-04	1,26E-03	Dof zinc finger protein5
Solyc05g006740.4	1,27	1,09E-11	1,49E-10	Glutathione S-transferase
Solyc07g061935.1	1,27	8,53E-08	7,28E-07	C2 domain-containing protein
Solyc08g061610.4	1,27	5,28E-12	7,47E-11	Copper-transporting ATPase PAA2, chloroplastic
Solyc05g015470.1	1,27	2,27E-09	2,43E-08	Chaperone protein dnaJ-like protein
Solyc08g067310.1	1,27	4,05E-09	4,16E-08	Non-specific serine/threonine protein kinase
Solyc08g062180.3	1,27	3,19E-05	1,83E-04	protein BIG GRAIN 1-like A
Solyc03g116340.3	1,27	3,33E-08	3,02E-07	bHLH transcription factor 025
Solyc01g107800.4	1,27	7,55E-06	4,81E-05	glucuronoxylan 4-O-methyltransferase 1-like
Solyc05g055010.4	1,27	5,35E-09	5,40E-08	RNA-binding protein 42
Solyc08g066860.2	1,27	9,55E-03	2,94E-02	Auxin canalization protein (DUF828)
Solyc08g078020.1	1,27	9,29E-09	9,12E-08	Methionine rich arabinogalactan
Solyc05g055840.4	1,27	6,36E-04	2,75E-03	Glycosyltransferase
Solyc01g057210.3	1,27	1,61E-09	1,76E-08	Mitochondrial pyruvate dehydrogenase kinase
Solyc10g032567.1	1,27	1,75E-06	1,23E-05	Unknown protein
Solyc10g055630.2	1,27	2,32E-09	2,48E-08	plasma membrane intrinsic protein 2.9
Solyc04g011510.4	1,27	7,82E-12	1,09E-10	Triosephosphate isomerase
Solyc05g054830.3	1,26	1,68E-04	8,32E-04	Ankyrin repeat-containing protein
Solyc01g102460.4	1,26	1,47E-07	1,22E-06	ubiquitin carboxyl-terminal hydrolase-like protein
Solyc02g067700.1	1,26	1,13E-05	7,00E-05	RING/U-box superfamily protein
Solyc02g065050.1	1,26	1,21E-05	7,48E-05	aspartic proteinase PCS1-like
Solyc06g076280.3	1,26	2,53E-08	2,34E-07	Transcription factor GRAS
Solyc08g061130.3	1,26	1,23E-07	1,03E-06	Transcription factor HY5
Solyc06g068980.4	1,26	3,12E-06	2,11E-05	MAP kinase kinase kinase 39
Solyc01g109180.4	1,26	5,42E-04	2,39E-03	Long chain acyl-CoA synthetase 4
Solyc07g016180.3	1,26	2,03E-06	1,42E-05	Auxin Response Factor 7A
Solyc06g084480.3	1,26	1,13E-08	1,09E-07	protease Do-like 2, chloroplastic
Solyc02g089940.4	1,26	1,04E-04	5,35E-04	BEL1-like homeodomain protein 4
Solyc06g011400.2	1,26	8,35E-03	2,62E-02	Chaperone protein ClpB
Solyc03g043700.3	1,26	4,10E-03	1,43E-02	U-box domain-containing protein 4-like
Solyc05g053070.4	1,26	9,08E-05	4,75E-04	Unknown protein
Solyc03g007240.3	1,26	2,53E-07	2,01E-06	spermine synthase,Pfam:PF01564
Solyc01g111960.3	1,26	5,67E-05	3,09E-04	GDSL esterase/lipase At5g55050-like
Solyc07g025457.1	1,26	9,74E-05	5,07E-04	40S ribosomal protein S15
Solyc02g090540.4	1,26	5,37E-03	1,80E-02	Glucose/ribitol dehydrogenase
Solyc01g106480.4	1,26	1,41E-12	2,14E-11	glyoxisomal malate dehydrogenase
Solyc10g009110.1	1,26	5,47E-04	2,40E-03	ethylene response factor F.5
Solyc12g099290.2	1,26	5,34E-07	4,05E-06	Aldehyde dehydrogenase
Solyc10g006240.3	1,26	2,12E-11	2,81E-10	Pyridoxal phosphate homeostasis protein
Solyc00g500062.1	1,25	9,96E-03	3,05E-02	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic
Solyc06g074620.3	1,25	3,00E-05	1,73E-04	hypothetical protein
Solyc08g016210.3	1,25	8,51E-07	6,27E-06	LOW QUALITY PROTEIN: LRR receptor-like serine/threonine-protein kinase GSO1
Solyc03g034070.1	1,25	1,46E-07	1,21E-06	anti-muellerian hormone type-2 receptor
Solyc06g075160.3	1,25	1,61E-09	1,76E-08	SIT4 phosphatase-associated family protein
Solyc10g055720.2	1,25	1,85E-05	1,11E-04	MAP kinase kinase kinase 75
Solyc11g005290.1	1,25	3,07E-03	1,11E-02	RING/U-box superfamily protein
Solyc01g110580.2	1,25	1,25E-03	5,03E-03	Small auxin up-regulated RNA5
Solyc08g079800.4	1,25	4,45E-04	1,99E-03	Growth-regulating factor 10
Solyc02g080510.1	1,25	1,66E-06	1,17E-05	Senescence regulator S40
Solyc06g043150.4	1,25	6,41E-03	2,09E-02	WD40 repeat
Solyc10g079110.2	1,25	1,08E-08	1,05E-07	1-acyl-sn-glycerol-3-phosphate acyltransferase 2
Solyc08g079700.3	1,25	2,26E-07	1,82E-06	Zinc finger A20 and AN1 domain stress-associated protein
Solyc06g075080.4	1,25	2,81E-09	2,97E-08	NADH pyrophosphatase-like, NUDIX hydrolase domain-like protein
Solyc06g150138.1	1,25	1,44E-06	1,03E-05	Unknown protein
Solyc03g115820.3	1,25	3,21E-09	3,36E-08	Ribulose-phosphate 3-epimerase-like
Solyc04g077470.3	1,24	1,35E-09	1,49E-08	Cellulose synthase-like C4, glycosyltransferase family 2
Solyc01g099990.3	1,24	6,20E-04	2,69E-03	F-box domain, Phloem protein 2-like protein
Solyc11g032220.2	1,24	4,04E-03	1,41E-02	12-oxophytodienoate reductase
Solyc01g008010.3	1,24	2,72E-07	2,16E-06	DUF220 domain-containing protein
Solyc02g077660.3	1,24	4,24E-03	1,47E-02	Homeobox domain-containing protein/DDT domain-containing protein
Solyc09g075230.1	1,24	6,22E-07	4,67E-06	DUF538 family protein
Solyc06g050620.3	1,23	1,96E-09	2,12E-08	DUF399 family protein, putative (DUF399 and DUF3411)
Solyc11g065740.2	1,23	4,20E-08	3,76E-07	Chaperonin-like RbcX
Solyc01g056850.3	1,23	1,41E-08	1,34E-07	CTP synthase
Solyc01g099030.4	1,23	1,07E-04	5,48E-04	GDSL esterase/lipase At5g03980-like
Solyc04g081400.3	1,23	6,11E-08	5,31E-07	plastidic hexokinase
Solyc08g079600.3	1,23	3,29E-06	2,22E-05	hypothetical protein
Solyc07g042440.3	1,23	5,29E-09	5,36E-08	Peroxiredoxin Q
Solyc03g121420.4	1,23	4,55E-06	3,01E-05	Inorganic pyrophosphatase 1
Solyc04g009430.3	1,23	6,87E-10	7,83E-09	NAD-dependent protein deacylase
Solyc02g021590.3	1,22	1,33E-09	1,47E-08	Protein male discoverer 2
Solyc08g006410.4	1,22	7,94E-08	6,79E-07	Glycosyltransferase
Solyc01g091130.4	1,22	1,91E-09	2,07E-08	Nitroreductase family protein
Solyc11g068730.2	1,22	4,87E-11	6,25E-10	Nitrilase
Solyc02g068600.3	1,22	1,31E-04	6,61E-04	Ankyrin repeat-containing protein
Solyc02g081250.3	1,22	8,90E-04	3,72E-03	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc10g083670.3	1,22	1,30E-07	1,08E-06	Glucomannan 4-beta-mannosyltransferase 2
Solyc05g017795.1	1,22	1,67E-02	4,71E-02	ATP-dependent DNA helicase
Solyc07g053630.4	1,22	6,40E-06	4,13E-05	Two-component response regulator
Solyc11g013010.2	1,22	5,34E-09	5,40E-08	Phosphatidylinositol-4-phosphate 5-kinase, putative
Solyc08g083330.2	1,22	7,07E-09	7,04E-08	Polyketide cyclase/dehydrase and lipid transport superfamily protein
Solyc07g006855.2	1,22	1,09E-02	3,28E-02	CASP-like protein
Solyc02g064640.4	1,22	2,85E-07	2,25E-06	ADP-ribosylation factor-like protein 8A
Solyc03g116160.1	1,22	1,45E-09	1,59E-08	protein PHYTOCHROME KINASE SUBSTRATE 3-like
Solyc02g093620.2	1,22	4,47E-09	4,57E-08	Pentatricopeptide repeat-containing protein
Solyc04g016330.3	1,22	1,25E-06	8,96E-06	Glycerol-3-phosphate dehydrogenase [NAD(+)]
Solyc01g060070.3	1,22	7,13E-06	4,56E-05	Outer envelope pore protein 16-2, chloroplastic
Solyc02g082740.1	1,21	1,51E-07	1,25E-06	Dirigent protein
Solyc10g024360.2	1,21	4,93E-05	2,72E-04	Potassium channel AKT2
Solyc12g006860.2	1,21	6,17E-05	3,34E-04	brassinosteroid hydroxylase
Solyc01g080750.3	1,21	1,45E-02	4,18E-02	ARM repeat superfamily protein
Solyc03g007770.3	1,21	4,36E-11	5,61E-10	S-type anion channel SLAH3
Solyc08g082900.4	1,21	2,01E-04	9,75E-04	WD40 repeat
Solyc08g005010.4	1,21	2,13E-12	3,17E-11	CAAX amino terminal protease
Solyc08g079530.3	1,21	3,99E-05	2,25E-04	Deoxyribodipyrimidine photo-lyase
Solyc11g012680.3	1,21	8,71E-11	1,09E-09	Heavy metal transport/detoxification superfamily protein
Solyc05g010320.4	1,21	2,56E-07	2,04E-06	Chalcone-flavonone isomerase family protein
Solyc01g044558.1	1,21	2,22E-04	1,07E-03	Cyclin-A1-1
Solyc05g025820.4	1,21	5,87E-08	5,12E-07	Protein kinase superfamily protein
Solyc11g069380.2	1,20	1,42E-05	8,66E-05	GcpE
Solyc01g007100.3	1,20	1,61E-06	1,14E-05	Digalactosyldiacylglycerol synthase 1, chloroplastic
Solyc07g054470.1	1,20	2,00E-03	7,62E-03	hypothetical protein
Solyc02g087030.1	1,20	1,44E-03	5,70E-03	NHL domain protein
Solyc11g044453.1	1,20	5,93E-03	1,96E-02	Serine/threonine-protein phosphatase 7 long form-like protein
Solyc07g062480.2	1,20	1,77E-02	4,93E-02	Epidermis-specific secreted glycoprotein EP1
Solyc07g007660.1	1,20	8,11E-05	4,29E-04	Armadillo-like helical
Solyc11g013480.3	1,20	5,83E-03	1,93E-02	Auxin Response Factor 17
Solyc07g053740.1	1,20	5,11E-05	2,81E-04	Ethylene Response Factor F.4
Solyc02g036370.3	1,20	5,38E-06	3,52E-05	Protein REVEILLE 7-like
Solyc09g064470.3	1,20	2,24E-09	2,40E-08	Xyloglucan galactosyltransferase KATAMARI1
Solyc06g054570.1	1,20	1,01E-02	3,09E-02	monothiol glutaredoxin-S3-like
Solyc02g093270.4	1,20	3,48E-05	1,98E-04	caffeoyl-CoA O-methyltransferase
Solyc06g035940.3	1,20	7,09E-03	2,28E-02	Homeobox-leucine zipper protein ROC5
Solyc08g062220.3	1,20	6,27E-11	7,98E-10	Glycosyltransferase
Solyc04g077150.3	1,20	6,36E-06	4,11E-05	Ergosterol biosynthetic protein 28

Solyc07g006480.4	1,20	2,96E-07	2,34E-06	Receptor-like kinase
Solyc06g062440.4	1,20	1,12E-03	4,56E-03	Disease resistance protein
Solyc04g078840.3	1,19	3,11E-06	2,11E-05	AREB
Solyc01g108570.3	1,19	1,13E-06	8,15E-06	Alpha/beta-Hydrolases superfamily protein
Solyc10g009365.1	1,19	3,33E-03	1,19E-02	Unknown protein
Solyc08g066800.4	1,19	3,13E-03	1,13E-02	phospholipase D
Solyc11g011780.3	1,19	1,04E-08	1,01E-07	60S ribosomal export protein NMD3
Solyc04g080710.4	1,19	5,15E-05	2,83E-04	Basic helix-loop-helix (BHLH) DNA-binding superfamily protein
Solyc03g111170.3	1,19	2,94E-07	2,32E-06	4-coumarate-CoA ligase
Solyc11g073010.1	1,19	4,89E-03	1,66E-02	Exocyst subunit Exo70 family protein
Solyc03g025410.4	1,19	2,07E-09	2,24E-08	NAD(P)-binding Rossmann-fold superfamily protein
Solyc06g075580.4	1,19	1,66E-02	4,69E-02	Kinesin
Solyc12g088530.2	1,19	2,32E-04	1,11E-03	cyclin A3.1
Solyc09g075080.3	1,19	2,26E-05	1,33E-04	Phytochrome A-associated F-box protein
Solyc05g054410.4	1,19	3,13E-04	1,45E-03	telomere binding protein 1
Solyc08g081060.3	1,19	1,50E-04	7,51E-04	DUF3527 domain-containing protein
Solyc12g094660.2	1,19	1,69E-05	1,02E-04	Disease resistance protein
Solyc11g066950.2	1,19	2,41E-03	9,00E-03	Stress responsive A/B barrel domain-containing protein
Solyc09g011720.3	1,19	1,58E-05	9,56E-05	DUF3527 domain-containing protein
Solyc02g065780.1	1,19	5,24E-09	5,32E-08	Protein RALF-like 27
Solyc05g051010.4	1,18	9,25E-06	5,81E-05	Dihydroflavonol-4-reductase
Solyc05g010813.1	1,18	6,80E-07	5,08E-06	Unknown protein
Solyc09g015170.4	1,18	6,38E-05	3,44E-04	Receptor-like kinase
Solyc02g072160.4	1,18	2,44E-08	2,27E-07	NAD(P)-binding Rossmann-fold superfamily protein
Solyc08g008610.3	1,18	1,63E-03	6,37E-03	Alpha/beta-Hydrolases superfamily protein
Solyc01g094890.4	1,18	3,15E-10	3,72E-09	Ferric reduction oxidase 2
Solyc01g097120.3	1,18	2,82E-05	1,64E-04	Protein WVD2-like 1
Solyc08g079790.1	1,18	1,03E-04	5,31E-04	Nucleotide-sugar transporter family protein
Solyc02g079190.3	1,18	1,80E-05	1,08E-04	Protein AUXIN SIGNALING F-BOX 3
Solyc06g053480.3	1,18	3,83E-12	5,51E-11	Acyl-[acyl-carrier-protein] desaturase
Solyc03g121550.3	1,18	5,37E-03	1,80E-02	Unknown protein
Solyc05g010516.1	1,18	1,02E-02	3,10E-02	Basic leucine zipper 43
Solyc03g032190.3	1,18	1,71E-02	4,80E-02	cyclinB2_7
Solyc04g077450.3	1,18	1,44E-06	1,02E-05	DNA binding protein
Solyc12g010800.2	1,18	2,45E-03	9,12E-03	Basic-leucine zipper (BZIP) transcription factor family protein
Solyc01g092950.3	1,18	1,96E-06	1,37E-05	MADS-box protein
Solyc05g012900.4	1,18	9,79E-03	3,00E-02	JJH-R-like protein
Solyc11g006640.3	1,18	1,10E-03	4,51E-03	Disease resistance protein
Solyc06g052020.2	1,17	1,32E-02	3,85E-02	protein PSY2 isoform X2
Solyc12g070270.2	1,17	1,26E-05	7,75E-05	ABC transporter B family member 26, chloroplastic
Solyc01g100650.3	1,17	1,22E-07	1,03E-06	NHL repeat-containing protein 2-like
Solyc11g069570.2	1,17	5,78E-08	5,05E-07	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc01g095620.3	1,17	6,36E-08	5,52E-07	Glycosyltransferase
Solyc10g005330.3	1,17	6,30E-05	3,40E-04	Homeobox-leucine zipper protein MERISTEM L1
Solyc07g052970.3	1,17	1,42E-05	8,69E-05	BTB domain-containing protein/NPH3 domain-containing protein
Solyc03g116100.3	1,17	2,53E-08	2,34E-07	R2R3MYB transcription factor 31
Solyc02g087340.3	1,17	2,75E-09	2,91E-08	Seed maturation-like protein
Solyc06g053760.3	1,17	1,23E-02	3,61E-02	Syntaxin-related protein KNOLLE
Solyc08g076060.3	1,17	1,45E-03	5,71E-03	Lectin protein kinase family protein
Solyc10g018300.3	1,17	7,61E-09	7,55E-08	Transketolase
Solyc06g084050.4	1,17	2,15E-08	2,01E-07	Photosystem II reaction center W protein, chloroplastic
Solyc03g120470.4	1,17	5,14E-05	2,83E-04	tonoplast intrinsic protein 2.2
Solyc05g053300.3	1,16	7,28E-12	1,02E-10	dihydrolipoamide dehydrogenase precursor
Solyc02g091000.4	1,16	6,36E-05	3,43E-04	Late embryogenesis abundant protein
Solyc05g012620.4	1,16	4,31E-09	4,42E-08	uvrB/uvrC motif-containing protein
Solyc05g015815.1	1,16	3,75E-04	1,71E-03	Unknown protein
Solyc01g112060.4	1,16	3,34E-08	3,03E-07	NAD(P)-binding domain-containing protein
Solyc04g015020.3	1,16	2,17E-08	2,03E-07	Heavy metal transport/detoxification superfamily protein
Solyc06g066620.4	1,16	1,46E-09	1,61E-08	Protein CURVATURE THYLAKOID 1C, chloroplastic
Solyc03g118710.3	1,16	7,85E-07	5,81E-06	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc01g100930.3	1,16	3,14E-07	2,47E-06	GDSL esterase/lipase
Solyc05g018300.3	1,16	1,73E-10	2,10E-09	Protein phosphatase 2C and cyclic nucleotide-binding/kinase domain-containing protein
Solyc08g083110.4	1,16	7,10E-07	5,29E-06	Methionine gamma-lyase
Solyc08g076470.4	1,16	1,35E-08	1,29E-07	glycerol-3-phosphate acyltransferase
Solyc07g066600.3	1,16	8,64E-09	8,52E-08	Phosphoglycerate kinase
Solyc09g074250.3	1,16	4,22E-03	1,46E-02	Protein kinase family protein
Solyc01g105370.4	1,16	1,41E-06	1,00E-05	2-nitropropane dioxygenase-like protein
Solyc07g053890.3	1,16	1,02E-07	8,61E-07	O-acyltransferase WSD1-like protein
Solyc06g060700.1	1,16	1,57E-02	4,48E-02	Inactive serine/threonine-protein kinase
Solyc02g092530.4	1,16	1,45E-06	1,03E-05	Acetamidase/Formamidase
Solyc10g083440.2	1,16	7,00E-07	5,22E-06	Glycosyltransferase
Solyc08g080770.3	1,15	5,82E-03	1,93E-02	LURP-one-like protein
Solyc09g075440.4	1,15	3,75E-07	2,91E-06	Never ripe-2
Solyc08g082630.3	1,15	4,58E-04	2,05E-03	Auxin Response Factor 9A
Solyc06g064450.3	1,15	8,59E-07	6,32E-06	E3 ubiquitin-protein ligase
Solyc07g063940.2	1,15	1,34E-07	1,12E-06	SCARECROW
Solyc04g009420.3	1,15	5,81E-07	4,37E-06	PsbP domain-containing protein
Solyc07g009380.4	1,15	4,93E-07	3,76E-06	xyloglucan endotransglucosylase-hydrolase 2
Solyc06g071030.3	1,15	3,85E-05	2,17E-04	isochorismate synthase
Solyc08g015780.3	1,15	3,05E-08	2,78E-07	Ankyrin repeat protein SKIP35
Solyc12g056950.2	1,15	1,36E-04	6,85E-04	FCS-Like Zinc finger 6
Solyc06g084080.4	1,15	7,46E-03	2,38E-02	Guanylate-binding protein
Solyc06g069820.4	1,15	4,10E-08	3,67E-07	DUF674 family protein
Solyc06g073920.3	1,15	5,77E-06	3,75E-05	CRABS CLAW-like protein 2a
Solyc07g025530.1	1,15	7,22E-07	5,38E-06	Methyltransf_11 domain-containing protein
Solyc02g088000.3	1,15	6,91E-11	8,74E-10	Starch synthase, chloroplastic/amyloplastic
Solyc08g083360.3	1,15	3,31E-07	2,60E-06	Photosynthetic NDH subcomplex B 3
Solyc01g006690.4	1,15	1,48E-03	5,84E-03	IRK-interacting protein
Solyc11g008620.2	1,15	4,59E-10	5,33E-09	Phosphoglycolate phosphatase
Solyc12g011020.2	1,15	1,12E-05	6,96E-05	Haloacid dehalogenase (HAD) superfamily protein
Solyc01g091710.4	1,15	7,08E-08	6,09E-07	F-box family protein
Solyc02g083590.3	1,15	3,26E-08	2,96E-07	dehydroquinate synthase
Solyc03g112460.3	1,15	9,22E-05	4,81E-04	Tryptophan aminotransferase-related protein 2
Solyc02g088560.4	1,15	2,26E-10	2,71E-09	Cyclic nucleotide-gated ion channel protein, putative
Solyc09g089640.2	1,14	4,90E-07	3,74E-06	Plant/protein (DUF668)
Solyc01g079880.3	1,14	6,44E-08	5,58E-07	Aluminum induced protein with YGL and LRDR motifs
Solyc03g118330.3	1,14	2,02E-04	9,79E-04	Receptor-like protein kinase
Solyc05g055850.3	1,14	2,47E-06	1,69E-05	Protein RESISTANCE TO PHYTOPHTHORA 1, chloroplastic
Solyc09g074050.3	1,14	4,56E-10	5,29E-09	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protein
Solyc07g052400.3	1,14	6,68E-07	5,00E-06	glutamate receptor-like 3.2
Solyc01g060170.4	1,14	5,76E-05	3,13E-04	Calmodulin-binding transcription activator
Solyc09g018170.4	1,14	2,87E-03	1,05E-02	MAP kinase kinase kinase 70
Solyc01g100660.4	1,14	3,46E-08	3,13E-07	Transcription factor
Solyc09g047900.2	1,14	8,40E-07	6,20E-06	Alpha/beta-Hydrolases superfamily protein
Solyc04g017720.3	1,14	7,52E-03	2,40E-02	Gibberellin regulated protein
Solyc03g116900.3	1,14	9,77E-09	9,57E-08	Metal transporter Nramp3
Solyc07g065660.4	1,14	9,37E-03	2,90E-02	Cellulose synthase-like protein E1
Solyc01g103760.3	1,14	3,06E-06	2,07E-05	magnesium transporter NIPA (DUF803)
Solyc09g074430.4	1,14	5,06E-04	2,25E-03	Flavin-containing monooxygenase
Solyc10g009320.3	1,14	2,61E-06	1,79E-05	NAD-dependent protein deacetylase HST1-like protein
Solyc06g069030.3	1,14	9,47E-10	1,07E-08	microbial collagenase
Solyc02g092670.1	1,14	1,03E-09	1,15E-08	Subtilisin-like protease
Solyc04g007000.2	1,13	7,54E-04	3,20E-03	AP2/B3 transcription factor family protein
Solyc08g078900.1	1,13	1,70E-03	6,58E-03	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc05g052590.1	1,13	1,89E-08	1,78E-07	Pkinase domain-containing protein
Solyc09g074520.3	1,13	9,82E-10	1,10E-08	Protein TRANSPORT INHIBITOR RESPONSE 1

Solyc01g095670.4	1,13	5,30E-10	6,12E-09	Rhodanese-like domain-containing protein 4, chloroplastic
Solyc01g059950.1	1,13	6,30E-03	2,06E-02	Transcription factor GRAS
Solyc03g083910.5	1,13	2,29E-08	2,14E-07	sucrose accumulator
Solyc09g008840.4	1,13	1,01E-06	7,33E-06	Pyruvate kinase
Solyc01g095900.4	1,13	1,98E-03	7,56E-03	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc05g005940.3	1,13	1,62E-02	4,58E-02	Protein NRT1/ PTR FAMILY 1.2
Solyc05g053200.3	1,13	2,58E-05	1,51E-04	PB1 domain-containing protein
Solyc05g012210.4	1,12	1,03E-06	7,46E-06	Ninja-family protein AFP3
Solyc03g005260.3	1,12	3,46E-09	3,59E-08	ATP sulfurylase
Solyc02g150128.1	1,12	2,56E-04	1,21E-03	Lrr receptor-like serinethreonine-protein kinase fls2
Solyc03g096770.1	1,12	2,92E-03	1,07E-02	Protein RESPONSE TO LOW SULFUR 2
Solyc01g099970.4	1,12	9,32E-10	1,05E-08	F-box family protein
Solyc07g064650.3	1,12	1,89E-03	7,25E-03	Senescence regulator S40
Solyc03g007440.4	1,12	5,86E-09	5,89E-08	Plastid division protein PDV1
Solyc03g111700.3	1,12	6,32E-10	7,22E-09	Metallo-hydrolase/oxidoreductase superfamily protein
Solyc11g020040.2	1,12	4,80E-03	1,64E-02	heat shock protein 70
Solyc10g051110.1	1,12	3,64E-07	2,83E-06	Protein TIC 62, chloroplastic
Solyc12g056850.2	1,12	1,42E-10	1,73E-09	Chaperone protein DnaJ
Solyc08g007950.3	1,12	1,06E-02	3,21E-02	30S ribosomal protein S1
Solyc05g010420.2	1,12	1,91E-07	1,55E-06	S-adenosylmethionine decarboxylase
Solyc09g075180.3	1,12	4,67E-10	5,42E-09	DNA photolyase
Solyc01g111760.4	1,12	1,19E-10	1,48E-09	Vacuolar ATP synthase subunit B
Solyc02g063150.3	1,12	2,34E-07	1,88E-06	RuBP carboxylase small subunit
Solyc09g008480.4	1,12	2,06E-06	1,43E-05	Phosphatidylinositol 4-phosphate 5-kinase
Solyc01g109910.4	1,12	1,24E-07	1,04E-06	RING/U-box superfamily protein
Solyc04g072230.4	1,12	2,39E-09	2,55E-08	Protein kinase superfamily protein
Solyc04g082000.4	1,12	1,60E-02	4,53E-02	Phospholipase D
Solyc01g107650.3	1,12	4,16E-06	2,77E-05	Ovary receptor kinase 1
Solyc05g008100.1	1,12	2,84E-05	1,65E-04	extensin
Solyc03g121910.1	1,12	1,01E-07	8,53E-07	Threonine synthase
Solyc12g044260.2	1,12	1,81E-06	1,27E-05	2-hydroxyacid dehydrogenase
Solyc09g075460.3	1,12	2,79E-10	3,30E-09	Pectin lyase-like superfamily protein
Solyc03g098330.2	1,11	5,94E-05	3,23E-04	Coiled coil protein
Solyc03g112700.1	1,11	2,40E-06	1,65E-05	Herbivore elicitor-regulated 1
Solyc04g082930.3	1,11	1,54E-07	1,27E-06	Chlorophyll a-b binding protein, chloroplastic
Solyc10g083340.3	1,11	1,76E-02	4,93E-02	Myb family transcription factor APL
Solyc03g065250.4	1,11	1,18E-09	1,31E-08	Fatty acid hydroxylase superfamily
Solyc06g010030.4	1,11	6,59E-08	5,70E-07	MLO-like protein
Solyc08g062290.4	1,11	8,81E-04	3,69E-03	Unknown protein
Solyc01g091540.3	1,11	7,09E-03	2,28E-02	Growth-regulating factor 10
Solyc02g086480.1	1,11	4,70E-03	1,61E-02	LOB domain-containing protein
Solyc03g115450.1	1,11	1,40E-02	4,07E-02	Zinc finger protein
Solyc02g064720.3	1,11	3,33E-04	1,54E-03	BTB/POZ domain-containing protein
Solyc07g062080.4	1,11	1,53E-07	1,26E-06	mitogen-activated protein kinase 11
Solyc01g100200.3	1,11	9,49E-06	5,95E-05	gras4
Solyc01g091950.4	1,10	3,18E-09	3,34E-08	Lysophospholipid acyltransferase LPEAT2
Solyc09g009040.3	1,10	4,19E-05	2,35E-04	Delta(14)-sterol reductase
Solyc03g123710.3	1,10	2,85E-05	1,66E-04	Unknown protein
Solyc04g080430.3	1,10	7,96E-06	5,04E-05	Cytosolic purine 5'-nucleotidase
Solyc04g071940.3	1,10	1,79E-07	1,46E-06	NAD(P)-binding Rossmann-fold superfamily protein
Solyc04g007640.3	1,10	1,83E-04	8,96E-04	RING-type E3 ubiquitin transferase
Solyc10g074930.1	1,10	2,22E-09	2,39E-08	Ribosomal protein S6 kinase
Solyc01g044556.1	1,10	8,01E-03	2,53E-02	TPX2 (targeting protein for Xklp2) protein family
Solyc09g092460.4	1,10	1,31E-07	1,09E-06	receptor-like kinase TMK4
Solyc10g054670.3	1,10	1,79E-05	1,08E-04	Unknown protein
Solyc04g009770.3	1,10	5,62E-08	4,92E-07	DnaJ protein
Solyc08g007210.4	1,10	3,42E-03	1,22E-02	Transferase domain-containing protein
Solyc05g053000.1	1,10	6,17E-05	3,34E-04	AT-hook motif nuclear-localized protein
Solyc09g009860.1	1,10	8,15E-03	2,57E-02	Glutaredoxin
Solyc10g006820.4	1,10	3,78E-06	2,53E-05	Myosin-2
Solyc01g008100.3	1,10	3,80E-07	2,95E-06	Transferring glycosyl group transferase
Solyc11g065780.3	1,10	1,54E-02	4,39E-02	CC-NBS-LRR type resistance-like protein
Solyc01g007770.2	1,10	1,07E-04	5,51E-04	hypothetical protein
Solyc12g056580.2	1,10	2,02E-10	2,44E-09	Cellulose synthase
Solyc09g008280.2	1,10	4,43E-05	2,47E-04	S-adenosyl-L-methionine synthetase Z24743
Solyc11g065350.2	1,10	5,30E-07	4,03E-06	ABC transporter G family member 12
Solyc07g061800.4	1,09	1,41E-02	4,09E-02	Heme-binding-like protein
Solyc08g082870.3	1,09	9,82E-07	7,15E-06	NAD(P)-binding Rossmann-fold superfamily protein
Solyc03g007530.3	1,09	1,08E-05	6,71E-05	ABC transporter C family member 10
Solyc10g081170.2	1,09	1,82E-07	1,48E-06	Calmodulin 2
Solyc07g062740.4	1,09	2,10E-04	1,02E-03	serine/arginine repetitive matrix protein
Solyc11g066040.2	1,09	2,91E-04	1,36E-03	RING-type E3 ubiquitin transferase
Solyc01g096670.4	1,09	2,75E-04	1,29E-03	Cytochrome P450
Solyc05g007895.1	1,09	8,67E-07	6,37E-06	RING/U-box superfamily protein
Solyc05g008300.3	1,09	7,20E-05	3,85E-04	Multicopper oxidase LPR1
Solyc02g089250.4	1,09	6,96E-05	3,72E-04	Pollen Ole e 1 allergen/extensin
Solyc12g099740.2	1,09	1,30E-06	9,28E-06	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein
Solyc05g007680.1	1,09	4,33E-06	2,88E-05	Arabinanase/levansucrase/invertase
Solyc08g081210.4	1,09	2,42E-05	1,42E-04	MAP kinase kinase kinase 66
Solyc06g061200.1	1,09	6,32E-04	2,73E-03	glycine-rich protein 1
Solyc06g082150.4	1,09	3,04E-05	1,75E-04	6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase
Solyc03g119860.3	1,09	3,74E-07	2,90E-06	Peptidyl-prolyl cis-trans isomerase
Solyc12g005840.2	1,08	1,11E-02	3,34E-02	Ras-related small GTP-binding family protein
Solyc05g055940.3	1,08	1,75E-05	1,05E-04	Protein PHR1-LIKE 1
Solyc07g063750.3	1,08	1,66E-03	6,46E-03	S receptor kinase
Solyc01g007020.4	1,08	7,52E-03	2,40E-02	RING-type E3 ubiquitin transferase
Solyc06g072580.3	1,08	2,24E-07	1,80E-06	Pyruvate dehydrogenase E1 component subunit beta
Solyc09g072800.3	1,08	2,88E-03	1,05E-02	Eisosome protein
Solyc02g065110.3	1,08	2,94E-07	2,32E-06	MAP kinase kinase kinase 15
Solyc03g121880.4	1,08	2,99E-05	1,73E-04	Protein phosphatase 2C 16
Solyc01g097460.3	1,08	4,52E-08	4,02E-07	Ribose 5-phosphate isomerase A
Solyc01g005220.3	1,08	4,53E-05	2,52E-04	MACPF domain-containing protein
Solyc03g033350.3	1,08	4,70E-03	1,61E-02	Aspartyl protease family protein 1
Solyc02g065220.4	1,08	5,86E-04	2,56E-03	Cytochrome P450
Solyc10g081720.2	1,08	8,45E-07	6,23E-06	Fasciclin-like arabinogalactan protein 17
Solyc12g006420.2	1,08	2,46E-08	2,28E-07	protein PAT1 homolog 1-like
Solyc07g052950.3	1,08	7,99E-05	4,23E-04	Unknown protein
Solyc10g006040.1	1,08	8,72E-06	5,50E-05	Serine acetyltransferase
Solyc09g091510.3	1,08	3,78E-04	1,72E-03	chalcone synthase 1
Solyc10g008410.1	1,07	4,06E-04	1,84E-03	E3 ubiquitin-protein ligase RMA1H1
Solyc10g005335.1	1,07	2,02E-03	7,67E-03	Unknown protein
Solyc10g075107.1	1,07	7,22E-03	2,32E-02	Non-specific lipid-transfer protein
Solyc04g071780.3	1,07	2,46E-08	2,29E-07	Cytochrome P450
Solyc02g089420.1	1,07	3,97E-03	1,39E-02	Basic leucine zipper 43
Solyc01g080640.3	1,07	1,59E-04	7,89E-04	ABC transporter C family member 4
Solyc12g019550.2	1,07	5,43E-08	4,76E-07	hypothetical protein
Solyc11g065090.2	1,07	1,77E-09	1,93E-08	magnesium transporter NIPA (DUF803)
Solyc01g088000.4	1,07	2,83E-07	2,24E-06	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc04g071930.4	1,07	1,75E-07	1,43E-06	Chlorophyll a/b binding protein domain-containing protein
Solyc12g006460.2	1,07	2,15E-05	1,28E-04	Cytochrome P450
Solyc02g069290.3	1,07	1,76E-02	4,91E-02	RING-type E3 ubiquitin transferase
Solyc06g071570.3	1,07	1,10E-02	3,31E-02	Protein NRT1/ PTR FAMILY 2.9
Solyc09g018890.3	1,07	7,77E-08	6,65E-07	DUF2996 family protein
Solyc02g084930.3	1,07	1,09E-04	5,58E-04	Cytochrome P450
Solyc08g080000.3	1,07	8,52E-07	6,27E-06	Calponin homology domain-containing protein
Solyc11g065700.2	1,07	1,02E-07	8,62E-07	Nuclear transcription factor Y subunit A-9

Solyc02g091780.1	1,07	3,20E-03	1,15E-02	Kinesin-like protein
Solyc10g080530.2	1,07	4,69E-05	2,60E-04	WRC protein
Solyc05g005460.3	1,07	1,84E-03	7,07E-03	DC1 domain-containing protein
Solyc04g072890.4	1,07	1,30E-04	6,57E-04	Transducin/WD40 repeat-like superfamily protein
Solyc03g117740.3	1,07	2,29E-09	2,45E-08	nuclear protein
Solyc12g096500.2	1,06	4,50E-05	2,51E-04	Zinc finger protein CONSTANS-LIKE 4
Solyc08g079100.3	1,06	3,54E-07	2,76E-06	CRABS CLAW 1b
Solyc01g098840.3	1,06	4,90E-07	3,74E-06	Mevalonate kinase
Solyc08g006980.3	1,06	3,23E-03	1,16E-02	RING/U-box superfamily protein
Solyc04g074180.4	1,06	3,28E-08	2,98E-07	cryptochrome 1
Solyc10g081750.1	1,06	2,66E-08	2,45E-07	Mal d 1-associated protein
Solyc05g056320.3	1,06	4,39E-09	4,49E-08	Smr (Small MutS-related) domain protein
Solyc08g075490.4	1,06	4,44E-09	4,54E-08	9-cis-epoxycarotenoid dioxygenase
Solyc01g081320.4	1,06	1,11E-02	3,33E-02	Pentatricopeptide repeat
Solyc11g011970.2	1,06	2,79E-07	2,20E-06	Protein-tyrosine phosphatase
Solyc02g083810.4	1,06	2,67E-10	3,16E-09	Ferredoxin--NADP reductase, chloroplastic
Solyc01g099160.4	1,06	1,73E-04	8,49E-04	lipoxygenase
Solyc09g018490.4	1,06	1,81E-03	6,98E-03	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc08g083370.4	1,06	6,72E-03	2,18E-02	Soluble inorganic pyrophosphatase
Solyc03g115940.4	1,06	5,87E-08	5,12E-07	Dof zinc finger protein
Solyc05g005890.2	1,06	1,46E-07	1,21E-06	Acyl-CoA N-acyltransferases (NAT) superfamily protein
Solyc09g092270.3	1,06	3,94E-08	3,54E-07	Transferase
Solyc02g085290.3	1,05	5,17E-05	2,84E-04	Maf-like protein
Solyc09g082990.3	1,05	8,14E-09	8,04E-08	GDP-mannose-3',5'-epimerase
Solyc06g068440.4	1,05	2,15E-07	1,73E-06	cinnamoyl-CoA reductase
Solyc07g063910.4	1,05	6,63E-08	5,73E-07	Unknown protein
Solyc03g117890.3	1,05	2,82E-08	2,58E-07	ACT domain-containing protein
Solyc03g118810.1	1,05	8,20E-05	4,34E-04	Calcium-binding allergen Ole e 8
Solyc01g088610.4	1,05	4,10E-05	2,30E-04	10 kDa chaperonin
Solyc09g063090.4	1,05	3,81E-03	1,34E-02	methyl-coenzyme M reductase II subunit gamma%2C putative (DUF3741)
Solyc07g066350.1	1,05	7,20E-04	3,08E-03	serine/arginine repetitive matrix-like protein
Solyc12g055720.2	1,05	1,36E-08	1,30E-07	protein STRUBBELIG-RECEPTOR FAMILY 6-like
Solyc08g076720.4	1,05	2,26E-03	8,48E-03	ABC transporter B family member 2
Solyc02g069450.3	1,05	4,92E-08	4,36E-07	Photosystem I reaction center subunit III, chloroplastic
Solyc07g063730.3	1,05	1,70E-02	4,77E-02	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc08g005300.3	1,05	1,35E-02	3,93E-02	DnaJ domain
Solyc06g068470.3	1,05	6,02E-03	1,99E-02	Phosphatidyl-N-methylethanolamine N-methyltransferase
Solyc01g099130.3	1,04	4,30E-08	3,84E-07	LysM domain-containing protein/F-box-like domain-containing protein
Solyc01g105230.4	1,04	8,70E-03	2,72E-02	Calmodulin-binding transcription activator 2
Solyc02g089780.3	1,04	3,45E-04	1,59E-03	dihydroflavonol 4-reductase/flavanone protein
Solyc09g097830.4	1,04	7,11E-08	6,12E-07	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc08g076970.3	1,04	6,82E-05	3,66E-04	Acetylornithine deacetylase
Solyc02g084900.2	1,04	1,16E-02	3,45E-02	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc08g076050.4	1,04	1,28E-04	6,49E-04	Receptor-like kinase
Solyc12g009570.3	1,04	1,23E-04	6,25E-04	calcineurin B-like interacting protein kinase
Solyc06g053670.1	1,04	1,21E-04	6,14E-04	Enoyl-CoA delta isomerase 2, peroxisomal
Solyc05g010810.1	1,04	1,39E-07	1,16E-06	Phosphatidylinositol 4-kinase gamma 7
Solyc08g066660.1	1,04	4,64E-03	1,59E-02	Ethylene-responsive transcription factor TINY
Solyc04g076220.3	1,04	1,97E-03	7,52E-03	AT-hook motif nuclear-localized protein
Solyc12g017970.1	1,04	7,66E-03	2,44E-02	GPI-anchored adhesin-like protein
Solyc10g011820.4	1,04	9,19E-07	6,71E-06	Delta(8)-fatty-acid desaturase
Solyc06g073720.3	1,04	5,39E-06	3,52E-05	EIL1
Solyc04g078810.4	1,04	5,19E-04	2,30E-03	Remorin family protein
Solyc09g060100.3	1,04	8,33E-06	5,27E-05	transmembrane protein
Solyc04g078930.4	1,04	3,38E-03	1,21E-02	Alpha-amylase
Solyc06g060230.3	1,04	6,92E-08	5,96E-07	NAC domain-containing protein
Solyc04g007690.3	1,04	4,44E-04	1,99E-03	SlPIN3
Solyc09g011600.3	1,04	5,17E-05	2,84E-04	glutathione S-transferase
Solyc06g060770.3	1,04	4,83E-05	2,66E-04	Formyltetrahydrofolate deformylase-like protein
Solyc01g095510.3	1,03	1,03E-05	6,42E-05	Mitochondrial carrier protein MTM1
Solyc01g099630.4	1,03	2,68E-05	1,56E-04	xyloglucan endotransglucosylase-hydrolase 1
Solyc01g006400.4	1,03	5,89E-07	4,43E-06	Pistil extensin like protein, partial CDS only
Solyc05g053810.3	1,03	1,48E-06	1,05E-05	Serine hydroxymethyltransferase
Solyc12g098810.2	1,03	1,55E-02	4,41E-02	Chitinase-like protein
Solyc01g104910.3	1,03	1,76E-08	1,66E-07	protein kinase family protein
Solyc02g081340.3	1,03	3,22E-05	1,84E-04	Glutathione S-transferase
Solyc04g010190.1	1,03	9,76E-07	7,11E-06	FKBP-type peptidyl-prolyl cis-trans isomerase
Solyc07g006180.3	1,03	1,73E-04	8,49E-04	ripening regulated protein (DDTFR5)
Solyc06g068720.3	1,03	1,47E-06	1,04E-05	Mitochondrial substrate carrier family protein
Solyc04g076480.3	1,03	1,34E-03	5,34E-03	MAP kinase kinase kinase 34
Solyc04g014220.1	1,03	1,75E-02	4,89E-02	RING/U-box superfamily protein
Solyc03g096050.3	1,03	1,12E-03	4,57E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc06g068460.3	1,03	8,99E-03	2,80E-02	WRKY transcription factor 40
Solyc08g074560.3	1,03	1,15E-04	5,88E-04	Protein kinase superfamily protein
Solyc02g090030.2	1,03	1,13E-08	1,09E-07	33 kDa oxygen-evolving protein
Solyc05g018640.3	1,03	1,82E-05	1,09E-04	Ultraviolet-B receptor UVR8
Solyc06g007110.3	1,03	5,79E-09	5,83E-08	SMR domain-containing protein At5g58720-like
Solyc01g110160.4	1,03	3,08E-03	1,12E-02	hypothetical protein
Solyc10g080600.3	1,02	2,18E-03	8,21E-03	Zinc finger protein 6
Solyc03g117530.1	1,02	4,28E-04	1,92E-03	Checkpoint protein
Solyc03g025990.1	1,02	1,61E-07	1,32E-06	6-phospho-3-hexuloisomerase
Solyc07g007790.3	1,02	5,60E-05	3,05E-04	sucrose-phosphate synthase
Solyc09g075580.1	1,02	1,16E-03	4,72E-03	leucine-rich repeat extensin-like protein 3
Solyc01g098430.3	1,02	1,69E-07	1,38E-06	Autophagy-related protein 18h
Solyc12g044290.2	1,02	1,28E-04	6,47E-04	Malonate--CoA ligase
Solyc03g121730.3	1,02	6,94E-09	6,92E-08	5'-nucleotidase SurE
Solyc07g055120.4	1,02	4,87E-05	2,69E-04	F-box protein MAX2
Solyc04g005800.3	1,02	5,24E-06	3,44E-05	Homeobox-leucine zipper protein HOX16
Solyc01g107820.2	1,02	9,41E-03	2,91E-02	TOMATO WOUND-INDUCED 1
Solyc07g064670.3	1,02	1,25E-04	6,34E-04	Hexosyltransferase
Solyc03g119810.1	1,02	3,02E-03	1,10E-02	At1g49000
Solyc12g096420.2	1,02	9,43E-05	4,91E-04	RING/U-box superfamily protein
Solyc04g081530.1	1,02	1,25E-04	6,34E-04	Chaperone protein DnaJ
Solyc03g097360.3	1,02	1,96E-07	1,59E-06	Protein BOLA4, chloroplastic/mitochondrial
Solyc01g110630.4	1,02	1,12E-02	3,36E-02	Small auxin up-regulated RNA9
Solyc05g025600.1	1,02	1,76E-07	1,43E-06	Photosystem II reaction center X protein
Solyc10g008910.1	1,02	1,21E-06	8,73E-06	Histone H3
Solyc02g065280.3	1,02	2,40E-07	1,92E-06	Methylesterase 1
Solyc10g079790.1	1,02	6,16E-03	2,02E-02	Plant calmodulin-binding-like protein
Solyc09g010950.3	1,02	4,01E-05	2,26E-04	ATP-dependent zinc metalloprotease FTSH 3, mitochondrial
Solyc06g068680.3	1,02	5,33E-03	1,79E-02	Respiratory burst oxidase homolog
Solyc02g092730.4	1,02	5,56E-04	2,44E-03	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial
Solyc07g054820.4	1,02	5,58E-08	4,88E-07	Protein THYLAKOID FORMATION1, chloroplastic
Solyc09g065180.3	1,01	7,05E-08	6,07E-07	binding protein precursor AF106660
Solyc10g006177.1	1,01	3,62E-03	1,28E-02	Unknown protein
Solyc03g116150.4	1,01	1,47E-04	7,33E-04	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc07g052690.4	1,01	1,96E-06	1,37E-05	Beta-amylase
Solyc07g055740.1	1,01	2,52E-07	2,00E-06	strictosidine synthase
Solyc03g044220.1	1,01	3,63E-06	2,44E-05	F-box protein
Solyc02g070480.4	1,01	4,83E-08	4,28E-07	F-box protein
Solyc07g056020.3	1,01	2,35E-04	1,13E-03	Translation initiation factor IF-2
Solyc09g075950.1	1,01	3,50E-03	1,25E-02	Heat shock protein 70 kDa
Solyc10g005620.3	1,01	5,36E-06	3,51E-05	FAD/NAD(P)-binding oxidoreductase family protein
Solyc02g083860.3	1,01	7,16E-06	4,58E-05	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc05g012650.4	1,01	1,69E-03	6,56E-03	DUF863 domain-containing protein
Solyc02g092550.3	1,01	9,64E-04	4,00E-03	LOB domain-containing protein 38

Solyc01g101240.4	1,01	1,14E-06	8,26E-06	aspartic protease precursor
Solyc11g007510.2	1,01	4,20E-04	1,90E-03	transmembrane protein
Solyc05g014470.3	1,00	5,92E-08	5,16E-07	glyceraldehyde 3-phosphate dehydrogenase
Solyc10g009080.4	1,00	3,37E-04	1,55E-03	Squamosa promoter binding protein 3
Solyc01g108490.3	1,00	2,15E-07	1,73E-06	Carboxypeptidase
Solyc06g069000.3	1,00	1,64E-04	8,10E-04	GPI-anchored protein
Solyc07g007160.3	1,00	1,20E-06	8,65E-06	RING/U-box superfamily protein
Solyc10g080690.2	1,00	6,06E-04	2,64E-03	Patatin
Solyc10g079420.1	1,00	7,33E-05	3,91E-04	Calcium-dependent protein kinase
Solyc01g007810.1	1,00	3,39E-03	1,21E-02	ovate family protein 3
Solyc12g099850.1	-1,00	8,96E-04	3,74E-03	Pentatricopeptide repeat
Solyc05g052780.4	-1,00	2,50E-05	1,47E-04	LIM domain-containing protein
Solyc08g005700.1	-1,00	1,08E-02	3,27E-02	Unknown protein
Solyc01g081510.4	-1,00	4,57E-04	2,05E-03	2-hydroxy-3-oxopropionate reductase
Solyc05g017900.3	-1,00	1,30E-04	6,57E-04	EamA domain-containing protein
Solyc09g064720.3	-1,00	2,51E-08	2,32E-07	endo-1,31,4-beta-D-glucanase-like
Solyc11g069290.2	-1,00	1,43E-05	8,70E-05	Pyridoxal 5'-phosphate synthase subunit PdxT
Solyc01g150126.1	-1,00	6,67E-05	3,59E-04	Calcium-binding EF-hand
Solyc05g051060.3	-1,00	3,29E-03	1,18E-02	Homeodomain-like superfamily protein
Solyc04g017690.3	-1,00	1,94E-09	2,10E-08	Protein EARLY RESPONSIVE TO DEHYDRATION 15
Solyc05g007060.4	-1,00	2,09E-05	1,24E-04	Plant/T7N9-9 protein
Solyc06g072250.3	-1,00	1,55E-05	9,40E-05	Methyltransferase
Solyc03g082840.3	-1,00	9,46E-03	2,92E-02	Dof zinc finger protein
Solyc04g051710.2	-1,00	1,70E-04	8,38E-04	thionin-like protein
Solyc08g075070.3	-1,00	2,19E-04	1,05E-03	Profilin family protein
Solyc10g007900.4	-1,01	5,18E-03	1,75E-02	Cytochrome
Solyc02g078350.3	-1,01	9,38E-03	2,90E-02	Pentatricopeptide repeat
Solyc08g042040.4	-1,01	3,79E-03	1,33E-02	Kinesin-like protein
Solyc03g117980.3	-1,01	1,64E-03	6,39E-03	whitefly-induced gp91-phox
Solyc10g082000.3	-1,01	1,44E-03	5,69E-03	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein
Solyc09g010565.1	-1,01	7,13E-04	3,05E-03	Unknown protein
Solyc10g005040.4	-1,01	1,55E-03	6,08E-03	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Solyc04g079950.4	-1,01	9,15E-05	4,78E-04	Methyltransferase-like protein 2
Solyc11g020960.2	-1,01	9,87E-05	5,13E-04	Proteinase inhibitor type-2
Solyc08g082300.3	-1,01	4,02E-05	2,26E-04	mitochondrial inner membrane protein OXA1-like
Solyc12g096250.2	-1,01	5,95E-03	1,97E-02	HXXXD-type acyl-transferase family protein
Solyc01g067295.1	-1,01	1,00E-03	4,14E-03	Fruit-specific protein
Solyc11g040065.1	-1,01	5,08E-03	1,72E-02	Ribosomal protein S3
Solyc12g100140.3	-1,01	9,57E-08	8,11E-07	Transcription factor bHLH80
Solyc04g049970.4	-1,01	5,48E-04	2,41E-03	complex 1 protein%2C LYR family protein
Solyc11g072610.3	-1,01	5,35E-04	2,36E-03	DNA repair (Rad51) family protein
Solyc11g010840.2	-1,01	1,09E-06	7,90E-06	KH domain-containing protein
Solyc08g075710.3	-1,01	8,85E-06	5,58E-05	Polyamine transporter PUT1
Solyc09g031590.4	-1,01	1,02E-02	3,12E-02	Sorting nexin 2B
Solyc04g078060.1	-1,01	1,91E-04	9,33E-04	transmembrane protein
Solyc11g007570.2	-1,02	1,37E-03	5,44E-03	Bifunctional TENA-E protein
Solyc12g009680.2	-1,02	7,44E-04	3,17E-03	Heptahelical transmembrane protein 1
Solyc08g079840.2	-1,02	5,38E-07	4,08E-06	LESUBENDO L.esculentum subtilisin-like endoprotease
Solyc08g023500.4	-1,02	5,38E-06	3,52E-05	Metallo-hydrolase/oxidoreductase superfamily protein
Solyc08g023440.3	-1,02	2,50E-07	1,99E-06	Early-responsive to dehydration stress protein (ERD4)
Solyc01g005370.3	-1,02	2,12E-03	8,00E-03	Calcium-dependent protein kinase
Solyc01g112020.3	-1,02	1,27E-06	9,10E-06	Pentatricopeptide repeat
Solyc03g119930.1	-1,02	7,60E-06	4,84E-05	Molybdate transporter like
Solyc06g076900.4	-1,02	2,65E-05	1,55E-04	Pentatricopeptide repeat
Solyc09g075810.3	-1,02	1,82E-03	7,01E-03	Mavicyanin
Solyc10g086630.2	-1,02	6,90E-03	2,23E-02	Legume-specific protein
Solyc05g006965.1	-1,02	3,60E-03	1,28E-02	Small multi-drug export protein
Solyc08g006000.3	-1,02	4,25E-05	2,37E-04	keratin-associated protein (DUF1218)
Solyc01g068270.3	-1,02	1,37E-05	8,37E-05	Protein kinase family protein
Solyc04g009380.3	-1,02	2,58E-05	1,51E-04	S-acyltransferase
Solyc09g091660.3	-1,02	4,14E-03	1,44E-02	Pleiotropic drug resistance protein
Solyc03g031940.4	-1,02	4,70E-07	3,60E-06	AMP-dependent synthetase/ligase
Solyc01g109710.3	-1,02	4,51E-05	2,51E-04	Adenine nucleotide alpha hydrolases-like superfamily protein
Solyc12g099190.1	-1,02	3,01E-04	1,40E-03	Pectinesterase inhibitor
Solyc02g081560.1	-1,02	4,94E-04	2,19E-03	Methionyl-tRNA synthetase
Solyc01g107860.3	-1,02	2,48E-05	1,45E-04	CBS domain-containing protein-like
Solyc12g043020.2	-1,02	8,76E-08	7,47E-07	Dihydroxy-acid dehydratase
Solyc12g008860.3	-1,02	1,28E-03	5,13E-03	transmembrane protein 258-like
Solyc08g080510.4	-1,02	6,45E-05	3,48E-04	Replication factor C subunit 2
Solyc03g119200.4	-1,02	4,54E-05	2,52E-04	L-Ala-D/L-amino acid epimerase
Solyc06g053380.3	-1,02	4,91E-03	1,67E-02	Chitinase
Solyc01g010480.3	-1,02	5,79E-07	4,36E-06	Protein TWIN LOV 1
Solyc10g006310.3	-1,02	4,02E-03	1,41E-02	Protein FATTY ACID EXPORT 6
Solyc08g076730.4	-1,02	3,61E-07	2,81E-06	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc03g111850.3	-1,02	1,64E-07	1,34E-06	Indole-3-glycerol phosphate synthase
Solyc08g082640.2	-1,02	3,58E-04	1,64E-03	Cellulose synthase
Solyc11g006190.3	-1,02	5,14E-05	2,82E-04	AT-hook motif nuclear-localized protein 1
Solyc01g112080.3	-1,03	7,99E-05	4,23E-04	Lysm domain GPI-anchored protein 2
Solyc03g123530.4	-1,03	1,26E-02	3,70E-02	CCAAT/enhancer-binding protein zeta
Solyc09g090710.3	-1,03	4,26E-06	2,83E-05	Unknown protein
Solyc08g074280.4	-1,03	1,33E-05	8,18E-05	Beta-lactamase domain-containing protein/ABC1 domain-containing protein/WaaY domain-containing protein
Solyc01g020520.4	-1,03	1,69E-03	6,56E-03	Membrane-bound transcription factor site-2 protease
Solyc04g008950.4	-1,03	2,79E-03	1,03E-02	GRAM domain-containing protein
Solyc12g096710.2	-1,03	3,57E-05	2,03E-04	probably inactive leucine-rich repeat receptor-like protein kinase At5g48380
Solyc04g015570.3	-1,03	3,08E-04	1,43E-03	Zinc finger AN1 and C2H2 domain-containing stress-associated protein 16
Solyc09g011910.3	-1,03	7,61E-05	4,05E-04	DUF674 family protein
Solyc06g005970.2	-1,03	1,99E-06	1,39E-05	Glycosyl hydrolase family protein
Solyc12g005070.2	-1,03	2,14E-03	8,07E-03	CASP-like protein
Solyc08g074890.4	-1,03	2,72E-03	1,00E-02	Unknown protein
Solyc04g007450.4	-1,03	4,92E-05	2,71E-04	Alpha/beta hydrolase family protein
Solyc02g088920.4	-1,03	8,79E-06	5,54E-05	Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain-containing protein
Solyc08g074490.4	-1,03	1,05E-03	4,33E-03	Nucleotide-diphospho-sugar transferase, nucleotide-diphospho-sugar transferase
Solyc03g093880.3	-1,03	6,44E-07	4,83E-06	U6 snRNA phosphodiesterase
Solyc03g025350.3	-1,03	9,70E-03	2,98E-02	Transporter arsB
Solyc02g150110.1	-1,03	1,67E-02	4,71E-02	Unknown protein
Solyc07g038100.3	-1,03	2,26E-03	8,48E-03	acyl-CoA synthetase family protein
Solyc06g035870.3	-1,03	6,86E-08	5,91E-07	Membrane steroid-binding protein
Solyc01g103400.4	-1,03	1,57E-04	7,79E-04	transmembrane protein
Solyc11g007860.1	-1,03	8,05E-03	2,54E-02	Cyclin-dependent protein kinase inhibitor SMR3
Solyc06g005350.3	-1,03	6,13E-03	2,02E-02	Rab family GTPase
Solyc11g071600.2	-1,03	1,52E-02	4,35E-02	aldehyde oxidase 3
Solyc10g081420.2	-1,03	4,92E-03	1,67E-02	Protein kinase
Solyc03g097750.4	-1,03	1,67E-02	4,71E-02	Translocon-associated protein subunit beta
Solyc09g064750.2	-1,03	3,13E-03	1,13E-02	Unknown protein
Solyc10g079600.2	-1,04	9,94E-05	5,16E-04	Two-component response regulator ARR9
Solyc08g067160.3	-1,04	4,71E-05	2,61E-04	Alpha/beta-Hydrolases superfamily protein
Solyc03g058940.4	-1,04	6,52E-06	4,20E-05	Hypersensitive-induced response protein
Solyc07g054330.4	-1,04	6,38E-03	2,09E-02	FBD-associated F-box protein
Solyc04g063350.3	-1,04	2,18E-05	1,29E-04	2-oxoisovalerate dehydrogenase subunit alpha 2, mitochondrial
Solyc01g102470.2	-1,04	1,71E-04	8,43E-04	Pentatricopeptide repeat
Solyc05g055260.4	-1,04	1,61E-04	7,99E-04	Small nuclear ribonucleoprotein G
Solyc10g079260.2	-1,04	2,85E-03	1,04E-02	Protein FATTY ACID EXPORT 1, chloroplastic
Solyc02g070280.3	-1,04	2,13E-08	1,99E-07	Cationic amino acid transporter

Solyc03g117330.4	-1,04	4,81E-04	2,14E-03	Proline-tRNA ligase
Solyc01g091690.3	-1,04	6,22E-06	4,02E-05	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc12g038570.3	-1,04	4,71E-03	1,61E-02	AP180 N-terminal homology (ANTH) domain-containing protein
Solyc03g063650.1	-1,04	1,15E-03	4,68E-03	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc12g015780.2	-1,04	2,67E-06	1,83E-05	DNA-directed RNA polymerase
Solyc06g074390.3	-1,04	3,59E-05	2,04E-04	Fatty acyl-CoA reductase
Solyc01g079450.3	-1,04	2,46E-09	2,62E-08	Peptidase S9
Solyc02g077640.1	-1,04	8,14E-03	2,57E-02	DUF679 domain-containing protein
Solyc01g087670.3	-1,04	2,11E-06	1,46E-05	WD40 repeat
Solyc02g093050.3	-1,04	6,73E-07	5,03E-06	WRKY transcription factor 8
Solyc12g094480.3	-1,04	5,09E-04	2,26E-03	hypothetical protein
Solyc02g084880.3	-1,04	1,06E-03	4,35E-03	Basic helix-loop-helix (BHLH) DNA-binding superfamily protein
Solyc03g005960.3	-1,05	7,20E-03	2,31E-02	protein kinase LESK1
Solyc01g081380.4	-1,05	3,61E-05	2,05E-04	nuclear matrix protein 1
Solyc01g108650.3	-1,05	7,75E-06	4,92E-05	embryo defective 1273
Solyc04g082590.3	-1,05	3,72E-03	1,31E-02	TLR4 regulator/MIR-interacting MSAP protein
Solyc06g008700.3	-1,05	4,26E-06	2,83E-05	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit
Solyc01g089890.3	-1,05	1,19E-02	3,53E-02	PRA1 family protein
Solyc01g088390.3	-1,05	4,91E-04	2,18E-03	Sister chromatid cohesion protein DCC1
Solyc08g077385.1	-1,05	1,52E-04	7,60E-04	Intron maturase, type II family protein
Solyc07g056530.3	-1,05	1,16E-03	4,71E-03	Nucleotide/sugar transporter family protein
Solyc07g066410.4	-1,05	5,34E-05	2,92E-04	WD repeat-containing protein 75
Solyc05g008210.4	-1,05	5,78E-04	2,53E-03	Plastid movement impaired protein
Solyc05g006570.1	-1,05	1,32E-03	5,25E-03	Inactive receptor kinase
Solyc03g110990.1	-1,05	7,97E-03	2,52E-02	Unknown protein
Solyc02g093310.3	-1,05	2,67E-03	9,86E-03	PI-PLC X domain-containing protein
Solyc07g007130.1	-1,05	8,66E-07	6,37E-06	NHL domain protein
Solyc10g008720.4	-1,05	1,21E-03	4,88E-03	GDSL esterase/lipase
Solyc12g049310.2	-1,05	3,79E-04	1,73E-03	Ubiquitin-like protein ATG12
Solyc05g013740.3	-1,05	1,06E-02	3,21E-02	Coilin-like protein
Solyc05g046270.3	-1,05	6,40E-03	2,09E-02	hypothetical protein
Solyc09g083350.3	-1,05	1,20E-02	3,55E-02	Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic
Solyc12g013560.2	-1,05	3,51E-04	1,61E-03	PAP-specific phosphatase HAL2-like
Solyc12g005850.2	-1,05	1,55E-06	1,10E-05	Protein DETOXIFICATION
Solyc10g079370.3	-1,05	2,50E-08	2,32E-07	Transcription initiation factor IIB
Solyc02g085360.4	-1,05	1,48E-03	5,82E-03	CYP90B3 mRNA for cytochrome P450
Solyc08g023660.3	-1,05	5,11E-03	1,73E-02	Kirola
Solyc09g065475.1	-1,06	1,08E-02	3,26E-02	Unknown protein
Solyc05g055820.3	-1,06	2,87E-04	1,34E-03	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Solyc07g056560.3	-1,06	5,06E-03	1,71E-02	Unknown protein
Solyc11g066000.1	-1,06	7,60E-03	2,42E-02	cyclin-dependent protein kinase inhibitor SMR3-like
Solyc02g090840.3	-1,06	6,09E-07	4,58E-06	DUF1685 domain-containing protein
Solyc03g083070.3	-1,06	2,46E-07	1,96E-06	Vesicle-associated membrane protein
Solyc01g104410.4	-1,06	6,03E-06	3,91E-05	Sterol 3-beta-glucosyltransferase
Solyc03g071720.4	-1,06	2,28E-08	2,13E-07	Phytol kinase 1, chloroplastic
Solyc02g068280.4	-1,06	1,57E-06	1,11E-05	subtilisin-like protein
Solyc03g119590.1	-1,06	1,28E-02	3,76E-02	NIMIN2c protein
Solyc11g018620.3	-1,06	3,13E-06	2,12E-05	SNARE associated Golgi protein
Solyc04g047670.2	-1,06	3,06E-03	1,11E-02	Vesicle transport protein
Solyc03g114480.4	-1,06	3,66E-03	1,30E-02	Tetraspanin
Solyc04g051540.3	-1,06	3,78E-03	1,33E-02	WRKY transcription factor 13
Solyc01g067630.3	-1,06	1,30E-07	1,09E-06	NAD(P)-binding Rossmann-fold superfamily protein
Solyc07g055980.3	-1,06	4,04E-06	2,69E-05	Haloacid dehalogenase (HAD) superfamily protein
Solyc10g086000.3	-1,06	8,78E-03	2,74E-02	Two-component response regulator-like APRR7
Solyc07g043550.3	-1,07	2,97E-05	1,72E-04	UDP-glucose 4-epimerase
Solyc06g076330.3	-1,07	1,20E-02	3,55E-02	Laccase
Solyc06g073190.3	-1,07	1,18E-04	6,02E-04	fructokinase 2
Solyc08g048290.4	-1,07	5,20E-04	2,30E-03	inositol transporter 2
Solyc12g089210.2	-1,07	1,80E-07	1,46E-06	Ornithine carbamoyltransferase
Solyc09g083080.4	-1,07	6,73E-04	2,89E-03	Nucleolar protein 58
Solyc06g069890.4	-1,07	4,69E-06	3,10E-05	Nucleosome assembly protein family
Solyc02g078910.3	-1,07	3,78E-03	1,33E-02	endonuclease AM238701
Solyc01g079530.4	-1,07	7,09E-04	3,03E-03	RING/FYVE/PHD zinc finger superfamily protein
Solyc10g054780.2	-1,07	1,61E-07	1,32E-06	Alpha/Beta hydrolase fold protein
Solyc10g086565.2	-1,07	1,55E-04	7,71E-04	S-acyltransferase
Solyc09g074290.1	-1,07	9,55E-03	2,94E-02	Ankyrin repeat-containing protein
Solyc11g066930.1	-1,07	1,20E-02	3,56E-02	DUF868 domain-containing protein
Solyc07g056160.4	-1,07	5,99E-05	3,25E-04	CYP724B2 mRNA for cytochrome P450
Solyc05g051530.4	-1,07	1,30E-05	7,98E-05	ABC transporter G family member 11
Solyc07g041070.3	-1,07	1,79E-03	6,92E-03	Hydroxyproline-rich glycoprotein family protein
Solyc03g119520.4	-1,07	7,45E-05	3,97E-04	BnaC05g48200D protein
Solyc04g049620.2	-1,07	9,32E-07	6,81E-06	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc12g009220.2	-1,07	2,26E-03	8,48E-03	jasmonate ZIM-domain protein 1
Solyc12g100310.2	-1,07	1,45E-07	1,20E-06	Protein kinase family protein
Solyc10g008100.3	-1,07	4,03E-04	1,83E-03	Glucosidase 2 subunit beta
Solyc05g006000.3	-1,07	1,48E-03	5,82E-03	protein NRT1/ PTR FAMILY 1.2-like
Solyc07g063420.3	-1,07	8,10E-04	3,42E-03	NAC domain-containing protein
Solyc05g014650.2	-1,07	3,37E-06	2,27E-05	Ribosomal silencing factor RsfS
Solyc08g007580.4	-1,07	3,70E-03	1,31E-02	Ycf49-like protein
Solyc03g119610.1	-1,07	4,92E-07	3,76E-06	hypothetical protein
Solyc10g081120.3	-1,07	5,26E-06	3,44E-05	alpha-L-arabinofuranosidase
Solyc07g062150.3	-1,08	8,89E-07	6,53E-06	NAD kinase
Solyc11g030700.1	-1,08	4,26E-04	1,92E-03	Unknown protein
Solyc06g062430.3	-1,08	8,01E-04	3,38E-03	Inositol oxygenase
Solyc07g049350.3	-1,08	4,27E-08	3,81E-07	G1/S-specific cyclin-E protein
Solyc04g074730.1	-1,08	4,54E-05	2,52E-04	classical arabinogalactan protein 5
Solyc10g083220.3	-1,08	1,48E-03	5,83E-03	Embryo defective 2735
Solyc03g093480.3	-1,08	1,21E-02	3,59E-02	ARM repeat superfamily protein
Solyc01g096900.3	-1,08	1,13E-03	4,59E-03	DNA gyrase subunit A
Solyc03g119840.3	-1,08	6,01E-03	1,98E-02	Adenine nucleotide alpha hydrolases-like superfamily protein
Solyc05g047610.3	-1,08	1,19E-03	4,82E-03	S-acyltransferase
Solyc01g014250.2	-1,08	2,68E-03	9,88E-03	Unknown protein
Solyc12g089290.3	-1,08	3,85E-04	1,75E-03	HVA22-like protein
Solyc03g044790.3	-1,08	5,46E-06	3,56E-05	methylesterase AY455313
Solyc03g083610.4	-1,08	6,28E-08	5,45E-07	UMP-CMP kinase
Solyc11g013330.3	-1,08	1,32E-03	5,26E-03	BPS1-like protein
Solyc10g062160.3	-1,08	4,59E-05	2,55E-04	Dynamin
Solyc05g007830.3	-1,08	7,36E-06	4,70E-05	expansin12
Solyc04g007210.3	-1,09	5,18E-08	4,57E-07	Zinc finger protein CONSTANS-LIKE 7
Solyc10g076450.2	-1,09	3,49E-04	1,60E-03	Ethylene-overproduction protein 1
Solyc12g040320.2	-1,09	2,38E-03	8,90E-03	Plant intracellular Ras-group-related LRR protein
Solyc01g111590.4	-1,09	1,09E-04	5,61E-04	WD-40 repeat-containing protein MSI1
Solyc02g077370.1	-1,09	8,14E-03	2,57E-02	Ethylene Response Factor C.5
Solyc09g092645.1	-1,09	3,29E-04	1,52E-03	Cytochrome
Solyc06g072030.1	-1,09	1,23E-03	4,97E-03	Unknown protein
Solyc12g088890.3	-1,09	1,58E-03	6,19E-03	DnaJ protein like
Solyc01g011100.2	-1,09	2,86E-05	1,66E-04	Phospholipid-transporting ATPase
Solyc05g032680.4	-1,09	3,37E-04	1,55E-03	3-hydroxyisobutyryl-CoA hydrolase 1
Solyc10g051140.3	-1,09	1,58E-04	7,86E-04	Protein ENHANCED DOWNY MILDEW 2
Solyc01g107340.4	-1,09	6,24E-04	2,70E-03	classical arabinogalactan protein 9
Solyc02g089980.3	-1,09	1,65E-04	8,16E-04	electron transporter%2C putative (Protein of unknown function%2C DUF547)
Solyc06g007170.4	-1,09	6,23E-04	2,70E-03	Protein trichome birefringence-like 45
Solyc06g068360.3	-1,09	7,09E-03	2,29E-02	Ethylene-responsive transcription factor
Solyc01g087020.2	-1,10	3,73E-03	1,32E-02	Unknown protein

Solyc07g005960.3	-1,10	2,01E-06	1,40E-05	Carboxypeptidase
Solyc03g095300.4	-1,10	2,36E-04	1,13E-03	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc04g077220.3	-1,10	1,09E-03	4,45E-03	Homeobox-leucine zipper protein HAT22
Solyc09g075770.3	-1,10	4,09E-03	1,43E-02	Long-chain acyl-CoA synthetase 6
Solyc05g056350.3	-1,10	3,82E-09	3,94E-08	cleft lip and palate transmembrane protein 1 homolog
Solyc07g062160.3	-1,10	1,10E-06	7,97E-06	Zinc finger, B-box
Solyc10g085900.3	-1,10	4,04E-05	2,27E-04	Protein SLOW GREEN 1, chloroplastic
Solyc01g010185.1	-1,10	3,05E-06	2,07E-05	Retrovirus-related Pol polyprotein from transposon TNT 1-94
Solyc04g072940.4	-1,10	1,59E-03	6,20E-03	nucleolar GTP-binding protein
Solyc09g059570.3	-1,10	1,02E-03	4,23E-03	B-cell receptor-associated protein 31-like protein
Solyc12g015970.3	-1,10	1,54E-04	7,66E-04	GPI-anchored protein LORELEI
Solyc06g074240.3	-1,10	8,82E-03	2,75E-02	Beta-carotene,Pfam:PF05834
Solyc08g066940.4	-1,10	5,65E-06	3,68E-05	Protein NRT1/ PTR FAMILY 1.2
Solyc04g082270.3	-1,10	6,56E-03	2,14E-02	DUF241 domain-containing protein
Solyc03g043940.4	-1,10	8,16E-04	3,44E-03	Unknown protein
Solyc03g119390.4	-1,10	1,12E-04	5,73E-04	bHLH transcription factor 026
Solyc02g070240.3	-1,10	9,09E-07	6,66E-06	Zinc finger transcription factor 17
Solyc07g042160.3	-1,10	3,45E-05	1,97E-04	Pectin lyase-like superfamily protein
Solyc07g062810.4	-1,10	1,87E-03	7,15E-03	D-amino-acid transaminase, chloroplastic
Solyc11g006070.3	-1,10	7,67E-07	5,69E-06	Peptidyl-prolyl cis-trans isomerase
Solyc06g069630.4	-1,10	2,04E-03	7,74E-03	T-box transcription factor%2C putative (DUF863)
Solyc12g009630.3	-1,10	5,37E-05	2,94E-04	Calmodulin-like protein 5
Solyc01g058020.4	-1,10	2,44E-04	1,16E-03	Neutral/alkaline invertase
Solyc11g005400.2	-1,10	4,15E-05	2,33E-04	DnaJ domain
Solyc05g013010.3	-1,11	5,90E-03	1,95E-02	Sulfotransferase
Solyc02g030225.1	-1,11	1,80E-05	1,08E-04	UDP-glucose 4-epimerase
Solyc07g005130.3	-1,11	9,84E-07	7,16E-06	Alpha/beta-Hydrolases superfamily protein
Solyc01g088460.3	-1,11	6,79E-03	2,20E-02	Unknown protein
Solyc06g068600.3	-1,11	1,09E-04	5,59E-04	Phosphate ABC transporter ATP-binding protein PstB
Solyc11g068480.2	-1,11	8,17E-05	4,32E-04	DNA polymerase epsilon subunit 3
Solyc01g108610.3	-1,11	1,24E-03	5,00E-03	Cyclin-dependent kinase inhibitor
Solyc07g062270.3	-1,11	3,82E-08	3,44E-07	Gamma-glutamyl hydrolase
Solyc04g079940.3	-1,11	4,18E-07	3,23E-06	NAC domain-containing protein
Solyc03g114760.3	-1,11	2,44E-06	1,68E-05	Protein MICROTUBULE BINDING PROTEIN 2C
Solyc08g078440.3	-1,11	2,21E-05	1,31E-04	sphingomyelin phosphodiesterase
Solyc05g020020.4	-1,11	3,73E-06	2,50E-05	Zinc finger protein CONSTANS-LIKE 9
Solyc09g015650.4	-1,11	1,07E-05	6,68E-05	Non-green plastid inner envelope membrane protein
Solyc07g039210.4	-1,11	3,86E-07	2,98E-06	PCI domain-containing protein
Solyc08g080220.3	-1,11	1,33E-02	3,87E-02	DNA-directed RNA polymerase subunit
Solyc11g031960.2	-1,11	7,21E-05	3,85E-04	GDSL esterase/lipase
Solyc11g007130.2	-1,11	1,01E-06	7,33E-06	Major facilitator superfamily
Solyc08g080270.3	-1,11	1,02E-02	3,12E-02	UDP-galactose/UDP-glucose transporter 2-like
Solyc12g094390.1	-1,11	3,60E-04	1,65E-03	Syringolide-induced protein 14-1-1
Solyc05g013210.3	-1,11	2,55E-04	1,21E-03	Ribonuclease
Solyc11g045220.2	-1,11	4,45E-06	2,95E-05	Pentatricopeptide repeat
Solyc02g092080.2	-1,11	8,70E-05	4,58E-04	60S ribosomal protein L23A
Solyc01g010430.4	-1,11	7,08E-06	4,54E-05	Actin cross-linking protein, putative (DUF569)
Solyc02g079540.2	-1,11	1,79E-02	4,98E-02	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc03g005690.3	-1,11	8,29E-07	6,11E-06	Cysteine-rich repeat secretory protein 3
Solyc05g042120.4	-1,12	5,95E-05	3,23E-04	Embryo defective 1381
Solyc04g082650.3	-1,12	3,06E-05	1,76E-04	S-acyltransferase
Solyc02g082970.1	-1,12	6,70E-05	3,60E-04	Pentatricopeptide repeat-containing protein
Solyc12g099600.2	-1,12	1,63E-07	1,34E-06	Protein phosphatase 2C
Solyc09g010510.4	-1,12	8,68E-04	3,64E-03	NAD(P)-binding Rossmann-fold superfamily protein
Solyc11g011920.2	-1,12	1,44E-09	1,58E-08	Glutamate decarboxylase
Solyc04g082420.3	-1,12	1,08E-07	9,10E-07	BTB/POZ domain-containing protein
Solyc03g007810.3	-1,12	1,73E-09	1,88E-08	Pyruvate kinase
Solyc02g066930.3	-1,12	1,22E-06	8,77E-06	RNA-binding protein
Solyc03g034320.3	-1,12	5,90E-03	1,95E-02	Class I glutamine amidotransferase-like superfamily protein
Solyc09g083200.4	-1,12	1,42E-05	8,66E-05	Protein kinase-like domain-containing protein
Solyc06g005940.3	-1,12	6,44E-08	5,58E-07	Protein disulfide-isomerase
Solyc06g053290.1	-1,12	3,12E-04	1,45E-03	SAUR-like auxin-responsive family protein
Solyc04g082040.3	-1,12	1,06E-07	8,94E-07	Mechanosensitive ion channel protein
Solyc05g048750.3	-1,12	5,34E-05	2,92E-04	coiled-coil protein
Solyc11g044560.3	-1,12	1,99E-08	1,88E-07	ABSCISIC ACID-INSENSITIVE 5-like protein 5
Solyc10g012030.4	-1,12	4,62E-07	3,54E-06	chorismate synthase
Solyc07g064920.3	-1,12	2,57E-06	1,76E-05	SWIB domain-containing protein
Solyc03g120390.3	-1,12	1,41E-07	1,17E-06	auxin-regulated IAA15
Solyc06g051750.3	-1,12	4,39E-08	3,91E-07	Cytochrome P450
Solyc12g095810.2	-1,12	2,12E-03	8,02E-03	Protein NRT1/ PTR FAMILY 1.1
Solyc02g036290.4	-1,13	2,63E-03	9,74E-03	Malonyl-CoA decarboxylase family protein
Solyc11g008050.1	-1,13	1,27E-03	5,08E-03	Pullulanase 1, chloroplastic
Solyc01g010230.2	-1,13	3,26E-04	1,51E-03	MDIS1-interacting receptor like kinase 2
Solyc03g025270.3	-1,13	5,08E-06	3,34E-05	Fibrillarin
Solyc05g012850.3	-1,13	1,96E-03	7,50E-03	transmembrane protein
Solyc01g050010.3	-1,13	2,79E-04	1,31E-03	Zinc finger BED domain-containing protein DAYSLEEPER
Solyc07g062440.1	-1,13	7,25E-03	2,33E-02	hypothetical protein
Solyc05g007150.4	-1,13	1,31E-05	8,06E-05	UDP-galactose/UDP-glucose transporter 3
Solyc03g025630.3	-1,13	1,29E-03	5,17E-03	Tripeptidyl-peptidase 2
Solyc02g080560.1	-1,13	8,26E-03	2,60E-02	Unknown protein
Solyc04g072550.3	-1,13	9,66E-03	2,97E-02	Mitochondrial transcription termination factor-like
Solyc08g065610.3	-1,13	4,08E-08	3,66E-07	Vacuolar-processing enzyme
Solyc05g041540.4	-1,13	1,24E-03	4,98E-03	Carboxypeptidase
Solyc04g079570.1	-1,13	3,46E-03	1,24E-02	Dof zinc finger protein
Solyc09g014860.3	-1,13	1,83E-03	7,04E-03	Protein LURP-one-related 15
Solyc07g054300.3	-1,13	1,27E-08	1,22E-07	Protein phosphatase 2C
Solyc06g060290.4	-1,13	2,30E-05	1,35E-04	Protein disulfide-isomerase
Solyc01g067080.3	-1,13	1,08E-04	5,57E-04	dynein beta chain%2C ciliary protein
Solyc01g098520.3	-1,13	6,10E-04	2,65E-03	MUTL protein homolog 3
Solyc11g010950.2	-1,13	3,74E-07	2,90E-06	Elongator complex protein 4
Solyc06g071860.3	-1,13	5,31E-07	4,03E-06	Zinc finger transcription factor 46
Solyc04g016560.2	-1,14	1,10E-02	3,31E-02	Folylpolyglutamate synthase
Solyc07g041730.4	-1,14	7,73E-05	4,11E-04	MOB kinase activator family
Solyc05g009390.3	-1,14	2,95E-06	2,00E-05	Alpha/beta-Hydrolases superfamily protein
Solyc04g076570.4	-1,14	2,64E-07	2,09E-06	CRT (Chloroquine-resistance transporter)-like transporter
Solyc12g005930.2	-1,14	1,16E-08	1,12E-07	Ypt/Rab-GAP domain of gyp1p superfamily protein
Solyc05g018600.3	-1,14	2,07E-06	1,44E-05	Actin-related protein 6
Solyc08g041710.3	-1,14	2,70E-08	2,48E-07	envelope glycoprotein B
Solyc10g007870.3	-1,14	1,55E-02	4,42E-02	Tumor-related protein
Solyc10g007440.3	-1,14	4,54E-08	4,03E-07	Zinc finger protein
Solyc04g072060.4	-1,14	4,80E-05	2,65E-04	Ras-related protein
Solyc08g029160.1	-1,14	2,08E-07	1,68E-06	Membrane steroid binding protein
Solyc04g009660.2	-1,14	1,13E-03	4,62E-03	Disease resistance protein
Solyc05g005320.1	-1,14	8,73E-05	4,59E-04	Unknown protein
Solyc03g080190.3	-1,14	1,68E-04	8,28E-04	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc02g085690.4	-1,14	9,56E-04	3,97E-03	Ubiquitin-conjugating enzyme
Solyc09g011340.3	-1,14	2,21E-06	1,53E-05	protein RETICULATA, chloroplastic-like
Solyc04g064545.1	-1,14	2,13E-04	1,03E-03	Unknown protein
Solyc01g088660.3	-1,14	2,25E-05	1,33E-04	FCS-Like Zinc finger 3
Solyc07g062860.3	-1,14	2,06E-06	1,43E-05	26S proteasome non-ATPase regulatory subunit 5
Solyc08g081570.3	-1,14	2,94E-07	2,32E-06	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
Solyc01g005253.1	-1,14	7,60E-06	4,84E-05	Sec14p-like phosphatidylinositol transfer family protein
Solyc01g096950.4	-1,14	1,03E-07	8,65E-07	WD40 repeat-containing protein
Solyc03g025850.3	-1,15	5,39E-05	2,94E-04	remorin 1

Solyc02g068730.3	-1,15	6,74E-07	5,03E-06	60 kDa chaperonin
Solyc01g010130.4	-1,15	1,05E-05	6,52E-05	bHLH transcription factor 001
Solyc01g090730.3	-1,15	7,91E-03	2,51E-02	Squamosa promoter binding protein 8b
Solyc09g091420.4	-1,15	4,76E-04	2,12E-03	Inosine triphosphate pyrophosphatase
Solyc05g006810.4	-1,15	7,15E-04	3,06E-03	2,4-dichlorophenol 6-monooxygenase
Solyc04g071520.3	-1,15	8,32E-03	2,61E-02	Transcription elongation factor (TFIIS) family protein
Solyc05g006330.2	-1,15	3,40E-04	1,57E-03	Unknown protein
Solyc11g011240.1	-1,15	5,99E-03	1,98E-02	geranylgeranyl pyrophosphate synthase 1
Solyc08g082110.4	-1,15	9,78E-05	5,09E-04	WRKY transcription factor 54
Solyc01g079360.4	-1,15	5,64E-08	4,93E-07	WRKY transcription factor 37
Solyc05g008820.4	-1,15	1,08E-04	5,56E-04	Lipid phosphate phosphatase
Solyc08g005260.2	-1,15	6,04E-05	3,28E-04	Homeodomain-like superfamily protein
Solyc05g052450.3	-1,15	9,80E-03	3,00E-02	Protein trichome birefringence-like 32
Solyc11g012510.3	-1,15	2,09E-04	1,01E-03	GRAS1
Solyc11g068690.2	-1,15	1,47E-02	4,22E-02	Plant intracellular ras-group-related lrr protein 4
Solyc10g008600.3	-1,15	6,93E-06	4,45E-05	embryo defective 1923
Solyc02g080300.3	-1,15	2,30E-06	1,59E-05	Beta-glucosidase 46
Solyc05g006120.3	-1,15	1,95E-03	7,45E-03	DNA polymerase lambda-like protein
Solyc05g007010.3	-1,15	6,76E-03	2,19E-02	Glyoxal oxidase
Solyc04g005560.3	-1,16	1,77E-03	6,84E-03	ARF guanine-nucleotide exchange factor GNOM
Solyc09g090020.4	-1,16	2,28E-05	1,34E-04	Germin-like protein subfamily 1 member 20
Solyc12g008580.2	-1,16	1,55E-05	9,42E-05	Glucan endo-1,3-beta-glucosidase 12
Solyc10g008960.1	-1,16	8,63E-03	2,70E-02	Protein kinase domain
Solyc06g008220.4	-1,16	1,03E-08	1,01E-07	Multiple organellar RNA editing factor 2, chloroplastic
Solyc02g069410.4	-1,16	2,36E-08	2,19E-07	Haloacid dehalogenase-like hydrolase domain-containing protein
Solyc02g086570.3	-1,16	8,33E-03	2,62E-02	Pentatricopeptide repeat
Solyc07g042190.3	-1,16	2,31E-08	2,16E-07	DUF581 domain-containing protein
Solyc04g015340.3	-1,16	1,11E-08	1,08E-07	Carboxypeptidase
Solyc11g069260.2	-1,16	3,88E-07	3,00E-06	ABC transporter ATP-binding protein
Solyc02g094190.3	-1,16	6,47E-07	4,85E-06	Major facilitator superfamily protein
Solyc06g007980.4	-1,16	2,35E-08	2,19E-07	Sterol 3-beta-glucosyltransferase
Solyc11g062400.2	-1,16	5,36E-05	2,93E-04	Protein kinase APK1B, chloroplastic
Solyc02g079730.4	-1,16	7,36E-07	5,47E-06	Thioredoxin-like fold protein
Solyc12g009520.2	-1,16	5,29E-04	2,34E-03	receptor-like protein 12
Solyc06g043060.1	-1,16	7,46E-03	2,38E-02	hypothetical protein
Solyc02g038750.3	-1,16	9,22E-08	7,84E-07	WD repeat-containing protein 55-like
Solyc10g080880.2	-1,16	1,34E-03	5,35E-03	SlPIN7
Solyc11g066400.1	-1,16	1,78E-03	6,89E-03	Zinc finger protein
Solyc09g009970.3	-1,16	3,19E-05	1,83E-04	Rho GTPase-activating protein 1
Solyc12g007030.3	-1,17	8,08E-07	5,98E-06	Aldehyde dehydrogenase
Solyc07g041340.2	-1,17	1,84E-03	7,07E-03	protein ELF4-LIKE 4-like
Solyc08g075680.4	-1,17	3,91E-03	1,37E-02	Ribonuclease P protein subunit P38-like protein
Solyc03g120910.4	-1,17	2,86E-08	2,62E-07	Homeobox leucine-zipper protein
Solyc04g082300.2	-1,17	6,76E-08	5,83E-07	WD40 repeat
Solyc11g032190.1	-1,17	1,37E-02	3,98E-02	Unknown protein
Solyc11g067060.3	-1,17	4,65E-07	3,57E-06	Protein-tyrosine phosphatase
Solyc10g078750.2	-1,17	1,86E-07	1,51E-06	Zinc finger transcription factor 59
Solyc01g005680.4	-1,17	3,15E-05	1,81E-04	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc10g086640.3	-1,17	7,56E-06	4,82E-05	BEL1-like homeodomain protein 9
Solyc02g080010.2	-1,17	2,06E-08	1,93E-07	Cysteine-rich receptor-like protein kinase 10
Solyc05g012920.3	-1,17	2,73E-03	1,01E-02	Pentatricopeptide repeat-containing protein
Solyc12g100180.2	-1,17	8,19E-04	3,45E-03	Pleiotropic drug resistance protein
Solyc07g063160.2	-1,17	1,79E-04	8,77E-04	Cytochrome c oxidase copper chaperone
Solyc11g065890.2	-1,17	8,97E-04	3,75E-03	1-acyl-sn-glycerol-3-phosphate acyltransferase (Putative)
Solyc05g014160.4	-1,17	2,18E-05	1,29E-04	Regulator of G-protein signaling 1
Solyc01g108440.2	-1,17	1,97E-03	7,51E-03	Herbivore elicitor-regulated 1
Solyc01g095480.4	-1,17	2,64E-08	2,43E-07	Exosome complex component Rrp41
Solyc12g100030.2	-1,17	1,17E-03	4,75E-03	receptor-like protein 12
Solyc12g044240.3	-1,17	5,17E-06	3,39E-05	Dynein light chain
Solyc01g079610.3	-1,17	8,68E-07	6,38E-06	DnaJ protein ERDJ3B
Solyc02g068890.3	-1,17	7,80E-05	4,14E-04	Pentatricopeptide repeat-containing protein
Solyc02g072310.3	-1,17	4,44E-04	1,99E-03	Protein NSP-INTERACTING KINASE 1
Solyc12g014270.3	-1,17	2,98E-06	2,02E-05	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
Solyc07g066320.3	-1,17	1,25E-08	1,20E-07	Protein RecA
Solyc07g008480.3	-1,17	1,28E-03	5,14E-03	Pentatricopeptide repeat-containing protein
Solyc12g099110.2	-1,17	4,81E-07	3,68E-06	30S ribosomal protein S1 protein
Solyc08g075400.3	-1,17	1,78E-06	1,25E-05	SWIb domain-containing protein
Solyc12g009980.2	-1,17	2,52E-08	2,33E-07	Nucleoid-associated protein
Solyc08g005490.3	-1,17	2,05E-12	3,06E-11	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc02g085615.1	-1,17	6,16E-03	2,02E-02	Unknown protein
Solyc08g067390.4	-1,17	3,09E-04	1,44E-03	EG45-like domain containing protein
Solyc09g010120.2	-1,18	5,19E-07	3,96E-06	hypothetical protein
Solyc12g040800.2	-1,18	1,61E-04	7,99E-04	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc03g051920.4	-1,18	5,86E-08	5,12E-07	DUF620 domain-containing protein
Solyc12g049210.1	-1,18	2,90E-03	1,06E-02	DUF3511 domain-containing protein
Solyc01g086730.4	-1,18	1,30E-02	3,81E-02	magnesium transporter%2C putative (DUF803)
Solyc01g109760.3	-1,18	3,12E-05	1,80E-04	Major facilitator superfamily
Solyc07g054170.3	-1,18	6,25E-04	2,71E-03	Expansin-B1
Solyc12g056930.2	-1,18	1,61E-07	1,32E-06	sulfate transporter 2
Solyc01g058390.3	-1,18	5,91E-10	6,78E-09	Galactokinase
Solyc02g087060.4	-1,18	7,12E-09	7,08E-08	WAT1-related protein
Solyc02g068640.3	-1,18	4,56E-07	3,50E-06	Pyrroline-5-carboxylate reductase
Solyc05g009090.3	-1,18	2,00E-04	9,71E-04	Receptor-like protein kinase
Solyc11g017400.2	-1,18	3,17E-04	1,47E-03	N-acetylglucosaminylphosphatidylinositol de-N-acetylase family protein
Solyc02g071090.3	-1,18	7,74E-09	7,67E-08	Purine permease
Solyc01g104640.3	-1,18	5,80E-05	3,15E-04	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc02g062040.3	-1,18	1,54E-06	1,09E-05	RING/U-box superfamily protein
Solyc08g013900.3	-1,18	9,02E-04	3,77E-03	Plant regulator RWP-RK family protein
Solyc04g064640.4	-1,19	8,01E-03	2,53E-02	Bidirectional sugar transporter SWEET
Solyc11g006350.1	-1,19	1,24E-05	7,68E-05	aspatate carbamoyltransferase
Solyc03g005030.3	-1,19	1,23E-08	1,18E-07	hypothetical protein
Solyc04g025450.3	-1,19	4,15E-04	1,87E-03	Acetate/butyrate--CoA ligase AAE7, peroxisomal
Solyc09g092530.4	-1,19	1,00E-08	9,78E-08	Protein TIC 22-like, chloroplastic
Solyc12g008760.3	-1,19	3,65E-09	3,77E-08	Protein arginine N-methyltransferase
Solyc01g111360.3	-1,19	3,14E-09	3,30E-08	Peptidyl-prolyl cis-trans isomerase
Solyc07g043250.1	-1,19	7,34E-04	3,13E-03	VQ motif-containing protein 22
Solyc02g083340.4	-1,19	3,96E-07	3,06E-06	Phospholipase D
Solyc01g111880.4	-1,19	1,08E-02	3,27E-02	MAP kinase kinase kinase 11
Solyc06g034230.2	-1,19	1,80E-04	8,85E-04	Plant organelle RNA recognition domain containing protein
Solyc07g055640.1	-1,19	2,91E-05	1,69E-04	Immunity to Fusarium wilt race 3
Solyc05g150152.1	-1,19	2,59E-04	1,23E-03	Photosystem I reaction centre subunit N protein
Solyc01g100030.5.1	-1,19	1,73E-07	1,41E-06	deoxyuridine triphosphatase
Solyc02g092880.3	-1,19	4,06E-03	1,42E-02	Maternal effect embryo arrest 59
Solyc10g086700.3	-1,19	2,44E-04	1,16E-03	RING/U-box superfamily protein
Solyc02g077290.2	-1,19	1,17E-02	3,48E-02	glutamate receptor-like 1.2
Solyc03g111350.3	-1,19	9,45E-05	4,93E-04	Deoxycytidylate deaminase
Solyc03g121890.1	-1,19	1,34E-06	9,58E-06	Hydroxyproline-rich glycoprotein family protein
Solyc11g012570.3	-1,19	7,30E-03	2,34E-02	Pentatricopeptide repeat-containing protein
Solyc10g085630.3	-1,19	2,32E-05	1,37E-04	3-hydroxyisobutyryl-CoA hydrolase-like protein mitochondrial-like
Solyc01g080040.3	-1,19	1,37E-05	8,38E-05	Dual specificity protein phosphatase 1
Solyc03g005450.3	-1,20	3,47E-08	3,13E-07	Cellulose synthase
Solyc06g063070.3	-1,20	1,72E-07	1,41E-06	Ethylene Response Factor A.3
Solyc08g066740.3	-1,20	3,89E-04	1,77E-03	Early nodulin-like protein 1
Solyc03g098730.1	-1,20	7,63E-04	3,24E-03	Kunitz-type protease inhibitor

Solyc07g056310.3	-1,20	1,21E-05	7,47E-05	Carbohydrate-binding X8 domain superfamily protein
Solyc01g098200.3	-1,20	3,14E-04	1,46E-03	Vesicle-associated protein 1-2
Solyc06g068290.1	-1,20	3,94E-06	2,63E-05	Triphosphate tunel metalloenzyme 3
Solyc08g077480.4	-1,20	4,72E-04	2,11E-03	FCS-Like Zinc finger 2
Solyc11g044750.3	-1,20	2,12E-07	1,71E-06	Single-stranded DNA-binding protein
Solyc03g044810.2	-1,20	9,82E-03	3,01E-02	Methyl jasmonate esterase
Solyc07g005775.1	-1,20	1,61E-04	7,98E-04	Unknown protein
Solyc09g009210.4	-1,20	1,33E-09	1,47E-08	Transcriptional activator (DUF662)
Solyc10g084620.3	-1,20	2,35E-06	1,62E-05	hypothetical protein
Solyc08g005210.3	-1,21	1,50E-04	7,49E-04	Dolichol phosphate-mannose biosynthesis regulatory protein
Solyc11g020955.1	-1,21	1,42E-04	7,11E-04	Unknown protein
Solyc02g062240.3	-1,21	2,96E-06	2,01E-05	Small nuclear ribonucleoprotein Sm D3
Solyc03g119960.3	-1,21	1,19E-05	7,39E-05	NPH3 domain
Solyc01g009030.4	-1,21	5,80E-08	5,07E-07	dgd1 suppressor 1
Solyc05g008190.3	-1,21	4,49E-05	2,50E-04	Transducin/WD40 repeat-like superfamily protein
Solyc06g005140.3	-1,21	1,09E-03	4,45E-03	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc12g006290.2	-1,21	4,34E-09	4,45E-08	Reticulon-like protein
Solyc02g150124.1	-1,21	4,45E-05	2,48E-04	Enolase
Solyc07g045350.4	-1,21	3,74E-06	2,50E-05	Acetyl-CoA C-acetyltransferase
Solyc04g078740.2	-1,22	5,70E-05	3,10E-04	Subtilisin-like protease-like protein
Solyc03g115465.1	-1,22	9,57E-03	2,95E-02	RING/U-box superfamily protein
Solyc10g079360.3	-1,22	1,95E-06	1,37E-05	Transcription initiation factor IIB
Solyc03g006990.1	-1,22	6,19E-03	2,03E-02	Pentatricopeptide repeat
Solyc08g078960.4	-1,22	1,25E-04	6,35E-04	Oxysterol-binding protein
Solyc11g006980.1	-1,22	1,09E-02	3,28E-02	Germin-like protein subfamily 3 member 2
Solyc04g076100.4	-1,22	1,25E-04	6,37E-04	transmembrane protein
Solyc01g103530.3	-1,22	3,43E-09	3,57E-08	Leucine-rich receptor-like protein kinase family protein, putative
Solyc06g009630.1	-1,22	7,27E-12	1,02E-10	Calvin cycle protein cp12 chloroplastic-like
Solyc04g081220.3	-1,22	1,11E-08	1,08E-07	39S ribosomal protein
Solyc07g055880.1	-1,22	1,09E-02	3,30E-02	vitellogenin-2 protein
Solyc11g007250.2	-1,22	2,42E-04	1,15E-03	Protein kinase G11A
Solyc01g067800.3	-1,22	6,26E-09	6,26E-08	Zinc finger protein
Solyc07g053530.1	-1,22	1,54E-03	6,05E-03	Fasciclin-like arabinogalactan protein 9
Solyc11g064790.2	-1,22	5,32E-09	5,39E-08	Signal peptide peptidase
Solyc11g033260.2	-1,22	2,08E-07	1,68E-06	Pseudouridine-5'-phosphate glycosidase
Solyc06g031690.4	-1,22	7,84E-08	6,71E-07	Ankyrin repeat family protein
Solyc12g014320.2	-1,22	1,62E-05	9,78E-05	Anaphase-promoting complex subunit 6
Solyc07g008710.3	-1,22	5,45E-05	2,97E-04	MLP-like protein 43
Solyc11g044330.3	-1,22	3,02E-05	1,74E-04	Zinc finger SWIM domain protein
Solyc07g052510.4	-1,23	6,62E-04	2,85E-03	peroxidase (TPX1)
Solyc02g078590.1	-1,23	1,09E-07	9,21E-07	Alpha 1,4-glycosyltransferase family protein
Solyc12g056340.2	-1,23	1,19E-04	6,09E-04	RNA helicase DEAD38
Solyc12g006250.3	-1,23	7,10E-06	4,55E-05	Vesicle transport protein
Solyc02g079280.3	-1,23	5,68E-03	1,89E-02	MYB transcription factor
Solyc12g049350.2	-1,23	2,84E-03	1,04E-02	R2R3MYB transcription factor 11
Solyc01g086975.1	-1,23	3,27E-03	1,17E-02	Unknown protein
Solyc10g048030.2	-1,23	4,81E-04	2,14E-03	MLP-like protein 43
Solyc05g005790.4	-1,23	1,32E-03	5,26E-03	RING-H2 finger protein ATL47-like
Solyc03g120420.3	-1,23	2,50E-04	1,19E-03	Unknown protein
Solyc06g066400.3	-1,23	7,74E-04	3,28E-03	Dolichol phosphate-mannose biosynthesis regulatory protein
Solyc05g008220.4	-1,23	1,36E-02	3,97E-02	Plastid movement impaired protein
Solyc08g081710.3	-1,23	1,32E-02	3,86E-02	membrane-associated kinase regulator
Solyc01g079620.4	-1,23	1,09E-05	6,77E-05	colorless fruit epidermis
Solyc09g011850.4	-1,23	1,34E-09	1,48E-08	Fructokinase-like protein 1
Solyc02g089990.1	-1,24	5,91E-04	2,58E-03	HTH-type transcriptional regulator
Solyc03g112960.1	-1,24	7,33E-06	4,68E-05	Pectinesterase
Solyc02g091650.4	-1,24	1,11E-02	3,34E-02	Glycine-rich domain-containing protein 2
Solyc04g049720.4	-1,24	3,44E-07	2,69E-06	Leukotriene A-4 hydrolase-like protein
Solyc07g008800.4	-1,24	2,00E-06	1,39E-05	10 kDa chaperonin
Solyc04g071280.3	-1,24	1,80E-06	1,26E-05	Pentatricopeptide repeat-containing protein
Solyc01g060130.3	-1,24	2,38E-05	1,40E-04	TOMGTPASE Mill. GTPase
Solyc02g082700.3	-1,24	4,98E-11	6,38E-10	High mobility group family
Solyc07g008770.4	-1,24	1,44E-09	1,59E-08	hypothetical protein
Solyc03g115570.1	-1,24	6,90E-03	2,23E-02	Pentatricopeptide repeat-containing protein
Solyc02g036310.4	-1,24	3,45E-04	1,59E-03	Malonyl-CoA decarboxylase family protein
Solyc05g018760.3	-1,24	1,20E-06	8,65E-06	RING/U-box superfamily protein
Solyc11g013450.2	-1,24	3,03E-04	1,41E-03	hypothetical protein
Solyc11g013090.2	-1,24	2,39E-06	1,65E-05	Penicillin-binding protein, 1A family
Solyc05g010470.4	-1,24	3,27E-07	2,56E-06	WD40 repeat
Solyc01g100220.3	-1,24	1,59E-04	7,89E-04	GATA transcription factor 23
Solyc06g072040.1	-1,24	2,55E-08	2,36E-07	CONSTANS interacting protein 2a
Solyc09g009490.4	-1,25	1,94E-04	9,43E-04	ABSCISIC ACID-INSENSITIVE 5-like protein 4
Solyc09g005640.3	-1,25	8,43E-09	8,33E-08	Protein SCO1-like protein 1, mitochondrial
Solyc11g066290.2	-1,25	1,14E-08	1,10E-07	Phosphatase DCR2
Solyc04g011650.3	-1,25	9,48E-04	3,94E-03	Telomere binding protein
Solyc02g086210.4	-1,25	2,38E-04	1,13E-03	Protein kinase family protein
Solyc02g078450.3	-1,25	3,05E-10	3,61E-09	tetraspanin-19-like
Solyc04g079900.3	-1,25	2,50E-10	2,97E-09	Metalloendopeptidase / zinc ion binding protein
Solyc08g066520.3	-1,25	1,41E-03	5,60E-03	BnaA10g30120D protein
Solyc06g005290.3	-1,25	5,47E-06	3,57E-05	UDP-galactose/UDP-glucose transporter 5B
Solyc06g005420.1	-1,25	4,18E-08	3,75E-07	Histone H4
Solyc04g076060.3	-1,25	7,02E-11	8,86E-10	tft10
Solyc05g006910.4	-1,25	1,29E-04	6,53E-04	AMP deaminase
Solyc02g089520.2	-1,25	5,80E-04	2,53E-03	Zinc finger protein CONSTANS-LIKE 2
Solyc08g081620.4	-1,25	4,01E-07	3,09E-06	LEU13054 endo-1,4-beta-glucanase precursor
Solyc05g009700.4	-1,25	3,98E-03	1,39E-02	Lysine histidine transporter-like 1
Solyc10g005780.3	-1,26	5,73E-08	5,01E-07	ER membrane protein complex subunit 8/9-like protein
Solyc09g097810.3	-1,26	1,65E-02	4,65E-02	SAR8.2 protein
Solyc09g090890.3	-1,26	2,73E-05	1,59E-04	DNA mismatch repair protein MSH1, mitochondrial
Solyc09g065040.1	-1,26	8,26E-04	3,47E-03	Cysteine-rich receptor-like protein kinase
Solyc02g062140.2	-1,26	2,73E-08	2,51E-07	Armadillo repeat only 1
Solyc10g083600.2	-1,26	3,54E-08	3,20E-07	Ribosome production factor 2-like protein
Solyc01g103390.3	-1,26	2,91E-03	1,06E-02	12-oxophytodienoate reductase 2
Solyc04g079850.2	-1,26	2,13E-03	8,05E-03	Pentatricopeptide repeat
Solyc02g079960.3	-1,26	1,30E-08	1,25E-07	Thioredoxin
Solyc01g008620.4	-1,26	6,38E-04	2,76E-03	Glucan endo-1,3-beta-glucosidase
Solyc05g056200.1	-1,26	1,55E-05	9,40E-05	Protein kinase domain
Solyc07g065940.1	-1,26	6,26E-04	2,71E-03	transmembrane protein
Solyc09g010710.4	-1,26	2,69E-04	1,27E-03	peptide transporter family protein
Solyc12g096350.2	-1,26	1,10E-03	4,49E-03	WRKY transcription factor 10
Solyc12g044230.2	-1,26	1,44E-05	8,80E-05	Sulfite exporter TauE/SafE family protein
Solyc12g010590.3	-1,26	2,39E-06	1,65E-05	O-acyltransferase WSD1-like protein
Solyc02g094290.1	-1,26	6,50E-03	2,12E-02	TCP transcription factor 27
Solyc01g109220.4	-1,26	5,74E-05	3,12E-04	Mitochondrial import receptor subunit TOM6-like protein
Solyc06g019200.4	-1,26	1,09E-11	1,49E-10	Ethylene-dependent gravitropism-deficient and yellow-green-like 2
Solyc05g014360.1	-1,27	1,54E-03	6,05E-03	Unknown protein
Solyc02g082430.4	-1,27	6,11E-08	5,31E-07	MLO-like protein
Solyc04g007820.3	-1,27	5,67E-04	2,49E-03	Sn-1 protein
Solyc02g090430.3	-1,27	3,04E-07	2,39E-06	MAP kinase kinase kinase 20
Solyc03g117860.3	-1,27	4,23E-05	2,36E-04	RBR-type E3 ubiquitin transferase
Solyc11g011890.2	-1,27	2,73E-03	1,01E-02	Zinc finger protein 1
Solyc11g007700.2	-1,27	5,25E-08	4,63E-07	mRNA cap guanine-N7 methyltransferase 2
Solyc05g010660.4	-1,27	4,81E-07	3,68E-06	DNA-directed RNA polymerase
Solyc01g006540.4	-1,27	9,03E-07	6,62E-06	lipoxygenase C

Solyc08g080620.1	-1,27	4,08E-04	1,84E-03	PR-5x
Solyc03g046270.4	-1,27	8,78E-05	4,61E-04	Protein trichome birefringence-like 19
Solyc10g085010.3	-1,27	5,25E-03	1,77E-02	PAR1-like protein
Solyc02g084770.3	-1,27	7,62E-05	4,06E-04	Mitochondrial carrier protein, expressed
Solyc03g119150.4	-1,27	2,09E-09	2,26E-08	Peptidylprolyl isomerase
Solyc02g078830.4	-1,28	5,21E-06	3,42E-05	p21-activated protein kinase-interacting protein 1-like
Solyc01g096080.3	-1,28	9,82E-08	8,31E-07	DUF688 domain-containing protein
Solyc04g081360.3	-1,28	1,47E-07	1,22E-06	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6
Solyc04g076360.4	-1,28	7,10E-06	4,55E-05	Homeodomain-like superfamily protein
Solyc01g066457.1	-1,28	2,13E-03	8,04E-03	Alpha/beta-Hydrolases superfamily protein
Solyc09g047840.3	-1,28	9,56E-04	3,97E-03	Ubiquitin-like-conjugating enzyme ATG10
Solyc05g056090.3	-1,28	1,10E-07	9,25E-07	Transmembrane protein 70 mitochondrial-like
Solyc05g047420.4	-1,28	3,39E-07	2,65E-06	Protein ECERIFERUM 7
Solyc03g117580.3	-1,28	1,50E-07	1,24E-06	GAG1At protein
Solyc12g017240.2	-1,28	4,43E-05	2,47E-04	xyloglucan endo-transglycosylase B1
Solyc03g006490.3	-1,28	3,81E-04	1,74E-03	Stem-specific protein TSJT1
Solyc06g031680.2	-1,28	2,13E-07	1,72E-06	hepatocyte growth factor-regulated tyrosine kinase substrate isoform X4
Solyc01g101260.2	-1,28	1,98E-03	7,55E-03	hypothetical protein
Solyc11g012290.2	-1,28	1,20E-04	6,09E-04	SWIB domain-containing protein
Solyc05g014560.3	-1,28	2,24E-03	8,41E-03	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic
Solyc03g116380.4	-1,28	1,42E-07	1,18E-06	WD repeat-containing protein 43-like
Solyc09g074230.4	-1,28	3,22E-09	3,36E-08	SlSFP7
Solyc01g111640.3	-1,28	9,76E-06	6,11E-05	SKP1-like protein
Solyc01g106500.4	-1,28	2,79E-05	1,63E-04	Receptor-like protein kinase
Solyc12g008680.3	-1,28	1,41E-04	7,06E-04	Unknown protein
Solyc12g010740.3	-1,28	1,17E-06	8,42E-06	protein STRUBBELIG-RECEPTOR FAMILY 3-like
Solyc11g066690.2	-1,28	3,12E-04	1,45E-03	RecQ-mediated instability-like protein
Solyc07g064160.3	-1,28	1,38E-13	2,31E-12	Thiamine thiazole synthase, chloroplastic
Solyc07g006075.1	-1,29	8,81E-03	2,75E-02	Unknown protein
Solyc08g077730.3	-1,29	2,57E-09	2,73E-08	phosphatidylinositol 4-phosphate 5-kinase 4-like
Solyc12g014330.1	-1,29	1,29E-04	6,53E-04	Pentatricopeptide repeat-containing protein
Solyc01g094830.4	-1,29	1,83E-06	1,29E-05	G-type lectin S-receptor-like serine/threonine-protein kinase SD2-2
Solyc07g064320.3	-1,29	7,51E-08	6,44E-07	hexon
Solyc02g080890.3	-1,29	1,27E-04	6,45E-04	WRKY transcription factor 6
Solyc03g113910.3	-1,29	2,24E-06	1,55E-05	Gibberellin-regulated protein 14
Solyc05g051870.3	-1,29	1,25E-05	7,69E-05	Pollen Ole e 1 allergen/extensin
Solyc04g074580.1	-1,29	2,33E-09	2,49E-08	Histone H3
Solyc11g069350.2	-1,29	3,25E-05	1,86E-04	Zinc finger, RING-CH-type, Zinc finger, RING/FYVE/PHD-type
Solyc12g098830.2	-1,29	2,98E-09	3,14E-08	5-nucleotidase
Solyc04g081240.2	-1,29	8,12E-07	6,00E-06	Auxin Response Factor 5
Solyc04g081960.1	-1,29	1,00E-02	3,07E-02	Syringolide-induced protein 14-1-1
Solyc02g078380.3	-1,29	1,10E-05	6,85E-05	Stem-specific protein TSJT1
Solyc01g087770.4	-1,29	6,56E-03	2,14E-02	Subtilisin-like protease
Solyc06g035790.3	-1,29	1,11E-04	5,67E-04	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc08g083130.4	-1,29	1,35E-06	9,63E-06	Homeobox-leucine zipper protein HOX6
Solyc09g008030.1	-1,29	7,52E-05	4,01E-04	TCP transcription factor 19
Solyc06g069280.4	-1,30	3,12E-05	1,79E-04	Protein LSM14-like protein A
Solyc03g063970.3	-1,30	4,20E-05	2,35E-04	Cornichon
Solyc12g087950.1	-1,30	3,12E-04	1,45E-03	AT-hook motif nuclear-localized protein
Solyc02g062230.1	-1,30	6,72E-04	2,89E-03	Small auxin up-regulated RNA32
Solyc08g079570.3	-1,30	1,08E-08	1,05E-07	Methylsterol monooxygenase 1-2
Solyc09g061280.4	-1,30	1,45E-04	7,27E-04	p27KIP1-related-protein 2
Solyc10g055770.2	-1,30	9,22E-03	2,86E-02	Major facilitator superfamily
Solyc06g035610.3	-1,30	1,65E-02	4,65E-02	RNA-binding protein
Solyc03g116840.3	-1,30	3,96E-04	1,80E-03	Pentatricopeptide repeat-containing protein
Solyc08g036503.1	-1,30	2,00E-03	7,62E-03	Unknown protein
Solyc02g078390.3	-1,30	5,29E-07	4,02E-06	DNA mismatch repair protein MutS
Solyc04g081580.4	-1,30	4,88E-03	1,66E-02	RNA helicase DEAD15
Solyc10g005100.3	-1,30	3,62E-12	5,22E-11	Plasma membrane-associated cation-binding protein 1
Solyc11g066320.2	-1,30	9,66E-08	8,18E-07	Exostosin family protein
Solyc05g008800.4	-1,30	2,27E-09	2,44E-08	lipid phosphate phosphatase 2-like
Solyc05g041820.1	-1,30	9,19E-04	3,83E-03	Unknown protein
Solyc02g094390.3	-1,30	1,41E-10	1,72E-09	S-acyltransferase
Solyc02g093670.3	-1,30	5,01E-03	1,70E-02	RPM1-interacting protein 4-like
Solyc03g114600.4	-1,30	4,07E-05	2,29E-04	Alternaria stem canker resistance
Solyc07g063860.4	-1,30	1,61E-04	8,00E-04	DUF538 domain-containing protein
Solyc12g088930.1	-1,30	3,61E-05	2,05E-04	protein MIZU-KUSSEI 1-like
Solyc05g009300.1	-1,30	2,74E-06	1,87E-05	transmembrane protein
Solyc03g122170.4	-1,30	1,42E-02	4,09E-02	Peroxisomal (S)-2-hydroxy-acid oxidase GLO4
Solyc11g007030.3	-1,30	8,88E-06	5,59E-05	Alpha/beta-Hydrolases superfamily protein
Solyc04g007170.3	-1,30	6,95E-07	5,18E-06	Ethylene-responsive transcription factor
Solyc10g080370.1	-1,30	2,66E-03	9,83E-03	Unknown protein
Solyc01g091840.4	-1,30	5,27E-07	4,01E-06	UDP-galactose/UDP-glucose transporter 2
Solyc04g080960.4	-1,30	3,39E-09	3,54E-08	pre-pro-cysteine proteinase
Solyc02g063140.4	-1,30	1,86E-05	1,11E-04	3-ketoacyl-CoA synthase
Solyc05g055650.3	-1,31	1,22E-03	4,92E-03	Quinoprotein alcohol dehydrogenase-like superfamily
Solyc02g081360.4	-1,31	4,52E-07	3,47E-06	AMP-dependent synthetase/ligase
Solyc02g005606.1	-1,31	6,30E-05	3,40E-04	serine/threonine-protein phosphatase 7 long form homolog
Solyc02g079580.4	-1,31	3,92E-03	1,38E-02	S-receptor kinase-like protein 1
Solyc02g081690.1	-1,31	2,59E-04	1,22E-03	Glycosyltransferase
Solyc12g099980.3	-1,31	4,59E-03	1,58E-02	receptor-like protein 12
Solyc03g051900.4	-1,31	1,73E-02	4,86E-02	Ribosomal protein S1
Solyc11g012520.1	-1,31	4,03E-04	1,82E-03	hypothetical protein
Solyc09g007850.3	-1,31	5,48E-07	4,15E-06	RNA-binding protein
Solyc02g072320.1	-1,31	7,35E-03	2,35E-02	Protein NSP-INTERACTING KINASE 1
Solyc12g049560.2	-1,31	2,21E-08	2,06E-07	Ethylene-responsive transcription factor
Solyc08g029360.4	-1,31	3,44E-05	1,96E-04	Unknown protein
Solyc11g073090.1	-1,31	2,75E-04	1,29E-03	Harbinger transposase-derived nuclease
Solyc02g085650.4	-1,31	4,76E-06	3,14E-05	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc02g077040.4	-1,31	1,10E-11	1,50E-10	phytophthora-inhibited protease 1
Solyc11g072010.3	-1,31	7,87E-06	4,99E-05	Homoserine dehydrogenase
Solyc10g049640.2	-1,31	4,22E-03	1,47E-02	Amino acid/polyamine transporter I
Solyc06g054315.1	-1,31	1,75E-02	4,91E-02	Mitogen-activated protein kinase kinase kinase 3
Solyc01g086860.3	-1,31	4,31E-08	3,85E-07	Expressed protein
Solyc03g123860.4	-1,31	1,34E-06	9,56E-06	Receptor-like protein kinase INRPK1c
Solyc10g051120.3	-1,31	2,07E-03	7,85E-03	Mitochondrial pyruvate carrier
Solyc10g006710.4	-1,32	3,60E-05	2,04E-04	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc01g066290.2	-1,32	1,26E-04	6,42E-04	Unknown protein
Solyc12g006840.2	-1,32	3,41E-03	1,22E-02	Lectin protein kinase family protein
Solyc02g081040.4	-1,32	1,52E-03	5,96E-03	Lyk11
Solyc03g098490.1	-1,32	7,62E-06	4,85E-05	DUF761 domain-containing protein/DUF4408 domain-containing protein
Solyc02g085580.4	-1,32	2,63E-10	3,13E-09	Protein indeterminate-domain 1
Solyc01g066060.4	-1,32	1,63E-07	1,33E-06	Multiple organellar RNA editing factor 3, mitochondrial
Solyc02g069770.3	-1,32	2,54E-04	1,20E-03	Transducin/WD40 repeat-like superfamily protein
Solyc10g006900.3	-1,32	7,86E-09	7,78E-08	light dependent NADH:protochlorophyllide oxidoreductase 3 s2
Solyc09g056360.3	-1,32	3,42E-09	3,57E-08	Cytochrome b561 and DOMON domain-containing protein
Solyc02g077220.3	-1,32	1,73E-03	6,71E-03	GDSL esterase/lipase
Solyc02g082420.3	-1,32	2,33E-04	1,11E-03	RING/U-box superfamily protein
Solyc10g081300.1	-1,32	1,40E-04	7,02E-04	Metacaspase-9
Solyc05g014150.4	-1,33	1,12E-02	3,35E-02	Very-long-chain 3-oxoacyl-CoA reductase-like protein
Solyc02g091250.1	-1,33	2,55E-03	9,46E-03	Mediator of RNA polymerase II transcription subunit
Solyc02g070540.3	-1,33	2,49E-09	2,65E-08	DUF642 domain-containing protein
Solyc10g078190.2	-1,33	3,88E-05	2,19E-04	cytosine-5 DNA methyltransferaseL1
Solyc05g051290.4	-1,33	1,45E-07	1,21E-06	HMG-Y-related protein A-like

Solyc03g097600.3	-1,33	1,57E-05	9,50E-05	Bidirectional sugar transporter SWEET
Solyc12g049030.1	-1,33	2,07E-04	1,00E-03	Fatty acid desaturase
Solyc05g018403.1	-1,33	1,38E-04	6,93E-04	Sigma-B regulation protein RsbQ
Solyc04g076680.2	-1,33	5,12E-03	1,73E-02	MADS box transcription factor AGAMOUS
Solyc07g052250.4	-1,33	7,11E-03	2,29E-02	Unknown protein
Solyc03g006630.3	-1,33	1,90E-04	9,26E-04	Sphingosine kinase 1
Solyc09g082060.3	-1,33	3,94E-13	6,28E-12	Cysteine synthase
Solyc04g078650.4	-1,33	1,73E-06	1,21E-05	wuschel related homobox 4
Solyc12g013990.3	-1,33	4,84E-07	3,71E-06	50S ribosomal protein L1
Solyc02g068910.3	-1,33	1,20E-12	1,83E-11	Trypsin family protein
Solyc06g051970.3	-1,33	6,74E-04	2,90E-03	Calcineurin B-like protein
Solyc11g005150.3	-1,33	4,56E-05	2,53E-04	entensin X55687
Solyc01g096170.4	-1,33	5,24E-03	1,76E-02	MAP kinase kinase kinase 5
Solyc02g071810.4	-1,34	1,79E-03	6,90E-03	Protein kinase domain
Solyc01g090120.3	-1,34	1,28E-02	3,76E-02	Uclacyanin-3
Solyc03g005180.1	-1,34	2,74E-04	1,29E-03	Ribosomal L18P L5E family protein
Solyc10g038060.2	-1,34	4,46E-03	1,54E-02	Ribosomal L28 family
Solyc02g087770.3	-1,34	1,29E-06	9,25E-06	Aldose 1-epimerase
Solyc10g074560.2	-1,34	7,75E-09	7,68E-08	nucleolar complex protein 4 homolog
Solyc01g098760.4	-1,34	1,61E-11	2,17E-10	Heavy metal-associated isoprenylated plant protein
Solyc07g054475.1	-1,34	8,09E-04	3,41E-03	Long chain acyl-CoA synthetase 1
Solyc02g092830.4	-1,34	5,36E-08	4,71E-07	hypothetical protein
Solyc09g007640.4	-1,34	4,06E-06	2,70E-05	Serine carboxypeptidase-like 50
Solyc05g013170.2	-1,34	8,69E-06	5,48E-05	GCK domain-containing protein
Solyc02g084590.4	-1,34	2,45E-07	1,95E-06	GATA transcription factor
Solyc10g007520.3	-1,34	3,01E-05	1,74E-04	Pentatricopeptide repeat-containing protein
Solyc04g079930.3	-1,34	2,82E-09	2,98E-08	Histone deacetylase complex subunit
Solyc05g010790.3	-1,34	6,39E-03	2,09E-02	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc01g095690.2	-1,34	2,08E-03	7,90E-03	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc09g015085.1	-1,34	1,54E-05	9,36E-05	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic
Solyc02g090310.1	-1,35	8,19E-04	3,45E-03	Dof zinc finger protein
Solyc09g056170.3	-1,35	4,50E-08	4,00E-07	Fimbrin-2
Solyc07g066560.1	-1,35	3,81E-06	2,54E-05	Small auxin up-regulated RNA65
Solyc07g055410.2	-1,35	1,37E-03	5,45E-03	Receptor-like protein kinase
Solyc09g092080.4	-1,35	7,02E-09	6,99E-08	Unknown protein
Solyc03g095450.3	-1,35	1,12E-07	9,38E-07	RING/U-box superfamily protein
Solyc05g050000.3	-1,35	2,34E-07	1,87E-06	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc02g024010.1	-1,35	6,05E-04	2,63E-03	transmembrane protein
Solyc04g016250.3	-1,35	2,51E-04	1,19E-03	Mitochondrial glycoprotein
Solyc03g114890.4	-1,35	2,88E-03	1,05E-02	COBRA-like protein
Solyc05g012430.1	-1,35	1,31E-02	3,84E-02	Leucine-rich repeat receptor-like protein kinase PXL1
Solyc01g087800.2	-1,35	3,91E-07	3,03E-06	Subtilisin-like protease
Solyc06g050250.1	-1,35	2,57E-09	2,73E-08	Adenine/guanine permease AZG1
Solyc06g007240.4	-1,35	4,92E-06	3,24E-05	BAG family molecular chaperone regulator 2-like
Solyc05g055440.1	-1,35	4,67E-12	6,66E-11	Histone H2B
Solyc10g005510.3	-1,35	1,12E-04	5,73E-04	Glyceraldehyde-3-phosphate dehydrogenase
Solyc06g063210.3	-1,35	8,51E-05	4,48E-04	glutamate receptor-like 2.5
Solyc10g054850.2	-1,35	3,32E-05	1,90E-04	Er lumen protein retaining receptor-like protein
Solyc06g007130.5.1	-1,36	8,42E-05	4,44E-04	omega-3 fatty acid desaturase -3
Solyc09g090040.3	-1,36	2,68E-06	1,83E-05	Germin-like protein subfamily 1 member 15
Solyc07g005850.3	-1,36	8,41E-03	2,64E-02	Pentatricopeptide repeat-containing protein
Solyc06g051620.3	-1,36	5,68E-04	2,49E-03	Phosphoinositide phospholipase C
Solyc01g010060.2	-1,36	9,73E-03	2,99E-02	Unknown protein
Solyc04g079520.3	-1,36	6,06E-05	3,28E-04	Major facilitator superfamily protein
Solyc04g079080.2	-1,36	1,02E-04	5,26E-04	EF-hand domain
Solyc04g076690.4	-1,36	3,94E-05	2,22E-04	Unknown protein
Solyc03g006220.4	-1,36	8,20E-04	3,45E-03	Protein trichome birefringence-like 39
Solyc02g067655.1	-1,36	2,58E-03	9,57E-03	Unknown protein
Solyc06g005340.3	-1,37	1,45E-02	4,18E-02	RAB GTPase homolog 8
Solyc05g043405.1	-1,37	3,46E-04	1,59E-03	Unknown protein
Solyc10g084660.2	-1,37	6,97E-03	2,25E-02	Actin-depolymerizing factor
Solyc08g068070.3	-1,37	3,42E-08	3,10E-07	Two-on-two hemoglobin-3
Solyc02g069580.3	-1,37	7,96E-12	1,11E-10	UDP-glucose 4-epimerase
Solyc03g118310.4	-1,37	1,08E-03	4,43E-03	bHLH transcription factor 083
Solyc05g025513.1	-1,37	5,15E-04	2,28E-03	Unknown protein
Solyc03g120110.3	-1,37	1,05E-03	4,32E-03	Lectin protein kinase family protein
Solyc03g113370.3	-1,37	7,46E-04	3,18E-03	Ubiquitin carboxyl-terminal hydrolase-like protein
Solyc07g006010.3	-1,37	3,58E-07	2,79E-06	Nuclear pore complex protein NUP43
Solyc03g033280.1	-1,37	1,18E-03	4,77E-03	Tracheary element differentiation-related 6
Solyc01g014180.3	-1,37	3,53E-13	5,66E-12	Zinc finger A20 and AN1 domain-containing stress-associated protein 8
Solyc01g100730.3	-1,37	2,03E-06	1,42E-05	Rhodanese-like domain-containing protein 6
Solyc06g061250.3	-1,38	1,15E-07	9,66E-07	RING/U-box superfamily protein
Solyc05g054545.1	-1,38	6,73E-05	3,61E-04	Ubiquitin conjugating enzyme
Solyc11g066800.2	-1,38	6,46E-03	2,11E-02	GABA transporter 1
Solyc09g075420.3	-1,38	1,10E-06	7,93E-06	ethylene response factor E.1
Solyc08g014300.4	-1,38	4,75E-08	4,21E-07	FAM136A-like protein (DUF842)
Solyc07g047790.3	-1,38	7,43E-04	3,16E-03	Heat shock protein
Solyc06g008360.3	-1,38	1,16E-02	3,45E-02	NAC domain-containing protein
Solyc12g027897.1	-1,38	6,12E-12	8,62E-11	Unknown protein
Solyc04g024420.3	-1,38	1,10E-07	9,21E-07	Proteasome subunit beta
Solyc01g103595.1	-1,38	1,37E-03	5,45E-03	Jasmonate ZIM domain protein l
Solyc09g009190.4	-1,38	2,30E-05	1,36E-04	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic
Solyc09g092750.3	-1,38	2,62E-05	1,53E-04	Unknown protein
Solyc03g123460.4	-1,38	1,56E-04	7,78E-04	DUF581 domain-containing protein
Solyc06g064500.3	-1,38	3,17E-06	2,14E-05	Myricetin O-methyltransferase 2
Solyc05g054490.3	-1,38	4,58E-08	4,07E-07	3-oxo-5-alpha-steroid 4-dehydrogenase
Solyc11g005820.1	-1,38	1,20E-02	3,56E-02	Pectinesterase inhibitor domain-containing protein
Solyc01g008460.3	-1,38	6,89E-07	5,14E-06	2Fe-2S ferredoxin
Solyc09g057960.1	-1,38	5,56E-03	1,86E-02	Cysteine-rich receptor-like protein kinase
Solyc04g079660.2	-1,39	4,00E-06	2,67E-05	Cytochrome P450
Solyc02g032660.3	-1,39	8,94E-08	7,61E-07	Protein DETOXIFICATION
Solyc02g077730.3	-1,39	4,90E-07	3,74E-06	Protein NUCLEAR FUSION DEFECTIVE 6, chloroplastic/mitochondrial
Solyc01g096120.3	-1,39	6,23E-06	4,03E-05	Dof zinc finger protein1
Solyc03g123620.4	-1,39	2,07E-08	1,95E-07	Pectinesterase
Solyc05g007940.3	-1,39	6,89E-03	2,23E-02	LERNALX L.esculentum ribonuclease lx
Solyc12g088840.1	-1,39	1,64E-05	9,89E-05	EF-hand domain
Solyc06g005520.4	-1,39	3,76E-09	3,88E-08	Protein kinase superfamily protein
Solyc05g055550.3	-1,39	3,28E-05	1,87E-04	vacuolar acid trehalase
Solyc09g008460.3	-1,39	9,14E-13	1,41E-11	RAB GTPase
Solyc04g081890.1	-1,39	1,05E-03	4,34E-03	RING/U-box superfamily protein
Solyc04g076120.3	-1,39	1,08E-03	4,41E-03	Serine carboxypeptidase-like 17
Solyc07g056000.2	-1,39	6,51E-03	2,12E-02	Xyloglucan endotransglucosylase/hydrolase
Solyc02g086970.4	-1,39	9,69E-09	9,49E-08	Aldehyde dehydrogenase
Solyc06g005410.3	-1,39	1,01E-04	5,23E-04	Unknown protein
Solyc08g079670.3	-1,40	1,28E-08	1,23E-07	SNARE associated Golgi protein
Solyc11g071620.3	-1,40	9,90E-04	4,10E-03	aldehyde oxidase 1
Solyc01g150165.1	-1,40	2,59E-03	9,60E-03	transmembrane protein 184C
Solyc05g014120.1	-1,40	6,34E-04	2,74E-03	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc02g063430.4	-1,40	5,41E-06	3,53E-05	bHLH transcription factor 078
Solyc05g046140.3	-1,40	2,53E-03	9,37E-03	Kirola
Solyc08g076870.1	-1,40	3,08E-05	1,78E-04	DUF740 domain-containing protein
Solyc03g079930.3	-1,40	6,09E-10	6,98E-09	Mitochondrial glycoprotein
Solyc02g081210.3	-1,40	9,12E-06	5,73E-05	Expansin
Solyc05g012510.3	-1,40	1,96E-03	7,50E-03	Alpha-1,4 glucan phosphorylase

Solyc02g087470.4	-1,40	2,02E-03	7,70E-03	CLAVATA3/ESR-RELATED 26
Solyc11g069110.2	-1,40	9,64E-04	4,00E-03	hypothetical protein
Solyc06g065820.3	-1,40	3,65E-03	1,29E-02	Ethylene Response Factor H.1
Solyc09g009895.1	-1,40	5,39E-07	4,09E-06	Unknown protein
Solyc07g053270.3	-1,40	9,04E-11	1,13E-09	HAD hydrolase
Solyc06g072070.2	-1,41	7,50E-07	5,57E-06	Transmembrane protein, putative (DUF 3339)
Solyc07g025110.1	-1,41	3,96E-05	2,23E-04	F-box protein CPR1
Solyc02g022830.3	-1,41	6,49E-06	4,18E-05	Twinkle-like protein, chloroplastic/mitochondrial
Solyc03g113950.4	-1,41	2,43E-11	3,21E-10	Calmodulin binding protein
Solyc08g068700.1	-1,41	6,50E-08	5,63E-07	Tyramine n-hydroxycinnamoyl transferase
Solyc08g074970.1	-1,41	6,97E-04	2,99E-03	UDP-Glycosyltransferase superfamily protein
Solyc04g054760.3	-1,41	1,01E-07	8,54E-07	FCS-Like Zinc finger 5
Solyc10g080360.1	-1,41	3,91E-05	2,21E-04	Unknown protein
Solyc01g102550.4	-1,41	3,53E-07	2,75E-06	nuclear pore complex protein NUP160 isoform X4
Solyc10g084080.3	-1,41	6,42E-06	4,14E-05	Pentatricopeptide repeat
Solyc01g008520.3	-1,42	1,57E-05	9,53E-05	Homolog of X-ray repair cross complementing 2 (XRCC2)
Solyc12g006850.2	-1,42	2,94E-09	3,10E-08	LELKT1GEN L.esculentum potassium channel
Solyc08g081260.1	-1,42	4,59E-03	1,58E-02	Disease resistance protein (TIR-NBS class)
Solyc03g006400.3	-1,42	5,74E-09	5,78E-08	MAP kinase kinase kinase 25
Solyc03g082670.3	-1,42	1,29E-09	1,42E-08	F-box-like domain-containing protein
Solyc06g053360.4	-1,42	1,42E-06	1,01E-05	Protein ENHANCED DISEASE RESISTANCE 2-like
Solyc04g074770.2	-1,42	5,29E-08	4,65E-07	Unknown protein
Solyc03g119080.4	-1,42	6,73E-09	6,72E-08	beta-mannosidase enzyme
Solyc03g111310.3	-1,42	4,91E-13	7,75E-12	Snf1-related protein kinase regulatory subunit gamma-1
Solyc02g085430.4	-1,42	3,59E-04	1,64E-03	Proline-rich receptor-like protein kinase PERK7
Solyc09g075350.4	-1,42	1,18E-05	7,34E-05	Pectinesterase
Solyc03g078110.1	-1,42	7,63E-03	2,43E-02	NAC domain-containing protein 16
Solyc11g011580.2	-1,42	5,35E-05	2,93E-04	GRAM domain
Solyc09g090990.2	-1,42	4,17E-04	1,88E-03	Major allergen Pru ar 1
Solyc07g063310.3	-1,42	1,15E-09	1,28E-08	LanC-like protein GCR2
Solyc04g015470.3	-1,42	9,93E-08	8,40E-07	Phosphatidylinositol 4-phosphate 5-kinase
Solyc01g067030.2	-1,42	5,36E-05	2,93E-04	F-box protein
Solyc02g079130.3	-1,43	3,54E-09	3,67E-08	SEC-C motif containing protein
Solyc12g011320.2	-1,43	1,03E-04	5,34E-04	Glutathione S-transferase
Solyc03g114010.3	-1,43	9,81E-03	3,01E-02	Pentatricopeptide repeat-containing protein
Solyc06g082810.3	-1,43	1,15E-12	1,75E-11	Oligoribonuclease
Solyc07g053470.4	-1,43	1,81E-09	1,98E-08	GTP-binding protein TypA
Solyc10g080960.1	-1,43	6,56E-07	4,91E-06	Two-component response regulator ARR1
Solyc01g009620.3	-1,43	2,76E-08	2,53E-07	Cleavage and polyadenylation specificity factor subunit 5
Solyc02g082160.2	-1,43	1,18E-02	3,51E-02	Pentatricopeptide repeat
Solyc11g012480.3	-1,43	4,59E-12	6,57E-11	Thymidine kinase
Solyc01g089880.3	-1,43	4,19E-05	2,35E-04	PRA1 family protein
Solyc01g006090.3	-1,43	2,13E-05	1,26E-04	Eukaryotic rRNA processing
Solyc10g005610.2	-1,43	2,58E-07	2,05E-06	serine/arginine repetitive matrix-like protein
Solyc04g077350.1	-1,43	1,11E-03	4,54E-03	Unknown protein
Solyc02g080950.3	-1,44	3,53E-04	1,62E-03	Pentatricopeptide repeat-containing protein
Solyc08g075280.4	-1,44	1,83E-08	1,73E-07	AT4g19390/T5K18_170
Solyc05g014790.3	-1,44	3,82E-04	1,74E-03	Lipoxygenase
Solyc11g017410.1	-1,44	2,47E-03	9,20E-03	protein BPS1, chloroplastic-like
Solyc01g097640.3	-1,44	3,40E-04	1,57E-03	Ribosome biogenesis protein BMS1-like protein
Solyc12g017690.3	-1,44	3,36E-09	3,51E-08	Queuine tRNA-ribosyltransferase accessory subunit 2
Solyc08g023270.3	-1,44	5,76E-06	3,75E-05	myosin heavy chain-like protein
Solyc11g010370.1	-1,44	9,18E-07	6,71E-06	ENTH/ANTH/VHS superfamily protein
Solyc02g062010.1	-1,44	1,31E-04	6,63E-04	Unknown protein
Solyc04g072310.3	-1,44	1,10E-05	6,83E-05	histone-lysine N-methyltransferase SETD1B-A
Solyc09g011220.3	-1,44	2,75E-08	2,52E-07	Glucose-1-phosphate adenylyltransferase family protein
Solyc02g082240.1	-1,44	1,77E-03	6,85E-03	Unknown protein
Solyc08g061650.4	-1,45	1,03E-03	4,25E-03	F-box/LRR-repeat protein 13
Solyc05g014630.2	-1,45	4,31E-06	2,86E-05	Unknown protein
Solyc07g055630.4	-1,45	9,46E-05	4,93E-04	Lectin-domain receptor-like kinase
Solyc01g067300.3	-1,45	3,00E-03	1,09E-02	CASP-like protein
Solyc01g096920.3	-1,45	1,39E-04	6,99E-04	GATA zinc finger protein
Solyc09g090980.3	-1,45	2,07E-05	1,23E-04	pathogenesis-related protein STH-2-like
Solyc01g008600.4	-1,45	7,28E-05	3,88E-04	Zinc finger transcription factor 6
Solyc02g014310.4	-1,45	2,20E-12	3,27E-11	glycine rich protein X55695
Solyc10g055740.2	-1,45	3,10E-03	1,12E-02	lysine histidine transporter-like 8
Solyc03g112210.1	-1,45	8,41E-14	1,44E-12	Unknown protein
Solyc01g090760.4	-1,45	2,11E-05	1,25E-04	GATA transcription factor
Solyc03g025140.1	-1,45	4,78E-03	1,63E-02	Unknown protein
Solyc05g056500.1	-1,45	3,41E-03	1,22E-02	RING-type E3 ubiquitin transferase
Solyc11g072820.3	-1,45	1,27E-02	3,74E-02	Kinesin
Solyc02g050210.2	-1,45	1,41E-02	4,09E-02	BREAST CANCER 2 like 2A
Solyc10g047120.2	-1,45	1,23E-09	1,37E-08	tRNA (Guanine(10)-N2)-methyltransferase homolog
Solyc12g014090.2	-1,45	3,16E-05	1,82E-04	TAF RNA polymerase I subunit A
Solyc03g094010.3	-1,45	1,17E-03	4,75E-03	Glutamate dehydrogenase
Solyc02g063090.3	-1,46	5,09E-11	6,52E-10	T-complex protein 1 subunit zeta
Solyc10g017960.2	-1,46	2,39E-03	8,95E-03	F-box protein PP2-A15
Solyc08g079080.5	-1,46	3,06E-03	1,11E-02	Lycopersicon esculentum invertase 9
Solyc11g065020.3	-1,46	1,44E-10	1,76E-09	GDP-mannose transporter GONST1
Solyc12g007045.1	-1,46	1,85E-03	7,11E-03	Arabinogalactan peptide 22
Solyc01g096100.2	-1,46	6,76E-06	4,35E-05	Transmembrane protein
Solyc02g079050.3	-1,46	6,24E-07	4,69E-06	Anaphase-promoting complex subunit 4
Solyc01g094280.3	-1,46	9,55E-09	9,36E-08	Bifunctional protein folD
Solyc02g070900.1	-1,46	1,19E-03	4,81E-03	Unknown protein
Solyc07g062820.1	-1,46	2,57E-09	2,73E-08	Pentatricopeptide repeat-containing protein
Solyc05g046280.3	-1,46	5,21E-05	2,85E-04	Pentatricopeptide repeat
Solyc03g025670.3	-1,46	2,37E-07	1,90E-06	PAR1
Solyc01g150164.1	-1,46	4,88E-06	3,21E-05	thionin-like protein
Solyc06g074850.3	-1,46	1,08E-09	1,21E-08	Carboxypeptidase
Solyc10g007070.4	-1,46	2,23E-06	1,54E-05	Early nodulin-like protein 1
Solyc11g007160.2	-1,46	6,45E-10	7,37E-09	RNA-binding (RRM/RBD/RNP motifs) family protein
Solyc01g010020.3	-1,46	6,48E-05	3,49E-04	Calmodulin
Solyc04g051390.2	-1,46	3,63E-03	1,29E-02	Unknown protein
Solyc03g031730.3	-1,46	4,45E-04	1,99E-03	Beta-glucosidase
Solyc06g007330.3	-1,46	9,63E-07	7,02E-06	gamma-interferon-inducible lysosomal thiol reductase-like
Solyc07g062220.3	-1,46	2,64E-06	1,81E-05	Protein trichome birefringence-like 41
Solyc09g011170.3	-1,46	4,97E-08	4,39E-07	Prf interactor 30137
Solyc04g051670.3	-1,47	5,49E-09	5,54E-08	RNA cytidine acetyltransferase
Solyc03g032040.3	-1,47	7,30E-10	8,30E-09	Tonoplast monosaccharide transporter 1
Solyc04g024840.3	-1,47	2,19E-05	1,30E-04	GDSL esterase/lipase
Solyc08g082940.2	-1,47	7,28E-07	5,42E-06	Transcription factor
Solyc01g109630.4	-1,47	5,25E-10	6,06E-09	Mitochondrial transcription termination factor family protein
Solyc01g097150.4	-1,47	2,34E-07	1,87E-06	Unknown protein
Solyc06g071460.3	-1,47	1,28E-09	1,42E-08	Exosome complex component rrp40-like protein
Solyc12g089385.1	-1,47	1,27E-04	6,45E-04	FAD/NAD(P)-binding oxidoreductase family protein
Solyc03g025860.3	-1,47	1,76E-03	6,82E-03	25.3 kDa vesicle transport protein
Solyc10g012060.3	-1,47	4,00E-09	4,12E-08	Mechanosensitive ion channel protein 1, mitochondrial
Solyc07g005870.3	-1,47	1,96E-07	1,59E-06	FAD dependent oxidoreductase
Solyc10g012430.3	-1,48	4,90E-12	6,96E-11	Signal peptide peptidase-like 4
Solyc03g098120.3	-1,48	2,72E-08	2,50E-07	40S ribosomal protein
Solyc02g081660.3	-1,48	1,01E-07	8,53E-07	GTP-binding protein ERG
Solyc01g006210.4	-1,48	3,29E-03	1,18E-02	Non-structural maintenance of chromosomes element 1
Solyc09g091810.1	-1,48	3,30E-03	1,19E-02	Unknown protein
Solyc04g014883.1	-1,48	3,77E-04	1,72E-03	LRR receptor-like serine/threonine-protein kinase EFR

Solyc04g064530.1	-1,48	4,32E-07	3,32E-06	polyadenylate-binding protein 1-B-binding protein
Solyc08g008305.1	-1,48	9,49E-06	5,95E-05	Ethylene-responsive transcription factor
Solyc12g013570.2	-1,48	3,81E-05	2,15E-04	Plant cadmium resistance 2, putative
Solyc01g102400.3	-1,48	9,00E-04	3,76E-03	Germin-like protein
Solyc09g008080.3	-1,48	7,26E-06	4,64E-05	Ubiquitin domain-containing protein
Solyc01g095740.4	-1,49	3,42E-12	4,95E-11	RNA helicase DEAD5
Solyc04g009910.3	-1,49	3,79E-07	2,94E-06	Phosphoenolpyruvate carboxylase kinase
Solyc03g114580.4	-1,49	1,14E-06	8,25E-06	Uridine kinase
Solyc07g007150.1	-1,49	9,09E-11	1,14E-09	hypothetical protein
Solyc06g010170.3	-1,49	2,44E-05	1,43E-04	Lysine ketoglutarate reductase trans-splicing protein (DUF707)
Solyc08g082480.3	-1,49	1,41E-08	1,34E-07	Phosphatidylinositol 4-kinase gamma 2
Solyc03g096460.4	-1,49	1,94E-07	1,57E-06	wound/stress protein AY568721
Solyc07g045370.3	-1,49	5,67E-09	5,72E-08	Las1-like family protein
Solyc02g070070.1	-1,49	4,75E-03	1,62E-02	FAD-binding Berberine family protein
Solyc07g007050.1	-1,49	1,75E-07	1,43E-06	hypothetical protein
Solyc01g086710.4	-1,49	1,61E-07	1,32E-06	DNA-directed RNA polymerase subunit beta
Solyc03g097930.3	-1,49	1,73E-04	8,53E-04	Unknown protein
Solyc08g075740.1	-1,49	2,71E-03	9,97E-03	Unknown protein
Solyc04g018130.1	-1,49	1,36E-03	5,41E-03	Unknown protein
Solyc01g106700.3	-1,49	9,02E-04	3,77E-03	MADS-box transcription factor 23
Solyc01g105600.3	-1,49	8,01E-04	3,38E-03	hypothetical protein
Solyc09g072680.2	-1,49	1,86E-09	2,02E-08	F-box domain
Solyc03g078240.3	-1,50	2,68E-03	9,89E-03	Glycosyltransferase
Solyc11g072100.2	-1,50	1,25E-10	1,54E-09	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc05g055560.1	-1,50	7,76E-04	3,29E-03	Protein MEF2BNB-like protein
Solyc04g072450.3	-1,50	4,02E-09	4,14E-08	acidic leucine-rich nuclear phosphoprotein 32 family member B
Solyc11g006590.2	-1,50	2,95E-09	3,11E-08	Cytochrome
Solyc05g026460.1	-1,50	1,59E-03	6,21E-03	Unknown protein
Solyc06g075150.3	-1,50	2,93E-08	2,68E-07	Auxin Response Factor 10B
Solyc03g051780.3	-1,50	4,25E-03	1,47E-02	Pentatricopeptide repeat-containing protein
Solyc03g119320.1	-1,50	9,01E-05	4,72E-04	hypothetical protein
Solyc01g088440.2	-1,50	1,30E-04	6,55E-04	RING/U-box superfamily protein
Solyc09g008300.2	-1,50	3,88E-05	2,19E-04	Pentatricopeptide repeat
Solyc01g066640.2	-1,50	3,61E-05	2,05E-04	Vitellogenin-like protein
Solyc12g015680.1	-1,50	6,52E-08	5,64E-07	Protein TIC 20-v, chloroplastic
Solyc05g054120.1	-1,50	4,06E-08	3,64E-07	Cysteine proteinase inhibitor
Solyc05g010780.1	-1,50	1,41E-04	7,09E-04	Pentatricopeptide repeat-containing protein
Solyc10g080350.3	-1,51	1,84E-03	7,07E-03	DNA-directed RNA polymerase subunit
Solyc01g100980.4	-1,51	6,71E-05	3,60E-04	Pectin lyase-like superfamily protein
Solyc06g036430.3	-1,51	1,02E-05	6,38E-05	Reticulon-like protein
Solyc03g078610.3	-1,51	4,03E-13	6,42E-12	Alpha-ketoglutarate-dependent dioxygenase alkB-like protein 2
Solyc09g090130.3	-1,51	1,35E-04	6,81E-04	R2R3MYB transcription factor 15
Solyc08g081960.3	-1,51	4,64E-04	2,07E-03	Solanum Lycopersicum Cytokinin Response Factor 2
Solyc07g005790.4	-1,51	2,15E-07	1,73E-06	Multipolar spindle 1
Solyc04g071900.4	-1,51	7,46E-12	1,04E-10	Peroxidase
Solyc09g008820.3	-1,51	7,88E-12	1,09E-10	F-box protein PP2-A15
Solyc02g078850.1	-1,51	1,18E-11	1,60E-10	glycine-rich protein
Solyc07g062930.3	-1,51	4,25E-08	3,81E-07	Ribosomal L11 methyltransferase
Solyc10g011810.4	-1,51	9,23E-12	1,27E-10	Delta(8)-fatty-acid desaturase
Solyc01g107080.3	-1,51	5,01E-03	1,70E-02	HXXXD-type acyl-transferase family protein
Solyc12g056360.1	-1,52	6,52E-04	2,81E-03	Pathogenesis-related thaumatin family protein
Solyc07g062040.3	-1,52	2,43E-04	1,16E-03	Receptor-like serine/threonine-protein kinase
Solyc02g063410.3	-1,52	5,13E-03	1,73E-02	Hydroxyproline-rich glycoprotein family protein
Solyc05g046200.3	-1,52	8,90E-03	2,77E-02	Unknown protein
Solyc06g008300.4	-1,52	1,25E-08	1,20E-07	Hcr2-5D
Solyc06g067950.3	-1,52	1,21E-07	1,02E-06	Alpha/beta-Hydrolases superfamily protein
Solyc10g078860.2	-1,52	3,41E-05	1,94E-04	DNA-directed RNA polymerase subunit beta
Solyc07g062510.2	-1,52	8,85E-05	4,64E-04	Cytochrome
Solyc03g118630.3	-1,52	7,12E-08	6,12E-07	transmembrane protein
Solyc12g011170.3	-1,52	5,30E-03	1,78E-02	Phospholipase D
Solyc06g075960.1	-1,52	1,75E-12	2,63E-11	Histone H4
Solyc11g006270.2	-1,53	1,14E-03	4,64E-03	3-oxo-5-alpha-steroid 4-dehydrogenase
Solyc08g075970.3	-1,53	5,98E-08	5,21E-07	Plant viral-response family protein
Solyc06g069190.4	-1,53	1,31E-14	2,40E-13	Eukaryotic aspartyl protease family protein
Solyc03g117550.1	-1,53	1,87E-10	2,26E-09	Receptor-like protein kinase
Solyc03g005980.3	-1,53	1,66E-05	1,00E-04	NOD26-like intrinsic protein 1.1
Solyc03g033490.3	-1,53	6,86E-07	5,12E-06	Thaumatin-like protein
Solyc01g097240.3	-1,53	1,93E-05	1,15E-04	Pathogenesis-related protein 4
Solyc08g006780.3	-1,54	6,02E-15	1,13E-13	Nucleoid-associated protein
Solyc06g053870.4	-1,54	8,37E-03	2,63E-02	3-ketoacyl-CoA synthase
Solyc05g054960.4	-1,54	3,92E-13	6,26E-12	Multiple organellar RNA editing factor 5, chloroplastic/mitochondrial
Solyc10g005210.4	-1,54	5,34E-09	5,40E-08	DNA-3-methyladenine glycosylase I
Solyc07g066010.3	-1,54	4,58E-13	7,25E-12	Amino acid transporter
Solyc12g019410.3	-1,54	2,90E-06	1,97E-05	Protein kinase domain
Solyc04g082210.3	-1,54	2,20E-07	1,77E-06	NADH-ubiquinone oxidoreductase chain
Solyc11g066890.1	-1,54	3,22E-10	3,79E-09	Arogenate dehydratase
Solyc08g082670.4	-1,54	3,26E-07	2,56E-06	Cellulose synthase
Solyc04g015610.3	-1,54	4,64E-03	1,59E-02	DUF642 domain-containing protein
Solyc02g087640.3	-1,54	4,63E-12	6,62E-11	Protein arginine methyltransferase NDUFAF7
Solyc07g048040.1	-1,54	8,99E-14	1,53E-12	Calcium-dependent lipid-binding domain-containing protein
Solyc01g011350.3	-1,54	2,97E-11	3,89E-10	DUF3755 domain-containing protein
Solyc09g083260.4	-1,55	4,28E-09	4,39E-08	Ion channel pollux-like protein
Solyc08g082470.1	-1,55	4,73E-05	2,62E-04	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Solyc05g050380.4	-1,55	5,88E-12	8,29E-11	Cyclic nucleotide-gated ion channel 1
Solyc11g007140.2	-1,55	3,84E-08	3,46E-07	Major facilitator superfamily
Solyc02g038806.1	-1,55	2,47E-10	2,95E-09	MLO-like protein
Solyc02g091620.3	-1,55	3,98E-03	1,39E-02	MUTL protein homolog 3
Solyc01g094650.4	-1,55	2,30E-03	8,63E-03	protein PAIR1 isoform X2
Solyc12g097010.1	-1,55	1,86E-03	7,13E-03	Disease resistance protein (TIR-NBS-LRR class)
Solyc12g010430.1	-1,55	7,70E-08	6,59E-07	hypothetical protein
Solyc07g056510.3	-1,55	9,13E-03	2,83E-02	Glutathione S-transferase-like protein
Solyc01g081620.3	-1,55	1,17E-02	3,49E-02	Vacuolar protein sorting-associated protein 62
Solyc05g050360.3	-1,55	2,19E-10	2,63E-09	Cyclic nucleotide-gated ion channel 1
Solyc01g005420.2	-1,55	9,29E-09	9,12E-08	C2 calcium-dependent membrane targeting
Solyc04g150163.1	-1,55	1,49E-07	1,23E-06	Unknown protein
Solyc01g095110.4	-1,55	9,91E-08	8,38E-07	Pentatricopeptide repeat-containing protein
Solyc01g109880.3	-1,56	7,16E-06	4,58E-05	BZIP transcription factor
Solyc02g080070.3	-1,56	3,10E-10	3,66E-09	Cysteine-rich receptor-like protein kinase 29
Solyc06g043070.4	-1,56	2,45E-07	1,95E-06	hypothetical protein
Solyc07g006500.3	-1,56	8,28E-14	1,42E-12	trehalose-6-phosphate synthase 1
Solyc11g068470.3	-1,56	2,14E-06	1,49E-05	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc05g012100.3	-1,56	1,02E-11	1,40E-10	Fructokinase-like protein 2
Solyc08g079850.3	-1,56	4,26E-08	3,81E-07	Subtilisin-like protease
Solyc11g072040.2	-1,56	4,73E-09	4,83E-08	GDSL esterase/lipase
Solyc02g089270.1	-1,56	6,25E-06	4,04E-05	Unknown protein
Solyc09g090510.3	-1,57	3,44E-14	6,11E-13	Cyclopropane-fatty-acyl-phospholipid synthase
Solyc09g090540.3	-1,57	1,88E-06	1,32E-05	hypothetical protein
Solyc07g054790.1	-1,57	7,39E-03	2,36E-02	Wound-responsive family protein
Solyc04g082450.3	-1,57	2,70E-08	2,48E-07	Integral membrane protein hemolysin-III-like protein
Solyc09g011610.3	-1,57	2,77E-03	1,02E-02	Glutathione S-transferase
Solyc11g008060.1	-1,57	3,63E-06	2,44E-05	Pullulanase 1, chloroplastic
Solyc09g090230.2	-1,57	1,13E-04	5,80E-04	Casein kinase I
Solyc05g006040.4	-1,57	8,91E-08	7,59E-07	Serine/Threonine-kinase
Solyc02g085560.3	-1,57	9,14E-07	6,69E-06	DNA-directed RNA polymerase III subunit Rpc5

Solyc04g047690.4	-1,57	6,56E-06	4,23E-05	Vesicle transport protein
Solyc12g009880.1	-1,57	3,37E-11	4,37E-10	Serine-rich protein
Solyc12g099810.2	-1,58	9,07E-08	7,72E-07	CRT (Chloroquine-resistance transporter)-like transporter
Solyc11g073080.3	-1,58	1,71E-03	6,62E-03	Methyl-CpG-binding domain-containing protein 6
Solyc07g014620.1	-1,58	7,48E-07	5,55E-06	Small auxin up-regulated RNA63
Solyc05g041920.3	-1,58	3,58E-09	3,71E-08	Dicer-like 3
Solyc03g114175.1	-1,58	6,86E-04	2,95E-03	Glycosyltransferase
Solyc10g086210.2	-1,58	8,10E-09	8,01E-08	translin-like
Solyc01g107580.4	-1,58	2,17E-07	1,74E-06	Pseudouridine synthase family protein
Solyc02g070100.3	-1,58	1,45E-08	1,38E-07	RNA helicase DEAD7
Solyc05g054480.3	-1,58	3,74E-10	4,37E-09	Actin
Solyc05g009230.3	-1,58	8,21E-05	4,34E-04	MYB transcription factor
Solyc10g076840.2	-1,59	8,42E-10	9,53E-09	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc11g007800.3	-1,59	1,61E-05	9,75E-05	Ribonucleases P/MRP protein subunit POP1
Solyc09g065590.3	-1,59	2,63E-10	3,13E-09	Auxin canalization protein (DUF828)
Solyc12g042300.2	-1,59	2,35E-05	1,38E-04	Major facilitator superfamily domain, general substrate transporter
Solyc09g090690.4	-1,59	4,11E-05	2,31E-04	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc09g092340.4	-1,59	1,76E-07	1,43E-06	Werner Syndrome-like exonuclease
Solyc08g083060.3	-1,59	6,53E-19	1,70E-17	Metal-nicotianamine transporter YSL1
Solyc05g052820.3	-1,59	5,84E-11	7,46E-10	proline transporter 3
Solyc02g077070.3	-1,59	3,69E-03	1,31E-02	Unknown protein
Solyc03g043740.4	-1,59	1,03E-08	1,01E-07	Hydroxyproline-rich glycoprotein family protein
Solyc06g065800.3	-1,59	4,29E-08	3,83E-07	Mitochondrial glycoprotein
Solyc04g077870.3	-1,59	8,28E-10	9,39E-09	Calcium-transporting ATPase
Solyc02g063220.3	-1,59	3,98E-12	5,73E-11	Mannose-6-phosphate isomerase
Solyc01g105070.3	-1,60	1,32E-04	6,64E-04	LECEVI16G peroxidase precursor
Solyc06g065330.4	-1,60	6,85E-11	8,67E-10	Receptor-like proteiny region, transmembrane domain-and RING domain-containing protein 2
Solyc04g051490.3	-1,60	5,62E-03	1,87E-02	Crossover junction endonuclease EME1B
Solyc08g006830.3	-1,60	3,42E-11	4,44E-10	Caffeoyl-CoA O-methyltransferase
Solyc09g089890.1	-1,60	1,45E-03	5,72E-03	RING/U-box superfamily protein
Solyc06g072620.4	-1,60	2,80E-05	1,63E-04	Bidirectional sugar transporter SWEET
Solyc01g087850.2	-1,60	7,89E-07	5,84E-06	serine protease SBT3
Solyc04g078120.3	-1,60	9,47E-10	1,07E-08	protein arginine N-methyltransferase 2
Solyc04g057970.3	-1,60	9,46E-06	5,94E-05	hypothetical protein
Solyc04g040130.1	-1,60	1,70E-04	8,37E-04	Fatty acid desaturase
Solyc03g119950.1	-1,60	5,35E-10	6,17E-09	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc10g085580.3	-1,60	3,92E-10	4,58E-09	Embryo sac development arrest 7
Solyc01g112000.4	-1,60	3,20E-11	4,16E-10	expansin-like protein precursor 1
Solyc06g074500.2	-1,61	1,06E-04	5,45E-04	DUF868 domain-containing protein
Solyc11g010420.3	-1,61	3,95E-06	2,64E-05	Dihydrofolate reductase-like protein
Solyc11g018560.2	-1,61	5,29E-09	5,36E-08	50S ribosomal protein L25
Solyc04g011530.3	-1,61	4,52E-09	4,62E-08	Cytochrome oxidase complex assembly protein
Solyc06g008920.3	-1,61	8,23E-14	1,41E-12	AMP-dependent synthetase/ligase
Solyc03g116510.1	-1,61	1,10E-03	4,49E-03	DUF761 domain-containing protein
Solyc01g006240.3	-1,61	9,25E-04	3,85E-03	Inactive protein restricted tev movement 1
Solyc09g090970.4	-1,61	3,16E-03	1,14E-02	pathogenesis-related protein STH-2-like
Solyc12g005860.2	-1,61	4,44E-20	1,24E-18	Aconitate hydratase
Solyc07g054310.3	-1,61	9,04E-03	2,81E-02	Cell wall protein
Solyc11g068430.3	-1,61	1,10E-07	9,21E-07	Ferredoxin
Solyc02g086360.3	-1,62	2,24E-10	2,69E-09	Octicosapeptide/Phox/Bem1p family protein
Solyc01g081400.3	-1,62	4,67E-12	6,67E-11	B3 domain-containing protein
Solyc06g054090.2	-1,62	2,67E-08	2,46E-07	N-acetyltransferase
Solyc07g007930.3	-1,62	5,06E-13	7,96E-12	Raffinose synthase family protein
Solyc02g069110.4	-1,62	1,41E-09	1,56E-08	Cathepsin B-like cysteine proteinase
Solyc05g010045.1	-1,62	9,10E-03	2,83E-02	Unknown protein
Solyc09g011330.3	-1,62	3,44E-10	4,03E-09	Receptor protein kinase ZmPK1
Solyc01g111420.3	-1,62	1,30E-09	1,43E-08	Ribosomal protein L1
Solyc05g051460.3	-1,62	1,36E-10	1,67E-09	Homeobox-leucine zipper protein HOX4
Solyc10g076820.2	-1,62	6,64E-06	4,27E-05	Transcription factor DIVARICATA
Solyc03g098240.3	-1,62	1,94E-05	1,16E-04	glutamate decarboxylase
Solyc08g062950.4	-1,63	5,79E-07	4,36E-06	Cytochrome P450 family protein
Solyc02g085300.4	-1,63	8,50E-16	1,73E-14	Unknown protein
Solyc09g075300.3	-1,63	8,71E-15	1,62E-13	Epoxide hydrolase 2
Solyc05g012200.3	-1,63	3,35E-04	1,55E-03	Asparagine synthase family protein
Solyc01g094380.2	-1,63	3,92E-03	1,38E-02	O-glucosyltransferase rumi-like protein
Solyc12g009300.3	-1,63	3,21E-12	4,67E-11	fruit sucrose synthase
Solyc01g008160.4	-1,63	3,51E-09	3,65E-08	Protein SLOW GREEN 1, chloroplastic
Solyc12g100260.1	-1,63	8,95E-05	4,69E-04	Fatty acid desaturase
Solyc12g098225.1	-1,63	1,17E-02	3,47E-02	glycine-rich cell wall structural protein
Solyc11g040040.2	-1,63	1,04E-09	1,17E-08	Phototropic-responsive NPH3 family protein
Solyc01g080800.3	-1,64	4,31E-08	3,84E-07	Basic secretory family protein
Solyc06g071260.4	-1,64	1,31E-07	1,10E-06	BnaA06g17060D protein
Solyc09g075030.3	-1,64	3,03E-13	4,90E-12	nucleolar protein 16-like
Solyc11g017010.2	-1,64	6,51E-12	9,13E-11	SISUT1,Pfam:PF13347
Solyc10g007930.4	-1,64	8,93E-12	1,23E-10	Cytochrome
Solyc02g084830.4	-1,64	1,21E-04	6,18E-04	Pentatricopeptide repeat-containing protein
Solyc04g009790.4	-1,64	3,45E-16	7,24E-15	Protein DETOXIFICATION
Solyc05g018230.4	-1,64	4,47E-14	7,83E-13	Sugar transporter protein 12
Solyc01g008290.3	-1,64	2,08E-09	2,25E-08	Dihydroorotate dehydrogenase (quinone), mitochondrial
Solyc06g069430.3	-1,64	3,42E-11	4,43E-10	FRUITFULL-like MADS-box 1
Solyc11g032120.2	-1,64	7,29E-03	2,34E-02	histone H3-like centromeric protein HTR12
Solyc10g009360.4	-1,64	1,58E-03	6,17E-03	Dof zinc finger protein
Solyc07g007180.4	-1,64	1,83E-14	3,32E-13	RING U-box superfamily protein
Solyc09g066150.2	-1,64	4,40E-09	4,50E-08	Cytochrome P450
Solyc05g007770.3	-1,64	1,49E-10	1,81E-09	NAC domain TF
Solyc07g017410.3	-1,65	4,29E-10	4,99E-09	hypothetical protein
Solyc06g071180.3	-1,65	2,81E-07	2,22E-06	Dynein light chain
Solyc02g071740.3	-1,65	2,47E-17	5,71E-16	MAP kinase kinase kinase 16
Solyc01g111600.3	-1,65	7,60E-18	1,84E-16	Heavy metal-associated isoprenylated plant protein
Solyc06g005300.4	-1,65	3,84E-07	2,98E-06	UPA23
Solyc08g067000.3	-1,65	3,62E-04	1,66E-03	muscle M-line assembly protein unc-89
Solyc07g049270.4	-1,65	1,86E-05	1,11E-04	RNA-binding protein
Solyc12g008800.3	-1,65	7,97E-06	5,05E-05	Transcription factor DIVARICATA
Solyc01g066260.2	-1,65	8,51E-06	5,37E-05	Unknown protein
Solyc04g007900.3	-1,65	2,30E-06	1,59E-05	protein PLANT CADMIUM RESISTANCE 2-like
Solyc07g014590.4	-1,65	2,51E-08	2,32E-07	Isoamylase 1, chloroplastic
Solyc01g079600.4	-1,65	9,38E-09	9,20E-08	Alpha/beta-Hydrolases superfamily protein
Solyc05g008000.3	-1,66	7,96E-09	7,88E-08	RNA pyrophosphohydrolase
Solyc04g076260.2	-1,66	1,08E-09	1,21E-08	thionin-like protein
Solyc04g008870.3	-1,66	2,49E-10	2,97E-09	Transcription factor DIVARICATA
Solyc02g078330.3	-1,66	3,39E-04	1,56E-03	Pentatricopeptide repeat
Solyc12g027540.3	-1,66	1,02E-08	9,98E-08	Unknown protein
Solyc03g097020.4	-1,66	8,88E-06	5,59E-05	ATPase family AAA domain-containing protein 3-like
Solyc02g070385.1	-1,66	1,94E-08	1,83E-07	Unknown protein
Solyc02g081680.4	-1,66	1,06E-05	6,58E-05	Nucleolar complex protein 2-like protein
Solyc05g005680.3	-1,66	9,69E-04	4,02E-03	Xyloglucan endotransglucosylase/hydrolase
Solyc07g042510.3	-1,66	4,89E-04	2,18E-03	Bax inhibitor 1-related
Solyc07g052700.3	-1,66	4,88E-12	6,94E-11	MADS-box transcription factor
Solyc12g005940.2	-1,66	1,07E-08	1,04E-07	1-aminocyclopropane-1-carboxylate oxidase 2
Solyc03g098480.1	-1,66	1,27E-10	1,56E-09	chromosome alignment-maintaining phosphoprotein 1-like isoform X2
Solyc11g020720.1	-1,66	3,64E-04	1,67E-03	Hydrolase-like protein family
Solyc06g063060.3	-1,66	3,10E-04	1,44E-03	Dormancy/auxin associated protein
Solyc12g056960.2	-1,66	7,74E-12	1,08E-10	putative glucan 1,3-beta-glucosidase
Solyc03g062710.4	-1,67	2,68E-17	6,17E-16	protein NDH-DEPENDENT CYCLIC ELECTRON FLOW 5

Solyc07g062730.1	-1,67	1,01E-04	5,25E-04	Serine/Threonine-kinase pakA-like protein
Solyc05g016320.2	-1,67	1,59E-02	4,50E-02	Exostosin-like
Solyc07g005800.2	-1,67	7,18E-05	3,84E-04	Multipolar spindle 1
Solyc09g009790.4	-1,67	2,88E-07	2,28E-06	Pentatricopeptide repeat
Solyc12g096960.2	-1,67	1,07E-02	3,24E-02	Major allergen Pru ar 1
Solyc10g078440.2	-1,67	1,56E-07	1,28E-06	Sigma factor binding protein 1, chloroplastic
Solyc06g051830.3	-1,67	3,19E-05	1,83E-04	Potassium transporter
Solyc01g103640.4	-1,67	2,59E-04	1,23E-03	Plant organelle RNA recognition domain
Solyc10g006920.3	-1,67	3,63E-03	1,29E-02	CBS domain
Solyc02g079210.3	-1,68	2,10E-12	3,13E-11	Multiple organellar RNA editing factor 5, mitochondrial
Solyc01g006170.4	-1,68	5,00E-08	4,42E-07	Eukaryotic rRNA processing
Solyc07g063230.3	-1,68	2,30E-15	4,46E-14	Choline transporter-like protein
Solyc01g081040.4	-1,68	1,27E-07	1,06E-06	RING/U-box superfamily protein
Solyc02g091850.1	-1,68	9,94E-05	5,16E-04	Unknown protein
Solyc06g062610.2	-1,68	1,06E-04	5,45E-04	Pentatricopeptide repeat
Solyc02g064950.3	-1,68	3,97E-19	1,05E-17	CBS domain-containing protein
Solyc02g078890.1	-1,68	1,41E-07	1,17E-06	BnaA08g25420D protein
Solyc02g090820.3	-1,68	1,55E-15	3,07E-14	Heat stress transcription factor B-1
Solyc01g079320.4	-1,68	1,49E-05	9,05E-05	Pentatricopeptide repeat
Solyc06g005840.4	-1,68	3,77E-04	1,72E-03	Mitochondrial import inner membrane translocase subunit TIM10
Solyc05g051480.2	-1,68	4,16E-04	1,88E-03	Unknown protein
Solyc02g068760.4	-1,68	2,29E-06	1,58E-05	Pentatricopeptide repeat-containing protein
Solyc08g082650.2	-1,68	1,00E-04	5,20E-04	Cellulose synthase
Solyc06g075360.3	-1,69	6,92E-09	6,90E-08	Tetraspanin-3
Solyc01g060420.2	-1,69	2,58E-03	9,57E-03	Zinc finger protein 8
Solyc09g061760.1	-1,69	1,86E-05	1,12E-04	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc01g006180.4	-1,69	2,67E-10	3,17E-09	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc02g079780.1	-1,69	3,70E-11	4,79E-10	hypothetical protein
Solyc06g005430.1	-1,69	4,69E-12	6,68E-11	Histone H4
Solyc01g100800.2	-1,69	9,04E-05	4,73E-04	Pentatricopeptide repeat
Solyc06g064880.3	-1,69	8,49E-07	6,26E-06	Nitrilase family protein (Carbon-nitrogen hydrolase)
Solyc01g010290.4	-1,69	1,05E-17	2,52E-16	Ureide permease
Solyc12g094610.3	-1,69	1,05E-02	3,18E-02	RING-type E3 ubiquitin transferase
Solyc06g084020.4	-1,69	1,62E-19	4,38E-18	histone H1
Solyc01g005280.3	-1,69	8,39E-06	5,30E-05	Sec14p-like phosphatidylinositol transfer family protein
Solyc07g054760.1	-1,69	1,07E-09	1,20E-08	Wound-responsive family protein
Solyc04g053145.1	-1,70	5,57E-08	4,88E-07	transmembrane protein
Solyc04g077780.3	-1,70	1,50E-14	2,74E-13	LIM domain-containing protein
Solyc12g036800.1	-1,70	3,33E-05	1,90E-04	Receptor like protein
Solyc06g075350.3	-1,70	2,08E-08	1,95E-07	tRNA-splicing endonuclease subunit Sen2-2
Solyc07g063170.1	-1,70	2,08E-04	1,01E-03	Unknown protein
Solyc05g054140.3	-1,70	7,58E-13	1,18E-11	DNA-directed RNA polymerase
Solyc11g069800.1	-1,71	1,71E-12	2,57E-11	Allene oxide synthase, chloroplastic
Solyc12g011140.3	-1,71	4,18E-06	2,78E-05	Subtilisin-like protease
Solyc05g009520.2	-1,71	5,42E-06	3,54E-05	hypothetical protein
Solyc12g038370.2	-1,71	6,91E-09	6,89E-08	Single-stranded DNA-binding protein
Solyc09g061340.1	-1,71	3,34E-06	2,25E-05	Pentatricopeptide repeat
Solyc02g093600.3	-1,71	3,00E-03	1,09E-02	Class I heat shock protein
Solyc06g072080.3	-1,71	2,55E-08	2,36E-07	ubiquitin activating enzyme
Solyc01g005470.3	-1,71	2,13E-05	1,26E-04	protein PLANT CADMIUM RESISTANCE 2-like
Solyc09g091830.4	-1,71	2,73E-14	4,90E-13	plastid transcriptionally active 5
Solyc10g080610.1	-1,71	4,11E-07	3,18E-06	F-box/kelch-repeat protein At1g15670-like
Solyc12g017460.1	-1,71	1,08E-10	1,34E-09	GDSL esterase/lipase At5g03980-like
Solyc10g011910.4	-1,71	2,96E-04	1,38E-03	WRKY transcription factor 25
Solyc03g121850.3	-1,71	4,58E-09	4,68E-08	hypothetical protein
Solyc05g007100.3	-1,71	1,25E-08	1,20E-07	Single-stranded DNA-binding protein WHY1, chloroplastic
Solyc01g079950.3	-1,71	4,20E-05	2,35E-04	Eukaryotic aspartyl protease family protein
Solyc09g090300.3	-1,71	7,41E-05	3,95E-04	dCTP pyrophosphatase-like protein
Solyc07g045340.4	-1,71	9,29E-08	7,89E-07	RPM1-interacting protein 4
Solyc07g064100.1	-1,71	4,46E-11	5,73E-10	Chlororespiratory reduction 41
Solyc07g052350.3	-1,71	5,81E-23	1,94E-21	Aconitate hydratase
Solyc12g088670.2	-1,71	8,91E-17	1,96E-15	cysteine protease CYP1
Solyc09g090600.3	-1,71	1,42E-02	4,11E-02	acid phosphatase 1-like
Solyc07g006990.3	-1,72	5,68E-03	1,89E-02	Pentatricopeptide repeat-containing protein
Solyc02g038815.1	-1,72	1,34E-03	5,35E-03	tail-anchored protein insertion receptor WRB-like protein
Solyc02g065350.3	-1,72	2,16E-09	2,33E-08	B3 domain-containing protein
Solyc01g009720.2	-1,72	1,11E-04	5,67E-04	E3 ubiquitin protein ligase DRIP2
Solyc04g005860.3	-1,72	2,14E-21	6,47E-20	Protein ENHANCED DISEASE RESISTANCE 2
Solyc05g054530.1	-1,72	5,56E-08	4,87E-07	transmembrane protein
Solyc01g109590.3	-1,72	4,72E-12	6,72E-11	Protein kinase domain
Solyc04g081060.3	-1,72	4,31E-03	1,49E-02	Kinesin-like protein NACK1
Solyc02g079220.4	-1,72	3,38E-11	4,38E-10	Sugar transporter protein 1
Solyc01g007140.3	-1,72	9,10E-06	5,72E-05	ARM repeat superfamily protein
Solyc04g015480.3	-1,72	1,10E-16	2,40E-15	BTB/POZ domain protein TNFAIP protein
Solyc12g087940.2	-1,73	1,30E-05	7,98E-05	Eukaryotic aspartyl protease family protein
Solyc03g113480.1	-1,73	1,79E-04	8,80E-04	extensin-like protein
Solyc11g065030.3	-1,73	2,14E-12	3,17E-11	GDP-mannose transporter
Solyc12g019540.2	-1,73	1,84E-05	1,10E-04	Unknown protein
Solyc03g114970.3	-1,73	1,11E-17	2,64E-16	Protein SPIRAL1
Solyc06g062370.4	-1,73	5,81E-04	2,54E-03	acid phosphatase 1-like
Solyc10g081590.2	-1,73	9,65E-09	9,46E-08	Protein-lysine N-methyltransferase
Solyc08g077120.2	-1,73	1,26E-16	2,73E-15	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc04g072000.4	-1,73	1,11E-05	6,89E-05	Chitinase
Solyc02g092290.4	-1,73	2,15E-12	3,18E-11	F-box/RNI-like superfamily protein
Solyc08g078210.3	-1,73	2,28E-19	6,09E-18	Nudix hydrolase 8
Solyc08g066570.3	-1,73	9,62E-15	1,78E-13	Regulator of chromosome condensation (RCC1) family protein
Solyc02g081770.2	-1,73	4,78E-03	1,63E-02	HXXXD-type acyl-transferase family protein
Solyc06g051250.1	-1,73	3,16E-09	3,32E-08	RING/U-box superfamily protein
Solyc07g005910.3	-1,73	1,57E-04	7,82E-04	Zein-binding domain-containing protein
Solyc05g006610.4	-1,73	8,95E-06	5,63E-05	CLAVATA3/ESR (CLE)-related protein 25-like
Solyc02g077910.4	-1,74	6,11E-13	9,54E-12	Mitochondrial substrate carrier family protein
Solyc05g050580.3	-1,74	1,33E-14	2,43E-13	E3 ubiquitin-protein ligase
Solyc09g008830.3	-1,74	5,46E-11	6,98E-10	Sequence-specific DNA binding transcription factor
Solyc03g062740.4	-1,74	2,50E-08	2,32E-07	Unknown protein
Solyc02g071280.3	-1,74	4,99E-18	1,22E-16	Ribosome maturation factor RimM
Solyc02g072400.1	-1,74	6,36E-04	2,75E-03	LRR receptor-like serine/threonine-protein kinase EFR
Solyc04g056425.1	-1,74	3,35E-09	3,49E-08	basic leucine zipper/W2 domain protein
Solyc12g014230.2	-1,74	1,04E-11	1,43E-10	Multiple organellar RNA editing factor 8, chloroplastic/mitochondrial
Solyc09g083110.3	-1,74	3,20E-05	1,83E-04	Pentatricopeptide repeat-containing protein
Solyc10g007940.1	-1,74	5,16E-03	1,74E-02	Pentatricopeptide repeat-containing protein
Solyc06g005795.2	-1,74	2,84E-05	1,65E-04	Non-specific lipid-transfer protein
Solyc02g090690.3	-1,74	5,12E-04	2,27E-03	Membrane protein
Solyc11g013310.2	-1,75	1,67E-06	1,17E-05	Auxin transporter-like protein 3
Solyc03g116540.1	-1,75	2,83E-04	1,33E-03	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc08g076520.3	-1,75	7,97E-13	1,23E-11	ribosome maturation factor
Solyc10g005770.4	-1,75	1,11E-09	1,23E-08	Protein kinase G11A
Solyc04g074680.1	-1,75	2,72E-03	1,00E-02	chromodomain-helicase-DNA-binding protein 9-like
Solyc05g052640.3	-1,75	2,29E-15	4,45E-14	Peroxisomal nicotinamide adenine dinucleotide carrier
Solyc04g054370.1	-1,75	6,07E-08	5,28E-07	RING/U-box superfamily protein
Solyc02g089350.3	-1,75	1,48E-17	3,50E-16	Gibberellin regulated protein
Solyc02g087560.1	-1,75	1,85E-11	2,47E-10	Pentatricopeptide repeat
Solyc07g009220.2	-1,75	7,87E-06	4,99E-05	Pentatricopeptide repeat-containing protein
Solyc07g032250.4	-1,75	2,40E-10	2,87E-09	nucleophosmin
Solyc06g073690.2	-1,75	1,42E-07	1,18E-06	Transducin/WD40 repeat-like superfamily protein

Solyc03g097160.4	-1,75	1,78E-11	2,37E-10	WD40 repeat
Solyc07g045180.4	-1,76	5,42E-14	9,46E-13	Zinc finger protein CONSTANS-LIKE 9
Solyc07g009520.2	-1,76	8,39E-04	3,52E-03	WEB family protein At4g27595, chloroplastic-like
Solyc08g061970.3	-1,76	3,24E-13	5,22E-12	putative spermine synthase,Pfam:PF01564
Solyc02g077420.3	-1,76	2,90E-08	2,65E-07	Phospholipase A1-II 1
Solyc03g007350.1	-1,76	6,09E-04	2,64E-03	Pentatricopeptide repeat
Solyc10g080010.2	-1,76	2,24E-11	2,97E-10	Glycosyltransferase family 61 protein
Solyc03g026360.1	-1,76	1,14E-03	4,65E-03	Peptidoglycan-binding LysM domain-containing protein
Solyc09g092240.3	-1,76	7,44E-06	4,75E-05	small subunit processome component 20 homolog isoform X1
Solyc06g062420.4	-1,76	8,52E-03	2,67E-02	Unknown protein
Solyc03g121070.3	-1,76	3,78E-14	6,68E-13	hexokinase
Solyc08g067610.3	-1,76	1,58E-05	9,59E-05	Pleiotropic drug resistance protein
Solyc02g062700.3	-1,76	5,99E-08	5,22E-07	ATPase family AAA domain-containing protein 3-like
Solyc01g066040.2	-1,76	1,21E-02	3,57E-02	Unknown protein
Solyc02g071560.4	-1,77	2,83E-06	1,92E-05	Subtilisin-like protease
Solyc04g049090.3	-1,77	3,81E-18	9,40E-17	SlMlo1
Solyc06g075470.3	-1,77	1,12E-04	5,74E-04	Nucleoside diphosphate kinase
Solyc03g112090.3	-1,77	5,88E-07	4,43E-06	High-affinity nitrate transporter
Solyc08g077140.1	-1,77	5,65E-13	8,84E-12	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc02g081840.4	-1,77	2,48E-10	2,96E-09	translocator assembly/maintenance protein
Solyc09g090350.3	-1,77	3,69E-06	2,47E-05	Long-chain-alcohol oxidase
Solyc07g066020.2	-1,77	2,90E-18	7,22E-17	Amino acid permease
Solyc07g047890.4	-1,77	9,15E-09	9,00E-08	Sterile alpha motif (SAM) domain-containing protein
Solyc05g007910.3	-1,77	1,16E-09	1,29E-08	50S ribosomal protein L18, chloroplastic
Solyc06g053850.4	-1,78	2,02E-04	9,79E-04	Pentatricopeptide repeat
Solyc09g082220.1	-1,78	1,69E-04	8,35E-04	Acyl-CoA N-acyltransferases (NAT) superfamily protein
Solyc01g081110.4	-1,78	4,96E-04	2,20E-03	Pentatricopeptide repeat
Solyc09g014930.1	-1,78	1,23E-04	6,28E-04	Pentatricopeptide repeat
Solyc02g065570.1	-1,78	2,11E-08	1,98E-07	DVL1
Solyc02g062910.3	-1,78	1,88E-11	2,50E-10	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc11g066010.2	-1,78	2,33E-08	2,17E-07	60S ribosomal protein L36
Solyc01g099000.1	-1,78	5,02E-06	3,30E-05	Pentatricopeptide repeat-containing protein
Solyc11g007940.2	-1,78	2,47E-07	1,96E-06	Protein BTR1
Solyc04g011910.3	-1,78	1,41E-03	5,57E-03	sorbin/SH3 domain protein
Solyc03g093240.4	-1,78	4,09E-18	1,01E-16	nitric oxide synthase 1
Solyc01g099230.3	-1,78	5,51E-07	4,17E-06	Zinc finger protein VAR3, chloroplastic
Solyc02g079790.3	-1,78	2,45E-07	1,95E-06	DUF538 domain-containing protein
Solyc01g100600.4	-1,78	1,28E-08	1,23E-07	LATE TERMINATION
Solyc02g081470.4	-1,78	8,22E-05	4,35E-04	Receptor-like protein kinase
Solyc08g016270.3	-1,78	1,72E-03	6,67E-03	LOW QUALITY PROTEIN: LRR receptor-like serine/threonine-protein kinase GSO1
Solyc07g008540.3	-1,78	4,11E-12	5,91E-11	Zinc finger protein CONSTANS-LIKE 2
Solyc10g076810.1	-1,78	1,24E-10	1,53E-09	3'-5' exonuclease domain
Solyc07g053550.3	-1,79	2,90E-10	3,43E-09	Glutaredoxin-C9
Solyc02g077330.3	-1,79	4,34E-11	5,58E-10	GDSL esterase/lipase
Solyc07g008620.1	-1,79	2,50E-10	2,97E-09	EIX receptor 1
Solyc12g011033.1	-1,79	3,82E-06	2,55E-05	Lipoxygenase
Solyc11g010730.3	-1,79	5,55E-13	8,71E-12	Receptor-like cytosolic serine/threonine-protein kinase RBK1
Solyc07g055040.1	-1,79	3,91E-05	2,20E-04	Agenet-like domain-containing protein
Solyc11g065340.2	-1,79	6,91E-04	2,96E-03	Transposase, Ptta/En/Spm, plant
Solyc09g066100.3	-1,79	4,98E-21	1,49E-19	Histone H1
Solyc01g049810.4	-1,79	1,53E-03	6,01E-03	Pentatricopeptide repeat
Solyc02g067710.3	-1,80	7,82E-04	3,31E-03	ARM repeat superfamily protein
Solyc02g077840.2	-1,80	1,14E-03	4,64E-03	Ethylene-responsive transcription factor 4
Solyc11g068950.3	-1,80	9,07E-21	2,67E-19	BEL1-like homeodomain protein 1
Solyc04g074400.1	-1,80	6,53E-03	2,13E-02	Protein EXORDIUM
Solyc02g091640.3	-1,80	2,02E-06	1,41E-05	Endoribonuclease E-like protein
Solyc02g081880.3	-1,80	1,28E-25	4,88E-24	Molybdenum cofactor sulfurase
Solyc10g074785.1	-1,80	3,46E-03	1,23E-02	Unknown protein
Solyc01g090710.3	-1,80	1,29E-04	6,52E-04	cytosolic malate dehydrogenase
Solyc03g007170.3	-1,80	5,27E-08	4,64E-07	Peptidylprolyl isomerase
Solyc10g007350.4	-1,80	1,32E-21	4,05E-20	Multiprotein bridging factor 1
Solyc04g074450.1	-1,81	2,25E-06	1,56E-05	Protein EXORDIUM-like 1
Solyc06g009810.4	-1,81	4,85E-04	2,16E-03	ethylene-responsive transcription factor CRF1
Solyc08g008170.4	-1,81	3,02E-17	6,90E-16	Calcium-dependent protein kinase
Solyc02g085830.4	-1,81	4,78E-09	4,87E-08	Regulator of Vps4 activity in the MVB pathway protein
Solyc07g042990.1	-1,81	5,53E-11	7,07E-10	Leucine-rich repeat receptor-like protein kinase
Solyc05g012350.4	-1,81	9,34E-05	4,87E-04	Alpha/beta-Hydrolases superfamily protein
Solyc12g009260.3	-1,81	7,77E-04	3,29E-03	3-oxoacyl-[acyl-carrier-protein] synthase
Solyc05g007640.3	-1,81	6,88E-03	2,23E-02	Non-specific serine/threonine protein kinase
Solyc10g054860.2	-1,81	3,78E-06	2,53E-05	Urb2/Npa2 family protein
Solyc04g074167.1	-1,81	1,86E-09	2,02E-08	classical arabinogalactan protein 26-like
Solyc03g006310.4	-1,82	2,37E-09	2,53E-08	Unknown protein
Solyc01g106060.3	-1,82	3,21E-07	2,52E-06	Glutamine amidotransferase
Solyc03g120840.3	-1,82	9,54E-11	1,19E-09	Ethylene-responsive transcription factor TINY
Solyc11g007850.2	-1,82	1,01E-17	2,41E-16	DNA-binding protein PD2
Solyc08g075950.3	-1,82	2,41E-09	2,57E-08	Growth-regulating factor 5
Solyc12g008660.1	-1,82	5,44E-10	6,27E-09	Zinc finger transcription factor 73
Solyc09g007550.3	-1,82	1,72E-11	2,31E-10	Protein indeterminate-domain 12
Solyc07g065810.2	-1,82	2,13E-05	1,26E-04	RING/U-box superfamily protein
Solyc01g102540.3	-1,82	6,60E-17	1,48E-15	hpoxia-induced protein 242
Solyc02g079770.3	-1,82	2,07E-22	6,64E-21	Multiple organellar RNA editing factor 9, chloroplastic
Solyc01g081020.1	-1,82	4,33E-04	1,95E-03	Pentatricopeptide repeat
Solyc01g090680.3	-1,83	8,74E-13	1,35E-11	Uncharacterized conserved protein (UCP012943)
Solyc01g109610.4	-1,83	2,05E-12	3,07E-11	Erythronate-4-phosphate dehydrogenase family protein
Solyc03g117430.3	-1,83	2,97E-21	8,93E-20	Cobalamin biosynthesis protein CobW
Solyc05g053430.3	-1,83	6,03E-09	6,05E-08	DNA-directed RNA polymerase subunit
Solyc05g006130.4	-1,83	1,42E-16	3,06E-15	RNA helicase DEAD17
Solyc11g072730.2	-1,83	7,39E-05	3,94E-04	DNA-directed RNA polymerase subunit
Solyc06g068620.3	-1,83	2,34E-18	5,87E-17	elongation factor
Solyc06g008030.3	-1,83	3,77E-07	2,92E-06	bHLH transcription factor 041
Solyc03g113720.3	-1,83	4,43E-07	3,41E-06	Two-component response regulator ARR3
Solyc08g078560.3	-1,84	3,73E-09	3,85E-08	hypothetical protein
Solyc06g054250.4	-1,84	1,04E-20	3,05E-19	5'-nucleotidase surE-like protein
Solyc06g082910.3	-1,84	2,80E-20	7,98E-19	Formin-like protein
Solyc06g071050.4	-1,84	6,29E-20	1,75E-18	Hypersensitive-induced response protein
Solyc03g119250.4	-1,84	5,46E-12	7,72E-11	Calmodulin binding protein-like
Solyc01g067620.3	-1,84	8,50E-05	4,48E-04	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc01g112070.4	-1,84	1,03E-05	6,45E-05	O-fucosyltransferase family protein
Solyc07g065200.3	-1,85	6,87E-14	1,19E-12	Mitochondrial import inner membrane translocase subunit TIM22-3
Solyc08g081170.4	-1,85	3,42E-18	8,47E-17	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase
Solyc12g096490.1	-1,85	6,16E-04	2,67E-03	Protein GLUTAMINE DUMPER 3
Solyc03g115380.3	-1,85	3,31E-08	3,01E-07	UDP-glucose 6-dehydrogenase
Solyc02g069390.2	-1,85	3,55E-05	2,02E-04	Myb-like domain-containing protein
Solyc11g007230.1	-1,85	1,85E-04	9,04E-04	pentatricopeptide repeat-containing protein At2g27610-like
Solyc02g031790.3	-1,85	3,94E-06	2,63E-05	Receptor-like protein kinase
Solyc01g099750.2	-1,85	1,42E-11	1,91E-10	Heparan-alpha-glucosaminide N-acetyltransferase-like protein (DUF1624)
Solyc04g071120.3	-1,85	1,56E-10	1,90E-09	Protein kinase domain
Solyc07g006770.2	-1,85	3,36E-07	2,63E-06	Receptor-like protein kinase
Solyc12g094550.2	-1,85	1,11E-11	1,51E-10	At1g76250
Solyc03g120610.3	-1,85	1,98E-11	2,63E-10	Cytochrome c-type biogenesis protein
Solyc08g005950.2	-1,85	5,88E-04	2,57E-03	guanine nucleotide-binding protein subunit gamma 2-like
Solyc04g079070.4	-1,85	6,87E-12	9,62E-11	Serine carboxypeptidase
Solyc05g009865.1	-1,85	3,92E-04	1,78E-03	Leucoanthocyanidin reductase
Solyc08g077500.4	-1,86	1,93E-03	7,38E-03	Pleckstrin homology domain

Solyc01g073720.2	-1,86	3,22E-04	1,49E-03	Transmembrane protein
Solyc10g084980.3	-1,86	4,85E-03	1,65E-02	Copper transporter
Solyc06g073560.4	-1,86	8,06E-17	1,78E-15	Isovaleryl-CoA dehydrogenase
Solyc04g005550.2	-1,86	2,96E-04	1,38E-03	Tsw
Solyc08g083500.2	-1,86	5,90E-03	1,95E-02	Cytochrome P450
Solyc09g008630.3	-1,87	5,90E-06	3,83E-05	DNA replication complex GINS protein PSF1
Solyc09g074550.3	-1,87	4,96E-09	5,05E-08	CASP-like protein
Solyc02g083400.3	-1,87	2,86E-11	3,76E-10	RING/U-box superfamily protein
Solyc02g088790.3	-1,87	5,69E-13	8,91E-12	RNA-binding protein
Solyc03g114150.3	-1,87	3,10E-24	1,11E-22	Aldehyde dehydrogenase
Solyc06g084190.3	-1,87	1,04E-02	3,15E-02	Non-specific lipid-transfer protein-like protein
Solyc09g048970.3	-1,87	2,72E-11	3,59E-10	DNA-directed RNA polymerase V subunit 7
Solyc01g006850.1	-1,87	4,54E-03	1,56E-02	Pentatricopeptide repeat
Solyc05g026600.3	-1,87	4,13E-03	1,44E-02	Terpene synthase
Solyc08g081890.4	-1,87	4,65E-06	3,07E-05	ABC transporter C family member 10
Solyc02g088340.4	-1,88	1,07E-13	1,81E-12	WRKY transcription factor 3
Solyc02g070390.3	-1,88	5,92E-19	1,55E-17	protein PLASTID TRANSCRIPTIONALLY ACTIVE 12
Solyc05g011980.4	-1,88	4,17E-11	5,38E-10	Unknown protein
Solyc06g083270.3	-1,88	6,75E-06	4,34E-05	ER lumen protein retaining receptor
Solyc01g100580.3	-1,88	3,14E-13	5,07E-12	Pentatricopeptide repeat
Solyc10g076480.2	-1,88	1,95E-06	1,36E-05	Ammonium transporter
Solyc07g005410.3	-1,88	1,22E-02	3,59E-02	Cytochrome c oxidase%2C subunit Vib family protein
Solyc06g005090.3	-1,88	1,76E-05	1,06E-04	LOB domain-containing protein
Solyc07g054460.4	-1,88	2,13E-14	3,85E-13	H/ACA ribonucleoprotein complex non-core subunit NAF1
Solyc06g069400.4	-1,88	7,02E-14	1,21E-12	Isoaspartyl peptidase/L-asparaginase
Solyc11g008040.3	-1,89	1,05E-05	6,54E-05	Pullulanase 1, chloroplastic
Solyc10g080670.2	-1,89	2,75E-13	4,45E-12	Transmembrane protein, putative
Solyc11g005650.1	-1,89	2,19E-06	1,52E-05	Ubiquitin
Solyc06g050130.3	-1,89	8,84E-16	1,80E-14	Alpha-galactosidase
Solyc08g008320.3	-1,90	8,29E-13	1,28E-11	Membrane insertase
Solyc05g005060.3	-1,90	5,63E-05	3,07E-04	Cysteine-rich receptor-like protein kinase 3
Solyc12g006230.3	-1,90	1,97E-16	4,21E-15	RING/U-box superfamily protein
Solyc05g016060.4	-1,90	4,66E-08	4,14E-07	cysteine-rich and transmembrane domain-containing protein WIH1
Solyc01g110000.3	-1,90	1,11E-20	3,25E-19	Beta-galactosidase
Solyc10g084630.2	-1,90	4,04E-09	4,16E-08	RNA binding protein
Solyc03g093120.5.1	-1,90	1,26E-02	3,71E-02	Xyloglucan endotransglucosylase/hydrolase
Solyc09g082210.4	-1,90	9,01E-12	1,24E-10	DUF581 domain-containing protein
Solyc07g054220.1	-1,90	3,92E-08	3,52E-07	Ethylene-responsive transcription factor
Solyc03g020010.1	-1,91	2,50E-04	1,19E-03	Lemir
Solyc04g074430.2	-1,91	4,80E-04	2,14E-03	Protein EXORDIUM-like 1
Solyc10g078540.3	-1,91	1,35E-08	1,29E-07	H/ACA ribonucleoprotein complex subunit
Solyc10g024410.2	-1,91	4,13E-26	1,61E-24	Ribose-phosphate pyrophosphokinase
Solyc06g007780.3	-1,91	2,66E-14	4,77E-13	Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain-containing protein
Solyc05g005050.3	-1,91	9,57E-05	4,98E-04	Cysteine-rich receptor-like protein kinase 3
Solyc07g045080.3	-1,92	2,60E-10	3,09E-09	2-alkenal reductase (NADP(+)-dependent)-like
Solyc08g078720.3	-1,92	4,26E-13	6,76E-12	14.7 kDa heat shock protein
Solyc10g007360.4	-1,92	1,48E-06	1,05E-05	Protein DETOXIFICATION
Solyc11g066360.2	-1,92	1,62E-05	9,77E-05	Enabled-like protein (DUF1635)
Solyc11g010910.3	-1,92	1,25E-10	1,53E-09	WD40 repeat
Solyc12g044310.2	-1,92	2,05E-15	4,02E-14	Protein NRT1/ PTR FAMILY 1.1
Solyc06g065100.3	-1,92	4,46E-13	7,07E-12	R2R3MYB transcription factor 3
Solyc04g079640.3	-1,92	1,07E-20	3,14E-19	Cytochrome P450
Solyc08g075920.4	-1,92	1,96E-13	3,23E-12	Protein BREVIS RADIX
Solyc05g024160.3	-1,92	2,76E-09	2,92E-08	Pyruvate dehydrogenase E1 component subunit beta
Solyc02g071820.4	-1,92	3,08E-07	2,42E-06	LRR_1 domain-containing protein/Pkinase_Tyr domain-containing protein/Malectin domain-containing protein
Solyc12g007070.2	-1,93	5,90E-12	8,31E-11	Heat shock transcription factor
Solyc01g094600.2	-1,93	5,72E-03	1,90E-02	Pentatricopeptide repeat-containing protein
Solyc07g053520.2	-1,93	1,43E-05	8,71E-05	Pentatricopeptide repeat-containing protein
Solyc12g094385.1	-1,93	1,47E-09	1,61E-08	RING/U-box superfamily protein
Solyc05g053100.3	-1,93	8,87E-12	1,23E-10	Dihydrolipoyl dehydrogenase-like protein
Solyc02g068400.3	-1,93	5,09E-03	1,72E-02	Pectin lyase-like superfamily protein
Solyc01g095680.2	-1,93	9,04E-20	2,49E-18	Plant organelle RNA recognition domain containing protein
Solyc03g093630.3	-1,93	3,85E-04	1,75E-03	Pentatricopeptide repeat-containing protein
Solyc10g045310.2	-1,94	7,21E-21	2,14E-19	DUF3531 domain-containing protein
Solyc06g059870.1	-1,94	1,67E-15	3,28E-14	Unknown protein
Solyc08g007550.1	-1,94	2,08E-04	1,01E-03	Unknown protein
Solyc04g079750.4	-1,94	8,09E-13	1,25E-11	Octanoyltransferase
Solyc01g008300.2	-1,94	3,17E-05	1,82E-04	HXXXD-type acyl-transferase family protein
Solyc03g118170.3	-1,94	1,06E-16	2,32E-15	Glycine--tRNA ligase
Solyc01g107100.3	-1,94	3,50E-05	1,99E-04	beta-1%2C4-xylosidase
Solyc11g008940.1	-1,94	3,17E-13	5,12E-12	Pentatricopeptide repeat-containing protein
Solyc07g053225.1	-1,94	1,30E-02	3,79E-02	Unknown protein
Solyc12g006120.3	-1,94	8,94E-17	1,96E-15	Nuclear transcription factor Y subunit B
Solyc09g010400.3	-1,94	1,57E-19	4,25E-18	Histone H2A
Solyc09g090770.2	-1,94	1,40E-07	1,17E-06	Unknown protein
Solyc03g046410.3	-1,94	2,95E-05	1,71E-04	Unknown protein
Solyc08g080960.4	-1,94	1,78E-08	1,68E-07	AT-hook motif nuclear-localized protein 10
Solyc10g083290.4	-1,95	6,40E-13	9,97E-12	invertase 6
Solyc07g016080.4	-1,95	1,97E-05	1,18E-04	Arginine decarboxylase-like protein
Solyc05g017840.4	-1,95	7,64E-08	6,55E-07	Protein PLANT CADMIUM RESISTANCE like
Solyc10g009130.4	-1,95	3,61E-07	2,81E-06	protein NUCLEAR FUSION DEFECTIVE 6, chloroplastic/mitochondrial -like isoform X1
Solyc07g007220.3	-1,95	1,23E-20	3,59E-19	Protein phosphatase 2C
Solyc11g017240.3	-1,95	2,88E-12	4,20E-11	chorismate mutase
Solyc03g026010.3	-1,95	5,42E-07	4,11E-06	transmembrane protein 161AB protein
Solyc05g051900.3	-1,95	2,97E-15	5,72E-14	Major facilitator superfamily
Solyc12g088050.2	-1,95	1,44E-14	2,63E-13	Rhamnogalacturonate lyase
Solyc12g035710.2	-1,96	4,25E-05	2,37E-04	DUF21 domain-containing protein
Solyc07g055490.4	-1,96	3,99E-04	1,81E-03	Cytochrome
Solyc04g016390.2	-1,96	8,15E-08	6,96E-07	50S ribosomal protein L33
Solyc12g057090.1	-1,96	2,08E-06	1,44E-05	purine permease 3-like
Solyc07g049370.2	-1,96	1,24E-10	1,53E-09	Glucan endo-1,3-beta-glucosidase 3
Solyc03g043860.2	-1,96	6,38E-09	6,39E-08	nudix hydrolase 1
Solyc07g049230.1	-1,96	1,42E-15	2,83E-14	RmlC-like cupins superfamily protein
Solyc06g053210.4	-1,96	5,42E-06	3,54E-05	ubiquitin-60S ribosomal protein L40
Solyc07g052730.3	-1,96	3,24E-08	2,94E-07	formin I2I isoform
Solyc12g008460.2	-1,96	6,18E-11	7,87E-10	Senescence/dehydration-associated protein-related protein
Solyc02g072170.3	-1,96	3,23E-05	1,85E-04	hypothetical protein
Solyc11g067210.1	-1,96	1,61E-02	4,56E-02	Pentatricopeptide repeat-containing protein
Solyc02g080350.1	-1,97	1,10E-03	4,51E-03	Pentatricopeptide repeat-containing protein
Solyc04g072570.3	-1,97	2,17E-15	4,23E-14	Receptor-like kinase
Solyc07g063465.1	-1,97	6,48E-04	2,80E-03	Unknown protein
Solyc05g010555.1	-1,97	8,42E-03	2,64E-02	Unknown protein
Solyc05g009040.3	-1,97	3,51E-09	3,65E-08	Receptor-like protein kinase
Solyc12g097060.1	-1,97	1,54E-03	6,04E-03	golgin subfamily A member 6-like protein 2
Solyc02g063280.4	-1,97	2,26E-12	3,34E-11	stress response protein
Solyc06g070900.3	-1,97	2,79E-14	5,00E-13	TCP transcription factor 17
Solyc08g076230.1	-1,97	8,20E-17	1,81E-15	GAGA-binding transcriptional activator
Solyc01g096430.4	-1,97	2,11E-13	3,48E-12	NADPH:quinone oxidoreductase-like
Solyc02g081390.3	-1,97	2,09E-19	5,62E-18	Lysine-specific histone demethylase 1
Solyc02g088270.3	-1,98	2,61E-05	1,52E-04	hypothetical protein (DUF1997)
Solyc09g025260.4	-1,98	6,45E-12	9,06E-11	Rho termination factor
Solyc01g111840.3	-1,98	1,32E-11	1,78E-10	Major facilitator superfamily protein
Solyc08g081350.2	-1,98	6,83E-03	2,21E-02	Zinc finger protein CONSTANS-LIKE 3

Solyc06g059840.4	-1,99	1,30E-03	5,19E-03	branched chain alpha-keto acid dehydrogenase E1-alpha subunit
Solyc12g008560.1	-1,99	3,95E-15	7,57E-14	Unknown protein
Solyc12g011200.3	-1,99	9,65E-04	4,00E-03	WRKY transcription factor 28
Solyc08g077360.3	-1,99	3,37E-06	2,27E-05	Dynamin
Solyc09g010600.1	-1,99	6,75E-04	2,90E-03	RING/U-box superfamily protein
Solyc09g011420.3	-1,99	9,20E-12	1,27E-10	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein
Solyc07g008650.4	-2,00	3,60E-12	5,19E-11	tRNA-specific adenosine deaminase
Solyc02g067050.3	-2,00	2,76E-12	4,05E-11	UPF0301 protein
Solyc03g006810.3	-2,00	1,28E-06	9,17E-06	Peroxidase
Solyc02g065520.1	-2,00	5,73E-06	3,72E-05	Lyk10
Solyc03g032220.3	-2,01	3,22E-06	2,17E-05	Caffeoyl-CoA O-methyltransferase
Solyc06g068130.3	-2,01	8,91E-05	4,67E-04	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc04g049710.3	-2,01	2,92E-17	6,69E-16	Protein TONNEAU 1b
Solyc06g005320.1	-2,01	5,85E-13	9,14E-12	Transcription factor MYB48
Solyc03g031980.4	-2,01	5,13E-08	4,52E-07	Lectin-receptor kinase
Solyc10g075110.2	-2,01	5,57E-07	4,21E-06	Non-specific lipid-transfer protein
Solyc07g056210.4	-2,01	6,37E-06	4,11E-05	Heavy metal-associated isoprenylated plant protein 47
Solyc01g098930.3	-2,01	1,78E-13	2,95E-12	cyclinU3_2
Solyc04g077380.2	-2,01	6,67E-04	2,87E-03	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc09g092430.3	-2,02	4,88E-30	2,36E-28	Selenium-binding protein
Solyc12g094460.2	-2,02	1,33E-04	6,73E-04	L-ascorbate oxidase-like protein
Solyc03g116670.3	-2,02	3,77E-28	1,64E-26	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc02g088780.4	-2,02	7,38E-14	1,27E-12	Ribosome biogenesis protein WDR12 homolog
Solyc05g009630.4	-2,02	4,72E-13	7,47E-12	Disease resistance protein
Solyc12g098360.2	-2,02	2,96E-12	4,30E-11	Protein arginine methyltransferase NDUFAF7
Solyc01g098400.3	-2,02	4,78E-09	4,88E-08	Histidine phosphotransfer protein
Solyc08g023640.1	-2,03	2,23E-05	1,32E-04	Pentatricopeptide repeat-containing protein
Solyc12g045020.2	-2,03	1,23E-07	1,03E-06	Cytochrome
Solyc05g006460.3	-2,03	5,10E-03	1,73E-02	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc10g078220.2	-2,03	2,83E-05	1,64E-04	Cytochrome P450
Solyc03g093340.4	-2,03	1,25E-14	2,30E-13	Uncharacterized conserved protein (UCP012943)
Solyc03g082370.1	-2,03	7,38E-06	4,71E-05	Avr9/Cf-9 rapidly elicited protein 65
Solyc08g048390.3	-2,03	5,89E-21	1,76E-19	TCP transcription factor 24
Solyc05g012190.3	-2,03	1,84E-15	3,61E-14	Cell division control protein 48-like protein B
Solyc12g056750.3	-2,03	1,01E-02	3,07E-02	WRKY transcription factor 61
Solyc02g077650.2	-2,03	1,42E-03	5,61E-03	Pentatricopeptide repeat-containing protein
Solyc05g054560.3	-2,04	5,19E-10	6,00E-09	CASP-like protein
Solyc04g078090.3	-2,04	3,80E-12	5,48E-11	Acyl-CoA-binding domain-containing protein 2
Solyc06g082595.1	-2,04	5,40E-14	9,43E-13	Ubiquitin-conjugating enzyme
Solyc01g081390.4	-2,04	4,45E-13	7,05E-12	Xylulose 5-phosphate/phosphate translocator, chloroplastic
Solyc07g053380.2	-2,04	4,57E-05	2,54E-04	Pentatricopeptide repeat
Solyc01g090390.1	-2,04	1,15E-04	5,88E-04	Pentatricopeptide repeat-containing protein
Solyc10g007030.2	-2,04	3,07E-11	4,01E-10	Transmembrane protein
Solyc10g054730.1	-2,04	5,53E-03	1,85E-02	Pentatricopeptide repeat
Solyc11g007740.2	-2,05	1,24E-12	1,88E-11	Ribosome recycling factor
Solyc03g097830.3	-2,05	1,13E-15	2,28E-14	Poly(A) polymerase I
Solyc01g109275.1	-2,05	8,85E-04	3,71E-03	Unknown protein
Solyc05g006450.3	-2,05	2,01E-05	1,20E-04	Carboxypeptidase
Solyc08g061450.3	-2,05	5,46E-07	4,14E-06	exosome complex exonuclease
Solyc03g117590.3	-2,05	6,53E-13	1,02E-11	Chaperone protein DnaJ
Solyc04g076330.3	-2,05	5,91E-04	2,58E-03	Pentatricopeptide repeat
Solyc09g005570.3	-2,05	2,09E-04	1,01E-03	hypothetical protein
Solyc12g088320.2	-2,06	1,94E-12	2,91E-11	LIM domain-containing protein
Solyc09g090470.3	-2,06	4,24E-15	8,08E-14	Protein NRT1/ PTR FAMILY 5.2
Solyc09g059575.1	-2,06	1,03E-06	7,51E-06	Pentatricopeptide repeat
Solyc11g067300.2	-2,06	2,87E-04	1,35E-03	ABC transporter B family member
Solyc09g011670.4	-2,06	2,25E-10	2,70E-09	Adenine nucleotide alpha hydrolases-like superfamily protein
Solyc12g057160.1	-2,06	1,69E-05	1,02E-04	Unknown protein
Solyc11g005635.1	-2,06	8,79E-09	8,65E-08	Ubiquitin
Solyc06g073090.3	-2,06	9,93E-16	2,01E-14	chloroplast-specific ribosomal protein chloroplast-specific ribosomal protein
Solyc09g091000.4	-2,07	1,01E-06	7,34E-06	Pathogenesis-related protein STH-2
Solyc06g083330.2	-2,07	1,44E-08	1,37E-07	acidic leucine-rich nuclear phosphoprotein 32 family B protein
Solyc11g005280.1	-2,07	3,29E-11	4,27E-10	RING-H2 finger protein ATL78
Solyc08g006690.1	-2,07	1,68E-10	2,04E-09	Plant invertase/pectin methylesterase inhibitor superfamily protein
Solyc08g082660.2	-2,07	9,25E-13	1,42E-11	Cellulose synthase
Solyc05g051735.1	-2,07	1,50E-05	9,11E-05	Unknown protein
Solyc03g112530.3	-2,07	2,73E-18	6,82E-17	WD40 repeat-containing protein
Solyc02g069100.4	-2,08	1,05E-26	4,24E-25	Cathepsin B-like cysteine proteinase
Solyc11g066420.1	-2,08	7,27E-05	3,88E-04	Zinc finger protein STAR3
Solyc03g007460.3	-2,08	6,61E-05	3,55E-04	Solanum lycopersicum Cytokinin Response Factor 4
Solyc02g086810.1	-2,08	3,38E-16	7,11E-15	Nipped-B-like protein
Solyc05g014550.1	-2,08	2,44E-06	1,68E-05	TRAM/LAG1/CLN8-like domain-containing protein
Solyc01g098320.4	-2,08	1,32E-12	2,00E-11	DNA-directed RNA polymerase V subunit 5A
Solyc02g087520.3	-2,08	2,01E-03	7,64E-03	Thaumatin
Solyc02g038740.4	-2,08	4,27E-12	6,13E-11	3-hydroxy-3-methylglutaryl coenzyme A reductase
Solyc11g005660.2	-2,08	1,27E-15	2,55E-14	Serine/threonine-protein kinase
Solyc03g111260.3	-2,09	4,41E-15	8,38E-14	Ribonuclease J
Solyc06g076080.3	-2,09	4,33E-04	1,95E-03	Unknown protein
Solyc06g009800.3	-2,09	3,49E-06	2,34E-05	Pentatricopeptide repeat-containing protein
Solyc04g008030.2	-2,09	8,74E-10	9,87E-09	Cleavage and polyadenylation specificity factor subunit 3-II
Solyc06g072075.1	-2,09	5,05E-03	1,71E-02	Unknown protein
Solyc08g005710.3	-2,09	1,62E-08	1,54E-07	Terpene synthase 41
Solyc09g075860.3	-2,09	6,17E-08	5,36E-07	Lipoxygenase
Solyc01g100420.3	-2,09	2,96E-18	7,34E-17	Peptide chain release factor 2
Solyc12g045035.1	-2,09	8,35E-06	5,28E-05	Fatty acid desaturase
Solyc03g031880.3	-2,09	6,52E-04	2,81E-03	Lysine-specific histone demethylase 1
Solyc01g102790.3	-2,10	7,45E-06	4,75E-05	Pentatricopeptide repeat-containing protein
Solyc01g091230.3	-2,10	1,70E-11	2,28E-10	Receptor-like kinase
Solyc07g005740.1	-2,10	2,23E-05	1,32E-04	Pentatricopeptide repeat
Solyc01g107090.2	-2,10	1,89E-04	9,21E-04	beta-1%2C4-xylosidase
Solyc10g008570.3	-2,10	1,31E-06	9,39E-06	Pentatricopeptide repeat-containing protein
Solyc01g100080.3	-2,10	1,27E-15	2,55E-14	Single-stranded DNA-binding protein, mitochondrial
Solyc02g031990.1	-2,10	1,55E-04	7,71E-04	VQ motif-containing protein 22
Solyc11g020870.3	-2,10	2,84E-17	6,51E-16	UPF0160 protein MYG1, mitochondrial
Solyc04g078870.4	-2,10	3,74E-27	1,56E-25	Non-specific serine/threonine protein kinase
Solyc03g096545.1	-2,10	6,27E-03	2,06E-02	PLAT/LH2 domain-containing protein
Solyc03g116170.3	-2,10	2,91E-16	6,15E-15	Nucleosome assembly protein family
Solyc10g076460.2	-2,11	1,23E-03	4,96E-03	Homeodomain-like superfamily protein
Solyc10g008590.1	-2,11	7,73E-05	4,11E-04	Pentatricopeptide repeat
Solyc02g071720.2	-2,11	7,35E-06	4,70E-05	GDSL esterase/lipase At1g29670-like
Solyc12g087860.3	-2,11	8,50E-06	5,37E-05	RING/U-box superfamily protein
Solyc05g015150.3	-2,11	2,08E-17	4,84E-16	Receptor protein kinase-like protein
Solyc07g005170.3	-2,11	3,28E-04	1,52E-03	Pentatricopeptide repeat-containing protein
Solyc05g008895.1	-2,11	3,45E-08	3,12E-07	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc10g085950.2	-2,12	1,23E-10	1,52E-09	ABC transporter protein
Solyc02g079330.3	-2,12	1,59E-09	1,74E-08	Equilibrative nucleotide transporter like
Solyc05g010620.3	-2,12	3,28E-05	1,88E-04	Pentatricopeptide repeat
Solyc02g065510.1	-2,12	3,51E-07	2,74E-06	Pentatricopeptide repeat-containing protein
Solyc10g081770.3	-2,12	1,23E-05	7,59E-05	Polyketide cyclase/dehydrase/lipid transport superfamily protein
Solyc06g050500.2	-2,12	3,71E-08	3,34E-07	abscisic acid receptor PYL4-like
Solyc11g068680.2	-2,13	3,26E-16	6,88E-15	NF-kappa-B inhibitor-like protein
Solyc02g067690.3	-2,13	8,18E-11	1,03E-09	Glycosyltransferase
Solyc09g098380.3	-2,13	9,76E-05	5,08E-04	Amino acid transporter
Solyc08g075500.4	-2,13	6,48E-06	4,18E-05	Pentatricopeptide repeat-containing protein

Solyc11g066020.2	-2,13	2,03E-26	8,03E-25	Ankyrin repeat family protein, putative, expressed
Solyc05g012250.3	-2,13	1,93E-10	2,34E-09	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc03g112820.4	-2,13	3,38E-07	2,65E-06	U3 small nucleolar ribonucleoprotein protein MPP10
Solyc08g082370.1	-2,14	4,19E-07	3,23E-06	Unknown protein
Solyc08g007980.3	-2,14	1,05E-04	5,39E-04	LURP-one-like protein
Solyc04g051480.1	-2,14	2,55E-04	1,21E-03	Pentatricopeptide repeat
Solyc03g083050.3	-2,14	3,64E-09	3,77E-08	hypothetical protein
Solyc05g010770.4	-2,14	6,93E-06	4,45E-05	Unknown protein
Solyc05g008810.4	-2,14	2,55E-22	8,08E-21	Lipid phosphate phosphatase
Solyc08g076430.3	-2,15	3,44E-14	6,11E-13	Survival motor neuron protein
Solyc04g005790.3	-2,15	4,23E-10	4,93E-09	Protein NRT1/ PTR FAMILY 4.6
Solyc12g005040.2	-2,15	5,58E-12	7,89E-11	Calcium-dependent protein kinase
Solyc07g043120.1	-2,15	2,24E-09	2,41E-08	Glycosyltransferase
Solyc06g005700.1	-2,15	5,56E-04	2,44E-03	Pentatricopeptide repeat-containing protein
Solyc12g010710.1	-2,16	1,58E-06	1,12E-05	Unknown protein
Solyc09g009950.4	-2,16	5,67E-07	4,28E-06	Pentatricopeptide repeat
Solyc06g033850.3	-2,16	8,37E-16	1,71E-14	Dehydration-responsive element-binding protein 2d-like
Solyc05g009470.4	-2,16	1,03E-13	1,75E-12	Glycoside hydrolase family 31
Solyc03g120080.4	-2,16	1,03E-17	2,46E-16	periodic tryptophan protein 2 homolog
Solyc06g007910.4	-2,16	2,95E-06	2,00E-05	Gibberellin regulated protein
Solyc03g150142.1	-2,16	1,10E-04	5,66E-04	Unknown protein
Solyc03g112100.3	-2,16	1,47E-09	1,61E-08	High-affinity nitrate transporter 3.2
Solyc09g090440.1	-2,16	1,56E-06	1,10E-05	Pentatricopeptide repeat
Solyc07g016210.1	-2,17	9,55E-06	5,98E-05	Specific tissue protein
Solyc01g107270.4	-2,17	1,46E-09	1,60E-08	Phosphoribosylformylglycinamidine synthase
Solyc06g053490.4	-2,17	4,74E-14	8,30E-13	FAM136A-like protein (DUF842)
Solyc04g079740.3	-2,17	4,09E-12	5,89E-11	tRNA-processing ribonuclease BN
Solyc01g111430.2	-2,18	1,04E-03	4,28E-03	Pentatricopeptide repeat
Solyc08g008020.1	-2,18	3,81E-06	2,54E-05	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
Solyc01g104090.4	-2,18	6,49E-04	2,80E-03	Pentatricopeptide repeat
Solyc11g006940.3	-2,18	2,23E-09	2,39E-08	Pentatricopeptide repeat
Solyc01g066200.1	-2,18	5,15E-08	4,54E-07	Unknown protein
Solyc09g074090.3	-2,18	1,70E-14	3,10E-13	Exosome complex component RRP4
Solyc01g006950.3	-2,19	2,34E-06	1,61E-05	syntaxin-121-like
Solyc09g042250.2	-2,19	1,16E-14	2,14E-13	Pentatricopeptide repeat
Solyc09g092150.1	-2,19	6,20E-03	2,04E-02	Pentatricopeptide repeat-containing protein
Solyc11g056620.3	-2,19	6,94E-20	1,93E-18	hypothetical protein
Solyc06g060710.4	-2,19	4,88E-06	3,21E-05	Glyco_transf_8 domain-containing protein
Solyc03g025600.3	-2,19	1,87E-12	2,80E-11	Pectin acetylesterase
Solyc09g150119.1	-2,19	1,26E-02	3,71E-02	Cytochrome P450
Solyc01g098480.3	-2,20	1,44E-04	7,23E-04	Pentatricopeptide repeat-containing protein
Solyc03g121640.3	-2,20	2,76E-22	8,70E-21	Chaperonin-60 kDa protein
Solyc06g064600.1	-2,20	1,19E-03	4,82E-03	Pentatricopeptide repeat-containing protein
Solyc03g083090.4	-2,20	1,51E-30	7,52E-29	Starch synthase, chloroplastic/amyloplastic
Solyc03g045110.3	-2,20	2,02E-04	9,80E-04	Ribosomal protein S5
Solyc01g007010.2	-2,20	8,18E-05	4,32E-04	RING-type E3 ubiquitin transferase
Solyc04g009220.2	-2,20	3,90E-11	5,03E-10	Pentatricopeptide repeat
Solyc05g009860.3	-2,20	2,03E-06	1,42E-05	leucoanthocyanidin reductase-like
Solyc01g087070.4	-2,21	4,32E-13	6,85E-12	ADP,ATP carrier protein, mitochondrial
Solyc02g077770.3	-2,21	3,37E-06	2,26E-05	F-box domain-containing protein
Solyc09g075890.3	-2,21	1,27E-19	3,47E-18	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Solyc03g082540.4	-2,22	1,57E-18	3,99E-17	plasminogen activator inhibitor
Solyc02g088650.1	-2,22	1,45E-05	8,84E-05	Pentatricopeptide repeat-containing protein
Solyc04g071140.3	-2,22	1,59E-12	2,39E-11	Serine decarboxylase
Solyc12g008650.2	-2,22	5,66E-06	3,68E-05	Inositol oxygenase
Solyc09g092050.4	-2,22	9,34E-11	1,16E-09	Pentatricopeptide repeat-containing protein
Solyc12g056650.2	-2,22	1,36E-15	2,71E-14	Protein GIGANTEA
Solyc02g079380.2	-2,23	1,40E-05	8,53E-05	Pentatricopeptide repeat-containing protein
Solyc01g106000.4	-2,23	2,12E-34	1,23E-32	Nicotinamidase 1
Solyc08g021820.3	-2,23	5,43E-05	2,97E-04	auxin-regulated IAA29
Solyc05g006800.2	-2,23	1,53E-07	1,26E-06	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc05g005300.2	-2,23	3,47E-04	1,60E-03	bHLH transcription factor 084
Solyc12g010570.1	-2,23	2,60E-11	3,43E-10	Tetraspanin
Solyc04g056530.2	-2,23	1,31E-09	1,45E-08	Ribosomal L18p/L5e family protein
Solyc04g074160.3	-2,23	2,63E-08	2,43E-07	Pentatricopeptide repeat
Solyc06g052050.4	-2,23	6,02E-04	2,62E-03	Heat shock protein 70 family
Solyc03g031420.1	-2,24	4,33E-06	2,87E-05	molybdenum cofactor sulfurase
Solyc12g056230.2	-2,24	2,17E-22	6,89E-21	glutathione peroxidase like encoding 2
Solyc09g065710.1	-2,24	2,26E-03	8,49E-03	Pentatricopeptide repeat-containing protein
Solyc01g090840.3	-2,24	3,19E-15	6,15E-14	Zinc finger protein
Solyc01g103470.2	-2,24	1,96E-06	1,37E-05	proline-rich receptor-like protein kinase PERK4
Solyc04g009400.4	-2,25	4,68E-05	2,59E-04	RING/FYVE/PHD zinc finger superfamily protein
Solyc04g015940.3	-2,25	6,13E-09	6,14E-08	ARM repeat superfamily protein
Solyc07g007770.2	-2,25	1,32E-03	5,26E-03	Unknown protein
Solyc09g010220.4	-2,25	1,89E-06	1,33E-05	lysosomal Pro-X carboxypeptidase
Solyc08g078550.1	-2,25	5,19E-06	3,41E-05	Metalloendoproteinase 1-like protein
Solyc09g011660.3	-2,25	7,62E-14	1,31E-12	Adenine nucleotide alpha hydrolases-like superfamily protein
Solyc07g055415.1	-2,25	5,63E-07	4,25E-06	Lectin-domain receptor-like kinase
Solyc02g093610.3	-2,25	2,59E-15	5,00E-14	BAG family molecular chaperone regulator 2-like
Solyc02g067560.1	-2,25	1,16E-18	2,98E-17	Inactive receptor kinase
Solyc01g006055.1	-2,26	8,19E-04	3,45E-03	Dirigent protein
Solyc03g097855.1	-2,26	2,01E-04	9,75E-04	Unknown protein
Solyc11g008970.1	-2,26	1,41E-09	1,56E-08	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc06g065650.3	-2,26	1,12E-27	4,72E-26	Tify domain-containing protein
Solyc09g092420.2	-2,26	1,65E-04	8,14E-04	Amino acid/polyamine transporter I
Solyc09g015770.3	-2,26	6,17E-17	1,39E-15	WRKY transcription factor 81
Solyc02g094125.1	-2,26	6,25E-03	2,05E-02	Pentatricopeptide repeat
Solyc05g012300.1	-2,27	4,27E-07	3,29E-06	WD40 repeat
Solyc07g062260.3	-2,27	4,96E-17	1,12E-15	BES1/BZR1
Solyc01g109010.3	-2,27	1,25E-05	7,71E-05	phox domain-containing protein
Solyc04g081550.3	-2,27	5,86E-16	1,21E-14	Thaumatin-like protein 1
Solyc02g080410.3	-2,27	1,32E-16	2,84E-15	18.8 kDa class V heat shock protein
Solyc02g087740.3	-2,27	1,17E-14	2,15E-13	Plant cysteine oxidase 2
Solyc08g080380.4	-2,27	2,57E-15	4,97E-14	Cytochrome P450
Solyc01g088400.4	-2,28	8,01E-13	1,24E-11	ECERIFERUM 1
Solyc06g062290.1	-2,28	7,18E-08	6,17E-07	Glycosyltransferase
Solyc01g096450.4	-2,28	3,65E-14	6,45E-13	Eukaryotic aspartyl protease family protein
Solyc03g007840.1	-2,28	3,17E-06	2,14E-05	Pentatricopeptide repeat
Solyc11g007830.2	-2,28	3,20E-33	1,78E-31	protein tyrosine phosphatase
Solyc11g045610.2	-2,28	1,40E-11	1,89E-10	Cyclin-dependent kinase C-1
Solyc01g109660.2	-2,28	7,92E-29	3,59E-27	meloidogyne-induced giant cell protein DB275
Solyc08g077530.3	-2,28	2,17E-13	3,56E-12	Beta-amylase
Solyc07g006600.1	-2,29	2,26E-13	3,70E-12	Protein GLUTAMINE DUMPER 3
Solyc06g005310.3	-2,29	1,17E-17	2,79E-16	Transcription factor MYB48
Solyc03g116060.4	-2,29	3,35E-13	5,39E-12	Gibberellin-regulated protein 6
Solyc04g009450.1	-2,29	1,53E-04	7,63E-04	Ethylene-responsive transcription factor
Solyc11g071810.2	-2,29	4,75E-09	4,85E-08	fasciated
Solyc01g096800.3	-2,29	2,80E-20	7,97E-19	Peter Pan-like protein
Solyc09g008940.4	-2,30	3,98E-18	9,79E-17	AT-hook motif nuclear-localized protein 10
Solyc07g053420.4	-2,30	4,24E-07	3,27E-06	RING/U-box superfamily protein
Solyc12g096630.2	-2,30	4,59E-10	5,33E-09	Inosine-uridine preferring nucleoside hydrolase family protein, expressed
Solyc12g005030.3	-2,30	5,10E-12	7,24E-11	Calcium-dependent protein kinase
Solyc12g087870.2	-2,30	9,44E-11	1,18E-09	purine permease 3-like
Solyc06g076850.3	-2,30	1,30E-32	7,15E-31	Tetratricopeptide repeat (TPR)-like superfamily protein

Solyc10g005790.3	-2,30	1,98E-23	6,85E-22	Transmembrane protein C9orf5 protein
Solyc03g005020.3	-2,31	2,90E-12	4,22E-11	Lipase
Solyc04g071430.2	-2,31	2,21E-03	8,34E-03	WAT1-related protein
Solyc01g100340.4	-2,31	1,49E-07	1,23E-06	Pentatricopeptide repeat-containing protein
Solyc01g091370.4	-2,31	4,97E-17	1,12E-15	AT-hook motif nuclear-localized protein 1
Solyc09g075820.3	-2,31	8,41E-16	1,72E-14	Sugar transporter protein 2
Solyc05g050570.3	-2,31	9,20E-11	1,15E-09	Cyclic pyranopterin monophosphate synthase accessory protein
Solyc03g114040.3	-2,31	4,43E-05	2,47E-04	Protein PRD1
Solyc03g025740.4	-2,32	1,99E-11	2,64E-10	Zf-CCHC domain-containing protein/Cofilin_ADF domain-containing protein
Solyc04g054290.3	-2,33	2,14E-05	1,27E-04	Pentatricopeptide repeat-containing protein
Solyc02g067360.3	-2,33	8,92E-23	2,95E-21	Protease Do-like 8, chloroplastic
Solyc01g066270.3	-2,33	1,94E-14	3,50E-13	Unknown protein
Solyc11g005960.1	-2,33	4,07E-04	1,84E-03	Pentatricopeptide repeat-containing protein
Solyc02g089330.3	-2,33	1,27E-07	1,06E-06	DNA-directed RNA polymerase
Solyc11g007710.2	-2,33	1,10E-16	2,39E-15	BnaA03g01310D protein
Solyc04g071770.3	-2,34	2,08E-04	1,01E-03	Ethylene-responsive transcription factor
Solyc09g092440.1	-2,34	1,90E-06	1,33E-05	Pentatricopeptide repeat
Solyc03g117080.4	-2,34	7,57E-14	1,30E-12	Mitochondrial glycoprotein
Solyc12g036530.1	-2,34	1,84E-03	7,08E-03	Pentatricopeptide repeat-containing protein
Solyc12g009180.2	-2,34	1,48E-21	4,53E-20	Cupin_5 domain-containing protein
Solyc08g077320.3	-2,34	6,32E-04	2,74E-03	Pentatricopeptide repeat-containing protein
Solyc02g090180.3	-2,35	1,54E-16	3,30E-15	Oligopeptidase B
Solyc06g084370.1	-2,35	3,10E-05	1,78E-04	Unknown protein
Solyc08g067840.3	-2,35	1,38E-23	4,80E-22	Photosystem II reaction center PsbP family protein
Solyc08g076300.3	-2,35	5,56E-14	9,69E-13	4-coumarate--CoA ligase-like 3
Solyc02g081920.3	-2,35	4,18E-32	2,23E-30	Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplastic
Solyc06g008940.4	-2,35	2,06E-13	3,39E-12	Elongation factor Tu
Solyc12g006575.1	-2,35	1,25E-08	1,20E-07	Pentatricopeptide repeat-containing protein
Solyc03g123580.4	-2,35	4,67E-08	4,15E-07	LL-diaminopimelate aminotransferase
Solyc12g094380.2	-2,36	2,20E-19	5,89E-18	Thioredoxin superfamily protein
Solyc08g081790.3	-2,36	6,03E-05	3,27E-04	Dirigent protein
Solyc02g079980.3	-2,36	3,51E-12	5,08E-11	Sulfite exporter TauE/SafE family protein 2
Solyc10g055390.2	-2,36	1,01E-15	2,05E-14	Major facilitator superfamily protein
Solyc03g113060.3	-2,36	9,44E-11	1,18E-09	ABC transporter A family member 7
Solyc10g083730.2	-2,37	5,74E-29	2,61E-27	F-box protein PP2-A15
Solyc09g090400.4	-2,37	1,63E-09	1,78E-08	Translation initiation factor eIF-2B subunit beta
Solyc04g082050.3	-2,37	3,10E-30	1,52E-28	Cellular retinaldehyde-binding/triple function, C-terminal
Solyc04g071260.3	-2,37	9,24E-04	3,85E-03	Actin
Solyc03g031560.4	-2,37	1,61E-12	2,43E-11	UDP-3-O-acylglucosamine N-acyltransferase
Solyc11g072600.3	-2,37	2,79E-29	1,30E-27	APETALA2d
Solyc03g063690.1	-2,38	1,11E-07	9,33E-07	Pentatricopeptide repeat
Solyc10g086100.2	-2,38	9,16E-05	4,78E-04	Proteinase inhibitor I-B
Solyc11g072830.1	-2,38	4,40E-11	5,65E-10	Chitinase
Solyc05g009180.1	-2,38	5,02E-04	2,23E-03	Zinc finger protein 8
Solyc12g099280.2	-2,38	2,10E-05	1,24E-04	Fip1 domain-containing protein
Solyc04g054500.3	-2,38	3,84E-17	8,71E-16	Heavy metal-associated isoprenylated plant protein
Solyc12g013700.2	-2,38	1,91E-08	1,80E-07	stem-specific protein TSJT1-like
Solyc07g055140.3	-2,39	1,95E-12	2,91E-11	DUF688 domain-containing protein
Solyc02g086980.3	-2,39	2,73E-11	3,60E-10	Unknown protein
Solyc01g010510.4	-2,39	1,32E-10	1,62E-09	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc01g110840.3	-2,39	2,12E-05	1,26E-04	Unknown protein
Solyc03g005700.1	-2,40	6,72E-11	8,52E-10	mitochondrial import receptor subunit TOM9-2-like
Solyc04g009860.4	-2,40	3,37E-17	7,67E-16	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc10g054727.1	-2,40	2,42E-04	1,15E-03	Unknown protein
Solyc01g066440.3	-2,40	2,19E-19	5,86E-18	hypothetical protein
Solyc06g007180.3	-2,40	2,23E-09	2,40E-08	asparagine synthetase 1
Solyc01g008400.3	-2,40	4,48E-05	2,50E-04	Unknown protein
Solyc12g010420.1	-2,41	1,17E-05	7,23E-05	hypothetical protein
Solyc11g005560.3	-2,41	2,17E-16	4,61E-15	Cellulose synthase
Solyc01g104900.3	-2,41	1,03E-05	6,44E-05	NAC domain-containing protein
Solyc09g090290.3	-2,41	9,94E-05	5,16E-04	RNA-binding (RRM/RBD/RNP motifs) family protein
Solyc03g098640.4	-2,42	1,81E-17	4,24E-16	Peroxisomal membrane MPV17/PMP22-like protein
Solyc03g116470.2	-2,42	7,31E-09	7,27E-08	transmembrane protein
Solyc04g079150.1	-2,42	2,62E-04	1,24E-03	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc01g091610.1	-2,42	1,55E-05	9,40E-05	Pentatricopeptide repeat-containing protein
Solyc02g062050.3	-2,42	3,33E-03	1,19E-02	Senescence/dehydration-associated protein-like protein
Solyc04g074410.2	-2,42	6,70E-15	1,25E-13	Protein EXORDIUM-like 1
Solyc04g072170.1	-2,42	2,27E-06	1,57E-05	Pentatricopeptide repeat-containing protein
Solyc08g008140.3	-2,42	4,61E-04	2,06E-03	E4 SUMO-protein ligase PIAL2 isoform X2
Solyc10g047300.2	-2,44	7,21E-17	1,60E-15	Outer envelope protein 64, mitochondrial
Solyc08g080670.1	-2,44	5,09E-07	3,88E-06	Pathogenesis-related 5-like protein
Solyc06g054620.4	-2,44	2,61E-05	1,52E-04	Zinc finger transcription factor 43
Solyc04g007410.4	-2,44	8,09E-14	1,39E-12	transmembrane protein
Solyc06g074420.1	-2,44	2,26E-05	1,33E-04	Cytochrome P450
Solyc09g007430.1	-2,44	2,95E-21	8,90E-20	Mitochondrial SBP40
Solyc08g081610.4	-2,45	1,16E-04	5,94E-04	WRKY family transcription factor
Solyc03g113860.2	-2,45	2,21E-11	2,93E-10	Ribosomal RNA small subunit methyltransferase G-like protein
Solyc06g075000.3	-2,45	8,90E-11	1,11E-09	MaoC_dehydratas domain-containing protein
Solyc12g099160.2	-2,45	9,21E-22	2,85E-20	Carboxypeptidase
Solyc01g094070.3	-2,45	5,13E-08	4,52E-07	Dihydroflavonol-4-reductase
Solyc01g091490.3	-2,45	3,84E-08	3,46E-07	Unknown protein
Solyc02g077430.4	-2,46	7,11E-16	1,46E-14	Phospholipase A1-II 1
Solyc10g055780.1	-2,46	6,91E-10	7,87E-09	Chitinase
Solyc06g008190.1	-2,46	4,10E-06	2,73E-05	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc03g083250.3	-2,46	1,69E-42	1,30E-40	ATP-dependent Clp protease ATP-binding subunit ClpX
Solyc02g065410.3	-2,46	9,13E-08	7,76E-07	Pentatricopeptide repeat
Solyc03g019710.3	-2,46	1,56E-06	1,10E-05	LETDR8
Solyc01g095600.4	-2,46	1,17E-03	4,74E-03	Pentatricopeptide repeat-containing protein
Solyc04g078980.4	-2,46	6,90E-04	2,96E-03	Hexosyltransferase
Solyc11g010710.2	-2,46	7,31E-07	5,44E-06	AP2-like ethylene-responsive transcription factor
Solyc02g005280.1	-2,47	5,73E-09	5,78E-08	Pentatricopeptide repeat
Solyc12g014360.2	-2,47	1,60E-11	2,15E-10	protein trichome birefringence-like 41
Solyc04g150172.1	-2,47	1,00E-11	1,37E-10	Protein RADIALIS-like 6
Solyc09g055180.4	-2,47	1,61E-20	4,67E-19	Protein kinase domain
Solyc03g095180.3	-2,48	2,33E-24	8,38E-23	Superoxide dismutase
Solyc01g098630.3	-2,48	4,28E-21	1,28E-19	Mitochondrial inner membrane translocase complex, subunit Tim44-related protein
Solyc02g036480.1	-2,48	6,14E-09	6,15E-08	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Solyc05g025790.3	-2,48	3,64E-06	2,44E-05	Potassium channel AKT2
Solyc02g091950.4	-2,49	2,79E-23	9,52E-22	Lysosomal Pro-X carboxypeptidase
Solyc09g009250.3	-2,49	7,31E-10	8,31E-09	Trihelix transcription factor GTL1
Solyc03g025690.4	-2,49	6,94E-11	8,77E-10	plastid transcriptionally active protein
Solyc03g117290.1	-2,49	4,00E-23	1,35E-21	Serine-rich protein
Solyc03g093080.3	-2,49	1,18E-03	4,76E-03	Xyloglucan endotransglucosylase/hydrolase
Solyc01g068130.4	-2,49	2,11E-32	1,15E-30	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase
Solyc02g070010.1	-2,49	1,85E-18	4,68E-17	Pentatricopeptide repeat-containing protein
Solyc06g150101.1	-2,50	1,24E-07	1,04E-06	Unknown protein
Solyc09g074560.3	-2,50	2,40E-31	1,23E-29	Zinc finger protein CONSTANS-LIKE 15
Solyc11g007750.3	-2,50	2,15E-07	1,73E-06	tRNA-thr(GGU) m(6)t(6)A37 methyltransferase
Solyc10g045490.2	-2,50	2,15E-15	4,20E-14	Plant organelle RNA recognition domain-containing protein
Solyc01g110060.3	-2,50	3,18E-27	1,33E-25	Purple acid phosphatase
Solyc10g052650.3	-2,51	4,57E-22	1,43E-20	F-box family protein
Solyc09g061790.1	-2,51	2,08E-04	1,01E-03	Pentatricopeptide repeat
Solyc06g034390.1	-2,51	6,73E-08	5,81E-07	Protein EXORDIUM-like 7
Solyc10g051130.3	-2,51	3,26E-11	4,23E-10	Protein DETOXIFICATION

Solyc12g095910.2	-2,51	4,19E-37	2,69E-35	cysteine protease
Solyc05g010340.3	-2,51	2,85E-12	4,17E-11	Uridine kinase
Solyc06g082190.3	-2,52	3,38E-16	7,11E-15	Protein kinase like protein
Solyc05g007070.2	-2,52	1,20E-26	4,85E-25	Alpha-amylase
Solyc02g087510.3	-2,52	2,79E-06	1,90E-05	Protein kinase G11A
Solyc03g119970.3	-2,52	1,46E-30	7,27E-29	ADP,ATP carrier protein
Solyc07g053210.3	-2,53	8,90E-04	3,72E-03	DNA repair metallo-beta-lactamase
Solyc02g021680.3	-2,53	4,52E-05	2,51E-04	WRKY transcription factor 35
Solyc10g017510.3	-2,53	1,30E-05	7,98E-05	Cytochrome
Solyc03g117570.3	-2,53	4,76E-13	7,53E-12	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc07g006420.1	-2,53	3,75E-07	2,91E-06	transmembrane protein
Solyc06g066380.1	-2,54	2,85E-17	6,54E-16	Pentatricopeptide repeat
Solyc07g055310.1	-2,54	8,05E-13	1,24E-11	Pentatricopeptide repeat-containing protein
Solyc01g081120.2	-2,54	1,26E-16	2,73E-15	Complex 1 LYR protein
Solyc11g007000.2	-2,55	3,41E-10	4,00E-09	Cytochrome c oxidase assembly protein COX15
Solyc12g099620.1	-2,55	8,83E-07	6,48E-06	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc07g045470.3	-2,55	1,57E-30	7,77E-29	alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
Solyc10g084540.3	-2,55	2,69E-05	1,57E-04	Pentatricopeptide repeat
Solyc09g092320.3	-2,55	2,29E-10	2,75E-09	RNA binding protein
Solyc03g117300.4	-2,55	1,23E-24	4,48E-23	Nodulin-like, Major facilitator superfamily domain protein
Solyc11g010260.3	-2,55	6,06E-06	3,93E-05	Pentatricopeptide repeat-containing protein
Solyc03g098795.1	-2,56	2,86E-05	1,66E-04	Proteinase inhibitor type-2
Solyc07g008140.3	-2,56	6,62E-14	1,15E-12	Umecyanin
Solyc02g076850.2	-2,56	9,83E-12	1,35E-10	Dof zinc finger protein4
Solyc04g077620.1	-2,56	5,13E-23	1,72E-21	Uncharacterized conserved protein UCP031279
Solyc11g042420.2	-2,56	2,06E-09	2,23E-08	Cytochrome c
Solyc09g066290.3	-2,56	9,31E-18	2,24E-16	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc02g090240.4	-2,57	1,17E-13	1,96E-12	Pentatricopeptide repeat
Solyc01g009810.3	-2,57	1,13E-05	6,99E-05	Leucine-rich repeat protein
Solyc02g091300.3	-2,58	2,52E-09	2,68E-08	Heavy metal-associated isoprenylated plant protein
Solyc09g074280.1	-2,58	1,61E-14	2,93E-13	Ankyrin repeat-containing protein
Solyc02g089340.4	-2,58	6,11E-10	7,00E-09	DNA-directed RNA polymerase
Solyc03g026130.3	-2,59	8,05E-25	2,95E-23	Cytochrome P450
Solyc11g006210.3	-2,59	6,86E-05	3,68E-04	Unknown protein
Solyc03g121030.2	-2,59	2,36E-23	8,12E-22	MMS19 nucleotide excision repair protein-like protein
Solyc07g055400.2	-2,59	1,52E-08	1,44E-07	Lectin-domain receptor-like kinase
Solyc01g106040.3	-2,59	1,90E-13	3,14E-12	GATA transcription factor 24
Solyc12g100270.2	-2,59	1,04E-05	6,49E-05	Fatty acid hydroxylase superfamily
Solyc01g096550.3	-2,60	6,18E-12	8,69E-11	Protein arginine N-methyltransferase
Solyc02g076750.3	-2,60	1,19E-17	2,82E-16	Cysteine protease CP14
Solyc10g079690.2	-2,60	5,28E-03	1,78E-02	Unknown protein
Solyc03g118080.4	-2,60	1,20E-11	1,63E-10	Pentatricopeptide repeat-containing protein
Solyc07g052460.3	-2,60	2,36E-05	1,39E-04	transmembrane protein
Solyc12g011037.1	-2,60	1,12E-08	1,08E-07	Lipoxygenase
Solyc04g072320.3	-2,61	2,70E-11	3,56E-10	ABC transporter C family member 8
Solyc07g008440.3	-2,61	1,72E-14	3,13E-13	Purine permease
Solyc02g094310.3	-2,61	1,60E-07	1,32E-06	Pentatricopeptide repeat
Solyc02g087610.1	-2,61	5,72E-07	4,31E-06	Pentatricopeptide repeat
Solyc11g008140.3	-2,61	8,02E-19	2,08E-17	Pectate lyase
Solyc02g091660.3	-2,62	1,75E-16	3,75E-15	transcription factor GTE2-like
Solyc02g076700.1	-2,62	2,86E-04	1,34E-03	Pentatricopeptide repeat
Solyc10g078590.2	-2,62	1,40E-19	3,80E-18	Jacalin-related lectin 3
Solyc04g082870.1	-2,63	4,03E-08	3,62E-07	Pentatricopeptide repeat-containing protein
Solyc09g007050.1	-2,63	5,07E-09	5,16E-08	Pentatricopeptide repeat-containing protein
Solyc04g063300.3	-2,63	1,27E-07	1,06E-06	Pentatricopeptide repeat-containing protein
Solyc11g009060.2	-2,64	7,03E-28	3,02E-26	ATP synthase subunit B
Solyc11g008200.2	-2,64	9,85E-12	1,35E-10	Major facilitator superfamily
Solyc10g076780.1	-2,64	2,73E-08	2,50E-07	Alpha 1,4-glycosyltransferase family protein
Solyc02g005003.1	-2,64	2,47E-03	9,21E-03	Unknown protein
Solyc08g075350.3	-2,64	4,61E-06	3,04E-05	Pentatricopeptide repeat-containing protein
Solyc09g011650.4	-2,64	1,96E-10	2,37E-09	Glutathione S-transferase
Solyc06g072550.3	-2,65	3,26E-04	1,51E-03	CASP-like protein
Solyc06g066080.1	-2,65	1,86E-07	1,51E-06	Pentatricopeptide repeat
Solyc03g019840.4	-2,65	3,54E-13	5,67E-12	hydroxyproline-rich glycoprotein family protein
Solyc11g005440.2	-2,65	3,46E-08	3,13E-07	Endonuclease or glycosyl hydrolase
Solyc06g007460.3	-2,66	2,85E-12	4,17E-11	EPIDERMAL PATTERNING FACTOR-like protein 6
Solyc05g006160.4	-2,66	2,08E-08	1,95E-07	Gibberellin regulated protein
Solyc10g078320.2	-2,66	2,19E-15	4,26E-14	Calmodulin-interacting protein
Solyc08g005390.1	-2,66	9,10E-07	6,67E-06	Pentatricopeptide repeat
Solyc11g008850.2	-2,66	7,24E-12	1,01E-10	protease Do-like 10, mitochondrial
Solyc01g100010.3	-2,67	1,18E-14	2,17E-13	F-box domain, Phloem protein 2-like protein
Solyc01g005040.3	-2,67	1,42E-06	1,01E-05	CASP-like protein
Solyc04g025650.3	-2,67	1,45E-19	3,93E-18	FAD/NAD(P)-binding oxidoreductase family protein
Solyc11g056650.2	-2,68	5,57E-29	2,54E-27	bHLH transcription factor 096
Solyc04g054510.4	-2,68	1,27E-16	2,75E-15	DNA-directed RNA polymerase subunit
Solyc06g061010.4	-2,68	2,43E-08	2,26E-07	FCS-Like Zinc finger 2
Solyc05g046150.3	-2,68	6,99E-04	2,99E-03	Kirola
Solyc03g093110.3	-2,68	4,86E-04	2,16E-03	Xyloglucan endotransglucosylase/hydrolase
Solyc02g080320.4	-2,68	2,02E-12	3,02E-11	RNA pseudouridine synthase 6, chloroplastic
Solyc11g010813.1	-2,68	5,56E-10	6,39E-09	UDP-glycosyltransferase 91A1
Solyc04g064750.2	-2,70	3,65E-09	3,77E-08	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc02g093380.1	-2,70	3,21E-06	2,17E-05	Pentatricopeptide repeat-containing protein
Solyc09g009400.4	-2,70	3,03E-20	8,59E-19	APO domain
Solyc04g039940.3	-2,71	1,39E-06	9,89E-06	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc02g084730.3	-2,72	6,86E-07	5,12E-06	rRNA adenine N(6)-methyltransferase
Solyc02g079820.4	-2,72	6,12E-06	3,97E-05	Pentatricopeptide repeat-containing protein
Solyc02g091700.3	-2,72	9,12E-16	1,85E-14	Hydroxyproline-rich glycoprotein
Solyc04g081910.4	-2,73	1,49E-11	2,01E-10	Calcium-dependent protein kinase
Solyc06g076570.4	-2,73	2,31E-15	4,48E-14	Class I heat shock protein
Solyc10g008400.1	-2,74	1,81E-22	5,85E-21	E3 ubiquitin-protein ligase RMA1H1
Solyc01g005350.4	-2,74	1,01E-03	4,19E-03	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc01g080020.2	-2,74	1,98E-21	6,01E-20	Eukaryotic aspartyl protease family protein
Solyc10g006120.2	-2,74	3,80E-06	2,54E-05	DUF3537 domain-containing protein
Solyc12g089140.2	-2,74	6,18E-33	3,42E-31	Erythronate-4-phosphate dehydrogenase family protein
Solyc06g018110.3	-2,74	4,15E-12	5,96E-11	RNA-binding (RRM/RBD/RNP motifs) family protein
Solyc03g111360.3	-2,75	2,30E-18	5,77E-17	Oxygen-independent coproporphyrinogen-III oxidase-like protein
Solyc05g005230.3	-2,75	1,33E-04	6,71E-04	Plant protein 1589 of Uncharacterized protein function
Solyc02g080960.3	-2,75	7,92E-06	5,02E-05	Transmembrane protein, putative (DUF1068)
Solyc11g072480.2	-2,75	5,02E-28	2,17E-26	Tetraspanin-3
Solyc08g077060.3	-2,76	2,79E-35	1,66E-33	Zinc finger, LSD1-type
Solyc04g083160.2	-2,76	9,32E-14	1,59E-12	Solyc04g083160
Solyc09g009480.1	-2,76	1,91E-06	1,34E-05	F-box protein
Solyc06g082880.2	-2,76	3,16E-09	3,32E-08	Pentatricopeptide repeat-containing protein
Solyc09g010390.2	-2,76	3,49E-15	6,70E-14	hypothetical protein
Solyc03g097850.1	-2,76	9,86E-07	7,18E-06	Pentatricopeptide repeat-containing protein
Solyc03g082420.3	-2,76	1,48E-05	8,99E-05	Small heat shock protein, chloroplastic
Solyc03g111210.4	-2,77	6,39E-15	1,20E-13	Pentatricopeptide repeat
Solyc12g100250.3	-2,77	1,09E-06	7,87E-06	Fatty acid desaturase
Solyc01g112200.3	-2,77	1,04E-12	1,59E-11	Pentatricopeptide repeat-containing protein
Solyc09g007440.3	-2,78	1,99E-11	2,64E-10	DEAD-box ATP-dependent RNA helicase 57
Solyc02g065560.1	-2,78	6,31E-11	8,03E-10	Pentatricopeptide repeat-containing protein
Solyc11g007530.2	-2,78	2,14E-22	6,82E-21	RING/U-box superfamily protein
Solyc03g031460.1	-2,78	4,74E-26	1,84E-24	Pentatricopeptide repeat
Solyc03g120690.3	-2,78	3,03E-04	1,41E-03	Dynein light chain

Solyc04g081560.3	-2,79	3,90E-08	3,51E-07	thaumatin-like protein
Solyc11g071370.1	-2,79	5,86E-10	6,73E-09	Pentatricopeptide repeat
Solyc10g086650.1	-2,79	1,65E-26	6,60E-25	Glyoxal oxidase
Solyc04g056370.3	-2,79	1,08E-23	3,77E-22	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc01g109100.2	-2,80	3,25E-07	2,55E-06	TMV resistance protein N
Solyc01g010910.2	-2,80	5,32E-03	1,79E-02	MYB transcription factor
Solyc02g077240.4	-2,81	2,14E-22	6,82E-21	Pyruvate decarboxylase
Solyc05g018050.1	-2,81	1,76E-11	2,36E-10	RING/U-box superfamily protein
Solyc06g075460.4	-2,82	1,03E-13	1,75E-12	Protein NRT1/ PTR FAMILY 2.7
Solyc05g009650.4	-2,82	3,77E-13	6,02E-12	Unknown protein
Solyc01g009260.1	-2,83	2,06E-08	1,94E-07	protein FAF-like, chloroplastic
Solyc07g008760.4	-2,83	2,76E-14	4,95E-13	tetratricopeptide repeat protein 27 homolog
Solyc04g015620.3	-2,83	1,37E-29	6,42E-28	DUF642 domain-containing protein
Solyc01g067910.3	-2,83	2,43E-17	5,64E-16	Unknown protein
Solyc01g080190.3	-2,83	7,90E-21	2,34E-19	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc10g055460.2	-2,83	1,84E-05	1,10E-04	Unknown protein
Solyc07g053493.1	-2,83	1,09E-04	5,59E-04	Cytochrome
Solyc02g081480.4	-2,84	6,34E-13	9,87E-12	Receptor-like protein kinase
Solyc06g069070.1	-2,84	5,53E-10	6,37E-09	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc08g007225.1	-2,84	6,45E-12	9,06E-11	Phospholipase A1-Ibeta2, chloroplastic
Solyc10g007880.4	-2,84	9,89E-09	9,67E-08	Cytochrome P450
Solyc01g109380.3	-2,85	4,10E-20	1,15E-18	UPF0496 protein
Solyc01g095270.3	-2,85	3,65E-38	2,46E-36	DUF2358 domain-containing protein
Solyc09g082780.3	-2,85	1,47E-29	6,89E-28	Aluminum induced protein with YGL and LRDR motifs
Solyc08g063090.2	-2,85	1,20E-33	6,78E-32	Fatty acid desaturase
Solyc08g014100.1	-2,85	3,04E-12	4,42E-11	Pentatricopeptide repeat-containing protein
Solyc08g080680.4	-2,85	2,85E-23	9,73E-22	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc12g042400.1	-2,85	1,91E-06	1,34E-05	Pentatricopeptide repeat
Solyc01g097000.3	-2,86	1,81E-33	1,01E-31	Glycosyl hydrolase family protein
Solyc10g051377.1	-2,86	2,42E-31	1,24E-29	RNA-binding protein
Solyc06g068990.4	-2,87	9,58E-28	4,07E-26	Mitogen-activated protein kinase
Solyc10g049600.3	-2,87	1,85E-41	1,38E-39	3-oxo-Delta(4,5)-steroid 5-beta-reductase
Solyc05g006340.3	-2,87	8,73E-29	3,94E-27	Transducin/WD40 repeat-like superfamily protein
Solyc04g008900.4	-2,87	1,67E-08	1,58E-07	Transmembrane protein, putative (DUF247)
Solyc03g093130.3	-2,87	1,41E-07	1,17E-06	xyloglucan endotransglucosylase-hydrolase 3
Solyc02g076730.3	-2,88	3,24E-26	1,28E-24	Cysteine protease CP14
Solyc02g077880.3	-2,88	6,08E-25	2,24E-23	Auxin-repressed protein
Solyc06g053640.1	-2,89	1,67E-04	8,25E-04	RING/U-box superfamily protein
Solyc11g005350.2	-2,89	2,03E-18	5,11E-17	WAT1-related protein
Solyc02g079710.4	-2,89	3,92E-20	1,10E-18	S receptor kinase
Solyc02g084005.1	-2,89	3,45E-03	1,23E-02	Auxin-responsive protein SAUR20
Solyc07g047827.1	-2,90	8,39E-04	3,52E-03	Unknown protein
Solyc05g012630.2	-2,91	8,27E-07	6,11E-06	Pentatricopeptide repeat
Solyc02g068170.1	-2,91	1,41E-10	1,73E-09	Unknown protein
Solyc07g006090.3	-2,91	2,35E-13	3,84E-12	Glutamine amidotransferase
Solyc10g054810.2	-2,92	5,87E-05	3,19E-04	X-intrinsic protein 1.3
Solyc07g005300.1	-2,92	5,26E-08	4,63E-07	Unknown protein
Solyc01g087060.4	-2,92	1,96E-20	5,64E-19	RING/U-box superfamily protein
Solyc02g080120.3	-2,92	3,70E-13	5,92E-12	Gibberellin 2-beta-dioxygenase 8
Solyc06g066020.3	-2,93	4,69E-05	2,60E-04	auxin-regulated IAA36
Solyc01g096440.4	-2,93	1,85E-12	2,77E-11	Pentatricopeptide repeat-containing protein
Solyc01g006150.3	-2,93	3,03E-43	2,44E-41	Cation efflux protein
Solyc03g006360.3	-2,93	4,80E-25	1,78E-23	Auxin-repressed protein
Solyc09g097840.2	-2,94	4,94E-12	7,02E-11	Pentatricopeptide repeat-containing protein
Solyc08g065870.4	-2,94	2,32E-40	1,68E-38	protein EARLY FLOWERING 3
Solyc01g081240.3	-2,94	2,54E-09	2,70E-08	Pentatricopeptide repeat-containing protein
Solyc10g008730.3	-2,95	8,20E-07	6,06E-06	transmembrane protein
Solyc01g096260.4	-2,95	1,10E-35	6,72E-34	NAD-dependent protein deacetylase HST1-like protein
Solyc11g062250.2	-2,97	5,66E-06	3,68E-05	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc05g026490.3	-2,97	2,49E-10	2,96E-09	Phosphomannomutase/phosphoglucomutase
Solyc04g007630.2	-2,97	1,95E-08	1,84E-07	Heavy metal-associated isoprenylated plant protein
Solyc01g096250.2	-2,97	1,35E-15	2,69E-14	proline-rich receptor-like protein kinase PERK2
Solyc02g092200.3	-2,97	9,50E-13	1,46E-11	hypothetical protein
Solyc10g079840.2	-2,97	2,31E-26	9,12E-25	Peptide chain release factor 2-like protein
Solyc04g025430.1	-2,98	9,88E-09	9,66E-08	Pentatricopeptide repeat-containing protein
Solyc09g074530.3	-2,98	2,39E-06	1,65E-05	Bidirectional sugar transporter SWEET
Solyc09g005710.3	-2,98	2,13E-10	2,56E-09	Pentatricopeptide repeat
Solyc10g055730.3	-2,99	1,00E-14	1,85E-13	HXXXD-type acyl-transferase family protein
Solyc01g068540.3	-2,99	9,82E-07	7,15E-06	Homeodomain-like superfamily protein
Solyc12g011400.3	-3,00	1,20E-13	2,01E-12	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc11g006200.2	-3,00	2,38E-07	1,90E-06	Homeobox domain-containing protein/DDT domain-containing protein
Solyc08g065260.4	-3,00	7,73E-23	2,57E-21	YCF36%2C putative (DUF1230)
Solyc08g005610.3	-3,00	7,35E-16	1,50E-14	Cytochrome P450
Solyc09g010605.1	-3,00	7,22E-08	6,20E-07	Unknown protein
Solyc09g090080.1	-3,00	1,20E-22	3,94E-21	Phosphate transporter
Solyc06g069700.4	-3,01	7,75E-09	7,68E-08	Pentatricopeptide repeat (PPR) superfamily protein
Solyc02g090810.4	-3,01	1,24E-16	2,69E-15	Calcium-binding protein CML19
Solyc09g082400.2	-3,01	1,19E-12	1,81E-11	Pentatricopeptide repeat-containing protein
Solyc04g063340.3	-3,01	1,20E-11	1,63E-10	Pentatricopeptide repeat-containing protein
Solyc03g063160.1	-3,01	1,71E-09	1,87E-08	Pentatricopeptide repeat
Solyc03g096830.4	-3,01	6,72E-17	1,50E-15	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc06g066420.4	-3,01	4,19E-15	7,99E-14	Oxidative stress 3
Solyc03g113600.4	-3,02	3,24E-09	3,39E-08	Myosin-binding protein 2
Solyc07g055530.3	-3,03	1,64E-15	3,22E-14	Cytochrome
Solyc02g079700.1	-3,03	6,22E-10	7,11E-09	S-receptor kinase-like protein
Solyc01g090510.2	-3,03	1,51E-05	9,16E-05	Pentatricopeptide repeat
Solyc05g052830.3	-3,04	1,46E-08	1,39E-07	Proline transporter 1
Solyc06g082030.3	-3,04	6,41E-15	1,20E-13	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc12g013710.2	-3,04	4,98E-32	2,63E-30	light dependent NADH:protochlorophyllide oxidoreductase 1
Solyc02g011680.4	-3,04	1,50E-08	1,42E-07	Pentatricopeptide repeat-containing protein
Solyc11g072380.2	-3,04	8,03E-10	9,11E-09	Cupin_1 domain-containing protein
Solyc01g014560.4	-3,05	1,33E-17	3,14E-16	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc02g090720.3	-3,05	5,20E-06	3,41E-05	BEST plant protein match is: (TAIR:plant.1) protein, putative
Solyc02g086600.3	-3,05	6,56E-17	1,47E-15	Polyribonucleotide nucleotidyltransferase
Solyc11g008640.1	-3,05	7,47E-04	3,18E-03	Flowering locus T
Solyc11g067140.2	-3,05	3,23E-07	2,54E-06	DNA polymerase epsilon catalytic subunit
Solyc03g019650.3	-3,06	2,82E-46	2,61E-44	Major facilitator superfamily protein
Solyc03g113130.3	-3,06	8,33E-10	9,44E-09	plant cysteine oxidase 2-like
Solyc01g098720.3	-3,07	1,33E-13	2,23E-12	Basic helix-loop-helix (BHLH) DNA-binding superfamily protein
Solyc11g005300.2	-3,08	8,98E-10	1,01E-08	RING/U-box superfamily protein
Solyc01g096040.4	-3,08	1,28E-34	7,51E-33	Eukaryotic aspartyl protease family protein
Solyc02g014360.3	-3,09	1,02E-22	3,36E-21	Pentatricopeptide repeat-containing protein
Solyc09g063150.3	-3,09	1,83E-10	2,22E-09	Glutathione S-transferase
Solyc09g031940.1	-3,09	4,39E-38	2,96E-36	protein RETICULATA-RELATED 3, chloroplastic-like
Solyc06g009500.1	-3,10	3,60E-10	4,22E-09	Pentatricopeptide repeat
Solyc04g051660.3	-3,11	2,88E-28	1,27E-26	protein SLOW GREEN 1, chloroplastic
Solyc02g085230.3	-3,13	5,40E-19	1,41E-17	U3 small nucleolar RNA-associated protein 22
Solyc01g067680.3	-3,13	3,67E-51	4,01E-49	Tubby-like F-box protein
Solyc07g006380.3	-3,13	8,18E-03	2,58E-02	Defensin-like protein
Solyc03g116480.1	-3,13	4,08E-16	8,53E-15	F-box/kelch-repeat protein At5g15710-like
Solyc06g048900.1	-3,13	2,15E-13	3,54E-12	Pentatricopeptide repeat-containing protein
Solyc05g005280.4	-3,14	8,61E-23	2,85E-21	Poly [ADP-ribose] polymerase
Solyc01g095160.3	-3,14	3,04E-05	1,75E-04	Pentatricopeptide repeat-containing protein
Solyc04g054690.3	-3,14	1,37E-10	1,68E-09	ascorbate oxidase

Solyc02g079240.1	-3,14	1,27E-05	7,80E-05	Unknown protein
Solyc03g034150.2	-3,14	2,02E-04	9,79E-04	Homeobox-leucine zipper protein HOX14
Solyc11g067110.2	-3,15	7,85E-06	4,98E-05	DNA polymerase epsilon catalytic subunit
Solyc01g094850.3	-3,15	1,38E-10	1,69E-09	Pentatricopeptide repeat-containing protein
Solyc03g032030.4	-3,16	4,35E-15	8,28E-14	Phosphate carrier protein mitochondrial-like
Solyc03g113460.1	-3,16	3,02E-32	1,62E-30	Short-chain dehydrogenase reductase 4
Solyc04g008730.3	-3,16	2,08E-43	1,70E-41	Alpha-galactosidase
Solyc08g077370.4	-3,17	1,63E-20	4,70E-19	Purine permease
Solyc02g065030.1	-3,17	2,37E-07	1,90E-06	Pentatricopeptide repeat
Solyc05g009400.3	-3,17	8,40E-10	9,52E-09	Pentatricopeptide repeat
Solyc02g090990.1	-3,17	4,44E-11	5,70E-10	MAP kinase kinase kinase 23
Solyc12g096660.3	-3,18	2,06E-08	1,93E-07	type I inositol polyphosphate 5-phosphatase 12-like
Solyc01g097670.4	-3,18	2,12E-12	3,16E-11	Pentatricopeptide repeat
Solyc02g076710.3	-3,18	6,87E-11	8,70E-10	Cysteine protease CP14
Solyc03g083480.4	-3,19	1,69E-17	3,97E-16	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.1
Solyc09g082450.1	-3,19	1,88E-17	4,40E-16	Pentatricopeptide repeat-containing protein
Solyc07g045530.2	-3,19	9,40E-07	6,86E-06	cilia- and flagella-associated protein 251-like
Solyc06g008750.1	-3,20	1,08E-13	1,83E-12	Glutaredoxin
Solyc04g054340.1	-3,20	1,96E-10	2,37E-09	hypothetical protein
Solyc06g084580.1	-3,20	1,07E-09	1,20E-08	Pentatricopeptide repeat
Solyc03g082830.2	-3,21	1,53E-16	3,29E-15	Pentatricopeptide repeat
Solyc09g082170.4	-3,22	1,23E-14	2,25E-13	Pentatricopeptide repeat-containing protein
Solyc03g005820.3	-3,22	2,94E-25	1,10E-23	Purine permease
Solyc12g044950.3	-3,23	1,16E-18	2,96E-17	lipid desaturase
Solyc11g017390.2	-3,23	2,88E-08	2,64E-07	hypothetical protein
Solyc08g014130.3	-3,23	1,31E-26	5,29E-25	Isopropylmalate synthase
Solyc01g104780.3	-3,23	2,49E-10	2,96E-09	Vacuolar iron transporter-like protein
Solyc11g072570.2	-3,23	1,45E-05	8,80E-05	protein NRT1/ PTR FAMILY 2.7-like
Solyc10g080070.3	-3,24	6,65E-15	1,24E-13	Ribosome biogenesis GTPase A
Solyc01g088490.3	-3,25	6,30E-08	5,47E-07	Pentatricopeptide repeat-containing protein
Solyc12g089145.1	-3,25	9,42E-15	1,75E-13	Unknown protein
Solyc09g009200.3	-3,27	1,49E-07	1,23E-06	Growth-regulating factor 3
Solyc01g087790.2	-3,28	5,12E-36	3,18E-34	Subtilisin-like protease
Solyc02g072020.3	-3,28	1,55E-08	1,47E-07	Pentatricopeptide repeat-containing protein
Solyc03g032090.1	-3,28	1,94E-22	6,25E-21	Amino acid transporter
Solyc11g071960.2	-3,28	3,36E-23	1,14E-21	Sulfhydryl oxidase
Solyc02g083310.3	-3,30	4,23E-59	6,02E-57	Bifunctional nuclease 2
Solyc06g024310.1	-3,33	2,21E-05	1,31E-04	Glycosyltransferase-like
Solyc09g014210.3	-3,33	4,51E-12	6,46E-11	Pentatricopeptide repeat-containing protein
Solyc03g032240.4	-3,34	7,19E-09	7,15E-08	cation/H(+) antiporter 2-like
Solyc02g072010.3	-3,34	6,44E-08	5,58E-07	Pentatricopeptide repeat-containing protein
Solyc03g096840.4	-3,36	2,35E-27	9,86E-26	hypothetical protein
Solyc02g071870.4	-3,36	3,33E-17	7,58E-16	Protein kinase domain
Solyc01g010280.3	-3,37	8,21E-07	6,06E-06	suppressor SRP40-like protein
Solyc01g095640.2	-3,37	2,50E-06	1,72E-05	MYB-like transcription factor TCL1
Solyc04g078860.4	-3,37	7,54E-26	2,90E-24	glutamate receptor-like 1.1
Solyc11g007870.1	-3,37	1,77E-08	1,68E-07	hypothetical protein
Solyc04g064920.4	-3,38	4,10E-16	8,56E-15	Glycolipid transfer protein 3
Solyc01g100230.3	-3,38	5,26E-31	2,67E-29	DnaJ-like protein subfamily B member 6
Solyc10g086380.1	-3,38	1,66E-26	6,61E-25	Transcription factor GRAS
Solyc08g077760.3	-3,38	7,48E-20	2,07E-18	Unknown protein
Solyc07g055170.1	-3,38	6,04E-06	3,92E-05	DNA repair protein XRCC3-like protein
Solyc03g031990.4	-3,39	1,64E-67	3,02E-65	Auxin efflux carrier
Solyc07g065500.2	-3,39	5,13E-46	4,69E-44	Nuclear transcription factor Y subunit B-3
Solyc06g006100.3	-3,39	4,09E-49	4,17E-47	Anthranilate synthase
Solyc08g014080.4	-3,40	3,34E-26	1,31E-24	RING/FYVE/PHD zinc finger superfamily protein
Solyc04g009210.1	-3,41	2,12E-09	2,29E-08	Pentatricopeptide repeat-containing protein
Solyc01g095140.4	-3,41	1,01E-09	1,14E-08	Desiccation protectant protein Lea14-like protein
Solyc01g006920.4	-3,43	1,14E-08	1,10E-07	Pentatricopeptide repeat-containing protein
Solyc08g078570.3	-3,43	1,91E-09	2,07E-08	Pentatricopeptide repeat (PPR) superfamily protein
Solyc11g066330.2	-3,44	2,44E-37	1,59E-35	Major facilitator superfamily
Solyc12g042770.3	-3,44	1,07E-48	1,07E-46	Post-illumination chlorophyll fluorescence increase
Solyc09g009430.3	-3,44	2,65E-67	4,85E-65	Cell division protein FtsZ
Solyc01g057430.3	-3,45	3,65E-12	5,27E-11	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha, chloroplastic
Solyc06g053220.3	-3,45	4,78E-34	2,74E-32	Homeobox-leucine zipper protein HOX6
Solyc03g123630.4	-3,45	1,55E-61	2,36E-59	pectin methylesterase pmeu1
Solyc12g008510.2	-3,46	6,31E-36	3,89E-34	hexokinase 3
Solyc02g068630.1	-3,46	9,90E-09	9,68E-08	Pentatricopeptide repeat
Solyc04g011750.3	-3,47	3,70E-07	2,88E-06	histone H3.v1
Solyc07g042760.1	-3,48	3,49E-15	6,70E-14	Pentatricopeptide repeat
Solyc06g068500.3	-3,48	1,78E-36	1,12E-34	Chaperone protein DnaJ
Solyc02g084240.3	-3,50	7,48E-56	9,33E-54	H1 histone-like protein
Solyc04g025880.4	-3,51	4,15E-10	4,83E-09	Potassium transporter
Solyc07g065730.1	-3,51	1,26E-10	1,54E-09	Pentatricopeptide repeat
Solyc12g005000.1	-3,52	2,74E-04	1,29E-03	Unknown protein
Solyc04g016200.1	-3,52	8,39E-17	1,84E-15	Glycosyltransferase
Solyc09g091050.4	-3,55	5,90E-30	2,82E-28	C2 calcium-dependent membrane targeting
Solyc10g080220.2	-3,55	6,26E-07	4,70E-06	Pentatricopeptide repeat
Solyc01g108330.2	-3,55	8,34E-14	1,43E-12	transmembrane protein
Solyc12g014350.3	-3,55	1,18E-30	5,92E-29	LRR receptor-like serine/threonine-protein kinase
Solyc06g083470.4	-3,55	4,12E-16	8,59E-15	NAD(P)-binding Rossmann-fold superfamily protein
Solyc02g084850.3	-3,57	2,23E-33	1,25E-31	Abscisic acid and environmental stress-inducible protein TAS14
Solyc03g116000.1	-3,57	4,96E-08	4,39E-07	Pentatricopeptide repeat-containing protein
Solyc07g054430.3	-3,58	5,24E-25	1,94E-23	folic acid binding / transferase
Solyc08g066450.1	-3,59	1,19E-13	2,00E-12	DUF1677 family protein (DUF1677)
Solyc08g062960.4	-3,59	8,09E-17	1,79E-15	Heat shock transcription factor
Solyc09g065840.3	-3,60	1,61E-40	1,17E-38	Single-stranded DNA-binding protein
Solyc11g045520.2	-3,60	3,58E-09	3,71E-08	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc06g061230.3	-3,61	6,42E-23	2,15E-21	metallocarboxypeptidase inhibitor precursor
Solyc06g008930.3	-3,62	7,81E-05	4,15E-04	Unknown protein
Solyc09g018020.3	-3,62	5,47E-29	2,50E-27	Expansin
Solyc01g099650.3	-3,62	2,32E-13	3,79E-12	Formin-like protein
Solyc09g005990.4	-3,64	5,53E-07	4,18E-06	Pentatricopeptide repeat-containing protein
Solyc06g071820.3	-3,64	7,04E-86	2,29E-83	BTB/POZ and TAZ domain-containing protein 1
Solyc06g006080.3	-3,65	1,77E-66	3,06E-64	Phosphomethylpyrimidine synthase
Solyc12g021160.1	-3,66	2,78E-22	8,76E-21	Unknown protein
Solyc03g083720.1	-3,66	3,83E-24	1,36E-22	Plant invertase/pectin methylesterase inhibitor superfamily protein, putative
Solyc01g068380.3	-3,67	3,07E-36	1,92E-34	Purple acid phosphatase
Solyc02g076910.3	-3,69	2,31E-09	2,48E-08	Cysteine protease
Solyc03g025700.2	-3,69	2,92E-11	3,82E-10	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc02g093590.3	-3,71	2,43E-45	2,17E-43	zinc finger protein CONSTANS-LIKE 16-like
Solyc11g011860.1	-3,71	1,77E-18	4,49E-17	Pentatricopeptide repeat-containing protein
Solyc09g014580.3	-3,71	1,46E-07	1,21E-06	MLP-like protein 43
Solyc11g007980.2	-3,72	5,23E-16	1,08E-14	Cytochrome
Solyc06g068270.3	-3,72	1,56E-12	2,36E-11	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc03g044630.2	-3,73	1,54E-22	4,99E-21	DUF309 domain protein
Solyc03g114100.1	-3,74	1,93E-23	6,70E-22	hypothetical protein
Solyc06g060050.1	-3,74	3,31E-09	3,46E-08	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc04g040170.3	-3,74	8,88E-45	7,79E-43	DNA-directed RNA polymerase V subunit 5A
Solyc07g007990.4	-3,74	1,27E-04	6,43E-04	Nucleotide/sugar transporter family protein
Solyc06g053980.3	-3,76	9,07E-40	6,35E-38	Chlorophyllase 2
Solyc01g096400.4	-3,77	4,94E-51	5,33E-49	Transglut_core2 domain-containing protein
Solyc02g067440.3	-3,78	4,81E-09	4,90E-08	meloidogyne-induced giant cell protein DB114
Solyc01g081560.2	-3,78	8,49E-10	9,59E-09	Pentatricopeptide repeat

Solyc09g090070.1	-3,78	4,00E-63	6,34E-61	phosphate transporter 1
Solyc06g008100.3	-3,78	1,67E-12	2,51E-11	Unknown protein
Solyc09g075170.1	-3,79	1,06E-11	1,45E-10	Pentatricopeptide repeat-containing protein
Solyc10g008270.3	-3,82	1,56E-36	9,86E-35	bHLH transcription factor 094
Solyc03g113850.1	-3,83	2,71E-20	7,73E-19	Transducin/WD40 repeat-like superfamily protein
Solyc04g071890.3	-3,84	7,39E-37	4,70E-35	Peroxidase
Solyc04g063210.3	-3,86	2,54E-40	1,83E-38	Caffeoyl-CoA O-methyltransferase
Solyc04g009000.1	-3,86	2,54E-08	2,34E-07	Pentatricopeptide repeat-containing protein
Solyc01g079830.3	-3,87	2,23E-13	3,66E-12	hypothetical protein
Solyc09g009530.4	-3,89	7,33E-47	6,93E-45	Alpha/beta-Hydrolases superfamily protein
Solyc08g080660.1	-3,90	2,07E-07	1,67E-06	Pathogenesis-related thaumatin family protein
Solyc03g083730.1	-3,90	7,40E-13	1,15E-11	Plant invertase/pectin methylesterase inhibitor superfamily protein, putative
Solyc03g031890.3	-3,91	2,41E-19	6,45E-18	Cold induced protein-like
Solyc01g067690.4	-3,92	2,01E-17	4,69E-16	Unknown protein
Solyc04g076780.4	-3,92	1,69E-42	1,30E-40	Oligopeptide transporter
Solyc04g064660.1	-3,94	7,17E-17	1,59E-15	Pentatricopeptide repeat-containing protein
Solyc03g115770.3	-3,94	6,38E-21	1,90E-19	Two-component response regulator-like APRR5
Solyc10g005450.2	-3,95	1,34E-06	9,58E-06	Equilibrative nucleotide transporter like
Solyc11g005970.1	-3,96	1,14E-08	1,10E-07	Pentatricopeptide repeat
Solyc04g080700.4	-3,97	3,73E-51	4,04E-49	Bifunctional nuclease 2
Solyc04g005460.1	-3,97	1,12E-06	8,08E-06	Pentatricopeptide repeat
Solyc03g031600.3	-3,97	2,50E-46	2,32E-44	Peroxisomal membrane protein PMP22
Solyc07g054780.1	-3,98	1,31E-17	3,11E-16	Wound induced protein
Solyc07g005190.3	-3,98	6,50E-64	1,07E-61	Lysosomal Pro-X carboxypeptidase
Solyc04g007140.1	-3,98	1,88E-09	2,04E-08	protein NIM1-INTERACTING 2-like
Solyc02g083880.3	-3,98	1,91E-14	3,46E-13	Gibberellin-regulated protein 3
Solyc12g014140.3	-4,00	7,28E-44	6,04E-42	SlTCP3
Solyc01g049880.3	-4,01	1,88E-48	1,84E-46	Unknown protein
Solyc01g088830.2	-4,01	3,04E-08	2,78E-07	Ankyrin repeat-containing protein
Solyc11g045530.3	-4,01	5,36E-22	1,67E-20	LOB domain-containing protein
Solyc05g009480.1	-4,02	4,97E-15	9,40E-14	Unknown protein
Solyc05g008130.4	-4,02	5,10E-32	2,68E-30	Unknown protein
Solyc12g089240.2	-4,03	7,66E-34	4,35E-32	B-box zinc finger protein 22
Solyc12g089220.3	-4,04	8,31E-73	1,81E-70	Bifunctional nuclease 2
Solyc11g006700.1	-4,06	3,21E-09	3,36E-08	Pentatricopeptide repeat-containing protein
Solyc01g079470.4	-4,07	9,42E-97	4,64E-94	Unknown protein
Solyc10g050210.3	-4,07	7,39E-11	9,31E-10	ABSCISIC ACID-INSENSITIVE 5-like protein 5
Solyc07g024000.3	-4,09	5,62E-90	1,96E-87	NAD(P)-binding Rossmann-fold superfamily protein
Solyc01g073890.3	-4,10	2,80E-13	4,54E-12	Cysteine/Histidine-rich C1 domain family protein
Solyc03g119530.3	-4,10	4,68E-34	2,69E-32	LOB domain-containing protein 41
Solyc03g114130.1	-4,11	5,07E-62	7,79E-60	NHL domain protein
Solyc01g096420.3	-4,12	3,60E-36	2,25E-34	NADPH quinone oxidoreductase
Solyc06g066590.4	-4,12	1,78E-19	4,79E-18	Protein PLANT CADMIUM RESISTANCE 8
Solyc11g071460.2	-4,13	1,23E-66	2,17E-64	NAD(P)-binding Rossmann-fold superfamily protein
Solyc11g072620.1	-4,14	1,66E-16	3,57E-15	Unknown protein
Solyc06g053960.3	-4,14	2,01E-35	1,21E-33	Heat shock transcription factor
Solyc07g005930.4	-4,14	4,97E-34	2,84E-32	DNA-directed RNA polymerase
Solyc01g102690.4	-4,16	1,85E-09	2,01E-08	Pentatricopeptide repeat-containing protein
Solyc10g018190.2	-4,16	5,08E-05	2,79E-04	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc05g052680.1	-4,16	1,39E-06	9,91E-06	HXXXD-type acyl-transferase family protein
Solyc12g005020.2	-4,17	9,65E-15	1,79E-13	RING/U-box superfamily protein
Solyc01g096820.4	-4,18	4,35E-15	8,27E-14	Calcium/calmodulin dependent protein kinase
Solyc10g050220.2	-4,19	1,58E-31	8,20E-30	hypothetical protein
Solyc01g005290.4	-4,23	5,14E-57	6,85E-55	Sec14p-like phosphatidylinositol transfer family protein
Solyc12g096810.2	-4,24	1,07E-13	1,81E-12	LETM1 domain-containing protein
Solyc08g079680.3	-4,25	5,41E-47	5,14E-45	Ycf49-like protein
Solyc03g111710.3	-4,27	1,60E-54	1,92E-52	BTB/POZ and TAZ domain-containing protein 2
Solyc01g073880.2	-4,27	2,40E-20	6,87E-19	Cysteine/Histidine-rich C1 domain family protein
Solyc02g062890.3	-4,28	6,60E-24	2,33E-22	polyol monosaccharide transporter 5
Solyc10g076760.3	-4,29	6,92E-49	6,99E-47	Protein kinase superfamily protein
Solyc11g011400.2	-4,31	8,48E-10	9,59E-09	Unknown protein
Solyc03g026050.3	-4,32	3,31E-23	1,13E-21	Terminal flower 1
Solyc09g055940.3	-4,32	1,01E-48	1,02E-46	Bile acid:sodium symporter
Solyc08g006770.3	-4,34	4,46E-82	1,21E-79	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc04g005770.3	-4,35	3,58E-08	3,23E-07	Pentatricopeptide repeat-containing protein
Solyc05g013560.3	-4,35	1,48E-63	2,37E-61	Serine-rich protein-like protein
Solyc01g103590.4	-4,36	2,12E-23	7,29E-22	Lactoylglutathione lyase / glyoxalase
Solyc07g042100.3	-4,37	2,35E-12	3,46E-11	hypothetical protein
Solyc07g041720.1	-4,41	2,58E-76	6,10E-74	Germin-like protein
Solyc06g009620.1	-4,42	1,73E-17	4,06E-16	Pentatricopeptide repeat
Solyc02g090390.4	-4,43	1,44E-66	2,52E-64	Protein kinase
Solyc07g041900.3	-4,44	1,07E-94	4,90E-92	cysteine proteinase
Solyc04g015560.4	-4,45	2,46E-32	1,33E-30	Glycosyl hydrolase family protein
Solyc04g076720.3	-4,47	1,62E-25	6,15E-24	autophagy-related protein 18a-like
Solyc06g053950.3	-4,47	3,16E-25	1,18E-23	Heat stress transcription factor A-2e
Solyc05g023900.1	-4,48	6,08E-14	1,06E-12	Pentatricopeptide repeat
Solyc01g095450.4	-4,51	5,25E-09	5,33E-08	GDSL esterase/lipase
Solyc06g009190.4	-4,54	2,68E-60	3,95E-58	Pectinesterase
Solyc11g010290.2	-4,55	2,50E-29	1,17E-27	Dicarboxylate transporter 2.1, chloroplastic
Solyc04g071990.3	-4,59	9,09E-91	3,35E-88	Protein GIGANTEA
Solyc05g055540.3	-4,60	8,94E-24	3,14E-22	Major facilitator superfamily
Solyc01g006670.2	-4,64	1,49E-38	1,01E-36	Glycosyltransferase
Solyc11g011990.2	-4,65	6,54E-83	1,85E-80	plastid terminal oxidase
Solyc02g070820.1	-4,68	6,93E-19	1,80E-17	Avr9/Cf-9 rapidly elicited protein 180
Solyc11g027840.2	-4,68	5,91E-55	7,27E-53	Alpha/beta-Hydrolases superfamily protein
Solyc02g064810.1	-4,70	5,19E-07	3,96E-06	Auxin-responsive GH3 family protein
Solyc01g006020.4	-4,70	2,05E-62	3,17E-60	BnaCnng41690D protein
Solyc03g096140.2	-4,71	4,41E-04	1,98E-03	Protein yippee-like
Solyc07g008560.3	-4,73	2,21E-43	1,80E-41	Purple acid phosphatase
Solyc03g093800.1	-4,73	9,06E-55	1,09E-52	glycine-rich cell wall structural protein 2
Solyc01g109090.2	-4,77	2,02E-16	4,32E-15	Unknown protein
Solyc01g091830.3	-4,79	1,31E-35	7,99E-34	hypothetical protein
Solyc06g082070.3	-4,80	1,49E-48	1,48E-46	Protein trichome birefringence-like 45
Solyc12g009110.3	-4,82	1,64E-68	3,17E-66	O-methyltransferase, putative
Solyc12g089190.1	-4,82	1,08E-23	3,78E-22	Protein RADIALIS-like 6
Solyc12g006260.1	-4,86	3,36E-35	2,00E-33	Glycine rich protein-interacting protein
Solyc06g060970.2	-4,90	2,99E-04	1,40E-03	Expansin-like B1
Solyc01g067330.3	-4,92	7,44E-16	1,52E-14	CASP-like protein
Solyc08g005960.2	-5,01	6,73E-42	5,06E-40	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc06g083650.3	-5,13	1,55E-47	1,49E-45	GDSL esterase/lipase
Solyc04g050620.3	-5,14	3,57E-91	1,34E-88	Cytochrome
Solyc05g008120.4	-5,16	1,70E-39	1,18E-37	DnaJ-like protein subfamily B member 6
Solyc02g070800.2	-5,21	1,86E-85	5,84E-83	DUF561 domain-containing protein
Solyc02g079560.1	-5,22	5,09E-23	1,72E-21	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc05g010240.4	-5,23	1,67E-22	5,40E-21	Chaperonin-60 beta4
Solyc04g007470.3	-5,24	3,67E-45	3,26E-43	Drought responsive Zinc finger protein
Solyc10g009310.4	-5,33	2,73E-40	1,96E-38	Cytochrome P450
Solyc12g057060.2	-5,38	3,66E-51	4,01E-49	Glycosyltransferase
Solyc05g009490.3	-5,43	7,06E-13	1,10E-11	Unknown protein
Solyc07g055050.3	-5,48	7,88E-113	5,60E-110	ATP synthase protein I-related protein
Solyc06g059740.4	-5,52	1,73E-90	6,16E-88	Alcohol dehydrogenase
Solyc11g021360.3	-5,52	5,57E-39	3,84E-37	Unknown protein
Solyc08g078080.2	-5,58	8,56E-20	2,37E-18	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc06g051660.1	-5,60	8,48E-73	1,83E-70	Protein EARLY FLOWERING 4

Solyc09g009810.1	-5,61	7,10E-17	1,58E-15	hypothetical protein
Solyc12g042950.2	-5,62	1,44E-91	5,74E-89	ADP,ATP carrier protein
Solyc09g092260.4	-5,62	8,97E-65	1,52E-62	Chaperone protein DnaJ
Solyc10g051215.1	-5,68	1,30E-37	8,66E-36	E3 ubiquitin-protein ligase ATL9
Solyc09g075880.3	-5,68	1,60E-10	1,94E-09	Unknown protein
Solyc04g074920.2	-5,73	1,95E-10	2,36E-09	Glycosyltransferase AER61
Solyc03g098030.3	-5,75	1,35E-15	2,69E-14	Type I inositol polyphosphate 5-phosphatase 5
Solyc01g066570.3	-5,78	2,08E-28	9,26E-27	FCS-Like Zinc finger 15
Solyc09g092110.4	-5,79	5,06E-40	3,60E-38	Light-regulated protein
Solyc03g093410.3	-5,82	9,56E-35	5,63E-33	Sugar transporter protein 16
Solyc11g068710.3	-5,83	2,40E-37	1,58E-35	F-box family protein
Solyc10g049420.2	-5,87	9,92E-37	6,28E-35	Unknown protein
Solyc10g085190.2	-5,87	3,35E-11	4,36E-10	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc10g078510.3	-5,97	1,71E-43	1,40E-41	Glucan endo-1,3-beta-glucosidase 5
Solyc01g096790.4	-5,97	4,04E-41	2,98E-39	B3 domain-containing protein
Solyc11g069093.1	-5,99	4,00E-20	1,12E-18	SAUR-like auxin-responsive protein family
Solyc10g084020.1	-6,00	3,79E-16	7,95E-15	SAUR-like auxin-responsive protein family
Solyc03g005330.1	-6,01	5,03E-42	3,81E-40	Non-specific serine/threonine protein kinase
Solyc04g010250.3	-6,01	5,54E-124	4,43E-121	Alpha/beta-Hydrolases superfamily protein
Solyc03g116460.4	-6,02	2,54E-128	2,32E-125	Aspartate racemase
Solyc02g079550.3	-6,10	1,77E-25	6,71E-24	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc06g076350.3	-6,26	1,96E-82	5,46E-80	LePCL1
Solyc06g006010.3	-6,28	4,00E-48	3,87E-46	Receptor-like protein kinase
Solyc02g081060.4	-6,31	1,10E-72	2,35E-70	Chaperonin-like RbcX
Solyc11g018660.2	-6,36	1,23E-06	8,80E-06	NAC domain
Solyc08g082680.3	-6,36	3,31E-53	3,83E-51	RING/U-box superfamily protein
Solyc07g014730.3	-6,38	7,74E-30	3,67E-28	Phospholipase A2-alpha
Solyc08g006765.1	-6,48	3,54E-50	3,71E-48	N-acetyltransferase
Solyc04g005555.1	-6,55	2,44E-39	1,69E-37	CASP-like protein 4A1 isoform X1
Solyc10g085940.1	-6,61	2,68E-07	2,13E-06	membrane-associated kinase regulator
Solyc01g100000.3	-6,69	4,79E-85	1,46E-82	F-box domain, Phloem protein 2-like protein
Solyc05g024010.3	-6,71	1,47E-67	2,76E-65	Zinc finger protein CONSTANS-LIKE 15
Solyc06g005100.3	-6,73	1,32E-04	6,65E-04	Phosphatidylinositol transfer protein
Solyc02g085910.4	-6,81	3,11E-09	3,27E-08	LOB domain-containing protein
Solyc09g150156.1	-6,86	1,57E-10	1,91E-09	Unknown protein
Solyc10g083580.2	-6,89	1,33E-07	1,11E-06	PHYTOSULFOKINE 3 PRECURSOR
Solyc12g006440.2	-6,91	4,85E-26	1,87E-24	transmembrane protein
Solyc10g078920.3	-6,93	4,05E-101	2,22E-98	Thioredoxin-like 3-1, chloroplastic
Solyc02g076690.3	-7,06	2,25E-84	6,75E-82	Cysteine protease CP14
Solyc07g053900.2	-7,08	2,06E-25	7,80E-24	DUF506 domain-containing protein
Solyc07g047990.1	-7,15	2,31E-12	3,41E-11	MAP kinase kinase kinase 49
Solyc06g073080.4	-7,18	1,03E-19	2,82E-18	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc06g072130.4	-7,36	5,54E-12	7,83E-11	tonoplast intrinsic protein 3.1
Solyc08g074895.1	-7,57	4,31E-05	2,41E-04	F-box/FBD/LRR-repeat protein isoform X2
Solyc01g057680.4	-7,60	4,14E-64	6,92E-62	Unknown protein
Solyc01g108100.3	-7,69	1,19E-34	6,98E-33	cold regulated protein 27
Solyc01g006680.4	-7,82	3,12E-133	2,99E-130	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc03g081240.3	-7,88	4,67E-78	1,16E-75	Two-component response regulator-like APRR9
Solyc01g111350.3	-8,04	1,61E-142	2,38E-139	Major facilitator superfamily protein
Solyc08g078420.2	-8,16	1,15E-15	2,31E-14	Ethylene-responsive transcription factor
Solyc06g005680.4	-8,31	4,80E-84	1,42E-81	Two-component response regulator
Solyc01g005300.4	-8,32	3,29E-89	1,13E-86	Adagio-like protein 1
Solyc02g014860.3	-8,95	1,13E-72	2,39E-70	Chaperone protein DnaJ
Solyc07g055720.4	-9,05	1,08E-209	1,04E-205	Heat shock protein, putative
Solyc03g083770.1	-9,05	6,20E-144	9,91E-141	Plant invertase/pectin methylesterase inhibitor superfamily protein, putative
Solyc09g082670.3	-9,08	1,60E-26	6,43E-25	Heat shock transcription factor
Solyc01g108910.4	-9,34	1,38E-212	2,65E-208	maternal effect embryo arrest 14
Solyc04g077640.4	-9,83	2,27E-92	9,27E-90	Serine carboxypeptidase
Solyc06g006000.3	-9,96	1,67E-141	2,29E-138	Maternal effect embryo arrest 59
Solyc08g007240.4	-10,01	5,15E-161	1,10E-157	Nudix hydrolase 8
Solyc05g009310.3	-10,04	5,80E-112	3,84E-109	Zinc finger protein CONSTANS-LIKE 7
Solyc12g006240.2	-10,36	2,51E-158	4,82E-155	Zinc finger protein CONSTANS-LIKE 9
Solyc06g051680.1	-11,35	1,61E-90	5,84E-88	Protein EARLY FLOWERING 4
Solyc03g026000.4	-11,73	1,99E-91	7,79E-89	bromodomain-containing protein DDB_G0271118-like
Solyc04g078880.3	-12,94	1,31E-121	9,67E-119	cold regulated protein 27

Tab. 2. List of differentially expressed genes identified in progeny lines

Gene ID	logFC	P-value	FDR	Gene description
Solyc08g066910.1	7,73	1,38E-04	1,15E-03	Unknown protein
Solyc03g093120.5.1	7,56	8,67E-10	6,37E-08	Xyloglucan endotransglucosylase/hydrolase
Solyc05g052400.3	7,21	7,87E-06	1,17E-04	Laccase
Solyc04g026020.3	7,10	6,13E-06	9,56E-05	Sieve element occlusion b
Solyc08g068030.1	6,85	5,79E-06	9,23E-05	zinc finger FYVE domain protein
Solyc05g017795.1	6,68	9,82E-05	8,74E-04	ATP-dependent DNA helicase
Solyc01g066614.1	6,64	1,20E-04	1,03E-03	Guanylate-binding family protein
Solyc02g087970.1	6,58	6,76E-04	4,12E-03	Mini zinc finger protein
Solyc08g074510.1	6,52	8,81E-07	2,00E-05	TATA-binding protein-associated factor BTAF1
Solyc03g124110.2	6,42	1,00E-06	2,24E-05	Dehydration-responsive element-binding transcription factor
Solyc08g074683.1	6,42	1,78E-06	3,57E-05	Polyphenol oxidase
Solyc03g118820.4	6,40	1,30E-02	4,11E-02	Ras-related protein RABA6a
Solyc05g017793.1	6,39	1,42E-04	1,18E-03	Unknown protein
Solyc03g093110.3	6,30	1,56E-16	8,37E-14	Xyloglucan endotransglucosylase/hydrolase
Solyc03g078620.1	6,13	7,34E-04	4,39E-03	C2 calcium/lipid-binding domain, CaLB
Solyc01g066616.1	5,39	2,27E-03	1,06E-02	replication protein A 70 kDa DNA-binding subunit B-like
Solyc01g087500.3	5,15	3,58E-09	2,11E-07	DNA topoisomerase 2
Solyc10g005740.3	4,93	1,32E-07	4,10E-06	Sec14p-like phosphatidylinositol transfer family protein
Solyc01g005320.2	4,78	9,67E-05	8,65E-04	3-oxo-5-alpha-steroid 4-dehydrogenase (DUF1295)
Solyc03g026270.3	4,72	1,68E-07	4,94E-06	CRT binding factor 3
Solyc11g011300.2	4,55	2,72E-05	3,15E-04	Rhamnogalacturonate lyase
Solyc09g084460.3	4,51	2,62E-10	2,27E-08	Protease inhibitor I
Solyc03g093080.3	4,31	2,34E-11	2,79E-09	Xyloglucan endotransglucosylase/hydrolase
Solyc01g094050.1	4,28	3,00E-16	1,40E-13	WD-40 repeat family protein / beige-like protein
Solyc05g005540.4	4,27	1,77E-33	3,31E-29	Polygalacturonase-1 non-catalytic subunit beta
Solyc05g047710.3	4,21	2,30E-05	2,77E-04	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc03g098420.3	4,18	1,05E-06	2,31E-05	Pentatricopeptide repeat
Solyc06g061200.1	4,11	1,33E-07	4,12E-06	glycine-rich protein 1
Solyc07g040960.1	4,10	6,68E-19	6,25E-16	Harbinger transposase-derived nuclease
Solyc07g042520.4	4,06	7,04E-04	4,25E-03	Sucrose synthase
Solyc04g050520.3	3,93	5,80E-11	6,14E-09	Translational activator GCN1
Solyc09g010990.3	3,86	8,99E-04	5,15E-03	Laccase
Solyc04g078970.3	3,84	1,87E-11	2,30E-09	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1
Solyc01g111740.3	3,82	5,36E-06	8,70E-05	DUF632 domain-containing protein/DUF630 domain-containing protein
Solyc01g060050.3	3,81	6,21E-07	1,52E-05	WD40 domain-containing protein
Solyc08g067500.1	3,81	2,12E-04	1,64E-03	Non-specific lipid-transfer protein
Solyc02g083480.3	3,77	1,66E-02	4,97E-02	Peroxidase
Solyc10g081200.1	3,72	4,11E-10	3,38E-08	Dentin sialophosphoprotein
Solyc10g011940.1	3,70	3,17E-03	1,37E-02	SNF2_N domain-containing protein/Chromo domain-containing protein
Solyc10g079300.2	3,68	2,82E-11	3,33E-09	Calcium-transporting ATPase
Solyc00g500066.1	3,68	8,70E-03	3,00E-02	Photosystem I assembly protein Ycf4
Solyc07g043170.4	3,67	1,53E-05	1,98E-04	Glycosyltransferase
Solyc04g078710.3	3,67	2,01E-03	9,65E-03	Subtilisin-like protease
Solyc07g049600.4	3,66	4,12E-05	4,39E-04	Fimbrin-5

Solyc07g056000.2	3,63	1,49E-17	1,07E-14	Xyloglucan endotransglucosylase/hydrolase
Solyc05g054870.3	3,62	2,94E-03	1,29E-02	protein RDM16 isoform X1
Solyc03g116070.1	3,62	2,12E-03	1,00E-02	Mini zinc finger protein 1
Solyc03g121900.1	3,60	1,80E-08	8,13E-07	Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain containing protein
Solyc02g072490.3	3,59	1,08E-07	3,48E-06	O-fucosyltransferase
Solyc09g009620.1	3,56	1,16E-03	6,25E-03	protein LITTLE ZIPPER 3
Solyc06g007890.3	3,52	1,17E-07	3,71E-06	Gibberellin regulated protein
Solyc11g006200.2	3,51	1,10E-04	9,56E-04	Homeobox domain-containing protein/DDT domain-containing protein
Solyc06g035700.1	3,50	1,57E-04	1,28E-03	Ethylene-responsive transcription factor
Solyc10g051010.3	3,50	4,02E-06	6,86E-05	Pentatricopeptide repeat-containing protein
Solyc02g069140.3	3,48	4,94E-04	3,17E-03	Leucine--tRNA ligase, cytoplasmic
Solyc05g015320.3	3,43	2,20E-04	1,68E-03	65-kDa microtubule-associated protein 8
Solyc11g005690.3	3,43	9,36E-06	1,35E-04	TONSOKU protein
Solyc11g045140.1	3,42	4,32E-03	1,74E-02	Vacuolar protein sorting-associated protein
Solyc03g115380.3	3,35	7,34E-08	2,56E-06	UDP-glucose 6-dehydrogenase
Solyc09g074700.2	3,32	3,53E-04	2,43E-03	Homeobox protein LUMINIDEPENDENS
Solyc10g009150.3	3,30	6,88E-05	6,60E-04	Organ specific protein
Solyc02g070380.1	3,29	1,42E-05	1,85E-04	Disease resistance protein
Solyc03g019890.3	3,27	7,49E-14	1,87E-11	beta-galactosidase 7
Solyc09g075480.3	3,27	3,10E-10	2,65E-08	Kinesin-4
Solyc04g049930.2	3,26	9,76E-06	1,40E-04	Unknown protein
Solyc12g098467.1	3,26	2,32E-06	4,41E-05	glutamic acid-rich protein-like
Solyc04g008430.1	3,25	1,49E-06	3,09E-05	Serine/threonine-protein kinase BRI1-like 2
Solyc04g080520.1	3,25	2,39E-04	1,80E-03	proteoglycan 4
Solyc05g013870.4	3,23	3,22E-20	4,03E-17	Sieve element occlusion b
Solyc03g058390.2	3,23	1,05E-08	5,22E-07	Eukaryotic translation initiation factor 5B
Solyc04g076640.3	3,21	3,62E-05	3,95E-04	Rhamnogalacturonate lyase
Solyc09g090550.3	3,20	4,35E-06	7,28E-05	Arp2/3 complex 34 kDa subunit
Solyc00g500065.1	3,19	5,41E-03	2,07E-02	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic
Solyc04g072840.3	3,17	1,17E-05	1,59E-04	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc04g077950.2	3,14	4,24E-04	2,80E-03	nucleic acid binding protein
Solyc11g062320.2	3,11	5,82E-06	9,25E-05	Proteasome-associated protein ECM29
Solyc09g055890.4	3,09	5,70E-05	5,72E-04	Lipoxygenase
Solyc12g013710.2	3,07	4,92E-08	1,86E-06	light dependent NADH:protochlorophyllide oxidoreductase 1
Solyc01g096960.3	3,06	7,87E-05	7,35E-04	Inactive protein RESTRICTED TEV MOVEMENT 2
Solyc02g093300.3	3,06	1,35E-07	4,17E-06	DNA polymerase
Solyc06g043150.4	3,05	2,13E-04	1,64E-03	WD40 repeat
Solyc02g094100.4	3,05	1,06E-03	5,85E-03	Fidgetin-like protein 1
Solyc10g005220.3	3,05	7,63E-05	7,18E-04	RING/U-box superfamily protein
Solyc05g054850.1	3,01	1,67E-04	1,35E-03	membrane-associated kinase regulator
Solyc03g122080.3	3,00	3,45E-05	3,80E-04	DUF936 domain-containing protein
Solyc02g081300.3	2,99	4,11E-09	2,33E-07	Sucrose synthase
Solyc09g014490.4	2,99	4,98E-07	1,25E-05	flocculation FLO11-like protein
Solyc11g010360.3	2,98	3,93E-03	1,62E-02	protein MIZU-KUSSEI 1-like
Solyc12g005310.2	2,97	5,13E-14	1,32E-11	Auxin-responsive GH3 family protein
Solyc06g069730.3	2,96	1,68E-07	4,95E-06	Chlorophyll a-b binding protein, chloroplastic
Solyc05g005230.3	2,94	3,82E-03	1,58E-02	Plant protein 1589 of Uncharacterized protein function
Solyc08g077360.3	2,94	1,79E-03	8,81E-03	Dynamin
Solyc03g111730.3	2,93	2,38E-03	1,10E-02	KDEL-tailed cysteine endopeptidase
Solyc10g084290.2	2,92	3,87E-04	2,62E-03	Interactor of constitutive active ROPs
Solyc01g103960.3	2,92	1,58E-04	1,29E-03	RNA helicase DEAH-box15
Solyc02g067010.3	2,91	2,60E-03	1,17E-02	ARF guanine-nucleotide exchange factor GNL1
Solyc06g036590.1	2,91	2,25E-06	4,29E-05	protein RDM16-like isoform X1
Solyc12g007020.2	2,91	2,50E-03	1,14E-02	DUF936 domain-containing protein
Solyc07g052510.4	2,91	2,65E-03	1,19E-02	peroxidase (TPX1)
Solyc10g085090.3	2,89	1,55E-04	1,27E-03	Laccase
Solyc12g098390.3	2,89	1,35E-04	1,13E-03	Ankyrin repeat-containing protein
Solyc06g076330.3	2,88	7,41E-07	1,76E-05	Laccase
Solyc05g054090.3	2,88	2,17E-06	4,16E-05	induced stolen tip protein TUB8-like
Solyc01g090120.3	2,87	1,36E-07	4,17E-06	Uclacyanin-3
Solyc01g101015.1	2,87	6,13E-05	6,04E-04	Unknown protein
Solyc06g053570.2	2,86	2,50E-08	1,05E-06	Nuclear-pore anchor protein
Solyc08g067510.1	2,86	3,44E-03	1,46E-02	Non-specific lipid-transfer protein
Solyc04g008040.4	2,85	3,43E-16	1,57E-13	Microtubule-associated protein 70
Solyc08g016060.1	2,85	3,73E-08	1,47E-06	Guanine nucleotide exchange factor SPIKE 1
Solyc01g057850.4	2,83	1,17E-04	1,00E-03	nuclear export mediator factor NEMF-like
Solyc03g025610.3	2,81	2,16E-11	2,59E-09	Tripeptidyl-peptidase 2
Solyc08g069040.3	2,81	1,35E-08	6,42E-07	Peroxidase
Solyc04g050160.4	2,81	6,50E-05	6,31E-04	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc02g014190.4	2,80	6,44E-05	6,26E-04	Zinc finger C3HC4 type (RING finger) protein
Solyc02g094530.1	2,79	3,12E-08	1,26E-06	Nuclear factor related to kappa-B-binding protein
Solyc12g014200.3	2,79	1,63E-03	8,15E-03	Protein trichome birefringence-like 31
Solyc10g006500.4	2,79	9,51E-07	2,14E-05	Hexosyltransferase
Solyc12g042180.1	2,77	1,33E-04	1,11E-03	Adp-ribosylation factor gtpase-activating protein agd3
Solyc03g006810.3	2,76	1,24E-08	5,94E-07	Peroxidase
Solyc10g076995.1	2,76	3,50E-06	6,15E-05	cardiomyopathy-associated protein
Solyc12g006270.2	2,74	3,46E-06	6,12E-05	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit
Solyc11g005760.3	2,73	2,32E-05	2,78E-04	Hexosyltransferase
Solyc06g070970.3	2,72	5,96E-05	5,90E-04	microtubule-associated futsch-like protein
Solyc10g076830.2	2,72	3,62E-05	3,95E-04	Laccase
Solyc08g061520.3	2,71	1,20E-05	1,62E-04	Myosin
Solyc08g079030.4	2,71	8,26E-03	2,88E-02	hypothetical protein (DUF863)
Solyc02g071000.1	2,71	7,12E-09	3,71E-07	Chlorophyll a-b binding protein, chloroplastic
Solyc10g085670.2	2,71	8,45E-12	1,16E-09	MAP kinase kinase kinase 79
Solyc04g076500.4	2,70	3,23E-07	8,57E-06	BEACH domain
Solyc09g075550.3	2,70	3,64E-04	2,49E-03	Cellulose synthase
Solyc07g062530.3	2,69	9,67E-05	8,65E-04	phosphoenolpyruvate carboxylase 2
Solyc10g005125.1	2,69	2,57E-07	7,03E-06	Endoribonuclease Dicer-like protein 1
Solyc01g105510.3	2,69	5,18E-04	3,30E-03	LMBR1-like membrane protein
Solyc08g080780.4	2,69	9,67E-15	3,18E-12	Myosin heavy chain-related protein
Solyc02g084510.3	2,69	2,31E-05	2,78E-04	Zinc finger CCCH domain-containing protein 19
Solyc10g074920.2	2,68	7,41E-20	8,67E-17	Mannan endo-1,4-beta-mannosidase
Solyc08g068920.4	2,67	7,24E-05	6,88E-04	Protein kinase superfamily protein
Solyc12g049500.3	2,67	3,83E-04	2,59E-03	DUF936 domain-containing protein
Solyc02g083640.4	2,67	2,93E-04	2,10E-03	Protein POLLENLESS 3-LIKE 2
Solyc09g072820.4	2,67	9,54E-11	9,30E-09	Cellulose synthase
Solyc03g096030.3	2,67	1,39E-07	4,23E-06	Protein trichome birefringence-like 28
Solyc12g036120.1	2,66	2,15E-04	1,65E-03	ABC transporter C family member 2
Solyc09g064490.3	2,66	1,44E-03	7,36E-03	Subtilisin-like protease SDD1-like protein
Solyc07g061750.4	2,66	1,54E-03	7,76E-03	Ankyrin repeat
Solyc03g063220.2	2,65	1,53E-05	1,97E-04	RNA helicase DEAH-box8
Solyc03g114900.3	2,64	5,00E-03	1,95E-02	COBRA-like protein
Solyc02g086430.4	2,64	5,37E-03	2,06E-02	Zinc finger transcription factor 21
Solyc04g014550.3	2,63	1,13E-02	3,67E-02	TPX2 (Targeting protein for Xklp2) protein family
Solyc04g079360.1	2,63	3,79E-04	2,57E-03	R2R3MYB transcription factor 77
Solyc08g067870.2	2,63	7,69E-04	4,54E-03	embryo defective 2410
Solyc04g077990.3	2,63	2,70E-03	1,21E-02	LOB domain-containing protein 37
Solyc09g060110.4	2,63	8,68E-15	2,95E-12	Protein kinase domain
Solyc09g010810.3	2,62	3,00E-03	1,31E-02	Kinesin-like protein
Solyc07g049680.4	2,62	1,70E-04	1,37E-03	Condensin complex subunit 2
Solyc09g091650.3	2,62	7,73E-05	7,25E-04	Replication factor C subunit 1
Solyc08g074520.2	2,62	1,10E-05	1,53E-04	TATA-binding protein-associated factor BTAF1
Solyc04g072260.3	2,61	1,35E-06	2,84E-05	Midasin
Solyc11g062220.2	2,59	2,06E-05	2,52E-04	Zinc finger CCCH domain-containing protein 44
Solyc09g059260.4	2,59	1,18E-04	1,01E-03	Unknown protein
Solyc04g010180.4	2,58	3,04E-07	8,14E-06	LOW QUALITY PROTEIN: uncharacterized protein LOC110670528
Solyc09g014240.4	2,58	4,09E-16	1,82E-13	Laccase
Solyc01g110130.3	2,57	1,23E-13	2,88E-11	DNA helicase
Solyc04g008900.4	2,57	1,38E-04	1,15E-03	Transmembrane protein, putative (DUF247)
Solyc02g085230.3	2,57	1,41E-04	1,17E-03	U3 small nucleolar RNA-associated protein 22
Solyc11g010410.2	2,56	3,92E-04	2,64E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein

Solyc03g026040.4	2,56	6,15E-06	9,57E-05	Leucine-rich repeat receptor protein kinase
Solyc10g086030.2	2,56	5,26E-09	2,86E-07	Interactor of constitutive active ROPs
Solyc03g006300.3	2,55	9,67E-05	8,65E-04	Receptor-like protein kinase
Solyc04g074740.4	2,55	4,49E-03	1,79E-02	Blue copper protein
Solyc03g119990.4	2,55	6,47E-06	9,91E-05	Alpha/beta-Hydrolases superfamily protein
Solyc02g070970.1	2,55	2,55E-07	6,97E-06	Chlorophyll a-b binding protein, chloroplastic
Solyc04g076100.4	2,55	1,48E-07	4,46E-06	transmembrane protein
Solyc01g079700.3	2,55	6,93E-04	4,20E-03	Helicase, C-terminal
Solyc03g093330.4	2,54	1,50E-05	1,94E-04	Leucine-rich repeat receptor-like protein kinase
Solyc08g081120.4	2,54	1,33E-06	2,81E-05	Kinesin-4
Solyc04g009600.3	2,54	2,10E-04	1,63E-03	TRAF-like superfamily protein
Solyc11g045160.3	2,54	2,68E-03	1,20E-02	Vacuolar protein sorting-associated protein, putative (DUF1162)
Solyc03g098290.4	2,54	5,65E-06	9,04E-05	Sucrose synthase
Solyc11g013240.3	2,54	3,88E-04	2,63E-03	serine/threonine-protein kinase mph1 isoform X4
Solyc08g068040.3	2,53	2,26E-05	2,72E-04	zinc finger FYVE domain protein
Solyc03g111810.2	2,53	8,97E-23	2,40E-19	Sieve element occlusion a
Solyc02g032480.3	2,53	1,49E-03	7,58E-03	Nuclear pore complex protein NUP214
Solyc02g072240.3	2,53	8,20E-11	8,17E-09	Cellulose synthase
Solyc03g118310.4	2,52	1,34E-04	1,12E-03	bHLH transcription factor 083
Solyc01g107890.3	2,52	1,99E-17	1,38E-14	Filament-like plant protein 7
Solyc04g074420.1	2,51	1,06E-02	3,51E-02	Protein EXORDIUM-like 1
Solyc04g076630.3	2,51	6,59E-05	6,37E-04	Rhamnogalacturonate lyase
Solyc09g007360.3	2,50	6,53E-08	2,34E-06	Interactor of constitutive active ROPs
Solyc03g026280.3	2,50	5,92E-06	9,32E-05	C-repeat binding factor 1
Solyc06g009680.4	2,50	7,58E-05	7,14E-04	BRCT domain-containing protein
Solyc08g079080.5	2,49	6,29E-03	2,32E-02	Lycopersicon esculentum invertase 9
Solyc11g043130.2	2,49	4,17E-09	2,35E-07	Phosphatidylinositol 4-kinase alpha 1
Solyc09g092510.3	2,48	1,38E-03	7,17E-03	hypothetical protein
Solyc06g083370.3	2,48	3,23E-05	3,63E-04	hypothetical protein
Solyc07g005500.2	2,48	2,07E-03	9,85E-03	Formin-like protein
Solyc04g007650.4	2,47	4,11E-06	6,97E-05	1-phosphatidylinositol-3-phosphate 5-kinase-like protein
Solyc05g007300.3	2,47	4,24E-03	1,72E-02	HVA22-like protein
Solyc02g070950.1	2,47	6,30E-09	3,33E-07	Chlorophyll a-b binding protein, chloroplastic
Solyc01g102520.4	2,46	9,88E-06	1,41E-04	MLO-like protein
Solyc07g025380.3	2,46	3,18E-04	2,24E-03	DNA ligase-like protein
Solyc07g045010.3	2,45	2,20E-05	2,66E-04	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit
Solyc04g077190.4	2,45	1,73E-12	2,95E-10	Endo-1,4-beta-xylanase 1
Solyc05g006550.4	2,45	1,26E-13	2,91E-11	Microtubule-associated protein TORTIFOLIA1
Solyc00g500064.1	2,45	4,73E-12	6,97E-10	Ycf15
Solyc05g046020.3	2,45	1,15E-04	9,88E-04	Peroxidase
Solyc07g063350.3	2,44	2,58E-09	1,61E-07	COP1-interacting protein 7
Solyc06g009670.3	2,44	6,20E-05	6,10E-04	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc04g005180.4	2,43	2,46E-03	1,12E-02	Protein PHYLLO, chloroplastic
Solyc01g111590.4	2,43	1,04E-05	1,47E-04	WD-40 repeat-containing protein MSI1
Solyc02g070780.4	2,43	2,81E-12	4,54E-10	DNA helicase
Solyc07g065880.4	2,42	1,34E-04	1,13E-03	Kinesin KP1
Solyc11g069670.2	2,42	3,11E-03	1,35E-02	CC-NBS-LRR type resistance-like protein
Solyc03g116360.2	2,41	4,62E-04	3,00E-03	Regulator of chromosome condensation (RCC1) family protein
Solyc07g056230.3	2,41	6,40E-03	2,36E-02	Cytochrome b561 domain-containing protein
Solyc01g080750.3	2,41	2,96E-04	2,12E-03	ARM repeat superfamily protein
Solyc01g081420.3	2,41	6,76E-04	4,12E-03	Armadillo-type fold
Solyc04g076400.3	2,40	5,53E-05	5,56E-04	VIN3-like protein 3
Solyc02g032490.3	2,40	2,88E-03	1,27E-02	Nuclear pore complex protein
Solyc10g005860.3	2,40	4,88E-04	3,14E-03	WW domain-containing protein
Solyc07g005020.3	2,40	7,37E-11	7,50E-09	DNA helicase
Solyc10g054080.3	2,39	2,49E-18	2,12E-15	Kinesin-related protein 11
Solyc09g074840.4	2,39	4,50E-04	2,94E-03	kinetochore protein
Solyc01g006360.4	2,39	6,41E-06	9,83E-05	Callose synthase 9
Solyc08g005610.3	2,38	1,60E-06	3,27E-05	Cytochrome P450
Solyc04g008410.3	2,38	3,82E-05	4,12E-04	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc10g080350.3	2,37	2,88E-08	1,18E-06	DNA-directed RNA polymerase subunit
Solyc01g095690.2	2,37	6,50E-05	6,31E-04	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc06g074730.4	2,37	2,52E-04	1,88E-03	Argonaute 5
Solyc11g012860.3	2,37	2,18E-13	4,81E-11	coiled-coil protein
Solyc04g008600.4	2,37	6,75E-04	4,11E-03	Zinc knuckle (CCHC-type) family protein
Solyc01g110190.4	2,36	1,97E-08	8,76E-07	Kinesin-related protein
Solyc03g033510.3	2,36	1,24E-03	6,58E-03	Armadillo repeat only 2
Solyc11g008970.1	2,36	6,13E-03	2,28E-02	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc08g080890.3	2,36	4,12E-04	2,75E-03	E1-E2_ATPase domain-containing protein/HMA domain-containing protein/Hydrolase domain-containing protein
Solyc03g116840.3	2,36	9,05E-05	8,23E-04	Pentatricopeptide repeat-containing protein
Solyc01g079570.3	2,35	2,57E-06	4,80E-05	Beta-D-xylosidase 1
Solyc04g082430.3	2,35	1,83E-03	8,92E-03	cyclinB2_4
Solyc03g093130.3	2,34	1,07E-03	5,90E-03	xyloglucan endotransglucosylase-hydrolase 3
Solyc09g009350.2	2,34	1,22E-03	6,51E-03	Calcium-dependent lipid-binding family protein
Solyc05g017980.3	2,34	4,80E-14	1,28E-11	Microtubule-associated protein 70
Solyc08g016270.3	2,33	7,38E-03	2,64E-02	LOW QUALITY PROTEIN: LRR receptor-like serine/threonine-protein kinase GSO1
Solyc10g017960.2	2,33	5,22E-03	2,01E-02	F-box protein PP2-A15
Solyc11g005150.3	2,33	8,05E-05	7,48E-04	entensin X55687
Solyc07g041510.3	2,33	2,10E-06	4,06E-05	RNA polymerase-associated protein CTR9-like protein
Solyc02g089050.4	2,32	3,06E-07	8,16E-06	protein LONGIFOLIA 1-like
Solyc07g064960.2	2,32	5,62E-04	3,53E-03	Phosphatidate cytidylyltransferase
Solyc12g011290.2	2,32	3,36E-03	1,43E-02	Kinesin-4
Solyc01g006370.3	2,31	4,99E-14	1,30E-11	Callose synthase
Solyc04g076190.1	2,31	7,29E-06	1,09E-04	Eukaryotic aspartyl protease family protein
Solyc12g094700.3	2,31	1,21E-15	4,74E-13	Xylem cysteine proteinase 1
Solyc11g012020.2	2,30	5,31E-04	3,36E-03	EH domain-containing protein 1
Solyc01g006585.1	2,30	1,09E-04	9,51E-04	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc02g069490.4	2,30	1,05E-09	7,45E-08	Delta(24)-sterol reductase
Solyc09g065800.4	2,30	1,21E-03	6,50E-03	3-ketoacyl-CoA synthase
Solyc01g006090.3	2,29	8,02E-04	4,69E-03	Eukaryotic rRNA processing
Solyc02g082180.3	2,29	2,15E-08	9,36E-07	DNA helicase
Solyc02g083490.3	2,28	2,32E-03	1,08E-02	Peroxidase
Solyc09g065570.4	2,28	1,81E-05	2,26E-04	Serine/threonine-protein kinase Nek2
Solyc02g089370.2	2,28	2,00E-05	2,46E-04	ARM repeat superfamily protein
Solyc01g098980.4	2,28	4,14E-04	2,76E-03	MAP kinase kinase kinase 8
Solyc04g005560.3	2,27	9,26E-09	4,63E-07	ARF guanine-nucleotide exchange factor GNOM
Solyc05g013850.2	2,27	8,65E-21	1,35E-17	Sieve element occlusion b
Solyc10g084320.3	2,26	4,32E-08	1,67E-06	Subtilisin-like protease
Solyc01g065700.3	2,25	1,32E-09	9,02E-08	Protein phosphatase 2C family protein
Solyc06g059960.4	2,25	9,92E-07	2,22E-05	Histone-lysine N-methyltransferase ASHH2
Solyc02g014180.2	2,25	9,23E-09	4,63E-07	Zinc finger C3HC4 type (RING finger) protein
Solyc04g045530.4	2,25	4,76E-04	3,08E-03	DNA primase large subunit
Solyc01g060040.3	2,25	9,63E-09	4,78E-07	WD40 domain-containing protein/Bromodomain domain-containing protein
Solyc12g017240.2	2,24	1,01E-09	7,28E-08	xyloglucan endo-transglycosylase B1
Solyc01g112340.3	2,24	8,21E-07	1,90E-05	Brefeldin A-inhibited guanine nucleotide-exchange protein 4
Solyc04g080830.4	2,23	2,10E-08	9,17E-07	Pentatricopeptide repeat-containing protein
Solyc01g109950.4	2,23	2,38E-03	1,10E-02	Kinase family protein
Solyc05g026070.1	2,22	7,67E-04	4,54E-03	glycine-rich protein
Solyc04g074450.1	2,21	1,68E-09	1,08E-07	Protein EXORDIUM-like 1
Solyc08g029050.4	2,21	2,05E-04	1,60E-03	TOPLESS 6
Solyc01g079500.4	2,20	5,77E-06	9,20E-05	DNA replication licensing factor MCM7
Solyc04g015750.3	2,20	7,51E-17	4,54E-14	CobN/magnesium chelatase
Solyc06g083480.4	2,20	9,21E-05	8,34E-04	NAD(P)-binding Rossmann-fold superfamily protein
Solyc09g008380.3	2,20	6,11E-05	6,02E-04	Pectate lyase
Solyc03g122040.4	2,20	6,78E-16	2,95E-13	COP1-interacting protein-like protein
Solyc11g071300.2	2,20	8,70E-03	3,00E-02	Myb
Solyc12g044920.3	2,20	5,19E-04	3,30E-03	Phospholipid-transporting ATPase
Solyc07g064180.4	2,19	1,67E-03	8,30E-03	pectin methylesterase 2
Solyc01g088380.3	2,19	5,19E-03	2,00E-02	DNA replication helicase
Solyc05g010680.2	2,19	6,22E-05	6,10E-04	Alpha/beta-Hydrolases superfamily protein
Solyc10g055260.2	2,19	2,69E-03	1,20E-02	Auxin transporter-like protein 3

Solyc02g063230.1	2,19	1,11E-04	9,64E-04	membrane-associated kinase regulator
Solyc06g008710.3	2,18	4,12E-03	1,68E-02	Cullin 1
Solyc12g099540.2	2,18	2,59E-06	4,83E-05	Kinesin-like protein
Solyc02g069440.3	2,18	3,47E-03	1,47E-02	LOB domain-containing protein 3
Solyc11g008460.1	2,17	2,80E-08	1,16E-06	SART-1 family protein DOT2
Solyc08g016070.3	2,17	7,93E-06	1,17E-04	Guanine nucleotide exchange factor SPIKE 1
Solyc04g012060.3	2,17	6,33E-12	8,99E-10	Ribonucleoside-diphosphate reductase
Solyc03g114690.4	2,17	1,80E-03	8,83E-03	Transducin family protein / WD-40 repeat family protein
Solyc02g062650.3	2,17	8,76E-05	8,01E-04	Laccase
Solyc03g025530.3	2,17	2,37E-16	1,17E-13	oxidoreductase/transition metal ion-binding protein
Solyc06g068910.3	2,16	1,24E-06	2,66E-05	Receptor-like kinase 1
Solyc01g095090.3	2,16	1,15E-03	6,23E-03	RING/U-box superfamily protein
Solyc03g059140.4	2,16	7,33E-03	2,63E-02	Ion channel CASTOR
Solyc02g085810.3	2,16	6,09E-10	4,69E-08	HEAT repeat-containing protein 5B
Solyc03g120230.3	2,16	1,80E-07	5,21E-06	MAR-binding filament-like protein 1
Solyc06g075220.1	2,15	2,02E-07	5,71E-06	Fasciclin-like arabinogalactan protein 11
Solyc05g014130.3	2,14	1,17E-03	6,33E-03	COP1-interacting protein 4
Solyc02g085120.3	2,14	3,45E-13	6,94E-11	Laccase
Solyc02g070980.1	2,14	9,58E-07	2,15E-05	Chlorophyll a-b binding protein, chloroplastic
Solyc02g082260.3	2,14	1,45E-02	4,48E-02	3-hydroxy-3-methylglutaryl CoA reductase
Solyc02g070990.1	2,13	6,97E-05	6,67E-04	Chlorophyll a-b binding protein, chloroplastic
Solyc08g068600.3	2,13	2,48E-05	2,92E-04	Serine decarboxylase
Solyc03g120120.3	2,13	1,30E-05	1,72E-04	Regulator of Vps4 activity in the MVB pathway protein
Solyc02g081420.3	2,13	7,39E-04	4,40E-03	P-loop containing nucleoside triphosphate hydrolase
Solyc09g015170.4	2,12	2,75E-05	3,18E-04	Receptor-like kinase
Solyc12g099260.2	2,12	1,09E-11	1,41E-09	Citrate synthase-like
Solyc10g081880.3	2,12	2,18E-03	1,02E-02	Pentatricopeptide repeat
Solyc02g032960.2	2,12	2,23E-05	2,69E-04	ATP-dependent zinc metalloprotease FtsH 2
Solyc03g053080.3	2,12	3,42E-05	3,78E-04	Kinesin
Solyc05g051370.3	2,12	6,96E-08	2,45E-06	transcription initiation factor TFIID subunit
Solyc06g054560.3	2,11	2,72E-16	1,31E-13	RNA helicase DEAH-box19
Solyc02g036270.4	2,11	3,03E-03	1,32E-02	Disease resistance protein
Solyc03g112660.3	2,11	1,08E-14	3,42E-12	protein MODIFIER OF SNC1 1-like isoform X1
Solyc03g063680.3	2,11	2,88E-04	2,07E-03	Zinc finger transcription factor 26
Solyc04g081675.1	2,11	7,71E-04	4,55E-03	Reverse transcriptase zinc-binding domain
Solyc06g048470.4	2,10	2,12E-12	3,54E-10	COP1-Interacting protein-related
Solyc02g085110.4	2,10	3,07E-05	3,48E-04	Laccase
Solyc10g008440.3	2,10	9,32E-06	1,34E-04	Expansin-B3
Solyc11g071560.2	2,10	1,34E-02	4,22E-02	Protein RESTRICTED TEV MOVEMENT 2
Solyc10g079730.3	2,10	9,57E-03	3,23E-02	Condensin complex subunit 1
Solyc10g076900.3	2,10	4,24E-05	4,50E-04	Calcium-dependent protein kinase
Solyc01g100020.4	2,09	1,17E-03	6,29E-03	Phospholipase
Solyc09g009380.3	2,09	7,73E-06	1,15E-04	Protein kinase G11A
Solyc07g008090.4	2,09	1,36E-06	2,85E-05	Transducin family protein / WD-40 repeat family protein
Solyc05g010080.3	2,09	5,60E-06	8,98E-05	lysine-rich arabinogalactan protein 19
Solyc03g117250.4	2,09	2,44E-13	5,32E-11	Flotillin-like protein 2
Solyc06g076860.4	2,08	1,20E-02	3,86E-02	Cell division control protein
Solyc01g091480.4	2,08	3,14E-06	5,63E-05	Kinesin-like protein
Solyc04g049840.4	2,08	3,93E-06	6,77E-05	RNA binding (RRM/RBD/RNP motifs) family protein
Solyc11g065160.3	2,08	1,32E-08	6,30E-07	Zinc finger protein
Solyc11g012770.2	2,07	6,93E-11	7,16E-09	Sister chromatid cohesion PDS5-like protein
Solyc10g083500.2	2,07	1,85E-16	9,63E-14	Protein kinase G11A
Solyc03g070440.4	2,07	1,57E-07	4,68E-06	COBRA-like protein
Solyc02g068720.3	2,07	9,98E-12	1,30E-09	Protein NAP1
Solyc10g049570.3	2,07	5,29E-03	2,03E-02	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc07g041180.4	2,07	5,46E-06	8,81E-05	protein PLASTID MOVEMENT IMPAIRED 1-RELATED 1
Solyc09g005330.3	2,07	5,92E-06	9,32E-05	HEAT repeat-containing protein
Solyc11g044340.3	2,07	7,22E-06	1,09E-04	Pre-mRNA-processing protein 40A
Solyc12g040640.2	2,06	9,80E-04	5,49E-03	Beta-glucosidase
Solyc08g021920.4	2,06	2,42E-08	1,03E-06	DnaJ-like protein subfamily C GRV2
Solyc10g084380.1	2,06	7,52E-08	2,61E-06	WRKY transcription factor 44
Solyc05g052450.3	2,06	1,73E-04	1,38E-03	Protein trichome birefringence-like 32
Solyc10g009480.4	2,06	4,92E-03	1,93E-02	Cytochrome and DOMON domain-containing protein
Solyc01g079520.3	2,05	5,46E-05	5,51E-04	DNA mismatch repair protein MutS
Solyc03g111500.3	2,05	4,51E-04	2,94E-03	B3 domain-containing protein
Solyc11g062100.1	2,05	1,97E-11	2,40E-09	E1-E2_ATPase domain-containing protein/HMA domain-containing protein/Hydrolase domain-containing protein
Solyc04g074430.2	2,05	1,16E-04	9,97E-04	Protein EXORDIUM-like 1
Solyc05g014540.3	2,05	3,78E-05	4,09E-04	DNA polymerase alpha subunit B
Solyc07g039500.4	2,05	1,81E-11	2,25E-09	Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic
Solyc12g009310.2	2,05	3,94E-05	4,24E-04	Protein kinase superfamily protein
Solyc05g054060.3	2,05	1,07E-03	5,88E-03	UTP--glucose-1-phosphate uridylyltransferase
Solyc01g067790.3	2,05	1,56E-04	1,27E-03	BRCT domain-containing DNA repair protein
Solyc02g091180.1	2,05	2,45E-03	1,12E-02	DUF4228 domain-containing protein
Solyc02g085030.4	2,05	4,78E-05	4,95E-04	Auxilin-like protein 1
Solyc07g055650.2	2,04	1,32E-02	4,14E-02	Receptor-like protein kinase
Solyc01g102810.3	2,04	2,86E-11	3,34E-09	DNA polymerase III subunit gamma/tau
Solyc10g086310.1	2,04	4,07E-04	2,72E-03	RAB GTPase
Solyc04g082900.4	2,03	9,02E-06	1,31E-04	Mitotic spindle checkpoint protein BUBR1
Solyc10g076570.2	2,03	6,07E-03	2,26E-02	Protein trichome birefringence-like 3
Solyc06g017970.4	2,03	3,74E-12	5,61E-10	TRAF-like family protein
Solyc01g009040.4	2,03	1,90E-04	1,50E-03	cyclinB1_4
Solyc01g008420.3	2,03	4,62E-04	3,00E-03	Protein DETOXIFICATION
Solyc01g103030.3	2,03	1,11E-07	3,54E-06	Major facilitator superfamily protein
Solyc06g036060.4	2,03	6,40E-03	2,36E-02	Zinc finger, C2H2
Solyc09g010995.1	2,03	9,31E-06	1,34E-04	Laccase
Solyc10g007290.4	2,03	1,05E-07	3,39E-06	phosphoenolpyruvate carboxylase
Solyc02g071350.3	2,03	1,03E-03	5,71E-03	ABC transporter B family member 9
Solyc12g007140.3	2,02	3,38E-05	3,75E-04	hypothetical protein
Solyc01g081540.4	2,02	4,97E-10	3,94E-08	Myosin-17
Solyc02g069680.3	2,02	9,22E-04	5,25E-03	vacuolar protein sorting-associated protein 2 homolog 2
Solyc02g068340.3	2,02	5,96E-12	8,53E-10	Kinesin-like protein
Solyc07g005840.2	2,02	1,33E-06	2,81E-05	Cellulose synthase
Solyc03g116770.3	2,02	7,53E-03	2,68E-02	seed dormancy control protein
Solyc09g074380.4	2,01	4,49E-04	2,93E-03	DCD (Development and Cell Death) domain protein
Solyc10g086180.2	2,01	7,78E-19	6,94E-16	Phenylalanine ammonia-lyase
Solyc12g006590.3	2,01	1,07E-03	5,89E-03	Zinc finger protein
Solyc06g072830.4	2,01	1,65E-03	8,23E-03	cell division cycle 20.2, cofactor of APC complex-like
Solyc08g080220.3	2,00	5,17E-05	5,26E-04	DNA-directed RNA polymerase subunit
Solyc03g115050.3	2,00	1,55E-05	1,99E-04	Replication protein A subunit
Solyc07g055180.3	2,00	7,96E-03	2,80E-02	Protein kinase superfamily protein
Solyc12g006620.2	2,00	5,61E-03	2,12E-02	Zinc finger transcription factor 72
Solyc06g069230.3	2,00	1,26E-04	1,07E-03	DNA mismatch repair protein MutS
Solyc12g055980.1	1,99	3,15E-04	2,22E-03	Endoglucanase
Solyc03g083440.4	1,99	4,72E-08	1,80E-06	Glutamate synthase
Solyc01g087590.3	1,99	1,54E-05	1,98E-04	Polyamine oxidase
Solyc04g071660.3	1,99	1,12E-02	3,64E-02	hypothetical protein
Solyc02g079850.4	1,99	7,18E-08	2,51E-06	Unknown protein
Solyc01g101030.4	1,99	3,49E-05	3,84E-04	FACT complex subunit SPT16
Solyc02g086330.4	1,98	2,94E-05	3,37E-04	HEAT repeat-containing protein-like
Solyc03g025280.4	1,98	8,44E-08	2,84E-06	RNA recognition motif (RRM)-containing protein
Solyc03g097050.3	1,98	3,45E-06	6,12E-05	Cellulose synthase
Solyc02g082840.3	1,98	7,61E-08	2,62E-06	Protein GRIP
Solyc03g025830.4	1,97	7,41E-05	7,00E-04	Myosin heavy chain-related protein
Solyc04g080200.4	1,97	3,79E-05	4,10E-04	hypothetical protein
Solyc02g084390.3	1,97	4,57E-14	1,24E-11	Kinesin-like protein
Solyc11g062310.2	1,97	5,45E-08	2,00E-06	proteasome-associated protein ECM29 homolog
Solyc02g080320.4	1,97	5,61E-03	2,12E-02	RNA pseudouridine synthase 6, chloroplastic
Solyc11g071250.3	1,96	1,84E-08	8,31E-07	protein EMBRYONIC FLOWER 1-like
Solyc01g104950.4	1,96	1,58E-13	3,52E-11	LEXYL2
Solyc10g084880.3	1,95	2,19E-05	2,65E-04	Avr9/Cf-9 rapidly elicited protein 137
Solyc03g115665.1	1,95	6,00E-03	2,24E-02	Unknown protein

Solyc08g066120.4	1,95	6,25E-03	2,31E-02	Polyribonucleotide nucleotidyltransferase
Solyc10g081770.3	1,95	1,98E-03	9,55E-03	Polyketide cyclase/dehydrase/lipid transport superfamily protein
Solyc09g018340.2	1,95	2,18E-04	1,67E-03	ARM repeat superfamily protein
Solyc02g086456.1	1,95	1,06E-06	2,33E-05	titin isoform X6
Solyc04g081210.4	1,95	2,54E-14	7,42E-12	SUN-like protein 14
Solyc01g091340.3	1,95	1,12E-04	9,67E-04	Peptidylprolyl isomerase
Solyc02g087520.3	1,94	4,98E-03	1,95E-02	Thaumatin
Solyc06g064550.3	1,94	8,46E-08	2,84E-06	Aspartokinase-homoserine dehydrogenase
Solyc12g009000.1	1,94	5,07E-05	5,18E-04	Harbinger transposase-derived nuclease
Solyc06g062580.3	1,94	9,30E-09	4,63E-07	Beta-galactosidase
Solyc06g019170.3	1,94	8,59E-05	7,89E-04	Delta-1-pyrroline-5-carboxylate synthase
Solyc09g072800.3	1,93	6,53E-04	4,01E-03	Eisosome protein
Solyc03g080100.4	1,93	1,66E-04	1,34E-03	Heavy metal-associated isoprenylated plant protein
Solyc11g043200.1	1,93	1,12E-04	9,68E-04	Dynamin related protein
Solyc02g077600.3	1,93	6,03E-07	1,48E-05	Guanylate-binding protein
Solyc06g011370.4	1,93	4,48E-04	2,93E-03	Chaperone protein ClpB
Solyc07g044930.3	1,92	2,59E-05	3,03E-04	DExH-box ATP-dependent RNA helicase DExH6-like
Solyc11g044880.3	1,92	9,69E-12	1,30E-09	Kinesin
Solyc03g111680.3	1,92	5,73E-05	5,74E-04	DNA polymerase III subunit gamma/tau
Solyc02g070210.3	1,92	4,47E-05	4,69E-04	Patellin-4
Solyc08g006903.1	1,91	6,80E-03	2,47E-02	Unknown protein
Solyc09g082500.4	1,91	1,98E-09	1,26E-07	Tesmin/TSO1-like CXC domain-containing protein
Solyc03g115120.1	1,91	2,38E-03	1,10E-02	DNAJ protein JJJ1 homolog
Solyc02g091197.1	1,91	8,11E-04	4,73E-03	Unknown protein
Solyc05g023770.4	1,91	4,60E-10	3,70E-08	Coiled-coil domain-containing protein SCD2
Solyc10g049580.2	1,91	1,16E-05	1,58E-04	classical arabinogalactan protein 9-like
Solyc04g076140.3	1,91	3,52E-04	2,43E-03	Rho GTPase-activating protein REN1
Solyc01g109580.4	1,91	3,22E-05	3,62E-04	Adenylyl cyclase-associated protein
Solyc11g066130.1	1,91	1,08E-04	9,44E-04	osmotin
Solyc02g080610.4	1,90	6,70E-05	6,46E-04	Ankyrin repeat
Solyc07g007850.2	1,90	1,19E-02	3,83E-02	SPOC domain / Transcription elongation factor S-II protein
Solyc04g025440.3	1,90	6,91E-05	6,62E-04	Pectin lyase-like superfamily protein
Solyc08g078330.4	1,90	4,93E-03	1,93E-02	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc04g007290.4	1,90	1,83E-05	2,28E-04	DUF639 domain-containing protein
Solyc07g064050.3	1,89	2,74E-04	1,99E-03	Hexosyltransferase
Solyc06g066610.4	1,89	4,48E-12	6,67E-10	Golgin candidate 5
Solyc08g005240.3	1,89	1,32E-04	1,11E-03	Transcription factor jumonji (Jmj) family protein / zinc finger (C5HC2 type) family protein
Solyc01g099630.4	1,89	7,55E-07	1,77E-05	xyloglucan endotransglucosylase-hydrolase 1
Solyc07g042260.4	1,89	1,83E-11	2,28E-09	Auxin Response Factor 7
Solyc06g066160.3	1,88	3,13E-05	3,53E-04	Isoflavone reductase
Solyc04g010300.4	1,88	1,59E-04	1,29E-03	ABC transporter B family member 20
Solyc01g081010.4	1,88	8,24E-16	3,35E-13	Nucleolar GTP-binding protein 1
Solyc08g005630.3	1,88	7,19E-07	1,71E-05	Long-chain-alcohol oxidase
Solyc09g010460.3	1,88	1,54E-16	8,37E-14	Eukaryotic translation initiation factor 3 subunit A
Solyc04g009560.3	1,88	3,85E-10	3,20E-08	Rab-GTPase-TBC domain
Solyc08g067200.2	1,88	1,51E-02	4,61E-02	Dicer-like protein 3
Solyc02g062780.4	1,88	7,23E-07	1,72E-05	ATP-dependent DNA helicase DDM1
Solyc07g047900.3	1,88	4,95E-05	5,08E-04	RNA-binding CRS1 / YhbY (CRM) domain protein
Solyc05g050210.4	1,88	1,25E-02	3,99E-02	GDSL esterase/lipase
Solyc07g062730.1	1,88	3,00E-12	4,73E-10	Serine/Threonine-kinase pakA-like protein
Solyc06g068230.4	1,87	1,03E-15	4,11E-13	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc11g073010.1	1,87	9,95E-04	5,56E-03	Exocyst subunit Exo70 family protein
Solyc02g091020.3	1,87	3,53E-03	1,49E-02	Nuclear pore complex protein NUP98A
Solyc01g110960.4	1,87	2,94E-08	1,20E-06	Prefoldin chaperone subunit family protein
Solyc08g068320.3	1,87	2,20E-05	2,67E-04	Myb
Solyc04g009950.3	1,87	1,01E-14	3,25E-12	cell division cycle 5
Solyc09g091430.4	1,87	1,09E-07	3,49E-06	Pectate lyase
Solyc07g032710.4	1,87	4,73E-05	4,91E-04	hypothetical protein
Solyc04g040110.3	1,87	2,24E-03	1,04E-02	Kinesin-related protein 4
Solyc09g083400.3	1,87	2,78E-13	5,77E-11	Protein WVD2-like 1
Solyc08g082820.4	1,87	3,43E-12	5,27E-10	TOMBIPGRBC Tomato BiP (binding protein)/grp78
Solyc06g009780.4	1,87	1,43E-05	1,87E-04	Kinesin-4
Solyc01g095895.1	1,87	3,38E-03	1,44E-02	Unknown protein
Solyc12g096530.1	1,86	8,83E-04	5,07E-03	Peroxidase
Solyc02g090940.3	1,86	3,99E-04	2,68E-03	Alpha/beta-Hydrolases superfamily protein
Solyc08g075940.4	1,86	5,26E-03	2,02E-02	DNA-directed RNA polymerase subunit beta
Solyc04g078810.4	1,86	5,26E-12	7,64E-10	Remorin family protein
Solyc11g068890.2	1,86	3,11E-03	1,35E-02	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Solyc07g065610.1	1,86	8,35E-03	2,90E-02	Pkinase domain-containing protein/Lectin_leg B domain-containing protein
Solyc02g078640.3	1,86	5,32E-15	1,88E-12	Protein MOR1
Solyc03g083060.3	1,85	2,49E-09	1,56E-07	Ribonuclease P protein subunit P38-like protein
Solyc04g071360.4	1,85	2,24E-10	2,01E-08	Trihelix transcription factor GTL1
Solyc03g121600.4	1,85	2,03E-06	3,97E-05	Glucose-methanol-choline (GMC) oxidoreductase family protein
Solyc02g093190.3	1,85	1,94E-03	9,39E-03	Histone-lysine N-methyltransferase
Solyc02g087880.3	1,85	5,86E-06	9,29E-05	Tubulin alpha chain
Solyc04g081100.3	1,85	2,04E-06	3,99E-05	Lysine-specific histone demethylase 1-like protein 3
Solyc01g090860.3	1,84	3,38E-07	8,92E-06	Non-canonical poly(A) RNA polymerase PAPD7
Solyc06g074850.3	1,84	9,22E-12	1,25E-09	Carboxypeptidase
Solyc04g076540.4	1,84	1,44E-11	1,84E-09	HYPERSENSITIVE TO PI STARVATION 4
Solyc02g089260.4	1,84	9,94E-12	1,30E-09	Auxin transport protein BIG
Solyc04g076550.3	1,84	3,54E-03	1,49E-02	HYPERSENSITIVE TO PI STARVATION 4
Solyc08g083240.3	1,84	2,70E-04	1,98E-03	SUN-like protein 24
Solyc09g011860.4	1,84	1,76E-05	2,20E-04	GDP-fucose protein O-fucosyltransferase protein
Solyc06g065680.3	1,83	1,34E-06	2,82E-05	cyclin A2
Solyc02g087440.4	1,83	2,85E-03	1,26E-02	DUF761 domain-containing protein
Solyc06g051320.3	1,83	2,39E-03	1,10E-02	HXXXD-type acyl-transferase family protein
Solyc09g074470.3	1,83	5,51E-03	2,10E-02	Kinase interacting (KIP1-like) protein
Solyc02g086452.1	1,83	7,58E-07	1,78E-05	titin isoform X3
Solyc11g069250.2	1,83	5,88E-04	3,67E-03	Fasciclin-like arabinogalactan protein 12
Solyc05g008780.4	1,83	1,26E-06	2,68E-05	Calponin-like domain protein
Solyc10g081810.3	1,83	3,40E-03	1,45E-02	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein
Solyc07g024070.3	1,82	1,47E-02	4,53E-02	Ubiquitin-conjugating enzyme
Solyc03g006840.4	1,82	5,37E-04	3,39E-03	LOW protein: M-phase inducer phosphatase-like protein
Solyc08g075420.4	1,82	7,00E-08	2,46E-06	zinc knuckle (CCHC-type) family protein
Solyc04g054480.3	1,82	1,50E-11	1,91E-09	U-box domain-containing protein
Solyc10g006260.3	1,82	3,28E-06	5,84E-05	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein
Solyc05g054930.3	1,82	1,50E-08	6,96E-07	CAP-gly domain linker
Solyc04g081260.3	1,82	2,78E-13	5,77E-11	filament-like plant protein 4
Solyc11g072820.3	1,82	1,69E-05	2,14E-04	Kinesin
Solyc03g120570.3	1,82	2,76E-04	2,01E-03	Protein NRT1/ PTR FAMILY 1.1
Solyc10g080390.2	1,81	8,76E-09	4,46E-07	serine/threonine-protein kinase Nek6-like isoform X1
Solyc05g014560.3	1,81	7,92E-04	4,65E-03	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic
Solyc03g114780.3	1,81	1,16E-04	9,98E-04	RNA helicase DEAH-box9
Solyc08g007280.2	1,81	3,13E-03	1,35E-02	Unknown protein
Solyc02g092820.4	1,81	4,23E-03	1,71E-02	IAA-amido synthetase 3-4
Solyc09g008840.4	1,81	1,94E-07	5,53E-06	Pyruvate kinase
Solyc08g081480.3	1,81	7,84E-11	7,89E-09	Pectin lyase-like superfamily protein
Solyc10g085550.3	1,80	3,29E-05	3,67E-04	Enolase
Solyc02g082680.4	1,80	2,78E-07	7,49E-06	RB1-inducible coiled-coil protein
Solyc07g018340.3	1,80	1,54E-06	3,19E-05	DNA mismatch repair protein MutS
Solyc12g098160.2	1,80	4,11E-10	3,38E-08	protein ALWAYS EARLY 3-like
Solyc12g049510.3	1,80	7,64E-07	1,79E-05	GPI-anchored adhesin-like protein
Solyc02g086840.3	1,80	2,87E-09	1,77E-07	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc03g097190.3	1,80	3,34E-10	2,83E-08	WEB family protein, chloroplastic
Solyc01g100280.4	1,80	5,86E-03	2,20E-02	RNA helicase DEAH-box4
Solyc04g005190.2	1,80	2,86E-04	2,06E-03	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase
Solyc09g007160.4	1,80	5,30E-08	1,98E-06	Rab-GTPase-TBC domain
Solyc07g056410.3	1,80	1,18E-06	2,55E-05	Leucine-rich receptor-like protein kinase family protein
Solyc08g060840.1	1,80	2,11E-05	2,56E-04	Protein FAR-RED IMPAIRED RESPONSE 1
Solyc06g075580.4	1,79	7,26E-13	1,38E-10	Kinesin
Solyc02g050200.2	1,79	8,24E-03	2,88E-02	BREAST CANCER 2 like 2A

Solyc10g006870.1	1,79	1,66E-12	2,87E-10	Receptor-like protein kinase THESEUS 1
Solyc03g026190.3	1,79	9,69E-04	5,45E-03	Transcriptional corepressor SEUSS
Solyc06g066730.3	1,79	2,38E-08	1,02E-06	Coatomer subunit beta'
Solyc07g005530.4	1,79	8,08E-16	3,35E-13	Ubiquitin carboxyl-terminal hydrolase 23
Solyc10g081730.2	1,79	6,22E-10	4,77E-08	Protein WVD2-like 1
Solyc01g100290.4	1,78	1,30E-10	1,23E-08	GPI-anchored adhesin-like protein
Solyc06g084120.4	1,78	6,07E-03	2,26E-02	Jasmonate ZIM domain protein k.1
Solyc05g009470.4	1,78	2,50E-10	2,20E-08	Glycoside hydrolase family 31
Solyc02g067830.3	1,78	4,89E-08	1,85E-06	Protein kinase G11A
Solyc01g099650.3	1,78	1,68E-03	8,33E-03	Formin-like protein
Solyc03g116260.3	1,78	2,09E-04	1,62E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc01g087450.3	1,78	1,05E-04	9,22E-04	Arm repeat superfamily protein
Solyc01g094060.4	1,78	7,20E-13	1,38E-10	BEACH domain-containing protein
Solyc02g093160.3	1,77	1,61E-09	1,04E-07	Filament-like plant protein 7
Solyc06g065670.4	1,77	1,75E-07	5,10E-06	Pleiotropic drug resistance protein 4
Solyc08g005655.1	1,77	3,59E-03	1,51E-02	Alkyl transferase
Solyc09g065240.3	1,77	1,65E-03	8,22E-03	Patatin
Solyc09g014970.4	1,77	1,61E-05	2,06E-04	Methylketone synthase Ib
Solyc03g116830.4	1,76	5,36E-05	5,43E-04	Phox (PX) domain-containing protein
Solyc08g005300.3	1,76	2,33E-08	1,01E-06	DnaJ domain
Solyc02g084210.1	1,76	7,54E-04	4,48E-03	GDP-mannose 4,6-dehydratase
Solyc06g084430.4	1,76	6,19E-03	2,30E-02	Histone H2A
Solyc04g049680.2	1,76	4,76E-06	7,86E-05	Pseudo-response regulator
Solyc10g050105.1	1,76	9,20E-03	3,13E-02	Rhomboid-like protein
Solyc02g024070.3	1,76	5,25E-10	4,13E-08	Homeobox leucine-zipper protein
Solyc10g086320.2	1,76	9,06E-03	3,09E-02	Phosphatidylinositol 4-phosphate 5-kinase
Solyc08g083290.4	1,76	1,50E-09	9,92E-08	PHD finger protein
Solyc05g010630.4	1,75	4,46E-03	1,79E-02	RING-type E3 ubiquitin transferase
Solyc01g005330.3	1,75	2,94E-12	4,66E-10	Microtubule-associated protein 70
Solyc04g072630.4	1,75	3,34E-06	5,95E-05	sporulation-specific protein
Solyc01g087850.2	1,75	5,39E-08	1,98E-06	serine protease SBT3
Solyc10g084670.3	1,75	8,23E-03	2,88E-02	Eukaryotic translation initiation factor 3 subunit A
Solyc07g025210.2	1,75	3,29E-03	1,41E-02	Pentatricopeptide repeat-containing protein
Solyc02g081810.4	1,75	2,80E-05	3,23E-04	H/ACA ribonucleoprotein complex subunit 4
Solyc06g065360.3	1,75	2,44E-04	1,83E-03	Erythroid differentiation-related factor 1-like protein
Solyc02g078390.3	1,75	2,55E-05	2,98E-04	DNA mismatch repair protein MutS
Solyc06g076040.3	1,75	9,01E-07	2,04E-05	RING-type E3 ubiquitin transferase
Solyc02g087980.3	1,74	1,14E-02	3,71E-02	Structural maintenance of chromosomes protein
Solyc05g026180.2	1,74	1,43E-03	7,33E-03	NAC domain
Solyc08g066810.3	1,74	5,86E-05	5,83E-04	Cellulase (Glycosyl hydrolase family 5) protein
Solyc09g065780.3	1,74	1,80E-07	5,20E-06	3-ketoacyl-CoA synthase
Solyc03g123620.4	1,74	6,54E-07	1,59E-05	Pectinesterase
Solyc07g061780.4	1,74	4,73E-10	3,77E-08	Ubiquitin carboxyl-terminal hydrolase 19
Solyc09g060080.4	1,74	3,31E-09	1,98E-07	Helicase/SANT-associated DNA-binding protein
Solyc06g068680.3	1,74	3,70E-08	1,46E-06	Respiratory burst oxidase homolog
Solyc12g088310.3	1,74	8,32E-05	7,70E-04	Unknown protein
Solyc11g040120.3	1,74	4,40E-08	1,70E-06	DNA helicase
Solyc02g090220.3	1,74	1,42E-02	4,38E-02	Dof zinc finger protein PBF
Solyc02g038740.4	1,74	6,42E-03	2,36E-02	3-hydroxy-3-methylglutaryl coenzyme A reductase
Solyc11g071620.3	1,73	1,59E-08	7,30E-07	aldehyde oxidase 1
Solyc02g078040.3	1,73	1,94E-06	3,83E-05	Pistil-specific extensin-like protein
Solyc01g080260.3	1,73	1,71E-03	8,48E-03	ARM repeat superfamily protein
Solyc06g034390.1	1,73	8,57E-03	2,97E-02	Protein EXORDIUM-like 7
Solyc11g008150.3	1,73	6,84E-10	5,17E-08	Transcription elongation factor Spt5
Solyc08g067150.4	1,73	5,27E-05	5,35E-04	CRC domain-containing protein TSO1
Solyc09g098270.4	1,73	8,86E-04	5,09E-03	Pectin lyase-like superfamily protein
Solyc07g006030.4	1,73	4,92E-14	1,30E-11	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc10g005690.3	1,73	1,08E-09	7,62E-08	Chloride channel protein
Solyc09g098260.3	1,73	3,59E-09	2,11E-07	Histone-lysine N-methyltransferase
Solyc06g050350.3	1,72	2,94E-07	7,88E-06	WEB family
Solyc06g034360.2	1,72	6,58E-03	2,41E-02	Pectinesterase
Solyc07g006320.4	1,71	1,52E-03	7,67E-03	auxin canalization protein (DUF828)
Solyc01g103090.4	1,71	4,34E-04	2,85E-03	Zinc finger transcription factor 14
Solyc09g007340.4	1,71	1,04E-02	3,45E-02	Tudor/PWWP/MBT superfamily protein
Solyc04g078610.4	1,71	1,36E-10	1,27E-08	Kinesin
Solyc02g083670.4	1,71	3,51E-09	2,08E-07	Histidine kinase 1
Solyc08g007670.1	1,71	2,46E-05	2,91E-04	Subtilisin-like protease
Solyc12g008390.3	1,71	1,11E-12	2,04E-10	Golgin candidate 1
Solyc11g066870.3	1,71	3,03E-11	3,46E-09	MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein
Solyc03g033550.3	1,71	1,25E-02	4,00E-02	WEB family protein
Solyc04g005810.3	1,70	1,34E-02	4,20E-02	Thioredoxin
Solyc03g116370.3	1,70	5,28E-03	2,03E-02	Microtubule-associated protein RP/EB family member 1C
Solyc09g011960.2	1,70	5,28E-07	1,32E-05	Laccase
Solyc03g007760.3	1,70	2,21E-08	9,62E-07	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc02g079300.3	1,70	8,02E-05	7,47E-04	Transcription factor jumonji (JmjC) domain-containing protein
Solyc02g063190.2	1,70	8,29E-03	2,89E-02	UDP-N-acetylenolpyruvoylglucosamine reductase
Solyc06g074070.3	1,70	1,53E-09	1,01E-07	receptor-like kinase TMK3
Solyc02g086454.1	1,70	7,98E-10	5,93E-08	titin isoform X6
Solyc06g075010.4	1,70	6,18E-09	3,29E-07	60 kDa chaperonin
Solyc09g098590.4	1,69	3,93E-09	2,26E-07	Sucrose synthase
Solyc01g087140.4	1,69	8,86E-03	3,04E-02	Late embryogenesis abundant protein
Solyc03g115660.3	1,69	4,04E-05	4,32E-04	Protein kinase superfamily protein
Solyc01g006830.3	1,69	7,86E-12	1,11E-09	Protein WVD2-like 1
Solyc03g006290.4	1,69	1,81E-03	8,86E-03	DUF599 domain-containing protein
Solyc12g017830.3	1,69	1,12E-08	5,47E-07	Brefeldin A-inhibited guanine nucleotide-exchange protein 5
Solyc12g098960.2	1,69	1,56E-07	4,66E-06	Protein kinase domain
Solyc10g006900.3	1,69	1,25E-04	1,06E-03	light dependent NADH:protochlorophyllide oxidoreductase 3 s2
Solyc03g114410.3	1,69	2,14E-06	4,11E-05	G patch domain-containing protein TGH
Solyc06g065380.4	1,69	4,02E-08	1,58E-06	Calcium-dependent protein kinase
Solyc06g083660.4	1,69	5,71E-10	4,45E-08	Methyl-coenzyme M reductase II subunit gamma, putative (DUF3741)
Solyc03g112950.4	1,69	6,84E-03	2,48E-02	Serine/threonine-protein kinase ATM
Solyc12g055910.3	1,69	4,02E-04	2,69E-03	RING/U-box protein
Solyc10g078860.2	1,69	2,66E-04	1,96E-03	DNA-directed RNA polymerase subunit beta
Solyc05g017890.4	1,68	1,21E-09	8,32E-08	THO complex subunit 2
Solyc10g086600.3	1,68	1,32E-03	6,90E-03	Subtilisin-like protease-like protein
Solyc06g050920.4	1,68	2,80E-04	2,03E-03	Protein trichome birefringence-like 32
Solyc02g070180.3	1,68	4,73E-08	1,80E-06	FAD-binding Berberine family protein
Solyc03g115980.1	1,68	2,83E-07	7,60E-06	Geranylgeranyl diphosphate reductase, chloroplastic
Solyc05g007130.4	1,67	1,45E-03	7,40E-03	SUN-like protein 15
Solyc02g031910.2	1,67	1,03E-06	2,29E-05	PB1 domain-containing protein/Pkinase_Tyr domain-containing protein
Solyc01g111570.3	1,67	1,63E-08	7,45E-07	proline-rich receptor-like protein kinase PERK7 isoform X1
Solyc02g072090.2	1,67	3,51E-07	9,21E-06	DNA polymerase III gamma-tau subunit
Solyc03g046270.4	1,67	4,56E-04	2,97E-03	Protein trichome birefringence-like 19
Solyc06g007790.1	1,67	2,91E-04	2,09E-03	acidic leucine-rich nuclear phosphoprotein 32 family B protein
Solyc04g055160.3	1,67	4,17E-06	7,06E-05	Alpha-ketoglutarate-dependent dioxygenase alkB-like protein 2
Solyc05g056530.4	1,67	9,16E-04	5,23E-03	DDT domain-containing protein
Solyc06g062380.3	1,67	3,57E-03	1,50E-02	acid phosphatase 1-like
Solyc06g066670.4	1,67	7,49E-03	2,67E-02	RNA helicase DEAH-box20
Solyc07g066200.4	1,67	2,29E-10	2,05E-08	hapless protein
Solyc01g086940.2	1,67	8,61E-07	1,98E-05	Zinc finger CCCH domain-containing protein
Solyc05g052490.3	1,67	4,88E-09	2,68E-07	Nucleoside phosphatase GDA1/CD39
Solyc01g096490.3	1,67	1,22E-12	2,17E-10	E3 ubiquitin-protein ligase KEG
Solyc11g071970.2	1,67	1,75E-05	2,19E-04	Serine/threonine-protein kinase Nek5
Solyc01g079490.2	1,67	3,88E-04	2,63E-03	Vacuolar protein sorting-associated protein 51-like protein
Solyc01g091930.3	1,67	1,24E-03	6,58E-03	Subtilisin-like protease SBT4.14
Solyc07g064030.4	1,67	7,32E-07	1,74E-05	Kinesin-like protein
Solyc08g082480.3	1,67	1,81E-03	8,86E-03	Phosphatidylinositol 4-kinase gamma 2
Solyc04g074720.3	1,66	5,45E-06	8,79E-05	FAM91 carboxy-terminus protein
Solyc07g052480.3	1,66	2,39E-10	2,11E-08	isocitrate lyase LEU18678
Solyc08g076883.1	1,66	6,37E-06	9,81E-05	Unknown protein
Solyc05g005640.4	1,66	2,14E-07	5,95E-06	methyl-CpG-binding domain-containing protein 9-like

Solyc03g095680.2	1,66	5,09E-03	1,97E-02	SNF2-related
Solyc01g112140.4	1,66	1,07E-03	5,87E-03	Flavin-containing monooxygenase
Solyc10g005910.2	1,66	1,64E-05	2,09E-04	GTPase Der
Solyc06g051630.5.1	1,66	1,15E-05	1,57E-04	Phosphoinositide phospholipase C
Solyc08g022030.3	1,66	3,88E-11	4,25E-09	Myosin heavy chain-related protein
Solyc10g076450.2	1,66	5,56E-05	5,60E-04	Ethylene-overproduction protein 1
Solyc10g077000.3	1,66	2,74E-07	7,41E-06	Dentin sialophosphoprotein
Solyc09g090270.3	1,66	4,58E-09	2,54E-07	COP1-interacting protein-like protein
Solyc06g071350.4	1,65	1,59E-09	1,03E-07	Bromo adjacent homology (BAH) domain
Solyc02g080200.4	1,65	2,22E-03	1,04E-02	Pectinesterase
Solyc09g065480.2	1,65	1,02E-03	5,66E-03	type I inositol polyphosphate 5-phosphatase 4-like
Solyc01g104040.4	1,65	4,73E-11	5,06E-09	UDP-glucose:glycoprotein glucosyltransferase
Solyc02g087350.3	1,65	5,91E-05	5,88E-04	Hexosyltransferase
Solyc07g042030.2	1,65	2,74E-05	3,17E-04	Pentatricopeptide repeat-containing protein
Solyc12g044290.2	1,65	5,35E-08	1,98E-06	Malonate--CoA ligase
Solyc03g115000.3	1,65	3,61E-09	2,12E-07	protein LONGIFOLIA 1-like
Solyc01g067890.4	1,65	4,05E-09	2,31E-07	1-D-deoxyxylulose 5-phosphate synthase
Solyc01g006100.4	1,65	1,16E-02	3,76E-02	cytosine-5 DNA methyltransferase1L
Solyc04g056410.3	1,65	1,29E-02	4,09E-02	Protein CHROMATIN REMODELING 25
Solyc07g055950.3	1,65	5,38E-05	5,44E-04	Protodermal factor 1
Solyc02g093330.4	1,65	3,94E-04	2,66E-03	nuclear pore complex protein NUP98A
Solyc04g078740.2	1,64	6,77E-10	5,13E-08	Subtilisin-like protease-like protein
Solyc04g074440.1	1,64	1,45E-05	1,88E-04	Protein EXORDIUM-like 1
Solyc08g008470.2	1,64	1,37E-06	2,87E-05	protein KINESIN LIGHT CHAIN-RELATED 1-like
Solyc08g014280.3	1,64	1,14E-09	7,93E-08	SUN-like protein 21
Solyc09g074110.4	1,64	7,70E-07	1,80E-05	Piezo-type mechanosensitive ion channel-like protein
Solyc05g049980.3	1,64	4,27E-06	7,16E-05	Pectin lyase-like superfamily protein
Solyc12g098900.2	1,64	1,66E-02	4,98E-02	Late embryogenesis abundant protein D-29
Solyc07g040980.3	1,64	1,57E-11	1,99E-09	Plant/F27B13-30 protein
Solyc09g007140.4	1,64	9,23E-04	5,25E-03	Protein RESTRICTED TEV MOVEMENT 2
Solyc11g040340.3	1,64	9,32E-04	5,29E-03	LEE14BDGL L.esculentum endo-1,4-beta-D-glucanase
Solyc03g095250.3	1,64	1,19E-08	5,74E-07	COP1-Interacting protein-related
Solyc01g006340.3	1,64	2,31E-04	1,75E-03	DEAD-box ATP-dependent RNA helicase 41
Solyc08g079890.2	1,64	2,14E-04	1,65E-03	Subtilisin-like protease
Solyc09g057910.3	1,64	1,32E-03	6,92E-03	N-alpha-acetyltransferase 25, NatB auxiliary subunit
Solyc03g034100.4	1,64	1,10E-02	3,61E-02	ovate family protein 6
Solyc11g065260.3	1,64	1,90E-06	3,77E-05	DnaJ domain-containing protein/TPR_1 domain-containing protein/TPR_11 domain-containing protein
Solyc10g007400.4	1,63	5,34E-03	2,05E-02	DNA polymerase delta subunit 3
Solyc03g119780.4	1,63	4,15E-08	1,62E-06	Transcription initiation factor TFIID subunit 2
Solyc01g091910.4	1,63	1,10E-06	2,40E-05	phospholipase PLDb2
Solyc07g061920.4	1,63	2,36E-03	1,09E-02	Callose synthase 1
Solyc10g083190.3	1,63	3,12E-09	1,90E-07	Plant/F24K9-26 protein
Solyc08g067330.1	1,63	2,16E-07	6,00E-06	Chlorophyll a-b binding protein, chloroplastic
Solyc10g083970.1	1,63	9,29E-09	4,63E-07	S-adenosylmethionine synthase
Solyc04g078310.3	1,63	9,53E-03	3,22E-02	cyclin A3_1
Solyc01g090440.2	1,63	2,05E-06	4,00E-05	cotton fiber protein
Solyc01g100120.4	1,63	2,68E-04	1,96E-03	Kinesin-like protein
Solyc01g109080.3	1,63	1,49E-03	7,56E-03	Serine/threonine-protein kinase SMG1
Solyc05g008200.4	1,62	3,61E-08	1,44E-06	1-phosphatidylinositol-3-phosphate 5-kinase FAB1A
Solyc03g093360.3	1,62	2,56E-06	4,78E-05	PLAT/LH2 domain
Solyc10g049890.3	1,62	1,77E-03	8,72E-03	D-3-phosphoglycerate dehydrogenase
Solyc01g066740.3	1,62	4,09E-04	2,73E-03	Transducin/WD40 repeat-like superfamily protein
Solyc07g018290.4	1,62	1,26E-03	6,69E-03	AP2-like ethylene-responsive transcription factor
Solyc01g091090.4	1,62	1,19E-02	3,84E-02	Tubulin-folding cofactor D
Solyc09g074670.4	1,62	3,24E-06	5,80E-05	Zinc finger, CW-type
Solyc12g056170.2	1,62	4,57E-06	7,57E-05	hypothetical protein
Solyc07g022760.4	1,62	9,34E-08	3,09E-06	Pre-mRNA-processing protein 40A
Solyc02g081550.3	1,62	2,31E-05	2,78E-04	LeftsH6FtsH protease
Solyc02g083900.3	1,62	6,85E-08	2,43E-06	Transformation/transcription domain associated protein
Solyc07g066040.1	1,62	1,40E-02	4,35E-02	RNA polymerase II elongation factor
Solyc09g150105.1	1,61	3,89E-05	4,19E-04	Laccase
Solyc01g102570.4	1,61	2,60E-04	1,92E-03	Eukaryotic translation initiation factor 3 subunit C
Solyc01g079750.3	1,61	1,39E-03	7,19E-03	MAP kinase kinase kinase 4
Solyc09g014980.4	1,61	4,84E-11	5,15E-09	Protein SCAR4
Solyc03g115250.4	1,61	1,00E-09	7,21E-08	Dentin sialophosphoprotein-like protein
Solyc03g095600.1	1,61	6,39E-06	9,81E-05	KIP1-like
Solyc04g076870.4	1,61	6,48E-08	2,33E-06	Glutamyl-tRNA reductase
Solyc02g084720.3	1,61	1,54E-07	4,61E-06	beta-galactosidase 6
Solyc12g056940.2	1,61	6,96E-11	7,16E-09	Acetyl CoA carboxylase
Solyc07g053610.3	1,61	1,44E-07	4,36E-06	Homeobox domain-containing protein/DDT domain-containing protein
Solyc02g085390.4	1,61	4,28E-03	1,73E-02	ATP-dependent DNA helicase DDM1
Solyc06g005710.3	1,61	1,50E-08	6,96E-07	Protein TIC 62, chloroplastic
Solyc08g068480.1	1,61	2,31E-03	1,07E-02	Auxin-responsive GH3 family protein
Solyc07g008820.3	1,60	3,96E-04	2,66E-03	Protein trichome birefringence-like 15
Solyc02g090070.3	1,60	2,18E-10	1,97E-08	BTB/POZ domain-containing protein
Solyc02g069500.1	1,60	4,78E-05	4,95E-04	Pentatricopeptide repeat-containing protein
Solyc05g047460.3	1,60	3,43E-12	5,27E-10	Auxin Response Factor 7B
Solyc02g087760.3	1,60	2,17E-10	1,97E-08	SUN-like protein 7
Solyc01g086990.3	1,60	4,62E-10	3,70E-08	Pre-mRNA-splicing factor SYF1
Solyc12g013790.3	1,60	1,54E-03	7,78E-03	RNA-binding protein 25
Solyc07g005930.4	1,60	7,52E-03	2,67E-02	DNA-directed RNA polymerase
Solyc10g074650.2	1,60	1,52E-06	3,14E-05	Hexosyltransferase
Solyc01g096700.4	1,60	1,31E-10	1,23E-08	DnaJ domain-containing protein
Solyc08g078530.4	1,60	8,43E-12	1,16E-09	Agenet domain-containing protein
Solyc05g006540.3	1,59	2,48E-07	6,83E-06	Paired amphipathic helix protein Sin3-like 4
Solyc07g062600.4	1,59	4,97E-08	1,88E-06	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein
Solyc02g089970.3	1,59	8,06E-11	8,08E-09	Histone-lysine N-methyltransferase SUVR5-like protein
Solyc09g082830.4	1,59	6,11E-08	2,21E-06	Argonaute 10a
Solyc02g031860.3	1,59	1,48E-06	3,06E-05	MAP kinase kinase kinase 12
Solyc11g008770.2	1,59	1,06E-06	2,33E-05	LETM1 domain-containing protein
Solyc01g068480.4	1,59	4,47E-11	4,81E-09	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc01g100130.3	1,59	8,09E-09	4,15E-07	Zinc finger protein
Solyc03g117730.3	1,59	6,96E-03	2,52E-02	Tubby-like protein 8
Solyc07g042580.3	1,59	1,11E-02	3,61E-02	microtubule-associated protein TORTIFOLIA1
Solyc08g081535.1	1,58	1,24E-03	6,59E-03	1-aminocyclopropane-1-carboxylate synthase
Solyc10g081510.2	1,58	4,60E-07	1,17E-05	ethylene-responsive methionine synthase
Solyc07g052210.2	1,58	1,88E-08	8,44E-07	glycine-rich cell wall structural protein 1-like
Solyc08g076720.4	1,58	2,80E-08	1,16E-06	ABC transporter B family member 2
Solyc05g005980.4	1,58	1,48E-05	1,92E-04	protein NRT1/ PTR FAMILY 1.2-like
Solyc11g066120.3	1,58	1,67E-02	5,00E-02	CLAVATA3/ESR (CLE)-related protein 46-like
Solyc08g068100.3	1,58	1,59E-09	1,03E-07	DUF632 domain-containing protein/DUF630 domain-containing protein
Solyc08g079880.2	1,58	2,78E-06	5,08E-05	Subtilisin-like protease
Solyc01g095210.3	1,58	1,35E-09	9,17E-08	Golgin candidate 4
Solyc06g008720.4	1,58	1,42E-07	4,32E-06	Zinc finger, CW-type
Solyc06g048460.2	1,58	1,64E-04	1,33E-03	anaphase-promoting complex subunit 1
Solyc10g079170.2	1,58	1,09E-05	1,53E-04	Leucine-rich repeat receptor-like tyrosine-protein kinase
Solyc07g066180.2	1,58	8,43E-03	2,93E-02	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc09g083130.3	1,58	8,72E-12	1,19E-09	Acylamino-acid-releasing enzyme
Solyc11g013280.1	1,58	3,10E-11	3,52E-09	transcription activator
Solyc09g082870.3	1,58	3,03E-03	1,32E-02	Calcium-transporting ATPase
Solyc08g067320.3	1,57	2,01E-08	8,86E-07	Chlorophyll a-b binding protein, chloroplastic
Solyc02g094000.1	1,57	4,35E-03	1,75E-02	EF_hand_5 domain-containing protein/EF_hand_6 domain-containing protein
Solyc05g012790.4	1,57	3,82E-11	4,21E-09	S-acyltransferase
Solyc07g064970.4	1,57	9,41E-07	2,13E-05	65-kDa microtubule-associated protein 1-like
Solyc12g049590.2	1,57	2,33E-04	1,76E-03	1-phosphatidylinositol-3-phosphate 5-kinase FAB1B
Solyc10g006250.3	1,57	6,04E-03	2,25E-02	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein
Solyc01g080640.3	1,57	2,65E-06	4,90E-05	ABC transporter C family member 4
Solyc04g008610.3	1,57	1,84E-07	5,28E-06	Histone acetyltransferase HAC12
Solyc09g066280.4	1,57	5,32E-06	8,65E-05	Transcription factor bHLH155-like protein
Solyc11g066140.2	1,57	1,76E-03	8,66E-03	Para-hydroxybenzoic acid efflux pump subunit AaeB/fusaric acid resistance protein
Solyc01g094800.4	1,57	2,19E-09	1,38E-07	ATP-dependent helicase BRM

Solyc03g120810.4	1,57	1,90E-11	2,33E-09	Kinesin-like protein
Solyc11g007020.2	1,57	1,14E-10	1,10E-08	mevalonate disphosphate decarboxylase
Solyc04g081580.4	1,57	2,80E-03	1,24E-02	RNA helicase DEAD15
Solyc04g050570.3	1,57	1,63E-02	4,90E-02	GDSL esterase/lipase
Solyc04g150104.1	1,57	3,28E-12	5,11E-10	Kirola
Solyc07g022860.4	1,56	3,51E-06	6,16E-05	Regulator of Vps4 activity in the MVB pathway protein
Solyc02g065170.3	1,56	1,66E-07	4,90E-06	L-ascorbate oxidase-like protein
Solyc08g074370.4	1,56	3,37E-11	3,74E-09	DDB1-and CUL4-associated factor-like protein 1
Solyc01g095710.3	1,56	3,98E-06	6,82E-05	RNA helicase DEAH-box3
Solyc02g080340.3	1,56	1,67E-06	3,40E-05	Patatin
Solyc09g008860.4	1,56	2,07E-05	2,53E-04	leucine-rich repeat receptor-like protein kinase PXC1
Solyc01g109510.3	1,56	5,67E-07	1,40E-05	SWI/SNF complex subunit SWI3D
Solyc01g091080.3	1,56	4,58E-05	4,77E-04	tubulin-folding cofactor D
Solyc02g086910.4	1,56	4,01E-07	1,04E-05	Peptidyl-prolyl cis-trans isomerase protein
Solyc07g043480.1	1,56	5,76E-10	4,46E-08	Glycosyltransferase
Solyc07g043620.3	1,56	7,96E-04	4,66E-03	Auxin Response Factor 6B
Solyc07g055530.3	1,56	9,09E-03	3,10E-02	Cytochrome
Solyc02g094520.3	1,56	2,57E-03	1,16E-02	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH4-like
Solyc04g008700.3	1,56	9,74E-08	3,20E-06	Pre-mRNA-processing protein 40C
Solyc02g081200.1	1,56	7,27E-07	1,73E-05	Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein
Solyc01g080430.4	1,55	2,04E-06	3,99E-05	RING/U-box superfamily protein
Solyc11g039650.2	1,55	1,71E-08	7,79E-07	Dynamin
Solyc08g081000.3	1,55	1,38E-06	2,88E-05	Transcription factor jumonji (JmjC) domain-containing protein
Solyc05g015050.3	1,55	3,60E-10	3,03E-08	GPT1
Solyc02g014350.4	1,55	2,39E-08	1,02E-06	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc02g080670.3	1,55	2,66E-04	1,96E-03	L-ascorbate oxidase-like protein
Solyc05g016460.2	1,55	1,09E-04	9,50E-04	mediator of RNA polymerase II transcription subunit 23
Solyc06g076700.1	1,55	2,80E-04	2,03E-03	UPF0503 protein, chloroplastic
Solyc12g039070.2	1,55	3,11E-03	1,35E-02	Strictosidine synthase family protein
Solyc03g115530.4	1,55	9,81E-06	1,40E-04	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1
Solyc09g082510.3	1,55	1,01E-07	3,30E-06	Kinase interacting (KIP1-like) family protein
Solyc07g052940.4	1,55	6,33E-08	2,28E-06	Histone-lysine N-methyltransferase ATXR3
Solyc02g067990.3	1,55	2,69E-08	1,12E-06	AUGMIN subunit 6-like
Solyc09g072753.1	1,55	3,24E-05	3,63E-04	Proteasome endopeptidase complex
Solyc10g018520.1	1,55	1,19E-07	3,75E-06	Polynucleotidyl transferase, ribonuclease H fold protein with HRDC domain-containing protein
Solyc07g042740.3	1,55	1,08E-03	5,92E-03	RNA-binding (RRM/RBD/RNP motifs) family protein
Solyc02g078670.3	1,54	5,45E-08	2,00E-06	COP1-interacting protein 7
Solyc01g091530.4	1,54	7,64E-08	2,62E-06	Fasciclin-like arabinogalactan protein
Solyc12g010110.3	1,54	4,84E-03	1,90E-02	Formin-like protein
Solyc10g085070.3	1,54	6,48E-10	4,93E-08	UPF0503 protein, chloroplastic
Solyc02g083630.3	1,54	5,94E-04	3,70E-03	Ascorbate peroxidase
Solyc03g113350.3	1,54	1,21E-05	1,63E-04	Zinc finger protein
Solyc04g073990.3	1,54	1,16E-06	2,51E-05	annexin p34
Solyc04g080240.4	1,54	8,46E-11	8,38E-09	GYF domain-containing protein
Solyc01g108300.3	1,54	2,18E-04	1,67E-03	Two-component response regulator ARR18
Solyc04g050170.4	1,54	4,56E-06	7,56E-05	Leucine-rich receptor-like protein kinase family protein
Solyc09g010570.1	1,54	1,40E-03	7,24E-03	Para-hydroxybenzoic acid efflux pump subunit AaeB/fusaric acid resistance protein
Solyc01g109860.3	1,54	7,69E-03	2,72E-02	Sec14p-like phosphatidylinositol transfer family protein
Solyc09g018960.4	1,54	1,06E-08	5,22E-07	Chaperone DnaJ-domain superfamily protein
Solyc11g010110.3	1,54	2,76E-08	1,15E-06	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc03g119980.3	1,53	1,36E-09	9,18E-08	Alpha/beta-Hydrolases superfamily protein
Solyc03g115140.4	1,53	4,26E-04	2,81E-03	DNAJ protein JJJ1 homolog
Solyc07g008900.4	1,53	2,92E-11	3,39E-09	Subtilisin-like protease-like protein
Solyc01g110000.3	1,53	1,30E-04	1,09E-03	Beta-galactosidase
Solyc02g090760.4	1,53	1,31E-10	1,23E-08	hypothetical protein
Solyc01g094340.3	1,53	4,10E-06	6,97E-05	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
Solyc12g099020.2	1,53	8,13E-03	2,85E-02	protein serine/threonine kinase
Solyc07g054480.3	1,53	7,45E-04	4,44E-03	Pentatricopeptide repeat-containing protein
Solyc12g019480.3	1,53	1,11E-03	6,06E-03	Formin-like protein
Solyc01g106770.4	1,53	7,67E-07	1,80E-05	Serine/threonine-protein kinase TOR
Solyc01g107200.4	1,53	1,10E-04	9,54E-04	QWRF motif-containing protein 2
Solyc03g082920.4	1,52	5,97E-09	3,20E-07	Heat shock protein 70 family
Solyc01g096010.4	1,52	2,73E-04	1,99E-03	Embryo defective 1703
Solyc01g087490.4	1,52	6,73E-07	1,63E-05	Protein OBERON
Solyc08g067860.2	1,52	7,06E-10	5,31E-08	embryo defective 2410
Solyc01g093970.4	1,52	1,04E-10	1,01E-08	Hexosyltransferase
Solyc01g057770.3	1,52	1,00E-07	3,27E-06	HCO3-transporter family
Solyc07g043240.4	1,52	3,99E-05	4,28E-04	Pectinesterase
Solyc10g006770.4	1,52	1,94E-07	5,53E-06	FACT complex subunit SPT16
Solyc11g008760.3	1,52	1,61E-03	8,08E-03	Pentatricopeptide repeat-containing protein
Solyc02g085560.3	1,52	7,28E-03	2,61E-02	DNA-directed RNA polymerase III subunit Rpc5
Solyc03g123570.3	1,52	8,36E-10	6,17E-08	1-phosphatidylinositol-3-phosphate 5-kinase FAB1B
Solyc03g113450.4	1,52	9,31E-05	8,39E-04	Receptor-like protein kinase
Solyc06g053710.3	1,52	2,08E-07	5,83E-06	ethylene receptor homolog (ETR4)
Solyc07g016170.4	1,52	2,27E-05	2,74E-04	L-arabinokinase-like
Solyc05g054170.4	1,52	3,00E-04	2,14E-03	Scarecrow-like protein 5
Solyc02g092450.3	1,52	2,66E-04	1,96E-03	Calcium-transporting ATPase
Solyc06g083580.4	1,52	7,64E-08	2,62E-06	Pectate lyase
Solyc04g072850.4	1,51	1,41E-09	9,34E-08	Beta-D-xylosidase
Solyc07g017510.3	1,51	4,22E-06	7,11E-05	1-phosphatidylinositol-3-phosphate 5-kinase FAB1B
Solyc03g113660.4	1,51	2,01E-04	1,57E-03	hypothetical protein
Solyc01g094620.3	1,51	2,96E-08	1,21E-06	Mediator of RNA polymerase II transcription subunit 12
Solyc08g074630.2	1,51	1,30E-03	6,85E-03	Polyphenol oxidase
Solyc08g067160.3	1,51	1,35E-02	4,24E-02	Alpha/beta-Hydrolases superfamily protein
Solyc10g005010.4	1,51	1,62E-02	4,88E-02	NAC domain-containing protein
Solyc11g008050.1	1,51	1,19E-02	3,82E-02	Pullulanase 1, chloroplastic
Solyc03g051790.3	1,51	1,04E-07	3,38E-06	Nucleolar GAR2-like protein
Solyc12g057020.2	1,51	1,33E-03	6,95E-03	Carbohydrate esterase, putative (DUF303)
Solyc06g061027.1	1,51	5,31E-05	5,39E-04	Cytochrome P450
Solyc09g091180.3	1,51	9,99E-04	5,58E-03	60 kDa chaperonin
Solyc04g050150.4	1,51	1,81E-06	3,62E-05	RNA helicase DEAH-box13
Solyc09g092250.3	1,51	1,22E-07	3,83E-06	Zinc finger transcription factor 55
Solyc08g045640.3	1,51	1,29E-04	1,09E-03	Remorin family protein
Solyc09g008240.3	1,51	1,14E-07	3,62E-06	ABC transporter
Solyc11g066770.3	1,51	9,19E-09	4,63E-07	AP-2 complex subunit alpha
Solyc11g011880.2	1,50	4,10E-06	6,97E-05	cysteine-rich receptor-like protein kinase 2
Solyc03g111390.4	1,50	1,35E-06	2,83E-05	kelch domain-containing protein 4
Solyc11g062270.2	1,50	9,85E-12	1,30E-09	Signal recognition particle subunit SRP72
Solyc12g099910.2	1,50	7,66E-08	2,62E-06	Protein CHROMATIN REMODELING 5
Solyc10g080550.2	1,50	2,63E-05	3,07E-04	Protein trichome birefringence
Solyc01g081430.4	1,50	1,38E-04	1,15E-03	Armadillo-type fold
Solyc02g021360.3	1,50	2,33E-08	1,01E-06	Katanin p80 WD40 repeat-containing subunit B1 homolog
Solyc11g008880.2	1,50	9,76E-03	3,28E-02	CRIB domain
Solyc01g101020.4	1,50	3,33E-11	3,73E-09	FACT complex subunit SPT16
Solyc06g050510.3	1,50	9,78E-06	1,40E-04	SNF2 domain-containing protein CLASSY 1
Solyc08g005640.4	1,49	1,22E-02	3,91E-02	Terpene synthase
Solyc08g067090.4	1,49	3,34E-09	2,00E-07	cyclophilin-like protein
Solyc03g124010.3	1,49	5,84E-05	5,82E-04	p-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc08g066360.3	1,49	2,44E-06	4,61E-05	Malic enzyme
Solyc06g083420.3	1,49	8,36E-07	1,93E-05	Helicase/SANT-associated DNA-binding protein
Solyc08g005540.2	1,49	3,53E-03	1,49E-02	Polyamine transporter PUT1
Solyc05g016390.4	1,49	1,08E-03	5,90E-03	Carbohydrate-binding X8 domain superfamily protein
Solyc05g015250.2	1,49	9,06E-03	3,09E-02	Mannosyl-oligosaccharide glucosidase GCS1
Solyc07g056260.4	1,49	1,15E-05	1,57E-04	Callose synthase 3
Solyc11g020810.2	1,49	7,22E-05	6,85E-04	AdoMet-dependent rRNA methyltransferase SPB1
Solyc04g049490.3	1,49	1,75E-10	1,62E-08	Vacuolar protein sorting-associated protein 53 A
Solyc09g092240.3	1,49	1,62E-03	8,12E-03	small subunit processome component 20 homolog isoform X1
Solyc07g022780.2	1,49	1,12E-03	6,09E-03	Calcium-transporting ATPase
Solyc05g009350.4	1,49	1,32E-03	6,90E-03	Zinc finger transcription factor 37
Solyc06g068860.3	1,49	2,86E-08	1,17E-06	Alpha-mannosidase
Solyc08g076030.3	1,49	3,26E-09	1,97E-07	TOPLESS 2

Solyc01g102340.3	1,49	3,06E-06	5,52E-05	R2R3MYB transcription factor 61
Solyc10g008710.3	1,49	9,14E-05	8,29E-04	GDSL esterase/lipase
Solyc09g011170.3	1,49	9,93E-10	7,18E-08	Prf interactor 30137
Solyc09g065880.4	1,49	2,32E-04	1,76E-03	F-box/LRR-repeat protein 17
Solyc08g061560.3	1,48	1,33E-06	2,81E-05	Receptor protein kinase
Solyc07g009130.4	1,48	6,40E-07	1,56E-05	Cadmium/zinc-transporting ATPase HMA2
Solyc11g013530.3	1,48	1,11E-08	5,47E-07	PHD finger family protein
Solyc06g072145.1	1,48	3,29E-05	3,67E-04	PB1 domain-containing protein
Solyc10g085850.1	1,48	1,46E-05	1,90E-04	TPSI1 protein
Solyc10g005920.4	1,48	6,25E-09	3,32E-07	enhancer of mRNA-decapping protein 4-like
Solyc08g007680.1	1,47	1,48E-04	1,22E-03	Subtilisin-like protease
Solyc03g120770.4	1,47	1,22E-03	6,52E-03	Phox (PX) domain-containing protein
Solyc10g081020.2	1,47	7,59E-10	5,66E-08	Transcription elongation factor spt6
Solyc07g005480.3	1,47	4,87E-05	5,02E-04	Formin-like protein
Solyc07g007550.3	1,47	1,59E-04	1,30E-03	Heparanase-like protein 3
Solyc03g097520.3	1,47	1,00E-06	2,24E-05	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein
Solyc02g088580.1	1,47	7,53E-06	1,12E-04	Plant calmodulin-binding protein-like protein
Solyc07g053730.4	1,47	2,65E-06	4,90E-05	Nucleolar GTP-binding protein 1
Solyc02g077660.3	1,47	2,68E-07	7,28E-06	Homeobox domain-containing protein/DDT domain-containing protein
Solyc03g111590.4	1,47	2,34E-08	1,01E-06	Lysine-specific demethylase REF6
Solyc03g096800.4	1,47	1,31E-05	1,73E-04	membrane protein of ER body-like protein
Solyc10g011690.3	1,47	6,78E-04	4,12E-03	protein SPA1-RELATED 2-like
Solyc09g074730.3	1,47	2,73E-04	1,99E-03	Homeobox protein LUMINIDEPENDENS
Solyc07g056010.3	1,47	5,31E-08	1,98E-06	Conserved oligomeric Golgi complex subunit 4
Solyc06g008040.3	1,47	4,86E-07	1,23E-05	CLIP-associated protein
Solyc12g009040.3	1,47	4,14E-03	1,68E-02	Long chain acyl-CoA synthetase
Solyc04g078000.3	1,47	1,01E-05	1,44E-04	QWRF motif-containing protein 2-like
Solyc05g054590.4	1,47	4,25E-05	4,50E-04	UDP-glucuronic acid decarboxylase
Solyc01g079240.3	1,47	8,22E-12	1,15E-09	Long chain acyl-CoA synthetase 1
Solyc10g009430.3	1,47	3,01E-03	1,31E-02	O-acyltransferase WSD1-like
Solyc09g061890.3	1,47	2,53E-05	2,96E-04	Pectate lyase
Solyc12g042170.3	1,47	7,33E-03	2,63E-02	Adp-ribosylation factor gtpase-activating protein agd3
Solyc01g080840.3	1,47	2,34E-08	1,01E-06	Protein translocase subunit SecA
Solyc03g005780.3	1,46	1,83E-05	2,28E-04	Chlorophyll a-b binding protein, chloroplastic
Solyc02g083350.4	1,46	5,01E-08	1,89E-06	RNA polymerase 2 largest subunit 1
Solyc11g071660.1	1,46	9,63E-07	2,16E-05	NF-kappa-B-activating protein
Solyc02g092950.3	1,46	1,30E-03	6,84E-03	Microtubule-associated protein RP/EB family member 1C
Solyc03g098070.3	1,46	1,87E-03	9,08E-03	C2H2-like zinc finger protein
Solyc06g060730.3	1,46	7,20E-06	1,08E-04	Zf-met domain-containing protein
Solyc05g055730.4	1,46	2,62E-03	1,18E-02	Methylenetetrahydrofolate reductase
Solyc12g011023.1	1,46	1,28E-03	6,78E-03	Xyloglucan endotransglucosylase/hydrolase
Solyc06g069300.1	1,46	4,27E-03	1,72E-02	Protein MIZU-KUSSEI 1
Solyc11g010850.2	1,46	6,93E-05	6,64E-04	1-deoxy-d-xylulose-5-phosphate synthase 1
Solyc01g079170.3	1,46	3,04E-03	1,33E-02	Hexosyltransferase
Solyc09g089560.4	1,46	1,11E-05	1,54E-04	MATH domain-containing protein
Solyc06g069500.3	1,46	2,06E-06	4,01E-05	Dentin sialophosphoprotein-like protein
Solyc08g075080.3	1,46	4,95E-05	5,08E-04	RING/U-box superfamily protein
Solyc03g063560.3	1,46	8,82E-11	8,70E-09	Glutamate synthase
Solyc05g007940.3	1,46	3,17E-04	2,24E-03	LERNALX L.esculentum ribonuclease lx
Solyc07g043390.4	1,46	1,09E-07	3,49E-06	Cellulose synthase
Solyc01g009300.3	1,46	4,06E-09	2,31E-07	Serine/threonine-protein kinase Nek2
Solyc02g068560.3	1,46	7,71E-07	1,80E-05	Protein CHROMATIN REMODELING 4
Solyc09g009080.4	1,46	1,63E-07	4,84E-06	DNA demethylase1
Solyc02g081070.4	1,45	2,03E-08	8,94E-07	Kinase
Solyc02g068780.4	1,45	2,63E-03	1,18E-02	Unknown protein
Solyc03g031420.1	1,45	3,86E-03	1,60E-02	molybdenum cofactor sulfurase
Solyc07g018070.4	1,45	1,17E-03	6,32E-03	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein
Solyc07g063440.3	1,45	3,32E-10	2,82E-08	Trafficking protein particle complex II-specific subunit-like protein
Solyc05g056170.3	1,45	7,08E-11	7,24E-09	Phenylalanine ammonia-lyase
Solyc03g118780.3	1,45	3,94E-04	2,65E-03	Thaumatin-like protein
Solyc06g010240.3	1,45	4,67E-08	1,79E-06	SNF2-related
Solyc02g093850.3	1,45	4,06E-04	2,72E-03	Ankyrin repeat
Solyc04g074640.4	1,45	9,56E-04	5,40E-03	Ascorbate peroxidase
Solyc05g055330.3	1,45	6,31E-06	9,75E-05	Pleiotropic drug resistance protein 2
Solyc02g020910.4	1,45	3,53E-09	2,09E-07	Unknown protein
Solyc12g014150.3	1,45	8,52E-06	1,25E-04	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc10g078180.3	1,44	2,99E-08	1,22E-06	cyclinT1_1
Solyc07g063130.4	1,44	9,84E-08	3,23E-06	Protein kinase domain
Solyc11g018720.1	1,44	1,10E-02	3,60E-02	ALBINO3-like protein 2, chloroplastic
Solyc07g056650.4	1,44	1,23E-04	1,04E-03	Interactor of constitutive active ROPS 1-like protein
Solyc04g008830.1	1,44	3,53E-03	1,49E-02	Leucine-rich repeat receptor-like protein kinase
Solyc06g071120.3	1,44	1,19E-06	2,56E-05	Ubiquitin carboxyl-terminal hydrolase-related protein
Solyc03g121440.4	1,44	2,54E-09	1,59E-07	Proline-rich receptor-like protein kinase PERK13
Solyc05g015930.4	1,44	7,37E-08	2,57E-06	GYF-like protein
Solyc07g018300.3	1,44	2,09E-03	9,92E-03	Replication protein A 32 kDa subunit A
Solyc07g065950.4	1,44	1,08E-07	3,48E-06	enhancer of mRNA-decapping protein 4-like
Solyc05g011930.4	1,44	1,80E-05	2,25E-04	DnaJ domain-containing protein
Solyc02g091890.3	1,44	4,48E-05	4,69E-04	myb-like protein X
Solyc06g150136.1	1,44	9,23E-03	3,14E-02	RING/U-box superfamily protein
Solyc06g072270.4	1,44	1,61E-03	8,06E-03	RING/U-box superfamily protein
Solyc09g098040.3	1,44	1,65E-08	7,53E-07	Phosphoglucan, water dikinase, chloroplastic
Solyc09g008280.2	1,44	8,85E-06	1,29E-04	S-adenosyl-L-methionine synthetase Z24743
Solyc09g066480.2	1,44	1,89E-07	5,41E-06	Protein CHROMATIN REMODELING 8
Solyc02g087410.4	1,44	1,49E-03	7,57E-03	ABC transporter B family member 18
Solyc08g007360.3	1,44	2,25E-06	4,30E-05	Protein transport protein sec16
Solyc03g020020.3	1,43	2,00E-07	5,66E-06	embryo defective 2016
Solyc03g046590.3	1,43	2,19E-06	4,20E-05	AUGMIN subunit 5
Solyc08g007340.3	1,43	1,35E-07	4,17E-06	Protein transport protein sec16
Solyc03g005170.3	1,43	2,74E-07	7,41E-06	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein
Solyc04g081520.3	1,43	1,18E-02	3,81E-02	L-ascorbate oxidase-like protein
Solyc10g046930.3	1,43	1,42E-07	4,33E-06	AdoMet-dependent rRNA methyltransferase SPB1
Solyc09g015660.4	1,43	3,24E-05	3,63E-04	transcription factor GTE6-like
Solyc10g047240.2	1,43	1,49E-03	7,58E-03	annexin 9
Solyc07g054200.4	1,43	1,24E-05	1,66E-04	Pre-mRNA splicing factor
Solyc03g097280.4	1,43	2,36E-05	2,82E-04	MIF4G-like domain containing protein
Solyc03g114240.4	1,43	1,61E-04	1,31E-03	BURP domain
Solyc09g015520.3	1,42	1,57E-06	3,23E-05	Leucine-rich repeat receptor-like protein kinase PXC2
Solyc09g030390.3	1,42	1,21E-07	3,80E-06	Serine/arginine repetitive matrix protein 1
Solyc04g016410.3	1,42	5,02E-06	8,21E-05	Heat shock protein DnaJ with tetratricopeptide repeat-containing protein
Solyc06g069630.4	1,42	2,41E-04	1,81E-03	T-box transcription factor%2C putative (DUF863)
Solyc03g043770.4	1,42	3,02E-05	3,44E-04	Leucine-rich receptor-like protein kinase family protein
Solyc03g005060.4	1,42	1,16E-03	6,27E-03	Nucleolar-like protein
Solyc02g090510.3	1,42	1,13E-06	2,45E-05	CDPK-related protein kinase
Solyc02g071260.3	1,42	6,64E-09	3,49E-07	Phytochrome
Solyc11g011490.2	1,42	3,86E-03	1,59E-02	Zinc ion binding protein
Solyc10g079010.3	1,42	5,37E-08	1,98E-06	hypothetical protein
Solyc04g072035.1	1,42	2,37E-06	4,49E-05	Inositol polyphosphate 5-phosphatase I
Solyc01g073950.4	1,42	6,29E-06	9,74E-05	Myb_DNA-binding domain-containing protein/Bromodomain domain-containing protein
Solyc11g072490.2	1,42	2,46E-08	1,04E-06	Interactor of constitutive active ROPs-like protein
Solyc06g076630.3	1,42	2,68E-07	7,28E-06	Peroxidase
Solyc03g118280.1	1,42	4,77E-03	1,88E-02	Pentatricopeptide repeat
Solyc05g054480.3	1,42	7,43E-04	4,42E-03	Actin
Solyc01g096670.4	1,42	1,54E-04	1,26E-03	Cytochrome P450
Solyc03g117510.4	1,42	5,98E-03	2,24E-02	Formamidopyrimidine-DNA glycosylase
Solyc03g121380.3	1,42	4,98E-06	8,15E-05	Mitochondrial outer membrane import complex protein METAXIN
Solyc08g077420.3	1,42	3,39E-09	2,02E-07	Regulator of nonsense transcripts 1-like protein
Solyc09g072750.2	1,42	7,51E-07	1,77E-05	Unknown protein
Solyc10g006330.3	1,42	1,19E-06	2,56E-05	protein PLASTID MOVEMENT IMPAIRED 1
Solyc05g050630.4	1,41	5,87E-06	9,30E-05	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc12g011030.3	1,41	3,85E-03	1,59E-02	xyloglucan endotransglucosylase-hydrolase 9
Solyc04g009200.3	1,41	1,39E-03	7,20E-03	glutamate 1-semialdehyde 2,1-aminomutase

Solyc05g005780.3	1,41	4,35E-10	3,52E-08	AP-1 complex subunit gamma
Solyc11g072810.2	1,41	6,30E-08	2,27E-06	Nuclear factor related to kappa-B-binding protein
Solyc04g015210.4	1,41	1,35E-02	4,22E-02	Disease resistance protein
Solyc06g060380.3	1,41	1,37E-03	7,11E-03	Sister chromatid cohesion protein PDS5-like protein A
Solyc09g014160.3	1,41	1,56E-04	1,27E-03	UPF0503 protein At3g09070, chloroplastic-like
Solyc11g069780.3	1,41	1,20E-06	2,59E-05	P-loop NTPase domain-containing protein LPA1-like protein 1
Solyc06g062600.3	1,41	4,19E-06	7,07E-05	Glucose-methanol-choline (GMC) oxidoreductase family protein
Solyc09g007420.4	1,41	9,13E-03	3,11E-02	Glycosyltransferases
Solyc04g076790.3	1,41	3,20E-11	3,61E-09	Serine hydroxymethyltransferase
Solyc05g051510.4	1,41	5,04E-03	1,96E-02	Prohibitin
Solyc03g115240.4	1,41	4,36E-10	3,52E-08	Protein LEO1-like protein
Solyc07g065630.4	1,41	1,71E-08	7,77E-07	E3 ubiquitin-protein ligase UPL2
Solyc02g093360.3	1,41	1,27E-08	6,10E-07	Stpk1 protein kinase
Solyc10g006390.3	1,41	3,43E-06	6,08E-05	Smad nuclear-interacting protein 1
Solyc08g067920.3	1,41	5,90E-06	9,32E-05	Enhancer of polycomb-like protein
Solyc11g011080.3	1,41	5,97E-04	3,71E-03	Disease resistance protein (TIR-NBS-LRR class)
Solyc09g007330.4	1,41	1,29E-02	4,09E-02	DNA helicase mcm8-like protein
Solyc12g100330.2	1,41	1,39E-06	2,89E-05	cytosine-5 DNA methyltransferase3L
Solyc01g109180.4	1,40	2,65E-06	4,90E-05	Long chain acyl-CoA synthetase 4
Solyc01g091230.3	1,40	1,50E-04	1,23E-03	Receptor-like kinase
Solyc06g008030.3	1,40	1,21E-06	2,59E-05	bHLH transcription factor 041
Solyc05g012650.4	1,40	2,08E-04	1,62E-03	DUF863 domain-containing protein
Solyc06g084420.1	1,40	9,88E-04	5,53E-03	Leucine-rich repeat receptor-like kinase
Solyc03g113060.3	1,40	1,17E-05	1,59E-04	ABC transporter A family member 7
Solyc01g095320.4	1,40	1,23E-05	1,65E-04	Bag family molecular chaperone regulator 6-like protein
Solyc02g088170.2	1,40	2,34E-03	1,08E-02	Pentatricopeptide repeat-containing protein
Solyc12g005010.2	1,40	1,69E-06	3,42E-05	Actin cytoskeleton-regulatory complex pan-like protein
Solyc01g111470.4	1,40	9,47E-03	3,21E-02	Pentatricopeptide repeat
Solyc12g044820.3	1,40	1,20E-04	1,03E-03	ABC transporter C family member 8
Solyc08g081380.3	1,40	1,08E-03	5,93E-03	BTB/POZ domain-containing protein
Solyc07g053590.4	1,40	8,82E-03	3,03E-02	NAC domain
Solyc09g059440.1	1,40	6,79E-03	2,47E-02	cell division control protein 45 homolog
Solyc05g007930.3	1,39	1,02E-05	1,45E-04	Beta-1,3-galactosyltransferase 15
Solyc01g107340.4	1,39	3,42E-05	3,78E-04	classical arabinogalactan protein 9
Solyc02g084520.3	1,39	1,45E-05	1,89E-04	Zinc finger transcription factor 20
Solyc12g006140.2	1,39	4,07E-04	2,72E-03	Cab-5 gene encoding chlorophyll a/b-binding protein
Solyc07g049370.2	1,39	3,33E-03	1,42E-02	Glucan endo-1,3-beta-glucosidase 3
Solyc05g013400.4	1,39	1,42E-02	4,41E-02	Pentatricopeptide repeat
Solyc11g011150.2	1,39	7,79E-04	4,59E-03	DNA repair protein Rad4 family
Solyc12g038490.2	1,39	5,91E-06	9,32E-05	Dentin sialophosphoprotein-like protein
Solyc12g007160.2	1,39	6,44E-03	2,37E-02	ABI family
Solyc10g006780.4	1,39	8,05E-06	1,19E-04	Telomere length regulation protein TEL2-like protein
Solyc06g082200.4	1,39	5,71E-04	3,58E-03	Rab3 GTPase-activating protein catalytic subunit
Solyc11g067200.2	1,39	8,46E-05	7,80E-04	Protein HIRA
Solyc04g054880.3	1,39	7,15E-04	4,30E-03	DUF632 domain-containing protein/DUF630 domain-containing protein
Solyc01g091460.3	1,39	1,92E-08	8,56E-07	Brefeldin A-inhibited guanine nucleotide-exchange protein 2
Solyc03g046450.3	1,38	4,97E-07	1,25E-05	ARM repeat superfamily protein
Solyc07g056660.4	1,38	5,58E-09	3,01E-07	Vacuolar sorting protein 39
Solyc02g086458.1	1,38	5,81E-09	3,13E-07	titin isoform X2
Solyc11g045215.1	1,38	8,20E-03	2,87E-02	DEAD-box ATP-dependent RNA helicase 50
Solyc02g062370.4	1,38	3,34E-05	3,71E-04	Zinc finger CCCH domain-containing protein 19
Solyc07g064870.3	1,38	3,92E-07	1,02E-05	Endoglucanase
Solyc03g115560.3	1,38	1,21E-06	2,59E-05	Flavin-containing monooxygenase
Solyc09g008490.4	1,38	2,65E-06	4,90E-05	Protein SHOOT GRAVITROPISM 6
Solyc09g072660.4	1,38	2,04E-04	1,59E-03	FAD-binding Berberine family protein
Solyc03g118530.3	1,38	1,00E-07	3,27E-06	Protein kinase domain
Solyc05g006570.1	1,38	1,25E-03	6,65E-03	Inactive receptor kinase
Solyc06g074480.3	1,38	1,37E-05	1,80E-04	Protein kinase G11A
Solyc06g008900.4	1,38	7,23E-03	2,60E-02	RING/U-box superfamily protein
Solyc03g097260.4	1,38	9,52E-06	1,36E-04	RING/FYVE/PHD zinc finger superfamily protein
Solyc11g017420.2	1,38	2,61E-04	1,93E-03	Transmembrane protein (DUF616)
Solyc02g076840.3	1,38	1,31E-07	4,07E-06	Protein SCAR1
Solyc07g063590.4	1,38	9,32E-06	1,34E-04	Myosin-2
Solyc08g007970.3	1,38	3,55E-05	3,89E-04	Myosin heavy chain-related protein
Solyc04g072860.3	1,38	2,83E-04	2,04E-03	Beta-D-xylosidase
Solyc05g051010.4	1,38	1,37E-03	7,11E-03	Dihydroflavonol-4-reductase
Solyc05g050540.4	1,38	2,05E-03	9,76E-03	Laccase
Solyc02g083780.3	1,38	1,43E-03	7,33E-03	Pentatricopeptide repeat
Solyc11g008680.2	1,37	7,23E-04	4,34E-03	Acyl-[acyl-carrier-protein] desaturase
Solyc04g071040.4	1,37	2,51E-06	4,72E-05	Regulator of chromosome condensation (RCC1) family protein
Solyc06g053920.4	1,37	2,70E-05	3,13E-04	hypothetical protein
Solyc02g076750.3	1,37	1,49E-03	7,56E-03	Cysteine protease CP14
Solyc01g006960.3	1,37	5,69E-06	9,09E-05	Trafficking protein particle complex subunit 8
Solyc09g065340.3	1,37	2,63E-04	1,94E-03	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein
Solyc09g005630.3	1,37	3,77E-03	1,57E-02	Protein trichome birefringence-like 3
Solyc01g088720.3	1,37	1,59E-06	3,26E-05	Transcription factor IIIB 90 kDa subunit
Solyc01g109540.4	1,37	1,29E-10	1,23E-08	Coatomer subunit gamma
Solyc02g089130.4	1,37	2,34E-03	1,08E-02	COBRA-like protein
Solyc03g118020.3	1,37	2,73E-06	5,00E-05	Nuclease domain-containing protein 1-like
Solyc01g009230.4	1,37	3,69E-07	9,63E-06	sitiens
Solyc02g083720.4	1,37	3,77E-05	4,08E-04	MLO-like protein
Solyc09g083380.4	1,37	3,10E-06	5,57E-05	Histone H1
Solyc01g090200.4	1,37	1,21E-08	5,84E-07	Glycine-tRNA ligase
Solyc04g063230.3	1,37	4,23E-09	2,36E-07	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc03g120970.3	1,37	1,17E-05	1,59E-04	Non-heme dioxygenase N-terminal domain
Solyc07g018360.3	1,37	1,76E-06	3,55E-05	Elongation factor Ts, mitochondrial
Solyc04g079520.3	1,36	3,49E-04	2,41E-03	Major facilitator superfamily protein
Solyc08g069231.1	1,36	1,74E-05	2,18E-04	L-arabinokinase
Solyc03g112140.4	1,36	3,67E-08	1,46E-06	MAP kinase kinase kinase 27
Solyc10g084280.2	1,36	1,29E-06	2,73E-05	SUN-like protein 29
Solyc01g087720.4	1,36	1,47E-04	1,21E-03	Structural maintenance of chromosomes protein 5
Solyc01g096390.4	1,36	5,29E-06	8,60E-05	DNA-directed RNA polymerase subunit
Solyc02g082540.4	1,36	2,29E-09	1,44E-07	Calcium-binding EF hand family protein
Solyc01g086720.3	1,36	8,67E-03	2,99E-02	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
Solyc04g005540.3	1,36	1,86E-04	1,47E-03	Pvr4
Solyc09g063030.4	1,36	9,23E-10	6,75E-08	CLIP-associated protein
Solyc07g047770.4	1,36	1,62E-05	2,07E-04	Histidine kinase 2
Solyc12g043000.3	1,36	9,09E-11	8,92E-09	Coatomer subunit beta'
Solyc06g034150.4	1,36	4,97E-03	1,94E-02	8-amino-7-oxononanoate synthase
Solyc11g005770.2	1,36	1,78E-03	8,76E-03	Pectinesterase
Solyc02g089940.4	1,36	1,37E-09	9,18E-08	BEL1-like homeodomain protein 4
Solyc04g057880.3	1,36	1,14E-05	1,57E-04	Histone-lysine N-methyltransferase ASHH2
Solyc01g065500.3	1,36	1,69E-03	8,37E-03	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
Solyc07g064330.3	1,36	3,79E-07	9,86E-06	DNA polymerase
Solyc03g098150.3	1,36	5,75E-08	2,09E-06	protein kinase 6
Solyc04g054190.3	1,36	1,37E-09	9,18E-08	Protein kinase superfamily protein
Solyc12g036150.1	1,36	6,68E-03	2,44E-02	ABC transporter C family member 2
Solyc02g089250.4	1,36	3,03E-03	1,32E-02	Pollen Ole e 1 allergen/extensin
Solyc01g068140.4	1,36	3,51E-03	1,48E-02	HXXXD-type acyl-transferase family protein
Solyc08g066530.4	1,36	2,38E-06	4,50E-05	acid phosphatase 1-like
Solyc09g075190.3	1,36	4,71E-05	4,89E-04	Gamma-tubulin complex component
Solyc07g047610.3	1,36	7,49E-07	1,77E-05	Transcriptional adapter
Solyc06g072340.3	1,35	1,46E-05	1,90E-04	Protein kinase domain
Solyc01g107410.3	1,35	1,50E-05	1,93E-04	Pathogenesis-related homeodomain protein
Solyc10g005720.1	1,35	4,91E-05	5,05E-04	Unknown protein
Solyc01g091590.3	1,35	2,95E-03	1,29E-02	BON1-associated protein 2-like
Solyc05g054910.3	1,35	2,50E-05	2,94E-04	SAC3/GANP/Nin1/mts3/eIF-3 p25
Solyc12g094460.2	1,35	4,22E-03	1,71E-02	L-ascorbate oxidase-like protein
Solyc11g005130.2	1,35	4,42E-05	4,65E-04	Wound-responsive family protein
Solyc07g019650.4	1,35	9,96E-07	2,22E-05	Pentatricopeptide repeat-containing protein
Solyc12g099290.2	1,35	1,98E-06	3,89E-05	Aldehyde dehydrogenase

Solyc02g071800.3	1,35	2,61E-03	1,17E-02	Protein kinase domain
Solyc05g010100.4	1,35	7,97E-05	7,43E-04	tRNA-specific adenosine deaminase
Solyc07g008670.3	1,35	5,59E-06	8,98E-05	protein LONGIFOLIA 1
Solyc09g063090.4	1,35	8,05E-05	7,48E-04	methyl-coenzyme M reductase II subunit gamma%2C putative (DUF3741)
Solyc04g016370.3	1,35	9,36E-05	8,43E-04	DNA helicase INO80
Solyc05g008090.3	1,35	6,70E-08	2,39E-06	TPX2 (Targeting protein for Xklp2) protein family
Solyc05g032750.3	1,35	5,02E-07	1,26E-05	protein PLASTID MOVEMENT IMPAIRED 1-RELATED 1
Solyc11g040170.3	1,35	5,19E-04	3,30E-03	mRNA capping enzyme family protein
Solyc09g075690.1	1,35	7,66E-03	2,71E-02	2-hydroxyisoflavanone dehydratase
Solyc06g066790.3	1,35	3,77E-09	2,19E-07	N-alpha-acetyltransferase 15, NatA auxiliary subunit-like
Solyc07g064580.3	1,35	1,04E-05	1,47E-04	Actin cytoskeleton-regulatory complex pan-like protein
Solyc07g045170.3	1,35	1,54E-04	1,26E-03	hypothetical protein
Solyc04g076860.3	1,35	2,52E-03	1,14E-02	Zinc finger (C3HC4-type RING finger) family protein
Solyc05g009700.4	1,34	1,44E-03	7,35E-03	Lysine histidine transporter-like 1
Solyc11g066380.3	1,34	7,03E-07	1,68E-05	Protein UPSTREAM OF FLC
Solyc09g060090.3	1,34	9,03E-06	1,31E-04	Sec14p-like phosphatidylinositol transfer family protein
Solyc09g064200.4	1,34	8,85E-06	1,29E-04	Myosin
Solyc12g099360.2	1,34	5,00E-03	1,95E-02	AMP-dependent synthetase/ligase
Solyc12g100360.1	1,34	2,91E-05	3,34E-04	calpain-type cysteine protease DEK1
Solyc09g009800.3	1,34	3,44E-04	2,39E-03	B-block binding subunit of TFIIIC
Solyc02g087620.3	1,34	4,72E-08	1,80E-06	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase
Solyc06g072110.4	1,34	1,83E-07	5,26E-06	testis-expressed sequence 2 protein-like
Solyc01g010460.4	1,34	7,52E-03	2,67E-02	5'-AMP-activated protein kinase subunit beta-2
Solyc02g082400.4	1,34	5,43E-05	5,49E-04	Transcription factor jumonji (JmjC) domain-containing protein
Solyc11g066100.2	1,34	3,47E-05	3,82E-04	Heat shock protein 70
Solyc08g077230.3	1,34	8,28E-08	2,79E-06	Two-component response regulator APRR2-like protein
Solyc04g079690.3	1,34	1,64E-05	2,08E-04	Protein kinase domain-containing protein
Solyc04g081280.3	1,34	1,76E-05	2,21E-04	5'-3' exoribonuclease
Solyc01g096850.4	1,34	7,21E-04	4,33E-03	Protein FAR1-RELATED SEQUENCE 3
Solyc03g044380.3	1,34	8,27E-06	1,22E-04	EZ2
Solyc12g055970.3	1,34	7,56E-05	7,12E-04	Endoglucanase
Solyc11g066670.1	1,34	9,50E-05	8,53E-04	Glycosyltransferase
Solyc01g088700.4	1,34	1,35E-07	4,16E-06	Eukaryotic translation initiation factor 4G
Solyc07g064910.3	1,34	1,07E-06	2,35E-05	EH domain-containing protein 1
Solyc11g007580.3	1,33	3,17E-05	3,57E-04	DNA demethylase 3
Solyc11g010560.3	1,33	1,47E-08	6,86E-07	Kinesin
Solyc02g071580.4	1,33	1,73E-08	7,84E-07	Subtilisin-like protease SBT5.3
Solyc05g008030.1	1,33	9,47E-03	3,21E-02	ATP-dependent DNA helicase RecG
Solyc04g015270.3	1,33	1,17E-09	8,10E-08	Hexosyltransferase
Solyc05g051640.4	1,33	8,89E-05	8,12E-04	Leucine-rich repeat receptor-like protein kinase
Solyc11g068360.1	1,33	7,52E-03	2,67E-02	CC-NBS-LRR type resistance protein
Solyc06g063010.4	1,33	4,42E-05	4,65E-04	nuclear receptor coactivator
Solyc07g008190.4	1,33	4,73E-08	1,80E-06	nuclear pore complex protein NUP1
Solyc11g069270.2	1,33	6,13E-07	1,50E-05	beta-galactosidase 5
Solyc07g032100.3	1,33	1,30E-08	6,20E-07	Coatomer subunit alpha
Solyc04g011650.3	1,33	6,23E-04	3,85E-03	Telomere binding protein
Solyc01g104570.4	1,33	2,01E-04	1,57E-03	kinetochore protein NDC80 homolog
Solyc07g041970.4	1,33	8,05E-05	7,48E-04	Subtilisin-like protease
Solyc03g096000.3	1,33	4,64E-08	1,79E-06	Clathrin heavy chain
Solyc11g008810.2	1,33	1,50E-08	6,96E-07	Beta-hexosaminidase
Solyc07g032230.3	1,33	9,50E-06	1,36E-04	Regulator of Vps4 activity in the MVB pathway protein
Solyc01g074000.3	1,33	2,45E-04	1,83E-03	Histone H3
Solyc03g078300.3	1,33	5,10E-03	1,98E-02	NBS-LRR resistance protein
Solyc01g096360.3	1,33	1,86E-09	1,19E-07	Rho GTPase-activating protein 3
Solyc08g083110.4	1,33	2,58E-03	1,16E-02	Methionine gamma-lyase
Solyc05g051680.4	1,33	1,58E-03	7,92E-03	Structural maintenance of chromosomes protein 6
Solyc07g053450.4	1,33	4,32E-04	2,85E-03	Basic-leucine zipper (BZIP) transcription factor family protein
Solyc01g088170.4	1,33	1,74E-07	5,10E-06	aldehyde oxidase 2
Solyc04g082330.3	1,32	3,30E-05	3,68E-04	pre-rRNA-processing protein TSR1 homolog
Solyc08g082750.3	1,32	2,62E-10	2,27E-08	Plant regulator RWP-RK family protein
Solyc04g009990.3	1,32	4,22E-07	1,08E-05	Transcription factor jumonji (Jmj) family protein / zinc finger (C5HC2 type) family protein
Solyc07g065710.3	1,32	8,99E-09	4,55E-07	Protein kinase G11A
Solyc05g054640.4	1,32	5,08E-08	1,91E-06	2-oxoglutarate dehydrogenase, E1 component
Solyc07g056020.3	1,32	8,80E-09	4,47E-07	Translation initiation factor IF-2
Solyc01g105020.3	1,32	2,59E-08	1,09E-06	Protein phosphatase 2C (PP2C)-like domain
Solyc09g009370.4	1,32	2,10E-04	1,63E-03	Calcium-dependent lipid-binding family protein
Solyc02g062180.3	1,32	1,45E-03	7,39E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc02g090200.3	1,32	6,87E-03	2,49E-02	Zinc-finger domain of monoamine-oxidase A repressor R1
Solyc09g005180.4	1,32	1,10E-02	3,60E-02	L-gulonolactone oxidase
Solyc01g106390.3	1,32	1,98E-03	9,53E-03	Glutamyl-tRNA reductase
Solyc04g082710.4	1,32	1,11E-05	1,53E-04	Papaya proteinase 4
Solyc10g005000.4	1,32	5,91E-03	2,21E-02	SUN-like protein 27
Solyc07g047790.3	1,32	2,76E-03	1,23E-02	Heat shock protein
Solyc02g062560.3	1,32	3,52E-08	1,41E-06	Tobacco mosaic virus resistance-1
Solyc02g094050.4	1,32	2,67E-04	1,96E-03	Blue copper protein
Solyc08g016050.4	1,32	4,16E-08	1,62E-06	Guanine nucleotide exchange factor SPIKE 1
Solyc02g083130.4	1,32	4,47E-04	2,92E-03	Regulator of Vps4 activity in the MVB pathway protein
Solyc02g032940.4	1,32	1,50E-03	7,60E-03	Aspartic proteinase
Solyc07g008880.3	1,32	5,04E-09	2,76E-07	Pre-mRNA-processing-splicing factor 8
Solyc07g064080.4	1,32	4,30E-05	4,55E-04	amino-terminal region of chorein
Solyc03g006140.3	1,32	3,83E-09	2,22E-07	Neutral ceramidase
Solyc02g091660.3	1,32	2,85E-03	1,26E-02	transcription factor GTE2-like
Solyc12g014490.3	1,32	7,72E-05	7,25E-04	65-kDa microtubule-associated protein 1-like
Solyc03g033530.4	1,32	1,30E-02	4,10E-02	DNA-(apurinic or apyrimidinic site) lyase
Solyc06g060960.3	1,31	1,59E-03	7,98E-03	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6
Solyc03g080010.3	1,31	4,31E-06	7,22E-05	DNA mismatch repair protein MutS
Solyc03g083970.3	1,31	2,21E-04	1,69E-03	BAG family molecular chaperone regulator 7-like
Solyc04g082140.3	1,31	9,88E-05	8,78E-04	pectinesterase
Solyc10g008320.1	1,31	4,90E-03	1,92E-02	microtubule-associated protein
Solyc12g094660.2	1,31	9,97E-08	3,27E-06	Disease resistance protein
Solyc06g008510.3	1,31	1,08E-02	3,56E-02	Cdt1-like protein chloroplastic-like
Solyc08g083070.3	1,31	1,76E-07	5,13E-06	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc07g008160.3	1,31	4,17E-08	1,62E-06	nuclear pore complex protein NUP155
Solyc09g065590.3	1,31	9,38E-04	5,31E-03	Auxin canalization protein (DUF828)
Solyc01g079510.3	1,31	1,22E-05	1,64E-04	WD40 domain-containing protein
Solyc06g073550.3	1,31	5,37E-08	1,98E-06	La-related protein 1
Solyc06g068770.3	1,31	5,23E-07	1,31E-05	DB279
Solyc05g054970.3	1,31	9,84E-07	2,21E-05	Ankyrin repeat
Solyc02g079190.3	1,31	1,16E-06	2,51E-05	Protein AUXIN SIGNALING F-BOX 3
Solyc05g008260.3	1,31	1,39E-07	4,24E-06	Peptidyl serine alpha-galactosyltransferase
Solyc08g077440.3	1,31	1,51E-09	9,96E-08	Lon protease homolog
Solyc06g074110.3	1,31	7,29E-04	4,37E-03	Transcription factor
Solyc06g083890.4	1,31	6,83E-06	1,04E-04	Pre-mRNA-splicing factor SLU7
Solyc07g025170.3	1,31	1,97E-06	3,89E-05	Exocyst complex component SEC3A
Solyc12g056300.3	1,31	2,02E-07	5,71E-06	Receptor kinase, putative
Solyc09g007200.4	1,31	2,28E-07	6,32E-06	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc02g078580.1	1,31	1,26E-06	2,68E-05	RNA polymerase-associated protein RTF1
Solyc04g049120.4	1,31	2,65E-06	4,90E-05	Nuclear receptor corepressor 1
Solyc03g111090.4	1,31	1,58E-07	4,69E-06	transcription factor GTE10-like
Solyc04g072920.4	1,30	5,63E-03	2,13E-02	Trehalose 6-phosphate phosphatase
Solyc01g006870.4	1,30	1,67E-05	2,12E-04	Polyketide cyclase/dehydrase/lipid transport superfamily protein
Solyc02g090260.3	1,30	2,32E-03	1,08E-02	golgin
Solyc08g007630.1	1,30	3,32E-03	1,42E-02	Disease resistance protein I2
Solyc07g006820.4	1,30	1,81E-05	2,26E-04	Transcription initiation factor TFIID subunit 1
Solyc02g094610.1	1,30	9,79E-06	1,40E-04	ARM repeat superfamily protein
Solyc02g093930.4	1,30	1,65E-02	4,95E-02	sister chromatid cohesion 1 protein 2
Solyc09g007940.3	1,30	1,17E-05	1,59E-04	Adenosine kinase
Solyc01g006880.4	1,30	3,72E-05	4,04E-04	Histone-lysine N-methyltransferase ATXR7
Solyc10g076730.1	1,30	5,13E-03	1,99E-02	Plant invertase/pectin methylesterase inhibitor superfamily protein
Solyc01g079350.3	1,30	2,93E-07	7,88E-06	HIT zinc finger and PAPA-1-like domain-containing protein
Solyc04g064700.4	1,30	1,62E-08	7,42E-07	Transcription elongation factor SPT5

Solyc04g014870.3	1,30	5,44E-07	1,35E-05	RNA-dependent RNA polymerase6a
Solyc12g044310.2	1,30	4,27E-05	4,52E-04	Protein NRT1/ PTR FAMILY 1.1
Solyc12g011140.3	1,30	2,60E-03	1,17E-02	Subtilisin-like protease
Solyc09g005760.3	1,30	1,17E-05	1,59E-04	U3 ribonucleoprotein (Utp) family protein
Solyc02g082660.3	1,30	2,22E-04	1,69E-03	DNA mismatch repair protein MLH3
Solyc12g096010.3	1,30	7,45E-03	2,66E-02	Protein kinase family protein
Solyc12g043120.2	1,30	7,14E-06	1,08E-04	Heat shock protein 70 family
Solyc05g055110.4	1,30	5,74E-04	3,59E-03	nuclear pore complex protein NUP1-like
Solyc03g120270.4	1,30	2,06E-08	9,02E-07	Coatomer subunit beta'
Solyc09g072890.2	1,30	2,29E-03	1,06E-02	Histone-lysine N-methyltransferase SUVR4
Solyc02g082100.4	1,30	3,24E-05	3,63E-04	RING/U-box superfamily protein
Solyc06g063170.3	1,30	2,55E-03	1,15E-02	Glutamate receptor
Solyc04g056270.4	1,30	1,57E-09	1,03E-07	ER66
Solyc11g013830.2	1,30	3,35E-04	2,34E-03	1-phosphatidylinositol-3-phosphate 5-kinase fab1d-like protein
Solyc12g043110.2	1,29	5,34E-08	1,98E-06	LETSW12
Solyc12g010050.2	1,29	3,78E-06	6,54E-05	DNA-3-methyladenine glycosylase I
Solyc01g086750.4	1,29	1,57E-08	7,24E-07	Clustered mitochondria protein
Solyc02g024000.4	1,29	4,96E-04	3,18E-03	WPP domain-associated protein
Solyc06g043030.4	1,29	1,88E-06	3,73E-05	AP-3 complex subunit beta
Solyc09g063010.4	1,29	5,01E-06	8,21E-05	bHLH transcription factor 058
Solyc01g006040.3	1,29	3,90E-03	1,60E-02	E3 ubiquitin protein ligase
Solyc02g071010.1	1,29	5,44E-04	3,43E-03	Chlorophyll a-b binding protein, chloroplastic
Solyc08g013900.3	1,29	1,35E-04	1,13E-03	Plant regulator RWP-RK family protein
Solyc03g117540.4	1,29	4,58E-03	1,82E-02	ABC transporter C family member 13
Solyc01g111240.4	1,29	2,63E-09	1,63E-07	Translocase of chloroplast, chloroplastic
Solyc03g006970.1	1,29	9,21E-05	8,34E-04	serine protease SBT2
Solyc06g051310.3	1,29	3,72E-08	1,47E-06	Clathrin heavy chain
Solyc01g096410.4	1,29	6,77E-05	6,51E-04	Phosphatidylinositol 4-phosphate 5-kinase
Solyc09g031970.3	1,29	8,81E-08	2,94E-06	Alpha-1,4 glucan phosphorylase
Solyc03g082945.1	1,29	1,39E-02	4,32E-02	protein PSY2-like
Solyc08g029130.3	1,29	3,81E-05	4,12E-04	Chromatin remodeling factor
Solyc05g010640.3	1,29	4,22E-03	1,71E-02	RING-type E3 ubiquitin transferase
Solyc11g008320.3	1,29	6,46E-07	1,57E-05	Lysine-specific histone demethylase 1-like protein 3
Solyc11g013370.3	1,29	1,22E-05	1,64E-04	E3 ubiquitin protein ligase
Solyc08g079090.4	1,29	6,75E-05	6,49E-04	Monocopper oxidase-like protein sku5
Solyc11g007900.3	1,29	4,25E-05	4,50E-04	EEIG1/EHBP1 N-terminal domain
Solyc04g008720.4	1,29	3,78E-05	4,09E-04	Katanin p80 WD40 repeat-containing subunit B1 homolog
Solyc02g077680.4	1,28	6,73E-08	2,39E-06	Alpha-1,4 glucan phosphorylase
Solyc12g016220.3	1,28	5,69E-04	3,57E-03	Disease resistance protein
Solyc02g072150.3	1,28	1,68E-05	2,13E-04	Trehalose-6-phosphate synthase
Solyc07g062940.4	1,28	5,56E-06	8,94E-05	Serine/threonine-protein kinase 24
Solyc06g068920.3	1,28	7,51E-07	1,77E-05	Protein kinase domain
Solyc04g082840.4	1,28	3,79E-03	1,57E-02	B2-type cyclin dependent kinase
Solyc02g083140.3	1,28	1,92E-05	2,37E-04	ribonuclease E
Solyc08g077800.4	1,28	1,10E-05	1,53E-04	DNA repair endonuclease UVH1
Solyc07g042380.4	1,28	2,76E-05	3,19E-04	RRP12-like protein
Solyc02g078260.3	1,28	2,63E-07	7,16E-06	RNA polymerase II subunit 2
Solyc03g123630.4	1,28	7,32E-09	3,79E-07	pectin methylesterase pmeu1
Solyc11g005250.3	1,28	7,28E-06	1,09E-04	SNF2 domain-containing protein / helicase domain-containing protein / F-box family protein
Solyc10g084050.2	1,28	1,49E-08	6,96E-07	Cell division cycle protein 48-like protein
Solyc05g053400.3	1,28	5,05E-04	3,23E-03	Glycosyltransferase
Solyc02g067930.3	1,28	8,01E-04	4,68E-03	Glycerol-3-phosphate dehydrogenase [NAD(+)]
Solyc07g056570.1	1,28	2,41E-08	1,03E-06	notabilis
Solyc09g064840.4	1,28	2,08E-06	4,03E-05	HUA2-like protein 2
Solyc03g059420.4	1,28	6,89E-06	1,04E-04	Sister chromatid cohesion protein
Solyc05g015070.4	1,28	4,22E-09	2,36E-07	RING-type E3 ubiquitin transferase
Solyc11g042470.1	1,28	1,84E-03	8,96E-03	Tubulin-folding cofactor E
Solyc06g065710.3	1,27	1,43E-08	6,75E-07	Sister chromatid cohesion PDS5-like protein
Solyc09g015840.4	1,27	6,09E-06	9,52E-05	receptor-like protein kinase FERONIA
Solyc02g084620.3	1,27	8,43E-08	2,84E-06	Forkhead-associated (FHA) domain
Solyc01g102510.4	1,27	2,50E-05	2,94E-04	Transducin/WD40 repeat-like superfamily protein
Solyc07g026810.3	1,27	3,75E-07	9,76E-06	Chaperone protein dnaJ
Solyc03g071550.3	1,27	1,24E-04	1,05E-03	Zinc finger, RING-type
Solyc01g007100.3	1,27	6,00E-08	2,17E-06	Digalactosyldiacylglycerol synthase 1, chloroplastic
Solyc05g053770.4	1,27	3,31E-04	2,32E-03	myb-like protein X
Solyc02g082280.3	1,27	1,27E-07	3,97E-06	Trafficking protein particle complex subunit 11
Solyc03g006550.4	1,27	5,71E-03	2,16E-02	Terpene synthase
Solyc08g067210.3	1,27	3,67E-05	4,00E-04	Dicer-like 3
Solyc03g098300.1	1,27	8,46E-03	2,93E-02	Ornithine decarboxylase
Solyc09g091860.4	1,27	4,74E-03	1,87E-02	Poly(A) RNA polymerase GLD2
Solyc05g009150.4	1,27	1,10E-05	1,53E-04	Zinc finger protein
Solyc05g018510.3	1,27	2,06E-08	9,02E-07	ABC transporter-like
Solyc08g067250.4	1,27	2,17E-04	1,66E-03	DNA cross-link repair protein SNM1
Solyc04g064760.3	1,27	2,33E-06	4,41E-05	Carboxypeptidase
Solyc01g103180.4	1,27	4,77E-03	1,88E-02	Protein FAR1-RELATED SEQUENCE 11
Solyc09g090020.4	1,27	2,09E-07	5,84E-06	Germin-like protein subfamily 1 member 20
Solyc04g077340.3	1,27	8,67E-06	1,27E-04	G-type lectin S-receptor-like serine/threonine-protein kinase
Solyc09g005750.3	1,27	8,23E-07	1,90E-05	DUF3741 domain-containing protein/DUF4378 domain-containing protein/VARLMGL domain-containing protein
Solyc07g007790.3	1,27	2,68E-08	1,12E-06	sucrose-phosphate synthase
Solyc07g062140.3	1,27	8,04E-07	1,87E-05	trehalose-phosphate synthase 1
Solyc02g086820.3	1,27	1,67E-03	8,30E-03	chloroplast carbonic anhydrase
Solyc01g088520.3	1,27	7,20E-07	1,71E-05	Dynamin-related protein 1E
Solyc01g111960.3	1,27	6,83E-03	2,48E-02	GDSL esterase/lipase At5g55050-like
Solyc09g064520.3	1,27	2,36E-03	1,09E-02	Leucine-rich repeat receptor-like protein kinase
Solyc02g077630.3	1,27	1,41E-05	1,84E-04	Receptor-like protein kinase
Solyc11g018670.3	1,27	4,32E-07	1,11E-05	DnaJ domain
Solyc06g071490.3	1,26	2,54E-07	6,95E-06	serine/threonine-protein kinase ATM
Solyc02g081250.3	1,26	3,37E-04	2,35E-03	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc11g069590.2	1,26	4,58E-05	4,77E-04	Receptor-like serine/threonine-protein kinase NCRK
Solyc01g068390.3	1,26	1,89E-08	8,45E-07	Zinc ion binding/nucleic acid binding protein
Solyc03g120350.3	1,26	1,92E-08	8,56E-07	N-alpha-acetyltransferase 15, NatA auxiliary subunit-like
Solyc04g080600.3	1,26	2,34E-03	1,08E-02	Auxilin-like protein 1
Solyc06g005990.4	1,26	5,69E-06	9,09E-05	ATP-dependent RNA helicase SKI2
Solyc08g013740.4	1,26	1,91E-03	9,27E-03	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc01g088250.4	1,26	7,34E-04	4,39E-03	SUN domain protein3
Solyc11g008670.2	1,26	2,35E-04	1,78E-03	Chromatin assembly factor 1 subunit FAS1
Solyc09g013080.3	1,26	1,06E-08	5,24E-07	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
Solyc07g066410.4	1,26	3,10E-04	2,20E-03	WD repeat-containing protein 75
Solyc12g015800.2	1,26	8,56E-03	2,97E-02	RING/U-box superfamily protein
Solyc11g008540.3	1,26	8,34E-05	7,71E-04	Dicer-like 2b
Solyc01g099360.3	1,26	4,49E-04	2,93E-03	Tudor/PWWP/MBT superfamily protein
Solyc05g007740.3	1,26	1,40E-03	7,22E-03	Pentatricopeptide repeat-containing protein
Solyc01g091500.3	1,26	1,23E-04	1,04E-03	SMAD/FHA domain protein
Solyc01g100500.3	1,26	1,81E-07	5,21E-06	microfibrillar-associated protein 1-like
Solyc01g086820.4	1,26	2,11E-04	1,63E-03	Histone H3
Solyc02g068280.4	1,26	1,52E-04	1,25E-03	subtilisin-like protein
Solyc09g091750.3	1,26	1,61E-07	4,78E-06	26S proteasome non-ATPase regulatory subunit 1 homolog
Solyc03g097370.4	1,26	1,46E-08	6,86E-07	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc01g099220.3	1,26	1,67E-03	8,29E-03	DNA polymerase
Solyc10g005490.4	1,26	6,54E-06	9,99E-05	Protein strawberry notch
Solyc11g010610.2	1,26	7,28E-09	3,78E-07	Mechanosensitive ion channel protein 2, chloroplastic
Solyc06g069880.1	1,26	2,03E-08	8,94E-07	protein PHYTOCHROME KINASE SUBSTRATE 3-like
Solyc06g007640.3	1,26	1,60E-09	1,04E-07	FRIGIDA-like protein
Solyc06g082910.3	1,26	3,56E-04	2,45E-03	Formin-like protein
Solyc08g061610.4	1,26	4,88E-07	1,23E-05	Copper-transporting ATPase PAA2, chloroplastic
Solyc06g065540.3	1,25	1,56E-07	4,67E-06	1-phosphatidylinositol-3-phosphate 5-kinase fab1d-like protein
Solyc03g031940.4	1,25	1,02E-02	3,40E-02	AMP-dependent synthetase/ligase
Solyc01g007850.2	1,25	2,48E-04	1,85E-03	Pentatricopeptide repeat
Solyc04g072570.3	1,25	6,87E-04	4,17E-03	Receptor-like kinase
Solyc02g069970.4	1,25	4,11E-04	2,74E-03	Receptor-like protein kinase
Solyc04g015490.4	1,25	7,32E-06	1,10E-04	Mg-protoporphyrin IX chelatase

Solyc04g049670.4	1,25	2,69E-06	4,94E-05	Pseudo-response regulator
Solyc03g019800.4	1,25	4,15E-04	2,76E-03	Cyclin-D-binding Myb-like transcription factor 1
Solyc01g081490.3	1,25	7,13E-05	6,78E-04	RNA polymerase sigma factor
Solyc06g053780.4	1,25	1,27E-05	1,70E-04	Protein WVD2-like 1
Solyc03g123390.4	1,25	1,64E-03	8,18E-03	Alpha/beta-Hydrolases superfamily protein
Solyc10g050160.2	1,25	1,42E-05	1,85E-04	Caffeoyl CoA O-methyltransferase
Solyc03g013340.3	1,25	1,66E-03	8,26E-03	NOD26-like intrinsic protein 2.1
Solyc06g074740.3	1,25	1,12E-06	2,44E-05	LEU86662 VPS41
Solyc03g083410.3	1,24	2,52E-05	2,95E-04	Histone-lysine N-methyltransferase
Solyc09g065720.4	1,24	6,12E-06	9,56E-05	Peptidyl-prolyl cis-trans isomerase
Solyc12g009930.3	1,24	6,08E-05	6,00E-04	Glycosyltransferase
Solyc06g052010.2	1,24	2,03E-04	1,58E-03	SUN-like protein 16
Solyc01g060090.1	1,24	3,15E-03	1,36E-02	serine/threonine-protein phosphatase 4 regulatory subunit 3-like
Solyc04g039950.4	1,24	6,52E-05	6,32E-04	Mediator of RNA polymerase II transcription subunit 13
Solyc08g062700.3	1,24	2,00E-03	9,59E-03	Peptidyl-prolyl cis-trans isomerase
Solyc09g048980.4	1,24	1,49E-02	4,56E-02	BTB domain-containing protein/NPH3 domain-containing protein
Solyc05g008430.4	1,24	5,18E-05	5,27E-04	BRO1 domain
Solyc07g066030.4	1,24	2,81E-05	3,24E-04	Proteasome activator subunit 4
Solyc02g090570.4	1,24	7,77E-07	1,81E-05	Transducin/WD40 repeat-like superfamily protein
Solyc11g007840.3	1,24	1,53E-03	7,71E-03	UDP-Glycosyltransferase superfamily protein
Solyc07g066660.4	1,24	2,11E-03	9,96E-03	cyclinB3_1
Solyc04g051570.4	1,24	3,74E-05	4,06E-04	spatacsin carboxy-terminus protein
Solyc06g082100.4	1,24	2,54E-07	6,95E-06	Helicase
Solyc11g008350.2	1,24	9,29E-03	3,16E-02	Kinesin-like protein
Solyc10g076910.2	1,24	5,21E-07	1,31E-05	ATP-dependent RNA helicase
Solyc10g006090.4	1,24	5,75E-05	5,76E-04	Protein ENHANCED DOWNY MILDEW 2
Solyc07g041150.4	1,24	5,93E-05	5,89E-04	Myosin-12
Solyc05g017760.4	1,24	4,10E-06	6,97E-05	Acetyl-CoA C-acetyltransferase
Solyc07g065080.4	1,24	4,31E-05	4,56E-04	Fimbrin-3
Solyc02g038812.1	1,24	5,97E-05	5,91E-04	Calcium-binding EF hand family protein
Solyc01g105890.3	1,24	1,36E-03	7,08E-03	Monoterpene synthase 1
Solyc12g070100.2	1,24	6,45E-06	9,89E-05	Mediator of RNA polymerase II transcription subunit 25
Solyc06g054020.3	1,24	1,77E-06	3,57E-05	p-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc01g105680.4	1,24	9,63E-06	1,38E-04	Phototropic-responsive NPH3 family protein
Solyc03g111380.3	1,24	3,71E-04	2,53E-03	Tubulin gamma chain
Solyc06g007440.4	1,24	9,51E-03	3,22E-02	Non-specific serine/threonine protein kinase
Solyc04g005430.4	1,23	3,62E-06	6,33E-05	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc12g017280.2	1,23	1,32E-03	6,90E-03	ARM repeat superfamily protein
Solyc01g106260.3	1,23	2,50E-04	1,86E-03	Heat shock protein 70 kDa
Solyc01g096110.3	1,23	4,75E-06	7,85E-05	Transducin family protein / WD-40 repeat family protein
Solyc03g115680.4	1,23	1,85E-04	1,46E-03	Formin-like protein
Solyc01g059870.4	1,23	1,13E-08	5,55E-07	phytochrome B1
Solyc12g063050.3	1,23	1,97E-06	3,89E-05	RNA polymerase II C-terminal domain phosphatase-like 3
Solyc02g080330.4	1,23	7,79E-04	4,59E-03	Cytochrome P450
Solyc09g065700.3	1,23	3,58E-06	6,27E-05	BEACH domain
Solyc08g061910.4	1,23	9,35E-03	3,18E-02	trihelix transcription factor GTL1-like
Solyc04g005500.3	1,23	2,95E-05	3,37E-04	T-box transcription factor%2C putative (DUF863)
Solyc02g080160.4	1,23	2,75E-03	1,23E-02	Xyloglucan endotransglucosylase/hydrolase
Solyc02g085360.4	1,23	9,89E-03	3,32E-02	CYP90B3 mRNA for cytochrome P450
Solyc12g013880.2	1,23	4,24E-03	1,72E-02	Origin recognition complex subunit 3
Solyc06g007190.4	1,23	9,83E-04	5,51E-03	Protein phosphatase 2C
Solyc09g092340.4	1,23	1,61E-04	1,31E-03	Werner Syndrome-like exonuclease
Solyc05g051580.3	1,23	9,54E-05	8,56E-04	Phototropic-responsive NPH3 family protein
Solyc11g040330.2	1,23	1,43E-03	7,32E-03	Endo-1,4-beta-xylanase
Solyc02g081730.3	1,23	1,75E-05	2,19E-04	3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 1
Solyc06g051810.4	1,23	4,01E-07	1,04E-05	XH/XS domain protein
Solyc01g067390.4	1,23	1,86E-07	5,34E-06	RNA helicase DEAH-box1
Solyc09g098100.4	1,23	2,80E-03	1,24E-02	NB-LRR tospovirus immune receptor
Solyc04g049770.4	1,23	2,51E-07	6,89E-06	Regulator of nonsense transcripts UPF2
Solyc09g008100.4	1,23	5,86E-06	9,30E-05	TSL-kinase interacting protein 1
Solyc03g117010.4	1,23	5,24E-04	3,32E-03	Sister chromatid cohesion PDS5-like protein
Solyc09g066140.3	1,23	2,55E-03	1,15E-02	myosin-binding protein 1-like
Solyc02g070540.3	1,23	5,55E-06	8,94E-05	DUF642 domain-containing protein
Solyc07g064230.4	1,23	1,22E-02	3,90E-02	Ypt/Rab-GAP domain of gyp1p superfamily protein
Solyc10g044670.3	1,23	2,42E-05	2,88E-04	phytochrome A
Solyc02g081910.2	1,23	1,33E-02	4,19E-02	DNA topoisomerase 1
Solyc09g074630.3	1,23	5,28E-04	3,35E-03	BTB domain-containing protein/NPH3 domain-containing protein
Solyc08g075840.3	1,23	1,07E-07	3,44E-06	Replication protein A subunit
Solyc10g078370.2	1,23	9,92E-03	3,32E-02	Auxin Efflux Facilitator 9
Solyc07g065760.3	1,23	2,42E-03	1,11E-02	Coiled-coil protein
Solyc04g064940.3	1,23	1,65E-06	3,36E-05	Receptor-like protein kinase 2
Solyc03g005960.3	1,22	3,26E-03	1,40E-02	protein kinase LESK1
Solyc11g008800.3	1,22	1,10E-05	1,53E-04	type I inositol polyphosphate 5-phosphatase 12-like
Solyc03g044150.4	1,22	1,01E-06	2,25E-05	Subtilisin-like protease
Solyc08g074620.3	1,22	4,08E-03	1,67E-02	Polyphenol oxidase
Solyc03g114520.3	1,22	1,42E-02	4,38E-02	Centromere protein Mis12
Solyc01g096200.4	1,22	2,19E-04	1,68E-03	RING-type E3 ubiquitin transferase
Solyc11g033270.2	1,22	2,80E-06	5,12E-05	MAP kinase kinase kinase 82
Solyc04g074110.4	1,22	1,12E-03	6,11E-03	Carbohydrate esterase, putative (DUF303)
Solyc11g018500.3	1,22	1,34E-02	4,20E-02	Beta-galactosidase
Solyc01g057760.4	1,22	6,67E-04	4,08E-03	RNA helicase DEAD2
Solyc05g055360.4	1,22	3,59E-05	3,93E-04	transcriptional regulator ATRX
Solyc04g071350.3	1,22	2,74E-07	7,41E-06	Exocyst complex component SEC5B
Solyc03g096830.4	1,22	1,28E-02	4,06E-02	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc04g011380.4	1,22	9,12E-04	5,21E-03	Zinc finger C3H1 domain protein
Solyc10g080100.3	1,22	1,43E-07	4,34E-06	Villin
Solyc07g053010.3	1,22	1,85E-04	1,46E-03	Disease resistance protein
Solyc04g078110.1	1,22	1,82E-05	2,27E-04	serine protease SBT1
Solyc12g008890.3	1,22	7,41E-03	2,65E-02	Zinc finger CCCH domain-containing protein 64-like
Solyc07g063740.2	1,22	3,27E-05	3,65E-04	Ferredoxin-like protein
Solyc08g077680.3	1,22	2,04E-05	2,49E-04	KIP1-like protein
Solyc01g008330.4	1,22	1,19E-05	1,61E-04	Biotin carboxylase
Solyc06g072660.4	1,22	1,37E-02	4,28E-02	DEK
Solyc02g069780.3	1,22	1,11E-04	9,60E-04	SIT4 phosphatase-associated family protein
Solyc06g053750.3	1,22	2,16E-06	4,14E-05	MATH domain-containing protein
Solyc02g087900.3	1,21	2,71E-06	4,98E-05	Cullin
Solyc04g057990.4	1,21	1,85E-03	9,03E-03	Zinc finger transcription factor 33
Solyc03g118340.3	1,21	7,16E-07	1,71E-05	ATP-dependent Clp protease ATP-binding subunit ClpC
Solyc06g074530.1	1,21	1,66E-04	1,34E-03	Arogenate dehydratase
Solyc06g008600.3	1,21	1,36E-04	1,14E-03	E3 ubiquitin protein ligase DRIP2
Solyc10g009160.3	1,21	7,81E-04	4,60E-03	Bromodomain
Solyc12g014220.3	1,21	2,40E-04	1,81E-03	muscle M-line assembly protein
Solyc06g066550.3	1,21	2,99E-03	1,31E-02	LETM1-like protein
Solyc03g121610.3	1,21	7,97E-05	7,43E-04	Serine/threonine-protein kinase PBS1
Solyc09g066100.3	1,21	3,86E-05	4,16E-04	Histone H1
Solyc09g010350.4	1,21	1,74E-06	3,51E-05	N-lysine methyltransferase
Solyc03g123490.1	1,21	7,39E-05	6,98E-04	Subtilisin-like protease-like protein
Solyc08g083310.3	1,21	1,59E-04	1,30E-03	Glucan endo-1,3-beta-glucosidase 11
Solyc02g093980.3	1,21	1,05E-06	2,31E-05	Nucleolar-like protein
Solyc01g110160.4	1,21	5,73E-04	3,59E-03	hypothetical protein
Solyc01g088020.3	1,21	1,23E-04	1,05E-03	Protein transport protein SEC31-like protein B
Solyc03g114060.3	1,21	6,70E-07	1,62E-05	Bromo adjacent homology (BAH) domain
Solyc06g066030.4	1,21	7,46E-07	1,76E-05	Protein WVD2-like 1
Solyc01g080010.2	1,21	1,62E-02	4,87E-02	xyloglucan endoglucanase inhibitor
Solyc03g117040.3	1,21	2,05E-06	3,99E-05	XH/XS domain-containing protein
Solyc03g097490.4	1,21	4,24E-04	2,80E-03	DEK
Solyc11g069540.3	1,21	2,30E-03	1,07E-02	Nucleotide/sugar transporter family protein
Solyc08g075500.4	1,21	1,66E-04	1,34E-03	Pentatricopeptide repeat-containing protein
Solyc06g008090.3	1,21	4,83E-04	3,12E-03	Myosin
Solyc08g044400.3	1,21	1,13E-05	1,56E-04	SacI homology domain-containing protein / WW domain-containing protein
Solyc12g088530.2	1,21	1,67E-02	4,98E-02	cyclin A3.1

Solyc03g117970.4	1,21	1,14E-05	1,57E-04	Poly [ADP-ribose] polymerase
Solyc08g005480.3	1,21	2,07E-05	2,53E-04	Unknown protein
Solyc07g054500.4	1,21	2,87E-06	5,23E-05	Protein STRUBBELIG-RECEPTOR FAMILY 3
Solyc06g060310.3	1,21	1,82E-06	3,63E-05	Chlorophyllide a oxygenase, chloroplastic
Solyc05g006630.4	1,21	5,14E-04	3,28E-03	Disease resistance protein (TIR-NBS-LRR class)
Solyc01g095720.3	1,21	4,40E-05	4,63E-04	Alpha/beta-Hydrolases superfamily protein
Solyc01g094410.3	1,21	5,15E-08	1,93E-06	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
Solyc03g120200.2	1,21	3,21E-03	1,38E-02	RNA helicase DEAH-box11
Solyc01g097040.4	1,20	2,14E-04	1,65E-03	Myosin-binding protein 1
Solyc04g064820.3	1,20	2,12E-06	4,09E-05	Vacuolar protein sorting-associated protein 45-like protein
Solyc01g106330.3	1,20	3,70E-05	4,02E-04	Glutamyl-tRNA(Gln) amidotransferase subunit A
Solyc04g008680.4	1,20	2,99E-04	2,14E-03	Cell division cycle and apoptosis regulator protein 1
Solyc01g098250.4	1,20	6,92E-07	1,66E-05	DnaJ domain-containing protein
Solyc11g072080.1	1,20	1,03E-02	3,43E-02	F-box/kelch-repeat protein
Solyc09g074940.3	1,20	1,36E-04	1,14E-03	(DB240) meloidogyne-induced giant cell protein
Solyc05g005620.4	1,20	2,47E-03	1,13E-02	RNA-binding protein 25-like
Solyc09g098510.3	1,20	8,63E-06	1,26E-04	Extensin-3
Solyc12g020000.3	1,20	5,85E-05	5,82E-04	pre-mRNA-splicing factor
Solyc12g099890.2	1,20	2,94E-05	3,36E-04	Protein SDA1
Solyc01g111530.3	1,20	2,57E-06	4,78E-05	E3 ubiquitin-protein ligase UPL3
Solyc08g007950.3	1,20	4,19E-06	7,07E-05	30S ribosomal protein S1
Solyc06g065730.3	1,20	1,49E-05	1,93E-04	CHD3-type chromatin-remodeling factor PICKLE
Solyc03g117360.4	1,20	1,25E-06	2,67E-05	TOPLESS1
Solyc05g052510.4	1,20	2,56E-08	1,07E-06	Clathrin heavy chain
Solyc02g087360.4	1,20	8,64E-08	2,89E-06	Paired amphipathic helix protein Sin3-like 1
Solyc02g091780.1	1,20	4,09E-04	2,73E-03	Kinesin-like protein
Solyc01g008120.4	1,20	1,39E-06	2,89E-05	Histone acetyltransferase HAC12
Solyc02g066950.4	1,20	7,56E-08	2,62E-06	Alpha-amylase isozyme 2A
Solyc01g087430.3	1,20	9,75E-05	8,70E-04	Zinc finger, FYVE/PHD-type
Solyc11g065110.2	1,20	4,58E-07	1,17E-05	Homeobox domain-containing protein
Solyc04g080980.2	1,20	3,55E-08	1,42E-06	Coatomer subunit alpha
Solyc01g095300.3	1,20	1,05E-07	3,39E-06	Glycosyl transferase, family 1
Solyc11g065930.3	1,20	3,21E-04	2,26E-03	Xanthine dehydrogenase
Solyc11g044480.2	1,20	1,18E-07	3,73E-06	Arm repeat superfamily protein
Solyc07g063240.4	1,20	2,35E-04	1,78E-03	Silencing defective 5
Solyc03g044060.4	1,20	1,22E-03	6,53E-03	Formin-like protein
Solyc04g050050.3	1,19	1,14E-05	1,57E-04	SUN-like protein 13
Solyc03g078650.4	1,19	1,12E-02	3,66E-02	DUF620 domain-containing protein
Solyc12g035670.3	1,19	1,13E-04	9,76E-04	SAC3/GANP/Nin1/mts3/eIF-3 p25
Solyc02g070460.3	1,19	3,84E-06	6,63E-05	Cullin
Solyc01g005080.3	1,19	5,81E-06	9,24E-05	65-kDa microtubule-associated protein 6
Solyc03g113680.4	1,19	2,49E-05	2,94E-04	Microtubule-associated protein TORTIFOLIA1
Solyc07g043560.4	1,19	2,78E-06	5,08E-05	Heat shock protein 70 kDa
Solyc01g087210.3	1,19	2,12E-06	4,09E-05	Cellulose synthase
Solyc06g084530.3	1,19	1,04E-06	2,30E-05	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc08g082410.4	1,19	4,37E-06	7,30E-05	LOW protein: zinc finger CCCH domain protein
Solyc11g010490.3	1,19	2,40E-05	2,86E-04	transmembrane protein
Solyc02g093810.3	1,19	3,77E-05	4,08E-04	AUGMIN subunit 6-like
Solyc02g080570.3	1,19	6,77E-07	1,63E-05	Soluble starch synthase
Solyc03g081260.4	1,19	5,23E-07	1,31E-05	Subtilisin-like protease SBT3.5
Solyc03g053000.4	1,19	1,12E-02	3,65E-02	C18orf8
Solyc12g096510.3	1,19	1,04E-02	3,44E-02	Pentatricopeptide repeat
Solyc04g016480.3	1,19	1,72E-04	1,38E-03	SUN-like protein 12
Solyc01g108630.3	1,19	1,09E-05	1,52E-04	nii1 nitrite reductase
Solyc04g077490.3	1,19	1,97E-03	9,50E-03	AP2-like ethylene-responsive transcription factor ANT
Solyc02g089560.4	1,19	4,63E-03	1,84E-02	Pentatricopeptide repeat
Solyc02g092780.3	1,19	4,37E-05	4,61E-04	Suppressor of RPS4-RLD 1
Solyc01g103690.4	1,19	5,15E-04	3,29E-03	RNA helicase family protein
Solyc09g075360.4	1,19	8,72E-04	5,03E-03	endo-1,4-beta-glucanase precursor
Solyc01g067640.3	1,19	3,94E-05	4,24E-04	Protein kinase domain
Solyc11g068960.2	1,19	1,41E-05	1,85E-04	Transcription factor LHW
Solyc01g091920.2	1,19	3,30E-03	1,41E-02	Subtilisin-like protease-like protein
Solyc12g042760.1	1,19	1,67E-02	4,99E-02	Leucine-rich repeat receptor-like protein kinase family protein
Solyc09g092550.4	1,18	9,22E-06	1,33E-04	Pentatricopeptide repeat (PPR) superfamily protein
Solyc08g082250.3	1,18	1,81E-04	1,43E-03	endo-beta-1,4-D-glucanase (Cel8)
Solyc07g063940.2	1,18	3,66E-06	6,39E-05	SCARECROW
Solyc06g051570.4	1,18	3,28E-03	1,40E-02	NF-X1-type zinc finger protein NFXL2
Solyc07g043460.3	1,18	4,32E-04	2,85E-03	Cytochrome P450
Solyc04g050960.3	1,18	4,11E-06	6,97E-05	Chromatin remodeling 4
Solyc12g044220.3	1,18	1,05E-04	9,20E-04	Phox-associated domain,Sorting nexin
Solyc11g008740.2	1,18	3,62E-06	6,33E-05	Sister chromatid cohesion 1 protein 4
Solyc10g007600.3	1,18	2,00E-05	2,46E-04	glycolate oxidase
Solyc02g078910.3	1,18	3,57E-03	1,50E-02	endonuclease AM238701
Solyc02g087870.3	1,18	3,08E-06	5,54E-05	ABC transporter
Solyc01g109990.4	1,18	4,81E-03	1,89E-02	RNA-binding protein 28
Solyc03g007610.4	1,18	1,45E-07	4,38E-06	DnaJ protein ERDJ2A
Solyc03g120290.3	1,18	7,85E-03	2,77E-02	To encode a PR protein, Belongs to the plant thionin family with the following members:, putative
Solyc01g102970.3	1,18	3,38E-06	6,01E-05	squamous cell carcinoma antigen recognized by T-cells 3-like
Solyc01g096190.3	1,18	7,57E-08	2,62E-06	Ca2+-ATPase
Solyc11g011470.2	1,18	2,01E-06	3,95E-05	NADH-quinone oxidoreductase
Solyc01g110380.3	1,18	4,51E-06	7,50E-05	Kinesin-like protein
Solyc03g113000.3	1,18	2,30E-06	4,37E-05	RINT1-like protein MAG2
Solyc01g105230.4	1,18	3,26E-05	3,65E-04	Calmodulin-binding transcription activator 2
Solyc06g074030.1	1,17	1,03E-05	1,46E-04	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
Solyc05g005160.3	1,17	4,09E-06	6,96E-05	ATP-citrate synthase
Solyc07g053640.1	1,17	2,45E-06	4,62E-05	Arabinogalactan-protein
Solyc11g066540.2	1,17	3,72E-07	9,69E-06	Unknown protein
Solyc06g008620.1	1,17	1,32E-03	6,90E-03	TolB protein-related protein
Solyc02g023950.3	1,17	9,36E-04	5,30E-03	Leucine-rich receptor-like protein kinase family protein
Solyc04g007640.3	1,17	4,16E-07	1,07E-05	RING-type E3 ubiquitin transferase
Solyc11g062010.3	1,17	3,50E-04	2,41E-03	Chromatin structure-remodeling complex protein SYD
Solyc05g053120.1	1,17	1,70E-03	8,40E-03	Glycosyltransferase
Solyc08g077240.3	1,17	9,98E-08	3,27E-06	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc11g073270.1	1,17	1,62E-02	4,88E-02	Pentatricopeptide repeat
Solyc12g009800.3	1,17	3,14E-06	5,63E-05	Purple acid phosphatase
Solyc03g006850.3	1,17	7,24E-03	2,60E-02	junctophilin-like protein
Solyc04g078160.4	1,17	8,54E-03	2,96E-02	C5orf35
Solyc04g008050.4	1,17	5,11E-05	5,22E-04	Two-component response regulator
Solyc05g050020.3	1,17	4,08E-03	1,67E-02	RING/U-box superfamily protein
Solyc08g077310.3	1,17	1,64E-05	2,08E-04	Suppressor of abi3-5
Solyc06g059750.3	1,17	3,49E-06	6,15E-05	Transcriptional corepressor SEUSS
Solyc07g042390.3	1,17	8,12E-04	4,73E-03	Plant invertase/pectin methylesterase inhibitor superfamily protein
Solyc02g082690.3	1,17	1,48E-04	1,22E-03	Transducin/WD40 repeat-like superfamily protein
Solyc01g008180.3	1,17	1,85E-05	2,29E-04	Remorin
Solyc02g078950.4	1,17	2,43E-04	1,82E-03	Beta-galactosidase
Solyc04g011640.3	1,17	2,55E-03	1,15E-02	Scarecrow-like protein 14
Solyc06g060350.4	1,17	4,05E-04	2,71E-03	Replication factor C subunit 1
Solyc07g007890.3	1,17	8,77E-06	1,28E-04	CCR4-NOT transcription complex subunit 10-like
Solyc11g032050.2	1,17	1,39E-02	4,31E-02	GDSL esterase/lipase
Solyc05g049960.4	1,17	6,66E-03	2,43E-02	ELM2 domain-containing protein
Solyc04g015620.3	1,17	8,40E-03	2,92E-02	DUF642 domain-containing protein
Solyc05g052500.4	1,17	2,10E-05	2,55E-04	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc04g071650.4	1,17	6,39E-06	9,81E-05	Cellulose synthase
Solyc04g074480.3	1,17	1,19E-05	1,61E-04	DAHP synthase 2 precursor
Solyc01g108160.3	1,17	2,07E-04	1,61E-03	autophagy-related protein 2-like
Solyc05g005560.4	1,17	2,07E-07	5,82E-06	polygalacturonase isoenzyme 1 beta subunit
Solyc03g117930.4	1,17	1,37E-03	7,09E-03	FRIGIDA-like protein
Solyc10g053970.2	1,17	7,13E-07	1,71E-05	Sec14p-like phosphatidylinositol transfer family protein
Solyc10g039190.2	1,16	7,01E-04	4,24E-03	WD40 repeat
Solyc07g066090.4	1,16	2,46E-05	2,91E-04	Sec14p-like phosphatidylinositol transfer family protein
Solyc08g079170.3	1,16	5,79E-08	2,10E-06	Hsp70-Hsp90 organizing protein 1

Solyc02g083560.3	1,16	2,40E-04	1,81E-03	Vacuolar protein sorting-associated protein 35
Solyc12g068070.2	1,16	1,27E-03	6,74E-03	Filament-like plant protein 3
Solyc03g116140.3	1,16	7,14E-06	1,08E-04	activating signal cointegrator 1
Solyc05g010120.4	1,16	1,99E-04	1,56E-03	Phospholipid-transporting ATPase
Solyc01g106220.4	1,16	6,81E-08	2,42E-06	DNA polymerase V
Solyc08g065220.3	1,16	2,04E-06	3,99E-05	glycine decarboxylase p-protein
Solyc04g072830.4	1,16	3,23E-05	3,62E-04	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc02g083820.1	1,16	1,08E-06	2,37E-05	Armadillo repeat only 2
Solyc12g010840.2	1,16	7,80E-03	2,75E-02	Ketol-acid reductoisomerase
Solyc03g095610.4	1,16	5,68E-05	5,71E-04	DUF3133 domain-containing protein
Solyc03g118640.3	1,16	3,11E-06	5,59E-05	Ketose-bisphosphate aldolase class-II family protein
Solyc09g010630.3	1,16	1,32E-04	1,11E-03	HSC2-like
Solyc12g009300.3	1,16	7,34E-03	2,63E-02	fruit sucrose synthase
Solyc02g088290.4	1,16	9,48E-05	8,52E-04	ARF guanine-nucleotide exchange factor GNL1
Solyc08g079740.3	1,16	1,08E-05	1,51E-04	Leucine-rich receptor-like protein kinase family protein
Solyc01g097000.3	1,16	2,08E-03	9,87E-03	Glycosyl hydrolase family protein
Solyc02g068590.3	1,16	2,11E-05	2,57E-04	Potassium transporter
Solyc02g076780.3	1,16	8,49E-04	4,91E-03	MAP kinase kinase kinase 17
Solyc04g063360.3	1,16	6,35E-04	3,91E-03	ATP-dependent zinc metalloprotease FtsH
Solyc12g099740.2	1,16	5,87E-06	9,30E-05	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain-containing protein
Solyc07g053650.4	1,16	2,08E-07	5,83E-06	26S proteasome non-ATPase regulatory subunit 2 homolog
Solyc04g009510.4	1,16	2,61E-06	4,85E-05	RNA binding (RRM/RBD/RNP motifs) family protein
Solyc05g006020.3	1,16	8,17E-04	4,76E-03	Nucleobase-ascorbate transporter 8
Solyc09g084450.3	1,16	1,23E-02	3,92E-02	Protease inhibitor I
Solyc09g014780.3	1,16	4,05E-06	6,91E-05	Regulatory-associated protein of TOR 1
Solyc08g081160.3	1,16	8,68E-04	5,00E-03	DUF3741 domain-containing protein/DUF4378 domain-containing protein
Solyc03g096900.4	1,16	8,68E-08	2,90E-06	GTP pyrophosphokinase
Solyc05g005020.4	1,16	4,59E-06	7,59E-05	Alpha-Glucan Water Dikinase
Solyc11g068640.2	1,16	1,31E-06	2,78E-05	Protein TPLATE
Solyc09g031580.3	1,16	8,40E-04	4,87E-03	Zinc finger, RING-type
Solyc06g076150.3	1,16	1,52E-05	1,97E-04	Eukaryotic translation initiation factor 3 subunit C
Solyc07g045350.4	1,16	4,58E-03	1,82E-02	Acetyl-CoA C-acetyltransferase
Solyc01g107350.3	1,16	1,74E-07	5,09E-06	DUF620 domain-containing protein
Solyc03g019770.4	1,15	1,89E-04	1,49E-03	testis-expressed sequence 2 protein-like
Solyc12g088760.1	1,15	5,59E-06	8,97E-05	Subtilisin-like protease preproenzyme
Solyc11g071270.2	1,15	7,67E-04	4,54E-03	target of Myb protein 1-like
Solyc02g065300.1	1,15	1,85E-05	2,29E-04	Leucine--tRNA ligase, cytoplasmic
Solyc07g053980.3	1,15	3,92E-06	6,76E-05	Callose synthase 12
Solyc04g078050.3	1,15	1,70E-03	8,44E-03	TBP-associated factor 4B
Solyc05g014490.3	1,15	1,21E-02	3,89E-02	Pentatricopeptide repeat
Solyc06g008500.3	1,15	1,23E-03	6,58E-03	Ankyrin repeat-containing protein
Solyc12g056200.2	1,15	3,24E-03	1,39E-02	DUF604 domain-containing protein
Solyc06g068980.4	1,15	5,12E-05	5,22E-04	MAP kinase kinase kinase 39
Solyc03g119450.3	1,15	1,46E-05	1,89E-04	Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic
Solyc07g022770.1	1,15	1,48E-02	4,54E-02	Calcium-transporting ATPase
Solyc04g082880.4	1,15	1,13E-03	6,13E-03	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha
Solyc11g006390.2	1,15	3,50E-05	3,85E-04	nuclear pore complex protein NUP1-like
Solyc07g054210.3	1,15	1,63E-03	8,14E-03	light dependent NADH:protochlorophyllide oxidoreductase 2
Solyc09g061860.4	1,15	3,15E-04	2,22E-03	Sterol 3-beta-glucosyltransferase
Solyc06g065640.3	1,15	6,44E-07	1,57E-05	Transcriptional corepressor LEUNIG
Solyc08g008410.3	1,15	2,82E-04	2,04E-03	Plant regulator RWP-RK family protein
Solyc05g056580.3	1,15	6,59E-08	2,35E-06	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc08g075440.4	1,15	9,44E-06	1,36E-04	conserved oligomeric Golgi complex subunit 6
Solyc05g007490.3	1,15	2,61E-06	4,85E-05	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc01g108400.3	1,15	2,08E-07	5,83E-06	CDPK-related protein kinase
Solyc04g010220.3	1,15	5,81E-06	9,24E-05	centrosomal protein of 135 kDa-like protein
Solyc01g103990.3	1,14	1,54E-05	1,98E-04	T-complex protein 11
Solyc03g121170.3	1,14	3,31E-08	1,33E-06	GDSL esterase/lipase
Solyc05g015920.3	1,14	1,28E-05	1,70E-04	GYF domain-containing protein
Solyc11g069990.2	1,14	2,40E-03	1,10E-02	I2C5
Solyc04g076480.3	1,14	1,41E-03	7,25E-03	MAP kinase kinase kinase 34
Solyc06g059760.3	1,14	4,91E-06	8,07E-05	Transcriptional corepressor SEUSS
Solyc03g098610.3	1,14	1,26E-05	1,68E-04	Plastid division protein CDP1, chloroplastic
Solyc04g049140.4	1,14	3,08E-04	2,18E-03	Transcription factor jumonji (JmjC) domain-containing protein
Solyc07g016180.3	1,14	1,07E-05	1,50E-04	Auxin Response Factor 7A
Solyc03g083900.4	1,14	9,80E-03	3,29E-02	monocopper oxidase-like protein SKU5
Solyc10g008950.3	1,14	8,49E-06	1,25E-04	Guanylate-binding family protein
Solyc01g074010.4	1,14	3,27E-06	5,84E-05	Protein kinase domain
Solyc12g044410.2	1,14	3,45E-07	9,07E-06	Homeobox leucine-zipper protein
Solyc04g082970.4	1,14	2,36E-05	2,82E-04	electron transporter%2C putative (Protein of unknown function%2C DUF547)
Solyc01g096450.4	1,14	2,00E-04	1,56E-03	Eukaryotic aspartyl protease family protein
Solyc02g086160.4	1,14	5,24E-07	1,31E-05	plastidic glucose translocator 1
Solyc10g080940.3	1,14	1,66E-03	8,26E-03	Tubulin beta chain
Solyc01g080810.3	1,14	2,77E-08	1,15E-06	Isoleucine--tRNA ligase
Solyc01g102330.3	1,13	3,60E-03	1,51E-02	Carbohydrate esterase, putative (DUF303)
Solyc11g017170.1	1,13	4,17E-03	1,69E-02	Phospholipid-transporting ATPase
Solyc04g077930.4	1,13	7,06E-04	4,26E-03	Activating signal cointegrator 1 complex subunit 2-like protein
Solyc01g103750.4	1,13	3,41E-03	1,45E-02	ATP phosphoribosyltransferase
Solyc09g007540.3	1,13	1,60E-06	3,27E-05	Valine--tRNA ligase
Solyc02g065600.3	1,13	1,02E-02	3,41E-02	Protein trichome birefringence-like 19
Solyc01g087800.2	1,13	2,22E-04	1,70E-03	Subtilisin-like protease
Solyc08g079850.3	1,13	2,49E-05	2,94E-04	Subtilisin-like protease
Solyc11g066780.3	1,13	2,51E-03	1,14E-02	PHD finger family protein
Solyc07g048090.2	1,13	6,19E-05	6,09E-04	Fasciclin-like arabinogalactan protein 7
Solyc01g095730.4	1,13	7,92E-05	7,40E-04	PAP/OAS1 substrate-binding domain superfamily
Solyc02g090930.3	1,13	1,03E-05	1,45E-04	Lipase
Solyc12g098463.1	1,13	7,67E-03	2,72E-02	myb-like protein X
Solyc03g120850.4	1,13	9,82E-04	5,50E-03	Chaperonin 60 beta
Solyc04g050990.3	1,13	2,66E-04	1,96E-03	F-box domain, Phloem protein 2-like protein
Solyc03g051900.4	1,13	9,39E-03	3,18E-02	Ribosomal protein S1
Solyc02g078800.4	1,13	3,40E-07	8,95E-06	Katanin p80 WD40 repeat-containing subunit B1
Solyc01g006330.4	1,13	6,93E-08	2,44E-06	Plastid-lipid associated protein PAP / fibrillin family protein
Solyc10g079770.3	1,13	3,86E-06	6,67E-05	triacylglycerol lipase SDP1-like
Solyc09g083080.4	1,13	1,19E-04	1,02E-03	Nucleolar protein 58
Solyc04g011350.3	1,13	1,09E-05	1,52E-04	2-oxoglutarate dehydrogenase, E1 component
Solyc02g092470.3	1,13	9,74E-05	8,69E-04	Formin-like protein
Solyc10g055800.2	1,13	1,03E-02	3,43E-02	Chitinase
Solyc01g109970.3	1,13	2,50E-05	2,94E-04	SNF2 domain-containing protein / helicase domain-containing protein
Solyc07g042010.4	1,13	2,40E-03	1,10E-02	RNA helicase DEAH-box22
Solyc03g113190.1	1,13	3,69E-04	2,52E-03	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
Solyc04g015130.3	1,13	4,91E-07	1,24E-05	Protein kinase G11A
Solyc05g044610.3	1,13	5,08E-03	1,97E-02	vacuolar protein sorting-associated protein 8 homolog
Solyc05g006640.4	1,13	1,10E-05	1,53E-04	Phospholipid-transporting ATPase
Solyc05g005670.1	1,13	6,27E-03	2,32E-02	RING-type E3 ubiquitin transferase
Solyc10g078340.2	1,13	1,68E-05	2,13E-04	Stomatal closure-related actin-binding protein 2
Solyc11g012760.2	1,13	1,11E-02	3,62E-02	tRNA (Guanine(9)-N1)-methyltransferase
Solyc07g055140.3	1,12	6,91E-03	2,50E-02	DUF688 domain-containing protein
Solyc08g068230.4	1,12	4,58E-07	1,17E-05	Pentatricopeptide repeat-containing protein
Solyc04g081570.3	1,12	1,84E-06	3,66E-05	Heat shock protein 90
Solyc01g103873.1	1,12	3,82E-03	1,58E-02	Basic-leucine zipper (BZIP) transcription factor family protein
Solyc02g091370.2	1,12	7,51E-03	2,67E-02	Glycosyltransferase
Solyc12g097070.3	1,12	2,10E-03	9,93E-03	BLISTER
Solyc01g073750.4	1,12	3,91E-04	2,64E-03	Callose synthase
Solyc01g044360.4	1,12	4,53E-05	4,73E-04	importin-5-like
Solyc06g010000.3	1,12	3,26E-05	3,64E-04	E3 SUMO-protein ligase SIZ1-like
Solyc05g013780.3	1,12	2,00E-05	2,46E-04	paramyosin
Solyc09g009710.4	1,12	4,14E-03	1,68E-02	Transducin/WD40 repeat-like superfamily protein
Solyc03g078390.3	1,12	4,70E-05	4,88E-04	Ubiquitin carboxyl-terminal hydrolase 26
Solyc12g009840.2	1,12	2,12E-03	9,99E-03	Pyrophosphate-energized vacuolar membrane proton pump
Solyc05g013960.3	1,12	5,94E-05	5,89E-04	Oxysterol-binding protein
Solyc03g077920.1	1,12	5,07E-06	8,28E-05	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein

Solyc02g079880.3	1,12	4,42E-04	2,90E-03	Eukaryotic translation initiation factor-related protein
Solyc03g097380.4	1,12	8,70E-06	1,27E-04	Heavy metal-associated isoprenylated plant protein
Solyc08g042100.3	1,12	3,12E-04	2,21E-03	RING-type E3 ubiquitin transferase
Solyc07g006540.3	1,12	3,43E-07	9,03E-06	Double CLP-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein
Solyc05g056450.3	1,12	2,26E-03	1,05E-02	Eukaryotic aspartyl protease family protein
Solyc08g074290.3	1,12	6,94E-07	1,67E-05	Myosin heavy chain-like protein
Solyc06g069440.3	1,12	1,58E-06	3,25E-05	Zinc finger transcription factor 45
Solyc11g072710.3	1,12	3,22E-06	5,77E-05	phototropin 1
Solyc08g006980.3	1,12	1,27E-05	1,69E-04	RING/U-box superfamily protein
Solyc03g115690.1	1,12	1,04E-02	3,45E-02	transmembrane protein
Solyc11g066040.2	1,12	2,00E-06	3,92E-05	RING-type E3 ubiquitin transferase
Solyc11g030600.3	1,12	1,00E-04	8,86E-04	cytosine-5 DNA methyltransferase
Solyc02g081900.4	1,12	1,47E-03	7,46E-03	Pentatricopeptide repeat
Solyc09g098580.3	1,11	1,07E-05	1,51E-04	GTP pyrophosphokinase, (P)ppGpp synthetase II Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase
Solyc01g100360.4	1,11	1,61E-04	1,31E-03	Dihydrolipoyl dehydrogenase
Solyc04g082480.3	1,11	1,84E-05	2,29E-04	Plant regulator RWP-RK family protein, putative
Solyc05g054260.3	1,11	1,62E-03	8,12E-03	Kinesin-like protein
Solyc03g082980.3	1,11	3,79E-07	9,86E-06	KH domain-containing protein
Solyc09g075830.3	1,11	1,25E-06	2,67E-05	Protein TIME FOR COFFEE
Solyc10g008120.4	1,11	8,14E-04	4,75E-03	O-methyltransferase
Solyc01g097770.4	1,11	6,07E-07	1,49E-05	phototropin 2
Solyc10g005640.4	1,11	1,56E-05	2,01E-04	Protein phosphatase 2C
Solyc09g055755.1	1,11	4,43E-05	4,65E-04	Myosin heavy chain-related protein
Solyc01g086810.2	1,11	5,80E-03	2,18E-02	disease resistance protein RPM1-like
Solyc08g078230.4	1,11	3,54E-06	6,21E-05	Zinc ion binding protein
Solyc12g019100.2	1,11	8,10E-03	2,84E-02	Valine--tRNA ligase
Solyc12g009160.2	1,11	1,36E-02	4,25E-02	Inter-alpha-trypsin inhibitor heavy chain-like protein
Solyc10g086500.1	1,11	2,71E-04	1,98E-03	steroid 5 alpha reductase DET2
Solyc01g111770.2	1,11	2,65E-04	1,95E-03	DUF616 domain-containing protein
Solyc11g008870.2	1,11	2,67E-06	4,91E-05	Methylenetetrahydrofolate reductase
Solyc01g100530.3	1,11	4,75E-05	4,93E-04	Arm repeat superfamily protein
Solyc10g005060.4	1,11	2,35E-05	2,81E-04	O-methyltransferase-like protein
Solyc02g032200.4	1,11	1,24E-02	3,96E-02	Disease resistance protein (TIR-NBS-LRR class)
Solyc03g065340.3	1,11	4,67E-07	1,19E-05	Alpha-1,4 glucan phosphorylase
Solyc03g114500.4	1,10	4,17E-04	2,77E-03	Enolase
Solyc03g095490.3	1,10	3,50E-06	6,15E-05	Leucine-rich repeat protein kinase family protein
Solyc05g056340.3	1,10	4,55E-07	1,16E-05	Zinc finger CCCH domain protein
Solyc03g120700.3	1,10	1,69E-06	3,42E-05	Vps51/Vps67 family (Components of vesicular transport) protein
Solyc01g098450.4	1,10	1,21E-03	6,47E-03	TATA box-binding protein associated factor RNA polymerase I subunit C
Solyc03g123700.4	1,10	2,36E-03	1,09E-02	muscle M-line assembly protein
Solyc07g066220.3	1,10	2,88E-06	5,24E-05	WRKY transcription factor 2
Solyc01g103480.3	1,10	1,79E-07	5,20E-06	Coatomer subunit delta
Solyc11g007330.2	1,10	1,55E-04	1,27E-03	RAB6-interacting golgin (DUF662)
Solyc01g102700.4	1,10	2,40E-05	2,86E-04	Leucine-rich repeat receptor-like protein kinase 1
Solyc01g110480.4	1,10	1,76E-06	3,54E-05	Basic-leucine zipper (BZIP) transcription factor family protein
Solyc01g100570.4	1,10	8,39E-05	7,74E-04	Nucleolar protein 56
Solyc02g069940.4	1,10	8,99E-04	5,15E-03	WPP domain associated protein
Solyc02g071880.3	1,10	4,67E-03	1,85E-02	Protein kinase domain
Solyc04g058190.3	1,10	8,18E-03	2,86E-02	PHD domain-containing protein
Solyc01g079690.4	1,10	2,65E-05	3,08E-04	Snf2 chromatin remodeling protein
Solyc06g083460.4	1,10	1,26E-04	1,07E-03	Transcriptional corepressor LEUNIG
Solyc12g005860.2	1,10	1,03E-05	1,45E-04	Aconitate hydratase
Solyc02g086180.4	1,10	4,34E-04	2,85E-03	Delta(7)-sterol-C5(6)-desaturase
Solyc03g025970.3	1,10	1,04E-03	5,77E-03	Methyl-CpG binding domain protein
Solyc10g085410.3	1,10	1,24E-05	1,65E-04	Cactin
Solyc02g062700.3	1,10	6,96E-03	2,52E-02	ATPase family AAA domain-containing protein 3-like
Solyc05g023740.3	1,10	1,71E-05	2,16E-04	Arabidopsis mei2-like protein
Solyc12g014350.3	1,10	2,85E-03	1,26E-02	LRR receptor-like serine/threonine-protein kinase
Solyc02g070290.3	1,10	2,70E-04	1,97E-03	Cation-chloride cotransporter 1
Solyc03g118620.3	1,10	2,45E-06	4,63E-05	Outer arm dynein light chain 1 protein
Solyc06g073780.4	1,10	4,93E-04	3,17E-03	SMC3
Solyc02g079415.1	1,10	1,89E-03	9,18E-03	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc07g005320.3	1,10	1,69E-06	3,41E-05	FIP1
Solyc09g042740.4	1,09	7,34E-05	6,95E-04	Formin-like protein
Solyc02g020980.4	1,09	1,54E-06	3,18E-05	4-alpha-glucanotransferase
Solyc07g062680.3	1,09	5,60E-07	1,39E-05	cycloidea
Solyc12g006000.1	1,09	1,20E-03	6,46E-03	Clathrin coat assembly protein
Solyc04g077980.1	1,09	7,02E-05	6,70E-04	C2H2-type zinc finger protein
Solyc09g098370.4	1,09	1,10E-04	9,54E-04	Fanconi-associated nuclease
Solyc02g085770.4	1,09	5,96E-03	2,23E-02	AWPM-19-like protein
Solyc11g012810.2	1,09	1,44E-03	7,36E-03	protein ANTI-SILENCING 1-like
Solyc02g079590.3	1,09	9,07E-04	5,18E-03	Receptor protein kinase
Solyc12g044400.3	1,09	6,25E-06	9,69E-05	ATP-dependent zinc metalloprotease FtsH
Solyc03g119270.1	1,09	1,77E-03	8,72E-03	AP-3 complex subunit delta
Solyc03g083100.3	1,09	6,99E-06	1,06E-04	SUN-like protein 10
Solyc04g076880.3	1,09	2,61E-05	3,04E-04	phosphoenolpyruvate carboxykinase
Solyc02g093770.3	1,09	3,01E-05	3,43E-04	GPI inositol-deacylase
Solyc11g006960.2	1,09	2,45E-05	2,90E-04	spectrin beta chain%2C brain
Solyc03g115230.3	1,09	2,70E-04	1,97E-03	Solanum lycopersicum heat shock protein
Solyc06g082990.4	1,09	6,42E-04	3,95E-03	RNA-binding CRS1 / YhbY (CRM) domain protein
Solyc04g078950.1	1,09	9,63E-03	3,25E-02	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1
Solyc08g080280.3	1,09	5,24E-03	2,02E-02	hypothetical protein
Solyc09g009190.4	1,09	2,43E-07	6,69E-06	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic
Solyc05g009930.3	1,09	3,03E-06	5,48E-05	Protein CHUP1, chloroplastic
Solyc11g066480.2	1,09	2,42E-05	2,88E-04	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein
Solyc06g083760.3	1,09	6,12E-04	3,79E-03	Histone-lysine N-methyltransferase SUVR1
Solyc05g013180.4	1,09	2,33E-03	1,08E-02	Phosphate transporter PHO1-like protein 10
Solyc03g150107.1	1,09	2,96E-04	2,12E-03	Unknown protein
Solyc01g105310.3	1,09	3,71E-06	6,46E-05	Metacaspase-1
Solyc01g080780.2	1,09	1,02E-04	9,01E-04	Translocase of chloroplast, chloroplastic
Solyc03g117680.4	1,09	1,50E-04	1,24E-03	ATP-dependent DNA helicase
Solyc08g068010.2	1,09	3,64E-04	2,49E-03	zinc finger FYVE domain protein
Solyc07g007040.4	1,08	1,80E-05	2,25E-04	G-patch domain-containing protein
Solyc08g042130.2	1,08	3,45E-03	1,46E-02	Phox (PX) domain-containing protein
Solyc04g055120.3	1,08	5,26E-06	8,58E-05	ABC transporter D family member 1
Solyc05g013040.3	1,08	3,62E-05	3,95E-04	ARF guanine-nucleotide exchange factor GNOM
Solyc02g067570.3	1,08	6,34E-05	6,20E-04	Paired amphipathic helix protein Sin3-like 1
Solyc06g082150.4	1,08	9,87E-06	1,41E-04	6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase
Solyc09g091930.3	1,08	5,03E-05	5,15E-04	Ubiquitinyl hydrolase 1
Solyc02g083620.3	1,08	5,16E-04	3,29E-03	Ascorbate peroxidase
Solyc05g056310.3	1,08	1,41E-03	7,25E-03	T-complex protein 1 subunit gamma
Solyc04g055200.3	1,08	1,82E-04	1,44E-03	Asparagine synthetase
Solyc07g048050.3	1,08	1,45E-02	4,47E-02	Cytochrome b561 and DOMON domain-containing protein
Solyc10g085120.3	1,08	1,34E-03	6,98E-03	Leucine-rich receptor-like kinase family protein
Solyc09g009970.3	1,08	4,24E-03	1,71E-02	Rho GTPase-activating protein 1
Solyc03g025150.4	1,08	5,12E-04	3,27E-03	Unknown protein
Solyc06g008330.2	1,08	4,48E-04	2,93E-03	Serine/threonine-protein kinase
Solyc11g069160.3	1,08	7,51E-06	1,12E-04	SUMO E3 ligase SIZ1
Solyc03g120890.3	1,08	9,31E-03	3,17E-02	GATA transcription factor
Solyc12g056510.3	1,08	7,40E-05	6,99E-04	Trihelix transcription factor GTL1
Solyc08g077690.3	1,08	9,62E-04	5,43E-03	SNF2-related
Solyc10g008070.4	1,08	7,76E-05	7,26E-04	Transcription factor GTE4
Solyc08g061100.3	1,08	4,56E-06	7,56E-05	Cellulose synthase
Solyc12g011010.2	1,08	2,31E-03	1,07E-02	Protodermal factor 1
Solyc09g016940.4	1,08	9,40E-05	8,46E-04	binder of USO1 and GRH1 protein 1 isoform X9
Solyc01g109960.3	1,08	1,19E-05	1,61E-04	SUMO-activating enzyme subunit 2
Solyc09g090420.4	1,08	1,51E-04	1,24E-03	U2 snRNP auxiliary factor large subunit
Solyc11g045110.3	1,08	2,00E-03	9,61E-03	Sucrose-phosphate synthase family protein
Solyc08g062630.3	1,08	1,44E-07	4,34E-06	Aminopeptidase
Solyc10g085610.2	1,08	3,29E-03	1,41E-02	Calmodulin-binding family protein, putative, expressed
Solyc05g011830.4	1,08	3,34E-04	2,34E-03	18S pre-ribosomal assembly protein gar2-like protein

Solyc04g072940.4	1,08	2,59E-03	1,17E-02	nucleolar GTP-binding protein
Solyc01g067480.4	1,08	2,08E-03	9,88E-03	Acyl-CoA-binding domain-containing protein 4-like
Solyc02g064680.4	1,08	1,16E-05	1,58E-04	Calcium-transporting ATPase
Solyc01g098740.4	1,07	2,11E-04	1,63E-03	Protein kinase superfamily protein
Solyc01g095900.4	1,07	3,67E-07	9,59E-06	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc10g007740.3	1,07	2,43E-04	1,82E-03	Magnesium transporter CorA-like family protein
Solyc04g011580.4	1,07	8,96E-05	8,16E-04	Pumilio-like protein 3
Solyc09g007870.3	1,07	2,93E-04	2,10E-03	ethylene signaling protein
Solyc04g082980.2	1,07	1,40E-02	4,34E-02	Tetratricopeptide repeat protein SKI3
Solyc01g094290.3	1,07	8,64E-07	1,98E-05	K(+) efflux antiporter 1, chloroplastic
Solyc04g082560.4	1,07	1,48E-05	1,91E-04	Calcium-binding ef-hand-containing protein
Solyc01g109590.3	1,07	7,38E-04	4,40E-03	Protein kinase domain
Solyc03g083130.3	1,07	1,44E-02	4,46E-02	Protein DEFECTIVE IN MERISTEM SILENCING 3
Solyc03g007485.1	1,07	5,75E-05	5,76E-04	Leucine-rich repeat protein kinase family protein
Solyc09g008040.3	1,07	8,70E-06	1,27E-04	RNA polymerase sigma factor
Solyc07g039190.4	1,07	2,93E-04	2,10E-03	hypothetical protein
Solyc01g108600.3	1,07	6,36E-06	9,81E-05	Presequence protease chloroplastic/mitochondrial-like
Solyc08g074500.2	1,07	8,76E-05	8,01E-04	SNF2-related
Solyc03g006570.3	1,07	7,92E-04	4,65E-03	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein
Solyc09g075860.3	1,07	2,53E-05	2,96E-04	Lipoxygenase
Solyc10g074940.2	1,07	2,60E-04	1,92E-03	Phospholipid-transporting ATPase
Solyc08g065230.1	1,07	8,88E-04	5,09E-03	serine/threonine-protein kinase EDR1-like
Solyc08g081410.3	1,07	2,62E-04	1,94E-03	Golgin candidate 6
Solyc04g076980.3	1,07	3,98E-03	1,63E-02	Receptor-like protein kinase
Solyc09g092130.3	1,07	9,30E-04	5,28E-03	Sucrose phosphate synthase
Solyc02g065500.4	1,07	7,21E-04	4,33E-03	ribosome 60S biogenesis amino-terminal protein
Solyc01g079230.4	1,07	1,42E-05	1,86E-04	Duf724 domain-containing protein 3
Solyc06g048950.3	1,07	1,19E-04	1,02E-03	Leucine-rich receptor-like kinase family protein
Solyc08g005400.4	1,07	1,40E-03	7,22E-03	DNA (Cytosine-5)-methyltransferase CMT2
Solyc03g007420.3	1,07	1,12E-03	6,13E-03	hypothetical protein
Solyc03g123780.4	1,07	9,96E-03	3,33E-02	Receptor kinase
Solyc03g113500.4	1,07	1,62E-04	1,31E-03	DDT domain-containing protein
Solyc06g071330.4	1,07	2,07E-03	9,85E-03	Nucleobase-ascorbate transporter 8
Solyc09g056350.4	1,07	1,89E-06	3,75E-05	Lipase class 3 family protein
Solyc12g019960.2	1,07	1,61E-05	2,06E-04	Telomerase activating protein Est1
Solyc02g091940.3	1,07	7,08E-04	4,27E-03	hypothetical protein
Solyc07g017860.3	1,07	1,10E-05	1,53E-04	Acetyl-coenzyme A synthetase
Solyc08g079710.3	1,07	1,33E-05	1,76E-04	Kinesin-like protein
Solyc03g033360.3	1,07	2,60E-03	1,17E-02	Eukaryotic aspartyl protease family protein
Solyc03g118510.3	1,07	4,95E-04	3,18E-03	Ovary receptor kinase 27
Solyc11g072390.2	1,07	9,00E-03	3,08E-02	Something about silencing protein 10
Solyc03g118260.3	1,06	5,37E-03	2,05E-02	Adp-ribosylation factor gtpase-activating protein agd3
Solyc10g076870.2	1,06	2,47E-04	1,84E-03	RNA binding protein
Solyc08g078520.4	1,06	1,60E-02	4,82E-02	electron transporter%2C putative (Protein of unknown function%2C DUF547)
Solyc11g017460.3	1,06	8,56E-04	4,94E-03	U-box domain-containing protein 13
Solyc08g080170.3	1,06	2,33E-05	2,79E-04	3-hydroxy-3-methylglutaryl coenzyme A synthase
Solyc04g076510.3	1,06	2,54E-04	1,89E-03	BEACH domain
Solyc05g009890.1	1,06	3,59E-04	2,46E-03	Eukaryotic aspartyl protease family protein
Solyc04g076180.4	1,06	3,97E-06	6,82E-05	ATPase family AAA domain-containing protein
Solyc09g090680.3	1,06	8,14E-03	2,86E-02	Cysteine-rich repeat secretory protein 3
Solyc11g040390.2	1,06	9,54E-04	5,39E-03	Aspartokinase-homoserine dehydrogenase
Solyc09g074060.3	1,06	8,15E-05	7,55E-04	BSD domain-containing protein
Solyc02g067670.4	1,06	1,04E-03	5,75E-03	DNA repair protein UVH3
Solyc01g097980.3	1,06	1,23E-05	1,65E-04	CTR1-like protein kinase 2
Solyc01g096600.4	1,06	3,20E-05	3,60E-04	THO complex subunit 1
Solyc09g007910.4	1,06	4,82E-04	3,11E-03	Phenylalanine ammonia-lyase
Solyc04g007150.3	1,06	2,48E-03	1,13E-02	Glycoside hydrolase family 31
Solyc04g081300.4	1,06	5,76E-05	5,76E-04	Endoglucanase
Solyc02g050280.4	1,06	5,00E-05	5,12E-04	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein
Solyc11g007270.3	1,06	1,89E-06	3,75E-05	Alkaline/neutral invertase
Solyc04g077660.3	1,06	4,19E-03	1,70E-02	Peptidylprolyl isomerase
Solyc01g106210.3	1,06	2,23E-04	1,70E-03	Heat shock protein 70 kDa
Solyc07g064740.3	1,06	4,63E-03	1,84E-02	Rab3 GTPase-activating protein catalytic subunit
Solyc11g069340.2	1,06	1,83E-05	2,28E-04	Zinc finger transcription factor 69
Solyc12g042200.2	1,06	8,06E-03	2,83E-02	Transducin family protein / WD-40 repeat family protein
Solyc02g030100.4	1,06	1,65E-02	4,93E-02	Vacuolar protein sorting-associated protein 54, chloroplastic
Solyc07g017490.3	1,06	1,27E-04	1,08E-03	Suppressor of mec-8 and unc-52 protein-like protein 2
Solyc02g078520.4	1,06	4,26E-06	7,16E-05	Mediator of rna polymerase ii transcription subunit 16
Solyc01g100060.4	1,06	6,68E-06	1,02E-04	Pre-mRNA-splicing factor 38A
Solyc09g010280.3	1,05	1,59E-06	3,26E-05	LETM1-like
Solyc08g078190.2	1,05	2,94E-03	1,29E-02	Ethylene-responsive transcription factor 5
Solyc02g082810.3	1,05	4,11E-03	1,67E-02	Poly(A) polymerase I
Solyc12g035250.3	1,05	1,75E-04	1,40E-03	Zinc finger transcription factor 77
Solyc08g081070.3	1,05	4,48E-05	4,69E-04	Mitochondrial substrate carrier family protein
Solyc11g062370.1	1,05	3,00E-04	2,14E-03	Stomatal closure-related actin-binding protein 1
Solyc11g069950.2	1,05	1,81E-06	3,62E-05	FtsH protease
Solyc08g067030.3	1,05	2,25E-04	1,72E-03	DUF642 domain-containing protein
Solyc09g018370.4	1,05	4,16E-04	2,76E-03	ARM repeat superfamily protein
Solyc05g010400.3	1,05	7,67E-04	4,54E-03	protein NSP-INTERACTING KINASE 1-like
Solyc03g118430.3	1,05	3,42E-06	6,08E-05	Peptidase M16
Solyc04g005060.3	1,05	3,61E-03	1,52E-02	TPX2 domain-containing protein
Solyc07g041070.3	1,05	9,33E-03	3,17E-02	Hydroxyproline-rich glycoprotein family protein
Solyc05g006490.4	1,05	8,49E-06	1,25E-04	TPX2 domain-containing protein
Solyc02g094540.4	1,05	1,15E-05	1,57E-04	nuclear factor kappa-B-binding protein
Solyc01g010030.3	1,05	6,20E-05	6,10E-04	Proline-rich receptor-like protein kinase PERK13
Solyc01g088750.3	1,05	1,49E-02	4,57E-02	Pentatricopeptide repeat-containing protein
Solyc07g053800.3	1,05	1,58E-03	7,96E-03	RING 1B
Solyc06g007130.5.1	1,05	2,85E-03	1,26E-02	omega-3 fatty acid desaturase -3
Solyc01g080460.3	1,05	2,12E-04	1,64E-03	Pyruvate, phosphate dikinase
Solyc07g064700.4	1,05	3,03E-05	3,44E-04	Bromodomain-containing protein
Solyc02g086510.4	1,05	3,52E-04	2,43E-03	Zinc finger transcription factor 22
Solyc06g069380.4	1,05	1,24E-05	1,66E-04	O-fucosyltransferase
Solyc03g110880.4	1,05	2,01E-06	3,95E-05	RNA polymerase 4 second largest subunit (RPD2)
Solyc04g015470.3	1,05	3,30E-03	1,41E-02	Phosphatidylinositol 4-phosphate 5-kinase
Solyc05g009660.4	1,05	4,25E-04	2,81E-03	Transcription factor PERIANTHIA
Solyc04g016240.3	1,05	1,18E-05	1,60E-04	Nuclear pore protein
Solyc08g074440.4	1,05	1,01E-05	1,43E-04	Pre-mRNA-splicing factor
Solyc07g064350.3	1,05	5,73E-03	2,16E-02	KRR1 family protein
Solyc11g066730.2	1,05	3,94E-05	4,24E-04	BTB/POZ domain-containing protein
Solyc01g097320.3	1,05	3,44E-04	2,39E-03	Mediator of RNA polymerase II transcription subunit 14
Solyc11g008700.2	1,05	4,01E-04	2,69E-03	splicing factor U2AF-associated protein 2
Solyc01g095790.4	1,05	1,90E-06	3,75E-05	Protein SDE2-like protein
Solyc01g098870.3	1,04	1,42E-04	1,18E-03	hypothetical protein
Solyc05g052570.3	1,04	2,92E-03	1,29E-02	Zinc finger transcription factor 39
Solyc01g098170.3	1,04	9,97E-05	8,84E-04	Protein HASTY 1
Solyc02g081980.3	1,04	2,61E-03	1,17E-02	Apyrase
Solyc11g056680.1	1,04	4,46E-03	1,79E-02	Leucine-rich repeat receptor-like protein
Solyc04g078680.4	1,04	2,09E-06	4,04E-05	RING/U-box superfamily protein
Solyc07g053440.4	1,04	8,68E-05	7,97E-04	hypothetical protein
Solyc05g023750.3	1,04	2,33E-06	4,42E-05	Adp-ribosylation factor gtpase-activating protein agd3
Solyc11g011020.2	1,04	4,59E-04	2,98E-03	Ovary receptor kinase 11
Solyc03g083240.4	1,04	1,74E-03	8,60E-03	Transcription factor jumonji (JmjC) domain-containing protein
Solyc10g084220.3	1,04	8,82E-04	5,07E-03	Protein FAR1-RELATED SEQUENCE 7
Solyc01g079180.4	1,04	5,04E-03	1,96E-02	Pectinesterase
Solyc07g005880.3	1,04	4,17E-04	2,77E-03	Replication factor C subunit 1
Solyc11g069720.2	1,04	2,52E-06	4,73E-05	Cell division cycle protein 48-like protein
Solyc08g007800.3	1,04	7,59E-03	2,69E-02	SPX domain-containing protein
Solyc10g083800.2	1,04	2,07E-04	1,61E-03	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein
Solyc06g051940.4	1,04	2,64E-05	3,08E-04	Protein phosphatase 2C
Solyc02g062810.4	1,04	2,84E-05	3,27E-04	Signal recognition particle subunit SRP68
Solyc01g112050.3	1,04	2,43E-04	1,82E-03	DUF630 family protein, putative (DUF630 and DUF632)

Solyc10g009200.3	1,04	9,69E-04	5,45E-03	Ribosomal RNA-processing protein
Solyc05g053410.4	1,04	1,69E-04	1,36E-03	phytochrome B2
Solyc01g103010.4	1,04	1,63E-06	3,33E-05	Cullin-associated NEDD8-dissociated protein 1
Solyc06g051960.3	1,04	2,52E-06	4,74E-05	Pectinesterase
Solyc12g056080.2	1,04	1,62E-06	3,32E-05	Crooked neck-like protein 1
Solyc02g081290.4	1,04	2,84E-06	5,19E-05	RNA helicase DEAD9
Solyc08g081640.3	1,04	1,78E-03	8,75E-03	Transducin/WD40 repeat-like superfamily protein
Solyc02g078790.4	1,04	3,31E-04	2,32E-03	Lysine-specific demethylase JMJ25
Solyc03g026180.1	1,04	3,96E-03	1,62E-02	Unknown protein
Solyc05g014640.3	1,03	7,73E-05	7,25E-04	Serine-rich adhesin for platelets-like protein
Solyc08g075530.3	1,03	5,71E-04	3,58E-03	Alpha glucosidase-like protein
Solyc02g021590.3	1,03	8,70E-07	1,99E-05	Protein male discoverer 2
Solyc07g062210.4	1,03	2,44E-03	1,12E-02	Protein trichome birefringence-like 43
Solyc09g098240.4	1,03	1,68E-06	3,40E-05	Importin beta-like SAD2
Solyc01g005020.3	1,03	5,71E-05	5,73E-04	Salt Overly Sensitive 1
Solyc03g005430.4	1,03	5,96E-06	9,35E-05	MATH domain-containing protein
Solyc09g083350.3	1,03	6,60E-05	6,37E-04	Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic
Solyc11g066370.2	1,03	6,78E-05	6,52E-04	DNA ligase
Solyc10g005080.3	1,03	1,02E-05	1,45E-04	Late elongated hypocotyl
Solyc01g096260.4	1,03	3,90E-03	1,61E-02	NAD-dependent protein deacetylase HST1-like protein
Solyc06g082840.4	1,03	1,39E-04	1,16E-03	Chaperone DnaJ-domain superfamily protein
Solyc02g065490.4	1,03	4,26E-03	1,72E-02	BEL1-like homeodomain protein 4
Solyc05g015650.3	1,03	1,88E-05	2,33E-04	Calmodulin-binding transcription activator 4
Solyc01g098180.3	1,03	7,90E-06	1,17E-04	translation initiation factor eIF-2B subunit epsilon isoform X1
Solyc03g006420.4	1,03	1,52E-03	7,69E-03	Origin recognition complex subunit 1
Solyc11g069620.3	1,03	1,09E-03	5,97E-03	CC-NBS-LRR type resistance protein
Solyc12g088990.2	1,03	4,02E-05	4,30E-04	Exocyst complex component SEC3A
Solyc02g086790.4	1,03	6,25E-05	6,12E-04	Protein kinase
Solyc07g052240.3	1,03	1,16E-03	6,26E-03	L-ascorbate oxidase-like protein
Solyc03g118370.3	1,03	1,15E-04	9,93E-04	Carboxypeptidase
Solyc11g065660.2	1,03	3,20E-03	1,38E-02	Calcium-dependent protein kinase
Solyc07g005360.3	1,03	4,70E-05	4,88E-04	Hexosyltransferase
Solyc04g008650.4	1,03	4,98E-03	1,95E-02	Inactive leucine-rich repeat receptor-like serinethreonine-protein kinase
Solyc10g006350.3	1,03	1,42E-04	1,18E-03	CONSTANS interacting protein 7
Solyc02g093000.3	1,03	1,94E-03	9,39E-03	phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and protein-tyrosine-phosphatase PTEN2A-like
Solyc05g054370.2	1,03	1,01E-06	2,25E-05	Acyl-CoA dehydrogenase family member 10
Solyc06g065970.1	1,03	9,24E-05	8,36E-04	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc02g091410.3	1,03	3,03E-05	3,44E-04	Protease Do-like 7
Solyc10g007950.4	1,03	2,16E-04	1,66E-03	Trehalose-6-phosphate synthase
Solyc11g033283.1	1,02	1,40E-05	1,83E-04	Protein NRT1/ PTR FAMILY 6.1
Solyc01g111400.4	1,02	1,09E-05	1,53E-04	Subtilisin-like protease-like protein
Solyc03g098630.4	1,02	6,71E-05	6,46E-04	DUF789 domain-containing protein
Solyc04g082950.4	1,02	1,35E-03	7,01E-03	galactan beta-1,4-galactosyltransferase GALS1
Solyc05g053240.4	1,02	1,85E-05	2,29E-04	Squamosa promoter binding protein12b
Solyc12g098700.1	1,02	3,96E-05	4,26E-04	RNA helicase DEAD42
Solyc07g006760.4	1,02	1,87E-05	2,31E-04	MAP kinase kinase kinase 43
Solyc04g014510.3	1,02	6,71E-04	4,10E-03	glutamine synthase
Solyc08g066600.4	1,02	1,24E-04	1,05E-03	DUF810 domain-containing protein
Solyc05g008630.4	1,02	1,10E-06	2,41E-05	Nuclear poly(A) polymerase 2
Solyc01g068590.4	1,02	1,06E-04	9,29E-04	Metal ion-binding protein
Solyc04g054470.3	1,02	2,54E-05	2,97E-04	Unknown protein
Solyc09g072570.3	1,02	3,05E-06	5,52E-05	Pre-mRNA-splicing factor SLU7
Solyc10g005330.3	1,02	3,72E-05	4,04E-04	Homeobox-leucine zipper protein MERISTEM L1
Solyc01g005560.3	1,02	1,55E-04	1,27E-03	Isocitrate dehydrogenase [NADP]
Solyc07g043490.1	1,02	2,00E-03	9,61E-03	Glycosyltransferase
Solyc06g051350.4	1,02	2,75E-03	1,22E-02	Protein trichome birefringence-like 28
Solyc06g069080.3	1,02	5,84E-03	2,19E-02	Tetratricopeptide repeat
Solyc03g025730.3	1,02	1,61E-05	2,06E-04	Tubulin beta chain
Solyc10g038190.2	1,02	1,07E-03	5,86E-03	Protein kinase G11A
Solyc10g050890.2	1,02	2,05E-03	9,78E-03	nitrite reductase 2
Solyc01g066860.3	1,02	1,03E-03	5,70E-03	hypothetical protein
Solyc05g013730.3	1,02	5,19E-05	5,28E-04	O-fucosyltransferase
Solyc06g082930.3	1,02	2,29E-06	4,36E-05	FRIGIDA-like protein
Solyc05g047520.4	1,02	3,92E-04	2,65E-03	Helicase
Solyc04g082320.3	1,02	7,33E-03	2,63E-02	Pentatricopeptide repeat
Solyc01g090780.3	1,02	1,60E-05	2,05E-04	CCR4-NOT transcription complex subunit 1
Solyc05g007430.4	1,02	1,26E-02	4,01E-02	Transmembrane protein (DUF616)
Solyc04g050510.3	1,01	5,93E-04	3,69E-03	Translational activator GCN1-like protein
Solyc04g012170.4	1,01	7,05E-06	1,07E-04	Serine/threonine-protein kinase
Solyc05g056210.4	1,01	7,86E-06	1,16E-04	N6-adenosine-methyltransferase subunit METTL14
Solyc06g036580.4	1,01	7,28E-05	6,90E-04	U4/U6 small nuclear ribonucleoprotein Prp3
Solyc09g010560.3	1,01	1,00E-05	1,43E-04	5-oxoprolinase
Solyc06g074090.3	1,01	7,43E-03	2,65E-02	7-dehydrocholesterol reductase
Solyc04g005270.1	1,01	8,11E-07	1,88E-05	Phosphatidylinositol 4-kinase gamma 7
Solyc09g010220.4	1,01	1,36E-02	4,26E-02	lysosomal Pro-X carboxypeptidase
Solyc12g100120.2	1,01	2,27E-06	4,33E-05	Proline-tRNA ligase (DUF1680)
Solyc11g071640.3	1,01	3,13E-05	3,53E-04	Glycosyl hydrolase family protein
Solyc02g078540.4	1,01	9,80E-05	8,73E-04	Clathrin light chain
Solyc11g072320.3	1,01	1,57E-03	7,89E-03	Something about silencing protein 10
Solyc01g099350.3	1,01	3,46E-04	2,39E-03	Acyl-CoA-binding domain-containing protein 4
Solyc01g079150.4	1,01	1,31E-05	1,73E-04	HCO3-transporter family
Solyc02g030480.4	1,01	7,83E-06	1,16E-04	Alcohol dehydrogenase superfamily
Solyc03g095970.3	1,01	1,67E-02	5,00E-02	Short-chain dehydrogenase reductase 4
Solyc09g064860.3	1,01	3,02E-06	5,48E-05	ELKS/Rab6-interacting/CAST family protein
Solyc08g080110.3	1,01	3,71E-04	2,53E-03	FAM63A-like protein (DUF544)
Solyc12g014530.3	1,01	2,31E-05	2,78E-04	L-aspartate oxidase
Solyc05g012640.3	1,01	1,32E-03	6,90E-03	T-box transcription factor%2C putative (DUF863)
Solyc01g103570.3	1,01	2,51E-03	1,14E-02	DNA-binding bromodomain-containing protein
Solyc11g072840.1	1,01	7,47E-03	2,66E-02	Histone H4
Solyc02g090580.3	1,01	1,44E-03	7,37E-03	ternary complex factor MIP1 leucine-zipper protein (Protein of unknown function%2C DUF547)
Solyc03g097290.4	1,01	5,85E-05	5,82E-04	DB199
Solyc05g056220.3	1,01	4,12E-05	4,39E-04	N6-adenosine-methyltransferase subunit METTL14
Solyc02g080260.4	1,00	3,38E-04	2,35E-03	Woolly
Solyc07g062130.3	1,00	6,21E-05	6,10E-04	trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1
Solyc11g071700.2	1,00	3,66E-05	3,99E-04	ubiquitin carboxyl-terminal hydrolase 12
Solyc05g026510.4	1,00	1,00E-03	5,58E-03	Sister-chromatid cohesion protein 3
Solyc02g092480.4	1,00	8,55E-05	7,87E-04	BTB domain-containing protein/NPH3 domain-containing protein
Solyc05g056140.4	1,00	1,20E-04	1,03E-03	Zinc finger (C3HC4-type RING finger) family protein
Solyc03g098460.3	1,00	9,93E-07	2,22E-05	NAD(P)-binding Rossmann-fold superfamily protein
Solyc03g121320.3	1,00	1,25E-03	6,63E-03	Tudor/PWWP/MBT superfamily protein
Solyc01g103350.3	1,00	1,81E-04	1,44E-03	Cyclin-dependent kinase C-2
Solyc02g085350.4	1,00	1,34E-05	1,76E-04	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
Solyc09g064440.4	1,00	2,67E-04	1,96E-03	ABC transporter C family member 13
Solyc05g006530.4	1,00	1,50E-04	1,24E-03	DEAD-box ATP-dependent RNA helicase ISE2, chloroplastic
Solyc02g090360.3	1,00	2,00E-05	2,46E-04	L-ascorbate oxidase-like protein
Solyc04g081240.2	1,00	1,35E-02	4,24E-02	Auxin Response Factor 5
Solyc11g012850.2	1,00	3,38E-05	3,75E-04	Chlorophyllide a oxygenase, chloroplastic
Solyc02g090430.3	1,00	5,40E-06	8,75E-05	MAP kinase kinase kinase 20
Solyc09g031650.3	1,00	8,45E-05	7,80E-04	Mediator of RNA polymerase II transcription subunit 12-like protein
Solyc01g111990.3	1,00	2,51E-04	1,87E-03	Alanine--tRNA ligase
Solyc01g107510.3	1,00	2,89E-04	2,08E-03	DNA repair protein REV1
Solyc04g079560.3	1,00	8,84E-03	3,04E-02	Lysine histidine transporter-like 8
Solyc05g025750.3	1,00	1,01E-05	1,44E-04	SH3 domain protein
Solyc03g119650.3	1,00	5,76E-04	3,60E-03	DENN domain and WD repeat-containing protein SCD1
Solyc03g119650.3	1,00	6,84E-03	2,48E-02	ABC transporter B family member
Solyc05g009500.3	-1,00	8,94E-06	1,30E-04	Protein NRT1/ PTR FAMILY 3.1
Solyc04g014400.4	-1,00	2,43E-03	1,11E-02	LOW QUALITY PROTEIN: LRR receptor-like serine/threonine-protein kinase GSO1
Solyc02g090010.3	-1,00	7,69E-05	7,23E-04	Molybdopterin synthase sulfur carrier subunit
Solyc10g078450.2	-1,00	3,47E-05	3,82E-04	Small nuclear ribonucleoprotein family protein
Solyc03g062740.4	-1,00	8,19E-03	2,86E-02	Unknown protein

Solyc07g017825.1	-1,00	6,64E-03	2,43E-02	Unknown protein
Solyc05g050360.3	-1,00	1,39E-03	7,20E-03	Cyclic nucleotide-gated ion channel 1
Solyc01g094220.3	-1,00	7,10E-03	2,56E-02	NAD(P)-binding Rossmann-fold superfamily protein
Solyc02g061990.3	-1,00	6,41E-04	3,95E-03	BZIP transcription factor FD
Solyc04g072640.3	-1,01	6,30E-06	9,74E-05	Membrane-anchored ubiquitin-fold protein
Solyc08g078060.3	-1,01	6,28E-05	6,14E-04	Transmembrane protein
Solyc11g069765.1	-1,01	2,23E-05	2,69E-04	SNF1-related protein kinase regulatory subunit beta-3
Solyc01g100940.2	-1,01	3,05E-04	2,17E-03	protein NIM1-INTERACTING 1-like isoform X2
Solyc11g011740.1	-1,01	1,35E-03	7,02E-03	Ethylene-responsive transcription factor
Solyc11g010870.2	-1,01	9,67E-03	3,26E-02	Unknown protein
Solyc01g095220.2	-1,01	6,25E-05	6,12E-04	Unknown protein
Solyc10g084620.3	-1,01	7,83E-04	4,61E-03	hypothetical protein
Solyc03g078150.3	-1,01	8,87E-04	5,09E-03	Amino acid transporter family protein
Solyc01g112170.3	-1,01	4,12E-06	6,97E-05	Calcium-dependent protein kinase SK5
Solyc05g007240.1	-1,01	1,75E-05	2,20E-04	zinc finger CCHC domain protein
Solyc07g045470.3	-1,01	6,44E-05	6,26E-04	alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
Solyc05g056480.3	-1,01	4,49E-04	2,93E-03	2-oxoisovalerate dehydrogenase subunit alpha 2, mitochondrial
Solyc09g009540.4	-1,01	8,21E-04	4,78E-03	Alpha/beta-Hydrolases superfamily protein
Solyc09g008760.1	-1,01	1,30E-03	6,83E-03	VQ motif-containing protein 29
Solyc11g071720.2	-1,01	1,59E-02	4,82E-02	Alpha/beta-Hydrolases superfamily protein
Solyc10g006520.3	-1,01	6,17E-04	3,82E-03	Thioredoxin domain-containing protein
Solyc09g010020.2	-1,01	2,25E-04	1,72E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc10g084120.2	-1,01	4,51E-03	1,80E-02	plasma membrane intrinsic protein 2.5
Solyc06g073890.3	-1,01	3,54E-05	3,88E-04	E3 ubiquitin-protein ligase RHF2A
Solyc03g080040.1	-1,01	1,13E-02	3,67E-02	Serine protease inhibitor, Kazal-type family protein
Solyc11g006590.2	-1,01	1,32E-05	1,74E-04	Cytochrome
Solyc06g069520.3	-1,02	2,92E-05	3,35E-04	Protein Asterix
Solyc11g006900.1	-1,02	4,19E-04	2,78E-03	hypothetical protein
Solyc05g018060.1	-1,02	1,52E-02	4,62E-02	Unknown protein
Solyc08g080940.3	-1,02	1,10E-06	2,40E-05	glutathione peroxidase like encoding 1
Solyc04g079080.2	-1,02	6,69E-04	4,09E-03	EF-hand domain
Solyc06g062960.3	-1,02	3,93E-06	6,76E-05	DUF1677 domain-containing protein
Solyc03g094160.3	-1,02	4,78E-06	7,89E-05	metacaspase-1-like
Solyc03g118880.3	-1,02	2,49E-04	1,86E-03	Unknown protein
Solyc06g050980.3	-1,02	5,57E-03	2,11E-02	Ferritin
Solyc09g091500.3	-1,02	2,18E-07	6,04E-06	U6 snRNA-associated Sm-like protein LSm5
Solyc11g011760.3	-1,02	3,48E-06	6,14E-05	voltage-dependent L-type calcium channel subunit
Solyc09g074430.4	-1,02	3,28E-04	2,30E-03	Flavin-containing monooxygenase
Solyc05g009520.2	-1,02	9,29E-05	8,39E-04	hypothetical protein
Solyc01g010185.1	-1,02	1,94E-05	2,40E-04	Retrovirus-related Pol polyprotein from transposon TNT 1-94
Solyc03g007360.3	-1,02	2,53E-05	2,97E-04	Bidirectional sugar transporter SWEET
Solyc08g080860.4	-1,02	4,69E-04	3,04E-03	patatin-like phospholipase domain protein
Solyc01g098590.3	-1,02	1,36E-05	1,79E-04	Phosphoglycerate mutase-like protein AT74
Solyc02g093010.3	-1,02	1,75E-05	2,20E-04	Protein RER1
Solyc10g076300.2	-1,03	3,65E-03	1,53E-02	CASP-like protein
Solyc07g007250.4	-1,03	1,33E-02	4,19E-02	Metallocarboxypeptidase inhibitor
Solyc01g049770.3	-1,03	1,32E-02	4,15E-02	Unknown protein
Solyc01g080890.2	-1,03	1,32E-04	1,11E-03	hypothetical protein
Solyc08g062360.3	-1,03	3,32E-03	1,42E-02	Ankyrin repeat family protein
Solyc05g013710.3	-1,03	3,74E-03	1,56E-02	SufE-like protein chloroplastic-like
Solyc09g098310.3	-1,03	7,72E-06	1,15E-04	Unknown protein
Solyc01g088090.3	-1,03	5,57E-07	1,38E-05	Pheophytinase, chloroplastic
Solyc09g005730.4	-1,03	4,98E-04	3,19E-03	Plant protein 1589 of Uncharacterized protein function
Solyc06g061230.3	-1,03	1,67E-03	8,32E-03	metallocarboxypeptidase inhibitor precursor
Solyc03g082720.3	-1,03	1,24E-05	1,66E-04	Protein yippee-like
Solyc05g008480.4	-1,03	2,37E-03	1,09E-02	Histone chaperone
Solyc12g056230.2	-1,03	6,70E-07	1,62E-05	glutathione peroxidase like encoding 2
Solyc03g032090.1	-1,03	9,00E-03	3,08E-02	Amino acid transporter
Solyc06g064560.4	-1,04	1,86E-03	9,05E-03	DNA ligase-like protein
Solyc05g046140.3	-1,04	1,51E-02	4,61E-02	Kirola
Solyc02g082060.2	-1,04	1,08E-04	9,41E-04	PPPDE putative thiol peptidase family protein
Solyc02g077880.3	-1,04	5,93E-06	9,33E-05	Auxin-repressed protein
Solyc02g081830.4	-1,04	4,48E-04	2,93E-03	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
Solyc06g036120.3	-1,04	1,13E-04	9,77E-04	Unknown protein
Solyc03g026370.1	-1,04	2,61E-04	1,93E-03	Peptidoglycan-binding LysM domain-containing protein
Solyc12g049290.2	-1,04	2,53E-06	4,74E-05	protein ELF4-LIKE 4
Solyc01g106310.3	-1,04	1,17E-04	1,01E-03	Unknown protein
Solyc12g087840.1	-1,04	7,31E-05	6,92E-04	RING/U-box superfamily protein
Solyc02g093050.3	-1,04	1,17E-06	2,53E-05	WRKY transcription factor 8
Solyc12g006160.2	-1,04	2,12E-06	4,09E-05	Sterile alpha motif (SAM) domain-containing protein
Solyc02g083280.4	-1,04	2,08E-05	2,53E-04	Rhodanese-like domain
Solyc10g051020.2	-1,04	1,04E-04	9,17E-04	Cytochrome P450
Solyc08g008330.3	-1,04	5,35E-06	8,69E-05	hypothetical protein
Solyc08g081455.1	-1,05	2,41E-04	1,81E-03	Unknown protein
Solyc06g075520.3	-1,05	2,92E-03	1,29E-02	Glutathione S-transferase
Solyc12g005660.2	-1,05	3,43E-05	3,78E-04	Zinc finger protein/CONSTANS-like protein
Solyc11g012690.3	-1,05	8,68E-07	1,99E-05	Heavy metal-associated isoprenylated plant protein
Solyc07g005210.3	-1,05	7,81E-06	1,16E-04	Outer membrane lipoprotein blc-like
Solyc06g050170.4	-1,05	1,35E-06	2,84E-05	Potassium transporter
Solyc09g074350.1	-1,05	2,55E-03	1,15E-02	phosphopantothenoylcysteine decarboxylase subunit VHS3
Solyc08g067390.4	-1,05	4,26E-04	2,81E-03	EG45-like domain containing protein
Solyc07g041340.2	-1,05	2,17E-04	1,66E-03	protein ELF4-LIKE 4-like
Solyc06g007510.3	-1,05	2,66E-06	4,91E-05	Ubiquitin-conjugating enzyme
Solyc03g063730.4	-1,05	1,07E-06	2,34E-05	Protein DETOXIFICATION
Solyc05g055310.3	-1,05	8,72E-05	7,99E-04	Heavy metal transport protein
Solyc01g080040.3	-1,05	6,43E-03	2,36E-02	Dual specificity protein phosphatase 1
Solyc06g075500.4	-1,05	1,95E-07	5,53E-06	Protein NRT1/ PTR FAMILY 2.7
Solyc02g065610.3	-1,05	3,76E-06	6,51E-05	Protein trichome birefringence-like 21
Solyc01g109810.2	-1,05	5,94E-05	5,89E-04	tRNA-methyltransferase non-catalytic subunit trm6MTase subunit
Solyc02g150141.1	-1,05	2,23E-03	1,04E-02	Cytochrome c oxidase subunit 5C
Solyc02g092540.2	-1,06	1,13E-03	6,15E-03	Unknown protein
Solyc01g009760.3	-1,06	1,13E-02	3,68E-02	GRAM domain family protein
Solyc01g080220.3	-1,06	3,24E-05	3,63E-04	endo-1,31,4-beta-D-glucanase-like
Solyc07g007170.3	-1,06	6,52E-06	9,97E-05	RING/U-box superfamily protein
Solyc11g072890.1	-1,06	2,13E-04	1,64E-03	hypothetical protein
Solyc12g009480.2	-1,06	1,63E-06	3,33E-05	SPX domain-containing protein
Solyc06g051740.1	-1,06	1,07E-03	5,89E-03	Unknown protein
Solyc04g053130.4	-1,06	1,80E-06	3,60E-05	Stress enhanced protein 2, chloroplastic
Solyc06g075090.4	-1,06	8,27E-06	1,22E-04	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc03g116570.3	-1,06	5,91E-06	9,32E-05	Thiol-disulfide oxidoreductase DCC family protein
Solyc02g067250.3	-1,06	2,94E-05	3,36E-04	Ribosomal protein L34e superfamily protein
Solyc06g064610.1	-1,06	1,32E-05	1,74E-04	hypothetical protein
Solyc09g011640.5.1	-1,06	5,23E-05	5,31E-04	Glutathione S-transferase-like protein
Solyc05g009420.1	-1,06	2,49E-05	2,94E-04	transmembrane protein
Solyc01g098020.2	-1,06	2,50E-06	4,71E-05	N-acetyltransferase
Solyc12g056760.2	-1,06	6,78E-03	2,47E-02	WD repeat protein
Solyc04g056425.1	-1,06	7,53E-04	4,47E-03	basic leucine zipper/W2 domain protein
Solyc04g081770.4	-1,06	3,46E-06	6,12E-05	GDSL esterase/lipase
Solyc10g080920.2	-1,07	9,27E-04	5,27E-03	Protein RADIALIS-like 2
Solyc09g008370.1	-1,07	1,13E-05	1,56E-04	Major facilitator superfamily
Solyc09g010160.3	-1,07	4,88E-05	5,02E-04	NAC domain-containing protein 90
Solyc07g056420.4	-1,07	1,78E-04	1,42E-03	glutathione S-transferase AY082341
Solyc02g072270.3	-1,07	9,71E-05	8,67E-04	RING/FYVE/PHD zinc finger superfamily protein
Solyc01g057445.1	-1,07	2,05E-07	5,78E-06	Mediator of RNA polymerase II transcription subunit 15a
Solyc08g065610.3	-1,07	3,40E-03	1,44E-02	Vacuolar-processing enzyme
Solyc12g056950.2	-1,07	9,50E-07	2,14E-05	FCS-Like Zinc finger 6
Solyc07g063860.4	-1,07	4,17E-07	1,07E-05	DUF538 domain-containing protein
Solyc02g092770.3	-1,07	3,67E-03	1,53E-02	Sigma-B regulation protein RsbQ
Solyc06g009390.3	-1,07	8,94E-07	2,03E-05	Protein phosphatase-2C
Solyc03g093340.4	-1,07	1,51E-04	1,24E-03	Uncharacterized conserved protein (UCP012943)
Solyc04g056340.4	-1,07	2,22E-06	4,25E-05	Tyrosine phosphatase family protein

Solyc09g082115.1	-1,08	3,74E-04	2,54E-03	Lactoylglutathione lyase / glyoxalase I family protein
Solyc08g006050.2	-1,08	5,78E-04	3,61E-03	Embryo defective 1303
Solyc05g006420.3	-1,08	1,28E-05	1,70E-04	Two-component response regulator ARR3
Solyc06g059860.3	-1,08	4,05E-07	1,04E-05	patatin-like phospholipase domain protein
Solyc09g013140.3	-1,08	1,66E-05	2,11E-04	DUF962 domain-containing protein
Solyc08g079590.3	-1,08	6,35E-05	6,20E-04	PPR containing protein
Solyc12g062690.2	-1,08	6,07E-06	9,49E-05	Unknown protein
Solyc10g017570.3	-1,08	1,56E-03	7,85E-03	NAD(P)-binding Rossmann-fold superfamily protein
Solyc03g096770.1	-1,08	1,28E-03	6,75E-03	Protein RESPONSE TO LOW SULFUR 2
Solyc01g020320.3	-1,08	2,66E-04	1,96E-03	hypothetical protein
Solyc09g090040.3	-1,09	1,66E-05	2,11E-04	Germin-like protein subfamily 1 member 15
Solyc04g009850.4	-1,09	1,06E-03	5,83E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc07g047700.4	-1,09	2,75E-07	7,42E-06	hypothetical protein
Solyc01g103770.3	-1,09	4,22E-05	4,49E-04	Unknown protein
Solyc04g074030.3	-1,09	2,61E-03	1,18E-02	Receptor protein kinase, putative
Solyc02g082850.3	-1,09	3,49E-06	6,15E-05	Serine acetyltransferase 2
Solyc04g011430.3	-1,09	6,48E-06	9,91E-05	Ubiquitin conjugating enzyme
Solyc06g072030.1	-1,09	5,91E-06	9,32E-05	Unknown protein
Solyc08g077480.4	-1,09	8,21E-08	2,79E-06	FCS-Like Zinc finger 2
Solyc03g096780.1	-1,09	2,12E-04	1,64E-03	Protein RESPONSE TO LOW SULFUR 2
Solyc03g033840.4	-1,09	2,10E-03	9,93E-03	AAA-ATPase At3g50940-like
Solyc08g007270.4	-1,09	3,37E-06	5,99E-05	homeobox-leucine zipper protein HAT4-like
Solyc03g031990.4	-1,09	1,68E-06	3,40E-05	Auxin efflux carrier
Solyc03g034050.3	-1,09	1,33E-06	2,81E-05	MIP18 family protein
Solyc07g056430.3	-1,10	1,05E-03	5,80E-03	Glutathione S-transferase
Solyc02g094350.3	-1,10	4,77E-07	1,21E-05	Membrane-anchored ubiquitin-fold protein
Solyc10g006270.4	-1,10	6,20E-06	9,63E-05	Autophagy-related protein
Solyc03g005030.3	-1,10	8,98E-06	1,30E-04	hypothetical protein
Solyc02g150124.1	-1,10	1,68E-06	3,40E-05	Enolase
Solyc01g005450.3	-1,10	1,33E-03	6,95E-03	F-box protein SKIP28
Solyc03g110930.3	-1,10	7,32E-03	2,62E-02	30S ribosomal protein S21, chloroplastic
Solyc01g108790.3	-1,10	8,22E-03	2,87E-02	3-hydroxyisobutyryl-CoA hydrolase 1
Solyc06g076140.4	-1,10	3,04E-06	5,49E-05	Metallothionein-like protein
Solyc04g016040.1	-1,10	1,06E-02	3,51E-02	Unknown protein
Solyc05g016060.4	-1,10	2,51E-05	2,95E-04	cysteine-rich and transmembrane domain-containing protein WIH1
Solyc04g081290.3	-1,10	3,39E-05	3,76E-04	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc01g105350.3	-1,10	5,87E-04	3,66E-03	Glycosyltransferase
Solyc08g013760.1	-1,10	9,85E-07	2,21E-05	F-box family protein
Solyc07g054600.3	-1,11	6,43E-03	2,36E-02	F-box protein
Solyc10g054670.3	-1,11	4,04E-08	1,58E-06	Unknown protein
Solyc04g080000.1	-1,11	5,00E-04	3,21E-03	peroxisomal membrane protein 11A
Solyc07g063410.3	-1,11	3,00E-04	2,14E-03	NAC domain protein
Solyc09g083100.1	-1,11	3,38E-06	6,01E-05	Non-specific serine/threonine protein kinase
Solyc05g009170.3	-1,11	1,39E-03	7,19E-03	Zinc finger protein 8
Solyc01g007770.2	-1,11	4,88E-05	5,03E-04	hypothetical protein
Solyc04g080620.3	-1,11	1,02E-02	3,39E-02	Mannan endo-1,4-beta-mannosidase 1
Solyc10g085880.1	-1,11	4,01E-07	1,04E-05	UDP-glycosyltransferase 73C4
Solyc05g016260.3	-1,11	2,15E-04	1,65E-03	Myosin family protein
Solyc04g081480.3	-1,12	2,72E-06	4,98E-05	Unknown protein
Solyc09g008250.4	-1,12	4,63E-04	3,01E-03	blind-like1
Solyc09g075470.2	-1,12	6,17E-07	1,51E-05	DnaJ-like protein subfamily B member 6
Solyc06g066700.1	-1,12	6,61E-05	6,38E-04	serine-rich protein-like protein
Solyc08g078820.3	-1,12	4,09E-08	1,60E-06	Autophagy-related protein
Solyc04g078290.4	-1,12	1,10E-05	1,53E-04	Cytochrome P450
Solyc01g096510.2	-1,12	1,97E-03	9,51E-03	Sigma factor binding protein 1, chloroplastic
Solyc09g083020.1	-1,12	3,10E-08	1,25E-06	inactive protein RESTRICTED TEV MOVEMENT 1-like
Solyc10g085030.1	-1,12	4,20E-06	7,07E-05	Heme-binding-like protein
Solyc06g084540.3	-1,12	1,25E-06	2,67E-05	Adenine nucleotide alpha hydrolases-like superfamily protein
Solyc05g051710.4	-1,12	6,52E-07	1,59E-05	sorbin/SH3 domain protein
Solyc10g082064.1	-1,12	2,76E-04	2,00E-03	furry
Solyc02g071110.3	-1,12	5,09E-07	1,28E-05	Purine permease
Solyc10g079860.2	-1,13	4,63E-03	1,84E-02	LEQB L.esculentum TomQ'b beta(1,3)glucanase
Solyc07g005090.4	-1,13	1,39E-07	4,23E-06	Glycosyl hydrolase family protein with chitinase insertion domain-containing protein
Solyc02g067520.4	-1,13	1,55E-04	1,27E-03	Unknown protein
Solyc09g059270.3	-1,13	1,18E-08	5,71E-07	ER lumen protein retaining receptor
Solyc04g080500.3	-1,13	4,73E-03	1,87E-02	Protein RADIALIS-like 6
Solyc04g072310.3	-1,13	6,18E-06	9,60E-05	histone-lysine N-methyltransferase SETD1B-A
Solyc01g016410.4	-1,13	3,11E-05	3,52E-04	RING/U-box superfamily protein
Solyc12g038453.1	-1,13	6,69E-05	6,45E-04	Unknown protein
Solyc12g098880.2	-1,13	1,02E-04	9,01E-04	SsrA-binding protein
Solyc04g150172.1	-1,13	8,03E-05	7,47E-04	Protein RADIALIS-like 6
Solyc12g070120.1	-1,13	5,31E-03	2,04E-02	Unknown protein
Solyc04g058150.3	-1,13	4,89E-05	5,03E-04	Metallothionein-like protein
Solyc01g080150.3	-1,13	4,73E-05	4,91E-04	Adenylate isopentenyltransferase
Solyc05g056430.3	-1,13	1,00E-04	8,89E-04	Small auxin up-regulated RNA56
Solyc07g066080.3	-1,13	5,99E-07	1,48E-05	Ubiquitin-conjugating enzyme
Solyc11g044515.1	-1,13	6,62E-06	1,01E-04	Unknown protein
Solyc08g068690.1	-1,14	2,02E-05	2,48E-04	Tyramine n-hydroxycinnamoyl transferase
Solyc02g084380.3	-1,14	7,74E-05	7,25E-04	Translation elongation factor EF1B/ribosomal protein S6 family protein
Solyc05g018050.1	-1,14	1,62E-02	4,87E-02	RING/U-box superfamily protein
Solyc05g015470.1	-1,14	1,04E-06	2,30E-05	Chaperone protein dnaJ-like protein
Solyc04g014220.1	-1,14	1,90E-03	9,24E-03	RING/U-box superfamily protein
Solyc01g088160.4	-1,14	5,05E-04	3,23E-03	cytokinin oxidase2
Solyc05g052940.3	-1,14	3,25E-05	3,64E-04	CASP-like protein
Solyc10g080230.2	-1,14	2,05E-05	2,51E-04	Remorin
Solyc04g011540.4	-1,14	1,13E-07	3,60E-06	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc04g080310.1	-1,14	5,68E-05	5,70E-04	Unknown protein
Solyc10g075070.3	-1,14	1,32E-04	1,11E-03	Non-specific lipid-transfer protein
Solyc07g043150.1	-1,14	1,34E-03	6,98E-03	Glycosyltransferase
Solyc08g082640.2	-1,14	5,94E-06	9,33E-05	Cellulose synthase
Solyc07g043550.3	-1,14	5,92E-03	2,22E-02	UDP-glucose 4-epimerase
Solyc08g065410.3	-1,14	1,17E-02	3,78E-02	Abscisic acid receptor PYL3
Solyc05g010530.3	-1,14	2,47E-04	1,85E-03	Protein kinase family protein
Solyc09g020190.3	-1,14	8,77E-07	2,00E-05	Non-specific phospholipase C1
Solyc02g081560.1	-1,14	8,89E-05	8,12E-04	Methionyl-tRNA synthetase
Solyc03g007870.3	-1,14	1,08E-06	2,37E-05	heavy metal-associated isoprenylated plant protein 3-like
Solyc02g078380.3	-1,14	2,44E-05	2,89E-04	Stem-specific protein TSJT1
Solyc12g009830.2	-1,15	1,07E-05	1,50E-04	RING/U-box superfamily protein
Solyc03g097200.3	-1,15	5,44E-08	2,00E-06	carboxypeptidase
Solyc03g026360.1	-1,15	1,60E-02	4,82E-02	Peptidoglycan-binding LysM domain-containing protein
Solyc06g083060.4	-1,15	1,13E-05	1,55E-04	MIP18 family protein
Solyc02g077760.2	-1,15	5,94E-05	5,89E-04	Unknown protein
Solyc07g065380.4	-1,15	3,66E-06	6,39E-05	zinc transporter EF026083
Solyc11g028080.2	-1,15	1,69E-07	4,96E-06	transmembrane protein
Solyc08g014080.4	-1,15	6,69E-03	2,44E-02	RING/FYVE/PHD zinc finger superfamily protein
Solyc01g091030.3	-1,15	1,16E-07	3,70E-06	Small auxin up-regulated RNA1
Solyc09g009650.3	-1,15	4,43E-05	4,65E-04	Unknown protein
Solyc02g061780.3	-1,15	2,84E-03	1,26E-02	NAC domain
Solyc09g014500.3	-1,15	6,00E-06	9,41E-05	Protein yippee-like
Solyc01g005370.3	-1,16	6,14E-03	2,28E-02	Calcium-dependent protein kinase
Solyc01g098140.4	-1,16	2,92E-05	3,35E-04	Alpha/beta-hydrolases superfamily protein
Solyc05g017955.1	-1,16	5,49E-05	5,53E-04	Unknown protein
Solyc02g091700.3	-1,16	1,16E-03	6,26E-03	Hydroxyproline-rich glycoprotein
Solyc02g077770.3	-1,16	1,73E-04	1,39E-03	F-box domain-containing protein
Solyc01g107250.3	-1,16	3,76E-09	2,19E-07	Leucine-rich repeat receptor-like protein kinase family
Solyc01g104150.4	-1,16	8,64E-03	2,99E-02	Unknown protein
Solyc05g016310.1	-1,16	3,57E-03	1,50E-02	Eukaryotic aspartyl protease family protein
Solyc05g018747.1	-1,17	5,49E-03	2,09E-02	Unknown protein
Solyc12g097000.2	-1,17	2,71E-03	1,21E-02	Disease resistance protein (TIR-NBS-LRR class) family
Solyc10g083290.4	-1,17	5,57E-05	5,60E-04	invertase 6
Solyc07g040890.1	-1,17	2,11E-05	2,56E-04	Alpha/beta-hydrolases superfamily protein

Solyc12g010710.1	-1,17	8,82E-04	5,07E-03	Unknown protein
Solyc07g065990.1	-1,17	7,61E-03	2,70E-02	oleosin S1-2-like
Solyc11g006030.1	-1,17	1,40E-02	4,35E-02	RING-type E3 ubiquitin transferase
Solyc06g150138.1	-1,17	8,08E-08	2,76E-06	Unknown protein
Solyc08g068860.3	-1,17	1,29E-06	2,74E-05	Eukaryotic aspartyl protease family protein
Solyc10g086380.1	-1,17	1,11E-02	3,62E-02	Transcription factor GRAS
Solyc09g055320.1	-1,17	1,27E-02	4,04E-02	Unknown protein
Solyc03g115170.1	-1,17	1,49E-02	4,57E-02	Unknown protein
Solyc05g051800.3	-1,17	1,02E-03	5,67E-03	RING/FYVE/PHD zinc finger superfamily protein
Solyc07g053550.3	-1,17	4,06E-06	6,93E-05	Glutaredoxin-C9
Solyc02g082740.1	-1,18	4,19E-05	4,46E-04	Dirigent protein
Solyc02g032660.3	-1,18	2,69E-07	7,30E-06	Protein DETOXIFICATION
Solyc06g008300.4	-1,18	1,55E-04	1,27E-03	Hcr2-5D
Solyc12g098190.2	-1,18	1,16E-05	1,58E-04	F-box protein
Solyc02g078840.4	-1,18	2,84E-08	1,17E-06	Secretory carrier-associated membrane protein
Solyc01g066290.2	-1,18	5,87E-05	5,84E-04	Unknown protein
Solyc09g014510.3	-1,18	3,61E-04	2,47E-03	Mitochondrial inner membrane protease subunit 2
Solyc12g019740.2	-1,18	1,36E-04	1,14E-03	Thioredoxin-like 1-1, chloroplastic
Solyc06g050810.3	-1,18	2,55E-05	2,98E-04	LURP-one-like protein (DUF567)
Solyc04g150108.1	-1,18	7,44E-07	1,76E-05	Unknown protein
Solyc07g008280.4	-1,18	4,35E-08	1,68E-06	cytochrome P450 family protein
Solyc10g049650.3	-1,18	7,75E-04	4,57E-03	histone deacetylase 6
Solyc06g060760.3	-1,18	8,49E-07	1,95E-05	tonoplast intrinsic protein 2.3
Solyc06g061130.4	-1,18	1,20E-03	6,45E-03	Gag-Pol polyprotein/retrotransposon
Solyc05g008820.4	-1,19	4,29E-04	2,82E-03	Lipid phosphate phosphatase
Solyc04g074950.3	-1,19	2,09E-07	5,84E-06	Dihydrofolate reductase
Solyc03g078370.1	-1,19	2,74E-03	1,22E-02	Receptor-like protein kinase
Solyc12g070157.1	-1,19	1,26E-03	6,69E-03	Unknown protein
Solyc10g007020.1	-1,20	1,02E-02	3,40E-02	Unknown protein
Solyc01g108190.3	-1,20	1,18E-07	3,73E-06	Calmodulin-like protein 1
Solyc11g007650.1	-1,20	5,08E-03	1,97E-02	F-box domain
Solyc04g076950.3	-1,20	2,95E-05	3,37E-04	Protein DETOXIFICATION
Solyc01g006300.3	-1,20	1,26E-07	3,94E-06	LECEVI1A
Solyc03g115650.4	-1,20	2,56E-06	4,78E-05	eukaryotic translation initiation factor 5A-1
Solyc04g051100.3	-1,20	1,28E-03	6,74E-03	Unknown protein
Solyc05g015780.1	-1,20	7,53E-08	2,61E-06	Unknown protein
Solyc06g150128.1	-1,20	6,91E-07	1,66E-05	hypothetical protein
Solyc08g008420.3	-1,20	1,98E-07	5,62E-06	Mitochondrial pyruvate carrier
Solyc09g074570.1	-1,20	2,03E-05	2,49E-04	Glutaredoxin
Solyc02g063510.1	-1,20	7,69E-04	4,54E-03	hypothetical protein
Solyc01g105410.4	-1,20	8,45E-09	4,32E-07	Protein EXORDIUM-like 2
Solyc07g065410.1	-1,20	4,87E-04	3,14E-03	hypothetical protein
Solyc07g006950.3	-1,20	1,94E-06	3,84E-05	Unknown protein
Solyc04g082020.3	-1,21	2,97E-06	5,39E-05	Zinc finger, DNL-type, Mitochondrial import protein TIM15
Solyc02g081690.1	-1,21	3,06E-03	1,33E-02	Glycosyltransferase
Solyc09g011710.4	-1,21	8,95E-06	1,30E-04	Class I heat shock protein
Solyc01g006200.3	-1,21	3,68E-06	6,42E-05	Unknown protein
Solyc09g065390.1	-1,21	3,70E-05	4,02E-04	DUF581 domain-containing protein
Solyc09g090710.3	-1,21	1,33E-07	4,12E-06	Unknown protein
Solyc12g096280.2	-1,21	2,82E-04	2,04E-03	Endonuclease V
Solyc02g071210.3	-1,21	1,74E-07	5,09E-06	Cold-regulated inner membrane protein 2, chloroplastic
Solyc09g074270.3	-1,21	2,32E-03	1,07E-02	Gibberellin receptor
Solyc11g017240.3	-1,21	1,49E-07	4,47E-06	chorismate mutase
Solyc11g045225.1	-1,21	2,31E-06	4,39E-05	Ankyrin repeat-containing protein
Solyc01g058350.1	-1,21	1,23E-02	3,94E-02	Unknown protein
Solyc05g006390.1	-1,21	1,35E-07	4,17E-06	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
Solyc01g090680.3	-1,22	5,51E-09	2,98E-07	Uncharacterized conserved protein (UCP012943)
Solyc04g076010.3	-1,22	7,61E-08	2,62E-06	zinc ion-binding protein
Solyc11g008020.2	-1,22	3,31E-05	3,68E-04	Ras-related protein RABC2a
Solyc08g082190.3	-1,22	3,69E-06	6,42E-05	Unknown protein
Solyc01g073910.4	-1,22	8,73E-05	8,00E-04	Homeobox-leucine zipper protein HOX27
Solyc07g049470.4	-1,22	1,79E-04	1,43E-03	Triacylglycerol lipase-like protein
Solyc01g110150.2	-1,22	3,95E-09	2,26E-07	Prostatic spermine-binding-like protein
Solyc04g015820.1	-1,22	1,14E-02	3,69E-02	Unknown protein
Solyc03g025430.1	-1,22	1,74E-03	8,59E-03	Transmembrane protein
Solyc11g010430.2	-1,22	4,95E-06	8,13E-05	Dihydrofolate reductase-like protein
Solyc04g014883.1	-1,22	1,46E-02	4,49E-02	LRR receptor-like serine/threonine-protein kinase EFR
Solyc09g014900.3	-1,22	1,56E-04	1,28E-03	Cytochrome P450
Solyc01g014250.2	-1,22	2,26E-03	1,06E-02	Unknown protein
Solyc04g074000.3	-1,23	1,75E-04	1,40E-03	Receptor protein kinase, putative
Solyc01g067120.4	-1,23	3,25E-07	8,61E-06	cullin-1-like
Solyc12g008330.3	-1,23	1,10E-05	1,53E-04	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1
Solyc07g065160.4	-1,23	4,13E-09	2,34E-07	Pirin-like protein
Solyc05g006610.4	-1,23	4,86E-03	1,91E-02	CLAVATA3/ESR (CLE)-related protein 25-like
Solyc01g100460.3	-1,23	6,68E-03	2,44E-02	BZIP transcription factor
Solyc10g006840.4	-1,23	4,01E-04	2,69E-03	Unknown protein
Solyc01g066700.4	-1,23	1,41E-02	4,38E-02	UDP-glucuronic acid decarboxylase
Solyc06g065820.3	-1,23	1,08E-02	3,55E-02	Ethylene Response Factor H.1
Solyc08g061250.3	-1,23	1,63E-02	4,91E-02	Receptor-like serine/threonine-protein kinase
Solyc08g079430.3	-1,23	1,86E-06	3,70E-05	partialcopper-containing amine oxidase
Solyc11g006300.2	-1,23	2,07E-06	4,02E-05	3-oxo-5-alpha-steroid 4-dehydrogenase
Solyc01g096340.3	-1,23	3,61E-07	9,44E-06	Small auxin up-regulated RNA2
Solyc09g008335.1	-1,24	7,04E-09	3,68E-07	transmembrane protein
Solyc07g041980.3	-1,24	9,78E-03	3,29E-02	Guanine nucleotide-binding protein subunit gamma 3
Solyc03g082880.1	-1,24	6,51E-03	2,39E-02	Unknown protein
Solyc02g071360.4	-1,24	6,96E-05	6,66E-04	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc07g055660.2	-1,24	1,38E-07	4,22E-06	glycine-rich protein
Solyc01g097150.4	-1,24	5,15E-05	5,25E-04	Unknown protein
Solyc01g087620.3	-1,24	8,99E-08	2,99E-06	Ubiquitin-like protein 5
Solyc12g019540.2	-1,24	8,18E-03	2,86E-02	Unknown protein
Solyc10g085350.2	-1,25	1,02E-03	5,68E-03	macrophage migration inhibitory factor homolog
Solyc05g008390.3	-1,25	2,95E-04	2,11E-03	RING/FYVE/PHD zinc finger superfamily protein
Solyc12g013920.2	-1,25	1,05E-09	7,45E-08	Protein yippee-like
Solyc12g045035.1	-1,25	1,68E-02	5,00E-02	Fatty acid desaturase
Solyc01g010250.4	-1,25	4,14E-09	2,34E-07	6-phosphogluconolactonase
Solyc04g081460.2	-1,25	9,48E-08	3,13E-06	F-box protein
Solyc01g100370.3	-1,25	9,70E-10	7,07E-08	Adenine nucleotide alpha hydrolases-like superfamily protein
Solyc12g056620.2	-1,25	1,60E-07	4,75E-06	Chlorophyll a/b binding protein domain-containing protein
Solyc02g068010.4	-1,25	6,91E-08	2,44E-06	TRAM/LAG1/CLN8-like domain-containing protein
Solyc04g009305.1	-1,25	4,69E-03	1,85E-02	transmembrane protein
Solyc08g007400.4	-1,25	3,06E-07	8,16E-06	autophagy-related protein 8f isoform X2
Solyc11g069570.2	-1,25	1,21E-09	8,32E-08	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc02g093860.3	-1,26	2,46E-08	1,04E-06	Lysine histidine transporter-like 1
Solyc08g066430.1	-1,26	1,97E-04	1,54E-03	Polyketide cyclase/dehydrase and lipid transport superfamily protein
Solyc02g063520.3	-1,26	6,56E-08	2,34E-06	Homeobox-leucine zipper protein HAT22
Solyc12g044940.2	-1,26	8,27E-08	2,79E-06	NAD(P)-binding Rossmann-fold superfamily protein
Solyc10g076540.1	-1,26	2,86E-06	5,21E-05	Wall-associated receptor kinase-like 9
Solyc01g060070.3	-1,26	3,26E-07	8,61E-06	Outer envelope pore protein 16-2, chloroplastic
Solyc12g013830.2	-1,26	7,49E-03	2,67E-02	Unknown protein
Solyc03g111993.1	-1,26	5,40E-04	3,41E-03	Cytochrome P450
Solyc01g014140.3	-1,26	3,04E-05	3,45E-04	receptor-like protein 12
Solyc07g026680.2	-1,26	5,43E-06	8,78E-05	Transcription factor DIVARICATA
Solyc02g065050.1	-1,27	1,81E-05	2,26E-04	aspartic proteinase PCS1-like
Solyc12g042550.2	-1,27	3,23E-03	1,39E-02	Unknown protein
Solyc07g053140.3	-1,27	4,03E-10	3,34E-08	Zinc finger protein/CONSTANS-like protein
Solyc11g066930.1	-1,27	2,28E-04	1,74E-03	DUF868 domain-containing protein
Solyc10g078570.1	-1,27	7,50E-06	1,12E-04	hypothetical protein
Solyc04g010285.1	-1,27	2,76E-09	1,70E-07	Plant protein 1589 of Uncharacterized protein function
Solyc08g076230.1	-1,27	1,35E-03	7,01E-03	GAGA-binding transcriptional activator
Solyc02g094250.4	-1,27	1,72E-03	8,48E-03	Unknown protein
Solyc04g058160.2	-1,27	8,40E-06	1,24E-04	Calcium-dependent protein kinase

Solyc11g045460.3	-1,27	5,77E-10	4,46E-08	Alpha/beta-Hydrolases superfamily protein
Solyc02g076900.4	-1,28	2,21E-04	1,69E-03	Dual specificity phosphatase
Solyc07g008210.4	-1,28	1,15E-04	9,94E-04	Tetratricopeptide repeat (TPR)-like superfamily protein
Solyc05g025870.4	-1,28	4,24E-04	2,80E-03	mast cell carboxypeptidase A
Solyc10g007070.4	-1,28	1,38E-07	4,22E-06	Early nodulin-like protein 1
Solyc07g055710.3	-1,28	3,73E-04	2,54E-03	Heat stress transcription factor A-5
Solyc11g007190.2	-1,28	4,06E-04	2,71E-03	Unknown protein
Solyc12g088250.2	-1,28	1,37E-09	9,18E-08	Serine carboxypeptidase
Solyc05g051460.3	-1,28	2,97E-07	7,96E-06	Homeobox-leucine zipper protein HOX4
Solyc09g074590.1	-1,28	8,84E-03	3,04E-02	Monothiol glutaredoxin-S2
Solyc05g018403.1	-1,28	1,12E-05	1,55E-04	Sigma-B regulation protein RsbQ
Solyc05g052210.3	-1,28	1,50E-04	1,24E-03	transmembrane protein
Solyc09g074040.1	-1,28	3,42E-04	2,37E-03	Unknown protein
Solyc02g088200.4	-1,28	5,64E-05	5,67E-04	Putative eukaryotic LigT
Solyc06g053980.3	-1,28	4,37E-06	7,30E-05	Chlorophyllase 2
Solyc02g062040.3	-1,29	2,26E-08	9,78E-07	RING/U-box superfamily protein
Solyc06g005330.3	-1,29	3,87E-04	2,62E-03	R2R3MYB transcription factor 59
Solyc04g005555.1	-1,29	9,22E-04	5,25E-03	CASP-like protein 4A1 isoform X1
Solyc01g099800.4	-1,29	8,53E-05	7,85E-04	Unknown protein
Solyc08g060920.4	-1,29	1,15E-05	1,57E-04	IDS4-like
Solyc01g010180.3	-1,29	3,17E-07	8,43E-06	Unknown protein
Solyc08g076860.3	-1,29	8,22E-07	1,90E-05	PLATZ transcription factor family protein
Solyc10g080010.2	-1,29	8,84E-03	3,04E-02	Glycosyltransferase family 61 protein
Solyc03g007220.3	-1,29	6,72E-09	3,53E-07	Membrane receptor-like protein 1
Solyc03g115220.4	-1,30	4,52E-06	7,50E-05	Flavonoid 3'-monooxygenase
Solyc04g079660.2	-1,30	1,50E-03	7,59E-03	Cytochrome P450
Solyc09g075820.3	-1,30	1,74E-09	1,12E-07	Sugar transporter protein 2
Solyc02g089660.2	-1,30	7,74E-09	3,99E-07	hypothetical protein
Solyc02g081450.2	-1,30	1,30E-03	6,85E-03	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Solyc08g061270.1	-1,30	5,02E-08	1,89E-06	DUF1677 family protein (DUF1677)
Solyc06g075310.4	-1,30	1,01E-03	5,62E-03	Adenylate kinase isoenzyme 6 homolog
Solyc07g056500.4	-1,30	2,38E-08	1,02E-06	glutathione S-transferase T5
Solyc05g012430.1	-1,30	3,28E-03	1,41E-02	Leucine-rich repeat receptor-like protein kinase PXL1
Solyc08g016580.1	-1,30	3,91E-03	1,61E-02	DUF538 domain-containing protein
Solyc07g006500.3	-1,30	3,34E-04	2,34E-03	trehalose-6-phosphate synthase 1
Solyc06g008100.3	-1,31	5,71E-04	3,58E-03	Unknown protein
Solyc02g031920.4	-1,31	1,78E-03	8,75E-03	pathogen-related protein-like
Solyc04g007800.4	-1,31	5,30E-07	1,32E-05	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc01g102870.3	-1,31	1,51E-02	4,62E-02	receptor-like protein kinase BRI1-like 3
Solyc04g082380.4	-1,31	2,91E-03	1,28E-02	cytochrome P450 86A8-like
Solyc06g050790.3	-1,31	3,72E-05	4,04E-04	Amino acid transporter
Solyc01g087070.4	-1,31	7,07E-03	2,55E-02	ADP,ATP carrier protein, mitochondrial
Solyc09g090070.1	-1,31	5,93E-11	6,24E-09	phosphate transporter 1
Solyc09g056200.3	-1,31	1,68E-04	1,35E-03	Unknown protein
Solyc01g150126.1	-1,31	1,05E-05	1,49E-04	Calcium-binding EF-hand
Solyc03g117610.2	-1,31	5,53E-07	1,37E-05	Unknown protein
Solyc11g069940.1	-1,32	1,17E-04	1,01E-03	Glutaredoxin
Solyc03g043940.4	-1,32	6,64E-03	2,43E-02	Unknown protein
Solyc03g006620.3	-1,32	1,08E-09	7,62E-08	Cotton fiber (DUF761)
Solyc05g008130.4	-1,32	1,34E-04	1,12E-03	Unknown protein
Solyc05g026500.1	-1,32	6,59E-03	2,41E-02	Unknown protein
Solyc06g009050.3	-1,32	1,81E-07	5,23E-06	Adenine nucleotide alpha hydrolases-like superfamily protein
Solyc10g085130.2	-1,32	3,10E-04	2,19E-03	RING/U-box superfamily protein
Solyc11g072470.3	-1,32	2,67E-03	1,20E-02	LOB domain-containing protein
Solyc02g092650.3	-1,32	3,95E-06	6,80E-05	Unknown protein
Solyc07g064650.3	-1,32	4,94E-03	1,93E-02	Senescence regulator S40
Solyc12g089130.2	-1,33	1,82E-03	8,90E-03	Sec14p-like phosphatidylinositol transfer family protein
Solyc08g016210.3	-1,33	2,41E-03	1,11E-02	LOW QUALITY PROTEIN: LRR receptor-like serine/threonine-protein kinase GSO1
Solyc12g088840.1	-1,33	2,63E-05	3,07E-04	EF-hand domain
Solyc04g054760.3	-1,33	1,15E-10	1,11E-08	FCS-Like Zinc finger 5
Solyc01g005420.2	-1,33	2,51E-08	1,05E-06	C2 calcium-dependent membrane targeting
Solyc11g020670.1	-1,33	2,96E-06	5,38E-05	TCP transcription factor 12
Solyc01g100230.3	-1,34	7,42E-10	5,56E-08	DnaJ-like protein subfamily B member 6
Solyc05g051425.2	-1,34	2,81E-08	1,16E-06	Dihydrofolate reductase-like protein
Solyc08g007980.3	-1,34	8,33E-03	2,90E-02	LURP-one-like protein
Solyc07g063160.2	-1,34	7,02E-06	1,06E-04	Cytochrome c oxidase copper chaperone
Solyc08g061130.3	-1,34	5,89E-06	9,31E-05	Transcription factor HY5
Solyc02g150126.1	-1,35	3,88E-03	1,60E-02	Unknown protein
Solyc05g007770.3	-1,35	1,54E-06	3,18E-05	NAC domain TF
Solyc06g048750.3	-1,35	8,39E-04	4,86E-03	Unknown protein
Solyc12g044930.3	-1,35	4,20E-06	7,08E-05	F-box protein
Solyc04g006950.4	-1,35	2,28E-03	1,06E-02	Unknown protein
Solyc01g011105.1	-1,35	1,75E-04	1,40E-03	CLAVATA3/ESR (CLE)-related protein 25-like
Solyc01g009860.3	-1,35	1,58E-06	3,25E-05	NAC domain-containing protein
Solyc04g078340.3	-1,35	2,35E-04	1,78E-03	Cytochrome P450
Solyc04g007980.3	-1,36	1,09E-05	1,53E-04	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc03g119600.1	-1,36	3,65E-09	2,14E-07	NIMIN2b protein
Solyc04g011880.1	-1,36	1,60E-02	4,84E-02	Monothiol glutaredoxin-S1
Solyc04g077170.3	-1,36	1,44E-06	2,99E-05	Epidermal patterning factor-like protein
Solyc11g010330.3	-1,36	7,15E-08	2,51E-06	RING/U-box superfamily protein
Solyc07g055400.2	-1,36	1,58E-02	4,76E-02	Lectin-domain receptor-like kinase
Solyc04g007900.3	-1,36	6,38E-11	6,68E-09	protein PLANT CADMIUM RESISTANCE 2-like
Solyc07g006480.4	-1,36	4,94E-06	8,11E-05	Receptor-like kinase
Solyc07g006090.3	-1,37	1,21E-02	3,87E-02	Glutamine amidotransferase
Solyc02g032100.4	-1,37	4,01E-06	6,86E-05	Zinc transporter protein
Solyc01g111230.3	-1,37	7,07E-03	2,55E-02	Dirigent protein
Solyc02g022850.1	-1,37	6,72E-04	4,10E-03	FAD-binding Berberine family protein
Solyc02g063020.3	-1,37	9,93E-05	8,81E-04	Major facilitator superfamily protein
Solyc10g086250.2	-1,37	2,43E-04	1,82E-03	R2R3MYB transcription factor 75
Solyc07g049530.3	-1,37	2,17E-05	2,63E-04	1-aminocyclopropane-1-carboxylate oxidase 1
Solyc07g063560.4	-1,37	7,70E-03	2,72E-02	Cotton fiber (DUF761)
Solyc01g106400.3	-1,37	1,30E-08	6,20E-07	Peptide-methionine (R)-S-oxide reductase
Solyc08g005120.3	-1,38	2,84E-03	1,26E-02	NAD(P)-binding Rossmann-fold superfamily protein
Solyc01g106890.2	-1,38	6,74E-07	1,63E-05	hypothetical protein
Solyc10g084400.2	-1,39	1,85E-10	1,69E-08	Glutathione S-transferase
Solyc07g006590.1	-1,39	7,87E-09	4,05E-07	hypothetical protein
Solyc07g008540.3	-1,39	7,54E-07	1,77E-05	Zinc finger protein CONSTANS-LIKE 2
Solyc02g089780.3	-1,39	7,33E-04	4,38E-03	dihydroflavonol 4-reductase/flavanone protein
Solyc06g066840.3	-1,39	1,99E-03	9,56E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc03g121010.4	-1,39	1,18E-05	1,59E-04	Unknown protein
Solyc02g150128.1	-1,39	2,87E-05	3,30E-04	Lrr receptor-like serinethreonine-protein kinase fls2
Solyc03g116910.3	-1,39	2,78E-09	1,71E-07	cinnamoyl-CoA reductase 2
Solyc08g042120.1	-1,40	6,00E-03	2,24E-02	PX domain-containing protein EREL1 isoform X3
Solyc08g077760.3	-1,40	1,37E-04	1,14E-03	Unknown protein
Solyc03g044810.2	-1,40	4,81E-03	1,89E-02	Methyl jasmonate esterase
Solyc11g070160.2	-1,40	3,89E-08	1,53E-06	SAWADEE HOMEODOMAIN protein
Solyc06g059870.1	-1,40	1,86E-08	8,36E-07	Unknown protein
Solyc01g109090.2	-1,40	4,25E-05	4,50E-04	Unknown protein
Solyc03g112210.1	-1,40	9,28E-08	3,08E-06	Unknown protein
Solyc06g036130.4	-1,40	1,16E-06	2,51E-05	Protein DETOXIFICATION
Solyc10g006150.3	-1,41	1,72E-05	2,17E-04	DUF761 domain-containing protein/DUF4408 domain-containing protein
Solyc06g010010.3	-1,41	1,27E-02	4,04E-02	MLO-like protein
Solyc06g005320.1	-1,41	7,11E-03	2,56E-02	Transcription factor MYB48
Solyc08g074960.3	-1,41	3,07E-07	8,18E-06	Major facilitator superfamily protein
Solyc02g062580.3	-1,41	4,28E-09	2,38E-07	Lipid phosphate phosphatase epsilon 2, chloroplastic
Solyc09g005840.2	-1,41	2,43E-03	1,11E-02	Exocyst subunit Exo70 family protein
Solyc08g016220.1	-1,41	2,00E-03	9,59E-03	Receptor like protein
Solyc04g009860.4	-1,41	3,89E-07	1,01E-05	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc08g078790.1	-1,42	9,41E-05	8,46E-04	hypothetical protein
Solyc04g005620.3	-1,42	4,10E-03	1,67E-02	Casparian strip membrane protein 1
Solyc06g005410.3	-1,42	4,38E-03	1,76E-02	Unknown protein

Solyc05g054750.3	-1,42	8,78E-04	5,06E-03	Plant protein 1589 of Uncharacterized protein function
Solyc01g099590.4	-1,43	1,03E-09	7,35E-08	glutathione-S-transferase
Solyc10g085140.2	-1,43	4,95E-07	1,25E-05	Alkyl transferase
Solyc03g033490.3	-1,43	7,91E-03	2,78E-02	Thaumatin-like protein
Solyc05g014280.4	-1,43	4,85E-05	5,00E-04	small heat shock protein 1
Solyc11g070150.2	-1,43	4,12E-05	4,39E-04	Histidine-containing phosphotransfer protein 4
Solyc04g011750.3	-1,44	1,43E-02	4,41E-02	histone H3.v1
Solyc07g056440.3	-1,44	5,64E-08	2,06E-06	Glutathione S-transferase
Solyc07g041000.4	-1,44	7,52E-03	2,67E-02	Cleavage and polyadenylation specificity factor subunit 5-like protein
Solyc10g080670.2	-1,44	9,27E-07	2,10E-05	Transmembrane protein, putative
Solyc02g050330.1	-1,45	1,34E-03	6,98E-03	Unknown protein
Solyc01g096330.2	-1,45	3,02E-04	2,15E-03	Unknown protein
Solyc01g066270.3	-1,45	1,50E-03	7,61E-03	Unknown protein
Solyc11g072620.1	-1,45	2,20E-04	1,68E-03	Unknown protein
Solyc04g007630.2	-1,45	8,71E-03	3,00E-02	Heavy metal-associated isoprenylated plant protein
Solyc08g066350.2	-1,45	3,13E-04	2,21E-03	Histidine-containing phosphotransfer protein 4
Solyc06g050500.2	-1,45	2,43E-05	2,88E-04	abscisic acid receptor PYL4-like
Solyc01g094140.3	-1,46	9,54E-05	8,56E-04	Cytochrome P450
Solyc02g150135.1	-1,46	4,99E-03	1,95E-02	Unknown protein
Solyc08g082370.1	-1,46	1,65E-07	4,88E-06	Unknown protein
Solyc07g056280.3	-1,46	2,66E-05	3,09E-04	WRKY transcription factor 30
Solyc01g150164.1	-1,46	2,28E-12	3,78E-10	thionin-like protein
Solyc12g099790.3	-1,46	4,40E-04	2,89E-03	Calcium-dependent protein kinase
Solyc03g122000.4	-1,46	5,95E-03	2,23E-02	Cytochrome b6-f complex subunit 4
Solyc04g007990.1	-1,46	1,50E-12	2,64E-10	hypothetical protein
Solyc06g008760.1	-1,46	4,18E-06	7,06E-05	Glutaredoxin
Solyc12g099550.1	-1,46	2,41E-07	6,66E-06	F-box domain-containing protein
Solyc11g011990.2	-1,46	1,35E-06	2,84E-05	plastid terminal oxidase
Solyc08g005320.3	-1,47	3,87E-03	1,60E-02	Histidinol-phosphate aminotransferase, chloroplastic
Solyc01g090840.3	-1,47	1,39E-04	1,16E-03	Zinc finger protein
Solyc10g055200.1	-1,47	9,25E-08	3,07E-06	Dirigent protein
Solyc09g064750.2	-1,47	7,49E-05	7,07E-04	Unknown protein
Solyc10g083690.3	-1,48	2,08E-04	1,61E-03	Cytochrome P450
Solyc12g087870.2	-1,48	2,09E-04	1,62E-03	purine permease 3-like
Solyc02g093700.3	-1,48	5,40E-05	5,45E-04	Cystinosin-like protein
Solyc09g005200.3	-1,48	1,75E-07	5,11E-06	transmembrane protein
Solyc12g089190.1	-1,48	3,20E-03	1,38E-02	Protein RADIALIS-like 6
Solyc12g010140.2	-1,48	2,77E-04	2,01E-03	Unknown protein
Solyc10g006950.1	-1,49	2,29E-04	1,74E-03	Unknown protein
Solyc03g113540.3	-1,49	2,89E-04	2,08E-03	Dynein light chain
Solyc10g078440.2	-1,49	1,44E-08	6,78E-07	Sigma factor binding protein 1, chloroplastic
Solyc04g014990.3	-1,49	1,58E-02	4,77E-02	Glycosyltransferase
Solyc02g080040.4	-1,49	9,93E-05	8,81E-04	Cysteine-rich receptor-like protein kinase 29
Solyc03g082640.3	-1,49	7,90E-03	2,78E-02	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc01g091840.4	-1,49	2,54E-05	2,97E-04	UDP-galactose/UDP-glucose transporter 2
Solyc12g096570.1	-1,50	2,90E-10	2,50E-08	auxin-regulated gene involved in organ size
Solyc06g072070.2	-1,50	8,29E-04	4,81E-03	Transmembrane protein, putative (DUF 3339)
Solyc04g077230.1	-1,50	1,25E-09	8,60E-08	Unknown protein
Solyc07g008440.3	-1,51	2,55E-12	4,19E-10	Purine permease
Solyc04g079600.3	-1,51	3,21E-05	3,62E-04	Homeodomain-like superfamily protein
Solyc02g032170.4	-1,51	2,53E-03	1,15E-02	Unknown protein
Solyc06g075530.1	-1,51	1,15E-03	6,22E-03	Unknown protein
Solyc08g029360.4	-1,51	1,26E-02	4,01E-02	Unknown protein
Solyc03g112300.3	-1,51	9,43E-07	2,13E-05	Octicosapeptide/phox/Bem1p domain kinase superfamily protein
Solyc04g081960.1	-1,52	1,04E-02	3,45E-02	Syringolide-induced protein 14-1-1
Solyc03g044630.2	-1,52	7,82E-04	4,61E-03	DUF309 domain protein
Solyc03g123510.3	-1,52	2,75E-03	1,22E-02	GDSL esterase/lipase 5-like
Solyc02g069390.2	-1,52	8,95E-03	3,06E-02	Myb-like domain-containing protein
Solyc08g023660.3	-1,52	6,86E-06	1,04E-04	Kirola
Solyc06g062330.3	-1,53	3,19E-03	1,37E-02	Glycosyltransferase
Solyc07g054060.3	-1,53	2,71E-13	5,77E-11	hypothetical protein
Solyc06g084170.3	-1,53	1,45E-04	1,20E-03	Unknown protein
Solyc10g018120.2	-1,54	8,93E-07	2,03E-05	Neuronal PAS domain protein
Solyc04g014790.1	-1,54	1,56E-06	3,21E-05	Cysteine proteinase inhibitor
Solyc09g011650.4	-1,54	1,61E-05	2,06E-04	Glutathione S-transferase
Solyc02g090440.3	-1,54	6,59E-04	4,04E-03	Unknown protein
Solyc03g078490.4	-1,54	7,20E-06	1,08E-04	Glycosyltransferase
Solyc04g009190.3	-1,54	6,99E-05	6,68E-04	UPF0664 stress-induced protein C29B12.11c
Solyc02g065240.3	-1,55	8,97E-15	3,00E-12	Methyl esterase 1
Solyc08g062870.1	-1,55	2,94E-03	1,29E-02	Unknown protein
Solyc08g042040.4	-1,55	2,82E-03	1,25E-02	Kinesin-like protein
Solyc02g077040.4	-1,55	7,75E-08	2,65E-06	phytophthora-inhibited protease 1
Solyc04g064530.1	-1,56	3,03E-11	3,46E-09	polyadenylate-binding protein 1-B-binding protein
Solyc11g070060.2	-1,56	7,34E-06	1,10E-04	hypothetical protein
Solyc09g007860.4	-1,56	1,26E-02	4,00E-02	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc04g072603.1	-1,56	1,35E-02	4,22E-02	Unknown protein
Solyc12g008800.3	-1,56	2,66E-04	1,96E-03	Transcription factor DIVARICATA
Solyc03g119310.3	-1,56	3,12E-09	1,90E-07	Unknown protein
Solyc03g118450.1	-1,56	2,63E-03	1,18E-02	Unknown protein
Solyc09g091810.1	-1,56	5,02E-05	5,14E-04	Unknown protein
Solyc03g006590.3	-1,56	4,16E-03	1,69E-02	multidrug resistance protein
Solyc05g041920.3	-1,56	1,57E-04	1,28E-03	Dicer-like 3
Solyc05g054820.1	-1,57	1,13E-05	1,56E-04	Exocyst subunit Exo70 family protein
Solyc06g034320.1	-1,57	3,66E-04	2,50E-03	transmembrane protein
Solyc05g010040.2	-1,57	2,58E-10	2,25E-08	Unknown protein
Solyc08g068710.1	-1,57	1,30E-02	4,11E-02	Tyramine n-hydroxycinnamoyl transferase
Solyc03g113690.1	-1,57	1,52E-02	4,64E-02	ABC transporter G family member 23
Solyc04g079230.4	-1,57	1,40E-14	4,30E-12	Patatin
Solyc07g008650.4	-1,58	3,75E-04	2,55E-03	tRNA-specific adenosine deaminase
Solyc09g011490.3	-1,58	2,25E-10	2,02E-08	Glutathione S-transferase
Solyc03g005330.1	-1,58	1,48E-02	4,55E-02	Non-specific serine/threonine protein kinase
Solyc01g081270.2	-1,58	3,01E-04	2,14E-03	Glutathione S-transferase
Solyc03g114480.4	-1,58	2,53E-06	4,74E-05	Tetraspanin
Solyc09g011590.4	-1,58	1,79E-07	5,20E-06	Glutathione S-transferase-like protein
Solyc10g007510.2	-1,59	2,72E-04	1,98E-03	Carbohydrate-binding X8 domain superfamily protein
Solyc12g056920.3	-1,59	1,08E-02	3,54E-02	Sulfate transporter-like protein
Solyc05g053330.3	-1,59	1,66E-04	1,34E-03	Transcription factor
Solyc02g089960.3	-1,59	3,40E-05	3,77E-04	transmembrane family 220 helix protein
Solyc09g008750.1	-1,59	1,70E-05	2,15E-04	VQ motif-containing protein 29
Solyc10g080240.1	-1,59	1,89E-06	3,75E-05	Remorin
Solyc10g080570.2	-1,60	2,25E-03	1,05E-02	E3 ubiquitin-protein ligase
Solyc02g079710.4	-1,60	5,72E-03	2,16E-02	S receptor kinase
Solyc10g078590.2	-1,60	5,15E-10	4,07E-08	Jacalin-related lectin 3
Solyc05g012820.2	-1,60	4,35E-05	4,58E-04	transmembrane protein
Solyc04g011770.2	-1,60	9,24E-05	8,36E-04	Unknown protein
Solyc10g084230.2	-1,60	2,90E-09	1,78E-07	hypothetical protein (DUF1685)
Solyc05g012550.4	-1,60	1,17E-02	3,79E-02	remorin isoform X2
Solyc01g101260.2	-1,60	7,68E-07	1,80E-05	hypothetical protein
Solyc11g005860.2	-1,61	9,69E-03	3,26E-02	Aminotransferase
Solyc03g031600.3	-1,61	6,16E-06	9,58E-05	Peroxisomal membrane protein PMP22
Solyc06g071180.3	-1,61	1,32E-05	1,74E-04	Dynein light chain
Solyc05g056440.3	-1,61	1,68E-06	3,40E-05	Small auxin up-regulated RNA57
Solyc02g071470.4	-1,62	4,63E-07	1,18E-05	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc01g089880.3	-1,62	6,48E-09	3,42E-07	PRA1 family protein
Solyc03g120110.3	-1,63	1,04E-02	3,46E-02	Lectin protein kinase family protein
Solyc03g095650.3	-1,63	1,09E-09	7,64E-08	MLO-like protein
Solyc02g071970.1	-1,63	3,10E-08	1,25E-06	N66 matrix protein
Solyc03g095940.1	-1,63	1,22E-12	2,17E-10	LOB domain-containing protein 21
Solyc06g005300.4	-1,63	2,31E-05	2,78E-04	UPA23
Solyc05g043405.1	-1,63	4,97E-04	3,19E-03	Unknown protein
Solyc06g035520.3	-1,63	1,09E-03	5,95E-03	Alpha/beta-hydrolases superfamily protein

Solyc01g067020.4	-1,64	2,37E-11	2,81E-09	Atypical receptor-like kinase 1
Solyc08g080770.3	-1,64	3,26E-03	1,40E-02	LURP-one-like protein
Solyc02g082737.1	-1,64	4,29E-03	1,73E-02	Unknown protein
Solyc04g010250.3	-1,64	4,28E-10	3,48E-08	Alpha/beta-Hydrolases superfamily protein
Solyc07g005420.2	-1,64	1,50E-08	6,96E-07	Unknown protein
Solyc04g079910.4	-1,65	5,20E-04	3,30E-03	Calcium uniporter protein 4, mitochondrial
Solyc04g040180.3	-1,65	3,63E-08	1,44E-06	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
Solyc06g053260.1	-1,65	1,30E-15	4,86E-13	Auxin-responsive protein SAUR32
Solyc05g006750.3	-1,65	1,93E-09	1,23E-07	Glutathione S-transferase
Solyc02g082900.3	-1,66	1,79E-07	5,20E-06	Protein STRICTOSIDINE SYNTHASE-LIKE 6
Solyc11g007140.2	-1,66	2,36E-04	1,78E-03	Major facilitator superfamily
Solyc03g115465.1	-1,66	4,64E-03	1,84E-02	RING/U-box superfamily protein
Solyc01g081170.3	-1,66	2,78E-04	2,02E-03	Beta-glucosidase 10
Solyc05g007895.1	-1,66	9,18E-13	1,72E-10	RING/U-box superfamily protein
Solyc07g043250.1	-1,66	5,83E-07	1,44E-05	VQ motif-containing protein 22
Solyc06g071830.2	-1,66	7,18E-04	4,32E-03	BTB/POZ and TAZ domain-containing protein 2
Solyc08g067610.3	-1,67	6,96E-05	6,66E-04	Pleiotropic drug resistance protein
Solyc12g017960.1	-1,67	2,33E-16	1,17E-13	hypothetical protein
Solyc09g061715.1	-1,67	3,79E-03	1,57E-02	hypothetical protein
Solyc05g008220.4	-1,67	1,41E-03	7,25E-03	Plastid movement impaired protein
Solyc02g079990.3	-1,67	4,38E-03	1,76E-02	Cysteine-rich receptor-like protein kinase 10
Solyc11g072830.1	-1,67	2,99E-06	5,43E-05	Chitinase
Solyc07g054620.4	-1,67	2,20E-03	1,03E-02	F-box domain
Solyc11g006230.3	-1,67	5,85E-09	3,14E-07	GRF1-interacting factor 1
Solyc04g072607.1	-1,68	1,17E-06	2,53E-05	Unknown protein
Solyc04g079210.3	-1,69	4,96E-12	7,25E-10	Patatin
Solyc01g105660.4	-1,69	1,43E-03	7,35E-03	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc02g090460.2	-1,70	2,81E-12	4,54E-10	Unknown protein
Solyc02g076920.3	-1,70	5,18E-03	2,00E-02	bHLH transcription factor 013
Solyc03g078240.3	-1,70	4,03E-04	2,70E-03	Glycosyltransferase
Solyc01g106830.4	-1,70	6,90E-05	6,61E-04	Phytosulfokine
Solyc02g032410.3	-1,70	1,43E-02	4,42E-02	Unknown protein
Solyc09g089650.1	-1,71	6,08E-15	2,11E-12	hypothetical protein
Solyc05g050130.4	-1,71	3,86E-09	2,23E-07	Acidic endochitinase
Solyc01g150176.1	-1,72	1,13E-06	2,46E-05	Gibberellin regulated protein
Solyc01g096420.3	-1,72	3,99E-06	6,83E-05	NADPH quinone oxidoreductase
Solyc12g009050.3	-1,72	3,40E-04	2,36E-03	Nuclear transcription factor Y subunit A-6
Solyc09g092640.3	-1,72	1,82E-10	1,68E-08	Cytochrome
Solyc04g082830.3	-1,72	1,83E-07	5,25E-06	Auxin efflux carrier
Solyc08g063035.1	-1,73	3,56E-04	2,45E-03	DDT domain-containing protein DDB_G0282237
Solyc03g116990.1	-1,74	6,33E-07	1,55E-05	Protein transport protein Sec61 subunit beta
Solyc05g009650.4	-1,74	4,66E-09	2,57E-07	Unknown protein
Solyc01g086670.3	-1,74	2,32E-03	1,07E-02	Unknown protein
Solyc09g091600.4	-1,74	6,81E-14	1,72E-11	Protein SULFUR DEFICIENCY-INDUCED 1
Solyc09g007790.1	-1,75	7,05E-05	6,72E-04	Senescence regulator
Solyc11g069770.2	-1,76	1,34E-04	1,12E-03	Agamous-like MADS-box protein AGL62
Solyc05g006855.1	-1,76	7,84E-04	4,61E-03	Thioredoxin
Solyc08g023645.1	-1,76	1,46E-07	4,40E-06	Unknown protein
Solyc12g056590.2	-1,76	6,26E-03	2,32E-02	Ethylene Response Factor D.2
Solyc04g007010.3	-1,77	2,12E-06	4,09E-05	Sn-2 protein
Solyc11g066270.3	-1,77	9,84E-10	7,14E-08	xyloglucan endotransglucosylase-hydrolase 6
Solyc07g039343.1	-1,77	2,88E-04	2,07E-03	Gag/pol polyprotein
Solyc09g009810.1	-1,77	1,95E-03	9,40E-03	hypothetical protein
Solyc07g052440.3	-1,77	2,00E-03	9,61E-03	transmembrane protein 97-like
Solyc10g085010.3	-1,78	2,97E-10	2,56E-08	PAR1-like protein
Solyc02g070020.1	-1,78	4,40E-04	2,89E-03	UDP-Glycosyltransferase superfamily protein
Solyc03g115930.3	-1,78	8,07E-05	7,49E-04	Calcium-binding EF-hand family protein
Solyc01g111640.3	-1,78	6,35E-10	4,85E-08	SKP1-like protein
Solyc03g121550.3	-1,78	8,59E-04	4,96E-03	Unknown protein
Solyc01g091000.4	-1,79	8,98E-03	3,07E-02	PLATZ transcription factor family protein
Solyc03g007150.3	-1,80	1,38E-06	2,87E-05	AT-hook motif nuclear-localized protein 1
Solyc07g043230.3	-1,80	2,27E-15	8,34E-13	Zinc transporter protein
Solyc06g053550.3	-1,80	2,96E-03	1,29E-02	Peroxisomal membrane protein PMP22
Solyc04g005610.3	-1,80	1,29E-09	8,84E-08	NAC domain-containing protein 2
Solyc02g086120.2	-1,80	8,57E-03	2,97E-02	Unknown protein
Solyc07g008020.3	-1,80	1,47E-16	8,32E-14	auxin-regulated 35
Solyc08g016415.1	-1,81	6,88E-03	2,49E-02	hypothetical protein
Solyc12g098130.1	-1,81	1,18E-02	3,82E-02	glycine-rich protein 5-like
Solyc09g011550.3	-1,81	8,68E-07	1,99E-05	Glutathione S-transferase
Solyc08g068870.3	-1,81	1,84E-10	1,69E-08	Eukaryotic aspartyl protease family protein, expressed
Solyc03g043700.3	-1,81	4,76E-03	1,88E-02	U-box domain-containing protein 4-like
Solyc12g056360.1	-1,81	1,15E-09	7,99E-08	Pathogenesis-related thaumatin family protein
Solyc06g069430.3	-1,82	1,53E-13	3,45E-11	FRUITFULL-like MADS-box 1
Solyc09g082820.3	-1,82	1,16E-12	2,10E-10	Unknown protein
Solyc04g072000.4	-1,82	2,00E-05	2,46E-04	Chitinase
Solyc05g015480.3	-1,82	1,89E-03	9,17E-03	molybdenum cofactor sulfurase-like
Solyc05g010030.4	-1,82	8,28E-10	6,13E-08	Unknown protein
Solyc08g062810.1	-1,83	5,20E-03	2,00E-02	DUF3511 domain-containing protein
Solyc01g108440.2	-1,83	8,02E-04	4,69E-03	Herbivore elicitor-regulated 1
Solyc01g086680.4	-1,84	1,14E-04	9,86E-04	glutathione S-transferase T1
Solyc11g056620.3	-1,85	7,32E-13	1,38E-10	hypothetical protein
Solyc06g005795.2	-1,85	2,91E-04	2,09E-03	Non-specific lipid-transfer protein
Solyc07g063420.3	-1,87	1,43E-08	6,74E-07	NAC domain-containing protein
Solyc09g074280.1	-1,87	6,53E-07	1,59E-05	Ankyrin repeat-containing protein
Solyc01g098520.3	-1,87	1,70E-03	8,42E-03	MUTL protein homolog 3
Solyc07g056640.1	-1,88	7,82E-06	1,16E-04	Unknown protein
Solyc10g084070.1	-1,88	1,96E-04	1,54E-03	Unknown protein
Solyc12g011320.2	-1,88	1,05E-05	1,48E-04	Glutathione S-transferase
Solyc07g066330.3	-1,89	1,50E-13	3,43E-11	NAC domain-containing protein
Solyc12g040800.2	-1,89	2,29E-07	6,32E-06	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc03g020010.1	-1,89	1,32E-03	6,92E-03	Lemir
Solyc12g005610.3	-1,89	4,03E-05	4,31E-04	Leucine-rich receptor-like kinase family protein
Solyc07g052250.4	-1,89	2,97E-04	2,12E-03	Unknown protein
Solyc06g035530.3	-1,89	1,14E-03	6,18E-03	gibberellin 20-oxidase-2
Solyc03g019700.1	-1,89	9,63E-13	1,79E-10	Transmembrane protein, putative (DUF 3339)
Solyc10g055230.1	-1,90	6,72E-03	2,45E-02	Dirigent protein
Solyc05g005280.4	-1,90	9,79E-12	1,30E-09	Poly [ADP-ribose] polymerase
Solyc06g051160.4	-1,90	1,46E-05	1,90E-04	DnaJ/Hsp40 cysteine-rich domain superfamily protein
Solyc02g070430.3	-1,90	6,78E-06	1,03E-04	Gibberellin 2-oxidase 1
Solyc07g056210.4	-1,91	3,19E-04	2,25E-03	Heavy metal-associated isoprenylated plant protein 47
Solyc05g012850.3	-1,91	8,65E-06	1,27E-04	transmembrane protein
Solyc12g056890.1	-1,92	6,34E-03	2,34E-02	DnaJ domain-containing protein/RRM_6 domain-containing protein
Solyc02g063440.3	-1,92	4,23E-10	3,46E-08	Unknown protein
Solyc08g075550.4	-1,92	4,57E-06	7,56E-05	alternative oxidase 1b
Solyc03g112100.3	-1,92	7,97E-06	1,18E-04	High-affinity nitrate transporter 3.2
Solyc06g005820.3	-1,92	7,14E-03	2,57E-02	Copper transporter 6
Solyc09g074475.1	-1,93	3,98E-03	1,63E-02	Unknown protein
Solyc07g066560.1	-1,93	2,37E-10	2,11E-08	Small auxin up-regulated RNA65
Solyc11g066800.2	-1,94	3,50E-10	2,95E-08	GABA transporter 1
Solyc07g055670.1	-1,94	6,92E-03	2,50E-02	Lectin-domain receptor-like kinase
Solyc04g079250.3	-1,95	5,02E-06	8,21E-05	Patatin
Solyc11g006290.2	-1,95	3,27E-14	9,13E-12	3-oxo-5-alpha-steroid 4-dehydrogenase
Solyc06g011350.3	-1,95	3,34E-11	3,73E-09	plasma membrane intrinsic protein 2.4
Solyc09g059400.4	-1,95	1,32E-05	1,74E-04	Unknown protein
Solyc03g112090.3	-1,95	1,73E-05	2,18E-04	High-affinity nitrate transporter
Solyc07g008205.1	-1,97	1,17E-08	5,67E-07	EPIDERMAL PATTERNING FACTOR-like protein 8
Solyc07g041925.1	-1,97	6,95E-06	1,05E-04	Unknown protein
Solyc02g031950.3	-1,97	2,50E-03	1,14E-02	pathogenesis-related family protein
Solyc01g073820.4	-1,98	4,66E-03	1,85E-02	Cysteine/Histidine-rich C1 domain family protein
Solyc03g113940.4	-1,98	1,51E-02	4,61E-02	Calmodulin binding protein-like
Solyc04g025530.3	-1,98	2,17E-03	1,02E-02	Glutamate decarboxylase

Solyc12g042480.3	-1,98	4,27E-11	4,65E-09	Cytochrome
Solyc12g005730.2	-1,98	7,69E-04	4,54E-03	DUF604 domain-containing protein
Solyc06g005310.3	-1,98	7,97E-07	1,85E-05	Transcription factor MYB48
Solyc01g066260.2	-1,98	4,59E-09	2,54E-07	Unknown protein
Solyc02g031990.1	-1,98	1,11E-05	1,54E-04	VQ motif-containing protein 22
Solyc11g069220.2	-1,99	1,17E-03	6,30E-03	MLO-like protein
Solyc04g077650.3	-1,99	6,12E-09	3,27E-07	Serine carboxypeptidase-like 17
Solyc09g063150.3	-1,99	2,44E-04	1,83E-03	Glutathione S-transferase
Solyc03g058433.1	-1,99	3,21E-03	1,38E-02	Unknown protein
Solyc05g009090.3	-1,99	7,22E-09	3,76E-07	Receptor-like protein kinase
Solyc08g005950.2	-1,99	9,75E-04	5,48E-03	guanine nucleotide-binding protein subunit gamma 2-like
Solyc04g080540.2	-1,99	4,54E-13	8,96E-11	DNA polymerase epsilon catalytic subunit A
Solyc12g005720.1	-1,99	3,81E-04	2,59E-03	Cysteine-rich receptor-like protein kinase
Solyc11g017280.2	-2,00	1,22E-07	3,83E-06	leucine-rich repeat receptor-like tyrosine-protein kinase PXC3
Solyc08g081700.1	-2,01	2,58E-13	5,55E-11	late embryogenesis abundant protein At1g64065-like
Solyc05g007950.4	-2,01	1,14E-05	1,57E-04	LERNALE L.esculentum ribonuclease le
Solyc09g090980.3	-2,02	5,11E-15	1,84E-12	pathogenesis-related protein STH-2-like
Solyc10g018150.2	-2,02	6,13E-04	3,80E-03	Cytochrome P450
Solyc09g042670.4	-2,02	9,04E-05	8,22E-04	Unknown protein
Solyc08g059700.2	-2,03	3,20E-04	2,25E-03	histone acetyltransferase
Solyc07g007770.2	-2,04	5,08E-03	1,97E-02	Unknown protein
Solyc07g066160.1	-2,04	3,79E-03	1,57E-02	Zinc finger, C2H2-like protein
Solyc09g014860.3	-2,04	1,27E-15	4,86E-13	Protein LURP-one-related 15
Solyc10g051120.3	-2,05	1,97E-08	8,76E-07	Mitochondrial pyruvate carrier
Solyc04g051241.1	-2,05	6,76E-04	4,12E-03	Unknown protein
Solyc07g045530.2	-2,05	8,59E-08	2,88E-06	cilia- and flagella-associated protein 251-like
Solyc12g009780.1	-2,06	4,66E-05	4,85E-04	receptor-like protein 12
Solyc04g056713.1	-2,06	4,23E-03	1,71E-02	Aldehyde dehydrogenase family 2 member mitochondrial-like
Solyc06g072650.1	-2,06	3,26E-05	3,64E-04	Small auxin up-regulated RNA61
Solyc03g114890.4	-2,06	7,06E-05	6,72E-04	COBRA-like protein
Solyc04g081700.3	-2,07	2,14E-14	6,48E-12	Unknown protein
Solyc01g009690.3	-2,07	7,79E-07	1,81E-05	SC0A
Solyc12g099980.3	-2,07	1,03E-03	5,69E-03	receptor-like protein 12
Solyc07g008140.3	-2,09	3,20E-06	5,73E-05	Umecyanin
Solyc11g005480.2	-2,09	2,16E-03	1,01E-02	Citrate binding protein
Solyc02g089630.3	-2,10	8,63E-04	4,98E-03	Proline dehydrogenase
Solyc05g051880.4	-2,10	2,57E-04	1,90E-03	Trehalose 6-phosphate phosphatase
Solyc08g068730.1	-2,10	1,27E-07	3,97E-06	Tyramine n-hydroxycinnamoyl transferase
Solyc12g005620.1	-2,10	8,40E-07	1,93E-05	receptor-like protein kinase
Solyc05g009550.3	-2,11	1,68E-05	2,12E-04	Regulator of Vps4 activity in the MVB pathway protein
Solyc04g071780.3	-2,12	1,12E-07	3,58E-06	Cytochrome P450
Solyc04g051690.4	-2,13	3,61E-12	5,50E-10	WRKY transcription factor 51
Solyc07g005100.4	-2,13	3,00E-11	3,46E-09	Chitinase/lysozyme
Solyc07g053225.1	-2,13	6,07E-05	6,00E-04	Unknown protein
Solyc09g089680.4	-2,13	1,11E-04	9,64E-04	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc09g011560.3	-2,13	2,78E-19	2,90E-16	Glutathione S-transferase
Solyc07g055490.4	-2,13	8,96E-04	5,13E-03	Cytochrome
Solyc06g069040.4	-2,13	1,05E-04	9,21E-04	glutathione S-transferase T4
Solyc03g098740.1	-2,13	5,27E-06	8,58E-05	Biotic cell death-associated protein
Solyc02g091380.1	-2,14	2,96E-18	2,41E-15	transmembrane protein
Solyc03g097230.1	-2,14	1,73E-20	2,50E-17	AIG2-like (Avirulence induced gene) family protein
Solyc05g051530.4	-2,15	1,01E-07	3,28E-06	ABC transporter G family member 11
Solyc03g025350.3	-2,15	3,27E-06	5,84E-05	Transporter arsB
Solyc12g026470.2	-2,16	5,73E-04	3,58E-03	Unknown protein
Solyc07g049610.1	-2,16	2,80E-17	1,87E-14	Xyloglucan galactosyltransferase KATAMARI1
Solyc05g052280.3	-2,16	4,52E-05	4,73E-04	Peroxidase
Solyc04g077810.1	-2,17	6,83E-04	4,15E-03	ZCF37
Solyc10g076480.2	-2,17	5,00E-05	5,12E-04	Ammonium transporter
Solyc09g011270.4	-2,18	9,93E-12	1,30E-09	Cysteine/histidine-rich C1 domain protein
Solyc06g006000.3	-2,18	3,18E-04	2,24E-03	Maternal effect embryo arrest 59
Solyc06g065060.1	-2,19	1,22E-02	3,92E-02	FAD-binding Berberine family protein
Solyc03g033770.1	-2,19	2,47E-06	4,65E-05	protein HYPER-SENSITIVITY-RELATED 4-like
Solyc06g050340.3	-2,19	5,26E-05	5,34E-04	high mobility group B protein 7 isoform X1
Solyc08g080090.3	-2,19	1,34E-10	1,25E-08	green flesh
Solyc05g051480.2	-2,19	2,84E-13	5,85E-11	Unknown protein
Solyc06g082240.2	-2,19	4,10E-03	1,67E-02	Laccase
Solyc09g082700.2	-2,20	2,03E-03	9,71E-03	Early light-induced protein, chloroplastic
Solyc02g070110.1	-2,20	9,85E-04	5,52E-03	FAD-binding Berberine family protein
Solyc07g056200.3	-2,21	8,45E-14	2,08E-11	Heavy metal-associated isoprenylated plant protein
Solyc11g068620.2	-2,21	2,13E-11	2,57E-09	NAC domain
Solyc07g061910.1	-2,22	4,52E-04	2,95E-03	Protein NRT1/ PTR FAMILY 7.3
Solyc12g011200.3	-2,24	6,06E-06	9,48E-05	WRKY transcription factor 28
Solyc10g076560.1	-2,25	1,72E-12	2,95E-10	Wall-associated receptor kinase 1
Solyc02g071130.4	-2,26	3,24E-04	2,27E-03	WRKY transcription factor 71
Solyc02g077370.1	-2,26	5,56E-10	4,35E-08	Ethylene Response Factor C.5
Solyc10g007900.4	-2,26	8,57E-05	7,88E-04	Cytochrome
Solyc01g008300.2	-2,26	9,20E-05	8,34E-04	HXXXD-type acyl-transferase family protein
Solyc08g066260.3	-2,26	2,57E-04	1,90E-03	Serine decarboxylase
Solyc01g097470.4	-2,27	4,01E-06	6,86E-05	Neurogenic locus notch-like protein
Solyc04g077755.1	-2,27	4,12E-03	1,68E-02	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial-like
Solyc12g010410.3	-2,28	1,50E-03	7,59E-03	Homeobox protein knotted-1-like 3
Solyc03g045110.3	-2,29	8,89E-04	5,09E-03	Ribosomal protein S5
Solyc11g068380.1	-2,31	1,81E-06	3,62E-05	hypothetical protein
Solyc09g083200.4	-2,32	1,40E-09	9,31E-08	Protein kinase-like domain-containing protein
Solyc02g085005.1	-2,32	1,06E-05	1,49E-04	hypothetical protein
Solyc01g009700.3	-2,32	5,38E-21	9,17E-18	NL0E
Solyc03g096180.4	-2,33	1,25E-04	1,06E-03	flocculation protein FLO11-like
Solyc05g009040.3	-2,33	2,18E-07	6,04E-06	Receptor-like protein kinase
Solyc08g077370.4	-2,33	5,15E-13	1,00E-10	Purine permease
Solyc09g092060.3	-2,34	9,12E-03	3,11E-02	F-box/kelch-repeat protein At3g23880-like
Solyc07g056080.1	-2,35	3,73E-03	1,55E-02	Unknown protein
Solyc03g120830.3	-2,38	3,67E-04	2,51E-03	transmembrane protein
Solyc01g006550.3	-2,38	2,01E-09	1,27E-07	Receptor-like protein Cf-9 homolog
Solyc01g006950.3	-2,39	1,24E-06	2,64E-05	syntaxin-121-like
Solyc08g060925.1	-2,40	1,29E-03	6,80E-03	Unknown protein
Solyc09g082810.3	-2,40	5,85E-07	1,44E-05	Unknown protein
Solyc12g011150.1	-2,40	5,05E-18	3,94E-15	Unknown protein
Solyc01g080480.4	-2,42	2,37E-04	1,79E-03	DNAse I-like superfamily protein
Solyc10g079810.1	-2,42	1,30E-07	4,05E-06	Unknown protein
Solyc09g011520.3	-2,43	9,27E-05	8,37E-04	Glutathione S-transferase-like protein
Solyc03g116690.3	-2,45	3,09E-08	1,25E-06	Umecyanin
Solyc12g096960.2	-2,45	2,98E-05	3,40E-04	Major allergen Pru ar 1
Solyc07g045000.4	-2,46	1,82E-03	8,89E-03	Homeodomain-like protein
Solyc07g066360.1	-2,46	4,55E-06	7,55E-05	proline-rich receptor-like protein kinase PERK2
Solyc03g045140.4	-2,48	1,07E-04	9,32E-04	Cyclopropane-fatty-acyl-phospholipid synthase
Solyc02g091300.3	-2,48	4,28E-06	7,17E-05	Heavy metal-associated isoprenylated plant protein
Solyc03g033795.1	-2,49	1,77E-12	2,99E-10	AAA-ATPase At3g50940-like
Solyc08g067340.4	-2,49	8,47E-06	1,24E-04	WRKY transcription factor 46
Solyc08g074890.4	-2,51	1,84E-04	1,45E-03	Unknown protein
Solyc08g074490.4	-2,51	4,89E-06	8,04E-05	Nucleotide-diphospho-sugar transferase, nucleotide-diphospho-sugar transferase
Solyc06g072520.2	-2,51	8,17E-04	4,76E-03	bHLH transcription factor GBOF-1
Solyc07g054760.1	-2,53	1,99E-08	8,82E-07	Wound-responsive family protein
Solyc03g113480.1	-2,53	6,91E-03	2,50E-02	extensin-like protein
Solyc08g008150.1	-2,54	1,36E-05	1,79E-04	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Solyc08g007460.3	-2,54	4,30E-19	4,24E-16	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Solyc09g098380.3	-2,54	5,56E-06	8,94E-05	Amino acid transporter
Solyc09g074290.1	-2,54	6,30E-06	9,74E-05	Ankyrin repeat-containing protein
Solyc01g057707.1	-2,54	1,77E-03	8,72E-03	Pentatricopeptide repeat-containing protein
Solyc05g012180.3	-2,55	2,03E-06	3,97E-05	Methyl esterase 11
Solyc01g081310.3	-2,56	1,91E-24	8,94E-21	glutathione S-transferase T3
Solyc11g039750.3	-2,57	6,79E-05	6,53E-04	MYB transcription factor

Solyc09g090970.4	-2,57	3,70E-04	2,52E-03	pathogenesis-related protein STH-2-like
Solyc02g093580.4	-2,57	2,34E-03	1,08E-02	Tomato 9612 mRNA
Solyc01g089890.3	-2,59	2,90E-12	4,65E-10	PRA1 family protein
Solyc01g005040.3	-2,59	8,28E-08	2,79E-06	CASP-like protein
Solyc10g007360.4	-2,60	1,34E-03	6,98E-03	Protein DETOXIFICATION
Solyc09g082690.3	-2,60	1,62E-28	1,01E-24	superoxide dismutase
Solyc05g015850.4	-2,62	7,83E-05	7,33E-04	WRKY transcription factor 75
Solyc08g067630.3	-2,64	2,52E-20	3,38E-17	histone deacetylase-like protein
Solyc05g046200.3	-2,65	1,07E-02	3,52E-02	Unknown protein
Solyc07g017980.1	-2,65	2,38E-04	1,80E-03	protein PELPK1
Solyc07g045030.4	-2,66	3,19E-09	1,93E-07	NAC domain-containing protein
Solyc03g044790.3	-2,66	8,69E-17	5,09E-14	methylesterase AY455313
Solyc09g090080.1	-2,67	1,80E-21	3,74E-18	Phosphate transporter
Solyc09g009980.3	-2,68	9,90E-04	5,54E-03	Small auxin up-regulated RNA70
Solyc09g098385.1	-2,69	1,86E-05	2,30E-04	Ubiquitin
Solyc04g072070.3	-2,70	9,04E-06	1,31E-04	WRKY transcription factor 55
Solyc03g116700.4	-2,71	1,62E-12	2,84E-10	Umecyanin
Solyc10g050880.2	-2,73	5,30E-03	2,04E-02	Alpha/beta-Hydrolases superfamily protein
Solyc02g062390.3	-2,73	8,59E-04	4,96E-03	abscisic acid and environmental stress-inducible protein TAS14
Solyc11g064980.1	-2,74	3,58E-08	1,43E-06	Unknown protein
Solyc06g066820.4	-2,74	8,95E-05	8,15E-04	Le3OH-13b-hydroxylase
Solyc12g009720.3	-2,75	2,64E-05	3,08E-04	receptor-like protein 12
Solyc02g082920.4	-2,75	7,78E-23	2,40E-19	acidic extracellular 26 kD chitinase
Solyc07g006420.1	-2,75	1,32E-07	4,10E-06	transmembrane protein
Solyc12g044950.3	-2,77	8,26E-08	2,79E-06	lipid desaturase
Solyc03g119590.1	-2,78	1,06E-05	1,50E-04	NIMIN2c protein
Solyc02g036480.1	-2,78	6,27E-17	3,91E-14	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Solyc04g014290.1	-2,79	4,89E-04	3,15E-03	protein PELPK1-like
Solyc01g080800.3	-2,79	5,14E-09	2,81E-07	Basic secretory family protein
Solyc01g096820.4	-2,79	3,75E-06	6,51E-05	Calcium/calmodulin dependent protein kinase
Solyc12g009730.3	-2,86	1,07E-13	2,55E-11	receptor-like protein 12
Solyc02g089210.4	-2,89	8,88E-03	3,05E-02	MADS box transcription factor
Solyc06g069710.3	-2,89	8,62E-07	1,98E-05	NAC domain-containing protein
Solyc02g076910.3	-2,89	1,26E-02	4,01E-02	Cysteine protease
Solyc01g009705.1	-2,89	3,79E-04	2,57E-03	Unknown protein
Solyc12g013680.3	-2,91	2,06E-06	4,00E-05	receptor-like protein 12
Solyc09g082270.4	-2,92	1,21E-08	5,83E-07	Lipid transfer protein
Solyc04g071600.3	-2,93	1,13E-06	2,45E-05	Abscisic acid stress ripening 5
Solyc12g045020.2	-2,95	3,16E-14	8,97E-12	Cytochrome
Solyc07g053420.4	-2,98	4,12E-08	1,61E-06	RING/U-box superfamily protein
Solyc06g065010.4	-3,00	1,45E-04	1,20E-03	GDSL esterase/lipase 2-like
Solyc06g051860.3	-3,01	5,64E-08	2,06E-06	mycorrhiza-inducible inorganic phosphate transporter 4
Solyc11g012705.2	-3,02	4,08E-05	4,35E-04	Pollen Ole e 1 allergen and extensin family protein
Solyc07g048070.3	-3,03	2,60E-08	1,09E-06	Cytochrome b561 and DOMON domain-containing protein
Solyc12g009695.1	-3,03	8,46E-05	7,80E-04	Calcium-dependent lipid-binding (CaLB domain) family protein
Solyc05g010000.1	-3,03	6,90E-04	4,18E-03	Protein IDA
Solyc05g054650.1	-3,05	8,70E-07	1,99E-05	Zinc finger protein
Solyc08g079540.4	-3,06	2,52E-04	1,87E-03	Unknown protein
Solyc07g008130.3	-3,07	9,36E-05	8,43E-04	Cupredoxin
Solyc07g045580.1	-3,07	5,08E-04	3,25E-03	Filament-like plant protein 4
Solyc10g008840.3	-3,07	6,90E-03	2,50E-02	RAB GTPase
Solyc06g062420.4	-3,11	9,43E-08	3,11E-06	Unknown protein
Solyc01g067300.3	-3,12	7,03E-05	6,70E-04	CASP-like protein
Solyc04g007380.3	-3,12	1,41E-05	1,84E-04	Receptor-like protein kinase
Solyc02g076980.5.1	-3,12	2,27E-14	6,74E-12	Cysteine protease-like protein
Solyc10g084960.2	-3,13	3,28E-09	1,97E-07	Glutathione S-transferase
Solyc04g040130.1	-3,17	3,56E-13	7,09E-11	Fatty acid desaturase
Solyc06g005620.3	-3,19	1,07E-06	2,34E-05	Zinc transporter 2
Solyc06g009480.3	-3,20	3,01E-05	3,43E-04	R2R3MYB transcription factor 24
Solyc09g090990.2	-3,23	4,48E-06	7,46E-05	Major allergen Pru ar 1
Solyc12g011100.2	-3,30	2,02E-05	2,48E-04	Unknown protein
Solyc03g118360.2	-3,31	4,47E-06	7,46E-05	ATP-dependent Clp protease ATP-binding subunit ClpC
Solyc02g080120.3	-3,31	1,61E-04	1,31E-03	Gibberellin 2-beta-dioxygenase 8
Solyc07g056510.3	-3,32	9,80E-14	2,38E-11	Glutathione S-transferase-like protein
Solyc01g057680.4	-3,32	1,27E-05	1,69E-04	Unknown protein
Solyc09g014820.3	-3,34	5,83E-05	5,82E-04	Protein LURP-one-related 15
Solyc02g079510.3	-3,36	1,23E-19	1,35E-16	Peroxidase
Solyc03g033750.2	-3,36	1,39E-06	2,90E-05	AAA-ATPase At3g50940-like
Solyc07g009230.3	-3,37	7,38E-08	2,57E-06	Defensin-like protein 1
Solyc06g053930.3	-3,38	8,79E-05	8,03E-04	Calmodulin
Solyc05g021090.4	-3,38	1,38E-06	2,87E-05	NAC domain
Solyc04g063317.1	-3,39	7,20E-04	4,33E-03	Unknown protein
Solyc11g068370.3	-3,39	4,55E-04	2,96E-03	Transcription factor
Solyc02g079350.3	-3,41	4,75E-04	3,07E-03	Equilibrative nucleotide transporter like
Solyc03g094110.4	-3,45	5,37E-06	8,70E-05	Nucleotide-diphospho-sugar transferase
Solyc06g067860.3	-3,46	3,11E-14	8,95E-12	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc11g013250.1	-3,56	7,28E-06	1,09E-04	C2 calcium-dependent membrane targeting
Solyc11g005840.2	-3,56	1,29E-04	1,09E-03	Aminotransferase
Solyc09g091000.4	-3,57	9,26E-09	4,63E-07	Pathogenesis-related protein STH-2
Solyc06g060470.1	-3,58	6,46E-06	9,90E-05	VQ motif-containing protein 20
Solyc09g011610.3	-3,60	5,20E-08	1,95E-06	Glutathione S-transferase
Solyc06g066590.4	-3,64	2,56E-06	4,78E-05	Protein PLANT CADMIUM RESISTANCE 8
Solyc10g085860.1	-3,65	1,19E-05	1,61E-04	Glycosyltransferase
Solyc06g005090.3	-3,65	2,65E-06	4,90E-05	LOB domain-containing protein
Solyc12g100270.2	-3,67	7,00E-07	1,68E-05	Fatty acid hydroxylase superfamily
Solyc11g068920.1	-3,69	1,24E-05	1,65E-04	RING-type E3 ubiquitin transferase
Solyc03g025670.3	-3,70	1,33E-29	1,24E-25	PAR1
Solyc08g078650.3	-3,70	5,15E-05	5,25E-04	Glyco_transf_8 domain-containing protein
Solyc07g026710.3	-3,71	2,11E-04	1,63E-03	Unknown protein
Solyc02g092120.3	-3,76	6,23E-05	6,11E-04	phytosulfokines-like
Solyc12g100240.1	-3,78	8,59E-09	4,38E-07	Fatty acid desaturase
Solyc02g079700.1	-3,78	2,95E-05	3,37E-04	S-receptor kinase-like protein
Solyc12g100250.3	-3,79	4,26E-09	2,38E-07	Fatty acid desaturase
Solyc08g080620.1	-3,80	3,46E-21	6,48E-18	PR-5x
Solyc07g056600.1	-3,83	8,77E-06	1,28E-04	VQ motif-containing protein
Solyc03g033740.4	-3,84	5,89E-03	2,21E-02	proteasome subunit beta type-1
Solyc01g103000.3	-3,86	4,12E-03	1,68E-02	Unknown protein
Solyc02g086700.4	-3,88	1,70E-11	2,13E-09	Glucan endo-1,3-beta-glucosidase
Solyc04g077750.2	-3,89	8,87E-04	5,09E-03	Unknown protein
Solyc01g009810.3	-3,93	6,82E-11	7,10E-09	Leucine-rich repeat protein
Solyc09g098080.4	-3,94	3,91E-09	2,25E-07	Glycosyltransferase
Solyc08g075560.1	-3,95	1,06E-05	1,49E-04	Unknown protein
Solyc01g097240.3	-3,97	1,24E-14	3,87E-12	Pathogenesis-related protein 4
Solyc10g075150.2	-3,97	3,18E-17	2,05E-14	Non-specific lipid-transfer protein
Solyc09g097810.3	-4,03	7,79E-11	7,89E-09	SAR8.2 protein
Solyc01g009930.3	-4,03	9,03E-07	2,05E-05	receptor-like protein 12
Solyc01g008620.4	-4,08	3,54E-24	1,33E-20	Glucan endo-1,3-beta-glucosidase
Solyc10g079380.2	-4,08	8,61E-05	7,91E-04	Heat stress transcription factor B-3
Solyc10g007580.1	-4,11	5,78E-08	2,10E-06	VQ-like protein
Solyc02g069960.4	-4,11	3,27E-13	6,65E-11	NAC domain-containing protein
Solyc09g089780.3	-4,11	1,92E-07	5,48E-06	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc03g033790.4	-4,14	5,37E-09	2,92E-07	P-loop containing nucleoside triphosphate hydrolases superfamily protein
Solyc08g023510.3	-4,42	4,44E-05	4,66E-04	Unknown protein
Solyc10g082066.1	-4,47	4,82E-08	1,83E-06	receptor-like protein kinase
Solyc12g100260.1	-4,54	1,04E-13	2,49E-11	Fatty acid desaturase
Solyc12g049030.1	-4,55	6,16E-18	4,61E-15	Fatty acid desaturase
Solyc12g150125.1	-4,58	3,24E-07	8,60E-06	Alpha/beta-hydrolases superfamily protein
Solyc01g090810.4	-4,65	3,26E-07	8,61E-06	beta-expansin precursor
Solyc11g007980.2	-4,65	3,54E-14	9,75E-12	Cytochrome
Solyc10g018190.2	-4,66	2,11E-07	5,88E-06	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Solyc01g105630.4	-4,68	1,16E-08	5,67E-07	Calmodulin

Solyc12g056750.3	-4,74	9,21E-05	8,34E-04	WRKY transcription factor 61
Solyc01g102910.4	-4,77	2,03E-07	5,73E-06	Germin-like protein subfamily 1 member
Solyc10g076460.2	-4,77	3,82E-10	3,20E-08	Homeodomain-like superfamily protein
Solyc10g078220.2	-4,92	3,74E-12	5,61E-10	Cytochrome P450
Solyc03g094120.3	-4,98	5,62E-12	8,09E-10	Nucleotide-diphospho-sugar transferase
Solyc09g007010.1	-5,11	3,65E-05	3,98E-04	Pathogenesis-related protein 1
Solyc04g014770.1	-5,45	1,93E-22	4,51E-19	Unknown protein
Solyc12g036820.2	-5,60	4,68E-04	3,03E-03	Unknown protein
Solyc12g036800.1	-5,89	7,02E-16	2,99E-13	Receptor like protein
Solyc10g018340.1	-6,00	4,34E-11	4,70E-09	Small auxin up-regulated RNA71
Solyc11g068940.1	-6,72	8,22E-08	2,79E-06	RING-type E3 ubiquitin transferase
Solyc02g033030.3	-6,86	1,61E-05	2,06E-04	Unknown protein
Solyc08g014090.1	-6,87	5,32E-08	1,98E-06	Unknown protein
Solyc07g007720.4	-7,49	1,21E-04	1,03E-03	Unknown protein
Solyc02g062815.1	-8,00	6,93E-04	4,20E-03	transcription initiation factor TFIID subunit
Solyc12g038430.3	-8,15	7,67E-04	4,54E-03	Transposase, Ptta/En/Spm, plant
Solyc08g074910.3	-8,22	9,64E-04	5,43E-03	F-box/FBD/LRR-repeat protein isoform X2
Solyc08g074895.1	-9,39	2,69E-04	1,97E-03	F-box/FBD/LRR-repeat protein isoform X2
Solyc12g042793.1	-9,78	2,32E-04	1,76E-03	coiled-coil domain-containing protein 18