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Investigations on the interactions between the endophyte nitrogen fixing bacterium *Gluconacetobacter diazotrophicus* and tomato plants.

Martina Franchini

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The University of Nottingham

Division of Plant Sciences

School of Biosciences

Sutton Bonington Campus

Loughborough, LE12 5RD, UK

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Abstract

The need to find new and more sustainable agricultural practices is a pressing matter of our times. The development and employment of microbial-based biofertilisers is one of the solutions advanced by science to reduce the amount of chemicals that are released in the environment to sustain high yield agricultural production.

Gluconacetobacter diazotrophicus (Gd) is a non-nodulating endophytic nitrogen-fixing bacterium, first isolated from sugarcane plants. It has been shown to be capable of colonising a wide range of crops and provide beneficial effects to the host plant thanks to both phytohormones production and nitrogen fixation.

The aim of this project was to investigate the effects elicited on tomato plants by the Gd strain AZ0019 and to elucidate the molecular mechanisms that lie behind Gd positive effect on plants health and yield.

Firstly, the achievement of a consistent microbial inoculation protocol for tomato plants was addressed in order to obtain a repeatable set up that would also allow molecular analyses on treated plants. In-soil colonisation experiments were initially tested with a promising outcome, showing improved growth in the wild type (WT) strain treated plants. However, the results scarce consistency, along with the high number of variables in this type of growth systems, led to the prioritisation of a more controllable setup. Bacterial inoculation on plants grown on MS agar or rockwool substrates was subsequently investigated, but low repeatability and inadequate colonisation success, in particular on the Money Maker tomato variety, discouraged further testing with this strategy. These attempts led to the development of a hydroponic system setup, in which the application of Gd through root dipping induced a consistent and repeatable growth promotion effect.

With the employment of the above-mentioned hydroponic setup, investigations on the effects of Gd on tomato plants, both from a phenotypical and a molecular point of view, were addressed. More specifically, the response induced by the inoculation of the WT Gd strain was compared to the one elicited by a N-fixation impaired mutant strain of Gd, *nifD*$^{-}$. The *nifD*$^{-}$ strain showed to be promoting the

plants growth to some extent, even though a stronger beneficial effect was obtained after the inoculation of the WT strain. This comparison provided insight on the relevance of N-fixation contribution to the general plant growth promoting (PGP) effect provided by Gd to the host plant. Moreover, thanks to the employment of GUS and GFP tagged bacterial strains and the setup of a consistent protocol for the quantification of the bacterial colonisation, Gd localisation in the root system and colonisation rate could be monitored. Gd was found to be mainly localised on the root surface and in the root intercellular spaces, however it also observed in correspondence of lateral roots emergence sites and adhering to root hairs. In some cases, indication of intracellular colonisation was detected.

Particular interest was posed on the molecular response of tomato plants to the interaction with Gd. A transcriptomic analysis was carried out on Gd-inoculated tomato roots in comparison to uninoculated plants, so to assess the plants molecular response to the interaction with either of the two Gd strains tested (WT or *nifD*$^{-}$) at different nitrogen levels in the growth substrate, at 1- and 14-days post bacterial inoculation (dpi).

1. Introduction

1.1. Historical background in-soil fertilisation management

Since the establishment of the first non-nomadic forms of settlement and the introduction of improved agricultural practices, soil fertility maintenance and optimisation of crops cultivation efficiency has been one of the main concerns to the human species.

In traditional farming systems, the favoured way to restore soil fertility was to include a period of fallow in the cropping rotation. Evidence of this practice was found starting from at least the time of Cato the Censor (234 -139 b.c.e.). Ancient Romans were already aware of the importance of fallowing in maintaining soil fertility, as well as applying crop rotation, liming acid soils, and adding manure [86].

In medieval Europe, between one-third and one-half of the arable land was left fallow. The portion of fallowing assigned lands progressively decreased until nearly disappearing due to the increase in population density. Spreading animal manures in the field, as well as inclusion of leguminous crops, helped to add nitrogen, a primary nutrient, to the soil. Legumes such as clover, beans, and peas can improve soil fertility thanks to their symbiotic association with specialised bacteria that attach themselves to plant roots and that can absorb elemental nitrogen from the atmosphere and convert it to a form that can be assimilated by the plants, a remarkable feat that higher plants are not able to perform on their own. Similarly, in the rice farming areas of Asia, the occurrence of blue-green algae (cyanobacteria) in the flooded rice paddies helps to supply nitrogen to the soil and maintain soil fertility. Application of organic residues, including human wastes, was not an uncommon strategy for nitrogen input in fields. The intensification of agricultural production was a direct consequence of the necessity to fulfill the growing population needs; the introduction of multiple cropping per year and with more nutrients removed from the fields as crops were harvested led to a progressive loss of soil fertility resulting from the depletion of essential nutrients. As a consequence, yields experienced a consistent decline [86].

On this basis, necessity impelled the development of artificial fertilisers, that could provide nutrients in forms readily available to plants. These chemical

substances mainly needed to contain sources of the three major nutrient elements that a crop needs: nitrogen, phosphorus, and potassium in addition to other "minor" elements that are required in smaller amounts [86].

1.2. Nitrogen fertilisation

1.2.1. Chemical nitrogen fertilisation

The first synthetic fertiliser was superphosphate, invented by the English agricultural chemist John Bennet Lawes. In 1842, he patented a process of treating phosphate rock with sulfuric acid to make the phosphate soluble, thus initiating the chemical fertiliser industry [41].

The problem remained how to supply sufficient nitrogen to satisfy crop needs. Nitrogen (N) is one of the most important nutrients for plant growth, being a primary constituent of nucleotides, proteins, and chlorophyll. Although the atmosphere is 78% nitrogen, its diatomic form makes it inaccessible to plants due to the presence of a triple bond [71]. In many cases, the limited natural N supply is a restriction to crop yield [195]; therefore, crop productivity heavily relies on N fertilisation.

Towards the end of the nineteenth and early part of the twentieth centuries, nitrogen fertilisation was mainly relying on saltpeter (sodium nitrate) deposits of Chile, and the guano (accumulated excrements of seabirds) in the islands off the shore of Peru. These fertiliser sources were too expensive and insecure due to the mining process required to obtain them, the long-range transport of these substances across the ocean and the frequent interruption of international trade by wars in the twentieth century [41].

In 1905, a solution to this supply problem was provided by the work of two German scientists, Fritz Haber and Carl Bosch. Haber discovered a way to synthesise ammonia under lab conditions. The process, as subsequently refined and industrialized by Bosch, requires energy that is generally obtained from fossil fuels [41].

The development and introduction of chemical fertilisers marked a revolutionary change in modern agriculture. In conjunction with the improvement of crop varieties (e.g. Borlaugh's dwarf wheat) and of methods to control diseases and

pests (Green Revolution, starting from 1968), and to prevent soil erosion, chemical fertilisers brought about a substantial increase in crop yields [41].

1.2.2. Drawbacks in chemical nitrogen fertilisation

The use of chemical N fertilisers has brought positive effects on cropping systems in terms of yield and productivity but came with huge energy costs as well as worrying environmental damages, as for example the well documented contribution to significantly increase the greenhouse gas emissions during the chemical N fertilisers production processes [252]. Nitrogen fertilisers are also very costly and their commercial cost quadrupled from 1999 to 2008 [256]. Additionally, many farmers tend to apply supra-optimal amounts of fertilisers to their fields as a means of risk management and insurance against possible nitrogen losses to ensure maximum attainable yields [256], [14], [175].

Nitrogen in the form of Nitrate is a mobile, reactive, and hard to contain compound making it very vulnerable to losses due to denitrification, volatilisation, and leaching [28], [222]. Leached reactive forms of nitrogen are capable of causing widespread environmental effects and severe consequences to human health [256], [251]–[257]. This underlines the importance of communication and correct technological transfer between researchers and farmers so that the correct use of agrochemicals or even new bio-based compounds is achieved.

In this context, developing strategies for improving nitrogen use efficiency is crucial for the establishment of a more sustainable agriculture and represents an important challenge of this century [27].

1.2.3. An alternative to chemical nitrogen fertilisers: nitrogen-fixing bacteria

Due to the above mentioned increased costs and detrimental effects on the environment associated with nitrogen fertilisers and negative field and yield effects resulting from continuous monoculture practices, farmers often rely on crop rotation to both provide benefits to the agricultural system and add fixed nitrogen into the soil through the process of biological nitrogen fixation (BNF) [178].

Biological nitrogen fixation can be defined as the reduction of dinitrogen to ammonia by means of a prokaryote [81]. Even though BNF has high potential in replacing chemical N fertilisers in agriculture, not all plants have acquired a symbiosis with a nitrogen fixing prokaryote [14], primarily due to the fact that known prokaryotes capable of BNF and internal plant colonisation, such as rhizobia, have a very selective host range [160]. Bacteria that are capable of nitrogen fixation are called diazotrophs [206]. These bacteria can be classified as plant growth promoting bacteria (PGPB) since they provide beneficial effects to their host plants [204].

One of the most investigated and best characterised symbiotic forms in which BNF-capable bacteria are found associated with plants is the nodule formation in legumes. The bacteria responsible for this type of association belong to the *rhizobium* genus of Gram negative proteobacteria [206]. The association requires an initial series of reciprocal molecular signals between the bacterium and host plant which leads to changes in the transcriptional regulation of genes, structural changes, and eventually the formation of a root nodule, the epicentre of BNF in legumes [73]. However, not all prokaryotes capable of BNF require nodules to fix nitrogen. These prokaryotes, some of which are endophytic, contain in many cases fewer requirements to establish a symbiotic relationship with a host plant. Recently, Hardoim et al. (2015) defined endophytes as microbes including bacteria, archaea, fungi, and protists that colonise the inner compartments of a plant regardless of the outcome of the association [80].

Bacterial endophytes are found across many phyla, including the Proteobacteria, Actinobacteria, Firmicutes and Bacteroidetes [80], [253]. Bacterial endophytes belonging to several genera such as *Azoarcus*, *Burkholderia*, *Gluconobacter*, *Herbaspirillum*, *Klebsiella*, *Pantoea* and *Rahnella* were found in many different plants, facilitating the growth of the host plant in scarce nutrient conditions [53], [200], [189], [193]. Common characteristics of endophytes include the ability to synthesise plant hormones such as indole-3-acetic acid (IAA), solubilise phosphate, secrete siderophores, and confer plant tolerance to biotic and abiotic stresses [68]-[13].

Some bacterial endophytes carry genes necessary for BNF, potentially enabling them to convert dinitrogen gas (N_2) into usable forms of nitrogen such as

ammonium and nitrate within the host plant [17], [206]. Symbiotic N-fixation by rhizobia in legume plants has been an active area of research for many years, however, the discovery of N-fixing bacterial endophytes in non-nodulating plants such as sugarcane during the late 1980's has widened the area of BNF research [77], [48].

N-fixation implies the reduction of the triple bonds of N_2 molecules, which requires significant amounts of energy. Given this energy demand, free-living N-fixers have rather limited applications in agriculture compared to plant-associated ones, which can, on the contrary, overcome the energy requirement of N-fixation by obtaining energy from the host plant [169].

Bacterial endophytes have been found to be located in the internal plant tissues which may be a favourable environment for N-fixation: this presumably minimises the competition with other microbes in the rhizosphere as well as possibly providing a microaerobic environment that is necessary for nitrogenase activity [188], [52].

Among the nitrogen fixing bacteria, are included some genera of the *Acetobacteraceae* family. These are aerobic bacteria capable of oxidizing ethanol to acetic acid. This family has been divided into ten genera *Acetobacter*, *Gluconacetobacter*, *Gluconobacter*, *Acidomonas*, *Kozakia*, *Asaia*, *Swaminathania*, *Saccharibacter*, *Granulibacter* and *Neoasaia* [176].

1.3. The case of *Gluconacetobacter diazotrophicus*

1.3.1. General characteristics

Among the members of Acetobacteraceae can be found the strain *Gluconacetobacter diazotrophicus.*

G. diazotrophicus (Gd) is a Gram negative nitrogen-fixing, acetic acid bacterium.

Under microscopic analysis, this bacterium presents rod shaped cells measuring 0.7-0.9 µm, motile by 1 to 3 lateral flagella and forming single, paired or chain-

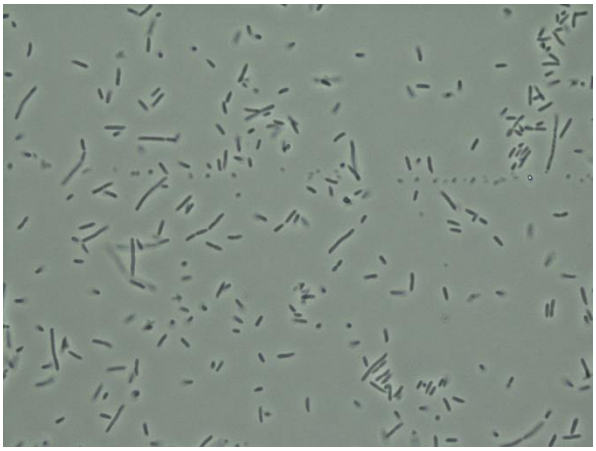


Fig. 1. G. diazotrophicus AZ0019 WT strain under Optical Microscope view. 100x magnification.

like structures (Fig. 1). It is an acid-tolerant bacterium, capable of growing at pH levels below 3.0, even though its optimum for growth is 5.5 [32], [59]. Growth and N_2 fixation can proceed at this acidity. Growth of *G. diazotrophicus* under laboratory conditions is frequently achieved through plating on LGIP medium (Section 3.1) due to the fact that it contains high sugar levels which are very similar to those found within sugarcane. The LGI medium, was developed starting from LG medium [126] by Baldani et al. (1984) [9] with the I derived from "Ivo" Baldani. Other media capable of sustaining *G. diazotrophicus* growth include but are not limited to DYGS [197], ATGUS [35], modified potato and SYP (Section 3.1). As found within the bacterium's natural host sugarcane, *G. diazotrophicus* requires a large amount of sucrose for adequate growth [48]. Sucrose is metabolised by secretion of an extracellular enzyme called levansucrase, which is able to hydrolyse it into glucose and levan polysaccharide [159].

The bacterium is capable of growing in sucrose levels up to 30%, even though the optimal concentration is achieved at sucrose levels of 10%. In addition to sucrose, *G. diazotrophicus* is capable of abundant growth on other carbon substrates including D-galactose, D-arabinose, D-fructose, and D-mannose [32]. Some compounds are listed as sources of both carbon and nitrogen for *G. diazotrophicus* cell division as for example some amino acids like Alanine, Serine, Glutamate and Histidine [83].

G. diazotrophicus was first isolated in 1988 from the internal compartments of sugarcane plants in Brazil. It has been classified as an obligate endophyte, since it has not been identified as free living in-soil, even though it has been isolated in the rhizosphere closely associated to roots, which are supposed to provide sugar and other nutrients that are fundamental for bacterial survival [216].

Studies have identified it to be resident mainly in the apoplast and xylem of the roots and stems of sugarcane plants [32] [51].

Besides sugarcane, *G. diazotrophicus* showed a wide range of host plants. Different studies have identified its association with other sugar- or starch-rich plants like sweet potato [174], pineapple [232] as well as coffee [105], tea, mango, banana, rice [159], corn [234] and sorghum 7. Among the suitable hosts for Gd can be found tomato, which, according to FAO, is the fourth most valuable crop worldwide, after wheat, rice and soybean. In Europe there are two major production systems for tomato. The Northern system is capital intensive and employs modern technology and practices like hydroponics, computerised climate control led glasshouses and integrated or biological crop protection. It is a highly intensive and productive system focused on fresh tomato production. The Southern system is highly focused on field tomato production for processing and also uses low-cost greenhouse technology for fresh tomato production [38].

Various studies have shown Gd to be able to significantly increase both number and weight of fruit production in inoculated tomato plants compared to non-inoculated controls [131].

The contribution of endophytic nitrogen fixation in sugarcane by *G. diazotrophicus* is as high as 150 Kg N ha^{-1} yr^{-1} [32], [160]. However, contribution of BNF varies with the host genotype.

Besides the nitrogen supply as a beneficial effect of *G. diazotrophicus,* plant growth promotion also occurs in $nif-$ mutant strains (impaired in N fixation), supporting the fact that additional plant-growth promoting benefits are provided by this bacterium [193]. *G. diazotrophicus* has been found to provide its host plants with phytohormones. Indole-3-acetic acid and the gibberellins A1 and A3 have been found to be produced by *G. diazotrophicus*; both phytohormones are critical for normal plant growth and development [67], [209], [13]. This bacterium has also been found to have phosphorous and zinc solubilisation capabilities [99], [39], [210]. Zinc and phosphorus, micro and macronutrients, respectively, are important for the growth, development, and yield of many plants.

1.3.2. Physiological features

G. diazotrophicus is able to fix N_2 in semisolid media under air but not in liquid media except when a starter dose of N is added. A peculiar characteristic of *G. diazotrophicus* is that it presents no nitrate reductase, which implies that the nitrogenase enzyme does not become inhibited by rising levels of nitrites and N_2 fixation proceeds at concentrations of NO_3^- as high as 10 mM. Additionally, the nitrogenase of *G. diazotrophicus* is only partially inhibited by the addition of ammonium, meaning that the bacterium is capable of undergoing nitrogen fixation in crops that are supplemented with low amounts of ammonium-based nitrogen fertilisers [228][62].

G. diazotrophicus also shows the ability of metabolising ethanol for its growth, "overoxidising" it to CO_2 and H_2O. Acetic and lactic acids are also oxidized to CO_2 and H_2O. Acids produced from glucose are consumed with precipitation of $CaCO_3$. Dark brown colonies are formed on potato agar with 10% sugar and dark orange colonies on N poor agar (20 mg yeast extract per 1L) containing bromothymol blue [32].

Interestingly, the high acidity of the growth medium enables *G. diazotrophicus* to solubilise insoluble zinc and phosphorous compounds even if Madhaiyan et al. (2006) demonstrated that this valuable characteristic is minimised in the presence of pesticides [134], [159].

1.3.3. N-fixation in *G. diazotrophicus*

An important question regarding associative and endophytic N-fixing bacteria is whether they contribute directly with fixed N to the plant. Discussions have been raised on whether death and subsequent mineralisation of diazotrophic bacteria could indirectly release significant amounts of fixed N [120], [122]. However, as described in legume nodules, the contribution of mineralisation is inefficient and delayed if compared with active release of immediate products of BNF by living bacteria [160].

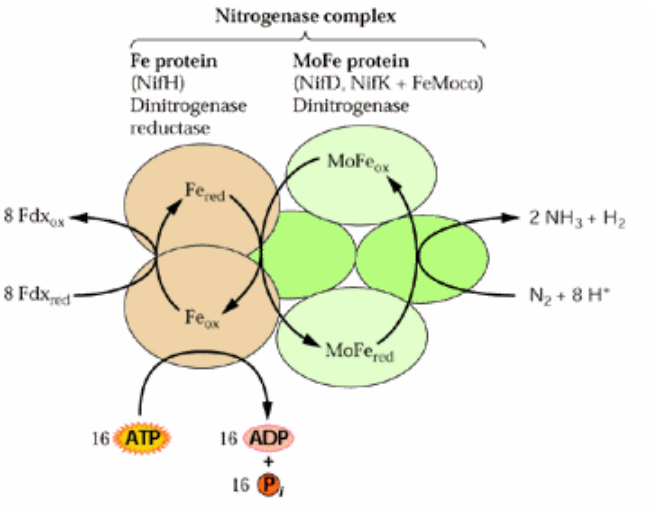


Fig. 2. Nitrogenase complex scheme as in Seefeldt et al. (2004).

The basic machinery of N fixation and regulation is very similar to those already well characterized in Rhizobium species [24], [160], [227], [151], as their genomes have an *nifHDK* operon, encoding both nitrogenase components: the dinitrogenase protein (MoFe protein, NifDK), which contains a molybdenum–iron cofactor that is the site of N_2 reduction; and the dinitrogenase reductase protein (Fe protein, NifH) that transfers electrons from an electron donor to the nitrogenase protein [24], [227], [151].

A few enzymes have been identified as key proteins in the nitrogen metabolising network of this bacterium: Nitrogenase, Levansucrase and Pyrroloquinoline Quinone-Linked Glucose Dehydrogenase. Removal or mutation of one of the three results in either the loss of nitrogen fixation ability, lack of the energy to power nitrogen fixation or of the environment to sustain this process [59].

1.3.3.1. Nitrogenase

The nitrogenase of *G. diazotrophicus* is a molybdenum-dependent system (Mo-nitrogenase) and is capable of providing its host with a substantial amount of fixed nitrogen [62]. ^{15}N-aided nitrogen balance studies have shown that certain genotypes of sugarcane are capable of having up to 200 kg of N per hectare fixed for them by *G. diazotrophicus*, providing approximately half of the crop's nitrogen needs [19], [124].

The Mo-nitrogenase is made up of two component proteins, the Fe protein containing the ATP-binding sites and the MoFe protein containing the substrate binding sites [187]. A feature which may make nitrogen-fixation in *G. diazotrophicus* unique is that early reports indicated that it does not contain a nitrate reductase protein [32]. Without a nitrate reductase protein in the bacterium, it was hypothesised that there would not be feedback inhibition of

nitrogenase by nitrate assimilation [32], [236]. However, more recent studies have suggested that the bacterium is inhibited to some extent by nitrate [236], [249]. Additionally, the nitrogenase of *G. diazotrophicus* appears not to be completely inhibited by the addition of ammonium and its growth under field conditions has been shown to be inhibited by high levels of nitrogen fertilisation (250-300 N ha^{-1} yr^{-1}) [67]. Therefore, the bacterium is capable of nitrogen fixation in crops that are supplemented with either nitrate-based fertilisers (no inhibition was detected up to 10 mM KNO_3 added to LGI growth medium) or with low amounts of ammonium-based fertilisers (no inhibition was detected up to 1 mM $(NH_4^+)_2SO_4$ added to LGI growth medium) [228].

1.3.3.2. Levansucrase

Since *G. diazotrophicus* is unable to transport or take up sucrose, it makes up for this incapability through the synthesis and export into the extracellular compartment of an enzyme called levansucrase, a fructosyltransferase exoenzyme which hydrolyses sucrose and polymerises the resultant fructose into fructooligosaccharides and levan [85], [138]. This enzyme is essential for bacterium survival and can represent over 70% of all secreted proteins by specific strains of *G. diazotrophicus* [85]. In addition to sucrose hydrolysis, levansucrase is also involved in tolerance to desiccation and NaCl as well as in biofilm formation [247]. For biofilm formation the expression of the *gumD* gene homologue is essential. This is a critical step in the production of exopolysaccharides, which along with levan, are a product of the hydrolysis of sucrose by levansucrase. The production of these particular compounds seems to lead to the formation of biofilm in *G. diazotrophicus* [247], [146]. The removal of either of these two factors has been shown to result in the bacterium becoming incapable of forming a biofilm. This leads to changes in colony morphology, tolerances, nitrogenase activity, and abilities to aggregate to abiotic and biotic surfaces, resulting in diminished colonisation abilities [247], [49].

1.3.3.3. Pyrroloquinoline Quinone-Linked Glucose Dehydrogenase

G. diazotrophicus also contains a pyrroloquinoline quinone-linked glucose dehydrogenase (PQQ-GDH), which oxidizes glucose into gluconic acid in the extracellular compartment [7], [69]. More importantly, the PQQ-GDH, which is primarily synthesised under nitrogen fixing conditions, produces a large amount of energy for the bacterium.

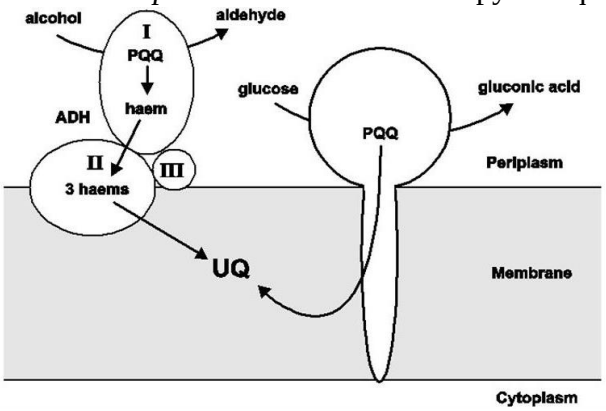


Fig. 3. Electron transport from membrane GDH and ADH. (Anthony et al., 1995)

The timing of the synthesis of this protein during the conversion of dinitrogen performed by the nitrogenase enzyme, provides the cell with the consistent amount of energy that is required for this process, showing the importance of this protein in the energetic balance of the bacterium [69]. While the principal pathway of glucose metabolism in *G. diazotrophicus* occurs through periplasmic oxidation via the PQQ-GDH, an alternate pathway exists, under specific environmental conditions, in an intracellular pathway via the nicotinamide adenine dinucleotide (NAD)-linked glucose dehydrogenase (GDH) [132].

1.3.3.4. Nitrogen utilisation by Gd

In *G. diazotrophicus*, the ammonium produced by the nitrogen fixation metabolism is mainly assimilated through the glutamine synthetase – glutamate synthase (GS/GOGAT) pathway [119] [180] (Fig. 4).

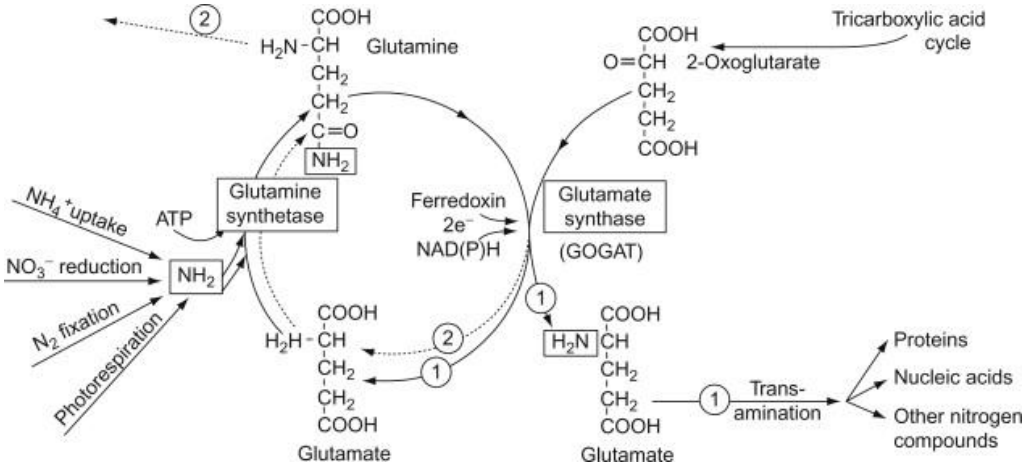


Fig. 4. Schematic model of ammonium assimilation via the glutamine synthetase–glutamate synthase cycle. Pathway at low (1) and at high (2) ammonium supply (Hawkesford et al., 2012).

Being BNF an energetically expensive process, bacteria do not usually fix N_2 in the presence of reactive N sources [21]. A number of mechanisms have been identified through which nitrogenase activity is inhibited, and *nif* gene expression is down-regulated, in response to increasing levels of NO_3^- and NH_4^+ in the environment [147].

As already mentioned, inhibition of nitrogenase activity as a consequence of the increase in NO_3^- levels is less pronounced in Gd due to the lack of a nitrate reductase enzyme [32]. Absence of this enzyme shifts the balance towards the accumulation of NH_4^+ (Fig. 5) towards which Gd nitrogenase shows to be more sensitive [228][62].



Fig. 5. Overview of part of the nitrogen cycle, showing the prominent enzymes involved in the interconversion of the different N forms. Red cross indicates interruption of this step in G. diazotrophicus, which lacks in the nitrate reductase enzyme (adapted from Timmons A.J. et al., 2015).

The lack of nitrate reductase has only been reported in two other diazotrophs that have shown the capability of fixing N_2 in the presence of nitrate, regardless its concentration: *Azotobacter paspali* [177][47] and *Bacillus azotofixans* [214].

1.3.4. Nitrogen role during host-microbe interaction

When dealing with plant associated or endophytic N-fixing bacteria, it must be taken into account the investigation of how N metabolism can affect plant interaction with these beneficial microorganisms. Different N forms such as ammonium, nitrate, and organic compounds are known for their ability to signal and regulate various metabolic processes, in both plants and bacteria, as well as regulating plant hormonal levels [114], [78], [46]. The architecture of plant root systems, which is the main interface of interaction between plants and microorganism, is modulated not only by hormones but also by Nitrogen. This makes clear how N is not only a fundamental molecule for plant nutrition and development, but also provides a major contribution to the establishment and maintenance of the beneficial plant-bacterial symbiosis.

Although BNF that comes with the interaction of associative and endophytic diazotrophic bacteria can offer a consistent contribution to the total N needs of plants, it rarely has been shown to be able to entirely replace the plants dependence on N fertilisers. It must be taken into consideration that the efficiency of BNF is highly affected by the composition and nutritional profile of the soil. This becomes rather clear taking as an example the case of sugarcane. Sugarcane plants inoculated with associative and endophytic diazotrophs and grown in-soil with different fertilisation levels showed a higher level of BNF when the N concentration was lower in the substrate [170]. This decrease in BNF contributions reported in high N content soils might be partially due to the control some N sources have over nitrogenase activity. Ammonium operates as one of the starting signals for the inactivation of nitrogenase through the reversible ADP-ribosylation of an Arg101 residue on one of the two homodimers of the Fe subunit [65][165]. Besides the control exerted on nitrogenase enzyme activity, studies have observed that N content in plant growth substrates can also affect the bacterial colonisation capacity. Fuentes-Ramirez et al. (1999) reported that sugarcane colonisation by *G. diazotrophicus* was inhibited at high concentrations of N fertilisers in the form of ammonium nitrate (11 mmol NH_4NO_3 per sugarcane plant grown in vermiculite/perlite 1:1) [66]. In addition to this, a study from Rodriguez-Blanco (2015), found a reduction in the number of diazotrophic bacteria isolated from plants of *Zea*

mays that were grown in the absence of N fertilisation in comparison to ones grown with the addition of either 40 kg N ha^{-1} or 80 kg N ha^{-1} as NH_4NO_3 [198]. It has been hypothesised that the presence of moderate amounts of N do not have a direct effect on bacteria but probably modify the plant physiological state that regulates its growth, root exudation patterns, and thus the abundance of the diazotrophic bacteria interacting with the plant [159] [50]. Furthermore, *G. diazotrophicus* growth is highly dependent on the type of N source. Ammonium and its derivative forms exert a suppression in *G. diazotrophicus* growth and colonisation rate in planta. Nitrates on the other hand appear to inhibit the bacterium functions to a lower extent [66], [170]. Some of the genes involved in the regulation of N and amino acid metabolism also play a consistent role in the modulation of the interaction between pathogenic bacteria and plants [224]. The plant defence response was also found to be induced by genes involved in the regulation of the C/N ratio, which governs plant growth [135].

Another N derivative, nitric oxide (NO), is a volatile compound involved in plant defence: it establishes cross-talk signalling involving salicylic acid and/or jasmonic acid [254]. This molecule has multiple effects besides the defence response. It can also act as a plant growth promoting molecule during plant association with diazotrophic bacteria. An example is the study of the interaction between tomato seedlings and the diazotrophic bacterium *A. brasilense* where NO formation led to the promotion of lateral root development [40].

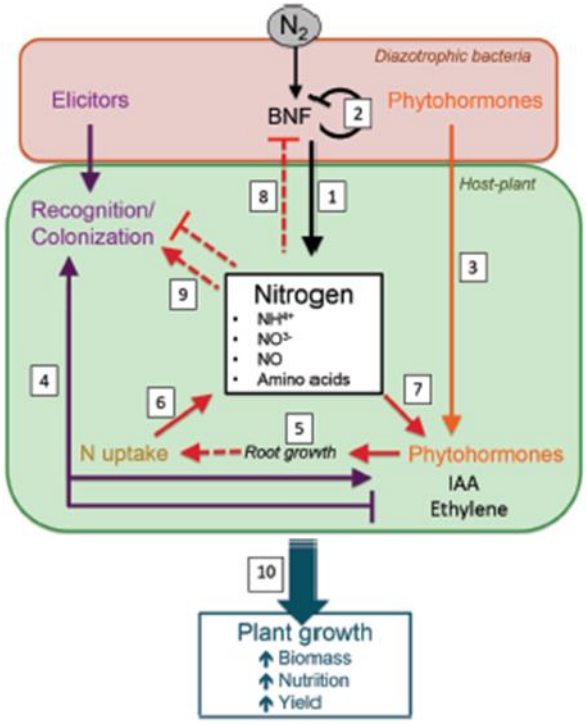


Fig. 6 Hypothetic model for levels of regulation occurring between bacteria and non-legume plants during association as in T. L. G. Carvalho et al. (2014).

In light of the strong modulation of nitrogen metabolism during plant-microbe interactions, hypotheses have been advanced about the possible role of N in regulating the efficacy of symbiosis establishment between hosts and beneficial associative and endophytic diazotrophs. Being involved in the modulation of plant defences and in the direct control of the BNF mechanism, it may have a key role in the regulation of colonisation levels. It has been shown that ammonium, glutamine, nitrate, and nitrite accumulation can suppress N_2 fixation by a negative feedback mechanism. This means that the bacterial colonisation rate can be strongly influenced by the N status of the soil, along with the endogenous plant and bacterial N content. It remains to be confirmed whether the endogenous N status would act as a signal for diazotrophic bacteria to start to interact with plants and establish a successful symbiosis only when the plant is in need of N nutrition. It is still unclear the exact mechanism through which the regulation of the association efficiency interacts with N metabolism and signalling to take advantage of this interaction.

A proposed model by Carvalho et al. (2014) for various levels of regulation that might take place within bacteria and plants during the association is presented in Fig. 6. The fixed nitrogen provided by plant growth promoting (PGP) diazotrophic bacteria is transferred to the plant, raising the endogenous N level in plant cells. Contemporarily, N fixation is autoregulated by a feedback mechanism: suppression is induced by high levels of ammonium, which can be both provided by the diazotrophs and by uptake from soil. PGP bacteria are often capable of also stimulating plant growth through the production of phytohormones, the biosynthesis and signalling pathways of which are modulated during the interaction with host plants. Hormonal stimulus frequently leads to an increase in root growth and root apparatus expansion. This has the double effect of providing more entry sites for the bacteria to enter the plant and fix N in the inner compartments and to increase the area for N uptake, thus raising the endogenous N levels. Moreover, nitrogen, in form of nitrate, ammonium, or organic N forms can control the endogenous hormonal balance, as well as bacterial recognition, colonisation, and the BNF processes. A perfect balance in all these mechanisms is important for the establishment of a beneficial and successful association, with positive effects on plant growth [27].

1.3.5. Sites of entry into host plants

Even though Gd is normally classified as an endophyte, the assignment to an associative or endophytic way of living is not always well defined since bacterial niches and numbers can be dynamically modulated during plant-bacteria interactions, in response to plant and environmental signals [211],[237],[170],[27].

Plant–bacterial interaction starts in the rhizosphere and seems to be induced by root exudates that attract diazotrophic bacteria**.** The presence of flagella, together with type IV pili and twitching motility, allow the bacterium to actively move towards the plant and come into contact with the roots thanks to a refined chemotaxis machinery.

G. diazotrophicus has been demonstrated to be capable of entering its host plant through roots, stems, or leaves [102].

With regards to the first interaction interface, the roots, the bacterium seems to penetrate through the root tips and cells of the root cap and meristem, at areas of lateral root emergence and through root hairs [102], [133], [201]. Root colonisation also depends on the adhesion and anchoring of the bacteria onto the root system, as well as microbial proliferation and the formation of biofilm structures at the root surface. Bacterial surface exopolysaccharides and lipopolysaccharides (LPSs) are involved in the adhesion and colonisation of roots [200], [96], [189].

For endophytic colonisation, the emergence points of lateral roots and, to some extent, differentiation and elongation zones near the root tip, where slightly disrupted or not completely differentiated tissues may facilitate penetration (Fig. 7), are considered sites for primary colonisation into roots [102], [96], [188]. Root intercellular spaces in the epidermal and cortical regions and lysed plant cells are major sites of colonisation, but vascular tissue and xylem cells may also

be invaded, an occurrence which is likely to allow systemic spreading into the shoots [188], [96],[200], [37].

Within the stems of host plants, specifically sugarcane, the bacterium is capable

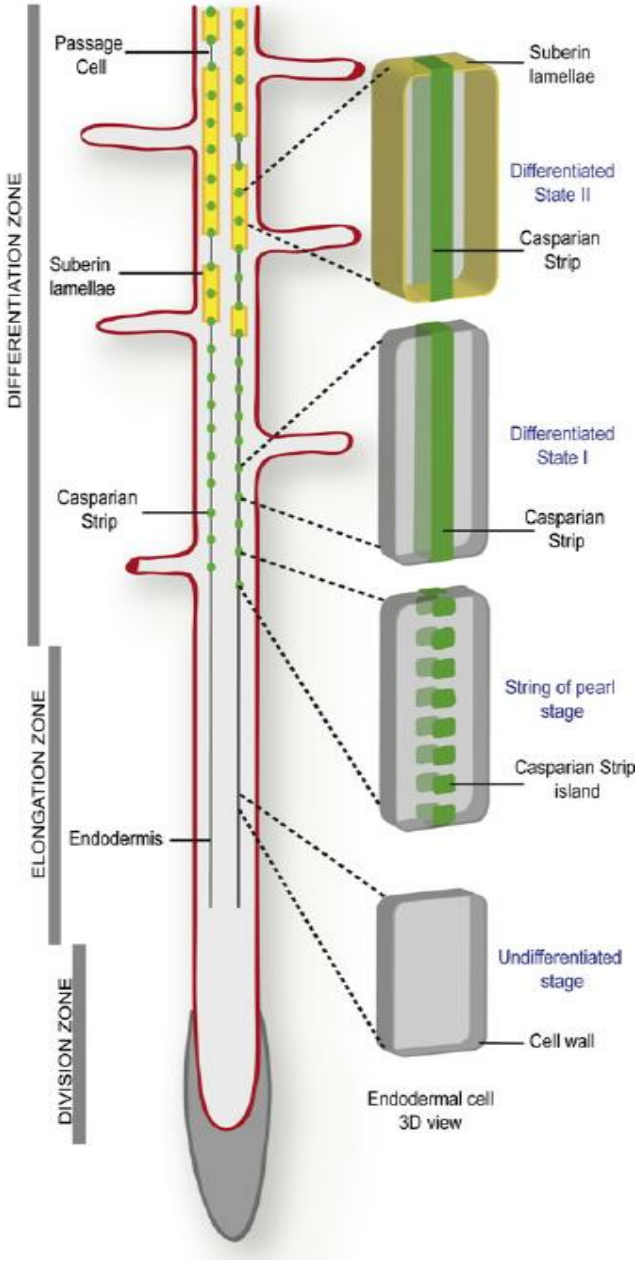


Fig. 7. The schematic representation shows the succession of events during endodermal differentiation (not to scale). The different stages are represented in a longitudinal view and in three-dimensional perspective to illustrate specific developmental steps. Endodermal differentiation starts with the deposition of Casparian strip islands (in green) in the anticlinal walls of endodermal cells (early differentiation), which fuse into a Casparian strip ring (differentiation state I). Later, suberin lamellae (in yellow) cover the entire endodermal cells except in the passage cells (differentiation state II) as in Barberon & Geldner (2014).

of entering at breaks caused by the separation of plantlets into individuals. Lastly, in the leaves, the bacterium's most probable site of entry would be through damaged stomata [102]. A peculiar additional mode of entry has been

observed: a plant sap-sucking insect, the pink sugarcane mealybug (*Saccharicoccus sacchari*), can function as a *G. diazotrophicus* propagation vector [64], [171]. Another vector that has shown to be involved in the transmission of Gd between plants are vesicular-arbuscular mycorrhizae (VAM) [174]. Paula et al. (1991), found the presence of *G. diazotrophicus* in spores of the vesicular-arbuscular mycorrhizal (VAM) fungus *Glomus clarum* obtained from sweet potatoes grown in soil inoculated with this fungus and with an enrichment culture of *G. diazotrophicus*. They then demonstrated that the inoculation of micropropagated sweet potatoes with a combination of *G. clarum* and *G. diazotrophicus* enhanced the number of both VAM spores and diazotroph cells on the inoculated tissue [174].

Once within the host plant, *G. diazotrophicus* was found to primarily inhabit intercellular apoplastic spaces, the xylem, and the xylem parenchyma [48], [102]. However, recent studies that employed β-glucuronidase (GUS)-labeled strains, suggest that this bacterium is also capable of intracellular colonisation within membrane-bound vesicles in its host plant [35]. Established *G. diazotrophicus* colonies are capable of growing up to 10^8 CFU per gram of tissue, as found within sugarcane [190]. The aforementioned modes of entry for *G. diazotrophicus* appear to be aided by hydrolytic enzymes. Within both PAL5 and UAP5541 strains, production of endoglucanase, endopolymethylgalacturonase and endoxygluconase was confirmed [1]. These enzymes have the potential to be responsible for both the bacterium's ability to enter its host plant and its mobility once inside [1], [59].

1.3.6. Colonisation mechanisms

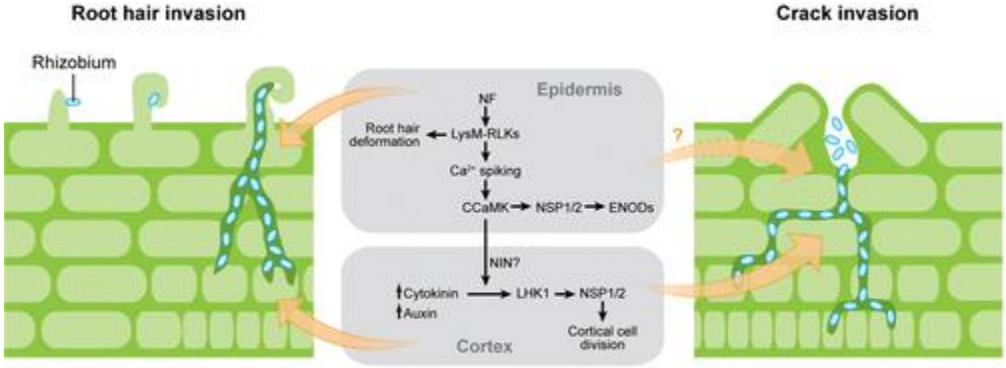
Three major groups include the heterotrophic nitrogen-fixing organisms that invade roots: 1) rhizobia, 2) *Frankia* and 3) other soil bacteria, including *Gluconacetobacter diazotrophicus* [34].

Among the different plant-diazotroph systems, the complex process of nodule formation and rhizobia symbiosis establishment is one of the best characterised BNF systems.

All nodulating rhizobia (with one known exception, *Aeschynomene* nodulating *Bradyrhizobium* strains) carry the common nodulation genes *nodABC*, which

encode enzymes responsible for the core structure of the lipochitooligosaccharide signal molecules (Nod factors) needed to induce nodule formation in host plants [125]. The entrance of rhizobia into the legume root, or stem in some cases, is a consequence of the dialogue between the bacterium and the plant, initiated by the presence of flavonoids and other excreted signalling molecules in the plant root exudate. The flavonoids play the role of inducers for the bacterial transcription of *nod* genes, leading to the formation and excretion of Nod factors [125]. The Nod factors are recognised by receptor-like kinases that contain sugar-binding LysM domains, which then induce gene expression changes in the plant. The components involved in the Nod-dependent signalling cascade are referred to as the Sym (symbiosis) pathway [113] [168]. Plant hormones, especially cytokinin, also play a role in the nodule formation [125].

During the early infection steps, rhizobia enter the plant following two main routes (Fig. 8). The most often mentioned is via root hair invasion. Following Nod-factors driven stimuli and rhizobial surface polysaccharides recognition, root hair cells curl around the bacteria, infection foci are formed, from which the infection thread extends transcellularly through the epidermis to reach the cortical cells allowing the rhizobia to reach the root inner compartments [107].



Oldroyd GED, Downie JA. 2008.
Annu. Rev. Plant Biol. 59:519–46.

Fig. 8. Coordinated root development during nodulation. The two bacterial infection strategies are presented. The bacteria can enter the plant either through root hair curls or cracks in the epidermis. During entry through root hair, epidermal responses are associated with nodulation (Nod) factors perception that leads to gene expression via a calcium spiking–dependent signaling pathway and root hair deformation via a signaling pathway independent of calcium spiking. Cortical responses are associated with increases in cytokinin and auxin; the main genes involved are noted. During crack invasion the epidermis is breached, and the bacteria gain direct access to cortical cells. Nod factor signalling is important in some species that undergo crack entry, but Nod factor–independent crack invasion also exists and may be associated with rhizobial modification of cytokinins. Abbreviations: ENODs, early nodulation genes; NIN, nodule inception, LysM-RLK, lysin motif receptor-like kinase (from Oldroyd and Downie, 2008).

Cortical cells ahead of the growing infection thread form specific cytoplasmic alterations, known as pre-infection threads, and these predict the path followed by the infection thread [240]. During growth in the infection thread, rhizobial surface polysaccharides are also thought to prevent plant defence responses [139][125]. The infection process via infection threads leads to the bacteria being trapped into plant membrane invaginations (symbiosomes) which develop into plant membrane encapsulated, differentiated rhizobia called bacteroids. Infection threads continue to grow and divide and thus deliver new symbiosomes to the growing nodule [125].

An ulterior route of colonisation is via wounds in the plant epidermis, often formed in correspondence of the emergence of lateral roots, or alternatively via infection between intact epidermal cells, followed by intracellular movement [167]. In this regards, there have been observations which document the production and isolation of cell-bound cellulases of white clover rhizobia that can erode a complete hole, slightly larger than the bacterial cell, that traverses the non-crystalline wall region of root hair apices of *T. repens* [34][140].

In most cases, Nod factors play a role both during their perception in the epidermis and during the invasion of rhizobia into the cortex, especially during transcellular invasion [125].

Another well-known symbiosis that legumes can initiate is the one with beneficial arbuscular mycorrhizal fungi (AMF) that facilitate the plant nutrient uptake, in particular of phosphate. The developmental ramifications of mycorrhizal fungal infection in the root are extremely different from the formation of nodules during rhizobial infection [113]. Nevertheless, these two symbioses utilize the same signalling Sym pathway, with components of the Nod factor signalling pathway playing a key role in the mycorrhizal association [166][168]. Utilisation of a communal signalling pathway, despite differences in the developmental outcomes of these two symbioses, poses a specificity problem [113]. For example, it has been observed that the activation of a specific protein kinase in the Sym pathway is sufficient for nodule formation in the rhizobia symbiosis establishment while the same kinase is activated in the AMF signalling cascade without inducing nodule formation [113]. This suggests that Nod factors signalling has inputs and outputs unique from the common Sym

pathway, and it seems likely that AMF signalling will also have analogous mycorrhizal-specific components [113].

The rhizobial nodule induction process is not dissimilar from the one observed during AMF symbiosis initiation; the conservation in both the AMF and rhizobial symbioses extends beyond early signalling and includes common cellular structures associated with intracellular microbial colonisation [168].
AM fungal infection is initiated with the formation of a swollen hyphal infection structure (hyphopodium) on the root surface and is accompanied by the assembly of a pre-penetration apparatus in the underlying cell. The pre-penetration apparatus is an intracellular structure composed of endoplasmic reticulum and cytoskeletal material that outlines the route for the subsequent hyphal growth across the cell lumen [74]. The development of pre-infection threads and pre-penetration apparatuses are the indicators that the plant cell is actively preparing for invasion by microsymbionts. This preparation is believed to be restricted to symbiosis, because analogous structures have not been observed during the compatible interaction of *M. truncatula* with a pathogenic fungus or upon mechanical stimulation of cells [76].

In addition to rhizobia and AMFs study, evaluations on the inoculation of non-legumes, especially cereals, with various diazotrophic bacteria such as *Azospirillum* and *Azotobacter* have a long history [34]. The plant mechanisms that permit bacterial colonisation in an endophytic and non-pathogenic manner, establishing a beneficial association, are not yet clear [130].

A successful endophytic association commonly involves an initial phase of bacterial attachment to the root surface. The subsequent endophytic colonisation is believed to involve bacterial cell-wall-degrading enzymes such as endoglucanases and pectinases [37].
The root attachment process has been studied in detail for the plant growth-promoting bacterial species *Azospirillum brasilense*. This species harbours surface-colonising strains, such as Sp7, which is not found inside plants, as well as strains such as Sp245, capable of endophytically colonising host plants [6][82]. In 1991, Michiels and associates [149] distinguished two phases in the surface attachment of the plant rhizosphere inhabiting *A. brasilense* Sp7 to roots

of wheat plants: 1) the initial weak binding of bacterial cells to the root surface, mediated by flagella and other proteins, was named the “adsorption” phase; 2) a subsequent irreversible attachment phase was named “anchoring”, during which the bacteria become irreversibly bound to the root surface. This anchoring phase was shown to require exopolysaccharides production. Exopolysaccharides are produced by a variety of bacteria, including nitrogen- fixing bacteria from genera such as *Azoarcus, Rhizobium*, *Azospirillum, Sinorhizobium, Burkholderia*, and *Bradyrhizobium* [63][79][95][152][221][238]. In these bacteria, exopolysaccharides, along with flagella, pili, bacterial exudates, and signalling molecules, have been shown to play a key role in the formation of biofilms and the first steps of the colonisation process [199].

As already mentioned, exopolysaccharides exert an analogue function in rhizobium–legume interactions, where are involved in the bacterial invasion of the plant, nodule development, bacterial release from the infection threads, bacteroid development, and protection against plant antimicrobial compounds [221]. Furthermore, exopolysaccharides contribute to growth and survival of bacteria inside the plant: they are noted to help creating a favourable microenvironment where exopolysaccharides may act as a barrier against plant defence mechanisms [55][194].

Referring to the *G. diazotrophicus* case, a number of genes probably involved in plant-bacteria interactions, such as genes coding for surface proteins (flagella and pili), genes involved in synthesis of capsular polysaccharides and lipopolysaccharides and *gum* genes have been found in the genome of *G. diazotrophicus* PAL5 strain [15]. A study from Meneses et al. (2011) [146] has noted the *gumD* gene as essential for exopolysaccharides production in *G. diazotrophicus* PAL5 strain and that exopolysaccharides production by this bacterium is determinant for biofilm formation and plant colonisation.

The precise infection and colonisation processes of *G. diazotrophicus* were initially studied in micro propagated sugarcane plants [102] [190] but this proved to be a laborious model system and it was discontinued in favour of hydroponics systems (applied mainly in rice) that demonstrated to be more effective and convenient for this type of study [201]. Nevertheless, the molecular mechanisms that enable *G. diazotrophicus* to colonise its host plants remain little studied [146].

It has been hypothesised that the action of *G. diazotrophicus* cell wall-degrading enzymes might weaken the primary cell walls of root meristems sufficiently, enabling this bacterium to directly interact with the plasma membrane of root cells. Endocytic uptake of *G. diazotrophicus* into membrane-bound vesicles in the cytoplasm could possibly result in the intracellular establishment of *G. diazotrophicus* in symbiosome-like structures, comparable to the one formed by rhizobia in root nodules [141]. It has also been suggested that if *G. diazotrophicus* reaches the intracellular compartment, it subsequently would be able to spread from the root tip meristem into cells of the elongating region of the root and into leaf cells of the shoot system in which the bacterium would associate closely with chloroplasts [45].

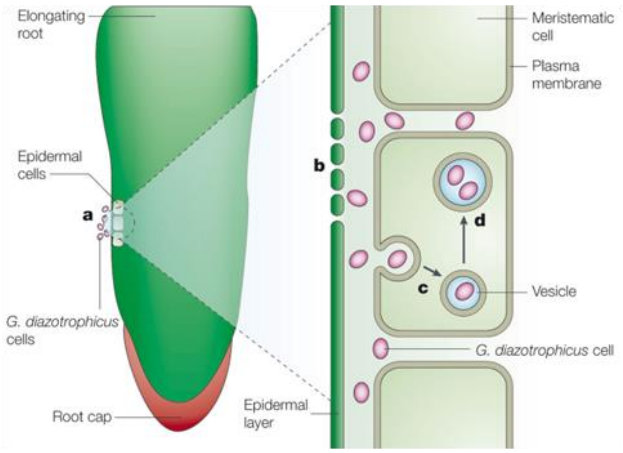


Fig. 9. Proposed entry mechanism of G. diazotrophicus in host plants roots. (a) meristematic zone of the elongating root; (b) G. diazotrophicus penetrates the epidermal cell wall by secretion of lytic enzymes; (c)the plasma membrane pinched off via endocytosis forms a membrane surrounding vesicles containing bacteria;(d) vesicles with G.diazotrophicus are surrounded by a membrane analogous to the symbiosome membrane of rhizobia. (Dent, 2015)

1.3.7. Further effects of *G. diazotrophicus* colonisation

1.3.7.1. Hormone production and nutrient uptake

Production of plant growth hormones by associative and endophytic bacteria is considered an important mechanism promoting host plant growth ([8]; [226]) and has been reported in several associative and endophytic diazotrophic bacteria such as *Azospirillum sp., Klebsiella sp., Gluconacetobacter sp., Azoarcus sp., Herbaspirillum sp., Enterobacter sp., and Azobacter sp.* [8].

Besides fixing N, *G. diazotrophicus* has been proven to produce a wide range of plant growth hormones, such as auxins and gibberellins (e.g. GA1 and GA3) [13],[226],[8]; several of these are predominant in regulating processes involved in determination of root architecture and are also reported to improve nutrient uptake [231], [192], [203]. Gibberellin production, for example, plays an

important role in the early stages of plant development by enhancing shoot and root growth and increasing root hair density [101], [191].

Among the auxins involved in plant growth promotion, IAA is one of the most relevant**.** Production of IAA by *G. diazotrophicus* in defined culture medium has been demonstrated and it was suggested that this could promote rooting and improve growth by a direct effect on metabolic processes [67]. According to studies by Suman et al., (2001) IAA production was present in almost all the *G. diazotrophicus* strains isolated from the diverse sugarcane genotypes maintained at the Indian Institute of Sugarcane Research, India. Interestingly, Madhaiyan et al. (2006) observed that, under laboratory conditions, the addition of pesticides to the growth media of pure cultures of *G. diazotrophicus* reduced the production of IAA and gibberellin A3 (GA3). Tests were led on different types of insecticides, herbicides and fungicides and, even though to different extents, all demonstrated to induce a reduction in Gd production of IAA and GA3.

A less clear topic is the mechanisms involved in increasing the host plant nutrient uptake; it could be indirectly related to the effects of these bacteria on plant development. In fact, studies have demonstrated the ability of *G. diazotrophicus* to produce siderophores and other molecules that help the solubilisation of important minerals such as phosphorus, potassium, and zinc [80], [37]. However, a bacterial-mediated increase in root weight, as well as the root length and root surface area, could lead to an increase in the volume of soil explored by the plant and thus favour the intake of many molecules [70], [16], [87], [249]. As an example of the *G. diazotrophicus* effect on the root system, an increase in root dry weight was observed after sugarcane inoculation with this bacterium in studies from Sevilla et al. (2001) and Oliveira et al. (2003). It is still not clear if this is the only mechanism involved in promoting nutrient uptake since some studies have observed an enhancement of the uptake with no parallel increment in root density and extension. Other, still uncharacterised, mechanisms could reside behind this phenomenon. Besides improving plant nutrition, promotion of root growth might also bring benefits to bacteria since root tissues are also the main habitat for associative and beneficial endophytic bacteria; however, it is still unclear how determinant it is for the success of bacterial colonisation [27].

1.4. Plants response to endophytes

Plant gene expression profiling studies are of foremost importance in helping to understand and integrate plant responses during association with beneficial microbes. These studies have the aim of elucidating the complex signalling interchange that occurs between the bacterium and its host while establishing a symbiotic relationship. The complexity of the plant-bacteria interaction leads to the involvement and modulation of a large number of genes and related pathways.

Here below are described the most relevant elements that have been reported in the literature to be involved in symbiosis establishment.

1.4.1. Plant receptors

A fundamental question to be addressed is whether plants react to the beneficial microorganisms as minor pathogens or develop a specific response towards them [184][241]. Molecular patterns on the surface of beneficial microbes are often similar to the ones of pathogens, and both types of microorganisms are similarly recognized by the plant [242]. However, recent findings have indicated that differences can be found between the molecular motifs in the structure of common bacterial MAMPs (microbe-associated molecular patterns) and the lipopolysaccharides (LPS) of pathogenic and plant growth-promoting rhizobacteria (PGPR). Moreover, the rhizobacterial LPS are capable of priming the plants for enhanced defence against a wide range of pathogens [161].

A recent review from Pinski et al. (2019) [183], summarized the current understanding of plant genetic responses to the interaction with endophytes. A number of plant receptors were indicated as involved in the recognition step of bacteria by plants: receptor-like kinases (RLK), which include a leucine-rich repeat that contains receptor-like kinases (LRR-RLKs), wall-associated kinases (WAK), lectin receptor-like kinases (LecRLKs) and Lys-motif receptors (LysM). These receptors are well known for their participation in the recognition of phytopathogens but only a few studies have showed their involvement in identifying PGPB [26].

1.4.2. Cell wall modulating enzymes

A number of cell wall modifications have been reported to be elicited during the interaction of plants with endophytes and associative bacteria. Several endophytes secrete cellulases and other enzymes that have the function to weaken the plant cell wall and thus facilitate the entrance in the plant inner compartments. Transcriptional analyses conducted on various plant species that had been inoculated with endophytic bacteria have indicated the modulation of sets of genes that are related to cell wall modifications, which are likely to favour the colonisation process. These include hydroxyproline-rich glycoproteins (HRGPs), expansins and pectinesterases. [106]

HRGPs are reported to be involved in many biological functions and are generally divided into three complex multigene families: arabinogalactan proteins (AGPs), extensins and proline-rich proteins [106]. The involvement of extensins in interactions with pathogenic and beneficial bacteria is well characterised. The increased expression of extensins that is observed following plants exposure to pathogens plays a critical role in plant defence by strengthening the cell wall. Interestingly, increases in extensins were also found in nodules that had been colonised by symbiotic *R. leguminosarum*. Extensins form part of the root mucilage together with AGPs, pectic polysaccharides, secondary metabolites, antimicrobial compounds and extracellular DNA. These compounds play a key role in root defence through the formation of a root extracellular trap. This structure is able to simultaneously enclose phytopathogens and attract beneficial microbes [29]. AGPs has also shown to have an influence on rhizosphere microbiome composition; for example, it can lead to an enrichment of the portion of bacteria present in the rhizosphere that can hydrolyse and metabolise AGPs-derived sugars for their growth [161].

Developmentally, expansins facilitate loosening of the cell wall components during division and pectinesterases catalyse the de-esterification of polygalacturonans. Both these proteins have been found to be features of endophytic interactions [100]. Upregulation of expansin gene expression was, for example, observed in rice roots inoculated with bacteria belonging to the *Azospirillum* species. Interestingly, the identical upregulation of this expansin

was observed regardless of the type of colonisation—rhizospheric or endophytic [56].

In endophytic colonisation, genes encoding pectinesterases, pectate lyase, fasciclin-like AGPs, extensin, cellulose synthase and COBRA-like proteins were among the upregulated genes [100]. Intriguingly, COBRA-like proteins have been pointed out as key regulators in the orientation of cell expansion and regulation of the status of cellulose crystallinity [163]. Furthermore, the upregulation of cell wall loosening enzymes may facilitate endophytic penetration and lead to systemic endophytic colonisation.

1.4.3. Plant hormones

As already mentioned, hormonal metabolism regulation plays a pivotal role in the host-bacteria communication.

In addition to phytohormone production by the bacterial side, plants might modulate endogenous biosynthesis of these growth regulators, and others, in response to association with microorganisms. The transcript profile of *in vitro* grown sugarcane plants inoculated with *G. diazotrophicus* revealed differentially expressed genes related to the auxin, gibberellin, and ethylene classes of growth hormones [164], [225][243]. Two ethylene receptors and one transcription factor showed opposite patterns of expression in response to beneficial diazotrophs and pathogenic bacteria, in two sugarcane genotypes with contrasting BNF efficiency [31].

The role of Ethylene, Salicylic Acid and Jasmonic Acid in regulating endophytic colonisation and the diversity of endophytic bacterial populations has been object of several studies. Sugarcane that had been colonised by *G. diazotrophicus* PAL5 and the other endophytic diazotroph *H. rubrisubalbicans* HCC103 exhibited increased expression of a putative ET receptor (SCER1) at 24 h as well as seven days after inoculation. Conversely, a decrease in the expression of SCER1 was observed after inoculation with pathogenic bacteria and virus [31]. It has been hypothesised that an increase in the Ethylene receptors may reduce the host's sensitivity to Ethylene in order to lower the plant defence mechanisms and allow colonisation [31].

Internal colonisation by *G. diazotrophicus* PAL5 strain and *S. enterica* serovar *Typhimurium* 14,028 was also found to be favoured in an *A. thaliana* mutant that was defective in the Salicylic Acid-mediated defence response [43]. As observed also in the case of other defence hormones, the disruption of the Salicylic Acid -mediated and Salicylic Acid -independent defence responses can exert a negative effect on the diversity of an endophytic bacterial community.

Similarly to observations for the Salicylic Acid response, Jasmonic Acid signalling was induced in rice roots colonised by *Azoarcus* sp. BH72 [148]. JA biosynthesis mutants (fad3/7/8) showed higher epiphytic colonisation. A very intriguing theory has been proposed based on the finding that Jasmonic Acid signalling pathways activation led in *A. thaliana* to an alteration in rhizosphere bacterial composition and to an enrichment of bacterial species that are closely related to one that is known to be involved in plant defence. This could suggest that plants may recruit useful microbes based on the current needs of the plant [25].

Another key player in the plant bacteria interaction is abscisic acid (ABA). This hormone regulates many processes involved in plant development and adaptation to biotic and abiotic stresses. ABA is synthetized by plants under stress conditions, and it initiate defence response mechanisms that typically involve the regulation of stomatal opening and expression of defence-related genes involved in the resistance to environmental stresses.

Several recent studies have demonstrated that ABA plays a critical role, not only in the control of water loss by transpiration, but also in pathogen response and that ABA signalling is highly interconnected with biotic and abiotic stress tolerance. Stomata are considered to be a main barrier against attacks from the outside thus the regulation of stomatal movement is an early stage of defence mechanism against pathogen entrance and consequent infection in the host plant [123].

ABA related plant responses to bacteria are not exclusively restricted to the defence response against pathogens. As previously mentioned, plant response towards pathogens is often similar and overlapping to the one towards plant growth promoting microorganisms and thus studies have shown how plant ABA status can mediate the interactions with beneficial microbes.

For example, *Bacillus. megaterium* inoculation led to a stimulation in growth of wild type tomato (*S. lycopersicum*), but inhibited shoot biomass accumulation of ABA-deficient tomato mutants [185].

Microbes can influence expression of the plant genes (e.g., *NCED3*, *ABA2* and *ABA3*) responsible for ABA biosynthesis *in planta* [244]. The inoculation of sugarcane (*Saccharum officinarum*) roots with *Gluconacetobacter diazotrophicus* led to differential transcription of genes responsible for ABA biosynthesis and signalling between inoculated and uninoculated plants: *G. diazotrophicus* stimulated ABA-dependent signalling genes in the shoots, which may confer drought resistance [244].

Nevertheless, it can be difficult to assess whether changes in plant ABA status can be ascribed to direct microbial ABA biosynthesis or to changes in ABA synthesis *in planta* deriving from changes in plant water status resulting from plant growth promotion [115].

1.4.4. Lignin synthesis

Among the defence responses identified as stimulated by endophytic interaction is lignin synthesis. Lignin is one of the main components of the plant cell wall and plays a key role in a number of physiological functions like growth, development, lodging resistance and responses to biotic and abiotic stresses [128].

The accumulation of lignin in the cell wall is an important response to phytopathogens and is a barrier against the spread of bacterial cells; it also poses a barrier to the attack of fungi, reducing the ability of their lytic enzymes and toxins to enter through the cell wall [128]. It may thus appear surprising that lignin accumulation can also occur in the case of beneficial endophytes colonisation. As an example of this, a higher lignin content was observed in the roots of cotton after inoculation with *Bacillus amyloliquefaciens* pb1 [100]. In some cases, an increase in the expression of the cell wall bound peroxidases and cinnamyl dehydrogenase (CAD), enzyme involved in cell wall lignification, is observed as a result of an endophytic colonisation [219] [230]. It may be hypothesised that the pattern and/or type of lignin that is produced in response to endophytes are distinctive to this type of interaction [183].

Elucidating the plant's response to the interaction with *G. diazotrophicus* is one of the major interests of this study; this way, a clearer picture of the setting in which the bacteria-plant interaction is happening can be obtained and thus lead to a stronger understanding of what the best conditions to establish a stable and fruitful symbiosis are.

1.5. Interaction between *G. diazotrophicus* and other soil microorganisms.

In addition to what has been previously reported about beneficial effects of these bacteria on plants, various experiments demonstrated that associative and endophytic bacteria may indirectly benefit plant growth by increasing the plant's tolerance to biotic and abiotic stresses [5], [200], [27].

G. diazotrophicus has demonstrated the ability to produce some advantageous molecule(s) that can exert an antimicrobial action towards plant pathogens as well as favour its own colonisation. Certain cell wall degrading enzymes such as endogluconase, endoxyloglucanase and endopolymethylgalacturonase in *G. diazotrophicus* [1], have been suggested as candidates that may help the bacteria to successfully outcompete other rhizosphere microorganisms and colonise the internal tissues of plant systems. *G. diazotrophicus* appears to be able to secrete proteins called bacteriocins that impede the growth of specific plant pathogens (e.g. *X. albilineans* for sugarcane) and impart a lysozyme-like activity on the innermost thick cell wall layer of the pathogen [18]. Recently, Blanco et al. (2010) studied the mechanism of inhibition of *X. albilineans* by *G. diazotrophicus* and concluded that xanthan is produced as a consequence of the infection of the pathogen *X. albilineans* in sugarcane stalks, but it was nullified by *G. diazotrophicus* when the endosymbiont is grown in plant tissues together with the pathogen. Mehnaz and Lazarovits (2006) also demonstrated a *G. diazotrophicus* dependent anti-fungal activity (both in wild-type and *nifD*-strains) against various *Fusarium spp.* (except *Fusarium culmorum* and *Helminthosporium carbonum*) when they were cultivated in PDA medium. In a study by Logeshwaran et al. (2011) the antibiotic pyoluteorin produced by *G. diazotrophicus* helped in the suppression of soil borne pathogenic fungus such as *F. oxysporum* in sweet potato. *G. diazotrophicus* was also found to be able to

carry out antagonistic activity on nematodes like *Meloidogyne incognita* by the production of volatile fatty acids [208].

Besides the favourable biocontrol activity against plant pathogens, *G. diazotrophicus* has shown enhanced plant growth promoting activities once co-inoculated with other microorganisms. Co-culturing with a specific amylolytic yeast strain, it has shown to release up to 48% of its fixed N and make it available to the yeast, suggesting that a similar process might occur during association with plants [36].

A positive synergistic interaction between strains of *Gluconacetobacter sp.* and *Burkholderia sp.* has also been observed for their plant growth promotion activity on rice (*Oryza sativa*) host plants. This was probably due to a bacterial driven enhancement of the plant's ability to uptake phosphorous and other nutrients from the soil [229].

In experiments conducted co-inoculating *G. diazotrophicus* and *Herbaspirillum spp.* in sugar cane plants, leaf N content analysis showed an enhanced quantity of N in *G. diazotrophicus* and *Herbaspirillum spp.* inoculated plants with and without N-fertilisation [157].

2. Aims of the project

The main aim of this project was to investigate the effects elicited on tomato plants by the nitrogen fixing diazotroph *Gluconacetobacter diazotrophicus* (AZ0019 strain from Azotic Technologies Ltd), to elucidate the mechanisms that lie behind its positive effect on tomato plant health and yield.

First, the setting up of a consistent microbial inoculation protocol for tomato plants was addressed. Preliminary investigations on different strategies were tested taking into consideration how the N content and the type of substrate could influence the plant-bacteria symbiosis establishment. A hydroponic set-up in which Gd was applied on plants through root dipping, was selected as the most efficient and consistent inoculation method.

To assess the differential effects elicited by the inoculation of either the WT or *nifD*$^-$ (N-fixation impaired mutant) strain of Gd, investigations were carried out using the above-mentioned hydroponic set up. The *nifD*$^-$ mutant was employed in order to evaluate the biological N-fixation (BNF) contribution in the plant growth promoting activity provided by Gd. In association with the characterisation of the phenotype induced in tomato plants by exposure to either the WT or the *nifD*$^-$ strain, a quantitative estimate of BNF was performed through the use of a ^{15}N tracer to monitor the fixed N incorporation in the plant chlorophyll.

To address the molecular response elicited in tomato plants by the interaction with either the WT or *nifD*$^-$ strains of Gd, a transcriptomic analysis was also carried out. Assessments were performed at both 1- and 14-days post inoculation (dpi) and in either the absence or the presence of KNO_3 in the plant growth substrate.

3. Materials and Methods

3.1. Growth media

Table 1. Composition of growth media employed for G. diazotrophicus growth.

Media	Component	Procedure	Sterilisation	Volume to add per l of media
LGI-P	Sugar	325 g sucrose in 650 ml H_2O	0.2 µm filter using 1L unit	200 ml
	Buffer	7 g dipotassium phosphate 21 g monopotassium phosphate in 350 ml H_2O pH 5.5 with acetic acid	autoclave	10 ml
	Nitrogen	1.75 g yeast extract in 350 ml H_2O pH 5.5 with acetic acid	autoclave	10 ml
	Minerals	0.2 g Sodium molybdate dihydrate in 100 ml H_2O	autoclave	1 ml
		1 g Calcium chloride dihydrate in 200 ml H_2O	autoclave	4 ml
		0.5 g Iron (iii) chloride hexahydrate in 200 ml H_2O	autoclave	4 ml
		1 g Magnesium sulfate heptahydrate in 200 ml H_2O	autoclave	4 ml
	Agar	15 g agar per l H_2O (solid)	autoclave	762 ml
ATGUS	Sugar	67.5 g glucose 45 g mannitol in 500 ml H_2O	0.2 µm filter using 500 ml unit	20 ml
	Buffer	84 g dipotassium phosphate 11.375 g monopotassium phosphate 77 g MES hydrate in 350 ml H_2O pH 6.5 with acetic acid	autoclave	20 ml
	Nitrogen	40.5 g yeast extract in 750 ml H_2O pH 6.5 with acetic acid	autoclave	50 ml
SYP	Sugar	325 g sucrose in 650 ml H_2O	0.2 µm filter using 1 l unit	20 ml

	Buffer	17.5 g dipotassium phosphate 52.5 g monopotassium phosphate in 350 ml H_2O pH 6.2 with acetic acid	autoclave	20 ml
	Nitrogen	45 g yeast extract in 750 ml H_2O	autoclave	50 ml
MS	Salts	-	autoclave	2.7 g M2909
AceLGI-P	Sugar	500 g sucrose in 1000 ml H_2O	0.2 µm filter using 1L unit	200 ml
	Buffer (20 mM, pH 4.0)	37.50 g monopotassium phosphate 47.36 ml acetic acid 17.67 g potassium acetate in 500 ml H_2O	autoclave	10 ml
	Nitrogen	1.75 g yeast extract in 350 ml H_2O pH 4 with acetic acid	autoclave	5 ml
	pH indicator	1 g bromothyol blue In 40 ml 1 M KOH (in 93% ethanol) Then top up to 200 ml with sterile deionised water	-	5 ml
	Minerals	0.2 g Sodium molybdate dihydrate in 100 ml H_2O	0.2 µm filter	1 ml
		1 g Calcium chloride dihydrate in 200 ml H_2O	autoclave	4 ml
		0.5 g Iron (iii) chloride hexahydrate in 200 ml H_2O	0.2 µm filter	4 ml
		1 g Magnesium sulfate heptahydrate in 200 ml H_2O	autoclave	4 ml
	Agar	15 g agar per l H_2O (solid)	autoclave	750 ml

3.2. Antibiotics working concentrations

Table 2. Stock and working concentrations of employed antibiotics.

Antibiotic	Stock Concentration	Working Concentration
Gentamycin	10 mg ml^{-1}	10 µg ml^{-1}
Kanamycin	50 mg ml^{-1}	50 µg ml^{-1}
Spectinomycin	50 mg ml^{-1}	50 µg ml^{-1}
Streptomycin	50 mg ml^{-1}	50 µg ml^{-1}

3.3. Bacterial strains and growth conditions

Table 3. Characteristics and source of strains used.

Bacterial strain	**Description and relevant characteristics**	**Source**
***G. diazotrophicus* AZ0019**		Azotic Technologies Ltd.
***G. diazotrophicus nifD*$^{-}$**	nifD- [Km^R]	R. Fray Lab, UoN
***E. coli* DH5α (chemically competent)**	F- Φ80lacZΔM15 Δ(lacZYA-argF) U169 recA1 endA1 hsdR17(rk-, mk+) phoA supE44 thi-1 gyrA96 relA1 λ-	Thermo Fisher Scientific
***E. coli β2163* (electrocompetent)**	(F-) RP4-2-Tc::Mu ΔdapA::(erm-pir) [Km^R; Em^R]	R. Fray Lab, UoN
***G. diazotrophicus GGG* (GUS, GFP Tagged)**	pBBR1MCS5 [Gm^R] pRGS561 [Spe^R; St^R]	R. Fray Lab, UoN
***G. diazotrophicus nifD*$^{-}$ (GUS Tagged)**	pRGS561 [Spe^R; St^R]	R. Fray Lab, UoN

Gluconacetobacter diazotrophicus AZ0019 strain employed in this study was provided by Azotic Technologies Ltd.

Escherichia coli DH5α chemically competent cells were purchased from Thermo Fisher Scientific.

The *nifD*$^{-}$ strain was produced in Fray's lab by conjugation of Gd with *E.coli β2163* carrying the pSW23T-nifD- plasmid. A disruption of the *nifD* gene was obtained through insertion of a Kanamycin cassette. The *nifD* gene encodes for the MoFe subunit of the nitrogenase enzyme; its disruption leads to the impossibility of synthetizing a functional form of the enzyme and thus to the impairment of the nitrogen fixation process.

The *G. diazotrophicus* GGG (GUS, GFP) was obtained by transformation by electroporation of WT AZ0019 Gd strain with the pBBR1MCS5 [Gm^R] GFP-cassette carrying plasmid and by conjugation between *E. coli β2163* that had been previously transformed by electroporation with the pRGS561 [Spe^R; St^R] GUS cassette-carrying plasmid. Screening of the positive colonies, respectively

to GFP and GUS phenotype, was carried out on ATGUS medium added with suitable antibiotics.

The *G. diazotrophicus nifD*$^{-}$ (GUS Tagging) was obtained by transformation by conjugation between *nifD*$^{-}$ strain and *E. coli β2163* that had previously been transformed by electroporation with the pRGS561 [Spe^{R}; St^{R}] GUS cassette-carrying plasmid.

The pRGS561 [Spe^{R}; St^{R}] GUS cassette-carrying plasmid was extracted from a Gd strain carrying this plasmid and kindly provided by Fuentes-Ramièrez E.L. [66]. Extraction was performed with a Sigma – Plasmid Extraction Kit. Screening of the positive colonies was performed on ATGUS medium added with suitable antibiotics.

All the Gd strains were grown in ATGUS or SYP or LGI-P media at 28 °C. For liquid cultures, incubator was set at a speed of 180 to 200 rpm.

All the *E. coli* strains were grown in Luria Beltrani (LB) medium at 37 °C. For liquid cultures, the incubator was set at a speed of 180 to 200 rpm. In the case of the *β2163* strain, Diaminopimelic Acid (DAP) was added to the medium at a working concentration of 300 µM.

3.4. Production of Gd electrocompetent cells

Gd cells (from -80 °C stock) were streaked on ATGUS Petri dishes and incubated for 48 hours at 28° C. Single colonies were scraped from the plate into 10 ml ATGUS liquid culture in a 100 ml flask. The flask was incubated overnight at 28 °C at 150 rpm. The overnight culture was used to prepare a new inoculum (200 ml liquid in 1 l flask) in ATGUS liquid media to a final OD_{600} of 0.07. A second incubation was performed by shaking at 200 rpm until the OD_{600} had reached 0.25. The culture was then chilled on ice for 15 min. Cells were then harvested by centrifugation at 4000 rpm/3800 g (Thermo Scientific™ TX-400 4 x 400 ml Swinging Bucket Rotor) for 15 min at 4°C. The supernatant was discarded, and the cells re-suspended in 100 ml ice cold 10% glycerol, gently mixing the cells to wash them and centrifuged again at 4000 rpm/3800 g (Thermo Scientific™ TX-400 4 x 400ml Swinging Bucket Rotor) for 15 min at 4 °C (with cells kept on ice at all times). The washing step was repeated twice,

ensuring cells were kept on ice at all times. Finally, the final washed cells were resuspended in 1 ml ice cold 10% glycerol. Aliquots of 40 µL were frozen in liquid nitrogen and stored at -80 °C.

3.5. *E. coli* DH5α competent cells transformation

E. coli DH5α were transformed according to the Subcloning Efficiency™ DH5α™ Competent Cells (Invitrogen) protocol [92].

3.6. Gd electroporation protocol

After thawing on ice one vial of electrocompetent Gd cells, 1 µg of plasmid was added to the cells. The cells and plasmid mix was then transferred to a chilled 2 mm electroporation cuvette. Electroporation was performed with a Gene Pulser apparatus at 1800 V with resulting time constant 4.0-4.8 ms. Immediately after electroporation, 1 ml ice cold ATGUS medium was added to the cuvette, cells are re-suspended gently and transferred to a 2 ml tube and incubated at 28 °C for 3 hrs at 100 rpm. The transformed cells were plated on ATGUS media with selective antibiotics and incubated at 28 °C for 2-3 days.

3.7. Gd conjugation protocol

Cultures of Gd and *E.coli β2163*-GUS cells (preferably without antibiotics) were grown overnight at suitable temperature; cells were pelleted at 4000 rpm/3800 g (Thermo Scientific™ TX-400 4 x 400 ml Swinging Bucket Rotor) at 22 °C for 10 minutes. Collected cells were washed once with ~5 ml of sterile (autoclaved) PBS Buffer ph 7.3. 50 µl of each bacterial culture was then re-suspended in ~5 ml of sterile $MgSO_4$ 10 mM (filter sterilised). Cell resuspension was vortexed briefly, transferred into a sterile syringe and filtered through a previously sterilised Millipore membrane. The membrane was then carefully transferred face up on a non-selective plate (PDA+DAP) and incubated overnight at 28 °C. After overnight growth, the filter was placed in a 15 ml tube filled with sterile PBS buffer and vortexed until the cells were well re-suspended. The cells were then diluted in 5% EtOH: this steps helps to more efficiently get rid of *E.coli* cells, since it has been demonstrated to effectively inactivate *E.coli* cells while Gd showed good capacity for surviving after overnight incubation at this concentration (Fig. 10). Suitable dilutions were then plated on selective media and incubated overnight until colonies were sufficiently big to perform

GUS/GFP screening. PCR with specific primers was later performed on re-streaked positive colonies in order to confirm the acquisition of the plasmid.

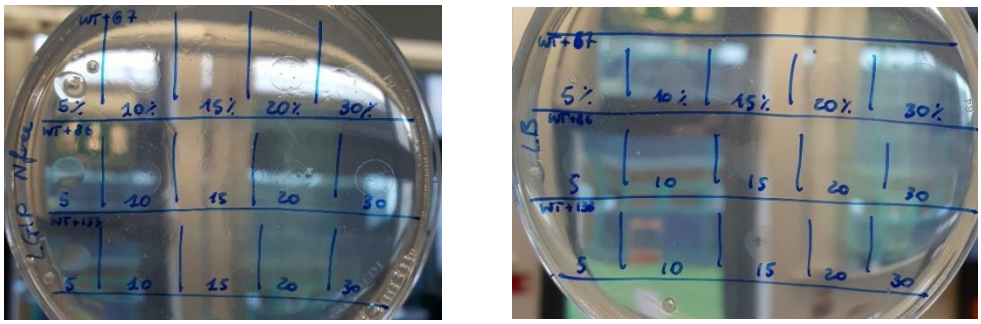


Fig. 10. Left: overnight growth of Gd in different concentrations of EtOH. Right: overnight growth of E. coli in different concentrations of EtOH; 5% showed high growth even after overnight incubation for Gd, while the same concentration resulted to be detrimental for E.coli and led to no growth.

3.8. Plant materials and plant growth conditions

Tomato (*Solanum lycopersicum*) seeds of Money Maker cultivar were purchased from B&Q, Just Seed and Mole's.

Tomato seeds of Micro Tom variety were kindly donated by Prof. G. Seymour's Lab, University of Nottingham.

For in vitro germination both Conviron and Growth Rooms were employed. Seed germination on MS Agar medium was performed in small, sterile, glass jars stored in a Conviron GEN1000 Plant Growth Chamber with a photoperiod of 16 hrs light and 8 hrs dark, at 28/20 °C (light/dark) and 65% humidity. In other cases, a Phytotron Growth Chamber was used for seed germination on MS Agar. If not differently stated, the photoperiod was set at 12/12 hrs light/dark at 28/20 °C (light/dark).

For rockwool experiments Grodan® rockwool plugs were employed for seed germination, plantlets were incubated in Growth Rooms with a photoperiod of 16 hrs light and 8 hrs dark, at 23/16 °C (light/dark). Bigger Grodan® rockwool cubes and slabs were employed for longer term experiments.

In glasshouse experiments, tomato plants were kept under a photoperiod of 16 hrs day/ 8 hrs light. The temperature was kept at an average of 26 °C during winter and of 28 °C during summer. The photoperiod, along with the temperature, was affected by seasonal changings.

Two types of soil were employed for glasshouse experiments:

- Levington M3 high nutrient potting soil, for seed germination. The main component of this compost is peat with a small amount of coir fibre to aid water uptake. This product is specifically designed for vigorous plants, including tomatoes. ph ranges from 5.3 to 6.0. Particle size: 0-10 mm. Nutrients added: 204N, 104P, 339K mg l^{-1}. No fertilisers were added during plants growth in this medium (1 month long).

- Klasmann Traysubstrate, employed for re-potting. pH of around 6.0. Conductivity: 0.35 dS m^{-1}. Nutrients Added: 12N 14P 24K kg m^3. This soil was mixed with 50% silver sand to further lower the N (and other nutrients) concentration.

Liquid fertiliser was used for the watering of plants in some experiments evaluating the nitrogen effect on plant-Gd interaction. Nutrients ratio was as follows: 15:7:30 N: P: K mg l^{-1}. Nitrogen was provided in the form of NH_4 NO_3.

3.9. GUS staining protocol

Table 4. Recipe for GUS Staining Solution.
**Ferricyanide and Ferrocyanide stock solutions were prepared in 0.2 M phosphate buffer, pH 7.0 and replaced every 6 weeks.*
This stock solution was stored at 4 °C in the dark.

Stock solution	**For 100 ml**
0.02 M Phosphate Buffer pH7	50 ml
Sterile Distilled Water	36.9 ml
0.5 mM EDTA	2 ml
0.1% (v/v) Triton X-100	100 µl
10 mM Potassium Ferricyanide*	5 ml
10 mM Potassium Ferrocyanide*	5 ml

Whole plants or plant material were placed in a suitable container so that the minimum amount of staining solution is needed. Preparation of the Staining Solution is reported in Table 4.

X-gluc (5-bromo-4chloro-3indolyl-beta-D-glucuronic acid cyclohexylammonium salt) was added to the Staining Solution just before use at

a concentration of 0.5 mg ml^{-1}. X-gluc was dissolved in a small volume (20-100 µl) of dimethylformamide.

The staining solution was then added to the vials containing the plant material in order to completely submerge the samples.

To favour the solution entry inside the plants tissue, a bench vacuum pump was used for 30 min.

The samples were kept in the dark at 28 °C (or at room temperature) overnight.

Plants aerial parts were then de-stained with 70% EtOH treatment until complete removal of the chlorophyll was achieved. To fix the tissues for long term conservation, samples were then preserved in 2% glutaraldehyde in 0.1 M phosphate buffer, pH 7.0.

3.10. Seed coating protocol

Gd from -80 ˚C stock culture was streaked on a fresh ATGUS plate and incubated at 28 ˚C for 48 hrs.

Around 10/15 Gd single colonies were picked and inoculated in 10 ml of liquid ATGUS and incubated overnight with shaking (~175 rpm) at 28 ˚C. This culture was used to inoculate 200 ml of fresh ATGUS. The fresh inoculum was incubated overnight with shaking (~175 rpm) at 28 ˚C. The 200ml culture was harvested in 50 ml Falcon tubes and cells were pelleted at 4000 rpm/3800 g (Thermo Scientific™ TX-400 4 x 400ml Swinging Bucket Rotor) for 10 minutes. The pellets were pooled together in one Falcon tube and re-suspended in less than 5 ml of supernatant. OD_{600} was measured with a spectrophotometer. The cell suspension was then mixed with N-Fix (3%) (a specific mixture that was being tested by Azotic Technologies Ltd as a sticky agent to favour bacterial adhesion to the seed surface) until a final OD_{600} of 2/2.5 was reached. Serial dilutions of this culture were performed and plated onto ATGUS media and after 48 hrs incubation at 28 ˚C, single colony counting provided the starting cell concentration (which was usually kept between 10^9 and 10^{11}).

Tomato Money-Maker seeds were soaked in around 5 ml of either N-Fix 3% only (UT) or N-fix-bacteria mix (treated samples) for 30 min, with occasional stirring.

After the 30 min incubation, seeds were drained from the liquid, spread on a sterile Petri dish and dried at room temperature under sterile conditions

overnight. Fully dried seeds were sown in 12 or 6 pot trays filled with Levington M3 soil.

3.11. Bacterial inoculum preparation for hydroponic system

WT and *nifD*- Gd were streaked on Petri dishes filled with solid ATGUS medium (with addition of Kanamycin for *nifD*-) from -80 °C stocks. After three days incubation at 28 °C, a first 20 ml liquid pre-inoculum was prepared starting from biomass collected from Petri dishes. Incubation overnight at 28 °C with shaking at 200 rpm.

A second inoculation (volume according to the amount of inoculum needed) was prepared in liquid ATGUS and grown overnight at 28 °C with shaking at 200 rpm. Bacteria were aliquoted in sterile 50 ml tubes and pelleted in a centrifuge at 4000 rpm/3800 g (Thermo Scientific™ TX-400 4 x 400 ml Swinging Bucket Rotor), 23 °C for 10 minutes. Bacteria were washed and re-pelleted twice with sterile distilled water. After washing, bacteria were re-suspended in the hydroponic nutrient solution to reach the desired OD_{600}, which was subsequently used for plants treatment.

After 72 hrs incubation, the nutrient solution was thoroughly removed from hydroponics boxes and substituted with fresh solution. Modified Hoagland solution (see 3.13 Section) was renewed once a week.

3.12. Seed sanification protocol

Tomato seeds were immersed for 10 minutes in 5% sodium hypochlorite and then carefully and repeatedly rinsed with sterile distilled water until the bleach was completely removed. Subsequently, seeds were incubated in 70% EtOH for 5 minutes. After incubation, a further and thorough wash with sterile distilled water was performed. Seeds were then dried on sterile Petri dishes kept under a bacteriological flow hood.

3.13. Modified Hoagland hydroponic nutrient solution

Table 5. Composition of N-deficient modified Hoagland nutrient solution employed in hydroponic experiments.

Compound	**Desired compound concentration (1xNS) mg l^{-1}**
K_2SO_4	261.39

$MgSO_4$ $7H_2O$	369.72
KH_2PO_4	136.09
NaCl	29.23
$Ca(H_2PO_4)_2$ H_2O	116.03
$CaCl_2$ $2H_20$	294.02
$FeSO_4.7H_20$ & EDTA 2Na $2H_20$	13.005
Micronutrients (See below for recipe)	0.5 (ml l^{-1})

Table 6. Composition of Micronutrients stock solution to be added to the nutrient solution employed in hydroponic experiments. When N was required in the nutrient solution: 10.5 ml of 1 M KNO3 was added to 1 l of Nutrient Solution (final concentration: 1.06 mg ml-1).

Micronutrients	**Concentration in NS mg l^{-1}**
$CuSO_4$ $5H_2O$	0.5
$ZnSO_4$ $7H_2O$	3
$MnSO_4$ $4H_2O$	2
H_3BO_3	4
Na_2MoO_4 $2H_2O$	0.5

3.14. Hydroponic system setup

Seeds of *Solanum lycopersicum* L. cv. Money Maker were first surface sanitised by soaking with 70% ethanol for 10 min, followed by vigorous washing with sterile distilled water and soaking in 5% sodium hypochlorite for a further 10 min in a 50 ml tube. Seeds were then washed several times with sterile distilled water. Surface-sanitised seeds were sown in sterile hydroponic boxes (15/20 seeds per box) each filled with 300 ml of half strength (0.5 x) modified Hoagland solution either in the absence of a nitrogen source (NoN condition) or with the addition of 2 mM KNO_3 (N condition). Five boxes were used for each treatment. Boxes were incubated in a growth chamber (Conviron GEN1000 / Binder kbwf720, Bohemina, NY, USA) set at 80% humidity, 16hrs photoperiod, at a temperature of 25±2 °C).

3.15. Acetylene Reduction Assay (ARA) protocol (GCMS FID)

Acetylene Reduction Assay is a standard method employed to measure the Nitrogenase activity of nitrogen fixing bacteria. It is based on the ability of the

Nitrogenase enzyme to reduce triple bounded substrates and in particular acetylene (C_2H_2) to ethylene (C_2H_4).

Previously autoclaved 30 ml glass vials were filled either with 15 ml MilliQ Water (Control) or 15 ml of bacterial liquid cultures of WT Gd / *nifD*$^-$ Gd in semi-solid ATGUS N-Free medium. Three replicates were set per each treatment. Incubation was carried out for 72 hrs at 28 °C.

After 3 days bacterial growth, vials were stoppered with sterilised (overnight in 70% EtOH) seal tight rubber stoppers with a pierceable septum and 1 ml of acetylene was added to the headspace with a 1 ml sterile syringe. Incubation was carried out for a further 72 hrs at 28 °C. Acetylene gas was developed from CaC_2 granules mixed with sterile distilled water. Calculations for the required amount of acetylene to be developed from CaC_2 were referred to the following proportion as recommended in Castle (2010) protocol [30] for Acetylene Reduction Assay: 1 g CaC_2= 130 ml of C_2H_2 gas.

Analysis of the headspace was performed with a GC equipped with a Flame Ionisation Detector (FID) set at 60 °C with the injector at 110 °C, with 3 ml min^{-1} flow rate of carrier gas. Injection was manually performed with 1 ml sterile syringes equipped with 23/25 gauge needles. 1 ml of the headspace was manually injected into the GC and the presence of peaks at 3/3.2 minutes retention time, corresponding to Ethylene, was evaluated. Quantification of analysed samples was calculated from the standard reference curve.

3.16. Acetylene Reduction Assay (ARA) protocol_(PTR-MS)

WT, *nifD*$^-$, *GUS nifD*$^-$, *GGG* strains were streaked on Petri dishes filled with solid ATGUS medium from -80 °C glycerol stocks. A 20 ml liquid inoculum was prepared in liquid ATGUS medium starting from biomass taken from Petri dishes. Incubation was done at 28 °C with shaking at 200 rpm.

Previously autoclaved 20 ml glass vials were filled with 5 ml of semisolid (0.7 %) N-free ATGUS medium. Ten vials per each treatment were inoculated with 100 µl of bacterial liquid cultures (≈10^8 for all strains) of either of the tested strains. Vials were stoppered with sterilised (UV light treated) seal tight stoppers with a pierceable septum. Each treatment was repeated for five times in order to

have material for measurements at 5 time points. Incubation was carried out for 72 hrs at 28 °C.

Acetylene (C_2H_2) was developed from CaC_2 reaction with H_2O (0.015 g of CaC_2 in a 20ml gas tight vial to which 1.5 ml of sterile distilled water was added) and injected into the headspace of each vial with a sterile syringe to reach a final concentration of 0.033% (v/v).

C_2H_2 was injected in 25 empty vials (Empty Control), in 25 vials filled with ATGUS medium only (Untreated) and in 25 vials inoculated with either of the tested bacterial strains. Further 25 vials where C_2H_2 was not injected were kept as a reference per each treatment.

Table 7. PTR-MS experimental samples setup.

Treatment	**N° of vials**	**N° of timepoints**	**TOT vials N°**
Empty	5	5	25
Empty + C_2H_2	5	5	25
Untreated (ATGUS)	5	5	25
Untreated (ATGUS + C_2H_2)	5	5	25
nifD$^-$	5	5	25
nifD$^-$ + C_2H_2	5	5	25
GUS nifD$^-$	5	5	25
GUS nifD$^-$ + C_2H_2	5	5	25
WT	5	5	25
WT + C_2H_2	5	5	25
GGG	5	5	25
GGG + C_2H_2	5	5	25

Analysis of the headspace was performed with a PTR-MS after 4 hrs from acetylene injection (T_0) and then every 24 hrs for four days (T_1 to T_3) and again at 6 days (T_6) post acetylene inoculation. At each time point, five vials were analysed per each treatment (Empty, Empty + C_2H_2, Untreated, Untreated + C_2H_2, *nifD*$^-$, *nifD*$^-$ + C_2H_2, *GUS nifD*$^-$, *GUS nifD*$^-$ + C_2H_2, WT, WT + C_2H_2, *GGG*, *GGG* + C_2H_2). All samples were kept at 28 °C for the duration of the experiment.

Oxygen was employed as a source gas in an Innsbruck PTR-MS instrument to produce O_2^+ ions as the chemical ionization reagent.

3.17. Chlorophyll extraction protocol

Chlorophyll extraction was adapted from Loh et al. (2012) [129]. For each treatment, around 0.1 g of freeze-dried tomato plants aerial parts (leaves and shoots) were finely pulverized using a sterilised mortar and pestle and mixed with 30 ml of hexane/ethanol/acetone/toluene (10:6:7:7, v/v/v/v) in a flask. The mixture was then shaken at room temperature for 1 h, followed by the addition of 15 ml of hexane, further shaking for 10 min and a final addition of 15 ml of 10% anhydrous sodium sulphate solution for partition. The upper phase containing chlorophylls was collected, and the lower phase was repeatedly extracted with 15 ml of hexane until the supernatant became colorless. Samples were then stored at -20 °C.

3.18. Bacterial re-isolation from plants

Fourteen days after inoculation, non-inoculated (UT) and bacterium-inoculated plants were collected, and roots and shoots were then detached and thoroughly washed twice with 10 mM $MgCl_2$ in order to remove loosely attached/non-adhering/non-interacting bacteria from plant surfaces. Roots and shoots were then separately ground in a mixer-mill disruptor (MM 400, Retsch, Haan, Germany) at 25 Hz for 1 min (or until completely macerated). For bigger plants, portions of roots or shoots and leaves were collected instead of whole organs. Samples were then re-suspended in 200 µL of sterile water and carefully vortexed. Each suspension was serially diluted and 10 µL aliquots were plated in triplicate on solid ATGUS or AceLGI-P medium (this second was the preferred medium for re-isolation being more selective for Gd). After incubation at 28 °C for three days, colony forming units (CFUs) of Gd per unit of plant fresh weight (CFUs g^{-1}) were calculated. As a standard method, three replicates (plants) were analysed for each treatment and the experiment was carried out at least twice.

3.19. Statistical analysis

Statistical data analysis was performed with Statistica 13.1 software (TIBCO Software, Palo Alto, CA, USA). Data were analysed according to non-parametric analysis. First, a multiple comparison analysis with Kruskal-Wallis was performed to demonstrate non-significant differences between repeated

experiments ($P > 0.05$). Furthermore, for hydroponics experiments in particular, data from the three experimental repetitions were pooled and significant differences among treatments were assessed again with Kruskal-Wallis ($P \leq 0.05$) for multiple comparisons.

3.20. Sample collection, RNA extraction, and Illumina Sequencing

For RNAseq experimental setup, non-inoculated plants and bacteria- inoculated plants grown in hydroponic systems containing half-strength Hoagland in either the absence (NoN condition) or addition of 2 mM (N condition) KNO_3 were collected at one- and fourteen- days post inoculation (dpi). Fifteen and nine plants were randomly collected from each treatment of NoN and N, respectively, and pooled into groups of five (NoN) or three (N) (replicate), roots and shoots were detached, and roots were placed into 2 ml Eppendorf tubes, immediately frozen in liquid nitrogen and stored at −80 °C. Root samples were then manually ground with sterile micropestles to a fine powder, with samples being frozen during the whole process. Total RNA was extracted following Hot Acid Phenol Extraction protocol (see 3.21 Section). Total RNA was quantified using a NanoDrop 1000 (Thermo Fisher Scientific) and RNA quality was checked using a 2100 Bioanalyser system (Agilent Technologies, Santa Clara, CA, USA). Each RNA sample was treated with Turbo DNA-*free*™ according to the product guidelines. For each treatment, three replicates (pool of five or three plants) were analysed.

RNA samples were subjected to RNA-Seq library construction, using the NEBNext® Ultra™ II Directional RNA Library Prep Kit for Illumina® (Illumina, SanDiego, CA, USA) and rRNA depletion with the RiboZero rRNA Removal Kit for plants according to the manufacturer's instructions (Illumina). Paired-end reads were obtained using a NextSeq500 instrument (Illumina) at the Deep Sequencing facility of University of Nottingham (Nottingham, UK) and sequences were deposited at the Sequence Read Archive of the National Center for Biotechnology under the BioProject numbers PRJNA666034 and PRJNA666036.

3.21. Hot acid phenol RNA extraction protocol

Plants material was finely ground with a sterile micro pestle, with the samples frozen all the time. The frozen powder was transferred in a 2 ml Eppendorf tube (not more than 500 µl volume for each sample). 600 µl of AE buffer (50 mM NaOAc-pH 5.3, 10 mM EDTA, previously sterilised) was added. 60 µl of SDS 10% (filter sterilised) was then immediately added. A thorough vortex round was performed (30") and equal volume of acid phenol (either AE buffer saturated of citrate saturated) was added. The sample was thoroughly vortexed (30") and incubated for 4 minutes at 65 °C. The phenol mixture was rapidly chilled using liquid N_2: the tube was dipped into liquid N_2 repeatedly, until phenol crystals formed. The sample was then spin down for 7-8 minutes, at top speed. In case the white particulate was not completely deposited, a 3 minutes spin round was performed. The upper phase was collected in a clean 1.5 ml tube and equal volume of phenol:chloroform mixture was added. Sample was thoroughly vortexed (30") and spinned for 3 minutes at top speed. The top layer was transferred into a clean 1.5 ml tube. Supernatant was repeatedly collected, added with phenol:chloroform mixture, vortexed and spinned twice. 1/10 (40 µl circa) of the volume of 3 M NaOAc (Sodium Acetate) was added; the sample was mixed and 2.5x volume (1 ml circa) of absolute EtOH was added. The sample was thoroughly mixed. The sample was then incubated overnight at -20 °C. On the second day of extraction, the sample was spin down (10 min at top speed). The upper phase was removed without discarding the pellet. A wash with 0.5 ml of 80% EtOH was performed. The sample was then spinned for 5 minutes at top speed. The EtOH was completely removed with a pipette and with the aid of a vacuum-dry pump (2 minutes) to completely dry the pellet. Finally, the pellet was resuspended in 25-30 µl of clean, sterile water. The samples were stored at -20 °C for short term storage and at -80 °C for long term storage.

3.22. Bioinformatic analysis and identification of differentially expressed genes

Differentially expressed genes (DEGs) were identified with the Limma-Voom package [234] which estimates the mean–variance relationship of log counts, generating a precision weight for each observation that is fed into the Limma empirical Bayes analysis pipeline [223]. A Volcano Plot was generated using

the Python programming language and the matplotlib package [94] and a double cut-off on P-value ($P \leq 0.01$) and minimum Log2 FC of one [Log2 (FC) ≥ 1 or Log2 (FC) ≤ -1] were used to select DEGs. Two pairwise comparisons were analysed for each growth condition [the absence of nitrogen (NoN) and 2 mM (N) KNO_3 added in plants growth solution], in order to identify DEGs modulated by either WT or *nifD*$^-$ strains of Gd: inoculated plants vs. controls at 1 days post inoculum (dpi) and at 14 dpi in NoN and N condition at each time point. The distribution of DEGs was summarised using Venn diagram [89] and DEGs were grouped in upregulated genes [$P \leq 0.01$ and Log2 (FC) ≥ 1] or downregulated genes [$P \leq 0.01$ and Log2 (FC) ≤ -1] in both NoN and N conditions, exclusively by WT in NoN condition (WT NoN) and exclusively by WT in N condition (WT N) for each time point (1 and 14 dpi). The same procedure was applied to analyse *nifD*$^-$ modulated genes. The heat map diagram of Log2-transformed FC values DEGs was visualised using the Java Treeview tool [237]. Gene Ontology (GO) terms and protein descriptions of tomato Heinz1706 genes [91] of the release ITAG3.2 were downloaded from the tomato genome browser [231]. GO terms significantly overrepresented ($P \leq 0.05$, Benjamin and Hochberg FDR correction) in the DEG lists in comparison to the whole tomato transcriptome were identified using the Biological Networks Gene Ontology (BiNGO) tool [136] and biological networks were visualised with Cytoscape version 3.7.1 [218].

3.23. qRT-PCR

Tomato genes were picked for quantitative real-time PCR (qPCR) analysis in order to validate transcriptomic data (Table S9). cDNA was synthesised from DNase-treated RNA using Superscript III (Invitrogen, Thermo Fisher Scientific) kit. For qPCR reactions, Platinum SYBR Green qPCR SuperMix-UDG (Invitrogen, Thermo Fisher Scientific) was employed; a Light Cycler 480 (Roche Diagnostics, Mannheim, Germany) was used for qPCR runs as previously described [179]. Briefly, the PCR conditions were as follows: 50°C for 5 min and 95°C for 3 min as initial steps, followed by 60 cycles of 95°C for 15 s and 60°C for 45 s. Each sample was examined with three technical replicates and dissociation curves were analysed to verify the specificity of each amplification reaction. The Light Cycler 480 SV1.5.0 software (Roche) was

used to extract Ct values based on the second derivative calculation and the LinReg software version 11.0 was used to calculate reaction efficiencies for each primer pair [202]. For each gene, the relative expression level (fold change) was calculated according to the Pfaffl equation [182] for each pairwise comparison between bacterium-inoculated and untreated plants. *ARD2* was selected as housekeeping gene for normalization. Three replicates (pool of five plants) were analysed for each treatment. Pearson correlation coefficient was 0.7, indicating a good correlation between transcriptomic and qRT PCR expression levels (Fig. 11).

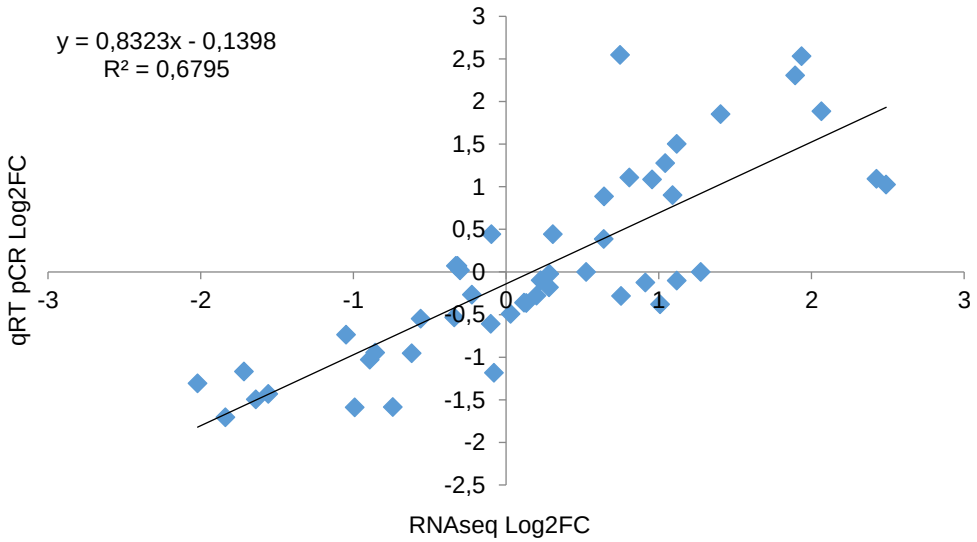


Fig. 11. Scatter plot comparing expression levels of tomato genes modulated by inoculation with either WT or nifD⁻ Gd strains obtained with either qRT PCR or RNA sequencing analyses.

4. Results and Discussion

4.1. Creation of GUS tagged WT and *nifD*$^{-}$ strains.

In order to obtain a rapid, visual method to detect Gd in *in planta* experiments, GUS tagged versions of both WT and *nifD*$^{-}$ strains were created. These strains were developed through conjugation between *E.coli β2163* cells harbouring the GUS reporter plasmid pRGS561 and either WT or *nifD*$^{-}$ strains. The pRGS561 plasmid leads the constitutive expression of the beta-glucuronidase enzyme. Positive conjugants were isolated on ATGUS medium supplemented with appropriate selective antibiotics and X-Gluc (5-bromo-4-chloro-3-indolyl-beta-D-glucuronic acid, cyclohexylammonium salt) reagent so as to identify colonies that contained the GUS carrying plasmid and that thus acquired the ability of synthetising the beta-glucuronidase enzyme that cleaves X-Gluc to produce colourless glucuronic acid and an intense blue precipitate of chloro-bromoindigo.

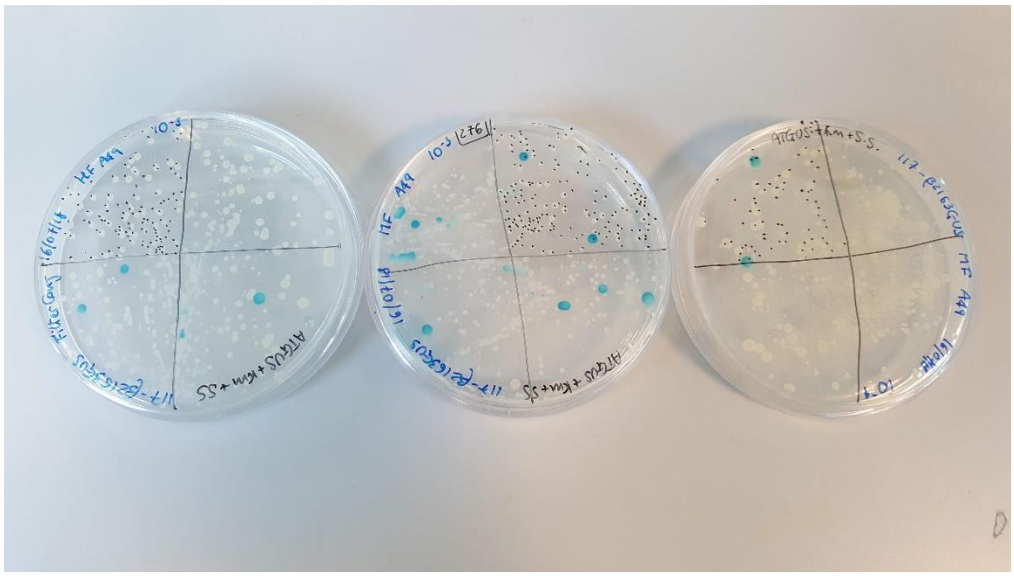


Fig. 12. Selective ATGUS medium Petri dishes for GUS tagged Gd strain selection after conjugation with E.coli β2163-GUS cells.

The obtained GUS tagged strains were employed in several preliminary experiments since this was the only method available at the time for Gd (qualitative) colonisation estimation. The GUS staining method (see 3.9 Section) was employed taking into consideration the limitations presented by this technique, particularly for in-soil experiments: several soil or rhizosphere

bacteria can synthetise glucuronidase enzymes and can thus impair the test reliability.

As the project progressed, a reliable and repeatable method for Gd colonisation quantification, involving plant material maceration, serial dilution, and plating (as described in 3.18 Section) was achieved and applied as later described for the hydroponics experiments that are presented in this work.

4.2. Preliminary inoculation experiments

Seed coating strategies are frequently used in agriculture for application of biocontrol or biostimulant products. In such approaches, seeds are imbibed in a bacterial suspension, often implemented with sticky agents that favour bacterial adhesion and permanence on the seed surface. During germination, the emerging root comes into contact with the bacterial coating and the seedling gets colonised. Many studies have shown most effective results in terms of plant growth promotion to be obtained when bacteria colonise meristematic cells and thus get to propagate throughout the whole plant system [248].

A seed inoculation protocol was tested for Gd colonisation of tomato plants, both in-soil and on artificial growth substrate (rockwool) experiments. Preliminary inoculation experiments involved seed coating and sowing in Levington M3 compost. These experiments were conducted at the very early stages of this project, when a consistent, repeatable, quantitative colonisation assay that could allow re-isolation of bacteria from plants and assessment of their colonisation efficiency was still under development. Data from these experiments are thus to be mainly considered as preliminary phenotypical evaluations of possible applications for in-soil and in solid substrate application of Gd on tomato plants. GUS staining was the only available rapid method to estimate the colonisation rate and was used to complement the gathered phenotypic data.

In-soil and in rockwool experiments had to be later set aside since less variable inoculation methods had to be prioritised so to obtain a suitable setup that would allow molecular analyses on plant samples.

4.2.1. Seed coating and in-soil sowing

Seed coating treatment was evaluated in an in-soil experimental setup.

In this case, N-Fix® 3% sticky agent was employed to favour bacterial adhesion to tomato seeds and mixed to the bacterial inoculum. Tomato (cultivar Money Maker) surface sanitised seeds were soaked for 30 minutes in a bacterial suspension of WT Gd strain, brought to a concentration of 10^9 CFU ml^{-1}.

Control seeds were soaked for an equal timespan in sterile N-Fix® 3% aqueous solution. Seeds were then air dried under sterile conditions before sowing into Levington M3 compost. Plants were grown in glasshouse environment with following settings: day temperature of 24 ˚C, night temperature of 20 ˚C, venting temperature 28 ˚C with the

lights running from 6 am until 10 pm.

Below are presented phenotypic data relative to the first seed coating inoculation and glasshouse growth experiment using 3 plants of WT GD inoculated seeds compared with 3 plants of seeds treated with N-Fix® 3% alone. Phenotype depicts plants at 2 months (Fig. 13) and 4 months (*Fig. 14*) after inoculation and sowing.

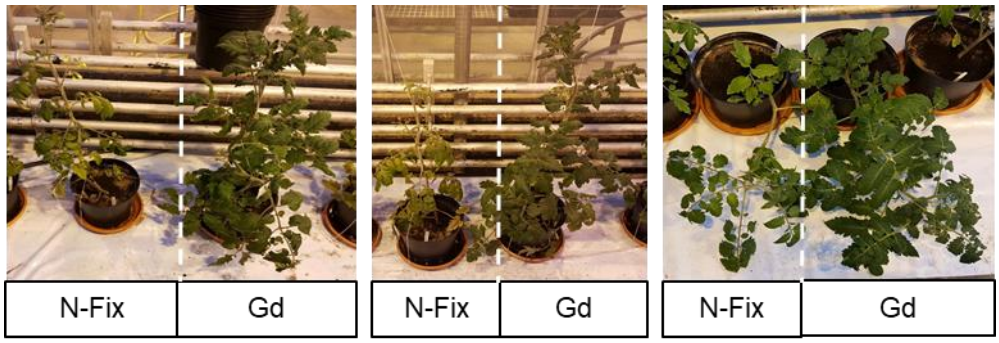


Fig. 13. Phenotype of seed coating Gd application. Three reps per each treatment. N-Fix® 3% (Control) treated plants (left in each picture) are compared to Gd 10^9 CFU ml^{-1} treated plants (right in each picture) at 2 months from sowing.

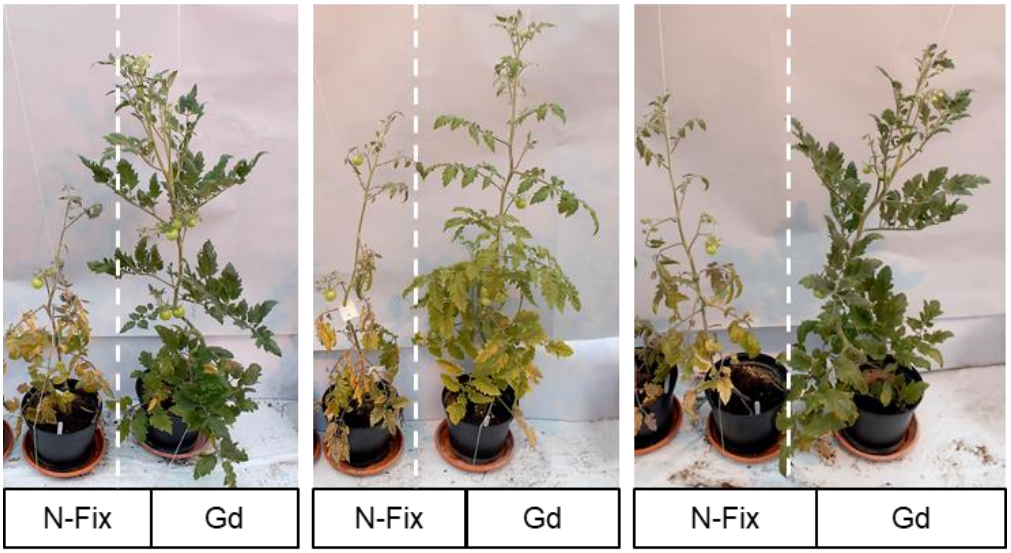


Fig. 14. Phenotype of seed coating Gd application. Three reps per each treatment. N-Fix® 3% (Control) treated plants (left in each picture) are compared to Gd 10^9 CFU ml^{-1} treated plants (right in each picture) at 4 months from sowing.

Inoculation with WT Gd led to an improvement in terms of plant biomass (Fig. 15a), side shoots production (Fig. 15b), yield (Fig. 16) and chlorophyll content (Fig. 17).

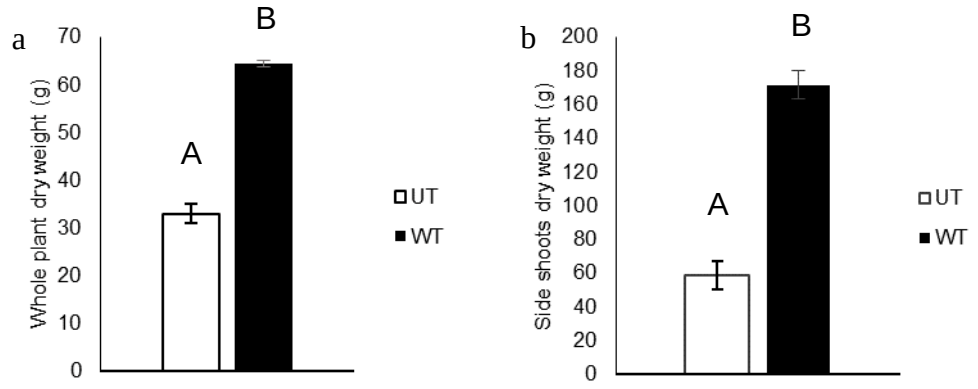


Fig. 15. Four months old whole plants dry weight (aerial parts) (a) and total side shoot dry biomass produced (b) by either untreated controls (UT) or WT Gd treated plants inoculated via the seed coating technique. Significance of differences between treatments was assessed by Kruskal-Wallis test to $P \leq 0.05$.

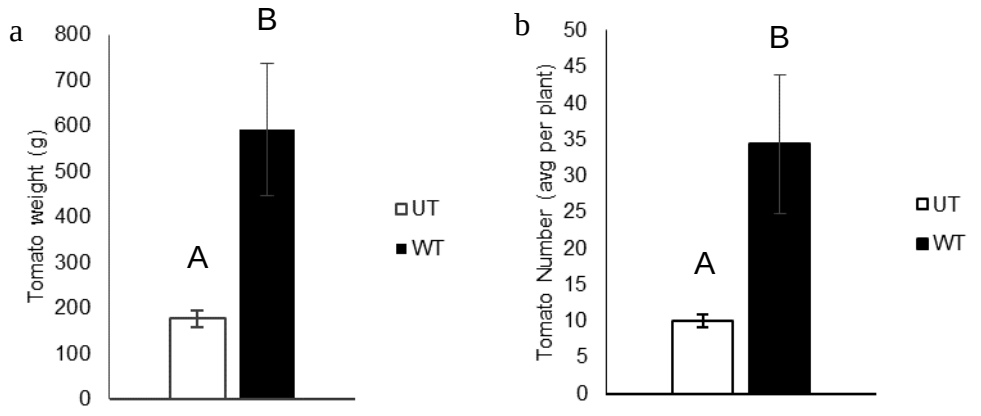


Fig. 16. Per plant average weight (a) and number (b) of tomatoes produced by either untreated controls (UT) or WT Gd treated four months old plants inoculated via the seed coating technique. Significance of differences between treatments was assessed by Kruskal-Wallis test to $P \leq 0.05$.

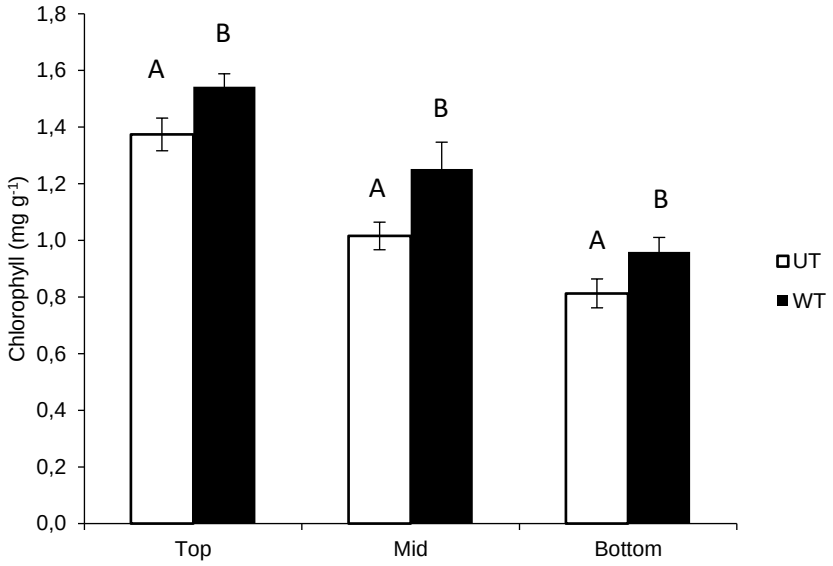


Fig. 17. Chlorophyll content in plants inoculated with WT Gd in comparison to untreated controls. SPAD measurement was performed on 10 different leaf blades from three parts of 4 months old tomato plants (Top, Middle, Bottom) and SPAD conversion to chlorophyll content was calculated as in Jiang et al. (2017). Significance of differences between treatments was assessed by Kruskal-Wallis test to $P \leq 0.05$.

In-soil experiment outcomes produced promising preliminary data. Although, results between experimental repeats were variable, even when experiments were conducted maintaining apparently identical conditions. The highly improved phenotype (mainly in terms of plant biomass, plant height and side shoot production) was, in most cases, visible only one month after inoculation and became less pronounced during later plant growth and maturation (Fig. 18).



Fig. 18. Phenotype of seed coating Gd application. In picture are presented representatives of the five reps evaluated per each treatment. N-Fix® 3% (Control) treated plants (left) are compared to WT Gd 10^9 CFU ml^{-1} treated plants (right) at 2 months from sowing. Germination and early growth was performed in Levington M3 compost; repotting of 1 month old plant was performed in Klasmann:Silversand (50:50) soil.

Nevertheless, even though the strength in the phenotype improvement was variable and plant height was oftentimes found to be unvaried, consistency was found in the plant growth promoting effects induced by the inoculation with WT

Gd bacterium: WT Gd inoculated plants always showed significantly improved phenotypes in comparison to the untreated controls, mainly in terms of improved plant chlorophyll content and fruit yield production.

4.2.2. Type of growing medium influence (Levington vs Klasmann)

The type and nutritional content of soils are among the main factors investigated for their influence on Gd colonisation efficiency and plant growth promoting (PGP) activity; additional experiments evaluating the effect of two different soils were carried out and provided interesting results. It is known from the literature that the plant's growth medium used and available nutrients have a strong influence on the bacterial activity and interaction with host plants [108].

In this experiment, the influence of different types of soil on the efficiency of symbiosis between tomato plants and Gd were assessed. The hypothesis was based on the assumption that N deficiency in-soil, and as a consequence the enhanced plant need for this element, could favour plant colonisation by Gd.



Fig. 19. Example of growth setup for different N content soils evaluation.

Gd coated tomato variety Money Maker seeds (Section 3.10) were sown both into Levington M3 (pH range - 5.3-6.0, Particle size - 0-10mm, Conductivity - 355-435s, Nutrients content - 204N 104P 339K mg l^{-1}) and Klasmann (pH - 6.0, Conductivity – 0.35 dS m^{-1}, Nutrient Added - 12N 14P 24K kg m^{3}) soil. Germination was performed in a controlled temperature and lighting room inside sterile 5 litres jars (Fig. 19). Two weeks after sowing, the GUS staining protocol (Section 3.9) was performed on whole plants. Five reps from each treatment were collected for assessments. As shown in Fig. 20 by the blue staining, Klasmann soil grown plantlets (left) showed higher colonisation in respect to the ones grown in Levington M3 soil (right).



Fig. 20. GUS staining of tomato seedlings a) Nfix® and WT Gd treated plants grown in low N (Klasmann) soil; b) right: Nfix® and WT Gd treated plants grown in high N containing (Levington) soil.

This result indicated that, in fact, the amount of available nitrogen in the plants' growth soil may influence the establishment of a host-bacterium interaction.

These results are not surprising since it has previously been reported how N concentration in-soil can strongly affect both biological nitrogen fixation (BNF) efficiency and bacterial colonisation rate. For example, sugarcane plants inoculated with associative and endophytic diazotrophs and grown in-soils with different fertilisation levels showed a higher BNF rate when the soil fertility was lower [170]. This decrease in BNF contribution, reported in high N content soils, might be to some extent ascribed to the control some N sources have over the nitrogenase enzyme activity: as an example, ammonium is among the starting signals leading to the inactivation of nitrogenase [65][165].

Besides the control exerted on the nitrogenase enzyme activity, studies have observed that N content in plants growth substrates can also affect the bacterial colonisation capacity. Fuentes-Ramirez et al. (1999) detected an inhibition in sugarcane colonisation by *G. diazotrophicus* when high concentrations of N fertilisers, in the form of ammonium nitrate, were supplied. Interestingly, a study from Rodriguez-Blanco (2015) has also found a reduction in the number of diazotrophic bacteria isolated from plants of *Zea mays* that were grown in the complete the absence of N fertilisation in comparison to ones grown with the addition of two different doses (either 40 kg N ha^{-1} or 80 kg N ha^{-1}) of ammonium nitrate [198]; this indicates that either too high or too low concentrations of N in growing medium can be detrimental for bacterial colonisation establishment and beneficial activity.

The same above-described experiment was repeated in a glasshouse environment with the following setup: day heating 24 ˚C, night heating 20 ˚C, venting temperature 28 ˚C. A photoperiod of 16 hrs day/ 8 hrs light was maintained.

In this case both WT (GUS tagged) and *nifD*$^{-}$ (not GUS tagged, since this experiment was performed prior to the creation of the *nifD*$^{-}$ GUS tagged strain) strains were employed.

In this experiment, in order to further increase the nutrient reduction, Klasmann soil was mixed with an equal volume of "Silver Sand" (50:50). In these conditions, no germination was observed in N-fix® 3% treated plants and very low germination rate (25%) in both *nifD*$^{-}$ and WT GUS inoculated plants. The WT GUS treated plants showed a healthier phenotype compared to the *nifD*$^{-}$ inoculated ones. Nevertheless, a strong variability was observed inside each treatment, suggesting differential colonisation among the individual plants (Fig. 21a). A more developed root structure was also observed in WT GUS treated plants compared to *nifD*$^{-}$ treated samples (Fig. 21b).



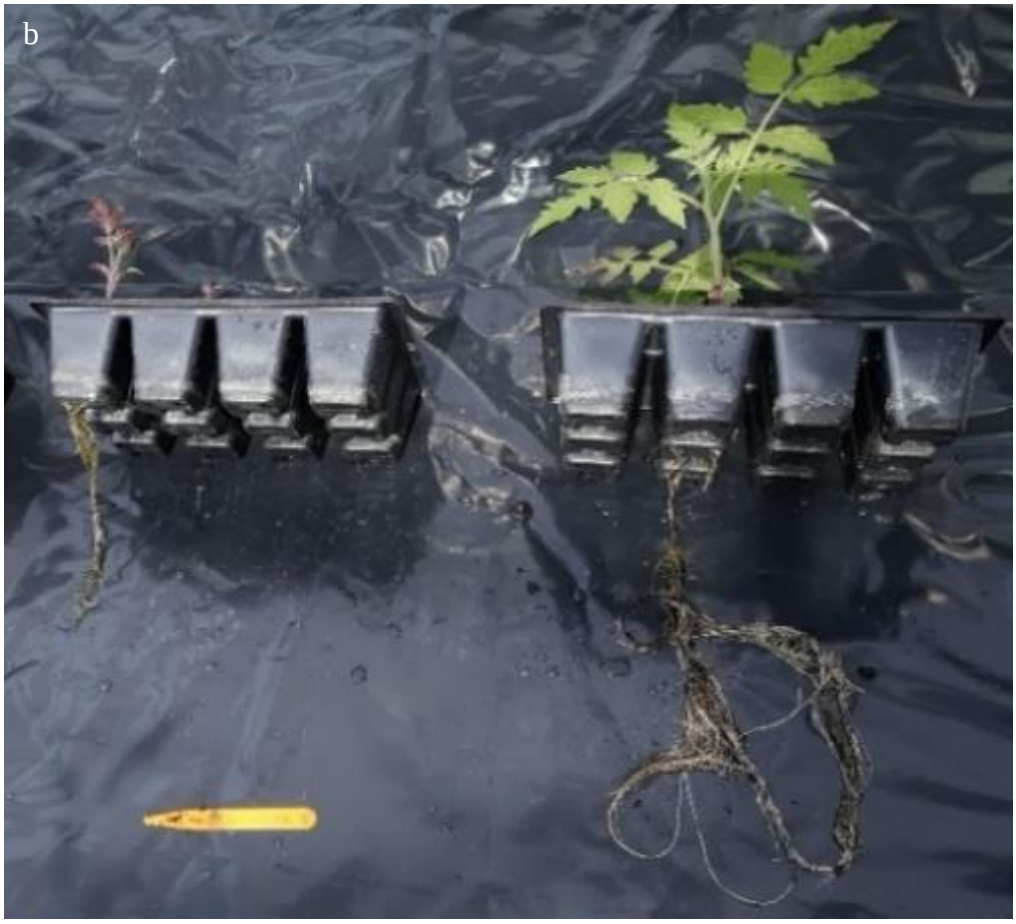


Fig. 21. Plants grown in Klasmann (low N) soil. a) from left to right: nifD$^-$ and GUS-GFP tagged Gd (GGG) treated plants (2 reps). b) from left to right: GUS-GFP tagged Gd (GGG) and nifD$^-$ treated plants (2 reps), detail of root apparatus.

GUS staining performed on thoroughly washed roots (Fig. 22), indicated high WT GUS Gd colonisation in roots while a less intense blue signal, probably noise caused by other soil microorganisms, was observed in plants treated with the non-tagged *nifD*$^-$ strain.

The above-mentioned seed coating method for in-soil colonisation experiments

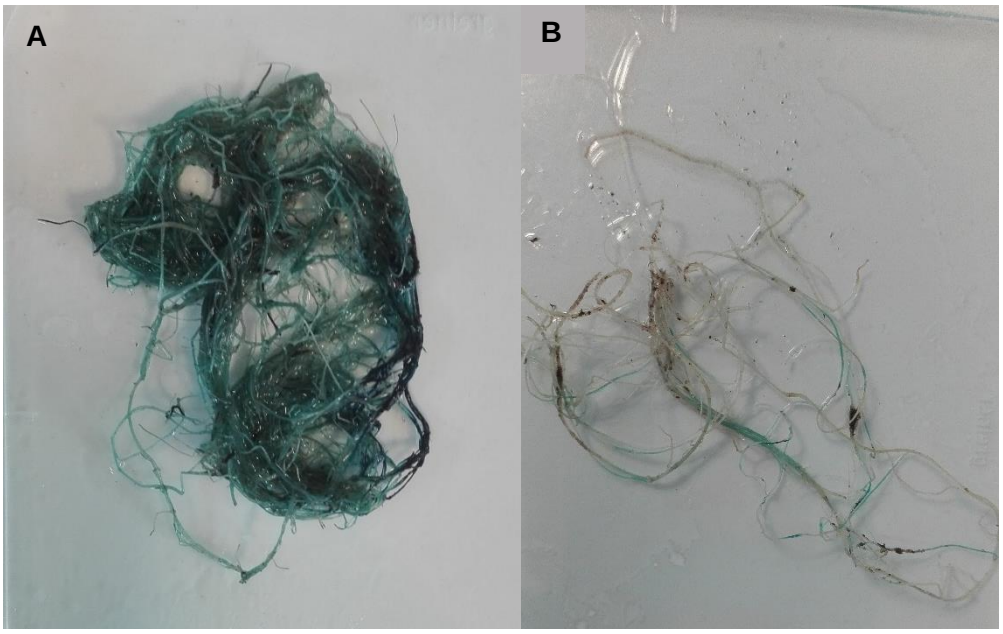


Fig. 22. GUS staining protocol performed on roots collected from plants grown in Klasmann (low N) soil and inoculated through seed coating with either (A) GUS-GFP tagged Gd (GGG) or nifD- strains of Gd (B). Strong blue signal is observed in WT Gd treated plants. Blue noise signal was detected in nifD- inoculated roots.

has been tested several times and, although preliminary data were encouraging, data collected did not present sufficient consistency, indicating that this system, given the very high number of variables involved, was not suitable to be employed for transcriptomic data collection, which was the main goal in this project.

The achievement of more controllable and less variable systems was thus to be prioritised in order to obtain a consistent, well-regulated and repeatable inoculation setup.

4.2.3. Seed coating and rockwool sowing

Europe is one of the main tomato producers worldwide, in particular for the fresh fruit market; the hydroponic based tomato production in Europe accounted for a 45 % share of the global tomato revenue in 2017 [217]. Since a substantial portion of tomato production in Europe is achieved through hydroponics systems in controlled glasshouse environments, it was thus decided to investigate the possibility of employing seed coating inoculation as an application for hydroponic production.

The seed coating protocol (Section 3.10) was performed on surface sanitised tomato Money Maker and MicroTom varieties, employing WT GUS tagged Gd strain in comparison to untreated (UT) plants that were treated with N-fix® 3% solution. Treated seeds were then sown into Grodan® rockwool plugs and germinated in a climate-controlled growth room. Watering was performed with N-free modified Hoagland solution. Two weeks after sowing, plants were transferred from plugs to bigger Rockwool cubes (7.5x7.5x7.5 cm). Two weeks after sowing, GUS staining protocol was performed on 3 replicates per treatment, but no blue signal was visible. This result suggests a low colonisation efficiency from this setup. Phenotypical differences were nevertheless detected: Gd inoculated plants showed improved greeness, height and early flowering in comparison to untreated controls. This observations were valid for both tomato varieties.



Fig. 23. Phenotype of MicroTom tomato seedlings 1 week after the inoculation through seed soaking with either N-fix® 3% (UT, left) or GUS tagged WT Gd strain (right). Rockwool was employed as plants growth substrate. Growth was performed in a climate-controlled chamber.

At later growth stages, after plants had been moved into bigger rockwool blocks, the improved phenotype of treated plants was lost.

No differences in plants' height or fruiting yield was observed in treated plants in comparison to untreated ones at these later growth stages (Fig. 24).

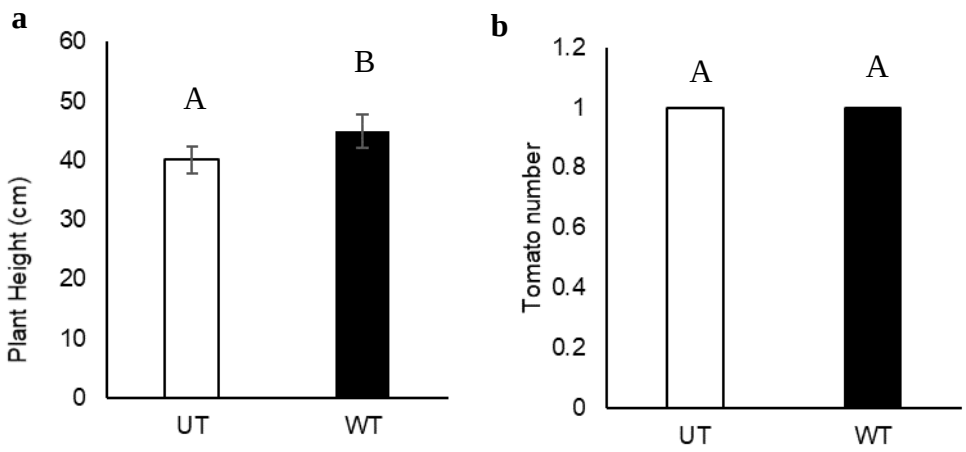


Fig. 24. Plant height (a) and average number of tomatoes produced per plant (b) by either untreated controls (UT) or WT Gd treated plants inoculated via the seed coating technique. Growth was performed on rockwool substrate. Five plants were assessed per each treatment (replicas). Significance of differences between treatments were assessed by Kruskal-Wallis test to $P \leq 0.05$.

The GUS staining and phenotypic assessment data indicated that this experimental setup, associated with the seed coating protocol, was not fully compatible for correct establishment of a plant bacteria symbiosis. The obtained improved early phenotype indicated that the bacterium could provide plant growth promotion to some extent but the absence of detectable GUS staining alongside the loss of a visible phenotype after a few months from sowing may indicate a non-effective long-term colonisation of Gd using rockwool substrate. It may also be considered that a completely N-free nutrient supply might have been too harsh a condition and may not be favourable for symbiosis establishment. Nevertheless, in support of the data here presented, parallel experiments conducted in our group, with the same setup but assessing different levels of nitrogen supply in the nutrient solution, showed similar results at all N concentrations tested.

4.2.4. Rockwool bacterial suspension inoculation

In parallel to the above-described seed coating and sowing on rockwool evaluation, a different inoculation strategy was tested for the same setup.

Surface sanitised seeds of both Money Maker and MicroTom tomato cultivars were pre-germinated in a growth chamber in petri dishes provided with moist

sterile paper. Pre-germinated seeds were transferred to rockwool plugs. Watering was performed with N-free modified Hoagland solution.

Inocula of either *GUS nifD*$^{-}$ or the GUS, GFP tagged WT strain (*GGG*) were grown on Petri dishes and then inoculated for overnight growth in liquid ATGUS medium. Cells were then pelleted in a centrifuge at 4000 rpm/3800 g (Thermo Scientific™ TX-400 4 x 400 ml Swinging Bucket Rotor) for 10 minutes. Bacterial cells were resuspended in sterile MilliQ water to reach a concentration of approximately 10^{8} CFU ml^{-1}. Bacterial suspensions were used to inoculate seedlings in rockwool plugs.

Each plug was injected with 5 ml of bacterial suspension (either *GUS nifD*$^{-}$ or *GGG*) and incubated to evaluate the plant phenotype. Untreated plants (UT) were watered with sterile MilliQ water only and used as controls.

Representative pictures of plantlets at five days (Fig. 25, Money Maker on the left and MicroTom on the right) and ten days (Fig. 26). MicroTom phenotype only is shown since difference was more relevant than in Money Maker) after bacterial treatment.

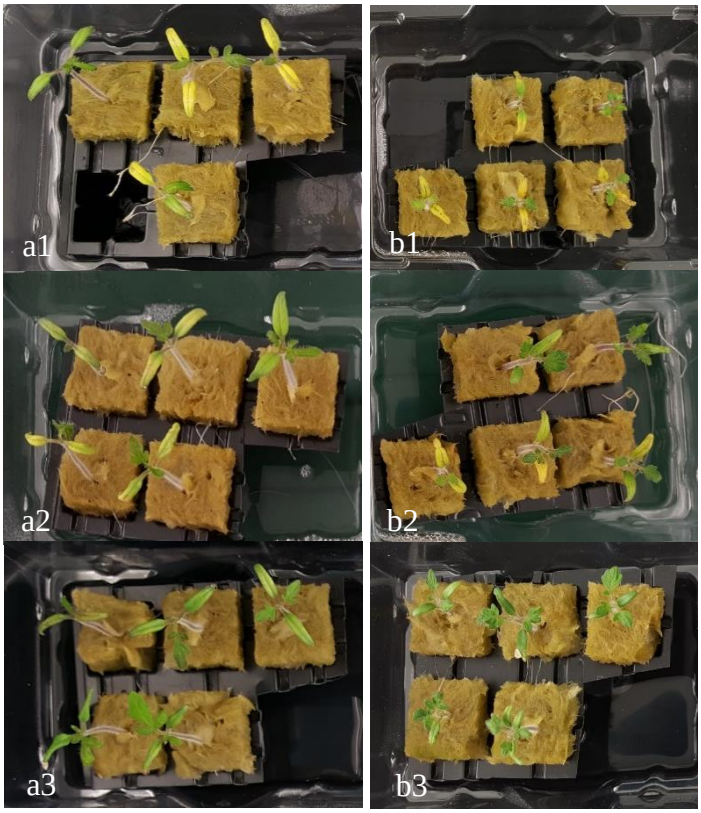


Fig. 25. Phenotype of Money Maker (a) MicroTom (b) tomato seedlings five days after the inoculation with either sterile water (UT, a1 and b1), GUS nifD- strain suspension (a2 and b2) or GUS-GFP tagged Gd (GGG) strain suspension (a3 and b3). Rockwool was employed as plants growth substrate. Growth was performed in a climate-controlled chamber.

Untreated plants had yellower leaves and lower number of leaves in comparison to both GUS *nifD*$^{-}$ and GGG treated ones; GUS *nifD*$^{-}$ treated plants, even though they showed improved phenotype in comparison to UT controls, had yellower leaf colour and slightly delayed plant development in comparison to GGG treated plants.



Fig. 26. MicroTom plantlets grown on Rockwool substrate. Bacterial inoculation was performed as bacterial suspension injected directly on growth substrate. Phenotype at ten days after bacterial inoculation. From left to right: UT, GUS nifD-, GUS-GFP tagged Gd (GGG) treated plant.

As observed in previously presented seed coating and in rockwool substrate growth experiments, the improved plant phenotype associated with Gd treatments was lost at two months after inoculation.

This inoculation strategy demonstrated not to be effective for the purpose of this study.

4.2.5. Root soaking

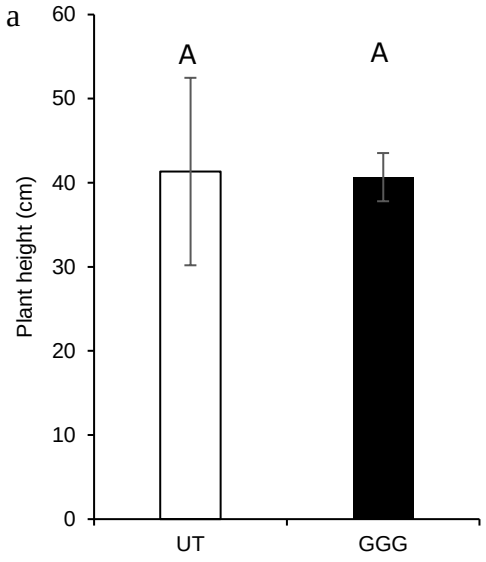
Tomato plants grown in Levington M3 compost for about one month (3 reps per experimental condition) were harvested, roots were carefully washed from soil and a few root tips were cut in order to create favourable entry sites for bacterial entrance into inner plant compartments. Plants roots were then submerged overnight in about 40 ml of cell culture suspension (concentration of around 10^8 CFU ml^{-1}) of *GGG*. Untreated (UT) plants were soaked for equal time in sterile distilled water. Plants were then re-potted in Klasmann low-N soil. N-free feeding was applied during plant growth in-soil. One week after inoculation and re-potting in-soil, leaf blades from lower and higher leaves were harvested and

GUS staining was performed. Blades from the plants' lower part, showed a blue signal while control ones remained unstained (

Fig. 27). This indicated the effective colonisation and spreading of bacteria in the above ground organs of tomato plants.

Fig. 27. Leaf blades collected from low leaves of tomato plants inoculated with GUS-GFP tagged Gd (GGG) strain through root soaking in bacterial suspension. Untreated sample (left) is compared to the GGG treated one (right). GUS stainingl was performed, and a blue signal could be detected in GGG treated leaf blades (right) while no signal was observed in control leaf blades (left).

No differences were detected in plant height between UT and *GGG* inoculated plants (Fig. 28a). However, an enhancement in plant side shoot production (strongly connected to plants N availability) and tomato yield production (Fig. 28b and c) was observed.



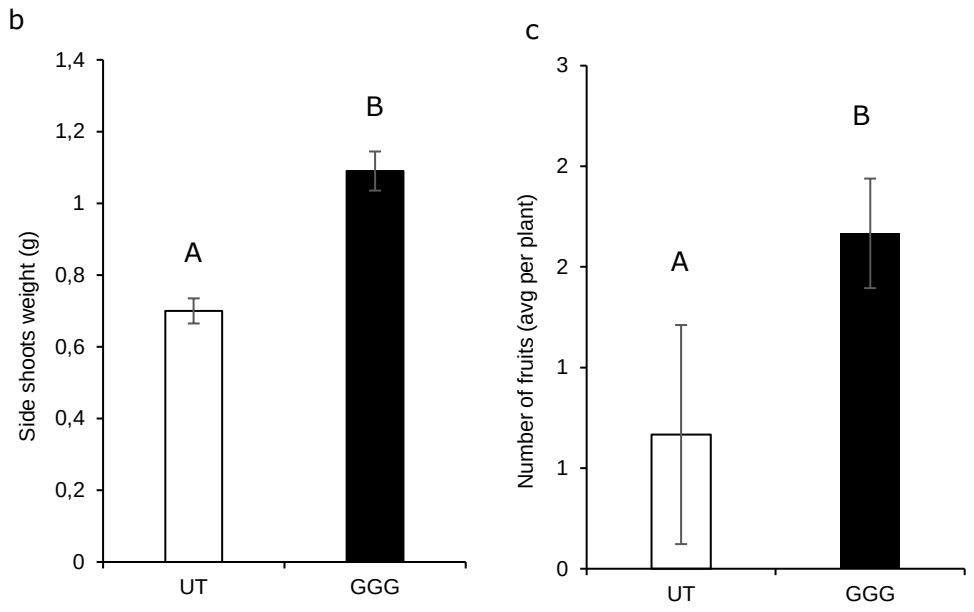


Fig. 28. Plant growth of Money Maker tomato plants inoculated with GUS-GFP tagged Gd (GGG) strain through root soaking. Plant height (a), total side shoot weight (b) and fruit number (c) (average per plant) of five GGG inoculated plants were measured and compared to those of untreated plants (UT). Significance of differences between treatments was assessed by Kruskal-Wallis test to $P \leq 0.05$.

This promising in-soil preliminary experiment set the basis for the realisation of the subsequent hydroponics setup.

In order to lower the number of variables in the growth system and obtain a setup that could be properly and finely tuned, convenient for molecular analyses of the interaction between tomato plants and Gd, more controllable methods were addressed as possible candidates for inoculation analyses.

4.3. Controlled inoculation strategies evaluation

The previous in-soil and in-rockwool inoculation experiments demonstrated how consistency between different experiments needed improvement and a simpler, more controllable and tuneable system for molecular analyses that was needed to investigate the genetic pathways involved in the interaction between Gd and tomato plants.

Considering this, the necessary next step of this work was to establish a reliable and repeatable inoculation method that would efficiently allow Gd to be inoculated with consistency in our target host plant, tomato.

In order to achieve this, different inoculation strategies were tested, evaluated, and colonisation was assessed, by GUS staining on treated plants tissues first

and by maceration, plating and counting once a proper bacterial re-isolation protocol was achieved.

4.3.1. MS agar inoculation

As previously published by Cocking et al. (2006) Gd colonisation of plants can be obtained by inoculation of very diluted cell suspensions onto small apical roots of seeds germinated on MS Agar.

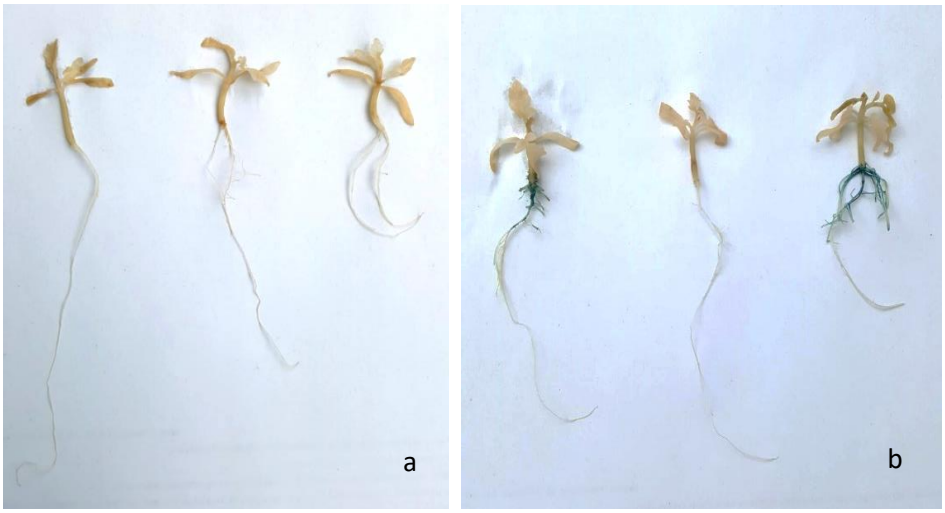
In this experiment the tomato variety MicroTom surface sanitized and sown in sterile glass jars (Ø around 5 cm) onto MS Agar 0.7% (N-free and without addition of sugars) until roots around 1 cm long emerged. Incubation was performed in a controlled growth chamber set at 80% humidity, 16 hrs photoperiod, at a temperature of 25±2 °C. Three jars were allocated for each condition tested. Inoculation of GUS tagged Gd was then performed at the proximity of the root emergence at different bacterial dilutions, in order to determine the best cell concentration for this set up. In fact, too high and too low concentrations of Gd had been previously demonstrated to be either ineffective or, in some cases, even detrimental for plant health (unpublished data from Azotic Technologies Ltd.). Different concentration dilutions of GUS tagged WT Gd strain were prepared in sterile water and a volume of 200 µl of either of the differential concentration solutions was pipetted per each germinated seed on root emergence sites. Untreated (UT) control seedlings were treated with 200 µl of sterile water.

All inoculated plants showed improved phenotypes in comparison to UT controls. To evaluate the best inoculum level among the ones tested, plantlets were thus evaluated for the elicited phenotype at different bacterial concentrations. Phenotypes of plantlets at two weeks after inoculation are shown in Fig. 29.



Fig. 29. Plantlets grown on MS agar 0.7%, treated with suspension of Gd at different concentrations. (a to f) UT, 5, 10, 50, 100 and 400 CFU ml^{-1}, respectively, n=3.

Two weeks after inoculation, plantlets were removed from the MS agar and GUS staining protocol was performed. Plantlets were incubated in Staining Solution either at 37 °C (steady) or at room temperature with slow shaking (20 rpm). In both conditions, treated plants presented blue staining after overnight incubation. No signal was detected in the untreated control plants. After incubation, staining solution was carefully removed, and a de-coloration step was performed in a 70% EtOH solution overnight. Plants tissues were then fixed via an incubation step in 0.1 M phosphate buffer ph7 with 2% glutaraldehyde. Results are presented in Fig. 30.



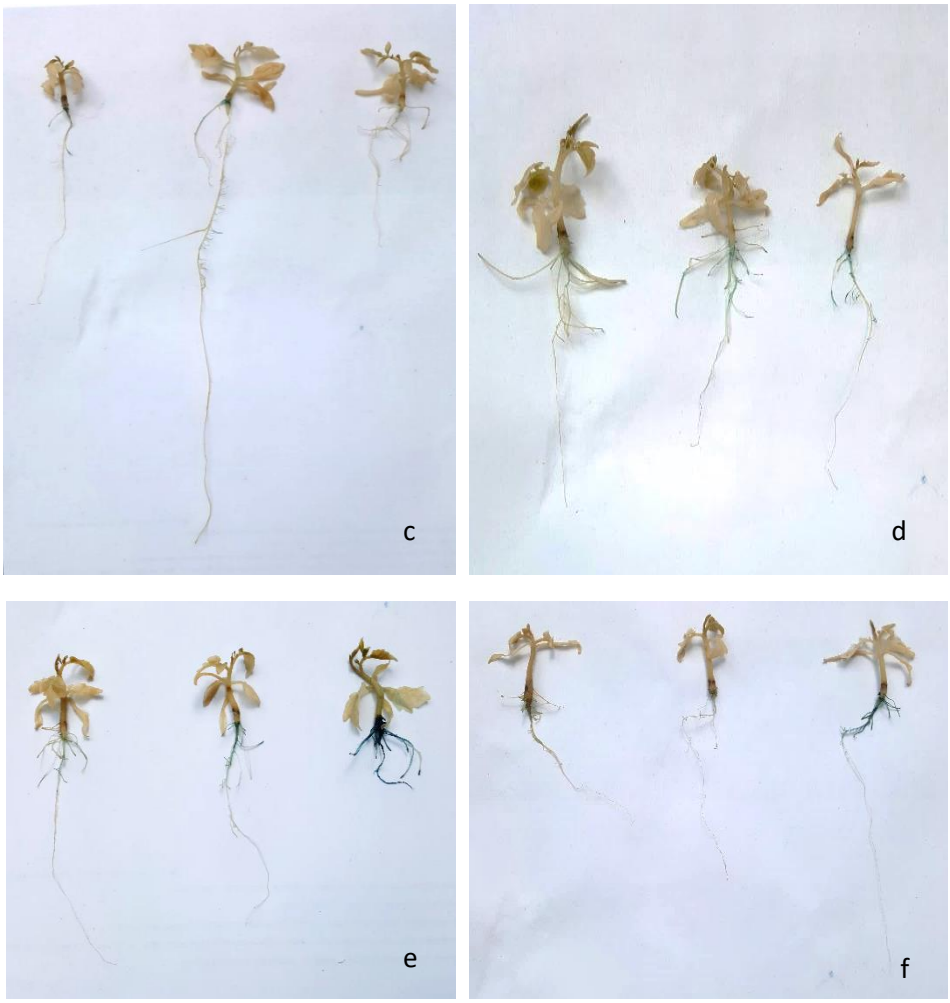


Fig. 30. MicroTom seedlings grown on MS agar 0.7%, treated with a suspension of Gd at different concentrations after GUS staining. (a to f) UT, 5, 10, 50, 100 and 400 CFU ml^{-1}, respectively, n=3.

Considering both plant phenotype and bacterial colonisation rate, assessed through GUS staining signal, the best inoculum concentration (Fig. 30e) was selected to be 100 CFU ml^{-1}.

The above-described setup was later tested for its consistency and surface sanitised tomato seeds (Money Maker and MicroTom) were sown (6 seeds per 5 jars for each treatment) on MS Agar 0.7% (nitrogen free and without sugars addition) in sterile glass jars and incubated in a controlled climate growth chamber set at 80% humidity, 16 hr photoperiod, at a temperature of 25±2 °C. One week after sowing, seedlings were treated with either sterile water (UT), WT strain or GUS-tagged WT Gd at a concentration of 100 CFU ml^{-1}. A volume of 200 µl per each plantlet was pipetted on roots emergence sites. Ten days from inoculation, plantlets were removed from agar substrate. GUS staining protocol

and plant tissue fixation was performed as above described. No de-coloration step was carried out. Results for MicroTom variety are presented in Fig. 31.



Fig. 31. MicroTom seedlings grown on MS agar and inoculated with 100 CFU ml^{-1} of either WT or GUS tagged WT strains of Gd after GUS staining protocol. a) from left to right: untreated, WT, GUS tagged WT strain inoculated seedlings. b) close up of GUS tagged WT Gd treated plantlet.

No blue signal was observed in UT nor WT inoculated plants, confirming the validity of the GUS staining method for *in vitro* inoculation tests; blue staining was detected in GUS-tagged WT inoculated MicroTom plants and was strictly confined to the root compartment. However, no signal was observed in the Money Maker variety.

Results from these two MS agar inoculation experiments have demonstrated how this method was not suitable for Money Maker variety inoculation, also suggesting the presence of some kind of structural and/or physiological difference between these two varieties that can affect Gd colonisation, interaction and growth on MS agar.

Since MicroTom is a dwarf variety of tomato, this was not a preferred model of study for molecular analyses. Moreover, Money Maker is one of the most commercially cultivated tomato varieties. In light of this, an inoculation method that worked on Money Maker variety was needed.

Furthermore, transferring MS agar grown plantlets from MS agar substrate to rockwool or soil substrates proved to be challenging: plants grown on MS agar were very delicate and dried out a few hours after transferring onto less hydrated substates even if the substrate was completely water or nutrient solution saturated.

4.3.2. Hydroponics setup

All the above-described inoculation methods proved to be inadequate for the need of establishing a repeatable, consistent, and controlled system where variables could be finely tuned in order to evaluate the effect of Gd inoculation of tomato Money Maker plants. Solid substrate tests showed too high a variability and thus fluctuations among trials were too strong. MS agar inoculations proved to be effective for the dwarf variety MicroTom but not suitable for Money Maker.

The promising results from the root soaking inoculation tests were the starting point for the setup of a hydroponics system that was later employed for seedling inoculation and growth of Money Maker plants for RNA sequencing analyses.

Seeds of Money Maker tomato were first surface sanitised and sown in sterile hydroponic boxes (15/20 seeds per box) each filled with 300 ml of half strength (0.5 x) modified Hoagland solution. Modified Hoagland solution was prepared *ad hoc*. Since one of the aims was to test the effect of nitrogen feed on the interaction between tomato plants and Gd, this system allowed us to be in control of the exact amount of N provided and was suitable also for the later described ^{15}N experiments. Five boxes were employed for each treatment. Boxes were incubated in a controlled climate growth chamber (Conviron GEN1000 / Binder kbwf720, Bohemina, NY, USA) set at 80% humidity, 16 hrs photoperiod, at a temperature of 25±2 °C.

WT Gd was streaked on Petri dishes with solid ATGUS medium from -80 °C stock. After three days of incubation at 28 °C, a first 20 ml liquid pre-inoculum was prepared starting from biomass collected from petri dishes with incubation overnight at 28 °C with shaking at 200 rpm.

A second inoculation (volume according to the amount of inoculum needed) was prepared in liquid ATGUS medium and grown overnight at 28 °C with shaking at 200 rpm. Bacteria were aliquoted in sterile 50 ml tubes and pelleted in a centrifuge at 4000 rpm/3800 g (Thermo Scientific™ TX-400 4 x 400 ml Swinging Bucket Rotor), 23 °C for 10 minutes. Bacteria were washed and re-pelleted twice with sterile distilled water. After washing, bacteria were re-suspended in hydroponics nutrient solution to reach a concentration that ranged between 10^8 and 10^9 CFU ml^{-1}) and used for plant treatment.

After a 72 hr incubation, nutrient solution was thoroughly removed from hydroponics boxes and substituted with fresh solution. Modified Hoagland solution was renewed once a week.

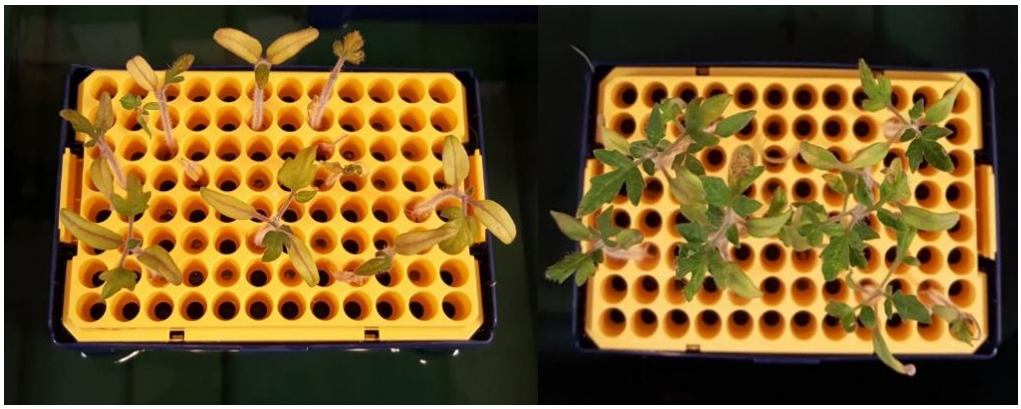


Fig. 32. Phenotype of hydroponically grown Money Maker tomato plants at 10 days post inoculum (dpi). Inoculation was perfomed through root dipping in bacterial suspension. No N source was additioned to plant growth nutrient solution (NoN). Untreated plants (left) phenotype was compared to the one of WT Gd inoculated ones.

Fig. 32 displays the phenotype observed after 10 days post inoculum (dpi) of seedlings grown in the absence of a N source in the growth nutrient solution, confirming an enhancement in height, growth and leaf chlorophyll of Gd treated plants in comparison to untreated ones.

This setup provided good inoculation results for the Money Maker variety. The reduced dimensions of the system were suitable for growth chamber incubations and several replicas could be obtained. Plants' roots could easily be accessed to

be sampled and assessed for bacterial colonisation through the employment of fluorescently tagged strains (Section 4.4.2). This setup also limited plant damage during harvest and provided clean roots, free from solid substrate material.

Various N levels were tested in order to set the best N concentration at which plants would show most significant phenotypic effects.
It was established to investigate the plants response to Gd in two conditions: complete the absence of N in modified Hoagland solution (stress condition) and at 2 mM KNO_3, concentration at which Gd effects were visible (previously tested).

4.4. Investigation of Gd-plant interactions and plant growth promotion

4.4.1. Phenotype WT vs *nifD*$^{-}$ Gd

The differentially elicited effects of the inoculation of either the WT or the nitrogen fixation-impaired strain (*nifD*$^{-}$) on tomato plants were evaluated. This is a key experiment for the evaluation of the significance of nitrogen fixation in the plant growth promoting effect of Gd on host plants.

4.4.1.1. Preliminary in-soil evaluation

For this type of comparative investigation, data collection was mainly performed on plants grown in hydroponics systems, which allowed a more controllable tuning of variables settings and more repeatable and consistent outcomes.

Nevertheless, an attempt at in-soil inoculation was performed at the beginning of the project. Data gained from this experimental setup are presented. These are to be considered as preliminary since data were not completely repeatable in subsequent experiments although identical inoculation and growth conditions were applied; this is probably to be ascribed to the increased variability in this type of less controllable setup.

Seed coating protocol was performed on the tomato variety Money Maker seeds with N-Fix® 3% formulation (UT), WT and *nifD*$^{-}$ strains at two different concentrations, as to evaluate possible differences in the effect of the inoculum concentration:

- WT 2 10^{10} CFU ml^{-1}
- WT 9 $10^{10} \approx 10^{11}$ CFU ml^{-1}
- *nifD*$^{-}$ 2.5 10^{10} CFU ml^{-1}
- *nifD*$^{-}$ 5 $10^{10} \approx 10^{11}$ CFU ml^{-1}



Fig. 33. From left to right: phenotype of one month old N-fix® 3% (UT), nifD^{-} *and WT inoculated plants sown in Levington M3 compost. Plants were grown in glasshouse conditions and inoculation was performed through seed soaking.*

Plants were sown in Levington M3 compost, grown for one month (Fig. 33) and then re-potted in 7 L pots filled with Klasmann:Silver Sand (50:50) mixture. Five reps for each treatment

were fed with 15% N Feed (15:7:30 N:P:K mg l^{-1}. Nitrogen was provided in the form of NH_4 NO_3) and five reps were kept under N-free feed until the fruiting stage.

Inoculated plants showed an improved phenotype in young plantlets: WT treated plants presented greener aerial parts and longer stems in comparison to both untreated controls and *nifD*$^-$ treated ones.

Following data are for phenotypes at 2 months from sowing and are from the first test of the experimental set up employing *nifD*$^-$ strain along with WT Gd. Five plants were analysed for each condition tested.

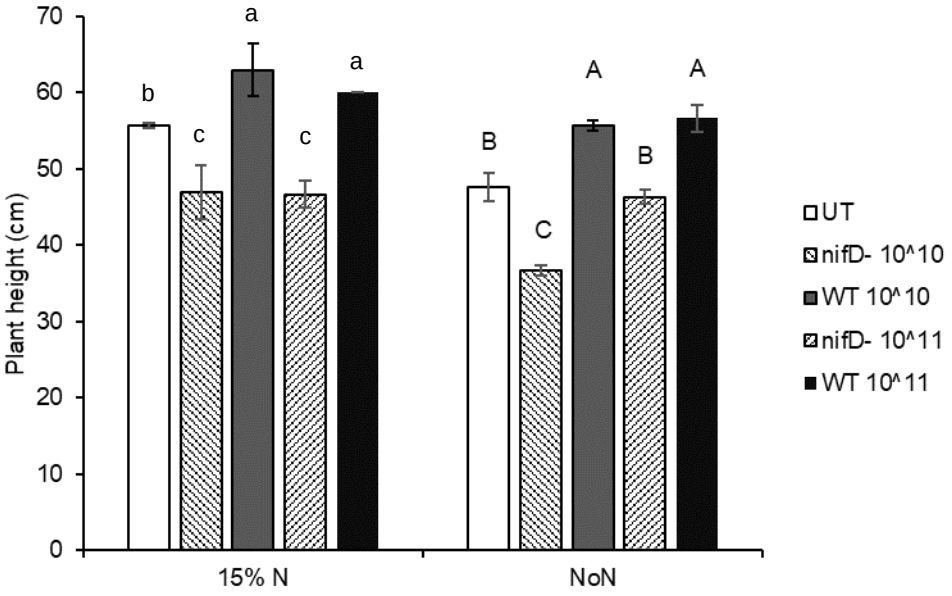


Fig. 34. Plant height (n=5) of 2 months old plants inoculated through seed coating protocol with two different concentrations (10^{10} and 10^{11} CFU ml^{-1}) of either WT or nifD$^-$ strains of Gd compared to untreated plants (UT). Growth was performed in-soil in glasshouse conditions. Two N-feed concentrations (0 and 15% N) were evaluated for their influence on the interaction between Gd and tomato plants. Columns marked with the same letter within each N treatment do not differ by Kruskal-Wallis test $P \leq 0.05$.

As shown in Fig. 34, Fig. 35 and Fig. 36, differences in plant height, biomass and yield could be observed in plants treated with either *nifD*$^-$ or the WT strain of Gd in comparison to UT plants.

Plant height was significantly improved by both WT inoculation levels, in both the presence and the absence of N in plant feed (Fig. 34). In the presence of N, both levels of inoculation with *nifD*$^{-}$ led to a reduction in plants height. In the absence of N in the feeding solution, height reduction was observed with a *nifD*$^{-}$ inoculation level of 10^{10} CFU ml^{-1}, while a concentration of 10^{11} CFU ml^{-1} led to no significant variations from UT plant height.

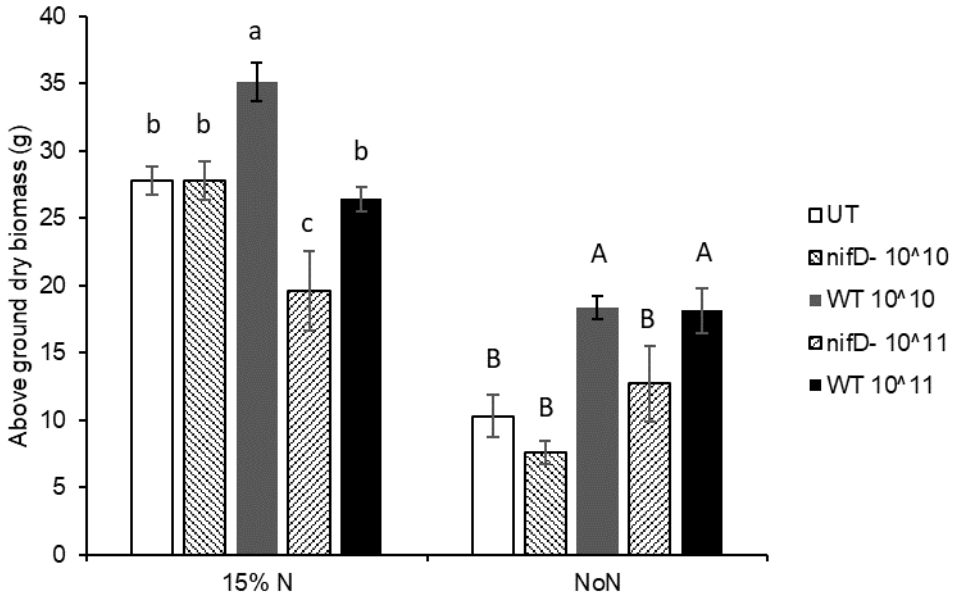


Fig. 35. Total above ground biomass (n=5) of 2 month old plants inoculated through seed coating protocol with two different concentrations (10^{10} and 10^{11} CFU ml^{-1}) of either WT or nifD^{-} strains of Gd compared to untreated plants (UT). Growth was performed in-soil in glasshouse conditions. Two N-feed concentrations (0 and 15% N) were evaluated for their influence on the interaction between Gd and tomato plants. Columns marked with the same letter within each N treatment do not differ by Kruskal-Wallis test $P \leq 0.05$.

In terms of dry biomass (Fig. 35), in the presence of 15% N in the plant feed, no significant variation from UT control plants was observed with the inoculation of *nifD*$^{-}$ strain at 10^{10} CFU ml^{-1} and of WT strain at 10^{11} CFU ml^{-1}. Inoculation with *nifD*$^{-}$ at 10^{11} CFU ml^{-1} led to a reduction in biomass accumulation whereas 10^{10} CFU ml^{-1} WT inoculation enhanced biomass formation. In the absence of N, no significant variation in dry biomass accumulation was observed after the inoculation of both concentrations of *nifD*$^{-}$ strain; however, both levels of WT inoculum gave rise to increased dry biomass accumulation in comparison to UT plants.

In the presence of N addition to the plant feed, no significant variation in the

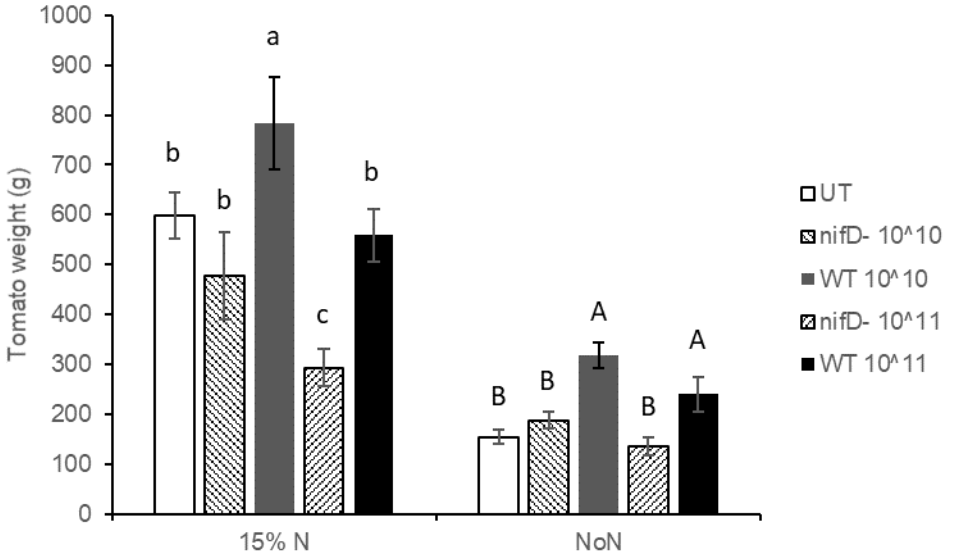


Fig. 36. Total weight of tomato fruits (n=5) from 2 month old plants inoculated through seed coating protocol with two different concentrations (10^{10} and 10^{11} CFU ml^{-1}) of either WT or nifD$^-$ strains of Gd compared to untreated plants (UT). Growth was performed in-soil in glasshouse conditions. Two N-feed concentrations were evaluated for their influence on the interaction between Gd and tomato plants. Columns marked with the same letter within each N treatment do not differ by Kruskal-Wallis test $P \leq 0.05$.

produced tomato weight (average weight of tomato produced per plant, Fig. 36) was observed neither after inoculation with 10^{10} CFU ml^{-1} *nifD*$^-$ nor 10^{11} CFU ml^{-1} WT. Reduction in tomato average weight was induced by inoculation with 10^{11} CFU ml^{-1} *nifD*$^-$ whereas 10^{10} CFU ml^{-1} WT inoculum led to an enhancement in tomato production. In the absence of N supplement, no yield enhancement was promoted by 10^{11} CFU ml^{-1} *nifD*$^-$ inoculation and only a slight, non-significant improvement with 10^{10} CFU ml^{-1} *nifD*$^-$. Yield improvement was observed after inoculation with both 10^{10} CFU ml^{-1} and 10^{11} CFU ml^{-1} concentrations of WT strain; 10^{10} CFU ml^{-1} induced a slightly higher yield promotion in comparison to 10^{11} CFU ml^{-1} WT concentration.

From these data it can be observed how the inoculum concentration has an influence on the bacterial growth promotion provided to tomato plants. This is also influenced by the amount of N available for plant consumption in the supplied feed.

In plants fed with 15% N, high concentrations of *nifD*$^-$ inoculum (10^{11} CFU ml^{-1}) led to reduced biomass and tomato fruit weight, indicating that the N-fixation impaired strain, when inoculated at concentrations as high as 10^{11} CFU ml^{-1} in

plants that are in no need of N, can lead to a reduction in plant growth. In fact, symbiotic bacteria not only provide nutrients and beneficial molecules for plant uptake, but also feed on plant produced sugars and other root exudates. This mutual exchange needs to be well balanced and thus the bacterial abundancy has a strong impact on the establishment of a fruitful cooperation.

Inoculation with WT at 10^{11} CFU ml^{-1} produced no variation in plant biomass and tomato fruit weight. This may be ascribable to the fact that a bacterial concentration of 10^{11} CFU ml^{-1} of the N-fixation functional WT strain may be perceived by the plant as a physiological burden and thus not favourable for growth promotion.

Inoculation with *nifD*$^{-}$ at 10^{10} CFU ml^{-1} seemed to lead to a less stressful interaction with the plant that experiences no significant growth promotion but neither a detrimental effect caused by the mutant strain.

Inoculum level of 10^{10} CFU ml^{-1} WT strain instead, showed a positive effect in terms of biomass and fruit weight production, indicating this as a good inoculation level for this type of treatment protocol to establish a fruitful symbiosis between Gd and tomato plants.

In the absence of N in the plant feed, both inocula concentrations of *nifD*$^{-}$ showed no difference between untreated controls and mutant strain treated plants indicating that, in this setup, no negative nor positive effect was provided by *nifD*$^{-}$ strain to tomato plants. On the other hand, both inoculations levels of WT strain led to an improvement of both biomass and tomato weight. This implies that a plant grown in N limiting conditions in this setup interacts differently from a N fed plant towards the same concentrations of inoculated bacteria. A more positive outcome is elicited by WT bacteria inoculation when the plant is in higher need of N supply, while *nifD*$^{-}$ inoculation has lower to no effects in this condition. When N is supplied in the feed (15% N condition), inoculation level becomes critical for bacteria-plant interaction establishment: for *nifD*$^{-}$, high inoculant levels (10^{11} CFU ml^{-1}) lead to a negative effect on tomato plants while 10^{10} CFU ml^{-1} induce no significant changes; in WT strain, inoculation at higher levels (10^{11} CFU ml^{-1}) provided no significant modulations while 10^{10} CFU ml^{-1} inoculation induced plant growth promotion in this setup.

No GUS tagged strains were available for Gd colonisation assessment at the time that these experiments were undertaken. BioPCR colonisation assessment was performed on leaves, but no positive results were obtained from this. Evidence suggested that this latter bacterial detection method was not completely reliable for our setup colonisation assessment. In addition, any plant colonisation may have been restricted to root tissues. A more reliable colonisation assay was achieved in later phases of the project and employed in later experiments (described below).

This in-soil test provided a good indication of the importance of the N-fixation ability of Gd on the PGP activity exerted towards tomato plants. It also underlined how the plant nutritional state is another crucial variable to be considered when investigating the interactions between plant associated bacteria and their host.

4.4.1.2. Gd effects on hydroponically grown plants

As already mentioned, in-soil experiments are subject to a much higher number of less controllable variables. One of our main goals was to investigate the interactions elicited by the contact between Gd and tomato plants from a molecular point of view and thus a less complex experimental setup was required. The previously described hydroponics setup was chosen as candidate for this analysis.

Money Maker plantlets were inoculated as previously described (Section 4.3.2). Two different levels of N were tested: the absence and 2 mM KNO_3 in plant growth solution. Bacterial inoculum of both tested strains (WT and *nifD*$^-$) was performed at a concentration of 10^9 CFU ml^{-1}.



Fig. 37. Phenotype of Money Maker plants two weeks after inoculation with either nifD- or WT Gd strain through root dipping. From left to right: UT, nifD- and WT. Evaluation was performed both in (a) the absence and (b) the presence of 2 mM KNO_3 in the nutrient solution.

Phenotypic data were collected two weeks after bacterial inoculation (14 dpi) (Fig. 37). Inoculation with either *nifD*- or WT Gd strains led to increased plant height and biomass (fresh weight) in comparison to UT control plants (Fig. 38). Nevertheless, the WT strain exhibited an enhanced effect compared to *nifD*- inoculated plants. A similar outcome was observed under both N nutrition conditions.

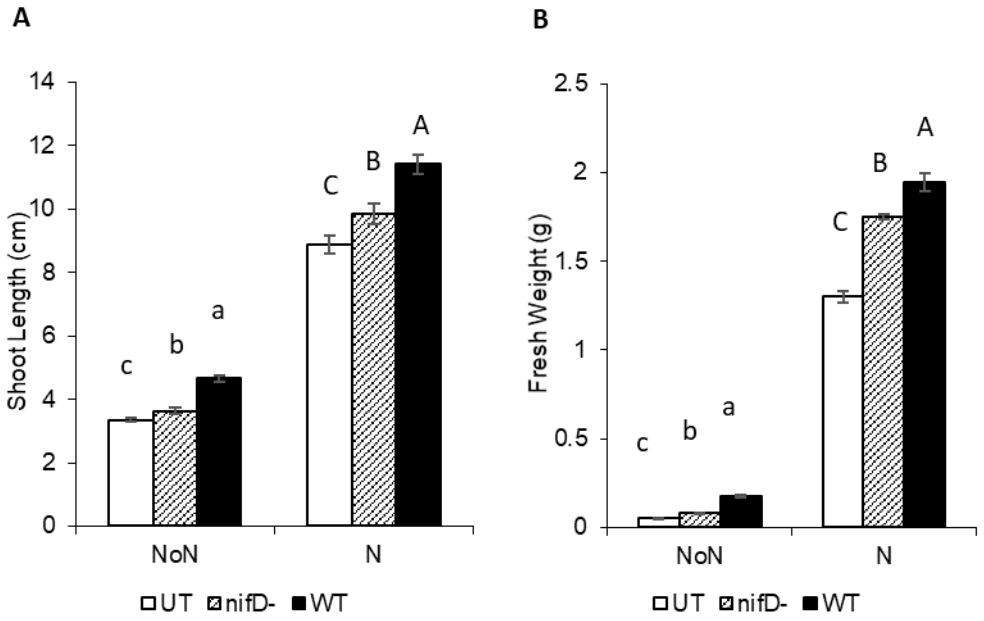


Fig. 38. Shoot length (A) and fresh weight (B) measurements of plants at 14 dpi through root dipping in a hydroponics system. Inoculation was performed with either WT or nifD- strains of Gd compared to untreated plants (UT). Two N concentrations were evaluated for their influence on the interaction between Gd and tomato plants: the absence of N supply (NoN) and addition of 2 mM KNO_3 (N). Columns marked with the same letter within each N treatment do not differ by Kruskal-Wallis test $P \leq 0.05$.

Interestingly, no significant differences from UT controls were observed in terms of chlorophyll content (Fig. 39) in *nifD*- inoculated plants while a higher chlorophyll content was detected in WT inoculated plants. Chlorophyll content is directly connected to the plant N availability, being one of the main sinks for this nutrient. These data support the suggestion of the importance of N fixation contribution to the PGP action of Gd in plants.

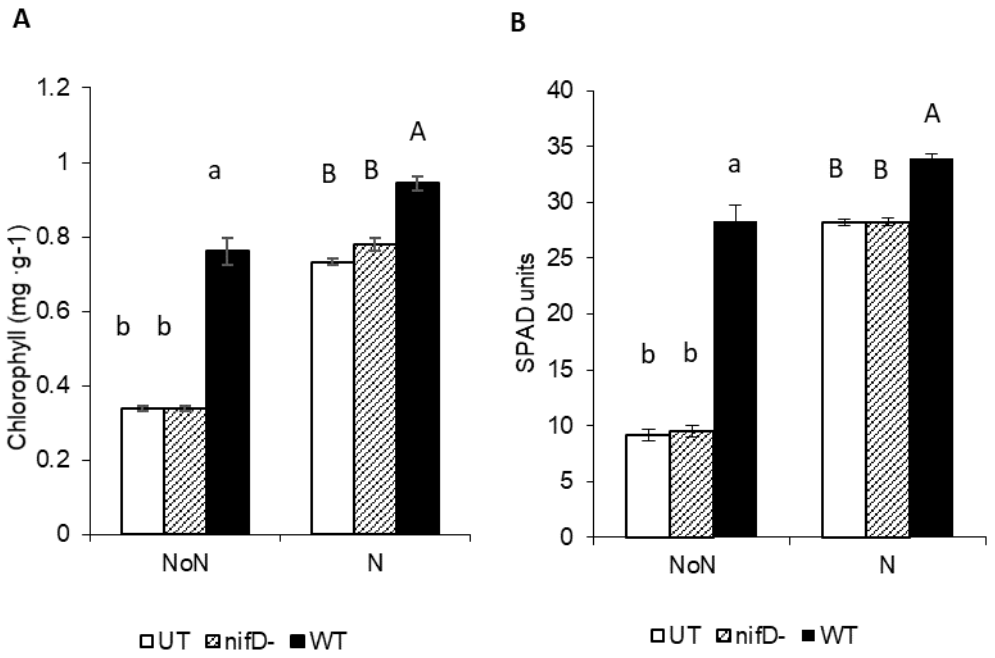


Fig. 39. Chlorophyll content (A) and corresponding SPAD unit (B) measurements of plants at 14 dpi through root dipping in hydroponics system. Inoculation was performed with either WT or nifD- strains of Gd compared to untreated plants (UT). Two N concentrations were evaluated for their influence on the interaction between Gd and tomato plants: the absence of N supply (NoN) and addition of 2 mM KNO_3 (N). Columns marked with the same letter within each N-treatment do not differ by Kruskal-Wallis test $P \leq 0.05$.

4.4.2. Gd localisation

4.4.2.1. GUS staining

For this experiment, an MS agar inoculation setup (Section 4.3.1) was employed. Two weeks after inoculation with the GUS tagged WT strain, GUS staining was performed on whole MicroTom plants using a concentration of 100 CFU ml^{-1}. The treatment showed good colonisation testified by GUS staining; nevertheless, bacteria were exclusively localized in the root system. Gd treated plants showed improved greenness and growth in comparison to untreated plants (Fig. 40).

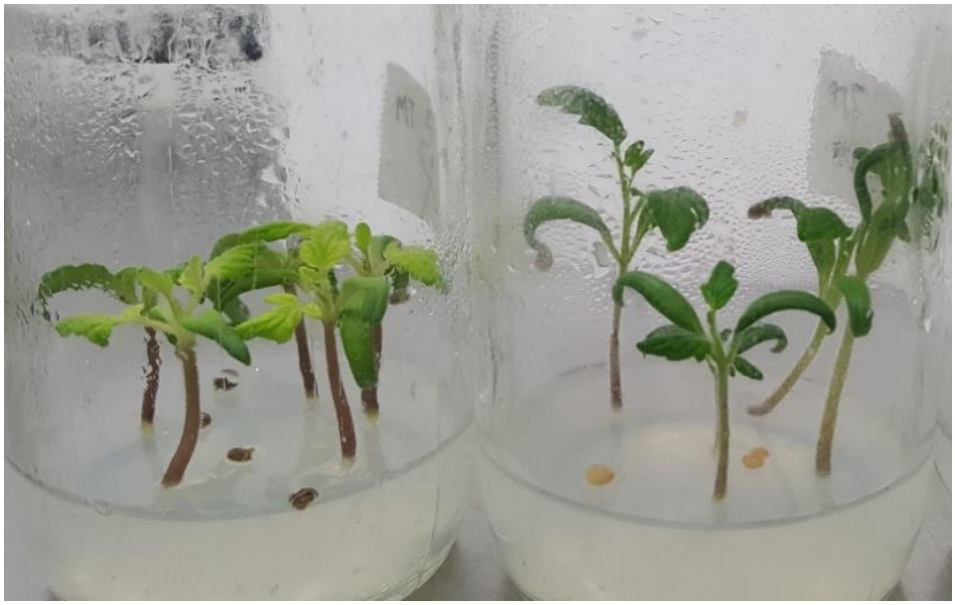


Fig. 40. Phenotype of MicroTom plants grown in MS agar medium in sterile glass jars. Untreated plants (left) are compared to WT Gd inoculated plants (right). Inoculation was performed on emerging roots at a bacterial concentration of 100 CFU ml^{-1}.

Plants were then removed from the MS agar substrate, carefully rinsed and, after overnight incubation in staining solution tissue was cleared using 70% EtOH solution overnight. Plants tissues were then fixed: an incubation step in 0.1 M phosphate buffer, ph7 with 2% Glutaraldehyde was performed. After tissue fixation, root samples were cross sectioned and observed under optical microscope to assess bacterial localisation.

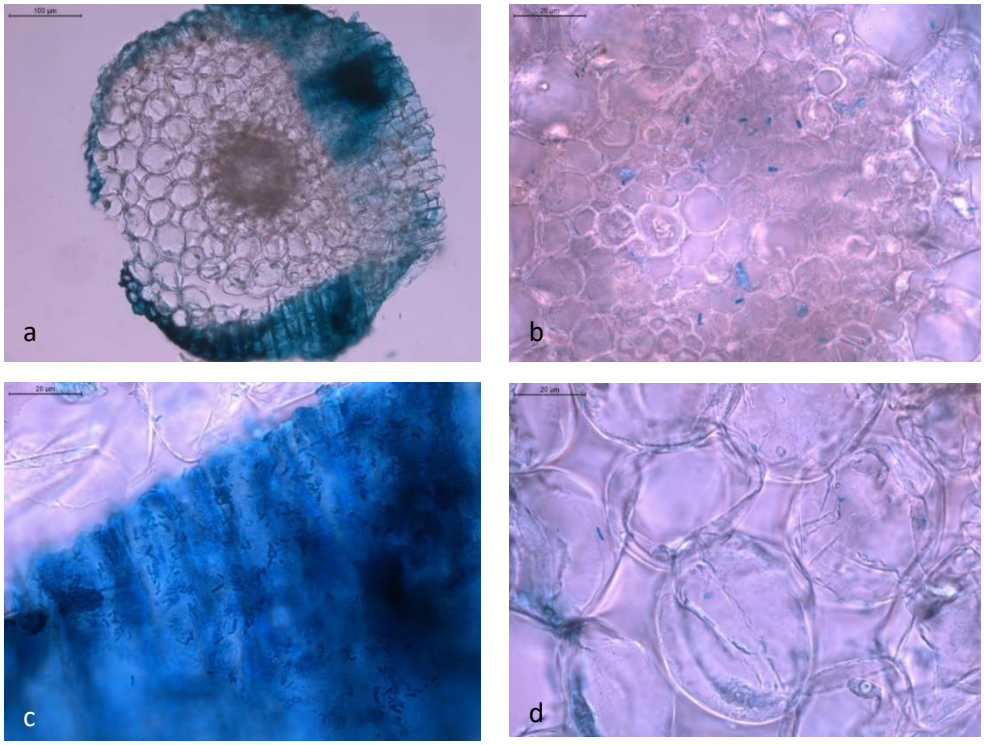


Fig. 41. a) cross section of tomato (MicroTom) roots from plants treated with GUS WT Gd after blue staining. b) blue stained bacterial cells in the vascular tissues of the root. c) root surface: majority of the stained cells localised on the root surface. d) blue stained bacterial cells probably in the cytoplasm of cortical root cells.

The bacterial cells appeared to be mainly localised on the root surface (Fig. 41c), while a small amount of cells could also be detected in the inner root layers and in the intracellular compartment as well (Fig. 41, b and d).

4.4.2.2. Fluorescence Microscopy

To gain a clearer method to visualise the bacterial localisation during the interaction with tomato root systems, the hydroponics setup was chosen to inoculate tomato plantlets with a GFP tagged strain of WT Gd (*GGG* strain). Root fragments were collected at different time points, thoroughly washed in either sterile distilled water or 10 mM $MgCl_2$ and observed under a fluorescence microscope (LMD7000, Leica Microsystem) provided with a GFP visualisation filter. This bacterial tagging proved to be very stable and allowed very sharp visualisation of bacterial cells, up to single cell resolution (Fig. 42). Furthermore, *GGG* fluorescent signal was still detected on hydroponically grown plants at 14 dpi and also in bacteria that were re-isolatad from inoculated plants through maceration.

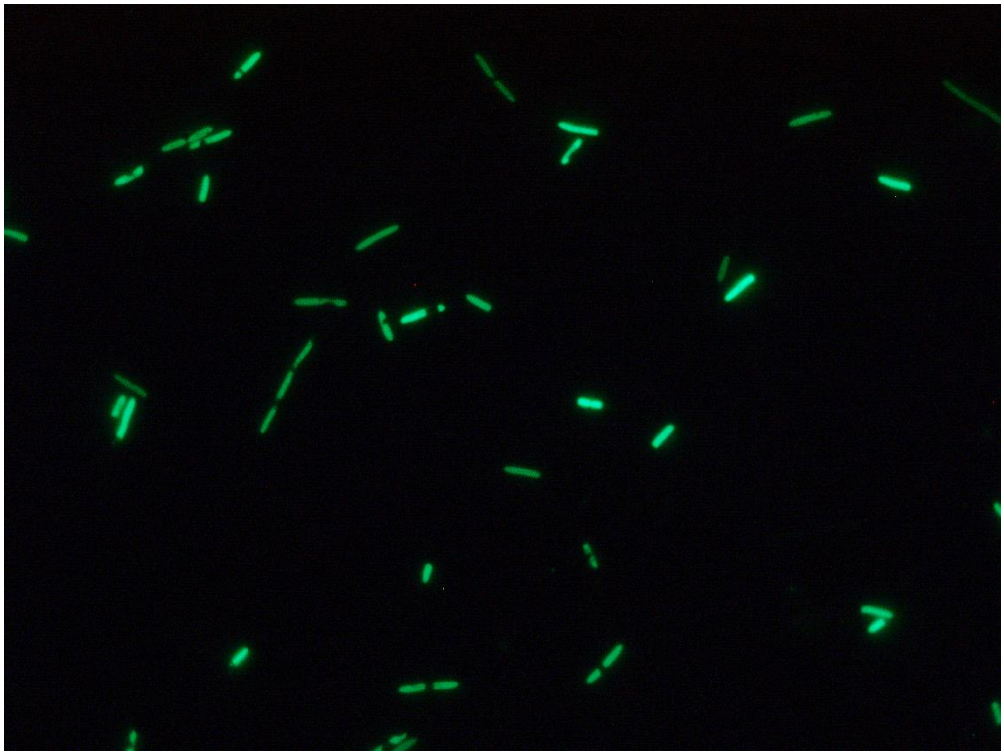


Fig. 42. Free GFP tagged cells of GGG Gd strain grown in ATGUS liquid medium.

From the following reported observations, backed up by the previously mentioned GUS staining visualisation data, bacteria mainly localised on the root

surface, mostly in proximity of the intercellular spaces between adjacent cells (Fig. 43 and Fig. 44).

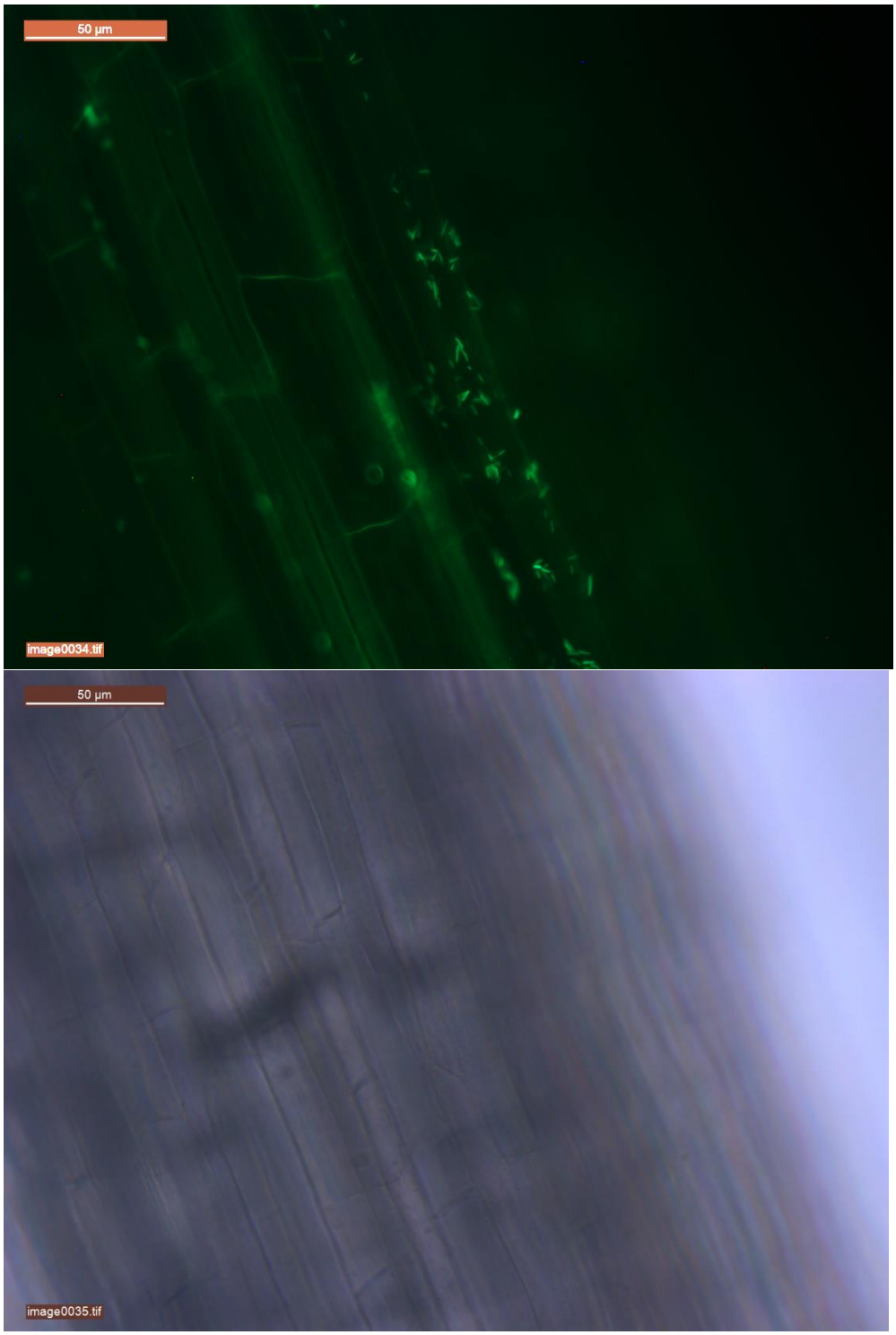


Fig. 43. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 6 dpi in the presence of 2mM KNO_3 in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

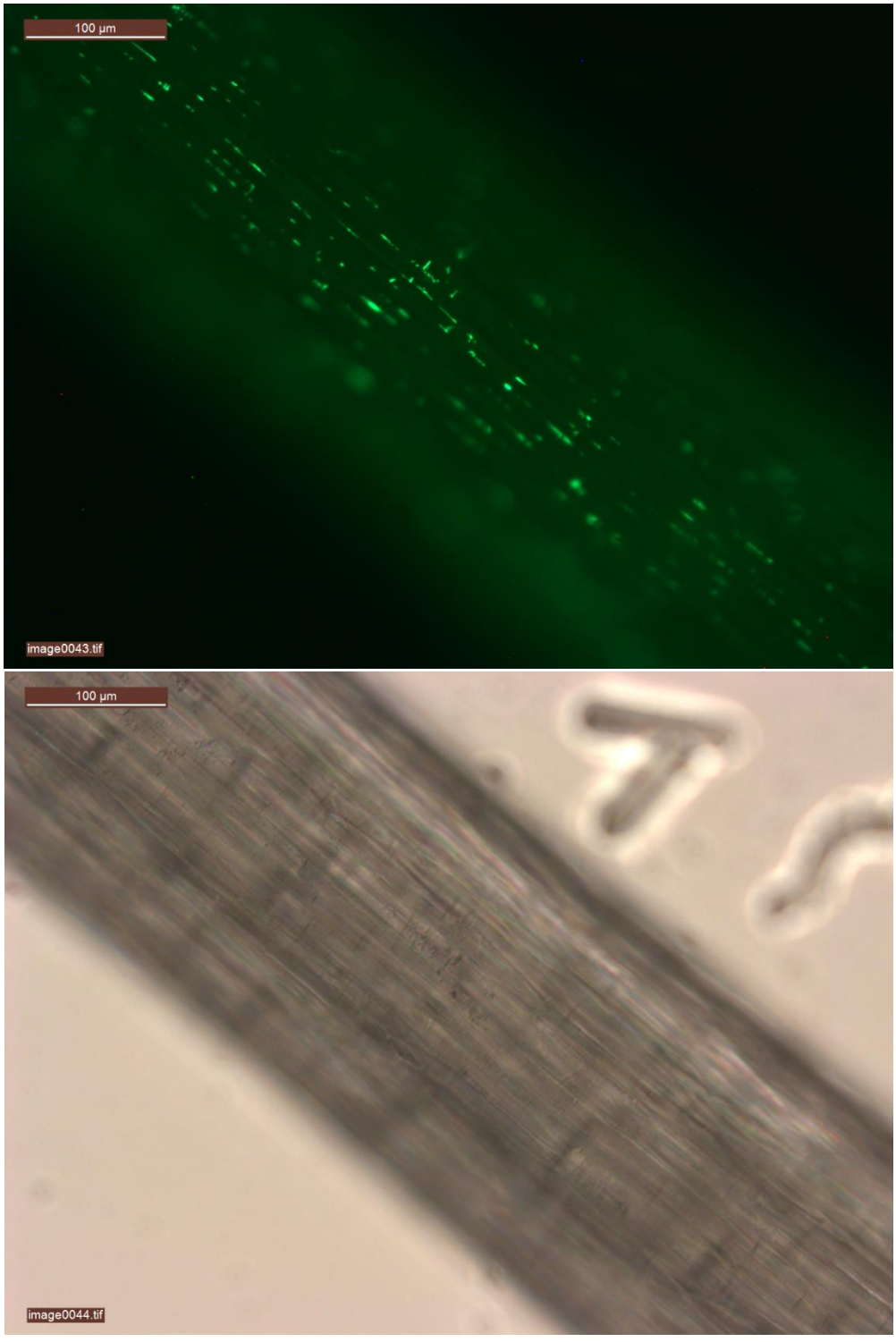


Fig. 44. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 1 dpi in the absence of a N source in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

Often, Gd cells could be found in clustered formations, with what appears to be an organic matrix to surround and maintain the aggregation (Fig. 45 and Fig. 46). Polysaccharidic matrix formation is known to be a key requirement for

biofilm formation and thus could favour bacterial adhesion to the plant root surfaces. Gd is in fact known to produce large amounts of Levan, an exopolysaccharide secreted in the external cellular compartment, that is involved in O_2 tolerance and biofilm formation [247].

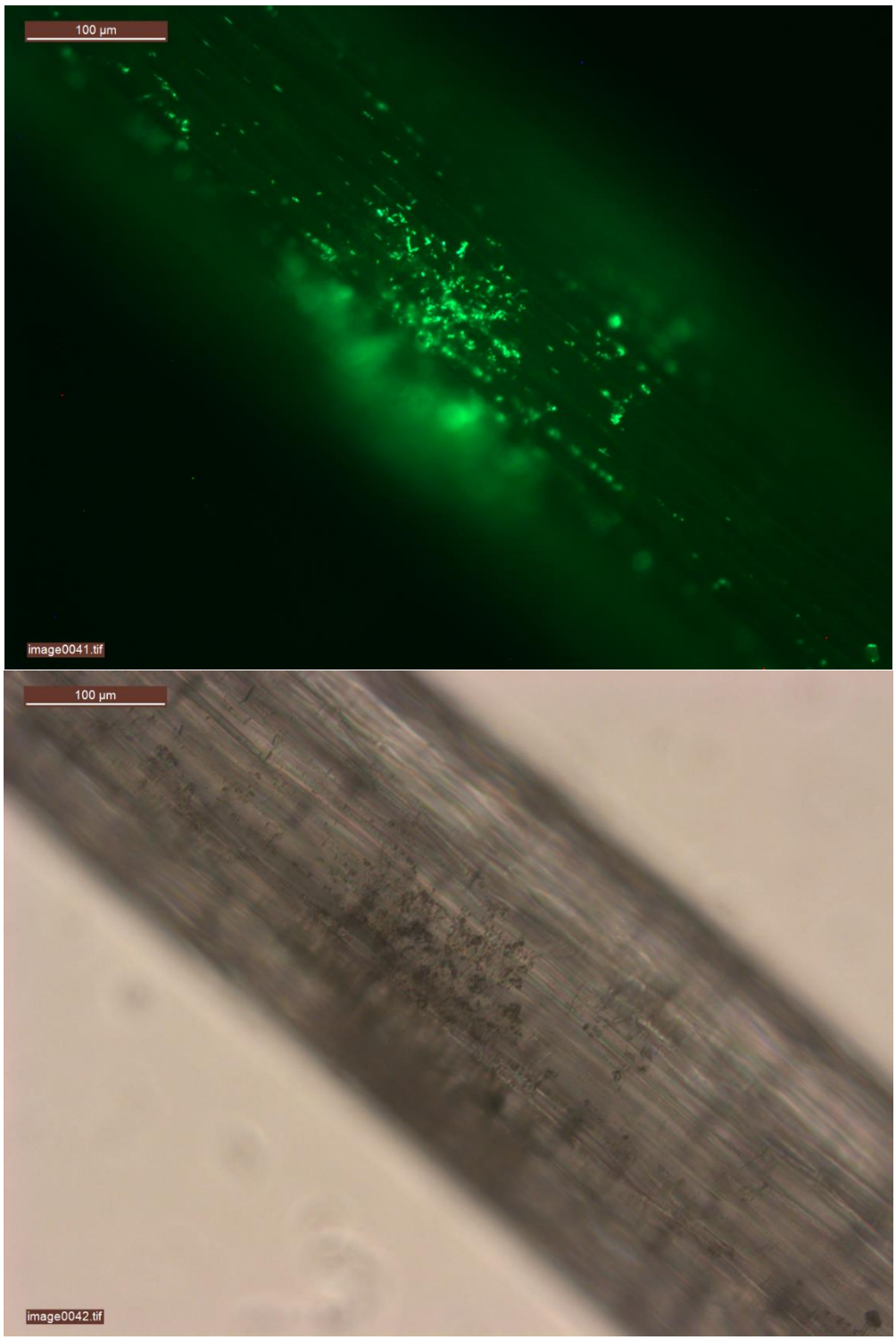


Fig. 45. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM

$MgCl_2$, at 1 dpi in the absence of N in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

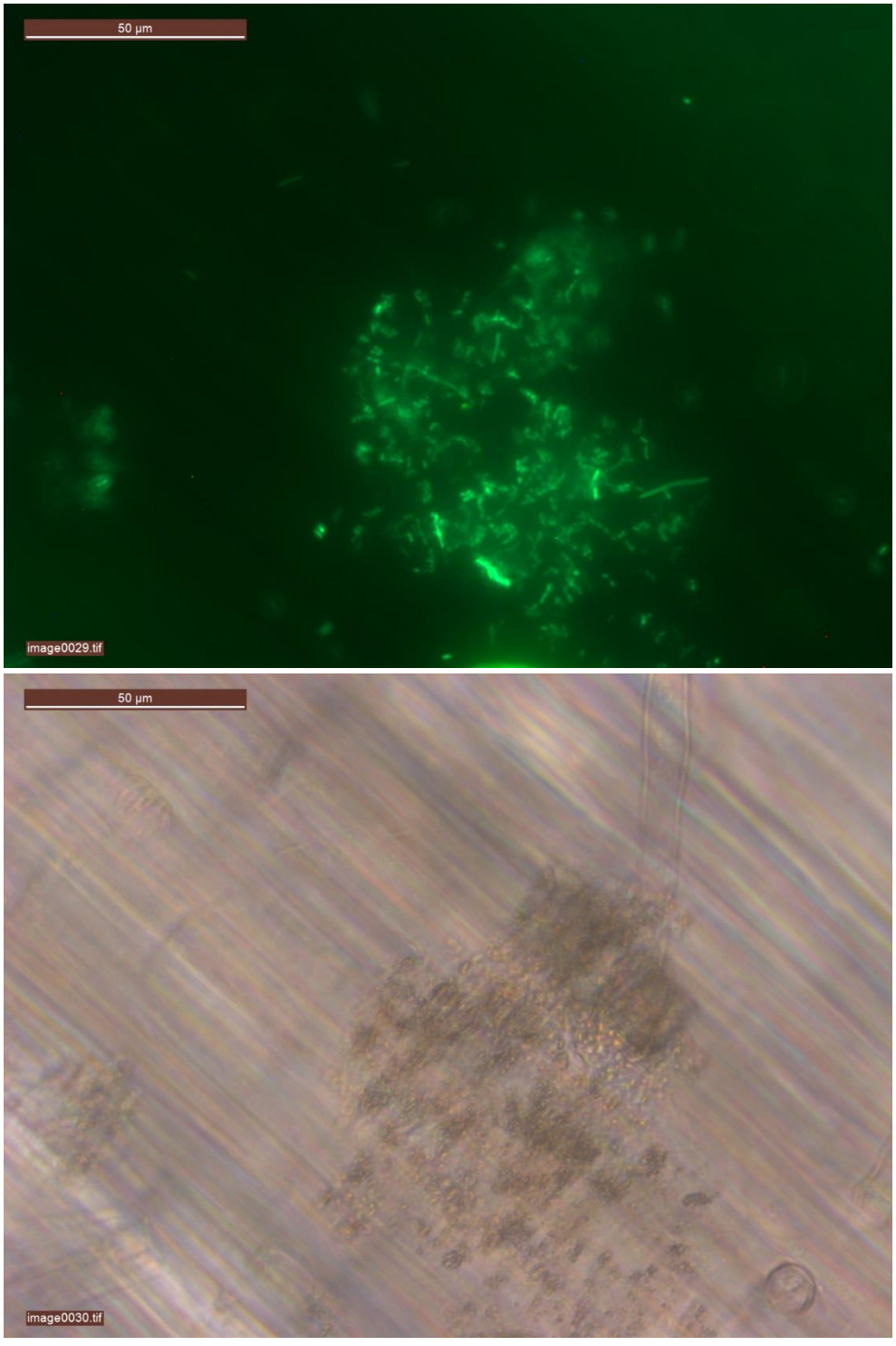


Fig. 46. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 1 dpi in the absence of N in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

In line with what has been previously reported in the literature [102] [133], Gd was also found to localise at lateral root emergence sites (Fig. 47). These areas

are thought to be a favoured entry sites for Gd colonisation since the integrity of the root surface is interrupted and this can be used by the bacterium to reach the inner compartments of the root.

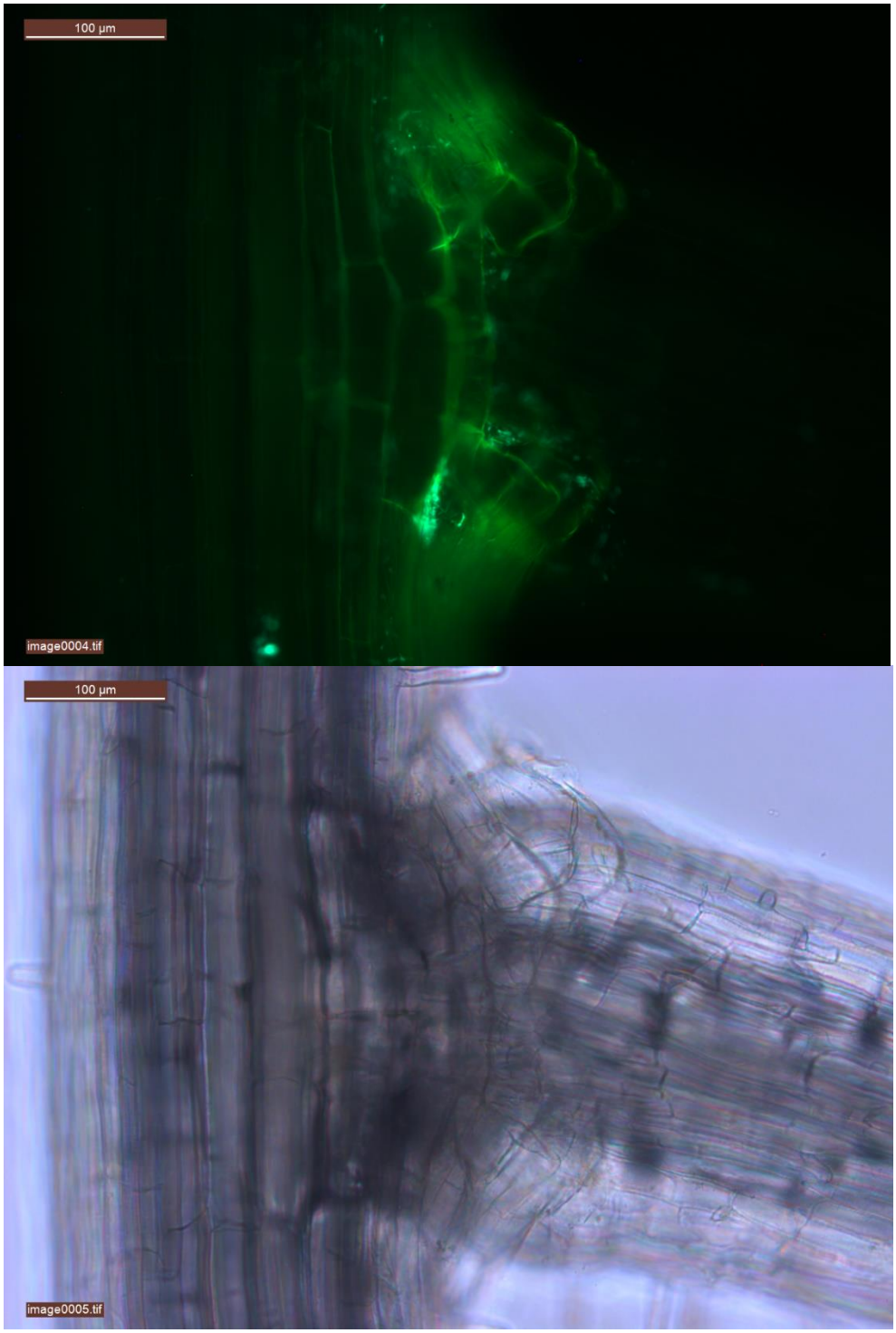


Fig. 47. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 6 dpi in the absence of N in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

In some cases, bacterial GFP tagged cell localisation seemed to be strictly confined inside the cell boundaries (Fig. 48 to Fig. 52), possibly indicating an established intracellular colonisation.

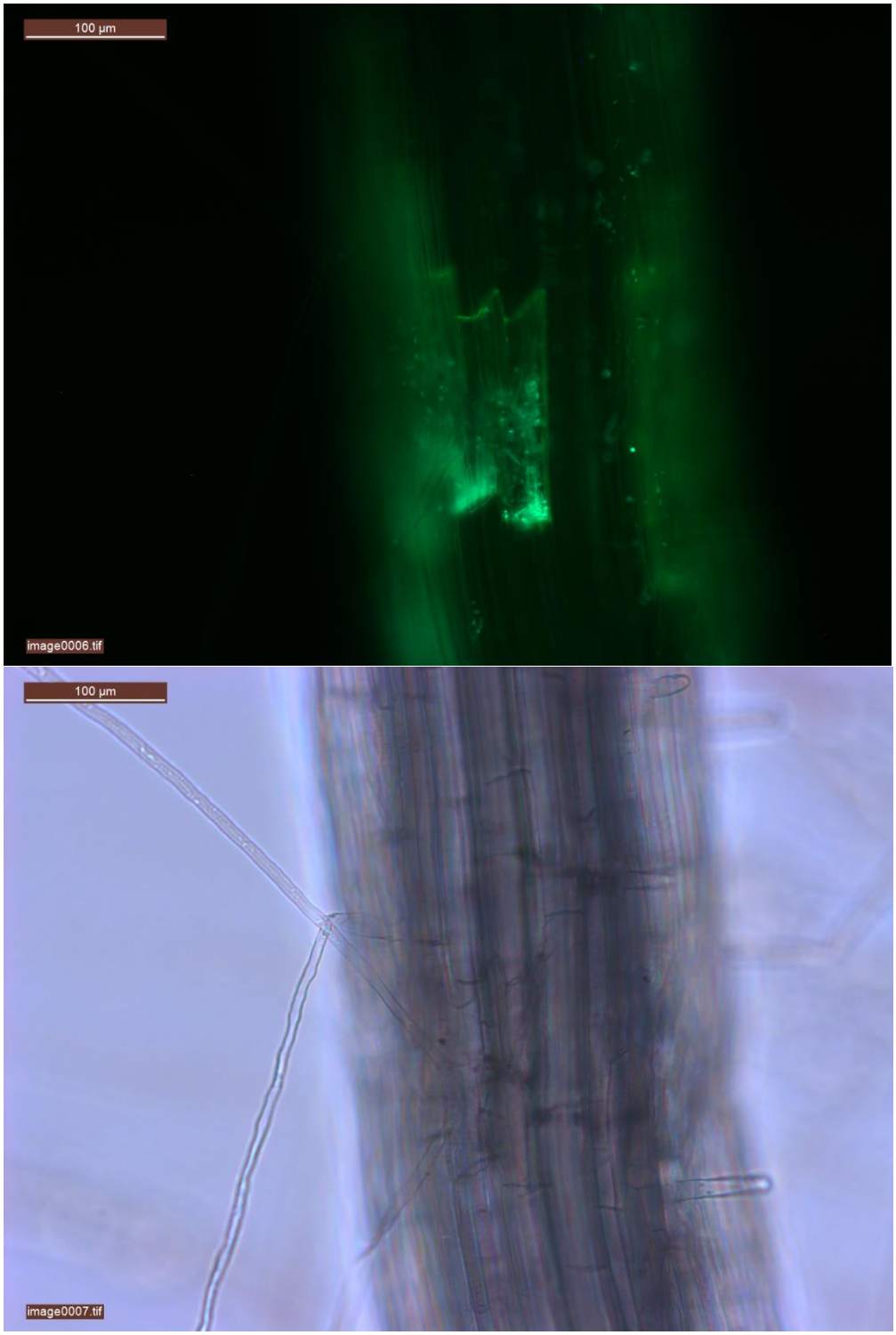


Fig. 48. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 6 dpi in the absence of N in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

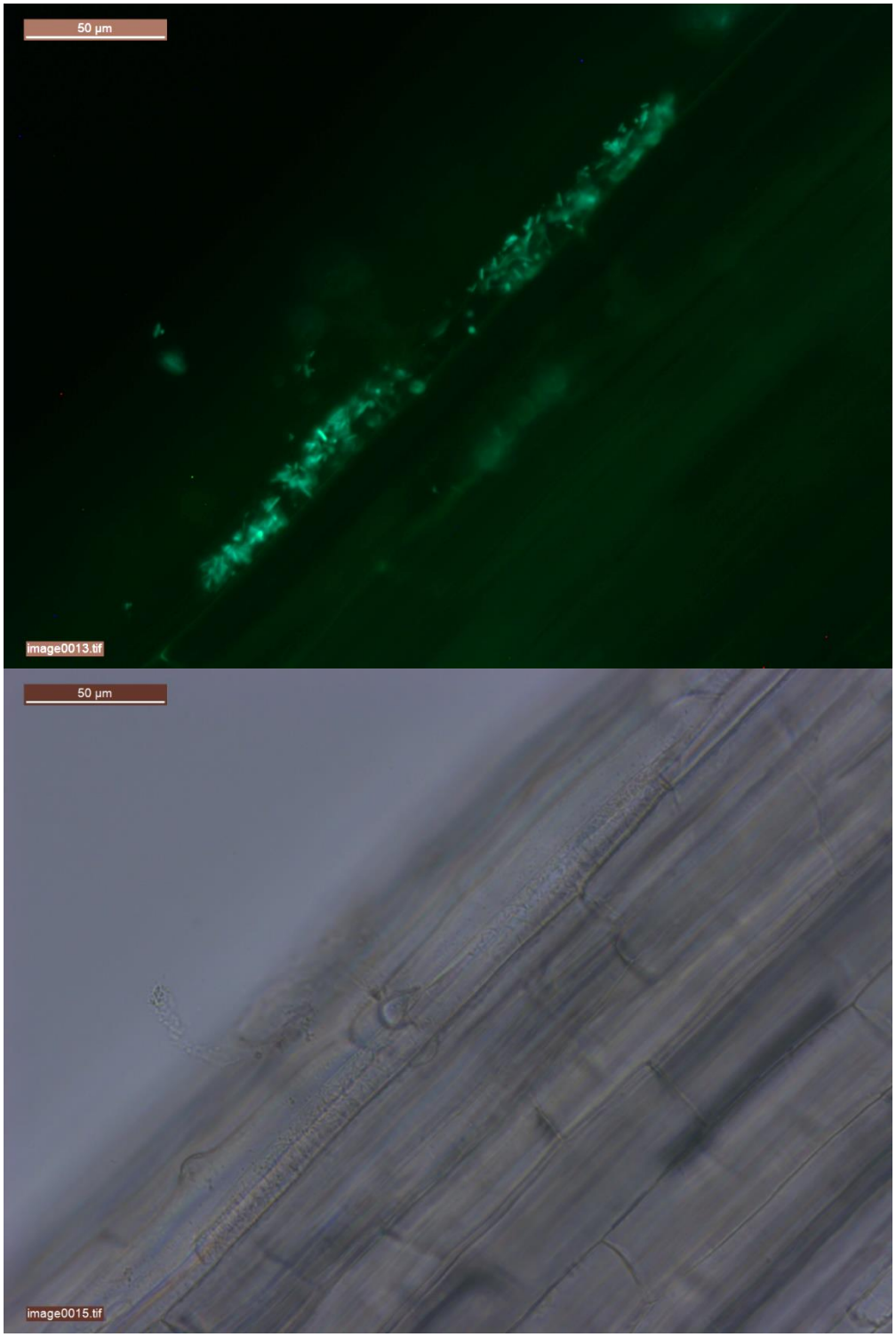


Fig. 49. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 2 dpi in the presence of 2mM KNO_3 in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

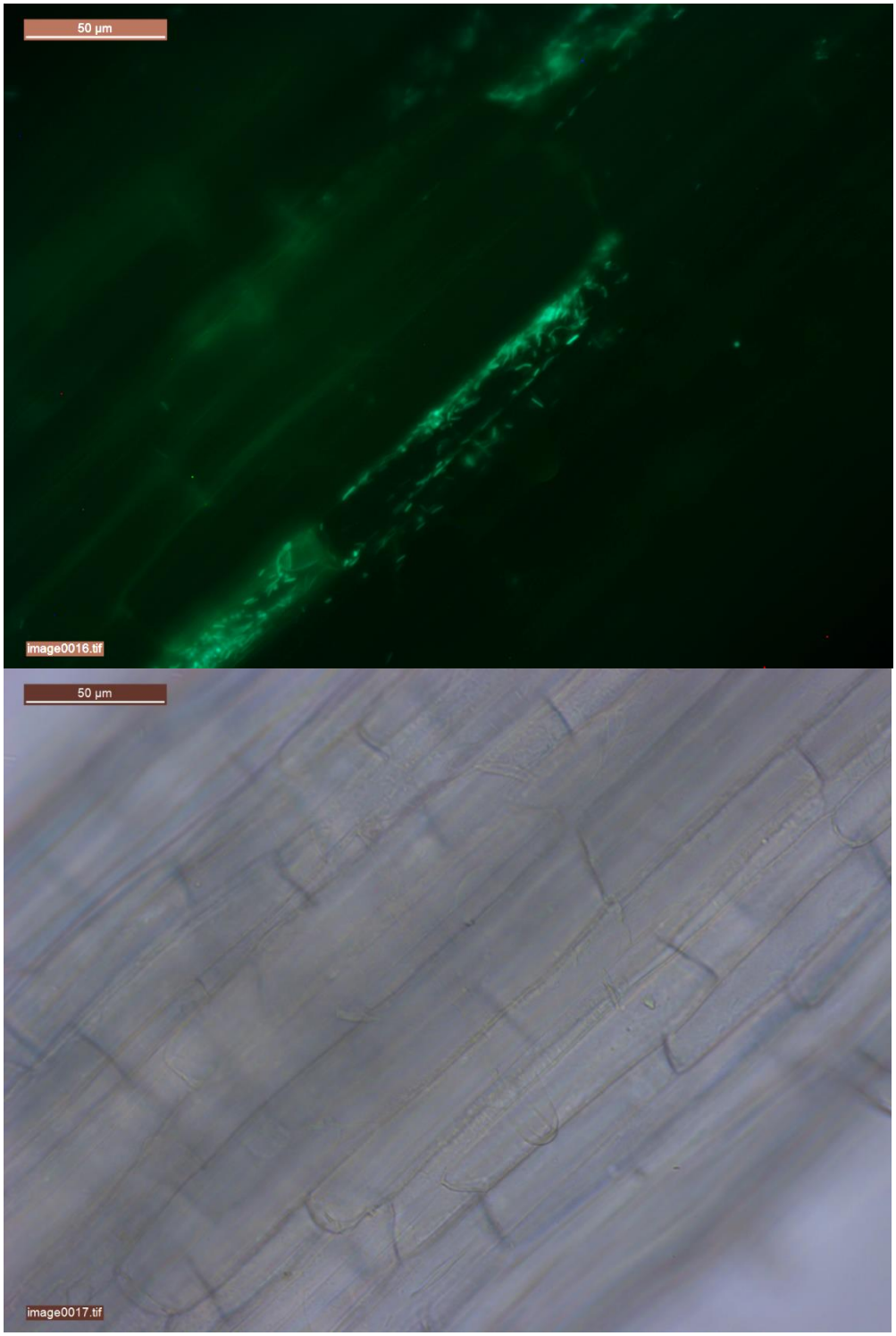


Fig. 50. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 2 dpi in the presence of 2mM KNO_3 in the modified Hoagland solution supplied. The corresponding brightfield picture is reported as a reference.

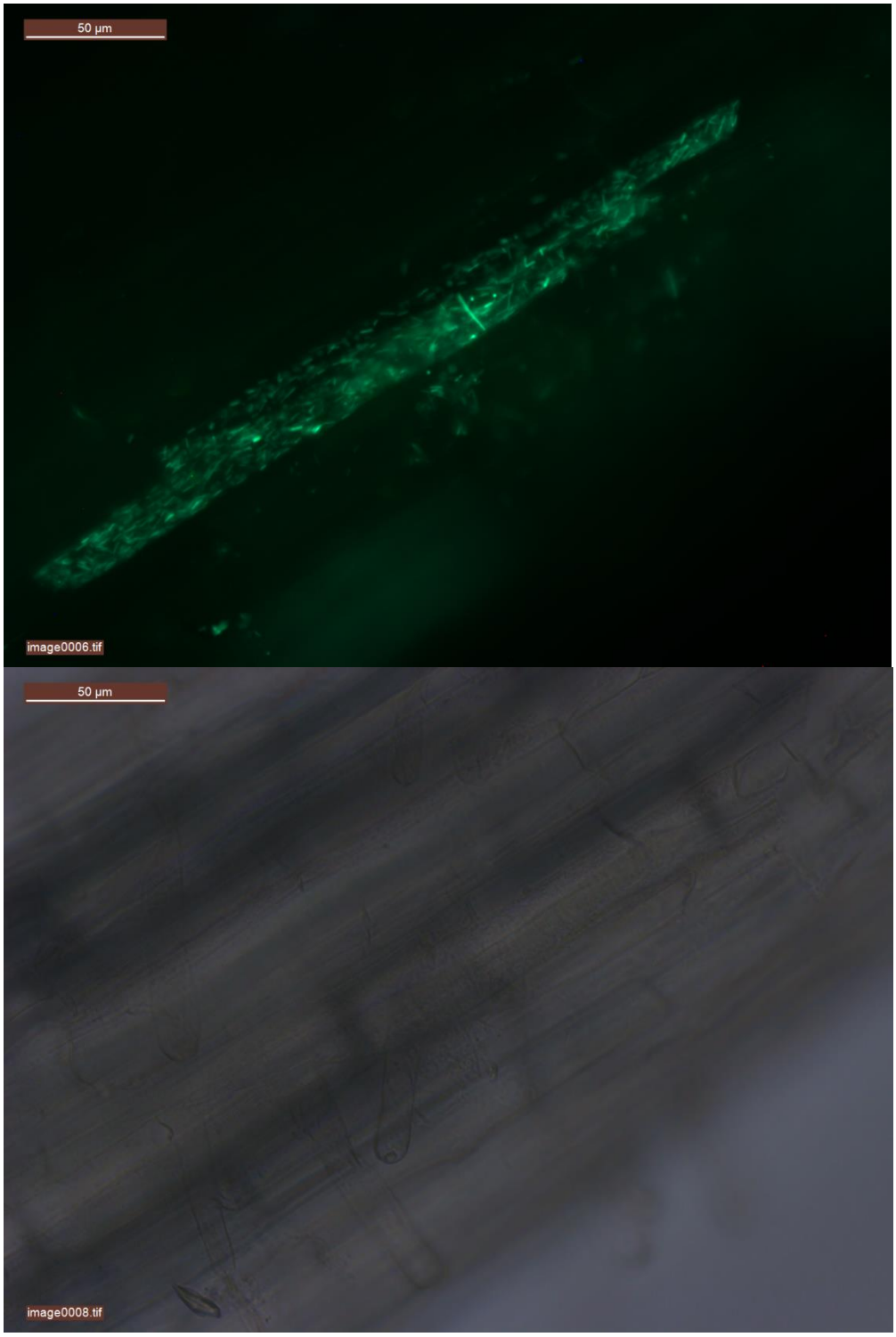


Fig. 51. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 2 dpi in the presence of 2 mM KNO_3 in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

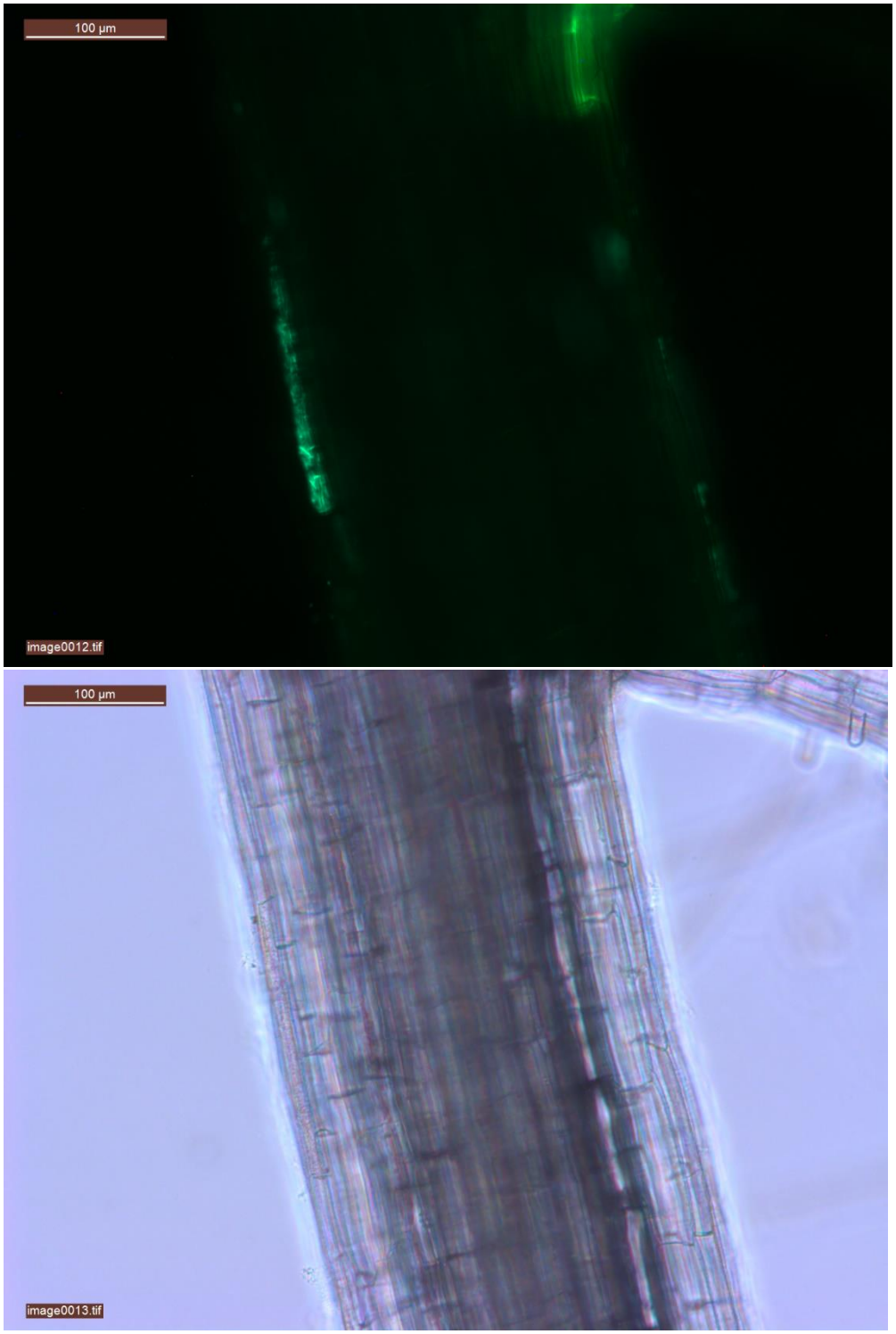


Fig. 52. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 6 dpi in the absence of N in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

Moreover, bacterial cells were also detected in proximity to the vascular tissues (Fig. 53). During sugarcane colonisation, Gd has proved to be able to reach the xylem and use it as a preferential route for whole plant colonisation [60].

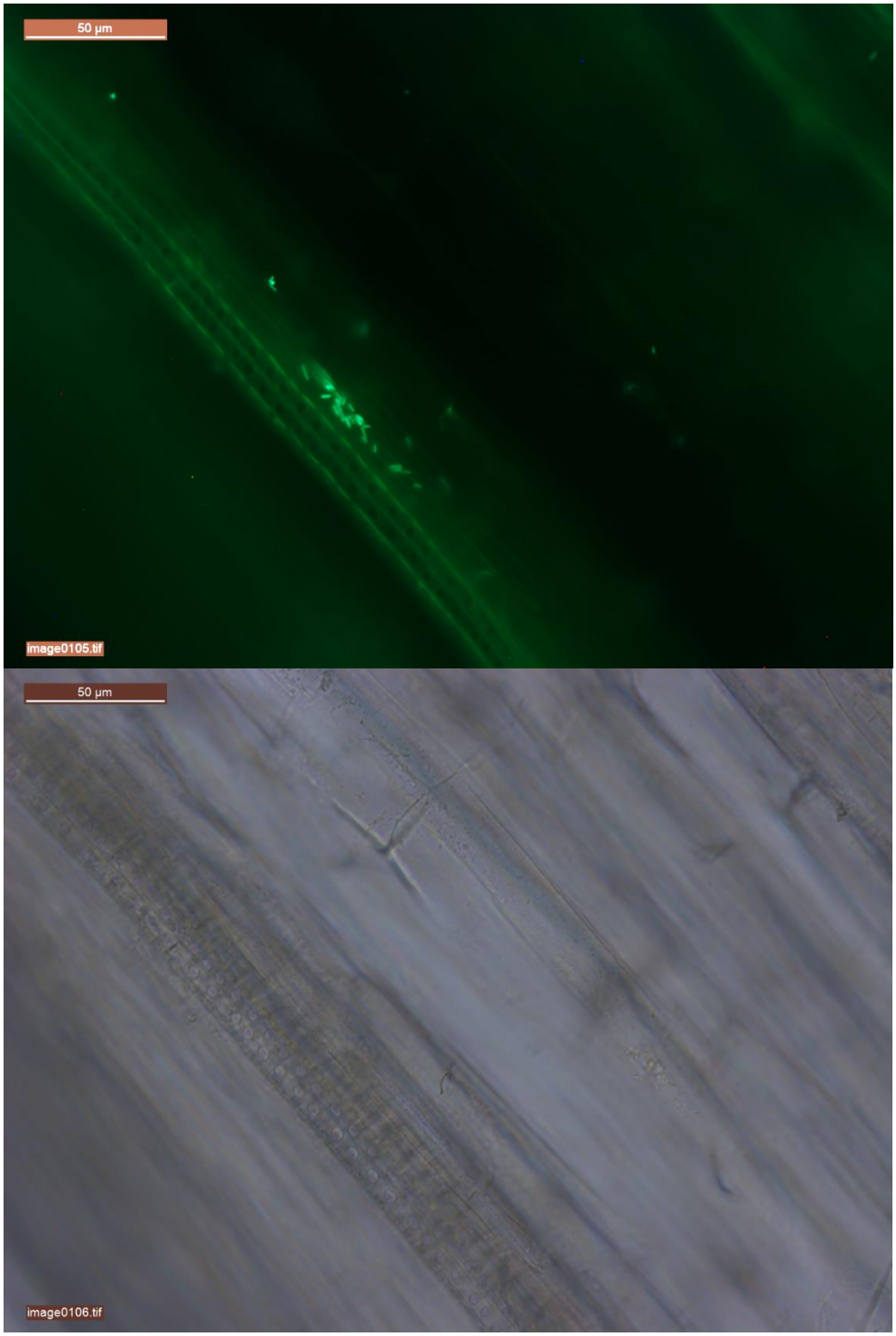


Fig. 53. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 2 dpi in the absence of N in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

Occasionally, Gd clusters could also be observed to be adhering, creating a coating like formation, to root hairs and very thin roots (Fig. 54).

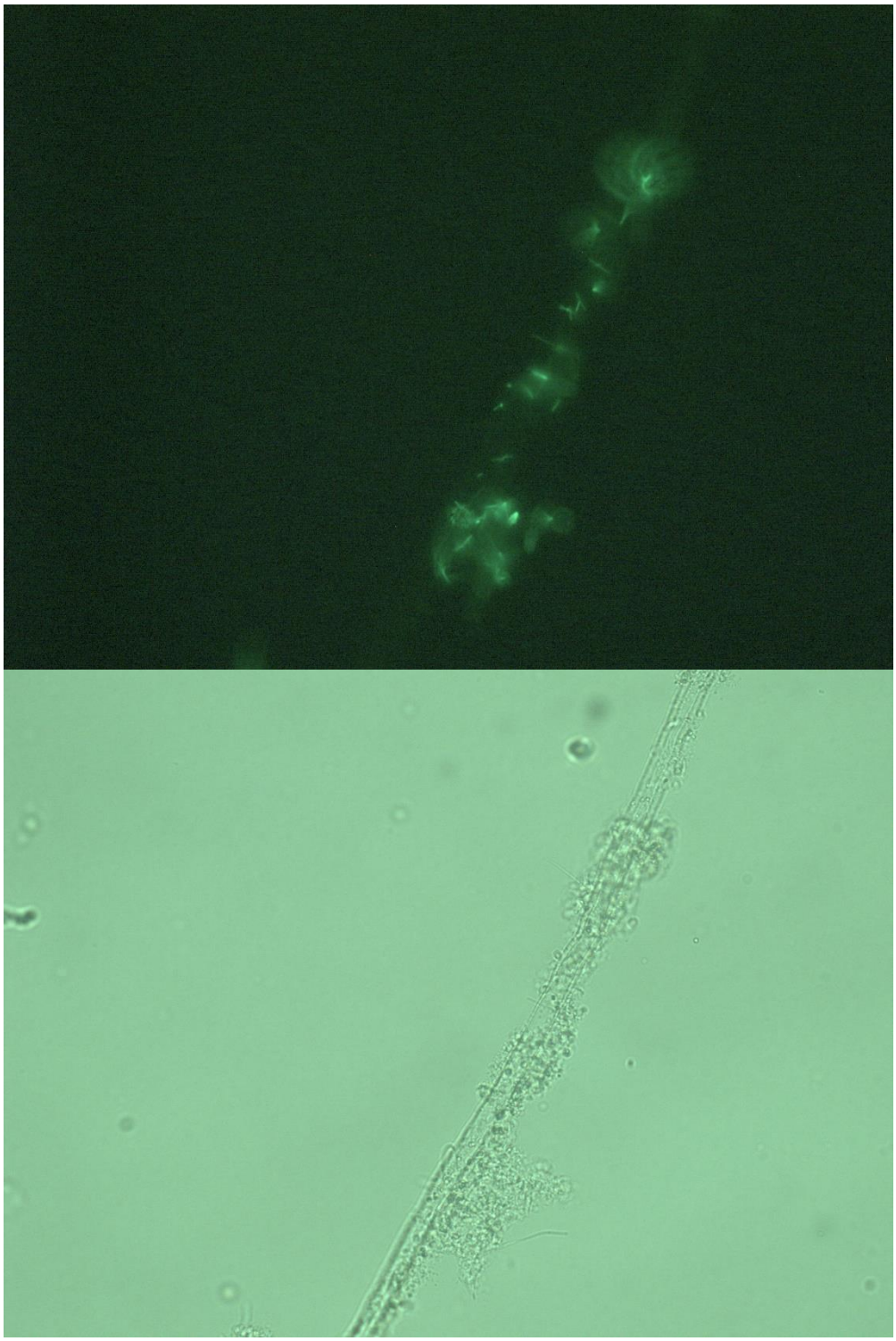


Fig. 54. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with GGG strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 7 dpi in the absence of N in the modified Hoagland solution. 40x magnification. The corresponding brightfield picture is reported as a reference.

From the observations in this study, the predominant interaction mechanism between Gd and tomato plants grown in a hydroponic system mainly implies root adhesion and intercellular colonisation with possible occurrence of intracellular establishment. The majority of bacterial biomass interacts with the plant strongly adhering to the root surface as rhizosphere associated bacteria. A portion of bacteria enters the root system and gets established either inside plants cells (intracellular colonisation) or moving in the intercellular compartment to reach the xylematic system, allowing the potential for bacterial spread towards above ground organs of the host plant. In this study, this was observed for both tomato cultivars analysed, both in MicroTom MS agar inoculation through GUS staining visualisation, and for Money Maker in hydroponic systems with GFP tagged strain inoculation.

4.4.2.3. Bacterial colonisation quantification: maceration and plating

The hydroponic system (Section 3.9) was employed for inoculation of Money Maker plants using either *nifD*$^-$ or WT strains of Gd at a concentration of 10^9 CFU ml^{-1}.

Plants were tested at two different levels of N (provided through modified Hoagland solution): the absence of nitrogen supply (NoN condition) and addition of 2 mM KNO_3 (N) so as to assess whether the presence or the absence of N could influence bacterial interaction and colonisation of plants in this specific production system.

Fourteen days after bacterial application, non-inoculated (UT) and bacterium-inoculated plants (either *nifD*$^-$ or WT strain) were collected, and roots and shoots were detached and thoroughly washed twice with 10 mM $MgCl_2$ in order to remove loosely attached/non-adhering/non-interacting bacteria from the surface. Roots and shoots were separately ground in a mixer-mill disruptor (MM 400, Retsch, Haan, Germany) at 25 Hz for 1 min (or until completely macerated). For bigger plants, portions of roots or shoots and leaves were collected to reach same weight in each sample instead of macerating whole organs. Samples were then re-suspended in 200 µL of sterile water and carefully vortexed. Each suspension was serially diluted and 10 µL aliquots were plated

in triplicate on solid AceLGI-P medium, that, from previous tests had shown to be appropriately selective for Gd re-isolation from plants tissues. After 72 hrs of incubation at 28 °C, colony forming units (CFUs) of Gd per unit of plant material fresh weight (CFUs g^{-1}) were calculated. As a standard method, three replicates (plants) were analysed for each treatment and the experiment was carried out at least twice.

Colony PCR was performed on bacterial colonies employing strain specific primers to confirm bacterial identification after re-isolation from plants.

Colonisation rate was evaluated as bacterial abundance in roots, shoots (stem and leaves) together with loose bacteria present in nutrient solution which were not directly interacting with plants.

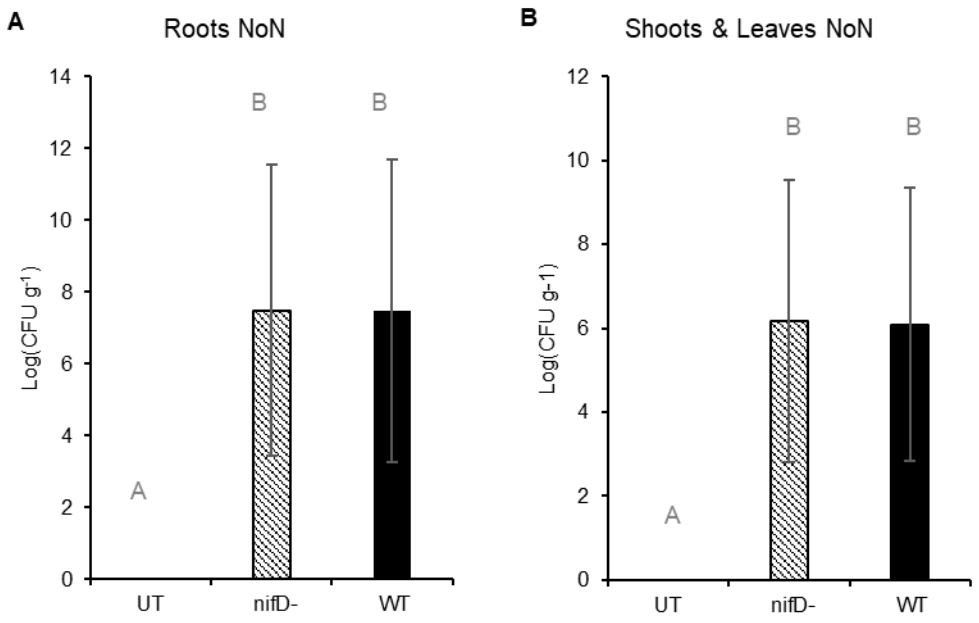


Fig. 55. Colonisation rate quantification following plant tissue maceration, serial dilution and plating. Data were collected from plants grown in the absence of N (NoN) in modified Hoagland nutrient solution at 14 dpi. Gd quantification was carried out on (A) roots and (B) shoots and leaves. Quantification was referred as CFU per g of macerated tissue. Significance of differences between treatments was assessed by Kruskal-Wallis test $P \leq 0.05$.

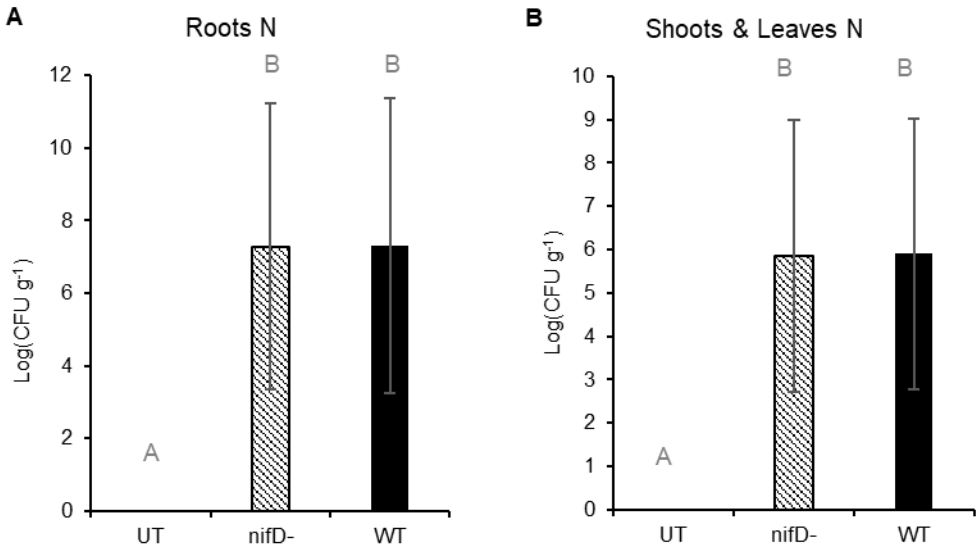


Fig. 56. Colonisation rate quantification following plant tissue maceration, serial dilution and plating. Data were collected from plants grown in the presence of 2 mM KNO^3 (N) in modified Hoagland nutrient solution at 14 dpi. Gd quantification was carried out on (A) roots and (B) shoots and leaves. Quantification was referred as CFU per g of macerated tissue. Columns marked with the same letter within each N treatment do not differ by Kruskal-Wallis test $P \leq 0.05$.

From these results, no difference was detected in root and shoot colonisation levels between the two N nutrition levels tested with no difference detected between the two strains tested (WT and *nifD*$^-$) (Fig. 55 and Fig. 56).

Root systems displayed a tenfold higher level of bacterial colonisation (10^7 CFU ml^{-1}) in comparison to shoots (10^6 CFU ml^{-1}), under both N and NoN conditions. This finding corroborates the understanding that Gd preferred site for symbiosis establishment is the root system.

Tenfold fewer bacteria were re-isolated from nutrient solution supplemented with 2 mM KNO_3 in comparison to the N-free nutrient solution (Fig. 57). This could indicate that bacterial survival in nutrient solution was dependent on the amount of N supplied and that N the presence could impair survival.

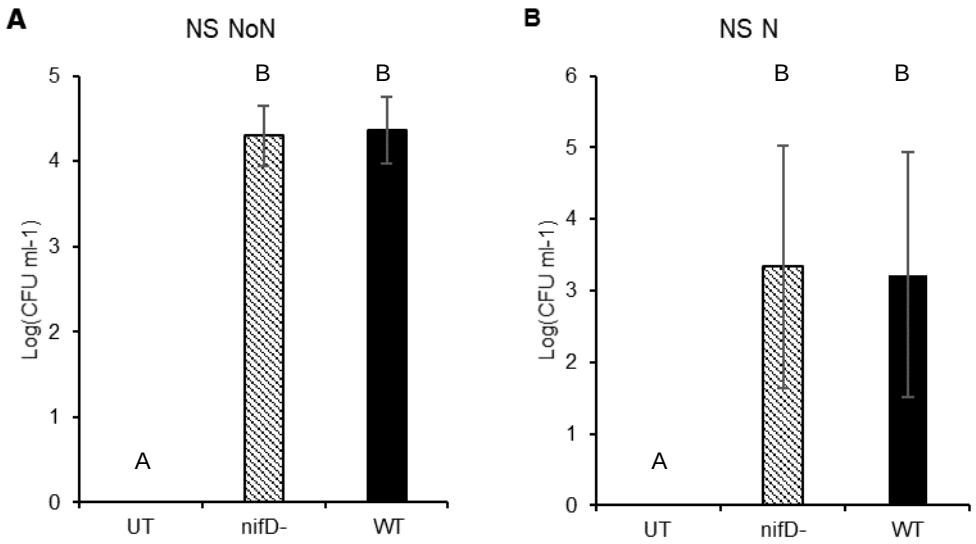


Fig. 57. Bacterial quantification through serial dilution and plating. Data were collected from plant growth nutrient solution, in either the (A) the absence or (B) the presence of 2 mM KNO_3 supply. Quantification was referred as CFU per ml of nutrient solution. Columns marked with the same letter within each N treatment do not differ by Kruskal-Wallis test $P \leq 0.05$.

It must be emphasised that bacterial growth in sole nutrient solution had been tested, in both the presence (Fig. 59 and Fig. 60) and the absence of N supply (Fig. 58), and no growth was observed when plants were not present in the system. This indicates that bacterial persistence in free living state in nutrient solution is dependent on the presence of plant root exudates.

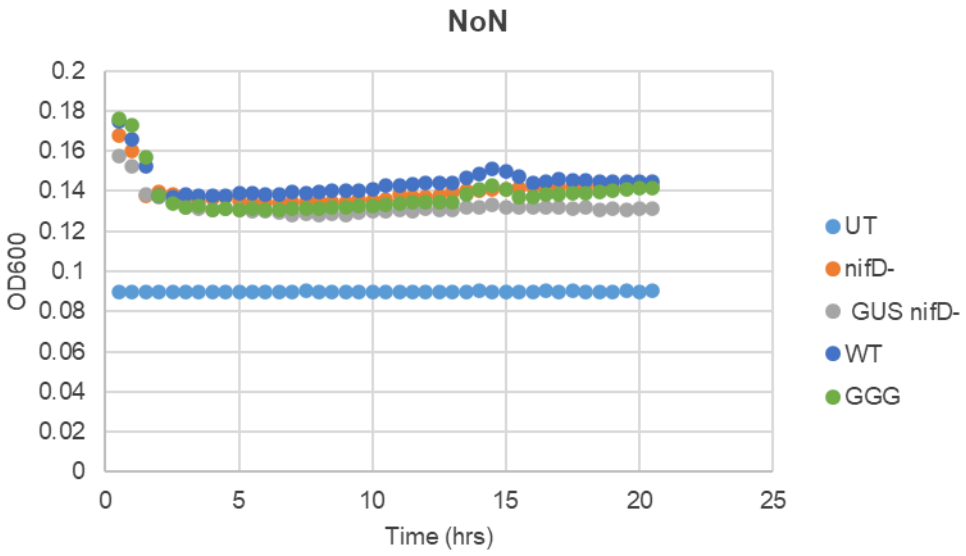


Fig. 58. Gd growth curve in modified Hoagland nutrient solution in the absence of N supply. Incubation during repeated measurements at OD_{600} was performed at 25 °C in a BioTek Synergy™ microplate reader.

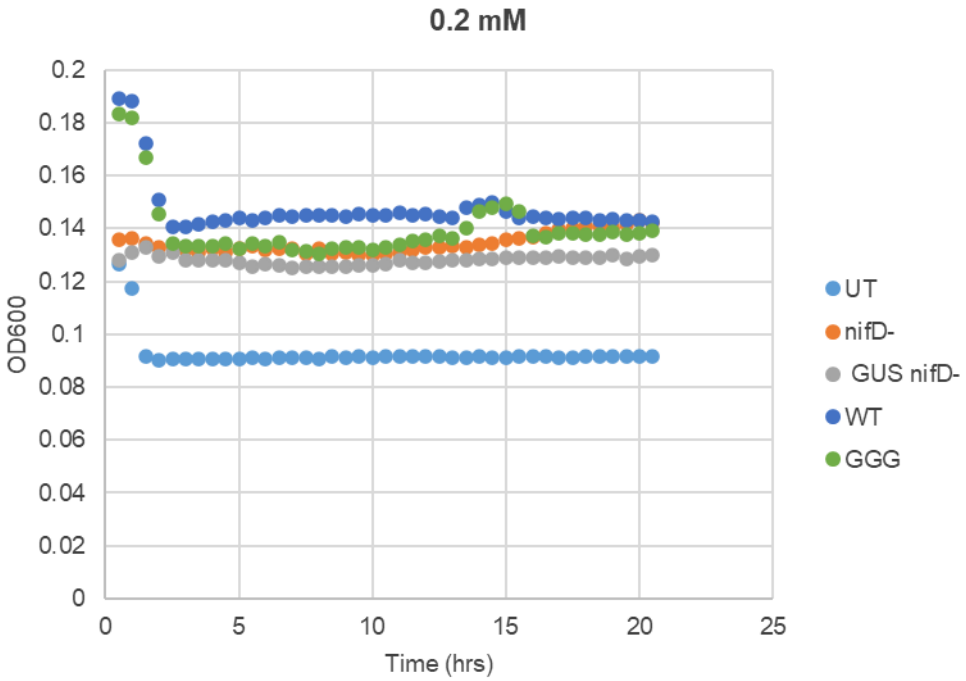


Fig. 59. Gd growth curve in modified Hoagland nutrient solution in the presence of 0.2 mM KNO_3 supply. Incubation during repeated measurements at OD_{600} was performed at 25 °C in a BioTek Synergy™ microplate reader.

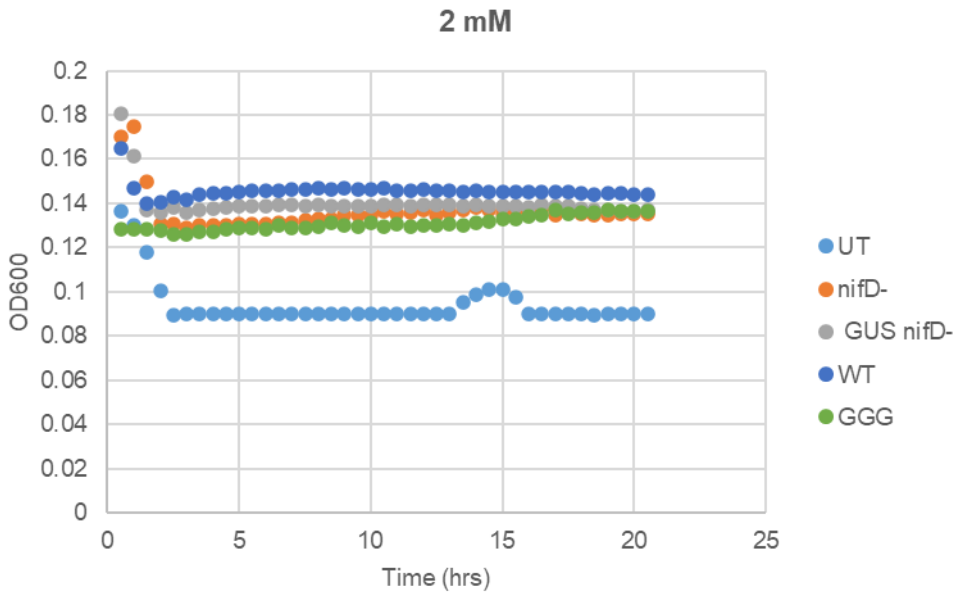


Fig. 60. Gd growth curve in modified Hoagland nutrient solution in the presence of 2 mM KNO_3 supply. Incubation during repeated measurements at OD_{600} was performed at 25 °C in a BioTek Synergy™ microplate reader.

The hydroponic setup used in this study proved to be a valid method of inoculation for tomato plants. Inoculation through root dipping in this system has been shown to lead to an efficient colonisation of the root system; the presence of bacteria was also detected in shoots, even if at lower concentrations in comparison to roots, indicating the successful migration of Gd from roots to aerial parts of the plant.

Moreover, when the *GGG* (GUS, GFP tagged) strain was employed in the same system, fluorescence could be detected in bacteria that were retrieved at 14 dpi through maceration and plating, facilitating bacterial identity confirmation.

4.4.3. Evaluation of N-fixation contribution

In order to evaluate the extent of the contribution of nitrogen fixation among the other beneficial effects provided by Gd to host plants, inoculation experiments were carried out employing the WT and the *nifD*$^{-}$ mutant strains (Section 4.4.1). In this comparison between the effect provided by either the WT strain or the nitrogen fixation impaired *nifD*$^{-}$ strain was analysed to clarify what influence the nitrogen fixation ability of Gd exerts on inoculated plants and, on the contrary, how the lack of this activity affects the promotion of plant growth.

Further analyses have been carried out to quantify the actual amount of bacterially fixed nitrogen in the plant.

4.4.3.1. Acetylene Assay

The first requirement for this experiment was to confirm the complete impairment of the *nifD*$^{-}$ strain to carry out nitrogen fixation, due to the mutation on the *nifD* gene. To assess the level of Nitrogenase activity in a comparative analysis between the WT and *nifD*$^{-}$ strain, an Acetylene Reduction Assay (ARA) was performed. This assay is normally used as a standard method for nitrogenase activity quantification. The bacterial strains to be analysed, grown in an air-tight system, are exposed to wcetylene gas, incubated and successively the measurement of the evolved ethylene is carried out. This assay is based on the ability of the nitrogenase enzyme to reduce triple bond- containing substrates (excepting HC≡N) [22]. Among the nitrogenase suitable substrates is acetylene (C_2H_2) which is reduced to ethylene (C_2H_4). The acetylene to ethylene conversion is thus used to quantify nitrogenase enzyme activity. Ethylene measurement is normally performed using a Gas Chromatograph fitted with a hydrogen Flame Ionization Detector (GC – FID) [22].

In this study, ARA was performed twice employing in one case the GC – FID setup and Proton Transfer Reaction Mass Spectrometry (PTR-MS).

4.4.3.1.1. GC-FID

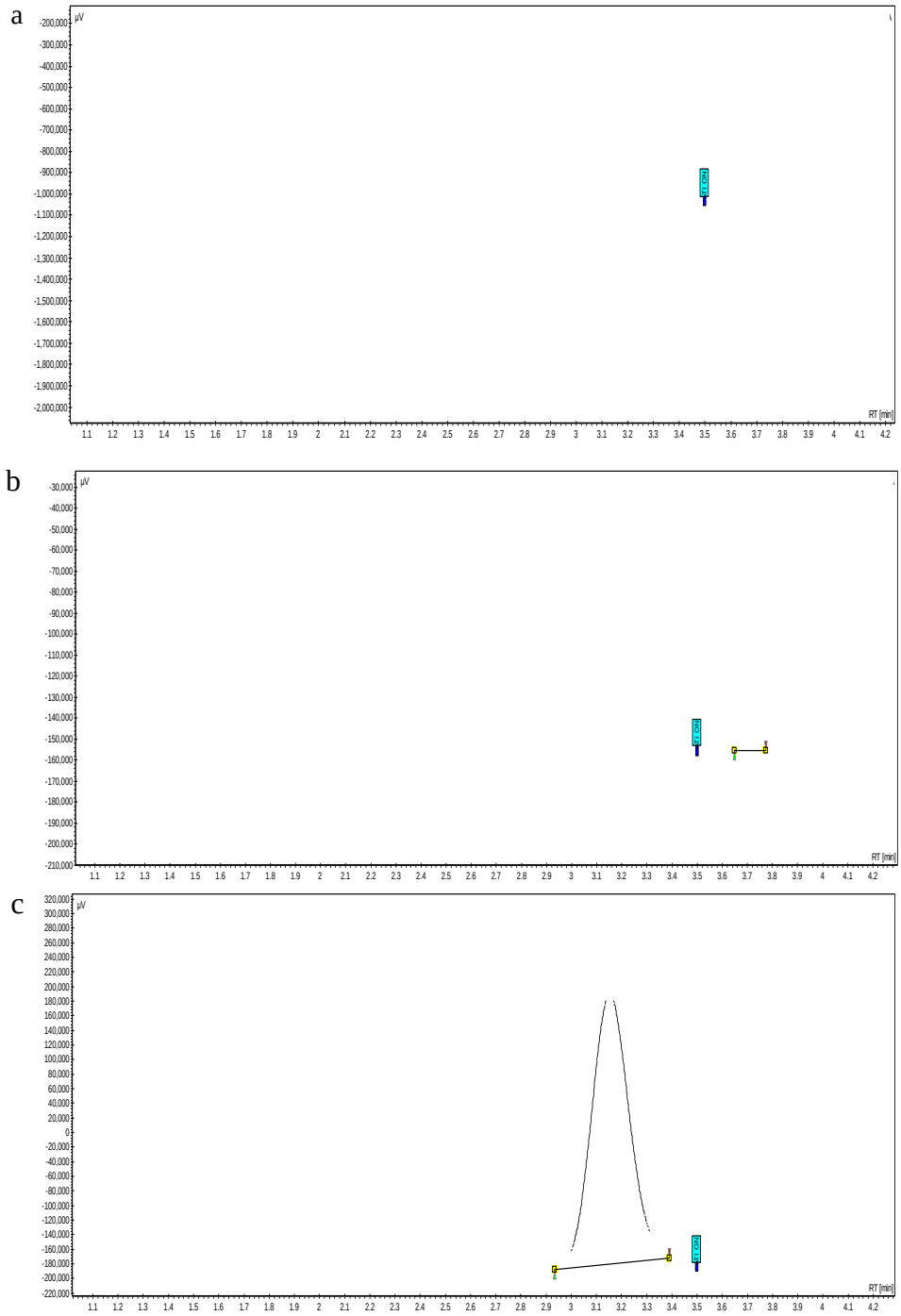


Fig. 61. GC-FID spectra resulting from analysis of a) control (sterile MilliQ water), b) nifD- strain and c) WT strain samples. Detected peaks are relative to the Ethylene retention time.

The analysis detected a conversion of acetylene (C_2H_2) to ethylene (C_2H_4) in the WT strain (Fig. 62c) while no ethylene production was observed in the *nifD*- (Fig. 63b) headspace as well as in the control samples (water) (Fig. 64a). This result confirmed the inactivation of the nitrogenase complex in the *nifD*- strain.

Ethylene standards were employed as reference to quantify the amount of acetylene reduced. The average concentration obtained for the three replicates relative to WT strain is 222.06 ± 141.76 ppm. No peaks were detected in Control and *nifD*$^{-}$ samples. However, quantification of developed ethylene was not the target of this analysis but rather a qualitative result was aimed for.

4.4.3.1.2. Proton Transfer Reaction – Mass Spectrometry (PTR-MS)

PTR-MS (Proton Transfer Reaction - Mass Spectrometry) is a method used for simultaneous real-time monitoring of volatile (organic) compounds (VOCs) present at very low concentrations in the analysed sample. PTR-MS analysis is not a technique that is normally employed in ARA measurements. To our knowledge, this analysis proved for the first time this technique to be suitable as a detector for this type of assay.

WT, *nifD*$^{-}$, *GUS nifD*$^{-}$ and *GGG* strains were streaked on Petri dishes filled with solid ATGUS medium from -80 °C glycerol stocks. A 20 ml liquid inoculum was prepared in liquid ATGUS medium starting from biomass taken from Petri dishes. Incubation was done at 28 °C with shaking at 200 rpm.

Previously autoclaved 20 ml glass vials were filled with 5 ml of semi-solid (0.7 %) N-free ATGUS medium. Ten vials per each treatment were inoculated with 100 µl of bacterial liquid cultures ($\approx 10^8$ for each strain) of the tested strains. Vials were stoppered with sterilised (UV light treated) seal tight stoppers with a pierceable septum. Each treatment was repeated five times in order to have material for analysis at 5 time points. Incubation was carried out for 72hrs at 28 °C.

Acetylene (C_2H_2) was generated from the reaction of CaC_2 with H_2O (0.015 g of CaC_2 in a 20 ml gas tight vial to which 1.5 ml of sterile distilled water was added) and injected into the headspace of each vial with a sterile syringe to reach a final concentration of 0.033% (v/v).

C_2H_2 was injected in 25 empty vials (Empty Control), in 25 vials filled with ATGUS medium only (Untreated) and in 25 vials inoculated with each of the tested bacterial strains. A further 25 vials where C_2H_2 was not injected were kept as a reference for each treatment.

Table 8. PTR-MS employing Acetylene Reduction Assay experimental setup.

Treatment	**N° of vials**	**N° of timepoints**	**TOT N° of vials**
Empty	5	5	25
Empty + C_2H_2	5	5	25
Untreated (ATGUS)	5	5	25
Untreated (ATGUS + C_2H_2)	5	5	25
nifD$^-$	5	5	25
nifD$^-$ + C_2H_2	5	5	25
GUS nifD$^-$	5	5	25
GUS nifD$^-$ + C_2H_2	5	5	25
WT	5	5	25
WT + C_2H_2	5	5	25
GGG	5	5	25
GGG + C_2H_2	5	5	25

Analysis of the headspace was performed with a PTR-MS after 4 hrs from acetylene injection (T_0) and then every 24 hrs for four days (T_1 to T_3) and again at 6 days (T_6) post acetylene inoculation. At each time point, five vials were analysed per each treatment (Empty, Empty + C_2H_2, Untreated, Untreated + C_2H_2, *nifD*$^-$, *nifD*$^-$ + C_2H_2, *GUS nifD*$^-$, *GUS nifD*$^-$ + C_2H_2, WT, WT + C_2H_2, *GGG*, *GGG* + C_2H_2). All samples were kept at 28 °C for the duration of the experiment.

Acetylene and ethylene profiles were plotted (Fig. 66 and Fig. 67).

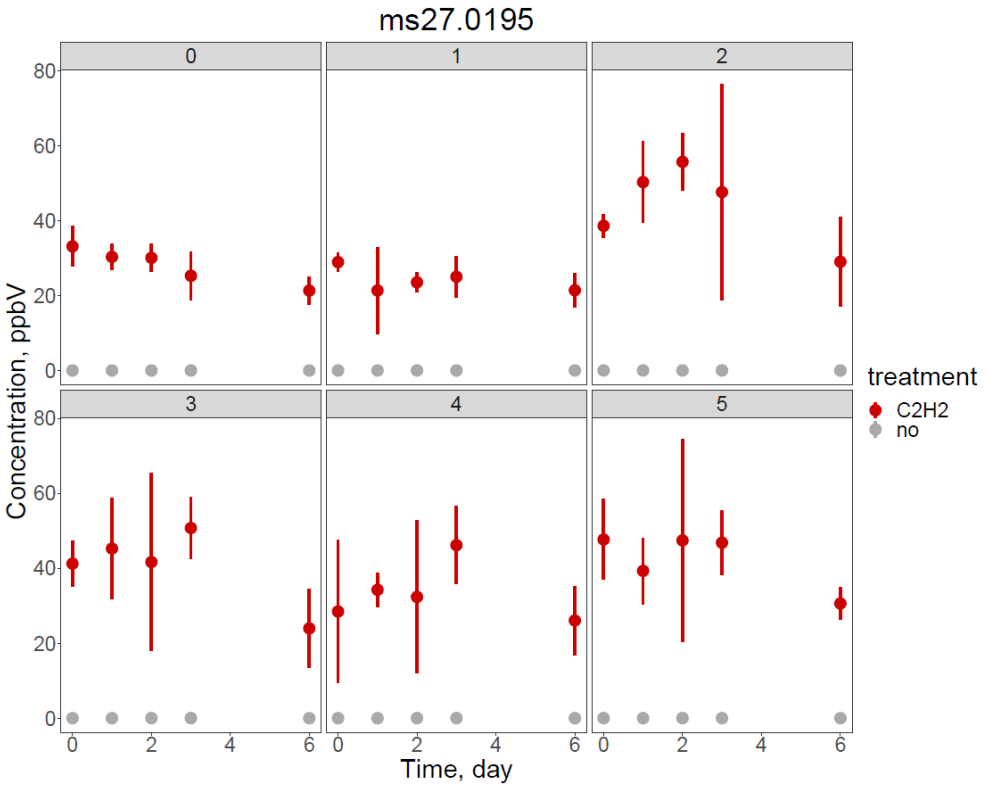


Fig. 65. PTR-MS detection of Acetylene (C_2H_2) signal. Measurements were carried out at 4 hrs post injection (T_0) and then every 24 hrs from the day of inoculation to day 4 (T_3) and then again at 6 days post inculation (T_6). Grey dots are relative to samples non injected with C_2H_2; red dots are relative to samples injected with C_2H_2. Grey boxes correspond to: 0) Empty vials, 1) ATGUS medium, 2) nifD$^-$ strain, 3) GUS nifD$^-$ strain, 4) WT strain, 5) GGG strain.

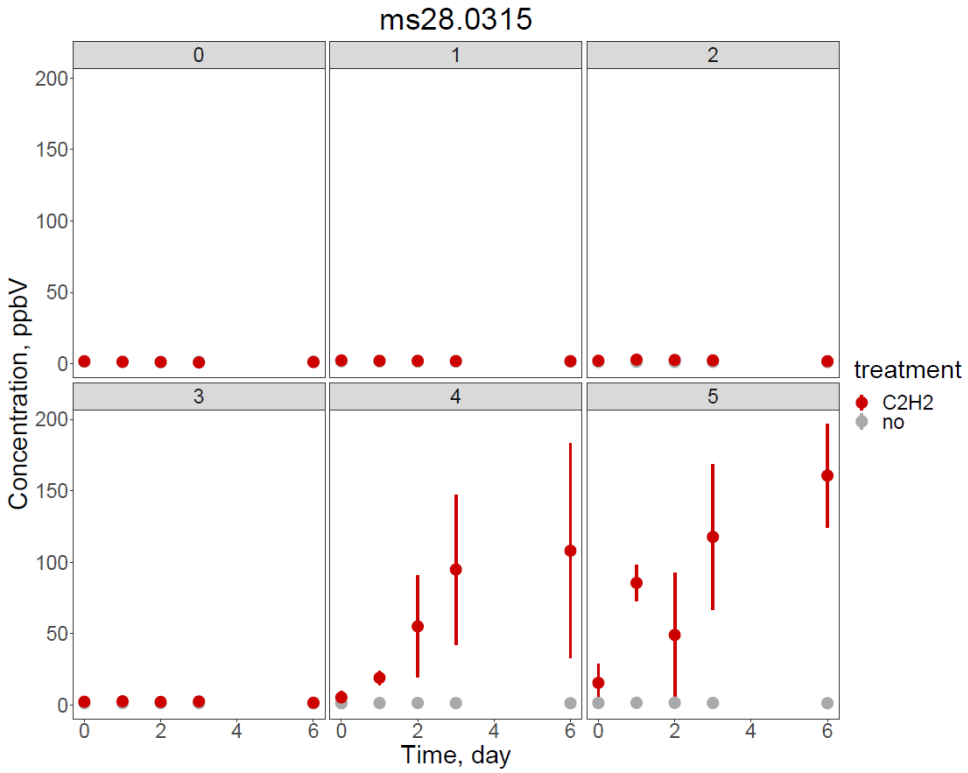


Fig. 68. PTR-MS detection of ethylene (C_2H_4) signal. Measurements were carried out at 4 hrs post injection (T_0) and then every 24 hrs from the day of inoculation to day 4 (T_3) and then again at 6 days post inculation (T_6). Grey dots are relative to samples non injected with C_2H_2; red dots are relative to samples injected with C_2H_2. Grey boxes correspond to: 0) Empty vials, 1) ATGUS medium, 2) nifD⁻ strain, 3) GUS nifD⁻ strain, 4) WT strain, 5) GGG strain.

PTR-MS analysis confirmed the capacity of Gd, both WT (Sample 4 in Fig. 68) and *GGG* (Sample 5 in Fig. 68) strains, to fix nitrogen while both *nifD*⁻ and *GUS nifD*⁻ showed no ethylene development after acetylene injection, indicating no nitrogenase functionality. The rapidity and automatisation of this Ethylene measurement procedure, as well as the possibility of maintaining samples at a constant temperature of 28 °C throughout the whole headspace sampling process, allowed monitoring of the ethylene production at different time points. In both WT and *GGG* strains, an increment in ethylene concentration was already detected at T0 and progressively raised during incubation.

4.4.3.2. Liquid ^{15}N Feeding

A ^{15}N tracer technique was employed to assess the contribution of nitrogen fixation to the PGP effect provided by Gd to tomato plants. ^{15}N isotope dilution techniques have been used to determine gross rates of nitrogen transformation in-soil [12]. These types of experiments are based on the concept for which a

known amount of ^{15}N is provided to the plant, in the form of gaseous N_2 for the study of N-fixing bacteria, and the amount of ^{15}N incorporated in chlorophyll molecules is calculated to estimate the N-fixation rate of the bacterium under test. In the setup employed in this study, ^{15}N was the only N source provided to the plant and thus a quantification of the atmospheric ^{14}N fixed by Gd was carried out. In comparison to normal in-soil ^{15}N dilution experiments, the highly controllable hydroponics setup allowed the only N pool available for plant uptake to be a ^{15}N labelled one. In order to minimise ^{14}N carryovers from the starting inoculum bacterial culture, Gd strains used were grown in N-free modified solid AceLGI-P medium, supplemented with ^{15}N nitrogen.

The above-mentioned hydroponic setup (Section 3.14) was employed to inoculate plants that were grown in the sole the presence of ^{15}N tracer (0.2 mM $K^{15}NO_3$). The bacterial inoculum of both WT and *nifD*- strains was grown on $K^{15}NO_3$ (10%) based LGI-P Petri dishes and bacteria were scraped and resuspended in Hoagland modified nutrient solution to reach a concentration of 10^8 cfu ml^{-1}. The bacterial suspension was then used to inoculate tomato plants. Fourteen days after inoculation (14 dpi), plant material was harvested, and chlorophyll was extracted (Section 3.17). Extracted chlorophyll was then analysed through Liquid Chromatography Mass Spectrometry (LC-MS) for the incorporation of fixed atmospheric ^{14}N in the chlorophyll.

Data relative to colonisation levels of plants' roots, shoots and free-living cells present in nutrient solution, collected at 14 dpi, are reported (Fig. 69).

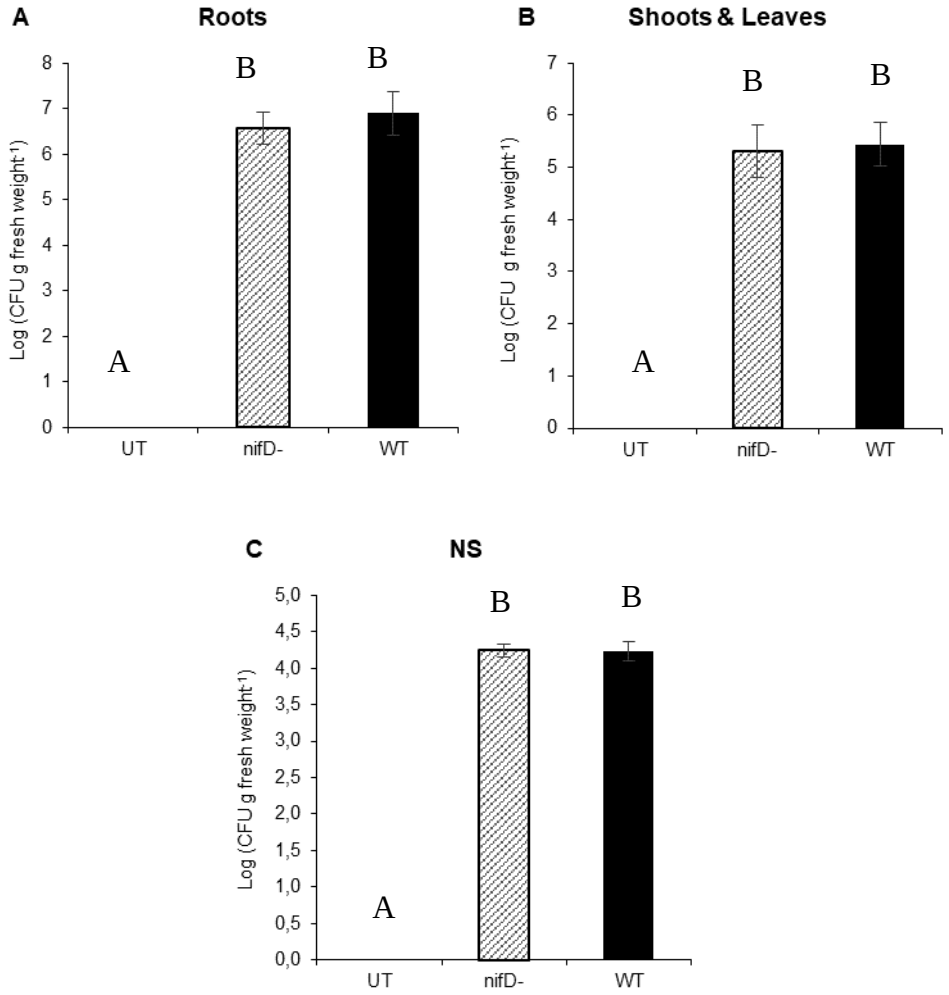


Fig. 70. Quantification of the colonisation rate following plant tissue maceration, serial dilution and plating. Plants were grown in the presence of 0.2 mM $K^{15}NO_3$ in modified Hoagland nutrient solution (NS) at 14 dpi. Gd quantification was carried out on (A) roots, (B) shoots and leaves and (C) in plant growth nutrient solution. Quantification was referred as either CFU per g of macerated tissue or CFU per ml of nutrient solution. Columns marked with the same letter within each N treatment do not differ by Kruskal-Wallis test $P \leq 0.05$.

Due to COVID19 restrictions, there was a strong delay in the analysis of these samples, which are currently being processed in the School of Chemistry at Nottingham University.

4.4.4. Discussion

Preliminary in-soil tests underlined how the plant nutritional state is a critical variable to be considered when investigating the interactions between plant associated bacteria and their host. In addition to this, the bacterial inoculum concentration was shown to have a strong influence on the plant growth promoting (PGP) effect provided by beneficial microorganisms. In fact, symbiotic bacteria not only provide nutrients and beneficial molecules for plant uptake, but also feed on plant produced sugars and other root exudates. The establishment of a fruitful cooperation between the host plant and beneficial microorganisms relies on a well-balanced mutual exchange of nutrients, and bacterial concentration is crucial for this symbiosis.

In plants fed with 15% N-feed, inoculum with high concentrations of either WT or *nifD*$^-$ strains (10^{11} CFU ml^{-1}) led to no variation or reduction of biomass production and tomato fruit weight. This may be attributable to the fact that bacterial concentrations as high as 10^{11} CFU ml^{-1} can be perceived by the plant as a physiological burden and thus not a favourable inoculum concentration for growth promotion.

Inoculation with 10^{10} CFU ml^{-1} of either WT or *nifD*$^-$ strains, led to, respectively, a positive effect or no variation from UT control plants, in terms of dry plant biomass and fruit weight. This indicated 10^{10} CFU ml^{-1} as a good concentration for WT strain seed coating inoculation and in-soil growth, when 15% N-feed is provided to plants.

In the absence of N in the plant feed, both inocula concentrations of *nifD*$^-$ showed no difference between untreated controls and mutant strain treated plants, indicating that, in this setup, no negative nor positive effect was provided by *nifD*$^-$ strain to tomato plants at these bacterial densities. On the contrary, both inoculations levels of the WT strain led to an increase of both dry biomass and total tomato fruit weight. This suggests that a plant grown in N limiting conditions, in this setup, reacts differently from a N fed plant in response to exposure to the same concentrations of inoculating bacteria.

In this setup, the impairment of N-fixation ability of the *nifD*$^-$ strain seems to lead to the loss of the PGP effect in this N-limiting condition. This suggested

that the N-fixation activity exerted by Gd gives a relevant contribution to the PGP effect on tomato host plants.

Similar data were collected in hydroponics setup experiments. Inoculation was performed through root dipping with either WT or *nifD*$^-$ at a concentration of 10^8 CFU ml^{-1}. Improved phenotype, in comparison to UT plants, was obtained in both WT and *nifD*$^-$ treated plants in terms of shoots length and plant fresh weight. Nevertheless, inoculation with WT showed a significant phenotypical enhancement in comparison to *nifD*$^-$. In particular, chlorophyll content was increased following WT inoculation. Chlorophyll abundance is directly related to plant N availability, being one of the main sinks for this nutrient after uptake.

Overall, data collected from both the preliminary in-soil experiments and hydroponic tests support the hypothesis for the ability of Gd to provide a beneficial effect to colonised plants is not entirely dependent on its N fixation capability, but this can provide further significant improvement to plant health.

Assessments of Gd localisation in inoculated plants showed that the predominant interaction mechanism between Gd and tomato plants grown in a hydroponic system is mainly through root adhesion and intercellular colonisation with the possible occurrence of intracellular localisation. Bacteria were also observed in association with the vascular tissues, which could allow the bacterial spread towards above-ground organs of the host plant. In fact, in root dipping inoculated plants, bacteria were found in aerial parts as well, indicating the migration of bacterial cells from the roots to shoots and leaves.
Root systems displayed a tenfold higher level of bacterial colonisation (10^7 CFU ml^{-1}) in comparison to shoots (10^6 CFU ml^{-1}), in both the presence and the absence of N in the nutrient solution. This finding supports the hypothesis for which Gd preferred compartment for symbiosis establishment is the root. Nevertheless, no difference in colonisation capability was detected between the two strains tested (WT and *nifD*$^-$) and no difference was detected in root and shoot colonisation level between the two N nutrition regimes tested. This latter finding is surprising, since previous studies have confirmed how Gd colonisation efficiency is affected by different N levels [50][159]. Moreover, further evidence (Section 4.13) collected in this study suggests a differential response

of the plants towards Gd grown at different N-levels. Based on previous findings [155], it can be hypothesised is that variations in Gd colonisation might occur at later stages then assessed in this experiment (14 dpi). Investigations at even later growth stages would be needed to clarify these population dynamics.

4.5. Transcriptomic Analysis

One of the main aims of this project was to investigate the molecular mechanisms involved in the establishment and conservation of a beneficial interaction between tomato plants and Gd. Transcriptomic data analysis on root samples of plants inoculated in the hydroponic system was chosen for this task. Root material was selected for assessment since this is the main interface in Gd-plant interaction and the plant area where highest bacterial localisation was found.

Hydroponics setup (Section 3.14) was employed to inoculate Money Maker surface sanitised seeds with either *nifD*- and WT Gd strains at a concentration of 10^8 cfu ml^{-1}. Plants were grown in either the absence of a nitrogen source (NoN) or with the addition of 2 mM KNO_3 (N) to the nutrient solution.



Fig. 71. Phenotype of Money Maker plants two weeks after inoculation with either nifD- or WT Gd strain through root dipping. From left to right: 3 replicas of UT, nifD- and WT inoculated plants. Evaluation was performed both in (A) the absence and (B) the presence of 2 mM KNO_3 in the nutrient solution.

Colonisation levels are here below presented.

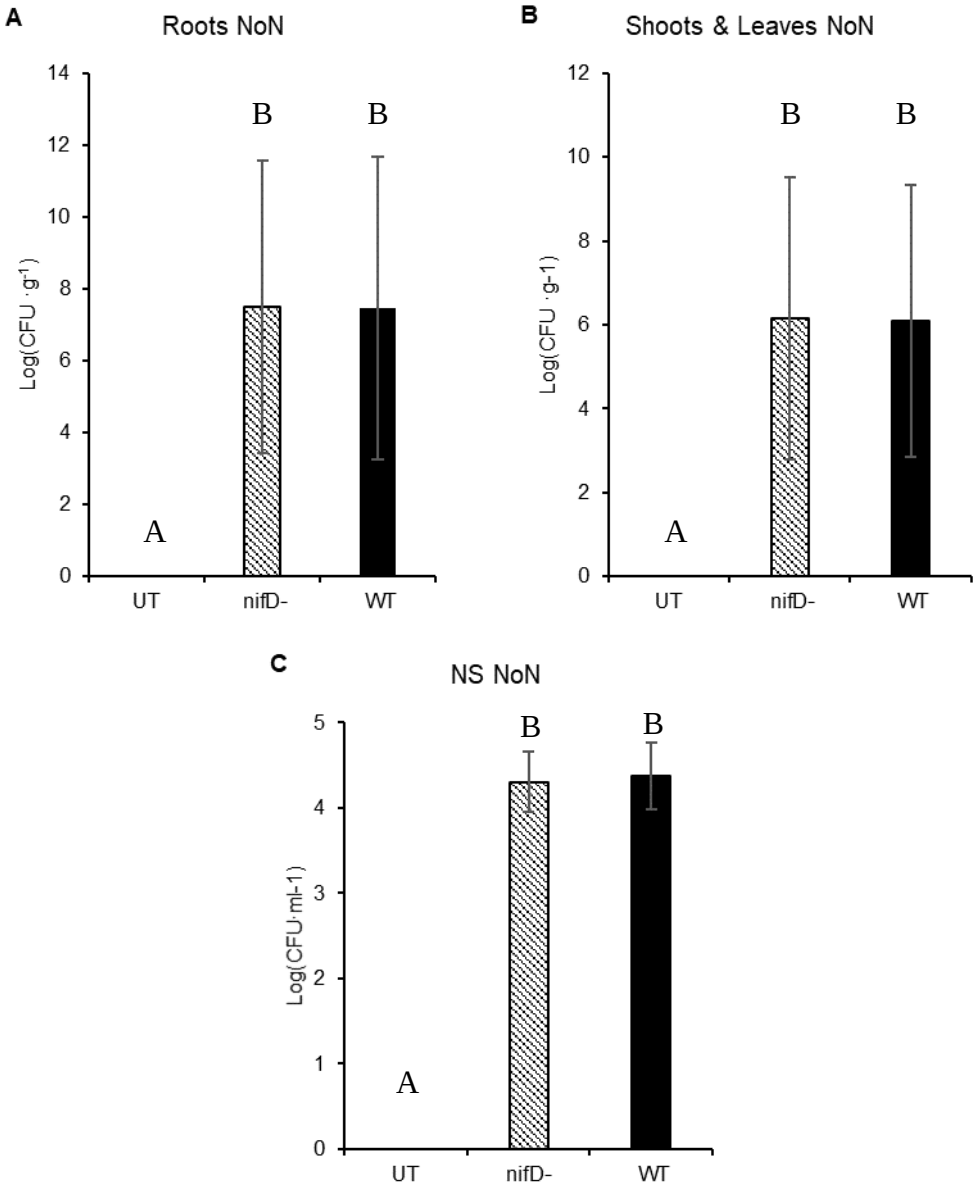


Fig. 72. Quantification of colonisation rate following plant tissue maceration, serial dilution and plating. Data were collected from plants grown in the absence of N (NoN) in modified Hoagland nutrient solution (NS) at 14 dpi. Gd quantification was carried out on (A) roots, (B) shoots and leaves and (C) in plant growth nutrient solution. Quantification was referred as either CFU per g of macerated tissue or CFU per ml of nutrient solution. Significant differences between treatments were assessed by Kruskal-Wallis test to $P \leq 0.05$.

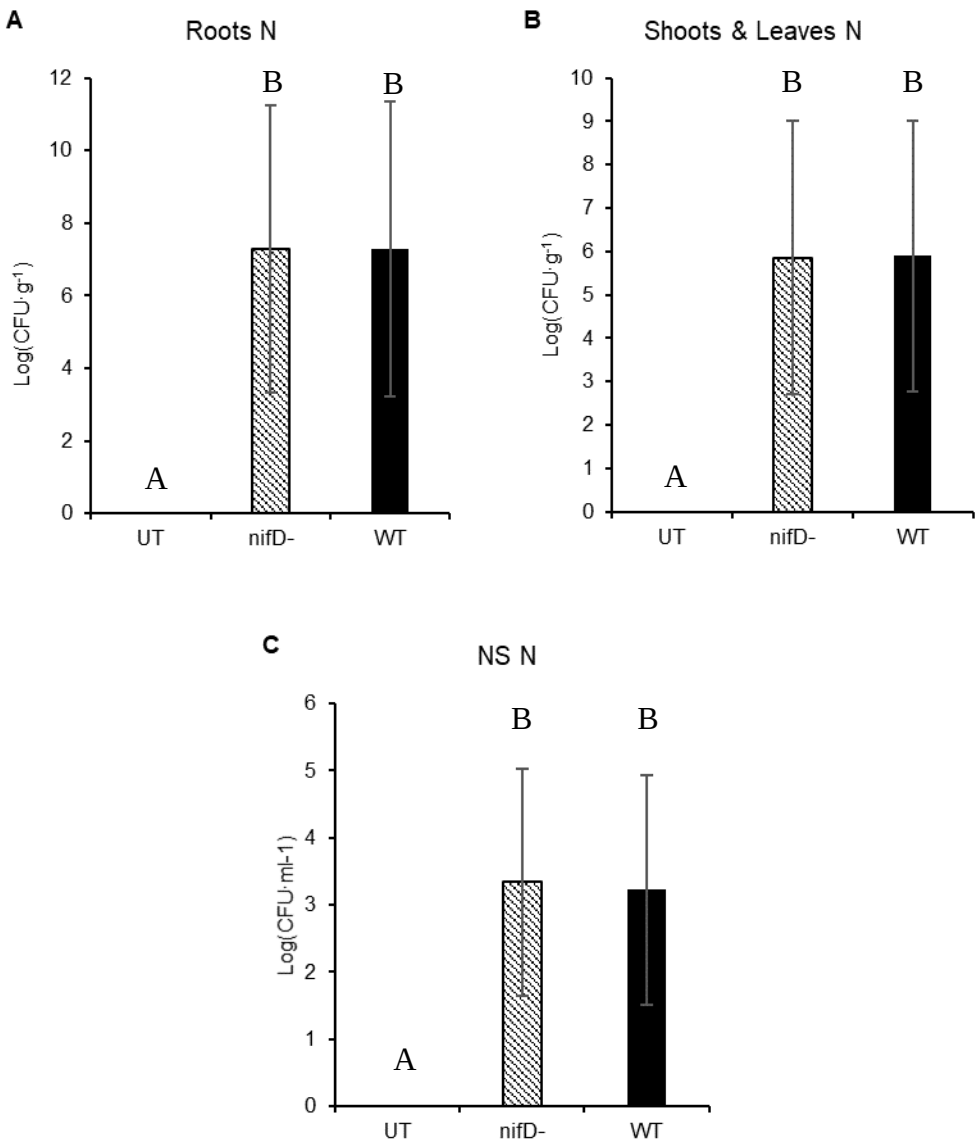


Fig. 73. Quantification of colonisation rate following plant tissue maceration, serial dilution and plating. Data were collected from plants grown in the presence of 2 mM KNO_3 (N) in modified Hoagland nutrient solution (NS) at 14 dpi. Gd quantification was carried out on (A) roots, (B) shoots and leave and (C) in plant growth nutrient solution. Quantification was referred as either CFU per g of macerated tissue or CFU per ml of nutrient solution. Significant differences between treatments were assessed by Kruskal-Wallis test to $P \leq 0.05$.

In order to evaluate the early and late response of the plant to the exposure to Gd, fifteen and nine plants were randomly collected from each treatment under NoN and N conditions, respectively, and pooled into groups of five (NoN) or three (N) (replicates) at one- and fourteen-days post inoculation (dpi). Roots were detached from shoots and were placed into 2 ml Eppendorf tubes, immediately frozen in liquid nitrogen and stored at −80 °C. Root samples were

then manually ground with a sterile micro pestle to a fine powder, ensuring the samples were frozen during the whole process. Total RNA was extracted following Hot Acid Phenol Extraction protocol (Section 3.21). Total RNA was quantified using a NanoDrop 1000 (Thermo Fisher Scientific) and RNA quality was checked using a 2100 Bioanalyser system (Agilent Technologies, Santa Clara, CA, USA). Each RNA sample was treated with Turbo DNA-*free*™ according to the product procedural guidelines.

RNA samples were subjected to RNA-Seq library construction, using the NEBNext® Ultra™ II Directional RNA Library Prep Kit for Illumina® (Illumina, SanDiego, CA, USA) and rRNA depletion with the RiboZero rRNA Removal Kit for plants according to the manufacturer's instructions (Illumina). Paired-end reads were obtained using a NextSeq500 instrument (Illumina) at the Deep Sequencing facility of the University of Nottingham (Nottingham, UK) and sequences were deposited at the Sequence Read Archive of the National Center for Biotechnology under the BioProject numbers PRJNA666034 and PRJNA666036.

A Venn clustering analysis was performed, and differentially expressed genes (DEG) were analysed accordingly (Fig. 74).

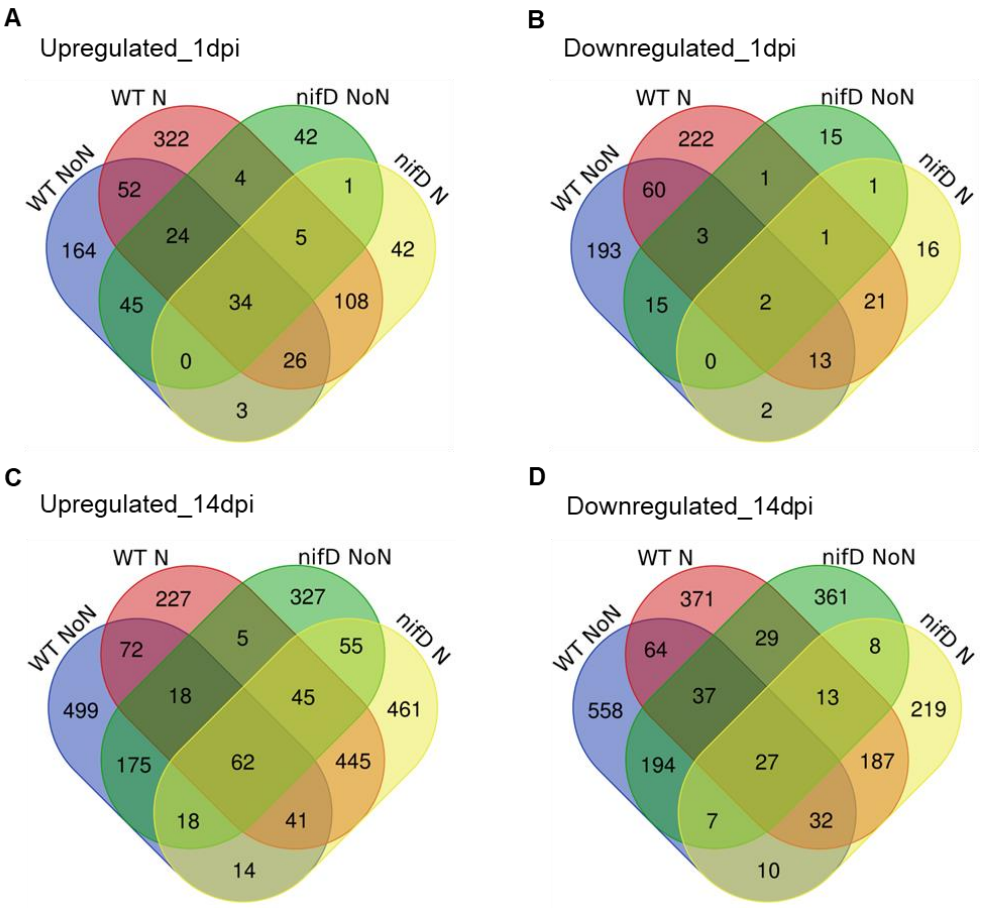


Fig. 74. Venn clustering of genes modulated (A and C upregulation, B and D downregulation) by either WT or nifD- Gd strains at 1dpi (A and B) and 14 dpi (C and D), in either the absence (NoN) or the presence of 2 mM KNO3 (N) in plant growth solution.

Up- and down-regulated functional classes are reported according to the main elicited response: upregulated genes are presented when upregulation prevails and *vice versa* for downregulation.

4.5.1. Transcriptional response induced in tomato roots following inoculation with Gd (both WT and *nifD*- strains) at one day post inoculation (dpi) (early response).

Below are reported genes belonging to the functional classes mainly modulated by the interaction with WT and *nifD*$^-$ mutant strain both in the absence of a nitrogen source and 2 mM KNO_3 added to the growth solution. The following data are considered as the general plant response to the bacterium during early interaction stages (1dpi), regardless of the nutritional conditions with respect to nitrogen (Table S2).

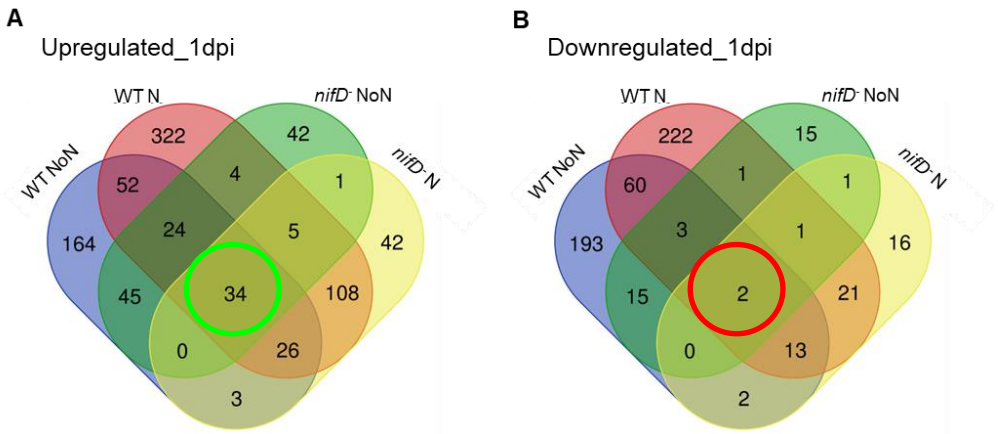


Fig. 76. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated; B downregulated) by either WT or nifD$^-$ Gd strains at 1dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by both Gd strains in both N and NoN conditions.

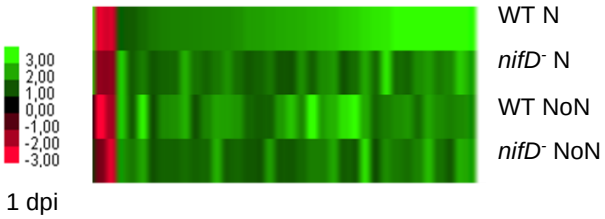


Fig. 75. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 1 dpi with G. diazotrophicus, WT and nifD$^-$ strains, in both the absence (NoN) and the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants.

Differentially Expressed Genes (DEGs) following bacterial inoculation showed a prevalence of gene upregulation. 34 genes are upregulated which predominantly belong to the following functional classes: **defence response** (e.g. one wound-responsive family protein, two defensin-like proteins), **hormonal metabolism** (e.g. one 1-aminocyclopropane-1-carboxylate oxidase 5, one GRAM domain-containing protein / ABA-responsive protein-related, two ethylene responsive factors), **gene expression regulation** (e.g. one zinc finger

family protein, one DNA polymerase epsilon catalytic subunit A, one inosine-uridine preferring nucleoside hydrolase family protein, one homeobox-leucine zipper protein family), and **oxidative stress** (one respiratory burst oxidase, two peroxidases).

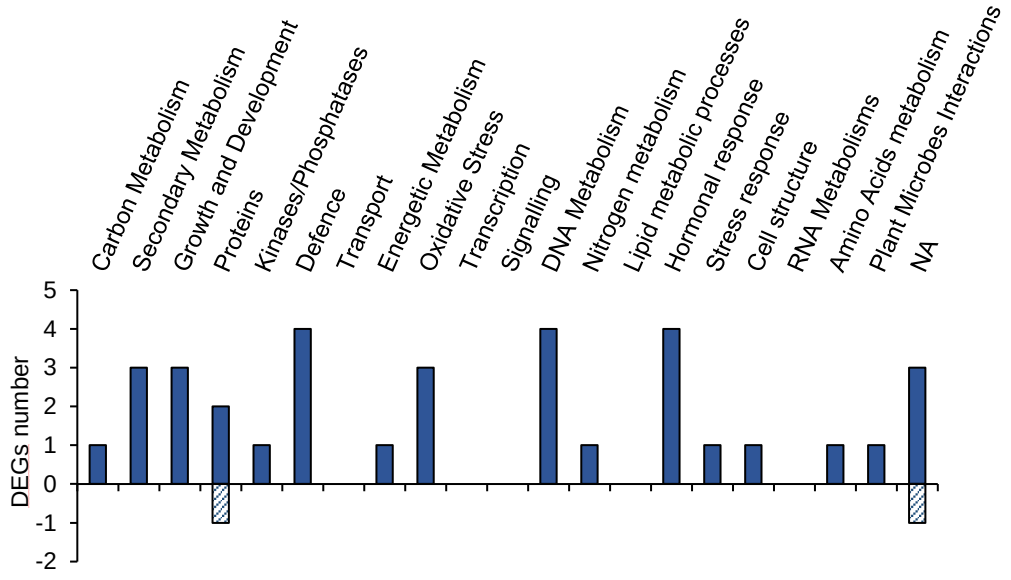


Fig. 77. ***General response, 1 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gluconacetobacter diazotrophicus WT and nifD- strains at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots both after inoculation with Gd WT and nifD- strains, in both the absence (NoN) and the presence of 2 mM KNO3 (N) in modified Hoagland growth solution, compared to non-inoculated plants.*

4.5.2. Transcriptional response induced in tomato roots following inoculation with Gd (both WT and *nifD*- strains) at 14 dpi (late response).

Here are reported the genes belonging to the functional classes mainly modulated by the interaction with WT and *nifD*- in both the absence and the presence of 2 mM KNO_3 added to the plant growth solution: the general plant response to the bacterium in late interaction stages (14 dpi), regardless of the nutritional conditions (Table S3).

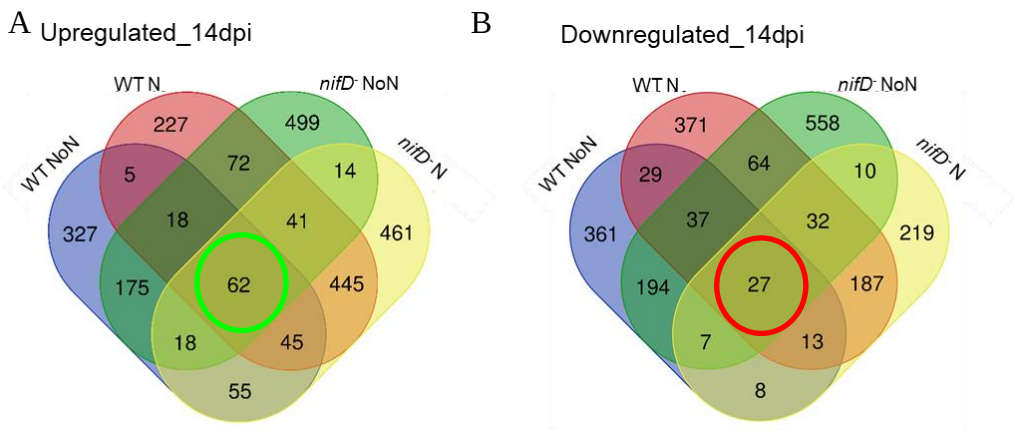


Fig. 79. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated, B downregulated) by either WT or nifD- Gd strains at 14 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by both Gd strains under both N and NoN conditions.

At 14 dpi, gene upregulation was again more apparent than downregulation. 62

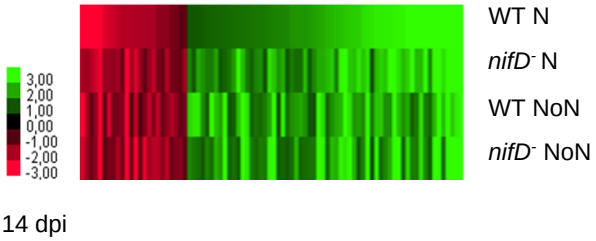


Fig. 78. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 14 dpi with G. diazotrophicus, WT and nifD- strains, in both the absence (NoN) and the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants (Control).

genes were upregulated represented by classes: **defence response** (e.g. one kunitz-type protease inhibitor, one hypersensitive response assisting protein, two RING/U-box superfamily proteins, one chitinase/lysozyme, one pathogen-induced protein, one osmotin-like protein, one thaumatin, pathogenesis-related protein), **transport** (e.g. one exocyst complex component 7, one potassium transporter, one purine permease-like protein, four Ycf1 proteins, one proton pump interactor 1, one heavy metal transport/detoxification superfamily protein), **growth and development** (e.g. one ovate family protein 9, one GIGANTEA protein, one thiamine biosynthesis protein ThiC, one CCAAT-binding transcription factor) and **DNA metabolism** (e.g. one inosine-uridine preferring nucleoside hydrolase family protein, one nudix hydrolase, one homeobox leucine zipper family protein, one essential meiotic endonuclease 1B, one zinc finger protein).

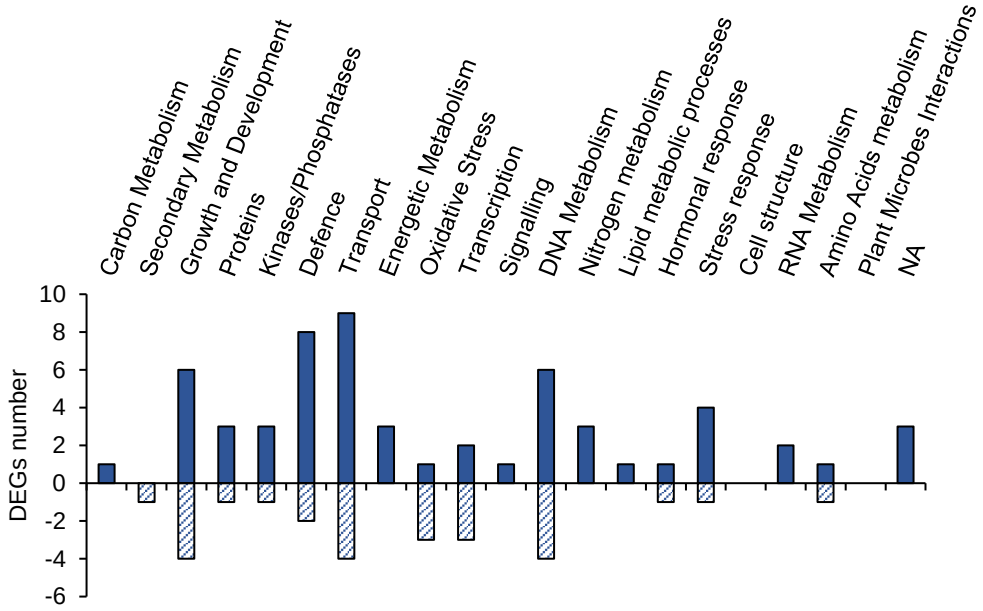


Fig. 80. ***General response, 14 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd WT and nifD- strains at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots both after inoculation with Gd WT and nifD- strains, in both the absence (NoN) and the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants.*

4.5.3. Transcriptional response induced in tomato roots following inoculation with Gd (both WT and *nifD*$^-$ strains) in the presence of nitrogen.

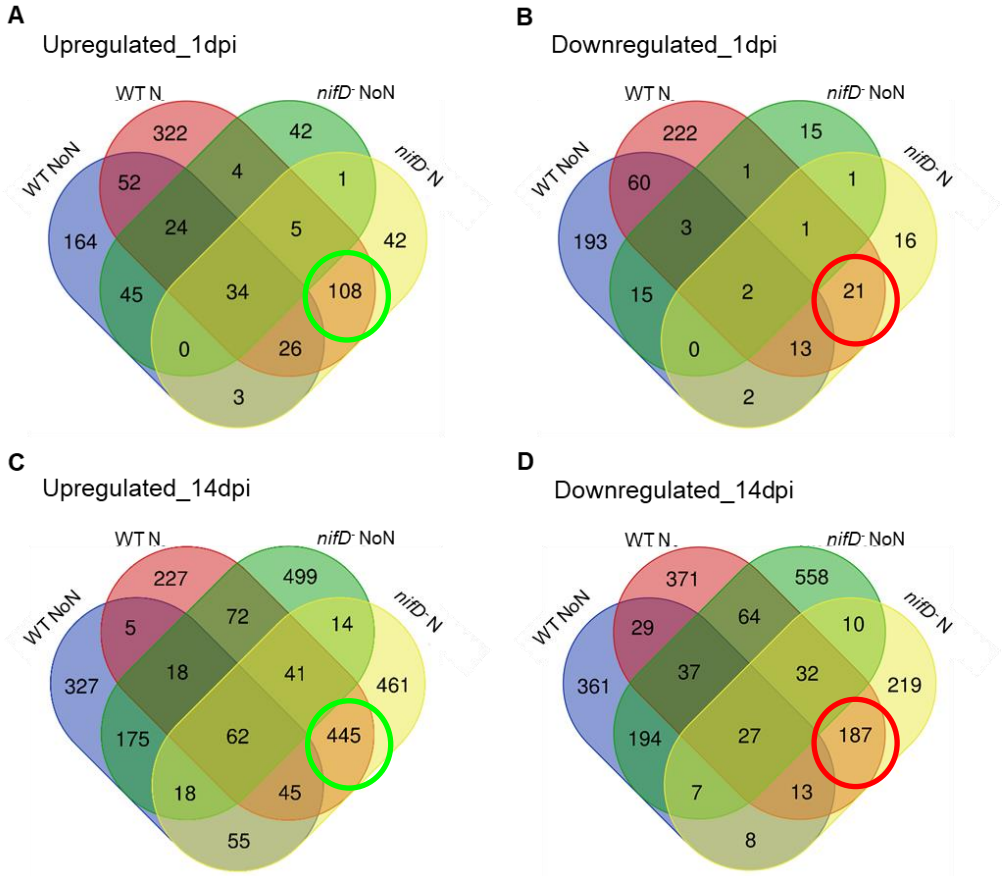
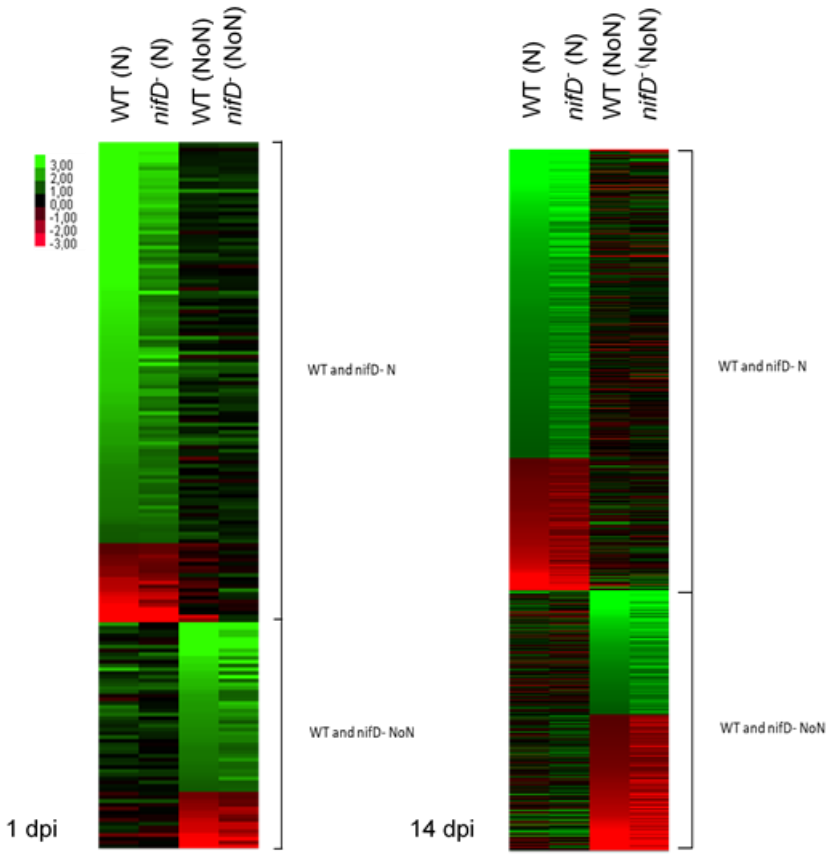


Fig. 81. Venn clustering of differentially expressed genes (DEGs) modulated (A, C upregulated, B, D downregulated) by either WT or nifD- Gd strains at 1 and 14 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by both Gd strains under N condition (presence of N).



108 genes were upregulated under these conditions at 1 dpi (early response;

Fig. 82. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 1 dpi and 14 dpi with G. diazotrophicus, WT and nifD- strains, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants (Control).

Table S4). The genes that were found to be most highly modulated belong to the **lipidic metabolism** (e.g. six GDSL esterase/lipases, one alpha/beta-Hydrolases superfamily protein, four 3-ketoacyl-CoA synthases, one phospholipase D, one non-specific lipid-transfer protein) and **transport** (e.g. one heavy metal transport/detoxification superfamily protein, seven ABC transporters, one nucleobase-ascorbate transporter-like).

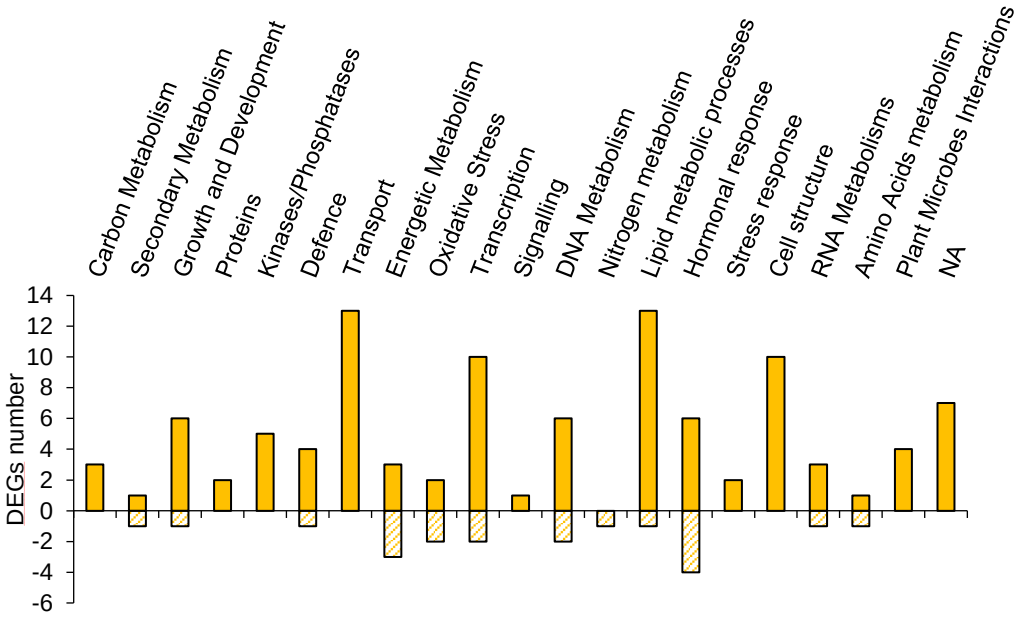


Fig. 83. ***Influence of nitrogen nutrition, N, 1 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd WT and nifD- strains at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots both after inoculation with Gd WT and nifD- strains, in the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants.*

At later stages of interaction (14 dpi) gene upregulation remained preponderant over downregulation (Table S5). 445 genes were upregulated with the mainly modulated functional classes being; **growth and development** (e.g. one APETALA2a, four bHLH transcription factors, one brassinazole-resistant 1 protein, one CONSTANS-like zinc finger protein, one flowering promoting factor, one light dependent short hypocotyls-like protein, three LOB domain-containing proteins, one ovate family protein, one monogalactosyldiacylglycerol synthase, one NAP1 protein, one purple acid phosphatase, one phytosulfokines 3 family protein, two R2R3MYB transcription factors, four senescence-associated family proteins, one SUN-like protein, one terminal flower 1-like protein, one zinc finger protein CONSTANS-LIKE), **transport** (e.g. one ABC transporter B family protein, three bidirectional sugar transporters SWEET, one cation calcium exchanger, two cation/H(+) antiporters, one chloride channel protein, one dynamin-related protein, one germin-like protein subfamily 1 member, five Ycf1 proteins, one magnesium transporter NIPA, three major facilitator superfamily proteins, one

outward rectifying potassium channel protein, two peptide transporters, one plant basic secretory family protein, one potassium channel, five purine permeases, one SlSFP7 protein, one S-type anion channel SLAH1, two sugar facilitator proteins, two sulfate transporters, two zinc transporter proteins), **defence response** (e.g. one acidic endochitinase, cinnamoyl-CoA reductase, one defensin-like protein one diacylglycerol kinase, one disease resistance protein, one hypersensitive-induced response protein, one late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family, two Avr9/Cf-9 rapidly elicited proteins, one Peptidoglycan-binding LysM domain-containing family protein, two RING/U-box superfamily proteins, three wound-responsive family proteins, one pathogenesis-related thaumatin family protein, one reticulon-like protein, eight RING/U-box superfamily proteins, one signal peptide peptidase-like protein) and **hormonal metabolism** (e.g. two 1-aminocyclopropane-1-carboxylate oxidases, three 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, one ABI3 protein, two abscisic acid stress ripening proteins, one abscisic acid responsive element-binding factor 1 family protein, one auxin efflux carrier family protein, one DELLA protein, two ethylene responsive factors, one GAI-like protein, one gibberellin 2-oxidase, one GRAM domain-containing protein / ABA-responsive protein, one jasmonate ZIM-domain protein, one linalool synthase, one WD40 domain-containing protein, one nicotinamidase, four small auxin up-regulated RNAs, four WAT1-related proteins).

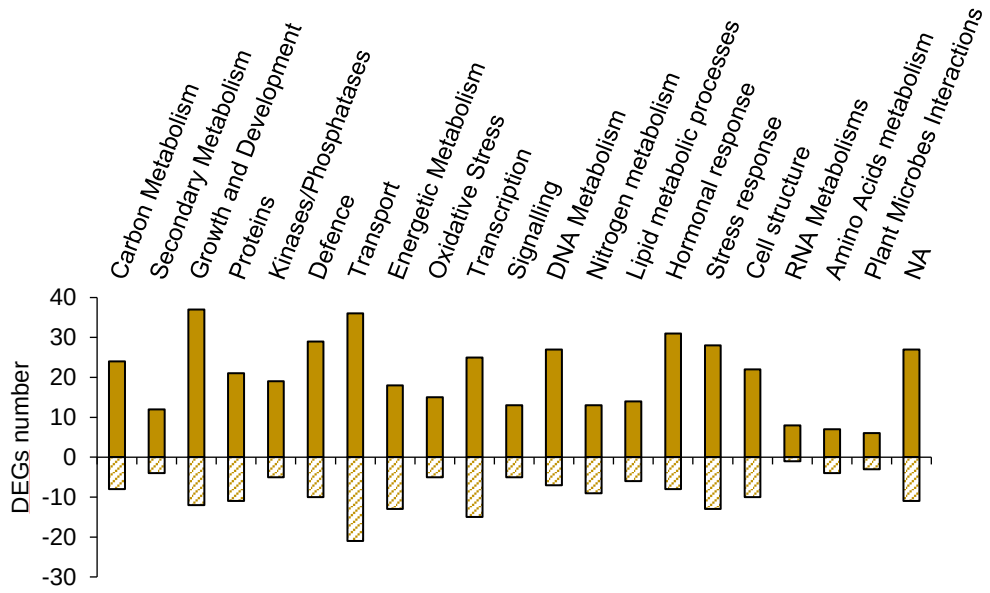


Fig. 84. ***Influence of nitrogen nutrition, N, 14 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd WT and nifD- strains at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots both after inoculation with Gd WT and nifD- strains, in the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants.*

4.5.4. Transcriptional response induced in tomato roots following inoculation with Gd (both WT and *nifD*$^-$ strains) in the absence of nitrogen.

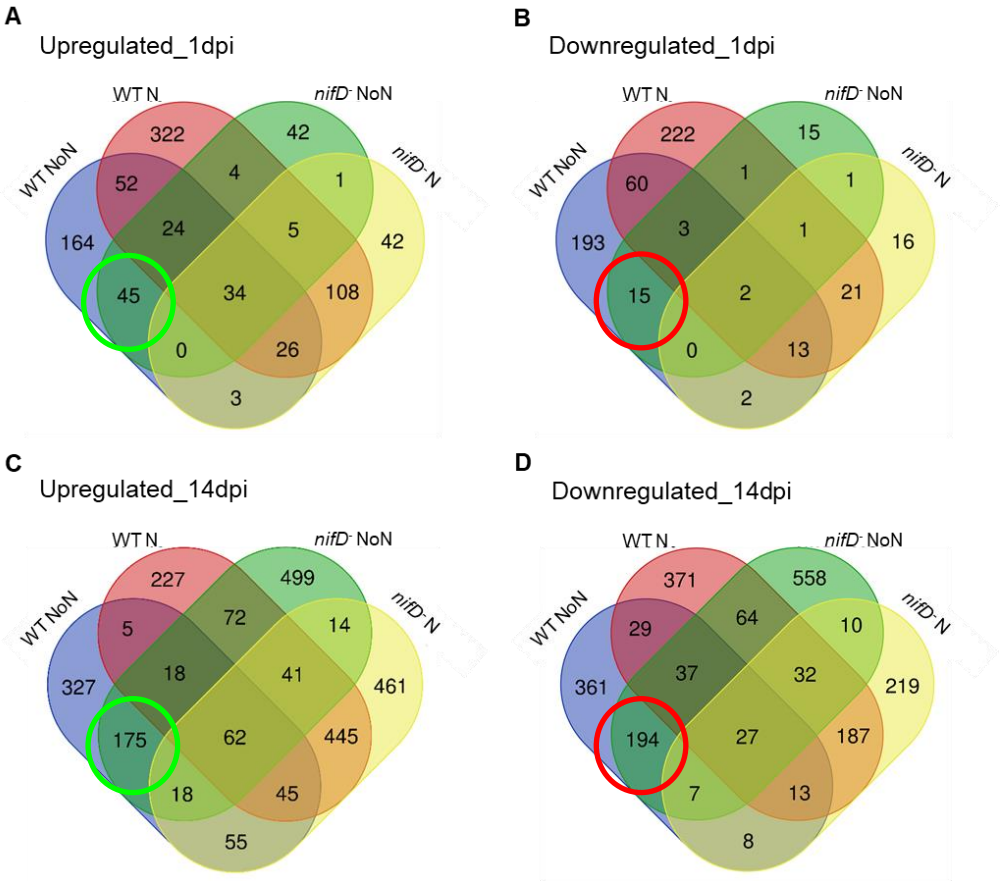


Fig. 85. Venn clustering of differentially expressed genes (DEGs) modulated (A, C upregulated; B, D downregulated) by either WT or nifD$^-$ Gd strains at 1 and 14 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by both Gd strains under NoN condition (absence of N).

The early gene response (1 dpi) that is elicited by both bacterial strains in the absence of nitrogen supply in plants growth solution is mainly upregulation (45 upregulated genes *vs* 15 downregulated) (Table S4). The mainly upregulated functional class is **stress response** (e.g. one subtilisin-like protease, three germin family proteins, one detoxification protein, one senescence/dehydration-associated protein, one carboxypeptidase).

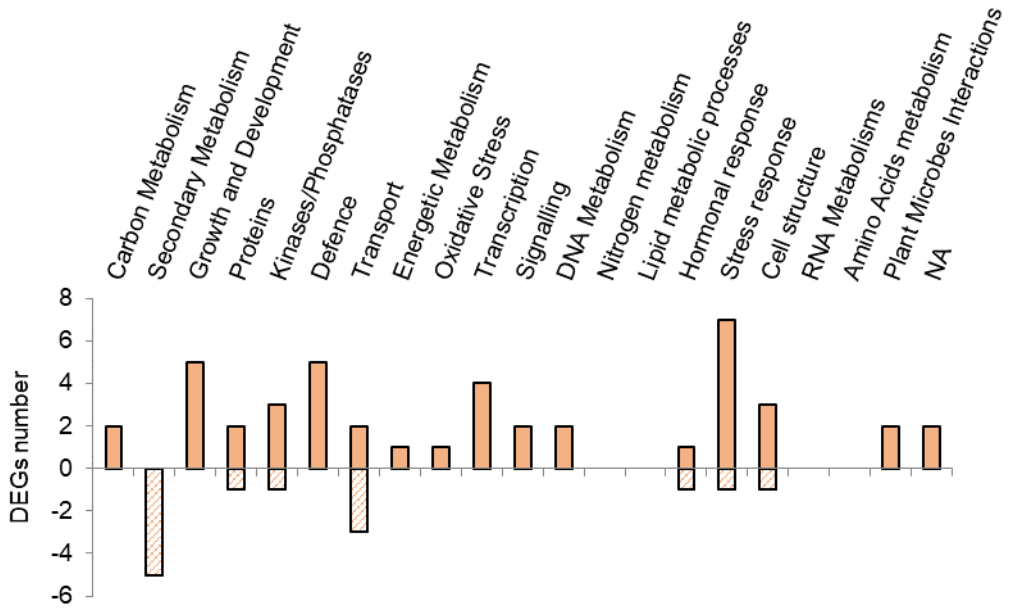


Fig. 86. ***Influence of nitrogen nutrition, NoN, 1 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd WT and nifD- strains at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots both after inoculation with Gd WT and nifD- strains, in the absence (NoN) of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

At later interaction stages, downregulation becomes prevalent (194 genes) in comparison to upregulation (175 genes) (Table S5). The most abundantly downregulated functional class was **cell structure modulation** (e.g. one ACT domain-containing family protein, four CASP-like proteins, two cellulose synthases, three dirigent proteins, two endoglucanases, one expansin, one extensin-like protein, two pectate lyases, one pectinesterase, two plant invertase/pectin methylesterase inhibitors, one trichome birefringence-like protein, one tubulin beta chain, one xyloglucan endotransglucosylase/hydrolase).

It is relevant in this case to consider two of the mainly upregulated functional classes (175 genes) as well. Namely, an upregulation was observed in the following classes of genes: **defence response** (e.g. two chitinases, one defensin-like protein, one glycine-rich protein family, three Kunitz trypsin inhibitors, one late embryogenesis abundant hydroxyproline-rich glycoprotein, one LURP-one-like protein, one major allergen, two pathogenesis-related proteins, one pin-II type proteinase inhibitor 69, two RING/U-box superfamily proteins, one thaumatin-like protein, one trypsin inhibitor) and **stress response** (e.g. three

glutathione S-transferase family proteins, three proteins DETOXIFICATION, two subtilisin-like proteases, one universal stress protein).

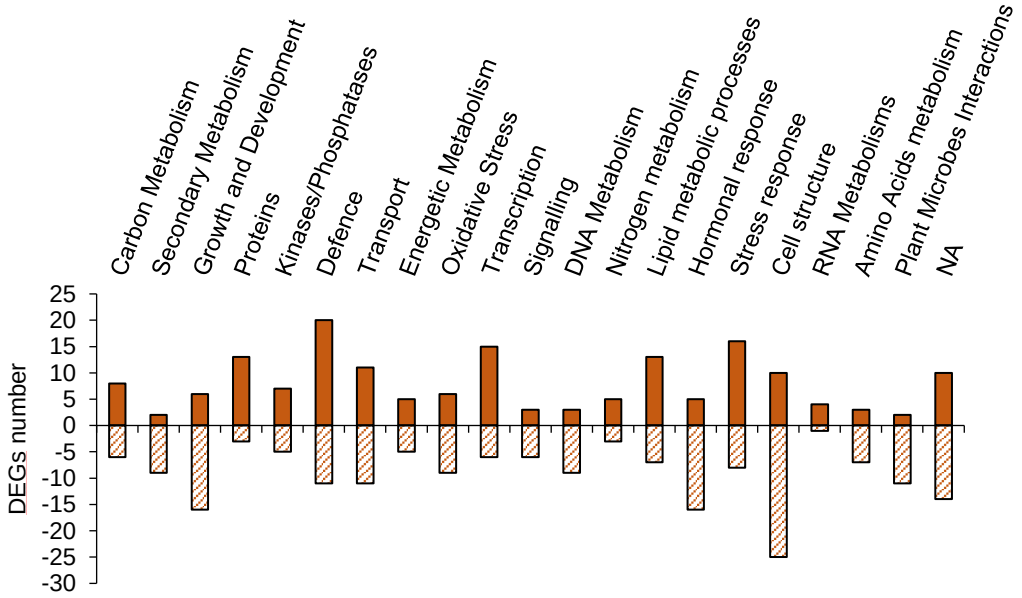


Fig. 87. ***Influence of nitrogen nutrition, NoN, 14 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd WT and nifD- strains at 14 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots both after inoculation with Gd WT and nifD- strains, in the absence (NoN) of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

4.5.5. Early (1dpi) transcriptional response to WT strain.

Genes that were specifically modulated in tomato plants by WT strain at 1 dpi were analysed as early response genes in either the absence of nitrogen or with 2 mM KNO_3 added to the plant growth solution (Table S6). Up- and downregulated gene classes will be alternatively reported according to the main elicited response. When available, Gene Ontology (GO) enrichment analysis results are presented for each condition.

4.5.5.1. N Condition

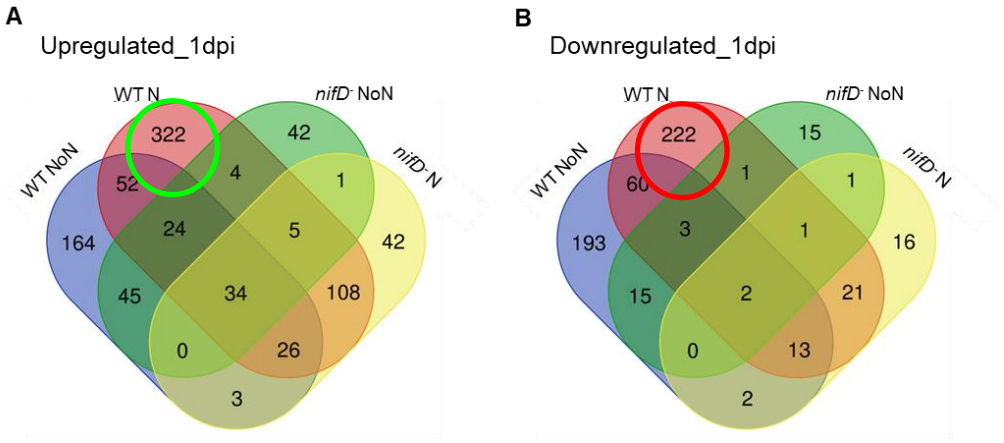


Fig. 88. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated; B downregulated) by either WT or nifD- Gd strains at 1 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by WT Gd strain under N condition (presence of N).

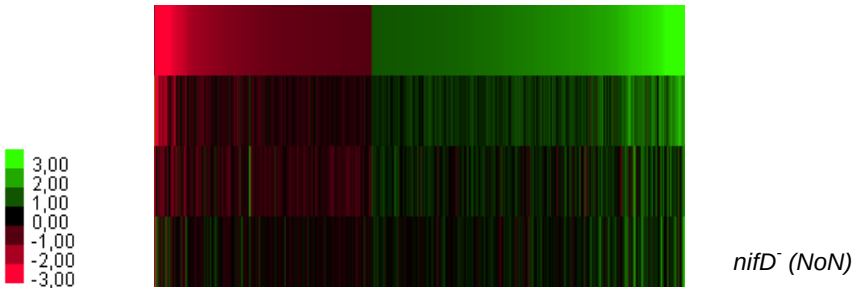


Fig. 89. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 1 dpi with G. diazotrophicus, WT strain, in the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants (Control).

322 genes were upregulated following inoculation with the WT strain in the presence of 2 mM KNO_3 (Table S6). The main classes that were upregulated in this condition belonged to **lipid metabolism** (e.g. two non-specific lipid-transfer proteins, two 3-ketoacyl-CoA synthases, two acyl-[acyl-carrier-protein] desaturases, one acyl-[acyl-carrier-protein] hydrolase, four GDSL esterases/lipases, four alpha/beta-Hydrolases superfamily proteins, one fatty acid amide hydrolase, one lipoxygenase), **protein metabolism** (e.g. two ankyrin repeat family proteins, one putative chaperone protein DNAj, two eukaryotic aspartyl protease family proteins, four F-box family proteins, one miraculin, one peptidase M28 family protein, five U-box domain-containing family proteins), **cell structure modulation** (e.g. three actin or actin related proteins, one dynein light chain family protein, one formin-like protein, one expansin-like protein,

one glycerol-3-phosphate acyltransferase, one cinnamyl alcohol dehydrogenase, two CASP-like proteins, three beta glucanases, three pectin lyase-like superfamily proteins, four pectinesterases), and **plant microbes interaction** related genes (e.g. two Clade IV and XVII lectin receptor kinases one digalactosyldiacylglycerol synthase, three early proteins, one laccase, four leucine-rich repeat receptor-like protein kinases , one PRA1 family protein). GO enrichment analysis highlighted an enrichment of genes related to lipid transport and localisation and fatty acids biosynthesis.

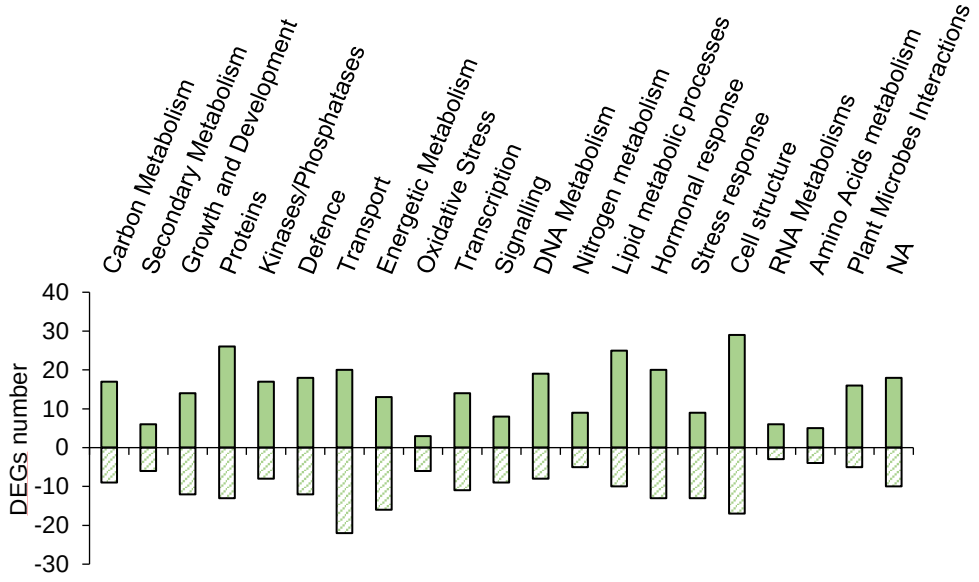


Fig. 90. ***WT strain specific response, N, 1 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd WT strain at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots specifically after inoculation with Gd WT, in the presence of 2 mM (N) KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

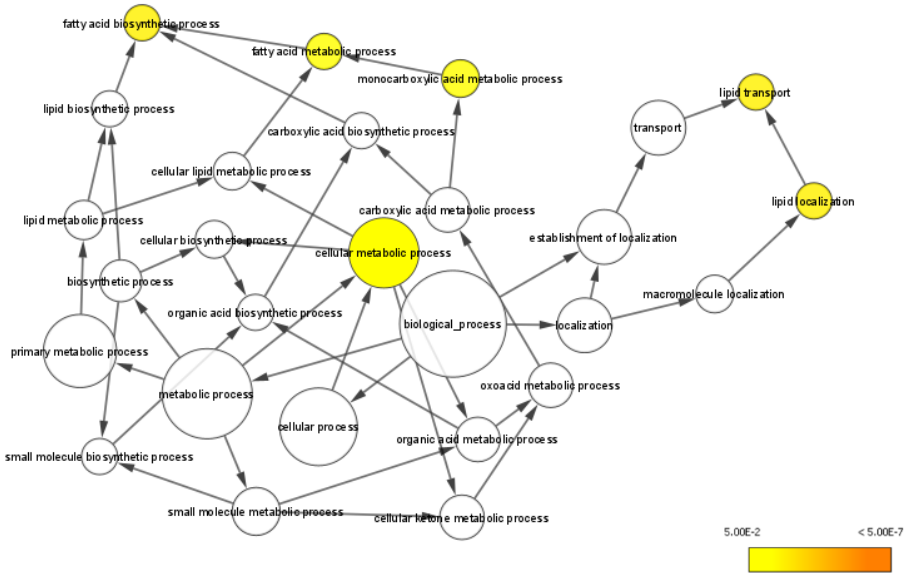


Fig. 91. Biological networks of significantly enriched ($P \leq 0.05$) Gene Ontology (GO) terms of genes upregulated at 14dpi in WT N condition were visualised using the BiNGO application in Cytoscape suite. The colour legend indicates the level of significance for enriched GO terms and white nodes indicate non significantly overrepresented categories.

4.5.5.2. NoN Condition

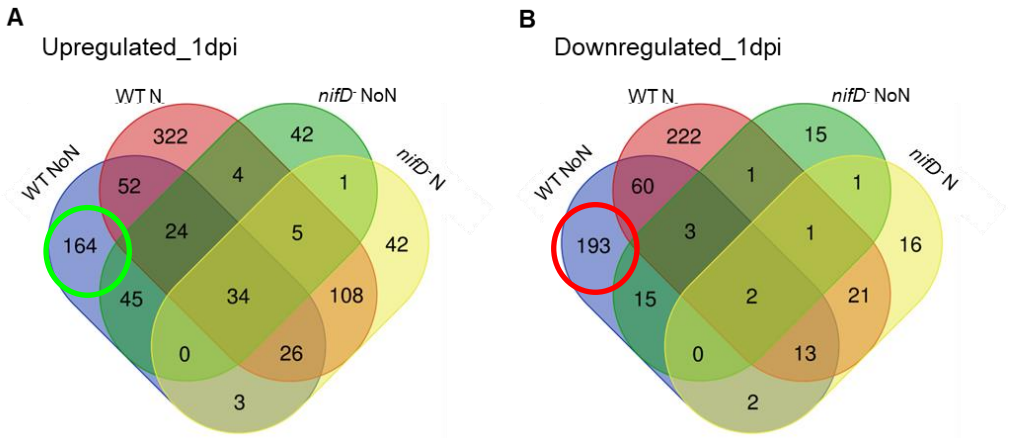


Fig. 92. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated; B downregulated) by either WT or nifD- Gd strains at 1 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by WT Gd strain in NoN condition (absence of N).

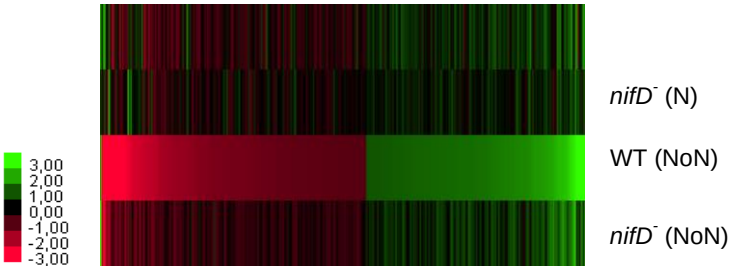


Fig. 93. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 1 dpi with G. diazotrophicus, WT strain, in the absence (NoN) of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants (Control).

193 genes were downregulated following inoculation with the WT strain in the absence of KNO_3 (Table S6). The genes that were found to be mainly modulated are included in the following classes: **growth and development** (e.g. one polyamine oxidase 5, one NAC domain containing protein 35, one self-pruning protein, one tomato 9612 mRNA, one bHLH transcription factor 058, one senescence regulator, two bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily proteins, two CONSTANS-like proteins, one cryptochrome 1) and **defence response** (e.g. two glycine rich proteins, one wound-responsive family protein, one pirin-like protein, one N-acetyl-D-glucosamine kinase, one defensin and one defensin-like protein, two RING/U-box superfamily proteins, one defensin-like protein, three Avr9/Cf-9 rapidly elicited proteins). In this case it is relevant to also consider the upregulated genes (165) that mainly belonged to **RNA processing**; in particular, thirty-five pentatricopeptide repeat-containing proteins were upregulated. GO enrichment analysis indicated an enrichment of downregulated gene categories relative to carotenoid and terpenoids biosynthesis, organ development and photosynthesis.

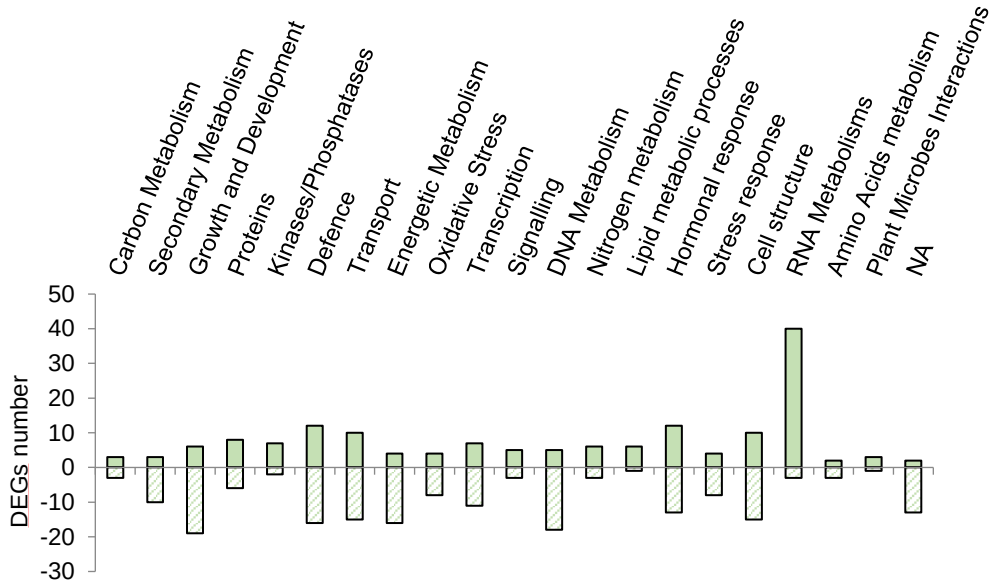


Fig. 95. ***WT strain specific response, NoN, 1 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd WT strain at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots specifically after inoculation with Gd WT, in the absence of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

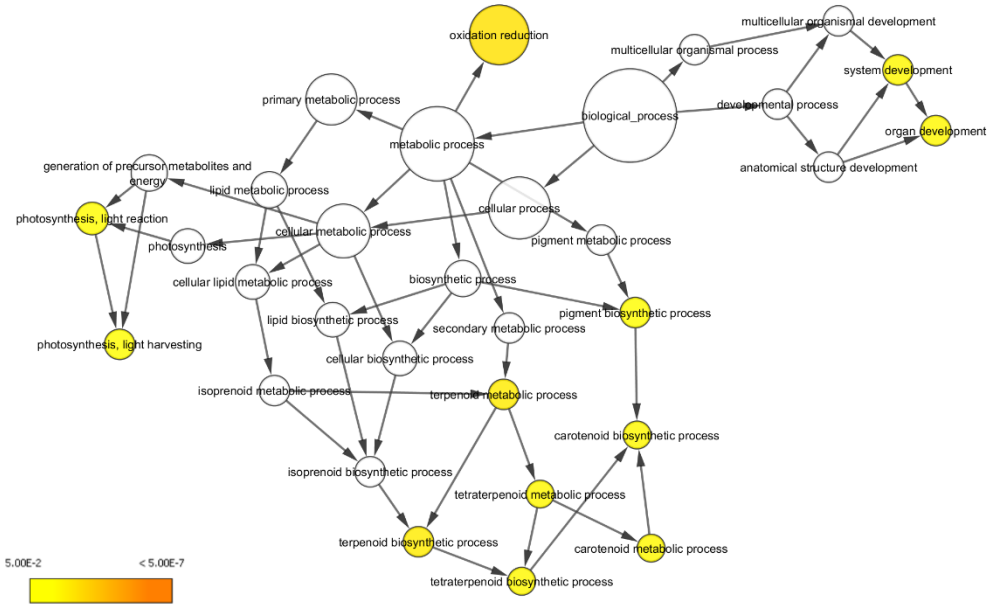


Fig. 94. Biological networks of significantly enriched ($P \leq 0.05$) Gene Ontology (GO) terms of genes downregulated at 1 dpi in WT NoN condition were visualised using the BiNGO application in Cytoscape suite. The colour legend indicates the level of significance for enriched GO terms and white nodes indicate non significantly overrepresented categories.

4.5.6. Late (14dpi) transcriptional response to WT strain.

Genes specifically modulated by WT strain at 14 dpi were analysed as late response genes either in the absence or in the presence of 2 mM KNO_3 added to the plant growth solution (Table S7).

4.5.6.1. N Condition

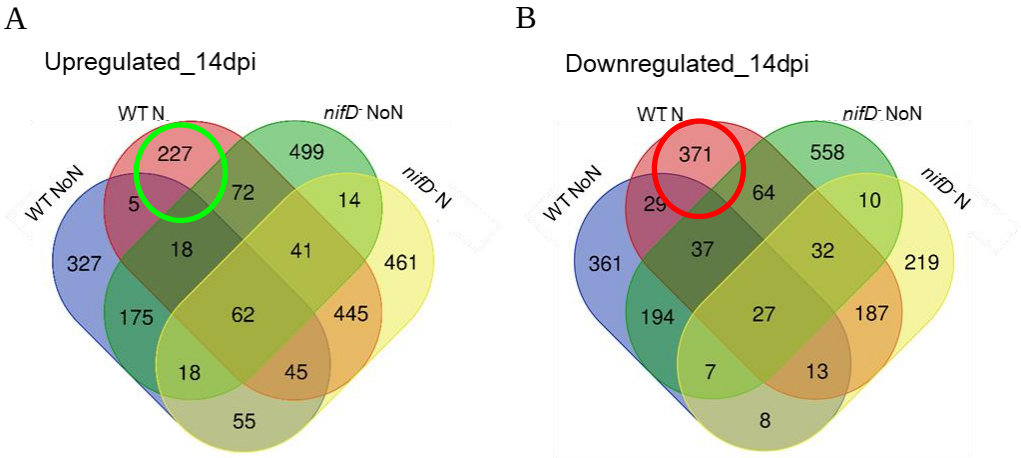


Fig. 96. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated; B downregulated) by either WT or nifD⁻ Gd strains at 14 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by WT Gd strain in N condition (presence of N).

371 genes were downregulated by the WT strain in the presence of 2 mM KNO_3

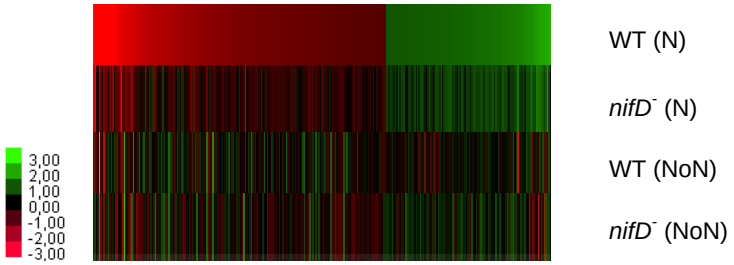


Fig. 97. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 14 dpi with G. diazotrophicus, WT strain, in the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants (Control).

(Table S7). The main classes that were downregulated in these conditions belonged to **transport** (e.g. three ABC transporter family proteins, one bidirectional sugar transporter SWEET, two calcium-transporting ATPases, two cation transporters, one ferric reductase oxidase and one ferritin, four kinesin-like, two nucleotide/sugar transporter) and **cell structure modulation** (e.g. one dynein light chain-like protein, one EXS family protein, one expansin-like protein, six extensin-like proteins, one glycerol-3-phosphate acyltransferase, one CASP-like protein, three pectinesterases, two xyloglucan endotransglucosylases/hydrolases, two pectin lyase-like superfamily proteins, one arabinogalactan protein, one cellulose synthase-like protein, one feruloyl transferase).

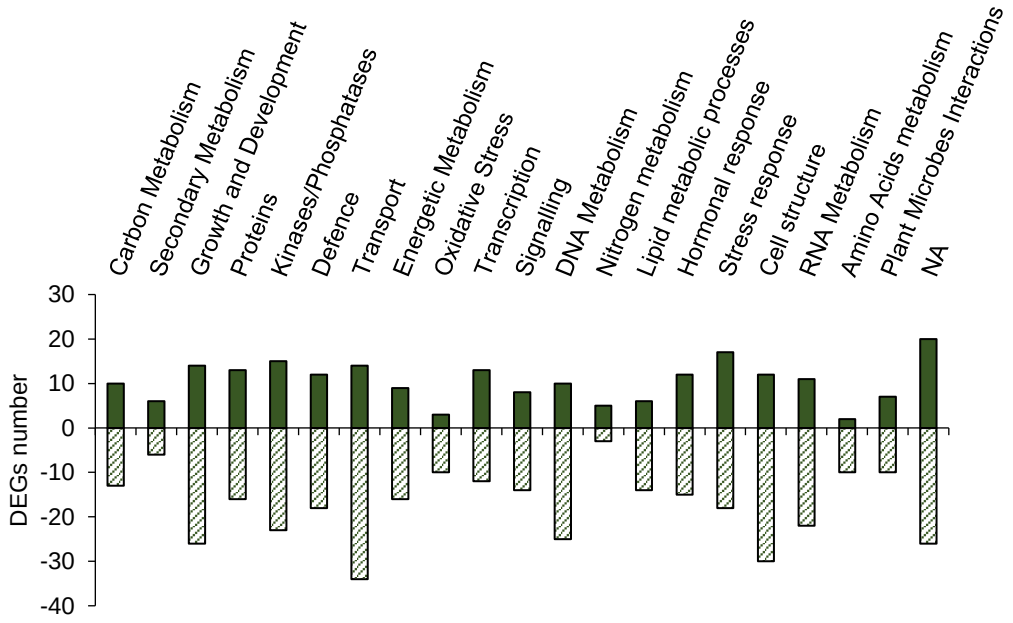


Fig. 98. ***WT strain specific response, N, 14 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd AZ0019 WT strain at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots specifically after inoculation with Gd AZ0019 WT, in the presence of 2 mM (N) KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

4.5.6.2. NoN Condition

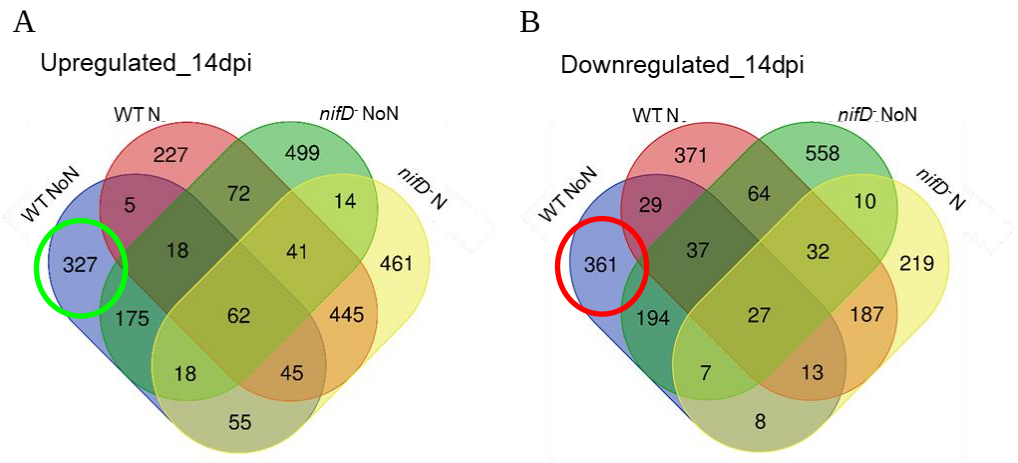


Fig. 99. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated; B downregulated) by either WT or nifD- Gd strains at 14 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by WT Gd strain in NoN condition (absence of N).

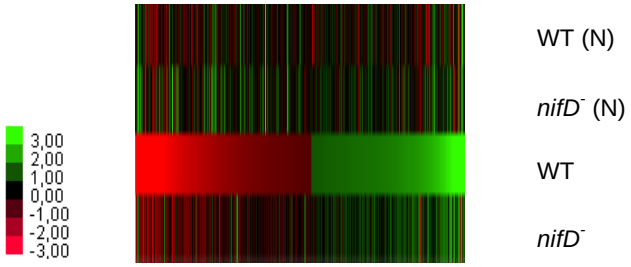


Fig. 100. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 14 dpi with G. diazotrophicus, WT strain, in the absence (NoN) of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants (Control).

The main modulation induced by WT inoculation in the absence of nitrogen in the nutrient solution was the downregulation of 361 genes (Table S7). The main functional classes modulated were **cell structure modulation** (e.g. two arabinogalactan proteins, two CASP-like proteins, seven dirigent proteins, one pectate and one pectine lyases, two trichome birefringence-like proteins, two xyloglucan endotransglucosylase/hydrolases, two xyloglucan galactosyltransferase KATAMARI1) and **oxidative stress related genes** (e.g. one caleosin-related family protein, one catalase, two glutaredoxins, fourteen peroxidases, three plant cadmium resistance 2, two respiratory burst oxidases). Gene upregulation (327 genes) was quantitatively similar to downregulation (361 genes). Elicitation of genes involved in **transport** (e.g. eight ABC

transporter family proteins, one annexin p34, one bidirectional sugar transporter SWEET, one calcium uniporter, mitochondrial, three heavy metal transport/detoxification superfamily proteins, three major facilitator superfamily proteins, one nodulin26-like intrinsic protein 31, two purine permeases, two zinc transporters) , **growth and development** (e.g. one basic blue protein, one cyclin A2_1, two D-type cyclins, five LOB domain-containing proteins, one LOV/LOV protein, one phototropic-responsive NPH3, one pollen Ole e 1 allergen and extensin family protein, one root meristem growth factor) and **hormonal response** (e.g. two AP2-like ethylene-responsive transcription factors, three auxin efflux carrier family proteins, one auxin Efflux Facilitator 9, one auxin-regulated IAA17, one BREVIS RADIX protein, one ethylene-responsive transcription factor, IAA-amino acid hydrolase ILR1, three jasmonate zim-domain proteins, two MLP, one notabilis, one S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase 1, one Tornado 1 protein) were found. Moreover, GO enrichment analysis indicated an upregulation of genes implicated in polysaccharides catabolism and polyamine biosynthesis. This latter finding correlates well with the enriched downregulation of oxidative stress related genes assessed in this condition (absence of N): it is reported that the stimulation of polyamine biosynthesis is associated with the scavenging or reactive oxygen species, H_2O_2 in particular, in plants cells [29][156].

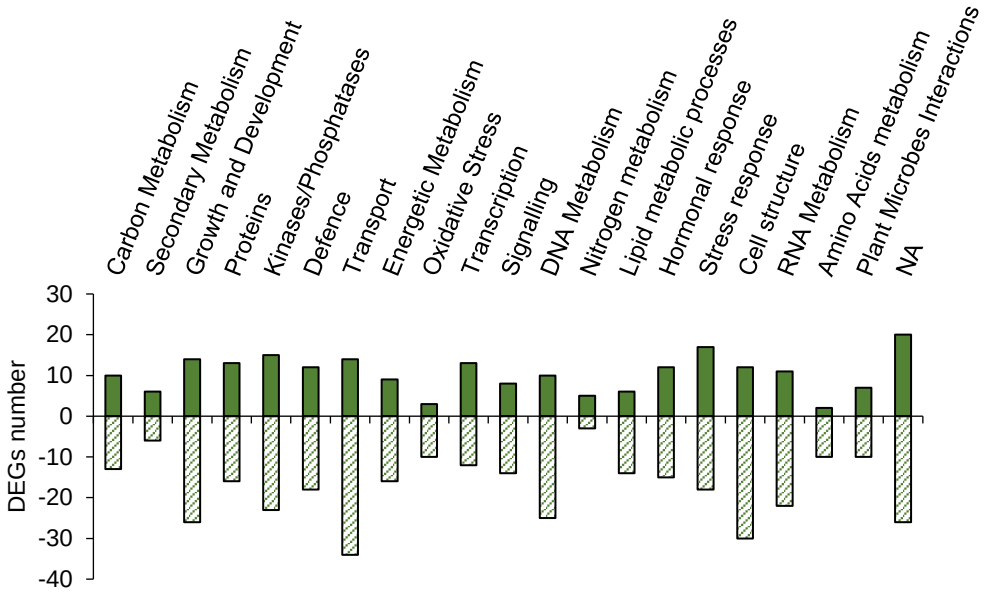


Fig. 102. ***WT strain specific response, NoN, 14 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd AZ0019 WT strain at 14 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots specifically after inoculation with Gd AZ0019 WT, in the absence of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

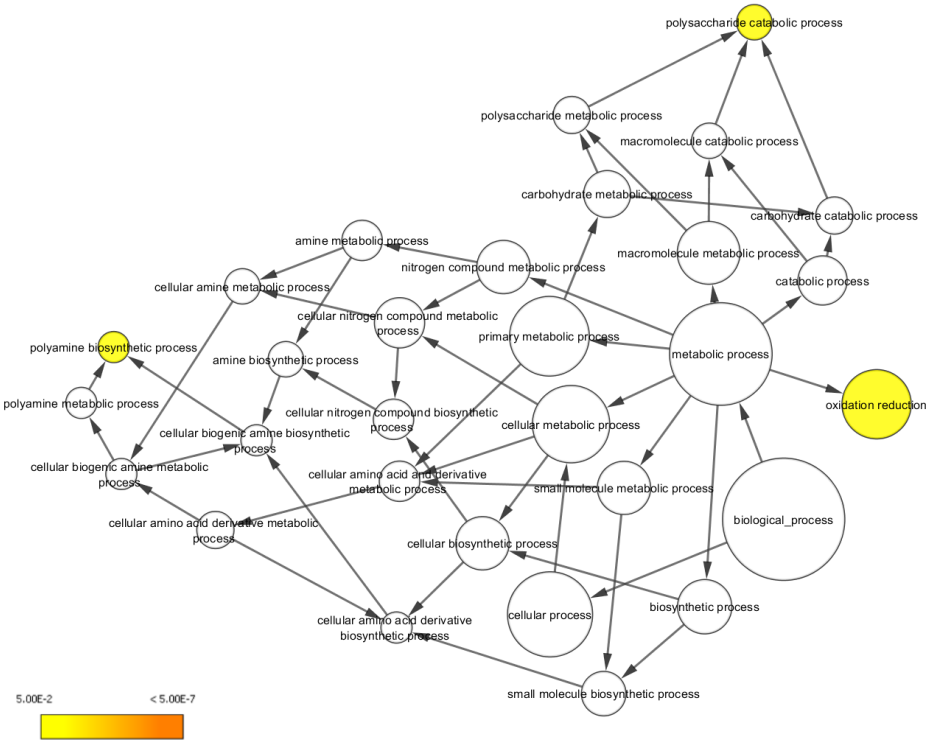


Fig. 101. Biological networks of significantly enriched ($P \leq 0.05$) Gene Ontology (GO) terms of genes upregulated at 14 dpi in WT NoN condition were visualised using the BiNGO application in Cytoscape suite. The colour scale legend indicates the level of significance for enriched GO terms and white nodes indicate non significantly overrepresented categories.

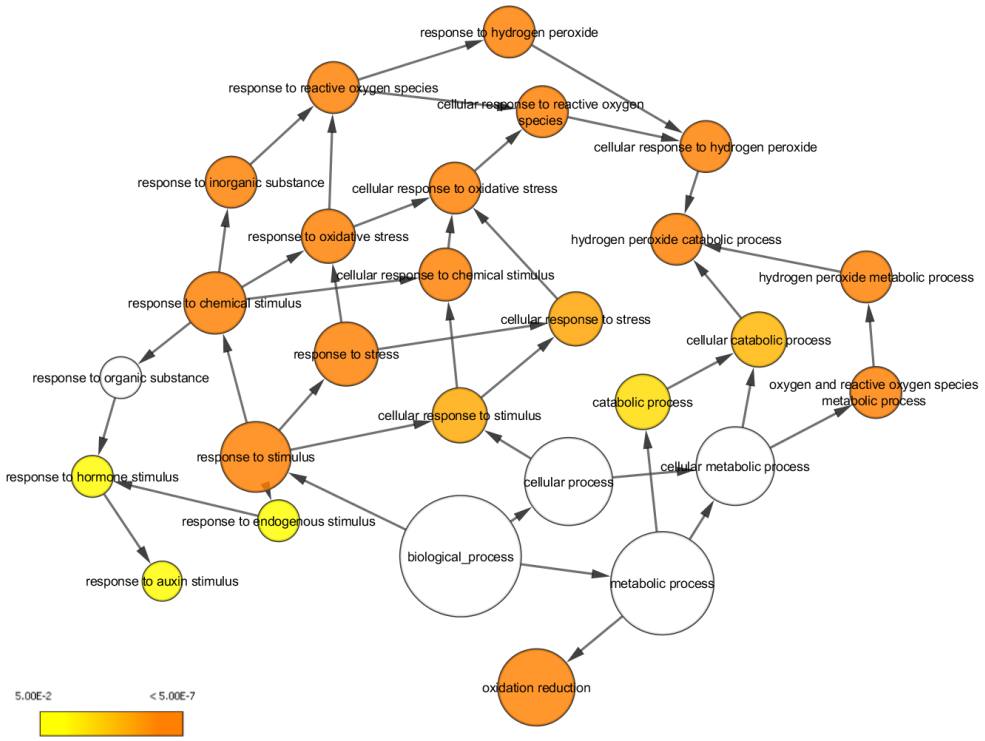


Fig. 103. Biological networks of significantly enriched ($P \leq 0.05$) Gene Ontology (GO) terms of genes downregulated at 14 dpi in WT NoN condition were visualised using the BiNGO application in Cytoscape suite. The colour scale legend indicates the level of significance for enriched GO terms and white nodes indicate non significantly overrepresented categories.

4.5.7. Early (1dpi) transcriptional response to *nifD*$^{-}$ mutant strain.

Genes that were specifically modulated in tomato plants by the *nifD*$^{-}$ mutant strain of *Gd* at 1 dpi were analysed as early response genes in either the absence of nitrogen or at 2 mM KNO_3 supplement to the plant growth solution (Table S8). Up- and downregulated gene classes are reported according to the main elicited response: upregulated genes are presented when upregulation prevails and the same for downregulation. When available, GO enrichment analysis results are presented for each condition.

1.1.1.1. N Condition

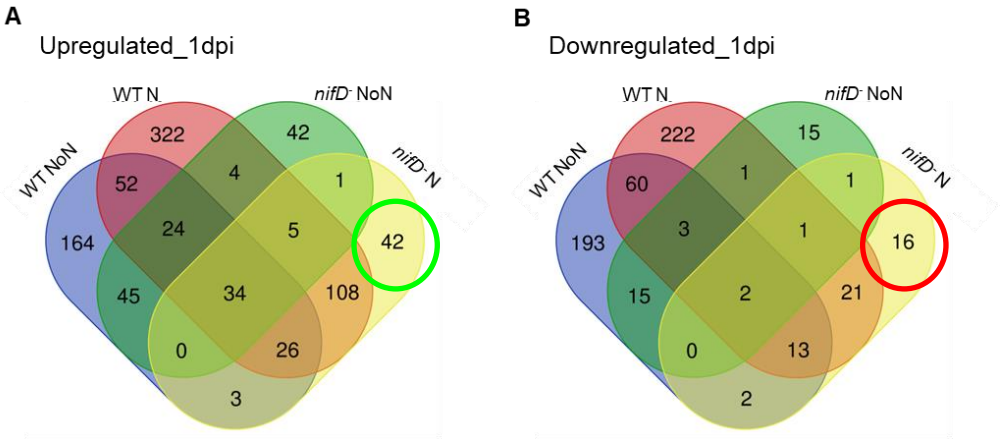


Fig. 105. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated; B downregulated) by either WT or nifD- Gd strains at 1 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N)) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by nifD- Gd strain in N condition (presence of N).

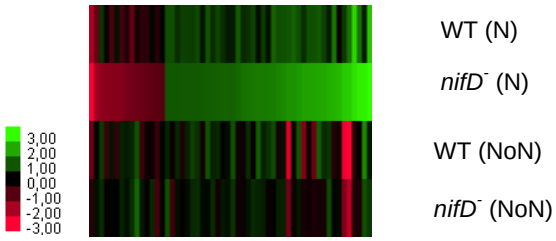


Fig. 104. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 1 dpi with G. diazotrophicus, nifD- strain, in the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants (Control).

42 genes were upregulated following inoculation with the *nifD*$^{-}$ in the presence of 2 mM KNO_3 (Table S8). The main functional classes modulated include

defence response (e.g. one pathogenesis-related protein, one defensin, one acidic endochitinase) and **hormonal response** (e.g one notabilis, three small auxin up-regulated RNAs, one ethylene-responsive transcription factor, one WAT1-related protein).

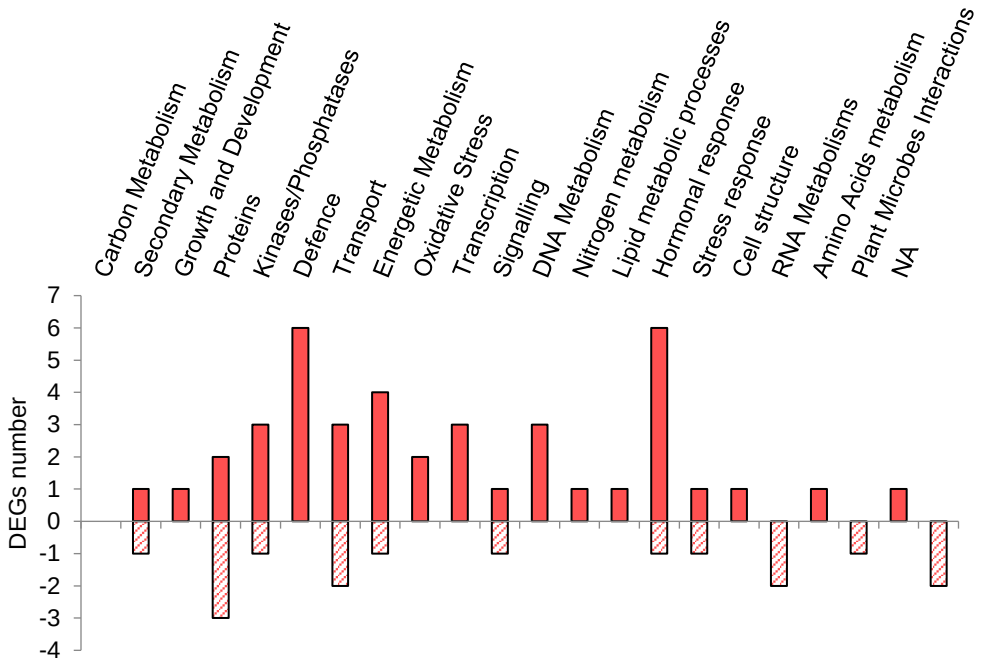


Fig. 106. ***nifD⁻ strain specific response, N, 1 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd nifD⁻ strain at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots specifically after inoculation with Gd nifD⁻ strain, in the presence of 2 mM (N) KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

1.1.1.2. NoN Condition

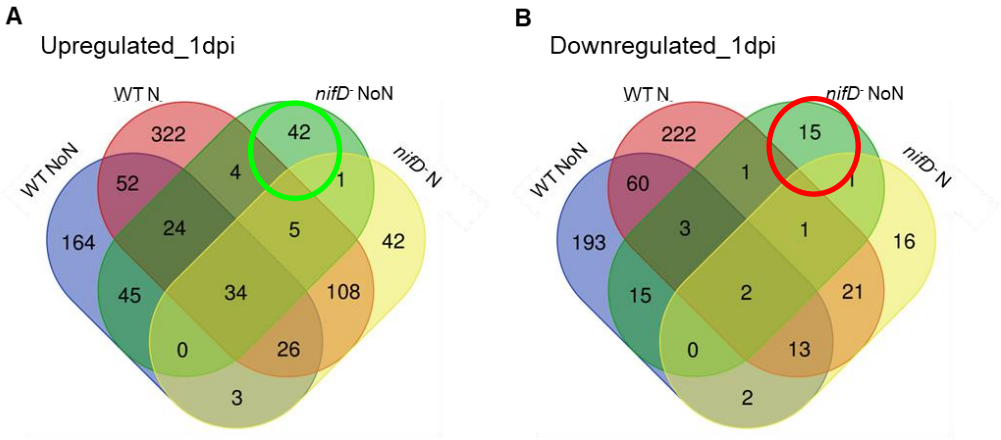


Fig. 108. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated; B downregulated) by either WT or nifD- Gd strains at 1 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by nifD- Gd strain in NoN condition (absence of N).

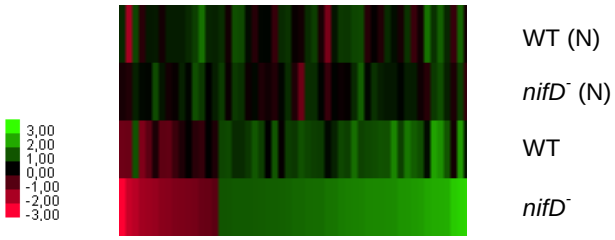


Fig. 107. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 1 dpi with G. diazotrophicus, nifD- strain, in the absence (NoN) of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants (Control).

Genes that were upregulated by the *nifD*- strain in the absence of KNO_3 were 42 (Table S8). Most relevant functional classes affected were: **cell structure modulation** (e.g. one pectinesterase, one alpha-1,4-glucan-protein synthase [UDP-forming], one xyloglucan-specific endoglucanase inhibitor protein 2, one CLIP-associating protein 1, one CASP-like protein, one expansin 6), **signalling** (e.g. one two-component response regulator, one receptor-like protein kinase, one Cysteine/Histidine-rich C1 domain family protein, one HXXXD-type acyl-transferase family protein), **defence response** (e.g. one NBS-LRR resistance protein, one pathogenesis-related protein 1, one defensin, one acidic endochitinase), **plant microbial interaction** related genes (e.g. two hydroxyproline-rich glycoprotein family proteins, two leucine-rich receptor-like kinase family proteins).

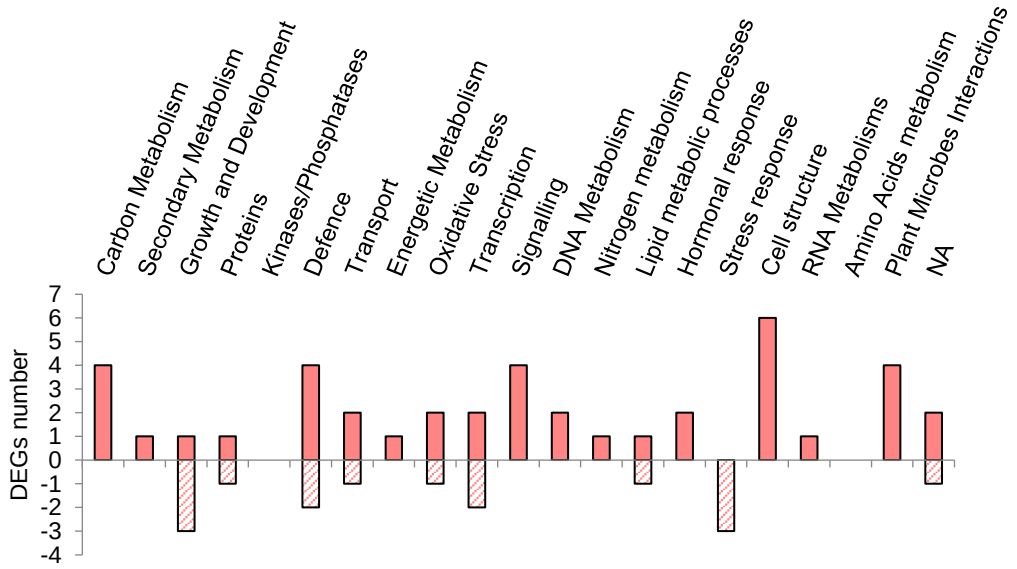


Fig. 109. ***nifD- strain specific response, NoN, 1 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd nifD- strain at 1 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots specifically after inoculation with Gd nifD- strain, in the absence of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

4.5.8. Late (14 dpi) response to *nifD-* mutant strain.

Genes that are specifically modulated by Gd *nifD-* at 14 dpi were analysed as late response genes in either the absence or at 2 mM KNO_3 added to the plant growth solution (Table S9).

4.5.8.1. N Condition

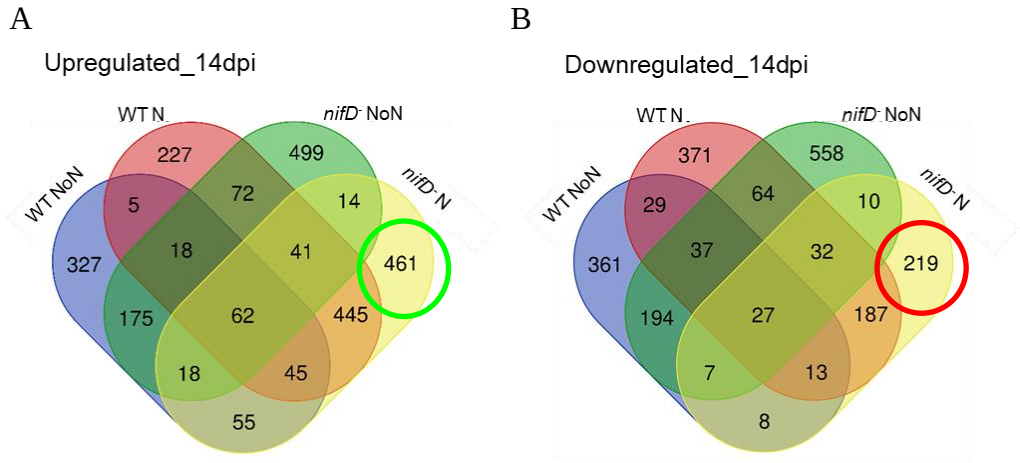


Fig. 111. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated; B downregulated) by either WT or nifD- Gd strains at 14 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circles indicate the considered gene clusters: genes up- (green) or down- (red) regulated by nifD- Gd strain in N condition (presence of N).

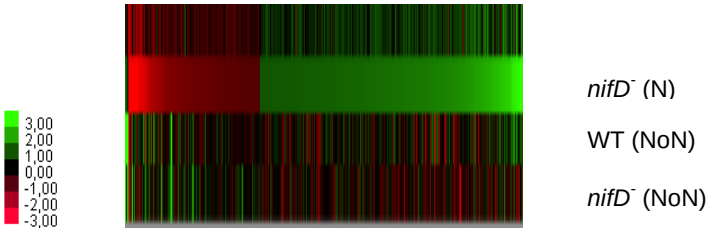


Fig. 110. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 14 dpi with G. diazotrophicus, nifD- strain, in the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution, compared to non-inoculated plants (Control).

Genes that were exclusively upregulated by *nifD-* in the presence of 2 mM KNO_3 in the plant growth solution were 461 (Table S9). The main functional classes upregulated in this condition belonged to: **cell structure modulation** (e.g. three actin cross-linking proteins, five CASP-like proteins, three cellulose synthases, one cinnamyl alcohol dehydrogenase, ten dirigent proteins, two endoglucanases, two expansins, two glucuronoxylan 4-O-methyltransferase-like proteins, one pectate lyase and one pectinesterase, two rhamnogalacturonate lyase family proteins, three trichome birefringence-like proteins), **transport** (e.g. one exocyst subunit exo70 family protein, one annexin 6, four ABC transporter B family proteins, five major facilitator superfamily proteins, three heavy metal transport/detoxification superfamily proteins, two bidirectional sugar

transporters SWEET, two sugar facilitator proteins) and **lipid metabolism** (e.g. eight alpha/beta-Hydrolases superfamily protein, three GDSL-like lipase/acylhydrolase superfamily proteins, five lipid transfer proteins, three phospholipases). GO analysis underlined an enrichment of categories relative to the response to inorganic nitrate and confirmed a stimulation of transport involved genes; in particular, it indicated an enhancement of nitrate transport.

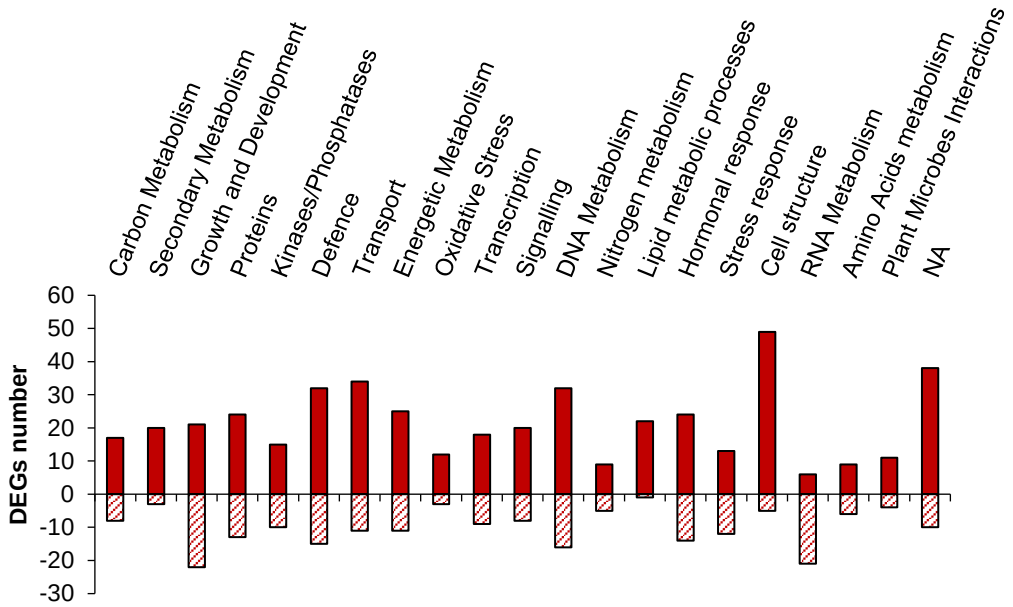


Fig. 112. ***nifD⁻ strain specific response, N, 14 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd nifD⁻ strain at 14 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots specifically after inoculation with Gd nifD⁻ strain, in the presence of 2 mM (N) KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

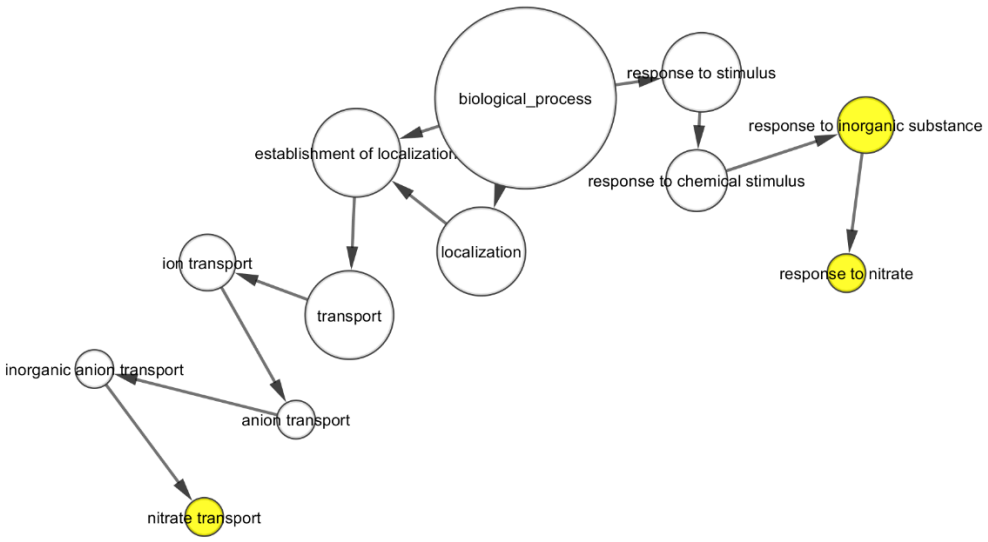


Fig. 113. Biological networks of significantly enriched (P ≤ 0.05) Gene Ontology (GO) terms of genes upregulated at 14 dpi in nifD⁻ N condition were visualised using the BiNGO application in Cytoscape suite. The colour scale legend indicates the level of significance for enriched GO terms and white nodes indicate non significantly overrepresented categories.

4.5.8.2. NoN Condition

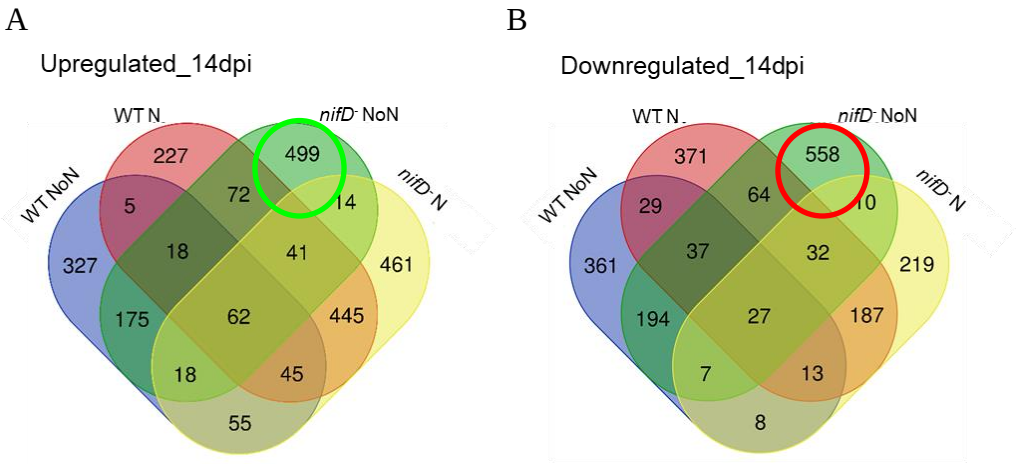


Fig. 114. Venn clustering of differentially expressed genes (DEGs) modulated (A upregulated; B downregulated) by either WT or nifD⁻ Gd strains at 14 dpi, in either the absence (NoN) or the presence of 2 mM KNO_3 (N) in modified Hoagland growth solution. Green and red circlesindicate the considered gene clusters: genes up- (green) or down- (red) regulated by nifD⁻ Gd strain in NoN condition (absence of N).

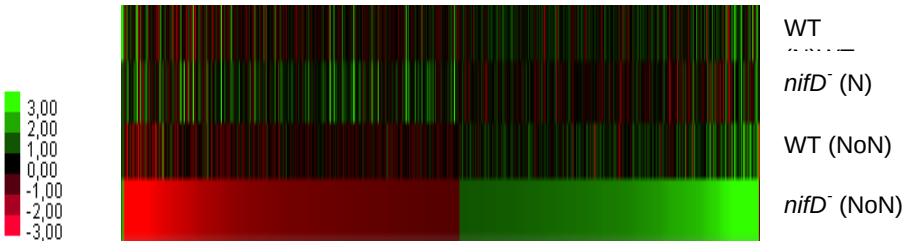


Fig. 115. Heat map of fold change values for differentially expressed genes (DEGs) identified in tomato roots at 14 dpi with G. diazotrophicus, nifD- strain, in the absence (NoN) of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants (Control).

The main modulation induced by *nifD*- strain inoculation in the absence of KNO_3 in the feed was the downregulation of 558 genes (Table S9). Main classes that were downregulated in this condition belonged to: **cell structure modulation** (e.g. four arabinogalactan peptides, four cellulose synthases, two COBRA proteins, four endoglucanases, five expansins, two formin-like proteins, two glucan endo-1,3-beta-glucosidases, two pectate and two pectine lyases, three S-adenosyl-L-methionine-dependent methyltransferases superfamily proteins, four trichome birefringence-like proteins,two xyloglucan galactosyltransferase KATAMARI), **transport** (e.g. two ABC transporter family proteins, one anthocyanin permease, two bidirectional sugar transporters SWEET, two boron transporters, two calcium-transporting ATPases, two dynamin family proteins, four kinesin motor family proteins, three major facilitator superfamily proteins, two peptide transporters, two potassium channels, one transport inhibitor response 1).

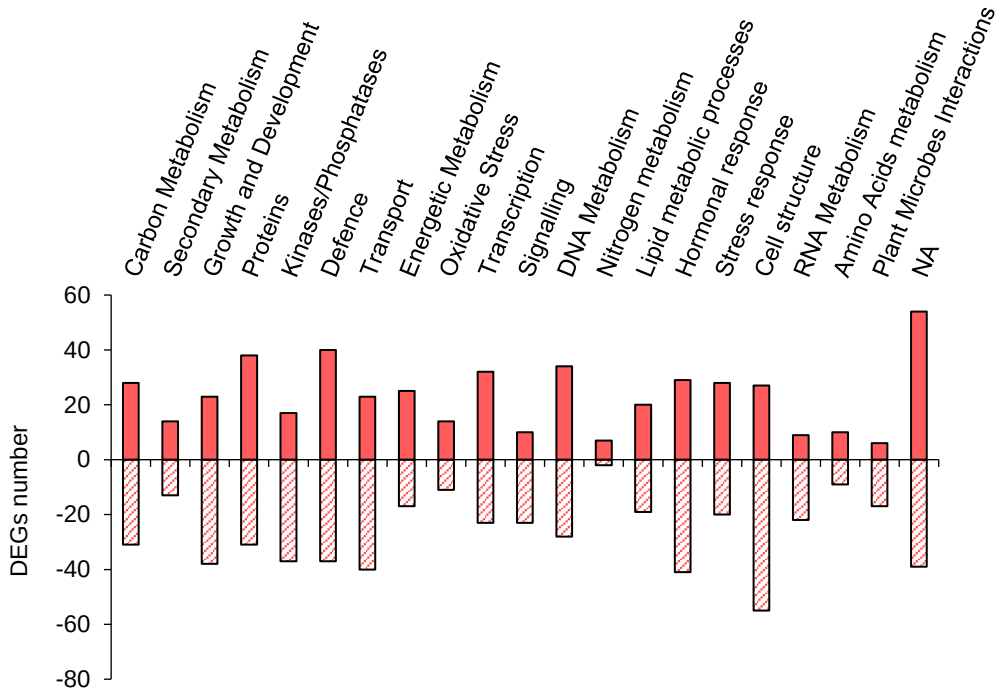


Fig. 116. ***nifD- strain specific response, NoN, 14 dpi****. Functional annotation of differentially expressed genes (DEGs) in tomato roots in response to Gd nifD- strain at 14 dpi. Functional classes were assigned on the basis of the function of genes. Plotted genes were found to be upregulated or downregulated in tomato roots specifically after inoculation with Gd nifD- strain, in the absence of KNO_3 in modified Hoagland growth solution, compared to non-inoculated plants.*

4.5.9. Transcriptomic data discussion

4.5.9.1. General response

The genes that were found to be commonly modulated in tomato plants by both *Gd* WT and *nifD-* strains in both the presence and the absence of nitrogen in the growth solution were considered to be a general response of plant roots to presence of the bacterium. Transcriptome analysis was undertaken at 1 dpi (early response) and 14 dpi (late response). In general, transcriptional upregulation was prevalent over downregulation at both early and late stages. At 1 dpi, the genes that were found to be mainly upregulated by both WT and *nifD-* strains belong to defence response, hormone metabolism and gene expression regulation categories. These results are in line with reported literature: defence response has been observed to be upregulated in plants exposed to plant growth promoting (PGP) microorganisms [37], having also a secondary beneficial effect in the

fight against plant pathogens [5]. The upregulation of hormone related genes, mainly ABA or ethylene responsive factors, is in line with previous studies in which sugarcane plants colonised by *Gd* PAL5 and *H. rubrisubalbicans* HCC103 exhibited an increased expression of a putative ethylene receptor at 24 h as well as seven days after inoculation [31]. It has been suggested that an increase in ethylene receptors might reduce the host's sensitivity to ethylene in order to lower the plant defence mechanisms and permit colonisation [31]. Abscisic acid also mediates plant adaptation to biotic and abiotic stresses. Under stress conditions, it is synthesised to initiate defence mechanisms, among which are the regulation of stomatal aperture and expression of defence-related genes conferring resistance to environmental stresses [123]. In plants, it has been suggested that microscopic surface openings, such as stomata, serve as passive ports of bacterial entry during infection, and further investigations have found stomatal closure to be part of a plant innate immune response to limit bacterial invasion [145]. In light of these findings, it could be hypothesised that ABA production in the early stages of tomato-Gd interaction is a plant attempt to limit the entry sites available for the bacteria.

As a possible additional defence mechanism against biotic stress, the tomato plant also upregulates oxidative burst related enzymes. The oxidative burst induction is not always a consequence of pathogenic bacteria challenge [4] but it can also occur when beneficial bacteria come into contact with host plants. The current finding of an upregulation of oxidative burst related enzymes is in line with what previously reported by Alqueres et al. [3] in the case of rice inoculation with Gd Pal 5 strain: in their study, they showed that reactive oxygen species (ROS) were produced at early stages of rice root colonisation.

Focusing on the late response (14 dpi), defence remains one of the main upregulated functional classes, indicating that the tomato plant seems to maintain an "alert" state even at later stages post inoculation. However, a growth promotion effect is evidenced by the upregulation of genes related to transport, growth and development. Previous work has demonstrated how *Gd* colonisation in hosts such as sugarcane, can enhance the uptake efficiency of certain nutrients [216]. This ability might partly reside in the production from the bacterial side of siderophores and other molecules that can help the solubilisation of important

minerals such as phosphorus, potassium, and zinc [37][80]. Furthermore, a bacteria-mediated increase in root weight, as well as root length and root surface area, is often reported as one of the effects induced by *Gd* inoculation; this could lead to an increase in the volume of substrate explored by the plant and thus favour the intake of nutrients [70][16][87][249]. Since no significant root biomass increase was observed in the hydroponic system setup used in this experiment, current data indicate that exposure to this bacterium, regardless of the nitrogen fixation capability, could significantly increase the expression of specific transporters in tomato plants roots, suggesting a direct effect on the ability of the root system to regulate the nutrient uptake. In support of this, for example, upregulation of a potassium transporter protein was observed as well as downregulation of the potassium starvation induced enzyme purple acid phosphatase [93].

Additionally, the second most upregulated gene (LogFC) was encoding for the exocyst complex component 7. The exocyst complex is a main component of the intracellular vescicular trafficking pathway and has been reported to be involved in the Solanaceae defence response to a number of pathogens such as *Phytophthora infestans* and *Pseudomonas syringae,* being also involved in callous deposition [57]. Exocyst subunits were also reported to play an important role during arbuscular mycorrhizal symbiosis, suggested by their accumulation at sites of microbial contact and role in the formation of the perifungal membrane [75][258]. Interestingly, one of the colonisation mechanisms proposed for *Gd* inter/intracellular establishment and migration inside host plants, involves the formation of vesicle-like structures [45].

Furthermore, at this colonisation stage downregulation of an aminocyclopropane 1- carboxylate oxidase protein, a key enzyme in ethylene synthesis, was found. This is in line with previous reports about the ability of some endophytic bacteria to improve plant growth by reducing the synthesis of stress ethylene in plants [88].

4.5.9.2. Influence of nitrogen on tomato plant response.

Modulation of tomato genes after the interaction with *Gd* was then analysed taking into consideration the presence or the absence of a nitrogen source in the hydroponic growth solution.

In plants grown in the presence of 2 mM KNO_3, the response at early (1 dpi) and late (14 dpi) stages is reported. At early stages, interaction with both Gd strains led to an upregulation of lipid metabolism. Lipids and their metabolites play diverse roles in plant growth as well as response to environmental stimuli. Lipids and their derivatives can be involved in a number of metabolic processes like energy production, cell membrane rearrangements, hormone production and plant growth. For example, evidence implicates lipids as signalling molecules mediating plant immunity [72]. In fact, lipases are presumed to be actively involved in plant defence responses. In particular, GDSL esterases/lipases, characterized by the conserved GDSL motif, are a subfamily of lipolytic enzymes with broad substrate specificity. Investigations on rice plants have identified two GDLS esterases/lipases whose overexpression significantly lowered plant disease resistance to pathogens [72]. Six GDLS esterases/lipases were found to be upregulated in tomato roots in the current experiments.

In addition to this, other genes that indicate a defence reaction of the plant were stimulated: response to ABA proteins, suberin, lignin and cutin biosynthesis and deposition.

Expression of transport related genes was also enhanced in the presence of nitrogen. Among other ion carrier proteins, seven ATP-binding cassette (ABC) transporter genes were upregulated. ABC transporters constitute a ubiquitous superfamily of integral membrane proteins that are responsible for the ATP-powered translocation of many substrates across membranes [186]. Among other functions, they have shown to be expressed in response to pathogen challenge by removing bacterial toxins from plant cells and by secreting antimicrobial secondary metabolites. Interestingly, among the secondary metabolites that ABC transporters can modulate the excretion of are also some compounds (like isoflavonoids) that act as attractants to beneficial microorganisms [110][181][215].

A mild overexpression of genes related to lateral root development was also observed in this condition. Lateral root emergence sites are considered to be a favourable entry point for endophytic bacteria colonisation.

At later stages, although a general response involving defence and ABA, JA and ethylene mediated stress response was still occurring, a plant growth promotion effect was visibly induced. In addition to a number of growth and development stimulating genes, a set of genes related to auxin transport and metabolism were enhanced. Auxin is a plant growth hormone known for its ability to stimulate differential growth in response to gravity or light stimuli. Indole-3-acetic acid (IAA), the main auxin in higher plants, has profound effects on plant growth and development [259]. Notably, previous investigations have shown that Gd is among the PGP bacteria that are able to actively synthetise IAA [173].
Furthermore, various transport related proteins, mainly involved in the uptake of nutrients like potassium, zinc, sulphate and sugars, were also upregulated.

In the case of plants grown in the absence of available nitrogen in the growth solution, the predominantly overexpressed genes at early plant-bacteria exposure stages were related to plant stress response and defence, and a minor modulation of growth and development and cell structure modification genes.
At 14 dpi, gene downregulation was slightly prevalent over upregulation. The most abundant negatively modulated genes belong to the cell structure modification functional class; among these genes, four CASP-like proteins and three dirigent proteins were downregulated: these proteins are responsible for lignin deposition at the Casparian strip and at the cell wall level respectively. These enzymes are often found to be elicited during pathogen challenge so to create a diffusion barrier towards external threats, like pathogenic bacteria [115][172]. Observing a reduction in the transcription of these enzymes could be a way of favouring bacterial establishment inside the plant. A number of polysaccharide structure rearranging enzymes were downregulated as well (two endoglucanases, two pectate lyases, one pectinesterase, one xyloglucan endotransglucosylase/hydrolase); this might be ascribed to a reduced active interaction of Gd with the external plant cell walls. At 14 dpi, the bacterial adhesion and penetration phase has been overcome and thus cell wall rearrangement genes, that were upregulated in the early colonisation stages are

now switched down. Auxin responsive genes, as well as a series of growth and development inducing genes, were also negatively regulated. A minor upregulation in defence and stress response related genes was also observed.

From these gene modulation patterns, it seems that a more positive response is elicited in plants that are not nitrogen starved: plant growth promotion is favoured by development-promoting genes, hormone-mediated growth stimulation and nutrient transport facilitation.

At early stages, both in the presence and the absence of KNO_3, tomato plants favour a general defence response, which seems to be stronger in the presence of KNO_3, where an upregulation of lignin, cutin and suberin synthesis and deposition genes was detected; arguably, a healthier plant can put in place a more efficient response to a possible threat. Nevertheless, a putative positive PGP effect (indicated by cell structure modification and development genes) can already be detected at 1 dpi in both conditions, although more evidently in non-N starved plants. Here the putative ABC-mediated plant-bacteria crosstalk, cell wall loosening enzymes and lateral root inducing genes upregulation might reflect the initial steps of the establishment of a positive symbiosis with the beneficial bacterium. Conversely, the downregulation of flavonoids biosynthesis was observed specifically in the NoN condition. Flavonoids production has been linked to the Rhizobia recruitment mechanism [181]. This might reflect a strategy for reducing attractiveness towards symbiotic bacteria and thus avoid the energetic burden of establishing a symbiosis under N starvation conditions.

At later interaction stages, the PGP effect (IAA response, growth and development enhancement, cell structure rearrangement), already discussed in the general response, is enhanced in tomato plants grown in the presence of nitrogen, while N-starved plants seem to be less positively influenced from the bacterial interaction.

It might be hypothesised that the presence of Gd on plants that grow in the absence of nitrogen can improve the plant fitness, but only up to a certain extent: the balance between the bacterial induced growth stimulus and the actual availability of nitrogen in the substrate exceeds a threshold after which the plant

cannot sustain accelerated growth anymore and needs to limit this biomass accumulation.

It could thus be inferred that the interaction of *Gd* with a physiologically stressed host might add to this stressful state and cause a reduction in the beneficial effects of the bacterium towards the plant.

Results presented in this work are in line with previously reported studies showing that the nitrogen level can affect the bacterial ability to establish a fruitful symbiosis with plants: very high or too low N concentrations can be detrimental for a positive plant-bacterial symbiosis [27][198][170].

4.5.9.3. Strain-related effects

To obtain a clearer picture of the influence of the nitrogen fixation ability of Gd on the tomato plant response, an analysis of the gene sets that were specifically modulated by inoculation with either the WT strain or *nifD*$^{-}$ mutant strain was carried out.

4.5.9.3.1. Early interaction stages (1 dpi)

Firstly, while at early stages the response induced by the WT strain was quantitatively higher in comparison to the one induced by the *nifD*$^{-}$ strain, the late response of the plant to the *nifD*$^{-}$ strain was quantitatively higher than the one towards WT. The bacterial inoculum concentration was kept constant for both bacterial strains.

The main response elicited by the WT strain at early interaction stages in the presence of nitrogen in the growth substrate is the upregulation of genes related to cell structure modulation, lipid metabolism and genes that have previously been recorded to be strictly involved in the plant microbial interaction. Finding an upregulation of genes involved in phospholipid or fatty acids catabolism (four GDSL esterases/lipases and four alpha/beta-Hydrolase superfamily proteins and two 3-ketoacyl-CoA synthases, two acyl-[acyl-carrier-protein] desaturases) and biosynthesis (one acyl-[acyl-carrier-protein] hydrolase), in combination to the enhanced synthesis of genes involved in polysaccharide catabolism (three pectin lyase-like superfamily proteins and four pectinesterases, three beta glucanases) would lead to hypothesise the elicitation of cell wall and membrane rearrangement following plant exposure to the bacterium. This would be in line

with that reported in literature for plant-bacteria interactions in which endophytes produce enzymes that weaken the cell boundaries in order to enter the plants inner compartments [100]. Moreover, three early nodulin or nodulin like proteins, reported to be involved in symbiosis establishment in non nodulating species, were also upregulated [44].

A number of lectin receptor kinases and leucine-rich repeat receptor-like protein kinases were elicited. These are described as receptors that are commonly involved in endophytic- or plant associated bacteria recognition by the host plant and cell downstream signalling [183].

Nevertheless, upregulation of genes responsible for lignin biosynthesis (one cinnamyl alcohol dehydrogenase) and deposition in the Casparian strip (two CASP-like proteins) support the idea that an early defence response is also displayed by the plant towards WT Gd. In fact, five U-box domain containing proteins were found to be upregulated as well. They are usually found to be involved in the protein ubiquitinilation, a posttranscriptional modification that usually leads to protein degradation, indicating a certain amount of stress induced in the early interaction stages. These data seem to overall indicate that in the early stages of interaction between tomato plants supplied with a nitrogen source and WT Gd, the plant undergoes modifications in terms of cell wall and membrane rearrangement, fundamental for plant-bacteria symbiosis establishment, as well as the upregulation of signalling proteins that transduce the bacterial recognition signal throughout the cell.

In the case of plants grown in the absence of a nitrogen source in the nutrient solution, WT strain inoculation mostly induced the early downregulation of growth and development involved genes and genes related to the defence response. This latter downregulation of defence response would seem in contrast with the previously reported results relative to both the plant general response towards Gd and plant response in the absence of nitrogen at early interaction stages (this study): an upregulation of defence responses was observed in both cases. Nevertheless, among these genes were found a few glycin-rich proteins that are often involved in stress sensing and signalling. Most of the time, it has been shown that their accumulation is mostly localised in the vascular tissues and that their synthesis is part of the plant's defence system. Other separate types of glycin rich proteins have structures and functions similar to animal

cytokeratins or by a domain with typical RNA-binding motifs [153]. Three Avr9/Cf-9 rapidly elicited proteins, involved in plant signalling after bacterial recognition were upregulated as well. It thus seems that a signalling component of the defence response towards Gd was attenuated in this particular condition. Genes that belonged to growth and development categories included some genes involved in cell fate specification (CLAVATA3/ESR (CLE)-related 25-like protein and phytosulfokine 3 and cyclin-dependent kinase D-1), in repression of negative regulation of flower development (self-pruning protein and NAC domain containing protein 35) and seed germination (bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily proteins).
In addition, a very high number of pentatricopeptide repeat-containing proteins were upregulated, which have been implicated in RNA modification and processing, although their role has not been narrowed down to a specific function yet [137]. In this particular condition, it appears that the reaction of a nutritionally stressed plant towards this bacterium is to alleviate some stress signalling related pathways and to attenuate the expression of some genes related to cell fate specification.

Early stages tomato plant response to *nifD*$^-$ strain and in the presence of nitrogen in the plants' growth solution, defence and hormonal responses were mainly upregulated. It must be underlined that the strength of the elicited response was far lower than the one towards WT Gd.
These results are in line with those in the case of the plant response towards WT Gd: tomato plants elicit a very early defence response towards Gd interaction; although, the upregulation of genes stimulated by auxins was also detected: this could be due to the plant sensing of exogenous auxins produced by Gd. In fact, Gd has been assessed for its ability to produce auxins like IAA [173].
In the absence of nitrogen, the main elicited response was the upregulation of cell structure modulation, signalling, defence response and plant microbial interaction genes. Cell structure modulation genes include genes involved in polysaccharide catabolism (pectinesterase) and polymerisation (alpha-1,4-glucan-protein synthase and xyloglucan-specific endoglucanase inhibitor protein 2) probably involved in the early establishment of bacterial adhesion and cell wall modifications that lead to Gd entrance into plant roots. Signalling and

defence response related protein transcription was also elicited during the early stages of interaction with *nifD*$^{-}$. The plant microbial interaction genes, in this case, are mainly receptors and signalling proteins that have been reported in the literature to be often involved in plant recognition of endophytes or plant interacting bacteria [183].

Overall, *nifD*$^{-}$ has shown to elicit an early response that comprises, in both nitrogen feeding conditions, bacterial interaction with cell wall recognition and downstream signalling that elicits a defence response towards the bacterium, even though the extent of the transcriptional reaction seems to be rather contained. Nevertheless, in the case of nitrogen addition to the growth medium, the upregulation of a hormonal driven response was also observed, suggesting the possibility of an enhanced role of the hormonal component in the plant-bacterial interaction when Gd ability to fix atmospheric nitrogen is impaired.

In general, tomato plants' early reaction towards both tested Gd strains do not denote relevant differences if not in terms of number of modulated genes: WT Gd provokes a significantly stronger gene modulation (544 genes in the presence of N and 346 in the absence of N) in comparison to the *nifD*$^{-}$ (57 in the presence of N and 57 in the absence of N).

4.5.9.3.2. Later interaction stages (14 dpi)

At later interaction stages, the WT strain in the presence of nitrogen induced a downregulation of genes involved in cell structure modulation and transport related genes. Among the cell structure modulating downregulated genes, seven extensins were found. An increased expression of extensins is observed following plant exposure to pathogens and it plays a critical role in plant defence by strengthening the cell wall [29]. In this regard, a CASP-like protein, responsible for lignin deposition in the Casparian Strip of the endodermis and often seen as a barrier to diffusion towards roots inner compartments [115][172], was also downregulated. The downregulation of the expression of these proteins could be related to the establishment of a positive symbiosis between tomato plants and Gd. Nevertheless, a downregulation of some cell wall loosening genes like pectinesterases, xyloglucan endotransglucosylases/hydrolases, pectin lyase-like superfamily proteins, and cellulose synthase-like proteins was observed. This might be due to the fact that these genes, initially required for cell wall

loosening and bacterial entrance favouring in roots, after two weeks from bacterial contact with roots, are no longer required and thus downregulated. Downregulation of genes like ABC transporters was also observed. As previously mentioned, these proteins are often involved in the excretion of toxic compounds and also of isoflavonoids, that are included in plant produced complex compounds that are capable of attracting beneficial microorganisms [181][215], but are not required once the symbiosis has established. Moreover, the downregulation of four kinesin proteins was found. It has been demonstrated how some kinesin-like proteins are involved in microtubule control of the oriented deposition of cellulose microfibrils [260]. The regulation of these genes, along with the downregulation of one cellulose synthase-like gene, can thus be implicated in the tuning of cellulose deposition and cell wall strength modulation.

In the absence of nitrogen, at later stages the WT strain mainly elicited a downregulation of cell structure modulation genes and oxidative stress genes. In particular, two CASP-like proteins and seven Dirigent proteins were found to be downregulated. Both proteins are involved in the lignin deposition in plant cells; the first one at the Casparian Strip level and the second one in the cell wall. Lignin deposition has been associated with the plants attempt to protect itself from esogenous attacks [115][172]. The observed downregulation of these proteins at 14 dpi could be related to a downturn in plants defence responses that had been elicited as a first reaction towards WT Gd. This also would be in line with the observed decreased synthesis of catalases, oxidases and respiratory burst oxidases. In fact, it has been reported that Gd can elicit a preliminary oxidative stress induction in host plants but later on, after symbiosis establishment, the defensive oxidative burst is decreased [3]. Current results are in line with this latter finding. GO enrichment analysis has confirmed an enrichment of downregulated pathways relative to oxidative stress but also an enrichment of auxin response genes. In this condition, the level of gene upregulation (327 genes) was similar to downregulation (361 genes). Elicitation of genes involved in transport, growth and development and hormonal response waere found. Transport genes included general molecules and nutrients transporters, which is in line with what previously found about Gd being able to

favour plant nutrient uptake for the host plant benefit [170][216]. Plant growth promoting genes were upregulated included root meristem growth factors, cell fate specification, phototropism regulation and general plant development involved genes. The mainly elicited hormonal response involved auxin efflux genes, jasmonic acid, ABA and ethylene responsive factors.

Interestingly, GO enrichment analysis also indicated an upregulation of genes implicated in polysaccharide catabolism and polyamine biosynthesis. This latter finding, correlates well with downregulation of the oxidative stress related genes found in response to this condition: it is reported that the stimulation of polyamine biosynthesis is associated with the scavenging or reactive oxygen species, H_2O_2 in particular, in plants cells [156][144]. Polyamines (PA), for their important roles in diverse plant growth and developmental processes and in environmental stress responses, are considered as a new kind of plant biostimulant [42]. Data from the literature indicate that changes in PA metabolism constitute a key adaptive response of the plant towards both pathogenic and beneficial bacteria and that their occurrence determines the development of the interaction. In turn, evidence suggests that some microorganisms are able to perturb plant PA metabolism in order to adjust it to their own requirements [104]. It has been shown that changes in PA concentration might affect, for example, the control of root nodule number and biomass [246][233]. Moreover, a common observation under nitrogen limiting conditions is the decrease in PAs total concentration in plants [239]. In light of this, the detection of an upregulation in PA transcription in plants supplied with no N and inoculated with the nitrogen fixing WT strain of Gd provides an interesting indication of how the inoculum with this bacterium benefits and modulates the host plant N metabolism.

In the case of the plant response to *nifD*$^-$ at 14 dpi in the presence of nitrogen, the upregulation of cell structure modulation, transport and lipid metabolism genes was predominant.

Many lignin deposition genes were elicited in this condition (five CASP-like proteins, one cinnamyl alcohol dehydrogenase, ten dirigent proteins). These results seem to display how the plant maintains high the defence barriers towards the mutant bacterium, even at late stages after inoculation.

Conversely, expansin genes, which are found to stimulate plant growth, cell wall loosening genes, like pectate lyases and endoglucanases, were also upregulated; these might be both involved in the establishment of plant-bacteria symbiosis and in plant cell accretion and development. Upregulation of genes involved in the general transport of nutrients and sugars was also detected, confirming the ability of Gd, independently from its ability of fixing nitrogen, to favour nutrient uptake for plant utilisation. Finally, hydrolases and phospholipases transcription was found to be elicited, probably concurring with the action of pectate lyases and endoglucanases for the establishment of plant bacteria symbiosis through cell membrane and cell wall modifications. Moreover, a number of GDSL-like lipase/acylhydrolase superfamily proteins were found to be upregulated: these proteins are reported to be involved in the plant defence reaction towards exogenous attacks [72]. Overall, the late response to *nifD*$^{-}$, in the presence of available nitrogen in the plant growth substrate, seems to involve the maintaining of the defence alert towards *nifD*$^{-}$ Gd, but also to experience a beneficial PGP effect provided by the improvement in nutrients transport and uptake and of cell growth and expansion. When plants are not excessively stressed, like in this experiment in the case of N supply to the growth medium, the nitrogen fixation impaired mutant strain can still provide a beneficial effect to plants.

In the absence of nitrogen, the plant main reaction towards *nifD*$^{-}$ is the downregulation of genes involved in transport and cell structure modulation. The downregulation of cell wall loosening enzymes like endoglucanases, pectate and pectine lyases, can be an indication of a reduction in the active interaction of bacteria with the plant cell wall. Moreover, downregulation of the transcription of cellulose synthases and expansins also indicate a diminished drive towards growth and development. This could be associated to the scarce availability of available nutrients that the plant could employ for growth. In this condition, also various nutrients and sugar transporters were downregulated. This might be in opposition to the previously observed, both in this and in previous studies, Gd behaviour of stimulating nutrient transport as part of its PGP effect. In fact, in the general response to Gd (this study), it was observed that an upregulation of nutrient transporters and carriers was induced at later

stages post inoculation by both WT and *nifD*$^{-}$ strains. This latter observation of some specific transporters to be downregulated by *nifD*$^{-}$ might be ascribable to a reduced drive of the plant towards active growth in a starvation condition.
It might thus be hypothesised that when the plant is already exposed to a nutritional stress the interaction with *nifD*$^{-}$ mutant becomes less favourable.

However, from the quantification through maceration data of the current study, no difference in colonisation rate was detected between the N and NoN conditions; this might be due to the fact that the defence response towards the bacterium is still in progress and its effect on bacterial colonisation is not yet detectable. In support of this theory, previous studies on sugarcane Gd inoculated plants have indicated that the bacterial population of Gd experiences a decline from 35 dpi onwards [155].

5. Conclusions and Future Perspectives

This work focused on the investigations of the interactions between the nitrogen fixing diazotroph *Gluconacetobacter diazotrophicus* (Gd) and tomato plants. This crop was chosen as target of our study for its commercial value in the worldwide economy and for its widespread cultivation both in Europe and overseas countries. The optimisation of Gd inoculation and agronomic employment on tomato growth would positively impact the efficiency of cultivation as well as its sustainability: the substitution of chemical N based fertilisers with biofertilisers would drive the agricultural practices towards a more virtuous management.

Primarily, an inoculation protocol that would consistently be applicable to tomato plants was needed to assess the nature of the interactions between Gd and tomato plants. Preliminary experiments were conducted on seed coating inoculation strategies and subsequent in-soil growth, as well as in rockwool substrate growth. In the last decades, seed coating has acquired increasing relevance as a mean of delivery of biofertilisers or biopesticides to the target crops [196]. Promising results were obtained in terms of plant growth promotion induced by the inoculated bacterium but, due to the high variability of such systems, experimental consistency was not always achievable. The most promising experimental setup implied a root soaking in bacterial suspension protocol that led to the achievement of a more controllable hydroponic system for bacterial inoculation. In fact, to obtain a sufficiently stable system where variables could be narrowed down and finely tuned, a hydroponic system in which plants inoculation was carried out through root dipping was tested. The hydroponic system in this study has proved to be a valid setup for consistent tomato plants inoculation with Gd and was used to investigate Gd effects on plants.

In this hydroponics setup, bacterial localisation on inoculated plants was also observed. This was done both quantitatively through maceration, serial dilution and colony counting, and qualitatively with the employment of GUS or GFP tagged strains of WT Gd. The most abundant bacterial concentration was found in the plant root system; a tenfold less abundant bacterial concentration was

detected in plants above-ground organs (leaves and shoots). Moreover, from microscopy analysis on root samples, bacteria showed to be mainly localised on the root surface; an organic matrix was frequently observed surrounding cell clutters adhering to the root. Gd is known to produce an extracellular polysaccharide called levan that has a strong role in O_2 tolerance and biofilm formation [247], [146]. The establishment of a biofilm like matrix could be one of the important steps in Gd attachment and interaction with the plant root system. Indications of bacterial intracellular colonisation were also evident from observations of bacterial cells strictly confined inside the plant cell boundaries. Furthermore, bacterial cells could also be spotted in proximity of the plant vascular tissues. This finding would support the proposed strategy for which Gd would spread from roots to above ground organs through colonisation of and movement through vascular tissues [45]. Further investigations will be needed to confirm how and in which conditions Gd enters the intracellular compartment. The production of protoplasts starting from Gd inoculated plant tissues would allow to visualise the internalisation of bacteria in the plant cell. This would also possibly be the starting point of the production of regenerated, already colonised shoots that would be harbouring Gd in their inner compartments. Given the fact that tomato cultivation methods in glasshouse often comprise grafting, this would pose the interesting perspective of testing the use of Gd inoculated, regenerated plants as either rootstock or scion.

The differential effect of the WT Gd strain in comparison to a *nifD*$^-$ nitrogen fixation impaired mutant strain was assessed. This latter experiment was crucial in evaluating the nitrogen fixation contribution to the plant growth promoting (PGP) effect provided by Gd. In fact, previous studies have demonstrated that Gd is able to provide a wide range of different beneficial effects to host plants: Gd can produce plant growth hormones, such as auxins and gibberellins [13],[8],[226]. In this study, the WT Gd inoculation led to an improvement in host plants growth (increased shoot height, plant fresh weight and chlorophyll content) in comparison to both untreated (UT) and *nifD*$^-$ treated plants; nevertheless, *nifD*$^-$ inoculated plants displayed an enhanced phenotype in terms of growth in comparison to UT plants, although no improvement in the chlorophyll content was observed. These data support the hypothesis for which

the ability of Gd to provide a beneficial effect to colonised plants is not entirely dependent to its N fixation capability, but this latter feature provides further significant improvement to plant health.

In light of this, to assess the amount of bacterially fixed nitrogen incorporated by tomato plants, a ^{15}N tracer experiment was conducted. A bacterial suspension of either the WT or *nifD*$^-$ strain was used to inoculate tomato plants through root dipping in the hydroponic system. Fourteen days after the inoculation (14 dpi), plant material was harvested, and chlorophyll was extracted. Obtained chlorophyll was sent to be analysed through Liquid Chromatography Mass Spectrometry (LC-MS) for the incorporation of fixed atmospheric ^{14}N in chlorophyll molecules. Due to COVID19 restrictions, a strong delay was experienced in the analysis of these samples, which are currently being processed in the School of Chemistry at Nottingham University. Further investigations on the quantification of the bacterially fixed nitrogen utilised by the host plant would give fundamental insights on the Gd-plant symbiosis outcome. The use of a gas tight chamber to supply the inoculated plants with a ^{15}N labelled gaseous mixture could be a complementary experiment that would strengthen the results coming from the liquid ^{15}N feeding experiment.

With the aim of optimising the inoculation efficiency and beneficial effect of Gd interaction with the host plant, the molecular reactions that are involved in the symbiosis establishment of Gd *in planta* were targeted with a transcriptomic analysis. Root samples were harvested at 1- and 14-days post inoculation (dpi) of plants inoculated with either the WT or *nifD*$^-$ Gd strain, in either the absence (NoN) or presence (N) of 2 mM KNO_3 in the plant growth solution. Modulated genes were categorised into functional classes and plant response to bacterial exposure was analysed in terms of a) general response of the plant to Gd, b) response of the plant towards Gd considering the N nutritional state of the plant and c) the strain specific elicited response, at either early or later interaction stages.

Firstly, the tomato plants general response was analysed. At early interaction stages, a general defence response mediated both by cell wall strengthening genes (lignin synthesis) and by hormonal response (ABA and Ethylene response) was observed. This was also accompanied by an upregulation of

oxidative burst inducing genes, in accordance with what reported in literature during the early interactions of the Gd Pal5 strain with rice roots [3].
At later interaction stages, defence response appeared to remain active, although this was complemented by an upregulation of growth promoting genes and nutrient transporters transcription. Moreover, a downregulation of ethylene synthesis genes was detected: a previous study has reported the ability of some endophytic bacteria to improve plant growth by reducing the synthesis of ethylene in plants [88].
Interestingly, the component 7 of the exocyst complex was also found to be upregulated: this protein complex is a major component of the intracellular vesicular trafficking pathway and has been reported to be involved in the Solanaceae defence response to a number of pathogens [57]. Exocyst subunits were also reported to play an important role during arbuscular mycorrhizal symbiosis, suggested by their accumulation at sites of microbial contact and role in the formation of the perifungal membrane [75][258]. Interestingly, one of the colonisation mechanisms proposed for Gd inter/intracellular establishment and migration inside host plants, involves the formation of vesicle-like structures [45].

Secondly, the influence of nitrogen nutritional level, in form of KNO_3, was assessed.
At early stages (1 dpi), in both the presence and absence of KNO_3, tomato plants put in place a general defence response, which appears to be stronger in the presence of KNO_3: upregulation of lignin, cutin and suberin synthesis and deposition genes was detected; possibly, a plant that is in an healthier physiological state can put up a stronger defence response towards to a possible threat. In fact, the early response of host plants towards beneficial microorganisms is often similar to the one elicited by pathogens. Nevertheless, in both conditions a putative positive PGP effect (underlined by upregulation of cell structure modification and development genes) can already be detected at 1 dpi, even though more evidently in non-N starved plants. The initial steps of the establishment of a positive symbiosis with the beneficial bacterium might be indicated by the observed elicitation of a potential ABC-mediated plant-bacteria crosstalk, cell wall loosening enzymes and lateral root inducing genes

upregulation. On the contrary, the downregulation of flavonoids biosynthesis was observed specifically in NoN condition. The production of these compounds has been noted to be involved in the recruitment mechanism of some beneficial microorganisms [181]. Hypothetically, downregulation of flavonoids could be a strategy for reducing attractiveness towards symbiotic bacteria: an already physiologically starved plant might be driven towards avoiding the establishment of a bacterial symbiosis, which is an energy demanding process.

At later interaction stages (14 dpi), the presence of N in the growth substrate appeared to enhance the PGP effect exerted by Gd if compared to plants grown in the absence of N: IAA response, growth and development enhancement, cell structure rearrangements were observed in N availability. Moreover, in N-starved plants, an upregulation of stress and defence response genes was still detected at later stages of interaction.

From these data it could be inferred that a reduction in the beneficial effects of the bacterium towards the plant can be ascribed to an additional stress that the interaction of Gd can cause to an already physiologically stressed host.

Arguably, Gd can improve the host plant growth in complete absence of nitrogen in the substrate only up to a certain extent. The accelerated growth promoted by the bacterium is dependent on the limiting nutrients concentration and thus, beyond a certain point, the plant will require to limit the resources devoted to the improved growth for the benefit of basal physiological functions.

Results presented in this work would corroborate previously reported studies that show how the nitrogen feeding level can affect the establishment of a fruitful symbiosis of Gd with host plants [27][198][170]. BNF in Gd is affected by the nutritional state of the host plant. Gd BNF was observed to be inhibited by high levels of nitrogen fertilisation (250-300 N ha^{-1} yr^{-1}) in field conditions [67], while a study by Stephan et al. (1991) has shown no BNF inhibition *in vitro* at up to 10 mM in KNO_3 added to LGI growth medium or at low amounts of ammonium-based fertilisers (no inhibition up to 1 mM $(NH_4^+)_2SO_4$ added to LGI growth medium) [228]. Moreover, colonisation efficiency is also influenced by the N presence in the growth substrate: abundance of diazotrophic bacteria isolated from maize plants grown in the absence of N fertilisation was shown to be reduced in comparison to the amount of bacteria retrieved from plants grown with the addition of either 40 kg N ha^{-1} or 80 kg N ha^{-1} as NH_4NO_3 [198].

Although, from the quantification through maceration data presented in this work, no difference in colonisation rate was detected between the N and NoN condition; this might be due to the fact that, at the time of the assessment, the plant defence response towards the bacterium was still in progress and its effect on the bacterial colonisation was not yet detectable. In support of this theory, a previous study on sugarcane Gd inoculated plants has shown how the bacterial population of Gd undergoes a decline from 35 dpi onwards [155]. It might thus be hypothesised that the timepoint at which the assessment of the colonisation rate was carried out in the present work was too early to observe any variations in the bacterial abundance. This particular aspect, also in light of the transcriptomic data outcome, will need further clarifications and investigations at more advanced growth stages.

Finally, genes that were specifically modulated by either WT or *nifD*$^-$ strains, at either late or early interaction stages and in either N or NoN nutritional state, were analysed.

Data collected seem to overall indicate that in the early stages of interaction of WT Gd with inoculated tomato plants supplied a with nitrogen source, the plant undergoes modifications in term of cell wall and membrane rearrangement, fundamental for plant-bacteria symbiosis establishment, as well as the upregulation of signalling proteins that transduce the bacterial recognition signal throughout the cell.

In the case of WT inoculation in NoN growth conditions, it appears that the reaction of a nutritionally stressed plant towards this bacterium is to alleviate some stress signalling related pathways and to attenuate the expression of some genes related to cell fate specification.

In the case of *nifD*$^-$ inoculation, the early response comprises, in both nitrogen feed conditions, genes involved in bacterial interaction with cell wall, recognition and downstream signalling that elicits a defence response, even though the extent of the transcriptional reaction seems to be quantitatively rather contained. Nevertheless, in the case of nitrogen addition to plants feed, the upregulation of a hormonal driven response was also observed, suggesting the possibility of an enhanced role of the hormonal component (auxin metabolism) in the plant-bacterial interaction when Gd ability to fix atmospheric nitrogen is

impaired. Overall, the tomato plant early reaction towards both tested Gd strains do not denote relevant differences, if not in terms of number of modulated genes: WT Gd provokes a significantly stronger gene modulation (544 genes in the presence of N and 346 in the absence of N) in comparison to the one induced by *nifD*$^{-}$ (57 in the presence of N and 57 in the absence of N).

Focusing on later interaction stages (14 dpi), the WT inoculation in the presence of N was firstly addressed. Downregulation was predominant on genes upregulation. Cell structure modulation was highly downregulated. The downregulation involved genes implicated in cell wall strengthening and lignin deposition at the Casparian strip level, generally involved in the early response towards the penetration of pathogens [29] [115][172]. The reduced expression of these proteins could be thus related to the establishment of a positive symbiosis between tomato plants and Gd. Nevertheless, a downregulation of some cell wall loosening genes was also observed. This might be ascribed to the fact that these genes, previously required for cell wall loosening and bacterial entrance favouring in roots, after two weeks from bacterial contact with roots, are no longer required and thus downregulated.

In the absence of nitrogen, at 14 dpi, WT strain mainly elicited a downregulation of cell structure modulation genes and oxidative stress involved genes. In particular, proteins that are involved in the lignin deposition in plant cells, both at the Casparian strip and at the cell wall level. The observed downregulation of these proteins at 14 dpi could be related to an attenuation of the plants defence responses that had been elicited as first reaction towards WT Gd. This also would be in line with the observed decreased synthesis of respiratory burst oxidases. In fact, it has been reported that Gd can elicit an initial oxidative stress induction in host plants but later on, after symbiosis establishment, the defensive oxidative burst is attenuated [3]. Results from the present study would be in line with this latter finding. In this condition, the gene upregulation (327 genes) was although quantitatively similar to downregulation (361 genes). Elicitation of genes involved in transport, growth and development (e.g., root meristem growth factors, cell fate specification, phototropism regulation and general plant development involved genes) and hormonal response (auxin transporters, Jasmonic Acid, ABA and Ethylene responsive factors) was found. Upregulated

transport genes included general molecules and nutrients transporters, and this is in line with what previously found about Gd being able to favour plants nutrients uptake for the host plant benefit [170][216].
Interestingly, GO enrichment analysis also indicated an upregulation of genes implicated in polysaccharides catabolism and polyamine biosynthesis. This latter finding, well correlates with the downregulation of the oxidative stress related genes that was found in this condition: it is reported that the stimulation of polyamine biosynthesis is associated with the scavenging or reactive oxygen species, H_2O_2 in particular, in plants cells [156][144]. Polyamines (PA), for their important roles in diverse plant growth and developmental processes and in environmental stress responses, are considered as a new category of plant biostimulants [42]. Moreover, a commonly observed indication of nitrogen limiting conditions is the decrease in PAs total concentration in plants [239]. In light of this, the detection of an upregulation in PA synthesis genes in plants supplied with no N source and inoculated with the nitrogen fixing WT strain of Gd provides an interesting indication of how the inoculation with this bacterium benefits and modulates the host plant N metabolism. Investigations on this aspect would be an interesting research topic to bring further. Quantification of these compounds in different growth conditions applied to inoculated plants so to assess the influence of Gd on their metabolism would provide important insight.

The late response to *nifD*$^-$, in the presence of available nitrogen in the plant growth substrate, seems to involve the maintaining of the defence alert towards *nifD*$^-$ Gd, but also to experience a beneficial PGP effect provided by the improvement in nutrients transport and uptake and of cell growth and expansion. When plants are not excessively stressed, like in the case of N condition in this experiment, the nitrogen fixation impaired mutant strain can still provide a beneficial effect to plants.

In the absence of nitrogen, the plant main reaction towards *nifD*$^-$ is the downregulation of genes involved in transport and cell structure modulation. The downregulation of cell wall loosening enzymes like endoglucanases, pectate and pectine lyases, can be an indication of a reduction in the active interaction of bacteria with the plant cell wall: the bacterium has probably already

established itself in the inner compartments of the host plant. Moreover, downregulation of transcription of cellulose synthases and expansins also seems to indicate a diminished drive towards growth and development. This could be associated to the scarce availability of available nutrients that the plant could employ for growth. In this condition, also various nutrients and sugar transporters were downregulated. This might seem in opposition to the previously observed, both in this and in previous studies, Gd behaviour of stimulating nutrients transport as part of its PGP effect. In fact, in the "General Response to Gd" section, it was observed that an upregulation of nutrient transporters and carriers was induced at 14 dpi by both WT and *nifD*$^-$ strains. This latter observation of some specific transporters to be downregulated by *nifD*$^-$ might be ascribable to a reduced drive of the plant towards active growth in a starvation condition. It might thus be hypothesised that when the plant is already exposed to a nutritional stress the interaction with the *nifD*$^-$ mutant becomes slightly less favourable.

Further investigations will be needed to clarify the nature of the interactions between tomato plants and Gd at later stages in order to better evaluate the dynamics of the plant and bacterial behaviour in long term symbiosis maintenance. Moreover, a key question to be addressed following this study would be to investigate the molecular pathways involved in the symbiosis establishment from the bacterial side. To assess the genes that are mainly implicated in plant recognition, attachment and entrance would be a key step. That would later lead to the creation of functional mutants of Gd to evaluate the importance of candidate genes in the bacterium colonisation strategy.

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8. Appendices

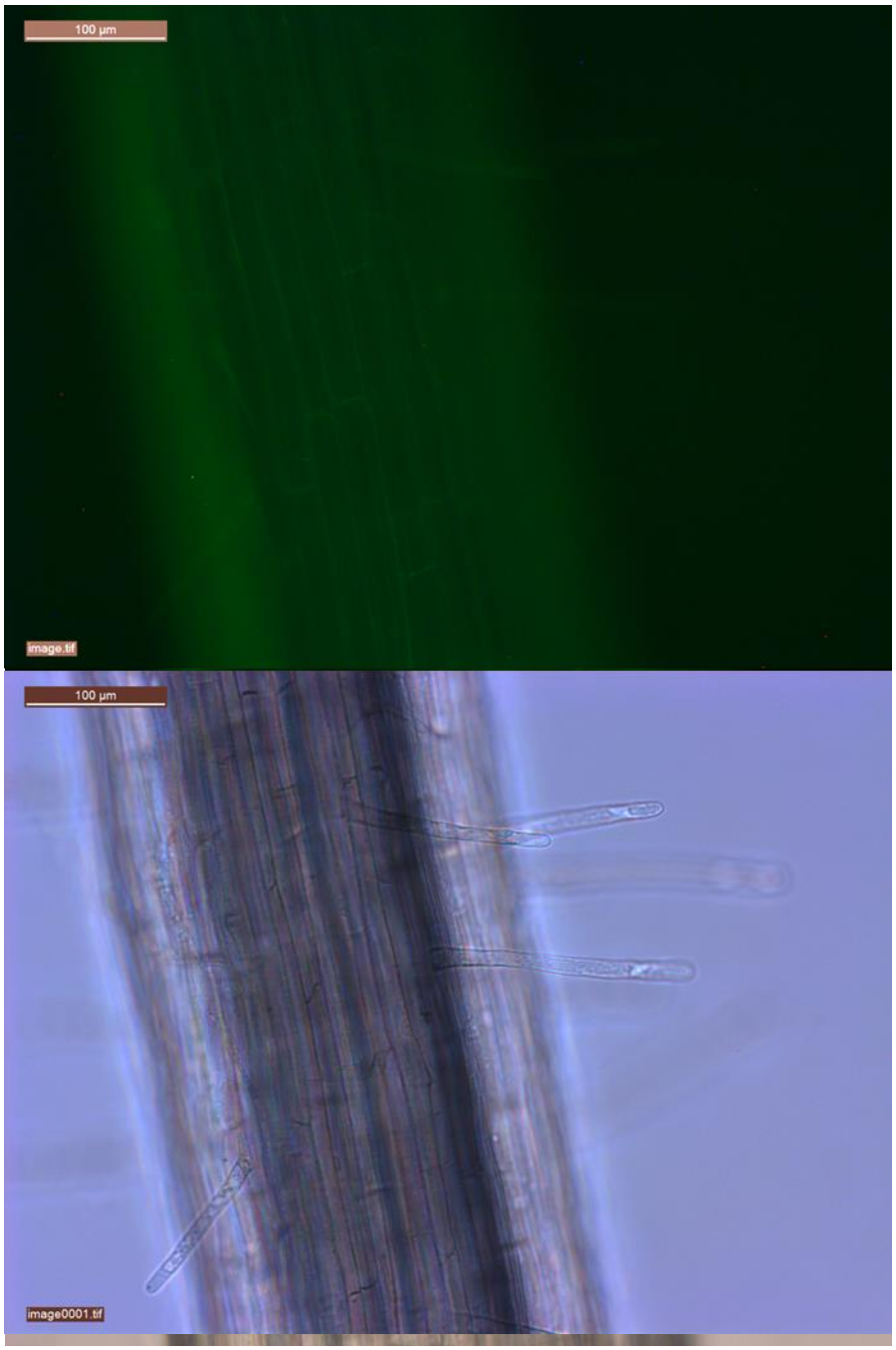


Fig. S 1. Fluorescence microscopy of roots of non-inoculated hydroponically grown Money Maker tomato plants. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 6 dpi in the presence of 2mM KNO_3 in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

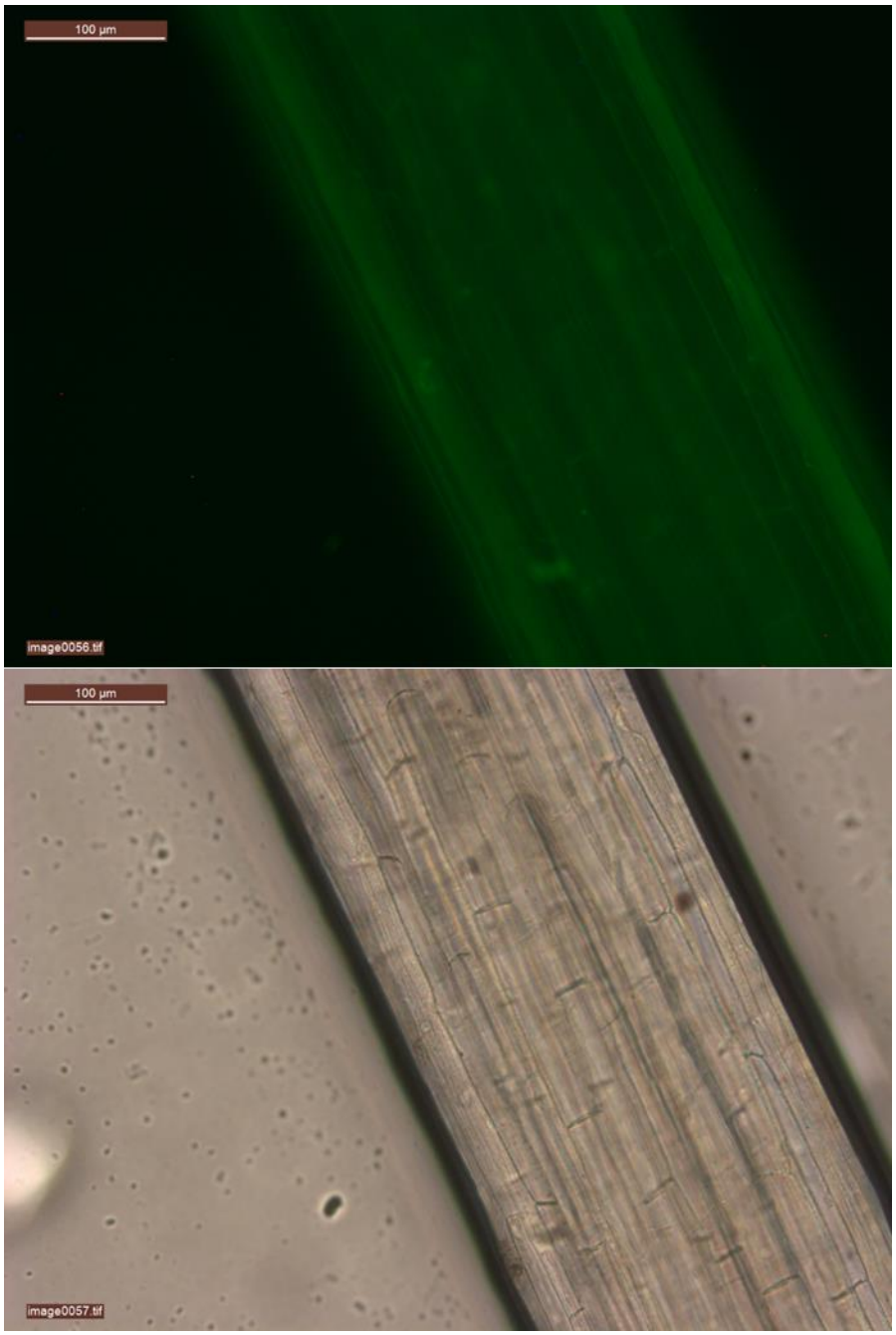


Fig. S 3. Fluorescence microscopy of roots of hydroponically grown Money Maker tomato plants inoculated with WT strain of Gd. Observation was carried out after thorough wash in 10 mM $MgCl_2$, at 1 dpi in the presence of 2mM KNO_3 in the modified Hoagland solution. The corresponding brightfield picture is reported as a reference.

Table S1. Legend of abbreviation codes for supplementary tables (S2 to S9).

Functional Annotation Classes Abbreviation	Description
C	Carbon metabolism (includes photosynthesis related genes)
2M	Secondary Metabolism
G	Growth and Development
P	Protein metabolism
K	Kinase/Phosphatase
D	Defence
TR	Transport
E	Energy metabolism
OX	Oxidative Stress
T	Transcription
S	Signal transduction
DNA	DNA metabolism and replication
N	Nitrogen metabolism
H	Hormonal response
STR	Response to Stress
CS	Cell Structure (Included Cell Wall Organisation)
RNA	RNA Metabolism and Interactions
AM	Aminoacid Metabolism
PMI	Plant Microbe Interaction
NA	Not Assignable

Table S 2. List of differentially expressed genes (DEGs) modulated in tomato roots both after inoculation with Gluconacetobacter diazotrophicus AZ0019 WT and nifD- strain at one day post inoculum (dpi), in both the absence and the presence of 2 mM KNO3 in plants growth medium: plant general early response. *Clustering results of the DEGs, classified as genes significantly modulated at 1 dpi (in bold, P ≤ 0.01 and Log2 (fold change) ≥ 1 or ≤ -1) by G. diazotrophicus AZ0019 WT and nifD- mutant strain in both the absence (WT & nifD- NoN) and the presence of 2 mM KNO3 (WT & nifD- N) in the growth substrate. Tomato gene identifier (ITAG3.2 release), Log2-transformed fold change values and P values calculated for each pairwise comparison between WT inoculated and nifD- inoculated simples are reported. Protein description and abbreviation codes of functional classes were assigned on the basis of the protein description and function. Gene ontology (GO) terms were based on the ITAG3.2 release (https://solgenomics.net/organism/Solanum_lycopersicum/genome).*

Gene ID	WT N	P.Value	*nifD* - N	P. Value	WT NoN	P. Value	*nifD*- NoN	P.Value	Cluster	Functional Class	Gene Description	GO
Solyc07g007420.3	**6.24E+00**	**2.18E-12**	**2.03E+00**	**4.15E-04**	**1.75E+00**	**1.78E-03**	**1.98E+00**	**5.36E-04**	General response 1dpi	PMI	F-box/LRR-repeat protein, putative (AHRD V3.3 *-* B9RVD1_RICCO)	
Solyc07g026650.3	**4.12E+00**	**1.67E-09**	**2.34E+00**	**2.25E-05**	**1.64E+00**	**1.30E-03**	**2.00E+00**	**1.60E-04**	General response 1dpi	H	1-aminocyclopropane-1-carboxylate oxidase 5	GO:0016491|GO:0055114|
Solyc06g059740.3	**3.44E+00**	**4.94E-17**	**1.63E+00**	**9.53E-10**	**1.53E+00**	**3.41E-09**	**1.12E+00**	**8.59E-07**	General response 1dpi	2M	Alcohol dehydrogenase (AHRD V3.3 *** ADH_MALDO)	GO:0055114|
Solyc01g099620.3	**3.35E+00**	**1.05E-14**	**1.49E+00**	**2.24E-07**	**1.66E+00**	**3.20E-08**	**1.39E+00**	**7.20E-07**	General response 1dpi	OX	Respiratory burst oxidase, putative (AHRD V3.3 *** B9RFA3_RICCO)	GO:0004601|GO:0050664|GO:0055114|GO:0005509
Solyc02g067440.3	**3.18E+00**	**2.60E-12**	**1.81E+00**	**2.04E-07**	**1.91E+00**	**7.59E-08**	**2.13E+00**	**1.09E-08**	General response 1dpi	D	meloidogyne-induced giant cell protein DB114	GO:0016702|GO:0055114|
Solyc02g090120.1	**3.18E+00**	**1.84E-14**	**1.64E+00**	**2.23E-08**	**1.35E+00**	**6.96E-07**	**1.57E+00**	**5.42E-08**	General response 1dpi	G	LOW QUALITY:Inositol 1,4,5-trisphosphate receptor-interacting protein-like 2 (AHRD V3.3 -** A0A1D1XL30_9ARAE)	
Solyc07g055690.1	**3.03E+00**	**1.71E-11**	**1.23E+00**	**1.02E-04**	**1.74E+00**	**6.82E-07**	**1.33E+00**	**3.58E-05**	General response 1dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** G4XXY5_NICAT)	GO:0048544|
Solyc02g077240.3	**3.00E+00**	**1.75E-14**	**1.33E+00**	**3.41E-07**	**1.66E+00**	**6.17E-09**	**1.43E+00**	**9.26E-08**	General response 1dpi	C	Pyruvate decarboxylase (AHRD V3.3 *** Q1I1D9_CITSI)	GO:0000287|GO:0030976|GO:0003824|GO:0030976
Solyc11g069240.2	**2.79E+00**	**3.35E-11**	**2.56E+00**	**2.07E-10**	**1.49E+00**	**3.54E-06**	**1.61E+00**	**1.10E-06**	General response 1dpi	DNA	Zinc finger family protein (AHRD V3.3 *** S8C619_9LAMI)	GO:0003676|GO:0046872
Solyc04g080540.2	**2.74E+00**	**5.58E-13**	**1.38E+00**	**4.96E-07**	**1.26E+00**	**1.97E-06**	**1.05E+00**	**2.73E-05**	General response 1dpi	DNA	DNA polymerase epsilon catalytic subunit A, putative (AHRD V3.3 *** A0A061FCM9_THECC)	
Solyc12g088000.2	**2.65E+00**	**7.58E-06**	**1.90E+00**	**4.63E-04**	**2.02E+00**	**2.46E-04**	**2.43E+00**	**2.43E-05**	General response 1dpi	AM	Tyrosine aminotransferase (AHRD V3.3 *** E2JFA7_PERFR)	GO:0003824|GO:0003824|GO:0009058|GO:0030170
Solyc11g011590.2	**2.51E+00**	**2.88E-08**	**1.30E+00**	**3.95E-04**	**2.92E+00**	**1.55E-09**	**1.13E+00**	**1.55E-03**	General response 1dpi	H	GRAM domain-containing protein / ABA-responsive protein-related (AHRD V3.3 *** A0A061E267_THECC)	
Solyc04g014510.3	**2.44E+00**	**9.92E-09**	**1.06E+00**	**1.30E-03**	**2.68E+00**	**1.57E-09**	**1.12E+00**	**7.42E-04**	General response 1dpi	N	glutamine synthase	GO:0003824|GO:0004356|GO:0006542|GO:0006807
Solyc01g066910.3	**2.29E+00**	**7.80E-08**	**1.74E+00**	**6.90E-06**	**2.13E+00**	**2.75E-07**	**1.88E+00**	**2.02E-06**	General response 1dpi	NA	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MM18_ARALL)	
Solyc12g087940.2	**2.22E+00**	**1.52E-04**	**1.64E+00**	**2.94E-03**	**1.94E+00**	**6.33E-04**	**1.51E+00**	**5.59E-03**	General response 1dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061FET5_THECC)	GO:0004190|GO:0006508|
Solyc01g080020.2	**2.16E+00**	**1.46E-05**	**1.20E+00**	**6.44E-03**	**3.40E+00**	**7.61E-09**	**1.48E+00**	**1.16E-03**	General response 1dpi	P	Eukaryotic aspartyl protease family protein, putative (AHRD V3.3 *** A0A061ELJ0_THECC)	GO:0004190|GO:0006508|
Solyc03g120870.3	**2.07E+00**	**2.19E-06**	**1.61E+00**	**7.20E-05**	**1.73E+00**	**2.88E-05**	**1.24E+00**	**1.25E-03**	General response 1dpi	CS	CASP-like protein (AHRD V3.3 *** K4BMN6_SOLLC)	
Solyc02g078160.3	**2.03E+00**	**4.90E-06**	**1.01E+00**	**8.13E-03**	**2.25E+00**	**1.00E-06**	**1.04E+00**	**6.77E-03**	General response 1dpi	NA	DUF506 family protein (AHRD V3.3 *** G7IPT8_MEDTR)	
Solyc02g082910.3	**2.01E+00**	**2.48E-09**	**1.02E+00**	**1.23E-04**	**1.81E+00**	**1.86E-08**	**1.08E+00**	**6.08E-05**	General response 1dpi	2M	CoA ligase (AHRD V3.3 *** A0A0K9NMT8_ZOSMR)	GO:0003824|GO:0008152|
Solyc07g054780.1	**1.94E+00**	**1.27E-09**	**1.37E+00**	**7.59E-07**	**1.17E+00**	**7.82E-06**	**1.75E+00**	**1.00E-08**	General response 1dpi	D	LOW QUALITY:Wound-responsive family protein (AHRD V3.3 *** AT4G10265.1)	
Solyc09g075420.3	**1.89E+00**	**2.15E-10**	**1.18E+00**	**1.30E-06**	**1.11E+00**	**3.30E-06**	**1.02E+00**	**1.14E-05**	General response 1dpi	H	ethylene response factor E.1	GO:0003677|GO:0003700|GO:0006355
Solyc02g090470.3	**1.86E+00**	**4.50E-07**	**1.07E+00**	**7.07E-04**	**1.24E+00**	**1.44E-04**	**1.05E+00**	**8.61E-04**	General response 1dpi	OX	Peroxidase (AHRD V3.3 *** K4BCJ6_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744
Solyc01g080570.3	**1.71E+00**	**1.66E-06**	**1.30E+00**	**7.57E-05**	**1.75E+00**	**1.17E-06**	**1.20E+00**	**2.00E-04**	General response 1dpi	DNA	inosine-uridine preferring nucleoside hydrolase family protein (AHRD V3.3 *** AT5G18860.2)	
Solyc08g007480.2	**1.65E+00**	**2.21E-06**	**1.69E+00**	**1.57E-06**	**1.88E+00**	**2.70E-07**	**1.15E+00**	**2.70E-04**	General response 1dpi	NA	DUF1442 family protein (AHRD V3.3 *** G7KG69_MEDTR)	
Solyc11g006730.1	**1.64E+00**	**1.56E-04**	**1.42E+00**	**7.14E-04**	**1.91E+00**	**2.24E-05**	**1.97E+00**	**1.43E-05**	General response 1dpi	STR	Germin-like protein 1 (AHRD V3.3 *** B9HVV6_POPTR)	GO:0030145|GO:0045735
Solyc07g043000.3	**1.60E+00**	**2.92E-04**	**1.21E+00**	**3.94E-03**	**1.55E+00**	**3.99E-04**	**1.25E+00**	**2.99E-03**	General response 1dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *-* AT3G22142.1)	
Solyc03g113130.3	**1.57E+00**	**9.70E-08**	**1.38E+00**	**8.50E-07**	**1.07E+00**	**3.66E-05**	**1.16E+00**	**1.19E-05**	General response 1dpi	E	2-aminoethanethiol dioxygenase (AHRD V3.3 *** A0A0B0PVN9_GOSAR)	GO:0016702|GO:0055114|
Solyc04g077220.3	**1.55E+00**	**3.46E-04**	**1.98E+00**	**1.75E-05**	**2.00E+00**	**1.48E-05**	**1.28E+00**	**2.22E-03**	General response 1dpi	DNA	Homeobox-leucine zipper protein family (AHRD V3.3 *** AT4G37790.1)	GO:0003677|GO:0003700|GO:0006355|GO:0043565
Solyc02g090450.3	**1.55E+00**	**9.38E-09**	**1.25E+00**	**4.41E-07**	**1.72E+00**	**1.23E-09**	**1.16E+00**	**1.35E-06**	General response 1dpi	OX	SI Peroxidase	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744
Solyc02g089250.3	**1.51E+00**	**3.76E-05**	**1.18E+00**	**6.53E-04**	**1.62E+00**	**1.44E-05**	**1.16E+00**	**7.51E-04**	General response 1dpi	G	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** A0A061EFL6_THECC)	
Solyc07g008980.3	**1.42E+00**	**3.97E-06**	**1.06E+00**	**1.90E-04**	**1.07E+00**	**1.68E-04**	**1.04E+00**	**2.38E-04**	General response 1dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952|
Solyc03g093270.3	**1.28E+00**	**4.86E-04**	**1.44E+00**	**1.28E-04**	**2.65E+00**	**9.82E-09**	**1.87E+00**	**3.84E-06**	General response 1dpi	2M	Aldo/keto reductase family oxidoreductase (AHRD V3.3 *** A0A072UK59_MEDTR)	GO:0016491|GO:0055114|
Solyc07g009090.3	**1.09E+00**	**2.65E-03**	**1.18E+00**	**1.34E-03**	**1.25E+00**	**7.94E-04**	**1.48E+00**	**1.25E-04**	General response 1dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952|
Solyc07g054220.1	**1.06E+00**	**5.06E-03**	**2.18E+00**	**1.09E-06**	**2.17E+00**	**1.16E-06**	**1.69E+00**	**4.42E-05**	General response 1dpi	H	Ethylene-responsive transcription factor ERF053 (AHRD V3.3 *** A0A0B2RF70_GLYSO)	GO:0003677|GO:0003700|GO:0006355
Solyc03g044580.1	**-2.46E+00**	**1.50E-04**	**-1.64E+00**	**6.50E-03**	**-1.97E+00**	**1.47E-03**	**-2.47E+00**	**1.46E-04**	General response 1dpi	NA	LOW QUALITY:transmembrane protein (AHRD V3.3 -** AT2G23440.1)	GO:0048364|
Solyc07g064410.1	**-2.62E+00**	**2.87E-06**	**-1.65E+00**	**8.94E-04**	**-5.53E+00**	**1.69E-12**	**-1.41E+00**	**3.48E-03**	General response 1dpi	P	Kua-ubiquitin conjugating enzyme hybrid, localization (AHRD V3.3 *** A0A103XYI2_CYNCS)	

Table S 3. List of differentially expressed genes (DEGs) modulated in tomato roots both after inoculation with Gluconacetobacter diazotrophicus AZ0019 WT and nifD- strain at 14 days post inoculum (dpi), in both the absence and the presence of 2 mM KNO3 in plants growth medium: plant general later response. *Clustering results of the DEGs, classified as genes significantly modulated at 14 dpi (in bold, P ≤ 0.01 and Log2 (fold change) ≥ 1 or ≤ -1) by G. diazotrophicus AZ0019 WT and nifD- mutant strain in both the absence (WT & nifD- NoN) and the presence of 2 mM KNO3 (WT & nifD- N) in the growth substrate. Tomato gene identifier (ITAG3.2 release), Log2-transformed fold change values and P values calculated for each pairwise comparison between WT inoculated and nifD- inoculated simples are reported. Protein description and abbreviation codes of functional classes were assigned on the basis of the protein description and function. Gene ontology (GO) terms were based on the ITAG3.2 release (https://solgenomics.net/organism/Solanum_lycopersicum/genome).*

Gene ID	WT N P.Value	nifD - N P. Value	WT NoN P. Value	nifD- NoN P.Value	Cluster	Functional Class	Gene Description	GO
Solyc02g005490.3	**5.50E+00 5.71E-06**	**5.51E+00 5.57E-06**	**4.79E+00 3.82E-05**	**3.03E+00 4.28E-03**	General response_14dpi	P	60S acidic ribosomal protein family (AHRD V3.3 *** AT5G24510.1),Pfam:PF00428	
Solyc10g081940.2	**5.13E+00 2.03E-08**	**4.47E+00 2.34E-07**	**3.79E+00 3.31E-06**	**2.83E+00 1.63E-04**	General response_14dpi	TR	Exocyst complex component 7 (AHRD V3.3 *** A0A151RD29_CAJCA)	GO:0000145|GO:0006887
Solyc12g017700.2	**3.91E+00 5.78E-05**	**2.99E+00 1.11E-03**	**3.62E+00 1.49E-04**	**2.47E+00 5.41E-03**	General response_14dpi	RNA	ATP-dependent RNA helicase (AHRD V3.3 *** A0A0K9PGQ5_ZOSMR)	GO:0003676|GO:0005524|GO:0008026|GO:0004386|GO:0004386
Solyc03g019690.1	**3.59E+00 6.16E-04**	**3.53E+00 7.21E-04**	**2.94E+00 3.63E-03**	**5.27E+00 5.13E-06**	General response_14dpi	D	Kunitz-type protease inhibitor (AHRD V3.3 *** Q3S481_SOLTU)	GO:0004866
Solyc12g056650.2	**3.55E+00 4.59E-21**	**2.66E+00 5.76E-18**	**1.34E+00 4.05E-11**	**2.32E+00 1.53E-16**	General response_14dpi	G	GIGANTEA (AHRD V3.3 *** F2Z6M2_IPONI)	GO:2000028
Solyc05g014300.1	**3.47E+00 3.75E-06**	**3.63E+00 1.88E-06**	**4.93E+00 9.24E-09**	**4.16E+00 1.99E-07**	General response_14dpi	G	LOW QUALITY:NAC domain containing protein 5 (AHRD V3.3 --* AT1G02250.1)	
Solyc09g074820.3	**3.45E+00 1.03E-04**	**4.91E+00 6.96E-07**	**2.99E+00 5.10E-04**	**2.18E+00 7.73E-03**	General response_14dpi	TR	Potassium transporter (AHRD V3.3 *** M1AT44_SOLTU)	GO:0015079|GO:0016020|GO:0071805
Solyc07g008440.3	**3.24E+00 8.92E-09**	**1.72E+00 1.57E-04**	**1.11E+00 8.10E-03**	**1.24E+00 3.67E-03**	General response_14dpi	TR	Purine permease-like protein (AHRD V3.3 *** G7J4H5_MEDTR)	GO:0005215|GO:0016021
Solyc08g066880.3	**3.19E+00 4.58E-10**	**3.18E+00 4.83E-10**	**1.60E+00 5.16E-05**	**1.47E+00 1.44E-04**	General response_14dpi	N	Bark storage protein A (AHRD V3.3 *** A0A151TDP1_CAJCA)	GO:0003824|GO:0009116
Solyc07g061800.3	**3.07E+00 5.01E-05**	**2.23E+00 1.59E-03**	**2.58E+00 3.79E-04**	**2.58E+00 3.83E-04**	General response_14dpi	S	SOUL heme-binding family protein (AHRD V3.3 *** AT1G17100.1)	
Solyc09g082670.3	**3.04E+00 5.62E-07**	**2.20E+00 6.01E-05**	**1.47E+00 3.58E-03**	**1.47E+00 3.69E-03**	General response_14dpi	STR	SolycHsfA6a	GO:0003700|GO:0005634|GO:0006355|GO:0043565
Solyc08g066890.3	**3.02E+00 8.91E-08**	**2.99E+00 1.01E-07**	**1.50E+00 1.15E-03**	**1.19E+00 7.59E-03**	General response_14dpi	N	Bark storage protein A (AHRD V3.3 *-* A0A0B2QEI9_GLYSO)	
Solyc11g021290.2	**3.00E+00 1.68E-05**	**2.49E+00 1.77E-04**	**2.50E+00 1.67E-04**	**1.97E+00 1.88E-03**	General response_14dpi	TR	Ycf1 (AHRD V3.3 *-* A0A0U1ZK62_SOLHA)	GO:0016021
Solyc03g013440.3	**2.92E+00 1.02E-08**	**2.23E+00 1.16E-06**	**1.23E+00 1.70E-03**	**1.74E+00 4.02E-05**	General response_14dpi	AM	Amino acid transporter, putative (AHRD V3.3 *** B9T0U1_RICCO)	
Solyc02g077610.3	**2.89E+00 1.93E-06**	**2.65E+00 7.06E-06**	**3.02E+00 9.47E-07**	**2.21E+00 8.01E-05**	General response_14dpi	T	NAC domain-containing protein (AHRD V3.3 *** A0A060A5P2_BOENI)	GO:0003677|GO:0006355
Solyc01g107400.2	**2.88E+00 2.10E-04**	**2.98E+00 1.40E-04**	**5.90E+00 2.93E-09**	**5.76E+00 4.69E-09**	General response_14dpi	H	IAA-amido synthetase	
Solyc08g066930.2	**2.83E+00 9.42E-05**	**3.23E+00 1.73E-05**	**2.04E+00 2.68E-03**	**1.71E+00 9.68E-03**	General response_14dpi	N	Bark storage protein A (AHRD V3.3 --* A0A0B2QEI9_GLYSO)	
Solyc11g021270.1	**2.82E+00 1.31E-05**	**2.36E+00 1.34E-04**	**1.61E+00 5.02E-03**	**1.69E+00 3.48E-03**	General response_14dpi	TR	Ycf1 (AHRD V3.3 *-* V5NDV5_9SOLN)	
Solyc04g080210.1	**2.81E+00 1.08E-06**	**2.49E+00 7.00E-06**	**1.27E+00 8.05E-03**	**2.36E+00 1.44E-05**	General response_14dpi	G	LOW QUALITY:ovate family protein 9	

Solyc09g065790.1	2.80E+00 5.12E-06	2.21E+00 1.21E-04	2.77E+00 6.06E-06	2.34E+00 5.86E-05	General response_14dpi	STR	ATP-dependent Clp protease proteolytic subunit (AHRD V3.3 *** K4CUK5_SOLLC)	GO:0004252|GO:0006508
Solyc04g071990.3	2.72E+00 3.41E-17	1.03E+00 5.20E-08	1.05E+00 3.76E-08	1.53E+00 1.84E-11	General response_14dpi	G	GIGANTEA (AHRD V3.3 *** F2Z6M2_IPONI)	GO:2000028
Solyc01g009870.3	2.69E+00 6.42E-03	2.61E+00 8.01E-03	3.25E+00 1.37E-03	2.93E+00 3.35E-03	General response_14dpi	L	Glycerophosphodiester phosphodiesterase, putative (AHRD V3.3 *** B9RM92_RICCO)	GO:0006629|GO:0008081
Solyc11g021240.2	2.60E+00 6.84E-05	2.38E+00 1.99E-04	1.58E+00 7.76E-03	1.70E+00 4.74E-03	General response_14dpi	TR	Ycf1 (AHRD V3.3 *-* A0A0U1ZHZ0_9SOLN)	
Solyc07g006570.3	2.45E+00 7.62E-09	2.69E+00 1.14E-09	1.09E+00 9.53E-04	1.87E+00 8.65E-07	General response_14dpi	RNA	Ribonuclease (AHRD V3.3 *** Q41722_ZINVI)	GO:0003723|GO:0033897
Solyc11g021280.1	2.42E+00 4.47E-04	2.29E+00 7.83E-04	2.10E+00 1.78E-03	1.83E+00 5.38E-03	General response_14dpi	TR	Ycf1 (AHRD V3.3 *-* A0A0U1ZJ99_SOLCI)	GO:0016021
Solyc09g091130.3	2.41E+00 7.27E-04	2.41E+00 7.23E-04	3.53E+00 6.87E-06	2.63E+00 2.86E-04	General response_14dpi	STR	Glutathione s-transferase, putative (AHRD V3.3 *** B9RWR5_RICCO)	GO:0005515
Solyc07g006560.3	2.34E+00 9.49E-04	3.33E+00 1.56E-05	2.72E+00 1.96E-04	5.29E+00 7.01E-09	General response_14dpi	D	Hypersensitive response assisting protein(AHRD V3.3 *** Q9SWC6_CAPAN)	GO:0003723|GO:0033897
Solyc08g014240.3	2.29E+00 1.14E-05	2.86E+00 3.64E-07	2.84E+00 3.96E-07	2.17E+00 2.44E-05	General response_14dpi	C	Isopropylmalate synthase (AHRD V3.3 *** A0A0G2T9V8_SOLPN)	GO:0003824|GO:0019752|GO:0046912|GO:0019752|GO:0046912
Solyc02g090430.3	2.25E+00 1.54E-05	1.56E+00 1.09E-03	2.13E+00 3.41E-05	2.01E+00 6.97E-05	General response_14dpi	K	MAP kinase kinase kinase 20	GO:0004672|GO:0005524|GO:0006468|GO:0005524|GO:0005524
Solyc02g032910.2	2.15E+00 2.02E-05	2.37E+00 5.25E-06	2.19E+00 1.56E-05	1.69E+00 3.73E-04	General response_14dpi	D	Glycine rich protein (AHRD V3.3 *** Q43498_SOLLC)	
Solyc09g008913.1	2.14E+00 3.98E-12	2.21E+00 2.02E-12	1.29E+00 9.81E-08	1.27E+00 1.30E-07	General response_14dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***Q8H0I7_PETHY)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc07g041500.3	2.01E+00 7.95E-04	2.04E+00 7.16E-04	2.83E+00 1.41E-05	2.53E+00 6.10E-05	General response_14dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** A0A061GL91_THECC)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc03g117860.3	1.97E+00 6.78E-03	2.02E+00 5.58E-03	4.55E+00 3.49E-07	3.18E+00 6.74E-05	General response_14dpi	D	RING/U-box superfamily protein (AHRDV3.3 *-* AT3G14250.1)	GO:0004842|GO:0016567
Solyc06g076570.3	1.93E+00 8.01E-06	1.60E+00 9.57E-05	1.47E+00 2.63E-04	1.03E+00 6.31E-03	General response_14dpi	STR	class I small heat shock protein	
Solyc06g006080.3	1.83E+00 3.55E-12	1.09E+00 1.11E-07	1.36E+00 1.88E-09	1.02E+00 3.56E-07	General response_14dpi	G	thiamine biosynthesis protein ThiC	GO:0009228|GO:0051536
Solyc01g080570.3	1.77E+00 9.77E-07	2.15E+00 3.60E-08	1.29E+00 8.71E-05	1.72E+00 1.55E-06	General response_14dpi	DNA	inosine-uridine preferring nucleoside hydrolase family protein (AHRD V3.3 *** AT5G18860.2)	
Solyc08g007240.3	1.76E+00 1.24E-07	1.30E+00 1.49E-05	1.21E+00 3.98E-05	1.99E+00 1.28E-08	General response_14dpi	DNA	Nudix hydrolase (AHRD V3.3 ***A0A061G4C5_THECC)	GO:0016787
Solyc08g075600.2	1.75E+00 4.10E-04	1.28E+00 6.35E-03	2.13E+00 4.29E-05	1.85E+00 2.24E-04	General response_14dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CMS7_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc12g087860.2	1.74E+00 4.72E-08	1.45E+00 1.07E-06	1.30E+00 5.67E-06	1.70E+00 6.64E-08	General response_14dpi	D	RING/U-box superfamily protein, putative(AHRD V3.3 *** A0A061FLH6_THECC)	GO:0005515|GO:0008270

Solyc10g087010.2	1.62E+00	1.59E-05	1.05E+00	1.97E-03	1.08E+00 1.53E-03	1.32E+00 1.97E-04	General response_14dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103XWG4_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc03g020010.1	1.58E+00	4.42E-04	2.01E+00	2.40E-05	1.19E+00 5.38E-03	2.77E+00 1.70E-07	General response_14dpi	P	miraculin	GO:0004866
Solyc09g008917.1	1.55E+00	1.96E-06	1.79E+00	1.81E-07	1.18E+00 8.75E-05	1.00E+00 5.25E-04	General response_14dpi	CYTP450	Cytochrome P450 (AHRD V3.3 --* A0A061DI80_THECC)	
Solyc12g006380.2	1.54E+00	6.32E-04	2.31E+00	3.89E-06	5.19E+00 6.69E-13	4.26E+00 4.95E-11	General response_14dpi	E	2-oxoglutarate-dependent dioxygenase	GO:0016491|GO:0055114
Solyc09g082220.1	1.49E+00	4.27E-03	2.63E+00	8.82E-06	2.88E+00 2.31E-06	1.97E+00 3.28E-04	General response_14dpi	NA	LOW QUALITY:Acetyltransferase (GNAT)domain protein (AHRD V3.3 *** A0A072U473_MEDTR)	GO:0008080
Solyc09g065840.3	1.44E+00	3.19E-04	1.04E+00	5.89E-03	1.46E+00 2.74E-04	1.49E+00 2.11E-04	General response_14dpi	DNA	single-stranded DNA binding protein-likeprotein	GO:0003697|GO:0003697|GO:0006260|GO:0003697|GO:0006260
Solyc04g054150.1	1.42E+00	3.02E-03	1.66E+00	7.22E-04	1.44E+00 2.56E-03	1.25E+00 7.64E-03	General response_14dpi	T	Nuclear transcription factor Y protein(AHRD V3.3 *** G7LB97_MEDTR)	GO:0005634|GO:0006355|GO:0043565|GO:0046982|GO:0046982
Solyc05g006980.3	1.41E+00	7.04E-07	1.57E+00	1.08E-07	1.25E+00 4.53E-06	1.34E+00 1.57E-06	General response_14dpi	DNA	Homeobox leucine zipper family protein(AHRD V3.3 *** G7K9R5_MEDTR)	GO:0003677|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565
Solyc01g100390.3	1.39E+00	5.88E-05	1.17E+00	4.09E-04	1.49E+00 2.18E-05	1.19E+00 3.56E-04	General response_14dpi	E	Pyrophosphate-energized vacuolar membrane proton pump (AHRD V3.3 *** AVP_VIGRR)	GO:0004427|GO:0009678|GO:0015992|GO:0016020
Solyc08g068850.3	1.37E+00	2.57E-04	1.48E+00	1.08E-04	2.71E+00 7.72E-09	2.64E+00 1.26E-08	General response_14dpi	TR	Proton pump interactor 1 (AHRD V3.3 *-* D5L6G0_SOLTU)	GO:0005783|GO:0005886|GO:0010155
Solyc04g051490.3	1.34E+00	9.88E-03	2.22E+00	9.23E-05	4.66E+00 4.50E-10	3.68E+00 4.25E-08	General response_14dpi	DNA	essential meiotic endonuclease 1B(AHRD V3.3 *-* AT2G22140.1)	GO:0003677|GO:0004518|GO:0005634|GO:0006281|GO:0048476|GO:0005634|GO:0006281|GO:0048476
Solyc01g067850.2	1.33E+00	1.58E-03	2.92E+00	3.50E-08	1.16E+00 5.07E-03	2.26E+00 2.58E-06	General response_14dpi	OX	Peroxidase (AHRD V3.3 *** K4AX33_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc07g005100.3	1.31E+00	8.82E-09	1.84E+00	8.12E-12	1.35E+00 5.33E-09	1.15E+00 9.97E-08	General response_14dpi	D	Chitinase/lysozyme (AHRD V3.3 *** Q43591_TOBAC)	GO:0004553|GO:0005975|GO:0004568|GO:0006032|GO:0004568|GO:0006032
Solyc09g064940.2	1.26E+00	2.97E-06	1.40E+00	5.74E-07	1.23E+00 4.25E-06	1.04E+00 4.39E-05	General response_14dpi	P	Phenazine biosynthesis PhzC/PhzF family protein (AHRD V3.3 ***B9HYD6_POPTR)	GO:0003824|GO:0009058
Solyc08g006470.3	1.24E+00	4.45E-03	1.19E+00	5.84E-03	3.33E+00 7.69E-09	2.90E+00 9.92E-08	General response_14dpi	DNA	Zinc finger protein (AHRD V3.3 *** A0A0B2RI16_GLYSO)	GO:0046872
Solyc03g080100.3	1.22E+00	1.33E-04	1.06E+00	6.28E-04	1.83E+00 4.12E-07	1.98E+00 1.10E-07	General response_14dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-*AT5G24580.4)	GO:0030001|GO:0046872
Solyc06g062420.3	1.19E+00	1.94E-04	1.88E+00	2.97E-07	2.10E+00 4.24E-08	2.28E+00 8.91E-09	General response_14dpi	NA	transmembrane protein (AHRD V3.3 -** AT3G21351.1)	
Solyc01g097270.3	1.17E+00	2.95E-03	1.47E+00	3.30E-04	1.32E+00 1.01E-03	3.00E+00 7.45E-09	General response_14dpi	D	pathogen-induced protein	GO:0008061|GO:0042742|GO:0050832|GO:0042742|GO:0050832

Solyc06g054640.2	1.17E+00	5.89E-05	1.47E+00	2.29E-06	1.52E+00 1.31E-06	1.16E+00 6.36E-05	General response_14dpi	NA	DUF506 family protein (AHRD V3.3 *** G7LD84_MEDTR)	
Solyc02g070090.1	1.13E+00	1.45E-04	1.75E+00	2.90E-07	1.10E+00 2.14E-04	1.66E+00 6.80E-07	General response_14dpi	E	FAD-binding Berberine family protein (AHRD V3.3 *** A0A061G7Z5_THECC)	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114
Solyc07g055690.1	1.05E+00	5.82E-04	1.97E+00	8.58E-08	1.30E+00 4.88E-05	2.74E+00 1.44E-10	General response_14dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** G4XXY5_NICAT)	GO:0048544
Solyc07g065500.2	1.02E+00	3.70E-04	1.09E+00	1.71E-04	1.43E+00 5.00E-06	2.75E+00 2.87E-11	General response_14dpi	G	CCAAT-binding transcription factor	GO:0005634|GO:0006355|GO:0043565|GO:0046982|GO:0046982
Solyc08g080650.3	1.01E+00	6.25E-04	1.53E+00	3.19E-06	1.58E+00 1.95E-06	2.46E+00 6.50E-10	General response_14dpi	D	Osmotin-like protein (Fragment) IPR001938 Thaumatin, pathogenesis-related	
Solyc01g100490.3	-1.09E+00	1.56E-03	-1,83E+00	2.78E-06	-1.12E+00 1.18E-03	-1.36E+00 1.53E-04	General response_14dpi	TR	chloronerva	GO:0030410|GO:0030418
Solyc05g055970.3	-1.09E+00	1.14E-04	-1,24E+00	2.32E-05	-1.59E+00 5.38E-07	-1.15E+00 6.29E-05	General response_14dpi	P	Ankyrin repeat-containing-like protein (AHRD V3.3 *-* A0A061FUD1_THECC)	GO:0016021|GO:0031347|GO:0071446|GO:2000031
Solyc08g083250.3	-1.40E+00	4.59E-03	-1,32E+00	7.09E-03	-1.55E+00 1.99E-03	-1.74E+00 6.66E-04	General response_14dpi	G	Purple acid phosphatase (AHRD V3.3 *-* K4CPW9_SOLLC)	
Solyc11g005320.1	-1.40E+00	5.32E-04	-1,43E+00	4.20E-04	-1.29E+00 1.15E-03	-2.08E+00 3.50E-06	General response_14dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT1G49230.1)	GO:0005515|GO:0008270
Solyc11g005280.1	-1.66E+00	8.97E-04	-2,10E+00	6.49E-05	-2.19E+00 3.76E-05	-1.66E+00 9.12E-04	General response_14dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT1G49230.1)	GO:0005515|GO:0008270
Solyc08g080290.3	-1.68E+00	1.18E-03	-1,28E+00	9.80E-03	-1.72E+00 9.31E-04	-1.35E+00 7.13E-03	General response_14dpi	STR	Dehydration responsive element bindingtranscription factor (AHRD V3.3 *** W6FIY4_9ROSA)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc01g101050.3	-1.70E+00	2.60E-03	-1,46E+00	8.37E-03	-2.14E+00 2.92E-04	-2.25E+00 1.65E-04	General response_14dpi	OX	Peroxidase (AHRD V3.3 *** K4B1D5_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc11g045520.2	-1.99E+00	1.86E-05	-2,25E+00	3.07E-06	-2.17E+00 5.19E-06	-1.64E+00 2.03E-04	General response_14dpi	H	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE-like protein	GO:0016491|GO:0055114
Solyc05g021540.2	-2.01E+00	9.54E-04	-1,76E+00	3.07E-03	-1.90E+00 1.64E-03	-2.23E+00 3.32E-04	General response_14dpi	2M	Alcohol dehydrogenase (AHRD V3.3 *-* Q4LAW8_CAPCH)	
Solyc06g075650.3	-2.03E+00	6.55E-11	-1,21E+00	1.04E-06	-2.65E+00 1.90E-13	-1.55E+00 1.45E-08	General response_14dpi	TR	tonoplast intrinsic protein 1.2	GO:0005215|GO:0006810|GO:0016020
Solyc03g063030.3	-2.05E+00	9.07E-07	-1,82E+00	5.78E-06	-1.33E+00 3.26E-04	-1.01E+00 4.18E-03	General response_14dpi	AM	Transmembrane amino acid transporterfamily protein (AHRD V3.3 *** AT2G39130.2)	
Solyc03g006720.1	-2.07E+00	9.59E-03	-2,53E+00	2.07E-03	-3.57E+00 5.33E-05	-2.27E+00 5.00E-03	General response_14dpi	K	Serine/threonine-protein kinase (AHRDV3.3 *** A0A059C900_EUCGR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g099320.3	-2.11E+00	6.61E-07	-1,98E+00	1.77E-06	-1.41E+00 1.82E-04	-1.09E+00 2.28E-03	General response_14dpi	T	Nuclear transcription factor Y protein(AHRD V3.3 *** G7I854_MEDTR)	GO:0005634|GO:0006355|GO:0043565|GO:0046982|GO:0046982
Solyc01g094910.3	-2.12E+00	4.41E-04	-3,04E+00	4.60E-06	-5.14E+00 4.04E-10	-4.37E+00 9.91E-09	General response_14dpi	TR	ferric-chelate reductase	GO:0016491|GO:0055114
Solyc06g073180.3	-2.13E+00	4.21E-13	-1,34E+00	6.51E-09	-1.44E+00 1.68E-09	-1.64E+00 1.16E-10	General response_14dpi	G	CONSTANS interacting protein 1	GO:0005622|GO:0008270
Solyc12g100300.2	-2.24E+00	1.13E-06	-1,87E+00	1.70E-05	-2.06E+00 4.20E-06	-1.42E+00 4.57E-04	General response_14dpi	TR	Metal tolerance protein (AHRD V3.3 *** D7RJ71_CARPA)	GO:0006812|GO:0008324|GO:0016021|GO:0055085

Solyc12g013840.2	**-2.40E+00**	**2.03E-12**	**-1,73E+00**	**1.85E-09**	**-1.40E+00**	**9.89E-08**	**-1.43E+00**	**7.01E-08**	General response_14dpi	G	SPA1-related 3 (AHRD V3.3 ***AT3G15354.3)	GO:0004672|GO:0005524|GO:0006468|GO:0005515|GO:0005515
Solyc05g052950.3	**-2.49E+00**	**2.36E-11**	**-1,79E+00**	**1.73E-08**	**-1.41E+00**	**1.08E-06**	**-2.49E+00**	**2.41E-11**	General response_14dpi	DNA	Regulator of chromosome condensation(RCC1) family protein (AHRD V3.3 *** AT3G55580.1)	
Solyc03g098320.3	**-2.69E+00**	**7.16E-14**	**-1,84E+00**	**2.93E-10**	**-1.14E+00**	**1.69E-06**	**-1.19E+00**	**8.86E-07**	General response_14dpi	T	Myb transcription factor (AHRD V3.3 *** A0A072UBN0_MEDTR)	GO:0003677
Solyc01g108710.3	**-2.95E+00**	**6.87E-07**	**-2,80E+00**	**1.59E-06**	**-4.72E+00**	**9.77E-11**	**-3.27E+00**	**1.15E-07**	General response_14dpi	T	transcription initiation factor TFIID subunit 1b-like protein (AHRD V3.3 -**AT3G19030.1)	
Solyc05g007880.3	**-3.01E+00**	**1.72E-13**	**-2,48E+00**	**1.33E-11**	**-1.78E+00**	**1.15E-08**	**-1.80E+00**	**8.47E-09**	General response_14dpi	DNA	Dof zinc finger protein (AHRD V3.3 *** W9S8B0_9ROSA)	GO:0003677|GO:0006355
Solyc02g067230.3	**-3.04E+00**	**3.32E-17**	**-2,14E+00**	**1.21E-13**	**-1.29E+00**	**5.56E-09**	**-1.13E+00**	**6.69E-08**	General response_14dpi	DNA	Dof zinc finger protein3	GO:0003677|GO:0006355
Solyc08g074270.3	**-3.15E+00**	**2.06E-10**	**-1,81E+00**	**4.31E-06**	**-1.88E+00**	**2.39E-06**	**-2.10E+00**	**4.30E-07**	General response_14dpi	DNA	Cryptochrome DASH, chloroplastic/mitochondrial (AHRD V3.3 *** CRYD_SOLLC)	GO:0003913|GO:0006281
Solyc09g082690.3	**-3.16E+00**	**4.74E-09**	**-1,24E+00**	**1.13E-05**	**-2.53E+00**	**2.66E-07**	**-3.44E+00**	**9.09E-10**	General response_14dpi	OX	superoxide dismutase	
Solyc04g057980.3	**-3.61E+00**	**6.63E-08**	**-1,32E+00**	**9.14E-05**	**-1.39E+00**	**7.85E-03**	**-1.79E+00**	**1.01E-03**	General response_14dpi	G	Orange Ripening	GO:0016655|GO:0055114
Solyc08g082590.3	**-4.20E+00**	**2.25E-16**	**-1,43E+00**	**7.32E-12**	**-2.81E+00**	**2.48E-12**	**-3.16E+00**	**1.76E-13**	General response_14dpi	OX	Glutaredoxin (AHRD V3.3 *** A0A103XR19_CYNCS)	GO:0009055|GO:0015035|GO:0045454
Solyc05g015350.3	**-5.60E+00**	**4.15E-06**	**-2,10E+00**	**7.94E-05**	**-3.12E+00**	**3.34E-03**	**-3.49E+00**	**1.26E-03**	General response_14dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103XVZ6_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114

Table S 4. List of differentially expressed genes (DEGs) modulated in tomato roots both after inoculation with Gluconacetobacter diazotrophicus AZ0019 WT and nifD- strain at one day post inoculum (dpi) in presence or absence of nitrogen in plants growth medium. *Clustering results of the DEGs, classified as genes significantly modulated at 1 dpi (in bold, P ≤ 0.01 and Log2 (fold change) ≥ 1 or ≤ -1) by G. diazotrophicus AZ0019 WT and nifD⁻ mutant strain in the absence (WT & nifD⁻ NoN) or presence of 2 mM KNO_3 (WT & nifD⁻ N) in the growth substrate. Tomato gene identifier (ITAG3.2 release), Log2-transformed fold change values and P values calculated for each pairwise comparison between WT inoculated and nifD⁻ inoculated simples are reported. Protein description and abbreviation codes of functional classes were assigned on the basis of the protein description and function. Gene ontology (GO) terms were based on the ITAG3.2 release (https://solgenomics.net/organism/Solanum_lycopersicum/genome).*

Gene ID	WT N	P.Value	*nifD* - N	P. Value	WT NoN	P. Value	*nifD*- NoN	P.Value	Cluster	Functional Class	Gene Description	GO
Solyc10g050980	**8.70E+00**	**4.66E-09**	**2.88E+00**	**8.34E-03**	-2.45E+00	2.00E-02	-2.21E+00	4.00E-02	WT & nifD- N 1 dpi	RNA	PAB-dependent poly(A)-specific ribonuclease subunit PAN2 (AHRD V3.3 -** A0A1D1XPR6_9ARAE)	
Solyc10g008810	**5.57E+00**	**9.41E-08**	**3.57E+00**	**7.64E-05**	6.70E-01	3.90E-01	7.00E-01	3.70E-01	WT & nifD- N 1 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2SKJ1_GLYSO)	GO:0016788
Solyc11g007180	**5.01E+00**	**8.81E-15**	**3.02E+00**	**6.24E-10**	5.37E-01	1.00E-01	6.78E-01	4.00E-02	WT & nifD- N 1 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2RXW1_GLYSO)	GO:0016788
Solyc04g074170	**4.80E+00**	**1.74E-09**	**3.12E+00**	**3.51E-06**	-1.63E-01	1.16E+00	-2.07E-01	1.10E+00	WT & nifD- N 1 dpi	T	MYB-related transcription factor (AHRD V3.3 *** A0A059PRU0_SALMI)	GO:0003677
Solyc06g076800	**4.63E+00**	**1.75E-12**	**2.76E+00**	**6.25E-08**	1.98E-01	1.00E+00	3.46E-01	3.60E-01	WT & nifD- N 1 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9SHY9_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114
Solyc09g014350	**4.40E+00**	**4.48E-10**	**2.91E+00**	**9.17E-07**	2.78E-01	5.50E-01	3.11E-01	5.00E-01	WT & nifD- N 1 dpi	CS	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7L6J6_MEDTR)	GO:0008152|GO:0016746
Solyc12g036480	**4.36E+00**	**5.06E-11**	**2.89E+00**	**1.52E-07**	3.09E-01	4.50E-01	2.92E-01	4.80E-01	WT & nifD- N 1 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061FUV1_THECC)	GO:0003677|GO:0006355

Solyc02g069730	**4.34E+00**	**1.10E-12**	**2.41E+00**	**1.53E-07**	3.19E-01	3.50E-01	3.70E-01	2.80E-01	WT & nifD- N 1 dpi	CS	CASP-like protein (AHRD V3.3 *** K4B7V5_SOLLC)	
Solyc10g039390	**4.33E+00**	**4.67E-10**	**1.92E+00**	**2.22E-04**	4.99E-01	2.80E-01	2.64E-01	5.60E-01	WT & nifD- N 1 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT1G29000.2)	GO:0030001|GO:0046872
Solyc05g010330	**4.33E+00**	**5.83E-11**	**2.55E+00**	**1.21E-06**	4.97E-01	2.30E-01	3.40E-01	4.10E-01	WT & nifD- N 1 dpi	OX	Peroxidase (AHRD V3.3 *** K4BXK6_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114GO:0004601|GO:0042744
Solyc11g011110	**4.12E+00**	**1.90E-09**	**2.52E+00**	**9.00E-06**	3.48E-01	4.50E-01	6.06E-01	2.00E-01	WT & nifD- N 1 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** W9S179_9ROSA)	GO:0016788
Solyc05g014150	**4.11E+00**	**1.63E-08**	**2.35E+00**	**9.76E-05**	9.98E-01	6.00E-02	7.01E-01	1.80E-01	WT & nifD- N 1 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT3G55290.2)	
Solyc01g006620	**3.94E+00**	**3.16E-07**	**2.40E+00**	**3.11E-04**	2.67E-01	1.05E+00	4.17E-01	4.80E-01	WT & nifD- N 1 dpi	H	C2 calcium/lipid-binding and GRAM domain protein (AHRD V3.3 *** A0A072ULK6_MEDTR)	GO:0005515
Solyc02g090210	**3.92E+00**	**3.35E-12**	**2.18E+00**	**3.46E-07**	3.41E-01	3.00E-01	4.47E-01	1.80E-01	WT & nifD- N 1 dpi	L	GDSL esterase/lipase family (AHRD V3.3 *** A0A151RJ07_CAJCA)	GO:0016788
Solyc05g005170	**3.83E+00**	**1.00E-05**	**2.50E+00**	**1.45E-03**	1.63E+00	3.00E-02	1.50E+00	4.00E-02	WT & nifD- N 1 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** A0A061E6B2_THECC)	GO:0004650|GO:0005975
Solyc06g050530	**3.82E+00**	**6.12E-10**	**2.27E+00**	**5.98E-06**	4.48E-01	2.70E-01	1.65E-01	1.08E+00	WT & nifD- N 1 dpi	PMI	Laccase (AHRD V3.3 *** I1M7Q3_SOYBN)	GO:0005507GO:0005507|GO:0016491|GO:0055114
Solyc09g065440	**3.82E+00**	**1.31E-09**	**2.13E+00**	**2.43E-05**	3.35E-01	4.30E-01	4.84E-01	2.50E-01	WT & nifD- N 1 dpi	NA	Protease inhibitor/seed storage/lipid transfer family protein (AHRD V3.3 *-* B9NBN8_POPTR)	
Solyc08g008610	**3.82E+00**	**4.56E-11**	**2.31E+00**	**6.45E-07**	5.25E-01	1.50E-01	6.96E-01	6.00E-02	WT & nifD- N 1 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061G3V4_THECC)	
Solyc06g065655	**3.77E+00**	**8.06E-05**	**2.60E+00**	**3.36E-03**	3.10E-01	1.10E+00	1.37E-01	1.27E+00	WT & nifD- N 1 dpi	TR	Drug resistance transporter-like ABC domain protein (AHRD V3.3 *-* G7JU55_MEDTR)	GO:0016020
Solyc06g048860	**3.75E+00**	**5.81E-07**	**2.18E+00**	**7.37E-04**	5.09E-01	3.80E-01	6.53E-01	2.60E-01	WT & nifD- N 1 dpi	PMI	Laccase (AHRD V3.3 *** A0A022PYV8_ERYGU)	GO:0005507GO:0005507|GO:0016491|GO:0055114
Solyc09g005970	**3.75E+00**	**1.70E-11**	**1.85E+00**	**7.09E-06**	1.81E-01	5.90E-01	6.71E-02	1.24E+00	WT & nifD- N 1 dpi	TR	ABC transporter family protein (AHRD V3.3 *** B9ICA5_POPTR)	GO:0005524|GO:0016887GO:0016020
Solyc05g046180	**3.74E+00**	**1.90E-09**	**2.10E+00**	**2.85E-05**	1.50E-01	1.12E+00	4.94E-01	2.40E-01	WT & nifD- N 1 dpi	E	LOW QUALITY:Alcohol dehydrogenase 2 (AHRD V3.3 --* ADH2_SOLLC)	
Solyc11g009100	**3.72E+00**	**1.39E-05**	**2.29E+00**	**2.86E-03**	4.42E-01	5.30E-01	7.64E-01	2.80E-01	WT & nifD- N 1 dpi	TR	ABC transporter G family member (AHRD V3.3 *** A0A0K9NWI5_ZOSMR)	GO:0005524|GO:0016887GO:0016020
Solyc01g106920	**3.67E+00**	**8.74E-10**	**1.97E+00**	**3.19E-05**	2.19E-01	5.80E-01	9.36E-02	1.21E+00	WT & nifD- N 1 dpi	TR	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7LFG1_MEDTR)	GO:0005215|GO:0006810|GO:0016020|GO:0055085
Solyc07g017980	**3.55E+00**	**3.09E-10**	**1.62E+00**	**1.25E-04**	3.74E-01	3.10E-01	4.39E-01	2.30E-01	WT & nifD- N 1 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** I3S1U4_MEDTR)	
Solyc06g054570	**3.51E+00**	**3.94E-08**	**2.39E+00**	**1.88E-05**	-3.78E-01	4.10E-01	-1.32E-01	1.18E+00	WT & nifD- N 1 dpi	OX	Glutaredoxin family protein (AHRD V3.3 *** D7LYE9_ARALL)	GO:0009055|GO:0015035|GO:0045454
Solyc04g014290	**3.38E+00**	**3.24E-08**	**1.59E+00**	**1.12E-03**	2.47E-01	5.70E-01	1.10E-01	1.20E+00	WT & nifD- N 1 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** A0A072V4P7_MEDTR)	
Solyc01g060260	**3.37E+00**	**2.40E-09**	**1.65E+00**	**1.88E-04**	2.87E-01	4.50E-01	6.71E-01	9.00E-02	WT & nifD- N 1 dpi	D	Glycine-rich protein family (AHRD V3.3 *-* AT5G49350.2)	
Solyc07g066360	**3.33E+00**	**7.92E-12**	**1.29E+00**	**1.17E-04**	3.34E-01	2.50E-01	2.57E-01	3.70E-01	WT & nifD- N 1 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 -** G7JV71_MEDTR)	
Solyc07g062630	**3.33E+00**	**7.29E-07**	**2.28E+00**	**1.45E-04**	4.58E-01	3.80E-01	7.59E-01	1.50E-01	WT & nifD- N 1 dpi	TR	ABC transporter family protein (AHRD V3.3 *** B9I1V7_POPTR)	GO:0005524|GO:0016887GO:0016020
Solyc04g007810	**3.31E+00**	**1.72E-10**	**1.40E+00**	**2.22E-04**	2.45E-01	4.60E-01	4.12E-01	2.20E-01	WT & nifD- N 1 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** I3S1U4_MEDTR)	
Solyc06g065670	**3.28E+00**	**6.95E-09**	**1.68E+00**	**1.98E-04**	8.12E-01	5.00E-02	2.26E-01	5.70E-01	WT & nifD- N 1 dpi	TR	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	GO:0005524|GO:0016887GO:0016020
Solyc01g100370	**3.26E+00**	**1.15E-15**	**1.23E+00**	**7.48E-07**	7.01E-01	0.00E+00	6.25E-01	0.00E+00	WT & nifD- N 1 dpi	DNA	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G62550.1)	GO:0006950
Solyc01g100070	**3.21E+00**	**3.59E-09**	**1.51E+00**	**3.51E-04**	3.07E-01	4.10E-01	3.01E-01	4.20E-01	WT & nifD- N 1 dpi	RNA	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 --* A0A1D1ZFE6_9ARAE)	
Solyc03g096660	**3.20E+00**	**1.38E-05**	**2.25E+00**	**8.89E-04**	-2.08E-01	1.13E+00	-5.83E-01	3.40E-01	WT & nifD- N 1 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561	GO:0016491
Solyc03g113690	**3.20E+00**	**5.95E-07**	**1.60E+00**	**2.89E-03**	7.73E-02	1.27E+00	-3.34E-02	1.35E+00	WT & nifD- N 1 dpi	TR	Abc transporter family protein (AHRD V3.3 *** D7LZ77_ARALL)	GO:0005524|GO:0016887GO:0016020

Solyc08g078030	**3.09E+00**	**3.36E-07**	**1.63E+00**	**1.36E-03**	1.24E-01	1.19E+00	-4.70E-02	1.32E+00	WT & nifD- N 1 dpi	NA	Transferase, putative (AHRD V3.3 *** B9T0L5_RICCO)	GO:0016747
Solyc04g014350	**3.06E+00**	**4.50E-07**	**1.35E+00**	**6.58E-03**	2.75E-01	5.50E-01	2.74E-01	5.50E-01	WT & nifD- N 1 dpi	H	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G69350.1)	
Solyc04g010200	**3.03E+00**	**1.88E-06**	**1.70E+00**	**2.04E-03**	6.55E-01	2.00E-01	2.62E-01	1.00E+00	WT & nifD- N 1 dpi	TR	ABC transporter G family member (AHRD V3.3 *** A0A0K9NPK2_ZOSMR)	GO:0005524|GO:0016887GO:0016020
Solyc02g014730	**3.00E+00**	**6.24E-08**	**1.60E+00**	**4.65E-04**	2.62E-01	5.20E-01	2.42E-01	5.50E-01	WT & nifD- N 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103YA00_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114GO:0016705|GO:0055114
Solyc06g069100	**2.95E+00**	**2.67E-06**	**1.37E+00**	**9.83E-03**	-6.27E-01	2.10E-01	2.03E-01	1.08E+00	WT & nifD- N 1 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061FUV1_THECC)	GO:0003677|GO:0006355
Solyc08g014110	**2.85E+00**	**1.04E-04**	**3.21E+00**	**2.31E-05**	8.01E-01	2.10E-01	1.15E+00	8.00E-02	WT & nifD- N 1 dpi	DNA	LOW QUALITY:B3 domain-containing protein REM13 (AHRD V3.3 --* AT2G24650.7)	
Solyc05g047530	**2.85E+00**	**1.29E-09**	**1.26E+00**	**3.94E-04**	7.17E-01	3.00E-02	7.12E-01	3.00E-02	WT & nifD- N 1 dpi	CS	trans-cinnamate 4-monooxygenase	GO:0005506|GO:0016705|GO:0020037|GO:0055114GO:0016705|GO:0055114
Solyc04g011600	**2.83E+00**	**5.19E-08**	**1.22E+00**	**3.15E-03**	2.72E-01	4.70E-01	1.01E-01	1.19E+00	WT & nifD- N 1 dpi	CS	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7KGS4_MEDTR)	GO:0008152|GO:0016746
Solyc06g074390	**2.82E+00**	**6.91E-07**	**1.44E+00**	**2.57E-03**	6.20E-02	1.29E+00	1.20E-01	1.18E+00	WT & nifD- N 1 dpi	CS	Fatty acyl-CoA reductase (AHRD V3.3 *** K4C9F7_SOLLC)	GO:0080019
Solyc01g009320	**2.81E+00**	**2.29E-05**	**1.57E+00**	**7.75E-03**	8.32E-01	1.40E-01	5.33E-01	3.40E-01	WT & nifD- N 1 dpi	P	U-box domain-containing family protein (AHRD V3.3 *** B9IIL0_POPTR)	GO:0004842|GO:0016567GO:0005488
Solyc02g079550	**2.74E+00**	**2.62E-07**	**1.36E+00**	**2.06E-03**	-4.90E-01	2.30E-01	-8.00E-02	1.24E+00	WT & nifD- N 1 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** B9H1U5_POPTR)	GO:0004672|GO:0005524|GO:0006468GO:0004672|GO:0006468
Solyc12g089350	**2.72E+00**	**1.90E-05**	**1.46E+00**	**9.65E-03**	1.45E-01	1.18E+00	4.69E-01	3.80E-01	WT & nifD- N 1 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2SN40_GLYSO)	GO:0016788
Solyc02g079140	**2.70E+00**	**8.71E-05**	**1.67E+00**	**7.95E-03**	5.79E-01	3.30E-01	1.41E-01	1.21E+00	WT & nifD- N 1 dpi	RNA	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (AHRD V3.3 *-* A0A1D1ZDK4_9ARAE)	GO:0005515
Solyc12g009680	**2.68E+00**	**3.76E-09**	**1.52E+00**	**3.85E-05**	-1.22E-01	1.09E+00	5.07E-02	1.27E+00	WT & nifD- N 1 dpi	H	ADIPOR-like receptor (AHRD V3.3 *** W9SGZ8_9ROSA)	GO:0016021
Solyc08g081630	**2.64E+00**	**3.91E-06**	**1.46E+00**	**3.40E-03**	4.45E-01	3.30E-01	4.12E-01	3.70E-01	WT & nifD- N 1 dpi	T	WRKY transcription factor 56	GO:0003700|GO:0006355|GO:0043565
Solyc02g078250	**2.62E+00**	**3.32E-08**	**1.30E+00**	**6.72E-04**	9.02E-02	1.19E+00	1.90E-01	5.80E-01	WT & nifD- N 1 dpi	CS	CASP-like protein (AHRD V3.3 *** K4B950_SOLLC)	
Solyc03g097500	**2.60E+00**	**5.96E-07**	**1.26E+00**	**3.77E-03**	-2.50E-01	5.30E-01	-4.01E-01	3.20E-01	WT & nifD- N 1 dpi	CS	Feruloyl transferase (AHRD V3.3 *** D5FPG8_SOLTU)	GO:0016747
Solyc03g098560	**2.56E+00**	**3.11E-04**	**2.03E+00**	**2.87E-03**	1.55E+00	2.00E-02	7.52E-01	2.30E-01	WT & nifD- N 1 dpi	DNA	zinc ion binding / nucleic acid binding protein (AHRD V3.3 --* AT3G43470.1)	
Solyc06g069640	**2.54E+00**	**5.00E-08**	**1.13E+00**	**2.35E-03**	4.86E-01	1.60E-01	-1.75E-01	1.01E+00	WT & nifD- N 1 dpi	DNA	dCTP pyrophosphatase 1 (AHRD V3.3 *** A0A151SL49_CAJCA)	GO:0047429
Solyc10g009240	**2.52E+00**	**2.62E-07**	**1.27E+00**	**1.75E-03**	1.20E-01	1.14E+00	9.26E-02	1.20E+00	WT & nifD- N 1 dpi	L	3-ketoacyl-CoA synthase (AHRD V3.3 *** B9GRP8_POPTR)	GO:0003824|GO:0008152GO:0006633|GO:0016020|GO:0016747
Solyc04g014650	**2.51E+00**	**6.79E-06**	**2.14E+00**	**6.04E-05**	1.19E-01	1.19E+00	9.43E-02	1.23E+00	WT & nifD- N 1 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* M1A662_SOLTU)	GO:0004672|GO:0005524|GO:0006468GO:0004672|GO:0006468
Solyc01g087810	**2.48E+00**	**2.99E-03**	**2.35E+00**	**4.56E-03**	1.61E+00	4.00E-02	1.40E+00	8.00E-02	WT & nifD- N 1 dpi	STR	subtilisin-like serine protease family protein	GO:0004252|GO:0006508
Solyc12g098590	**2.47E+00**	**9.37E-04**	**2.77E+00**	**2.92E-04**	-4.56E-01	5.00E-01	-4.66E-01	4.90E-01	WT & nifD- N 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DHN2_SOLLC)	GO:0008152|GO:0016758
Solyc09g008070	**2.44E+00**	**7.33E-07**	**1.54E+00**	**3.76E-04**	4.18E-01	2.80E-01	2.31E-01	5.40E-01	WT & nifD- N 1 dpi	G	cell division cycle 48 (AHRD V3.3 *** AT3G09840.1)	GO:0005524GO:0016787
Solyc09g098120	**2.42E+00**	**6.83E-03**	**2.76E+00**	**2.47E-03**	1.40E+00	1.00E-01	1.18E+00	1.60E-01	WT & nifD- N 1 dpi	H	Oil body-associated protein 1A (AHRD V3.3 *** OBP1A_ARATH)	
Solyc01g109390	**2.41E+00**	**7.11E-07**	**1.53E+00**	**3.45E-04**	8.96E-01	2.00E-02	9.09E-01	2.00E-02	WT & nifD- N 1 dpi	NA	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MM18_ARALL)	
Solyc01g103300	**2.41E+00**	**3.24E-05**	**1.34E+00**	**9.61E-03**	1.14E+00	2.00E-02	8.81E-01	8.00E-02	WT & nifD- N 1 dpi	DNA	SWIB/MDM2 and Plus-3 and GYF domain-containing protein (AHRD V3.3 *-* AT5G08430.1)	
Solyc04g072890	**2.40E+00**	**3.97E-08**	**1.74E+00**	**7.69E-06**	9.22E-01	1.00E-02	1.06E-01	1.14E+00	WT & nifD- N 1 dpi	G	Transducin/WD40 repeat protein (AHRD V3.3 *-* G8A379_MEDTR)	
Solyc06g035480	**2.40E+00**	**7.19E-08**	**1.69E+00**	**1.92E-05**	5.24E-01	1.20E-01	8.94E-01	1.00E-02	WT & nifD- N 1 dpi	K	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)	

Solyc03g005320	**2.39E+00**	**4.01E-08**	**1.58E+00**	**2.79E-05**	1.43E-01	1.05E+00	-1.74E-01	5.80E-01	WT & nifD- N 1 dpi	L	3-ketoacyl-CoA synthase (AHRD V3.3 *** M1A6B6_SOLTU)	GO:0003824|GO:0008152GO:0006633|GO:0016020|GO:0016747
Solyc08g067260	**2.37E+00**	**2.45E-06**	**1.24E+00**	**4.08E-03**	4.38E-01	2.70E-01	5.45E-01	1.80E-01	WT & nifD- N 1 dpi	L	3-ketoacyl-CoA synthase (AHRD V3.3 *** A0A0V0IHH6_SOLCH)	GO:0003824|GO:0008152GO:0006633|GO:0016020|GO:0016747
Solyc09g007020	**2.36E+00**	**8.63E-08**	**1.98E+00**	**1.66E-06**	3.64E-01	2.70E-01	9.41E-01	1.00E-02	WT & nifD- N 1 dpi	D	pathogenesis-related protein	GO:0005576
Solyc03g117690	**2.29E+00**	**1.20E-03**	**1.99E+00**	**3.95E-03**	9.79E-01	1.30E-01	6.91E-01	2.80E-01	WT & nifD- N 1 dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061GAK7_THECC)	GO:0004190|GO:0006508
Solyc12g009650	**2.25E+00**	**4.34E-08**	**1.30E+00**	**1.53E-04**	2.28E-01	4.40E-01	4.37E-01	1.50E-01	WT & nifD- N 1 dpi	PMI	SI proline-rich protein	
Solyc00g050430	**2.24E+00**	**8.74E-12**	**1.41E+00**	**9.15E-08**	1.45E-02	1.34E+00	3.98E-01	5.00E-02	WT & nifD- N 1 dpi	T	bHLH transcription factor 073	GO:0046983
Solyc07g042550	**2.18E+00**	**1.12E-16**	**1.36E+00**	**5.64E-12**	9.22E-01	0.00E+00	5.86E-01	0.00E+00	WT & nifD- N 1 dpi	C	Sucrose synthase (AHRD V3.3 *** SUS2_SOLTU)	GO:0005985|GO:0016157
Solyc05g010517	**2.13E+00**	**8.45E-08**	**1.12E+00**	**6.35E-04**	2.63E-01	3.70E-01	5.91E-01	5.00E-02	WT & nifD- N 1 dpi	T	BZip transcription factor (AHRD V3.3 *** Q9AT29_PHAVU)	GO:0003700|GO:0006355|GO:0043565
Solyc02g062900	**2.11E+00**	**3.45E-03**	**2.27E+00**	**1.87E-03**	8.48E-01	2.10E-01	1.21E-01	1.26E+00	WT & nifD- N 1 dpi	G	Polyol transporter (AHRD V3.3 --* I1W6X3_CAMSI)	
Solyc01g100020	**2.08E+00**	**4.66E-05**	**1.39E+00**	**3.18E-03**	-7.42E-02	1.26E+00	7.15E-02	1.27E+00	WT & nifD- N 1 dpi	L	Phospholipase D (AHRD V3.3 *** I1NJ37_SOYBN)	GO:0003824
Solyc07g006370	**2.04E+00**	**1.21E-03**	**1.65E+00**	**6.87E-03**	-2.28E-01	1.09E+00	8.51E-02	1.28E+00	WT & nifD- N 1 dpi	TR	Cation calcium exchanger (AHRD V3.3 *** A0A072U799_MEDTR)	GO:0016021|GO:0055085
Solyc01g096940	**1.96E+00**	**1.91E-04**	**1.48E+00**	**2.90E-03**	1.16E+00	2.00E-02	1.07E+00	3.00E-02	WT & nifD- N 1 dpi	S	Receptor-like kinase 17 (AHRD V3.3 *** A5A0Y6_SOLCH)	GO:0004672|GO:0005524|GO:0006468GO:0004672|GO:0006468
Solyc09g065390	**1.94E+00**	**1.17E-05**	**1.07E+00**	**6.01E-03**	3.49E-01	3.40E-01	1.31E-02	1.37E+00	WT & nifD- N 1 dpi	RNA	LOW QUALITY:Pre-mRNA cleavage complex 2 protein Pcf11, putative isoform 2 (AHRD V3.3 *-* A0A061GBF7_THECC)	
Solyc08g077910	**1.92E+00**	**3.12E-07**	**1.40E+00**	**3.68E-05**	2.86E-01	3.20E-01	9.55E-01	0.00E+00	WT & nifD- N 1 dpi	CS	Expansin-like protein (AHRD V3.3 *** W9S0F1_9ROSA)	GO:0005576
Solyc06g083590	**1.89E+00**	**7.35E-08**	**1.17E+00**	**1.05E-04**	7.27E-01	1.00E-02	4.46E-01	9.00E-02	WT & nifD- N 1 dpi	H	ABI3	GO:0003677
Solyc12g007160	**1.87E+00**	**7.89E-04**	**1.46E+00**	**6.23E-03**	1.28E+00	1.00E-02	1.16E+00	3.00E-02	WT & nifD- N 1 dpi	H	ABIL1-like protein (AHRD V3.3 *** B7FL53_MEDTR)	
Solyc04g008230	**1.87E+00**	**1.11E-04**	**2.04E+00**	**3.75E-05**	1.01E+00	2.00E-02	7.42E-01	8.00E-02	WT & nifD- N 1 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G48100.1)	GO:0004650|GO:0005975
Solyc08g078770	**1.78E+00**	**3.67E-04**	**1.52E+00**	**1.68E-03**	-2.79E-01	5.30E-01	1.56E-01	1.12E+00	WT & nifD- N 1 dpi	NA	LOW QUALITY:Plant/MNJ7-17 protein, putative (AHRD V3.3 *** G7JIX8_MEDTR)	
Solyc03g007380	**1.74E+00**	**8.95E-05**	**1.13E+00**	**6.01E-03**	3.17E-01	4.10E-01	9.54E-01	2.00E-02	WT & nifD- N 1 dpi	T	WRKY transcription factor 52	GO:0003700|GO:0006355|GO:0043565
Solyc02g083250	**1.69E+00**	**3.25E-10**	**1.16E+00**	**3.91E-07**	3.40E-01	6.00E-02	2.54E-01	1.50E-01	WT & nifD- N 1 dpi	NA	Ganglioside-induced differentiation-associated protein 2 (AHRD V3.3 *** A0A199VGA4_ANACO)	
Solyc09g065660	**1.67E+00**	**5.38E-04**	**1.30E+00**	**4.95E-03**	-1.01E+00	2.00E-02	3.09E-01	4.70E-01	WT & nifD- N 1 dpi	T	SolycHsfA7	GO:0003700|GO:0005634|GO:0006355|GO:0043565
Solyc04g012090	**1.65E+00**	**7.51E-05**	**1.23E+00**	**1.66E-03**	-1.63E-01	1.05E+00	-1.66E-01	1.04E+00	WT & nifD- N 1 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BPR1_SOLLC)	GO:0004672|GO:0005524|GO:0006468GO:0004672|GO:0006468
Solyc04g054340	**1.55E+00**	**2.98E-06**	**1.20E+00**	**9.83E-05**	7.76E-01	1.00E-02	3.12E-01	2.40E-01	WT & nifD- N 1 dpi	NA	LOW QUALITY:transmembrane protein (AHRD V3.3 --* AT5G65440.9)	
Solyc08g074300	**1.53E+00**	**3.84E-03**	**1.41E+00**	**6.87E-03**	-2.73E-02	1.36E+00	5.06E-01	3.00E-01	WT & nifD- N 1 dpi	T	NAC domain-containing protein (AHRD V3.3 *-* I6YR01_9CARY)	GO:0003677|GO:0006355
Solyc02g073571	**1.51E+00**	**3.44E-03**	**1.57E+00**	**2.57E-03**	-2.41E-02	1.36E+00	-1.28E-01	1.19E+00	WT & nifD- N 1 dpi	NA	UPF0183 protein family (AHRD V3.3 *-* A0A151TIL6_CAJCA)	
Solyc04g007150	**1.50E+00**	**1.15E-05**	**1.07E+00**	**6.56E-04**	5.79E-01	5.00E-02	1.71E-01	5.40E-01	WT & nifD- N 1 dpi	C	Alpha-glucosidase (AHRD V3.3 *** Q9LEC9_SOLTU)	GO:0003824GO:0003824|GO:0005975|GO:0030246
Solyc05g012520	**1.47E+00**	**9.36E-03**	**1.53E+00**	**7.19E-03**	-3.84E-01	4.70E-01	-4.13E-01	4.40E-01	WT & nifD- N 1 dpi	PMI	SNAP25 like protein SNAP33 (AHRD V3.3 *** A0A0B2SW23_GLYSO)	GO:0005515
Solyc04g072895	**1.46E+00**	**7.34E-11**	**1.15E+00**	**9.23E-09**	5.06E-01	0.00E+00	2.20E-01	1.20E-01	WT & nifD- N 1 dpi	G	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT1G78070.1)	GO:0005515
Solyc11g005070	**1.46E+00**	**7.39E-04**	**1.12E+00**	**6.88E-03**	-2.24E-02	1.35E+00	4.06E-01	3.00E-01	WT & nifD- N 1 dpi	AM	amino acid transporter 3	

Solyc04g055250	**1.43E+00**	**3.98E-06**	**1.06E+00**	**2.07E-04**	4.99E-01	5.00E-02	2.51E-01	3.20E-01	WT & nifD- N 1 dpi	DNA	Adenine deaminase 2 (AHRD V3.3 *-* A0A0B0PKM7_GOSAR)	
Solyc05g051890	**1.43E+00**	**2.04E-03**	**1.50E+00**	**1.32E-03**	1.50E-01	1.12E+00	3.49E-02	1.33E+00	WT & nifD- N 1 dpi	D	LOW QUALITY:Late embryogenesis abundant hydroxyproline-rich glycoprotein (AHRD V3.3 *** G7K2X8_MEDTR)	
Solyc00g006820	**1.40E+00**	**1.40E-05**	**1.20E+00**	**1.03E-04**	4.70E-01	8.00E-02	4.06E-01	1.30E-01	WT & nifD- N 1 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** A0A097PNX1_SOLLC)	GO:0005215|GO:0006810|GO:0016020GO:0005215|GO:0006857|GO:0016020
Solyc05g056470	**1.39E+00**	**1.19E-04**	**1.07E+00**	**1.85E-03**	4.48E-01	1.60E-01	5.74E-01	7.00E-02	WT & nifD- N 1 dpi	TR	ABC transporter family protein (AHRD V3.3 *** B9H498_POPTR)	GO:0005524|GO:0016887GO:0016020
Solyc07g008740	**1.38E+00**	**1.39E-03**	**1.71E+00**	**1.52E-04**	-1.28E-01	1.14E+00	7.03E-01	8.00E-02	WT & nifD- N 1 dpi	K	Kinase family protein (AHRD V3.3 *-* D7LXZ8_ARALL)	GO:0004672|GO:0005524|GO:0006468
Solyc08g078930	**1.38E+00**	**1.20E-08**	**1.16E+00**	**2.51E-07**	4.13E-01	2.00E-02	3.63E-01	4.00E-02	WT & nifD- N 1 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12520.1)	
Solyc01g081600	**1.35E+00**	**6.88E-05**	**1.44E+00**	**3.22E-05**	-2.08E-01	4.70E-01	4.00E-01	1.70E-01	WT & nifD- N 1 dpi	L	Non-specific lipid-transfer protein (AHRD V3.3 *** K4AY52_SOLLC)	GO:0006869|GO:0008289
Solyc06g065530	**1.31E+00**	**1.64E-04**	**1.25E+00**	**2.77E-04**	2.49E-01	4.10E-01	4.84E-01	1.10E-01	WT & nifD- N 1 dpi	L	GDSL-like lipase/acylhydrolase superfamily protein	GO:0016788
Solyc01g105800	**1.22E+00**	**3.72E-03**	**1.25E+00**	**3.09E-03**	7.45E-01	6.00E-02	6.62E-02	1.26E+00	WT & nifD- N 1 dpi	T	MADS box transcription factor (AHRD V1 **-- Q2NNB9_ELAGV)%3B contains Interpro domain(s) IPR002100 Transcription factor%2C MADS-box	GO:0000165|GO:0000977|GO:0045944GO:0003677|GO:0046983
Solyc11g072990	**1.07E+00**	**9.73E-03**	**1.10E+00**	**8.21E-03**	3.92E-01	3.20E-01	2.55E-01	5.10E-01	WT & nifD- N 1 dpi	L	3-ketoacyl-CoA synthase (AHRD V3.3 *** K4DB05_SOLLC)	GO:0003824|GO:0008152GO:0006633|GO:0016020|GO:0016747
Solyc03g113570	**1.07E+00**	**3.85E-07**	**1.05E+00**	**5.26E-07**	2.88E-01	8.00E-02	3.93E-01	2.00E-02	WT & nifD- N 1 dpi	STR	Germin-like protein	GO:0030145GO:0045735
Solyc03g121920	**1.04E+00**	**9.28E-06**	**1.12E+00**	**3.51E-06**	9.82E-01	0.00E+00	2.23E-01	2.50E-01	WT & nifD- N 1 dpi	TR	Mitochondrial carrier protein (AHRD V3.3 *** F8WLA3_CITUN)	GO:0055085
Solyc06g050760	**1.04E+00**	**4.68E-06**	**1.10E+00**	**2.02E-06**	7.84E-01	0.00E+00	4.22E-01	3.00E-02	WT & nifD- N 1 dpi	D	Wound-induced protein 1 (AHRD V3.3 *** WUN1_SOLTU)	
Solyc07g009080	**1.01E+00**	**5.92E-06**	**1.05E+00**	**3.00E-06**	1.24E-01	4.90E-01	7.01E-01	0.00E+00	WT & nifD- N 1 dpi	2M	AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT1G21530.1)	
Solyc01g099320	**-1.01E+00**	**4.41E-03**	**-1.10E+00**	**2.23E-03**	-9.95E-01	0.00E+00	-3.34E-01	3.10E-01	WT & nifD- N 1 dpi	T	Nuclear transcription factor Y protein (AHRD V3.3 *** G7I854_MEDTR)	GO:0005634|GO:0006355|GO:0043565GO:0046982
Solyc05g006310	**-1.03E+00**	**2.62E-03**	**-1.12E+00**	**1.25E-03**	-6.58E-01	4.00E-02	-1.79E-01	5.70E-01	WT & nifD- N 1 dpi	DNA	Zinc finger protein, putative (AHRD V3.3 *-* B9RSL7_RICCO)	GO:0003676GO:0046872
Solyc01g091030	**-1.06E+00**	**3.70E-05**	**-1.16E+00**	**1.03E-05**	-2.51E-01	2.50E-01	3.56E-01	1.10E-01	WT & nifD- N 1 dpi	H	Small auxin up-regulated RNA1	GO:0009733
Solyc12g096480	**-1.25E+00**	**1.54E-03**	**-1.54E+00**	**1.86E-04**	-3.91E-01	2.80E-01	-1.45E-01	1.08E+00	WT & nifD- N 1 dpi	AM	Glutamine dumper 4, putative (AHRD V3.3 *** A0A061GHE4_THECC)	
Solyc01g088160	**-1.31E+00**	**4.05E-03**	**-1.29E+00**	**4.59E-03**	-1.06E+00	2.00E-02	-3.61E-01	3.90E-01	WT & nifD- N 1 dpi	H	cytokinin oxidase2	GO:0003824|GO:0016614|GO:0050660|GO:0055114GO:0003824|GO:0050660|GO:0055114
Solyc08g083115	**-1.35E+00**	**3.49E-03**	**-1.17E+00**	**9.85E-03**	-6.24E-02	1.28E+00	1.68E-01	1.09E+00	WT & nifD- N 1 dpi	AM	Cystathionine gamma-synthase, putative (AHRD V3.3 *** B9RYU1_RICCO)	GO:0003824GO:0030170
Solyc06g064990	**-1.54E+00**	**1.40E-05**	**-1.16E+00**	**4.68E-04**	-7.94E-01	1.00E-02	-2.37E-01	4.20E-01	WT & nifD- N 1 dpi	L	Lipase, GDSL (AHRD V3.3 *** A0A124SDS7_CYNCS)	GO:0006629|GO:0016298GO:0016788
Solyc11g072620	**-1.60E+00**	**7.59E-07**	**-1.10E+00**	**1.46E-04**	-6.57E-01	1.00E-02	-2.84E-01	2.60E-01	WT & nifD- N 1 dpi	DNA	LOW QUALITY:G patch domain-containing protein 1 (AHRD V3.3 --* A0A1D1XCL3_9ARAE)	
Solyc11g072670	**-1.60E+00**	**2.35E-03**	**-1.38E+00**	**7.44E-03**	4.03E-01	4.00E-01	8.40E-01	9.00E-02	WT & nifD- N 1 dpi	RNA	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT4G00830.6)	
Solyc01g059950	**-2.10E+00**	**4.59E-04**	**-1.53E+00**	**7.14E-03**	-3.90E-01	4.60E-01	-1.03E-02	1.38E+00	WT & nifD- N 1 dpi	H	LOW QUALITY:GAI-like protein 1	
Solyc03g119590	**-2.12E+00**	**1.41E-03**	**-2.37E+00**	**4.95E-04**	-8.56E-01	1.60E-01	9.03E-02	1.28E+00	WT & nifD- N 1 dpi	D	LOW QUALITY:NIMIN2c protein (AHRD V3.3 *** A0FJY4_TOBAC)	
Solyc11g012130	**-2.17E+00**	**5.70E-08**	**-1.00E+00**	**1.80E-03**	-9.92E-01	0.00E+00	-2.00E-01	4.90E-01	WT & nifD- N 1 dpi	E	Blue copper protein (AHRD V3.3 *** A0A0B2RLQ3_GLYSO)	GO:0009055
Solyc05g050870	**-2.23E+00**	**3.11E-04**	**-1.74E+00**	**3.32E-03**	-1.85E-01	1.13E+00	1.42E+00	1.00E-02	WT & nifD- N 1 dpi	OX	Peroxidase (AHRD V3.3 *** K4C1C0_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114GO:0004601|GO:0042744
Solyc10g050730	**-2.54E+00**	**3.90E-03**	**-2.28E+00**	**8.56E-03**	-8.61E-01	2.90E-01	4.61E-01	5.70E-01	WT & nifD- N 1 dpi	E	Plastocyanin-like domain protein (AHRD V3.3 *** G7JMH1_MEDTR)	GO:0009055
Solyc02g094860	**-2.75E+00**	**6.17E-08**	**-2.44E+00**	**4.64E-07**	-5.34E-02	1.29E+00	3.72E-01	3.20E-01	WT & nifD- N 1 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9RSK4_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114

Solyc04g051690	**-2.82E+00**	**6.45E-07**	**-1.47E+00**	**2.17E-03**	-7.38E-01	1.00E-01	-4.75E-01	2.80E-01	WT & nifD- N 1 dpi	T	WRKY transcription factor 51	GO:0003700|GO:0006355|GO:0043565
Solyc01g105870	**-3.26E+00**	**7.48E-05**	**-1.99E+00**	**8.10E-03**	1.97E-01	1.18E+00	-3.18E-01	1.05E+00	WT & nifD- N 1 dpi	2M	(E)-beta-ocimene synthase (AHRD V1 **** Q5CD81_CITUN)%3B contains Interpro domain(s) IPR005630 Terpene synthase%2C metal-binding domain	GO:0000287|GO:0010333|GO:0016829GO:0008152|GO:0010333|GO:0016829
Solyc10g078270	**-3.79E+00**	**2.75E-03**	**-3.78E+00**	**2.84E-03**	-3.34E-02	1.38E+00	-3.68E-01	1.15E+00	WT & nifD- N 1 dpi	H	WAT1-related protein (AHRD V3.3 *** K4D269_SOLLC)	GO:0016020|GO:0016021GO:0016021|GO:0022857
Solyc05g053150	**-3.80E+00**	**4.88E-04**	**-3.24E+00**	**2.18E-03**	6.98E-02	1.34E+00	7.95E-02	1.33E+00	WT & nifD- N 1 dpi	G	R2R3MYB transcription factor 71	GO:0003677
Solyc06g082420	**-4.14E+00**	**1.93E-03**	**-3.76E+00**	**4.28E-03**	-2.49E+00	5.00E-02	5.17E-01	1.07E+00	WT & nifD- N 1 dpi	OX	Peroxidase (AHRD V3.3 *-* K4CAA1_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114GO:0004601|GO:0042744
Solyc01g108350	**-4.52E+00**	**1.86E-03**	**-3.75E+00**	**7.89E-03**	-1.56E+00	2.40E-01	5.46E-01	1.08E+00	WT & nifD- N 1 dpi	E	Plastocyanin-like domain protein (AHRD V3.3 *** G7JMH4_MEDTR)	GO:0009055
Solyc08g080700	2.15E+00	1.00E-02	1.24E+00	0.00E+00	**2.50E+00**	**3.82E-03**	**2.63E+00**	**2.51E-03**	WT & nifD- NoN 1 dpi	NA	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)	
Solyc04g077990	1.81E+00	3.00E-02	2.82E-02	0.00E+00	**4.59E+00**	**4.06E-06**	**3.49E+00**	**1.55E-04**	WT & nifD- NoN 1 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9SND0_RICCO)	
Solyc07g061720	1.36E+00	2.00E-02	1.65E-01	0.00E+00	**1.81E+00**	**3.33E-03**	**2.07E+00**	**9.94E-04**	WT & nifD- NoN 1 dpi	H	gibberellin 2-oxidase 4	GO:0016491|GO:0055114
Solyc05g052650	1.24E+00	3.00E-02	1.19E+00	0.00E+00	**1.75E+00**	**3.55E-03**	**1.76E+00**	**3.37E-03**	WT & nifD- NoN 1 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *-* V5PZN5_9CARY)	GO:0016747
Solyc02g089710	1.19E+00	2.20E-01	1.10E+00	0.00E+00	**3.45E+00**	**1.22E-03**	**4.34E+00**	**1.09E-04**	WT & nifD- NoN 1 dpi	CS	Trichome birefringence-like protein (AHRD V3.3 *** A0A072TUJ8_MEDTR)	
Solyc10g080620	1.14E+00	7.00E-02	1.20E+00	0.00E+00	**2.13E+00**	**1.51E-03**	**1.90E+00**	**3.87E-03**	WT & nifD- NoN 1 dpi	E	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 2 A, chloroplastic (AHRD V3.3 -* NU2C1_HORVU)	
Solyc06g007580	1.04E+00	2.00E-02	3.34E-01	0.00E+00	**1.81E+00**	**1.76E-04**	**1.55E+00**	**8.83E-04**	WT & nifD- NoN 1 dpi	NA	LOW QUALITY:DUF506 family protein (AHRD V3.3 *** G7LF52_MEDTR)	
Solyc07g062490	1.01E+00	2.00E-02	3.55E-01	0.00E+00	**1.56E+00**	**7.21E-04**	**1.49E+00**	**1.12E-03**	WT & nifD- NoN 1 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A067JEE7_JATCU)	
Solyc10g055820	9.68E-01	1.00E-02	3.66E-01	0.00E+00	**2.53E+00**	**6.68E-08**	**1.17E+00**	**1.92E-03**	WT & nifD- NoN 1 dpi	D	Chitinase (AHRD V3.3 *** B9VRK7_CAPAN)	GO:0004568|GO:0005975GO:0004568|GO:0006032|GO:0016998
Solyc10g085500	9.53E-01	3.00E-02	9.07E-01	1.00E-02	**-1.54E+00**	**1.11E-03**	**-1.18E+00**	**9.35E-03**	WT & nifD- NoN 1 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9SRM6_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114GO:0016705|GO:0055114
Solyc01g106610	9.44E-01	0.00E+00	3.52E-01	0.00E+00	**2.00E+00**	**2.58E-07**	**1.12E+00**	**6.23E-04**	WT & nifD- NoN 1 dpi	D	LEPR1A1A	GO:0005576
Solyc01g102875	9.06E-01	1.00E-02	6.22E-01	0.00E+00	**1.27E+00**	**6.05E-04**	**1.36E+00**	**3.02E-04**	WT & nifD- NoN 1 dpi	STR	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)	GO:0030145GO:0045735
Solyc04g009040	8.86E-01	8.00E-02	1.05E+00	0.00E+00	**2.19E+00**	**1.31E-04**	**2.28E+00**	**7.84E-05**	WT & nifD- NoN 1 dpi	S	Receptor-kinase, putative (AHRD V3.3 *** B9SZK5_RICCO)	GO:0004672|GO:0005524|GO:0006468GO:0004672|GO:0006468
Solyc08g079900	8.16E-01	2.00E-01	3.73E-01	0.00E+00	**3.71E+00**	**2.38E-06**	**2.35E+00**	**7.39E-04**	WT & nifD- NoN 1 dpi	STR	subtilisin-like protease	GO:0004252|GO:0006508
Solyc10g087010	7.65E-01	2.00E-02	4.22E-02	0.00E+00	**1.40E+00**	**1.03E-04**	**1.03E+00**	**2.25E-03**	WT & nifD- NoN 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103XWG4_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114GO:0016705|GO:0055114
Solyc03g114180	7.59E-01	0.00E+00	7.52E-01	0.00E+00	**2.65E+00**	**9.26E-12**	**1.63E+00**	**1.31E-07**	WT & nifD- NoN 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BKS0_SOLLC)	GO:0008152|GO:0016758
Solyc11g005970	7.55E-01	1.60E-01	1.81E-02	1.00E-02	**1.72E+00**	**2.70E-03**	**1.46E+00**	**9.06E-03**	WT & nifD- NoN 1 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JUV1_CYNCS)	GO:0005515GO:0008270
Solyc07g022830	7.55E-01	0.00E+00	4.64E-01	0.00E+00	**2.20E+00**	**1.25E-11**	**1.14E+00**	**2.69E-06**	WT & nifD- NoN 1 dpi	CS	EXS family protein (AHRD V3.3 *** B9MXW8_POPTR)	GO:0016021
Solyc02g005280	6.28E-01	9.00E-02	-1.21E-01	0.00E+00	**1.47E+00**	**3.39E-04**	**1.13E+00**	**3.78E-03**	WT & nifD- NoN 1 dpi	RNA	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061E854_THECC)	
Solyc02g088987	6.26E-01	2.90E-01	-7.03E-02	0.00E+00	**3.80E+00**	**5.49E-07**	**2.92E+00**	**2.84E-05**	WT & nifD- NoN 1 dpi	DNA	LOW QUALITY:Arginine/serine-rich splicing factor, putative (AHRD V3.3 --* B9T7V5_RICCO)	GO:0003676|GO:0008270
Solyc02g085910	6.02E-01	4.00E-02	3.99E-02	0.00E+00	**1.38E+00**	**4.95E-05**	**1.13E+00**	**5.24E-04**	WT & nifD- NoN 1 dpi	G	LOB domain-containing protein (AHRD V3.3 *** A0A0K9PUI8_ZOSMR)	
Solyc02g084600	6.01E-01	8.00E-02	5.84E-01	0.00E+00	**1.24E+00**	**9.60E-04**	**1.28E+00**	**7.03E-04**	WT & nifD- NoN 1 dpi	PMI	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** A0A061DFG6_THECC)	GO:0005515
Solyc07g064450	5.85E-01	4.80E-01	-4.57E-01	1.00E-02	**-2.47E+00**	**5.87E-03**	**-2.31E+00**	**9.39E-03**	WT & nifD- NoN 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A061FD55_THECC)	GO:0005506|GO:0016705|GO:0020037|GO:0055114GO:0016705|GO:0055114

Solyc06g036467	5.75E-01	1.30E-01	5.79E-01	0.00E+00	**1.61E+00**	**1.78E-04**	**1.24E+00**	**2.37E-03**	WT & nifD- NoN 1 dpi	K	Protein kinase, putative (AHRD V3.3 *-* Q1EP57_MUSBA)	
Solyc01g102890	5.18E-01	2.00E-01	1.53E-01	0.00E+00	**1.83E+00**	**8.55E-05**	**2.30E+00**	**3.60E-06**	WT & nifD- NoN 1 dpi	STR	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)	GO:0030145GO:0045735
Solyc07g043170	5.14E-01	4.00E-02	5.52E-01	0.00E+00	**1.68E+00**	**1.08E-07**	**1.02E+00**	**1.66E-04**	WT & nifD- NoN 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CEH7_SOLLC)	GO:0008152|GO:0016758
Solyc08g080640	5.11E-01	6.00E-02	3.56E-01	0.00E+00	**1.32E+00**	**2.19E-05**	**1.19E+00**	**8.73E-05**	WT & nifD- NoN 1 dpi	D	Osmotin-like protein (Fragment) IPR017949 Thaumatin, conserved site IPR001938	
Solyc08g080310	4.89E-01	4.10E-01	1.34E+00	0.00E+00	**3.16E+00**	**1.08E-05**	**2.72E+00**	**7.91E-05**	WT & nifD- NoN 1 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4CP31_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc10g084085	4.49E-01	1.50E-01	-9.67E-02	0.00E+00	**1.38E+00**	**1.15E-04**	**1.76E+00**	**4.23E-06**	WT & nifD- NoN 1 dpi	D	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT5G41540.1)	
Solyc06g075970	4.38E-01	4.30E-01	1.01E+00	0.00E+00	**2.30E+00**	**2.52E-04**	**3.96E+00**	**1.01E-07**	WT & nifD- NoN 1 dpi	TR	P-hydroxybenzoic acid efflux pump subunit aaeB (AHRD V3.3 *** A0A061GW63_THECC)	
Solyc03g031450	3.70E-01	1.70E-01	9.51E-01	0.00E+00	**1.65E+00**	**9.98E-07**	**1.61E+00**	**1.55E-06**	WT & nifD- NoN 1 dpi	DNA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G61660.7)	GO:0046983
Solyc02g063410	3.68E-01	6.80E-01	-3.15E-01	0.00E+00	**3.47E+00**	**4.84E-04**	**3.81E+00**	**1.75E-04**	WT & nifD- NoN 1 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)	
Solyc03g119180	3.58E-01	4.50E-01	-4.29E-01	0.00E+00	**-2.52E+00**	**1.31E-05**	**-1.74E+00**	**9.88E-04**	WT & nifD- NoN 1 dpi	P	LOW QUALITY:Lysine--tRNA ligase (AHRD V3.3 --* V7B2W1_PHAVU)	
Solyc08g066710	2.82E-01	6.50E-01	5.95E-01	0.00E+00	**-2.44E+00**	**5.17E-04**	**-2.30E+00**	**9.34E-04**	WT & nifD- NoN 1 dpi	2M	Carotenoid 9,10(9',10')-cleavage dioxygenase 1, putative isoform 1 (AHRD V3.3 *-* A0A061GK16_THECC)	
Solyc07g062200	2.72E-01	5.20E-01	4.25E-01	1.00E-02	**2.36E+00**	**6.99E-06**	**1.20E+00**	**8.48E-03**	WT & nifD- NoN 1 dpi	T	bHLH transcription factor 088	GO:0003677GO:0046983
Solyc02g083690	2.64E-01	5.20E-01	4.09E-01	0.00E+00	**1.61E+00**	**4.84E-04**	**1.66E+00**	**3.49E-04**	WT & nifD- NoN 1 dpi	STR	LOW QUALITY:Senescence/dehydration-associated protein-like protein (AHRD V3.3 *** AT2G17840.1)	
Solyc07g063930	2.13E-01	5.80E-01	-1.10E-01	0.00E+00	**1.19E+00**	**4.07E-03**	**1.88E+00**	**3.56E-05**	WT & nifD- NoN 1 dpi	TR	Organic cation transporter, putative (AHRD V3.3 *** B9SY49_RICCO)	GO:0005215|GO:0016021|GO:0055085GO:0016021|GO:0022857|GO:0055085
Solyc02g090480	2.00E-01	3.70E-01	1.12E-01	0.00E+00	**1.08E+00**	**4.14E-05**	**1.08E+00**	**3.92E-05**	WT & nifD- NoN 1 dpi	P	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0V0I8Y4_SOLCH)	GO:0000413|GO:0003755|GO:0006457GO:0003755|GO:0006457
Solyc01g094910	1.86E-01	7.30E-01	-7.77E-02	0.00E+00	**-5.87E+00**	**2.47E-11**	**-2.74E+00**	**2.09E-05**	WT & nifD- NoN 1 dpi	TR	ferric-chelate reductase	GO:0016491|GO:0055114
Solyc01g102910	1.64E-01	7.60E-01	3.20E-01	0.00E+00	**3.58E+00**	**4.06E-07**	**2.37E+00**	**1.46E-04**	WT & nifD- NoN 1 dpi	STR	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)	GO:0030145GO:0045735
Solyc01g108450	1.11E-01	7.20E-01	8.66E-02	0.00E+00	**1.05E+00**	**1.90E-03**	**1.13E+00**	**9.53E-04**	WT & nifD- NoN 1 dpi	STR	Carboxypeptidase (AHRD V3.3 *** K4B360_SOLLC)	GO:0004185|GO:0006508
Solyc06g053850	1.06E-01	6.70E-01	-2.25E-02	0.00E+00	**1.53E+00**	**1.34E-06**	**1.50E+00**	**1.79E-06**	WT & nifD- NoN 1 dpi	RNA	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9RTF6_RICCO)	GO:0005515
Solyc07g063830	1.03E-01	6.10E-01	5.74E-01	0.00E+00	**1.38E+00**	**2.97E-07**	**1.34E+00**	**5.31E-07**	WT & nifD- NoN 1 dpi	T	bHLH transcription factor142	GO:0046983
Solyc06g005310	6.49E-04	1.00E+00	5.35E-02	0.00E+00	**1.28E+00**	**1.04E-04**	**1.17E+00**	**3.04E-04**	WT & nifD- NoN 1 dpi	T	MYB transcription factor	GO:0003677
Solyc11g045520	-2.00E-02	9.60E-01	4.69E-02	0.00E+00	**-1.96E+00**	**2.28E-05**	**-1.89E+00**	**3.65E-05**	WT & nifD- NoN 1 dpi	H	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE-like protein	GO:0016491|GO:0055114
Solyc01g059965	-7.14E-02	9.40E-01	-2.24E-01	0.00E+00	**3.55E+00**	**1.46E-03**	**3.53E+00**	**1.53E-03**	WT & nifD- NoN 1 dpi	CS	Beta-1,3-glucanase (AHRD V3.3 *** G9G7S0_HEVBR)	GO:0004553|GO:0005975GO:0005975
Solyc03g006720	-1.16E-01	8.80E-01	-1.44E-01	0.00E+00	**-2.97E+00**	**4.39E-04**	**-3.91E+00**	**1.56E-05**	WT & nifD- NoN 1 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** A0A059C900_EUCGR)	GO:0004672|GO:0005524|GO:0006468GO:0004672|GO:0006468
Solyc01g100100	-1.22E-01	6.80E-01	7.26E-01	0.00E+00	**1.12E+00**	**8.63E-04**	**1.05E+00**	**1.49E-03**	WT & nifD- NoN 1 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061E1W0_THECC)	GO:0005515|GO:0008270
Solyc12g100300	-1.45E-01	6.90E-01	-2.39E-01	0.00E+00	**-2.02E+00**	**5.79E-06**	**-1.36E+00**	**7.09E-04**	WT & nifD- NoN 1 dpi	TR	Metal tolerance protein (AHRD V3.3 *** D7RJ71_CARPA)	GO:0006812|GO:0008324|GO:0016021|GO:0055085
Solyc02g083860	-1.55E-01	6.10E-01	-3.61E-01	0.00E+00	**-1.65E+00**	**9.40E-06**	**-1.11E+00**	**1.01E-03**	WT & nifD- NoN 1 dpi	2M	flavanone 3-dioxygenase	GO:0016491|GO:0055114
Solyc12g096890	-1.72E-01	8.30E-01	-4.70E-02	0.00E+00	**2.64E+00**	**3.16E-03**	**2.99E+00**	**1.04E-03**	WT & nifD- NoN 1 dpi	P	F-box protein PP2 (AHRD V3.3 *** A0A059PC27_CICAR)	
Solyc01g107190	-2.34E-01	3.80E-01	-2.12E-01	0.00E+00	**1.89E+00**	**1.39E-07**	**1.12E+00**	**2.39E-04**	WT & nifD- NoN 1 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9SGY6_RICCO)	

Solyc01g100490	-2.43E-01	4.40E-01	-1.67E-01	0.00E+00	**-1.35E+00**	**1.64E-04**	**-1.01E+00**	**2.91E-03**	WT & nifD- NoN 1 dpi	TR	chloronerva	GO:0030410|GO:0030418
Solyc01g067440	-3.06E-01	5.90E-01	1.82E-01	0.00E+00	**3.17E+00**	**5.23E-06**	**2.27E+00**	**3.68E-04**	WT & nifD- NoN 1 dpi	OX	Glutaredoxin family protein (AHRD V3.3 *** AT3G21460.1)	GO:0009055|GO:0015035|GO:0045454
Solyc09g065750	-4.92E-01	4.10E-01	6.66E-02	1.00E-02	**-3.23E+00**	**8.30E-06**	**-1.67E+00**	**8.23E-03**	WT & nifD- NoN 1 dpi	2M	Beta-carotene isomerase D27 (AHRD V3.3 *** R4HZ96_MEDTR)	
Solyc11g071830	-6.07E-01	1.10E-01	1.99E-01	1.00E-02	**-1.32E+00**	**1.45E-03**	**-1.06E+00**	**8.24E-03**	WT & nifD- NoN 1 dpi	STR	DnaJ protein homolog (AHRD V3.3 *** DNJH_CUCSA)	GO:0005524|GO:0006457|GO:0009408|GO:0051082GO:0006457|GO:0051082
Solyc08g065500	-7.28E-01	2.00E-02	-7.70E-03	0.00E+00	**1.88E+00**	**9.92E-07**	**1.19E+00**	**4.53E-04**	WT & nifD- NoN 1 dpi	K	Phosphatase 2C family protein (AHRD V3.3 *** A0A061GL17_THECC)	GO:0003824GO:0004722|GO:0006470
Solyc10g018150	-7.28E-01	7.00E-02	-2.46E-01	1.00E-02	**-2.31E+00**	**2.46E-06**	**-1.18E+00**	**5.08E-03**	WT & nifD- NoN 1 dpi	2M	SlCytochromeP450	GO:0005506|GO:0016705|GO:0020037|GO:0055114GO:0016705|GO:0055114
Solyc07g063610	-8.64E-01	1.60E-01	6.17E-02	0.00E+00	**-1.71E+00**	**7.95E-03**	**-2.03E+00**	**2.10E-03**	WT & nifD- NoN 1 dpi	CS	Dynein light chain family protein (AHRD V3.3 *** B9N570_POPTR)	GO:0007017|GO:0030286
Solyc01g005940	-1.18E+00	3.00E-02	-1.40E+00	0.00E+00	**-2.93E+00**	**5.10E-06**	**-2.22E+00**	**1.90E-04**	WT & nifD- NoN 1 dpi	2M	Phytoene synthase (AHRD V3.3 *** A0A0K1L5A0_MALDO)	GO:0004310|GO:0006696|GO:0051996GO:0009058|GO:0016740

Table S 5. List of differentially expressed genes (DEGs) modulated in tomato roots both after inoculation with Gluconacetobacter diazotrophicus AZ0019 WT and nifD- strain at fourteen days post inoculum (dpi) in presence or absence of nitrogen in plants growth medium. *Clustering results of the DEGs, classified as genes significantly modulated at 14 dpi (in bold, P ≤ 0.01 and Log2 (fold change) ≥ 1 or ≤ -1) by G. diazotrophicus AZ0019 WT and nifD- mutant strain in the absence (WT & nifD- NoN) or presence of 2 mM KNO_3 (WT & nifD- N) in the growth substrate. Tomato gene identifier (ITAG3.2 release), Log2-transformed fold change values and P values calculated for each pairwise comparison between WT inoculated and nifD- inoculated simples are reported. Protein description and abbreviation codes of functional classes were assigned on the basis of the protein description and function. Gene ontology (GO) terms were based on the ITAG3.2 release (https://solgenomics.net/organism/Solanum_lycopersicum/genome).*

Gene ID	WT N	P.Value	*nifD* - N	P. Value	WT NoN	P. Value	*nifD*- NoN	P.Value	Cluster	Functional Class	Gene Description	GO
Solyc08g065680.2	**6.40E+00**	**2.68E-15**	**6.68E+00**	**9.77E-16**	-7.66E-01	5.65E-02	9.63E-01	1.87E-02	WT & nifD- N 14 dpi	K	Phosphatase 2C family protein (AHRD V3.3 *** A0A061GL17_THECC)	GO:0003824|GO:0004722|GO:0006470|GO:0004722|GO:0006470
Solyc09g082280.3	**6.39E+00**	**7.13E-07**	**5.38E+00**	**9.81E-06**	2.29E+00	2.79E-02	1.54E+00	1.29E-01	WT & nifD- N 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** Q5MJA5_CAPAN)	
Solyc04g079505.1	**6.23E+00**	**6.29E-12**	**6.51E+00**	**2.39E-12**	7.64E-02	8.85E-01	2.03E-01	7.02E-01	WT & nifD- N 14 dpi	P	Serpin-like protein (AHRD V3.3 *-* G7J5S6_MEDTR)	GO:0005615
Solyc03g122360.3	**5.85E+00**	**6.91E-15**	**7.09E+00**	**6.94E-17**	4.61E-01	2.18E-01	-6.89E-01	7.03E-02	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q0PNH1_CAPCH)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc03g078500.3	**5.53E+00**	**2.56E-06**	**6.96E+00**	**5.38E-08**	-3.79E+00	3.51E-04	-2.26E+00	2.10E-02	WT & nifD- N 14 dpi	2M	UDP-glucuronosyltransferase	GO:0008152|GO:0016758
Solyc01g059900.3	**5.34E+00**	**9.75E-10**	**6.34E+00**	**2.80E-11**	-2.50E+00	1.79E-04	-2.15E+00	8.77E-04	WT & nifD- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4AW97_SOLLC)	
Solyc00g134620.2	**5.29E+00**	**1.09E-07**	**2.95E+00**	**4.18E-04**	-1.57E+00	4.04E-02	-7.52E-01	3.11E-01	WT & nifD- N 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *-* A0A061G9X2_THECC)	GO:0016747
Solyc08g013900.3	**5.26E+00**	**2.34E-10**	**5.72E+00**	**4.07E-11**	-3.26E-01	5.41E-01	1.31E-02	9.80E-01	WT & nifD- N 14 dpi	DNA	Plant regulator RWP-RK family protein (AHRD V3.3 *** AT2G43500.9)	GO:0005515
Solyc08g065540.3	**5.23E+00**	**2.73E-16**	**5.87E+00**	**1.66E-17**	7.55E-03	9.79E-01	3.20E-01	2.72E-01	WT & nifD- N 14 dpi	K	Phosphatase 2C family protein (AHRD V3.3 *** A0A061GL17_THECC)	GO:0003824|GO:0004722|GO:0006470|GO:0004722|GO:0006470
Solyc07g014580.3	**5.10E+00**	**6.03E-09**	**4.29E+00**	**1.44E-07**	-3.25E+00	1.14E-05	-3.03E+00	3.06E-05	WT & nifD- N 14 dpi	S	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061G8N7_THECC)	GO:0016747
Solyc08g079300.3	**5.00E+00**	**1.76E-08**	**5.88E+00**	**7.56E-10**	-2.71E+00	1.91E-04	-2.24E+00	1.32E-03	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc00g040290.2	**5.00E+00**	**1.80E-06**	**3.52E+00**	**2.03E-04**	-9.58E-01	2.50E-01	-6.55E-01	4.28E-01	WT & nifD- N 14 dpi	S	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT1G32910.1)	GO:0016747
Solyc03g097610.3	**4.75E+00**	**3.69E-05**	**5.57E+00**	**3.94E-06**	-1.64E+00	9.82E-02	1.32E+00	1.78E-01	WT & nifD- N 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJH8_SOLLC)	GO:0016021
Solyc07g006370.1	**4.61E+00**	**1.19E-08**	**4.95E+00**	**3.13E-09**	7.05E-01	2.21E-01	6.97E-01	2.26E-01	WT & nifD- N 14 dpi	TR	Cation calcium exchanger (AHRD V3.3 *** A0A072U799_MEDTR)	GO:0016021|GO:0055085

Solyc03g097870.3	**4.59E+00**	**2.44E-06**	**5.31E+00**	**2.29E-07**	-2.78E+00	1.21E-03	-1.18E-01	8.79E-01	WT & nifD- N 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJK4_SOLLC)	GO:0016021
Solyc10g045580.1	**4.54E+00**	**2.51E-04**	**3.86E+00**	**1.28E-03**	-1.46E+00	1.83E-01	1.27E+00	2.45E-01	WT & nifD- N 14 dpi	E	Cytochrome c oxidase subunit 5C (AHRD V3.3 *** Q9ZTN1_PETHY)	GO:0005746
Solyc09g066050.2	**4.41E+00**	**1.30E-04**	**2.88E+00**	**6.92E-03**	1.13E+00	2.58E-01	1.01E+00	3.13E-01	WT & nifD- N 14 dpi	DNA	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072UAM9_MEDTR)	GO:0008289
Solyc03g122330.1	**4.24E+00**	**1.57E-05**	**4.26E+00**	**1.45E-05**	1.23E+00	1.37E-01	-4.87E-01	5.48E-01	WT & nifD- N 14 dpi	C	LOW QUALITY:trehalose-6-phosphatase synthase S8 (AHRD V3.3 --* AT1G70290.2)	
Solyc02g030480.3	**4.22E+00**	**1.66E-05**	**4.68E+00**	**3.76E-06**	-3.12E-02	9.69E-01	-1.20E+00	1.46E-01	WT & nifD- N 14 dpi	2M	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9R8D9_RICCO)	GO:0008270|GO:0016491|GO:0055114|GO:0016491|GO:0016491
Solyc04g006950.3	**4.19E+00**	**2.10E-07**	**6.13E+00**	**1.47E-10**	-1.40E+00	2.75E-02	-7.94E-01	1.97E-01	WT & nifD- N 14 dpi	DNA	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1 (AHRD V3.3 --* A0A1D1YML1_9ARAE)	
Solyc06g074995.1	**4.18E+00**	**1.85E-05**	**4.33E+00**	**1.14E-05**	6.61E-01	4.14E-01	1.10E+00	1.79E-01	WT & nifD- N 14 dpi	N	High affinity nitrate transporter protein (AHRD V3.3 *-* Q84MZ9_TOBAC)	
Solyc01g095820.2	**4.17E+00**	**8.00E-17**	**4.42E+00**	**1.93E-17**	-3.05E-01	1.69E-01	1.69E-01	4.40E-01	WT & nifD- N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G25410.1)	GO:0005515|GO:0008270
Solyc01g009580.2	**4.13E+00**	**2.21E-03**	**4.19E+00**	**1.94E-03**	1.49E+00	2.30E-01	-5.19E-01	6.73E-01	WT & nifD- N 14 dpi	G	Terminal flower 1-like protein (AHRD V3.3 *** A0A0S1LKM5_CHRMO)	
Solyc03g005420.2	**4.05E+00**	**5.92E-05**	**3.26E+00**	**6.78E-04**	1.47E+00	9.37E-02	-2.77E-01	7.46E-01	WT & nifD- N 14 dpi	P	SPFH/Band 7/PHB domain-containing membrane-associated protein family (AHRD V3.3 *** AT5G25260.1)	
Solyc10g086680.1	**4.00E+00**	**2.83E-04**	**4.30E+00**	**1.25E-04**	1.84E+00	6.43E-02	1.21E+00	2.14E-01	WT & nifD- N 14 dpi	STR	Class I heat shock protein (AHRD V3.3 *** F4YBC5_SOLNI)	
Solyc02g021220.1	**3.96E+00**	**3.47E-04**	**4.61E+00**	**5.77E-05**	2.52E+00	1.45E-02	8.96E-01	3.59E-01	WT & nifD- N 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** W9R4Z9_9ROSA)	GO:0004252|GO:0006508
Solyc06g053950.2	**3.75E+00**	**1.23E-07**	**2.56E+00**	**4.13E-05**	2.78E-01	5.97E-01	1.39E+00	1.26E-02	WT & nifD- N 14 dpi	STR	Heat shock transcription factor (AHRD V3.3 *-* A0A076L230_GOSHI)	
Solyc03g006120.3	**3.73E+00**	**7.93E-08**	**3.45E+00**	**3.06E-07**	-5.56E-01	2.79E-01	5.50E-03	9.91E-01	WT & nifD- N 14 dpi	T	transcription factor-like protein (AHRD V3.3 *** AT3G14880.2)	GO:0006351|GO:0043565
Solyc06g053960.3	**3.71E+00**	**7.21E-07**	**2.54E+00**	**1.48E-04**	1.59E-01	7.82E-01	1.08E+00	6.94E-02	WT & nifD- N 14 dpi	STR	SolycHsfA6b	GO:0003700|GO:0005634|GO:0006355|GO:00
Solyc11g069750.2	**3.70E+00**	**4.73E-16**	**3.84E+00**	**2.02E-16**	-1.88E+00	1.52E-09	1.26E-01	5.48E-01	WT & nifD- N 14 dpi	N	High-affinity nitrate transporter (AHRD V3.3 *** Q76IJ7_PRUPE)	GO:0016021|GO:0055085
Solyc08g065670.3	**3.70E+00**	**2.25E-14**	**4.10E+00**	**2.06E-15**	-4.40E-02	8.58E-01	2.90E-01	2.43E-01	WT & nifD- N 14 dpi	K	Phosphatase 2C family protein (AHRD V3.3 *** A0A061GL17_THECC)	GO:0003824|GO:0004722|GO:0006470|GO:0004722|GO:0006470
Solyc10g078270.2	**3.68E+00**	**3.52E-03**	**5.78E+00**	**3.01E-05**	-7.40E-01	5.24E-01	-1.35E+00	2.50E-01	WT & nifD- N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4D269_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc12g098270.1	**3.66E+00**	**2.78E-04**	**3.42E+00**	**5.63E-04**	-2.27E-01	7.96E-01	3.05E-01	7.29E-01	WT & nifD- N 14 dpi	NA	LOW QUALITY:Unknown protein (AHRD V3.3)	
Solyc05g050010.3	**3.52E+00**	**7.69E-05**	**3.19E+00**	**2.42E-04**	4.22E-01	5.78E-01	1.34E+00	8.64E-02	WT & nifD- N 14 dpi	H	1-aminocyclopropane-1-carboxylic acid synthase-4	GO:0003824|GO:0003824|GO:0009058|GO:0030170|GO:0003824|GO:0009058|GO:0030170
Solyc03g098030.3	**3.45E+00**	**8.41E-10**	**3.00E+00**	**1.30E-08**	-1.19E-01	7.48E-01	-1.34E-01	7.18E-01	WT & nifD- N 14 dpi	S	Type I inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 *** G7KHW0_MEDTR)	GO:0046856
Solyc03g005910.3	**3.44E+00**	**2.73E-06**	**3.65E+00**	**1.07E-06**	1.96E-01	7.36E-01	9.08E-01	1.27E-01	WT & nifD- N 14 dpi	L	Lipase, GDSL (AHRD V3.3 *** A0A103XTV4_CYNCS)	GO:0016788
Solyc06g072550.3	**3.44E+00**	**1.92E-08**	**3.77E+00**	**3.28E-09**	-8.02E-01	7.34E-02	-3.61E-01	4.08E-01	WT & nifD- N 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4C8X5_SOLLC)	
Solyc07g061830.1	**3.43E+00**	**4.81E-06**	**2.80E+00**	**7.59E-05**	6.52E-01	2.83E-01	7.07E-01	2.46E-01	WT & nifD- N 14 dpi	S	LOW QUALITY:Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 --* AT1G19650.3)	
Solyc03g032080.3	**3.40E+00**	**2.27E-08**	**2.16E+00**	**3.14E-05**	4.39E-02	9.19E-01	-2.98E-01	4.93E-01	WT & nifD- N 14 dpi	H	Auxin efflux carrier family protein (AHRD V3.3 *** AT2G17500.4)	GO:0016021|GO:0055085
Solyc07g064120.2	**3.34E+00**	**3.74E-04**	**4.49E+00**	**9.38E-06**	6.09E-01	4.62E-01	-9.91E-01	2.36E-01	WT & nifD- N 14 dpi	TR	ABC transporter B family protein (AHRD V3.3 *** G7JF16_MEDTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO:0016887
Solyc01g099990.3	**3.30E+00**	**1.20E-05**	**2.41E+00**	**5.57E-04**	1.81E-01	7.69E-01	1.41E+00	2.92E-02	WT & nifD- N 14 dpi	P	F-box protein (AHRD V3.3 *** G7KWK0_MEDTR)	GO:0005515
Solyc09g082550.3	**3.25E+00**	**5.33E-06**	**4.56E+00**	**1.86E-08**	7.86E-01	1.79E-01	-2.00E+00	1.66E-03	WT & nifD- N 14 dpi	TR	Sulfate transporter (AHRD V3.3 *** D7LTZ8_ARALL)	GO:0008271|GO:0008272|GO:0008271|GO:0008272|GO:0016020|GO:0055085|GO:0008271|GO:0008272|GO:0016020|GO:0055085

Solyc12g014260.1	**3.24E+00**	**9.32E-05**	**3.64E+00**	**2.09E-05**	6.10E-01	3.93E-01	-3.40E-01	6.32E-01	WT & nifD- N 14 dpi	G	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT2G42610.2)	
Solyc11g021300.1	**3.21E+00**	**2.70E-05**	**3.29E+00**	**1.95E-05**	1.59E+00	1.82E-02	9.49E-01	1.44E-01	WT & nifD- N 14 dpi	TR	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0U1ZG15_SOLCE)	GO:0016021
Solyc07g008290.3	**3.21E+00**	**3.08E-04**	**3.86E+00**	**3.31E-05**	-2.00E-01	7.97E-01	-1.24E-01	8.74E-01	WT & nifD- N 14 dpi	C	O-fucosyltransferase family protein (AHRD V3.3 *** AT3G21190.1)	
Solyc04g054740.3	**3.21E+00**	**2.51E-04**	**4.79E+00**	**1.07E-06**	1.30E+00	9.63E-02	-2.02E-01	7.92E-01	WT & nifD- N 14 dpi	H	myo-inositol-1-phosphate synthase	GO:0004512|GO:0006021|GO:0008654
Solyc01g112190.3	**3.18E+00**	**3.68E-16**	**3.68E+00**	**1.11E-17**	-6.17E-01	1.66E-03	-2.00E-01	2.64E-01	WT & nifD- N 14 dpi	DNA	Plant regulator RWP-RK family protein (AHRD V3.3 *** AT4G35270.4)	GO:0005515
Solyc08g068000.2	**3.18E+00**	**3.38E-06**	**2.60E+00**	**5.48E-05**	-4.65E-01	3.97E-01	-8.40E-01	1.32E-01	WT & nifD- N 14 dpi	TR	Potassium channel (AHRD V3.3 *** B6ECZ4_TOBAC)	GO:0005216|GO:0006811|GO:0016020|GO:0055085|GO:0005249|GO:0006813|GO:0016020|GO:0005249|GO:0006813|GO:0016020
Solyc02g071100.3	**3.17E+00**	**1.21E-05**	**3.81E+00**	**7.52E-07**	-8.97E-02	8.80E-01	4.78E-02	9.36E-01	WT & nifD- N 14 dpi	TR	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)	GO:0005215|GO:0016021
Solyc02g070670.3	**3.16E+00**	**1.75E-20**	**3.38E+00**	**3.29E-21**	2.19E-01	7.03E-02	4.07E-01	1.64E-03	WT & nifD- N 14 dpi	N	urease accessory protein G (AHRD V3.3 *** AT2G34470.2)	GO:0003924|GO:0006807|GO:0016151
Solyc03g097600.3	**3.15E+00**	**1.86E-08**	**3.02E+00**	**4.01E-08**	3.71E-01	3.54E-01	2.83E-01	4.78E-01	WT & nifD- N 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJH7_SOLLC)	GO:0016021
Solyc12g042980.2	**3.14E+00**	**2.99E-05**	**5.38E+00**	**4.27E-09**	-8.09E-01	2.04E-01	-1.33E+00	4.23E-02	WT & nifD- N 14 dpi	E	2-oxoglutarate-dependent dioxygenase (AHRD V3.3 *** A0A061G9S7_THECC)	GO:0016491|GO:0055114
Solyc02g083527.1	**3.13E+00**	**2.15E-05**	**2.46E+00**	**3.86E-04**	-8.73E-01	1.60E-01	-6.15E-01	3.18E-01	WT & nifD- N 14 dpi	D	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *** AT3G51325.1)	GO:0005515|GO:0008270|GO:0008270|GO:0008270
Solyc07g054790.1	**3.11E+00**	**6.74E-08**	**3.52E+00**	**6.86E-09**	-1.30E+00	4.44E-03	-4.22E-01	3.21E-01	WT & nifD- N 14 dpi	D	Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)	
Solyc08g065210.1	**3.09E+00**	**2.39E-06**	**3.36E+00**	**6.13E-07**	9.41E-02	8.56E-01	-1.08E+00	4.44E-02	WT & nifD- N 14 dpi	S	LOW QUALITY:Type I inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 --* A0A072UDV5_MEDTR)	
Solyc01g067130.3	**3.08E+00**	**1.25E-10**	**2.99E+00**	**2.26E-10**	-4.06E-01	1.86E-01	-1.15E-01	7.03E-01	WT & nifD- N 14 dpi	T	Nuclear transcription factor Y protein (AHRD V3.3 *** G7JKC3_MEDTR)	GO:0046982
Solyc04g071610.3	**3.07E+00**	**2.93E-18**	**2.89E+00**	**1.32E-17**	-7.61E-02	5.88E-01	8.82E-02	5.30E-01	WT & nifD- N 14 dpi	H	Abscicic acid stress ripening 1	GO:0006950
Solyc01g095810.3	**3.03E+00**	**6.90E-15**	**3.39E+00**	**4.82E-16**	-7.38E-01	6.02E-04	6.88E-02	7.19E-01	WT & nifD- N 14 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DTM6_THECC)	GO:0005515|GO:0008270|GO:0030247|GO:0030247
Solyc01g066980.3	**3.01E+00**	**6.77E-06**	**2.32E+00**	**1.99E-04**	-6.87E-01	2.11E-01	1.10E-01	8.38E-01	WT & nifD- N 14 dpi	G	Flowering promoting factor 1 (AHRD V3.3 *** A0A061EW40_THECC)	
Solyc08g062570.1	**2.99E+00**	**1.26E-05**	**3.05E+00**	**9.36E-06**	8.91E-01	1.20E-01	1.16E+00	4.60E-02	WT & nifD- N 14 dpi	STR	Glutathione s-transferase, putative (AHRD V3.3 *-* B9R999_RICCO)	GO:0005515
Solyc12g056180.2	**2.98E+00**	**1.67E-05**	**3.13E+00**	**8.54E-06**	-3.51E+00	1.48E-06	-3.18E+00	6.68E-06	WT & nifD- N 14 dpi	P	Sl 1-aminocyclopropane-1-carboxylate synthase	GO:0003824|GO:0003824|GO:0009058|GO:0030170|GO:0003824|GO:0009058|GO:0030170
Solyc04g054730.3	**2.97E+00**	**4.06E-04**	**2.28E+00**	**4.48E-03**	1.73E-01	8.15E-01	-3.01E-01	6.83E-01	WT & nifD- N 14 dpi	TR	Sulfate transporter (AHRD V3.3 *** A7YGJ3_POPCN)	GO:0008271|GO:0008272|GO:0008271|GO:0008272|GO:0016020|GO:0055085|GO:0008271|GO:0008272|GO:0016020|GO:0055085
Solyc06g083590.3	**2.95E+00**	**1.05E-11**	**2.57E+00**	**2.03E-10**	-3.83E-01	1.45E-01	-2.01E-01	4.38E-01	WT & nifD- N 14 dpi	H	ABI3	GO:0003677
Solyc12g088190.2	**2.95E+00**	**7.88E-04**	**3.11E+00**	**4.65E-04**	4.61E-01	5.58E-01	-1.26E+00	1.17E-01	WT & nifD- N 14 dpi	AM	Amino acid permease (AHRD V3.3 *** A0A0K9P9F3_ZOSMR)	
Solyc00g244290.1	**2.95E+00**	**2.05E-04**	**2.19E+00**	**3.54E-03**	9.60E-01	1.71E-01	9.37E-01	1.82E-01	WT & nifD- N 14 dpi	E	LOW QUALITY:NADH dehydrogenase subunit 2 (AHRD V3.3 *-* A0A1C9I9Q6_9ROSI)	
Solyc03g118760.3	**2.92E+00**	**7.00E-04**	**3.26E+00**	**2.19E-04**	-3.92E+00	2.25E-05	-2.77E+00	1.17E-03	WT & nifD- N 14 dpi	CS	Tubulin beta chain (AHRD V3.3 *** TBB_HORVU)	GO:0003924|GO:0005200|GO:0005525|GO:0005874|GO:0007017|GO:0005200|GO:0005525
Solyc01g066040.2	**2.89E+00**	**4.54E-03**	**4.17E+00**	**1.34E-04**	7.36E-01	4.36E-01	-6.62E-01	4.82E-01	WT & nifD- N 14 dpi	H	LOW QUALITY:WD40 domain-containing protein (AHRD V3.3 --* AT2G47410.6)	
Solyc07g018370.2	**2.88E+00**	**1.70E-07**	**3.43E+00**	**6.96E-09**	7.05E-01	9.51E-02	7.67E-01	7.04E-02	WT & nifD- N 14 dpi	T	mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** AT4G28840.1)	
Solyc01g066570.3	**2.85E+00**	**8.26E-10**	**1.62E+00**	**1.34E-05**	-2.14E-01	4.87E-01	7.54E-01	1.96E-02	WT & nifD- N 14 dpi	G	senescence-associated family protein (DUF581) (AHRD V3.3 *** AT1G22160.1)	
Solyc06g074350.3	**2.82E+00**	**3.09E-03**	**4.77E+00**	**8.58E-06**	-4.67E-02	9.57E-01	-8.60E-01	3.28E-01	WT & nifD- N 14 dpi	G	self-pruning	

Solyc11g021310.1	**2.78E+00**	**4.78E-04**	**3.66E+00**	**1.78E-05**	1.77E+00	1.73E-02	1.20E+00	9.72E-02	WT & nifD- N 14 dpi	TR	Ycf1 (AHRD V3.3 *-* A0A0U1ZKJ5_SOLPI)	GO:0016021
Solyc11g068780.1	**2.78E+00**	**8.90E-04**	**2.99E+00**	**4.24E-04**	2.52E-01	7.36E-01	1.60E-01	8.30E-01	WT & nifD- N 14 dpi	G	LOW QUALITY:ovate family protein 30	
Solyc08g075570.3	**2.77E+00**	**1.42E-11**	**3.44E+00**	**1.08E-13**	-5.77E-01	2.48E-02	-1.70E-01	4.87E-01	WT & nifD- N 14 dpi	N	Sodium:solute symporter family protein (AHRD V3.3 *** G7K6S1_MEDTR)	GO:0005215|GO:0006810|GO:0016020|GO:0055085|GO:0015204|GO:0016021|GO:0071918|GO:0015204|GO:0016021|GO:0071918
Solyc08g079600.3	**2.76E+00**	**6.45E-06**	**2.69E+00**	**9.71E-06**	1.03E+00	4.49E-02	2.59E-01	6.02E-01	WT & nifD- N 14 dpi	NA	BnaA07g13420D protein (AHRD V3.3 *** A0A078ETL1_BRANA)	
Solyc11g069940.1	**2.75E+00**	**1.76E-14**	**3.32E+00**	**2.11E-16**	4.54E-01	1.74E-02	-3.16E-01	8.87E-02	WT & nifD- N 14 dpi	OX	Glutaredoxin (AHRD V3.3 *** A0A118JSL8_CYNCS)	GO:0009055|GO:0015035|GO:0045454
Solyc06g063040.1	**2.75E+00**	**1.85E-05**	**2.38E+00**	**1.14E-04**	1.31E+00	1.92E-02	-4.01E-02	9.40E-01	WT & nifD- N 14 dpi	OX	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** A0A072TWU1_MEDTR)	GO:0016491|GO:0055114|GO:0055114
Solyc03g096770.1	**2.73E+00**	**1.15E-04**	**3.52E+00**	**3.70E-06**	-1.19E+00	5.87E-02	-1.86E+00	4.73E-03	WT & nifD- N 14 dpi	STR	Response to low sulfur protein, putative (AHRD V3.3 *** G7J9Q1_MEDTR)	
Solyc03g006110.3	**2.70E+00**	**7.56E-04**	**2.34E+00**	**2.76E-03**	2.81E-01	6.94E-01	-4.42E-01	5.37E-01	WT & nifD- N 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IH06_SOLCH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g065610.3	**2.70E+00**	**8.45E-17**	**2.47E+00**	**6.97E-16**	-5.09E-01	1.22E-03	5.31E-01	8.11E-04	WT & nifD- N 14 dpi	C	Vacuolar processing enzyme (AHRD V3.3 *** V9M6Z0_9ROSA)	GO:0006508|GO:0008233
Solyc10g005010.3	**2.68E+00**	**1.01E-05**	**2.34E+00**	**6.39E-05**	1.27E+00	1.55E-02	1.07E+00	3.79E-02	WT & nifD- N 14 dpi	T	NAC domain-containing protein, putative (AHRD V3.3 *** B9SVG2_RICCO)	GO:0003677|GO:0006355
Solyc12g088140.2	**2.68E+00**	**3.79E-08**	**2.87E+00**	**1.10E-08**	-1.13E+00	3.27E-03	-1.26E+00	1.26E-03	WT & nifD- N 14 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)	
Solyc12g056160.2	**2.64E+00**	**7.03E-04**	**3.70E+00**	**1.26E-05**	5.37E-01	4.41E-01	1.20E-01	8.63E-01	WT & nifD- N 14 dpi	TR	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NMD6_ZOSMR)	GO:0006812|GO:0015299|GO:0016021|GO:0055085
Solyc08g016000.1	**2.63E+00**	**8.14E-03**	**2.90E+00**	**3.98E-03**	2.08E+00	3.17E-02	1.02E+00	2.75E-01	WT & nifD- N 14 dpi	TR	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0U1ZJ99_SOLCI)	GO:0016021
Solyc02g092680.1	**2.62E+00**	**5.80E-04**	**2.10E+00**	**4.16E-03**	1.82E-01	7.87E-01	-1.43E-01	8.32E-01	WT & nifD- N 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** A9XG40_TOBAC)	GO:0004252|GO:0006508
Solyc04g071340.4	**2.60E+00**	**7.78E-05**	**1.91E+00**	**1.95E-03**	2.57E-01	6.46E-01	-1.51E-02	9.78E-01	WT & nifD- N 14 dpi	C	fructose-1%2C6-bisphosphatase%2C cytosolic	
Solyc11g021260.1	**2.59E+00**	**7.93E-05**	**2.53E+00**	**1.05E-04**	1.43E+00	1.57E-02	1.16E+00	4.61E-02	WT & nifD- N 14 dpi	TR	Ycf1 (AHRD V3.3 *-* A0A0U1ZG15_SOLCE)	
Solyc09g065750.3	**2.59E+00**	**1.50E-04**	**3.06E+00**	**1.80E-05**	-7.53E-01	2.08E-01	-1.10E+00	7.06E-02	WT & nifD- N 14 dpi	2M	Beta-carotene isomerase D27 (AHRD V3.3 *** R4HZ96_MEDTR)	
Solyc01g105660.3	**2.55E+00**	**5.02E-06**	**1.72E+00**	**6.61E-04**	1.07E+00	2.32E-02	5.02E-01	2.68E-01	WT & nifD- N 14 dpi	E	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061E128_THECC)	GO:0016491|GO:0055114
Solyc09g015880.3	**2.53E+00**	**4.59E-06**	**1.94E+00**	**1.59E-04**	6.11E-01	1.75E-01	6.28E-01	1.64E-01	WT & nifD- N 14 dpi	E	Cytochrome c oxidase subunit 2 (AHRD V3.3 *-* A0A0C5B2A3_HYONI)	GO:0004129|GO:0005507|GO:0016020|GO:0005507|GO:0005507
Solyc06g074990.2	**2.53E+00**	**9.68E-11**	**3.21E+00**	**5.42E-13**	-9.31E-01	7.04E-04	-7.40E-01	5.14E-03	WT & nifD- N 14 dpi	N	putative high affinity nitrate transporter 2	GO:0016021|GO:0055085
Solyc11g072130.2	**2.52E+00**	**8.97E-05**	**3.18E+00**	**3.80E-06**	1.21E+00	3.47E-02	6.13E-01	2.70E-01	WT & nifD- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G55290.1)	GO:0016491|GO:0055114
Solyc12g042890.2	**2.52E+00**	**1.47E-06**	**2.69E+00**	**5.11E-07**	1.05E+00	1.54E-02	3.56E-01	3.88E-01	WT & nifD- N 14 dpi	P	Acyl-protein thioesterase 2 (AHRD V3.3 *** A0A0B0PZC3_GOSAR)	GO:0016787
Solyc08g062970.1	**2.52E+00**	**1.70E-09**	**3.54E+00**	**1.22E-12**	-1.44E-01	6.07E-01	-1.09E+00	5.73E-04	WT & nifD- N 14 dpi	OX	Glutaredoxin (AHRD V3.3 *** A0A118JSL8_CYNCS)	GO:0009055|GO:0015035|GO:0045454
Solyc01g098490.3	**2.50E+00**	**8.71E-04**	**3.10E+00**	**8.50E-05**	1.03E+00	1.35E-01	6.07E-01	3.69E-01	WT & nifD- N 14 dpi	TR	Sugar facilitator protein 1	GO:0005215|GO:0016021|GO:0055085|GO:0016020|GO:0022891|GO:0055085|GO:0016020
Solyc02g086950.1	**2.50E+00**	**2.08E-11**	**2.78E+00**	**1.91E-12**	-7.63E-02	7.34E-01	8.58E-01	6.82E-04	WT & nifD- N 14 dpi	D	LOW QUALITY:RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FV20_THECC)	GO:0005515|GO:0008270
Solyc04g064900.1	**2.48E+00**	**1.19E-03**	**3.48E+00**	**2.49E-05**	-1.05E+00	1.34E-01	-2.22E+00	3.05E-03	WT & nifD- N 14 dpi	CS	Endoglucanase (AHRD V3.3 *-* A0A067LEU1_JATCU)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc07g016215.1	**2.47E+00**	**1.97E-08**	**3.10E+00**	**2.21E-10**	4.69E-01	1.41E-01	-1.15E-02	9.71E-01	WT & nifD- N 14 dpi	NA	Organ specific protein (AHRD V3.3 *** A0A103YKI8_CYNCS)	
Solyc03g112030.2	**2.46E+00**	**3.51E-03**	**2.21E+00**	**7.80E-03**	1.57E+00	5.10E-02	1.38E+00	8.38E-02	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103XWH5_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705

Solyc07g049240.3	**2.46E+00**	**1.97E-10**	**3.04E+00**	**2.14E-12**	-5.23E-02	8.32E-01	1.37E-02	9.55E-01	WT & nifD- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4CF27_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc04g008930.2	**2.46E+00**	**6.87E-03**	**2.37E+00**	**8.69E-03**	-4.33E-01	6.09E-01	1.43E+00	9.88E-02	WT & nifD- N 14 dpi	H	GRAM domain-containing protein / ABA-responsive protein-related (AHRD V3.3 *** A0A061E267_THECC)	
Solyc02g071090.3	**2.44E+00**	**8.70E-14**	**2.42E+00**	**1.11E-13**	-2.72E-01	1.22E-01	1.70E-01	3.28E-01	WT & nifD- N 14 dpi	TR	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)	GO:0005215|GO:0016021
Solyc12g009050.2	**2.43E+00**	**4.48E-14**	**3.03E+00**	**2.34E-16**	-6.32E-01	7.08E-04	-2.45E-01	1.48E-01	WT & nifD- N 14 dpi	T	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)	GO:0003677|GO:0016602|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc01g100230.3	**2.41E+00**	**3.03E-15**	**1.34E+00**	**1.20E-09**	1.54E-01	2.99E-01	6.88E-01	6.78E-05	WT & nifD- N 14 dpi	STR	DnaJ-like protein (AHRD V3.3 *** D5FNB3_SOYBN)	
Solyc11g017390.2	**2.39E+00**	**9.65E-06**	**2.84E+00**	**6.69E-07**	7.92E-01	8.05E-02	6.70E-01	1.36E-01	WT & nifD- N 14 dpi	RNA	LOW QUALITY:RNA-binding KH domain-containing protein (AHRD V3.3 --* AT5G46190.4)	
Solyc08g078170.1	**2.38E+00**	**9.22E-06**	**2.62E+00**	**2.22E-06**	-6.63E-02	8.79E-01	-2.32E-01	5.97E-01	WT & nifD- N 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *** A0A024CAT9_BRAJU)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc04g076950.3	**2.37E+00**	**4.71E-05**	**2.20E+00**	**1.22E-04**	-4.20E-01	3.96E-01	-1.28E+00	1.38E-02	WT & nifD- N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4BUD2_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc08g062450.1	**2.37E+00**	**9.05E-04**	**3.21E+00**	**2.79E-05**	5.35E-01	4.04E-01	9.16E-02	8.86E-01	WT & nifD- N 14 dpi	STR	Heat-shock protein, putative (AHRD V3.3 *** B9RQT7_RICCO)	
Solyc12g014500.2	**2.33E+00**	**1.25E-05**	**4.11E+00**	**6.56E-10**	7.59E-01	9.10E-02	2.01E-01	6.46E-01	WT & nifD- N 14 dpi	H	S-adenosyl-L-methionine:carboxyl methyltransferase family protein (AHRD V3.3 *** B9GJG7_POPTR)	GO:0008168
Solyc09g073030.3	**2.32E+00**	**7.99E-07**	**1.96E+00**	**1.04E-05**	-1.64E-01	6.53E-01	-5.13E-01	1.65E-01	WT & nifD- N 14 dpi	N	carbamoyl phosphate synthetase A (AHRD V3.3 --* AT3G27740.2)	
Solyc10g007570.3	**2.31E+00**	**2.22E-06**	**1.96E+00**	**2.39E-05**	-8.40E-01	3.68E-02	4.33E-02	9.10E-01	WT & nifD- N 14 dpi	H	Gibberellin 2-oxidase 2 (AHRD V3.3 *** I0B5A7_PETHY)	GO:0016491|GO:0055114
Solyc01g104434.1	**2.31E+00**	**2.58E-03**	**2.80E+00**	**4.14E-04**	3.31E-01	6.36E-01	6.86E-01	3.30E-01	WT & nifD- N 14 dpi	OX	Thioredoxin reductase (AHRD V3.3 --* I1GYQ0_BRADI)	
Solyc08g014090.1	**2.30E+00**	**9.67E-04**	**2.05E+00**	**2.73E-03**	-1.94E-01	7.56E-01	-1.18E+00	6.84E-02	WT & nifD- N 14 dpi	RNA	LOW QUALITY:Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT3G09040.3)	
Solyc12g089220.2	**2.30E+00**	**2.14E-11**	**1.49E+00**	**1.12E-07**	-5.28E-01	1.63E-02	6.83E-01	2.65E-03	WT & nifD- N 14 dpi	D	Bifunctional nuclease 1 (AHRD V3.3 *** BBD1_ARATH)	GO:0004518
Solyc04g078300.3	**2.29E+00**	**1.49E-05**	**1.55E+00**	**1.35E-03**	-2.68E-01	5.40E-01	8.63E-02	8.43E-01	WT & nifD- N 14 dpi	T	MADS-box transcription factor family protein (AHRD V3.3 *** G7ZXM5_MEDTR)	GO:0000165|GO:0000977|GO:0045944|GO:0003677|GO:0046983|GO:0003677|GO:0046983
Solyc03g083090.3	**2.28E+00**	**2.01E-06**	**1.84E+00**	**4.29E-05**	-4.70E-02	9.01E-01	-6.29E-01	1.04E-01	WT & nifD- N 14 dpi	D	transcription factor jumonji (jmjC) domain-containing protein (AHRD V3.3 --* AT1G63490.4)	
Solyc04g007410.3	**2.27E+00**	**1.10E-06**	**1.58E+00**	**1.71E-04**	1.07E-01	7.68E-01	8.58E-01	2.43E-02	WT & nifD- N 14 dpi	NA	transmembrane protein (AHRD V3.3 *** AT3G45050.4)	GO:0031072|GO:0051082
Solyc06g069430.3	**2.26E+00**	**1.34E-05**	**1.56E+00**	**1.05E-03**	6.13E-01	1.58E-01	6.80E-01	1.19E-01	WT & nifD- N 14 dpi	DNA	FRUITFULL-like MADS-box 1	GO:0000165|GO:0000977|GO:0045944|GO:0003677|GO:0046983|GO:0003677|GO:0046983
Solyc09g074560.3	**2.25E+00**	**7.26E-11**	**2.04E+00**	**5.51E-10**	9.08E-01	2.34E-04	7.96E-01	9.24E-04	WT & nifD- N 14 dpi	G	CONSTANS-like zinc finger protein (AHRD V3.3 *** A0A0H3YNS5_9ROSI)	GO:0005515|GO:0005622|GO:0008270|GO:0005622|GO:0008270
Solyc03g083770.1	**2.25E+00**	**1.58E-04**	**1.71E+00**	**2.36E-03**	6.93E-01	1.85E-01	1.05E+00	4.85E-02	WT & nifD- N 14 dpi	CS	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** AT5G62360.1)	GO:0004857
Solyc03g118000.1	**2.23E+00**	**4.98E-08**	**2.87E+00**	**3.73E-10**	-1.35E-01	6.50E-01	7.06E-01	2.37E-02	WT & nifD- N 14 dpi	S	Inositol polyphosphate multikinase (AHRD V3.3 *** K4BLV1_SOLLC)	GO:0008440
Solyc01g100020.3	**2.20E+00**	**2.19E-05**	**1.24E+00**	**7.41E-03**	-2.08E-01	6.30E-01	-7.73E-01	8.09E-02	WT & nifD- N 14 dpi	L	Phospholipase D (AHRD V3.3 *** I1NJ37_SOYBN)	GO:0003824
Solyc08g065550.1	**2.20E+00**	**1.14E-05**	**1.97E+00**	**4.98E-05**	-3.22E-01	4.35E-01	4.01E-01	3.32E-01	WT & nifD- N 14 dpi	E	LOW QUALITY:NADH dehydrogenase subunit 9 (AHRD V3.3 *-* ATMG00070.1)	GO:0008137|GO:0055114
Solyc04g014830.2	**2.20E+00**	**8.84E-06**	**1.66E+00**	**3.10E-04**	1.98E-01	6.23E-01	6.33E-01	1.24E-01	WT & nifD- N 14 dpi	T	GRAS family transcription factor (AHRD V3.3 *** G7JLR5_MEDTR)	
Solyc09g008770.3	**2.19E+00**	**3.76E-04**	**1.90E+00**	**1.53E-03**	-8.31E-02	8.78E-01	5.74E-01	2.94E-01	WT & nifD- N 14 dpi	STR	Late embryogenesis abundant protein, putative (AHRD V3.3 *** G7I9D0_MEDTR)	
Solyc10g050210.2	**2.18E+00**	**2.29E-05**	**1.29E+00**	**5.35E-03**	-1.16E-02	9.78E-01	-1.71E+00	4.28E-04	WT & nifD- N 14 dpi	H	Abscisic acid responsive element-binding factor 1 family protein (AHRD V3.3 *** U5GLH1_POPTR)	GO:0003700|GO:0006355|GO:0043565
Solyc03g006150.2	**2.17E+00**	**3.21E-08**	**1.61E+00**	**4.74E-06**	7.55E-01	1.19E-02	7.10E-01	1.73E-02	WT & nifD- N 14 dpi	T	LOW QUALITY:MYB-like transcription factor family protein (AHRD V3.3 *** A0A072TT31_MEDTR)	GO:0003677
Solyc01g009645.1	**2.16E+00**	**3.51E-05**	**1.84E+00**	**2.32E-04**	4.32E-01	3.26E-01	6.29E-01	1.57E-01	WT & nifD- N 14 dpi	T	MYB-related transcription factor (AHRD V3.3 *** A0A059PSP5_SALMI)	GO:0003677

Solyc12g005670.2	**2.15E+00**	**1.15E-08**	**2.94E+00**	**2.05E-11**	-3.42E-01	2.02E-01	-5.55E-01	4.32E-02	WT & nifD- N 14 dpi	NA	HAK5	GO:0015079|GO:0016020|GO:0071805
Solyc02g070070.1	**2.14E+00**	**9.44E-03**	**3.88E+00**	**2.78E-05**	-6.47E-02	9.33E-01	-2.39E+00	4.27E-03	WT & nifD- N 14 dpi	E	FAD-binding Berberine family protein (AHRD V3.3 *** AT2G34790.1)	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114
Solyc01g108745.1	**2.14E+00**	**3.12E-05**	**2.63E+00**	**1.49E-06**	-2.25E+00	1.55E-05	-1.22E+00	7.89E-03	WT & nifD- N 14 dpi	2M	Polyneuridine-aldehyde esterase-like protein (AHRD V3.3 *** A0A075F1V8_TOBAC)	
Solyc04g051247.1	**2.13E+00**	**8.04E-04**	**2.35E+00**	**2.92E-04**	9.43E-01	1.06E-01	4.37E-01	4.44E-01	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q0PNH1_CAPCH)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc05g052830.3	**2.13E+00**	**2.52E-04**	**2.69E+00**	**1.32E-05**	5.32E-01	2.98E-01	5.12E-01	3.16E-01	WT & nifD- N 14 dpi	N	proline transporter 1 (AHRD V3.3 *** AT2G39890.2)	
Solyc09g009530.3	**2.13E+00**	**1.50E-15**	**2.18E+00**	**8.45E-16**	7.03E-01	6.35E-06	4.59E-01	1.06E-03	WT & nifD- N 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G36290.1)	
Solyc08g081680.2	**2.12E+00**	**2.36E-03**	**2.30E+00**	**1.12E-03**	6.37E-01	3.20E-01	5.27E-01	4.09E-01	WT & nifD- N 14 dpi	CS	Protein LURP-one-related 17 (AHRD V3.3 *** A0A0B2R169_GLYSO)	
Solyc12g006430.2	**2.11E+00**	**1.45E-07**	**2.14E+00**	**1.20E-07**	-9.29E-01	4.19E-03	2.72E-01	3.66E-01	WT & nifD- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DBI0_SOLLC)	GO:0008152|GO:0016758
Solyc00g227860.1	**2.08E+00**	**3.66E-06**	**1.45E+00**	**3.69E-04**	1.14E-01	7.51E-01	1.84E-01	6.09E-01	WT & nifD- N 14 dpi	C	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XS50_DAUCA)	GO:0008152|GO:0016758
Solyc05g006500.3	**2.07E+00**	**1.24E-03**	**2.33E+00**	**3.85E-04**	5.61E-01	3.36E-01	-2.86E-01	6.22E-01	WT & nifD- N 14 dpi	STR	Germin-like protein subfamily 1 member 1 (AHRD V3.3 *** A0A0B2NVG1_GLYSO)	GO:0030145|GO:0045735|GO:0045735
Solyc01g096730.2	**2.07E+00**	**4.06E-03**	**1.85E+00**	**9.19E-03**	1.16E+00	8.90E-02	1.10E+00	1.08E-01	WT & nifD- N 14 dpi	TR	zinc induced facilitator-like 1 (AHRD V3.3 *** AT5G13750.1)	GO:0016021|GO:0055085
Solyc09g064365.1	**2.07E+00**	**6.78E-03**	**2.85E+00**	**4.20E-04**	4.14E-01	5.61E-01	4.05E-01	5.69E-01	WT & nifD- N 14 dpi	DNA	BED zinc finger,hAT family dimerization domain (AHRD V3.3 *** A0A061DK10_THECC)	GO:0003676|GO:0046983|GO:0046983
Solyc01g006320.3	**2.06E+00**	**9.51E-03**	**2.63E+00**	**1.43E-03**	2.28E-01	7.60E-01	-8.10E-01	2.81E-01	WT & nifD- N 14 dpi	D	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT3G20600.1)	
Solyc03g096780.1	**2.06E+00**	**1.10E-05**	**2.86E+00**	**5.51E-08**	-9.84E-01	1.53E-02	-1.27E+00	2.47E-03	WT & nifD- N 14 dpi	STR	Response to low sulfur protein, putative (AHRD V3.3 *** G7J9Q1_MEDTR)	
Solyc02g071750.3	**2.05E+00**	**2.51E-10**	**1.64E+00**	**1.96E-08**	9.57E-01	8.48E-05	6.22E-01	5.53E-03	WT & nifD- N 14 dpi	RNA	RNA ligase/cyclic nucleotide phosphodiesterase family protein (AHRD V3.3 *** A0A097PLR7_SOLLC)	GO:0004112
Solyc04g079490.1	**2.04E+00**	**3.90E-03**	**3.10E+00**	**5.54E-05**	-4.52E-01	4.89E-01	-2.59E-01	6.91E-01	WT & nifD- N 14 dpi	P	Serpin-like protein (AHRD V3.3 *-* G7IW05_MEDTR)	GO:0005615
Solyc04g054745.1	**2.04E+00**	**1.11E-03**	**4.11E+00**	**8.15E-08**	8.30E-01	1.48E-01	-5.70E-01	3.15E-01	WT & nifD- N 14 dpi	T	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 --* AT5G64360.7)	
Solyc12g057060.2	**2.03E+00**	**3.89E-18**	**1.74E+00**	**1.72E-16**	3.97E-01	2.35E-04	5.09E-01	9.97E-06	WT & nifD- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** M1AG38_SOLTU)	GO:0008152|GO:0016758
Solyc07g008980.3	**2.03E+00**	**8.26E-09**	**1.67E+00**	**2.87E-07**	-3.43E+00	1.34E-13	-1.10E+00	1.18E-04	WT & nifD- N 14 dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952
Solyc11g007530.2	**2.03E+00**	**2.10E-12**	**1.22E+00**	**6.81E-08**	2.78E-01	1.01E-01	3.33E-01	5.16E-02	WT & nifD- N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** A0A061DVK5_THECC)	GO:0005515|GO:0008270
Solyc03g116910.3	**2.03E+00**	**8.39E-05**	**3.78E+00**	**4.00E-09**	-8.71E-01	5.59E-02	-3.02E-01	4.94E-01	WT & nifD- N 14 dpi	D	cinnamoyl-CoA reductase 2	GO:0003824|GO:0050662
Solyc05g006870.3	**2.02E+00**	**1.96E-03**	**2.36E+00**	**4.55E-04**	8.49E-01	1.60E-01	-5.74E-02	9.23E-01	WT & nifD- N 14 dpi	OX	Thioredoxin H (AHRD V3.3 *** Q4U0W0_NICAL)	GO:0006662|GO:0015035|GO:0045454|GO:0045454|GO:0045454
Solyc04g007685.1	**2.02E+00**	**4.01E-08**	**2.42E+00**	**1.31E-09**	1.85E-01	4.89E-01	-3.82E-01	1.58E-01	WT & nifD- N 14 dpi	G	Hydroxyproline-rich glycoprotein (AHRD V3.3 -** B9HJA6_POPTR)	
Solyc11g045530.2	**2.00E+00**	**1.20E-07**	**2.17E+00**	**2.97E-08**	-5.51E-01	5.76E-02	-7.68E-01	1.02E-02	WT & nifD- N 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9RI26_RICCO)	
Solyc12g008380.1	**2.00E+00**	**2.80E-04**	**2.73E+00**	**5.29E-06**	-7.36E-01	1.35E-01	-1.48E+00	4.48E-03	WT & nifD- N 14 dpi	D	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** I3SWH2_MEDTR)	
Solyc07g064160.3	**2.00E+00**	**2.75E-04**	**2.61E+00**	**9.70E-06**	4.13E-01	3.93E-01	7.20E-04	9.99E-01	WT & nifD- N 14 dpi	G	Thiamine thiazole synthase, chloroplastic (AHRD V3.3 *** K4CH99_SOLLC)	GO:0006950|GO:0009228|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc02g092120.3	**1.98E+00**	**6.04E-03**	**2.30E+00**	**1.76E-03**	-4.12E-01	5.38E-01	6.66E-01	3.23E-01	WT & nifD- N 14 dpi	G	Phytosulfokines 3 family protein (AHRD V3.3 *** B9IBM1_POPTR)	GO:0005576|GO:0008083|GO:0008283
Solyc09g082720.3	**1.97E+00**	**2.29E-13**	**2.08E+00**	**7.07E-14**	5.57E-01	6.30E-04	-2.24E-01	1.31E-01	WT & nifD- N 14 dpi	2M	Aldo_keto reductase family protein IPR001395 Aldo_keto reductase	

Solyc08g082680.3	**1.96E+00**	**5.53E-10**	**1.31E+00**	**8.51E-07**	-5.50E-01	1.23E-02	6.16E-01	5.71E-03	WT & nifD- N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT4G24015.1)	GO:0005515|GO:0008270
Solyc05g050130.3	**1.96E+00**	**1.77E-07**	**3.05E+00**	**3.27E-11**	7.19E-01	1.55E-02	-5.58E-01	5.45E-02	WT & nifD- N 14 dpi	D	Acidic endochitinase (AHRD V3.3 *** CHIA_TOBAC)	GO:0004553|GO:0005975|GO:0005975|GO:00
Solyc04g054990.3	**1.96E+00**	**9.66E-14**	**2.20E+00**	**6.09E-15**	9.09E-01	5.06E-07	-1.32E-02	9.24E-01	WT & nifD- N 14 dpi	G	PLAT domain-containing protein 1 (AHRD V3.3 *** PLAT1_ARATH)	GO:0005515
Solyc03g034120.3	**1.95E+00**	**2.42E-03**	**2.51E+00**	**2.02E-04**	-1.39E+00	2.41E-02	7.04E-01	2.35E-01	WT & nifD- N 14 dpi	DNA	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9MXR7_POPTR)	GO:0003677|GO:0006355|GO:0043565|GO:00 06355|GO:0043565
Solyc10g018150.2	**1.94E+00**	**3.10E-05**	**2.97E+00**	**3.62E-08**	-2.70E+00	1.88E-07	-2.49E+00	7.46E-07	WT & nifD- N 14 dpi	2M	SlCytochromeP450	GO:0005506|GO:0016705|GO:0020037|GO:00 55114|GO:0016705|GO:0055114|GO:0016705
Solyc03g123550.1	**1.93E+00**	**7.19E-07**	**1.52E+00**	**2.61E-05**	-2.48E+00	8.59E-09	-1.87E+00	1.21E-06	WT & nifD- N 14 dpi	H	Small auxin up-regulated RNA39	GO:0009733
Solyc05g050870.3	**1.93E+00**	**1.37E-03**	**2.45E+00**	**1.07E-04**	-3.44E-02	9.49E-01	2.12E-02	9.69E-01	WT & nifD- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4C1C0_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:00 55114|GO:0004601|GO:0042744|GO:0004601
Solyc05g024010.3	**1.92E+00**	**1.43E-12**	**1.01E+00**	**4.61E-07**	2.40E-01	1.25E-01	8.48E-01	7.23E-06	WT & nifD- N 14 dpi	G	Zinc finger protein CONSTANS-LIKE 14 (AHRD V3.3 *** B9GMQ8_POPTR)	GO:0005515|GO:0005622|GO:0008270|GO:00 05622|GO:0008270
Solyc04g049670.3	**1.92E+00**	**4.83E-19**	**1.35E+00**	**2.36E-15**	4.02E-01	3.57E-05	6.59E-01	1.30E-08	WT & nifD- N 14 dpi	T	Pseudo-response regulator (AHRD V3.3 *** X5I0R0_IPONI)	GO:0000160|GO:0005515|GO:0005515
Solyc08g082120.2	**1.91E+00**	**1.14E-06**	**2.50E+00**	**1.03E-08**	3.44E-01	2.66E-01	4.57E-01	1.43E-01	WT & nifD- N 14 dpi	STR	Methanol inducible protein (AHRD V3.3 *** D1MAX5_NICBE)	
Solyc05g051880.3	**1.91E+00**	**1.55E-10**	**1.55E+00**	**1.05E-08**	3.42E-02	8.56E-01	9.14E-01	4.68E-05	WT & nifD- N 14 dpi	K	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** K4C1L9_SOLLC)	GO:0003824|GO:0005992
Solyc09g074810.3	**1.90E+00**	**2.46E-08**	**1.96E+00**	**1.36E-08**	7.73E-01	3.57E-03	8.75E-01	1.23E-03	WT & nifD- N 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT5G51790.2)	GO:0003677|GO:0046983|GO:0046983
Solyc06g075100.3	**1.90E+00**	**5.56E-05**	**1.68E+00**	**2.42E-04**	-2.11E-01	5.98E-01	-4.16E-01	3.02E-01	WT & nifD- N 14 dpi	C	Glycosyl transferase, family 2 (AHRD V3.3 *** A0A124SHF0_CYNCS)	
Solyc08g082190.3	**1.90E+00**	**1.97E-08**	**2.57E+00**	**4.57E-11**	2.03E-01	4.00E-01	1.27E-01	5.96E-01	WT & nifD- N 14 dpi	D	diacylglycerol kinase 5 (AHRD V3.3 --* AT2G20900.4)	
Solyc02g069960.3	**1.89E+00**	**7.70E-04**	**2.25E+00**	**1.15E-04**	8.58E-01	9.50E-02	9.00E-01	8.06E-02	WT & nifD- N 14 dpi	T	NAC domain-containing protein, putative (AHRD V3.3 *** B9RI29_RICCO)	GO:0003677|GO:0006355
Solyc10g078590.2	**1.88E+00**	**5.09E-14**	**1.21E+00**	**7.50E-10**	-6.23E-01	4.90E-05	3.88E-01	5.49E-03	WT & nifD- N 14 dpi	NA	transmembrane protein (AHRD V3.3 *** AT5G18130.1)	
Solyc12g005300.2	**1.87E+00**	**4.87E-03**	**1.94E+00**	**3.73E-03**	1.04E+00	9.90E-02	-3.12E-01	6.13E-01	WT & nifD- N 14 dpi	P	Chlorophyllase (AHRD V3.3 *** A0A165YG74_POAPR)	GO:0015996|GO:0047746
Solyc09g008320.3	**1.85E+00**	**2.97E-05**	**1.86E+00**	**2.87E-05**	-9.13E-01	1.96E-02	-1.43E+00	6.07E-04	WT & nifD- N 14 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4CQM0_SOLLC)	GO:0004553|GO:0005975|GO:0005618|GO:00 06073|GO:0016762|GO:0048046|GO:0005618 |GO:0006073|GO:0016762|GO:0048046
Solyc00g125990.2	**1.85E+00**	**2.55E-04**	**1.86E+00**	**2.41E-04**	1.16E+00	1.34E-02	3.98E-01	3.71E-01	WT & nifD- N 14 dpi	E	NADH dehydrogenase subunit 2 (AHRD V3.3 *-* A0A1C9I9Q6_9ROSI)	
Solyc09g009520.3	**1.85E+00**	**2.45E-11**	**1.32E+00**	**2.21E-08**	4.27E-01	1.61E-02	3.56E-01	4.14E-02	WT & nifD- N 14 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ETT5_THECC)	
Solyc04g082180.4	**1.85E+00**	**1.84E-04**	**1.68E+00**	**5.26E-04**	-1.54E+00	1.20E-03	-9.23E-01	3.83E-02	WT & nifD- N 14 dpi	2M	alcohol dehydrogenase	
Solyc09g008350.3	**1.84E+00**	**2.13E-16**	**1.59E+00**	**6.66E-15**	2.19E-01	3.67E-02	1.05E-01	3.00E-01	WT & nifD- N 14 dpi	CS	ACT domain-containing family protein (AHRD V3.3 *** B9GIE7_POPTR)	GO:0008152|GO:0016597
Solyc03g115600.3	**1.83E+00**	**2.95E-03**	**2.62E+00**	**7.50E-05**	3.80E-01	5.01E-01	-8.17E-01	1.54E-01	WT & nifD- N 14 dpi	DNA	Zinc finger protein (AHRD V3.3 *-* A0A0B0MNI3_GOSAR)	GO:0003676|GO:0008270
Solyc04g054930.3	**1.82E+00**	**1.83E-11**	**1.46E+00**	**1.77E-09**	6.28E-01	6.07E-04	3.41E-01	4.37E-02	WT & nifD- N 14 dpi	K	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** M1BUG9_SOLTU)	GO:0003824|GO:0005992
Solyc11g073130.2	**1.81E+00**	**7.55E-14**	**1.08E+00**	**4.78E-09**	5.00E-01	4.95E-04	9.39E-01	6.43E-08	WT & nifD- N 14 dpi	L	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase (AHRD V3.3 *** K4DB19_SOLLC)	
Solyc12g035400.2	**1.81E+00**	**8.03E-15**	**1.75E+00**	**1.70E-14**	3.07E-01	1.20E-02	3.74E-02	7.45E-01	WT & nifD- N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4DE01_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:00 22857|GO:0016021|GO:0022857
Solyc08g079140.1	**1.80E+00**	**3.13E-04**	**2.00E+00**	**9.47E-05**	-8.84E-01	5.15E-02	3.55E-01	4.19E-01	WT & nifD- N 14 dpi	H	Small auxin up-regulated RNA67	GO:0009733
Solyc06g035710.1	**1.79E+00**	**1.10E-04**	**1.50E+00**	**7.70E-04**	7.07E-01	8.36E-02	6.20E-01	1.26E-01	WT & nifD- N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4C4U3_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:00 16020|GO:0055085

Solyc05g009590.3	**1.79E+00**	**7.65E-08**	**2.46E+00**	**1.56E-10**	-4.41E-01	7.93E-02	-1.20E+00	3.61E-05	WT & nifD- N 14 dpi	G	aluminum activated malate transporter family protein (AHRD V3.3 *** AT1G18420.1)	GO:0015743
Solyc07g049460.3	**1.78E+00**	**4.18E-08**	**2.31E+00**	**2.89E-10**	-6.04E-01	1.54E-02	-3.90E-01	1.06E-01	WT & nifD- N 14 dpi	PMI	laccase	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc01g108330.2	**1.78E+00**	**1.14E-07**	**1.81E+00**	**8.76E-08**	5.28E-01	4.10E-02	-5.40E-01	3.71E-02	WT & nifD- N 14 dpi	NA	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7J5T0_MEDTR)	
Solyc07g045460.3	**1.78E+00**	**3.89E-05**	**2.58E+00**	**1.33E-07**	-2.68E-01	4.63E-01	-1.00E+00	9.58E-03	WT & nifD- N 14 dpi	C	SNF1-related protein kinase regulatory subunit beta-2 (AHRD V3.3 *** AT4G16360.1)	GO:0005515|GO:0009744|GO:0043562|GO:0009744|GO:0043562
Solyc05g012520.3	**1.78E+00**	**2.27E-03**	**1.63E+00**	**4.46E-03**	-9.25E-01	8.94E-02	5.61E-01	2.95E-01	WT & nifD- N 14 dpi	PMI	SNAP25 like protein SNAP33 (AHRD V3.3 *** A0A0B2SW23_GLYSO)	GO:0005515
Solyc02g086480.1	**1.78E+00**	**1.75E-03**	**1.53E+00**	**5.78E-03**	1.02E+00	5.61E-02	1.16E+00	3.05E-02	WT & nifD- N 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9S640_RICCO)	
Solyc01g009810.3	**1.78E+00**	**3.53E-06**	**1.96E+00**	**7.20E-07**	9.68E-01	3.57E-03	7.71E-02	8.01E-01	WT & nifD- N 14 dpi	PMI	Leucine-rich repeat receptor-like kinase protein (AHRD V3.3 *-* A0A060H1D1_ELAGV)	GO:0005515
Solyc02g090390.3	**1.77E+00**	**7.73E-17**	**1.07E+00**	**9.98E-12**	5.14E-02	5.80E-01	9.74E-01	6.74E-11	WT & nifD- N 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9N888_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc11g066020.2	**1.77E+00**	**9.81E-16**	**1.35E+00**	**5.02E-13**	1.50E-01	1.53E-01	6.85E-01	4.06E-07	WT & nifD- N 14 dpi	P	Ankyrin repeat family protein (AHRD V3.3 *** B9GJP4_POPTR)	GO:0005515|GO:0005515|GO:0008270|GO:0005515|GO:0008270
Solyc12g010940.1	**1.77E+00**	**2.68E-09**	**2.18E+00**	**3.63E-11**	-1.15E+00	4.42E-06	-5.66E-01	8.70E-03	WT & nifD- N 14 dpi	NA	LOW QUALITY:DUF1685 family protein (AHRD V3.3 *** A0A072V475_MEDTR)	
Solyc04g079040.3	**1.77E+00**	**3.79E-05**	**2.08E+00**	**3.81E-06**	-5.01E-01	1.71E-01	3.48E-01	3.37E-01	WT & nifD- N 14 dpi	STR	Serine carboxypeptidase, putative (AHRD V3.3 *-* Q9FX26_ARATH)	GO:0004185|GO:0006508
Solyc03g007860.1	**1.76E+00**	**1.82E-05**	**1.57E+00**	**8.15E-05**	-2.56E-01	4.53E-01	7.63E-01	3.17E-02	WT & nifD- N 14 dpi	E	Protein PAM68, chloroplastic (AHRD V3.3 *-* PAM68_ARATH)	
Solyc07g017600.3	**1.76E+00**	**1.33E-06**	**2.35E+00**	**8.17E-09**	3.18E-01	2.67E-01	-6.25E-01	3.50E-02	WT & nifD- N 14 dpi	CS	Pectinesterase (AHRD V3.3 *** K4CCH4_SOLLC)	GO:0004857|GO:0005618|GO:0030599|GO:0042545|GO:0005618|GO:0030599|GO:0042545
Solyc04g072030.1	**1.75E+00**	**9.71E-09**	**1.78E+00**	**6.77E-09**	4.62E-01	3.75E-02	-1.33E+00	1.19E-06	WT & nifD- N 14 dpi	TR	Dynamin-related protein (AHRD V3.3 *** A0A1B0UTC3_TOBAC)	GO:0003924|GO:0005525|GO:0005525|GO:0005525
Solyc02g032660.3	**1.75E+00**	**4.52E-12**	**1.70E+00**	**8.61E-12**	-7.62E-02	6.03E-01	-4.02E-01	1.02E-02	WT & nifD- N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4B5L0_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc07g066020.2	**1.74E+00**	**2.61E-13**	**1.47E+00**	**1.16E-11**	2.09E-01	1.12E-01	-9.53E-02	4.61E-01	WT & nifD- N 14 dpi	AM	Amino acid transporter, putative (AHRD V3.3 *** B9T658_RICCO)	
Solyc01g020200.1	**1.74E+00**	**7.74E-03**	**2.99E+00**	**3.72E-05**	7.83E-01	2.05E-01	8.58E-01	1.66E-01	WT & nifD- N 14 dpi	TR	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0C5C9W8_SOLLC)	
Solyc05g014140.2	**1.73E+00**	**5.23E-03**	**3.47E+00**	**1.90E-06**	4.82E-03	9.93E-01	-2.36E-01	6.81E-01	WT & nifD- N 14 dpi	G	beta-ketoacyl reductase 1 (AHRD V3.3 *-* AT1G67730.1)	
Solyc04g080390.3	**1.72E+00**	**1.89E-10**	**1.06E+00**	**1.53E-06**	-3.59E-03	9.83E-01	2.40E-01	1.71E-01	WT & nifD- N 14 dpi	NA	plasma membrane fusion protein (AHRD V3.3 *** AT5G42765.1)	
Solyc08g065500.2	**1.72E+00**	**4.15E-06**	**2.54E+00**	**4.80E-09**	-4.30E-01	1.58E-01	2.35E-01	4.34E-01	WT & nifD- N 14 dpi	K	Phosphatase 2C family protein (AHRD V3.3 *** A0A061GL17_THECC)	GO:0003824|GO:0004722|GO:0006470|GO:0004722|GO:0006470
Solyc02g080550.1	**1.72E+00**	**1.56E-08**	**1.59E+00**	**6.07E-08**	3.19E-01	1.45E-01	1.49E-01	4.90E-01	WT & nifD- N 14 dpi	NA	SH3 domain-binding protein 1, putative (AHRD V3.3 *** A0A061F5K7_THECC)	
Solyc10g024490.2	**1.72E+00**	**7.51E-04**	**1.89E+00**	**2.82E-04**	-1.12E-01	8.05E-01	-6.80E-01	1.42E-01	WT & nifD- N 14 dpi	TR	Peptide transporter, putative (AHRD V3.3 *** B9S1I2_RICCO)	GO:0005215|GO:0006810|GO:0016020
Solyc06g071290.3	**1.72E+00**	**2.58E-03**	**1.54E+00**	**6.10E-03**	9.81E-01	6.75E-02	7.95E-01	1.34E-01	WT & nifD- N 14 dpi	STR	putative betaine aldehyde dehyrogenase	GO:0008152|GO:0016491|GO:0016620|GO:0055114|GO:0008152|GO:0016491|GO:0055114|GO:0008152|GO:0016491|GO:0055114
Solyc08g082690.2	**1.71E+00**	**1.54E-05**	**1.01E+00**	**4.49E-03**	1.78E-01	5.87E-01	8.14E-01	1.83E-02	WT & nifD- N 14 dpi	R	Ribosomal protein S6 (AHRD V3.3 *** A0A103XFW4_CYNCS)	GO:0003735|GO:0005840|GO:0006412|GO:0019843
Solyc03g121190.3	**1.71E+00**	**6.18E-05**	**1.87E+00**	**1.92E-05**	1.23E-01	7.34E-01	5.39E-01	1.45E-01	WT & nifD- N 14 dpi	NA	transmembrane protein (AHRD V3.3 -** AT1G51920.1)	
Solyc06g062670.3	**1.71E+00**	**7.07E-10**	**1.24E+00**	**2.92E-07**	8.26E-01	1.05E-04	8.26E-01	1.05E-04	WT & nifD- N 14 dpi	DNA	zinc finger family protein	GO:0003676|GO:0046872|GO:0046872
Solyc06g054250.3	**1.70E+00**	**4.05E-14**	**1.68E+00**	**5.89E-14**	7.24E-01	1.19E-06	3.45E-01	5.89E-03	WT & nifD- N 14 dpi	DNA	5'-nucleotidase surE (AHRD V3.3 *** W9QLZ8_9ROSA)	GO:0008252|GO:0016787|GO:0016787
Solyc07g038110.2	**1.70E+00**	**6.26E-07**	**1.21E+00**	**8.44E-05**	2.20E-01	4.02E-01	7.31E-02	7.80E-01	WT & nifD- N 14 dpi	C	Beta-galactosidase (AHRD V3.3 *-* V7C958_PHAVU)	GO:0004553|GO:0005975|GO:0030246|GO:00

Solyc08g074495.1	**1.70E+00**	**4.49E-12**	**2.16E+00**	**1.85E-14**	-4.20E-01	6.09E-03	7.10E-01	3.05E-05	WT & nifD- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** A0A022RAZ3_ERYGU)	
Solyc06g050160.3	**1.69E+00**	**1.95E-04**	**2.05E+00**	**1.75E-05**	2.56E-01	5.16E-01	1.97E-01	6.18E-01	WT & nifD- N 14 dpi	DNA	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072TNH2_MEDTR)	GO:0003677|GO:0008289|GO:0008289
Solyc12g087880.2	**1.69E+00**	**4.67E-03**	**1.56E+00**	**8.46E-03**	6.98E-01	2.12E-01	7.72E-01	1.69E-01	WT & nifD- N 14 dpi	TR	Purine permease-like protein (AHRD V3.3 *-* G7J4H5_MEDTR)	GO:0005215|GO:0016021
Solyc07g054770.1	**1.69E+00**	**9.19E-07**	**1.69E+00**	**9.03E-07**	-5.48E-01	4.77E-02	-4.01E-01	1.40E-01	WT & nifD- N 14 dpi	D	Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)	
Solyc12g057075.1	**1.69E+00**	**1.96E-04**	**1.68E+00**	**1.98E-04**	3.25E-01	4.10E-01	5.60E-01	1.62E-01	WT & nifD- N 14 dpi	TR	Purine permease-like protein (AHRD V3.3 *-* G7J4H5_MEDTR)	GO:0005215|GO:0016021
Solyc11g005350.2	**1.69E+00**	**1.09E-04**	**2.15E+00**	**4.13E-06**	9.51E-01	1.61E-02	7.91E-01	4.20E-02	WT & nifD- N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4D4E8_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc05g050240.3	**1.68E+00**	**8.32E-03**	**1.80E+00**	**5.22E-03**	-1.10E-01	8.53E-01	-2.06E+00	1.70E-03	WT & nifD- N 14 dpi	E	Plastid division protein PDV1 (AHRD V3.3 *-* A0A199W2F8_ANACO)	
Solyc01g008620.3	**1.68E+00**	**1.04E-05**	**1.80E+00**	**3.67E-06**	1.58E-01	6.11E-01	-9.33E-02	7.64E-01	WT & nifD- N 14 dpi	CS	Beta-1,3-glucanase (AHRD V3.3 *** Q9SYX6_TOBAC)	GO:0004553|GO:0005975|GO:0005975|GO:00
Solyc08g074970.1	**1.67E+00**	**2.21E-08**	**1.37E+00**	**7.15E-07**	1.61E-01	4.53E-01	-3.25E-01	1.36E-01	WT & nifD- N 14 dpi	C	LOW QUALITY:Glycosyltransferase family protein (AHRD V3.3 *** G7L745_MEDTR)	
Solyc03g078490.3	**1.67E+00**	**1.31E-08**	**1.03E+00**	**3.22E-05**	3.18E-01	1.31E-01	6.72E-01	2.88E-03	WT & nifD- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BHS7_SOLLC)	GO:0008152|GO:0016758
Solyc09g098190.3	**1.66E+00**	**8.32E-10**	**1.77E+00**	**2.28E-10**	9.98E-02	5.77E-01	4.36E-01	2.06E-02	WT & nifD- N 14 dpi	D	Signal peptide peptidase-like protein (AHRD V3.3 *-* A0A072TX77_MEDTR)	GO:0004190|GO:0016021
Solyc07g062200.2	**1.66E+00**	**5.59E-04**	**1.29E+00**	**4.98E-03**	8.60E-01	5.13E-02	7.59E-01	8.29E-02	WT & nifD- N 14 dpi	T	bHLH transcription factor 088	GO:0003677|GO:0046983|GO:0046983
Solyc08g079430.3	**1.65E+00**	**3.84E-11**	**1.72E+00**	**1.62E-11**	2.17E-01	1.64E-01	-7.01E-02	6.47E-01	WT & nifD- N 14 dpi	N	partialcopper-containing amine oxidase	GO:0005507|GO:0008131|GO:0009308|GO:0048038|GO:0055114
Solyc06g066830.3	**1.64E+00**	**4.52E-09**	**1.83E+00**	**4.91E-10**	-2.20E-01	2.58E-01	-1.37E+00	1.18E-07	WT & nifD- N 14 dpi	E	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)	GO:0016491|GO:0055114
Solyc08g062210.3	**1.63E+00**	**3.83E-17**	**1.65E+00**	**2.94E-17**	-2.74E-01	2.54E-03	1.12E-01	1.84E-01	WT & nifD- N 14 dpi	T	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)	GO:0003677|GO:0016602|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc03g116970.2	**1.63E+00**	**2.88E-07**	**1.23E+00**	**2.19E-05**	2.67E-01	2.72E-01	-2.40E-01	3.22E-01	WT & nifD- N 14 dpi	CS	Sister chromatid cohesion PDS5 B-B (AHRD V3.3 *-* A0A0B0PPN5_GOSAR)	GO:0005488
Solyc04g080990.2	**1.63E+00**	**1.44E-04**	**1.47E+00**	**4.38E-04**	1.30E-01	7.24E-01	-1.23E+00	2.38E-03	WT & nifD- N 14 dpi	TR	S-type anion channel SLAH1 (AHRD V3.3 *** SLAH1_ARATH)	GO:0006873|GO:0008308|GO:0016021|GO:0016021|GO:0055085|GO:0016021|GO:0055085
Solyc03g111260.3	**1.63E+00**	**8.28E-11**	**1.11E+00**	**1.29E-07**	3.00E-01	6.31E-02	6.94E-01	1.30E-04	WT & nifD- N 14 dpi	RNA	Ribonuclease J (AHRD V3.3 *** A0A0B0P255_GOSAR)	
Solyc10g007900.3	**1.62E+00**	**7.97E-09**	**1.85E+00**	**6.38E-10**	-8.79E-02	6.54E-01	5.05E-02	7.96E-01	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *-* A0A124SAX2_CYNCS)	GO:0004497|GO:0005506|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0
Solyc07g054780.1	**1.62E+00**	**4.11E-08**	**1.69E+00**	**1.75E-08**	-8.13E-01	6.86E-04	1.69E-01	4.31E-01	WT & nifD- N 14 dpi	D	LOW QUALITY:Wound-responsive family protein (AHRD V3.3 *** AT4G10265.1)	
Solyc06g082030.3	**1.59E+00**	**5.95E-07**	**1.61E+00**	**4.99E-07**	7.21E-01	6.18E-03	6.41E-01	1.35E-02	WT & nifD- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G58660.1)	GO:0016491|GO:0055114
Solyc08g077070.3	**1.58E+00**	**2.75E-03**	**2.02E+00**	**2.56E-04**	6.49E-02	8.93E-01	-9.08E-01	6.79E-02	WT & nifD- N 14 dpi	G	Protein NAP1 (AHRD V3.3 --* NCKP1_ARATH)	
Solyc01g107540.3	**1.58E+00**	**4.76E-04**	**2.72E+00**	**2.77E-07**	-1.98E-01	6.19E-01	1.05E+00	1.31E-02	WT & nifD- N 14 dpi	TR	Plant basic secretory family protein (AHRD V3.3 *** B9GHT3_POPTR)	
Solyc03g119310.3	**1.57E+00**	**8.11E-06**	**1.48E+00**	**1.90E-05**	7.51E-02	7.93E-01	-5.17E-01	7.96E-02	WT & nifD- N 14 dpi	E	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 --* RBL_ANTLU)	
Solyc10g039270.2	**1.57E+00**	**8.31E-04**	**1.42E+00**	**2.12E-03**	7.31E-01	9.04E-02	1.40E-01	7.39E-01	WT & nifD- N 14 dpi	P	Peptidyl-prolyl cis-trans isomerase (AHRD V3.3 *** A0A0K9PKM9_ZOSMR)	
Solyc01g098190.3	**1.57E+00**	**1.98E-03**	**1.68E+00**	**1.09E-03**	5.08E-01	2.76E-01	-4.58E-01	3.25E-01	WT & nifD- N 14 dpi	E	(Sodium/potassium)/proton exchanger 4	GO:0005774|GO:0005886|GO:0006814|GO:0009651|GO:0055075|GO:0006812|GO:0015299|GO:0016021|GO:0006812|GO:0015299|GO:0
Solyc03g080150.3	**1.57E+00**	**1.86E-10**	**2.37E+00**	**2.11E-14**	5.44E-01	1.68E-03	-1.38E-01	3.81E-01	WT & nifD- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4BHZ1_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc12g095910.2	**1.56E+00**	**4.48E-17**	**1.42E+00**	**4.32E-16**	3.76E-01	6.42E-05	7.33E-01	1.10E-09	WT & nifD- N 14 dpi	G	cysteine protease	GO:0006508|GO:0008233

Solyc06g007350.3	**1.56E+00**	**1.26E-06**	**1.40E+00**	**6.89E-06**	2.79E-01	2.71E-01	-6.08E-01	2.15E-02	WT & nifD- N 14 dpi	K	Protein phosphatase 2C family protein (AHRD V3.3 *** AT2G30170.1)	GO:0003824
Solyc10g086380.1	**1.55E+00**	**1.54E-09**	**1.33E+00**	**2.94E-08**	4.21E-01	2.04E-02	5.10E-01	6.03E-03	WT & nifD- N 14 dpi	H	GAI-like protein 1 (AHRD V3.3 *** A1YWN9_9ROSI)	GO:0000989|GO:0005634
Solyc06g073940.3	**1.55E+00**	**3.10E-08**	**1.97E+00**	**2.93E-10**	2.21E-01	2.77E-01	-3.25E-01	1.15E-01	WT & nifD- N 14 dpi	H	Protein FAF-like, chloroplastic (AHRD V3.3 *** A0A0B2RVL4_GLYSO)	
Solyc02g083620.3	**1.55E+00**	**3.77E-05**	**1.92E+00**	**1.80E-06**	3.67E-01	2.50E-01	7.38E-01	2.58E-02	WT & nifD- N 14 dpi	OX	L-ascorbate peroxidase 5	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0055114|GO:0004601
Solyc11g012050.1	**1.54E+00**	**1.80E-06**	**1.43E+00**	**5.93E-06**	5.15E-01	5.10E-02	-4.07E-01	1.18E-01	WT & nifD- N 14 dpi	K	MAP kinase kinase kinase 81	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g087240.3	**1.54E+00**	**1.54E-11**	**1.43E+00**	**6.68E-11**	7.17E-02	5.99E-01	2.83E-01	4.60E-02	WT & nifD- N 14 dpi	T	nuclear transcription factor Y subunit A-9	GO:0003677|GO:0016602|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc01g100900.3	**1.53E+00**	**5.91E-06**	**1.90E+00**	**1.88E-07**	-7.22E-02	7.92E-01	-1.08E+00	4.66E-04	WT & nifD- N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4B1C1_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc01g073660.3	**1.53E+00**	**2.14E-11**	**1.04E+00**	**5.09E-08**	-1.27E-02	9.27E-01	5.58E-01	3.84E-04	WT & nifD- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT2G44280.4),Pfam:PF13347	
Solyc03g113130.3	**1.53E+00**	**1.55E-07**	**1.61E+00**	**6.30E-08**	-4.71E-01	3.74E-02	6.44E-02	7.67E-01	WT & nifD- N 14 dpi	E	2-aminoethanethiol dioxygenase (AHRD V3.3 *** A0A0B0PVN9_GOSAR)	GO:0016702|GO:0055114
Solyc01g060240.3	**1.52E+00**	**8.65E-12**	**1.24E+00**	**6.13E-10**	1.66E-01	2.14E-01	7.01E-01	1.26E-05	WT & nifD- N 14 dpi	NA	cAMP-regulated phosphoprotein 19-related protein (AHRD V3.3 --* AT4G16146.1)	
Solyc03g114860.3	**1.51E+00**	**9.52E-04**	**1.79E+00**	**1.66E-04**	-2.62E-01	5.24E-01	-1.81E-01	6.59E-01	WT & nifD- N 14 dpi	CS	UDP-arabinose mutase-like protein	GO:0016866|GO:0030244
Solyc08g074980.3	**1.51E+00**	**1.01E-13**	**1.17E+00**	**2.74E-11**	-4.37E-01	3.42E-04	7.91E-01	6.82E-08	WT & nifD- N 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9H049_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g116630.3	**1.51E+00**	**5.90E-11**	**1.68E+00**	**5.30E-12**	-1.85E-01	2.00E-01	4.28E-01	5.33E-03	WT & nifD- N 14 dpi	CYTP450	cytochrome P450 family protein (AHRD V3.3 *** AT1G52565.1)	
Solyc05g014790.3	**1.50E+00**	**1.44E-15**	**1.05E+00**	**4.83E-12**	2.11E-01	2.36E-02	1.53E-01	9.29E-02	WT & nifD- N 14 dpi	L	Lipoxygenase (AHRD V3.3 *** A0A0V0IV84_SOLCH)	GO:0005515|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc06g060710.3	**1.50E+00**	**6.59E-10**	**1.29E+00**	**1.23E-08**	1.60E-01	3.18E-01	9.08E-01	4.76E-06	WT & nifD- N 14 dpi	NA	Nucleotide-diphospho-sugar transferases superfamily protein (AHRD V3.3 *** AT4G16600.1)	
Solyc01g066770.3	**1.50E+00**	**7.49E-06**	**1.21E+00**	**1.26E-04**	6.63E-01	2.04E-02	5.00E-01	7.39E-02	WT & nifD- N 14 dpi	P	Chaperone protein dnaJ, putative (AHRD V3.3 *** B9RT65_RICCO)	
Solyc11g072560.2	**1.50E+00**	**5.05E-05**	**2.24E+00**	**1.06E-07**	-2.08E+00	3.88E-07	-1.25E+00	4.17E-04	WT & nifD- N 14 dpi	TR	Major Facilitator Superfamily protein (AHRD V3.3 *** Q6L3J2_SOLDE)	GO:0005215|GO:0006810|GO:0016020|GO:0005215|GO:0006857|GO:0016020|GO:0005215
Solyc08g014130.3	**1.50E+00**	**8.58E-15**	**1.07E+00**	**1.51E-11**	-6.14E-02	5.21E-01	8.62E-01	1.48E-09	WT & nifD- N 14 dpi	C	Isopropylmalate synthase (AHRD V3.3 *** K4CJ46_SOLLC)	GO:0003824|GO:0003852|GO:0009098|GO:0003852|GO:0009098
Solyc07g066560.1	**1.50E+00**	**1.68E-03**	**1.27E+00**	**6.14E-03**	-5.83E-01	1.83E-01	-1.26E+00	6.57E-03	WT & nifD- N 14 dpi	H	Small auxin up-regulated RNA65	GO:0009733
Solyc01g010350.3	**1.49E+00**	**1.98E-06**	**2.40E+00**	**3.43E-10**	1.73E-01	4.85E-01	-1.04E-01	6.73E-01	WT & nifD- N 14 dpi	C	Glucose-6-phosphate translocator	GO:0005215|GO:0006810|GO:0016021
Solyc01g105940.3	**1.49E+00**	**3.15E-04**	**1.24E+00**	**1.87E-03**	5.31E-01	1.50E-01	7.10E-01	5.81E-02	WT & nifD- N 14 dpi	H	Linalool synthase (AHRD V3.3 *-* Q1XBU5_SOLLC)	GO:0000287|GO:0010333|GO:0016829
Solyc03g026360.1	**1.49E+00**	**1.07E-10**	**2.17E+00**	**2.44E-14**	-7.32E-01	2.57E-05	3.42E-02	8.13E-01	WT & nifD- N 14 dpi	D	LOW QUALITY:Peptidoglycan-binding LysM domain-containing family protein (AHRD V3.3 *** B9ID24_POPTR)	
Solyc03g026130.3	**1.49E+00**	**3.86E-15**	**1.21E+00**	**4.67E-13**	1.87E-01	4.84E-02	3.15E-01	1.81E-03	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A0N9HM28_9MAGN)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc10g079460.1	**1.48E+00**	**1.43E-05**	**1.30E+00**	**7.71E-05**	6.70E-02	8.11E-01	8.77E-03	9.75E-01	WT & nifD- N 14 dpi	T	BTB/POZ ankyrin repeat protein (AHRD V3.3 *** G8GTN4_MEDTR)	GO:0005515
Solyc09g075320.1	**1.47E+00**	**1.22E-04**	**2.11E+00**	**8.18E-07**	-1.26E-02	9.70E-01	5.79E-01	8.76E-02	WT & nifD- N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT4G15975.1)	GO:0005515|GO:0008270
Solyc08g082670.3	**1.47E+00**	**2.56E-09**	**1.42E+00**	**4.96E-09**	-2.46E-01	1.50E-01	-3.10E-03	9.85E-01	WT & nifD- N 14 dpi	CS	Cellulose synthase (AHRD V3.3 *** A0A118JUI8_CYNCS)	GO:0016020|GO:0016760|GO:0030244
Solyc03g033660.3	**1.47E+00**	**1.15E-04**	**1.61E+00**	**3.62E-05**	2.80E-01	3.93E-01	3.55E-01	2.81E-01	WT & nifD- N 14 dpi	T	GATA transcription factor (AHRD V3.3 *** K4BFN8_SOLLC)	GO:0003677|GO:0005634|GO:0045893|GO:0003700|GO:0006355|GO:0008270|GO:0043565|GO:0003700|GO:0006355|GO:0008270|GO:0
Solyc01g065980.3	**1.46E+00**	**4.18E-07**	**2.19E+00**	**2.12E-10**	-4.44E-01	5.18E-02	-4.76E-01	3.82E-02	WT & nifD- N 14 dpi	H	Ethylene Response Factor E.4	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355

Solyc01g010290.3	**1.46E+00**	**3.37E-14**	**1.53E+00**	**1.10E-14**	-7.56E-02	4.46E-01	-1.16E-02	9.06E-01	WT & nifD- N 14 dpi	N	Ureide permease (AHRD V3.3 *** A0A124SG70_CYNCS)	GO:0016021|GO:0071705|GO:0071705|GO:00
Solyc04g071620.3	**1.45E+00**	**5.81E-04**	**1.54E+00**	**3.09E-04**	-3.29E-01	3.83E-01	-8.14E-01	3.74E-02	WT & nifD- N 14 dpi	H	Abscicic acid stress ripening 4	GO:0006950
Solyc07g007690.3	**1.45E+00**	**1.43E-11**	**1.04E+00**	**1.23E-08**	-9.18E-01	1.13E-07	-1.23E-01	3.42E-01	WT & nifD- N 14 dpi	TR	Chloride channel protein (AHRD V3.3 *** M1D0Y1_SOLTU)	GO:0005216|GO:0055085|GO:0005247|GO:00 06821|GO:0016020|GO:0005247|GO:0006821
Solyc05g012700.3	**1.43E+00**	**2.15E-13**	**1.33E+00**	**1.12E-12**	5.27E-01	2.82E-05	8.00E-01	3.81E-08	WT & nifD- N 14 dpi	NA	integral membrane family protein (AHRD V3.3 *** AT1G28140.1)	
Solyc01g099620.3	**1.43E+00**	**4.18E-07**	**1.28E+00**	**2.50E-06**	-1.05E+00	4.08E-05	-2.19E-01	3.13E-01	WT & nifD- N 14 dpi	OX	Respiratory burst oxidase, putative (AHRD V3.3 *** B9RFA3_RICCO)	GO:0004601|GO:0050664|GO:0055114|GO:00 05509|GO:0005509
Solyc04g054760.3	**1.43E+00**	**7.07E-10**	**1.50E+00**	**2.78E-10**	2.05E-01	1.85E-01	2.48E-03	9.87E-01	WT & nifD- N 14 dpi	G	senescence-associated family protein (DUF581) (AHRD V3.3 *** AT1G22160.1)	
Solyc03g095300.3	**1.43E+00**	**2.32E-03**	**1.65E+00**	**5.88E-04**	9.51E-01	3.31E-02	4.33E-01	3.15E-01	WT & nifD- N 14 dpi	STR	Calcium-dependent lipid-binding (CaLB domain) family protein, putative (AHRD V3.3 *** A0A072VBE8_MEDTR)	GO:0005515
Solyc09g018430.3	**1.43E+00**	**9.33E-03**	**1.98E+00**	**6.13E-04**	-5.68E-01	2.73E-01	-1.54E+00	5.55E-03	WT & nifD- N 14 dpi	NA	Gamma-interferon-inducible lysosomal thiol reductase (AHRD V3.3 *-* A0A151RU75_CAJCA)	
Solyc12g099190.1	**1.42E+00**	**5.83E-11**	**1.02E+00**	**4.45E-08**	4.29E-01	3.44E-03	3.34E-01	1.87E-02	WT & nifD- N 14 dpi	C	LOW QUALITY:Invertase inhibitor (AHRD V3.3 *** C1KBP2_SOLTU)	GO:0004857|GO:0004857|GO:0043086|GO:00 04857|GO:0043086
Solyc06g061010.3	**1.42E+00**	**7.42E-03**	**2.13E+00**	**1.87E-04**	-2.28E-01	6.44E-01	-3.73E-01	4.53E-01	WT & nifD- N 14 dpi	G	senescence-associated family protein (DUF581) (AHRD V3.3 *-* AT4G17670.1)	
Solyc04g078650.3	**1.42E+00**	**4.82E-03**	**1.75E+00**	**7.92E-04**	1.34E-01	7.73E-01	-7.71E-01	1.05E-01	WT & nifD- N 14 dpi	G	wuschel related homobox 4	GO:0003677
Solyc01g107660.3	**1.42E+00**	**3.65E-13**	**1.12E+00**	**6.67E-11**	4.49E-01	2.37E-04	6.90E-01	6.23E-07	WT & nifD- N 14 dpi	STR	Stress enhanced protein 1, chloroplastic (AHRD V3.3 *** STEP1_ARATH)	
Solyc01g094140.3	**1.42E+00**	**6.49E-12**	**1.10E+00**	**1.27E-09**	-1.25E-01	3.07E-01	-4.80E-02	6.91E-01	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** B9IC22_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:00 55114|GO:0016705|GO:0055114|GO:0016705
Solyc12g098170.1	**1.41E+00**	**1.45E-03**	**2.00E+00**	**2.95E-05**	-2.28E+00	4.84E-06	-4.02E-01	3.20E-01	WT & nifD- N 14 dpi	P	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *** S1RTT0_THECC)	
Solyc10g085350.2	**1.41E+00**	**2.69E-03**	**1.99E+00**	**7.73E-05**	8.30E-01	6.13E-02	2.83E-01	5.11E-01	WT & nifD- N 14 dpi	NA	Macrophage migration inhibitory factor (AHRD V3.3 *** A0A103YL90_CYNCS)	
Solyc01g079880.3	**1.41E+00**	**2.42E-08**	**1.27E+00**	**1.40E-07**	2.23E-02	9.01E-01	-3.61E-01	5.30E-02	WT & nifD- N 14 dpi	NA	Stem-specific TSJT1 (AHRD V3.3 *** A0A0B0MRD0_GOSAR)	
Solyc06g069385.1	**1.40E+00**	**8.44E-07**	**1.67E+00**	**4.06E-08**	1.58E-01	4.74E-01	-1.29E-01	5.57E-01	WT & nifD- N 14 dpi	DNA	Dof zinc finger protein (AHRD V3.3 *** W9RP28_9ROSA)	GO:0003677|GO:0006355
Solyc01g088650.3	**1.40E+00**	**8.39E-12**	**1.38E+00**	**1.04E-11**	-2.60E-01	3.84E-02	6.35E-01	1.48E-05	WT & nifD- N 14 dpi	P	ALG6, ALG8 glycosyltransferase family (AHRD V3.3 *** AT2G44660.1)	GO:0005789|GO:0016758
Solyc12g005790.2	**1.40E+00**	**5.67E-05**	**1.97E+00**	**3.40E-07**	-3.14E+00	4.41E-11	-3.08E+00	7.01E-11	WT & nifD- N 14 dpi	OX	Peroxidase 27	GO:0004601|GO:0006979|GO:0020037|GO:00 55114|GO:0004601|GO:0042744|GO:0004601
Solyc05g009630.3	**1.39E+00**	**1.52E-14**	**1.21E+00**	**3.57E-13**	1.00E-01	2.75E-01	4.27E-02	6.38E-01	WT & nifD- N 14 dpi	D	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)	GO:0043531
Solyc01g090740.3	**1.39E+00**	**3.54E-04**	**1.32E+00**	**5.92E-04**	-3.22E-01	3.49E-01	1.14E-01	7.38E-01	WT & nifD- N 14 dpi	DNA	Zinc finger protein (AHRD V3.3 *** A0A0B0MVF4_GOSAR)	
Solyc07g053420.3	**1.38E+00**	**2.32E-06**	**1.81E+00**	**2.20E-08**	3.13E-01	1.81E-01	-2.70E-01	2.46E-01	WT & nifD- N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT2G42360.1)	GO:0005515|GO:0008270
Solyc01g106000.3	**1.37E+00**	**3.02E-11**	**1.03E+00**	**9.43E-09**	8.46E-02	5.01E-01	-1.20E-01	3.44E-01	WT & nifD- N 14 dpi	H	nicotinamidase 1 (AHRD V3.3 *** AT2G22570.1)	GO:0003824|GO:0008152
Solyc09g075970.3	**1.37E+00**	**3.26E-09**	**1.22E+00**	**3.10E-08**	4.35E-01	9.76E-03	6.14E-01	5.61E-04	WT & nifD- N 14 dpi	S	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G05370.1)	
Solyc02g079350.3	**1.37E+00**	**1.01E-04**	**1.88E+00**	**1.15E-06**	-7.10E-01	2.49E-02	-1.64E+00	9.42E-06	WT & nifD- N 14 dpi	DNA	Equilibrative nucleoside transporter family protein (AHRD V3.3 *** B9H1Z9_POPTR)	GO:0005337|GO:0006810|GO:0016021
Solyc03g114705.1	**1.37E+00**	**3.13E-03**	**1.56E+00**	**1.01E-03**	-9.27E-01	3.63E-02	-1.52E+00	1.25E-03	WT & nifD- N 14 dpi	H	DELLA protein (AHRD V3.3 --* Q0HA73_MALDO)	
Solyc04g079520.3	**1.36E+00**	**1.06E-07**	**1.96E+00**	**9.32E-11**	-7.38E-03	9.69E-01	-5.97E-01	3.78E-03	WT & nifD- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** A0A061FB74_THECC)	GO:0005215|GO:0006810|GO:0016020
Solyc03g083095.1	**1.36E+00**	**4.13E-07**	**1.10E+00**	**1.15E-05**	2.86E-01	1.71E-01	-2.87E-01	1.69E-01	WT & nifD- N 14 dpi	C	Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 *** K4BI85_SOLLC)	GO:0004373
Solyc11g068710.2	**1.36E+00**	**1.60E-04**	**1.26E+00**	**3.68E-04**	4.46E-01	1.60E-01	9.19E-01	6.17E-03	WT & nifD- N 14 dpi	P	F-box family protein (AHRD V3.3 *** B9MYU0_POPTR)	

Solyc07g055260.3	**1.36E+00**	**6.00E-05**	**1.32E+00**	**8.12E-05**	6.87E-01	2.27E-02	4.39E-01	1.34E-01	WT & nifD- N 14 dpi	STR	DnaJ (AHRD V3.3 *** A0A126DIH0_ARAHY)	
Solyc01g105310.3	**1.35E+00**	**6.15E-08**	**1.75E+00**	**4.48E-10**	-2.16E-01	2.42E-01	6.52E-02	7.20E-01	WT & nifD- N 14 dpi	P	metacaspase 2,Pfam:PF00656	
Solyc02g081360.3	**1.35E+00**	**6.17E-03**	**2.22E+00**	**4.45E-05**	4.94E-01	2.86E-01	-9.92E-01	3.78E-02	WT & nifD- N 14 dpi	2M	CoA ligase (AHRD V3.3 *** A0A0K9NMT8_ZOSMR)	GO:0003824|GO:0008152
Solyc02g068250.3	**1.35E+00**	**1.92E-03**	**2.12E+00**	**1.11E-05**	-4.03E-01	3.11E-01	3.09E-01	4.36E-01	WT & nifD- N 14 dpi	G	microspore-specific promoter 2 (AHRD V3.3 *-* AT5G46795.1)	
Solyc09g074230.3	**1.34E+00**	**2.85E-11**	**1.42E+00**	**8.09E-12**	-5.31E-01	1.79E-04	-4.55E-02	7.11E-01	WT & nifD- N 14 dpi	TR	SlSFP7	GO:0005215|GO:0016021|GO:0055085|GO:0016021|GO:0022857|GO:0055085|GO:0016021
Solyc11g011400.2	**1.34E+00**	**4.41E-06**	**1.20E+00**	**2.24E-05**	-3.92E-01	1.03E-01	-8.66E-02	7.12E-01	WT & nifD- N 14 dpi	L	Linoleate 9S-lipoxygenase (AHRD V3.3 --* LOXB_PHAVU)	
Solyc09g090470.3	**1.34E+00**	**5.39E-07**	**1.54E+00**	**5.02E-08**	4.12E-01	5.25E-02	-8.76E-02	6.69E-01	WT & nifD- N 14 dpi	TR	Peptide transporter (AHRD V3.3 *** G7I4R9_MEDTR)	GO:0005215|GO:0006810|GO:0016020
Solyc10g085500.2	**1.34E+00**	**3.79E-03**	**1.98E+00**	**7.25E-05**	-2.10E+00	3.52E-05	-8.36E-01	5.72E-02	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9SRM6_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc01g009430.3	**1.33E+00**	**1.06E-07**	**1.33E+00**	**1.06E-07**	1.33E-01	4.74E-01	5.36E-01	7.10E-03	WT & nifD- N 14 dpi	NA	BnaA07g13420D protein (AHRD V3.3 *** A0A078ETL1_BRANA)	
Solyc10g007110.3	**1.33E+00**	**6.97E-05**	**2.52E+00**	**2.08E-09**	6.11E-01	3.90E-02	9.40E-01	2.52E-03	WT & nifD- N 14 dpi	AM	Tyrosine aminotransferase (AHRD V3.3 *** E2JFA7_PERFR)	GO:0003824|GO:0003824|GO:0009058|GO:0030170|GO:0003824|GO:0009058|GO:0030170
Solyc09g011870.2	**1.33E+00**	**4.92E-04**	**1.87E+00**	**7.04E-06**	1.99E-01	5.55E-01	-6.36E-01	6.70E-02	WT & nifD- N 14 dpi	AM	Arogenate dehydrogenase 2 (AHRD V3.3 *** F1BPV6_SOLPN)	GO:0004665|GO:0006571|GO:0008977|GO:0055114|GO:0055114|GO:0055114
Solyc09g090730.2	**1.33E+00**	**3.10E-10**	**1.62E+00**	**4.14E-12**	-8.08E-01	2.46E-06	1.05E-01	4.42E-01	WT & nifD- N 14 dpi	N	AMT1	GO:0008519|GO:0015696|GO:0016020|GO:0008519|GO:0016020|GO:0072488|GO:0008519
Solyc05g011980.3	**1.33E+00**	**1.45E-09**	**1.40E+00**	**4.78E-10**	8.70E-01	2.52E-06	2.26E-01	1.30E-01	WT & nifD- N 14 dpi	E	Photosystem II reaction center protein M (AHRD V3.3 --* PSBM_PHYPA)	
Solyc03g044300.3	**1.32E+00**	**8.54E-08**	**1.32E+00**	**8.18E-08**	5.09E-02	7.79E-01	1.72E-01	3.46E-01	WT & nifD- N 14 dpi	G	APETALA2a	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc06g071050.3	**1.32E+00**	**7.56E-16**	**1.04E+00**	**1.75E-13**	2.02E-01	1.20E-02	8.14E-01	4.19E-11	WT & nifD- N 14 dpi	D	Hypersensitive-induced response protein (AHRD V3.3 *** A6YGE4_CARPA)	
Solyc04g054370.1	**1.32E+00**	**3.70E-08**	**1.23E+00**	**1.27E-07**	2.16E-01	2.17E-01	-1.89E-01	2.77E-01	WT & nifD- N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *-* AT5G41400.1)	GO:0005515|GO:0008270
Solyc10g085610.2	**1.31E+00**	**3.50E-04**	**1.50E+00**	**7.69E-05**	-9.76E-01	5.11E-03	-5.46E-01	9.86E-02	WT & nifD- N 14 dpi	DNA	Calmodulin binding protein, putative (AHRD V3.3 *** B9T5N0_RICCO)	GO:0005515
Solyc02g069090.2	**1.31E+00**	**6.49E-08**	**1.34E+00**	**4.45E-08**	4.43E-01	1.80E-02	5.14E-01	6.98E-03	WT & nifD- N 14 dpi	STR	Cathepsin B-like cysteine proteinase (AHRD V3.3 *** Q40413_NICRU)	GO:0004197|GO:0050790|GO:0006508|GO:0008234|GO:0006508|GO:0008234
Solyc03g033330.3	**1.31E+00**	**4.59E-06**	**1.02E+00**	**1.25E-04**	-5.43E-01	2.43E-02	2.82E-01	2.25E-01	WT & nifD- N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** A0A061DF87_THECC)	GO:0005515|GO:0008270
Solyc03g120450.3	**1.31E+00**	**9.71E-11**	**1.38E+00**	**3.35E-11**	1.33E-01	2.99E-01	4.63E-01	1.03E-03	WT & nifD- N 14 dpi	AM	Aspartate aminotransferase (AHRD V3.3 *** W9S4V9_9ROSA)	GO:0003824|GO:0003824|GO:0009058|GO:0030170|GO:0003824|GO:0009058|GO:0030170
Solyc06g073460.3	**1.31E+00**	**2.12E-13**	**1.13E+00**	**5.79E-12**	4.84E-01	2.52E-05	7.66E-01	1.51E-08	WT & nifD- N 14 dpi	OX	phospholipid hydroperoxide glutathione peroxidase	GO:0004602|GO:0006979|GO:0055114
Solyc11g017240.2	**1.30E+00**	**2.25E-07**	**1.28E+00**	**3.02E-07**	2.59E-01	1.78E-01	1.30E-01	4.92E-01	WT & nifD- N 14 dpi	AM	chorismate mutase	GO:0004106|GO:0009073|GO:0046417|GO:00
Solyc12g100250.2	**1.30E+00**	**9.83E-04**	**1.88E+00**	**1.33E-05**	9.86E-01	9.14E-03	-4.32E-03	9.90E-01	WT & nifD- N 14 dpi	2M	Fatty acid desaturase (AHRD V3.3 *** E5D7U7_9GENT)	GO:0006629|GO:0016717|GO:0055114|GO:0016717|GO:0055114
Solyc11g068950.2	**1.30E+00**	**1.43E-05**	**1.25E+00**	**2.42E-05**	7.49E-02	7.61E-01	-9.42E-03	9.69E-01	WT & nifD- N 14 dpi	T	BEL1-related homeotic protein 11 (AHRD V3.3 *** Q8LLE3_SOLTU)	GO:0003677|GO:0003677|GO:0006355|GO:0003677|GO:0006355
Solyc11g066270.2	**1.30E+00**	**1.68E-07**	**1.59E+00**	**3.78E-09**	-4.33E-01	2.57E-02	-3.98E-01	3.86E-02	WT & nifD- N 14 dpi	CS	xyloglucan endotransglucosylase-hydrolase 6	GO:0004553|GO:0005975|GO:0005618|GO:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc07g064870.3	**1.29E+00**	**4.44E-06**	**2.07E+00**	**1.12E-09**	-9.99E-01	1.38E-04	-1.51E+00	3.87E-07	WT & nifD- N 14 dpi	CS	Endoglucanase (AHRD V3.3 *** M1C0J8_SOLTU)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc07g041900.3	**1.29E+00**	**2.40E-09**	**1.37E+00**	**7.81E-10**	4.64E-01	3.62E-03	7.05E-02	6.31E-01	WT & nifD- N 14 dpi	G	cysteine proteinase	GO:0006508|GO:0008234|GO:0008234|GO:00
Solyc03g119350.2	**1.29E+00**	**1.53E-03**	**1.12E+00**	**4.83E-03**	-2.26E-01	5.39E-01	-9.78E-01	1.24E-02	WT & nifD- N 14 dpi	P	peptidase M50B-like protein (AHRD V3.3 *-* AT1G67060.1)	

Solyc02g081040.3	**1.29E+00**	**2.63E-08**	**1.34E+00**	**1.29E-08**	-3.44E-01	4.55E-02	6.81E-02	6.80E-01	WT & nifD- N 14 dpi	S	Receptor protein kinase, putative (AHRD V3.3 *** B9SH40_RICCO)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g093890.1	**1.28E+00**	**4.36E-03**	**1.49E+00**	**1.23E-03**	9.57E-01	2.76E-02	2.93E-01	4.82E-01	WT & nifD- N 14 dpi	P	Emb|CAB62340.1 (AHRD V3.3 *** Q9FKS6_ARATH)	
Solyc06g053980.3	**1.28E+00**	**2.59E-03**	**1.40E+00**	**1.11E-03**	7.26E-01	6.90E-02	2.82E-02	9.42E-01	WT & nifD- N 14 dpi	P	Chlorophyllase (AHRD V3.3 *** F1BPW6_SOLPN)	GO:0015996|GO:0047746
Solyc04g012090.2	**1.27E+00**	**1.21E-03**	**1.36E+00**	**6.30E-04**	-3.02E+00	4.57E-09	-1.29E+00	1.05E-03	WT & nifD- N 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BPR1_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g005440.1	**1.27E+00**	**5.25E-10**	**1.18E+00**	**2.30E-09**	3.04E-02	8.20E-01	-2.60E-01	6.04E-02	WT & nifD- N 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CB16_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g005840.2	**1.27E+00**	**4.31E-04**	**1.59E+00**	**3.12E-05**	8.86E-01	9.31E-03	2.46E-01	4.42E-01	WT & nifD- N 14 dpi	TR	Outward rectifying potassium channel protein (AHRD V3.3 *** A0A072UNK3_MEDTR)	
Solyc05g015150.3	**1.27E+00**	**4.22E-07**	**1.39E+00**	**8.92E-08**	3.22E-01	1.01E-01	-2.48E-01	2.02E-01	WT & nifD- N 14 dpi	S	Receptor-like kinase (AHRD V3.3 *** G7KTA0_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc06g069070.1	**1.27E+00**	**7.86E-03**	**1.92E+00**	**1.80E-04**	9.65E-01	3.76E-02	-4.18E-02	9.25E-01	WT & nifD- N 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** S4TID2_GOSHI)	GO:0006869
Solyc08g081780.1	**1.27E+00**	**1.86E-03**	**2.33E+00**	**9.77E-07**	-2.96E+00	1.55E-08	-1.14E+00	4.29E-03	WT & nifD- N 14 dpi	CS	Dirigent protein	
Solyc06g072430.2	**1.27E+00**	**1.20E-03**	**1.00E+00**	**7.72E-03**	-3.26E-01	3.56E-01	-1.01E+00	7.24E-03	WT & nifD- N 14 dpi	P	BAG family molecular chaperone regulator 5 (AHRD V3.3 *-* W9QTU5_9ROSA)	GO:0005515|GO:0051087|GO:0051087
Solyc03g045120.1	**1.26E+00**	**4.19E-03**	**2.06E+00**	**2.61E-05**	-3.26E-01	4.25E-01	7.05E-02	8.62E-01	WT & nifD- N 14 dpi	CS	jacalin-related lectin 22 (AHRD V3.3 --* AT2G39310.4)	
Solyc01g094170.3	**1.26E+00**	**2.27E-09**	**1.59E+00**	**1.77E-11**	-3.61E-01	1.63E-02	-1.12E-01	4.31E-01	WT & nifD- N 14 dpi	PMI	Digalactosyldiacylglycerol synthase (AHRD V3.3 *** A2Q3N6_MEDTR)	
Solyc01g106460.3	**1.25E+00**	**1.92E-07**	**1.97E+00**	**2.83E-11**	-1.22E-01	4.99E-01	-5.11E-01	8.18E-03	WT & nifD- N 14 dpi	T	bHLH transcription factor 007	GO:0046983
Solyc09g010800.4	**1.25E+00**	**1.17E-06**	**1.14E+00**	**4.59E-06**	-7.27E-02	7.16E-01	2.45E-01	2.27E-01	WT & nifD- N 14 dpi	NA	metallothionein II-like protein	
Solyc02g071070.3	**1.24E+00**	**1.30E-06**	**2.10E+00**	**7.61E-11**	-7.47E-01	8.75E-04	1.16E-01	5.63E-01	WT & nifD- N 14 dpi	TR	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NMD6_ZOSMR)	GO:0006812|GO:0015299|GO:0016021|GO:0055085
Solyc10g085950.2	**1.24E+00**	**2.49E-08**	**1.83E+00**	**9.86E-12**	-1.72E+00	3.62E-11	-1.03E+00	7.08E-07	WT & nifD- N 14 dpi	S	aluminum sensitive 3 (AHRD V3.3 *** AT2G37330.1)	
Solyc05g056440.2	**1.24E+00**	**2.00E-04**	**1.64E+00**	**5.08E-06**	-5.74E-01	5.58E-02	-1.06E+00	1.05E-03	WT & nifD- N 14 dpi	H	Small auxin up-regulated RNA57	GO:0009733
Solyc00g022103.1	**1.24E+00**	**6.35E-03**	**1.93E+00**	**9.31E-05**	5.08E-01	2.35E-01	6.81E-01	1.16E-01	WT & nifD- N 14 dpi	G	Transducin family protein / WD-40 repeat family protein (AHRD V3.3 --* AT5G43930.4)	
Solyc02g084930.3	**1.24E+00**	**1.79E-09**	**1.15E+00**	**8.50E-09**	-8.54E-01	1.43E-06	-7.95E-01	4.28E-06	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** G7LDW2_MEDTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc06g059740.3	**1.24E+00**	**1.64E-07**	**1.87E+00**	**5.80E-11**	-9.42E-01	1.25E-05	-2.94E-01	1.05E-01	WT & nifD- N 14 dpi	2M	Alcohol dehydrogenase (AHRD V3.3 *** ADH_MALDO)	GO:0055114
Solyc10g007030.2	**1.24E+00**	**7.79E-13**	**1.19E+00**	**1.86E-12**	-9.96E-02	3.04E-01	4.36E-01	1.00E-04	WT & nifD- N 14 dpi	NA	Transmembrane protein, putative (AHRD V3.3 *** G7IPT2_MEDTR)	
Solyc11g008440.2	**1.23E+00**	**3.78E-10**	**1.16E+00**	**1.33E-09**	2.15E-01	1.01E-01	6.91E-01	1.00E-05	WT & nifD- N 14 dpi	AM	Amino acid transporter family protein (AHRD V3.3 *** B9HLH9_POPTR)	
Solyc03g005020.3	**1.23E+00**	**4.38E-05**	**1.08E+00**	**2.21E-04**	7.37E-01	6.93E-03	-5.45E-01	3.94E-02	WT & nifD- N 14 dpi	L	Lipase (AHRD V3.3 *** K4BDS6_SOLLC)	GO:0006629|GO:0016788|GO:0016788
Solyc03g025870.3	**1.23E+00**	**7.09E-05**	**1.61E+00**	**1.60E-06**	-7.98E-01	5.06E-03	-1.06E+00	3.87E-04	WT & nifD- N 14 dpi	G	R2R3MYB transcription factor 19	GO:0003677
Solyc04g074380.3	**1.23E+00**	**3.35E-03**	**1.30E+00**	**2.10E-03**	-7.04E-01	7.58E-02	-1.81E+00	6.58E-05	WT & nifD- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *-* M1D1E1_SOLTU)	GO:0008152|GO:0016758
Solyc02g087090.3	**1.23E+00**	**2.11E-07**	**1.70E+00**	**4.68E-10**	-1.89E+00	4.83E-11	8.68E-02	6.25E-01	WT & nifD- N 14 dpi	OX	alpha-DOX2	GO:0004601|GO:0006979|GO:0020037|GO:00
Solyc08g082870.3	**1.23E+00**	**3.29E-09**	**1.35E+00**	**4.74E-10**	7.70E-03	9.56E-01	-3.55E-01	1.75E-02	WT & nifD- N 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein	
Solyc11g013150.1	**1.22E+00**	**3.59E-08**	**1.57E+00**	**3.03E-10**	-2.05E-01	2.07E-01	-1.98E-01	2.21E-01	WT & nifD- N 14 dpi	T	GRAS family transcription factor (AHRD V3.3 *** A0A061FHT3_THECC)	
Solyc01g010295.1	**1.22E+00**	**8.24E-07**	**1.52E+00**	**1.79E-08**	-1.17E-03	9.95E-01	-8.25E-02	6.66E-01	WT & nifD- N 14 dpi	N	Ureide permease, putative (AHRD V3.3 *-* B9REE2_RICCO)	GO:0016021|GO:0071705|GO:0071705|GO:00

Solyc11g010900.2	**1.21E+00**	**3.53E-03**	**1.57E+00**	**3.26E-04**	4.62E-01	2.32E-01	3.15E-01	4.12E-01	WT & nifD- N 14 dpi	RNA	tRNA/rRNA methyltransferase family protein (AHRD V3.3 *** D7M9L1_ARALL)	GO:0003723|GO:0006396|GO:0008173
Solyc04g080960.3	**1.21E+00**	**2.75E-12**	**1.07E+00**	**4.01E-11**	3.87E-01	5.58E-04	7.60E-01	3.58E-08	WT & nifD- N 14 dpi	P	pre-pro-cysteine proteinase	GO:0006508|GO:0008234|GO:0008234|GO:00
Solyc02g067440.3	**1.21E+00**	**7.72E-05**	**1.34E+00**	**2.16E-05**	1.08E-01	6.78E-01	5.19E-01	5.45E-02	WT & nifD- N 14 dpi	D	meloidogyne-induced giant cell protein DB114	GO:0016702|GO:0055114
Solyc02g071080.2	**1.21E+00**	**6.10E-05**	**1.94E+00**	**4.09E-08**	-2.68E-01	2.98E-01	-5.84E-01	2.90E-02	WT & nifD- N 14 dpi	TR	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)	GO:0005215|GO:0016021
Solyc09g074780.3	**1.21E+00**	**1.08E-05**	**1.58E+00**	**1.49E-07**	5.38E-02	8.10E-01	-6.28E-01	8.86E-03	WT & nifD- N 14 dpi	DNA	Zinc finger protein (AHRD V3.3 *** E9NZV2_PHAVU)	GO:0003676|GO:0046872|GO:0046872
Solyc07g007620.3	**1.21E+00**	**2.02E-05**	**1.25E+00**	**1.19E-05**	6.82E-02	7.71E-01	-4.38E-01	7.03E-02	WT & nifD- N 14 dpi	G	Monogalactosyldiacylglycerol synthase (AHRD V3.3 *** A0A087G8S7_ARAAL)	GO:0009247|GO:0016758|GO:0016758|GO:00 16758
Solyc02g076920.3	**1.20E+00**	**6.73E-08**	**1.82E+00**	**1.82E-11**	-1.45E-01	3.75E-01	-5.57E-01	1.90E-03	WT & nifD- N 14 dpi	T	bHLH transcription factor 013	GO:0046983
Solyc08g077300.3	**1.20E+00**	**5.82E-06**	**1.28E+00**	**2.18E-06**	2.62E-01	2.26E-01	7.03E-01	2.63E-03	WT & nifD- N 14 dpi	K	UMP-CMP kinase (AHRD V3.3 *** K4CN90_SOLLC)	GO:0004127|GO:0006207|GO:0006221|GO:00 09041|GO:0005524|GO:0006139|GO:0019205 |GO:0005524|GO:0006139|GO:0019205
Solyc06g060070.3	**1.20E+00**	**1.84E-05**	**1.59E+00**	**2.36E-07**	7.50E-01	2.94E-03	7.40E-01	3.25E-03	WT & nifD- N 14 dpi	H	1-aminocyclopropane-1-carboxylate oxidase (AHRD V3.3 *** A0A0G3FFL2_FICCA)	GO:0016491|GO:0055114
Solyc08g066650.3	**1.19E+00**	**2.03E-06**	**2.00E+00**	**1.52E-10**	1.49E-01	4.53E-01	-1.41E+00	1.32E-07	WT & nifD- N 14 dpi	2M	Carotenoid Cleavage Dioxygenase 8	GO:0016702|GO:0055114
Solyc05g006850.3	**1.19E+00**	**3.36E-04**	**2.06E+00**	**1.46E-07**	9.35E-02	7.48E-01	-5.39E-01	7.22E-02	WT & nifD- N 14 dpi	OX	Thioredoxin family protein (AHRD V3.3 *** B9IJS4_POPTR)	GO:0006662|GO:0015035|GO:0045454|GO:00 45454|GO:0045454
Solyc07g007220.3	**1.18E+00**	**3.59E-07**	**1.12E+00**	**8.50E-07**	1.88E-01	2.91E-01	-4.88E-02	7.82E-01	WT & nifD- N 14 dpi	K	Protein phosphatase 2c, putative (AHRD V3.3 *** B9T2N5_RICCO)	GO:0003824|GO:0004722|GO:0006470|GO:00 04722|GO:0006470
Solyc02g085170.3	**1.18E+00**	**2.88E-03**	**1.03E+00**	**7.55E-03**	1.23E-01	7.32E-01	-3.66E-01	3.14E-01	WT & nifD- N 14 dpi	TR	Sugar facilitator protein 10	GO:0005215|GO:0016021|GO:0055085|GO:00 16020|GO:0022891|GO:0055085|GO:0016020
Solyc02g032840.1	**1.17E+00**	**5.42E-09**	**1.52E+00**	**2.93E-11**	-3.77E-01	1.08E-02	-6.63E-01	5.46E-05	WT & nifD- N 14 dpi	L	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, putative (AHRD V3.3 --* A0A061FTS5_THECC)	
Solyc11g010400.2	**1.17E+00**	**2.63E-05**	**1.81E+00**	**2.67E-08**	-5.43E-01	2.61E-02	-8.72E-01	8.23E-04	WT & nifD- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G24530.1)	GO:0016491|GO:0055114
Solyc12g005400.2	**1.17E+00**	**8.57E-04**	**1.29E+00**	**3.16E-04**	1.93E-01	5.41E-01	6.90E-01	3.55E-02	WT & nifD- N 14 dpi	S	Cyclic nucleotide-gated ion channel, putative (AHRD V3.3 *** B9SIE1_RICCO)	GO:0005216|GO:0006811|GO:0016020|GO:00 55085
Solyc01g104910.3	**1.17E+00**	**3.81E-10**	**1.47E+00**	**2.83E-12**	-3.42E-01	8.42E-03	-4.49E-01	9.10E-04	WT & nifD- N 14 dpi	NA	Loricrin-like protein (AHRD V3.3 *** A0A072UZF2_MEDTR)	
Solyc01g006930.3	**1.17E+00**	**8.93E-11**	**1.32E+00**	**6.26E-12**	6.09E-02	5.89E-01	2.00E-01	8.44E-02	WT & nifD- N 14 dpi	T	Nuclear transcription factor Y subunit A-10, putative (AHRD V3.3 *** A0A061EVQ6_THECC)	GO:0003700|GO:0006355
Solyc01g095170.2	**1.16E+00**	**5.76E-05**	**1.89E+00**	**2.75E-08**	-3.93E-02	8.72E-01	9.17E-02	7.07E-01	WT & nifD- N 14 dpi	CS	LOW QUALITY:cell wall protein SlTFR88	
Solyc00g009070.1	**1.16E+00**	**5.29E-03**	**1.92E+00**	**2.99E-05**	-6.79E-01	8.62E-02	4.61E-01	2.37E-01	WT & nifD- N 14 dpi	NA	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7ZYN0_MEDTR)	
Solyc02g062390.3	**1.16E+00**	**1.93E-04**	**1.93E+00**	**1.10E-07**	3.22E-01	2.37E-01	9.36E-01	1.63E-03	WT & nifD- N 14 dpi	STR	Dehydrin (AHRD V3.3 *** E7BXD9_JATCU)	GO:0006950|GO:0009415
Solyc11g010340.2	**1.15E+00**	**2.46E-03**	**1.74E+00**	**2.89E-05**	-7.43E-01	4.01E-02	-2.50E+00	1.07E-07	WT & nifD- N 14 dpi	T	bHLH transcription factor 069	GO:0046983
Solyc07g039190.3	**1.15E+00**	**8.31E-03**	**1.20E+00**	**6.30E-03**	-1.10E-01	7.87E-01	-1.32E-01	7.45E-01	WT & nifD- N 14 dpi	RNA	nuclear pore complex protein (DUF3414) (AHRD V3.3 --* AT5G51200.3)	
Solyc03g080020.3	**1.15E+00**	**7.65E-09**	**1.12E+00**	**1.35E-08**	-3.92E-01	8.17E-03	1.20E-01	3.88E-01	WT & nifD- N 14 dpi	NA	UNC93-like protein (AHRD V3.3 *** A0A0B2SHJ9_GLYSO)	
Solyc07g007050.1	**1.15E+00**	**2.74E-05**	**1.05E+00**	**8.82E-05**	7.40E-01	2.97E-03	6.36E-01	9.15E-03	WT & nifD- N 14 dpi	DNA	Zinc finger, SWIM-type (AHRD V3.3 *** A0A118JSI3_CYNCS)	
Solyc01g095650.3	**1.15E+00**	**2.56E-04**	**1.25E+00**	**9.68E-05**	2.24E-01	4.16E-01	1.63E-01	5.51E-01	WT & nifD- N 14 dpi	DNA	Histone H3 like protein (AHRD V3.3 *-* Q7XIZ8_TURGL)	GO:0000786|GO:0003677|GO:0003677|GO:00
Solyc01g057275.1	**1.14E+00**	**2.05E-04**	**1.53E+00**	**4.46E-06**	-4.59E-01	9.46E-02	-1.99E-01	4.59E-01	WT & nifD- N 14 dpi	T	Calmodulin-binding transcription activator (AHRD V3.3 *-* A0A072TUJ0_MEDTR)	GO:0005515
Solyc05g006740.3	**1.14E+00**	**1.77E-03**	**1.29E+00**	**5.58E-04**	-2.91E-01	3.81E-01	-4.59E-01	1.71E-01	WT & nifD- N 14 dpi	STR	Sl Glutathione S-transferase	GO:0005515

Solyc03g025855.1	**1.14E+00**	**1.17E-03**	**1.24E+00**	**5.05E-04**	-9.19E-01	6.60E-03	-6.14E-02	8.45E-01	WT & nifD- N 14 dpi	CS	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT3G17365.1)	
Solyc11g045610.2	**1.14E+00**	**4.28E-06**	**1.25E+00**	**9.59E-07**	-1.42E-01	4.76E-01	1.15E-01	5.62E-01	WT & nifD- N 14 dpi	K	Protein kinase family protein (AHRD V3.3 *** Q9LQ29_ARATH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc12g009480.2	**1.13E+00**	**4.00E-06**	**1.14E+00**	**3.89E-06**	-2.09E-02	9.15E-01	8.62E-01	1.53E-04	WT & nifD- N 14 dpi	STR	SPX domain-containing family protein (AHRD V3.3 *** B9IMZ5_POPTR)	GO:0016036
Solyc03g031760.3	**1.13E+00**	**3.14E-08**	**1.27E+00**	**3.53E-09**	-3.70E-01	1.70E-02	-2.69E-01	7.54E-02	WT & nifD- N 14 dpi	DNA	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9GU68_POPTR)	GO:0008289
Solyc02g089920.1	**1.13E+00**	**2.72E-04**	**1.82E+00**	**3.58E-07**	-6.59E-01	2.08E-02	-8.11E-01	5.55E-03	WT & nifD- N 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9HEM3_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g079970.1	**1.12E+00**	**7.21E-05**	**1.06E+00**	**1.39E-04**	-2.63E-01	2.79E-01	6.95E-01	7.05E-03	WT & nifD- N 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)	GO:0004252|GO:0006508
Solyc12g006290.2	**1.12E+00**	**8.39E-12**	**1.04E+00**	**4.37E-11**	2.77E-01	7.68E-03	4.26E-01	1.46E-04	WT & nifD- N 14 dpi	D	Reticulon-like protein (AHRD V3.3 *** M1CT78_SOLTU)	
Solyc09g005630.3	**1.12E+00**	**6.05E-03**	**1.96E+00**	**1.87E-05**	-9.76E-01	1.49E-02	-1.04E+00	1.01E-02	WT & nifD- N 14 dpi	CS	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT5G01360.1)	
Solyc03g083100.3	**1.12E+00**	**8.43E-03**	**1.43E+00**	**1.16E-03**	8.16E-01	4.69E-02	3.14E-01	4.29E-01	WT & nifD- N 14 dpi	G	SUN-like protein 10	GO:0005515
Solyc02g077240.3	**1.11E+00**	**5.53E-06**	**1.65E+00**	**7.09E-09**	-1.29E-01	5.14E-01	-8.78E-02	6.56E-01	WT & nifD- N 14 dpi	C	Pyruvate decarboxylase (AHRD V3.3 *** Q1I1D9_CITSI)	GO:0000287|GO:0030976|GO:0003824|GO:0030976|GO:0003824|GO:0030976
Solyc11g007160.2	**1.11E+00**	**1.77E-04**	**1.20E+00**	**6.77E-05**	7.51E-02	7.70E-01	-4.47E-01	9.02E-02	WT & nifD- N 14 dpi	RNA	RNA binding protein, putative (AHRD V3.3 *** B9SG63_RICCO)	GO:0000166|GO:0003676|GO:0003676
Solyc09g091910.2	**1.11E+00**	**2.11E-06**	**1.10E+00**	**2.44E-06**	-7.68E-01	2.81E-04	6.53E-01	1.43E-03	WT & nifD- N 14 dpi	G	Purple acid phosphatase (AHRD V3.3 *** K4CWL7_SOLLC)	GO:0003993|GO:0046872|GO:0016787|GO:00
Solyc06g074240.2	**1.11E+00**	**4.33E-04**	**1.12E+00**	**3.84E-04**	-2.26E-02	9.35E-01	-3.82E-01	1.76E-01	WT & nifD- N 14 dpi	2M	Beta-carotene	GO:0006810|GO:0016021|GO:0016192|GO:0016021|GO:0016192
Solyc05g013710.3	**1.11E+00**	**3.14E-03**	**1.31E+00**	**6.70E-04**	-2.14E-01	5.33E-01	-8.94E-01	1.41E-02	WT & nifD- N 14 dpi	E	Quinolinate synthase A (AHRD V3.3 *-* W9RJG8_9ROSA)	
Solyc02g079330.3	**1.10E+00**	**7.46E-03**	**1.21E+00**	**3.80E-03**	-9.28E-01	2.17E-02	-1.02E+00	1.26E-02	WT & nifD- N 14 dpi	DNA	Equilibrative nucleoside transporter family protein (AHRD V3.3 *** B9H1Z9_POPTR)	GO:0005337|GO:0006810|GO:0016021
Solyc02g080520.3	**1.10E+00**	**5.54E-03**	**1.22E+00**	**2.39E-03**	8.65E-01	2.49E-02	1.11E-01	7.61E-01	WT & nifD- N 14 dpi	NA	F11F12.2 protein (AHRD V3.3 *** Q9LPT5_ARATH)	
Solyc11g017380.2	**1.10E+00**	**3.52E-05**	**1.29E+00**	**3.67E-06**	-2.82E-01	2.11E-01	-3.37E-01	1.37E-01	WT & nifD- N 14 dpi	TR	magnesium transporter NIPA (DUF803) (AHRD V3.3 *** AT4G13800.8)	GO:0015095|GO:0015693|GO:0016021
Solyc09g091270.2	**1.09E+00**	**2.03E-07**	**1.20E+00**	**3.76E-08**	4.53E-01	7.44E-03	-8.26E-01	1.61E-05	WT & nifD- N 14 dpi	NA	cotton fiber protein (AHRD V3.3 *** AT5G13880.2)	
Solyc04g074330.3	**1.09E+00**	**1.36E-05**	**1.88E+00**	**1.24E-09**	-3.71E-01	8.07E-02	-1.26E+00	1.69E-06	WT & nifD- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BTX1_SOLLC)	GO:0008152|GO:0016758
Solyc06g076550.3	**1.09E+00**	**6.93E-04**	**1.64E+00**	**4.70E-06**	5.59E-01	5.96E-02	-6.76E-02	8.14E-01	WT & nifD- N 14 dpi	C	UDP-glycosyltransferase (AHRD V3.3 *** A0A164TMY6_DAUCA)	GO:0008152|GO:0016758
Solyc02g085430.3	**1.09E+00**	**7.58E-03**	**1.64E+00**	**1.91E-04**	8.37E-01	3.54E-02	-4.86E-01	2.09E-01	WT & nifD- N 14 dpi	K	Protein kinase superfamily protein (AHRD V3.3 *** AT4G34440.2)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g062260.3	**1.09E+00**	**6.83E-03**	**2.05E+00**	**8.53E-06**	5.96E-01	1.20E-01	-3.92E-01	3.00E-01	WT & nifD- N 14 dpi	G	Brassinazole-resistant 1 protein (AHRD V3.3 *** G7IR04_MEDTR)	GO:0003700|GO:0006351|GO:0009742
Solyc10g084540.2	**1.09E+00**	**8.54E-03**	**1.20E+00**	**4.26E-03**	6.69E-01	9.24E-02	6.27E-01	1.13E-01	WT & nifD- N 14 dpi	L	Phosphatidate phosphatase LPIN2-like protein (AHRD V3.3 *-* A0A0B2P3Z9_GLYSO)	
Solyc12g009110.2	**1.08E+00**	**6.47E-06**	**1.18E+00**	**1.74E-06**	1.96E-01	3.18E-01	-4.40E-01	3.07E-02	WT & nifD- N 14 dpi	P	O-methyltransferase, putative (AHRD V3.3 *** B9SUX6_RICCO)	GO:0008168|GO:0008171|GO:0008171
Solyc04g007400.3	**1.08E+00**	**8.33E-07**	**1.35E+00**	**1.80E-08**	6.25E-01	9.82E-04	1.14E-01	5.02E-01	WT & nifD- N 14 dpi	K	Protein kinase family protein (AHRD V3.3 *-* AT5G38210.2)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g083760.3	**1.08E+00**	**6.81E-09**	**1.37E+00**	**5.48E-11**	5.16E-01	4.32E-04	-1.19E-01	3.61E-01	WT & nifD- N 14 dpi	D	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** G7JWA0_MEDTR)	
Solyc05g007420.1	**1.08E+00**	**5.64E-04**	**1.18E+00**	**2.10E-04**	-8.53E-01	4.47E-03	-6.73E-01	2.10E-02	WT & nifD- N 14 dpi	T	TCP transcription factor 23	
Solyc07g063370.2	**1.07E+00**	**8.20E-04**	**1.57E+00**	**8.49E-06**	-3.37E-01	2.45E-01	-7.44E-01	1.44E-02	WT & nifD- N 14 dpi	C	Beta-glucosidase (AHRD V3.3 *** B4FQQ6_MAIZE)	GO:0004553|GO:0005975|GO:0005975|GO:00
Solyc06g054240.3	**1.07E+00**	**7.51E-06**	**1.14E+00**	**2.99E-06**	5.48E-01	8.41E-03	-4.28E-02	8.25E-01	WT & nifD- N 14 dpi	DNA	5'-nucleotidase surE (AHRD V3.3 *** W9QLZ8_9ROSA)	GO:0008252|GO:0016787|GO:0016787

Solyc01g080480.3	**1.07E+00**	**1.28E-05**	**1.64E+00**	**1.07E-08**	8.97E-01	1.27E-04	-1.02E-01	6.12E-01	WT & nifD- N 14 dpi	DNA	Endonuclease/exonuclease/phosphatase family protein (AHRD V3.3 *** B9HM94_POPTR)	GO:0003723|GO:0006396|GO:0008173
Solyc08g062760.1	**1.07E+00**	**2.07E-03**	**1.31E+00**	**2.86E-04**	-2.39E-02	9.39E-01	-1.78E-01	5.73E-01	WT & nifD- N 14 dpi	CS	LOW QUALITY:villin 4 (AHRD V3.3 --* AT4G30160.4)	
Solyc04g074120.3	**1.07E+00**	**4.85E-03**	**1.39E+00**	**4.62E-04**	-7.31E-01	4.43E-02	-1.01E+00	7.11E-03	WT & nifD- N 14 dpi	DNA	Synaptonemal complex protein 1 (AHRD V3.3 *** A0A151TZS6_CAJCA)	
Solyc05g051860.3	**1.07E+00**	**5.99E-07**	**1.46E+00**	**1.83E-09**	3.08E-01	6.86E-02	1.75E-01	2.89E-01	WT & nifD- N 14 dpi	G	senescence-associated family protein, putative (DUF581) (AHRD V3.3 *** AT1G78020.1)	
Solyc12g099180.2	**1.06E+00**	**1.41E-03**	**1.37E+00**	**9.08E-05**	1.65E-01	5.83E-01	-8.03E-01	1.19E-02	WT & nifD- N 14 dpi	RNA	Poly(A) polymerase, putative (AHRD V3.3 *** B9RZU0_RICCO)	GO:0003723|GO:0016779|GO:0031123|GO:0003723|GO:0043631|GO:0003723|GO:0043631
Solyc06g053610.3	**1.06E+00**	**7.34E-07**	**1.18E+00**	**1.14E-07**	1.88E-01	2.59E-01	7.65E-02	6.43E-01	WT & nifD- N 14 dpi	G	R2R3MYB transcription factor 14	GO:0003677
Solyc07g014730.3	**1.06E+00**	**5.95E-03**	**2.00E+00**	**5.68E-06**	9.91E-01	9.19E-03	4.68E-02	8.95E-01	WT & nifD- N 14 dpi	L	Phospholipase A2 (AHRD V3.3 *** Q5CCT8_TOBAC)	GO:0004623|GO:0005509|GO:0016042|GO:0004623|GO:0006644|GO:0050482|GO:0004623
Solyc03g097670.3	**1.05E+00**	**7.90E-06**	**1.89E+00**	**2.58E-10**	7.99E-01	2.72E-04	-8.53E-01	1.28E-04	WT & nifD- N 14 dpi	DNA	ATP/DNA binding protein (AHRD V3.3 *** AT3G48770.2)	
Solyc06g066520.1	**1.05E+00**	**4.20E-03**	**1.10E+00**	**2.91E-03**	-1.42E+00	2.47E-04	-2.43E+00	1.14E-07	WT & nifD- N 14 dpi	D	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 146 (AHRD V3.3 *** Q9FQZ6_TOBAC)	
Solyc04g080290.3	**1.05E+00**	**4.03E-11**	**1.01E+00**	**8.40E-11**	9.16E-01	6.43E-10	5.81E-01	2.30E-06	WT & nifD- N 14 dpi	S	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 *** AT1G75170.2)	GO:0005215|GO:0005622|GO:0006810
Solyc01g014375.1	**1.05E+00**	**2.81E-03**	**1.24E+00**	**5.97E-04**	1.37E-02	9.66E-01	6.44E-03	9.84E-01	WT & nifD- N 14 dpi	DNA	DNA double-strand break repair rad50 ATPase (AHRD V3.3 *** A0A061GZ54_THECC)	
Solyc00g072100.3	**1.04E+00**	**3.05E-03**	**1.13E+00**	**1.59E-03**	2.87E-01	3.77E-01	-5.80E-01	8.12E-02	WT & nifD- N 14 dpi	NA	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151S5P0_CAJCA)	
Solyc07g049160.3	**1.04E+00**	**7.24E-07**	**1.35E+00**	**7.79E-09**	5.30E-01	2.79E-03	-3.93E-01	2.12E-02	WT & nifD- N 14 dpi	RNA	Ribonuclease 3 family protein (AHRD V3.3 *** B9GTV4_POPTR)	GO:0004525|GO:0006396
Solyc08g076840.3	**1.04E+00**	**3.20E-09**	**1.14E+00**	**4.88E-10**	3.58E-01	5.61E-03	2.22E-02	8.53E-01	WT & nifD- N 14 dpi	G	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *** AT2G35410.1)	GO:0000166|GO:0003676|GO:0003676
Solyc01g066860.3	**1.04E+00**	**1.37E-03**	**1.11E+00**	**7.21E-04**	1.74E-01	5.54E-01	-7.10E-02	8.08E-01	WT & nifD- N 14 dpi	NA	LOW QUALITY:BnaCnng45880D protein (AHRD V3.3 *** A0A078JHJ1_BRANA)	
Solyc04g079070.3	**1.04E+00**	**1.30E-05**	**1.01E+00**	**1.85E-05**	-1.26E-01	5.20E-01	-2.47E-01	2.12E-01	WT & nifD- N 14 dpi	STR	Serine carboxypeptidase, putative (AHRD V3.3 *** B9R6Y4_RICCO)	GO:0004185|GO:0006508
Solyc01g103600.3	**1.03E+00**	**6.86E-03**	**1.12E+00**	**3.69E-03**	6.24E-02	8.61E-01	-6.28E-01	8.64E-02	WT & nifD- N 14 dpi	H	Jasmonate ZIM-domain protein 4 (AHRD V3.3 *** T1WMV9_TOBAC)	
Solyc12g042010.1	**1.03E+00**	**5.88E-05**	**1.26E+00**	**3.98E-06**	-3.84E-02	8.60E-01	-1.41E-01	5.18E-01	WT & nifD- N 14 dpi	T	LOW QUALITY:Transcription factor, putative (AHRD V3.3 *** B9TBR8_RICCO)	GO:0046983
Solyc02g080530.3	**1.03E+00**	**7.93E-08**	**1.35E+00**	**4.70E-10**	4.32E-01	4.67E-03	9.49E-02	5.03E-01	WT & nifD- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4B9S4_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc07g018430.3	**1.03E+00**	**5.41E-07**	**1.53E+00**	**3.53E-10**	-1.74E-01	2.75E-01	-1.52E-01	3.38E-01	WT & nifD- N 14 dpi	P	F-box family protein (AHRD V3.3 --* AT3G60040.3)	
Solyc09g098030.3	**1.03E+00**	**1.03E-05**	**1.02E+00**	**1.08E-05**	1.37E-01	4.71E-01	-1.18E-02	9.50E-01	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103Y530_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc07g065930.3	**1.02E+00**	**1.32E-08**	**1.24E+00**	**2.85E-10**	2.48E-01	5.85E-02	5.18E-02	6.83E-01	WT & nifD- N 14 dpi	T	BTB/POZ domain-containing protein (AHRD V3.3 *** A0A097PQ10_SOLLC)	GO:0005515
Solyc02g090300.3	**1.02E+00**	**9.22E-03**	**1.36E+00**	**9.11E-04**	5.50E-02	8.81E-01	-1.18E-01	7.47E-01	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc02g032100.3	**1.02E+00**	**1.59E-03**	**1.74E+00**	**2.52E-06**	5.75E-01	5.71E-02	-6.40E-01	3.58E-02	WT & nifD- N 14 dpi	TR	Zinc transporter protein (AHRD V3.3 *** A5BDR3_VITVI)	GO:0005385|GO:0016021|GO:0071577|GO:0016020|GO:0030001|GO:0046873|GO:0055085|GO:0016020|GO:0030001|GO:0046873|GO:0
Solyc10g011810.3	**1.02E+00**	**1.54E-07**	**1.10E+00**	**4.00E-08**	9.60E-01	4.25E-07	9.88E-01	2.66E-07	WT & nifD- N 14 dpi	L	Fatty acid/sphingolipid desaturase (AHRD V3.3 *-* AT2G46210.1)	GO:0006629
Solyc01g081560.2	**1.02E+00**	**9.86E-03**	**1.20E+00**	**2.97E-03**	2.98E-01	4.22E-01	-1.37E-02	9.70E-01	WT & nifD- N 14 dpi	RNA	LOW QUALITY:Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A199UML1_ANACO)	GO:0005515|GO:0008270|GO:0008270
Solyc01g079130.2	**1.02E+00**	**1.20E-04**	**1.63E+00**	**1.15E-07**	-5.30E-01	2.60E-02	-1.13E+00	3.30E-05	WT & nifD- N 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G02460.1)	GO:0004650|GO:0005975
Solyc12g038970.2	**1.01E+00**	**1.71E-09**	**1.36E+00**	**3.46E-12**	-2.18E-02	8.47E-01	-4.71E-02	6.77E-01	WT & nifD- N 14 dpi	N	EMB1873 protein (AHRD V3.3 *** A0A097PRP8_SOLLC)	GO:0004668|GO:0009446|GO:0009446|GO:0047632|GO:0009446|GO:0047632

Solyc04g054310.3	**1.01E+00**	**6.00E-09**	**1.00E+00**	**7.31E-09**	-1.03E-01	3.94E-01	6.25E-02	6.04E-01	WT & nifD- N 14 dpi	N	Alanine-glyoxylate aminotransferase, putative (AHRD V3.3 *** B9T1D1_RICCO)	GO:0003824|GO:0008483|GO:0030170|GO:0008483|GO:0030170
Solyc06g084460.3	**1.01E+00**	**1.89E-03**	**1.36E+00**	**8.99E-05**	1.16E-01	6.96E-01	-5.15E-01	9.04E-02	WT & nifD- N 14 dpi	C	Shikimate dehydrogenase, 3-dehydroquinate dehydratase (AHRD V3.3 *** A0A0K9PLS3_ZOSMR)	GO:0003824|GO:0003855|GO:0003855
Solyc06g069900.3	**1.01E+00**	**4.79E-06**	**1.46E+00**	**8.95E-09**	-1.93E-01	2.82E-01	-3.97E-01	3.25E-02	WT & nifD- N 14 dpi	E	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061FWB6_THECC)	GO:0016491|GO:0055114
Solyc01g100240.3	**1.01E+00**	**4.76E-04**	**1.67E+00**	**5.36E-07**	-1.61E-01	5.29E-01	-7.00E-01	1.03E-02	WT & nifD- N 14 dpi	DNA	Calmodulin-binding protein (AHRD V3.3 *** AT2G18750.3)	GO:0005516|GO:0006950
Solyc08g060920.3	**1.01E+00**	**2.32E-05**	**1.39E+00**	**1.75E-07**	-5.06E-01	1.58E-02	-6.67E-01	2.17E-03	WT & nifD- N 14 dpi	STR	IDS4-like	
Solyc05g009320.3	**1.01E+00**	**2.27E-03**	**1.58E+00**	**1.55E-05**	2.40E-01	4.26E-01	9.75E-01	2.96E-03	WT & nifD- N 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9T058_RICCO)	
Solyc03g119080.4	**1.00E+00**	**6.47E-03**	**1.51E+00**	**1.42E-04**	5.65E-01	1.08E-01	7.05E-02	8.37E-01	WT & nifD- N 14 dpi	C	beta-mannosidase enzyme	
Solyc03g118410.3	**-1.00E+00**	**2.25E-04**	**-1.25E+00**	**1.41E-05**	-9.81E-01	2.89E-04	1.24E+00	1.53E-05	WT & nifD- N 14 dpi	L	Acyl carrier protein (AHRD V3.3 *** Q672Q9_SOLLC)	GO:0006633
Solyc03g095985.1	**-1.01E+00**	**3.14E-05**	**-1.23E+00**	**1.76E-06**	-1.06E-01	5.99E-01	1.57E-01	4.40E-01	WT & nifD- N 14 dpi	NA	Differentiation-associated protein 1, putative isoform 2 (AHRD V3.3 *** A0A061FKZ1_THECC)	
Solyc05g050710.3	**-1.01E+00**	**1.07E-03**	**-1.66E+00**	**2.30E-06**	2.91E-01	3.00E-01	5.95E-01	3.96E-02	WT & nifD- N 14 dpi	L	Lecithin-cholesterol acyltransferase-like 1 (AHRD V3.3 *** A0A0B2SJV8_GLYSO)	GO:0006629|GO:0008374
Solyc03g116540.1	**-1.02E+00**	**5.94E-03**	**-1.20E+00**	**1.59E-03**	-1.31E-01	7.02E-01	-2.23E-01	5.17E-01	WT & nifD- N 14 dpi	RNA	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SY25_RICCO)	GO:0005515
Solyc02g092530.3	**-1.03E+00**	**7.97E-04**	**-1.15E+00**	**2.56E-04**	-6.60E-01	2.28E-02	2.65E-01	3.40E-01	WT & nifD- N 14 dpi	N	Acetamidase/Formamidase family protein (AHRD V3.3 *** AT4G37560.1)	GO:0016811
Solyc02g082557.1	**-1.04E+00**	**2.29E-03**	**-1.33E+00**	**1.89E-04**	-6.31E-01	4.94E-02	-7.22E-01	2.62E-02	WT & nifD- N 14 dpi	DNA	CTP synthase family protein (AHRD V3.3 --* AT4G20320.6)	
Solyc05g010780.1	**-1.04E+00**	**1.11E-03**	**-1.09E+00**	**6.59E-04**	-5.26E-01	7.41E-02	-9.84E-01	1.78E-03	WT & nifD- N 14 dpi	RNA	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9HWT8_POPTR)	GO:0005515
Solyc03g059155.1	**-1.05E+00**	**5.32E-04**	**-1.17E+00**	**1.64E-04**	-5.20E-01	5.99E-02	-1.11E-01	6.78E-01	WT & nifD- N 14 dpi	D	Pathogenesis-related thaumatin superfamily protein (AHRD V3.3 --* AT1G77700.1)	
Solyc07g005530.3	**-1.07E+00**	**4.35E-12**	**-1.06E+00**	**5.01E-12**	-7.70E-01	3.91E-09	-4.08E-01	9.71E-05	WT & nifD- N 14 dpi	P	Ubiquitin carboxyl-terminal hydrolase, putative (AHRD V3.3 *** A0A061GR07_THECC)	GO:0006511|GO:0036459|GO:0016579|GO:0036459|GO:0016579|GO:0036459
Solyc12g006860.2	**-1.07E+00**	**2.54E-08**	**-1.19E+00**	**3.78E-09**	-4.70E-01	1.96E-03	-2.32E-01	1.01E-01	WT & nifD- N 14 dpi	H	brassinosteroid hydroxylase	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc12g015880.2	**-1.08E+00**	**4.61E-05**	**-1.07E+00**	**5.33E-05**	-1.67E-02	9.41E-01	-7.97E-01	1.35E-03	WT & nifD- N 14 dpi	STR	Heat shock protein 90-1	GO:0005524|GO:0006457|GO:0006950|GO:00
Solyc02g090210.3	**-1.09E+00**	**2.19E-03**	**-1.12E+00**	**1.75E-03**	1.62E+00	2.98E-05	1.04E+00	3.24E-03	WT & nifD- N 14 dpi	L	GDSL esterase/lipase family (AHRD V3.3 *** A0A151RJ07_CAJCA)	GO:0016788
Solyc12g044330.2	**-1.10E+00**	**3.31E-05**	**-1.06E+00**	**4.85E-05**	-4.63E-01	4.40E-02	2.09E+00	5.89E-10	WT & nifD- N 14 dpi	TR	tonoplast intrinsic protein 2.1	GO:0005215|GO:0006810|GO:0016020
Solyc09g063015.1	**-1.11E+00**	**1.76E-06**	**-1.24E+00**	**2.70E-07**	-8.14E-01	1.23E-04	-4.35E-01	2.32E-02	WT & nifD- N 14 dpi	G	Transcription factor PIF1-like protein (AHRD V3.3 *-* A0A0B0P1J2_GOSAR)	
Solyc06g050530.3	**-1.11E+00**	**9.92E-03**	**-1.15E+00**	**7.84E-03**	1.39E+00	1.85E-03	8.86E-01	3.59E-02	WT & nifD- N 14 dpi	PMI	Laccase (AHRD V3.3 *** I1M7Q3_SOYBN)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc04g015710.3	**-1.12E+00**	**1.53E-04**	**-1.61E+00**	**9.96E-07**	-2.51E-01	3.30E-01	-5.84E-01	2.92E-02	WT & nifD- N 14 dpi	DNA	SANTA (SANT associated) protein (AHRD V3.3 *-* A0A072VWG5_MEDTR)	
Solyc00g007150.3	**-1.12E+00**	**1.66E-03**	**-1.11E+00**	**1.80E-03**	-4.01E-01	2.21E-01	-3.79E-01	2.46E-01	WT & nifD- N 14 dpi	H	LOW QUALITY:WAT1-related protein (AHRD V3.3 --* R0HAL8_9BRAS)	
Solyc05g011960.3	**-1.12E+00**	**1.56E-04**	**-1.02E+00**	**4.61E-04**	-1.35E-01	5.99E-01	-2.67E-01	3.03E-01	WT & nifD- N 14 dpi	STR	DnaJ domain-containing protein (AHRD V3.3 *-* A0A103YBW3_CYNCS)	
Solyc03g059150.3	**-1.12E+00**	**4.44E-06**	**-1.38E+00**	**1.63E-07**	-9.04E-01	8.53E-05	-5.98E-01	4.85E-03	WT & nifD- N 14 dpi	TR	Ion channel DMI1 (AHRD V3.3 *** DMI1_MEDTR)	GO:0006813|GO:0008324
Solyc02g069730.3	**-1.14E+00**	**2.44E-03**	**-1.14E+00**	**2.44E-03**	1.69E+00	3.57E-05	1.29E+00	7.43E-04	WT & nifD- N 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4B7V5_SOLLC)	
Solyc01g099160.3	**-1.14E+00**	**5.83E-04**	**-1.43E+00**	**4.53E-05**	3.83E-01	2.00E-01	6.53E-02	8.25E-01	WT & nifD- N 14 dpi	L	Lipoxygenase (AHRD V1 **** Q9FT17_SOLLC)%3B contains Interpro domain(s) IPR001246 Lipoxygenase%2C plant	GO:0005515|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc02g069860.3	**-1.15E+00**	**2.80E-08**	**-1.11E+00**	**5.22E-08**	-3.99E-01	1.14E-02	-6.43E-02	6.64E-01	WT & nifD- N 14 dpi	T	Nuclear transcription factor Y subunit (AHRD V3.3 *-* A0A0K9P8V1_ZOSMR)	GO:0003677|GO:0016602|GO:0003700|GO:0006355|GO:0003700|GO:0006355

Solyc07g045540.3	**-1.15E+00**	**1.25E-05**	**-1.94E+00**	**1.72E-09**	1.22E-01	5.74E-01	1.25E-01	5.66E-01	WT & nifD- N 14 dpi	C	Glucose-6-phosphate 1-dehydrogenase (AHRD V3.3 *** K4CEW0_SOLLC)	GO:0004345|GO:0006006|GO:0050661|GO:0055114|GO:0004345|GO:0006006|GO:0055114|GO:0004345|GO:0006006|GO:0055114
Solyc03g006970.1	**-1.17E+00**	**6.20E-03**	**-1.19E+00**	**5.31E-03**	7.19E-01	7.82E-02	6.63E-01	1.03E-01	WT & nifD- N 14 dpi	STR	serine protease SBT2	GO:0004252|GO:0006508
Solyc11g006410.2	**-1.17E+00**	**1.92E-04**	**-1.24E+00**	**9.46E-05**	-2.56E-02	9.25E-01	-3.70E-02	8.92E-01	WT & nifD- N 14 dpi	NA	EEIG1/EHBP1 N-terminal domain-containing protein (AHRD V3.3 *** A0A103PZW1_CYNCS)	
Solyc01g007100.3	**-1.18E+00**	**4.43E-08**	**-1.01E+00**	**5.98E-07**	-1.76E-01	2.63E-01	-2.35E-01	1.39E-01	WT & nifD- N 14 dpi	PMI	Digalactosyldiacylglycerol synthase 1 (AHRD V3.3 *** W8SVK3_TOBAC)	
Solyc11g044250.2	**-1.18E+00**	**7.13E-05**	**-1.15E+00**	**9.94E-05**	-6.27E-01	1.87E-02	-4.76E-01	6.79E-02	WT & nifD- N 14 dpi	TR	K(+) efflux antiporter (AHRD V3.3 *** A0A0K9NYY6_ZOSMR)	GO:0006812|GO:0015299|GO:0016021|GO:0055085|GO:0006813|GO:0006813
Solyc02g089520.2	**-1.20E+00**	**3.21E-06**	**-1.13E+00**	**7.59E-06**	-1.78E-01	3.90E-01	-1.41E-01	4.95E-01	WT & nifD- N 14 dpi	G	CONSTANS protein (AHRD V3.3 *** C0Z3T8_SOLTU)	GO:0005515|GO:0005622|GO:0008270|GO:0005622|GO:0008270
Solyc12g056920.2	**-1.21E+00**	**1.52E-09**	**-1.06E+00**	**1.73E-08**	-1.57E-01	2.46E-01	5.51E-02	6.80E-01	WT & nifD- N 14 dpi	TR	Sulfate transporter, putative (AHRD V3.3 *** B9RJF7_RICCO)	GO:0008271|GO:0008272|GO:0016020|GO:0055085|GO:0008272|GO:0015116|GO:0008272
Solyc02g014220.3	**-1.21E+00**	**1.27E-03**	**-1.01E+00**	**5.70E-03**	-8.45E-01	1.77E-02	-4.40E-01	1.98E-01	WT & nifD- N 14 dpi	CS	Endoglucanase (AHRD V3.3 *** K4B4M1_SOLLC)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc07g066310.3	**-1.22E+00**	**7.02E-06**	**-1.46E+00**	**4.20E-07**	-5.63E-01	1.54E-02	2.84E-01	2.03E-01	WT & nifD- N 14 dpi	E	Photosystem II 10 kDa polypeptide family protein (AHRD V3.3 *** A9PH94_POPTR)	GO:0009523|GO:0009654|GO:0015979|GO:0042651
Solyc01g107240.3	**-1.25E+00**	**3.91E-04**	**-1.11E+00**	**1.28E-03**	2.92E-01	3.49E-01	4.67E-01	1.39E-01	WT & nifD- N 14 dpi	OX	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT4G33905.1)	GO:0016021
Solyc09g091950.1	**-1.25E+00**	**2.72E-09**	**-1.26E+00**	**2.27E-09**	9.60E-01	3.32E-07	-2.83E-03	9.84E-01	WT & nifD- N 14 dpi	H	Ethylene-responsive transcription factor ERF062 (AHRD V3.3 *** ERF62_ARATH)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc02g082720.3	**-1.25E+00**	**3.93E-03**	**-1.28E+00**	**3.35E-03**	-5.54E-01	1.73E-01	-7.58E-01	6.64E-02	WT & nifD- N 14 dpi	P	Trypsin-like peptidase domain protein (AHRD V3.3 *** G7KBB1_MEDTR)	GO:0004252|GO:0006508|GO:0005515|GO:0005515
Solyc10g081570.2	**-1.27E+00**	**1.83E-03**	**-1.18E+00**	**3.43E-03**	9.23E-02	8.03E-01	-1.49E-01	6.86E-01	WT & nifD- N 14 dpi	NA	Marmande	
Solyc12g096500.2	**-1.28E+00**	**3.31E-09**	**-1.14E+00**	**2.69E-08**	-2.61E-01	8.47E-02	1.26E+00	4.12E-09	WT & nifD- N 14 dpi	G	CONSTANS-like protein (AHRD V3.3 *** Q0MQL9_SOLTU)	GO:0005515|GO:0005622|GO:0008270|GO:0005622|GO:0008270
Solyc02g068080.3	**-1.28E+00**	**4.87E-10**	**-1.98E+00**	**3.18E-14**	-4.38E-01	2.73E-03	-3.01E-01	3.10E-02	WT & nifD- N 14 dpi	TR	Chloride channel protein (AHRD V3.3 *** M1A9T9_SOLTU)	GO:0005216|GO:0055085|GO:0005247|GO:0006821|GO:0016020|GO:0005247|GO:0006821
Solyc07g053280.3	**-1.28E+00**	**1.06E-11**	**-1.82E+00**	**3.96E-15**	-3.60E-01	3.20E-03	9.33E-02	4.08E-01	WT & nifD- N 14 dpi	E	Ketol-acid reductoisomerase (AHRD V3.3 *** K4CFM5_SOLLC)	GO:0004455|GO:0009082|GO:0055114|GO:0004455|GO:0055114|GO:0004455|GO:0055114
Solyc09g065440.3	**-1.28E+00**	**4.75E-03**	**-1.20E+00**	**7.90E-03**	8.64E-01	4.76E-02	8.04E-01	6.41E-02	WT & nifD- N 14 dpi	NA	Protease inhibitor/seed storage/lipid transfer family protein (AHRD V3.3 *-* B9NBN8_POPTR)	
Solyc12g007100.2	**-1.29E+00**	**2.64E-15**	**-1.02E+00**	**5.95E-13**	-3.60E-01	8.29E-05	-4.78E-01	1.59E-06	WT & nifD- N 14 dpi	E	AAA-type ATPase family protein / ankyrin repeat family protein (AHRD V3.3 *** AT3G24530.1)	GO:0005515|GO:0005524|GO:0005524
Solyc11g006710.2	**-1.29E+00**	**1.95E-03**	**-1.59E+00**	**2.45E-04**	3.08E-01	4.18E-01	1.07E+00	8.04E-03	WT & nifD- N 14 dpi	AM	Cationic amino acid transporter, putative (AHRD V3.3 *** B9RPW6_RICCO)	GO:0003333|GO:0015171|GO:0016020
Solyc02g069320.1	**-1.30E+00**	**8.02E-05**	**-1.14E+00**	**3.39E-04**	-6.96E-02	8.03E-01	-1.80E-01	5.21E-01	WT & nifD- N 14 dpi	T	LOW QUALITY:Mitochondrial transcription termination factor family protein, putative (AHRD V3.3 *** A0A061GDK1_THECC)	GO:0003690|GO:0006355
Solyc06g072220.1	**-1.30E+00**	**2.71E-06**	**-1.24E+00**	**5.80E-06**	-3.27E-01	1.46E-01	3.91E-01	8.46E-02	WT & nifD- N 14 dpi	D	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)	GO:0004866
Solyc02g089530.3	**-1.30E+00**	**7.36E-05**	**-1.52E+00**	**9.70E-06**	2.08E-01	4.59E-01	4.62E-01	1.07E-01	WT & nifD- N 14 dpi	2M	AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT5G35930.3)	
Solyc09g090510.3	**-1.31E+00**	**2.05E-06**	**-1.42E+00**	**5.43E-07**	-2.66E-01	2.26E-01	-9.38E-01	1.81E-04	WT & nifD- N 14 dpi	L	Cyclopropane-fatty-acyl-phospholipid synthase (AHRD V3.3 *** AT3G23510.1)	GO:0016491|GO:0055114
Solyc01g102900.3	**-1.31E+00**	**3.05E-04**	**-1.93E+00**	**1.77E-06**	3.98E-01	2.17E-01	-3.97E-01	2.18E-01	WT & nifD- N 14 dpi	STR	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)	GO:0030145|GO:0045735|GO:0045735
Solyc11g065830.2	**-1.31E+00**	**1.65E-12**	**-1.10E+00**	**8.31E-11**	-1.25E-01	2.42E-01	-1.97E-01	7.03E-02	WT & nifD- N 14 dpi	N	2-oxoglutarate/malate translocator, chloroplastic (AHRD V3.3 *** A0A0B0P837_GOSAR)	GO:0005215|GO:0006814|GO:0016020|GO:0055085
Solyc10g083220.2	**-1.31E+00**	**8.24E-09**	**-1.55E+00**	**2.94E-10**	4.87E-01	4.61E-03	1.88E-01	2.42E-01	WT & nifD- N 14 dpi	G	embryo defective 2735 (AHRD V3.3 *** AT5G06240.1)	
Solyc02g067120.3	**-1.32E+00**	**9.21E-10**	**-1.03E+00**	**9.94E-08**	-1.96E-01	1.76E-01	-7.02E-01	3.60E-05	WT & nifD- N 14 dpi	NA	DUF1997 family protein (AHRD V3.3 *** G7KKZ0_MEDTR)	
Solyc08g081520.1	**-1.32E+00**	**9.49E-05**	**-1.33E+00**	**8.52E-05**	-3.70E-01	2.08E-01	1.38E-01	6.33E-01	WT & nifD- N 14 dpi	NA	LOW QUALITY:Plant/F1M20-13 protein (AHRD V3.3 *** A0A072TUL8_MEDTR)	

Solyc01g008220.3	**-1.33E+00**	**1.46E-03**	**-1.62E+00**	**1.96E-04**	6.82E-01	7.91E-02	4.63E-01	2.25E-01	WT & nifD- N 14 dpi	STR	UPF0664 stress-induced protein C29B12.11c (AHRD V3.3 *** A0A0B2PCL5_GLYSO)	
Solyc09g075210.3	**-1.34E+00**	**1.59E-04**	**-2.68E+00**	**2.78E-09**	5.24E-01	9.52E-02	8.62E-01	8.52E-03	WT & nifD- N 14 dpi	STR	Late embryogenesis abundant protein Lea5 (AHRD V3.3 *** F2VPP8_SOLNI)	GO:0006950
Solyc12g014470.2	**-1.34E+00**	**1.43E-03**	**-1.27E+00**	**2.39E-03**	6.08E-01	1.18E-01	3.91E-01	3.08E-01	WT & nifD- N 14 dpi	P	GrpE protein homolog (AHRD V3.3 *** K4DCY2_SOLLC)	GO:0000774|GO:0006457|GO:0042803|GO:0051087|GO:0006457|GO:0006457
Solyc12g011450.2	**-1.34E+00**	**2.64E-03**	**-1.29E+00**	**3.68E-03**	-4.43E-01	2.82E-01	5.94E-01	1.53E-01	WT & nifD- N 14 dpi	E	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** M1AG46_SOLTU)	GO:0009765|GO:0016020
Solyc03g063730.3	**-1.35E+00**	**9.63E-04**	**-1.87E+00**	**2.16E-05**	-9.87E-01	1.12E-02	-3.06E-01	4.05E-01	WT & nifD- N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** M1AVC8_SOLTU)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc02g079430.3	**-1.35E+00**	**3.34E-04**	**-1.01E+00**	**4.74E-03**	-3.89E-01	2.46E-01	-3.05E-01	3.61E-01	WT & nifD- N 14 dpi	DNA	Zinc finger, B-box (AHRD V3.3 *-* A0A103Y479_CYNCS)	GO:0005622|GO:0008270
Solyc02g094860.2	**-1.36E+00**	**1.01E-03**	**-2.14E+00**	**3.78E-06**	-9.95E-01	1.15E-02	-5.43E-01	1.50E-01	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9RSK4_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc02g089540.3	**-1.36E+00**	**1.37E-05**	**-1.13E+00**	**1.42E-04**	-4.84E-01	6.74E-02	-2.66E-01	3.04E-01	WT & nifD- N 14 dpi	G	CONSTANS 1	GO:0005515|GO:0005622|GO:0008270|GO:0005622|GO:0008270
Solyc07g066360.1	**-1.36E+00**	**6.12E-05**	**-1.03E+00**	**1.21E-03**	1.28E+00	1.27E-04	1.20E+00	2.69E-04	WT & nifD- N 14 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 -** G7JV71_MEDTR)	
Solyc00g009120.3	**-1.36E+00**	**7.50E-08**	**-1.05E+00**	**5.40E-06**	-3.43E-01	7.32E-02	-5.27E-01	8.18E-03	WT & nifD- N 14 dpi	D	Short-chain dehydrogenase/reductase family protein (AHRD V3.3 *** D7LXC9_ARALL)	
Solyc02g094110.1	**-1.37E+00**	**1.85E-04**	**-1.36E+00**	**1.97E-04**	-4.38E-02	8.90E-01	5.47E-02	8.63E-01	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9RBJ0_RICCO)	GO:0004497|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0
Solyc01g080230.3	**-1.38E+00**	**4.42E-06**	**-1.27E+00**	**1.37E-05**	1.16E+00	4.86E-05	9.26E-02	7.00E-01	WT & nifD- N 14 dpi	CS	Endo-1,3-1,4-beta-d-glucanase, putative (AHRD V3.3 *** B9RSS4_RICCO)	GO:0016787
Solyc05g050430.1	**-1.38E+00**	**8.10E-11**	**-1.24E+00**	**7.33E-10**	-5.74E-01	1.72E-04	9.46E-03	9.43E-01	WT & nifD- N 14 dpi	D	LOW QUALITY:NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)	GO:0043531
Solyc01g106920.3	**-1.38E+00**	**1.61E-03**	**-1.18E+00**	**5.83E-03**	1.01E+00	1.62E-02	8.70E-01	3.51E-02	WT & nifD- N 14 dpi	TR	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7LFG1_MEDTR)	GO:0005215|GO:0006810|GO:0016020|GO:0055085
Solyc03g025720.3	**-1.38E+00**	**9.90E-09**	**-2.28E+00**	**2.68E-13**	4.05E-01	2.26E-02	7.60E-01	1.13E-04	WT & nifD- N 14 dpi	CS	4-coumarate:CoA ligase-like protein (AHRD V3.3 *** A0A0A1ETC4_ALBBR)	GO:0003824|GO:0008152
Solyc11g018530.2	**-1.39E+00**	**3.66E-05**	**-1.19E+00**	**2.42E-04**	-6.18E-01	3.64E-02	-1.82E-01	5.21E-01	WT & nifD- N 14 dpi	TR	root-specific metal transporter	GO:0005215|GO:0006810|GO:0016020
Solyc03g059140.3	**-1.40E+00**	**4.86E-03**	**-1.52E+00**	**2.52E-03**	-1.00E+00	3.71E-02	-3.01E-01	5.14E-01	WT & nifD- N 14 dpi	TR	Ion channel CASTOR (AHRD V3.3 *-* A0A1D1ZL57_9ARAE)	
Solyc09g015770.3	**-1.41E+00**	**5.59E-03**	**-1.33E+00**	**8.24E-03**	-9.78E-01	4.57E-02	-8.82E-01	6.96E-02	WT & nifD- N 14 dpi	T	WRKY transcription factor 81	GO:0003700|GO:0006355|GO:0043565
Solyc01g111880.3	**-1.41E+00**	**8.42E-07**	**-2.26E+00**	**1.26E-10**	9.10E-01	3.19E-04	2.02E+00	1.25E-09	WT & nifD- N 14 dpi	K	MAP kinase kinase kinase 11	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g043160.1	**-1.42E+00**	**3.79E-08**	**-1.12E+00**	**1.87E-06**	-5.39E-01	6.88E-03	-2.52E-01	1.83E-01	WT & nifD- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CEH6_SOLLC)	GO:0008152|GO:0016758
Solyc01g107190.3	**-1.43E+00**	**1.11E-05**	**-1.66E+00**	**1.18E-06**	1.29E+00	4.33E-05	2.07E+00	2.62E-08	WT & nifD- N 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9SGY6_RICCO)	
Solyc00g009140.3	**-1.44E+00**	**1.60E-05**	**-1.08E+00**	**5.00E-04**	-1.16E-01	6.74E-01	-5.27E-01	6.37E-02	WT & nifD- N 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G09750.1)	
Solyc08g007540.3	**-1.44E+00**	**1.19E-05**	**-1.39E+00**	**1.89E-05**	5.23E-01	6.04E-02	-4.81E-02	8.58E-01	WT & nifD- N 14 dpi	CS	ACT domain-containing family protein (AHRD V3.3 *** B9N3K8_POPTR)	GO:0008152|GO:0016597
Solyc02g092550.3	**-1.44E+00**	**1.48E-04**	**-1.71E+00**	**1.71E-05**	9.28E-01	8.34E-03	1.23E+00	7.94E-04	WT & nifD- N 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9SGY6_RICCO)	
Solyc08g016080.3	**-1.45E+00**	**2.35E-14**	**-1.28E+00**	**4.19E-13**	-7.50E-01	2.71E-08	-7.93E-01	9.57E-09	WT & nifD- N 14 dpi	E	high chlorophyll fluorescence phenotype 173 (AHRD V3.3 *** AT1G16720.1)	
Solyc05g015950.3	**-1.50E+00**	**5.81E-12**	**-1.78E+00**	**1.28E-13**	-2.15E-01	9.94E-02	-1.29E-02	9.20E-01	WT & nifD- N 14 dpi	C	Glucose-6-phosphate 1-dehydrogenase (AHRD V3.3 *** K4BYW1_SOLLC)	GO:0004345|GO:0006006|GO:0050661|GO:0055114|GO:0004345|GO:0006006|GO:0055114|GO:0004345|GO:0006006|GO:0055114
Solyc02g068140.3	**-1.51E+00**	**2.50E-03**	**-1.45E+00**	**3.59E-03**	-2.68E-01	5.58E-01	-7.61E-01	1.04E-01	WT & nifD- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT3G01930.2)	
Solyc07g062500.3	**-1.54E+00**	**1.72E-10**	**-1.27E+00**	**8.66E-09**	-1.20E-01	4.35E-01	-4.34E-01	8.25E-03	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:00

Solyc08g076710.3	**-1.55E+00**	**2.75E-03**	**-1.31E+00**	**9.35E-03**	1.02E+00	3.91E-02	1.29E+00	1.05E-02	WT & nifD- N 14 dpi	T	R2R3MYB transcription factor 39	GO:0003677
Solyc03g096050.3	**-1.55E+00**	**1.93E-04**	**-1.33E+00**	**9.31E-04**	-4.80E-01	1.91E-01	8.21E-01	2.97E-02	WT & nifD- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G05600.1)	GO:0016491|GO:0055114
Solyc12g006850.2	**-1.56E+00**	**2.81E-06**	**-1.40E+00**	**1.34E-05**	-1.40E-01	5.95E-01	2.16E-02	9.35E-01	WT & nifD- N 14 dpi	TR	LELKT1GEN L.esculentum potassium channel	GO:0005216|GO:0006811|GO:0016020|GO:0055085|GO:0005249|GO:0006813|GO:0016020|GO:0005249|GO:0006813|GO:0016020
Solyc09g064910.1	**-1.56E+00**	**4.03E-03**	**-2.31E+00**	**7.71E-05**	-3.26E-01	5.14E-01	-1.24E+00	1.87E-02	WT & nifD- N 14 dpi	H	Adenylate isopentenyltransferase (AHRD V3.3 *** I0IUP8_SOLLC)	GO:0008033
Solyc01g088160.3	**-1.56E+00**	**9.36E-04**	**-1.45E+00**	**1.84E-03**	5.61E-01	1.90E-01	-7.16E-01	9.78E-02	WT & nifD- N 14 dpi	H	cytokinin oxidase2	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114
Solyc11g011980.3	**-1.56E+00**	**2.12E-05**	**-1.41E+00**	**7.76E-05**	6.70E-01	3.48E-02	4.19E-01	1.75E-01	WT & nifD- N 14 dpi	G	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT2G32950.1)	GO:0005515|GO:0005515|GO:0008270|GO:0005515|GO:0008270
Solyc03g007530.3	**-1.57E+00**	**5.09E-04**	**-1.23E+00**	**4.44E-03**	-3.89E-01	3.33E-01	-9.82E-01	1.94E-02	WT & nifD- N 14 dpi	TR	ABC transporter family protein (AHRD V3.3 *** U5FPJ5_POPTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO:0016887
Solyc02g062300.3	**-1.57E+00**	**2.67E-05**	**-1.05E+00**	**2.15E-03**	-3.20E-01	3.06E-01	-2.45E-01	4.32E-01	WT & nifD- N 14 dpi	STR	BURP domain protein RD22 (AHRD V3.3 *-* RD22_ARATH)	
Solyc12g008990.2	**-1.57E+00**	**3.61E-05**	**-1.39E+00**	**1.60E-04**	-3.97E-01	2.19E-01	-8.31E-01	1.39E-02	WT & nifD- N 14 dpi	K	Kinase family protein (AHRD V3.3 *** D7MM98_ARALL)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc00g009110.3	**-1.57E+00**	**2.95E-10**	**-1.10E+00**	**2.36E-07**	-6.66E-01	2.88E-04	-5.47E-01	1.98E-03	WT & nifD- N 14 dpi	S	inositol-1,4,5-triphosphate-5-phosphatase 2	GO:0046856
Solyc02g067085.1	**-1.58E+00**	**2.36E-05**	**-1.00E+00**	**3.10E-03**	3.10E-02	9.20E-01	-3.03E-01	3.32E-01	WT & nifD- N 14 dpi	E	NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic (AHRD V3.3 --* NU5C_EUCGG)	
Solyc01g065700.3	**-1.58E+00**	**9.20E-15**	**-1.21E+00**	**3.84E-12**	-2.67E-03	9.79E-01	-9.92E-01	2.86E-10	WT & nifD- N 14 dpi	K	Protein phosphatase 2C family protein (AHRD V3.3 *** AT5G27930.2)	GO:0003824|GO:0004722|GO:0006470|GO:0004722|GO:0006470
Solyc05g009720.3	**-1.59E+00**	**2.85E-04**	**-2.15E+00**	**5.73E-06**	4.03E-01	2.97E-01	1.30E+00	2.08E-03	WT & nifD- N 14 dpi	S	Two-component response regulator (AHRD V3.3 *** W9RG69_9ROSA)	GO:0003677
Solyc05g046180.1	**-1.61E+00**	**6.28E-04**	**-1.31E+00**	**3.99E-03**	1.66E+00	4.74E-04	1.55E+00	9.21E-04	WT & nifD- N 14 dpi	E	LOW QUALITY:Alcohol dehydrogenase 2 (AHRD V3.3 --* ADH2_SOLLC)	
Solyc03g111710.3	**-1.62E+00**	**1.51E-07**	**-2.43E+00**	**5.72E-11**	6.59E-01	7.37E-03	2.81E+00	2.45E-12	WT & nifD- N 14 dpi	T	BTB/POZ and TAZ domain protein (AHRD V3.3 *** G7JMM8_MEDTR)	GO:0003712|GO:0004402|GO:0005634|GO:0006355|GO:0008270|GO:0005515|GO:0005515
Solyc10g084860.1	**-1.62E+00**	**4.34E-06**	**-1.19E+00**	**2.33E-04**	-4.35E-01	1.32E-01	-5.35E-01	6.64E-02	WT & nifD- N 14 dpi	PMI	Clade XI lectin receptor kinase (AHRD V3.3 *** K4D3S0_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g026230.1	**-1.64E+00**	**1.73E-04**	**-2.45E+00**	**6.36E-07**	5.49E-01	1.55E-01	1.23E+00	2.97E-03	WT & nifD- N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4BF96_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc02g064770.3	**-1.64E+00**	**1.15E-03**	**-2.05E+00**	**1.10E-04**	-4.71E-01	3.05E-01	-6.35E-01	1.70E-01	WT & nifD- N 14 dpi	G	Sigma factor sigb regulation protein rsbq, putative (AHRD V3.3 *** B9SG47_RICCO)	GO:0010223|GO:1901601
Solyc04g054190.3	**-1.65E+00**	**4.24E-14**	**-1.38E+00**	**2.22E-12**	-5.74E-01	2.31E-05	-7.25E-01	7.06E-07	WT & nifD- N 14 dpi	TR	ABC1 protein (AHRD V3.3 *** D2XP29_MAIZE)	
Solyc11g010460.2	**-1.66E+00**	**2.62E-03**	**-1.90E+00**	**7.82E-04**	-6.77E-01	1.86E-01	-9.75E-01	6.16E-02	WT & nifD- N 14 dpi	G	cyclinD4_1	GO:0005634
Solyc01g102270.2	**-1.69E+00**	**2.73E-05**	**-1.39E+00**	**2.94E-04**	-8.31E-01	1.88E-02	7.81E-01	2.64E-02	WT & nifD- N 14 dpi	CS	Jojoba acyl CoA reductase-related male sterility protein (AHRD V3.3 --* AT4G33790.2)	
Solyc03g119200.3	**-1.71E+00**	**9.45E-17**	**-1.79E+00**	**2.78E-17**	2.98E-01	2.51E-03	2.13E-01	2.41E-02	WT & nifD- N 14 dpi	AM	L-Ala-D/L-Glu epimerase (AHRD V3.3 *** A0A061FV22_THECC)	
Solyc12g094580.2	**-1.72E+00**	**2.19E-07**	**-1.53E+00**	**1.46E-06**	-6.30E-01	1.66E-02	5.71E-01	2.84E-02	WT & nifD- N 14 dpi	DNA	AT hook motif DNA-binding family protein (AHRD V3.3 --* AT5G46640.1)	
Solyc05g005480.2	**-1.72E+00**	**1.33E-06**	**-1.08E+00**	**5.84E-04**	9.68E-02	7.28E-01	-3.86E-01	1.72E-01	WT & nifD- N 14 dpi	E	Quinone oxidoreductase-like protein (AHRD V3.3 *** W9RNB1_9ROSA)	GO:0008270|GO:0016491|GO:0016491|GO:0016491
Solyc12g006997.1	**-1.72E+00**	**5.60E-09**	**-1.13E+00**	**7.31E-06**	-5.43E-01	1.24E-02	-4.46E-01	3.62E-02	WT & nifD- N 14 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A061GN86_THECC)	GO:0030001|GO:0046872
Solyc06g076630.3	**-1.73E+00**	**6.01E-13**	**-1.09E+00**	**1.00E-08**	2.27E-01	9.59E-02	-4.59E-01	1.73E-03	WT & nifD- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4CA23_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc12g014530.2	**-1.74E+00**	**1.81E-11**	**-1.26E+00**	**1.19E-08**	4.64E-01	5.71E-03	-3.56E-01	2.88E-02	WT & nifD- N 14 dpi	AM	L-aspartate oxidase (AHRD V3.3 *** K4DCY8_SOLLC)	GO:0005737|GO:0008734|GO:0009435|GO:0055114|GO:0016491|GO:0055114|GO:0016491
Solyc10g085830.2	**-1.74E+00**	**2.17E-08**	**-1.38E+00**	**1.17E-06**	-2.87E-01	2.02E-01	-5.91E-01	1.21E-02	WT & nifD- N 14 dpi	CS	Caffeic acid O-methyltransferase (AHRD V3.3 *** A0A072VA70_MEDTR)	GO:0008168|GO:0008171|GO:0008171

Solyc08g078950.3	**-1.74E+00**	**1.67E-11**	**-1.27E+00**	**1.03E-08**	9.83E-02	5.28E-01	-1.76E-01	2.61E-01	WT & nifD- N 14 dpi	N	NIT1	GO:0005215|GO:0006810|GO:0016020|GO:0005215|GO:0006857|GO:0016020|GO:0005215
Solyc01g091705.1	**-1.76E+00**	**2.22E-07**	**-1.09E+00**	**1.97E-04**	-2.49E-02	9.22E-01	-5.49E-01	3.91E-02	WT & nifD- N 14 dpi	R	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein (AHRD V3.3 *-* AT4G12600.2)	GO:0003723|GO:0005730
Solyc11g010380.2	**-1.76E+00**	**1.51E-10**	**-1.00E+00**	**4.11E-06**	9.46E-01	9.48E-06	7.46E-02	6.69E-01	WT & nifD- N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4D5J9_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc07g032385.1	**-1.78E+00**	**3.32E-06**	**-1.55E+00**	**2.53E-05**	-7.36E-01	2.19E-02	1.23E-01	6.86E-01	WT & nifD- N 14 dpi	RNA	Pentatricopeptide repeat-containing-like protein (AHRD V3.3 *** A0A0B0N0N5_GOSAR)	GO:0005515
Solyc10g084370.2	**-1.78E+00**	**2.48E-11**	**-1.69E+00**	**7.35E-11**	-9.16E-01	5.29E-06	-4.50E-01	9.39E-03	WT & nifD- N 14 dpi	T	MYB transcription factor (AHRD V3.3 *** B5TV64_CAMSI)	GO:0003677
Solyc10g050510.1	**-1.79E+00**	**5.78E-03**	**-2.21E+00**	**9.64E-04**	-1.13E+00	6.73E-02	1.98E+00	2.62E-03	WT & nifD- N 14 dpi	T	LOW QUALITY:transcription initiation factor TFIID subunit 1b-like protein (AHRD V3.3 -** AT3G19030.1)	
Solyc02g089495.1	**-1.79E+00**	**2.48E-03**	**-1.72E+00**	**3.55E-03**	-3.80E-01	4.84E-01	1.38E-02	9.80E-01	WT & nifD- N 14 dpi	P	Eukaryotic translation initiation factor 3 subunit D (AHRD V3.3 --* M8BC43_AEGTA)	
Solyc08g079490.3	**-1.80E+00**	**7.51E-12**	**-1.90E+00**	**2.14E-12**	-4.12E-02	7.90E-01	-5.36E-02	7.29E-01	WT & nifD- N 14 dpi	P	Class I peptide chain release factor (AHRD V3.3 *** AT1G62850.3)	GO:0003747|GO:0006415
Solyc12g013620.2	**-1.81E+00**	**9.45E-07**	**-1.21E+00**	**2.23E-04**	2.61E-01	3.63E-01	1.51E+00	1.36E-05	WT & nifD- N 14 dpi	H	jasmonic acid 2	GO:0003677|GO:0006355
Solyc11g012850.2	**-1.84E+00**	**4.69E-09**	**-1.57E+00**	**8.80E-08**	-7.86E-01	1.10E-03	-5.05E-01	2.61E-02	WT & nifD- N 14 dpi	P	Chlorophyllide a oxygenase (AHRD V3.3 *** W9SD87_9ROSA)	GO:0005506|GO:0016705|GO:0051537|GO:0055114|GO:0010277|GO:0055114|GO:0010277
Solyc02g072260.3	**-1.84E+00**	**2.47E-10**	**-1.43E+00**	**3.47E-08**	-4.79E-01	1.56E-02	-3.20E-01	9.56E-02	WT & nifD- N 14 dpi	T	SAP-like protein BP-73 (AHRD V3.3 *-* M8BMZ0_AEGTA)	GO:0006353
Solyc11g007180.2	**-1.85E+00**	**3.92E-06**	**-1.77E+00**	**7.34E-06**	1.48E+00	8.11E-05	1.38E+00	1.89E-04	WT & nifD- N 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2RXW1_GLYSO)	GO:0016788
Solyc02g089490.3	**-1.85E+00**	**8.66E-04**	**-1.80E+00**	**1.16E-03**	-6.05E-01	2.30E-01	-5.81E-01	2.48E-01	WT & nifD- N 14 dpi	RNA	Plant Tudor-like RNA-binding protein (AHRD V3.3 --* AT4G32440.3)	
Solyc08g081530.3	**-1.85E+00**	**1.84E-15**	**-1.44E+00**	**5.94E-13**	2.27E-01	4.81E-02	-2.56E-01	2.71E-02	WT & nifD- N 14 dpi	E	monodehydroascorbate reductase	GO:0016491|GO:0055114
Solyc03g031860.3	**-1.85E+00**	**8.41E-14**	**-2.13E+00**	**3.34E-15**	-2.49E-01	6.44E-02	-1.30E-01	3.21E-01	WT & nifD- N 14 dpi	2M	Phytoene synthase 1	GO:0004310|GO:0006696|GO:0051996|GO:0009058|GO:0016740|GO:0009058|GO:0016740
Solyc09g057903.1	**-1.87E+00**	**3.48E-03**	**-1.72E+00**	**6.57E-03**	6.23E-02	9.16E-01	-6.77E-01	2.56E-01	WT & nifD- N 14 dpi	S	Type I inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 *-* A0A0K9NH83_ZOSMR)	
Solyc11g011500.2	**-1.90E+00**	**4.79E-10**	**-1.76E+00**	**2.12E-09**	-5.26E-01	1.27E-02	4.85E-01	2.05E-02	WT & nifD- N 14 dpi	TR	Potassium channel	GO:0005216|GO:0006811|GO:0016020|GO:0055085|GO:0005249|GO:0006813|GO:0016020|GO:0005249|GO:0006813|GO:0016020
Solyc12g087840.1	**-1.90E+00**	**2.58E-08**	**-1.12E+00**	**9.17E-05**	-8.35E-01	1.93E-03	-6.18E-01	1.68E-02	WT & nifD- N 14 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FG67_THECC)	GO:0005515|GO:0008270
Solyc04g081230.3	**-1.93E+00**	**3.33E-17**	**-1.77E+00**	**2.43E-16**	2.76E-01	8.10E-03	1.62E-01	1.05E-01	WT & nifD- N 14 dpi	NA	TLD-domain containing nucleolar protein (AHRD V3.3 *** AT5G39590.1)	
Solyc08g081700.1	**-1.95E+00**	**8.42E-08**	**-1.62E+00**	**1.79E-06**	-1.60E-01	5.49E-01	-6.68E-01	1.77E-02	WT & nifD- N 14 dpi	D	LOW QUALITY:Late embryogenesis abundant hydroxyproline-rich glycofamily protein, putative (AHRD V3.3 *** A0A061G5L2_THECC)	
Solyc06g069100.2	**-1.97E+00**	**4.80E-04**	**-2.08E+00**	**2.72E-04**	2.07E+00	2.78E-04	1.74E+00	1.56E-03	WT & nifD- N 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061FUV1_THECC)	GO:0003677|GO:0006355
Solyc05g050805.1	**-2.01E+00**	**5.02E-04**	**-2.32E+00**	**9.98E-05**	1.11E-01	8.28E-01	-1.38E-02	9.78E-01	WT & nifD- N 14 dpi	STR	DnaJ protein (AHRD V3.3 *-* A0A199V6W4_ANACO)	
Solyc03g111120.3	**-2.02E+00**	**2.39E-07**	**-1.42E+00**	**4.71E-05**	7.96E-02	7.86E-01	-9.13E-01	4.19E-03	WT & nifD- N 14 dpi	C	Malate synthase (AHRD V3.3 *** M1B824_SOLTU)	GO:0003824|GO:0004474|GO:0006097|GO:0004474|GO:0006097
Solyc04g016200.1	**-2.02E+00**	**1.12E-04**	**-1.98E+00**	**1.45E-04**	9.12E-01	5.00E-02	-2.35E-01	6.01E-01	WT & nifD- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** Q8RXA4_SOLLC)	GO:0008152|GO:0016758
Solyc06g072840.3	**-2.04E+00**	**5.08E-04**	**-1.93E+00**	**8.79E-04**	2.50E+00	4.66E-05	1.59E+00	4.54E-03	WT & nifD- N 14 dpi	OX	Hydrogen peroxide induced protein 1 (AHRD V3.3 *** J7F198_CAMSI)	
Solyc06g036260.3	**-2.04E+00**	**4.10E-16**	**-1.36E+00**	**4.99E-12**	-4.99E-01	1.60E-04	-8.35E-01	8.17E-08	WT & nifD- N 14 dpi	2M	beta-carotene hydroxylase-1	GO:0005506|GO:0006633|GO:0016491|GO:00
Solyc02g081250.2	**-2.05E+00**	**1.79E-14**	**-1.31E+00**	**3.31E-10**	-7.96E-02	5.55E-01	-8.23E-01	1.59E-06	WT & nifD- N 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *-* A0A103Y0J8_CYNCS)	GO:0005515|GO:0046872|GO:0046872
Solyc11g013810.2	**-2.06E+00**	**8.70E-07**	**-1.72E+00**	**1.35E-05**	1.29E+00	4.58E-04	4.01E-01	2.23E-01	WT & nifD- N 14 dpi	N	Nitrate reductase (AHRD V3.3 *** K4D6I5_SOLLC)	GO:0006809|GO:0042128|GO:0050464|GO:0016491|GO:0030151|GO:0055114|GO:0016491

Solyc10g084120.2	**-2.08E+00**	**2.29E-10**	**-1.43E+00**	**2.87E-07**	6.73E-01	3.30E-03	8.27E-01	5.06E-04	WT & nifD- N 14 dpi	TR	plasma membrane intrinsic protein 2.5	GO:0005215|GO:0006810|GO:0016020
Solyc11g069760.1	**-2.09E+00**	**1.04E-03**	**-3.28E+00**	**4.35E-06**	-6.35E-01	2.72E-01	-3.45E-01	5.48E-01	WT & nifD- N 14 dpi	N	LOW QUALITY:High affinity nitrate transporter protein (AHRD V3.3 *-* Q84MZ8_TOBAC)	
Solyc03g113280.3	**-2.11E+00**	**1.44E-10**	**-1.29E+00**	**1.33E-06**	-2.45E-03	9.91E-01	-7.89E-01	7.47E-04	WT & nifD- N 14 dpi	NA	Integral membrane HPP family protein (AHRD V3.3 *** AT3G47980.1)	
Solyc09g009830.3	**-2.14E+00**	**3.36E-07**	**-1.07E+00**	**2.30E-03**	1.05E-01	7.40E-01	-8.34E-01	1.37E-02	WT & nifD- N 14 dpi	C	Carbonic anhydrase family protein (AHRD V3.3 *** D7LUA2_ARALL)	GO:0004089|GO:0006730|GO:0008270
Solyc05g050420.1	**-2.16E+00**	**2.37E-06**	**-2.50E+00**	**2.23E-07**	-5.28E-01	1.52E-01	-4.95E-01	1.79E-01	WT & nifD- N 14 dpi	D	LOW QUALITY:Disease resistance protein (AHRD V3.3 *-* Q9SBC3_SOLLC)	
Solyc02g088070.3	**-2.16E+00**	**2.87E-14**	**-1.72E+00**	**4.73E-12**	-1.80E-02	9.01E-01	4.46E-01	4.47E-03	WT & nifD- N 14 dpi	DNA	Dof zinc finger protein (AHRD V3.3 *** W9QEV1_9ROSA)	GO:0003677|GO:0006355
Solyc05g005040.3	**-2.17E+00**	**1.64E-10**	**-1.18E+00**	**8.17E-06**	-1.89E-01	3.82E-01	-6.86E-01	3.42E-03	WT & nifD- N 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G26610.1)	GO:0004650|GO:0005975
Solyc07g051860.1	**-2.20E+00**	**5.46E-07**	**-2.43E+00**	**9.87E-08**	2.35E-01	4.86E-01	-5.62E-01	1.03E-01	WT & nifD- N 14 dpi	K	MAP kinase kinase kinase 50	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g007360.3	**-2.22E+00**	**6.58E-09**	**-2.08E+00**	**2.30E-08**	9.16E-01	1.75E-03	5.67E-02	8.31E-01	WT & nifD- N 14 dpi	TR	Nodulin MtN3	GO:0016021
Solyc09g072750.2	**-2.25E+00**	**7.55E-06**	**-1.69E+00**	**2.97E-04**	1.43E-01	7.27E-01	1.99E-01	6.27E-01	WT & nifD- N 14 dpi	CS	LOW QUALITY:Carbohydrate-binding X8 domain superfamily protein (AHRD V3.3 --* AT1G29380.3)	
Solyc10g084680.1	**-2.27E+00**	**9.64E-11**	**-1.27E+00**	**3.58E-06**	4.39E-01	5.36E-02	3.40E-01	1.29E-01	WT & nifD- N 14 dpi	TR	Sulfate transporter, putative (AHRD V3.3 *** A0A061GW43_THECC)	GO:0015098|GO:0015689|GO:0015098|GO:0015689|GO:0016021|GO:0015098|GO:0015689
Solyc06g011350.3	**-2.28E+00**	**2.79E-15**	**-1.20E+00**	**3.19E-09**	7.33E-01	1.35E-05	-9.14E-01	4.59E-07	WT & nifD- N 14 dpi	TR	plasma membrane intrinsic protein 2.4	GO:0005215|GO:0006810|GO:0016020
Solyc06g008980.3	**-2.28E+00**	**7.65E-08**	**-1.01E+00**	**2.86E-03**	-5.69E-02	8.55E-01	-2.67E-01	3.95E-01	WT & nifD- N 14 dpi	P	F-box/WD repeat-containing 10 (AHRD V3.3 *** A0A0B0NKC4_GOSAR)	
Solyc12g097080.2	**-2.29E+00**	**2.16E-11**	**-1.93E+00**	**7.42E-10**	-1.90E-01	3.62E-01	-8.44E-02	6.83E-01	WT & nifD- N 14 dpi	STR	Glutathione s-transferase, putative (AHRD V3.3 *** B9RWR5_RICCO)	GO:0005515
Solyc10g086730.2	**-2.32E+00**	**3.77E-14**	**-1.62E+00**	**1.02E-10**	-7.97E-02	6.13E-01	-7.50E-01	5.53E-05	WT & nifD- N 14 dpi	C	Fructose-1,6-bisphosphatase (AHRD V3.3 *** W9S5L8_9ROSA)	GO:0005975|GO:0016791|GO:0042132|GO:0042132
Solyc11g044260.2	**-2.35E+00**	**6.26E-07**	**-1.67E+00**	**8.78E-05**	-8.77E-01	2.17E-02	-7.64E-01	4.28E-02	WT & nifD- N 14 dpi	TR	K(+) efflux antiporter (AHRD V3.3 *-* A0A0K9NYY6_ZOSMR)	GO:0006812|GO:0015299|GO:0016021|GO:00
Solyc02g036370.3	**-2.37E+00**	**2.12E-11**	**-2.01E+00**	**6.71E-10**	-2.04E-01	3.44E-01	-1.09E-01	6.11E-01	WT & nifD- N 14 dpi	T	Myb family transcription factor	GO:0003677
Solyc04g082630.3	**-2.41E+00**	**4.71E-03**	**-2.27E+00**	**7.41E-03**	-6.37E-01	4.21E-01	-1.13E+00	1.60E-01	WT & nifD- N 14 dpi	C	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** K4BVZ0_SOLLC)	GO:0006006|GO:0016620|GO:0050661|GO:0051287|GO:0055114|GO:0016620|GO:0055114
Solyc07g009260.3	**-2.44E+00**	**4.59E-05**	**-4.16E+00**	**8.50E-09**	-8.58E-01	9.70E-02	-1.01E+00	5.22E-02	WT & nifD- N 14 dpi	D	Defensin-like protein (AHRD V3.3 *-* A0A072TKV9_MEDTR)	GO:0006952
Solyc12g006640.2	**-2.45E+00**	**1.18E-11**	**-1.82E+00**	**5.02E-09**	-8.63E-01	4.00E-04	-8.97E-01	2.62E-04	WT & nifD- N 14 dpi	STR	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** AT1G80160.3)	
Solyc10g050890.2	**-2.45E+00**	**1.50E-10**	**-1.54E+00**	**9.17E-07**	-1.31E-02	9.57E-01	-3.72E-01	1.32E-01	WT & nifD- N 14 dpi	N	nitrite reductase 2	GO:0016491|GO:0020037|GO:0051536|GO:0055114|GO:0016491|GO:0055114|GO:0016491
Solyc08g008630.3	**-2.48E+00**	**5.14E-05**	**-1.94E+00**	**7.92E-04**	-6.63E-01	2.06E-01	-6.32E-01	2.27E-01	WT & nifD- N 14 dpi	2M	beta-carotene isomerase D27 (AHRD V3.3 *** AT1G64680.2)	
Solyc10g083230.1	**-2.57E+00**	**8.70E-11**	**-2.50E+00**	**1.57E-10**	-2.14E-01	3.90E-01	-3.51E-01	1.64E-01	WT & nifD- N 14 dpi	P	F-box family protein (AHRD V3.3 *** B9NEF0_POPTR)	GO:0005515
Solyc07g061790.3	**-2.63E+00**	**2.29E-06**	**-1.78E+00**	**3.82E-04**	7.94E-01	7.99E-02	1.93E-01	6.61E-01	WT & nifD- N 14 dpi	S	SOUL heme-binding family protein (AHRD V3.3 *** AT1G17100.1)	
Solyc06g075970.3	**-2.65E+00**	**4.56E-05**	**-3.51E+00**	**7.78E-07**	-3.97E-01	4.70E-01	9.51E-01	9.10E-02	WT & nifD- N 14 dpi	TR	P-hydroxybenzoic acid efflux pump subunit aaeB (AHRD V3.3 *** A0A061GW63_THECC)	
Solyc10g055260.2	**-2.76E+00**	**1.55E-04**	**-1.82E+00**	**7.13E-03**	4.91E-01	4.37E-01	-1.46E+00	2.72E-02	WT & nifD- N 14 dpi	H	SlLAX5	
Solyc08g007130.3	**-2.76E+00**	**8.16E-09**	**-2.10E+00**	**9.82E-07**	-2.93E-01	3.83E-01	4.60E-01	1.75E-01	WT & nifD- N 14 dpi	CS	Beta-amylase (AHRD V3.3 *** K4CIK0_SOLLC)	GO:0000272|GO:0016161|GO:0005975|GO:00
Solyc07g064410.1	**-2.81E+00**	**9.12E-07**	**-2.88E+00**	**6.23E-07**	-1.06E-01	8.11E-01	1.84E-01	6.79E-01	WT & nifD- N 14 dpi	P	Kua-ubiquitin conjugating enzyme hybrid, localization (AHRD V3.3 *** A0A103XYI2_CYNCS)	
Solyc00g090860.2	**-2.81E+00**	**2.00E-06**	**-3.83E+00**	**9.69E-09**	-6.35E-01	1.81E-01	-3.45E-01	4.62E-01	WT & nifD- N 14 dpi	N	LOW QUALITY:High affinity nitrate transporter protein (AHRD V3.3 *-* Q84MZ8_TOBAC)	

Solyc07g008240.3	**-3.01E+00**	**3.77E-08**	**-2.00E+00**	**2.46E-05**	1.01E+00	1.62E-02	9.41E-01	2.35E-02	WT & nifD- N 14 dpi	TR	Non-symbiotic hemoglobin 1 (AHRD V3.3 *** HBL1_GOSHI)	GO:0019825|GO:0020037
Solyc01g067870.3	**-3.04E+00**	**7.19E-05**	**-2.52E+00**	**6.03E-04**	-1.07E+00	1.09E-01	-3.21E-01	6.23E-01	WT & nifD- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4AX35_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc06g050760.1	**-3.08E+00**	**1.69E-15**	**-2.44E+00**	**3.55E-13**	2.04E+00	1.98E-11	5.22E-01	7.79E-03	WT & nifD- N 14 dpi	D	Wound-induced protein 1 (AHRD V3.3 *** WUN1_SOLTU)	
Solyc08g077820.3	**-3.09E+00**	**5.42E-06**	**-1.55E+00**	**8.16E-03**	-1.38E+00	1.68E-02	-1.17E+00	3.96E-02	WT & nifD- N 14 dpi	AM	Cationic amino acid transporter, putative (AHRD V3.3 *-* A0A061G4V0_THECC)	
Solyc04g011850.1	**-3.30E+00**	**9.36E-04**	**-2.79E+00**	**4.06E-03**	-1.06E-01	9.05E-01	1.84E-01	8.37E-01	WT & nifD- N 14 dpi	OX	Glutaredoxin family protein (AHRD V3.3 *** B9I9V9_POPTR)	GO:0009055|GO:0015035|GO:0045454
Solyc06g083160.1	**-3.40E+00**	**7.50E-04**	**-3.55E+00**	**4.89E-04**	3.60E+00	4.26E-04	2.86E+00	3.51E-03	WT & nifD- N 14 dpi	NA	LOW QUALITY:DUF506 family protein (AHRD V3.3 *** G7LF52_MEDTR)	
Solyc10g085030.1	**-3.53E+00**	**1.13E-05**	**-2.51E+00**	**6.82E-04**	-5.58E-01	3.99E-01	-1.04E+00	1.21E-01	WT & nifD- N 14 dpi	S	SOUL heme-binding family protein (AHRD V3.3 *** AT2G37970.1)	
Solyc03g111887.1	**-3.57E+00**	**8.85E-05**	**-2.21E+00**	**7.96E-03**	1.18E+00	1.38E-01	2.57E-01	7.41E-01	WT & nifD- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *-* A0A103XWG4_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc12g011060.2	**-3.59E+00**	**1.20E-03**	**-3.62E+00**	**1.10E-03**	1.39E-01	8.89E-01	-3.45E-01	7.29E-01	WT & nifD- N 14 dpi	DNA	Zinc finger protein-like protein (AHRD V3.3 *** Q3S345_GOSHI)	GO:0008270
Solyc08g006860.3	**-3.66E+00**	**1.32E-04**	**-5.17E+00**	**1.09E-06**	1.50E+00	7.82E-02	2.91E+00	1.44E-03	WT & nifD- N 14 dpi	P	Patatin (AHRD V3.3 *** K4CIH4_SOLLC)	GO:0006629|GO:0008152|GO:0008152
Solyc07g051890.1	**-3.77E+00**	**3.13E-06**	**-2.01E+00**	**3.98E-03**	-3.63E-01	5.72E-01	1.18E+00	7.40E-02	WT & nifD- N 14 dpi	K	MAP kinase kinase kinase 53	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc09g011080.3	**-3.78E+00**	**1.18E-06**	**-4.38E+00**	**1.01E-07**	1.48E+00	2.06E-02	-1.12E+00	7.35E-02	WT & nifD- N 14 dpi	E	Ribulose bisphosphate carboxylase/oxygenase activase (AHRD V3.3 *** V9IMY5_NICAT)	GO:0005524
Solyc11g006910.2	**-3.92E+00**	**5.37E-14**	**-2.74E+00**	**1.47E-10**	9.77E-01	1.17E-03	-7.45E-02	7.83E-01	WT & nifD- N 14 dpi	E	Ferredoxin family protein (AHRD V3.3 *** B9MYW6_POPTR)	GO:0009055|GO:0022900|GO:0051537|GO:0009055|GO:0051536|GO:0009055|GO:0051536
Solyc02g078130.3	**-3.96E+00**	**3.29E-07**	**-1.70E+00**	**7.09E-03**	5.06E-01	3.92E-01	-5.12E-01	3.86E-01	WT & nifD- N 14 dpi	T	bHLH transcription factor 079	GO:0003677|GO:0046983|GO:0046983
Solyc03g094000.3	**-3.96E+00**	**5.90E-05**	**-6.92E+00**	**8.01E-09**	1.20E+00	1.60E-01	1.84E-01	8.26E-01	WT & nifD- N 14 dpi	E	Light induced like protein (AHRD V3.3 *** C1E3F8_MICCC)	
Solyc06g066710.1	**-3.99E+00**	**1.71E-05**	**-3.34E+00**	**1.66E-04**	-2.05E+00	1.20E-02	-1.90E+00	1.87E-02	WT & nifD- N 14 dpi	NA	LOW QUALITY:NHL domain-containing protein, putative (AHRD V3.3 --* A0A061EBN2_THECC)	
Solyc07g052620.1	**-4.38E+00**	**4.93E-05**	**-2.67E+00**	**6.34E-03**	1.60E+00	8.64E-02	-2.15E+00	2.44E-02	WT & nifD- N 14 dpi	DNA	LOW QUALITY:Zinc finger, B-box (AHRD V3.3 *** A0A118JXT6_CYNCS)	GO:0005622|GO:0008270
Solyc11g045410.1	**-4.50E+00**	**5.60E-05**	**-3.86E+00**	**3.32E-04**	-1.18E-01	9.01E-01	-1.19E+00	2.12E-01	WT & nifD- N 14 dpi	D	LOW QUALITY:Disease resistance protein (AHRD V3.3 *-* A0A068EW38_SOLLC)	
Solyc02g075625.1	**-4.62E+00**	**2.38E-11**	**-4.41E+00**	**6.39E-11**	-1.06E-01	7.99E-01	1.84E-01	6.61E-01	WT & nifD- N 14 dpi	T	LOW QUALITY:transcription factor-like protein (AHRD V3.3 *** AT3G14880.2)	GO:0006351|GO:0043565
Solyc06g071830.2	**-4.65E+00**	**9.94E-05**	**-3.83E+00**	**8.36E-04**	1.47E+00	1.58E-01	2.58E+00	1.71E-02	WT & nifD- N 14 dpi	T	BTB/POZ and TAZ domain protein (AHRD V3.3 *** G7JMM8_MEDTR)	GO:0003712|GO:0004402|GO:0005634|GO:0006355|GO:0008270|GO:0005515|GO:0005515
Solyc03g034320.3	**-5.04E+00**	**4.07E-07**	**-3.81E+00**	**2.79E-05**	2.46E+00	3.00E-03	2.78E+00	1.00E-03	WT & nifD- N 14 dpi	N	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *** AT5G38200.1)	GO:0006541|GO:0016787
Solyc03g119180.1	**-6.02E+00**	**1.08E-12**	**-5.16E+00**	**3.11E-11**	5.12E-01	2.85E-01	-1.12E+00	2.41E-02	WT & nifD- N 14 dpi	P	LOW QUALITY:Lysine--tRNA ligase (AHRD V3.3 --* V7B2W1_PHAVU)	
Solyc07g053370.1	**-6.33E+00**	**9.58E-07**	**-4.83E+00**	**4.72E-05**	1.36E+00	1.82E-01	1.84E-01	8.54E-01	WT & nifD- N 14 dpi	NA	LOW QUALITY:Clavata3/ESR (CLE) gene family member (AHRD V3.3 -** A0A072TRR8_MEDTR)	
Solyc08g007430.2	**-9.87E+00**	**1.59E-10**	**-1.10E+01**	**1.52E-11**	-9.13E-02	9.26E-01	-5.06E-01	6.05E-01	WT & nifD- N 14 dpi	N	NIT2	GO:0005215|GO:0006810|GO:0016020|GO:0005215|GO:0006857|GO:0016020|GO:0005215|GO:0006857|GO:0016020
Solyc01g101180.3	-4.71E-02	9.72E-01	-6.42E-01	6.38E-01	**5.03E+00**	**9.55E-04**	**8.04E+00**	**2.83E-06**	WT & nifD- NoN 14 dpi	2M	viridiflorene synthase	GO:0000287|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829
Solyc04g015635.1	2.80E+00	3.13E-01	3.02E+00	2.78E-01	**8.60E+00**	**4.03E-03**	**7.69E+00**	**9.05E-03**	WT & nifD- NoN 14 dpi	DNA	BED zinc finger,hAT family dimerization domain, putative (AHRD V3.3 *-* A0A061FD65_THECC)	GO:0003676|GO:0003677|GO:0003677
Solyc03g006650.2	2.00E+00	8.85E-02	8.27E-01	4.71E-01	**5.42E+00**	**5.90E-05**	**5.74E+00**	**2.79E-05**	WT & nifD- NoN 14 dpi	TR	Sugar transporter protein 10	GO:0005215|GO:0016021|GO:0055085|GO:0016020|GO:0022891|GO:0055085|GO:0016020
Solyc00g174330.3	2.11E+00	9.60E-02	1.39E-01	9.10E-01	**6.07E+00**	**3.69E-05**	**5.71E+00**	**8.00E-05**	WT & nifD- NoN 14 dpi	D	Pathogenesis-related protein 1 (AHRD V3.3 *-* Q75QH2_CAPCH)	

Solyc02g067750.3	-1.68E-01	9.13E-01	5.39E-01	7.26E-01	**5.76E+00**	**8.43E-04**	**4.98E+00**	**3.09E-03**	WT & nifD- NoN 14 dpi	C	Carbonic anhydrase (AHRD V3.3 *** B1VK36_SOLLC)	GO:0004089|GO:0008270|GO:0004089|GO:0008270|GO:0015976|GO:0004089|GO:0008270
Solyc11g011600.2	8.11E-01	2.28E-01	1.62E+00	2.07E-02	**2.84E+00**	**1.98E-04**	**4.70E+00**	**1.39E-07**	WT & nifD- NoN 14 dpi	H	GRAM domain protein/ABA-responsive-like protein (AHRD V3.3 *** AT5G23350.1)	
Solyc05g053860.3	-4.33E-01	5.61E-01	-2.72E-01	7.15E-01	**2.48E+00**	**2.37E-03**	**4.68E+00**	**1.05E-06**	WT & nifD- NoN 14 dpi	TR	Organic cation/carnitine transporter (AHRD V3.3 *** A0A072TPM4_MEDTR)	GO:0016021|GO:0022857|GO:0055085
Solyc01g106130.1	-8.21E-01	1.75E-01	-4.45E-01	4.56E-01	**4.96E+00**	**7.22E-09**	**4.68E+00**	**2.16E-08**	WT & nifD- NoN 14 dpi	P	LOW QUALITY:F-box protein (AHRD V3.3 *** G7I272_MEDTR)	
Solyc01g079930.2	5.89E-01	5.35E-01	1.92E+00	5.09E-02	**3.23E+00**	**1.95E-03**	**4.57E+00**	**4.74E-05**	WT & nifD- NoN 14 dpi	CS	Xyloglucan-specific endoglucanase inhibitor 9 (AHRD V3.3 *** G8GYH9_SOLTU)	GO:0004190|GO:0006508
Solyc08g080310.1	-1.20E+00	4.93E-02	-7.88E-01	1.86E-01	**4.18E+00**	**1.24E-07**	**4.56E+00**	**2.61E-08**	WT & nifD- NoN 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4CP31_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc03g098760.2	2.39E-01	8.47E-01	1.27E+00	3.10E-01	**5.70E+00**	**8.92E-05**	**4.54E+00**	**1.04E-03**	WT & nifD- NoN 14 dpi	D	Kunitz-type protease inhibitor-like protein (AHRD V3.3 *** Q2XPY0_SOLTU)	GO:0004866
Solyc10g076320.2	3.60E-01	6.69E-01	9.19E-01	2.80E-01	**4.77E+00**	**5.11E-06**	**4.49E+00**	**1.25E-05**	WT & nifD- NoN 14 dpi	K	Protein phosphatase-2c, putative (AHRD V3.3 *** B9SL27_RICCO)	GO:0003824|GO:0004722|GO:0006470|GO:0004722|GO:0006470
Solyc05g054380.2	3.60E-01	7.46E-01	-2.35E-01	8.33E-01	**4.57E+00**	**3.22E-04**	**4.46E+00**	**4.15E-04**	WT & nifD- NoN 14 dpi	D	Major allergen d 1 (AHRD V3.3 *** Q8L6K9_MALDO)	GO:0006952|GO:0009607
Solyc10g044967.1	-3.17E-01	7.27E-01	4.19E-01	6.46E-01	**3.27E+00**	**1.21E-03**	**4.46E+00**	**3.88E-05**	WT & nifD- NoN 14 dpi	T	MADS-box transcription factor (AHRD V3.3 *** A0A059Q1L5_9POAL)	GO:0000165|GO:0000977|GO:0045944|GO:0003677|GO:0046983|GO:0003677|GO:0046983
Solyc02g086300.3	-9.13E-01	3.66E-02	-1.49E+00	1.36E-03	**3.10E+00**	**6.45E-08**	**4.05E+00**	**3.80E-10**	WT & nifD- NoN 14 dpi	N	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *** AT5G38200.1)	GO:0006541|GO:0016787
Solyc00g174340.2	1.58E+00	1.73E-01	4.12E-01	7.17E-01	**4.84E+00**	**2.17E-04**	**4.01E+00**	**1.46E-03**	WT & nifD- NoN 14 dpi	D	Pathogenesis-related protein 1 (AHRD V3.3 *** Q75QH2_CAPCH)	GO:0005576
Solyc03g006490.3	1.48E-01	6.70E-01	-3.61E-01	3.03E-01	**1.20E+00**	**1.76E-03**	**3.93E+00**	**1.38E-11**	WT & nifD- NoN 14 dpi	NA	glutaminase domain-containing protein	
Solyc04g017740.1	1.25E+00	2.35E-01	1.71E+00	1.08E-01	**4.05E+00**	**5.46E-04**	**3.89E+00**	**8.18E-04**	WT & nifD- NoN 14 dpi	AM	LOW QUALITY:pyridoxal-phosphate-dependent serine hydroxymethyltransferase, putative (DUF632) (AHRD V3.3 --* AT3G51290.3)	
Solyc01g080020.2	5.08E-01	2.20E-01	-4.29E-02	9.16E-01	**1.69E+00**	**2.90E-04**	**3.85E+00**	**6.61E-10**	WT & nifD- NoN 14 dpi	P	Eukaryotic aspartyl protease family protein, putative (AHRD V3.3 *** A0A061ELJ0_THECC)	GO:0004190|GO:0006508
Solyc12g099930.2	-1.01E+00	2.43E-01	-2.27E+00	1.20E-02	**2.87E+00**	**2.15E-03**	**3.74E+00**	**1.51E-04**	WT & nifD- NoN 14 dpi	AM	alanine:glyoxylate aminotransferase (AHRD V3.3 *** AT2G13360.3)	GO:0003824
Solyc07g061720.3	1.02E+00	7.94E-02	4.82E-01	3.96E-01	**3.65E+00**	**6.75E-07**	**3.73E+00**	**4.55E-07**	WT & nifD- NoN 14 dpi	H	gibberellin 2-oxidase 4	GO:0016491|GO:0055114
Solyc01g057000.3	1.54E+00	1.35E-01	-7.46E-02	9.41E-01	**3.55E+00**	**1.44E-03**	**3.68E+00**	**1.05E-03**	WT & nifD- NoN 14 dpi	STR	Universal stress protein	GO:0006950
Solyc03g098740.1	3.13E-01	7.34E-01	4.47E-01	6.27E-01	**2.80E+00**	**4.98E-03**	**3.67E+00**	**4.44E-04**	WT & nifD- NoN 14 dpi	D	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)	GO:0004866
Solyc08g079900.3	1.43E+00	2.81E-02	1.03E+00	1.06E-01	**2.83E+00**	**9.79E-05**	**3.50E+00**	**5.69E-06**	WT & nifD- NoN 14 dpi	STR	subtilisin-like protease	GO:0004252|GO:0006508
Solyc07g054430.3	4.45E-01	6.84E-02	2.69E-02	9.09E-01	**1.82E+00**	**3.37E-08**	**3.20E+00**	**2.74E-13**	WT & nifD- NoN 14 dpi	N	Glutamate formiminotransferase 1 (AHRD V3.3 *** B4F7V5_MAIZE)	GO:0005542|GO:0008152|GO:0016740
Solyc04g071780.3	-1.88E-01	8.66E-01	3.41E-01	7.60E-01	**3.20E+00**	**7.64E-03**	**3.12E+00**	**9.12E-03**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A0B0NSU6_GOSAR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc05g051820.3	1.24E+00	5.10E-02	-8.75E-02	8.87E-01	**2.32E+00**	**7.64E-04**	**2.96E+00**	**4.67E-05**	WT & nifD- NoN 14 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** G7LAE8_MEDTR)	GO:0030001|GO:0046872
Solyc10g083880.2	2.21E-01	4.83E-01	-3.37E-01	2.88E-01	**1.63E+00**	**1.76E-05**	**2.89E+00**	**9.97E-10**	WT & nifD- NoN 14 dpi	TR	tonoplast intrinsic protein 1.3	GO:0005215|GO:0006810|GO:0016020
Solyc03g020030.3	1.43E+00	1.82E-02	-1.32E+00	2.76E-02	**2.01E+00**	**1.56E-03**	**2.87E+00**	**2.97E-05**	WT & nifD- NoN 14 dpi	D	Pin-II type proteinase inhibitor 69 (AHRD V3.3 *** A0A097J9C9_CAPAN)	GO:0004867
Solyc08g077910.3	-1.62E-01	5.69E-01	-7.81E-01	9.97E-03	**2.45E+00**	**3.72E-09**	**2.87E+00**	**1.53E-10**	WT & nifD- NoN 14 dpi	CS	Expansin-like protein (AHRD V3.3 *** W9S0F1_9ROSA)	GO:0005576
Solyc06g083160.1	-3.40E+00	7.50E-04	-3.55E+00	4.89E-04	**3.60E+00**	**4.26E-04**	**2.86E+00**	**3.51E-03**	WT & nifD- NoN 14 dpi	NA	LOW QUALITY:DUF506 family protein (AHRD V3.3 *** G7LF52_MEDTR)	
Solyc10g055820.2	9.51E-01	9.27E-03	9.65E-01	8.40E-03	**1.79E+00**	**1.65E-05**	**2.85E+00**	**7.08E-09**	WT & nifD- NoN 14 dpi	D	Chitinase (AHRD V3.3 *** B9VRK7_CAPAN)	GO:0004568|GO:0005975|GO:0004568|GO:0006032|GO:0016998|GO:0004568|GO:0006032

Solyc09g007790.1	3.30E-01	3.08E-01	-5.83E-01	7.82E-02	**1.14E+00**	**1.37E-03**	**2.83E+00**	**2.49E-09**	WT & nifD- NoN 14 dpi	G	LOW QUALITY:Senescence regulator (AHRD V3.3 *** G7IRS7_MEDTR)	
Solyc03g034320.3	-5.04E+00	4.07E-07	-3.81E+00	2.79E-05	**2.46E+00**	**3.00E-03**	**2.78E+00**	**1.00E-03**	WT & nifD- NoN 14 dpi	N	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *** AT5G38200.1)	GO:0006541|GO:0016787
Solyc01g006530.1	-1.81E+00	1.98E-03	6.90E-01	2.01E-01	**2.22E+00**	**2.73E-04**	**2.78E+00**	**1.68E-05**	WT & nifD- NoN 14 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** K4ASL9_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g011680.2	-4.06E-02	9.36E-01	-3.60E-01	4.81E-01	**2.41E+00**	**6.01E-05**	**2.70E+00**	**1.29E-05**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A061DI80_THECC)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc09g091670.3	-1.43E+00	5.39E-02	-1.65E+00	2.78E-02	**2.21E+00**	**4.34E-03**	**2.70E+00**	**7.67E-04**	WT & nifD- NoN 14 dpi	TR	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc03g116120.2	9.59E-01	6.13E-03	-3.48E-01	2.89E-01	**1.33E+00**	**3.36E-04**	**2.63E+00**	**1.26E-08**	WT & nifD- NoN 14 dpi	STR	Glutathione s-transferase, putative (AHRD V3.3 *** B9R999_RICCO)	GO:0005515
Solyc02g083690.2	-1.32E-01	7.45E-01	-1.28E+00	3.89E-03	**1.42E+00**	**1.58E-03**	**2.57E+00**	**9.77E-07**	WT & nifD- NoN 14 dpi	STR	LOW QUALITY:Senescence/dehydration-associated protein-like protein (AHRD V3.3 *** AT2G17840.1)	
Solyc08g014000.3	-1.22E+00	6.57E-05	-6.99E-01	1.17E-02	**2.77E+00**	**5.29E-11**	**2.54E+00**	**3.15E-10**	WT & nifD- NoN 14 dpi	L	lipoxygenase A	GO:0005515|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc03g058213.1	1.57E+00	5.37E-02	2.09E+00	1.20E-02	**3.06E+00**	**5.34E-04**	**2.52E+00**	**3.22E-03**	WT & nifD- NoN 14 dpi	P	50S ribosomal protein L16, chloroplastic (AHRD V3.3 *** RK16_GUIAB)	GO:0003735|GO:0005840|GO:0006412|GO:0003735|GO:0006412|GO:0019843|GO:0003735
Solyc01g106520.1	-3.05E-02	8.99E-01	-4.84E-01	5.14E-02	**2.51E+00**	**7.17E-11**	**2.50E+00**	**7.64E-11**	WT & nifD- NoN 14 dpi	P	LOW QUALITY:F-box protein SKIP23 (AHRD V3.3 *-* A0A151TCP0_CAJCA)	
Solyc02g070110.1	2.42E-01	7.73E-01	-3.36E-01	6.89E-01	**3.28E+00**	**5.28E-04**	**2.50E+00**	**5.67E-03**	WT & nifD- NoN 14 dpi	E	FAD-binding Berberine family protein (AHRD V3.3 *** A0A061GF79_THECC)	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114
Solyc09g065410.3	-7.52E-01	1.83E-01	8.88E-01	1.19E-01	**1.99E+00**	**1.27E-03**	**2.44E+00**	**1.51E-04**	WT & nifD- NoN 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** B7FGM2_MEDTR)	GO:0006869|GO:0008289
Solyc11g069700.2	6.85E-01	7.29E-03	5.26E-01	3.41E-02	**2.56E+00**	**3.99E-11**	**2.43E+00**	**1.19E-10**	WT & nifD- NoN 14 dpi	P	Elongation factor 1-alpha (AHRD V3.3 *** EF1A_SOLLC)	GO:0003746|GO:0005525|GO:0005737|GO:0006414|GO:0003924|GO:0005525|GO:0003924
Solyc10g079860.2	7.55E-01	9.54E-02	-1.04E+00	2.54E-02	**2.61E+00**	**2.68E-06**	**2.42E+00**	**8.17E-06**	WT & nifD- NoN 14 dpi	CS	LEQB L.esculentum TomQ'b beta(1,3)glucanase	GO:0004553|GO:0005975|GO:0005975|GO:00
Solyc02g078150.3	3.76E-02	9.26E-01	6.05E-02	8.82E-01	**1.28E+00**	**3.93E-03**	**2.41E+00**	**2.77E-06**	WT & nifD- NoN 14 dpi	NA	DUF506 family protein (AHRD V3.3 *** G7IPT8_MEDTR)	
Solyc05g009620.3	-8.70E-01	4.68E-02	-2.03E+00	4.73E-05	**1.83E+00**	**1.74E-04**	**2.39E+00**	**5.01E-06**	WT & nifD- NoN 14 dpi	OX	Protein PLANT CADMIUM RESISTANCE 2 (AHRD V3.3 *** A0A1D1Y359_9ARAE)	
Solyc10g048065.1	1.43E+00	1.56E-02	1.39E+00	1.83E-02	**2.63E+00**	**6.06E-05**	**2.35E+00**	**2.29E-04**	WT & nifD- NoN 14 dpi	TR	Transport membrane protein (AHRD V3.3 *** A0A0C5ARU2_HYONI)	GO:0016021
Solyc07g056100.1	1.09E+00	1.72E-01	9.52E-01	2.31E-01	**2.77E+00**	**1.43E-03**	**2.34E+00**	**5.71E-03**	WT & nifD- NoN 14 dpi	NA	LOW QUALITY:ArgH (DUF639) (AHRD V3.3 --* AT2G21720.2)	
Solyc01g056850.3	8.72E-01	1.80E-03	7.68E-01	5.07E-03	**1.29E+00**	**2.37E-05**	**2.31E+00**	**1.23E-09**	WT & nifD- NoN 14 dpi	DNA	CTP synthase (AHRD V3.3 *** W8SVJ8_TOBAC)	GO:0003883|GO:0006221|GO:0003883|GO:0006241|GO:0003883|GO:0006241
Solyc01g090980.1	-1.35E-01	8.30E-01	7.86E-01	2.19E-01	**2.33E+00**	**9.35E-04**	**2.31E+00**	**1.01E-03**	WT & nifD- NoN 14 dpi	S	LOW QUALITY:cyclic nucleotide-gated channel 6 (AHRD V3.3 --* AT2G23980.9)	
Solyc10g055800.2	1.41E-03	9.96E-01	4.71E-01	1.32E-01	**1.74E+00**	**4.75E-06**	**2.31E+00**	**4.54E-08**	WT & nifD- NoN 14 dpi	D	Chitinase (AHRD V3.3 *** B9VRK7_CAPAN)	GO:0004568|GO:0005975|GO:0004568|GO:0006032|GO:0016998|GO:0004568|GO:0006032
Solyc03g098730.1	-7.20E-01	6.37E-02	-4.52E-01	2.35E-01	**2.19E+00**	**3.40E-06**	**2.30E+00**	**1.57E-06**	WT & nifD- NoN 14 dpi	D	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)	GO:0004866
Solyc01g005500.3	1.32E+00	2.98E-02	1.53E+00	1.32E-02	**2.23E+00**	**6.30E-04**	**2.27E+00**	**5.43E-04**	WT & nifD- NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061EUQ7_THECC),Pfam:PF13561	
Solyc07g049200.3	1.07E+00	1.60E-02	8.04E-01	6.38E-02	**2.47E+00**	**2.93E-06**	**2.21E+00**	**1.47E-05**	WT & nifD- NoN 14 dpi	NA	Coiled-coil domain-containing protein 21, putative isoform 2 (AHRD V3.3 *** A0A061DLJ7_THECC)	
Solyc11g006740.2	-6.30E-01	1.72E-01	-1.49E+00	2.64E-03	**2.72E+00**	**2.13E-06**	**2.17E+00**	**5.09E-05**	WT & nifD- NoN 14 dpi	P	F-box protein PP2 (AHRD V3.3 *** A0A059PC27_CICAR)	GO:0005515
Solyc03g117270.1	1.35E+00	1.65E-02	9.10E-01	9.49E-02	**2.71E+00**	**2.29E-05**	**2.17E+00**	**3.40E-04**	WT & nifD- NoN 14 dpi	P	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *** A0A061F027_THECC)	GO:0005515
Solyc10g086090.2	-6.33E-01	4.05E-02	-1.50E+00	2.47E-05	**1.68E+00**	**5.27E-06**	**2.17E+00**	**8.24E-08**	WT & nifD- NoN 14 dpi	D	Trypsin inhibitor 1 (AHRD V3.3 *** ITR1_NICSY)	GO:0004867|GO:0009611
Solyc03g113810.1	5.01E-01	3.28E-01	4.31E-01	4.00E-01	**1.90E+00**	**8.43E-04**	**2.17E+00**	**2.16E-04**	WT & nifD- NoN 14 dpi	L	LOW QUALITY:CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, putative (AHRD V3.3 *** A0A061FTS5_THECC)	

Solyc06g072880.2	4.57E-01	4.73E-01	1.08E+00	9.83E-02	**2.91E+00**	**9.11E-05**	**2.16E+00**	**1.98E-03**	WT & nifD- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4C908_SOLLC)	GO:0008152|GO:0016758
Solyc03g043880.3	9.50E-01	6.21E-04	2.56E-02	9.17E-01	**1.17E+00**	**5.93E-05**	**2.15E+00**	**3.06E-09**	WT & nifD- NoN 14 dpi	NA	SlBCAT4	GO:0003824|GO:0008152|GO:0004084|GO:0009081|GO:0004084|GO:0009081
Solyc01g106140.1	-1.20E+00	1.55E-02	-4.97E-01	2.92E-01	**2.55E+00**	**8.93E-06**	**2.10E+00**	**1.13E-04**	WT & nifD- NoN 14 dpi	P	LOW QUALITY:F-box protein family-like (AHRD V3.3 *-* Q6ZCS3_ORYSJ)	
Solyc01g106710.1	-1.83E-01	6.14E-01	-7.90E-01	3.63E-02	**2.40E+00**	**4.34E-07**	**2.09E+00**	**3.87E-06**	WT & nifD- NoN 14 dpi	T	Transcription factor, MADS-box (AHRD V3.3 *** A0A103YIH6_CYNCS)	GO:0000165|GO:0000977|GO:0045944|GO:0003677|GO:0046983|GO:0003677|GO:0046983
Solyc07g007240.3	7.97E-01	4.02E-03	-2.21E-01	3.90E-01	**1.34E+00**	**1.49E-05**	**2.09E+00**	**1.05E-08**	WT & nifD- NoN 14 dpi	STR	Metallocarboxypeptidase inhibitor (AHRD V3.3 *** A0A0A0VBW2_SOLTU)	GO:0004866
Solyc01g107190.3	-1.43E+00	1.11E-05	-1.66E+00	1.18E-06	**1.29E+00**	**4.33E-05**	**2.07E+00**	**2.62E-08**	WT & nifD- NoN 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9SGY6_RICCO)	
Solyc04g076880.3	6.01E-01	2.71E-04	1.69E-01	2.47E-01	**1.20E+00**	**7.00E-09**	**2.03E+00**	**1.00E-13**	WT & nifD- NoN 14 dpi	C	phosphoenolpyruvate carboxykinase	GO:0004611|GO:0006094|GO:0017076|GO:0004612|GO:0005524|GO:0006094|GO:0004612
Solyc02g079930.3	2.53E-01	5.98E-01	1.31E+00	1.04E-02	**4.71E+00**	**2.89E-10**	**2.02E+00**	**2.47E-04**	WT & nifD- NoN 14 dpi	STR	phosphosulfolactate synthase	GO:0003824
Solyc07g065590.3	-3.74E-01	2.83E-01	-1.21E+00	1.46E-03	**2.23E+00**	**6.23E-07**	**2.00E+00**	**3.58E-06**	WT & nifD- NoN 14 dpi	E	Nicotinamide-nucleotide adenylyltransferase (AHRD V3.3 *** K4CHN7_SOLLC)	GO:0003824|GO:0009058|GO:0009435|GO:0016779|GO:0009435|GO:0016779
Solyc12g010950.2	1.03E+00	6.66E-02	-8.05E-02	8.82E-01	**3.03E+00**	**6.21E-06**	**1.98E+00**	**1.02E-03**	WT & nifD- NoN 14 dpi	OX	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** A0A072TLD5_MEDTR)	GO:0055114
Solyc06g064445.1	4.47E-01	2.81E-01	-5.18E-01	2.13E-01	**1.30E+00**	**3.60E-03**	**1.97E+00**	**4.96E-05**	WT & nifD- NoN 14 dpi	T	DNA-directed RNA polymerase subunit beta (AHRD V3.3 --* RPOB_PINKO)	
Solyc11g042710.2	1.57E+00	3.47E-02	5.36E-01	4.53E-01	**2.11E+00**	**6.01E-03**	**1.97E+00**	**9.59E-03**	WT & nifD- NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT2G24190.2)	
Solyc04g077220.3	2.41E-03	9.95E-01	-2.18E-01	5.68E-01	**1.38E+00**	**1.12E-03**	**1.94E+00**	**2.31E-05**	WT & nifD- NoN 14 dpi	DNA	Homeobox-leucine zipper protein family (AHRD V3.3 *** AT4G37790.1)	GO:0003677|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565
Solyc02g079140.2	6.92E-01	2.44E-01	1.01E+00	9.39E-02	**1.94E+00**	**2.57E-03**	**1.90E+00**	**2.97E-03**	WT & nifD- NoN 14 dpi	RNA	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (AHRD V3.3 *-* A0A1D1ZDK4_9ARAE)	GO:0005515
Solyc12g005940.2	3.12E-01	8.07E-03	6.49E-01	2.86E-06	**1.36E+00**	**1.97E-12**	**1.90E+00**	**9.50E-16**	WT & nifD- NoN 14 dpi	H	1-aminocyclopropane-1-carboxylate oxidase 1 (AHRD V3.3 *** ACCO1_SOLLC)	GO:0016491|GO:0055114
Solyc02g072210.1	5.94E-01	1.04E-01	-5.03E-01	1.65E-01	**1.22E+00**	**1.85E-03**	**1.86E+00**	**1.62E-05**	WT & nifD- NoN 14 dpi	NA	LOW QUALITY:DUF1685 family protein (AHRD V3.3 *** A0A072V475_MEDTR)	
Solyc12g008670.2	2.47E-01	4.54E-01	6.93E-01	4.23E-02	**1.47E+00**	**1.16E-04**	**1.86E+00**	**5.12E-06**	WT & nifD- NoN 14 dpi	G	blind-like4	GO:0003677
Solyc05g051890.1	-8.59E-01	4.89E-02	-7.35E-01	8.88E-02	**3.00E+00**	**1.23E-07**	**1.84E+00**	**1.61E-04**	WT & nifD- NoN 14 dpi	D	LOW QUALITY:Late embryogenesis abundant hydroxyproline-rich glycoprotein (AHRD V3.3 *** G7K2X8_MEDTR)	
Solyc06g061080.3	1.95E-01	3.96E-01	-3.70E-01	1.14E-01	**1.40E+00**	**1.65E-06**	**1.82E+00**	**1.70E-08**	WT & nifD- NoN 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061GAH7_THECC)	GO:0003677|GO:0006355
Solyc12g049550.2	-5.40E-01	4.14E-02	-3.10E-01	2.29E-01	**1.66E+00**	**5.33E-07**	**1.82E+00**	**1.21E-07**	WT & nifD- NoN 14 dpi	L	GDSL esterase/lipase 5 (AHRD V3.3 *** GLIP5_ARATH)	GO:0016788
Solyc06g048790.1	8.51E-01	1.49E-01	1.04E+00	8.00E-02	**2.13E+00**	**9.72E-04**	**1.80E+00**	**4.15E-03**	WT & nifD- NoN 14 dpi	OX	Plant cadmium resistance 10-like protein (AHRD V3.3 *** A0A0B0N332_GOSAR)	
Solyc08g061560.3	-3.65E-01	2.11E-01	-7.72E-01	1.18E-02	**1.23E+00**	**2.09E-04**	**1.79E+00**	**1.22E-06**	WT & nifD- NoN 14 dpi	S	Receptor protein kinase (AHRD V3.3 *** A0A0U5BM22_RORAQ)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g009280.3	-1.90E-03	9.97E-01	-4.50E-01	4.46E-01	**1.70E+00**	**7.01E-03**	**1.78E+00**	**5.11E-03**	WT & nifD- NoN 14 dpi	D	potyvirus VPg interacting protein (DUF1423) (AHRD V3.3 --* AT3G07780.3)	
Solyc02g092410.3	2.66E-01	1.73E-01	6.94E-02	7.18E-01	**1.29E+00**	**3.51E-07**	**1.77E+00**	**1.06E-09**	WT & nifD- NoN 14 dpi	K	Adenylyl-sulfate kinase (AHRD V3.3 *** K4BD37_SOLLC)	GO:0000103|GO:0004020|GO:0005524
Solyc12g096930.2	9.82E-01	8.53E-02	6.28E-01	2.63E-01	**1.66E+00**	**5.46E-03**	**1.76E+00**	**3.62E-03**	WT & nifD- NoN 14 dpi	OX	Caleosin (AHRD V3.3 *** S8C3C9_9LAMI)	
Solyc06g008620.1	-2.45E-01	4.92E-01	-4.29E-01	2.33E-01	**1.43E+00**	**3.89E-04**	**1.75E+00**	**3.56E-05**	WT & nifD- NoN 14 dpi	P	LOW QUALITY:tolB protein-like protein (AHRD V3.3 *** AT4G01870.2)	
Solyc06g010005.1	-4.14E-01	3.76E-01	-1.01E+00	3.74E-02	**1.46E+00**	**3.80E-03**	**1.75E+00**	**7.93E-04**	WT & nifD- NoN 14 dpi	D	MLO-like protein (AHRD V3.3 *-* K4C428_SOLLC)	GO:0006952|GO:0016021
Solyc06g069100.2	-1.97E+00	4.80E-04	-2.08E+00	2.72E-04	**2.07E+00**	**2.78E-04**	**1.74E+00**	**1.56E-03**	WT & nifD- NoN 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061FUV1_THECC)	GO:0003677|GO:0006355
Solyc07g066390.1	3.88E-01	3.06E-01	-3.30E-02	9.30E-01	**1.70E+00**	**1.11E-04**	**1.74E+00**	**8.21E-05**	WT & nifD- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103Y4I4_CYNCS)	GO:0005515

Solyc04g071890.3	1.48E-01	4.90E-01	5.47E-01	1.55E-02	**1.58E+00**	**6.81E-08**	**1.73E+00**	**1.21E-08**	WT & nifD- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4BTH6_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc03g120900.2	-4.57E-01	1.13E-01	-4.67E-01	1.05E-01	**2.00E+00**	**1.33E-07**	**1.72E+00**	**1.63E-06**	WT & nifD- NoN 14 dpi	G	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G01340.2)	GO:0005515
Solyc08g080585.1	8.06E-01	1.35E-01	-8.13E-01	1.32E-01	**1.90E+00**	**1.23E-03**	**1.69E+00**	**3.29E-03**	WT & nifD- NoN 14 dpi	D	Thaumatin-like protein (AHRD V3.3 *** TLP_ACTDE)	
Solyc09g050050.1	9.83E-01	5.66E-02	1.19E-01	8.12E-01	**1.65E+00**	**2.47E-03**	**1.69E+00**	**2.00E-03**	WT & nifD- NoN 14 dpi	T	LOW QUALITY:DNA-directed RNA polymerase subunit beta (AHRD V3.3 *-* A0A151UEH4_CAJCA)	
Solyc01g091160.4	5.18E-01	1.04E-01	-6.39E-01	4.77E-02	**1.02E+00**	**2.79E-03**	**1.69E+00**	**9.63E-06**	WT & nifD- NoN 14 dpi	N	arginase 1 ARG1	
Solyc09g014910.3	-4.15E-01	3.81E-01	-2.29E-01	6.26E-01	**1.52E+00**	**3.14E-03**	**1.68E+00**	**1.29E-03**	WT & nifD- NoN 14 dpi	D	LURP-one-like protein (AHRD V3.3 *** G7KW21_MEDTR)	
Solyc04g018130.1	-7.50E-01	8.98E-02	-5.54E-01	2.04E-01	**1.29E+00**	**5.57E-03**	**1.68E+00**	**5.57E-04**	WT & nifD- NoN 14 dpi	PMI	Leucine-rich repeat protein kinase family protein (AHRD V3.3 --* AT2G04300.2)	
Solyc05g051920.3	3.07E-01	3.00E-01	7.15E-01	2.09E-02	**1.68E+00**	**4.57E-06**	**1.67E+00**	**5.11E-06**	WT & nifD- NoN 14 dpi	TR	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)	GO:0016021|GO:0055085
Solyc06g064660.3	7.51E-01	4.14E-02	4.84E-01	1.78E-01	**1.73E+00**	**3.91E-05**	**1.64E+00**	**7.99E-05**	WT & nifD- NoN 14 dpi	K	Protein kinase family protein (AHRD V3.3 *** Q9LQ29_ARATH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g071850.1	4.25E-01	1.20E-02	7.04E-01	1.37E-04	**1.59E+00**	**2.03E-10**	**1.62E+00**	**1.34E-10**	WT & nifD- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BHL4_SOLLC)	GO:0008152|GO:0016758
Solyc06g072840.3	-2.04E+00	5.08E-04	-1.93E+00	8.79E-04	**2.50E+00**	**4.66E-05**	**1.59E+00**	**4.54E-03**	WT & nifD- NoN 14 dpi	OX	Hydrogen peroxide induced protein 1 (AHRD V3.3 *** J7F198_CAMSI)	
Solyc12g036480.2	6.70E-01	1.10E-01	-4.85E-01	2.42E-01	**1.99E+00**	**4.44E-05**	**1.59E+00**	**5.70E-04**	WT & nifD- NoN 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061FUV1_THECC)	GO:0003677|GO:0006355
Solyc06g008360.3	5.49E-01	1.30E-01	8.47E-01	2.31E-02	**1.22E+00**	**1.85E-03**	**1.55E+00**	**1.56E-04**	WT & nifD- NoN 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061DNM9_THECC)	GO:0003677|GO:0006355
Solyc05g046180.1	-1.61E+00	6.28E-04	-1.31E+00	3.99E-03	**1.66E+00**	**4.74E-04**	**1.55E+00**	**9.21E-04**	WT & nifD- NoN 14 dpi	E	LOW QUALITY:Alcohol dehydrogenase 2 (AHRD V3.3 --* ADH2_SOLLC)	
Solyc12g009680.2	-4.09E-01	1.95E-01	-7.47E-01	2.21E-02	**1.66E+00**	**1.19E-05**	**1.54E+00**	**3.28E-05**	WT & nifD- NoN 14 dpi	H	ADIPOR-like receptor (AHRD V3.3 *** W9SGZ8_9ROSA)	GO:0016021
Solyc03g083480.3	6.83E-01	1.38E-01	5.01E-01	2.72E-01	**1.29E+00**	**7.68E-03**	**1.53E+00**	**2.07E-03**	WT & nifD- NoN 14 dpi	S	Membrane receptor-like protein 1 (AHRD V3.3 *** B3TJG2_CAPAN)	GO:0030247
Solyc09g092400.2	3.90E-02	9.32E-01	7.12E-01	1.29E-01	**1.66E+00**	**1.12E-03**	**1.52E+00**	**2.52E-03**	WT & nifD- NoN 14 dpi	K	Apyrase (AHRD V3.3 *** APY_SOLTU)	GO:0016787
Solyc10g009260.1	-8.40E-01	8.49E-02	-8.91E-01	6.88E-02	**1.80E+00**	**7.06E-04**	**1.52E+00**	**3.36E-03**	WT & nifD- NoN 14 dpi	D	LOW QUALITY:Cytochrome b5 isoform 1 (AHRD V3.3 -** M8A0M0_TRIUA)	
Solyc06g084330.3	3.85E-02	9.32E-01	-1.47E-01	7.46E-01	**3.35E+00**	**6.93E-08**	**1.52E+00**	**2.34E-03**	WT & nifD- NoN 14 dpi	STR	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 *** AT4G02900.4)	GO:0016020
Solyc07g043170.3	-7.44E-01	3.50E-03	-2.65E-01	2.62E-01	**1.94E+00**	**8.29E-09**	**1.51E+00**	**6.90E-07**	WT & nifD- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CEH7_SOLLC)	GO:0008152|GO:0016758
Solyc03g005320.3	6.46E-01	4.80E-02	2.25E-02	9.43E-01	**1.05E+00**	**2.27E-03**	**1.50E+00**	**5.41E-05**	WT & nifD- NoN 14 dpi	L	3-ketoacyl-CoA synthase (AHRD V3.3 *** M1A6B6_SOLTU)	GO:0003824|GO:0008152|GO:0006633|GO:0016020|GO:0016747|GO:0006633|GO:0016020
Solyc12g008430.2	-2.53E-01	5.68E-01	5.52E-02	9.00E-01	**2.18E+00**	**3.65E-05**	**1.49E+00**	**2.20E-03**	WT & nifD- NoN 14 dpi	C	Malic enzyme (AHRD V3.3 *** M0ZHN3_SOLTU)	GO:0004470|GO:0004471|GO:0006108|GO:0055114|GO:0004471|GO:0051287|GO:0055114|GO:0004471|GO:0051287|GO:0055114
Solyc07g006740.3	8.49E-01	3.02E-04	3.52E-01	9.54E-02	**1.48E+00**	**1.08E-07**	**1.46E+00**	**1.31E-07**	WT & nifD- NoN 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4CBE5_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc07g009290.3	8.47E-01	2.03E-04	8.26E-01	2.67E-04	**1.23E+00**	**1.20E-06**	**1.46E+00**	**6.75E-08**	WT & nifD- NoN 14 dpi	D	defensin-like protein (AHRD V3.3 -** AT1G19610.1)	GO:0006952
Solyc10g009310.3	7.73E-01	1.52E-02	-2.20E-02	9.42E-01	**1.20E+00**	**4.16E-04**	**1.44E+00**	**5.01E-05**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** F4YF83_9APIA)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc01g087007.1	-2.79E-01	4.74E-01	-2.71E-01	4.87E-01	**1.21E+00**	**4.08E-03**	**1.44E+00**	**8.97E-04**	WT & nifD- NoN 14 dpi	RNA	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *-* AT1G63080.3)	
Solyc10g076610.2	7.58E-02	7.20E-01	-9.00E-02	6.71E-01	**1.33E+00**	**1.06E-06**	**1.44E+00**	**2.84E-07**	WT & nifD- NoN 14 dpi	RNA	lysyl-tRNA synthetase	GO:0000166|GO:0004812|GO:0005524|GO:0006418|GO:0000166|GO:0004824|GO:0005524|GO:0005737|GO:0006430|GO:0000166|GO:0004824|GO:0005524|GO:0005737|GO:000643
Solyc10g085850.1	-9.07E-01	6.61E-03	-1.44E+00	7.78E-05	**1.18E+00**	**7.01E-04**	**1.43E+00**	**8.14E-05**	WT & nifD- NoN 14 dpi	PMI	LOW QUALITY:S-locus lectin protein kinase family protein (AHRD V3.3 --* AT1G61360.1)	

Solyc01g109720.3	2.27E-01	1.36E-01	8.49E-02	5.70E-01	**1.09E+00**	**7.94E-08**	**1.42E+00**	**5.20E-10**	WT & nifD- NoN 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G18360.1)	GO:0003824
Solyc12g096820.1	6.44E-02	8.57E-01	7.25E-01	5.16E-02	**2.77E+00**	**3.01E-08**	**1.42E+00**	**4.74E-04**	WT & nifD- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DHF5_SOLLC)	GO:0008152|GO:0016758
Solyc00g042840.1	-2.91E-02	9.29E-01	-6.27E-04	9.98E-01	**1.66E+00**	**2.25E-05**	**1.42E+00**	**1.62E-04**	WT & nifD- NoN 14 dpi	P	LOW QUALITY:F-box family protein (AHRD V3.3 *** B9H429_POPTR)	GO:0005515
Solyc10g009483.1	1.37E+00	1.07E-02	9.16E-01	7.79E-02	**1.69E+00**	**2.32E-03**	**1.42E+00**	**8.73E-03**	WT & nifD- NoN 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 --* AT2G46494.1)	
Solyc01g100100.3	-9.44E-01	3.80E-03	-1.14E+00	7.14E-04	**1.14E+00**	**7.18E-04**	**1.42E+00**	**6.29E-05**	WT & nifD- NoN 14 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061E1W0_THECC)	GO:0005515|GO:0008270
Solyc02g089630.3	7.83E-01	2.24E-02	5.41E-01	1.05E-01	**1.29E+00**	**4.79E-04**	**1.41E+00**	**1.83E-04**	WT & nifD- NoN 14 dpi	AM	Proline dehydrogenase (AHRD V3.3 *** A0A0H4CNX3_BETPL)	GO:0004657|GO:0006562
Solyc11g012290.2	2.39E-01	6.19E-02	2.65E-01	3.98E-02	**1.02E+00**	**8.84E-09**	**1.38E+00**	**1.92E-11**	WT & nifD- NoN 14 dpi	T	Upstream activation factor subunit spp27 (AHRD V3.3 *** W9QUP5_9ROSA)	GO:0003677|GO:0005515|GO:0005515
Solyc08g014010.3	-7.57E-02	8.36E-01	-2.63E-01	4.73E-01	**1.06E+00**	**7.12E-03**	**1.38E+00**	**7.74E-04**	WT & nifD- NoN 14 dpi	NA	Transmembrane protein, putative (AHRD V3.3 *** A0A072VMY8_MEDTR)	
Solyc11g007180.2	-1.85E+00	3.92E-06	-1.77E+00	7.34E-06	**1.48E+00**	**8.11E-05**	**1.38E+00**	**1.89E-04**	WT & nifD- NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2RXW1_GLYSO)	GO:0016788
Solyc11g066700.2	-4.11E-01	3.48E-01	-4.99E-01	2.57E-01	**2.13E+00**	**3.96E-05**	**1.35E+00**	**4.15E-03**	WT & nifD- NoN 14 dpi	L	GDSL esterase/lipase family protein	GO:0006629|GO:0016298|GO:0016788|GO:00
Solyc08g083280.3	6.34E-01	1.18E-06	9.23E-01	1.36E-09	**1.19E+00**	**6.30E-12**	**1.34E+00**	**5.07E-13**	WT & nifD- NoN 14 dpi	2M	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9RYV6_RICCO)	GO:0008270|GO:0016491|GO:0055114|GO:00 55114|GO:0055114
Solyc03g096055.1	-2.52E-01	4.73E-01	3.23E-01	3.60E-01	**1.37E+00**	**5.46E-04**	**1.33E+00**	**6.88E-04**	WT & nifD- NoN 14 dpi	T	DNA-directed RNA polymerase II protein (AHRD V3.3 --* AT1G77890.5)	
Solyc09g090020.3	-3.16E-01	1.03E-01	-1.96E-01	3.05E-01	**1.42E+00**	**4.92E-08**	**1.33E+00**	**1.62E-07**	WT & nifD- NoN 14 dpi	STR	Germin-like protein 1 (AHRD V3.3 *** A8QK89_VITVI)	GO:0030145|GO:0045735|GO:0045735
Solyc09g014350.3	-1.01E+00	3.53E-02	-1.04E+00	2.99E-02	**2.03E+00**	**1.37E-04**	**1.33E+00**	**6.97E-03**	WT & nifD- NoN 14 dpi	CS	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7L6J6_MEDTR)	GO:0008152|GO:0016746
Solyc07g056480.3	-2.63E-01	5.06E-01	-6.16E-02	8.76E-01	**1.44E+00**	**1.06E-03**	**1.33E+00**	**2.16E-03**	WT & nifD- NoN 14 dpi	STR	glutathione S-transferase/peroxidase	GO:0005515
Solyc11g008530.2	4.88E-01	1.61E-01	8.87E-01	1.45E-02	**2.27E+00**	**4.36E-07**	**1.32E+00**	**5.96E-04**	WT & nifD- NoN 14 dpi	RNA	Dicer-like 2d	GO:0004525|GO:0006396|GO:0005515|GO:00
Solyc02g069730.3	-1.14E+00	2.44E-03	-1.14E+00	2.44E-03	**1.69E+00**	**3.57E-05**	**1.29E+00**	**7.43E-04**	WT & nifD- NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4B7V5_SOLLC)	
Solyc04g071590.3	-1.62E+00	5.58E-05	-6.41E-01	6.84E-02	**1.72E+00**	**2.66E-05**	**1.29E+00**	**7.69E-04**	WT & nifD- NoN 14 dpi	STR	Abscisic acid stress ripening 3%2C ASR3	GO:0006950
Solyc10g009290.1	-5.21E-01	8.83E-02	-7.30E-01	1.99E-02	**1.28E+00**	**1.97E-04**	**1.28E+00**	**1.97E-04**	WT & nifD- NoN 14 dpi	T	bHLH transcription factor155	GO:0046983
Solyc08g083080.3	9.02E-01	1.49E-02	-9.21E-02	7.92E-01	**1.10E+00**	**3.86E-03**	**1.28E+00**	**1.05E-03**	WT & nifD- NoN 14 dpi	CS	esterase/lipase/thioesterase family protein (AHRD V3.3 *-* AT3G50790.2)	
Solyc09g056430.3	-4.91E-02	8.70E-01	2.32E-01	4.44E-01	**1.96E+00**	**5.89E-07**	**1.28E+00**	**2.25E-04**	WT & nifD- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9GQP3_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:00 04672|GO:0006468|GO:0004672|GO:0006468
Solyc06g082340.2	2.72E-01	5.25E-01	2.06E-02	9.61E-01	**1.30E+00**	**4.82E-03**	**1.27E+00**	**5.79E-03**	WT & nifD- NoN 14 dpi	P	F-box family protein (AHRD V3.3 *** AT3G06240.1)	GO:0005515
Solyc10g039390.1	-1.01E+00	3.21E-02	-2.21E+00	4.16E-05	**1.40E+00**	**4.43E-03**	**1.26E+00**	**9.06E-03**	WT & nifD- NoN 14 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT1G29000.2)	GO:0030001|GO:0046872
Solyc04g071070.2	-1.42E-01	6.79E-01	8.01E-01	2.62E-02	**1.47E+00**	**1.96E-04**	**1.25E+00**	**1.09E-03**	WT & nifD- NoN 14 dpi	CS	Extensin (AHRD V3.3 *** Q06446_SOLTU)	GO:0005199|GO:0009664
Solyc01g060260.3	2.36E-01	5.38E-01	7.67E-01	5.27E-02	**1.90E+00**	**3.30E-05**	**1.24E+00**	**3.02E-03**	WT & nifD- NoN 14 dpi	D	Glycine-rich protein family (AHRD V3.3 *-* AT5G49350.2)	
Solyc07g017980.1	-1.14E+00	3.99E-03	-6.05E-01	1.04E-01	**1.41E+00**	**5.99E-04**	**1.23E+00**	**2.02E-03**	WT & nifD- NoN 14 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** I3S1U4_MEDTR)	
Solyc08g008610.3	-1.13E+00	3.50E-03	-7.91E-01	3.36E-02	**1.45E+00**	**3.64E-04**	**1.22E+00**	**1.87E-03**	WT & nifD- NoN 14 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061G3V4_THECC)	
Solyc08g007120.3	2.51E-01	1.16E-01	6.88E-01	1.42E-04	**1.30E+00**	**7.18E-09**	**1.22E+00**	**2.43E-08**	WT & nifD- NoN 14 dpi	RNA	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT1G32740.1)	GO:0004842|GO:0005634|GO:0016567|GO:00 31347|GO:0005515|GO:0008270|GO:0005515
Solyc03g007230.3	-8.39E-02	7.93E-01	-4.00E-01	2.18E-01	**2.20E+00**	**2.31E-07**	**1.22E+00**	**7.05E-04**	WT & nifD- NoN 14 dpi	K	Protein phosphatase 2c, putative (AHRD V3.3 *** B9RIK1_RICCO)	GO:0003824|GO:0004722|GO:0006470|GO:00 04722|GO:0006470

Solyc04g074760.3	4.54E-01	5.68E-03	4.11E-01	1.13E-02	**1.24E+00**	**1.08E-08**	**1.21E+00**	**1.67E-08**	WT & nifD- NoN 14 dpi	NA	BEST plant protein match is: (TAIR:plant.1) protein, putative (AHRD V3.3 *** G7J4G3_MEDTR)	
Solyc01g067300.3	7.99E-01	1.95E-06	7.55E-02	5.69E-01	**1.02E+00**	**3.14E-08**	**1.21E+00**	**1.10E-09**	WT & nifD- NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4AWX9_SOLLC)	
Solyc05g056500.1	3.88E-01	1.99E-01	5.14E-01	9.24E-02	**1.60E+00**	**1.12E-05**	**1.21E+00**	**3.53E-04**	WT & nifD- NoN 14 dpi	P	U-box domain-containing protein 25 (AHRD V3.3 *** W9QUC2_9ROSA)	GO:0004842|GO:0016567|GO:0005488|GO:0005488
Solyc04g007810.1	-5.28E-01	1.17E-01	-3.54E-01	2.88E-01	**1.29E+00**	**5.16E-04**	**1.21E+00**	**1.03E-03**	WT & nifD- NoN 14 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** I3S1U4_MEDTR)	
Solyc08g061930.3	-6.28E-01	3.62E-03	-7.18E-01	1.14E-03	**1.20E+00**	**1.94E-06**	**1.20E+00**	**1.79E-06**	WT & nifD- NoN 14 dpi	H	Cytokinin oxidase/dehydrogenase-like (AHRD V3.3 *** I0IUQ5_SOLLC)	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0003824
Solyc11g007200.2	-2.53E-01	1.22E-01	-2.73E-02	8.65E-01	**1.27E+00**	**1.92E-08**	**1.20E+00**	**4.94E-08**	WT & nifD- NoN 14 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G27690.1)	GO:0030001|GO:0046872
Solyc04g078340.3	4.03E-01	1.37E-01	-8.41E-01	3.62E-03	**1.27E+00**	**5.16E-05**	**1.20E+00**	**1.08E-04**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** C5NM78_TOBAC)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc01g094700.3	3.33E-01	1.50E-01	3.04E-01	1.88E-01	**1.54E+00**	**2.88E-07**	**1.20E+00**	**1.46E-05**	WT & nifD- NoN 14 dpi	CS	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7LBQ7_MEDTR)	GO:0008152|GO:0016746
Solyc07g066360.1	-1.36E+00	6.12E-05	-1.03E+00	1.21E-03	**1.28E+00**	**1.27E-04**	**1.20E+00**	**2.69E-04**	WT & nifD- NoN 14 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 -** G7JV71_MEDTR)	
Solyc12g009800.2	-2.16E-01	3.59E-01	2.69E-01	2.55E-01	**1.94E+00**	**7.71E-09**	**1.17E+00**	**2.81E-05**	WT & nifD- NoN 14 dpi	G	Purple acid phosphatase (AHRD V3.3 *** K4DC68_SOLLC)	GO:0003993|GO:0046872|GO:0016787|GO:00
Solyc01g081600.3	-2.74E-01	3.47E-01	-5.18E-01	8.15E-02	**2.34E+00**	**1.21E-08**	**1.16E+00**	**4.12E-04**	WT & nifD- NoN 14 dpi	L	Non-specific lipid-transfer protein (AHRD V3.3 *** K4AY52_SOLLC)	GO:0006869|GO:0008289
Solyc11g005960.1	-1.34E-01	7.26E-01	4.68E-02	9.02E-01	**1.05E+00**	**9.69E-03**	**1.15E+00**	**5.44E-03**	WT & nifD- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103YER7_CYNCS)	GO:0005515|GO:0008270|GO:0008270
Solyc10g084320.2	9.66E-02	7.94E-01	-1.19E-01	7.48E-01	**2.06E+00**	**6.89E-06**	**1.13E+00**	**4.73E-03**	WT & nifD- NoN 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** O82777_SOLLC)	GO:0004252|GO:0006508
Solyc04g078800.3	6.43E-01	3.11E-02	7.50E-01	1.33E-02	**1.60E+00**	**6.11E-06**	**1.13E+00**	**4.60E-04**	WT & nifD- NoN 14 dpi	L	Lipase (AHRD V3.3 *** A0A0B2PU23_GLYSO)	GO:0006629
Solyc06g034340.2	-3.79E-01	2.77E-01	-1.59E-01	6.45E-01	**1.14E+00**	**2.59E-03**	**1.11E+00**	**3.10E-03**	WT & nifD- NoN 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061G781_THECC)	GO:0003677|GO:0006355
Solyc06g076800.3	-7.93E-01	4.08E-02	-9.02E-01	2.15E-02	**1.82E+00**	**4.02E-05**	**1.10E+00**	**6.13E-03**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9SHY9_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc12g009300.3	3.53E-01	2.06E-01	7.26E-01	1.29E-02	**1.21E+00**	**1.43E-04**	**1.09E+00**	**4.60E-04**	WT & nifD- NoN 14 dpi	C	sucrose synthase (SuSy)	GO:0005985|GO:0016157
Solyc03g120330.1	5.49E-01	4.60E-03	1.83E-01	3.10E-01	**1.21E+00**	**2.97E-07**	**1.09E+00**	**1.72E-06**	WT & nifD- NoN 14 dpi	P	F-box/kelch-repeat protein (AHRD V3.3 *** W9S4X9_9ROSA)	GO:0005515
Solyc10g011815.1	6.43E-01	1.01E-02	7.58E-01	3.00E-03	**1.39E+00**	**2.51E-06**	**1.09E+00**	**7.70E-05**	WT & nifD- NoN 14 dpi	L	Desaturase/cytochrome b5 protein (AHRD V3.3 *-* Q9ZTY9_RICCO)	
Solyc09g074640.3	9.60E-01	8.22E-05	9.23E-01	1.31E-04	**2.23E+00**	**4.53E-11**	**1.08E+00**	**1.67E-05**	WT & nifD- NoN 14 dpi	T	Zinc finger transcription factor 54	GO:0046872
Solyc09g007860.3	9.71E-01	1.11E-06	1.38E-01	3.76E-01	**1.04E+00**	**3.73E-07**	**1.06E+00**	**2.43E-07**	WT & nifD- NoN 14 dpi	STR	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT5G04220.2)	GO:0005515|GO:0008289|GO:0008289
Solyc06g005070.2	-7.68E-01	8.48E-04	-2.18E-01	2.93E-01	**1.58E+00**	**3.49E-08**	**1.06E+00**	**2.03E-05**	WT & nifD- NoN 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT1G68570.1)	GO:0005215|GO:0006810|GO:0016020
Solyc07g065340.1	2.34E-02	8.29E-01	-1.16E-01	2.90E-01	**1.10E+00**	**1.27E-10**	**1.05E+00**	**3.34E-10**	WT & nifD- NoN 14 dpi	AM	Serine acetyltransferase (AHRD V3.3 *** Q6STL5_NICPL)	GO:0005737|GO:0006535|GO:0009001|GO:0016740|GO:0016740
Solyc02g090210.3	-1.09E+00	2.19E-03	-1.12E+00	1.75E-03	**1.62E+00**	**2.98E-05**	**1.04E+00**	**3.24E-03**	WT & nifD- NoN 14 dpi	L	GDSL esterase/lipase family (AHRD V3.3 *** A0A151RJ07_CAJCA)	GO:0016788
Solyc02g084900.2	-1.89E-01	2.18E-01	-2.22E-01	1.49E-01	**1.39E+00**	**1.02E-09**	**1.03E+00**	**2.56E-07**	WT & nifD- NoN 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT2G18193.1)	GO:0005524
Solyc03g118970.3	-1.00E-01	6.68E-01	-2.04E-01	3.86E-01	**2.35E+00**	**1.64E-10**	**1.03E+00**	**1.44E-04**	WT & nifD- NoN 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4BM46_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc10g047643.1	8.93E-01	4.45E-03	5.36E-01	7.27E-02	**1.19E+00**	**3.05E-04**	**1.02E+00**	**1.41E-03**	WT & nifD- NoN 14 dpi	CS	CHCH-like protein (AHRD V3.3 *** A0A103XM78_CYNCS)	
Solyc10g084400.2	3.49E-01	1.36E-01	9.96E-02	6.65E-01	**1.55E+00**	**3.07E-07**	**1.02E+00**	**1.33E-04**	WT & nifD- NoN 14 dpi	STR	Glutathione S-transferase family protein (AHRD V3.3 *** AT5G02790.1)	GO:0005515
Solyc08g083090.2	5.30E-01	1.11E-01	4.12E-01	2.11E-01	**1.50E+00**	**8.44E-05**	**1.01E+00**	**4.13E-03**	WT & nifD- NoN 14 dpi	NA	DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G24130.1)	

Solyc04g057940.3	1.19E-02	9.54E-01	1.94E-01	3.53E-01	**-1.02E+00**	**3.83E-05**	**-1.01E+00**	**4.21E-05**	WT & nifD- NoN 14 dpi	G	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** A0A061EZ85_THECC)	GO:0004842|GO:0016567|GO:0005488|GO:0005488
Solyc08g005240.2	4.71E-02	8.66E-01	8.17E-01	6.56E-03	**-1.02E+00**	**1.07E-03**	**-1.01E+00**	**1.13E-03**	WT & nifD- NoN 14 dpi	DNA	Lysine-specific demethylase (AHRD V3.3 *** A0A199VZ18_ANACO)	
Solyc11g008630.2	6.17E-01	4.13E-02	1.30E+00	1.15E-04	**-1.47E+00**	**2.63E-05**	**-1.02E+00**	**1.56E-03**	WT & nifD- NoN 14 dpi	S	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT1G65450.1)	GO:0016747
Solyc10g085950.2	1.24E+00	2.49E-08	1.83E+00	9.86E-12	**-1.72E+00**	**3.62E-11**	**-1.03E+00**	**7.08E-07**	WT & nifD- NoN 14 dpi	S	aluminum sensitive 3 (AHRD V3.3 *** AT2G37330.1)	
Solyc02g079920.3	7.16E-01	2.47E-02	3.79E-01	2.18E-01	**-1.78E+00**	**3.17E-06**	**-1.03E+00**	**2.09E-03**	WT & nifD- NoN 14 dpi	DNA	C2H2-like zinc finger protein (AHRD V3.3 *** G7JF39_MEDTR)	GO:0003950|GO:0046872|GO:0046872
Solyc01g100120.3	-9.71E-01	2.86E-03	-3.16E-01	2.93E-01	**-1.47E+00**	**3.55E-05**	**-1.04E+00**	**1.65E-03**	WT & nifD- NoN 14 dpi	TR	Kinesin-like protein (AHRD V3.3 *** B9I798_POPTR)	GO:0003777|GO:0005524|GO:0007018|GO:0003777|GO:0005524|GO:0007018|GO:0008017|GO:0003777|GO:0005524|GO:0007018|GO:0
Solyc07g047740.3	8.58E-01	1.58E-03	1.45E+00	2.80E-06	**-2.15E+00**	**2.82E-09**	**-1.04E+00**	**2.36E-04**	WT & nifD- NoN 14 dpi	OX	TOMTPX2A peroxidase	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc07g009080.3	6.60E-01	9.68E-04	5.17E-01	7.18E-03	**-1.83E+00**	**1.28E-10**	**-1.04E+00**	**3.57E-06**	WT & nifD- NoN 14 dpi	2M	AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT1G21530.1)	
Solyc09g082560.3	-5.47E-01	8.25E-02	5.81E-03	9.85E-01	**-2.03E+00**	**4.53E-07**	**-1.04E+00**	**2.00E-03**	WT & nifD- NoN 14 dpi	G	SUN-like protein 26	GO:0005515
Solyc01g102340.3	-1.45E-01	6.65E-01	7.34E-01	3.60E-02	**-2.31E+00**	**2.30E-07**	**-1.04E+00**	**4.22E-03**	WT & nifD- NoN 14 dpi	G	R2R3MYB transcription factor 61	GO:0003677
Solyc08g078930.1	2.05E-01	2.34E-01	1.10E+00	6.63E-07	**-1.22E+00**	**1.11E-07**	**-1.05E+00**	**1.48E-06**	WT & nifD- NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12520.1)	
Solyc10g079110.2	-3.09E-01	2.60E-01	-1.55E-01	5.68E-01	**-1.04E+00**	**6.51E-04**	**-1.05E+00**	**5.85E-04**	WT & nifD- NoN 14 dpi	L	1-acyl-sn-glycerol-3-phosphate acyltransferase (AHRD V3.3 *** Q2Z1Y8_PRUMU)	GO:0008152|GO:0016746
Solyc06g054290.2	-6.26E-01	1.01E-01	1.11E+00	5.83E-03	**-1.41E+00**	**7.07E-04**	**-1.05E+00**	**8.10E-03**	WT & nifD- NoN 14 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EKQ6_THECC)	GO:0008152|GO:0016787
Solyc05g046020.3	-2.23E-01	5.38E-01	8.79E-01	2.07E-02	**-2.43E+00**	**3.24E-07**	**-1.06E+00**	**6.46E-03**	WT & nifD- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4C0T5_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc02g031750.3	-1.56E-01	6.78E-01	-5.24E-01	1.71E-01	**-2.09E+00**	**7.18E-06**	**-1.06E+00**	**8.53E-03**	WT & nifD- NoN 14 dpi	D	Phloem protein 2-like protein (AHRD V3.3 *** A0A103Y5W1_CYNCS)	
Solyc04g007090.1	-2.17E-01	5.13E-01	3.00E-01	3.69E-01	**-1.68E+00**	**2.50E-05**	**-1.06E+00**	**3.32E-03**	WT & nifD- NoN 14 dpi	D	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT1G69550.1)	
Solyc05g007790.3	7.16E-01	9.82E-03	1.63E+00	1.07E-06	**-2.29E+00**	**2.39E-09**	**-1.06E+00**	**3.37E-04**	WT & nifD- NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4BWV4_SOLLC)	
Solyc09g010200.3	5.83E-01	4.98E-02	1.56E+00	8.85E-06	**-1.93E+00**	**3.16E-07**	**-1.06E+00**	**8.79E-04**	WT & nifD- NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4CR48_SOLLC)	
Solyc08g075760.3	7.94E-01	3.50E-06	4.03E-01	6.13E-03	**-1.04E+00**	**3.53E-08**	**-1.08E+00**	**1.94E-08**	WT & nifD- NoN 14 dpi	PMI	CYCLOPS/IPD3-like protein	
Solyc01g079370.3	-2.11E-01	4.40E-01	5.37E-02	8.44E-01	**-1.19E+00**	**1.60E-04**	**-1.09E+00**	**4.28E-04**	WT & nifD- NoN 14 dpi	T	GRAS family transcription factor, putative (AHRD V3.3 *** A0A061EWU1_THECC)	
Solyc03g007580.2	-9.68E-01	1.55E-08	-7.02E-01	3.61E-06	**-1.32E+00**	**3.06E-11**	**-1.09E+00**	**1.55E-09**	WT & nifD- NoN 14 dpi	NA	DUF21 domain-containing protein (AHRD V3.3 *-* A0A199V808_ANACO)	
Solyc03g034410.1	-3.07E-01	3.84E-01	7.57E-01	3.80E-02	**-1.93E+00**	**7.62E-06**	**-1.09E+00**	**4.06E-03**	WT & nifD- NoN 14 dpi	NA	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7IAV0_MEDTR)	
Solyc06g007370.1	7.02E-02	8.44E-01	7.81E-01	3.59E-02	**-1.78E+00**	**3.10E-05**	**-1.09E+00**	**4.69E-03**	WT & nifD- NoN 14 dpi	2M	LOW QUALITY:6,7-dimethyl-8-ribityllumazine synthase (AHRD V3.3 *** AT2G30230.1)	
Solyc06g062580.3	-7.19E-01	4.92E-02	6.90E-02	8.44E-01	**-1.05E+00**	**5.72E-03**	**-1.10E+00**	**4.10E-03**	WT & nifD- NoN 14 dpi	C	Beta-galactosidase (AHRD V3.3 *** BGAL_SOLLC)	GO:0004553|GO:0005975|GO:0005975|GO:00
Solyc07g008980.3	2.03E+00	8.26E-09	1.67E+00	2.87E-07	**-3.43E+00**	**1.34E-13**	**-1.10E+00**	**1.18E-04**	WT & nifD- NoN 14 dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952
Solyc05g005580.3	4.14E-01	1.15E-01	9.23E-01	1.21E-03	**-1.44E+00**	**5.99E-06**	**-1.11E+00**	**1.82E-04**	WT & nifD- NoN 14 dpi	NA	DUF936 family protein (AHRD V3.3 *** G7K1E3_MEDTR)	
Solyc02g032030.1	-2.69E-03	9.86E-01	1.05E+00	2.12E-07	**-1.34E+00**	**2.39E-09**	**-1.12E+00**	**6.52E-08**	WT & nifD- NoN 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4B5E9_SOLLC)	
Solyc04g014470.3	-7.71E-01	7.21E-04	9.03E-01	1.30E-04	**-1.16E+00**	**4.42E-06**	**-1.12E+00**	**7.60E-06**	WT & nifD- NoN 14 dpi	G	R2R3MYB transcription factor 20	GO:0003677

Solyc10g049280.2	-9.83E-01	7.93E-09	-3.96E-01	2.32E-03	**-1.43E+00**	**3.28E-12**	**-1.12E+00**	**5.82E-10**	WT & nifD- NoN 14 dpi	TR	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7LFG1_MEDTR)	GO:0005215|GO:0006810|GO:0016020|GO:0055085
Solyc09g013150.3	-5.55E-01	5.80E-03	4.08E-01	3.60E-02	**-1.03E+00**	**8.05E-06**	**-1.12E+00**	**2.09E-06**	WT & nifD- NoN 14 dpi	TR	Phosphate transporter (AHRD V3.3 *** A0A0B5WYW1_MANES)	GO:0016021|GO:0055085
Solyc03g114940.3	3.01E-02	9.24E-01	1.75E-01	5.80E-01	**-1.79E+00**	**5.55E-06**	**-1.13E+00**	**1.29E-03**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103Y3J6_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc08g081780.1	1.27E+00	1.86E-03	2.33E+00	9.77E-07	**-2.96E+00**	**1.55E-08**	**-1.14E+00**	**4.29E-03**	WT & nifD- NoN 14 dpi	CS	Dirigent protein	
Solyc02g088240.3	-9.87E-01	1.08E-08	-4.73E-01	5.40E-04	**-1.04E+00**	**4.15E-09**	**-1.15E+00**	**5.88E-10**	WT & nifD- NoN 14 dpi	STR	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A0B0MVV1_GOSAR)	GO:0016021
Solyc01g009760.3	3.01E-01	1.03E-01	7.29E-01	3.66E-04	**-1.05E+00**	**3.09E-06**	**-1.15E+00**	**8.08E-07**	WT & nifD- NoN 14 dpi	H	GRAM domain protein/ABA-responsive-like protein (AHRD V3.3 *** G7KW78_MEDTR)	
Solyc06g062600.3	8.56E-01	5.99E-03	6.19E-01	3.98E-02	**-1.60E+00**	**7.31E-06**	**-1.15E+00**	**4.35E-04**	WT & nifD- NoN 14 dpi	NA	Glucose-methanol-choline (GMC) oxidoreductase family protein (AHRD V3.3 *** AT1G72970.1)	GO:0016491|GO:0055114|GO:0016614|GO:0050660|GO:0055114|GO:0016614|GO:0050660
Solyc05g013650.2	-1.09E-02	9.78E-01	-8.83E-01	3.11E-02	**-1.88E+00**	**5.01E-05**	**-1.16E+00**	**6.05E-03**	WT & nifD- NoN 14 dpi	AM	LOW QUALITY:lysine ketoglutarate reductase trans-splicing protein (DUF707) (AHRD V3.3 *** AT1G67850.7)	
Solyc01g006780.3	-4.83E-01	6.29E-02	2.96E-01	2.44E-01	**-1.53E+00**	**1.80E-06**	**-1.16E+00**	**8.34E-05**	WT & nifD- NoN 14 dpi	N	LOW QUALITY:Nitrate reductase [NADH] 1 (AHRD V3.3 --* NIA1_PHAVU)	
Solyc02g069690.1	-2.11E-02	9.07E-01	5.59E-01	4.13E-03	**-1.01E+00**	**5.84E-06**	**-1.17E+00**	**5.97E-07**	WT & nifD- NoN 14 dpi	E	FAD-binding Berberine family protein (AHRD V3.3 *** AT5G44400.1)	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114
Solyc06g053830.3	2.20E-01	5.41E-01	6.19E-01	9.36E-02	**-1.84E+00**	**2.14E-05**	**-1.17E+00**	**2.90E-03**	WT & nifD- NoN 14 dpi	H	auxin-regulated IAA7	GO:0005515|GO:0005634|GO:0006355|GO:0005634|GO:0006355
Solyc10g076480.2	-1.36E-01	4.55E-01	4.33E-01	2.29E-02	**-1.25E+00**	**2.14E-07**	**-1.17E+00**	**6.52E-07**	WT & nifD- NoN 14 dpi	N	Ammonium transporter (AHRD V3.3 *** K4D1Z0_SOLLC)	GO:0008519|GO:0015696|GO:0016020|GO:0008519|GO:0016020|GO:0072488|GO:0008519
Solyc02g067410.2	4.37E-02	9.02E-01	1.48E-01	6.79E-01	**-2.02E+00**	**5.18E-06**	**-1.18E+00**	**2.54E-03**	WT & nifD- NoN 14 dpi	DNA	Homeobox associated leucine zipper protein (AHRD V3.3 *** A0A072U5Q1_MEDTR)	GO:0003677|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565
Solyc05g005870.3	9.51E-01	1.60E-05	9.22E-01	2.45E-05	**-1.09E+00**	**2.07E-06**	**-1.18E+00**	**5.71E-07**	WT & nifD- NoN 14 dpi	TR	nodulin-related MtN21 family protein	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc02g071640.2	-3.42E-01	3.82E-01	-2.65E-01	4.98E-01	**-1.86E+00**	**5.33E-05**	**-1.19E+00**	**4.82E-03**	WT & nifD- NoN 14 dpi	L	Lipase, GDSL (AHRD V3.3 *-* A0A103XTV4_CYNCS)	
Solyc05g006670.1	3.61E-01	2.92E-01	-1.62E-01	6.33E-01	**-1.54E+00**	**1.03E-04**	**-1.20E+00**	**1.45E-03**	WT & nifD- NoN 14 dpi	PMI	LOW QUALITY:Leucine-rich repeat receptor protein kinase family protein (AHRD V3.3 *** A0A061E5L2_THECC)	GO:0005515
Solyc01g109320.3	-5.08E-01	2.12E-01	3.17E-01	4.32E-01	**-3.01E+00**	**5.29E-08**	**-1.20E+00**	**5.72E-03**	WT & nifD- NoN 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4B3E5_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc01g005320.2	-3.79E-01	3.71E-01	1.60E-02	9.70E-01	**-1.86E+00**	**1.38E-04**	**-1.20E+00**	**7.76E-03**	WT & nifD- NoN 14 dpi	L	3-oxo-5-alpha-steroid 4-dehydrogenase (AHRD V3.3 *** G7ZZ33_MEDTR)	GO:0005737|GO:0006629|GO:0016021|GO:0016627
Solyc01g108745.1	2.14E+00	3.12E-05	2.63E+00	1.49E-06	**-2.25E+00**	**1.55E-05**	**-1.22E+00**	**7.89E-03**	WT & nifD- NoN 14 dpi	2M	Polyneuridine-aldehyde esterase-like protein (AHRD V3.3 *** A0A075F1V8_TOBAC)	
Solyc11g006890.2	-5.17E-01	6.99E-02	-6.00E-01	3.73E-02	**-1.09E+00**	**4.94E-04**	**-1.22E+00**	**1.40E-04**	WT & nifD- NoN 14 dpi	G	sterol 4-alpha-methyl-oxidase 2-2 (AHRD V3.3 --* AT2G29390.3)	
Solyc01g091530.3	-7.72E-01	9.68E-03	-4.31E-02	8.77E-01	**-1.23E+00**	**1.40E-04**	**-1.24E+00**	**1.39E-04**	WT & nifD- NoN 14 dpi	PMI	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** E3WHD6_9ROSI)	
Solyc03g034057.1	5.17E-01	4.90E-03	1.01E+00	2.48E-06	**-1.91E+00**	**1.57E-11**	**-1.24E+00**	**8.37E-08**	WT & nifD- NoN 14 dpi	D	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT4G08450.2)	
Solyc03g114750.3	3.86E-01	2.96E-03	1.09E+00	1.15E-09	**-1.67E+00**	**1.19E-13**	**-1.24E+00**	**8.04E-11**	WT & nifD- NoN 14 dpi	CS	18S pre-ribosomal assembly protein gar2-like protein (AHRD V3.3 *-* AT2G03810.7)	
Solyc11g072560.2	1.50E+00	5.05E-05	2.24E+00	1.06E-07	**-2.08E+00**	**3.88E-07**	**-1.25E+00**	**4.17E-04**	WT & nifD- NoN 14 dpi	TR	Major Facilitator Superfamily protein (AHRD V3.3 *** Q6L3J2_SOLDE)	GO:0005215|GO:0006810|GO:0016020|GO:0005215|GO:0006857|GO:0016020|GO:0005215
Solyc12g006970.1	-9.09E-01	2.37E-02	-1.57E-01	6.82E-01	**-1.12E+00**	**6.57E-03**	**-1.25E+00**	**2.72E-03**	WT & nifD- NoN 14 dpi	P	50S ribosomal protein L22, chloroplastic (AHRD V3.3 --* RK22_OENPA)	
Solyc01g091670.3	-5.74E-03	9.89E-01	8.23E-01	4.76E-02	**-1.67E+00**	**2.64E-04**	**-1.25E+00**	**3.90E-03**	WT & nifD- NoN 14 dpi	NA	Progesterone 5-beta-reductase (AHRD V3.3 *** D6N9X0_NEROL)	
Solyc12g036390.2	8.99E-02	8.42E-01	5.80E-01	2.05E-01	**-1.31E+00**	**7.10E-03**	**-1.26E+00**	**9.09E-03**	WT & nifD- NoN 14 dpi	DNA	Calmodulin binding protein-like, putative (AHRD V3.3 *** A0A061G202_THECC)	GO:0005516|GO:0006950
Solyc12g088140.2	2.68E+00	3.79E-08	2.87E+00	1.10E-08	**-1.13E+00**	**3.27E-03**	**-1.26E+00**	**1.26E-03**	WT & nifD- NoN 14 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)	

Solyc09g011960.2	-8.52E-01	3.96E-02	-2.50E-01	5.30E-01	**-1.41E+00**	**1.34E-03**	**-1.27E+00**	**3.44E-03**	WT & nifD- NoN 14 dpi	PMI	Laccase (AHRD V3.3 *** A0A067L6R3_JATCU)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc10g084280.2	-5.59E-01	1.18E-04	4.35E-02	7.27E-01	**-1.14E+00**	**1.15E-09**	**-1.28E+00**	**1.07E-10**	WT & nifD- NoN 14 dpi	G	SUN-like protein 29	GO:0005515
Solyc04g012090.2	1.27E+00	1.21E-03	1.36E+00	6.30E-04	**-3.02E+00**	**4.57E-09**	**-1.29E+00**	**1.05E-03**	WT & nifD- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BPR1_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g078660.1	3.68E-01	2.63E-03	1.10E+00	2.60E-10	**-1.45E+00**	**6.47E-13**	**-1.29E+00**	**8.46E-12**	WT & nifD- NoN 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT5G42830.1)	GO:0016747
Solyc08g079650.3	-9.45E-01	1.19E-07	-9.17E-01	2.01E-07	**-1.07E+00**	**1.28E-08**	**-1.30E+00**	**2.81E-10**	WT & nifD- NoN 14 dpi	CS	ACT domain-containing family protein (AHRD V3.3 *** B9N3K8_POPTR)	GO:0008152|GO:0016597
Solyc12g015690.2	9.09E-01	6.35E-03	6.00E-01	6.05E-02	**-1.17E+00**	**7.31E-04**	**-1.30E+00**	**2.42E-04**	WT & nifD- NoN 14 dpi	PMI	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7K0M1_MEDTR)	
Solyc03g083840.3	-3.97E-01	2.95E-01	-7.49E-02	8.42E-01	**-1.28E+00**	**1.92E-03**	**-1.31E+00**	**1.64E-03**	WT & nifD- NoN 14 dpi	CS	Pectinesterase (AHRD V3.3 *** K4BIF9_SOLLC)	GO:0004857|GO:0005618|GO:0030599|GO:0042545|GO:0005618|GO:0030599|GO:0042545
Solyc08g081890.3	5.02E-01	4.89E-02	5.87E-01	2.31E-02	**-1.28E+00**	**1.79E-05**	**-1.31E+00**	**1.24E-05**	WT & nifD- NoN 14 dpi	TR	ABC transporter family protein (AHRD V3.3 *** U5FPJ5_POPTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO:0016887
Solyc04g055000.3	-1.60E-01	4.45E-01	3.76E-01	8.05E-02	**-1.10E+00**	**1.49E-05**	**-1.32E+00**	**9.72E-07**	WT & nifD- NoN 14 dpi	H	tetratricopeptide repeat (TPR)-containing protein (AHRD V3.3 *** AT5G65160.1)	GO:0005515
Solyc10g039290.2	-3.72E-01	9.81E-02	6.98E-01	3.47E-03	**-1.29E+00**	**2.95E-06**	**-1.32E+00**	**1.97E-06**	WT & nifD- NoN 14 dpi	N	Nitrate transporter protein 1.2-like protein (AHRD V3.3 *** A0A0H3WEV3_CAMSI)	GO:0005215|GO:0006810|GO:0016020
Solyc05g018730.3	3.60E-01	3.47E-01	-6.39E-03	9.87E-01	**-1.26E+00**	**2.54E-03**	**-1.33E+00**	**1.60E-03**	WT & nifD- NoN 14 dpi	TR	calcium uniporter-like protein (DUF607) (AHRD V3.3 --* AT1G09575.2)	
Solyc01g105225.1	-8.74E-01	7.06E-02	-6.81E-01	1.54E-01	**-1.42E+00**	**5.12E-03**	**-1.33E+00**	**8.12E-03**	WT & nifD- NoN 14 dpi	DNA	Protein DA1-related 1 (AHRD V3.3 *** DAR1_ARATH)	
Solyc06g071700.1	-6.14E-01	1.82E-02	-5.95E-01	2.17E-02	**-1.69E+00**	**2.30E-07**	**-1.33E+00**	**1.03E-05**	WT & nifD- NoN 14 dpi	AM	LOW QUALITY:Amine oxidase (AHRD V3.3 *** K4C8P2_SOLLC)	GO:0005507|GO:0008131|GO:0009308|GO:0048038|GO:0055114
Solyc01g005630.2	3.50E-01	4.12E-01	8.29E-01	5.87E-02	**-2.29E+00**	**1.03E-05**	**-1.34E+00**	**3.65E-03**	WT & nifD- NoN 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *** W9SBA4_9ROSA)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc12g009650.2	-1.88E-01	5.28E-01	6.51E-01	3.55E-02	**-1.70E+00**	**4.25E-06**	**-1.36E+00**	**8.91E-05**	WT & nifD- NoN 14 dpi	PMI	Sl proline-rich protein	
Solyc08g075320.3	9.19E-01	4.27E-05	1.01E+00	1.19E-05	**-1.49E+00**	**2.07E-08**	**-1.36E+00**	**9.97E-08**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 family ABA 8'-hydroxylase (AHRD V3.3 *** G7L7U3_MEDTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc01g100890.3	-1.13E-01	8.15E-01	7.50E-01	1.29E-01	**-1.90E+00**	**5.11E-04**	**-1.37E+00**	**8.18E-03**	WT & nifD- NoN 14 dpi	H	WAT1-related protein (AHRD V3.3 *-* K4B1C0_SOLLC)	GO:0016021|GO:0022857
Solyc02g067190.3	4.05E-01	3.01E-01	1.16E+00	5.72E-03	**-2.28E+00**	**2.96E-06**	**-1.37E+00**	**1.41E-03**	WT & nifD- NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4B751_SOLLC)	
Solyc01g112140.3	-9.27E-01	3.33E-07	-3.85E-01	8.99E-03	**-1.00E+00**	**8.37E-08**	**-1.38E+00**	**1.75E-10**	WT & nifD- NoN 14 dpi	OX	Flavin-containing monooxygenase (AHRD V3.3 *** M1B691_SOLTU)	GO:0004499|GO:0050660|GO:0050661|GO:0055114|GO:0016491|GO:0055114|GO:0016491
Solyc04g076690.3	1.43E+00	8.72E-04	7.32E-01	6.44E-02	**-1.13E+00**	**6.24E-03**	**-1.39E+00**	**1.13E-03**	WT & nifD- NoN 14 dpi	NA	Protein with RNI-like/FBD-like domain (AHRD V3.3 --* AT3G26930.1)	
Solyc03g031800.3	-6.74E-01	3.34E-03	-4.45E-01	4.26E-02	**-1.04E+00**	**3.52E-05**	**-1.41E+00**	**3.67E-07**	WT & nifD- NoN 14 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4BFF2_SOLLC)	GO:0004553|GO:0005975|GO:0005618|GO:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc11g005710.2	4.62E-01	8.98E-02	3.96E-01	1.43E-01	**-1.26E+00**	**5.67E-05**	**-1.42E+00**	**1.12E-05**	WT & nifD- NoN 14 dpi	H	Transducin/WD-like repeat-protein (AHRD V3.3 *** A0A0C3Y5Y4_MEDTR)	GO:0005515
Solyc02g082120.3	-3.30E-01	2.00E-01	7.97E-01	3.88E-03	**-1.46E+00**	**4.28E-06**	**-1.44E+00**	**5.21E-06**	WT & nifD- NoN 14 dpi	DNA	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9SVU2_RICCO)	GO:0003824|GO:0006281|GO:0006284|GO:0008725|GO:0006284|GO:0008725
Solyc05g014000.3	-5.02E-03	9.90E-01	-1.98E-01	6.12E-01	**-1.27E+00**	**2.90E-03**	**-1.44E+00**	**9.51E-04**	WT & nifD- NoN 14 dpi	CS	Pectate lyase (AHRD V3.3 *** M1AQF5_SOLTU)	
Solyc11g010630.3	-4.79E-01	8.15E-02	2.10E-01	4.34E-01	**-1.01E+00**	**7.81E-04**	**-1.45E+00**	**9.60E-06**	WT & nifD- NoN 14 dpi	K	Kinase interacting (KIP1-like) family protein (AHRD V3.3 *** AT2G22560.1)	GO:0003779
Solyc06g074910.3	1.02E-01	7.08E-01	7.98E-01	6.63E-03	**-2.30E+00**	**6.13E-09**	**-1.46E+00**	**1.15E-05**	WT & nifD- NoN 14 dpi	G	potato leaf	GO:0003677
Solyc01g066560.3	3.71E-01	2.17E-01	5.64E-01	6.57E-02	**-1.20E+00**	**3.84E-04**	**-1.47E+00**	**3.49E-05**	WT & nifD- NoN 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4AWQ7_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc10g075175.1	-5.89E-01	1.90E-01	9.51E-01	3.91E-02	**-2.07E+00**	**6.90E-05**	**-1.49E+00**	**2.12E-03**	WT & nifD- NoN 14 dpi	AM	Aspartate aminotransferase (AHRD V3.3 *** B9HDA1_POPTR)	GO:0003824|GO:0006520|GO:0008483|GO:0006520|GO:0008483

Solyc01g067370.3	-1.77E-02	9.58E-01	5.09E-01	1.35E-01	**-1.72E+00**	**2.01E-05**	**-1.50E+00**	**1.09E-04**	WT & nifD- NoN 14 dpi	NA	TSB	
Solyc03g120650.3	-1.18E+00	3.22E-02	-7.20E-01	1.78E-01	**-1.93E+00**	**9.94E-04**	**-1.51E+00**	**7.50E-03**	WT & nifD- NoN 14 dpi	C	GDP-mannose pyrophosphorylase	GO:0005089
Solyc02g083980.3	6.78E-01	7.09E-02	5.72E-01	1.24E-01	**-2.65E+00**	**8.92E-08**	**-1.51E+00**	**2.77E-04**	WT & nifD- NoN 14 dpi	CS	Endoglucanase (AHRD V3.3 *** K4BAR6_SOLLC)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc07g009090.3	7.79E-01	2.57E-02	1.03E+00	4.22E-03	**-1.39E+00**	**2.65E-04**	**-1.53E+00**	**8.96E-05**	WT & nifD- NoN 14 dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952
Solyc02g090540.3	1.79E-01	6.63E-01	1.07E+00	1.36E-02	**-3.24E+00**	**1.93E-08**	**-1.54E+00**	**7.94E-04**	WT & nifD- NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061DHS1_THECC)	
Solyc08g066660.1	6.00E-01	4.51E-03	1.26E+00	6.38E-07	**-1.45E+00**	**6.00E-08**	**-1.56E+00**	**1.56E-08**	WT & nifD- NoN 14 dpi	H	Ethylene-responsive transcription factor TINY (AHRD V3.3 *** TINY_ARATH)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc03g063040.3	-9.49E-01	1.67E-03	-9.79E-01	1.26E-03	**-1.23E+00**	**1.10E-04**	**-1.57E+00**	**4.20E-06**	WT & nifD- NoN 14 dpi	AM	Amino acid transporter family protein (AHRD V3.3 *-* B9HLH9_POPTR)	
Solyc01g094610.3	-5.95E-01	1.77E-01	-5.20E-01	2.36E-01	**-1.48E+00**	**1.92E-03**	**-1.58E+00**	**1.08E-03**	WT & nifD- NoN 14 dpi	DNA	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9RDS3_RICCO)	GO:0005089
Solyc10g008030.3	-1.36E-01	8.11E-01	1.06E+00	7.07E-02	**-2.26E+00**	**4.51E-04**	**-1.62E+00**	**8.00E-03**	WT & nifD- NoN 14 dpi	CS	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)	
Solyc01g110590.3	-1.04E+00	3.84E-02	-6.56E-01	1.80E-01	**-2.84E+00**	**2.85E-06**	**-1.62E+00**	**2.18E-03**	WT & nifD- NoN 14 dpi	H	Small auxin up-regulated RNA6	GO:0009733
Solyc04g074310.3	-1.15E+00	4.20E-02	-6.12E-01	2.64E-01	**-2.57E+00**	**5.93E-05**	**-1.63E+00**	**5.38E-03**	WT & nifD- NoN 14 dpi	RNA	RNA-binding family protein, putative (AHRD V3.3 *-* A0A061G9K2_THECC)	GO:0000166|GO:0003676|GO:0003676
Solyc06g051680.1	-1.68E-01	7.35E-01	-2.35E-01	6.37E-01	**-1.94E+00**	**5.46E-04**	**-1.65E+00**	**2.47E-03**	WT & nifD- NoN 14 dpi	G	Protein EARLY FLOWERING 4 (AHRD V3.3 *-* A0A0B2RPG0_GLYSO)	
Solyc02g065190.3	7.47E-01	5.64E-02	-3.46E-02	9.27E-01	**-2.40E+00**	**8.91E-07**	**-1.65E+00**	**1.58E-04**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc12g100220.2	-8.74E-01	7.18E-02	-3.34E-01	4.80E-01	**-1.88E+00**	**4.20E-04**	**-1.69E+00**	**1.22E-03**	WT & nifD- NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G55290.2)	GO:0016491
Solyc12g010800.2	-8.30E-01	1.69E-01	-5.17E-01	3.86E-01	**-2.53E+00**	**2.13E-04**	**-1.70E+00**	**7.58E-03**	WT & nifD- NoN 14 dpi	T	BZIP family transcription factor (AHRD V3.3 *** G7ZUL8_MEDTR)	GO:0003700|GO:0006355|GO:0043565
Solyc04g071650.3	-2.51E-01	1.13E-01	2.90E-01	6.81E-02	**-1.09E+00**	**1.50E-07**	**-1.71E+00**	**2.23E-11**	WT & nifD- NoN 14 dpi	CS	Cellulose synthase (AHRD V3.3 *** M1A8I3_SOLTU)	GO:0005515|GO:0008270|GO:0016020|GO:0016760|GO:0030244|GO:0016020|GO:0016760
Solyc02g085110.3	-6.39E-01	4.00E-02	3.84E-01	2.06E-01	**-2.02E+00**	**3.26E-07**	**-1.71E+00**	**4.34E-06**	WT & nifD- NoN 14 dpi	PMI	Laccase (AHRD V3.3 *** I1J8U1_SOYBN)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc11g012580.2	-1.20E-01	7.70E-01	2.56E-01	5.33E-01	**-1.54E+00**	**7.71E-04**	**-1.72E+00**	**2.45E-04**	WT & nifD- NoN 14 dpi	C	Carbohydrate-binding X8 domain superfamily protein (AHRD V3.3 *** A0A061GP73_THECC)	
Solyc03g116370.3	8.76E-01	2.04E-02	1.51E+00	2.37E-04	**-2.68E+00**	**5.40E-08**	**-1.73E+00**	**4.90E-05**	WT & nifD- NoN 14 dpi	G	RP/EB family microtubule-associated protein (AHRD V3.3 *** A0A072TJV8_MEDTR)	GO:0005515|GO:0008017|GO:0008017
Solyc03g095310.3	-1.19E-01	3.42E-01	1.84E-01	1.48E-01	**-1.82E+00**	**4.55E-14**	**-1.73E+00**	**1.49E-13**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 protein (AHRD V3.3 *** A0A0B0P3Q6_GOSAR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc07g042470.3	-4.14E-01	4.36E-01	-2.31E-01	6.62E-01	**-1.89E+00**	**1.27E-03**	**-1.73E+00**	**2.74E-03**	WT & nifD- NoN 14 dpi	H	Small auxin up-regulated RNA64	GO:0009733
Solyc05g050090.3	-4.94E-01	3.30E-01	8.09E-02	8.72E-01	**-1.69E+00**	**2.17E-03**	**-1.77E+00**	**1.44E-03**	WT & nifD- NoN 14 dpi	L	Fatty acid/sphingolipid desaturase (AHRD V3.3 *** AT2G46210.1)	GO:0006629|GO:0006629|GO:0016021|GO:0016491|GO:0006629|GO:0016021|GO:0016491
Solyc02g093230.3	7.42E-01	3.52E-03	1.67E+00	1.20E-07	**-1.16E+00**	**3.25E-05**	**-1.79E+00**	**3.62E-08**	WT & nifD- NoN 14 dpi	2M	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** CAMT_SOLTU)	GO:0008171
Solyc03g117790.2	-8.70E-01	1.60E-02	-4.44E-01	1.99E-01	**-1.23E+00**	**1.20E-03**	**-1.79E+00**	**1.57E-05**	WT & nifD- NoN 14 dpi	K	Kinase (AHRD V3.3 *** D7KWK7_ARALL)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g062650.3	-4.60E-01	2.97E-01	5.18E-01	2.41E-01	**-2.52E+00**	**4.00E-06**	**-1.81E+00**	**2.92E-04**	WT & nifD- NoN 14 dpi	PMI	Laccase (AHRD V3.3 *** I1J8U1_SOYBN)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc12g098840.2	3.94E-01	1.33E-01	8.00E-01	4.11E-03	**-1.12E+00**	**1.56E-04**	**-1.82E+00**	**1.37E-07**	WT & nifD- NoN 14 dpi	TR	ABC transporter B family protein (AHRD V3.3 *** G7IBR0_MEDTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO:0016887
Solyc01g067510.3	-1.93E-01	6.73E-01	3.70E-01	4.20E-01	**-1.42E+00**	**4.27E-03**	**-1.85E+00**	**3.75E-04**	WT & nifD- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9GNF8_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc12g098770.2	-4.37E-01	3.34E-01	2.52E-01	5.74E-01	**-3.12E+00**	**1.97E-07**	**-1.85E+00**	**3.04E-04**	WT & nifD- NoN 14 dpi	2M	strictosidine synthase-like 3 (AHRD V3.3 --* AT1G08470.1)	
Solyc02g065220.3	1.68E+00	7.62E-04	1.01E+00	2.96E-02	**-3.08E+00**	**2.13E-07**	**-1.85E+00**	**2.75E-04**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103Y530_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705

Solyc03g123550.1	1.93E+00	7.19E-07	1.52E+00	2.61E-05	**-2.48E+00**	**8.59E-09**	**-1.87E+00**	**1.21E-06**	WT & nifD- NoN 14 dpi	H	Small auxin up-regulated RNA39	GO:0009733
Solyc11g072800.2	-6.35E-01	2.16E-01	-6.50E-01	2.06E-01	**-2.53E+00**	**3.09E-05**	**-1.87E+00**	**9.52E-04**	WT & nifD- NoN 14 dpi	OX	Respiratory burst oxidase-like protein (AHRD V3.3 *** G7L3G1_MEDTR)	GO:0004601|GO:0050664|GO:0055114|GO:0005509|GO:0005509
Solyc03g113720.3	-2.83E-01	3.34E-01	-3.45E-01	2.42E-01	**-1.54E+00**	**1.35E-05**	**-1.87E+00**	**7.27E-07**	WT & nifD- NoN 14 dpi	S	Two-component response regulator (AHRD V3.3 *** W9S9I1_9ROSA)	GO:0000160
Solyc08g007435.1	5.46E-01	3.87E-01	4.32E-01	4.93E-01	**-2.52E+00**	**4.04E-04**	**-1.93E+00**	**4.62E-03**	WT & nifD- NoN 14 dpi	H	Auxin responsive SAUR protein (AHRD V3.3 *** A0A103XGA7_CYNCS)	GO:0009733
Solyc12g055960.1	-9.74E-01	1.64E-01	4.10E-01	5.51E-01	**-2.99E+00**	**1.65E-04**	**-1.93E+00**	**8.71E-03**	WT & nifD- NoN 14 dpi	P	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061GNR0_THECC)	GO:0008375|GO:0016020
Solyc08g081490.3	-3.36E-01	3.66E-01	8.03E-02	8.28E-01	**-1.45E+00**	**5.07E-04**	**-1.94E+00**	**1.51E-05**	WT & nifD- NoN 14 dpi	K	mitogen-activated protein kinase 7	
Solyc08g080070.1	-3.77E-01	3.61E-01	-5.21E-01	2.10E-01	**-1.95E+00**	**5.64E-05**	**-1.96E+00**	**5.29E-05**	WT & nifD- NoN 14 dpi	NA	LOW QUALITY:transmembrane protein, putative (DUF1191) (AHRD V3.3 *** AT4G22900.1)	
Solyc06g009780.3	-3.71E-01	2.68E-01	-9.52E-02	7.74E-01	**-1.06E+00**	**3.29E-03**	**-1.98E+00**	**2.28E-06**	WT & nifD- NoN 14 dpi	TR	Kinesin-like protein (AHRD V3.3 *** F8UN41_TOBAC)	GO:0003777|GO:0005524|GO:0007018|GO:0008017|GO:0005515|GO:0005515
Solyc09g011270.3	1.04E+00	2.30E-02	1.81E+00	2.64E-04	**-1.91E+00**	**1.43E-04**	**-1.98E+00**	**9.15E-05**	WT & nifD- NoN 14 dpi	S	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G37820.1)	
Solyc09g059473.1	4.86E-01	1.93E-02	1.41E+00	1.23E-07	**-2.35E+00**	**4.29E-12**	**-1.99E+00**	**1.53E-10**	WT & nifD- NoN 14 dpi	D	S-norcoclaurine synthase 1 (AHRD V3.3 *** A0A061FEF4_THECC)	GO:0006952|GO:0009607
Solyc03g083820.2	4.19E-01	3.71E-01	9.07E-01	5.98E-02	**-2.47E+00**	**1.34E-05**	**-2.00E+00**	**1.94E-04**	WT & nifD- NoN 14 dpi	CS	Endoglucanase (AHRD V3.3 *-* K4BIF7_SOLLC)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc11g005300.2	-1.65E+00	2.19E-02	-1.39E+00	5.03E-02	**-2.44E+00**	**1.31E-03**	**-2.02E+00**	**6.15E-03**	WT & nifD- NoN 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT1G49230.1)	GO:0005515|GO:0008270
Solyc04g050170.3	-7.85E-01	1.66E-01	1.04E-01	8.51E-01	**-2.65E+00**	**5.70E-05**	**-2.03E+00**	**1.06E-03**	WT & nifD- NoN 14 dpi	PMI	Clavata1 receptor kinase family protein (AHRD V3.3 *** B9I5Q8_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g078950.3	3.17E-01	2.89E-01	7.22E-01	2.06E-02	**-1.57E+00**	**1.34E-05**	**-2.03E+00**	**2.40E-07**	WT & nifD- NoN 14 dpi	C	Beta-galactosidase (AHRD V3.3 *** M1C1C4_SOLTU)	GO:0004553|GO:0005975|GO:0005975|GO:00
Solyc07g061840.1	5.43E-01	3.82E-01	7.32E-01	2.41E-01	**-1.82E+00**	**6.29E-03**	**-2.05E+00**	**2.40E-03**	WT & nifD- NoN 14 dpi	G	LOW QUALITY:Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 -** AT1G66850.1)	
Solyc02g083860.3	-2.16E-01	4.77E-01	5.15E-01	9.80E-02	**-1.36E+00**	**1.14E-04**	**-2.06E+00**	**2.95E-07**	WT & nifD- NoN 14 dpi	2M	flavanone 3-dioxygenase	GO:0016491|GO:0055114
Solyc09g098380.2	-4.71E-02	9.50E-01	-2.35E-01	7.53E-01	**-2.07E+00**	**9.53E-03**	**-2.09E+00**	**9.08E-03**	WT & nifD- NoN 14 dpi	AM	Transmembrane amino acid transporter family protein (AHRD V3.3 *-* G7JBE3_MEDTR)	
Solyc06g008240.3	-5.54E-01	4.64E-01	-3.18E-01	6.72E-01	**-3.56E+00**	**6.08E-05**	**-2.09E+00**	**9.31E-03**	WT & nifD- NoN 14 dpi	H	ROP-interactive CRIB motif protein (AHRD V3.3 *** A0A072U2K9_MEDTR)	
Solyc09g091700.3	-1.64E-01	8.14E-01	-1.06E+00	1.34E-01	**-2.95E+00**	**2.32E-04**	**-2.11E+00**	**5.15E-03**	WT & nifD- NoN 14 dpi	OX	NADP-dependent alkenal double bond reductase (AHRD V3.3 *** I3SE71_MEDTR)	GO:0016491|GO:0055114|GO:0055114
Solyc02g091440.2	-6.10E-01	3.81E-01	6.51E-01	3.51E-01	**-2.84E+00**	**3.24E-04**	**-2.11E+00**	**4.80E-03**	WT & nifD- NoN 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT2G14760.1)	GO:0046983
Solyc06g066800.2	-8.68E-01	2.14E-02	-9.29E-01	1.45E-02	**-1.14E+00**	**3.57E-03**	**-2.12E+00**	**2.68E-06**	WT & nifD- NoN 14 dpi	NA	Nucleotide-diphospho-sugar transferases superfamily protein (AHRD V3.3 *** AT1G64980.2)	
Solyc10g075170.2	-1.87E-01	6.86E-01	1.04E+00	3.12E-02	**-1.95E+00**	**2.44E-04**	**-2.12E+00**	**9.06E-05**	WT & nifD- NoN 14 dpi	AM	Aspartate aminotransferase (AHRD V3.3 *-* A0A067JJ16_JATCU)	GO:0003824|GO:0006520|GO:0008483|GO:0006520|GO:0008483
Solyc01g059900.3	5.34E+00	9.75E-10	6.34E+00	2.80E-11	**-2.50E+00**	**1.79E-04**	**-2.15E+00**	**8.77E-04**	WT & nifD- NoN 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4AW97_SOLLC)	
Solyc04g025750.3	-9.02E-01	1.85E-01	-4.34E-01	5.18E-01	**-5.15E+00**	**3.22E-08**	**-2.16E+00**	**3.09E-03**	WT & nifD- NoN 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4BR19_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc08g075830.3	5.04E-01	4.69E-01	1.46E+00	4.36E-02	**-4.13E+00**	**2.45E-06**	**-2.17E+00**	**4.03E-03**	WT & nifD- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4CMV0_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc09g091880.3	-8.82E-01	1.30E-05	-2.79E-01	1.02E-01	**-1.14E+00**	**2.32E-07**	**-2.21E+00**	**3.77E-13**	WT & nifD- NoN 14 dpi	T	Myb family transcription factor APL (AHRD V3.3 *** A0A0B0NIP7_GOSAR)	GO:0003677|GO:0005515|GO:0005515
Solyc02g084210.1	-1.35E+00	9.87E-02	-6.82E-01	3.93E-01	**-2.20E+00**	**9.54E-03**	**-2.21E+00**	**9.22E-03**	WT & nifD- NoN 14 dpi	C	GDP-mannose 4,6 dehydratase 1 (AHRD V3.3 *** GMD1_ARATH)	GO:0008446|GO:0019673
Solyc05g047580.3	7.59E-01	4.15E-03	9.09E-01	8.60E-04	**-1.93E+00**	**1.84E-08**	**-2.23E+00**	**1.17E-09**	WT & nifD- NoN 14 dpi	2M	Terpene cyclase/mutase family member (AHRD V3.3 *** O82141_PANGI)	GO:0016866

Solyc08g079300.3	5.00E+00	1.76E-08	5.88E+00	7.56E-10	**-2.71E+00**	**1.91E-04**	**-2.24E+00**	**1.32E-03**	WT & nifD- NoN 14 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc10g007970.2	-4.46E-01	1.07E-01	2.36E-01	3.85E-01	**-1.47E+00**	**9.70E-06**	**-2.24E+00**	**7.91E-09**	WT & nifD- NoN 14 dpi	T	WRKY transcription factor 77	GO:0003700|GO:0006355|GO:0043565
Solyc04g011470.2	2.90E-02	9.69E-01	1.14E+00	1.32E-01	**-4.25E+00**	**4.53E-06**	**-2.29E+00**	**4.55E-03**	WT & nifD- NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4BPK0_SOLLC)	
Solyc00g020545.1	1.11E+00	1.15E-01	-3.58E-01	6.05E-01	**-2.64E+00**	**6.67E-04**	**-2.35E+00**	**1.97E-03**	WT & nifD- NoN 14 dpi	TR	Ferric reductase oxidase (AHRD V3.3 *-* V9HYU8_MANES)	
Solyc03g034413.1	4.67E-01	5.63E-01	8.57E-01	2.93E-01	**-3.56E+00**	**1.44E-04**	**-2.38E+00**	**6.19E-03**	WT & nifD- NoN 14 dpi	E	V-type proton ATPase subunit F (AHRD V3.3 --* A0A0D2VC83_GOSRA)	
Solyc03g090990.1	2.75E-01	6.17E-01	3.82E-01	4.87E-01	**-3.24E+00**	**2.76E-06**	**-2.41E+00**	**1.49E-04**	WT & nifD- NoN 14 dpi	H	SlCortical cell-delineating protein	
Solyc06g066520.1	1.05E+00	4.20E-03	1.10E+00	2.91E-03	**-1.42E+00**	**2.47E-04**	**-2.43E+00**	**1.14E-07**	WT & nifD- NoN 14 dpi	D	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 146 (AHRD V3.3 *** Q9FQZ6_TOBAC)	
Solyc09g009230.2	6.29E-01	2.36E-01	-9.64E-01	7.46E-02	**-2.33E+00**	**1.34E-04**	**-2.48E+00**	**6.12E-05**	WT & nifD- NoN 14 dpi	NA	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT2G36430.1)	
Solyc10g018150.2	1.94E+00	3.10E-05	2.97E+00	3.62E-08	**-2.70E+00**	**1.88E-07**	**-2.49E+00**	**7.46E-07**	WT & nifD- NoN 14 dpi	2M	SlCytochromeP450	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705
Solyc07g066510.3	-8.81E-01	3.34E-01	1.09E+00	2.34E-01	**-2.64E+00**	**6.70E-03**	**-2.60E+00**	**7.54E-03**	WT & nifD- NoN 14 dpi	G	Zinc finger protein CONSTANS (AHRD V3.3 *** W9R0E5_9ROSA)	GO:0005515
Solyc09g010993.1	-1.36E+00	6.50E-02	-6.68E-01	3.51E-01	**-2.39E+00**	**2.23E-03**	**-2.63E+00**	**9.42E-04**	WT & nifD- NoN 14 dpi	PMI	Laccase (AHRD V3.3 *-* M1AHJ4_SOLTU)	GO:0005507|GO:0055114|GO:0055114
Solyc12g009820.2	6.27E-01	1.15E-01	1.20E+00	4.48E-03	**-1.97E+00**	**2.56E-05**	**-2.67E+00**	**2.39E-07**	WT & nifD- NoN 14 dpi	G	Monogalactosyldiacylglycerol synthase (AHRD V3.3 *** G7JGJ5_MEDTR)	GO:0009247|GO:0016758|GO:0016758|GO:0016758
Solyc07g062710.3	-6.65E-01	1.89E-01	-2.83E-01	5.70E-01	**-2.55E+00**	**2.18E-05**	**-2.70E+00**	**9.97E-06**	WT & nifD- NoN 14 dpi	T	BZIP family transcription factor (AHRD V3.3 *** G8A005_MEDTR)	GO:0003700|GO:0006355|GO:0043565
Solyc01g090970.3	-1.06E+00	2.57E-01	-1.73E+00	6.90E-02	**-2.76E+00**	**5.49E-03**	**-2.72E+00**	**6.18E-03**	WT & nifD- NoN 14 dpi	CS	14 kDa proline-rich protein DC2.15 (AHRD V3.3 *** A0A151QNX1_CAJCA)	
Solyc03g118760.3	2.92E+00	7.00E-04	3.26E+00	2.19E-04	**-3.92E+00**	**2.25E-05**	**-2.77E+00**	**1.17E-03**	WT & nifD- NoN 14 dpi	CS	Tubulin beta chain (AHRD V3.3 *** TBB_HORVU)	GO:0003924|GO:0005200|GO:0005525|GO:0005874|GO:0007017|GO:0005200|GO:0005525
Solyc06g034370.1	-8.87E-01	2.34E-02	-4.47E-02	9.04E-01	**-1.35E+00**	**1.11E-03**	**-2.81E+00**	**4.62E-08**	WT & nifD- NoN 14 dpi	CS	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** AT5G62350.1)	GO:0004857
Solyc01g097700.1	-7.53E-01	3.93E-02	4.26E-02	9.03E-01	**-3.65E+00**	**8.56E-11**	**-2.83E+00**	**1.36E-08**	WT & nifD- NoN 14 dpi	CS	LOW QUALITY:Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)	
Solyc09g009010.3	8.78E-01	6.43E-02	6.58E-01	1.59E-01	**-1.39E+00**	**5.15E-03**	**-2.86E+00**	**1.23E-06**	WT & nifD- NoN 14 dpi	CS	Cellulose synthase-like protein (AHRD V3.3 *** L0ASI8_POPTO)	
Solyc12g019120.2	5.35E-01	4.77E-01	6.91E-01	3.60E-01	**-3.44E+00**	**8.94E-05**	**-2.87E+00**	**6.72E-04**	WT & nifD- NoN 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT2G43890.1)	GO:0004650|GO:0005975
Solyc02g066960.3	1.29E-01	6.29E-01	5.37E-01	5.16E-02	**-2.16E+00**	**1.20E-08**	**-2.93E+00**	**2.49E-11**	WT & nifD- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4B728_SOLLC)	GO:0008152|GO:0016758
Solyc08g079200.1	1.23E-02	9.89E-01	1.04E+00	2.65E-01	**-3.64E+00**	**4.68E-04**	**-2.95E+00**	**3.28E-03**	WT & nifD- NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12490.1)	
Solyc11g071720.2	9.22E-03	9.81E-01	4.33E-01	2.61E-01	**-1.39E+00**	**1.06E-03**	**-3.02E+00**	**1.95E-08**	WT & nifD- NoN 14 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GZL6_THECC)	GO:0008152|GO:0016787
Solyc07g014580.3	5.10E+00	6.03E-09	4.29E+00	1.44E-07	**-3.25E+00**	**1.14E-05**	**-3.03E+00**	**3.06E-05**	WT & nifD- NoN 14 dpi	S	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061G8N7_THECC)	GO:0016747
Solyc07g009310.3	1.28E+00	1.20E-01	1.28E+00	1.19E-01	**-2.71E+00**	**2.16E-03**	**-3.06E+00**	**7.06E-04**	WT & nifD- NoN 14 dpi	D	LOW QUALITY:defensin-like protein (AHRD V3.3 -** AT1G19610.1)	GO:0006952
Solyc02g084580.2	-1.24E+00	1.11E-01	5.11E-01	5.03E-01	**-3.76E+00**	**3.46E-05**	**-3.06E+00**	**3.93E-04**	WT & nifD- NoN 14 dpi	NA	LOW QUALITY:(S)-N-methylcoclaurine 3'-hydroxylase isozyme 1 (AHRD V3.3 --* C80B1_ESCCA)	
Solyc12g049350.2	1.59E+00	5.63E-02	1.23E+00	1.35E-01	**-3.36E+00**	**2.69E-04**	**-3.07E+00**	**6.93E-04**	WT & nifD- NoN 14 dpi	T	R2R3MYB transcription factor 11	GO:0003677
Solyc12g005790.2	1.40E+00	5.67E-05	1.97E+00	3.40E-07	**-3.14E+00**	**4.41E-11**	**-3.08E+00**	**7.01E-11**	WT & nifD- NoN 14 dpi	OX	Peroxidase 27	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc01g110570.3	-1.47E+00	9.20E-02	1.47E+00	9.28E-02	**-2.83E+00**	**2.41E-03**	**-3.09E+00**	**1.08E-03**	WT & nifD- NoN 14 dpi	H	Small auxin up-regulated RNA4	GO:0009733
Solyc01g005940.3	3.60E-01	4.87E-01	-2.35E-01	6.50E-01	**-1.94E+00**	**8.14E-04**	**-3.11E+00**	**2.09E-06**	WT & nifD- NoN 14 dpi	2M	Phytoene synthase (AHRD V3.3 *** A0A0K1L5A0_MALDO)	GO:0004310|GO:0006696|GO:0051996|GO:0009058|GO:0016740|GO:0009058|GO:0016740

Solyc12g005785.1	4.70E-01	5.51E-01	1.25E+00	1.19E-01	**-3.80E+00**	**4.66E-05**	**-3.12E+00**	**4.55E-04**	WT & nifD- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *-* M1C971_SOLTU)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0055114|GO:0004601
Solyc12g056180.2	2.98E+00	1.67E-05	3.13E+00	8.54E-06	**-3.51E+00**	**1.48E-06**	**-3.18E+00**	**6.68E-06**	WT & nifD- NoN 14 dpi	P	Sl 1-aminocyclopropane-1-carboxylate synthase	GO:0003824|GO:0003824|GO:0009058|GO:0030170|GO:0003824|GO:0009058|GO:0030170
Solyc07g008420.3	-1.08E+00	1.16E-01	-6.69E-01	3.23E-01	**-3.32E+00**	**3.52E-05**	**-3.20E+00**	**5.59E-05**	WT & nifD- NoN 14 dpi	E	Blue copper (AHRD V3.3 *** A0A0B0N2W0_GOSAR)	GO:0009055
Solyc06g030590.2	-7.62E-01	3.58E-01	-5.53E-01	5.03E-01	**-2.31E+00**	**8.69E-03**	**-3.25E+00**	**4.89E-04**	WT & nifD- NoN 14 dpi	L	Serine palmitoyltransferase (AHRD V3.3 *** B3Y000_NICBE)	GO:0003824|GO:0008152|GO:0016740|GO:0008152|GO:0016740
Solyc03g112240.1	-5.82E-01	4.87E-01	1.95E-01	8.15E-01	**-2.49E+00**	**5.60E-03**	**-3.27E+00**	**5.30E-04**	WT & nifD- NoN 14 dpi	AM	LOW QUALITY:pyrroline-5-carboxylate reductase (AHRD V3.3 *-* AT4G03600.1)	
Solyc09g064810.3	1.27E-01	8.21E-01	5.95E-01	2.93E-01	**-1.69E+00**	**5.27E-03**	**-3.27E+00**	**3.37E-06**	WT & nifD- NoN 14 dpi	STR	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 *** AT4G02900.4)	GO:0016020
Solyc10g018320.1	-1.10E+00	2.04E-01	-1.05E+00	2.27E-01	**-3.71E+00**	**1.71E-04**	**-3.38E+00**	**4.70E-04**	WT & nifD- NoN 14 dpi	CS	Plant invertase/pectin methylesterase inhibitor (AHRD V3.3 *** G7KG88_MEDTR)	GO:0004857
Solyc06g082560.2	-1.87E+00	7.11E-02	3.37E-01	7.38E-01	**-2.93E+00**	**6.72E-03**	**-3.44E+00**	**1.92E-03**	WT & nifD- NoN 14 dpi	T	Chaperone protein (AHRD V3.3 *** W9RSC3_9ROSA)	GO:0005524|GO:0019538|GO:0019538
Solyc07g063210.3	1.03E-01	8.92E-01	-4.06E-01	5.94E-01	**-3.05E+00**	**4.08E-04**	**-3.70E+00**	**4.30E-05**	WT & nifD- NoN 14 dpi	CS	Expansin (AHRD V3.3 *** G4XZZ0_9GENT)	GO:0005576|GO:0009664|GO:0009664
Solyc10g080640.2	-5.47E-01	4.71E-01	-5.05E-02	9.47E-01	**-2.90E+00**	**6.51E-04**	**-3.76E+00**	**3.16E-05**	WT & nifD- NoN 14 dpi	DNA	calmodulin-binding family protein (AHRD V3.3 *** AT3G13600.2)	
Solyc01g107710.2	-4.52E-01	6.29E-01	1.57E+00	1.02E-01	**-5.23E+00**	**6.28E-06**	**-3.79E+00**	**3.66E-04**	WT & nifD- NoN 14 dpi	STR	LOW QUALITY:Late embryogenesis abundant protein-like protein (AHRD V3.3 *** F4JB74_ARATH)	
Solyc06g073220.1	2.39E-01	7.51E-01	-7.63E-01	3.16E-01	**-2.86E+00**	**7.35E-04**	**-3.80E+00**	**2.68E-05**	WT & nifD- NoN 14 dpi	G	Stigma-specific protein Stig1 (AHRD V3.3 *** A0A103Y3M1_CYNCS)	
Solyc05g021550.2	-1.91E+00	8.49E-02	-2.02E+00	7.00E-02	**-3.39E+00**	**3.81E-03**	**-3.88E+00**	**1.22E-03**	WT & nifD- NoN 14 dpi	CS	Sister-chromatide cohesion protein 3 (AHRD V3.3 *-* D7M8Q0_ARALL)	
Solyc04g009690.2	-4.11E-01	2.00E-01	1.29E-01	6.82E-01	**-2.67E+00**	**5.38E-09**	**-3.93E+00**	**1.72E-12**	WT & nifD- NoN 14 dpi	D	LOW QUALITY:Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)	GO:0043531
Solyc06g034410.3	-9.18E-01	2.53E-01	9.23E-02	9.07E-01	**-2.59E+00**	**2.83E-03**	**-3.96E+00**	**3.05E-05**	WT & nifD- NoN 14 dpi	NA	DUF1442 family protein (AHRD V3.3 *** B7FH79_MEDTR)	
Solyc10g018200.2	-2.50E-01	6.72E-01	-1.70E-01	7.73E-01	**-3.23E+00**	**8.64E-06**	**-4.14E+00**	**1.68E-07**	WT & nifD- NoN 14 dpi	NA	DUF1442 family protein (AHRD V3.3 *** G7KG71_MEDTR)	
Solyc09g014940.2	-7.93E-01	1.56E-01	1.68E+00	4.79E-03	**-1.53E+00**	**9.35E-03**	**-4.25E+00**	**2.86E-08**	WT & nifD- NoN 14 dpi	D	Wound-induced protein 1 (AHRD V3.3 *** A0A0B2R5F9_GLYSO)	
Solyc04g076770.3	-1.35E+00	1.07E-01	1.50E+00	7.63E-02	**-3.30E+00**	**3.94E-04**	**-4.47E+00**	**8.87E-06**	WT & nifD- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4BUB5_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601
Solyc06g034130.2	-1.25E+00	2.10E-01	4.47E-01	6.51E-01	**-4.52E+00**	**8.88E-05**	**-4.52E+00**	**9.06E-05**	WT & nifD- NoN 14 dpi	STR	LOW QUALITY:Late embryogenesis abundant protein-like protein (AHRD V3.3 *** F4JB74_ARATH)	
Solyc03g091010.1	-1.11E-04	1.00E+00	-6.28E-01	4.18E-01	**-4.55E+00**	**2.86E-06**	**-4.64E+00**	**2.12E-06**	WT & nifD- NoN 14 dpi	NA	Sl Cortical cell-delineating protein	
Solyc11g073150.1	-4.14E-01	6.91E-01	-4.80E-01	6.45E-01	**-4.48E+00**	**1.90E-04**	**-4.97E+00**	**5.53E-05**	WT & nifD- NoN 14 dpi	STR	LOW QUALITY:Late embryogenesis abundant protein-like protein (AHRD V3.3 *** F4JB74_ARATH)	
Solyc04g079510.2	3.60E-01	6.67E-01	-2.35E-01	7.79E-01	**-4.61E+00**	**7.83E-06**	**-5.17E+00**	**1.38E-06**	WT & nifD- NoN 14 dpi	TR	Peptide transporter	GO:0005215|GO:0006810|GO:0016020
Solyc04g007590.2	2.92E+05	7.60E-02	2.45E+05	5.10E-03	**-2.72E+05**	**4.52E-03**	**-4.00E+05**	**1.13E-07**	WT & nifD- NoN 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4BNR6_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc01g107720.3	-2.56E+04	1.01E-01	1.65E+05	8.44E-01	**-3.23E+05**	**9.58E-04**	**-4.23E+03**	**3.33E-05**	WT & nifD- NoN 14 dpi	STR	Late embryogenesis abundant protein-like protein (AHRD V3.3 *** F4JB74_ARATH)	

Table S 6. List of differentially expressed genes (DEGs) identified in tomato roots 1 day post inoculation (dpi) with Gluconacetobacter diazotrophicus WT strain. *Fold change values of DEGs identified in tomato roots with G. diazotrophicus WT strain as compared to uninoculated plants (Control) in modified Hoagland in the absence (WT NoN) or presence of 2 mM KNO_3 (WT N) in hydroponic systems at 1dpi. Tomato gene identifier (ITAG3.2 release), Log2-transformed fold change values and P values calculated for each pairwise comparison between bacterium-inoculated and uninoculated samples are reported. Clustering results of the DEGs, classified as genes significantly modulated (in bold, $P \leq 0.01$ and Log2(fold change) ≥ 1 or ≤ -1) by WT in either N or NoN condition. Protein description and abbreviation codes of functional classes were assigned on the basis of the protein description and function. Gene ontology (GO) terms were based on the ITAG3.2 release (https://solgenomics.net/organism/Solanum_lycopersicum/genome).*

Gene ID	WT N	P.Value	*nifD* - N	P. Value	WT NoN	P. Value	*nifD*- NoN	P.Value	Cluster	Functional Class	Gene Description	GO
Solyc02g089140.2	**7.47E+00**	**5.27E-07**	2.37E+00	4.51E-02	-1.58E-01	8.89E-01	6.72E-01	5.56E-01	WT N 1 dpi	T	LOW QUALITY:SIN3-like 1 (AHRD V3.3 --* AT3G01320.2)	
Solyc10g050990.1	**7.41E+00**	**2.33E-06**	2.26E+00	7.74E-02	2.25E+00	7.82E-02	2.21E+00	8.40E-02	WT N 1 dpi	C	Pyruvate kinase (AHRD V3.3 --* A9TZX1_PHYPA)	
Solyc06g050870.3	**6.69E+00**	**1.18E-05**	2.11E+00	9.90E-02	1.38E+00	2.75E-01	2.62E+00	4.35E-02	WT N 1 dpi	E	Hypoxia-responsive family protein(AHRD V3.3 *** A0A061FYY0_THECC)	
Solyc07g007410.3	**5.46E+00**	**9.19E-09**	1.72E+00	1.44E-02	1.61E+00	2.12E-02	1.78E+00	1.17E-02	WT N 1 dpi	PMI	Leucine-rich repeat family protein(AHRD V3.3 *** AT1G15740.1)	GO:0005515
Solyc12g006680.2	**4.59E+00**	**6.52E-03**	1.35E+00	3.94E-01	1.12E+00	4.76E-01	1.50E+00	3.43E-01	WT N 1 dpi	PMI	Early nodulin 93 protein (AHRDV3.3 *** A3FGC9_9ROSI)	
Solyc05g046190.1	**4.28E+00**	**1.23E-05**	2.08E+00	1.47E-02	5.64E-01	4.84E-01	4.07E-01	6.12E-01	WT N 1 dpi	G	LOW QUALITY:1-phosphatidylinositol-4-phosphate 5-kinase 3 (AHRD V3.3 --* AT2G26420.3)	
Solyc02g079690.1	**4.06E+00**	**2.07E-04**	2.00E+00	4.30E-02	-2.05E-02	9.83E-01	-9.63E-02	9.19E-01	WT N 1 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *-* M1B357_SOLTU)	GO:0048544
Solyc12g088130.2	**3.98E+00**	**1.74E-04**	2.46E+00	1.19E-02	-6.98E-01	4.49E-01	-7.37E-01	4.24E-01	WT N 1 dpi	DNA	basic helix-loop-helix (bHLH) DNA- binding superfamily protein (AHRD V3.3 *** AT5G10570.1)	GO:0046983
Solyc01g103070.2	**3.98E+00**	**1.41E-03**	2.24E+00	5.42E-02	1.38E+00	2.25E-01	1.29E+00	2.56E-01	WT N 1 dpi	DNA	LOW QUALITY:homeobox protein(AHRD V3.3 *** AT4G24265.2)	
Solyc05g055930.2	**3.79E+00**	**5.13E-04**	1.69E+00	8.85E-02	2.81E-01	7.71E-01	1.89E-01	8.45E-01	WT N 1 dpi	S	Cysteine-rich repeat secretoryprotein (AHRD V3.3 *** A0A0K9P487_ZOSMR)	
Solyc06g005770.1	**3.52E+00**	**5.31E-04**	1.94E+00	3.85E-02	1.45E-01	8.72E-01	-3.73E-01	6.78E-01	WT N 1 dpi	L	Non-specific lipid-transfer protein(AHRD V3.3 *** K4C359_SOLLC)	GO:0006869|GO:0008289
Solyc01g106600.2	**3.49E+00**	**3.01E-04**	1.93E+00	2.97E-02	1.23E+00	1.55E-01	2.19E+00	1.48E-02	WT N 1 dpi	D	Pathogenesis-related protein 1 (AHRD V3.3 *** E2GEU1_9ROSI)	GO:0005576
Solyc05g009280.3	**3.46E+00**	**2.35E-04**	1.34E+00	1.10E-01	6.43E-02	9.37E-01	4.05E-01	6.21E-01	WT N 1 dpi	L	3-ketoacyl-CoA synthase (AHRDV3.3 *** M1B5V3_SOLTU)	GO:0003824|GO:0008152
Solyc12g055770.1	**3.40E+00**	**4.93E-03**	1.51E+00	1.84E-01	9.26E-01	4.10E-01	1.05E+00	3.49E-01	WT N 1 dpi	TR	LOW QUALITY:Exocyst complex exo70-like protein (AHRD V3.3 ***G7I5R5_MEDTR)	GO:0000145|GO:0006887
Solyc02g089150.3	**3.39E+00**	**1.51E-04**	1.50E+00	6.09E-02	3.97E-01	6.08E-01	3.44E-01	6.56E-01	WT N 1 dpi	L	PI-PLC X domain-containing protein(AHRD V3.3 *** A0A0B2PWM6_GLYSO)	GO:0006629|GO:0008081
Solyc09g082290.3	**3.30E+00**	**4.71E-05**	1.52E+00	3.35E-02	1.11E-01	8.71E-01	1.32E-01	8.47E-01	WT N 1 dpi	NA	Protease inhibitor/seed storage/lipidtransfer family protein (AHRD V3.3	

											*** B9NBN8_POPTR)	
Solyc06g048780.1	**3.29E+00**	**6.07E-03**	2.29E+00	4.74E-02	2.31E+00	4.56E-02	8.90E-01	4.27E-01	WT N 1 dpi	2M	LOW QUALITY:PLAC8 family protein (AHRD V3.3 *-*AT3G10980.1)	
Solyc04g014330.1	**3.23E+00**	**4.81E-08**	6.74E-01	1.25E-01	3.90E-01	3.67E-01	-7.82E-02	8.55E-01	WT N 1 dpi	NA	LOW QUALITY:Leguminosin group485 secreted peptide (AHRDV3.3 *** G7KAF8_MEDTR)	
Solyc07g064120.2	**3.21E+00**	**5.65E-04**	2.04E+00	1.89E-02	-4.55E-01	5.82E-01	-2.18E-01	7.91E-01	WT N 1 dpi	TR	ABC transporter B family protein (AHRD V3.3 *** G7JF16_MEDTR)	GO:0005524|GO:0006810|GO :0016021|GO:0042626|GO:00 55085
Solyc03g044960.2	**3.15E+00**	**1.02E-03**	-4.22E-01	6.24E-01	2.01E+00	2.61E-02	1.84E+00	4.02E-02	WT N 1 dpi	E	Calcium uniporter protein, mitochondrial (AHRD V3.3 ***A0A0B2SA24_GLYSO)	GO:0003674|GO:0005215|GO :0005575|GO:0005622|GO:00 05623|GO:0005737|GO:0005 739|GO:0006810|GO:000815 0|GO:0015291|GO:0015292|G O:0022804|GO:0022857|GO:0 043226|GO:0043227|GO:004 3229|GO:0043231|GO:00444 24|GO:0044444|GO:0044464| GO:0051179|GO:0051234|GO :0055085
Solyc01g105770.2	**2.64E+00**	**8.23E-06**	9.52E-01	5.57E-02	4.46E-01	3.56E-01	2.99E-01	5.35E-01	WT N 1 dpi	NA	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** A0A072UVS4_MEDTR)	
Solyc04g025530.3	**2.60E+00**	**3.13E-06**	6.75E-01	1.36E-01	7.60E-01	9.53E-02	7.58E-01	9.59E-02	WT N 1 dpi	N	glutamate decarboxylase (AHRD V3.3 *** AT5G17330.1)	GO:0003824
Solyc09g065420.3	**2.59E+00**	**6.75E-06**	1.19E+00	1.57E-02	4.36E-02	9.25E-01	-2.65E-01	5.71E-01	WT N 1 dpi	L	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)	GO:0006869|GO:0008289
Solyc07g007010.1	**2.59E+00**	**2.67E-04**	5.95E-01	3.41E-01	2.11E-01	7.34E-01	3.20E-01	6.06E-01	WT N 1 dpi	NA	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *** AT3G02645.1)	
Solyc06g076160.3	**2.58E+00**	**4.17E-03**	1.48E+00	8.24E-02	1.57E+00	6.67E-02	8.12E-01	3.32E-01	WT N 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *-* C5NM77_TOBAC)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc08g077900.3	**2.55E+00**	**1.91E-06**	-7.07E-01	1.02E-01	8.90E-01	4.24E-02	7.52E-01	8.29E-02	WT N 1 dpi	CS	Expansin-like protein (AHRD V3.3 *** W9S0F1_9ROSA)	GO:0005576
Solyc07g008360.2	**2.54E+00**	**5.64E-06**	1.21E+00	1.18E-02	1.08E-01	8.11E-01	4.36E-02	9.23E-01	WT N 1 dpi	R	ribosomal protein L30/L7 family protein	GO:0003824|GO:0008152
Solyc10g078220.2	**2.53E+00**	**4.09E-03**	1.02E+00	2.14E-01	1.22E+00	1.42E-01	1.23E+00	1.39E-01	WT N 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A9ZT63_COPJA)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc08g014360.2	**2.53E+00**	**1.73E-03**	1.45E+00	5.51E-02	1.10E+00	1.40E-01	2.76E-01	7.06E-01	WT N 1 dpi	CS	Cinnamyl alcohol dehydrogenase(AHRD V3.3 *** A0A1B0YY99_DAUCA)	GO:0016491
Solyc09g072885.1	**2.52E+00**	**6.44E-03**	1.33E+00	1.30E-01	1.00E+00	2.49E-01	1.91E+00	3.39E-02	WT N 1 dpi	G	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 --* AT4G21130.1)	
Solyc01g103275.1	**2.49E+00**	**4.91E-03**	9.00E-01	2.76E-01	1.83E+00	3.25E-02	1.60E+00	5.90E-02	WT N 1 dpi	N	glutamate receptor 3.4 (AHRD V3.3 -* AT1G05200.7)	
Solyc10g075100.2	**2.46E+00**	**8.18E-05**	1.39E+00	1.41E-02	-2.61E-01	6.25E-01	2.62E-02	9.61E-01	WT N 1 dpi	L	Non-specific lipid-transfer protein (AHRD V3.3 *** Q4A1N1_SOLLC)	GO:0006869|GO:0008289
Solyc03g115960.3	**2.46E+00**	**1.97E-05**	9.72E-01	4.96E-02	-1.06E-01	8.25E-01	-1.40E-01	7.69E-01	WT N 1 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2P2I1_GLYSO)	GO:0016788
Solyc05g047590.3	**2.46E+00**	**2.24E-04**	1.44E+00	1.82E-02	5.06E-01	3.85E-01	1.27E+00	3.54E-02	WT N 1 dpi	CS	SI Pectinesterase	GO:0004857

Solyc01g079160.3	**2.43E+00**	**6.27E-07**	8.02E-01	3.96E-02	-6.23E-01	1.04E-01	-1.02E-01	7.85E-01	WT N 1 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** W9R6R2_9ROSA)	GO:0016788
Solyc05g051550.2	**2.43E+00**	**1.00E-03**	1.32E+00	5.33E-02	-3.27E-02	9.60E-01	-5.23E-02	9.37E-01	WT N 1 dpi	T	MYB-related transcription factor(AHRD V3.3 *** A0A059PRU0_SALMI)	GO:0003677
Solyc01g099580.2	**2.42E+00**	**8.22E-03**	7.22E-01	4.01E-01	1.17E+00	1.79E-01	1.17E+00	1.78E-01	WT N 1 dpi	S	Cysteine/Histidine-rich C1 domain family protein, putative (AHRD V3.3 *-* A0A061EYK7_THECC)	
Solyc04g016190.1	**2.41E+00**	**9.13E-03**	1.08E+00	2.18E-01	2.12E+00	2.00E-02	2.01E+00	2.66E-02	WT N 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BQB9_SOLLC)	GO:0008152|GO:0016758
Solyc03g098010.3	**2.41E+00**	**7.04E-03**	1.53E+00	7.36E-02	1.47E+00	8.54E-02	1.42E+00	9.55E-02	WT N 1 dpi	STR	phosphate starvation inducible gene TPSI1	GO:0003993
Solyc02g086700.3	**2.41E+00**	**3.49E-03**	1.55E+00	4.91E-02	-1.01E+00	1.89E-01	-3.19E-01	6.73E-01	WT N 1 dpi	CS	Beta-1,3-glucanase (AHRD V3.3 *** Q9SYX6_TOBAC)	GO:0004553|GO:0005975
Solyc07g042100.3	**2.38E+00**	**2.36E-04**	7.13E-01	2.13E-01	4.99E-01	3.79E-01	3.20E-01	5.72E-01	WT N 1 dpi	H	Early auxin response protein (AHRD V3.3 *** Q69P88_ORYSJ)	
Solyc06g059840.3	**2.37E+00**	**6.29E-03**	1.88E+00	2.62E-02	5.13E-01	5.26E-01	5.90E-01	4.66E-01	WT N 1 dpi	AM	branched chain alpha-keto acid dehydrogenase E1-alpha subunit	GO:0008152|GO:0016624
Solyc04g054960.1	**2.37E+00**	**5.35E-03**	2.11E+00	1.20E-02	-3.71E-01	6.38E-01	-8.05E-01	3.11E-01	WT N 1 dpi	D	LOW QUALITY:Late embryogenesisabundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT5G21130.1)	
Solyc03g118140.3	**2.29E+00**	**6.28E-03**	1.67E+00	3.97E-02	-7.32E-01	3.50E-01	2.59E-01	7.39E-01	WT N 1 dpi	TR	Protein kish (AHRD V3.3 *** K4BLW5_SOLLC)	
Solyc04g056620.2	**2.26E+00**	**3.75E-03**	1.66E+00	2.73E-02	1.13E+00	1.23E-01	1.71E+00	2.35E-02	WT N 1 dpi	H	Auxin Efflux Facilitator 10	GO:0016021|GO:0055085
Solyc06g054610.2	**2.23E+00**	**1.33E-06**	9.60E-01	1.23E-02	2.55E-01	4.80E-01	5.44E-01	1.39E-01	WT N 1 dpi	E	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 --* NDHK_HELAN)	
Solyc12g011390.1	**2.22E+00**	**6.27E-03**	1.53E+00	5.08E-02	1.88E+00	1.83E-02	1.91E+00	1.68E-02	WT N 1 dpi	NA	LOW QUALITY:SNOWY COTYLEDON protein (DUF566) (AHRD V3.3 --* AT3G19570.4)	
Solyc06g054625.1	**2.21E+00**	**3.32E-08**	7.13E-01	1.92E-02	4.37E-01	1.38E-01	7.25E-01	1.74E-02	WT N 1 dpi	DNA	Zinc finger CCCH domain- containing protein 32 (AHRD V3.3 *-* A0A151STD4_CAJCA)	GO:0046872
Solyc10g076510.2	**2.21E+00**	**4.92E-12**	8.46E-01	1.00E-04	5.24E-01	8.58E-03	3.72E-01	5.37E-02	WT N 1 dpi	C	Pyruvate decarboxylase (AHRD V3.3 *** Q8H9C6_SOLTU)	GO:0000287|GO:0030976
Solyc08g065560.1	**2.21E+00**	**2.03E-03**	1.55E+00	2.36E-02	9.33E-01	1.59E-01	4.36E-01	5.04E-01	WT N 1 dpi	P	Core-2/I-branching beta-1%2C6-N-acetylglucosaminyltransferase familyprotein (AHRD V3.3 --* AT4G31350.4)	
Solyc04g056310.3	**2.19E+00**	**1.45E-06**	9.72E-01	1.05E-02	-5.74E-01	1.15E-01	-2.82E-01	4.31E-01	WT N 1 dpi	T	Myb transcription factor (AHRD V3.3 *-* A0A072V9U0_MEDTR)	GO:0003677
Solyc03g006110.3	**2.18E+00**	**4.83E-03**	4.48E-01	5.32E-01	-1.66E+00	2.73E-02	-7.51E-02	9.16E-01	WT N 1 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IH06_SOLCH)	GO:0004672|GO:0005524|GO :0006468
Solyc06g031710.3	**2.18E+00**	**1.83E-05**	8.71E-01	4.57E-02	-3.57E-02	9.32E-01	-2.84E-01	4.99E-01	WT N 1 dpi	PMI	SI Nodulin-like protein	GO:0016020|GO:0016021
Solyc01g107100.3	**2.12E+00**	**3.36E-07**	8.79E-01	9.02E-03	1.12E-01	7.22E-01	5.87E-01	7.04E-02	WT N 1 dpi	CS	LOW QUALITY:beta-1,4-xylosidase(AHRD V3.3 *** AT3G19615.1)	
Solyc12g005030.2	**2.09E+00**	**3.97E-08**	5.61E-01	4.93E-02	2.09E-01	4.49E-01	-2.42E-01	3.81E-01	WT N 1 dpi	K	Protein kinase (AHRD V3.3 *** Q9AR92_MEDSA)	GO:0004672|GO:0005524|GO :0006468

Solyc01g103060.3	**2.09E+00**	**9.45E-07**	7.60E-01	2.80E-02	-3.06E-01	3.58E-01	-7.72E-02	8.15E-01	WT N 1 dpi	L	Lipid transfer protein (AHRD V3.3 *** A0A072UG85_MEDTR)	GO:0006869|GO:0008289
Solyc07g065410.1	**2.06E+00**	**7.01E-03**	5.85E-01	4.14E-01	3.68E-01	6.05E-01	9.09E-01	2.08E-01	WT N 1 dpi	NA	LOW QUALITY:Melanin- concentrating hormone receptor 1(AHRD V3.3 *** A0A1D1ZFH6_9ARAE)	
Solyc12g042890.2	**2.06E+00**	**2.82E-05**	8.41E-01	4.79E-02	9.52E-02	8.16E-01	8.73E-01	4.04E-02	WT N 1 dpi	P	Acyl-protein thioesterase 2 (AHRD V3.3 *** A0A0B0PZC3_GOSAR)	GO:0016787
Solyc02g043900.1	**2.03E+00**	**8.64E-04**	-7.07E-01	2.00E-01	4.48E-01	4.13E-01	2.05E-01	7.06E-01	WT N 1 dpi	2M	LOW QUALITY:UDP-Glycosyltransferase superfamilyprotein (AHRD V3.3 --* AT1G16570.2)	
Solyc03g007690.1	**2.03E+00**	**9.50E-04**	1.15E+00	4.36E-02	8.74E-01	1.20E-01	7.61E-01	1.74E-01	WT N 1 dpi	TR	ABC transporter family protein (AHRD V3.3 *** U5FQ57_POPTR)	GO:0005524|GO:0016887
Solyc01g094700.3	**2.03E+00**	**1.93E-09**	7.18E-01	3.70E-03	1.94E-01	3.95E-01	-1.87E-02	9.34E-01	WT N 1 dpi	CS	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7LBQ7_MEDTR)	GO:0008152|GO:0016746
Solyc11g068940.1	**2.02E+00**	**3.94E-09**	8.37E-01	1.30E-03	7.31E-01	4.08E-03	4.06E-01	9.16E-02	WT N 1 dpi	P	U-box domain-containing familyprotein (AHRD V3.3 *** B9IIL0_POPTR)	GO:0004842|GO:0016567
Solyc04g028460.1	**2.01E+00**	**3.90E-03**	-8.26E-02	8.97E-01	-7.17E-02	9.11E-01	1.96E-01	7.59E-01	WT N 1 dpi	RNA	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) familyprotein (AHRD V3.3 --* AT4G00830.6)	
Solyc04g076600.2	**1.98E+00**	**3.73E-03**	7.57E-01	2.34E-01	8.91E-01	1.63E-01	1.11E+00	8.61E-02	WT N 1 dpi	CS	CHCH-like protein (AHRD V3.3 *-* A0A103XM78_CYNCS)	
Solyc09g005110.3	**1.95E+00**	**1.62E-03**	8.09E-01	1.57E-01	-3.37E-02	9.52E-01	8.29E-01	1.47E-01	WT N 1 dpi	C	Pyruvate decarboxylase (AHRDV3.3 *** Q8H9C6_SOLTU)	GO:0000287|GO:0030976
Solyc09g010250.1	**1.95E+00**	**4.04E-03**	2.36E-01	7.06E-01	1.03E+00	1.07E-01	-4.06E-01	5.18E-01	WT N 1 dpi	PMI	importin alpha isoform 4 (AHRDV3.3 --* AT1G09270.3)	
Solyc03g098260.2	**1.94E+00**	**2.06E-03**	7.07E-01	2.23E-01	5.30E-01	3.58E-01	4.74E-01	4.10E-01	WT N 1 dpi	T	Myb transcription factor (AHRD V3.3 *-* G7KJN3_MEDTR)	GO:0003677
Solyc03g118000.1	**1.93E+00**	**6.07E-07**	9.64E-01	2.95E-03	3.01E-01	3.16E-01	1.92E-01	5.19E-01	WT N 1 dpi	S	Inositol polyphosphate multikinase(AHRD V3.3 *** K4BLV1_SOLLC)	GO:0008440
Solyc02g092630.2	**1.93E+00**	**5.51E-03**	-5.43E-02	9.33E-01	5.63E-01	3.84E-01	-4.19E-01	5.16E-01	WT N 1 dpi	RNA	LOW QUALITY:Maturase K (AHRDV3.3 --* MATK_LIRMU)	
Solyc06g076090.3	**1.92E+00**	**1.27E-04**	1.10E+00	1.64E-02	2.75E-01	5.26E-01	3.75E-01	3.88E-01	WT N 1 dpi	CS	Actin (AHRD V3.3 *** ACT1_TOBAC)	GO:0005575|GO:0005622|GO:0005623|GO:0005856|GO:0043226|GO:0043228|GO:0043229|GO:0043232|GO:0044424|GO:0044464
Solyc07g006700.1	**1.92E+00**	**3.81E-03**	1.42E+00	2.68E-02	9.34E-01	1.35E-01	4.21E-01	4.92E-01	WT N 1 dpi	D	Pathogenesis-related family protein(AHRD V3.3 *** B9IM28_POPTR)	GO:0005576
Solyc08g023510.2	**1.92E+00**	**3.42E-03**	9.06E-01	1.41E-01	9.47E-01	1.25E-01	5.51E-01	3.64E-01	WT N 1 dpi	CS	Serine incorporator 4 (AHRD V3.3 *** A0A1D1XYQ2_9ARAE)	
Solyc03g005550.3	**1.92E+00**	**3.93E-03**	1.30E+00	4.23E-02	1.45E-01	8.13E-01	1.54E+00	1.77E-02	WT N 1 dpi	K	Serine/threonine protein phosphatase 7 long form isogeny(AHRD V3.3 *** A0A151SGZ7_CAJCA)	

Solyc07g006090.2	**1.92E+00**	**6.07E-03**	9.43E-01	1.53E-01	7.99E-01	2.24E-01	8.44E-01	2.00E-01	WT N 1 dpi	N	Class I glutamine amidotransferase(AHRD V3.3 *-* G7JV26_MEDTR)	GO:0003674|GO:0003824|GO:0005575|GO:0005622|GO:0005623|GO:0005737|GO:0005829|GO:0006082|GO:0006508|GO:0006725|GO:0006790|GO:0006807|GO:0008150|GO:0008152|GO:0008233|GO:0008238|GO:0008242|GO:0009058|GO:0009403|GO:0009404|GO:0009700|GO:0009987|GO:0010120|GO:0016143|GO:0016787|GO:0018130|GO:0019438|GO:0019538|GO:0019748|GO:0019757|GO:0019760|GO:0034641|GO:0034722|GO:0042430|GO:0042435|GO:0043170|GO:0043436|GO:0044237|GO:0044238|GO:0044249|GO:0044271|GO:0044272|GO:0044281|GO:0044424|GO:0044444|GO:0044464|GO:0044550|GO:0046217|GO:0046483|GO:0052314|GO:0052315|GO:0052317|GO:0070011|GO:0071704|GO:0140096|GO:1901135|GO:1901360|GO:1901362|GO:1901564|GO:1901566|GO:1901576|GO:1901657
Solyc01g090810.4	**1.91E+00**	**2.96E-03**	9.83E-01	1.04E-01	8.39E-01	1.62E-01	6.48E-01	2.76E-01	WT N 1 dpi	CS	beta-expansin precursor	
Solyc11g012705.1	**1.91E+00**	**5.01E-08**	9.72E-01	6.65E-04	7.49E-03	9.76E-01	8.02E-02	7.52E-01	WT N 1 dpi	G	Pollen Ole e 1 allergen and extensinfamily protein (AHRD V3.3 *** AT5G47635.1)	
Solyc05g046290.3	**1.90E+00**	**2.76E-03**	-5.02E-01	3.90E-01	2.83E-01	6.26E-01	5.30E-01	3.64E-01	WT N 1 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4C0W2_SOLLC)	GO:0004553|GO:0005975
Solyc01g079880.3	**1.90E+00**	**6.33E-11**	9.50E-01	1.42E-05	-6.98E-01	5.80E-04	-2.79E-02	8.77E-01	WT N 1 dpi	NA	Stem-specific TSJT1 (AHRD V3.3 *** A0A0B0MRD0_GOSAR)	
Solyc02g067580.3	**1.89E+00**	**8.56E-11**	4.76E-01	1.36E-02	7.18E-01	4.84E-04	8.71E-01	5.20E-05	WT N 1 dpi	STR	B12D (AHRD V3.3 *** D2XQY6_WOLAR)	
Solyc05g054620.3	**1.88E+00**	**5.39E-12**	7.61E-01	5.19E-05	6.68E-01	2.46E-04	1.11E-01	4.85E-01	WT N 1 dpi	CS	ACT domain-containing protein(AHRD V3.3 *** AT2G39570.1)	GO:0008152|GO:0016597
Solyc07g014730.3	**1.86E+00**	**1.68E-05**	9.19E-01	1.48E-02	3.32E-01	3.54E-01	4.05E-01	2.60E-01	WT N 1 dpi	L	Phospholipase A2 (AHRD V3.3 *** Q5CCT8_TOBAC)	GO:0004623|GO:0005509|GO:0016042
Solyc03g083100.3	**1.85E+00**	**7.15E-05**	9.66E-01	2.04E-02	8.19E-01	4.63E-02	7.03E-01	8.42E-02	WT N 1 dpi	G	SUN-like protein 10	GO:0005515
Solyc01g099990.3	**1.84E+00**	**5.70E-03**	-9.90E-01	1.17E-01	-3.82E-01	5.37E-01	1.23E+00	5.50E-02	WT N 1 dpi	P	F-box protein (AHRD V3.3 *** G7KWK0_MEDTR)	GO:0005515
Solyc01g007955.1	**1.84E+00**	**6.04E-09**	7.44E-01	1.97E-03	-5.77E-02	7.91E-01	1.03E-01	6.37E-01	WT N 1 dpi	L	alpha/beta-Hydrolases superfamilyprotein (AHRD V3.3 *** AT1G10740.4)	
Solyc07g065980.3	**1.83E+00**	**1.91E-09**	4.83E-01	2.48E-02	8.26E-01	3.90E-04	1.40E-01	4.96E-01	WT N 1 dpi	C	alkaline alpha-galactosidase seedimbibition protein	GO:0003824
Solyc04g079910.3	**1.82E+00**	**2.47E-10**	8.61E-01	7.05E-05	-5.26E-01	7.69E-03	-1.91E-02	9.17E-01	WT N 1 dpi	E	Calcium uniporter protein, mitochondrial (AHRD V3.3 ***A0A0B2QLC6_GLYSO)	

Solyc07g049560.3	**1.80E+00**	**1.61E-04**	-1.03E-02	9.80E-01	4.42E-01	2.88E-01	2.94E-01	4.76E-01	WT N 1 dpi	K	Tyrosine specific protein phosphatase family protein (AHRDV3.3 *** Q32W70_CAPAN)	GO:0004725
Solyc08g060920.3	**1.79E+00**	**1.50E-09**	7.51E-01	7.28E-04	-1.74E+00	2.56E-09	-6.60E-01	2.37E-03	WT N 1 dpi	STR	IDS4-like	
Solyc07g008620.1	**1.79E+00**	**4.86E-05**	8.93E-01	2.22E-02	9.04E-01	2.07E-02	6.27E-01	9.93E-02	WT N 1 dpi	D	EIX receptor 1	GO:0005515
Solyc07g064010.3	**1.78E+00**	**5.51E-03**	2.09E-01	7.26E-01	1.83E-01	7.59E-01	4.93E-01	4.10E-01	WT N 1 dpi	CS	Formin-like protein (AHRD V3.3 *** K4CH84_SOLLC)	
Solyc07g007800.3	**1.78E+00**	**5.48E-04**	1.04E+00	3.02E-02	1.53E-02	9.73E-01	-1.22E-01	7.89E-01	WT N 1 dpi	H	ADIPOR-like receptor (AHRD V3.3 *** W9SGZ8_9ROSA)	GO:0016021
Solyc07g065810.2	**1.78E+00**	**6.32E-07**	7.08E-01	1.50E-02	-1.19E-01	6.65E-01	3.45E-03	9.90E-01	WT N 1 dpi	D	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 ***AT5G55970.2)	GO:0005515|GO:0008270
Solyc07g054810.1	**1.78E+00**	**2.74E-03**	3.47E-01	5.24E-01	-7.18E-01	1.93E-01	4.57E-01	4.03E-01	WT N 1 dpi	E	LOW QUALITY:glutamate-1- semialdehyde 2,1-aminomutase 2(AHRD V3.3 --* AT3G48730.1)	
Solyc01g080990.3	**1.77E+00**	**4.17E-03**	6.12E-01	2.87E-01	1.34E+00	2.52E-02	3.50E-01	5.39E-01	WT N 1 dpi	H	Carboxyl methyltransferase (AHRDV3.3 *** Q70T29_BIXOR)	GO:0008168
Solyc01g103310.3	**1.76E+00**	**1.65E-07**	5.64E-01	3.12E-02	1.26E-01	6.15E-01	1.45E-01	5.64E-01	WT N 1 dpi	DNA	Binding protein, putative isoform 3(AHRD V3.3 *-* A0A061DJC6_THECC)	GO:0003677
Solyc11g005840.2	**1.75E+00**	**2.15E-13**	6.05E-01	6.55E-05	3.21E-01	1.79E-02	5.42E-01	2.37E-04	WT N 1 dpi	AM	Cysteine desulfurase (AHRD V3.3 *** A0A0K9Q199_ZOSMR)	GO:0003824
Solyc04g006970.3	**1.75E+00**	**4.30E-10**	2.19E-01	2.35E-01	9.77E-02	5.93E-01	6.14E-02	7.36E-01	WT N 1 dpi	C	Phosphoenolpyruvate carboxylase(AHRD V3.3 *** A6YM33_RICCO)	GO:0003824
Solyc03g112750.3	**1.74E+00**	**4.44E-03**	5.72E-01	3.17E-01	1.03E+00	7.81E-02	2.30E-02	9.67E-01	WT N 1 dpi	H	Tornado 1 (AHRD V3.3 *** A0A061F576_THECC)	GO:0005515
Solyc01g089890.3	**1.73E+00**	**3.95E-08**	5.30E-01	2.65E-02	1.05E-01	6.44E-01	7.39E-02	7.45E-01	WT N 1 dpi	PMI	PRA1 family protein (AHRD V3.3 *** K4AYT0_SOLLC)	
Solyc12g019230.2	**1.73E+00**	**4.15E-03**	9.04E-01	1.12E-01	-5.42E-01	3.33E-01	-6.07E-01	2.79E-01	WT N 1 dpi	CS	Pectin lyase-like superfamily protein(AHRD V3.3 *** AT3G59850.2)	GO:0004650|GO:0005975
Solyc04g016330.3	**1.72E+00**	**2.46E-08**	7.11E-01	3.16E-03	2.56E-01	2.52E-01	1.61E-01	4.68E-01	WT N 1 dpi	C	Glycerol-3-phosphate dehydrogenase [NAD(+)] (AHRDV3.3 *** K4BQD3_SOLLC)	GO:0004367|GO:0005975|GO :0055114
Solyc06g054030.2	**1.72E+00**	**4.86E-03**	7.26E-01	2.05E-01	-6.27E-01	2.72E-01	-5.54E-01	3.31E-01	WT N 1 dpi	NA	LOW QUALITY:Protease inhibitor/seed storage/lipid transferfamily protein (AHRD V3.3 *** B9NBN8_POPTR)	
Solyc07g065970.1	**1.72E+00**	**7.95E-07**	9.18E-01	1.93E-03	5.77E-01	3.94E-02	5.46E-01	5.03E-02	WT N 1 dpi	P	Chaperone protein DNAj, putative(AHRD V3.3 *** B9SXA3_RICCO)	GO:0005575|GO:0005622|GO :0005623|GO:0005634|GO:00 05737|GO:0009507|GO:0009 536|GO:0043226|GO:004322 7|GO:0043229|GO:0043231|G O:0044424|GO:0044444|GO:0 044464
Solyc02g093970.3	**1.72E+00**	**1.47E-06**	7.75E-01	9.37E-03	9.09E-01	2.87E-03	2.80E-01	3.19E-01	WT N 1 dpi	PMI	Leucine-rich repeat protein kinasefamily protein (AHRD V3.3 *** AT5G14210.2)	GO:0004672|GO:0005524|GO :0006468
Solyc02g093910.3	**1.72E+00**	**4.72E-07**	3.69E-01	1.63E-01	2.05E-01	4.32E-01	-1.01E-01	6.98E-01	WT N 1 dpi	E	Kelch repeat-containing proteinfamily (AHRD V3.3 *** A0A151RD96_CAJCA)	GO:0005515
Solyc08g078850.3	**1.70E+00**	**1.21E-06**	4.90E-01	8.08E-02	-6.32E-02	8.16E-01	2.77E-01	3.14E-01	WT N 1 dpi	C	lactate dehydrogenase	GO:0003824|GO:0005975|GO :0016616|GO:0055114

Solyc08g077070.3	**1.69E+00**	**1.56E-03**	4.13E-01	3.94E-01	4.97E-02	9.18E-01	1.66E-01	7.30E-01	WT N 1 dpi	G	Protein NAP1 (AHRD V3.3 --* NCKP1_ARATH)	
Solyc07g049550.3	**1.69E+00**	**2.46E-06**	3.32E-02	9.06E-01	9.86E-01	1.62E-03	1.77E-01	5.32E-01	WT N 1 dpi	H	1-aminocyclopropane-1-carboxylate oxidase 1 (AHRD V3.3 *** ACCO1_SOLLC)	GO:0016491|GO:0055114
Solyc08g078940.1	**1.68E+00**	**9.48E-03**	1.16E+00	6.46E-02	1.19E+00	5.84E-02	1.12E+00	7.24E-02	WT N 1 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT1G12100.1)	
Solyc09g083050.3	**1.67E+00**	**1.59E-03**	7.75E-01	1.13E-01	-1.13E-01	8.14E-01	2.37E-01	6.21E-01	WT N 1 dpi	L	3-ketoacyl-CoA synthase (AHRD V3.3 *** M1A6B6_SOLTU)	GO:0003824|GO:0008152
Solyc08g083090.2	**1.66E+00**	**2.16E-05**	8.76E-01	1.14E-02	-3.63E-01	2.69E-01	-1.60E-01	6.22E-01	WT N 1 dpi	NA	DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G24130.1)	
Solyc07g054430.3	**1.66E+00**	**1.74E-07**	7.84E-01	2.51E-03	6.01E-01	1.63E-02	2.53E-01	2.89E-01	WT N 1 dpi	N	Glutamate formiminotransferase 1 (AHRD V3.3 *** B4F7V5_MAIZE)	GO:0005542|GO:0008152|GO :0016740
Solyc02g077290.2	**1.65E+00**	**2.01E-07**	6.67E-01	8.98E-03	-6.37E-02	7.89E-01	-3.63E-01	1.36E-01	WT N 1 dpi	N	glutamate receptor 1.2	GO:0004970|GO:0016020
Solyc03g006230.1	**1.65E+00**	**1.65E-06**	3.10E-01	2.57E-01	3.74E-01	1.74E-01	3.91E-02	8.85E-01	WT N 1 dpi	NA	LOW QUALITY:Integral membraneprotein TmpA (AHRD V3.3 *** A0A0K9PA02_ZOSMR)	
Solyc06g074140.1	**1.65E+00**	**3.04E-06**	7.42E-01	1.31E-02	9.00E-02	7.49E-01	8.22E-02	7.70E-01	WT N 1 dpi	P	LOW QUALITY:U-box domain- containing family protein (AHRD V3.3 *** B9IIL0_POPTR)	GO:0004842|GO:0016567
Solyc02g092290.3	**1.65E+00**	**1.05E-09**	4.67E-01	1.41E-02	3.10E-01	9.30E-02	1.87E-01	3.02E-01	WT N 1 dpi	P	F-box family protein (AHRD V3.3 *** B9GFH4_POPTR)	GO:0005515
Solyc10g081780.2	**1.64E+00**	**3.33E-03**	-2.16E-02	9.66E-01	-1.18E+00	2.76E-02	-5.62E-01	2.77E-01	WT N 1 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT2G35910.1)	GO:0005515|GO:0008270
Solyc06g074170.3	**1.64E+00**	**7.46E-05**	4.00E-01	2.60E-01	-4.83E-01	1.76E-01	-1.93E-01	5.83E-01	WT N 1 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061GVZ7_THECC)	GO:0003677|GO:0006355
Solyc03g116870.3	**1.63E+00**	**1.34E-04**	8.94E-01	2.11E-02	-3.59E-03	9.92E-01	1.73E-01	6.39E-01	WT N 1 dpi	E	NAD(P)H dehydrogenase subunit 48(AHRD V3.3 *** A0A0F7GZU3_9ROSI)	GO:0005575|GO:0005622|GO :0005623|GO:0005737|GO:00 06091|GO:0008150|GO:0008 152|GO:0009507|GO:000953 4|GO:0009535|GO:0009536|G O:0009579|GO:0009767|GO:0 009773|GO:0009987|GO:001 0598|GO:0015979|GO:00160 20|GO:0019684|GO:0022900| GO:0031976|GO:0031984|GO :0032991|GO:0034357|GO:00 42651|GO:0043226|GO:0043 227|GO:0043229|GO:004323 1|GO:0044237|GO:0044422|G O:0044424|GO:0044425|GO:0 044434|GO:0044435|GO:004 4436|GO:0044444|GO:00444 46|GO:0044464|GO:0055035| GO:0055114|GO:0098796
Solyc03g006100.3	**1.63E+00**	**4.82E-03**	6.98E-01	1.97E-01	2.20E-01	6.81E-01	4.14E-01	4.40E-01	WT N 1 dpi	S	Receptor-kinase, putative (AHRD V3.3 *** B9RVA8_RICCO)	GO:0004672|GO:0005524|GO :0006468
Solyc01g005390.3	**1.62E+00**	**4.82E-08**	7.37E-01	1.93E-03	1.85E-01	3.95E-01	6.48E-02	7.64E-01	WT N 1 dpi	DNA	Nudix hydrolase (AHRD V3.3 *** A0A061E9N4_THECC)	GO:0016787
Solyc08g065550.1	**1.62E+00**	**4.85E-04**	1.11E+00	1.10E-02	1.44E-01	7.26E-01	1.27E-01	7.56E-01	WT N 1 dpi	E	LOW QUALITY:NADH dehydrogenase subunit 9 (AHRDV3.3 *-* ATMG00070.1)	GO:0008137|GO:0055114

Solyc06g068270.3	**1.62E+00**	**2.27E-03**	-5.11E-02	9.16E-01	-2.69E-01	5.77E-01	3.25E-01	5.02E-01	WT N 1 dpi	H	2-oxoglutarate (2OG) and Fe(II)- dependent oxygenase superfamilyprotein (AHRD V3.3 *** AT1G49390.1)	GO:0016491|GO:0055114
Solyc02g078510.3	**1.61E+00**	**1.20E-04**	7.96E-01	3.37E-02	8.03E-01	3.23E-02	2.02E-02	9.55E-01	WT N 1 dpi	C	Acylsugar acyltransferase 3 (AHRDV3.3 *-* A0A0B5JC18_SOLHA)	GO:0016747
Solyc10g078410.2	**1.60E+00**	**3.60E-06**	8.48E-01	4.44E-03	-1.45E-01	5.97E-01	-7.33E-02	7.90E-01	WT N 1 dpi	P	F-box family protein (AHRD V3.3 *** AT2G32560.1)	GO:0005515
Solyc06g062670.3	**1.59E+00**	**3.00E-09**	8.02E-01	1.49E-04	6.68E-01	1.02E-03	3.90E-01	4.03E-02	WT N 1 dpi	DNA	zinc finger family protein	GO:0003676
Solyc03g123610.3	**1.59E+00**	**1.59E-12**	4.57E-01	1.21E-03	5.62E-01	1.40E-04	2.55E-01	5.26E-02	WT N 1 dpi	N	alanine aminotransferase 2 (AHRD V3.3 *** AT1G72330.1)	GO:0003824
Solyc09g074450.1	**1.59E+00**	**5.65E-04**	8.76E-01	3.92E-02	-1.22E-01	7.65E-01	2.54E-01	5.35E-01	WT N 1 dpi	G	LOW QUALITY:Hydroxyproline-richglycoprotein (AHRD V3.3 *** B9I9X0_POPTR)	GO:0005575|GO:0008150|GO :0009628|GO:0016020|GO:00 31224|GO:0031225|GO:0044 425|GO:0050896|GO:008016 7
Solyc01g066720.3	**1.58E+00**	**1.77E-10**	4.36E-01	9.78E-03	-4.02E-02	7.99E-01	1.42E-01	3.73E-01	WT N 1 dpi	E	Hypoxia-responsive family protein (AHRD V3.3 *** G7I8Q8_MEDTR)	
Solyc03g078100.3	**1.58E+00**	**1.82E-03**	1.01E+00	3.56E-02	-1.02E-01	8.25E-01	3.13E-01	4.98E-01	WT N 1 dpi	CS	Pectinesterase (AHRD V3.3 *** K4BHP0_SOLLC)	GO:0004857
Solyc04g071580.3	**1.58E+00**	**4.49E-06**	5.84E-01	4.24E-02	3.44E-01	2.20E-01	5.78E-02	8.34E-01	WT N 1 dpi	H	ASR2	GO:0006950
Solyc06g010010.2	**1.57E+00**	**2.58E-03**	2.96E-01	5.34E-01	-2.68E-01	5.74E-01	-2.00E-01	6.73E-01	WT N 1 dpi	D	MLO-like protein (AHRD V3.3 *-* K4C428_SOLLC)	GO:0006952|GO:0016021
Solyc03g020010.1	**1.56E+00**	**4.87E-04**	9.22E-01	2.64E-02	7.07E-01	8.24E-02	7.47E-01	6.74E-02	WT N 1 dpi	P	miraculin	GO:0004866
Solyc01g005990.3	**1.56E+00**	**4.07E-04**	9.06E-01	2.61E-02	3.51E-01	3.69E-01	6.53E-01	1.01E-01	WT N 1 dpi	L	Lipid transfer protein (AHRD V3.3 *** A0A072TPI6_MEDTR)	
Solyc11g027840.2	**1.55E+00**	**3.69E-04**	3.48E-01	3.68E-01	5.43E-01	1.65E-01	1.31E-01	7.32E-01	WT N 1 dpi	CS	1,4-beta-D-glucanase (AHRD V3.3 *** B4FHX7_MAIZE)	GO:0016787
Solyc01g109800.2	**1.54E+00**	**2.58E-04**	8.14E-01	3.43E-02	4.49E-01	2.29E-01	2.73E-01	4.60E-01	WT N 1 dpi	NA	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *-*G7J762_MEDTR)	
Solyc07g056640.1	**1.53E+00**	**1.29E-04**	-1.60E-01	6.42E-01	1.59E-01	6.45E-01	7.30E-01	4.16E-02	WT N 1 dpi	G	cycling DOF factor 2 (AHRD V3.3 --*AT5G39660.3)	
Solyc03g083770.1	**1.53E+00**	**5.81E-03**	3.39E-01	5.11E-01	4.74E-01	3.59E-01	-3.16E-02	9.51E-01	WT N 1 dpi	CS	Plant invertase/pectin methylesterase inhibitor superfamilyprotein (AHRD V3.3 *** AT5G62360.1)	GO:0004857
Solyc05g047550.3	**1.51E+00**	**3.43E-03**	5.48E-01	2.54E-01	4.57E-01	3.39E-01	1.24E-01	7.94E-01	WT N 1 dpi	K	Kinase (AHRD V3.3 *** D7LHK4_ARALL)	GO:0004672|GO:0005524|GO :0006468
Solyc03g093140.3	**1.51E+00**	**1.62E-10**	9.27E-01	1.38E-06	1.45E-01	3.37E-01	1.45E-01	3.37E-01	WT N 1 dpi	TR	Glycerol-3-phosphate transporter,putative (AHRD V3.3 *** B9R9S6_RICCO)	GO:0005215|GO:0006810|GO :0016021
Solyc10g083400.1	**1.51E+00**	**8.89E-09**	4.94E-03	9.78E-01	2.35E-01	2.06E-01	2.28E-01	2.20E-01	WT N 1 dpi	CYTP450	Cytochrome P450, putative (AHRDV3.3 *** B9T5M5_RICCO)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc12g014500.2	**1.50E+00**	**1.79E-03**	7.09E-01	1.13E-01	1.08E+00	1.90E-02	9.25E-01	4.20E-02	WT N 1 dpi	H	S-adenosyl-L-methionine:carboxylmethyltransferase family protein (AHRD V3.3 *** B9GJG7_POPTR)	GO:0008168
Solyc08g077060.3	**1.50E+00**	**5.73E-05**	6.46E-01	4.86E-02	1.67E-01	5.98E-01	5.06E-01	1.17E-01	WT N 1 dpi	DNA	Zinc finger, LSD1-type (AHRD V3.3 *** A0A103XQX8_CYNCS)	

Solyc09g011990.1	**1.50E+00**	**2.34E-06**	5.30E-01	4.21E-02	6.28E-01	1.77E-02	5.02E-01	5.35E-02	WT N 1 dpi	PMI	Clade IV lectin receptor kinase (AHRD V3.3 *** K4CRM4_SOLLC)	GO:0004672|GO:0005524|GO :0006468
Solyc03g005210.3	**1.49E+00**	**4.92E-03**	9.01E-01	7.47E-02	-8.72E-01	8.38E-02	-8.59E-01	8.83E-02	WT N 1 dpi	CS	Alpha-amylase inhibitor, lipid transfer and seed storage protein(AHRD V3.3 *** A0A075BNW0_SOLTU)	
Solyc02g093650.3	**1.49E+00**	**6.35E-03**	7.16E-01	1.64E-01	1.92E-01	7.05E-01	7.03E-01	1.72E-01	WT N 1 dpi	PMI	Early nodulin-like protein (AHRDV3.3 *** A0A072U7R7_MEDTR)	GO:0009055
Solyc09g065430.3	**1.48E+00**	**5.52E-05**	6.13E-01	5.67E-02	-7.02E-01	3.08E-02	-6.16E-01	5.55E-02	WT N 1 dpi	L	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)	GO:0006869|GO:0008289
Solyc03g095860.3	**1.47E+00**	**1.55E-05**	7.17E-01	1.58E-02	3.05E-01	2.81E-01	1.60E-01	5.69E-01	WT N 1 dpi	P	Ankyrin repeat-containing protein(AHRD V3.3 *** A0A103YIY1_CYNCS)	GO:0005515
Solyc08g067630.3	**1.47E+00**	**1.06E-04**	5.65E-01	9.09E-02	-3.90E-01	2.37E-01	-1.67E-01	6.08E-01	WT N 1 dpi	DNA	histone deacetylase-like protein(AHRD V3.3 *** AT2G25625.2)	
Solyc01g105435.1	**1.47E+00**	**8.26E-05**	3.23E-01	3.15E-01	-5.66E-02	8.59E-01	-2.88E-01	3.70E-01	WT N 1 dpi	TR	ABC transporter G family member(AHRD V3.3 *** A0A0K9NWI5_ZOSMR)	GO:0005524|GO:0016887
Solyc01g106173.1	**1.47E+00**	**2.19E-03**	1.95E-01	6.55E-01	1.98E-01	6.51E-01	-7.67E-01	8.78E-02	WT N 1 dpi	STR	PDI-like 2-3 (AHRD V3.3 --* AT2G32920.1)	
Solyc04g015120.3	**1.47E+00**	**4.08E-05**	9.63E-01	3.27E-03	-6.75E-01	3.17E-02	-1.02E-01	7.35E-01	WT N 1 dpi	P	U-box domain-containing protein 33(AHRD V3.3 *** W9RCI3_9ROSA)	
Solyc07g065110.1	**1.47E+00**	**4.87E-03**	6.90E-01	1.59E-01	1.80E-01	7.09E-01	6.48E-01	1.85E-01	WT N 1 dpi	L	Lipid transfer protein (AHRD V3.3 *** G7J041_MEDTR)	
Solyc12g006430.2	**1.46E+00**	**3.95E-05**	8.57E-01	7.55E-03	-8.41E-02	7.78E-01	-5.01E-02	8.67E-01	WT N 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DBI0_SOLLC)	GO:0008152|GO:0016758
Solyc09g090470.3	**1.46E+00**	**1.27E-07**	7.31E-01	1.31E-03	3.19E-01	1.28E-01	4.49E-01	3.55E-02	WT N 1 dpi	TR	Peptide transporter (AHRD V3.3 *** G7I4R9_MEDTR)	GO:0005215|GO:0006810|GO :0016020
Solyc02g090440.3	**1.46E+00**	**1.49E-03**	1.05E+00	1.62E-02	4.06E-01	3.31E-01	4.99E-01	2.35E-01	WT N 1 dpi	P	ankyrin repeat family protein (AHRDV3.3 --* AT4G05040.7)	
Solyc03g097390.3	**1.46E+00**	**9.83E-05**	7.12E-01	3.32E-02	-2.21E-01	4.91E-01	-2.38E-01	4.59E-01	WT N 1 dpi	L	Acyl-[acyl-carrier-protein] hydrolase(AHRD V3.3 *** K4BJF6_SOLLC)	GO:0006633|GO:0016790

Solyc05g047540.3	**1.45E+00**	**1.58E-04**	7.70E-01	2.71E-02	5.34E-01	1.16E-01	-6.59E-01	5.56E-02	WT N 1 dpi	RNA	Pentatricopeptide repeat superfamily protein, putative (AHRDV3.3 *** A0A061GYI5_THECC)	GO:0003674|GO:0003676|GO:0003723|GO:0003824|GO:0004518|GO:0004519|GO:0005488|GO:0005575|GO:0005622|GO:0005623|GO:0005737|GO:0005739|GO:0006139|GO:0006417|GO:0006446|GO:0006725|GO:0006807|GO:0008150|GO:0008152|GO:0009451|GO:0009507|GO:0009536|GO:0009889|GO:0009891|GO:0009893|GO:0009987|GO:0010468|GO:0010556|GO:0010557|GO:0010604|GO:0010608|GO:0010628|GO:0016070|GO:0016787|GO:0016788|GO:0019222|GO:0031323|GO:0031325|GO:0031326|GO:0031328|GO:0032268|GO:0032270|GO:0034248|GO:0034250|GO:0034641|GO:0043170|GO:0043226|GO:0043227|GO:0043229|GO:0043231|GO:0043412|GO:0044237|GO:0044238|GO:0044424|GO:0044444|GO:0044464|GO:0045727|GO:0045948|GO:0046483|GO:0048518|GO:0048522|GO:0050789|GO:0050794|GO:0051171|GO:00
Solyc07g054270.3	**1.44E+00**	**1.72E-07**	8.83E-01	1.97E-04	9.24E-01	1.16E-04	4.52E-01	3.53E-02	WT N 1 dpi	NA	Plant/F9H3-4 protein (AHRD V3.3 *** A0A072VLR0_MEDTR)	
Solyc01g090140.2	**1.44E+00**	**1.75E-03**	1.06E+00	1.64E-02	3.60E-01	3.90E-01	-6.15E-01	1.48E-01	WT N 1 dpi	H	2-oxoglutarate (2OG) and Fe(II)- dependent oxygenase superfamilyprotein (AHRD V3.3 *** AT2G44800.1)	GO:0016491|GO:0055114
Solyc01g094990.2	**1.43E+00**	**2.22E-03**	6.05E-01	1.64E-01	1.18E-01	7.82E-01	1.45E-01	7.34E-01	WT N 1 dpi	C	LOW QUALITY:transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)	
Solyc05g050210.3	**1.43E+00**	**6.86E-04**	5.60E-01	1.44E-01	-4.11E-02	9.13E-01	2.50E-01	5.06E-01	WT N 1 dpi	L	GDSL esterase/lipase family (AHRDV3.3 *** A0A151QZV0_CAJCA)	GO:0016788
Solyc12g009880.1	**1.43E+00**	**1.28E-06**	9.43E-01	3.28E-04	2.67E-01	2.53E-01	8.93E-02	6.98E-01	WT N 1 dpi	D	LOW QUALITY:Serine-rich protein-related (AHRD V3.3 *** A0A061GN42_THECC)	
Solyc02g069960.3	**1.43E+00**	**7.86E-03**	6.20E-01	2.22E-01	2.47E-01	6.22E-01	1.40E-01	7.80E-01	WT N 1 dpi	T	NAC domain-containing protein,putative (AHRD V3.3 *** B9RI29_RICCO)	GO:0003677|GO:0006355
Solyc04g009870.1	**1.41E+00**	**2.61E-05**	4.70E-02	8.67E-01	4.14E-01	1.47E-01	9.90E-01	1.40E-03	WT N 1 dpi	2M	Beta-carotene hydroxylase 2,chloroplastic (AHRD V3.3 --* BCH2_CAPAN)	
Solyc12g089220.2	**1.40E+00**	**3.10E-07**	7.39E-02	7.22E-01	4.96E-01	2.32E-02	1.25E-01	5.48E-01	WT N 1 dpi	D	Bifunctional nuclease 1 (AHRD V3.3 *** BBD1_ARATH)	GO:0004518
Solyc01g009430.3	**1.40E+00**	**4.42E-08**	7.30E-01	4.97E-04	4.30E-01	2.71E-02	2.73E-01	1.49E-01	WT N 1 dpi	NA	BnaA07g13420D protein (AHRD V3.3 *** A0A078ETL1_BRANA)	

Solyc01g107540.3	**1.39E+00**	**1.58E-03**	6.96E-01	8.93E-02	3.30E-01	4.10E-01	4.85E-01	2.30E-01	WT N 1 dpi	TR	Plant basic secretory family protein(AHRD V3.3 *** B9GHT3_POPTR)	
Solyc05g056450.3	**1.39E+00**	**9.55E-07**	6.75E-01	4.63E-03	1.80E-02	9.35E-01	-7.18E-02	7.44E-01	WT N 1 dpi	P	Eukaryotic aspartyl protease familyprotein (AHRD V3.3 *** AT2G03200.1)	GO:0004190|GO:0006508
Solyc12g008550.2	**1.39E+00**	**4.87E-09**	6.78E-01	2.85E-04	3.68E-01	3.16E-02	2.27E-01	1.72E-01	WT N 1 dpi	P	Peptidase M28 family protein (AHRD V3.3 *-* AT5G19740.1)	
Solyc02g092880.3	**1.39E+00**	**8.48E-09**	4.80E-01	7.65E-03	6.92E-01	3.03E-04	5.76E-01	1.83E-03	WT N 1 dpi	G	maternal effect embryo arrest 59 (AHRD V3.3 *** AT4G37300.1)	
Solyc07g005900.3	**1.38E+00**	**1.64E-03**	5.96E-01	1.41E-01	-2.76E-01	4.87E-01	-1.60E-01	6.86E-01	WT N 1 dpi	D	Calcium-binding EF-hand familyprotein (AHRD V3.3 *** A0A061GQP8_THECC)	GO:0005509
Solyc01g105497.1	**1.38E+00**	**6.37E-04**	7.51E-01	4.41E-02	4.86E-01	1.83E-01	-2.06E-01	5.66E-01	WT N 1 dpi	N	ureide permease 2 (AHRD V3.3 --* AT2G03530.5)	
Solyc07g053200.3	**1.36E+00**	**1.85E-06**	9.24E-02	6.80E-01	8.46E-01	7.59E-04	-1.14E-01	6.11E-01	WT N 1 dpi	DNA	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT1G11360.4)	GO:0006950
Solyc12g044200.2	**1.35E+00**	**3.42E-03**	6.62E-01	1.26E-01	-6.22E-01	1.50E-01	-1.25E+00	6.26E-03	WT N 1 dpi	D	Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *** A0A072VNI6_MEDTR)	GO:0043531
Solyc08g078170.1	**1.35E+00**	**4.53E-03**	2.23E-01	6.11E-01	4.25E-01	3.36E-01	-5.30E-02	9.04E-01	WT N 1 dpi	H	Ethylene-responsive transcriptionfactor (AHRD V3.3 *** A0A024CAT9_BRAJU)	GO:0003677
Solyc06g064895.1	**1.35E+00**	**6.60E-03**	6.17E-01	1.87E-01	-3.61E-01	4.35E-01	-4.91E-01	2.91E-01	WT N 1 dpi	STR	Aldehyde dehydrogenase, putative (AHRD V3.3 *-* B9SH74_RICCO)	GO:0008152|GO:0016491|GO :0055114
Solyc08g061230.3	**1.34E+00**	**5.68E-04**	7.65E-01	3.37E-02	1.27E-01	7.14E-01	-6.02E-02	8.61E-01	WT N 1 dpi	L	alpha/beta-Hydrolases superfamilyprotein (AHRD V3.3 *-* AT4G33180.1)	
Solyc02g071970.1	**1.34E+00**	**8.32E-03**	1.50E-01	7.51E-01	6.59E-03	9.89E-01	1.07E-01	8.21E-01	WT N 1 dpi	PMI	LOW QUALITY:F-box and LeucineRich Repeat domains containing protein (AHRD V3.3 --* AT1G80960.6)	
Solyc02g076830.1	**1.33E+00**	**4.20E-08**	3.81E-01	3.80E-02	3.86E-01	3.57E-02	2.17E-01	2.23E-01	WT N 1 dpi	K	Serine/threonine-protein kinase(AHRD V3.3 *-* A0A199VI10_ANACO)	
Solyc09g074700.2	**1.33E+00**	**1.28E-04**	7.10E-01	2.41E-02	5.15E-01	9.36E-02	-6.86E-02	8.19E-01	WT N 1 dpi	DNA	Homeobox protein LUMINIDEPENDENS (AHRD V3.3 *- * A0A0B2R2D8_GLYSO)	
Solyc10g084910.2	**1.31E+00**	**1.56E-05**	8.08E-01	3.12E-03	7.50E-01	5.54E-03	4.48E-01	8.21E-02	WT N 1 dpi	DNA	C2H2 zinc finger protein (AHRDV3.3 *-* A5JUQ4_SOYBN)	GO:0003676
Solyc10g049870.1	**1.31E+00**	**2.10E-04**	5.33E-01	9.11E-02	6.35E-02	8.36E-01	2.07E-01	5.02E-01	WT N 1 dpi	DNA	Zinc finger protein, putative (AHRDV3.3 *** B9SNA3_RICCO)	GO:0046872
Solyc02g070890.3	**1.30E+00**	**7.98E-08**	5.77E-01	3.01E-03	7.56E-01	2.23E-04	6.83E-01	6.60E-04	WT N 1 dpi	NA	Ontology_term=GO:0004675	GO:0004672|GO:0005524|GO :0006468
Solyc11g019910.1	**1.30E+00**	**1.43E-04**	5.41E-01	7.55E-02	-3.38E-01	2.57E-01	3.10E-01	2.97E-01	WT N 1 dpi	CS	LOW QUALITY:Plant invertase/pectin methylesteraseinhibitor (AHRD V3.3 *** I3T947_MEDTR)	GO:0004857
Solyc01g091060.1	**1.30E+00**	**5.20E-06**	6.86E-01	5.60E-03	5.48E-02	8.11E-01	1.90E-01	4.11E-01	WT N 1 dpi	CS	Pectinesterase (AHRD V3.3 ***K4AZ46_SOLLC)	GO:0004857

Solyc11g006030.1	**1.29E+00**	**3.70E-04**	5.92E-01	7.23E-02	5.40E-01	9.97E-02	3.78E-01	2.42E-01	WT N 1 dpi	P	U-box domain-containing familyprotein (AHRD V3.3 *** U5FLQ4_POPTR)	GO:0004842|GO:0016567
Solyc09g075610.3	**1.29E+00**	**8.06E-03**	7.85E-01	9.31E-02	-1.88E-01	6.80E-01	1.53E-01	7.37E-01	WT N 1 dpi	T	GATA transcription factor, putative(AHRD V3.3 *** B9RNI7_RICCO)	GO:0003700|GO:0006355|GO :0008270|GO:0043565
Solyc03g113890.1	**1.29E+00**	**6.44E-05**	8.50E-01	4.23E-03	3.67E-01	1.87E-01	1.53E-02	9.55E-01	WT N 1 dpi	DNA	LOW QUALITY:Zinc finger familyprotein (AHRD V3.3 *-* B9HJ48_POPTR)	GO:0003676
Solyc01g094170.3	**1.29E+00**	**1.42E-09**	2.88E-01	5.06E-02	-1.60E-01	2.65E-01	-5.08E-02	7.21E-01	WT N 1 dpi	PMI	Digalactosyldiacylglycerol synthase(AHRD V3.3 *** A2Q3N6_MEDTR)	
Solyc05g052420.2	**1.29E+00**	**2.37E-06**	5.68E-01	1.32E-02	7.38E-01	1.90E-03	7.19E-01	2.36E-03	WT N 1 dpi	H	Abscisic acid receptor (AHRD V3.3 *** G7JKP6_MEDTR)	
Solyc07g043580.3	**1.27E+00**	**4.49E-04**	2.08E-01	5.18E-01	3.21E-01	3.21E-01	1.39E-01	6.64E-01	WT N 1 dpi	T	bHLH transcription factor 052	GO:0046983
Solyc04g078410.3	**1.27E+00**	**6.41E-07**	6.85E-01	1.58E-03	8.06E-01	3.20E-04	3.04E-01	1.29E-01	WT N 1 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** M0ZUR7_SOLTU)	GO:0004672|GO:0005524|GO :0006468
Solyc08g067610.3	**1.27E+00**	**4.02E-10**	1.93E-01	1.50E-01	2.52E-01	6.32E-02	-8.06E-02	5.41E-01	WT N 1 dpi	TR	Pleiotropic drug resistance ABCtransporter (AHRD V3.3 *** W0TUG3_ACAMN)	GO:0005524|GO:0016887
Solyc02g077880.3	**1.26E+00**	**7.45E-07**	5.99E-01	4.86E-03	4.86E-01	1.91E-02	3.10E-01	1.23E-01	WT N 1 dpi	H	auxin repressed/dormancyassociated protein	
Solyc09g066150.1	**1.26E+00**	**6.64E-04**	3.05E-01	3.58E-01	2.46E-01	4.57E-01	2.97E-01	3.70E-01	WT N 1 dpi	CYTP450	Cytochrome P450, putative (AHRDV3.3 *** B9S4U5_RICCO)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc06g005070.2	**1.26E+00**	**1.59E-06**	4.77E-01	2.70E-02	5.50E-02	7.89E-01	-3.90E-01	6.64E-02	WT N 1 dpi	TR	Major facilitator superfamily protein(AHRD V3.3 *** AT1G68570.1)	GO:0005215|GO:0006810|GO :0016020
Solyc06g071890.3	**1.26E+00**	**8.53E-03**	7.83E-02	8.60E-01	6.08E-01	1.80E-01	2.51E-01	5.75E-01	WT N 1 dpi	C	Mitochondrial pyruvate carrier (AHRD V3.3 *** K4C8R1_SOLLC)	GO:0005743|GO:0006850
Solyc03g025455.1	**1.25E+00**	**1.22E-04**	5.82E-01	4.58E-02	4.44E-01	1.22E-01	-5.09E-01	7.77E-02	WT N 1 dpi	P	U-box domain-containing familyprotein (AHRD V3.3 *-* B9I8K1_POPTR)	
Solyc04g072310.3	**1.25E+00**	**1.80E-08**	7.90E-01	2.93E-05	6.45E-01	3.33E-04	-4.50E-02	7.75E-01	WT N 1 dpi	D	Elicitor peptide 1 (AHRD V3.3 --* A0A087GE76_ARAAL)	
Solyc02g079533.1	**1.25E+00**	**4.55E-05**	2.43E-01	3.51E-01	1.20E-01	6.42E-01	9.78E-02	7.05E-01	WT N 1 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** E5D7E5_TOBAC)	GO:0004672|GO:0005524|GO :0006468
Solyc09g098160.3	**1.24E+00**	**5.07E-09**	6.91E-01	6.15E-05	2.26E-01	1.30E-01	-1.25E-01	3.94E-01	WT N 1 dpi	D	pirin	
Solyc08g061240.2	**1.23E+00**	**2.21E-07**	6.37E-01	1.31E-03	6.90E-01	6.07E-04	1.64E-01	3.62E-01	WT N 1 dpi	L	alpha/beta-Hydrolases superfamilyprotein (AHRD V3.3 *** AT4G33180.1)	
Solyc06g072550.3	**1.23E+00**	**8.14E-03**	1.00E+00	2.73E-02	7.23E-01	1.05E-01	4.78E-01	2.76E-01	WT N 1 dpi	CS	CASP-like protein (AHRD V3.3 *** K4C8X5_SOLLC)	
Solyc10g076250.2	**1.23E+00**	**1.93E-05**	5.28E-01	3.36E-02	5.62E-01	2.45E-02	1.76E-01	4.60E-01	WT N 1 dpi	N	Alanine-glyoxylate aminotransferase, putative (AHRDV3.3 *** B9SZ94_RICCO)	GO:0003824
Solyc04g007160.1	**1.23E+00**	**9.97E-07**	7.93E-01	3.48E-04	-2.13E-03	9.91E-01	1.26E-01	5.19E-01	WT N 1 dpi	C	Alpha-glucosidase (AHRD V3.3 *-*Q9LEC9_SOLTU)	GO:0004553|GO:0005975
Solyc02g093975.1	**1.21E+00**	**4.89E-06**	4.43E-01	4.51E-02	1.53E-01	4.73E-01	4.52E-01	4.11E-02	WT N 1 dpi	S	Receptor protein kinase-like protein(AHRD V3.3 *-* Q9FMT0_ARATH)	GO:0004672|GO:0005524|GO :0006468
Solyc03g032040.3	**1.20E+00**	**5.22E-06**	3.25E-01	1.34E-01	6.86E-01	3.10E-03	5.56E-02	7.94E-01	WT N 1 dpi	TR	Tonoplast monosaccharidetransporter 1	GO:0005215|GO:0016021|GO :0055085

Solyc03g120690.3	**1.20E+00**	**9.66E-03**	7.18E-01	1.07E-01	8.27E-01	6.58E-02	4.98E-01	2.57E-01	WT N 1 dpi	CS	Dynein light chain family protein (AHRD V3.3 *** B9GXB1_POPTR)	GO:0007017|GO:0030286
Solyc01g106177.1	**1.20E+00**	**1.22E-06**	4.01E-01	4.51E-02	2.87E-03	9.88E-01	1.89E-01	3.31E-01	WT N 1 dpi	T	MADS-box transcription factor (AHRD V3.3 *** G7IS85_MEDTR)	GO:0003700|GO:0005634|GO :0006355
Solyc01g099080.3	**1.20E+00**	**9.11E-03**	5.03E-01	2.47E-01	-3.23E-01	4.54E-01	1.52E-01	7.23E-01	WT N 1 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A199UFA2_ANACO)	
Solyc11g069125.1	**1.20E+00**	**4.78E-03**	2.40E-01	5.41E-01	-6.37E-02	8.71E-01	-2.78E-01	4.79E-01	WT N 1 dpi	C	beta glucosidase 7 (AHRD V3.3 --*AT3G62740.2)	
Solyc11g040040.2	**1.19E+00**	**5.41E-09**	5.78E-01	3.19E-04	5.92E-01	2.46E-04	2.17E-01	1.32E-01	WT N 1 dpi	G	Phototropic-responsive NPH3 familyprotein (AHRD V3.3 *** AT3G19850.1)	GO:0005515
Solyc01g008620.3	**1.19E+00**	**6.64E-04**	4.01E-01	2.04E-01	5.05E-01	1.13E-01	5.56E-01	8.25E-02	WT N 1 dpi	CS	Beta-1,3-glucanase (AHRD V3.3 *** Q9SYX6_TOBAC)	GO:0004553|GO:0005975
Solyc12g005660.2	**1.19E+00**	**2.83E-05**	4.81E-01	5.02E-02	1.78E-01	4.54E-01	-1.78E-01	4.54E-01	WT N 1 dpi	DNA	Zinc finger, B-box (AHRD V3.3 *-* A0A103Y7X2_CYNCS)	GO:0005622|GO:0008270
Solyc01g106200.2	**1.18E+00**	**8.91E-03**	3.15E-01	4.58E-01	1.38E-01	7.44E-01	4.98E-01	2.45E-01	WT N 1 dpi	TR	Oligopeptide transporter, putative(AHRD V3.3 *** B9RX59_RICCO)	GO:0055085
Solyc12g045020.2	**1.18E+00**	**1.70E-05**	4.11E-01	7.83E-02	-5.57E-01	1.99E-02	2.22E-01	3.31E-01	WT N 1 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW5_POPTR)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc05g025890.2	**1.18E+00**	**1.97E-03**	6.33E-01	7.63E-02	4.59E-01	1.92E-01	7.77E-01	3.20E-02	WT N 1 dpi	H	Acyl-CoA N-acyltransferases (NAT) superfamily protein (AHRD V3.3 *** AT2G06025.6)	GO:0008080
Solyc09g092420.2	**1.17E+00**	**3.83E-06**	6.30E-01	4.20E-03	2.47E-01	2.30E-01	-1.08E-02	9.57E-01	WT N 1 dpi	AM	Amino acid permease family protein(AHRD V3.3 *** AT1G31830.1)	GO:0003333|GO:0015171|GO :0016020
Solyc06g050160.3	**1.17E+00**	**5.77E-03**	4.55E-01	2.54E-01	-8.02E-01	4.98E-02	-4.01E-01	3.13E-01	WT N 1 dpi	DNA	Homeobox leucine zipper protein(AHRD V3.3 *** A0A072TNH2_MEDTR)	GO:0003677
Solyc03g097030.3	**1.17E+00**	**8.62E-04**	7.47E-01	2.36E-02	-5.21E-01	1.05E-01	-3.35E-02	9.15E-01	WT N 1 dpi	2M	4-coumarate--CoA ligase	GO:0003824|GO:0008152
Solyc03g112755.1	**1.16E+00**	**4.54E-04**	3.93E-01	1.86E-01	-1.32E-01	6.51E-01	2.94E-01	3.20E-01	WT N 1 dpi	H	Tornado 1 (AHRD V3.3 *-* A0A061F576_THECC)	
Solyc12g056090.2	**1.16E+00**	**3.47E-09**	1.56E-01	2.49E-01	-4.58E-02	7.32E-01	1.64E-01	2.26E-01	WT N 1 dpi	E	Cox19-like CHCH family protein(AHRD V3.3 *-* AT4G23760.1)	
Solyc03g118450.1	**1.16E+00**	**5.57E-03**	1.04E+00	1.12E-02	1.08E-01	7.80E-01	-4.66E-02	9.04E-01	WT N 1 dpi	P	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolasessuperfamily protein (AHRD V3.3 --*AT2G28290.6)	
Solyc05g054890.3	**1.16E+00**	**3.43E-05**	5.21E-01	3.29E-02	-2.13E-01	3.65E-01	-8.85E-02	7.05E-01	WT N 1 dpi	TR	ABC transporter family protein (AHRD V3.3 *** B9HTY6_POPTR)	GO:0005524|GO:0016887
Solyc01g008640.3	**1.15E+00**	**4.28E-05**	6.94E-01	6.49E-03	-2.45E-02	9.17E-01	-1.86E-01	4.34E-01	WT N 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc00g233480.1	**1.15E+00**	**4.93E-04**	3.61E-01	2.22E-01	-2.18E-02	9.40E-01	-2.75E-01	3.50E-01	WT N 1 dpi	TR	ABC transporter (AHRD V3.3 *-* H1A8M9_DIOKA)	GO:0005524|GO:0016887
Solyc06g036110.1	**1.15E+00**	**1.73E-05**	4.03E-01	7.60E-02	-2.60E-01	2.44E-01	-2.69E-01	2.28E-01	WT N 1 dpi	S	LOW QUALITY:Calcium-dependentlipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT5G23950.2)	GO:0005515
Solyc02g092410.3	**1.15E+00**	**2.43E-06**	7.95E-01	2.98E-04	4.79E-01	1.84E-02	8.85E-02	6.45E-01	WT N 1 dpi	K	Adenylyl-sulfate kinase (AHRD V3.3 *** K4BD37_SOLLC)	GO:0000103|GO:0004020|GO :0005524

Solyc09g009490.3	**1.14E+00**	**8.70E-04**	5.16E-01	1.01E-01	-2.62E-01	3.97E-01	-2.76E-02	9.28E-01	WT N 1 dpi	H	Abscisic acid insensitive (AHRD V3.3 *** B3U2B5_CUCSA)	GO:0003700|GO:0005634|GO :0009737|GO:0045893
Solyc01g096090.3	**1.14E+00**	**1.87E-13**	3.57E-01	1.92E-04	3.98E-01	5.14E-05	5.82E-02	4.85E-01	WT N 1 dpi	NA	Transmembrane protein, putative(AHRD V3.3 *** A0A072U5P8_MEDTR)	
Solyc07g018370.2	**1.14E+00**	**9.68E-03**	3.81E-02	9.26E-01	2.69E-01	5.14E-01	7.29E-01	8.48E-02	WT N 1 dpi	T	mediator of RNA polymerase II transcription subunit (AHRD V3.3 *** AT4G28840.1)	
Solyc03g095780.2	**1.13E+00**	**8.05E-10**	5.22E-01	1.92E-04	8.78E-01	9.88E-08	6.53E-01	1.10E-05	WT N 1 dpi	H	Abscisic acid receptor (AHRD V3.3 *** G7JKP6_MEDTR)	
Solyc01g080910.2	**1.13E+00**	**3.34E-04**	6.11E-01	3.39E-02	1.33E-02	9.61E-01	2.33E-01	4.01E-01	WT N 1 dpi	RNA	LOW QUALITY:polyadenylate- binding protein 1-B-binding protein (AHRD V3.3 *** AT4G19950.1)	
Solyc06g048410.3	**1.12E+00**	**1.91E-07**	3.61E-01	3.23E-02	3.03E-01	6.85E-02	3.98E-01	1.94E-02	WT N 1 dpi	OX	iron superoxide dismutase	GO:0004784|GO:0006801|GO :0046872|GO:0055114
Solyc10g047810.2	**1.12E+00**	**1.27E-05**	9.75E-01	7.87E-05	-6.45E-03	9.75E-01	1.68E-01	4.26E-01	WT N 1 dpi	PMI	Clade XVII lectin receptor kinase (AHRD V3.3 *** K4D043_SOLLC)	GO:0004672|GO:0005524|GO :0006468
Solyc06g019200.3	**1.12E+00**	**8.03E-03**	6.54E-01	1.05E-01	-2.42E-01	5.40E-01	-6.59E-02	8.67E-01	WT N 1 dpi	H	Ethylene-dependent gravitropism-deficient and yellow-green-like 2 isoform 2 (AHRD V3.3 *** A0A061FLR5_THECC)	
Solyc01g102675.1	**1.12E+00**	**2.50E-03**	6.99E-01	4.63E-02	5.47E-01	1.13E-01	-4.56E-01	1.84E-01	WT N 1 dpi	PMI	Leucine-rich repeat receptor-likeprotein kinase (AHRD V3.3 *-* Q8GY50_ARATH)	
Solyc08g059700.2	**1.12E+00**	**4.42E-03**	2.61E-01	4.71E-01	-8.67E-01	2.26E-02	-8.84E-01	2.04E-02	WT N 1 dpi	DNA	Histone acetyltransferase (AHRD V3.3 *** A0A0B0NK56_GOSAR)	
Solyc01g098410.3	**1.11E+00**	**1.52E-03**	6.83E-01	3.90E-02	3.07E-01	3.37E-01	3.91E-01	2.24E-01	WT N 1 dpi	S	Receptor protein kinase, putative (AHRD V3.3 *** B9RXG1_RICCO)	GO:0004672|GO:0005524|GO :0006468
Solyc03g031760.3	**1.11E+00**	**4.24E-08**	6.72E-01	9.04E-05	-6.66E-02	6.50E-01	-8.76E-02	5.51E-01	WT N 1 dpi	DNA	Homeobox-leucine zipper familyprotein (AHRD V3.3 *** B9GU68_POPTR)	GO:0008289
Solyc08g081480.3	**1.11E+00**	**1.54E-08**	7.53E-01	9.68E-06	4.13E-02	7.66E-01	-1.40E-01	3.18E-01	WT N 1 dpi	CS	Pectin lyase-like superfamily protein(AHRD V3.3 *** AT4G23500.1)	GO:0004650|GO:0005975
Solyc01g049925.1	**1.11E+00**	**5.02E-05**	-5.57E-02	8.09E-01	3.27E-01	1.65E-01	-3.01E-01	1.99E-01	WT N 1 dpi	E	Cytochrome b (AHRD V3.3 --* CYB_VICFA)	
Solyc01g108100.3	**1.11E+00**	**8.03E-03**	5.85E-01	1.42E-01	4.32E-01	2.74E-01	2.86E-01	4.66E-01	WT N 1 dpi	G	Cold regulated gene 27, putativeisoform 1 (AHRD V3.3 *** A0A061DZZ1_THECC)	
Solyc03g098730.1	**1.11E+00**	**6.17E-03**	6.86E-01	7.63E-02	4.65E-01	2.22E-01	6.32E-01	1.01E-01	WT N 1 dpi	D	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)	GO:0004866
Solyc08g005420.3	**1.10E+00**	**2.53E-03**	6.73E-01	5.17E-02	2.39E-01	4.76E-01	3.91E-02	9.07E-01	WT N 1 dpi	P	WD40 repeat-containing protein(AHRD V3.3 *** A0A103YEC3_CYNCS)	GO:0005515
Solyc04g016010.3	**1.10E+00**	**1.48E-03**	9.82E-01	3.91E-03	8.56E-01	1.04E-02	-6.92E-02	8.25E-01	WT N 1 dpi	OX	Thioredoxin reductase (AHRD V3.3 *** M1C6N0_SOLTU)	GO:0016491|GO:0055114
Solyc12g008660.1	**1.10E+00**	**3.14E-06**	8.98E-01	5.48E-05	2.71E-01	1.57E-01	6.32E-02	7.37E-01	WT N 1 dpi	T	Zinc finger transcription factor 73	GO:0046872
Solyc03g116520.1	**1.10E+00**	**7.87E-03**	4.77E-01	2.23E-01	7.50E-01	6.01E-02	4.57E-01	2.42E-01	WT N 1 dpi	NA	LOW QUALITY:cotton fiber protein(AHRD V3.3 --* AT1G15385.1)	

Solyc01g066260.2	**1.10E+00**	**4.00E-04**	8.16E-01	5.70E-03	1.49E-01	5.87E-01	3.48E-01	2.10E-01	WT N 1 dpi	P	LOW QUALITY:dyggve-melchior-clausen syndrome protein (AHRD V3.3 --* AT1G04200.2)	
Solyc10g009487.1	**1.10E+00**	**7.52E-04**	4.78E-01	1.08E-01	2.80E-01	3.40E-01	2.62E-02	9.28E-01	WT N 1 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G46494.1)	GO:0005515|GO:0008270
Solyc08g065320.3	**1.10E+00**	**1.64E-09**	7.21E-01	2.79E-06	4.03E-01	2.62E-03	2.69E-01	3.48E-02	WT N 1 dpi	H	green ripe-like 1	
Solyc11g069570.2	**1.10E+00**	**6.79E-05**	7.80E-01	2.37E-03	6.04E-01	1.48E-02	-8.22E-02	7.25E-01	WT N 1 dpi	H	Cytokinin riboside 5'- monophosphate phosphoribohydrolase (AHRD V3.3 *** K4DAB3_SOLLC)	
Solyc09g072880.3	**1.10E+00**	**2.09E-06**	1.12E-01	5.42E-01	-2.05E-01	2.67E-01	-3.99E-01	3.61E-02	WT N 1 dpi	E	Fluorescent in blue light, chloroplastic-like protein (AHRD V3.3 *** A0A0B0PKQ3_GOSAR)	GO:0005515
Solyc09g064940.2	**1.10E+00**	**2.20E-05**	-3.01E-02	8.88E-01	4.91E-01	2.87E-02	1.63E-01	4.47E-01	WT N 1 dpi	P	Phenazine biosynthesis PhzC/PhzFfamily protein (AHRD V3.3 *** B9HYD6_POPTR)	GO:0003824|GO:0009058
Solyc09g074690.3	**1.10E+00**	**7.46E-04**	4.13E-01	1.61E-01	7.67E-01	1.27E-02	-2.17E-01	4.54E-01	WT N 1 dpi	G	Homeobox LUMINIDEPENDENS-like protein (AHRD V3.3 *-* A0A0B0NNT5_GOSAR)	GO:0003677
Solyc02g083730.3	**1.09E+00**	**5.55E-09**	1.15E-01	3.78E-01	-7.03E-01	9.60E-06	-3.25E-01	1.76E-02	WT N 1 dpi	P	Rhodanese-related sulfurtransferase(AHRD V3.3 *** G7JXI1_MEDTR)	
Solyc02g068400.3	**1.09E+00**	**5.17E-03**	1.47E-01	6.83E-01	-4.29E-01	2.41E-01	-3.28E-01	3.66E-01	WT N 1 dpi	CS	Pectin lyase-like superfamily protein(AHRD V3.3 *** AT4G20050.5)	
Solyc04g049670.3	**1.09E+00**	**3.59E-13**	5.07E-01	1.25E-06	6.06E-01	6.09E-08	3.77E-01	8.20E-05	WT N 1 dpi	T	Pseudo-response regulator (AHRD V3.3 *** X5I0R0_IPONI)	GO:0000160
Solyc09g007535.1	**1.09E+00**	**7.15E-03**	6.82E-01	7.87E-02	7.00E-01	7.15E-02	7.35E-02	8.45E-01	WT N 1 dpi	DNA	chromatin remodeling 38 (AHRD V3.3 --* AT3G42670.4)	
Solyc07g054230.3	**1.09E+00**	**1.14E-05**	5.03E-01	1.87E-02	-1.23E-01	5.46E-01	-7.85E-02	6.99E-01	WT N 1 dpi	TR	Regulator of Vps4 activity in theMVB pathway protein, putative (AHRD V3.3 *** A0A061E4V2_THECC)	GO:0015031
Solyc07g061890.1	**1.09E+00**	**1.38E-05**	5.71E-01	9.26E-03	4.89E-01	2.34E-02	2.18E-01	2.93E-01	WT N 1 dpi	STR	LOW QUALITY:Heat stress transcription factor B-4b, putative(AHRD V3.3 *** A0A061FAG8_THECC)	
Solyc08g066160.3	**1.08E+00**	**1.74E-08**	2.76E-01	4.92E-02	3.91E-02	7.72E-01	1.75E-01	2.03E-01	WT N 1 dpi	PMI	Early nodulin 93 (AHRD V3.3 *** G7I281_MEDTR)	
Solyc02g086360.3	**1.08E+00**	**4.97E-06**	1.85E-01	3.32E-01	4.21E-01	3.31E-02	1.25E-01	5.10E-01	WT N 1 dpi	K	Phox/Bem1p (AHRD V3.3 *** A0A124SEH3_CYNCS)	GO:0005515
Solyc11g044960.2	**1.08E+00**	**8.79E-03**	6.77E-01	8.61E-02	6.09E-01	1.20E-01	-4.17E-01	2.81E-01	WT N 1 dpi	K	Protein kinase family protein GCN2(AHRD V3.3 *-* A0A0N7AH70_TOBAC)	GO:0005515
Solyc03g080100.3	**1.07E+00**	**5.54E-04**	7.52E-01	1.05E-02	6.62E-01	2.24E-02	-7.59E-02	7.83E-01	WT N 1 dpi	TR	Heavy metal transport/detoxificationsuperfamily protein (AHRD V3.3 *-* AT5G24580.4)	GO:0030001|GO:0046872
Solyc01g009810.3	**1.07E+00**	**1.50E-03**	8.55E-01	8.86E-03	-2.14E-01	4.85E-01	4.30E-02	8.88E-01	WT N 1 dpi	PMI	Leucine-rich repeat receptor-likekinase protein (AHRD V3.3 *-* A0A060H1D1_ELAGV)	GO:0005515
Solyc06g060010.3	**1.07E+00**	**2.07E-04**	5.71E-01	2.98E-02	6.82E-01	1.09E-02	-1.23E-01	6.23E-01	WT N 1 dpi	2M	Terpene synthase (AHRD V3.3 *** G5CV42_SOLLC)	GO:0008152|GO:0010333|GO:0016829

Solyc02g071950.1	**1.07E+00**	**1.16E-06**	4.80E-01	8.73E-03	-8.52E-02	6.19E-01	-1.81E-01	2.94E-01	WT N 1 dpi	AM	LOW QUALITY:asparagine synthetase 2 (AHRD V3.3 --* AT5G65010.1)	
Solyc05g052750.3	**1.07E+00**	**3.21E-07**	8.99E-01	4.80E-06	6.47E-01	3.23E-04	3.64E-03	9.82E-01	WT N 1 dpi	L	Alpha/beta hydrolase related protein(AHRD V3.3 *** A0A061FLN1_THECC)	
Solyc01g088660.3	**1.06E+00**	**3.70E-06**	2.39E-01	2.00E-01	2.37E-01	2.04E-01	1.45E-01	4.32E-01	WT N 1 dpi	G	senescence-associated family protein (DUF581) (AHRD V3.3 *** AT2G44670.1)	
Solyc10g017490.2	**1.06E+00**	**7.26E-04**	5.66E-01	5.13E-02	1.03E-01	7.14E-01	-3.84E-01	1.78E-01	WT N 1 dpi	K	MAP kinase kinase kinase 74	GO:0004672|GO:0005524|GO :0006468
Solyc01g067300.3	**1.06E+00**	**1.51E-08**	4.10E-01	4.29E-03	-7.97E-02	5.47E-01	1.90E-01	1.58E-01	WT N 1 dpi	CS	CASP-like protein (AHRD V3.3 *** K4AWX9_SOLLC)	
Solyc07g017990.3	**1.06E+00**	**2.13E-04**	2.75E-01	2.74E-01	6.50E-01	1.38E-02	-4.79E-01	6.22E-02	WT N 1 dpi	DNA	DNA ligase (AHRD V3.3 *** K4CCL3_SOLLC)	GO:0003677|GO:0003910|GO :0005524|GO:0006281|GO:00 51103
Solyc06g053310.3	**1.05E+00**	**6.18E-12**	1.91E-01	3.97E-02	-2.82E-02	7.52E-01	3.58E-02	6.88E-01	WT N 1 dpi	C	Hydroxyacylglutathione hydrolase (AHRD V3.3 *** G7IS04_MEDTR)	GO:0004416|GO:0019243
Solyc09g090020.3	**1.05E+00**	**7.34E-06**	1.80E-01	3.45E-01	4.24E-02	8.23E-01	2.20E-01	2.51E-01	WT N 1 dpi	STR	Germin-like protein 1 (AHRD V3.3 *** A8QK89_VITVI)	GO:0030145
Solyc01g106340.3	**1.05E+00**	**1.44E-03**	4.66E-02	8.75E-01	1.97E-02	9.47E-01	1.31E-01	6.60E-01	WT N 1 dpi	L	fatty acid amide hydrolase (AHRD V3.3 *** AT5G64440.1)	GO:0004040
Solyc09g075270.1	**1.04E+00**	**3.24E-03**	4.43E-01	1.80E-01	-4.18E-01	2.05E-01	-6.87E-01	4.23E-02	WT N 1 dpi	NA	transmembrane protein, putative(Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G02360.1)	
Solyc10g078550.3	**1.04E+00**	**3.21E-05**	8.10E-01	6.01E-04	7.58E-01	1.15E-03	-1.98E-01	3.48E-01	WT N 1 dpi	N	glutamate dehydrogenase	GO:0004352
Solyc05g054820.1	**1.04E+00**	**1.59E-04**	3.13E-01	1.95E-01	7.02E-01	6.27E-03	6.73E-01	8.37E-03	WT N 1 dpi	TR	LOW QUALITY:Exocyst subunit EXO70 family protein (AHRD V3.3 *** B9HTX5_POPTR)	GO:0000145|GO:0006887
Solyc12g036340.1	**1.04E+00**	**1.30E-03**	3.87E-01	1.92E-01	4.11E-01	1.66E-01	3.12E-01	2.89E-01	WT N 1 dpi	RNA	Pentatricopeptide repeat (PPR-like)superfamily protein (AHRD V3.3 --* AT1G05670.3)	
Solyc00g227860.1	**1.04E+00**	**6.90E-03**	7.54E-01	4.33E-02	9.35E-01	1.39E-02	3.74E-01	3.02E-01	WT N 1 dpi	C	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XS50_DAUCA)	GO:0008152|GO:0016758
Solyc12g008650.2	**1.04E+00**	**2.69E-03**	9.65E-02	7.61E-01	9.61E-01	5.00E-03	1.99E-01	5.30E-01	WT N 1 dpi	S	Myo-inositol oxygenase (AHRD V3.3 *** C6K2L2_SOLLC)	GO:0005506|GO:0005737|GO :0019310|GO:0050113|GO:00 55114
Solyc04g008075.1	**1.04E+00**	**1.06E-04**	6.54E-01	7.86E-03	2.11E-01	3.60E-01	2.83E-01	2.23E-01	WT N 1 dpi	D	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)	GO:0004866
Solyc06g053480.3	**1.03E+00**	**2.04E-09**	1.42E-01	2.28E-01	-4.57E-02	6.94E-01	1.40E-01	2.35E-01	WT N 1 dpi	L	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A0V0I9I2_SOLCH)	GO:0006631|GO:0045300|GO :0055114
Solyc06g035790.3	**1.03E+00**	**5.11E-03**	5.11E-02	8.81E-01	2.24E-01	5.13E-01	-4.48E-02	8.95E-01	WT N 1 dpi	CS	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G00750.1)	GO:0008168
Solyc01g094340.3	**1.03E+00**	**4.93E-04**	1.96E-01	4.56E-01	5.33E-01	4.97E-02	-2.72E-01	3.03E-01	WT N 1 dpi	L	Carboxyltransferase alpha Subunit(AHRD V3.3 *** A0A0G2SJ78_SALMI)	GO:0003989|GO:0006633|GO :0009317
Solyc05g052610.3	**1.03E+00**	**6.58E-06**	3.83E-01	4.58E-02	1.98E-01	2.88E-01	2.35E-02	8.99E-01	WT N 1 dpi	T	Myb family transcription factor familyprotein (AHRD V3.3 *** B9HT09_POPTR)	GO:0003677

Solyc03g112320.3	**1.03E+00**	**1.12E-05**	8.79E-01	8.75E-05	6.84E-01	1.28E-03	1.43E-01	4.56E-01	WT N 1 dpi	TR	Ferric reduction oxidase 8 (AHRD V3.3 *** W9RI94_9ROSA)	GO:0016020|GO:0016491|GO :0055114
Solyc01g087200.3	**1.03E+00**	**2.32E-04**	1.57E-01	5.20E-01	-9.06E-03	9.70E-01	7.73E-02	7.50E-01	WT N 1 dpi	D	Disease resistance protein (AHRD V3.3 *** A0A118JXS4_CYNCS)	GO:0043531
Solyc01g102850.2	**1.03E+00**	**7.15E-05**	2.08E-01	3.46E-01	3.64E-01	1.06E-01	6.71E-03	9.76E-01	WT N 1 dpi	D	Disease resistance protein (TIR- NBS-LRR class) family (AHRD V3.3 *** AT5G36930.2)	GO:0005515
Solyc06g082260.3	**1.03E+00**	**3.37E-03**	5.18E-01	1.15E-01	6.88E-02	8.30E-01	-6.20E-01	6.18E-02	WT N 1 dpi	PMI	Laccase (AHRD V3.3 *** A0A1B0YZD2_DAUCA)	GO:0005507
Solyc03g006700.3	**1.02E+00**	**1.22E-08**	5.65E-01	1.23E-04	5.19E-01	3.22E-04	3.95E-01	4.01E-03	WT N 1 dpi	OX	Peroxidase (AHRD V3.3 *** K4BE93_SOLLC)	GO:0004601|GO:0006979|GO :0020037|GO:0055114
Solyc08g029000.3	**1.02E+00**	**5.47E-05**	1.40E-01	5.14E-01	8.33E-01	5.49E-04	5.20E-01	2.09E-02	WT N 1 dpi	L	Lipoxygenase (AHRD V3.3 *** Q43800_TOBAC)	GO:0005515
Solyc02g068660.2	**1.02E+00**	**4.67E-07**	9.88E-01	7.28E-07	5.64E-01	1.01E-03	3.84E-01	1.82E-02	WT N 1 dpi	K	Kinase, putative (AHRD V3.3 *** B9RE26_RICCO)	GO:0004672|GO:0005524|GO :0006468
Solyc12g088050.2	**1.01E+00**	**3.78E-06**	3.65E-01	4.47E-02	5.00E-01	7.70E-03	1.62E-01	3.59E-01	WT N 1 dpi	CS	Rhamnogalacturonate lyase familyprotein (AHRD V3.3 *** AT1G09890.4)	GO:0003824|GO:0005975|GO :0030246
Solyc01g102410.3	**1.01E+00**	**1.72E-09**	2.55E-01	3.06E-02	5.53E-01	3.86E-05	2.71E-01	2.24E-02	WT N 1 dpi	RNA	Glutamyl-tRNA synthetase (AHRDV3.3 *** G7IAE3_MEDTR)	GO:0000166|GO:0004812|GO :0005524|GO:0005737|GO:00 06418
Solyc12g010430.1	**1.01E+00**	**1.25E-06**	4.19E-01	1.50E-02	4.94E-01	4.99E-03	1.74E-01	2.89E-01	WT N 1 dpi	P	LOW QUALITY:NHL domain protein(AHRD V3.3 --* AT3G01430.1)	
Solyc01g010350.3	**1.01E+00**	**3.38E-04**	2.01E-01	4.18E-01	9.92E-03	9.68E-01	-1.49E-01	5.48E-01	WT N 1 dpi	C	Glucose-6-phosphate translocator	GO:0005215|GO:0006810|GO :0016021
Solyc08g076170.1	**1.01E+00**	**6.15E-06**	7.49E-01	2.75E-04	3.52E-01	5.84E-02	5.94E-01	2.58E-03	WT N 1 dpi	P	LOW QUALITY:50S ribosomal protein L22, chloroplastic (AHRD V3.3 -** RK22_CHLAT)	
Solyc02g087580.3	**1.01E+00**	**8.23E-04**	3.68E-01	1.78E-01	4.89E-01	7.73E-02	7.26E-01	1.13E-02	WT N 1 dpi	CS	Actin cross-linking (AHRD V3.3 *** A0A103Y4S4_CYNCS)	
Solyc06g071410.3	**1.01E+00**	**1.63E-07**	5.98E-01	2.67E-04	-1.79E-01	2.17E-01	-1.81E-01	2.13E-01	WT N 1 dpi	K	MAP kinase kinase kinase 40	GO:0004672|GO:0005524|GO :0006468
Solyc07g005110.3	**1.00E+00**	**7.55E-05**	3.98E-01	7.35E-02	9.36E-01	1.72E-04	5.58E-01	1.47E-02	WT N 1 dpi	K	Receptor-like kinase CHRK1 (AHRDV3.3 *** Q9SWX8_TOBAC)	GO:0004553|GO:0005975
Solyc01g067690.3	**1.00E+00**	**1.41E-03**	3.73E-01	1.95E-01	2.90E-01	3.10E-01	7.50E-01	1.28E-02	WT N 1 dpi	T	Sgf11 (Transcriptional regulationprotein) protein (AHRD V3.3 --* A0A072TU18_MEDTR)	
Solyc09g075920.1	**1.00E+00**	**5.96E-04**	5.10E-01	5.71E-02	5.78E-01	3.28E-02	-5.39E-02	8.35E-01	WT N 1 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** K4CVG9_SOLLC)	GO:0004672|GO:0005524|GO :0006468
Solyc10g080610.1	**1.00E+00**	**2.86E-04**	6.48E-01	1.17E-02	9.33E-01	6.07E-04	3.25E-01	1.86E-01	WT N 1 dpi	P	F-box/kelch-repeat protein (AHRD V3.3 *** A0A172MAC1_VITPS)	GO:0005515
Solyc01g005680.3	**-1.00E+00**	**2.05E-05**	-3.03E-01	1.29E-01	-7.58E-01	5.76E-04	-3.60E-01	7.33E-02	WT N 1 dpi	H	Cytokinin riboside 5'- monophosphate phosphoribohydrolase (AHRD V3.3 *** K4ASD4_SOLLC)	
Solyc07g017220.3	**-1.01E+00**	**4.57E-10**	-3.64E-01	1.72E-03	-7.46E-01	1.37E-07	-2.68E-01	1.59E-02	WT N 1 dpi	G	senescence-associated family protein, putative (DUF581) (AHRD V3.3 *** AT5G20700.1)	
Solyc10g085130.2	**-1.01E+00**	**8.40E-06**	-3.51E-01	6.49E-02	-8.83E-01	5.19E-05	-3.50E-01	6.57E-02	WT N 1 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT5G01520.1)	GO:0005515|GO:0008270

Solyc07g018300.3	**-1.01E+00**	**1.16E-03**	-3.27E-01	2.47E-01	-7.47E-02	7.89E-01	2.51E-01	3.73E-01	WT N 1 dpi	DNA	Replication protein A subunit (AHRDV3.3 *** A0A1D1Z493_9ARAE)	GO:0003676
Solyc07g062220.3	**-1.01E+00**	**3.97E-03**	-2.66E-01	4.12E-01	-2.59E-01	4.25E-01	-2.46E-02	9.39E-01	WT N 1 dpi	CS	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)	
Solyc10g084950.2	**-1.01E+00**	**3.09E-06**	-2.57E-02	8.82E-01	-1.41E-01	4.17E-01	-5.57E-01	3.09E-03	WT N 1 dpi	TR	Major facilitator superfamily protein(AHRD V3.3 *** AT2G37900.1)	GO:0005215|GO:0006810|GO :0016020
Solyc08g081350.2	**-1.01E+00**	**8.93E-03**	-7.24E-01	5.37E-02	-2.60E-01	4.74E-01	-3.78E-01	3.00E-01	WT N 1 dpi	G	LOW QUALITY:Zinc finger protein CONSTANS-LIKE 3 (AHRD V3.3 *** W9QPI7_9ROSA)	GO:0005515
Solyc03g116280.3	**-1.01E+00**	**6.04E-04**	2.96E-01	2.64E-01	-2.74E-01	3.01E-01	6.69E-01	1.60E-02	WT N 1 dpi	H	1-aminocyclopropane-1-carboxylate oxidase 2 (AHRD V3.3 *-* M7YEU7_TRIUA)	GO:0016491|GO:0055114
Solyc06g065010.3	**-1.01E+00**	**1.32E-06**	-5.56E-01	2.02E-03	-6.78E-01	2.90E-04	-2.91E-01	8.45E-02	WT N 1 dpi	L	Lipase, GDSL (AHRD V3.3 *** A0A124SDS7_CYNCS)	GO:0016788
Solyc06g009130.3	**-1.01E+00**	**7.25E-07**	-1.91E-01	2.31E-01	-4.89E-01	4.30E-03	-2.87E-01	7.77E-02	WT N 1 dpi	TR	Magnesium/proton exchanger family member (AHRD V3.3 *** K4C3U3_SOLLC)	GO:0016021|GO:0055085
Solyc03g117470.3	**-1.01E+00**	**2.92E-03**	-6.82E-01	3.62E-02	1.24E-02	9.68E-01	7.69E-02	8.05E-01	WT N 1 dpi	D	Calcium-binding EF-hand familyprotein (AHRD V3.3 *** AT3G18430.3)	GO:0005509
Solyc07g062500.3	**-1.02E+00**	**4.54E-07**	-5.61E-01	1.04E-03	-5.89E-01	6.46E-04	-5.34E-01	1.63E-03	WT N 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc07g043390.3	**-1.02E+00**	**3.90E-03**	-3.42E-01	2.96E-01	-7.60E-01	2.57E-02	-2.94E-01	3.67E-01	WT N 1 dpi	CS	Cellulose synthase (AHRD V3.3 *** A0A118J5T2_CYNCS)	GO:0016020|GO:0016760|GO :0030244
Solyc12g043150.2	**-1.02E+00**	**2.41E-04**	-3.76E-01	1.28E-01	-7.98E-01	2.55E-03	-2.11E-01	3.85E-01	WT N 1 dpi	TR	Regulator of Vps4 activity in theMVB pathway protein, putative (AHRD V3.3 *** A0A061GBK3_THECC)	GO:0015031
Solyc02g081600.3	**-1.02E+00**	**6.56E-03**	-1.87E-01	5.92E-01	-6.66E-01	6.40E-02	-6.00E-01	9.33E-02	WT N 1 dpi	TR	Zinc transporter protein (AHRD V3.3 *** A5BDR3_VITVI)	GO:0005385|GO:0016021|GO :0071577
Solyc11g007730.2	**-1.02E+00**	**2.60E-03**	1.41E-01	6.48E-01	-7.65E-01	1.91E-02	-6.89E-01	3.31E-02	WT N 1 dpi	N	Bark storage protein A (AHRD V3.3 *** W9SCI4_9ROSA)	GO:0003824|GO:0009116
Solyc10g085610.2	**-1.02E+00**	**3.55E-03**	-5.73E-01	8.41E-02	-8.48E-01	1.32E-02	1.68E-01	6.02E-01	WT N 1 dpi	DNA	Calmodulin binding protein, putative(AHRD V3.3 *** B9T5N0_RICCO)	GO:0005515
Solyc10g005020.3	**-1.03E+00**	**1.81E-06**	-5.28E-01	4.09E-03	-5.23E-01	4.37E-03	-1.81E-01	2.89E-01	WT N 1 dpi	NA	DUF4228 domain protein (AHRD V3.3 *** G7LHF9_MEDTR)	
Solyc01g096435.1	**-1.03E+00**	**3.97E-06**	-4.12E-01	2.75E-02	-4.33E-01	2.12E-02	-2.20E-01	2.23E-01	WT N 1 dpi	D	NADPH:quinone oxidoreductase (AHRD V3.3 *** AT3G27890.1)	GO:0016491
Solyc05g056120.3	**-1.03E+00**	**8.33E-06**	-5.01E-01	1.22E-02	-7.21E-01	6.49E-04	-4.74E-01	1.70E-02	WT N 1 dpi	T	GATA transcription factor (AHRD V3.3 *** K4C2T6_SOLLC)	GO:0003677|GO:0005634|GO :0045893
Solyc07g043420.3	**-1.03E+00**	**5.23E-05**	-3.34E-01	1.30E-01	-7.66E-01	1.35E-03	8.63E-02	6.89E-01	WT N 1 dpi	E	2-oxoglutarate-dependent dioxygenase 2	GO:0016491|GO:0055114
Solyc04g073940.3	**-1.04E+00**	**3.52E-03**	-4.61E-01	1.64E-01	-2.59E-01	4.29E-01	-1.55E-01	6.34E-01	WT N 1 dpi	OX	TPR repeat-containing thioredoxinTTL1-like protein (AHRD V3.3 *** A0A0B2PI95_GLYSO)	GO:0005515
Solyc09g009130.3	**-1.04E+00**	**7.34E-04**	-3.48E-01	2.12E-01	-9.83E-01	1.25E-03	-3.80E-01	1.73E-01	WT N 1 dpi	G	Phytosulfokine 3, putative (AHRD V3.3 *** A0A061ESV9_THECC)	GO:0005576|GO:0008083|GO :0008283
Solyc06g084820.2	**-1.04E+00**	**3.40E-06**	-3.83E-01	3.98E-02	-8.34E-01	7.38E-05	-2.12E-01	2.41E-01	WT N 1 dpi	CYTP450	Cytochrome P450, putative (AHRDV3.3 *** A0A061G7Z4_THECC)	GO:0005506|GO:0016705|GO :0020037|GO:0055114

Solyc04g078470.3	**-1.04E+00**	**1.84E-03**	-3.64E-01	2.37E-01	-6.84E-01	3.14E-02	1.47E-01	6.30E-01	WT N 1 dpi	G	D-type cyclin-3	GO:0005634
Solyc08g008050.3	**-1.05E+00**	**2.19E-05**	-1.53E-01	4.56E-01	-9.78E-01	5.27E-05	-8.86E-02	6.65E-01	WT N 1 dpi	TR	plasma membrane intrinsic protein 1.1	GO:0005215|GO:0006810|GO:0016020
Solyc01g068640.3	**-1.05E+00**	**4.88E-08**	-4.70E-01	2.13E-03	-4.17E-01	5.46E-03	-1.84E-01	1.92E-01	WT N 1 dpi	K	aarF domain-containing protein kinase	
Solyc03g026080.3	**-1.05E+00**	**8.12E-11**	-4.25E-01	2.31E-04	-6.37E-01	9.18E-07	-6.60E-01	5.07E-07	WT N 1 dpi	P	Rhomboid-like protein (AHRD V3.3 *** K4BF81_SOLLC)	GO:0004252|GO:0006508|GO:0016021
Solyc04g016060.1	**-1.05E+00**	**2.25E-06**	-6.37E-01	1.09E-03	-6.49E-01	9.15E-04	-2.40E-02	8.91E-01	WT N 1 dpi	E	MIZU-KUSSEI-like protein (Proteinof unknown function, DUF617) (AHRD V3.3 *** AT2G41660.1)	
Solyc11g011330.2	**-1.05E+00**	**2.28E-07**	-6.38E-01	2.57E-04	-4.00E-01	1.34E-02	-4.60E-01	5.15E-03	WT N 1 dpi	2M	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9T7R7_RICCO)	GO:0008270|GO:0016491|GO:0055114
Solyc09g056340.3	**-1.05E+00**	**2.35E-07**	-4.50E-01	6.20E-03	-4.84E-01	3.56E-03	-1.39E-01	3.67E-01	WT N 1 dpi	NA	Ras family (AHRD V3.3 *** A0A191UMR0_SOLDE)	GO:0005525
Solyc10g081910.2	**-1.05E+00**	**4.82E-07**	-2.64E-01	1.06E-01	-6.07E-01	6.97E-04	-2.96E-01	7.15E-02	WT N 1 dpi	S	Receptor-kinase-like protein (AHRDV3.3 *** A0A072U3D4_MEDTR)	GO:0004672|GO:0005524|GO:0006468
Solyc07g052230.3	**-1.06E+00**	**8.98E-05**	-2.51E-01	2.83E-01	-5.11E-01	3.49E-02	-5.89E-01	1.63E-02	WT N 1 dpi	D	L-ascorbate oxidase like (AHRD V3.3 *** A0A0B2S927_GLYSO)	GO:0005507
Solyc03g098490.1	**-1.06E+00**	**1.16E-06**	-3.59E-01	4.31E-02	-8.51E-01	3.07E-05	-3.52E-01	4.67E-02	WT N 1 dpi	NA	LOW QUALITY:Cotton fiber expressed protein (AHRD V3.3 *** A0A109XNG5_GOSHI)	
Solyc12g009270.1	**-1.07E+00**	**2.54E-03**	-3.60E-01	2.69E-01	-3.54E-01	2.76E-01	-1.44E-01	6.55E-01	WT N 1 dpi	CS	Plant invertase/pectin methylesterase inhibitor superfamilyprotein (AHRD V3.3 *** A0A061GSW0_THECC)	GO:0004857
Solyc04g015520.3	**-1.07E+00**	**1.05E-07**	-7.02E-02	6.36E-01	-6.06E-01	3.37E-04	-4.08E-01	9.97E-03	WT N 1 dpi	PMI	Remorin family protein (AHRD V3.3 *** A0A061F452_THECC)	
Solyc01g096430.3	**-1.07E+00**	**1.89E-03**	-4.11E-01	1.96E-01	-4.32E-01	1.74E-01	-9.29E-02	7.66E-01	WT N 1 dpi	RNA	Maturase K (AHRD V3.3 --* MATK_PAESU)	
Solyc08g081710.3	**-1.07E+00**	**3.74E-03**	-5.50E-01	1.14E-01	-1.85E-01	5.87E-01	-2.02E-01	5.55E-01	WT N 1 dpi	S	membrane-associated kinaseregulator (AHRD V3.3 *** AT1G64080.1)	
Solyc09g065770.1	**-1.08E+00**	**1.25E-05**	1.08E-01	5.91E-01	-8.88E-01	1.46E-04	-1.73E-01	3.94E-01	WT N 1 dpi	P	LOW QUALITY:Ubiquitin- conjugating enzyme/RWD-like protein, putative (AHRD V3.3 *** A0A061DQB8_THECC)	GO:0006464|GO:0015031
Solyc05g012330.3	**-1.08E+00**	**4.09E-06**	-4.15E-01	3.36E-02	-9.75E-01	1.68E-05	-4.00E-01	4.00E-02	WT N 1 dpi	N	Ureide permease (AHRD V3.3 *-* A0A124SG70_CYNCS)	GO:0016021|GO:0071705
Solyc02g032030.1	**-1.08E+00**	**1.29E-07**	4.92E-02	7.45E-01	-7.25E-01	5.19E-05	-2.18E-01	1.57E-01	WT N 1 dpi	CS	Dirigent protein (AHRD V3.3 *** K4B5E9_SOLLC)	
Solyc10g083950.1	**-1.08E+00**	**9.25E-06**	-4.56E-01	2.80E-02	-8.14E-01	3.14E-04	-2.69E-01	1.81E-01	WT N 1 dpi	PMI	LOW QUALITY:Nodulin-like / MajorFacilitator Superfamily protein (AHRD V3.3 *** A0A0K9NWX1_ZOSMR)	GO:0016021|GO:0055085
Solyc09g059970.3	**-1.08E+00**	**1.34E-03**	-5.19E-01	9.56E-02	-8.27E-01	1.06E-02	-1.70E-01	5.75E-01	WT N 1 dpi	P	Small ubiquitin-related modifier (AHRD V3.3 *** Q9SMD1_SOLLC)	GO:0005515
Solyc03g078630.3	**-1.08E+00**	**1.77E-09**	-3.92E-01	2.91E-03	-3.28E-01	1.06E-02	-1.48E-01	2.25E-01	WT N 1 dpi	P	Polyubiquitin (AHRD V3.3 *-* UBI2P_PETCR)	GO:0005515
Solyc01g021600.3	**-1.08E+00**	**3.11E-04**	-1.10E-01	6.76E-01	-8.08E-01	4.47E-03	1.32E-01	6.15E-01	WT N 1 dpi	CS	Dirigent protein (AHRD V3.3 *** K4AV41_SOLLC)	

Solyc01g102940.3	**-1.08E+00**	**3.31E-08**	-1.99E-01	1.67E-01	-1.35E-01	3.44E-01	-6.87E-02	6.27E-01	WT N 1 dpi	NA	methionine S-methyltransferase (AHRD V3.3 *** AT5G49810.1)	GO:0003824
Solyc06g073320.3	**-1.09E+00**	**2.84E-08**	-4.71E-01	2.26E-03	-5.88E-01	2.59E-04	-2.63E-01	7.00E-02	WT N 1 dpi	D	GDP-L-galactose phosphorylase 1 (AHRD V3.3 *** AT4G26850.1)	GO:0080048
Solyc02g078860.3	**-1.09E+00**	**3.34E-03**	-6.00E-01	8.67E-02	-8.62E-02	8.00E-01	4.14E-01	2.31E-01	WT N 1 dpi	STR	3(2),5-bisphosphate nucleotidaseHAL2 (AHRD V3.3 *** A0A118JXE0_CYNCS)	GO:0006790|GO:0008441
Solyc03g095310.3	**-1.09E+00**	**2.67E-09**	-1.40E-01	2.67E-01	-5.92E-01	5.78E-05	-4.50E-01	1.18E-03	WT N 1 dpi	CYTP450	Cytochrome P450 protein (AHRD V3.3 *** A0A0B0P3Q6_GOSAR)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc04g079080.2	**-1.09E+00**	**2.06E-06**	-5.90E-01	2.97E-03	-5.87E-01	3.08E-03	-2.13E-01	2.46E-01	WT N 1 dpi	D	LOW QUALITY:Calcium-binding EF-hand (AHRD V3.3 *-* A0A103YCM4_CYNCS)	GO:0005509
Solyc01g111610.3	**-1.10E+00**	**9.68E-03**	1.32E-01	7.39E-01	-3.04E-01	4.45E-01	-2.75E-01	4.90E-01	WT N 1 dpi	RNA	SBP (S-ribonuclease binding protein) family protein (AHRD V3.3 *** AT4G35070.1)	GO:0004842|GO:0005634|GO :0016567|GO:0031347
Solyc02g089700.3	**-1.10E+00**	**1.52E-08**	-2.20E-01	1.17E-01	-4.27E-01	4.20E-03	-3.18E-01	2.74E-02	WT N 1 dpi	CS	Trichome birefringence-like protein(AHRD V3.3 *** A0A072TUJ8_MEDTR)	
Solyc03g115060.3	**-1.10E+00**	**4.93E-03**	-6.27E-01	9.20E-02	1.39E-01	7.00E-01	-7.71E-02	8.31E-01	WT N 1 dpi	N	Assimilatory nitrate reductase catalytic subunit (AHRD V3.3 *** A0A0B0NYS4_GOSAR)	
Solyc11g012040.2	**-1.10E+00**	**9.17E-03**	-9.01E-02	8.20E-01	-1.07E-01	7.87E-01	-1.57E-01	6.91E-01	WT N 1 dpi	P	Ubiquitin-specific protease family C19-related protein (AHRD V3.3 *** AT4G22290.1)	
Solyc07g042500.3	**-1.11E+00**	**8.80E-07**	-8.25E-01	6.24E-05	-5.34E-01	4.78E-03	-5.32E-01	4.90E-03	WT N 1 dpi	L	Alpha/beta-Hydrolases superfamilyprotein, putative (AHRD V3.3 *** A0A061GM37_THECC)	GO:0016020
Solyc02g078900.3	**-1.11E+00**	**3.04E-09**	-4.42E-01	1.70E-03	-4.89E-01	6.53E-04	-1.66E-01	1.99E-01	WT N 1 dpi	E	Internal alternative NAD(P)H- ubiquinone oxidoreductase A1,mitochondrial (AHRD V3.3 *** A0A199VZH3_ANACO)	GO:0016491|GO:0055114
Solyc12g049210.1	**-1.11E+00**	**3.53E-03**	-6.59E-01	6.79E-02	-8.29E-01	2.42E-02	-6.05E-02	8.63E-01	WT N 1 dpi	NA	LOW QUALITY:DUF3511 domain protein (AHRD V3.3 *** G7IS34_MEDTR)	
Solyc05g005040.3	**-1.11E+00**	**1.88E-05**	2.53E-01	2.45E-01	-9.36E-01	1.69E-04	-9.65E-03	9.64E-01	WT N 1 dpi	CS	Pectin lyase-like superfamily protein(AHRD V3.3 *** AT3G26610.1)	GO:0004650|GO:0005975
Solyc04g007685.1	**-1.11E+00**	**2.53E-04**	4.49E-02	8.66E-01	8.82E-02	7.40E-01	3.07E-01	2.54E-01	WT N 1 dpi	G	Hydroxyproline-rich glycoprotein (AHRD V3.3 -** B9HJA6_POPTR)	
Solyc11g069590.2	**-1.12E+00**	**2.96E-08**	-2.60E-01	8.05E-02	-2.76E-02	8.48E-01	-2.81E-01	6.06E-02	WT N 1 dpi	K	Kinase, putative (AHRD V3.3 *** B9SVB0_RICCO)	GO:0004672|GO:0005524|GO :0006468
Solyc11g065620.2	**-1.12E+00**	**5.88E-08**	-5.66E-01	7.73E-04	-8.09E-01	1.08E-05	-2.95E-01	5.80E-02	WT N 1 dpi	AM	Sulfite reductase (AHRD V3.3 *** H6WYS2_SOLLC)	GO:0016491|GO:0020037|GO :0051536|GO:0055114
Solyc01g073670.3	**-1.12E+00**	**3.98E-05**	-4.17E-01	7.66E-02	-7.94E-01	1.67E-03	-3.48E-01	1.36E-01	WT N 1 dpi	TR	Major facilitator superfamily protein(AHRD V3.3 *** AT3G60070.5),Pfam:PF13347	
Solyc12g006110.2	**-1.13E+00**	**3.31E-06**	2.35E-01	2.29E-01	-1.67E-01	3.90E-01	-9.19E-02	6.34E-01	WT N 1 dpi	PMI	Fasciclin-like arabinogalactanprotein (AHRD V3.3 *** G7K0M1_MEDTR)	
Solyc07g007990.3	**-1.13E+00**	**8.69E-04**	-9.85E-01	2.98E-03	-6.40E-01	4.27E-02	-4.32E-02	8.87E-01	WT N 1 dpi	TR	Nucleotide/sugar transporter familyprotein (AHRD V3.3 *** AT4G32272.1)	

Solyc01g095390.3	**-1.13E+00**	**8.31E-04**	-7.34E-01	2.12E-02	9.92E-02	7.43E-01	5.48E-01	7.84E-02	WT N 1 dpi	TR	Intracellular protein transporter USO1-like protein (AHRD V3.3 ***G7KAQ1_MEDTR)	
Solyc03g043930.3	**-1.13E+00**	**1.03E-04**	-3.86E-01	1.30E-01	-8.83E-01	1.43E-03	-5.39E-01	3.84E-02	WT N 1 dpi	H	ADIPOR-like receptor protein(AHRD V3.3 *** A0A0B0MUN3_GOSAR)	GO:0016021
Solyc12g009570.2	**-1.14E+00**	**3.03E-12**	-3.03E-01	3.08E-03	-3.46E-01	9.39E-04	-1.10E-01	2.44E-01	WT N 1 dpi	S	calcineurin B-like interacting proteinkinase	GO:0004672|GO:0005524|GO :0006468
Solyc01g111260.2	**-1.14E+00**	**4.21E-09**	-5.49E-01	3.03E-04	-7.59E-01	4.66E-06	-4.62E-01	1.66E-03	WT N 1 dpi	L	1-phosphatidylinositol phosphodiesterase-related familyprotein (AHRD V3.3 *** B9H168_POPTR)	GO:0006629|GO:0008081
Solyc04g054257.1	**-1.14E+00**	**9.39E-04**	-5.82E-01	6.82E-02	-6.63E-01	3.94E-02	1.59E-01	6.08E-01	WT N 1 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW5_POPTR)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc05g054470.3	**-1.14E+00**	**2.08E-03**	-4.13E-01	2.27E-01	-9.68E-01	7.49E-03	-2.49E-01	4.61E-01	WT N 1 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamilyprotein (AHRD V3.3 --* AT2G28290.6)	
Solyc01g006310.3	**-1.15E+00**	**4.48E-03**	-6.77E-01	7.82E-02	-1.12E-01	7.64E-01	3.58E-01	3.41E-01	WT N 1 dpi	OX	SlPeroxidase	GO:0004601|GO:0006979|GO :0020037|GO:0055114
Solyc02g071060.3	**-1.15E+00**	**7.50E-04**	-4.36E-01	1.60E-01	-5.35E-01	8.76E-02	-1.41E-01	6.43E-01	WT N 1 dpi	TR	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)	GO:0005215|GO:0016021
Solyc04g007705.1	**-1.15E+00**	**1.32E-03**	-2.82E-01	3.87E-01	-6.90E-01	4.07E-02	-1.89E-01	5.61E-01	WT N 1 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 --*AT5G53090.1)	
Solyc02g061850.3	**-1.16E+00**	**3.33E-03**	-2.03E-01	5.76E-01	-1.30E-01	7.21E-01	-5.26E-01	1.54E-01	WT N 1 dpi	L	Phospholipase D (AHRD V3.3 *** K4B675_SOLLC)	GO:0003824
Solyc05g013680.3	**-1.16E+00**	**3.04E-07**	-7.22E-01	2.39E-04	-8.91E-01	1.76E-05	-2.44E-01	1.62E-01	WT N 1 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** W9RN10_9ROSA)	GO:0016788
Solyc10g085920.2	**-1.16E+00**	**6.84E-04**	-4.06E-01	1.89E-01	-6.86E-01	3.11E-02	-4.34E-01	1.61E-01	WT N 1 dpi	CS	UDP-glucuronate decarboxylaseprotein 1 (AHRD V3.3 *** N0A9W0_POPTO)	
Solyc07g043460.3	**-1.17E+00**	**7.00E-04**	-7.14E-01	2.70E-02	-8.15E-01	1.27E-02	-1.48E-01	6.32E-01	WT N 1 dpi	CYTP450	Cytochrome P450, putative (AHRDV3.3 *** A0A061E4E7_THECC)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc09g074780.3	**-1.17E+00**	**1.62E-05**	2.20E-03	9.92E-01	-2.12E-01	3.49E-01	3.27E-01	1.53E-01	WT N 1 dpi	DNA	Zinc finger protein (AHRD V3.3 *** E9NZV2_PHAVU)	GO:0003676
Solyc11g066670.1	**-1.17E+00**	**9.63E-04**	-6.28E-01	5.69E-02	-5.12E-01	1.17E-01	-9.88E-02	7.56E-01	WT N 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4D9S4_SOLLC)	GO:0008152|GO:0016758
Solyc01g097340.3	**-1.18E+00**	**7.67E-06**	4.61E-02	8.28E-01	-7.08E-01	2.46E-03	-3.95E-01	7.22E-02	WT N 1 dpi	2M	GDP-mannose 3',5'-epimerase (AHRD V3.3 *** C6K2K9_SOLLC)	GO:0003824|GO:0050662
Solyc01g011510.3	**-1.18E+00**	**1.78E-07**	-1.37E-01	4.17E-01	-3.04E-01	7.95E-02	-2.47E-01	1.50E-01	WT N 1 dpi	STR	Aldehyde dehydrogenase (AHRDV3.3 *** K4ATY6_SOLLC)	GO:0004030|GO:0006081|GO :0055114
Solyc07g043500.1	**-1.18E+00**	**2.43E-03**	-5.96E-01	1.01E-01	-7.65E-01	3.85E-02	-9.12E-02	7.97E-01	WT N 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CEK8_SOLLC)	GO:0008152|GO:0016758
Solyc02g094300.3	**-1.18E+00**	**2.71E-08**	9.16E-02	5.47E-01	-5.79E-01	6.96E-04	-4.62E-01	4.90E-03	WT N 1 dpi	CS	ACT domain-containing protein(AHRD V3.3 *-* A0A103Y4L4_CYNCS)	GO:0008152|GO:0016597
Solyc01g098570.2	**-1.18E+00**	**2.86E-03**	-5.79E-01	1.18E-01	-9.22E-01	1.61E-02	-5.07E-01	1.68E-01	WT N 1 dpi	G	LOW QUALITY:FANTASTIC four-like protein (DUF3049) (AHRD V3.3 *-* AT1G54740.1)	

Solyc09g011570.3	**-1.18E+00**	**1.91E-06**	-6.79E-01	1.63E-03	-2.86E-01	1.50E-01	-6.14E-02	7.53E-01	WT N 1 dpi	STR	Glutathione S-transferase-likeprotein (AHRD V3.3 *** A8DUB0_SOLLC)	GO:0005515
Solyc03g116260.3	**-1.18E+00**	**3.69E-08**	-1.05E-01	4.98E-01	-5.94E-01	6.41E-04	-3.00E-01	6.07E-02	WT N 1 dpi	E	2-oxoglutarate and Fe(II)-dependentoxygenase superfamily protein, putative (AHRD V3.3 *** A0A061FWB6_THECC)	GO:0016491|GO:0055114
Solyc09g018460.1	**-1.19E+00**	**4.79E-05**	-2.68E-01	2.80E-01	-3.62E-01	1.49E-01	-1.15E-01	6.40E-01	WT N 1 dpi	T	LOW QUALITY:GRAS5	
Solyc02g077000.3	**-1.19E+00**	**2.20E-08**	-1.14E-01	4.55E-01	-2.15E-01	1.66E-01	-2.43E-01	1.19E-01	WT N 1 dpi	L	Phospholipase A1 (AHRD V3.3 *** A5YW95_CAPAN)	GO:0006629
Solyc05g021390.3	**-1.20E+00**	**4.20E-04**	-9.57E-01	3.30E-03	-1.20E-01	6.88E-01	8.09E-01	1.11E-02	WT N 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A161ABB0_OCIBA)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc05g011860.1	**-1.20E+00**	**2.26E-05**	-2.51E-01	2.90E-01	-3.48E-01	1.46E-01	-3.48E-01	1.45E-01	WT N 1 dpi	TR	Sulfotransferase (AHRD V3.3 *** K4BXQ9_SOLLC)	GO:0008146
Solyc03g114860.3	**-1.20E+00**	**6.67E-03**	-2.31E-01	5.74E-01	-5.92E-02	8.85E-01	2.98E-02	9.42E-01	WT N 1 dpi	CS	UDP-arabinose mutase-like protein	GO:0016866|GO:0030244
Solyc01g100850.3	**-1.20E+00**	**5.19E-10**	-6.07E-01	4.77E-05	-6.52E-01	1.88E-05	-2.36E-01	6.91E-02	WT N 1 dpi	TR	ABC transporter family protein(AHRD V3.3 *** A0A097P9U5_HEVBR)	GO:0005524|GO:0016887
Solyc02g089850.3	**-1.20E+00**	**1.42E-06**	-7.28E-01	8.57E-04	-5.97E-01	4.68E-03	-2.39E-01	2.26E-01	WT N 1 dpi	E	Calcium uniporter protein, mitochondrial (AHRD V3.3 *-*A0A0B2RWG8_GLYSO)	
Solyc11g013810.2	**-1.21E+00**	**8.98E-04**	-3.59E-01	2.73E-01	-1.99E-01	5.40E-01	-1.58E-01	6.27E-01	WT N 1 dpi	N	Nitrate reductase (AHRD V3.3 *** K4D6I5_SOLLC)	GO:0006809|GO:0042128|GO :0050464
Solyc01g098500.3	**-1.21E+00**	**9.03E-03**	-5.66E-01	1.99E-01	-1.03E+00	2.42E-02	-4.69E-01	2.84E-01	WT N 1 dpi	TR	Sugar facilitator protein 5	GO:0005215|GO:0016021|GO :0055085
Solyc03g123550.1	**-1.21E+00**	**3.79E-04**	-7.94E-02	7.91E-01	-4.72E-01	1.24E-01	-2.33E-02	9.38E-01	WT N 1 dpi	H	Small auxin up-regulated RNA39	GO:0009733
Solyc11g069360.2	**-1.21E+00**	**6.16E-10**	-5.82E-01	1.03E-04	-4.89E-01	7.07E-04	-3.20E-01	1.83E-02	WT N 1 dpi	T	DHBP synthase RibB-like alpha/beta domain-containingprotein (AHRD V3.3 *** AT5G60590.2)	GO:0003725
Solyc12g088760.1	**-1.23E+00**	**2.28E-05**	-6.08E-02	8.00E-01	-6.50E-01	1.12E-02	2.06E-01	3.95E-01	WT N 1 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** W9SHY0_9ROSA)	GO:0004252|GO:0006508
Solyc07g016215.1	**-1.23E+00**	**5.05E-04**	7.79E-02	8.03E-01	6.19E-01	5.56E-02	3.74E-01	2.36E-01	WT N 1 dpi	NA	Organ specific protein (AHRD V3.3 *** A0A103YKI8_CYNCS)	
Solyc07g007560.3	**-1.23E+00**	**5.48E-06**	-5.29E-01	2.14E-02	-8.66E-01	4.61E-04	-3.77E-01	9.25E-02	WT N 1 dpi	TR	phosphate transporter 4-5 (AHRDV3.3 *** AT5G20380.2)	GO:0016021|GO:0055085
Solyc12g099000.2	**-1.23E+00**	**8.58E-11**	-5.90E-01	3.19E-05	-2.59E-01	3.67E-02	-1.85E-01	1.27E-01	WT N 1 dpi	H	S-adenosylmethionine synthase (AHRD V3.3 *** M1A0F3_SOLTU)	GO:0004478|GO:0005524|GO :0006556
Solyc11g073260.2	**-1.24E+00**	**9.95E-04**	-6.20E-01	7.47E-02	-6.43E-01	6.53E-02	-7.39E-02	8.27E-01	WT N 1 dpi	DNA	Histone H2A (AHRD V3.3 *** K4DB32_SOLLC)	GO:0000786|GO:0003677|GO :0005634
Solyc11g010400.2	**-1.24E+00**	**1.20E-05**	-4.06E-01	8.96E-02	-3.24E-01	1.70E-01	-3.74E-01	1.17E-01	WT N 1 dpi	H	2-oxoglutarate (2OG) and Fe(II)- dependent oxygenase superfamilyprotein (AHRD V3.3 *** AT5G24530.1)	GO:0016491|GO:0055114
Solyc12g011370.2	**-1.25E+00**	**1.95E-06**	-4.13E-01	5.37E-02	-8.13E-01	4.99E-04	-5.61E-01	1.08E-02	WT N 1 dpi	AM	Cationic amino acid transporter,putative (AHRD V3.3 *** B9RY28_RICCO)	GO:0003333|GO:0015171|GO :0016020
Solyc11g072560.2	**-1.26E+00**	**3.87E-04**	2.43E-01	4.38E-01	-8.40E-01	1.14E-02	-8.91E-02	7.75E-01	WT N 1 dpi	TR	Major Facilitator Superfamily protein(AHRD V3.3 *** Q6L3J2_SOLDE)	GO:0005215|GO:0006810|GO :0016020
Solyc02g091080.2	**-1.27E+00**	**2.06E-05**	-1.38E-01	5.78E-01	-2.32E-01	3.53E-01	8.02E-02	7.46E-01	WT N 1 dpi	STR	Protein DETOXIFICATION (AHRDV3.3 *** K4BCQ7_SOLLC)	GO:0006855|GO:0015238|GO :0015297|GO:0016020|GO:00 55085

Solyc05g009590.3	**-1.27E+00**	**1.66E-05**	-7.02E-01	7.31E-03	-6.61E-01	1.10E-02	-2.54E-01	3.03E-01	WT N 1 dpi	G	aluminum activated malate transporter family protein (AHRD V3.3 *** AT1G18420.1)	GO:0015743
Solyc11g065010.1	**-1.28E+00**	**6.95E-04**	7.50E-02	8.23E-01	-4.50E-01	1.86E-01	1.18E-01	7.24E-01	WT N 1 dpi	S	LOW QUALITY:AR781, pheromonereceptor-like protein (DUF1645) (AHRD V3.3 *-* AT2G26530.1)	
Solyc12g044920.2	**-1.28E+00**	**9.20E-06**	-4.13E-01	8.69E-02	-9.71E-01	2.94E-04	-3.07E-01	1.97E-01	WT N 1 dpi	L	Phospholipid-transporting ATPase(AHRD V3.3 *** A0A0V0IZF4_SOLCH)	GO:0000166
Solyc07g043480.1	**-1.28E+00**	**3.34E-03**	-7.65E-01	6.48E-02	-7.01E-01	8.89E-02	-9.29E-02	8.16E-01	WT N 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** A0A0A1WC49_NICAT)	GO:0008152|GO:0016758
Solyc06g074710.1	**-1.30E+00**	**5.69E-03**	2.94E-01	5.01E-01	-2.19E-01	6.16E-01	2.50E-01	5.68E-01	WT N 1 dpi	2M	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase (AHRD V3.3 *** AT5G48930.1)	GO:0016747
Solyc03g005260.3	**-1.30E+00**	**2.54E-09**	-6.91E-01	7.33E-05	-6.37E-01	1.94E-04	-1.93E-01	1.99E-01	WT N 1 dpi	S	ATP-sulfurylase (AHRD V3.3 *** Q1W2K0_CAMSI)	GO:0000103|GO:0004781
Solyc01g008440.3	**-1.30E+00**	**2.68E-11**	-4.62E-01	5.64E-04	-5.25E-01	1.42E-04	-3.43E-01	7.20E-03	WT N 1 dpi	S	Calcium-dependent protein kinase (AHRD V3.3 *** F8V179_HEVBR)	GO:0004672|GO:0005524|GO :0006468
Solyc03g083615.1	**-1.31E+00**	**4.89E-06**	-8.59E-01	8.32E-04	-6.86E-01	5.64E-03	-1.29E-01	5.76E-01	WT N 1 dpi	CS	Plant invertase/pectin methylesterase inhibitor superfamilyprotein (AHRD V3.3 *** AT5G62350.1)	GO:0004857
Solyc10g084240.2	**-1.31E+00**	**4.75E-03**	-7.85E-01	7.48E-02	-4.72E-01	2.75E-01	8.24E-01	6.24E-02	WT N 1 dpi	OX	Peroxidase (AHRD V3.3 *** K4D3L0_SOLLC)	GO:0004601|GO:0006979|GO :0020037|GO:0055114
Solyc10g081700.2	**-1.31E+00**	**1.57E-04**	-6.20E-01	4.59E-02	-6.41E-01	3.95E-02	-2.67E-01	3.75E-01	WT N 1 dpi	E	ATP synthase subunit b, chloroplastic (AHRD V3.3 --* ATPF_PIPCE)	
Solyc03g078150.3	**-1.31E+00**	**2.01E-03**	-6.56E-01	9.76E-02	-2.72E-01	4.83E-01	-4.16E-01	2.85E-01	WT N 1 dpi	AM	Amino acid transporter familyprotein (AHRD V3.3 *** D7LGK0_ARALL)	
Solyc08g066660.1	**-1.32E+00**	**3.24E-07**	-6.36E-01	2.84E-03	-8.15E-01	2.62E-04	-4.76E-01	2.05E-02	WT N 1 dpi	H	Ethylene-responsive transcriptionfactor TINY (AHRD V3.3 *** TINY_ARATH)	GO:0003677
Solyc09g098770.2	**-1.32E+00**	**2.11E-03**	-1.81E-01	6.44E-01	-1.02E-01	7.94E-01	2.40E-01	5.39E-01	WT N 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc02g063510.1	**-1.33E+00**	**8.03E-05**	-2.52E-01	3.83E-01	-6.04E-01	4.25E-02	-9.12E-02	7.50E-01	WT N 1 dpi	NA	LOW QUALITY:GTPase-activatingprotein pac-1 (AHRD V3.3 *** A0A1D1Y9Q3_9ARAE)	
Solyc08g076120.3	**-1.34E+00**	**1.06E-07**	-9.47E-01	2.39E-05	-5.48E-01	6.27E-03	-4.21E-02	8.21E-01	WT N 1 dpi	P	MIP18 family protein (AHRD V3.3 *** A0A0B2S844_GLYSO)	
Solyc11g011740.1	**-1.34E+00**	**7.21E-03**	-6.36E-01	1.79E-01	-7.04E-01	1.38E-01	-6.20E-01	1.90E-01	WT N 1 dpi	H	Ethylene-responsive transcriptionfactor (AHRD V3.3 *** F2Y9E9_COFAR)	GO:0003677
Solyc12g008350.2	**-1.37E+00**	**7.65E-05**	-6.82E-01	2.73E-02	-7.39E-01	1.77E-02	-1.93E-01	5.14E-01	WT N 1 dpi	STR	dehydration responsive element binding protein 2	GO:0003677
Solyc03g119350.2	**-1.38E+00**	**8.32E-04**	-1.93E-01	6.00E-01	-8.61E-01	2.57E-02	-2.21E-01	5.49E-01	WT N 1 dpi	P	peptidase M50B-like protein (AHRD V3.3 *-* AT1G67060.1)	
Solyc06g035710.1	**-1.38E+00**	**1.61E-03**	1.06E+00	1.22E-02	3.10E+00	2.41E-08	1.07E+00	1.14E-02	WT N 1 dpi	STR	Protein DETOXIFICATION (AHRDV3.3 *** K4C4U3_SOLLC)	GO:0006855|GO:0015238|GO :0015297|GO:0016020|GO:00 55085

Solyc01g106140.1	**-1.39E+00**	**5.94E-03**	-2.41E-01	6.07E-01	1.81E-02	9.69E-01	-1.29E-01	7.82E-01	WT N 1 dpi	P	LOW QUALITY:F-box protein family-like (AHRD V3.3 *-* Q6ZCS3_ORYSJ)	
Solyc11g056320.1	**-1.39E+00**	**6.25E-04**	-7.67E-01	4.18E-02	-3.60E-01	3.24E-01	-1.39E-01	7.02E-01	WT N 1 dpi	E	LOW QUALITY:Photosystem II CP47 reaction center protein (AHRD V3.3 --* PSBB_SPIOL)	
Solyc08g075020.3	**-1.39E+00**	**3.92E-04**	-4.14E-01	2.38E-01	-4.08E-01	2.44E-01	-4.42E-01	2.08E-01	WT N 1 dpi	CS	Pectinacetylesterase family protein (AHRD V3.3 *** AT4G19420.2)	GO:0016787
Solyc01g108570.3	**-1.40E+00**	**5.04E-04**	-2.80E-01	4.31E-01	-6.02E-01	9.83E-02	-2.66E-01	4.56E-01	WT N 1 dpi	H	Gibberellin receptor GID1L2 IPR013094 Alpha_beta hydrolase fold-3	GO:0008152|GO:0016787
Solyc04g071620.3	**-1.40E+00**	**8.64E-04**	-4.55E-01	2.31E-01	3.01E-03	9.94E-01	-5.64E-01	1.41E-01	WT N 1 dpi	H	Abscicic acid stress ripening 4	GO:0006950
Solyc05g011850.1	**-1.41E+00**	**3.39E-05**	-1.61E-01	5.72E-01	-4.52E-01	1.20E-01	-1.96E-01	4.93E-01	WT N 1 dpi	TR	Sulfotransferase (AHRD V3.3 *** K4BXQ8_SOLLC)	GO:0008146
Solyc06g076300.3	**-1.43E+00**	**4.67E-03**	-8.74E-01	6.94E-02	-4.92E-01	2.95E-01	2.04E-01	6.62E-01	WT N 1 dpi	K	Haloacid dehalogenase-likehydrolase (AHRD V3.3 *** G7JUV7_MEDTR)	GO:0008152|GO:0016787
Solyc12g088140.2	**-1.43E+00**	**3.55E-04**	-6.60E-01	6.90E-02	1.07E-01	7.60E-01	1.37E+00	5.58E-04	WT N 1 dpi	G	hydroxyproline-rich glycoproteinfamily protein (AHRD V3.3 *** AT5G65660.1)	
Solyc08g007080.3	**-1.43E+00**	**1.40E-06**	-3.89E-01	1.02E-01	-9.10E-01	5.16E-04	-1.62E-01	4.85E-01	WT N 1 dpi	S	Type I inositol-1,4,5-trisphosphate 5-phosphatase (AHRD V3.3 *** G7JZV2_MEDTR)	GO:0046856
Solyc06g074990.2	**-1.46E+00**	**2.31E-06**	6.26E-01	1.57E-02	6.75E-01	9.78E-03	4.13E-01	9.98E-02	WT N 1 dpi	N	putative high affinity nitrate transporter 2	GO:0016021|GO:0055085
Solyc05g008895.1	**-1.47E+00**	**7.35E-04**	-7.72E-01	5.51E-02	-8.99E-01	2.73E-02	-5.62E-01	1.55E-01	WT N 1 dpi	L	Lipid transfer protein (AHRD V3.3 *** I0IK55_9MYRT)	GO:0006869
Solyc09g074760.1	**-1.48E+00**	**6.34E-07**	-8.88E-01	5.61E-04	-5.77E-01	1.67E-02	-3.88E-01	9.73E-02	WT N 1 dpi	T	Nuclear transcription factor Yprotein (AHRD V3.3 *** A0A072TR10_MEDTR)	GO:0005634|GO:0006355|GO :0043565
Solyc01g105660.3	**-1.48E+00**	**2.60E-03**	-1.15E+00	1.51E-02	-2.99E-01	5.06E-01	3.59E-01	4.26E-01	WT N 1 dpi	E	2-oxoglutarate and Fe(II)-dependentoxygenase superfamily protein, putative (AHRD V3.3 *** A0A061E128_THECC)	GO:0016491|GO:0055114
Solyc08g008420.3	**-1.48E+00**	**7.36E-11**	-5.88E-01	2.91E-04	-8.55E-01	2.02E-06	-3.58E-01	1.70E-02	WT N 1 dpi	C	Mitochondrial pyruvate carrier (AHRD V3.3 *** K4CIX6_SOLLC)	GO:0005743|GO:0006850
Solyc09g075820.3	**-1.49E+00**	**1.21E-06**	-7.77E-01	2.94E-03	-1.47E-01	5.39E-01	3.41E-01	1.61E-01	WT N 1 dpi	TR	Sugar transporter protein 2	GO:0005215|GO:0016021|GO :0055085
Solyc08g075540.4	**-1.49E+00**	**1.13E-05**	-9.67E-01	1.61E-03	-5.93E-01	4.03E-02	-1.90E-01	4.95E-01	WT N 1 dpi	D	alternative oxidase 1au	
Solyc00g014830.3	**-1.49E+00**	**1.10E-03**	-2.51E-01	5.42E-01	8.47E-02	8.36E-01	6.87E-03	9.87E-01	WT N 1 dpi	E	NADH dehydrogenase subunit 7(AHRD V3.3 *** A0A0C5B9X5_9SOLA)	GO:0016651|GO:0048038|GO :0051287|GO:0055114
Solyc03g005980.3	**-1.49E+00**	**5.16E-06**	-4.44E-01	1.01E-01	-2.15E-01	4.16E-01	2.54E-02	9.23E-01	WT N 1 dpi	TR	NOD26-like intrinsic protein 1.1	GO:0005215|GO:0006810|GO :0016020
Solyc06g066830.3	**-1.50E+00**	**2.39E-08**	-2.79E-01	1.54E-01	-3.61E-01	6.89E-02	-3.44E-01	8.17E-02	WT N 1 dpi	E	2-oxoglutarate-dependent dioxygenase-related family protein(AHRD V3.3 *** B9GL08_POPTR)	GO:0016491|GO:0055114
Solyc12g009930.2	**-1.50E+00**	**2.38E-07**	-7.68E-01	1.52E-03	-8.51E-01	5.67E-04	-2.19E-01	3.22E-01	WT N 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DC81_SOLLC)	GO:0008152|GO:0016758
Solyc12g056710.2	**-1.51E+00**	**7.95E-03**	3.60E-01	4.98E-01	-1.14E+00	3.88E-02	-5.54E-01	3.00E-01	WT N 1 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 ***AT1G52340.1),Pfam:PF13561	

Solyc02g078600.3	**-1.51E+00**	**8.49E-07**	-4.60E-01	6.08E-02	-7.15E-01	5.26E-03	-4.83E-01	4.94E-02	WT N 1 dpi	TR	polyol monosaccharide transporter 1	GO:0005215|GO:0016021|GO :0055085
Solyc03g123400.1	**-1.54E+00**	**1.74E-09**	-5.54E-01	3.05E-03	-8.24E-01	4.96E-05	-2.73E-01	1.19E-01	WT N 1 dpi	T	GRAS16	
Solyc08g065430.3	**-1.57E+00**	**6.14E-10**	-3.96E-01	2.37E-02	-5.29E-01	3.52E-03	-4.11E-01	1.93E-02	WT N 1 dpi	G	Pollen specific protein sf21, putative(AHRD V3.3 *** B9RRU1_RICCO)	
Solyc02g092840.1	**-1.57E+00**	**4.49E-08**	-6.23E-01	5.56E-03	-6.55E-01	3.81E-03	-5.19E-01	1.82E-02	WT N 1 dpi	CS	Xyloglucan galactosyltransferase KATAMARI1, putative (AHRD V3.3 *** B9R9L8_RICCO)	
Solyc09g008320.3	**-1.58E+00**	**2.05E-04**	-3.07E-01	4.10E-01	-3.79E-01	3.11E-01	-3.66E-01	3.27E-01	WT N 1 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4CQM0_SOLLC)	GO:0004553|GO:0005975
Solyc01g088550.3	**-1.59E+00**	**2.58E-14**	-7.76E-01	7.87E-08	-5.34E-01	2.72E-05	-5.01E-01	6.24E-05	WT N 1 dpi	TR	Purine permease family protein (AHRD V3.3 *** B9I8W9_POPTR)	GO:0005215|GO:0016021
Solyc08g067700.1	**-1.60E+00**	**7.60E-08**	-3.19E-01	1.50E-01	-9.69E-01	1.26E-04	1.63E-01	4.57E-01	WT N 1 dpi	K	LOW QUALITY:Serine/threonineprotein kinase, putative isoform 1(AHRD V3.3 --* A0A061GQI4_THECC)	
Solyc03g115930.2	**-1.60E+00**	**1.10E-03**	-5.09E-01	2.54E-01	-4.73E-01	2.89E-01	-4.74E-02	9.14E-01	WT N 1 dpi	D	Calcium-binding EF-hand familyprotein (AHRD V3.3 *-* AT5G39670.1)	GO:0005509
Solyc03g096670.3	**-1.61E+00**	**2.79E-03**	-3.32E-01	5.00E-01	1.92E-01	6.96E-01	-1.90E-01	6.99E-01	WT N 1 dpi	K	Protein phosphatase 2C (AHRDV3.3 *** Q8RVG0_TOBAC)	GO:0003824
Solyc09g015770.3	**-1.62E+00**	**1.83E-03**	-6.03E-01	2.07E-01	-5.98E-01	2.11E-01	-3.05E-01	5.19E-01	WT N 1 dpi	T	WRKY transcription factor 81	GO:0003700|GO:0006355|GO :0043565
Solyc05g055220.1	**-1.63E+00**	**3.01E-08**	-4.75E-01	3.18E-02	-8.79E-01	2.82E-04	-5.03E-02	8.12E-01	WT N 1 dpi	T	ovate family protein 10	
Solyc10g048065.1	**-1.64E+00**	**6.26E-03**	4.55E-01	4.16E-01	-4.39E-01	4.33E-01	5.26E-01	3.48E-01	WT N 1 dpi	TR	Transport membrane protein (AHRDV3.3 *** A0A0C5ARU2_HYONI)	GO:0016021
Solyc07g009333.1	**-1.66E+00**	**6.66E-05**	-4.18E-02	9.06E-01	2.29E-01	5.17E-01	2.10E-01	5.52E-01	WT N 1 dpi	P	60S acidic ribosomal protein P3 (AHRD V3.3 *** B9HPG0_POPTR)	
Solyc02g091070.3	**-1.66E+00**	**1.42E-04**	-1.41E-01	7.08E-01	5.71E-01	1.37E-01	9.61E-01	1.57E-02	WT N 1 dpi	STR	Protein DETOXIFICATION (AHRDV3.3 *** K4BCQ6_SOLLC)	GO:0006855|GO:0015238|GO :0015297|GO:0016020|GO:00 55085
Solyc01g100980.3	**-1.66E+00**	**8.45E-03**	-4.63E-01	4.35E-01	-6.38E-01	2.84E-01	4.89E-01	4.10E-01	WT N 1 dpi	CS	Pectin lyase-like superfamily protein(AHRD V3.3 *** AT1G02460.1)	GO:0004650|GO:0005975
Solyc01g095770.3	**-1.67E+00**	**1.73E-03**	-4.73E-01	3.31E-01	-5.22E-01	2.84E-01	-1.77E-01	7.14E-01	WT N 1 dpi	S	Cyclic nucleotide-gated channel(AHRD V3.3 *** A0A0K9PRG4_ZOSMR)	GO:0005216|GO:0006811|GO :0016020|GO:0055085
Solyc03g083320.3	**-1.67E+00**	**2.00E-10**	-3.48E-01	4.59E-02	7.27E-02	6.65E-01	4.88E-02	7.71E-01	WT N 1 dpi	S	calcium sensor calcineurin B	GO:0005509
Solyc02g065430.1	**-1.68E+00**	**6.34E-03**	-2.53E-01	6.59E-01	-1.02E-01	8.58E-01	7.71E-02	8.93E-01	WT N 1 dpi	NA	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7K9H8_MEDTR)	
Solyc04g080210.1	**-1.70E+00**	**7.09E-04**	-7.42E-01	1.06E-01	1.99E-01	6.57E-01	1.01E+00	3.17E-02	WT N 1 dpi	G	LOW QUALITY:ovate family protein9	
Solyc07g009280.3	**-1.71E+00**	**6.81E-03**	-8.12E-01	1.75E-01	-9.24E-01	1.24E-01	-3.75E-01	5.24E-01	WT N 1 dpi	D	potyvirus VPg interacting protein(DUF1423) (AHRD V3.3 --* AT3G07780.3)	

Solyc09g098620.2	**-1.72E+00**	**8.22E-07**	-2.56E-01	3.45E-01	-5.90E-01	3.55E-02	-2.10E-02	9.38E-01	WT N 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A061ETV7_THECC)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc07g006140.3	**-1.74E+00**	**3.88E-03**	-8.46E-01	1.35E-01	-7.60E-01	1.77E-01	7.66E-01	1.74E-01	WT N 1 dpi	P	Eukaryotic peptide chain release factor subunit 1-1 (AHRD V3.3 *-*A0A0A9G2E9_ARUDO)	
Solyc06g083130.3	**-1.75E+00**	**2.73E-07**	-7.40E-01	7.27E-03	2.13E-01	4.09E-01	1.61E-01	5.31E-01	WT N 1 dpi	DNA	dCTP pyrophosphatase 1 (AHRDV3.3 *** A0A151QMJ8_CAJCA)	GO:0047429
Solyc03g119600.1	**-1.78E+00**	**1.12E-09**	-7.57E-01	5.49E-04	-9.36E-01	4.73E-05	-3.81E-01	5.77E-02	WT N 1 dpi	D	LOW QUALITY:NIMIN2b protein (AHRD V3.3 *** Q0MR95_TOBAC)	
Solyc05g008020.3	**-1.79E+00**	**4.31E-03**	-1.71E-01	7.68E-01	5.33E-01	3.61E-01	6.85E-01	2.43E-01	WT N 1 dpi	K	mitogen-activated protein kinase 15	GO:0004672|GO:0005524|GO :0006468
Solyc00g136565.1	**-1.81E+00**	**3.30E-03**	-1.18E+00	4.52E-02	-6.28E-01	2.72E-01	7.47E-02	8.95E-01	WT N 1 dpi	E	2-oxoglutarate-dependent dioxygenase-related family protein(AHRD V3.3 *** B9GL08_POPTR)	GO:0016491|GO:0055114
Solyc12g042980.2	**-1.81E+00**	**7.23E-03**	-9.57E-01	1.36E-01	2.25E-01	7.21E-01	-4.00E-01	5.25E-01	WT N 1 dpi	E	2-oxoglutarate-dependent dioxygenase (AHRD V3.3 ***A0A061G9S7_THECC)	GO:0016491|GO:0055114
Solyc02g079280.3	**-1.82E+00**	**4.52E-03**	-5.62E-01	3.47E-01	-3.22E-01	5.87E-01	-5.28E-01	3.76E-01	WT N 1 dpi	T	MYB transcription factor (AHRDV3.3 *** A0A0U3IU11_MESCR)	GO:0003677
Solyc12g008430.2	**-1.84E+00**	**2.71E-04**	-1.13E+00	1.59E-02	-8.57E-01	6.08E-02	-2.56E-01	5.63E-01	WT N 1 dpi	C	Malic enzyme (AHRD V3.3 *** M0ZHN3_SOLTU)	GO:0004470|GO:0004471|GO :0006108|GO:0055114
Solyc09g092500.1	**-1.86E+00**	**5.13E-03**	-7.81E-01	2.11E-01	-1.10E+00	8.24E-02	-4.18E-01	4.98E-01	WT N 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CWS6_SOLLC)	GO:0008152|GO:0016758
Solyc06g006040.2	**-1.87E+00**	**7.22E-03**	-5.08E-01	4.35E-01	-1.56E-01	8.09E-01	-1.33E-01	8.38E-01	WT N 1 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 ***M1ANR5_SOLTU)	GO:0004672|GO:0005524|GO :0006468
Solyc08g016440.3	**-1.87E+00**	**4.42E-03**	-1.48E+00	2.09E-02	-1.50E+00	1.94E-02	-1.42E-01	8.14E-01	WT N 1 dpi	RNA	Polynucleotidyl transferase, ribonuclease H-like superfamilyprotein (AHRD V3.3 --* AT2G13980.1)	
Solyc12g005790.2	**-1.88E+00**	**7.46E-07**	1.26E-01	6.68E-01	-8.58E-01	6.56E-03	-2.93E-01	3.22E-01	WT N 1 dpi	OX	Peroxidase 27	GO:0004601|GO:0006979|GO :0020037|GO:0055114
Solyc03g116270.3	**-1.90E+00**	**5.60E-13**	-5.74E-01	4.67E-04	-9.93E-01	2.52E-07	-5.32E-01	9.93E-04	WT N 1 dpi	E	2-oxoglutarate and Fe(II)-dependentoxygenase superfamily protein, putative (AHRD V3.3 *** A0A061FWB6_THECC)	GO:0016491|GO:0055114
Solyc01g108700.3	**-1.92E+00**	**3.05E-03**	2.69E-01	6.50E-01	-5.12E-02	9.31E-01	-5.41E-01	3.65E-01	WT N 1 dpi	T	LOW QUALITY:transcription initiation factor TFIID subunit 1b-likeprotein (AHRD V3.3 -** AT3G19030.1)	
Solyc10g050210.2	**-1.93E+00**	**1.11E-04**	-2.59E-01	5.46E-01	2.28E-01	5.95E-01	-3.24E-01	4.51E-01	WT N 1 dpi	H	Abscisic acid responsive element-binding factor 1 family protein (AHRD V3.3 *** U5GLH1_POPTR)	GO:0003700|GO:0006355|GO :0043565
Solyc05g005280.3	**-1.93E+00**	**6.20E-07**	-8.03E-01	1.14E-02	-5.14E-01	9.29E-02	6.19E-02	8.35E-01	WT N 1 dpi	DNA	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4BW59_SOLLC)	GO:0003950
Solyc03g123540.3	**-1.97E+00**	**4.47E-03**	-6.45E-01	3.18E-01	-9.68E-01	1.39E-01	-3.40E-01	5.97E-01	WT N 1 dpi	STR	Heat-shock protein, putative (AHRDV3.3 *** B9ST51_RICCO)	
Solyc04g040120.1	**-1.98E+00**	**1.21E-04**	-1.22E-01	7.82E-01	-4.27E-01	3.38E-01	-2.29E-01	6.05E-01	WT N 1 dpi	2M	Fatty acid desaturase (AHRD V3.3 *** I3RV99_9ERIC)	GO:0006629

Solyc06g072880.2	**-2.00E+00**	**3.78E-03**	-1.25E+00	5.71E-02	-6.85E-01	2.85E-01	-1.29E-01	8.39E-01	WT N 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4C908_SOLLC)	GO:0008152|GO:0016758
Solyc02g084980.3	**-2.00E+00**	**1.23E-05**	2.13E-01	5.70E-01	-3.11E-01	4.09E-01	-1.84E-01	6.23E-01	WT N 1 dpi	P	Hexosyltransferase (AHRD V3.3 *** K4BB12_SOLLC)	GO:0006012|GO:0047216
Solyc03g111120.3	**-2.11E+00**	**1.11E-07**	-1.15E-01	6.97E-01	-1.29E-01	6.60E-01	1.47E-01	6.17E-01	WT N 1 dpi	C	Malate synthase (AHRD V3.3 *** M1B824_SOLTU)	GO:0003824
Solyc07g014680.3	**-2.18E+00**	**2.38E-04**	-3.11E-01	5.48E-01	-3.57E-01	4.91E-01	3.04E-01	5.57E-01	WT N 1 dpi	TR	sodium transporter HKT1,2	GO:0006812|GO:0008324|GO :0055085
Solyc05g050890.2	**-2.25E+00**	**1.63E-03**	-1.54E+00	2.30E-02	-1.07E+00	1.07E-01	1.44E+00	3.35E-02	WT N 1 dpi	OX	Peroxidase (AHRD V3.3 ***K4C1C1_SOLLC)	GO:0004601|GO:0006979|GO :0020037|GO:0055114
Solyc05g055460.1	**-2.30E+00**	**1.11E-03**	-1.10E+00	8.95E-02	-1.45E+00	2.92E-02	-6.36E-01	3.19E-01	WT N 1 dpi	NA	LOW QUALITY:Unknown protein(AHRD V3.3)	
Solyc03g115750.1	**-2.31E+00**	**2.79E-03**	-3.41E-01	6.30E-01	-1.36E+00	6.25E-02	-4.91E-01	4.89E-01	WT N 1 dpi	CS	Xyloglucan galactosyltransferaseKATAMARI1 (AHRD V3.3 *** W9RU56_9ROSA)	
Solyc11g066270.2	**-2.33E+00**	**1.35E-12**	-8.72E-01	6.35E-05	1.77E-01	3.43E-01	-2.91E-01	1.23E-01	WT N 1 dpi	CS	xyloglucan endotransglucosylase-hydrolase 6	GO:0004553|GO:0005975
Solyc10g080920.2	**-2.42E+00**	**1.10E-04**	-6.12E-01	2.60E-01	-8.33E-01	1.29E-01	-1.06E+00	5.67E-02	WT N 1 dpi	T	Myb family transcription factor familyprotein (AHRD V3.3 *** B9GRM8_POPTR)	GO:0003677
Solyc02g082890.1	**-2.44E+00**	**1.07E-03**	2.41E-01	7.20E-01	1.28E-01	8.48E-01	5.64E-01	4.02E-01	WT N 1 dpi	D	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-*AT2G29840.1)	GO:0005515|GO:0008270
Solyc12g049250.2	**-2.45E+00**	**1.12E-03**	-2.38E-01	7.25E-01	-1.11E+00	1.10E-01	-7.16E-01	2.95E-01	WT N 1 dpi	G	alpha-L-arabinofuranosidase 1(AHRD V3.3 --* AT3G10740.4)	
Solyc02g080120.2	**-2.48E+00**	**1.08E-05**	-1.09E+00	2.36E-02	-7.04E-01	1.34E-01	-1.45E-01	7.52E-01	WT N 1 dpi	H	Gibberellin 2-beta- dioxygenase 7	GO:0016491|GO:0055114
Solyc07g066510.3	**-2.51E+00**	**9.59E-03**	-6.77E-01	4.56E-01	6.00E-01	5.09E-01	2.92E-02	9.74E-01	WT N 1 dpi	G	Zinc finger protein CONSTANS (AHRD V3.3 *** W9R0E5_9ROSA)	GO:0005515
Solyc06g072865.1	**-2.52E+00**	**7.87E-03**	-4.71E-01	5.95E-01	-5.40E-01	5.42E-01	1.42E-01	8.73E-01	WT N 1 dpi	K	Protein phosphatase 2C familyprotein (AHRD V3.3 --* AT2G46920.4)	
Solyc07g061850.1	**-2.60E+00**	**5.92E-03**	2.53E-01	7.73E-01	-1.80E+00	4.79E-02	-1.32E-01	8.80E-01	WT N 1 dpi	DNA	LOW QUALITY:AT hook motif DNA-binding family protein (AHRD V3.3 -- * AT1G63480.7)	
Solyc01g107710.2	**-2.61E+00**	**9.14E-03**	-1.85E+00	5.56E-02	-8.93E-01	3.43E-01	-5.97E-01	5.24E-01	WT N 1 dpi	STR	LOW QUALITY:Late embryogenesis abundant protein-like protein (AHRD V3.3 *** F4JB74_ARATH)	
Solyc01g108390.3	**-2.67E+00**	**2.05E-03**	-2.01E+00	1.57E-02	-3.91E-01	6.20E-01	3.96E-01	6.15E-01	WT N 1 dpi	D	Proteinase inhibitor (AHRD V3.3 *** A0A0R4WFE3_TOBAC)	GO:0004867|GO:0009611
Solyc12g099930.2	**-2.77E+00**	**2.92E-03**	-1.61E+00	6.75E-02	-1.44E+00	9.87E-02	-2.07E-02	9.81E-01	WT N 1 dpi	AM	alanine:glyoxylate aminotransferase(AHRD V3.3 *** AT2G13360.3)	GO:0003824
Solyc09g074570.1	**-2.80E+00**	**1.00E-03**	-6.79E-01	3.76E-01	-1.37E+00	8.01E-02	-7.59E-01	3.23E-01	WT N 1 dpi	OX	Glutaredoxin (AHRD V3.3 *** B3F8F2_SOLTU)	GO:0009055|GO:0015035|GO :0045454
Solyc08g067340.3	**-2.86E+00**	**5.22E-05**	-1.61E+00	1.15E-02	-1.36E+00	2.98E-02	-1.22E+00	4.86E-02	WT N 1 dpi	T	WRKY transcription factor 46	GO:0003700|GO:0006355|GO :0043565
Solyc05g009640.3	**-2.99E+00**	**6.82E-09**	-3.34E-02	9.26E-01	-5.42E-01	1.38E-01	-1.43E-02	9.68E-01	WT N 1 dpi	T	bHLH transcription factor 037	GO:0046983
Solyc12g096620.1	**-3.01E+00**	**3.09E-03**	-6.73E-01	4.72E-01	6.78E-02	9.42E-01	1.38E+00	1.47E-01	WT N 1 dpi	L	GDSL esterase	GO:0016788
Solyc06g064590.2	**-3.04E+00**	**7.02E-04**	-1.07E+00	1.85E-01	6.53E-02	9.35E-01	1.64E-01	8.37E-01	WT N 1 dpi	T	bHLH transcription factor 045	GO:0046983
Solyc05g015350.3	**-3.06E+00**	**3.89E-03**	-4.50E-01	6.44E-01	-1.80E+00	7.33E-02	-1.37E+00	1.68E-01	WT N 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103XVZ6_CYNCS)	GO:0005506|GO:0016705|GO :0020037|GO:0055114

Solyc09g073040.3	**-3.08E+00**	**4.44E-03**	-2.65E+00	1.27E-02	1.67E-01	8.67E-01	9.24E-01	3.58E-01	WT N 1 dpi	NA	amino-terminal region of chorein (AHRD V3.3 --* AT3G20720.2)	
Solyc12g049030.1	**-3.09E+00**	**7.59E-03**	-2.00E+00	7.18E-02	-3.75E-01	7.28E-01	1.16E+00	2.86E-01	WT N 1 dpi	2M	Fatty acid desaturase (AHRD V3.3 *** B3SP99_CAPAN)	GO:0006629
Solyc09g097950.2	**-3.13E+00**	**2.33E-03**	-1.78E+00	6.53E-02	-7.70E-01	4.13E-01	-5.37E-01	5.67E-01	WT N 1 dpi	2M	Aldo/keto reductase family oxidoreductase (AHRD V3.3 *-* G7KTT7_MEDTR)	
Solyc08g006860.3	**-3.31E+00**	**4.02E-04**	-1.75E+00	4.09E-02	-1.60E+00	6.00E-02	-7.52E-01	3.65E-01	WT N 1 dpi	P	Patatin (AHRD V3.3 *** K4CIH4_SOLLC)	GO:0006629
Solyc04g072700.3	**-3.32E+00**	**1.50E-03**	-1.67E+00	8.59E-02	-9.75E-01	3.07E-01	4.56E-01	6.30E-01	WT N 1 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT4G08570.1)	GO:0030001|GO:0046872
Solyc02g085880.2	**-3.43E+00**	**4.97E-04**	-1.45E+00	1.04E-01	-1.06E+00	2.28E-01	5.07E-01	5.61E-01	WT N 1 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9RSK4_RICCO)	GO:0005506|GO:0016705|GO :0020037|GO:0055114
Solyc01g107720.3	**-3.53E+00**	**6.78E-03**	-2.78E+00	2.84E-02	-1.42E+00	2.48E-01	-1.29E+00	2.90E-01	WT N 1 dpi	STR	Late embryogenesis abundant protein-like protein (AHRD V3.3 *** F4JB74_ARATH)	
Solyc04g005260.2	**-3.66E+00**	**6.70E-04**	-8.54E-01	3.75E-01	-8.68E-01	3.67E-01	2.37E-02	9.80E-01	WT N 1 dpi	DNA	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9RLG1_RICCO)	GO:0003824|GO:0006281
Solyc06g067980.3	**-3.86E+00**	**6.76E-05**	-1.88E+00	2.90E-02	-7.05E-01	3.94E-01	8.70E-01	2.95E-01	WT N 1 dpi	STR	Late embryogenesis abundantprotein (AHRD V3.3 --* Q2QKE8_CATRO)	
Solyc08g007840.2	**-3.92E+00**	**4.96E-03**	-2.99E+00	2.72E-02	-1.44E+00	2.71E-01	-1.19E+00	3.60E-01	WT N 1 dpi	STR	Dehydration-responsive elementbinding factor (AHRD V3.3 *** X2JR99_POPNI)	GO:0003677
Solyc02g084850.3	**-4.27E+00**	**4.93E-03**	-3.67E+00	1.36E-02	2.07E-01	8.83E-01	1.21E+00	3.89E-01	WT N 1 dpi	H	Abscisic acid and environmentalstress-inducible protein TAS14 (AHRD V3.3 *** TAS14_SOLLC)	GO:0006950|GO:0009415
Solyc01g108360.3	**-4.34E+00**	**6.48E-04**	-2.56E+00	3.03E-02	2.85E-01	8.01E-01	1.30E+00	2.57E-01	WT N 1 dpi	E	Blue copper protein (AHRD V3.3 *** A0A199VY96_ANACO)	GO:0009055
Solyc09g008500.2	**-5.11E+00**	**1.17E-03**	-2.78E+00	5.79E-02	-3.27E+00	2.77E-02	-3.85E+00	1.07E-02	WT N 1 dpi	L	Non-specific lipid-transfer protein (AHRD V3.3 *** K4CQN8_SOLLC)	GO:0006869|GO:0008289
Solyc03g006410.3	2.68E+00	1.24E-02	6.27E-01	1.13E-01	**4.20E+00**	**2.65E-04**	1.63E+00	1.13E-01	WT NoN 1 dpi	N A	DUF506 family protein (AHRD V3.3 *** G7IPT8_MEDTR)	
Solyc09g097760.3	2.20E+00	1.91E-01	1.00E+00	4.59E-02	**-4.74E+00**	**7.66E-03**	-3.44E+00	4.59E-02	WT NoN 1 dpi	D	Glycine rich protein (AHRD V3.3 *-* Q94CG1_TOBAC)	
Solyc12g013710.2	2.08E+00	1.32E-02	9.85E-01	7.87E-02	**2.67E+00**	**2.15E-03**	1.43E+00	7.87E-02	WT NoN 1 dpi	E	light dependent NADH:protochlorophyllide oxidoreductase 1	GO:0016630|GO:0055114|
Solyc05g021555.1	2.06E+00	4.52E-02	7.64E-01	7.81E-01	**3.45E+00**	**1.62E-03**	2.76E-01	7.81E-01	WT NoN 1 dpi	2M	Alcohol dehydrogenase (AHRD V3.3 *** Q4LAW8_CAPCH)	
Solyc09g082810.3	1.94E+00	2.18E-01	-8.90E-01	2.71E-02	**-4.78E+00**	**4.50E-03**	-3.60E+00	2.71E-02	WT NoN 1 dpi	D	Glycine-rich protein (AHRD V3.3 *-* D2K2U0_TOBAC)	
Solyc09g074590.1	1.80E+00	9.55E-02	4.68E-01	8.14E-01	**2.99E+00**	**7.99E-03**	2.47E-01	8.14E-01	WT NoN 1 dpi	OX	Glutaredoxin (AHRD V3.3 *** A0A103Y7J3_CYNCS)	GO:0009055|GO:0015035|GO :0045454|
Solyc08g060920.3	1.79E+00	1.50E-09	7.51E-01	2.37E-03	**-1.74E+00**	**2.56E-09**	-6.60E-01	2.37E-03	WT NoN 1 dpi	STR	IDS4-like	
Solyc06g076170.3	1.71E+00	2.40E-02	1.09E+00	7.61E-02	**2.22E+00**	**4.62E-03**	1.32E+00	7.61E-02	WT NoN 1 dpi	CS	Glucan endo-1,3-beta-glucosidase,putative (AHRD V3.3 *** B9T3M9_RICCO)	GO:0004553|GO:0005975|GO :0005506|GO:0016705|GO:00 20037|GO:0055114

Solyc07g062480.1	1.64E+00	1.87E-02	1.25E+00	1.86E-01	**2.16E+00**	**2.79E-03**	8.87E-01	1.86E-01	WT NoN 1 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *-* M1CRP0_SOLTU)	
Solyc03g093290.2	1.58E+00	7.04E-02	1.80E+00	1.01E-02	**2.93E+00**	**1.68E-03**	2.32E+00	1.01E-02	WT NoN 1 dpi	2M	Aldo/keto reductase family oxidoreductase (AHRD V3.3 *** A0A072UK59_MEDTR)	GO:0016491|GO:0055114|
Solyc03g062910.3	1.55E+00	1.04E-02	8.75E-01	7.75E-01	**1.68E+00**	**6.02E-03**	-1.62E-01	7.75E-01	WT NoN 1 dpi	DNA	Copia protein (AHRD V3.3 *-* A0A151SBM2_CAJCA)	
Solyc07g053370.1	1.54E+00	1.32E-01	1.88E+00	2.32E-01	**4.25E+00**	**2.23E-04**	1.21E+00	2.32E-01	WT NoN 1 dpi	NA	LOW QUALITY:Clavata3/ESR (CLE) gene family member (AHRD V3.3 -** A0A072TRR8_MEDTR)	
Solyc02g089770.3	1.43E+00	5.84E-02	3.49E-01	7.49E-01	**-2.41E+00**	**2.59E-03**	-2.34E-01	7.49E-01	WT NoN 1 dpi	2M	Dihydroflavonol-4-reductase-binding domain	GO:0003854|GO:0006694|GO :0016616|GO:0055114|
Solyc04g079510.2	1.34E+00	1.18E-01	2.43E+00	1.32E-02	**-3.74E+00**	**1.22E-04**	-2.20E+00	1.32E-02	WT NoN 1 dpi	TR	Peptide transporter	GO:0005215|GO:0006810|GO :0016020|
Solyc08g075630.3	1.30E+00	4.37E-02	2.28E-02	1.09E-01	**2.43E+00**	**5.30E-04**	1.02E+00	1.09E-01	WT NoN 1 dpi	D	NBS-LRR resistance protein (AHRD V3.3 *** B6E013_SOLBU)	GO:0005515|GO:0043531
Solyc01g081290.3	1.21E+00	3.20E-02	4.80E-01	6.16E-01	**1.87E+00**	**1.75E-03**	2.71E-01	6.16E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103Y132_CYNCS)	GO:0005515|GO:0008270
Solyc04g005660.3	1.20E+00	2.27E-01	9.65E-01	2.48E-02	**3.61E+00**	**9.78E-04**	2.32E+00	2.48E-02	WT NoN 1 dpi	T	Transcription factor protein (AHRD V3.3 *** A0A0B0MSC8_GOSAR)	GO:0046983|
Solyc03g119390.3	1.12E+00	3.69E-02	7.86E-01	9.03E-01	**1.56E+00**	**5.29E-03**	-6.28E-02	9.03E-01	WT NoN 1 dpi	T	bHLH transcription factor 026	GO:0046983|
Solyc04g008180.2	1.08E+00	2.11E-02	8.01E-01	7.96E-01	**1.38E+00**	**4.30E-03**	-1.15E-01	7.96E-01	WT NoN 1 dpi	D	Hero resistance protein (AHRD V3.3 *** Q8GT46_SOLLC)	GO:0043531|
Solyc06g048790.1	1.07E+00	7.37E-02	1.51E-01	1.48E-01	**1.63E+00**	**8.59E-03**	8.51E-01	1.48E-01	WT NoN 1 dpi	OX	Plant cadmium resistance 10-likeprotein (AHRD V3.3 *** A0A0B0N332_GOSAR)	
Solyc06g072455.1	1.03E+00	2.86E-01	-5.13E-01	1.35E-01	**3.42E+00**	**1.23E-03**	1.45E+00	1.35E-01	WT NoN 1 dpi	RNA	LOW QUALITY:Agenet-like domain-containing protein (AHRD V3.3 *** A0A103YGJ9_CYNCS)	
Solyc06g062610.2	1.02E+00	1.23E-02	5.27E-01	1.84E-01	**1.07E+00**	**8.72E-03**	5.16E-01	1.84E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103YL18_CYNCS)	
Solyc08g079300.3	1.00E+00	1.20E-01	1.73E+00	3.78E-02	**-2.66E+00**	**2.36E-04**	-1.36E+00	3.78E-02	WT NoN 1 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)	GO:0005506|GO:0016705|GO :0020037|GO:0055114|GO:00 16705|GO:0055114
Solyc01g109140.3	9.95E-01	3.93E-04	7.44E-01	1.49E-03	**1.44E+00**	**3.28E-06**	8.69E-01	1.49E-03	WT NoN 1 dpi	L	divinyl ether synthase	GO:0004497|GO:0005506|GO :0016705|GO:0020037|GO:00 55114|GO:0005506|GO:0016 705|GO:0020037|GO:005511 4
Solyc01g059990.3	9.95E-01	5.33E-02	6.72E-01	1.32E-02	**2.26E+00**	**9.83E-05**	1.31E+00	1.32E-02	WT NoN 1 dpi	K	Serine/threonine protein phosphatase 7 long form isogeny(AHRD V3.3 *-* A0A151SHP6_CAJCA)	
Solyc11g013293.1	9.83E-01	1.33E-02	6.04E-01	7.41E-01	**1.23E+00**	**2.61E-03**	1.24E-01	7.41E-01	WT NoN 1 dpi	CS	Protein PIR (AHRD V3.3 *-* PIR_ARATH)	
Solyc02g077190.2	9.58E-01	1.85E-04	7.18E-01	4.19E-02	**1.09E+00**	**3.69E-05**	4.70E-01	4.19E-02	WT NoN 1 dpi	DNA	chromatin remodeling factor18(AHRD V3.3 -* AT1G48310.2)	

Solyc02g085310.3	9.53E-01	5.73E-08	4.33E-01	1.97E-06	**2.21E+00**	**8.40E-16**	7.72E-01	1.97E-06	WT NoN 1 dpi	CS	plant invertase/pectin methylesterase inhibitor superfamilyprotein (AHRD V3.3 --* AT3G17227.1)	
Solyc06g074420.1	9.50E-01	6.98E-03	2.74E-01	6.06E-02	**1.42E+00**	**1.74E-04**	6.36E-01	6.06E-02	WT NoN 1 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** B9HQW0_POPTR)	GO:0005506|GO:0016705|GO :0020037|GO:0055114|
Solyc08g078870.2	9.48E-01	4.20E-05	5.72E-01	5.89E-05	**1.28E+00**	**4.76E-07**	9.23E-01	5.89E-05	WT NoN 1 dpi	CS	14 kDa proline-rich protein DC2.15,putative (AHRD V3.3 *** B9RD76_RICCO)	
Solyc10g006250.3	9.47E-01	2.28E-02	4.27E-01	7.07E-01	**1.27E+00**	**3.25E-03**	1.49E-01	7.07E-01	WT NoN 1 dpi	RNA	Protein suppressor of white apricot(AHRD V3.3 *-* A0A151U2B3_CAJCA)	
Solyc09g098610.2	9.45E-01	1.63E-02	2.94E-01	3.72E-01	**-1.26E+00**	**2.12E-03**	-3.34E-01	3.72E-01	WT NoN 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q8H0I6_PETHY)	GO:0005506|GO:0016705|GO :0020037|GO:0055114|GO:00 16705|GO:0055114
Solyc04g072320.2	9.34E-01	3.87E-02	9.52E-01	5.01E-01	**1.88E+00**	**1.74E-04**	2.92E-01	5.01E-01	WT NoN 1 dpi	RNA	RNA polymerase I subunit 43 (AHRD V3.3 --* AT1G60620.2)	
Solyc12g094580.2	9.15E-01	9.62E-04	1.56E-01	2.86E-01	**1.04E+00**	**2.64E-04**	2.68E-01	2.86E-01	WT NoN 1 dpi	DNA	AT hook motif DNA-binding familyprotein (AHRD V3.3 --* AT5G46640.1)	
Solyc04g077930.3	9.14E-01	2.53E-02	5.24E-01	7.81E-01	**1.25E+00**	**3.22E-03**	1.08E-01	7.81E-01	WT NoN 1 dpi	P	Ubiquitin system component Cueprotein (AHRD V3.3 --* AT1G27752.1)	
Solyc11g072310.2	9.04E-01	1.17E-01	5.89E-01	4.57E-02	**1.83E+00**	**2.91E-03**	1.17E+00	4.57E-02	WT NoN 1 dpi	H	gibberellin 20-oxidase-3	GO:0016491|GO:0055114|
Solyc11g017370.2	9.01E-01	2.05E-02	2.28E-01	6.35E-01	**1.10E+00**	**5.89E-03**	1.75E-01	6.35E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A172CHJ1_POPTO)	GO:0005515|
Solyc07g054770.1	8.91E-01	2.30E-03	4.73E-01	8.93E-01	**-1.17E+00**	**1.46E-04**	-3.58E-02	8.93E-01	WT NoN 1 dpi	D	Wound-responsive family protein(AHRD V3.3 *** A0A061E3U8_THECC)	
Solyc01g090660.3	8.89E-01	3.20E-01	2.69E-01	8.73E-02	**-2.51E+00**	**8.31E-03**	-1.56E+00	8.73E-02	WT NoN 1 dpi	2M	carotenoid cleavage dioxygenase7	GO:0016702|GO:0055114|
Solyc02g090545.1	8.86E-01	2.35E-01	3.19E-01	5.52E-02	**2.28E+00**	**4.32E-03**	1.46E+00	5.52E-02	WT NoN 1 dpi	TR	Calcium-transporting ATPase (AHRD V3.3 *** M5X6S2_PRUPE)	GO:0000166|
Solyc03g111710.3	8.43E-01	9.73E-04	6.37E-01	6.80E-01	**1.34E+00**	**3.33E-06**	9.45E-02	6.80E-01	WT NoN 1 dpi	T	BTB/POZ and TAZ domain protein(AHRD V3.3 *** G7JMM8_MEDTR)	GO:0003712|GO:0004402|GO :0005634|GO:0006355|GO:00 08270|GO:0005515
Solyc06g063090.3	8.39E-01	6.03E-06	7.27E-01	3.86E-06	**1.10E+00**	**6.96E-08**	8.65E-01	3.86E-06	WT NoN 1 dpi	N	alanine aminotransferase 2 (AHRDV3.3 *** AT1G72330.1)	GO:0003824|GO:0009058|GO :0030170
Solyc09g092710.3	8.39E-01	1.36E-01	7.87E-01	1.46E-02	**-2.50E+00**	**9.97E-05**	-1.42E+00	1.46E-02	WT NoN 1 dpi	D	Glycine-rich protein (AHRD V3.3 *** D2K2T8_TOBAC)	
Solyc01g112340.3	8.38E-01	2.96E-02	5.37E-01	5.95E-01	**1.18E+00**	**3.28E-03**	-1.96E-01	5.95E-01	WT NoN 1 dpi	TR	Brefeldin A-inhibited guanine nucleotide-exchange protein (AHRDV3.3 *-* G7KFH4_MEDTR)	
Solyc02g063200.2	8.36E-01	6.38E-02	1.24E-01	1.99E-01	**1.30E+00**	**5.70E-03**	5.69E-01	1.99E-01	WT NoN 1 dpi	L	alpha/beta-Hydrolases superfamilyprotein (AHRD V3.3 *** AT5G16120.2)	
Solyc08g082670.3	8.24E-01	3.76E-05	2.59E-01	7.59E-04	**1.25E+00**	**5.38E-08**	6.33E-01	7.59E-04	WT NoN 1 dpi	CS	Cellulose synthase (AHRD V3.3 *** A0A118JUI8_CYNCS)	GO:0016020|GO:0016760|GO :0030244|
Solyc08g066650.3	8.19E-01	2.90E-04	1.97E-01	8.01E-05	**-1.02E+00**	**1.97E-05**	-9.15E-01	8.01E-05	WT NoN 1 dpi	2M	Carotenoid Cleavage Dioxygenase 8	GO:0016702|GO:0055114|

Solyc10g055810.2	7.92E-01	2.36E-03	1.97E-01	2.43E-03	**1.41E+00**	**2.56E-06**	7.89E-01	2.43E-03	WT NoN 1 dpi	D	chitinase Z15140	GO:0004568|GO:0005975|GO :0004568|GO:0006032|GO:00 16998
Solyc08g061060.2	7.66E-01	6.65E-02	-1.52E-01	5.66E-01	**1.59E+00**	**5.13E-04**	2.32E-01	5.66E-01	WT NoN 1 dpi	D	Barwin-like endoglucanase (AHRD V3.3 *** A0A103XZL4_CYNCS)	
Solyc04g017690.3	7.65E-01	2.05E-08	6.56E-01	4.91E-05	**1.01E+00**	**8.58E-11**	4.67E-01	4.91E-05	WT NoN 1 dpi	STR	ERD15 (AHRD V3.3 *** A0EPI4_CAPAN)	
Solyc02g081980.3	7.62E-01	9.49E-03	6.52E-01	2.12E-02	**-1.16E+00**	**2.30E-04**	-6.67E-01	2.12E-02	WT NoN 1 dpi	K	Apyrase (AHRD V3.3 *** APY_SOLTU)	GO:0016787|
Solyc02g089010.2	7.53E-01	3.15E-04	-2.04E-01	2.19E-03	**1.49E+00**	**1.16E-08**	6.16E-01	2.19E-03	WT NoN 1 dpi	S	Receptor protein kinase, putative (AHRD V3.3 *-* B9RXG1_RICCO)	GO:0004672|GO:0005524|GO :0006468|GO:0004672|GO:00 06468
Solyc08g014485.1	7.46E-01	6.90E-02	6.96E-01	5.97E-01	**1.19E+00**	**5.43E-03**	2.11E-01	5.97E-01	WT NoN 1 dpi	C	glycoside hydrolase family 2 protein(AHRD V3.3 *-* AT3G54440.2)	GO:0004553|GO:0005975|
Solyc07g065590.3	7.41E-01	3.90E-02	-1.49E-02	1.04E-02	**1.08E+00**	**3.78E-03**	9.41E-01	1.04E-02	WT NoN 1 dpi	E	Nicotinamide-nucleotide adenylyltransferase (AHRD V3.3 *** K4CHN7_SOLLC)	GO:0003824|GO:0009058|GO :0009435|GO:0016779
Solyc12g036310.1	7.38E-01	1.57E-01	-6.67E-01	1.99E-01	**-1.77E+00**	**1.70E-03**	-6.67E-01	1.99E-01	WT NoN 1 dpi	E	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic (AHRD V3.3 --*NU5C_CHLSC)	
Solyc03g113420.3	7.36E-01	2.55E-02	3.02E-01	1.58E-01	**1.46E+00**	**7.51E-05**	4.51E-01	1.58E-01	WT NoN 1 dpi	TR	Major facilitator superfamily protein(AHRD V3.3 *** AT5G62680.1)	GO:0005215|GO:0006810|GO :0016020|
Solyc09g007050.1	7.34E-01	1.05E-01	-5.24E-02	2.65E-01	**1.48E+00**	**2.25E-03**	4.98E-01	2.65E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A118JTY1_CYNCS)	GO:0005515|
Solyc12g013660.2	7.25E-01	3.17E-01	7.97E-01	8.74E-02	**2.54E+00**	**1.42E-03**	1.26E+00	8.74E-02	WT NoN 1 dpi	H	ethylene-responsive transcriptionfactor (AHRD V3.3 *-* AT5G07580.1)	GO:0003677|GO:0003700|GO :0006355
Solyc02g085285.1	7.18E-01	6.73E-03	3.80E-01	7.32E-03	**1.81E+00**	**7.51E-08**	7.10E-01	7.32E-03	WT NoN 1 dpi	G	Protein with RING/U-box and TRAF-like domain (AHRD V3.3 --* AT1G66660.1)	
Solyc12g096660.2	6.96E-01	1.12E-01	-4.87E-02	1.29E-01	**1.52E+00**	**1.35E-03**	6.65E-01	1.29E-01	WT NoN 1 dpi	STR	Type II inositol 5-phosphatase,putative (AHRD V3.3 *** B9RM01_RICCO)	GO:0005515|GO:0046856
Solyc04g054260.3	6.94E-01	6.43E-03	4.74E-01	6.74E-03	**1.21E+00**	**2.20E-05**	6.89E-01	6.74E-03	WT NoN 1 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW5_POPTR)	GO:0005506|GO:0016705|GO :0020037|GO:0055114|GO:00 16705|GO:0055114
Solyc12g049550.2	6.92E-01	1.07E-02	2.04E-01	5.34E-04	**1.78E+00**	**1.71E-07**	9.94E-01	5.34E-04	WT NoN 1 dpi	L	GDSL esterase/lipase 5 (AHRDV3.3 *** GLIP5_ARATH)	GO:0016788|
Solyc12g049350.2	6.90E-01	3.95E-01	2.40E+00	6.08E-02	**-2.82E+00**	**1.54E-03**	-1.56E+00	6.08E-02	WT NoN 1 dpi	T	R2R3MYB transcription factor 11	GO:0003677|
Solyc05g052030.1	6.86E-01	7.24E-03	3.61E-01	4.44E-02	**1.06E+00**	**1.25E-04**	4.97E-01	4.44E-02	WT NoN 1 dpi	H	ethylene response factor 4	GO:0003677|GO:0003700|GO :0006355
Solyc04g011990.2	6.82E-01	8.65E-02	4.03E-01	6.71E-02	**1.11E+00**	**7.70E-03**	7.32E-01	6.71E-02	WT NoN 1 dpi	D	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-*AT5G38350.1)	GO:0043531|
Solyc00g100880.3	6.68E-01	1.23E-01	4.44E-01	9.48E-02	**1.29E+00**	**4.99E-03**	7.27E-01	9.48E-02	WT NoN 1 dpi	D	LURP-one-like protein (AHRD V3.3 *** AT1G53875.1)	
Solyc03g096550.3	6.66E-01	4.84E-03	1.93E-01	6.97E-03	**1.27E+00**	**3.48E-06**	6.34E-01	6.97E-03	WT NoN 1 dpi	G	PLAT domain-containing protein 1(AHRD V3.3 *** PLAT1_ARATH)	GO:0005515|

Solyc03g115790.1	6.55E-01	5.43E-03	4.14E-01	1.88E-02	**1.14E+00**	**1.63E-05**	5.41E-01	1.88E-02	WT NoN 1 dpi	RNA	LOW QUALITY:Pentatricopeptiderepeat-containing protein (AHRD V3.3 *** A0A0B2QFK0_GLYSO)	GO:0005515|
Solyc05g046280.2	6.52E-01	1.51E-01	1.21E-01	6.12E-02	**1.45E+00**	**2.89E-03**	8.63E-01	6.12E-02	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103XBJ8_CYNCS)	GO:0005515|
Solyc01g090740.3	6.28E-01	7.40E-02	-5.28E-02	7.94E-01	**-1.28E+00**	**8.15E-04**	8.90E-02	7.94E-01	WT NoN 1 dpi	DNA	Zinc finger protein (AHRD V3.3 *** A0A0B0MVF4_GOSAR)	
Solyc07g005920.2	6.25E-01	1.05E-02	1.25E-01	2.21E-02	**1.11E+00**	**4.51E-05**	5.51E-01	2.21E-02	WT NoN 1 dpi	PMI	Leucine-rich receptor-like proteinkinase family protein (AHRD V3.3 *** AT2G24130.2)	GO:0004672|GO:0005524|GO :0006468|GO:0004672|GO:00 06468
Solyc01g094640.3	6.25E-01	4.64E-01	6.93E-01	5.62E-02	**2.71E+00**	**3.44E-03**	1.68E+00	5.62E-02	WT NoN 1 dpi	S	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein (AHRD V3.3 *** A0A072TN99_MEDTR)	
Solyc03g025610.2	6.18E-01	4.18E-02	3.46E-01	7.14E-01	**1.00E+00**	**1.82E-03**	-1.07E-01	7.14E-01	WT NoN 1 dpi	P	Tripeptidyl-peptidase 2 (AHRD V3.3 *-* A0A151T4Q0_CAJCA)	GO:0004252|GO:0006508|
Solyc10g080460.2	6.14E-01	1.04E-03	3.97E-01	1.02E-05	**1.58E+00**	**6.53E-10**	9.09E-01	1.02E-05	WT NoN 1 dpi	T	Myb family transcription factor familyprotein (AHRD V3.3 *** B9HAD3_POPTR)	GO:0003677|
Solyc03g119720.3	6.08E-01	5.63E-05	2.56E-01	1.69E-01	**1.14E+00**	**2.02E-09**	1.78E-01	1.69E-01	WT NoN 1 dpi	L	Lipase family protein (AHRD V3.3 *** B9I2Q8_POPTR)	GO:0006629|
Solyc04g014530.1	6.06E-01	8.88E-02	6.64E-01	1.36E-02	**1.40E+00**	**3.77E-04**	9.07E-01	1.36E-02	WT NoN 1 dpi	H	Ethylene Response Factor C.2	GO:0003677|GO:0003700|GO :0006355
Solyc10g084540.2	6.04E-01	1.26E-01	2.95E-01	3.60E-01	**1.14E+00**	**6.31E-03**	3.56E-01	3.60E-01	WT NoN 1 dpi	L	Phosphatidate phosphatase LPIN2-like protein (AHRD V3.3 *-* A0A0B2P3Z9_GLYSO)	
Solyc05g010790.2	6.04E-01	3.11E-01	-2.60E-01	3.65E-01	**1.69E+00**	**7.57E-03**	5.39E-01	3.65E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *-* B9RLG0_RICCO)	
Solyc05g010780.1	6.01E-01	4.30E-02	2.54E-01	3.19E-01	**1.22E+00**	**1.97E-04**	2.87E-01	3.19E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingfamily protein (AHRD V3.3 *** B9HWT8_POPTR)	GO:0005515|
Solyc01g011095.1	6.01E-01	2.14E-01	-3.95E-03	9.40E-01	**-1.72E+00**	**1.19E-03**	3.60E-02	9.40E-01	WT NoN 1 dpi	G	CLAVATA3/ESR (CLE)-related 25-like protein (AHRD V3.3 *-* A0A0B0NFL0_GOSAR)	
Solyc04g071890.3	5.94E-01	9.26E-03	1.02E-01	7.64E-04	**1.05E+00**	**3.95E-05**	8.06E-01	7.64E-04	WT NoN 1 dpi	OX	Peroxidase (AHRD V3.3 *** K4BTH6_SOLLC)	GO:0004601|GO:0006979|GO :0020037|GO:0055114|GO:00 04601|GO:0042744
Solyc11g065960.2	5.91E-01	1.27E-01	4.28E-01	8.74E-01	**1.13E+00**	**5.73E-03**	-6.00E-02	8.74E-01	WT NoN 1 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 --* M0ZPQ7_SOLTU)	
Solyc04g076980.3	5.87E-01	7.00E-02	4.10E-01	7.00E-01	**1.12E+00**	**1.27E-03**	-1.21E-01	7.00E-01	WT NoN 1 dpi	PMI	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *-* AT1G09970.2)	
Solyc05g051200.1	5.80E-01	6.77E-02	-1.29E-01	8.75E-02	**1.21E+00**	**4.98E-04**	5.40E-01	8.75E-02	WT NoN 1 dpi	H	ethylene-responsive factor 1	GO:0003677|GO:0003700|GO :0006355
Solyc02g087070.3	5.77E-01	7.38E-03	4.28E-01	1.58E-02	**1.20E+00**	**2.22E-06**	5.13E-01	1.58E-02	WT NoN 1 dpi	OX	alpha-DOX1	GO:0004601|GO:0006979|GO :0020037|GO:0055114|
Solyc12g010110.2	5.61E-01	3.29E-02	4.95E-01	9.78E-01	**1.16E+00**	**8.31E-05**	7.01E-03	9.78E-01	WT NoN 1 dpi	CS	Formin-like protein (AHRD V3.3 *** K4DC98_SOLLC)	GO:0005515|

Solyc03g082725.1	5.61E-01	3.15E-01	-3.56E-01	3.66E-02	**1.53E+00**	**9.58E-03**	1.21E+00	3.66E-02	WT NoN 1 dpi	S	Protein IQ-DOMAIN 1 (AHRD V3.3 * * W9RRW9_9ROSA)	GO:0005515|
Solyc01g103610.3	5.60E-01	1.33E-01	7.64E-01	5.01E-02	**1.05E+00**	**7.43E-03**	7.42E-01	5.01E-02	WT NoN 1 dpi	D	Disease resistance protein (AHRDV3.3 *** A0A103XDQ0_CYNCS)	GO:0043531|
Solyc10g083260.1	5.38E-01	2.62E-02	4.40E-01	9.51E-03	**1.78E+00**	**3.12E-08**	6.39E-01	9.51E-03	WT NoN 1 dpi	G	LOW QUALITY:senescence regulator (Protein of unknown function, DUF584) (AHRD V3.3 *-*AT3G15040.1)	
Solyc06g069410.3	5.32E-01	2.17E-04	3.31E-01	1.66E-02	**1.17E+00**	**8.02E-10**	3.17E-01	1.66E-02	WT NoN 1 dpi	TR	ADP,ATP carrier protein, mitochondrial (AHRD V3.3 ***ADT_ORYSJ)	GO:0005215|GO:0005743|GO :0006810|GO:0055085|GO:00 55085
Solyc11g045610.2	5.32E-01	1.16E-02	2.43E-01	4.71E-03	**1.01E+00**	**2.39E-05**	6.05E-01	4.71E-03	WT NoN 1 dpi	K	Protein kinase family protein (AHRDV3.3 *** Q9LQ29_ARATH)	GO:0004672|GO:0005524|GO :0006468|GO:0004672|GO:00 06468
Solyc02g078665.1	5.24E-01	3.71E-01	4.36E-01	1.08E-01	**1.93E+00**	**2.42E-03**	9.58E-01	1.08E-01	WT NoN 1 dpi	G	Hydroxyproline-rich glycoprotein family protein, putative (AHRD V3.3 - -* A0A072UP10_MEDTR)	
Solyc09g090220.3	5.23E-01	1.14E-01	3.12E-01	2.95E-01	**1.01E+00**	**3.89E-03**	-3.41E-01	2.95E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** D7L3A6_ARALL)	GO:0005515|GO:0008270
Solyc05g012257.1	5.02E-01	1.58E-01	3.06E-01	6.60E-01	**1.31E+00**	**8.45E-04**	1.54E-01	6.60E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9RV44_RICCO)	
Solyc09g089930.2	4.99E-01	1.83E-01	2.25E-01	3.75E-02	**1.79E+00**	**4.37E-05**	8.01E-01	3.75E-02	WT NoN 1 dpi	H	ethylene responsive factor E.2	GO:0003677|GO:0003700|GO :0006355
Solyc01g111080.3	4.94E-01	7.82E-03	4.42E-01	2.44E-05	**-1.19E+00**	**2.27E-07**	-8.79E-01	2.44E-05	WT NoN 1 dpi	NA	Unknown protein (AHRD V3.3)	
Solyc09g090440.1	4.90E-01	8.78E-02	7.31E-02	2.27E-01	**1.33E+00**	**5.48E-05**	3.41E-01	2.27E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103Y2G7_CYNCS)	
Solyc05g021550.2	4.86E-01	6.52E-01	-1.46E-01	6.88E-02	**3.91E+00**	**1.12E-03**	2.03E+00	6.88E-02	WT NoN 1 dpi	CS	Sister-chromatide cohesion protein 3 (AHRD V3.3 *-* D7M8Q0_ARALL)	
Solyc04g007000.1	4.86E-01	2.61E-01	1.06E+00	8.01E-02	**1.64E+00**	**6.61E-04**	7.71E-01	8.01E-02	WT NoN 1 dpi	T	AP2/B3 transcription factor familyprotein (AHRD V3.3 *** AT1G25560.1)	GO:0003677|GO:0003700|GO :0006355
Solyc08g006770.3	4.82E-01	6.89E-04	2.70E-01	6.86E-02	**1.04E+00**	**9.39E-09**	2.37E-01	6.86E-02	WT NoN 1 dpi	E	2-oxoglutarate and Fe(II)-dependentoxygenase superfamily protein, putative (AHRD V3.3 *** A0A061E128_THECC)	GO:0016491|GO:0055114|
Solyc06g066080.1	4.81E-01	1.72E-01	7.92E-02	8.45E-01	**1.47E+00**	**2.11E-04**	6.77E-02	8.45E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103XZP2_CYNCS)	GO:0005515|GO:0008270
Solyc02g032480.2	4.78E-01	1.60E-01	1.83E-01	5.60E-01	**1.49E+00**	**1.32E-04**	-1.96E-01	5.60E-01	WT NoN 1 dpi	RNA	Nuclear pore complex proteinNup214 (AHRD V3.3 *-* W6JJ76_NICBE)	GO:0005515|
Solyc04g009000.1	4.75E-01	1.26E-01	1.78E-01	7.42E-01	**1.02E+00**	**2.32E-03**	1.00E-01	7.42E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103XCD9_CYNCS)	GO:0005515|GO:0008270
Solyc12g011450.2	4.74E-01	2.51E-01	6.25E-01	2.27E-01	**-1.34E+00**	**2.77E-03**	-5.00E-01	2.27E-01	WT NoN 1 dpi	E	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** M1AG46_SOLTU)	GO:0009765|GO:0016020|

Solyc02g080170.1	4.71E-01	4.02E-01	8.48E-02	3.58E-02	**1.91E+00**	**1.94E-03**	1.23E+00	3.58E-02	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingfamily protein (AHRD V3.3 *** B9H1G1_POPTR)	GO:0005515|
Solyc06g061200.1	4.65E-01	1.05E-01	3.14E-01	5.06E-02	**1.01E+00**	**1.20E-03**	5.67E-01	5.06E-02	WT NoN 1 dpi	D	glycine-rich protein 1	
Solyc01g081420.2	4.62E-01	3.88E-01	-1.28E-02	6.49E-01	**1.60E+00**	**5.51E-03**	-2.42E-01	6.49E-01	WT NoN 1 dpi	RNA	Serrate RNA effector molecule(AHRD V3.3 *-* A0A1D1Y9V9_9ARAE)	
Solyc03g096540.3	4.60E-01	1.33E-01	1.30E-01	1.67E-02	**1.55E+00**	**1.96E-05**	7.59E-01	1.67E-02	WT NoN 1 dpi	G	PLAT domain-containing protein 1 (AHRD V3.3 *** PLAT1_ARATH)	GO:0005515|
Solyc12g010420.1	4.33E-01	2.78E-01	1.23E-01	1.82E-01	**1.29E+00**	**2.77E-03**	5.36E-01	1.82E-01	WT NoN 1 dpi	P	LOW QUALITY:NHL domain protein(AHRD V3.3 --* AT5G14895.1)	
Solyc02g083980.3	4.32E-01	2.41E-01	3.16E-01	1.32E-02	**-3.53E+00**	**3.59E-10**	-9.58E-01	1.32E-02	WT NoN 1 dpi	CS	Endoglucanase (AHRD V3.3 *** K4BAR6_SOLLC)	GO:0003824|GO:0004553|GO :0005975
Solyc03g097600.3	4.30E-01	2.84E-01	-6.27E-01	4.90E-01	**-1.13E+00**	**7.95E-03**	-2.75E-01	4.90E-01	WT NoN 1 dpi	TR	Bidirectional sugar transporterSWEET (AHRD V3.3 *** K4BJH7_SOLLC)	GO:0016021|
Solyc05g021540.2	4.18E-01	4.46E-01	-1.78E-01	4.03E-01	**1.59E+00**	**6.69E-03**	-4.59E-01	4.03E-01	WT NoN 1 dpi	2M	Alcohol dehydrogenase (AHRD V3.3 *-* Q4LAW8_CAPCH)	
Solyc01g090390.1	4.15E-01	1.42E-01	2.06E-01	5.42E-01	**1.15E+00**	**2.99E-04**	1.70E-01	5.42E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat (PPR-like)superfamily protein (AHRD V3.3 *** AT2G44880.2)	GO:0005515|
Solyc01g006920.3	4.11E-01	3.41E-01	1.16E-01	3.83E-01	**1.38E+00**	**3.06E-03**	3.76E-01	3.83E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A0B2S1E2_GLYSO)	GO:0005515|GO:0008270
Solyc04g050440.3	4.07E-01	3.74E-02	7.83E-01	9.92E-04	**2.37E+00**	**1.23E-12**	6.88E-01	9.92E-04	WT NoN 1 dpi	N	ammonium transporter	GO:0008519|GO:0015696|GO :0016020|GO:0008519|GO:00 16020|GO:0072488
Solyc01g095160.3	4.01E-01	2.01E-01	2.47E-02	1.45E-01	**1.22E+00**	**4.80E-04**	4.60E-01	1.45E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 *** AT4G37170.1)	GO:0005515|GO:0008270
Solyc01g091160.4	4.00E-01	2.04E-01	-3.88E-01	2.66E-02	**1.13E+00**	**1.07E-03**	7.22E-01	2.66E-02	WT NoN 1 dpi	N	arginase 1 ARG1	
Solyc06g005220.2	3.88E-01	3.01E-01	4.25E-01	2.52E-02	**1.19E+00**	**3.20E-03**	8.73E-01	2.52E-02	WT NoN 1 dpi	RNA	LOW QUALITY:Pentatricopeptiderepeat protein (AHRD V3.3 *** A0A1B3IPW0_CAPAN)	GO:0005515|
Solyc02g084900.2	3.79E-01	1.75E-02	4.58E-01	8.42E-05	**1.14E+00**	**4.81E-08**	6.96E-01	8.42E-05	WT NoN 1 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamilyprotein (AHRD V3.3 *** AT2G18193.1)	GO:0005524|
Solyc09g082400.2	3.78E-01	2.47E-01	1.10E-01	5.05E-01	**1.48E+00**	**8.96E-05**	2.16E-01	5.05E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9SPW3_RICCO)	GO:0005515|
Solyc11g067210.1	3.77E-01	3.11E-01	2.88E-01	1.77E-01	**1.80E+00**	**4.23E-05**	5.07E-01	1.77E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103XH63_CYNCS)	GO:0005515|GO:0008270
Solyc01g066870.3	3.70E-01	7.66E-03	3.64E-01	1.99E-02	**1.13E+00**	**2.87E-09**	3.18E-01	1.99E-02	WT NoN 1 dpi	K	Protein phosphatase 2C familyprotein (AHRD V3.3 *** AT3G16560.4)	GO:0003824|GO:0004722|GO :0006470
Solyc12g099600.2	3.63E-01	1.39E-01	1.23E-01	2.04E-01	**1.09E+00**	**1.03E-04**	3.11E-01	2.04E-01	WT NoN 1 dpi	K	Protein phosphatase 2C familyprotein (AHRD V3.3 *** AT3G16560.4)	GO:0003824|GO:0004722|GO :0006470

Solyc04g063300.2	3.63E-01	1.68E-01	2.52E-01	9.23E-03	**1.17E+00**	**1.02E-04**	7.20E-01	9.23E-03	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9SVS3_RICCO)	
Solyc06g009500.1	3.60E-01	1.54E-01	2.32E-01	3.64E-02	**1.00E+00**	**3.87E-04**	5.42E-01	3.64E-02	WT NoN 1 dpi	RNA	LOW QUALITY:Pentatricopeptiderepeat-containing protein (AHRD V3.3 *** A0A0B2SEE4_GLYSO)	GO:0005515|
Solyc01g099530.3	3.57E-01	3.63E-01	1.08E-01	9.17E-01	**1.34E+00**	**1.79E-03**	-4.05E-02	9.17E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103XQU8_CYNCS)	GO:0005515|
Solyc12g009070.1	3.56E-01	7.17E-01	3.62E-01	2.27E-01	**-3.35E+00**	**1.93E-03**	-1.20E+00	2.27E-01	WT NoN 1 dpi	DNA	Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 --* A0A151SSR0_CAJCA)	
Solyc02g070940.1	3.51E-01	4.28E-01	7.98E-01	7.71E-02	**-1.36E+00**	**4.32E-03**	-8.02E-01	7.71E-02	WT NoN 1 dpi	E	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** Q41422_SOLTU)	GO:0009765|GO:0016020|
Solyc03g080075.1	3.45E-01	7.29E-01	7.25E-01	5.60E-01	**3.96E+00**	**4.46E-04**	5.82E-01	5.60E-01	WT NoN 1 dpi	H	WAT1-related protein (AHRD V3.3 *** K4BHY3_SOLLC)	GO:0016020|GO:0016021|GO :0016021|GO:0022857
Solyc09g075940.3	3.39E-01	1.98E-01	9.25E-01	5.41E-01	**-1.40E+00**	**1.04E-05**	-1.59E-01	5.41E-01	WT NoN 1 dpi	AM	Amine oxidase (AHRD V3.3 *** K4CVH1_SOLLC)	GO:0005507|GO:0008131|GO :0009308|GO:0048038|GO:00 55114|
Solyc03g007360.3	3.33E-01	2.15E-01	2.94E-01	3.45E-03	**-1.04E+00**	**5.03E-04**	-8.45E-01	3.45E-03	WT NoN 1 dpi	TR	Nodulin MtN3	GO:0016021|
Solyc01g097700.1	3.31E-01	3.49E-01	4.14E-02	4.41E-02	**-1.02E+00**	**6.76E-03**	-7.35E-01	4.41E-02	WT NoN 1 dpi	CS	LOW QUALITY:Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)	
Solyc02g086300.3	3.29E-01	4.35E-01	-1.81E-01	8.98E-01	**1.28E+00**	**4.85E-03**	-5.34E-02	8.98E-01	WT NoN 1 dpi	N	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *** AT5G38200.1)	GO:0006541|GO:0016787|
Solyc02g092820.3	3.12E-01	4.15E-01	6.45E-01	5.86E-01	**1.15E+00**	**5.22E-03**	-2.07E-01	5.86E-01	WT NoN 1 dpi	H	IAA-amido synthetase 3-4	
Solyc08g081680.2	3.03E-01	6.34E-01	4.93E-01	1.81E-02	**1.94E+00**	**4.75E-03**	1.59E+00	1.81E-02	WT NoN 1 dpi	CS	Protein LURP-one-related 17(AHRD V3.3 *** A0A0B2R169_GLYSO)	
Solyc08g014100.1	3.02E-01	1.65E-02	7.38E-02	1.38E-05	**1.33E+00**	**1.73E-11**	6.30E-01	1.38E-05	WT NoN 1 dpi	RNA	Pentatricopeptide repeat superfamily protein (AHRD V3.3 ***A0A061EU55_THECC)	GO:0005515|GO:0008270
Solyc03g096830.3	2.93E-01	3.63E-01	-2.76E-01	8.65E-02	**1.07E+00**	**2.39E-03**	5.64E-01	8.65E-02	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9S1X8_RICCO)	GO:0005515|
Solyc08g077320.2	2.92E-01	5.15E-01	2.67E-01	2.76E-01	**1.48E+00**	**2.52E-03**	4.93E-01	2.76E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A0B2QIA0_GLYSO)	GO:0005515|
Solyc03g025380.3	2.88E-01	5.19E-01	5.23E-01	5.79E-01	**-1.25E+00**	**8.63E-03**	-2.48E-01	5.79E-01	WT NoN 1 dpi	OX	Peroxidase (AHRD V3.3 ***K4BF11_SOLLC)	GO:0004601|GO:0006979|GO :0020037|GO:0055114|GO:00 04601|GO:0042744
Solyc10g052650.2	2.87E-01	2.18E-01	-1.28E-01	7.96E-03	**-1.09E+00**	**5.67E-05**	-6.55E-01	7.96E-03	WT NoN 1 dpi	P	F-box protein (AHRD V3.3 *-* A0A0B2RZB4_GLYSO)	
Solyc04g014220.1	2.86E-01	4.30E-01	9.51E-01	9.94E-03	**1.24E+00**	**1.84E-03**	9.93E-01	9.94E-03	WT NoN 1 dpi	D	LOW QUALITY:RING/U-box superfamily protein, putative (AHRDV3.3 *** A0A061E293_THECC)	GO:0005515|GO:0008270|
Solyc08g080660.1	2.84E-01	2.73E-01	-3.05E-02	1.35E-03	**1.82E+00**	**1.44E-07**	9.12E-01	1.35E-03	WT NoN 1 dpi	D	Osmotin-like protein (AHRD V3.3 *** OLPA_TOBAC)	
Solyc06g074350.3	2.82E-01	7.46E-01	6.66E-02	2.73E-01	**-2.51E+00**	**7.24E-03**	-9.66E-01	2.73E-01	WT NoN 1 dpi	G	self-pruning	

Solyc01g006640.1	2.82E-01	7.36E-01	4.74E-01	6.96E-01	**3.11E+00**	**8.73E-04**	-3.26E-01	6.96E-01	WT NoN 1 dpi	P	LOW QUALITY:AMP-dependent synthetase and ligase family protein(AHRD V3.3 *** A0A061GTM3_THECC)	GO:0003824|GO:0008152|GO :0004096|GO:0020037|GO:00 55114
Solyc02g061990.3	2.82E-01	7.54E-01	-9.90E-01	4.26E-01	**-3.27E+00**	**1.12E-03**	-7.21E-01	4.26E-01	WT NoN 1 dpi	T	Bzip transcription factor (AHRD V3.3 *** A0A087GK23_ARAAL)	GO:0003700|GO:0006355|GO :0043565|
Solyc09g008360.2	2.82E-01	7.14E-01	6.66E-02	1.51E-01	**-2.51E+00**	**2.91E-03**	-1.13E+00	1.51E-01	WT NoN 1 dpi	NA	LOW QUALITY:Heparan-alpha- glucosaminide N-acetyltransferase(AHRD V3.3 *** A0A0B2STS8_GLYSO)	
Solyc09g014210.2	2.65E-01	3.11E-01	-1.32E-01	7.18E-01	**1.33E+00**	**2.08E-05**	9.35E-02	7.18E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingfamily protein (AHRD V3.3 *** B9IG54_POPTR)	GO:0005515|
Solyc04g073990.3	2.61E-01	1.04E-01	7.31E-02	7.57E-05	**1.31E+00**	**6.86E-09**	7.28E-01	7.57E-05	WT NoN 1 dpi	TR	annexin p34	GO:0005509|GO:0005544|
Solyc07g041000.3	2.54E-01	6.18E-01	4.70E-01	1.22E-01	**-1.72E+00**	**2.05E-03**	-8.05E-01	1.22E-01	WT NoN 1 dpi	RNA	Cleavage and polyadenylation specificity factor subunit 5 (AHRD V3.3 *** A0A0B2R9M0_GLYSO)	GO:0003729|GO:0005849|GO :0006378|GO:0016787
Solyc05g055990.3	2.53E-01	2.48E-01	2.54E-01	1.31E-03	**1.26E+00**	**3.68E-06**	7.73E-01	1.31E-03	WT NoN 1 dpi	TR	plasma membrane intrinsic protein 2.12	GO:0005215|GO:0006810|GO :0016020|
Solyc07g053380.2	2.50E-01	6.18E-01	9.13E-01	2.16E-01	**1.55E+00**	**4.34E-03**	6.28E-01	2.16E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103XH40_CYNCS)	GO:0005515|
Solyc12g056527.1	2.43E-01	6.06E-01	5.28E-01	4.12E-01	**1.59E+00**	**2.20E-03**	3.89E-01	4.12E-01	WT NoN 1 dpi	TR	Exocyst complex component,putative (AHRD V3.3 *-* B9T2G4_RICCO)	GO:0000145|GO:0006893|
Solyc01g096280.2	2.30E-01	3.57E-01	-2.76E-02	4.33E-01	**1.07E+00**	**1.76E-04**	1.96E-01	4.33E-01	WT NoN 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** F4YF83_9APIA)	GO:0005506|GO:0016705|GO :0020037|GO:0055114|GO:00 16705|GO:0055114
Solyc08g016588.1	2.11E-01	5.82E-01	5.63E-02	8.11E-02	**-1.06E+00**	**9.43E-03**	-6.87E-01	8.11E-02	WT NoN 1 dpi	DNA	Zinc finger CCCH domain- containing protein 54 (AHRD V3.3 -- * C3H54_ORYSJ)	
Solyc01g102690.3	2.05E-01	4.47E-01	-1.31E-02	2.90E-02	**1.35E+00**	**2.90E-05**	6.14E-01	2.90E-02	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingfamily protein (AHRD V3.3 *** B9IBN2_POPTR)	GO:0005515|GO:0008270
Solyc08g007130.3	2.04E-01	5.41E-01	7.07E-01	2.19E-02	**-1.16E+00**	**1.67E-03**	-8.05E-01	2.19E-02	WT NoN 1 dpi	CS	Beta-amylase (AHRD V3.3 *** K4CIK0_SOLLC)	GO:0000272|GO:0016161|GO :0005975
Solyc04g063245.1	2.01E-01	3.64E-01	5.69E-01	1.57E-01	**-1.11E+00**	**2.52E-05**	-3.17E-01	1.57E-01	WT NoN 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)	GO:0005506|GO:0016705|GO :0020037|GO:0055114|GO:00 16705|GO:0055114
Solyc06g082190.3	1.90E-01	3.73E-01	-4.62E-02	2.13E-03	**1.01E+00**	**5.03E-05**	7.14E-01	2.13E-03	WT NoN 1 dpi	K	Protein kinase, putative (AHRDV3.3 *** B9SKV0_RICCO)	GO:0004672|GO:0005524|GO :0006468|GO:0004672|GO:00 06468
Solyc12g049520.2	1.78E-01	8.31E-01	5.49E-01	8.40E-02	**3.26E+00**	**5.35E-04**	1.48E+00	8.40E-02	WT NoN 1 dpi	H	COP1-interacting-like protein (AHRD V3.3 *-* G7L8C6_MEDTR)	
Solyc02g088470.1	1.73E-01	4.46E-01	1.81E-01	1.50E-01	**1.01E+00**	**1.30E-04**	3.32E-01	1.50E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103YHC4_CYNCS)	GO:0005515|
Solyc07g005170.2	1.63E-01	7.26E-01	-7.12E-01	1.91E-01	**1.61E+00**	**1.71E-03**	6.17E-01	1.91E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9S4A9_RICCO)	GO:0005515|

Solyc08g079150.1	1.44E-01	7.26E-01	8.32E-01	1.95E-02	**1.72E+00**	**2.62E-04**	1.01E+00	1.95E-02	WT NoN 1 dpi	H	SAUR-like auxin-responsive proteinfamily (AHRD V3.3 *** AT4G22620.1)	GO:0009733|
Solyc01g090510.2	1.37E-01	7.16E-01	-2.09E-02	9.29E-01	**1.23E+00**	**2.85E-03**	-3.33E-02	9.29E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** A0A061GHG1_THECC)	GO:0005515|GO:0008270
Solyc04g078660.1	1.35E-01	2.34E-01	5.30E-01	4.34E-06	**-1.30E+00**	**7.73E-12**	-6.40E-01	4.34E-06	WT NoN 1 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT5G42830.1)	GO:0016747|
Solyc08g076710.3	1.24E-01	7.94E-01	6.55E-01	5.64E-02	**-1.41E+00**	**5.77E-03**	-9.34E-01	5.64E-02	WT NoN 1 dpi	T	R2R3MYB transcription factor 39	GO:0003677|
Solyc12g088970.1	1.14E-01	9.08E-01	2.07E-01	3.93E-02	**-5.36E+00**	**9.71E-06**	-2.12E+00	3.93E-02	WT NoN 1 dpi	CYTP450	CytochromeP450	GO:0005506|GO:0016705|GO :0020037|GO:0055114|GO:00 16705|GO:0055114
Solyc07g047850.3	1.04E-01	7.92E-01	4.16E-01	2.14E-01	**-1.22E+00**	**4.28E-03**	-4.96E-01	2.14E-01	WT NoN 1 dpi	E	Chlorophyll a-b binding protein,chloroplastic (AHRD V3.3 *** CB23_ORYSI)	GO:0009765|GO:0016020|
Solyc02g069200.3	1.01E-01	8.91E-01	-2.03E-01	4.79E-02	**-4.54E+00**	**1.40E-06**	-1.51E+00	4.79E-02	WT NoN 1 dpi	TR	iron-regulated transporter 1	GO:0005385|GO:0016021|GO :0071577|GO:0016020|GO:00 30001|GO:0046873|GO:0055 085
Solyc01g101260.2	9.81E-02	7.35E-01	-7.92E-01	3.75E-01	**-1.40E+00**	**4.97E-05**	-2.59E-01	3.75E-01	WT NoN 1 dpi	DNA	DNA-(apurinic or apyrimidinic site)lyase (AHRD V3.3 --* A0A067FYM9_CITSI)	
Solyc04g051480.1	9.01E-02	8.27E-01	2.17E-01	2.64E-01	**1.35E+00**	**2.73E-03**	4.65E-01	2.64E-01	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103XF42_CYNCS)	GO:0005515|GO:0008270
Solyc10g079700.2	8.96E-02	7.41E-01	-3.60E-01	1.57E-02	**1.25E+00**	**8.18E-05**	6.95E-01	1.57E-02	WT NoN 1 dpi	S	Two-component response regulator(AHRD V3.3 *** A0A059T9P7_ROSCN)	GO:0000160|
Solyc08g061010.3	8.71E-02	7.30E-01	7.19E-02	8.63E-01	**1.17E+00**	**7.62E-05**	-4.37E-02	8.63E-01	WT NoN 1 dpi	TR	Major facilitator superfamily protein(AHRD V3.3 *** AT2G26690.1)	GO:0005215|GO:0006810|GO :0016020|GO:0005215|GO:00 06857|GO:0016020
Solyc07g005870.3	6.41E-02	8.59E-01	-1.61E-01	1.51E-02	**1.51E+00**	**2.46E-04**	9.28E-01	1.51E-02	WT NoN 1 dpi	E	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT4G30720.1)	GO:0016491|GO:0055114|GO :0071949
Solyc06g005320.1	6.00E-02	8.73E-01	1.36E-01	2.65E-02	**1.20E+00**	**3.42E-03**	8.75E-01	2.65E-02	WT NoN 1 dpi	T	MYB-related transcription factor(AHRD V3.3 *-* A0A059PRS8_SALMI)	GO:0003677|
Solyc02g090400.3	5.88E-02	8.92E-01	2.07E-01	1.43E-02	**1.94E+00**	**1.15E-04**	1.12E+00	1.43E-02	WT NoN 1 dpi	S	Two-component response regulator(AHRD V3.3 *** W9S3N8_9ROSA)	GO:0003677|
Solyc08g074682.1	5.82E-02	8.77E-01	3.41E-01	1.41E-01	**1.24E+00**	**2.68E-03**	5.67E-01	1.41E-01	WT NoN 1 dpi	2M	polyphenol oxidase precursor	GO:0004097|GO:0046148|GO :0055114|GO:0004097|GO:00 55114
Solyc02g089720.2	5.74E-02	7.59E-01	3.25E-01	1.87E-02	**1.06E+00**	**5.26E-06**	4.65E-01	1.87E-02	WT NoN 1 dpi	C	Glycoside hydrolase, family 81(AHRD V3.3 *** A0A103YH72_CYNCS)	GO:0052861|
Solyc01g087830.1	5.07E-02	8.37E-01	6.95E-01	8.24E-03	**1.21E+00**	**3.70E-05**	6.96E-01	8.24E-03	WT NoN 1 dpi	P	LOW QUALITY:Subtilisin-likeprotease (AHRD V3.3 *-* O82777_SOLLC)	GO:0004252|GO:0006508|

Solyc08g061920.2	3.14E-02	9.32E-01	-1.75E-01	1.47E-02	**2.08E+00**	**5.63E-06**	9.57E-01	1.47E-02	WT NoN 1 dpi	H	cytokinin oxidase/dehydrogenase 3	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660
Solyc04g016440.3	1.85E-02	9.42E-01	-2.81E-01	7.84E-04	**-1.08E+00**	**2.26E-04**	-9.56E-01	7.84E-04	WT NoN 1 dpi	NA	Transmembrane proteins 14C (AHRD V3.3 *** AT3G57280.1)	GO:0016020|
Solyc06g009620.1	1.39E-02	9.71E-01	-4.67E-01	1.22E-02	**1.28E+00**	**2.39E-03**	1.02E+00	1.22E-02	WT NoN 1 dpi	RNA	Pentatricopeptide repeat superfamily protein, putative (AHRDV3.3 *** A0A061F8B1_THECC)	GO:0005515|
Solyc03g093250.2	1.33E-02	9.73E-01	2.11E-01	3.03E-01	**1.10E+00**	**8.96E-03**	4.07E-01	3.03E-01	WT NoN 1 dpi	DNA	Structural maintenance of chromosomes protein (AHRD V3.3 *** A0A068V0V7_COFCA)	GO:0005515|GO:0005524|GO:0005694|GO:0051276|
Solyc09g091700.3	2.41E-03	9.97E-01	2.32E-01	3.59E-02	**-2.47E+00**	**1.40E-03**	-1.53E+00	3.59E-02	WT NoN 1 dpi	OX	NADP-dependent alkenal doublebond reductase (AHRD V3.3 ***I3SE71_MEDTR)	GO:0016491|GO:0055114
Solyc02g011815.1	-2.09E-02	9.83E-01	2.87E-01	3.35E-02	**2.74E+00**	**9.25E-03**	2.18E+00	3.35E-02	WT NoN 1 dpi	P	30S ribosomal protein S15, chloroplastic (AHRD V3.3 *-* RR15_SOLLC)	GO:0003735|GO:0005622|GO:0005840|GO:0006412|GO:0003735|GO:0005840|GO:0006412
Solyc03g115910.2	-2.85E-02	9.65E-01	-2.12E-01	3.61E-01	**-2.30E+00**	**1.28E-03**	-5.93E-01	3.61E-01	WT NoN 1 dpi	T	Transcription factor, MADS-box(AHRD V3.3 *** A0A118JYM5_CYNCS)	GO:0003677|GO:0046983|
Solyc01g104090.3	-2.87E-02	9.69E-01	1.21E-01	1.56E-02	**2.26E+00**	**5.06E-03**	1.91E+00	1.56E-02	WT NoN 1 dpi	RNA	Pentatricopeptide repeat-containingprotein (AHRD V3.3 *** A0A103YKX6_CYNCS)	GO:0005515|GO:0008270
Solyc08g080540.3	-3.61E-02	8.88E-01	-3.66E-01	7.53E-02	**-1.30E+00**	**2.45E-05**	-4.70E-01	7.53E-02	WT NoN 1 dpi	STR	SolycHsfB2b	GO:0003700|GO:0005634|GO:0006355|GO:0043565|
Solyc03g044560.1	-4.13E-02	9.43E-01	1.57E-01	4.72E-01	**-1.90E+00**	**2.48E-03**	-4.14E-01	4.72E-01	WT NoN 1 dpi	G	LOW QUALITY:NAC domain containing protein 35 (AHRD V3.3 -- * AT2G02450.2)	GO:0048364|
Solyc04g076303.1	-5.03E-02	8.02E-01	1.57E-02	5.82E-01	**1.01E+00**	**2.74E-05**	1.11E-01	5.82E-01	WT NoN 1 dpi	TR	Mechanosensitive ion channel-likeprotein (AHRD V3.3 *** G7J535_MEDTR)	GO:0016020|GO:0055085|
Solyc11g005280.1	-7.27E-02	8.71E-01	-1.58E-01	2.42E-01	**-1.56E+00**	**1.60E-03**	-5.29E-01	2.42E-01	WT NoN 1 dpi	D	RING/U-box superfamily protein(AHRD V3.3 *** AT1G49230.1)	GO:0005515|GO:0008270|
Solyc07g009290.3	-7.28E-02	7.13E-01	-1.88E-01	6.53E-02	**-1.19E+00**	**1.98E-06**	-3.77E-01	6.53E-02	WT NoN 1 dpi	D	defensin-like protein (AHRD V3.3 -** AT1G19610.1)	GO:0006952|
Solyc07g019450.3	-8.13E-02	8.19E-01	-3.46E-02	3.81E-01	**-1.13E+00**	**3.50E-03**	-3.14E-01	3.81E-01	WT NoN 1 dpi	H	auxin-regulated IAA33	GO:0005515|GO:0005634|GO:0006355
Solyc02g080060.1	-8.39E-02	8.92E-01	5.30E-01	2.15E-02	**2.22E+00**	**1.29E-03**	1.50E+00	2.15E-02	WT NoN 1 dpi	D	Cysteine-rich receptor-kinase-likeprotein (AHRD V3.3 *** A0A072VRC1_MEDTR)	
Solyc07g054145.1	-8.61E-02	6.74E-01	-3.92E-01	2.89E-03	**-1.30E+00**	**9.16E-07**	-6.66E-01	2.89E-03	WT NoN 1 dpi	P	CAAX amino terminal proteasefamily protein (AHRD V3.3 *** AT2G20725.1)	GO:0016020|
Solyc04g058100.3	-9.48E-02	5.54E-01	-1.84E-01	5.77E-06	**-1.55E+00**	**3.74E-10**	-9.00E-01	5.77E-06	WT NoN 1 dpi	NA	Metallothionein-like protein type 2(AHRD V3.3 *** MT2X_SOLLC)	GO:0046872|
Solyc07g066310.3	-1.04E-01	6.35E-01	-2.78E-01	7.74E-02	**-1.12E+00**	**2.32E-05**	-3.99E-01	7.74E-02	WT NoN 1 dpi	E	Photosystem II 10 kDa polypeptidefamily protein (AHRD V3.3 *** A9PH94_POPTR)	GO:0009523|GO:0009654|GO:0015979|GO:0042651|
Solyc05g055343.1	-1.09E-01	7.22E-01	-2.56E-01	9.45E-02	**-1.02E+00**	**2.32E-03**	-5.25E-01	9.45E-02	WT NoN 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CEK8_SOLLC)	GO:0008152|GO:0016758|

Solyc10g009260.1	-1.23E-01	7.96E-01	-6.57E-01	5.83E-02	**-1.98E+00**	**2.72E-04**	-9.29E-01	5.83E-02	WT NoN 1 dpi	D	LOW QUALITY:Cytochrome b5 isoform 1 (AHRD V3.3 -** M8A0M0_TRIUA)	
Solyc10g050890.2	-1.43E-01	5.57E-01	1.85E-01	5.20E-02	**1.18E+00**	**4.06E-05**	4.88E-01	5.20E-02	WT NoN 1 dpi	N	nitrite reductase 2	GO:0016491|GO:0020037|GO :0051536|GO:0055114|GO:00 16491|GO:0055114
Solyc01g097810.3	-1.46E-01	1.42E-01	-1.79E-01	4.23E-08	**-1.24E+00**	**9.95E-13**	-7.38E-01	4.23E-08	WT NoN 1 dpi	2M	zeta-carotene desaturase	GO:0016117|GO:0016719|GO :0055114|GO:0016491|GO:00 55114
Solyc10g007510.2	-1.50E-01	8.00E-01	1.84E-01	5.54E-02	**-1.81E+00**	**4.64E-03**	-1.17E+00	5.54E-02	WT NoN 1 dpi	CS	Glucan endo-1,3-beta-glucosidase(AHRD V3.3 *** A0A0B0NBZ5_GOSAR)	
Solyc02g084930.3	-1.55E-01	2.70E-01	-1.33E-02	8.24E-07	**-1.17E+00**	**5.99E-09**	-8.84E-01	8.24E-07	WT NoN 1 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** G7LDW2_MEDTR)	GO:0005506|GO:0016705|GO :0020037|GO:0055114|GO:00 16705|GO:0055114
Solyc12g017350.2	-1.61E-01	7.74E-01	-3.18E-01	9.51E-02	**-2.17E+00**	**6.24E-04**	-9.63E-01	9.51E-02	WT NoN 1 dpi	TR	Cation diffusion facilitator 9	GO:0006812|GO:0008324|GO :0016021|GO:0055085|
Solyc12g100180.2	-1.71E-01	6.98E-01	3.39E-01	8.75E-01	**-1.25E+00**	**8.19E-03**	-6.90E-02	8.75E-01	WT NoN 1 dpi	TR	Pleiotropic drug resistance ABCtransporter (AHRD V3.3 *** W0TUG3_ACAMN)	GO:0005524|GO:0016887|GO :0016020
Solyc10g079650.2	-1.79E-01	7.00E-01	-4.12E-01	9.84E-02	**-3.34E+00**	**1.09E-07**	-7.87E-01	9.84E-02	WT NoN 1 dpi	T	bHLH transcription factor 066	GO:0003677|GO:0046983
Solyc01g106820.3	-1.82E-01	5.98E-01	-3.44E-02	7.60E-02	**-1.48E+00**	**2.01E-04**	-6.32E-01	7.60E-02	WT NoN 1 dpi	DNA	Sterol regulatory element-binding protein site 2 protease, putative (AHRD V3.3 *** B9S7Z4_RICCO)	
Solyc05g025620.2	-1.89E-01	5.79E-01	-7.38E-03	3.36E-01	**1.18E+00**	**1.69E-03**	3.29E-01	3.36E-01	WT NoN 1 dpi	L	alpha/beta-Hydrolases superfamilyprotein (AHRD V3.3 *-* AT3G47560.4)	
Solyc04g009030.3	-1.95E-01	6.88E-01	3.86E-01	2.97E-01	**-1.38E+00**	**8.36E-03**	-5.12E-01	2.97E-01	WT NoN 1 dpi	C	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 ***K4BP59_SOLLC)	GO:0006006|GO:0016620|GO :0050661|GO:0051287|GO:00 55114|GO:0016620|GO:0055 114
Solyc06g008760.1	-2.01E-01	4.04E-01	-5.39E-01	2.66E-01	**-1.01E+00**	**2.35E-04**	-2.69E-01	2.66E-01	WT NoN 1 dpi	OX	Glutaredoxin (AHRD V3.3 ***B3F8F2_SOLTU)	GO:0009055|GO:0015035|GO :0045454|
Solyc11g018530.2	-2.04E-01	4.73E-01	-2.19E-01	7.68E-03	**-1.66E+00**	**3.18E-06**	-8.09E-01	7.68E-03	WT NoN 1 dpi	TR	root-specific metal transporter	GO:0005215|GO:0006810|GO :0016020|
Solyc09g076030.3	-2.08E-01	7.39E-01	4.44E-01	1.55E-01	**-1.78E+00**	**7.71E-03**	-9.01E-01	1.55E-01	WT NoN 1 dpi	E	Photosystem II protein (AHRD V3.3 *-* A0A1D1ZBF0_9ARAE)	GO:0010207|
Solyc05g051220.3	-2.24E-01	1.45E-01	1.43E-02	8.64E-02	**1.17E+00**	**2.81E-08**	2.66E-01	8.64E-02	WT NoN 1 dpi	TR	Potassium channel TORK1 (AHRDV3.3 *** Q5NT78_TOBAC)	GO:0005216|GO:0006811|GO :0016020|GO:0055085|GO:00 05249|GO:0006813|GO:0016 020
Solyc11g068515.1	-2.32E-01	7.16E-01	4.52E-02	6.06E-01	**-1.76E+00**	**9.96E-03**	-3.29E-01	6.06E-01	WT NoN 1 dpi	K	Protein kinase superfamily protein(AHRD V3.3 --* AT1G54610.3)	
Solyc06g036770.1	-2.36E-01	5.32E-01	2.86E-01	1.21E-01	**1.05E+00**	**8.88E-03**	5.97E-01	1.21E-01	WT NoN 1 dpi	CS	LOW QUALITY:CASP-like protein(AHRD V3.3 --* A0A0L9UWM4_PHAAN)	
Solyc04g011680.2	-2.38E-01	6.40E-01	-2.51E-02	9.98E-01	**1.45E+00**	**7.82E-03**	-1.26E-03	9.98E-01	WT NoN 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A061DI80_THECC)	GO:0005506|GO:0016705|GO :0020037|GO:0055114|GO:00 16705|GO:0055114
Solyc11g007140.2	-2.45E-01	1.49E-01	-1.70E-02	1.84E-03	**-1.01E+00**	**1.88E-06**	-5.73E-01	1.84E-03	WT NoN 1 dpi	NA	Hippocampus abundant transcript-like protein 1 (AHRD V3.3 *-* W9QGN7_9ROSA)	GO:0016021|GO:0055085|

Solyc06g006090.1	-2.55E-01	4.61E-01	-3.02E-01	1.11E-01	**-1.05E+00**	**4.88E-03**	-5.61E-01	1.11E-01	WT NoN 1 dpi	NA	LOW QUALITY:JOSEPHIN-like protein, putative (AHRD V3.3 *-* A0A061GWC4_THECC)	
Solyc11g013110.2	-2.69E-01	3.64E-01	1.66E-03	7.92E-03	**-1.01E+00**	**1.82E-03**	-8.38E-01	7.92E-03	WT NoN 1 dpi	2M	Flavonol synthase (AHRD V3.3 *** C0LUV3_SOLTU)	GO:0016491|GO:0055114|
Solyc06g074240.2	-2.70E-01	3.35E-01	7.47E-01	3.10E-03	**-1.07E+00**	**6.45E-04**	-8.96E-01	3.10E-03	WT NoN 1 dpi	2M	Beta-carotene	GO:0006810|GO:0016021|GO :0016192
Solyc10g079860.2	-2.71E-01	5.41E-01	-5.70E-01	2.44E-01	**-1.22E+00**	**9.55E-03**	-5.20E-01	2.44E-01	WT NoN 1 dpi	CS	LEQB L.esculentum TomQ'b beta(1,3)glucanase	GO:0004553|GO:0005975|GO :0005975
Solyc04g053050.3	-2.71E-01	6.13E-01	-2.59E-01	7.71E-01	**-1.52E+00**	**8.08E-03**	-1.56E-01	7.71E-01	WT NoN 1 dpi	E	2-oxoglutarate-dependent dioxygenase-related family protein(AHRD V3.3 *-* B9GL08_POPTR)	
Solyc09g005500.3	-2.77E-01	3.39E-01	-3.12E-01	2.36E-02	**1.27E+00**	**1.41E-04**	6.84E-01	2.36E-02	WT NoN 1 dpi	H	MLP (AHRD V3.3 *** G8DRV9_GOSBA)	GO:0006952|GO:0009607|
Solyc08g014240.3	-2.87E-01	5.03E-01	-2.54E-01	4.25E-01	**1.27E+00**	**5.65E-03**	3.42E-01	4.25E-01	WT NoN 1 dpi	C	Isopropylmalate synthase (AHRDV3.3 *** A0A0G2T9V8_SOLPN)	GO:0003824|GO:0019752|GO :0046912
Solyc11g010850.2	-2.89E-01	3.12E-01	-1.81E-01	1.80E-03	**-1.41E+00**	**3.33E-05**	-9.77E-01	1.80E-03	WT NoN 1 dpi	C	1-deoxy-D-xylulose 5-phosphatesynthase (AHRD V3.3 *** B6E973_STERE)	GO:0003824|GO:0008152|GO :0008661|GO:0016114
Solyc08g065670.3	-2.92E-01	2.40E-01	4.64E-01	1.25E-03	**1.37E+00**	**6.89E-06**	8.80E-01	1.25E-03	WT NoN 1 dpi	K	Phosphatase 2C family protein(AHRD V3.3 *** A0A061GL17_THECC)	GO:0003824|GO:0004722|GO :0006470
Solyc10g083340.2	-3.08E-01	2.65E-01	-7.65E-01	2.12E-02	**-1.18E+00**	**1.83E-04**	-6.64E-01	2.12E-02	WT NoN 1 dpi	T	Myb family transcription factor APL(AHRD V3.3 *** A0A0B2R6R9_GLYSO)	GO:0003677|
Solyc06g062960.2	-3.18E-01	1.37E-02	-2.88E-01	9.39E-03	**-1.09E+00**	**1.82E-09**	-3.37E-01	9.39E-03	WT NoN 1 dpi	NA	DUF1677 family protein (DUF1677)(AHRD V3.3 *** AT1G72510.2)	
Solyc10g079660.2	-3.24E-01	6.60E-01	-1.39E+00	3.10E-02	**-4.34E+00**	**2.81E-06**	-1.66E+00	3.10E-02	WT NoN 1 dpi	STR	bHLH transcription factor 067	GO:0003677|GO:0005488
Solyc10g012240.3	-3.31E-01	8.27E-02	1.27E-01	4.82E-02	**-1.06E+00**	**4.72E-06**	-3.80E-01	4.82E-02	WT NoN 1 dpi	S	Ubiquitin-conjugating enzyme E2(AHRD V3.3 *** A0A1D1ZAB9_9ARAE)	
Solyc04g015750.3	-3.32E-01	1.36E-01	-1.27E-01	3.03E-02	**-1.12E+00**	**2.19E-05**	-4.94E-01	3.03E-02	WT NoN 1 dpi	H	Magnesium chelatase H subunit (AHRD V3.3 *** F8SPG3_CAMSI)	GO:0009058|GO:0015995|GO :0016851
Solyc07g006740.3	-3.38E-01	1.08E-01	2.26E-01	2.68E-03	**1.23E+00**	**2.22E-06**	6.75E-01	2.68E-03	WT NoN 1 dpi	STR	Protein DETOXIFICATION (AHRDV3.3 *** K4CBE5_SOLLC)	GO:0006855|GO:0015238|GO :0015297|GO:0016020|GO:00 55085|
Solyc09g008917.1	-3.39E-01	1.92E-01	-8.13E-02	2.91E-02	**1.17E+00**	**9.05E-05**	5.86E-01	2.91E-02	WT NoN 1 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 --* A0A061DI80_THECC)	
Solyc10g079640.2	-3.67E-01	3.91E-01	-3.71E-01	8.40E-02	**-1.90E+00**	**1.25E-04**	-7.57E-01	8.40E-02	WT NoN 1 dpi	H	IAA-amino acid hydrolase ILR1,putative (AHRD V3.3 *** B9RJ28_RICCO)	GO:0008152|GO:0016787|GO :0016787
Solyc05g015700.1	-3.69E-01	2.97E-01	-6.08E-01	1.84E-01	**-1.11E+00**	**3.71E-03**	-4.73E-01	1.84E-01	WT NoN 1 dpi	NA	LOW QUALITY:transmembrane protein, putative (DUF 3339) (AHRDV3.3 *** AT3G48660.1)	
Solyc01g108300.3	-3.71E-01	1.33E-01	-3.78E-01	8.77E-02	**1.18E+00**	**3.87E-05**	4.24E-01	8.77E-02	WT NoN 1 dpi	T	Myb family transcription factor	GO:0003677|
Solyc03g111700.3	-3.78E-01	3.26E-01	3.07E-01	4.43E-01	**-1.56E+00**	**3.25E-04**	-2.94E-01	4.43E-01	WT NoN 1 dpi	NA	Metallo-hydrolase/oxidoreductase superfamily protein (AHRD V3.3 *** AT1G29700.2),Pfam:PF13483	
Solyc02g090610.1	-3.80E-01	4.53E-01	-1.23E+00	2.64E-02	**-1.69E+00**	**2.24E-03**	-1.18E+00	2.64E-02	WT NoN 1 dpi	G	LOW QUALITY:Cyclin-dependentkinase D-1 (AHRD V3.3 --* CDKD1_ORYSI)	GO:0048364|

Solyc04g014600.3	-3.96E-01	4.60E-02	-9.08E-01	2.18E-03	**-1.31E+00**	**2.56E-07**	-6.44E-01	2.18E-03	WT NoN 1 dpi	DNA	Adenine nucleotide alpha hydrolases-like superfamily protein(AHRD V3.3 *** AT3G03270.2)	GO:0006950|
Solyc05g015480.3	-3.97E-01	3.29E-04	-1.19E-01	2.34E-05	**-1.12E+00**	**9.49E-12**	-4.94E-01	2.34E-05	WT NoN 1 dpi	H	Molybdenum cofactor sulfurase(AHRD V3.3 *** A0A1D1Y5S2_9ARAE)	
Solyc05g012230.3	-4.14E-01	1.56E-01	-6.42E-01	5.11E-02	**-1.08E+00**	**7.85E-04**	-5.79E-01	5.11E-02	WT NoN 1 dpi	CS	Protein POLAR LOCALIZATION DURING ASYMMETRIC DIVISIONAND REDISTRIBUTION (AHRD V3.3 --* A0A199UMI0_ANACO)	
Solyc06g054270.3	-4.14E-01	3.54E-01	-4.18E-01	3.75E-02	**-1.45E+00**	**2.78E-03**	-9.62E-01	3.75E-02	WT NoN 1 dpi	TR	Sugar transporter protein 11	GO:0005215|GO:0016021|GO:0055085|GO:0016020|GO:0022891|GO:0055085
Solyc06g009010.1	-4.16E-01	1.15E-01	-8.42E-02	1.28E-01	**-1.00E+00**	**5.72E-04**	-4.01E-01	1.28E-01	WT NoN 1 dpi	T	Nuclear transcription factor Yprotein (AHRD V3.3 *** I3TAW4_MEDTR)	GO:0005634|GO:0006355|GO:0043565|GO:0046982
Solyc02g078910.3	-4.17E-01	7.05E-02	-4.50E-01	3.53E-01	**-1.13E+00**	**2.54E-05**	-2.09E-01	3.53E-01	WT NoN 1 dpi	DNA	endonuclease AM238701	GO:0003676|GO:0004519|GO:0006308|GO:0016788
Solyc10g083230.1	-4.18E-01	9.94E-02	-3.59E-01	1.35E-03	**1.15E+00**	**7.56E-05**	8.80E-01	1.35E-03	WT NoN 1 dpi	P	F-box family protein (AHRD V3.3 *** B9NEF0_POPTR)	GO:0005515|
Solyc01g109880.3	-4.26E-01	6.61E-02	-5.36E-01	1.53E-01	**-1.40E+00**	**1.22E-06**	-3.27E-01	1.53E-01	WT NoN 1 dpi	T	BZIP transcription factor (AHRDV3.3 *** C0KYN1_SOLLC)	GO:0003700|GO:0006355|GO:0043565|
Solyc01g090340.2	-4.27E-01	1.61E-01	-1.67E-01	7.90E-01	**-1.01E+00**	**2.17E-03**	-7.98E-02	7.90E-01	WT NoN 1 dpi	H	Ethylene-responsive transcriptionfactor, putative (AHRD V3.3 *** B9RD03_RICCO)	GO:0003677|GO:0003700|GO:0006355
Solyc10g084370.2	-4.29E-01	1.27E-02	-1.67E-01	3.38E-03	**-1.04E+00**	**7.14E-07**	-5.17E-01	3.38E-03	WT NoN 1 dpi	T	MYB transcription factor (AHRDV3.3 *** B5TV64_CAMSI)	GO:0003677|
Solyc11g073110.2	-4.34E-01	3.69E-01	2.26E-01	9.39E-01	**-1.42E+00**	**6.20E-03**	3.69E-02	9.39E-01	WT NoN 1 dpi	G	UPSTREAM OF FLC protein(DUF966) (AHRD V3.3 *** AT5G59790.1)	
Solyc09g090790.3	-4.52E-01	5.06E-01	-1.09E+00	1.29E-02	**1.98E+00**	**6.73E-03**	1.79E+00	1.29E-02	WT NoN 1 dpi	G	R2R3MYB transcription factor 79	GO:0003677|
Solyc07g044750.3	-4.63E-01	3.18E-03	1.25E-01	1.75E-04	**-1.10E+00**	**3.50E-08**	-6.24E-01	1.75E-04	WT NoN 1 dpi	D	N-acetyl-D-glucosamine kinase(AHRD V3.3 *** A0A0B0P7N8_GOSAR)	
Solyc10g006330.3	-4.64E-01	5.86E-01	1.51E-01	1.00E+00	**-2.50E+00**	**6.21E-03**	6.78E-06	1.00E+00	WT NoN 1 dpi	H	Plastid movement impaired protein(AHRD V3.3 *** G7LD87_MEDTR)	GO:0009902|
Solyc02g089540.3	-4.75E-01	7.22E-02	-2.66E-01	7.39E-03	**-1.29E+00**	**2.62E-05**	-7.37E-01	7.39E-03	WT NoN 1 dpi	G	CONSTANS 1	GO:0005515|GO:0005622|GO:0008270
Solyc11g066880.2	-4.88E-01	1.20E-02	-5.67E-01	3.46E-01	**-1.75E+00**	**4.30E-10**	-1.73E-01	3.46E-01	WT NoN 1 dpi	G	Phytosulfokine 3, putative (AHRDV3.3 *** A0A061ESV9_THECC)	GO:0005576|GO:0008083|GO:0008283|
Solyc07g066000.3	-4.92E-01	5.17E-01	-5.87E-01	8.20E-02	**2.12E+00**	**8.98E-03**	1.36E+00	8.20E-02	WT NoN 1 dpi	AM	Amino acid permease (AHRD V3.3 *-* S8CYC9_9LAMI)	
Solyc05g009180.1	-4.94E-01	4.38E-03	-8.62E-01	2.30E-03	**-1.32E+00**	**8.59E-09**	-5.35E-01	2.30E-03	WT NoN 1 dpi	DNA	LOW QUALITY:Zinc finger familyprotein (AHRD V3.3 *** B9HWF8_POPTR)	GO:0003676|GO:0046872
Solyc12g011100.2	-5.08E-01	3.12E-01	2.61E-01	2.51E-01	**-1.45E+00**	**6.72E-03**	5.77E-01	2.51E-01	WT NoN 1 dpi	CS	glycerol-3-phosphate acyltransferase 3 (AHRD V3.3 --*AT4G01950.2)	

Solyc05g005480.2	-5.09E-01	7.56E-02	-1.73E-01	2.16E-02	**-1.23E+00**	**1.33E-04**	-6.73E-01	2.16E-02	WT NoN 1 dpi	E	Quinone oxidoreductase-like protein(AHRD V3.3 *** W9RNB1_9ROSA)	GO:0008270|GO:0016491|GO :0016491
Solyc03g121280.3	-5.10E-01	1.42E-03	-2.72E-01	1.15E-02	**-1.07E+00**	**6.15E-08**	-3.88E-01	1.15E-02	WT NoN 1 dpi	P	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase familyprotein (AHRD V3.3 *** AT3G21310.3)	GO:0008375|GO:0016020|
Solyc09g008970.1	-5.11E-01	1.55E-01	1.16E-01	6.10E-01	**-1.38E+00**	**5.42E-04**	-1.80E-01	6.10E-01	WT NoN 1 dpi	OX	LOW QUALITY:AT3g10020/T22K18_16 (AHRD V3.3 *** Q9SR67_ARATH)	
Solyc01g080380.3	-5.19E-01	2.21E-01	2.12E-01	7.58E-02	**1.51E+00**	**1.16E-03**	7.67E-01	7.58E-02	WT NoN 1 dpi	N	S-adenosylmethionine decarboxylase proenzyme (AHRDV3.3 *** A0A068TRL8_COFCA)	GO:0004014|GO:0004014|GO :0006597|GO:0008295
Solyc11g072470.2	-5.19E-01	3.79E-01	-3.96E-01	4.76E-01	**-1.70E+00**	**6.98E-03**	4.20E-01	4.76E-01	WT NoN 1 dpi	G	LOB domain-containing protein,putative (AHRD V3.3 *** B9SK21_RICCO)	
Solyc02g079430.3	-5.31E-01	1.17E-01	-1.65E-01	7.54E-01	**-1.14E+00**	**1.84E-03**	-1.04E-01	7.54E-01	WT NoN 1 dpi	DNA	Zinc finger, B-box (AHRD V3.3 *-* A0A103Y479_CYNCS)	GO:0005622|GO:0008270|
Solyc04g074120.3	-5.37E-01	1.32E-01	-2.06E-01	4.59E-01	**1.04E+00**	**5.76E-03**	2.60E-01	4.59E-01	WT NoN 1 dpi	DNA	Synaptonemal complex protein 1(AHRD V3.3 *** A0A151TZS6_CAJCA)	
Solyc08g067000.3	-5.41E-01	1.70E-01	-2.14E-01	1.31E-01	**-1.08E+00**	**9.06E-03**	-5.97E-01	1.31E-01	WT NoN 1 dpi	RNA	Serine/arginine repetitive matrix protein 2 isoform 1 (AHRD V3.3 --* A0A061DPI3_THECC)	
Solyc01g059900.3	-5.43E-01	3.51E-01	-9.92E-01	4.20E-02	**-2.21E+00**	**6.74E-04**	-1.22E+00	4.20E-02	WT NoN 1 dpi	CS	Dirigent protein (AHRD V3.3 *** K4AW97_SOLLC)	
Solyc02g067190.3	-5.46E-01	1.67E-01	-1.28E-01	8.92E-01	**-1.10E+00**	**8.25E-03**	-5.27E-02	8.92E-01	WT NoN 1 dpi	CS	CASP-like protein (AHRD V3.3 *** K4B751_SOLLC)	
Solyc02g080510.1	-5.46E-01	7.60E-05	-5.91E-01	4.85E-05	**-1.49E+00**	**1.06E-12**	-5.66E-01	4.85E-05	WT NoN 1 dpi	G	Senescence regulator (AHRD V3.3 *** A0A103XFA1_CYNCS)	
Solyc06g066490.1	-5.47E-01	3.14E-01	-1.29E+00	7.35E-01	**-1.92E+00**	**1.28E-03**	-1.82E-01	7.35E-01	WT NoN 1 dpi	D	Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *-* G7II06_MEDTR)	
Solyc04g057940.3	-5.48E-01	1.29E-02	9.66E-02	1.74E-04	**-1.20E+00**	**3.89E-06**	-8.99E-01	1.74E-04	WT NoN 1 dpi	G	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 ***A0A061EZ85_THECC)	GO:0004842|GO:0016567|GO :0005488
Solyc09g059473.1	-5.48E-01	9.26E-03	1.38E-01	1.19E-03	**-1.37E+00**	**1.84E-07**	-7.10E-01	1.19E-03	WT NoN 1 dpi	D	S-norcoclaurine synthase 1 (AHRDV3.3 *** A0A061FEF4_THECC)	GO:0006952|GO:0009607|
Solyc08g080050.3	-5.51E-01	1.69E-01	-2.57E-01	2.24E-01	**-1.34E+00**	**1.95E-03**	-4.84E-01	2.24E-01	WT NoN 1 dpi	NA	PGRL1A transmembrane protein(AHRD V3.3 *** A0A0F7GZP2_9ROSI)	
Solyc12g044420.1	-5.59E-01	6.11E-02	-3.06E-01	1.51E-01	**-1.42E+00**	**3.78E-05**	-4.23E-01	1.51E-01	WT NoN 1 dpi	D	LOW QUALITY:Avr9/Cf-9 rapidlyelicited protein (AHRD V3.3 *** G7LFZ0_MEDTR)	
Solyc05g007880.3	-5.63E-01	1.49E-02	-1.51E-01	5.39E-03	**-1.78E+00**	**1.11E-08**	-6.56E-01	5.39E-03	WT NoN 1 dpi	DNA	Dof zinc finger protein (AHRD V3.3 *** W9S8B0_9ROSA)	GO:0003677|GO:0006355|
Solyc05g007940.3	-5.64E-01	4.46E-02	-6.64E-01	3.82E-01	**-1.07E+00**	**4.52E-04**	-2.38E-01	3.82E-01	WT NoN 1 dpi	RNA	LERNALX L.esculentum ribonuclease lx	GO:0003723|GO:0033897|
Solyc09g007710.3	-5.66E-01	3.37E-01	-1.98E-01	1.91E-01	**1.78E+00**	**4.95E-03**	7.76E-01	1.91E-01	WT NoN 1 dpi	D	Disease resistance protein (TIR- NBS-LRR class) family (AHRD V3.3 *** AT5G36930.2)	GO:0005515|GO:0005515|GO :0007165
Solyc10g018300.2	-5.67E-01	2.34E-01	-2.48E-02	3.44E-01	**-1.42E+00**	**5.28E-03**	-4.48E-01	3.44E-01	WT NoN 1 dpi	E	Transketolase (AHRD V3.3 *** AT3G60750.1)	GO:0003824|GO:0008152|GO :0004802

Solyc04g076130.3	-5.89E-01	4.79E-02	-1.69E-01	6.35E-01	**-1.28E+00**	**1.24E-04**	-1.36E-01	6.35E-01	WT NoN 1 dpi	STR	Serine carboxypeptidase, putative (AHRD V3.3 *-* B9R6Y4_RICCO)	GO:0004185|GO:0006508|
Solyc03g120120.3	-5.89E-01	1.43E-04	-7.74E-01	1.13E-03	**-1.23E+00**	**1.10E-09**	-4.84E-01	1.13E-03	WT NoN 1 dpi	TR	Regulator of Vps4 activity in theMVB pathway protein, putative (AHRD V3.3 *** A0A061GBK3_THECC)	GO:0015031|
Solyc04g080650.3	-5.90E-01	5.97E-02	-2.50E-01	6.52E-03	**-1.15E+00**	**7.43E-04**	-8.86E-01	6.52E-03	WT NoN 1 dpi	2M	LOW QUALITY:Cytochrome P450,putative (AHRD V3.3 *** B9R7Y0_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|
Solyc07g065165.1	-5.99E-01	1.24E-01	2.24E-01	7.59E-02	**-1.37E+00**	**1.19E-03**	-6.97E-01	7.59E-02	WT NoN 1 dpi	D	Pirin-like protein (AHRD V3.3 *** A0A0B2SAS7_GLYSO)	
Solyc07g039310.1	-6.06E-01	2.09E-04	-5.72E-01	2.59E-05	**-1.05E+00**	**6.57E-08**	-7.18E-01	2.59E-05	WT NoN 1 dpi	G	Polyamine oxidase 5 (AHRD V3.3 *** A0A1C8M5K2_MALDO)	GO:0016491|GO:0055114|
Solyc03g034010.3	-6.09E-01	8.15E-02	-1.46E-01	4.68E-02	**-1.05E+00**	**4.39E-03**	-7.01E-01	4.68E-02	WT NoN 1 dpi	P	U-box domain-containing familyprotein (AHRD V3.3 *-* U5GHQ7_POPTR)	
Solyc09g065740.2	-6.12E-01	4.14E-01	4.74E-01	5.23E-02	**-3.73E+00**	**2.93E-05**	-1.50E+00	5.23E-02	WT NoN 1 dpi	N	Ammonium transporter (AHRD V3.3 *** K4CUK0_SOLLC)	GO:0008519|GO:0015696|GO:0016020|GO:0008519|GO:0016020|GO:0072488
Solyc07g061840.1	-6.14E-01	3.24E-01	2.80E-01	5.38E-01	**-2.78E+00**	**1.10E-04**	3.81E-01	5.38E-01	WT NoN 1 dpi	G	LOW QUALITY:Bifunctional inhibitor/lipid-transfer protein/seedstorage 2S albumin superfamily protein (AHRD V3.3 -** AT1G66850.1)	
Solyc09g061310.3	-6.15E-01	4.81E-04	-3.12E-01	1.26E-01	**-1.14E+00**	**8.40E-08**	-2.44E-01	1.26E-01	WT NoN 1 dpi	P	PPPDE putative thiol peptidasefamily protein (AHRD V3.3 *** AT3G07090.2)	
Solyc10g084060.2	-6.15E-01	4.06E-02	-3.11E-01	1.17E-01	**-1.03E+00**	**1.27E-03**	-4.63E-01	1.17E-01	WT NoN 1 dpi	STR	cysteine-rich TM module stress tolerance protein (AHRD V3.3 *** AT5G04080.1)	
Solyc03g112460.3	-6.35E-01	1.24E-01	-3.29E-01	5.41E-02	**-1.26E+00**	**4.11E-03**	-8.05E-01	5.41E-02	WT NoN 1 dpi	H	Tryptophan aminotransferase related 2, putative (AHRD V3.3 *** A0A061FUE1_THECC)	GO:0003824|GO:0016846
Solyc09g091880.3	-6.46E-01	5.62E-04	1.82E-01	1.68E-01	**-1.12E+00**	**3.38E-07**	-2.33E-01	1.68E-01	WT NoN 1 dpi	T	Myb family transcription factor APL(AHRD V3.3 *** A0A0B0NIP7_GOSAR)	GO:0003677|GO:0005515
Solyc06g060620.3	-6.48E-01	9.33E-02	-4.77E-01	2.17E-02	**-1.35E+00**	**1.25E-03**	-9.09E-01	2.17E-02	WT NoN 1 dpi	N	Nitrate transporter (AHRD V3.3 *** Q852P7_TOBAC)	GO:0005215|GO:0006810|GO:0016020|GO:0005215|GO:0006857|GO:0016020
Solyc10g078610.1	-6.54E-01	3.13E-03	-3.56E-02	7.64E-03	**-1.03E+00**	**2.30E-05**	-5.81E-01	7.64E-03	WT NoN 1 dpi	H	Ethylene-responsive transcriptionfactor (AHRD V3.3 *** W9RCL9_9ROSA)	GO:0003677|GO:0003700|GO:0006355
Solyc01g096380.1	-6.61E-01	1.32E-02	2.67E-01	4.12E-01	**-1.06E+00**	**2.42E-04**	-2.07E-01	4.12E-01	WT NoN 1 dpi	CS	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamilyprotein (AHRD V3.3 *** AT1G01180.1)	
Solyc09g082460.3	-6.67E-01	9.95E-02	-6.24E-01	6.52E-01	**-1.18E+00**	**5.45E-03**	-1.78E-01	6.52E-01	WT NoN 1 dpi	AM	Homocysteine S-methyltransferase(AHRD V3.3 *** M1P405_PRUPE)	

Solyc11g012850.2	-6.68E-01	4.41E-03	-1.43E-01	2.42E-02	**-1.14E+00**	**1.53E-05**	-5.13E-01	2.42E-02	WT NoN 1 dpi	P	Chlorophyllide a oxygenase (AHRDV3.3 *** W9SD87_9ROSA)	GO:0005506|GO:0016705|GO :0051537|GO:0055114|GO:00 10277|GO:0055114
Solyc04g005800.3	-6.68E-01	1.95E-02	-6.32E-03	3.94E-02	**-1.35E+00**	**3.05E-05**	-5.82E-01	3.94E-02	WT NoN 1 dpi	DNA	Homeobox leucine zipper familyprotein (AHRD V3.3 *** G7K9R5_MEDTR)	GO:0003677|GO:0003700|GO :0006355|GO:0043565
Solyc06g059710.3	-6.90E-01	4.86E-01	1.03E-01	5.79E-01	**-3.01E+00**	**4.86E-03**	-5.50E-01	5.79E-01	WT NoN 1 dpi	L	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A118HPD5_CYNCS)	GO:0006631|GO:0045300|GO :0055114|GO:0016491|GO:00 55114
Solyc10g081690.1	-6.93E-01	3.07E-03	5.64E-02	8.11E-02	**-1.04E+00**	**4.59E-05**	-3.85E-01	8.11E-02	WT NoN 1 dpi	NA	LOW QUALITY:Transmembraneprotein, putative (AHRD V3.3 *** A0A072UES2_MEDTR)	
Solyc06g064610.1	-6.95E-01	5.37E-04	-4.38E-01	9.76E-06	**-1.44E+00**	**1.26E-08**	-9.65E-01	9.76E-06	WT NoN 1 dpi	CS	LOW QUALITY:Glucan endo-1,3-beta-glucosidase (AHRD V3.3 -** A0A0B0PK92_GOSAR)	
Solyc12g044240.2	-7.00E-01	9.86E-03	-6.72E-02	3.47E-02	**-1.26E+00**	**3.40E-05**	-5.60E-01	3.47E-02	WT NoN 1 dpi	CS	Dynein light chain family protein (AHRD V3.3 *** B9GXB1_POPTR)	GO:0007017|GO:0030286|
Solyc07g061860.2	-7.01E-01	4.13E-01	2.32E-01	9.88E-01	**-2.57E+00**	**5.25E-03**	-1.23E-02	9.88E-01	WT NoN 1 dpi	CS	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamilyprotein (AHRD V3.3 --* AT1G08125.2)	
Solyc07g017570.2	-7.05E-01	2.31E-02	7.35E-02	6.20E-02	**-1.35E+00**	**9.33E-05**	-5.69E-01	6.20E-02	WT NoN 1 dpi	D	Defensin protein (AHRD V3.3 -** B1N682_SOLPI)	GO:0006952|
Solyc06g036260.3	-7.20E-01	1.00E-06	-5.07E-01	4.38E-02	**-1.18E+00**	**1.03E-10**	-2.40E-01	4.38E-02	WT NoN 1 dpi	2M	beta-carotene hydroxylase-1	GO:0005506|GO:0006633|GO :0016491|GO:0055114|
Solyc10g086580.2	-7.25E-01	1.52E-01	1.86E-01	6.74E-02	**-1.90E+00**	**6.71E-04**	-9.38E-01	6.74E-02	WT NoN 1 dpi	E	Ribulose bisphosphate carboxylase/oxygenase activase (AHRD V3.3 *** V9IMY5_NICAT)	GO:0005524|
Solyc02g084790.3	-7.28E-01	2.71E-02	2.53E-01	4.59E-01	**-1.18E+00**	**8.07E-04**	2.33E-01	4.59E-01	WT NoN 1 dpi	OX	Peroxidase (AHRD V3.3 *** K4BAZ4_SOLLC)	GO:0004601|GO:0006979|GO :0020037|GO:0055114|GO:00 04601|GO:0042744
Solyc06g064620.3	-7.35E-01	1.45E-03	9.88E-02	7.05E-01	**-1.00E+00**	**4.93E-05**	-7.87E-02	7.05E-01	WT NoN 1 dpi	CS	Cell wall invertase (AHRD V3.3 *** H6V7I5_MANES)	GO:0004553|GO:0005975|
Solyc09g007760.3	-7.39E-01	4.60E-04	-1.89E-02	2.79E-02	**-1.49E+00**	**1.64E-08**	-4.29E-01	2.79E-02	WT NoN 1 dpi	TR	plasma membrane intrinsic protein 2.10	GO:0005215|GO:0006810|GO :0016020|
Solyc10g075160.1	-7.45E-01	1.85E-02	3.26E-01	1.25E-01	**-2.25E+00**	**4.77E-08**	-4.69E-01	1.25E-01	WT NoN 1 dpi	E	Ferredoxin (AHRD V3.3 *** A0A0K0PY61_NICBE)	GO:0009055|GO:0022900|GO :0051537|GO:0009055|GO:00 51536
Solyc09g091600.3	-7.74E-01	7.80E-03	-8.02E-01	1.79E-01	**-1.34E+00**	**3.50E-05**	-3.71E-01	1.79E-01	WT NoN 1 dpi	H	Tetratricopeptide repeat-like superfamily protein (AHRD V3.3 *** A0A061EKH3_THECC)	GO:0005515|
Solyc05g052950.3	-7.78E-01	1.75E-03	-4.42E-01	2.66E-04	**-1.81E+00**	**1.43E-08**	-9.41E-01	2.66E-04	WT NoN 1 dpi	DNA	Regulator of chromosome condensation (RCC1) family protein(AHRD V3.3 *** AT3G55580.1)	
Solyc11g011340.2	-7.81E-01	2.43E-01	-9.06E-01	2.75E-01	**-1.98E+00**	**5.54E-03**	-7.28E-01	2.75E-01	WT NoN 1 dpi	OX	cultivar Rio Grande ELI3	GO:0008270|GO:0016491|GO :0055114|GO:0016491
Solyc12g094690.1	-7.85E-01	2.08E-04	-8.34E-02	2.14E-02	**-1.57E+00**	**4.49E-09**	-4.45E-01	2.14E-02	WT NoN 1 dpi	D	RING/U-box superfamily protein,putative (AHRD V3.3 *** A0A061FF49_THECC)	GO:0005515|GO:0008270|

Solyc02g032860.3	-7.94E-01	1.17E-04	-7.45E-01	1.41E-03	**-1.43E+00**	**1.38E-08**	-6.26E-01	1.41E-03	WT NoN 1 dpi	OX	5'-adenylylsulfate reductase (AHRDV3.3 *** A0A072V4H5_MEDTR)	GO:0003824|GO:0008152|GO :0016671|GO:0019419|GO:00 55114
Solyc03g097570.3	-8.08E-01	1.71E-01	-1.43E+00	1.76E-02	**-2.35E+00**	**3.74E-04**	-1.46E+00	1.76E-02	WT NoN 1 dpi	TR	Bidirectional sugar transporterSWEET (AHRD V3.3 *** K4BJH4_SOLLC)	GO:0016021|
Solyc09g063010.3	-8.08E-01	1.12E-02	-2.05E-01	2.58E-01	**-1.18E+00**	**4.72E-04**	-3.42E-01	2.58E-01	WT NoN 1 dpi	T	bHLH transcription factor 058	
Solyc02g067230.3	-8.45E-01	7.64E-06	-4.22E-01	8.34E-05	**-1.34E+00**	**2.98E-09**	-7.07E-01	8.34E-05	WT NoN 1 dpi	DNA	Dof zinc finger protein3	GO:0003677|GO:0006355|
Solyc10g079680.2	-8.49E-01	1.74E-01	-1.57E+00	1.96E-02	**-3.49E+00**	**5.01E-06**	-1.51E+00	1.96E-02	WT NoN 1 dpi	T	bHLH transcription factor 068	GO:0003677|GO:0046983
Solyc01g099450.3	-8.51E-01	3.19E-02	1.02E-02	8.42E-02	**-1.13E+00**	**5.65E-03**	-6.74E-01	8.42E-02	WT NoN 1 dpi	DNA	ATP-dependent DNA helicase Q-like SIM (AHRD V3.3 *-* W9S050_9ROSA)	
Solyc07g045000.3	-8.51E-01	9.55E-03	-2.00E-01	8.13E-01	**-1.21E+00**	**5.05E-04**	-7.28E-02	8.13E-01	WT NoN 1 dpi	E	Homeodomain-like superfamilyprotein (AHRD V3.3 *-* AT2G02060.2)	GO:0003677|
Solyc08g062970.1	-8.54E-01	4.87E-03	-6.35E-01	2.09E-01	**-1.39E+00**	**3.35E-05**	-3.58E-01	2.09E-01	WT NoN 1 dpi	OX	Glutaredoxin (AHRD V3.3 *** A0A118JSL8_CYNCS)	GO:0009055|GO:0015035|GO :0045454|
Solyc03g097510.1	-8.62E-01	4.45E-02	-1.29E-01	6.19E-02	**-1.43E+00**	**1.69E-03**	-7.96E-01	6.19E-02	WT NoN 1 dpi	H	Small auxin up-regulated RNA38	GO:0009733|
Solyc01g080230.3	-8.81E-01	1.01E-03	-3.05E-01	3.33E-04	**-2.01E+00**	**6.69E-09**	-9.84E-01	3.33E-04	WT NoN 1 dpi	CS	Endo-1,3-1,4-beta-d-glucanase, putative (AHRD V3.3 *** B9RSS4_RICCO)	GO:0016787|
Solyc08g081195.1	-8.83E-01	4.41E-06	-3.17E-01	7.76E-02	**-1.30E+00**	**5.84E-09**	-2.80E-01	7.76E-02	WT NoN 1 dpi	TR	heavy metal * atpase (AHRD V3.3 -- 3AT4G30120.2)	
Solyc05g008880.1	-8.89E-01	5.55E-02	8.07E-03	3.43E-02	**1.27E+00**	**8.07E-03**	9.90E-01	3.43E-02	WT NoN 1 dpi	AM	LOW QUALITY:proline transporter 2(AHRD V3.3 --* AT3G55740.3)	
Solyc07g045185.1	-9.00E-01	3.24E-06	-3.77E-01	3.52E-04	**-1.04E+00**	**3.12E-07**	-6.26E-01	3.52E-04	WT NoN 1 dpi	G	CONSTANS-like zinc finger protein(AHRD V3.3 *-* A0A023GS52_SOYBN)	GO:0005515|
Solyc06g069300.1	-9.08E-01	1.06E-02	-1.96E-01	3.32E-01	**-1.11E+00**	**2.44E-03**	-3.26E-01	3.32E-01	WT NoN 1 dpi	E	MIZU-KUSSEI-like protein (Proteinof unknown function, DUF617) (AHRD V3.3 *** AT5G23100.1)	
Solyc04g074180.4	-9.20E-01	4.78E-06	-3.74E-01	9.30E-03	**-1.02E+00**	**9.63E-07**	-4.49E-01	9.30E-03	WT NoN 1 dpi	G	cryptochrome 1	
Solyc03g098320.3	-9.24E-01	3.69E-05	-5.45E-01	7.07E-04	**-1.78E+00**	**5.47E-10**	-7.14E-01	7.07E-04	WT NoN 1 dpi	T	Myb transcription factor (AHRD V3.3 *** A0A072UBN0_MEDTR)	GO:0003677|
Solyc09g007765.1	-9.24E-01	3.10E-02	-2.32E-03	3.10E-01	**-1.20E+00**	**6.52E-03**	-4.20E-01	3.10E-01	WT NoN 1 dpi	TR	Aquaporin-like protein (AHRD V3.3 * * A0A103XNC2_CYNCS)	GO:0005215|GO:0006810|GO :0016020|
Solyc06g060340.3	-9.43E-01	2.43E-01	1.30E-02	1.94E-02	**-2.96E+00**	**9.23E-04**	-1.97E+00	1.94E-02	WT NoN 1 dpi	E	photosystem II subunit S	
Solyc04g007530.3	-9.57E-01	1.78E-02	-4.50E-01	3.64E-01	**-1.10E+00**	**7.23E-03**	-3.49E-01	3.64E-01	WT NoN 1 dpi	STR	Protein DETOXIFICATION (AHRDV3.3 *** K4BNR0_SOLLC)	GO:0006855|GO:0015238|GO :0015297|GO:0016020|GO:00 55085|
Solyc06g011350.3	-9.57E-01	2.10E-07	-1.50E-01	2.08E-01	**-1.11E+00**	**1.43E-08**	-1.77E-01	2.08E-01	WT NoN 1 dpi	TR	plasma membrane intrinsic protein2.4	GO:0005215|GO:0006810|GO :0016020|
Solyc03g111730.3	-9.59E-01	1.34E-02	5.30E-02	1.68E-01	**-1.05E+00**	**7.56E-03**	-5.13E-01	1.68E-01	WT NoN 1 dpi	D	KDEL-tailed cysteine endopeptidase	GO:0006508|GO:0008234|GO :0008234
Solyc07g052250.3	-9.66E-01	1.56E-01	-9.37E-01	7.25E-02	**-2.21E+00**	**2.54E-03**	-1.24E+00	7.25E-02	WT NoN 1 dpi	NA	Unknown protein (AHRD V3.3)	
Solyc01g007100.3	-9.88E-01	8.65E-07	-5.58E-01	3.52E-05	**-1.08E+00**	**1.97E-07**	-7.68E-01	3.52E-05	WT NoN 1 dpi	PMI	Digalactosyldiacylglycerol synthase1 (AHRD V3.3 *** W8SVK3_TOBAC)	
Solyc01g111630.3	-1.04E+00	2.52E-02	-2.16E-01	2.41E-01	**-1.52E+00**	**1.74E-03**	-5.22E-01	2.41E-01	WT NoN 1 dpi	AM	D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *-*AT4G34200.1)	GO:0008152|GO:0016616|GO :0051287|GO:0055114|GO:00 51287|GO:0055114

Solyc07g061820.1	-1.05E+00	4.64E-02	-4.27E-01	1.41E-01	**-2.86E+00**	**5.54E-06**	-7.63E-01	1.41E-01	WT NoN 1 dpi	DNA	LOW QUALITY:Replication factor-A protein 1-like protein (AHRD V3.3 --*AT4G19130.2)	
Solyc02g084430.3	-1.05E+00	2.10E-02	-2.91E-01	8.84E-02	**-1.67E+00**	**6.32E-04**	-7.60E-01	8.84E-02	WT NoN 1 dpi	DNA	B-box type zinc finger family protein(AHRD V3.3 *-* A0A061E6F9_THECC)	
Solyc02g078400.3	-1.08E+00	2.64E-02	-7.29E-01	1.29E-01	**-1.59E+00**	**1.87E-03**	-7.20E-01	1.29E-01	WT NoN 1 dpi	N	allantoinase (AHRD V3.3 *** AT4G04955.1)	GO:0000256|GO:0004038|GO :0008270|GO:0050897|GO:00 16787
Solyc04g078710.2	-1.09E+00	1.24E-01	8.77E-01	7.53E-02	**-2.24E+00**	**3.01E-03**	-1.27E+00	7.53E-02	WT NoN 1 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** A0A151U5K8_CAJCA)	GO:0004252|GO:0006508|
Solyc06g050900.3	-1.09E+00	3.53E-02	-7.51E-01	1.57E-01	**-1.50E+00**	**5.13E-03**	-7.16E-01	1.57E-01	WT NoN 1 dpi	TR	Major facilitator superfamily protein(AHRD V3.3 *** AT2G40460.1)	GO:0005215|GO:0006810|GO :0016020|
Solyc02g092760.3	-1.13E+00	1.06E-02	-8.30E-01	1.98E-01	**-1.38E+00**	**2.46E-03**	-5.43E-01	1.98E-01	WT NoN 1 dpi	G	Sigma factor sigb regulation proteinrsbq, putative (AHRD V3.3 *** B9SG47_RICCO)	GO:0010223|GO:1901601|
Solyc02g084420.3	-1.14E+00	1.34E-02	-6.37E-01	1.30E-01	**-1.95E+00**	**1.17E-04**	-6.72E-01	1.30E-01	WT NoN 1 dpi	DNA	B-box zinc finger family protein(AHRD V3.3 *** AT2G21320.1)	GO:0005622|GO:0008270|
Solyc01g108745.1	-1.16E+00	1.13E-02	-3.15E-01	2.62E-01	**-1.26E+00**	**6.47E-03**	-4.86E-01	2.62E-01	WT NoN 1 dpi	2M	Polyneuridine-aldehyde esterase-like protein (AHRD V3.3 *** A0A075F1V8_TOBAC)	
Solyc11g072110.2	-1.17E+00	7.07E-02	-3.07E-01	3.06E-01	**-1.78E+00**	**8.21E-03**	-6.50E-01	3.06E-01	WT NoN 1 dpi	H	2-oxoglutarate (2OG) and Fe(II)- dependent oxygenase superfamilyprotein (AHRD V3.3 *** AT1G55290.1)	GO:0016491|GO:0055114|
Solyc06g005090.3	-1.20E+00	4.68E-02	-4.01E-01	9.19E-01	**-2.31E+00**	**4.58E-04**	-5.88E-02	9.19E-01	WT NoN 1 dpi	G	LOB domain-containing protein,putative (AHRD V3.3 *** B9SK21_RICCO)	
Solyc08g008630.3	-1.21E+00	2.54E-02	-2.72E-01	9.57E-02	**-1.79E+00**	**1.70E-03**	-8.84E-01	9.57E-02	WT NoN 1 dpi	2M	beta-carotene isomerase D27 (AHRD V3.3 *** AT1G64680.2)	
Solyc12g008380.1	-1.23E+00	1.63E-02	-7.52E-01	3.53E-01	**-2.07E+00**	**1.95E-04**	-4.51E-01	3.53E-01	WT NoN 1 dpi	D	LOW QUALITY:Avr9/Cf-9 rapidlyelicited protein (AHRD V3.3 *** I3SWH2_MEDTR)	
Solyc09g015870.3	-1.25E+00	6.27E-02	-8.40E-01	8.23E-01	**-1.82E+00**	**8.92E-03**	-1.45E-01	8.23E-01	WT NoN 1 dpi	E	Cytochrome c oxidase subunit 2 (AHRD V3.3 *-* J7MFY4_MALDO)	GO:0004129|GO:0005507|GO :0016020|GO:0016021|GO:00 22900
Solyc02g093580.3	-1.26E+00	2.61E-02	-6.61E-01	4.54E-01	**-1.57E+00**	**6.97E-03**	4.06E-01	4.54E-01	WT NoN 1 dpi	G	Tomato 9612 mRNA	
Solyc11g068620.2	-1.28E+00	2.04E-02	-1.09E+00	3.51E-01	**-2.17E+00**	**2.94E-04**	-4.93E-01	3.51E-01	WT NoN 1 dpi	DNA	NAC-domain protein	GO:0003677|GO:0006355|
Solyc07g061830.1	-1.34E+00	3.30E-02	-4.44E-01	1.33E-01	**-3.66E+00**	**1.72E-06**	-9.23E-01	1.33E-01	WT NoN 1 dpi	S	LOW QUALITY:Sec14p-like phosphatidylinositol transfer familyprotein (AHRD V3.3 --* AT1G19650.3)	
Solyc03g091020.1	-1.38E+00	3.03E-02	-6.89E-01	7.46E-01	**-1.90E+00**	**4.05E-03**	-1.97E-01	7.46E-01	WT NoN 1 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12520.1)	
Solyc06g035710.1	-1.38E+00	1.61E-03	1.06E+00	1.14E-02	**3.10E+00**	**2.41E-08**	1.07E+00	1.14E-02	WT NoN 1 dpi	STR	Protein DETOXIFICATION (AHRDV3.3 *** K4C4U3_SOLLC)	GO:0006855|GO:0015238|GO :0015297|GO:0016020|GO:00 55085|
Solyc07g005685.1	-1.73E+00	7.42E-02	-6.44E-01	3.68E-01	**-3.26E+00**	**1.65E-03**	-8.50E-01	3.68E-01	WT NoN 1 dpi	STR	Carboxypeptidase (AHRD V3.3 *-* M1ARY0_SOLTU)	GO:0004185|GO:0006508|

Solyc07g056100.1	-1.91E+00	2.10E-02	5.74E-01	2.02E-01	**-2.35E+00**	**5.51E-03**	-1.02E+00	2.02E-01	WT NoN 1 dpi	NA	LOW QUALITY:ArgH (DUF639) (AHRD V3.3 --* AT2G21720.2)	
Solyc09g061700.3	-1.98E+00	1.33E-02	-1.70E+00	1.07E-01	**-2.27E+00**	**5.20E-03**	-1.24E+00	1.07E-01	WT NoN 1 dpi	H	Tetratricopeptide repeat (TPR)-likesuperfamily protein (AHRD V3.3 *** AT5G48850.1)	GO:0005515|
Solyc03g025710.3	-2.20E+00	1.20E-02	-6.91E-01	4.70E-02	**-3.31E+00**	**4.04E-04**	-1.70E+00	4.70E-02	WT NoN 1 dpi	H	Acyl-CoA N-acyltransferases-likeprotein (AHRD V3.3 *** Q9C7G6_ARATH)	GO:0008080|
Solyc02g085950.3	-2.28E+00	6.87E-02	-2.66E-01	6.03E-01	**-3.60E+00**	**5.97E-03**	-6.32E-01	6.03E-01	WT NoN 1 dpi	E	cell wall protein X77373	

Table S 7. List of differentially expressed genes (DEGs) identified in tomato roots 14 days post inoculation (dpi) with Gluconacetobacter diazotrophicus WT strain. *Fold change values of DEGs identified in tomato roots with G. diazotrophicus WT strain as compared to uninoculated plants (Control) in modified Hoagland in the absence (WT NoN) or presence of 2 mM KNO_3 (WT N) in hydroponic systems at 14 dpi. Tomato gene identifier (ITAG3.2 release), Log2-transformed fold change values and P values calculated for each pairwise comparison between bacterium-inoculated and uninoculated samples are reported. Clustering results of the DEGs, classified as genes significantly modulated (in bold, P ≤ 0.01 and Log2(fold change) ≥ 1 or ≤ -1) by WT in either N or NoN condition. Protein description and abbreviation codes of functional classes were assigned on the basis of the protein description and function. Gene ontology (GO) terms were based on the ITAG3.2 release (https://solgenomics.net/organism/Solanum_lycopersicum/genome).*

Gene ID	WT N	P.Value	*nifD* - N	P. Value	WT NoN	P. Value	*nifD*- NoN	P.Value	Cluster	Functional Class	Gene Description	GO
Solyc04g071400.3	**3.68E+00**	**2.63E-03**	2.75E+00	1.97E-02	8.45E-01	4.52E-01	1.15E-01	9.18E-01	WT N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4BTD2_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc09g092110.3	**3.51E+00**	**8.37E-03**	-3.55E-02	9.77E-01	7.92E-02	9.49E-01	2.06E+00	1.06E-01	WT N 14 dpi	G	Light-regulated (AHRD V3.3 *** A0A0B0P5I2_GOSAR)	
Solyc06g009190.3	**3.29E+00**	**9.27E-03**	2.51E+00	4.15E-02	-2.20E+00	7.14E-02	-1.70E+00	1.57E-01	WT N 14 dpi	CS	Pectinesterase (AHRD V3.3 ***K4C3U9_SOLLC)	GO:0004857|GO:0005618|GO:0030599|GO:0042545|GO:0005618|GO:0030599|GO:0042545
Solyc07g043400.1	**3.28E+00**	**7.55E-05**	1.91E+00	1.10E-02	1.71E+00	2.11E-02	-2.73E-01	6.99E-01	WT N 14 dpi	T	LOW QUALITY:C2H2 and C2HC zinc fingers superfamily protein (AHRD V3.3 --*AT5G26749.2)	
Solyc01g014700.2	**3.25E+00**	**1.08E-03**	2.01E+00	3.17E-02	7.21E-01	4.22E-01	1.12E+00	2.15E-01	WT N 14 dpi	K	LOW QUALITY:Serine/threonine-protein kinase (AHRD V3.3 *-* K4ASL8_SOLLC)	
Solyc04g049400.3	**3.24E+00**	**3.29E-03**	2.60E+00	1.50E-02	1.55E+00	1.34E-01	1.26E+00	2.20E-01	WT N 14 dpi	K	Kinase family protein (AHRD V3.3 ***D7MB86_ARALL)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g098300.1	**2.99E+00**	**4.51E-03**	2.40E+00	1.93E-02	8.04E-01	4.10E-01	-6.10E-01	5.31E-01	WT N 14 dpi	N	Ornithine decarboxylase 2 (AHRD V3.3 ***A0A060IIA7_ATRBE)	GO:0003824|GO:0006596|GO:0006596
Solyc05g009860.2	**2.87E+00**	**1.35E-03**	1.86E+00	2.82E-02	5.98E-01	4.60E-01	9.90E-02	9.02E-01	WT N 14 dpi	2M	Leucoanthocyanidin reductase (AHRD V3.3 *-* J7M947_9ERIC)	
Solyc06g072320.3	**2.84E+00**	**7.97E-03**	1.47E+00	1.48E-01	1.36E+00	1.81E-01	1.87E+00	7.01E-02	WT N 14 dpi	L	Serine palmitoyltransferase (AHRD V3.3 *** B3Y000_NICBE)	GO:0003824|GO:0008152|GO:0016740|GO:0008152|GO:0016740
Solyc02g079700.1	**2.72E+00**	**9.03E-03**	2.22E+00	2.94E-02	7.44E-01	4.47E-01	6.91E-02	9.43E-01	WT N 14 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *-* M1B352_SOLTU)	
Solyc12g042830.2	**2.34E+00**	**2.53E-03**	7.80E-01	2.75E-01	3.24E-01	6.48E-01	-3.72E-01	6.00E-01	WT N 14 dpi	STR	Small heat-shock protein, putative (AHRDV3.3 *** B9RV59_RICCO)	
Solyc12g096310.2	**2.27E+00**	**1.86E-05**	1.20E+00	1.04E-02	8.26E-01	6.82E-02	-8.55E-01	5.96E-02	WT N 14 dpi	NA	plant/protein (Protein of unknown function, DUF599) (AHRD V3.3 *** AT5G10580.4)	
Solyc04g054430.2	**2.21E+00**	**1.41E-05**	9.73E-01	2.68E-02	2.43E-01	5.63E-01	1.03E+00	1.94E-02	WT N 14 dpi	NA	Retrovirus-related Pol polyprotein fromtransposon 17.6 (AHRD V3.3 --* A0A151SX10_CAJCA)	
Solyc02g079980.3	**2.19E+00**	**7.45E-03**	1.75E+00	2.81E-02	-1.72E+00	3.08E-02	-2.19E+00	7.44E-03	WT N 14 dpi	P	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT1G61740.1)	GO:0016021
Solyc11g010290.2	**2.18E+00**	**5.30E-03**	1.77E+00	2.05E-02	-3.02E-01	6.77E-01	5.22E-01	4.73E-01	WT N 14 dpi	N	2-oxoglutarate/malate translocator,chloroplastic (AHRD V3.3 *** A0A1D1ZLG4_9ARAE)	GO:0005215|GO:0006814|GO:0016020|GO:0055085

Solyc10g049470.1	**2.15E+00**	**4.20E-03**	1.29E+00	7.12E-02	1.34E+00	6.21E-02	7.54E-01	2.81E-01	WT N 14 dpi	TR	Ycf1 (AHRD V3.3 *-* A0A0U1ZJ99_SOLCI)	GO:0016021
Solyc00g022100.1	**2.12E+00**	**7.81E-03**	1.25E+00	9.95E-02	1.10E+00	1.44E-01	1.94E+00	1.39E-02	WT N 14 dpi	R	Ribosomal protein L10 (AHRD V3.3 ***E0D3E6_SOLLC)	
Solyc09g015240.1	**2.11E+00**	**3.08E-03**	1.55E+00	2.38E-02	-4.26E-01	5.16E-01	7.43E-01	2.61E-01	WT N 14 dpi	K	Protein kinase family protein (AHRD V3.3 *** B5RHV5_MUSBA)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g078207.1	**2.09E+00**	**9.54E-03**	1.50E+00	5.57E-02	5.06E-01	5.05E-01	-2.05E+00	1.08E-02	WT N 14 dpi	P	RING-H2 finger protein ATL22 (AHRDV3.3 *** A0A0B2SEF9_GLYSO)	
Solyc06g068180.3	**2.09E+00**	**1.28E-03**	1.78E-02	9.76E-01	-3.10E-01	5.96E-01	9.44E-02	8.71E-01	WT N 14 dpi	P	Ubiquitin system component Cue protein (AHRD V3.3 *-* AT5G32440.2)	
Solyc06g033870.1	**2.08E+00**	**6.44E-03**	1.51E+00	4.02E-02	-3.47E-02	9.61E-01	4.11E-01	5.62E-01	WT N 14 dpi	T	LOW QUALITY:R2R3MYB transcriptionfactor 105	GO:0003677
Solyc09g010120.2	**2.07E+00**	**3.75E-05**	8.97E-01	4.04E-02	9.75E-01	2.70E-02	7.84E-01	7.05E-02	WT N 14 dpi	CS	Alpha-amylase (AHRD V3.3 *** A0A1D1XX21_9ARAE)	
Solyc11g006570.2	**2.03E+00**	**7.92E-07**	7.52E-01	2.41E-02	9.99E-02	7.53E-01	1.97E-01	5.36E-01	WT N 14 dpi	S	Myo-inositol oxygenase (AHRD V3.3 ***C6K2L2_SOLLC)	GO:0005506|GO:0005737|GO:0019310|GO:0050113|GO:0055114
Solyc09g090790.3	**1.99E+00**	**6.44E-03**	1.75E+00	1.49E-02	-7.26E-01	2.88E-01	-1.66E+00	2.03E-02	WT N 14 dpi	G	R2R3MYB transcription factor 79	GO:0003677
Solyc12g005360.2	**1.97E+00**	**4.57E-03**	1.53E+00	2.35E-02	4.40E-01	4.94E-01	-8.13E-01	2.11E-01	WT N 14 dpi	K	MAP kinase kinase kinase 83	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g069810.2	**1.96E+00**	**1.06E-04**	9.88E-01	2.97E-02	-1.24E+00	7.95E-03	1.15E+00	1.29E-02	WT N 14 dpi	T	Bromo-adjacent-like (BAH) domain protein(AHRD V3.3 *-* A0A072VCT6_MEDTR)	GO:0003682
Solyc10g005880.3	**1.96E+00**	**2.61E-08**	7.98E-01	3.56E-03	3.14E-01	2.18E-01	8.76E-01	1.63E-03	WT N 14 dpi	K	Uridine kinase (AHRD V3.3 *** A0A022QIW2_ERYGU)	GO:0005524|GO:0008152|GO:0016301|GO:0009116|GO:0009116
Solyc08g066370.2	**1.94E+00**	**1.83E-03**	7.32E-01	2.02E-01	-1.31E+00	2.72E-02	-3.38E+00	2.34E-06	WT N 14 dpi	K	Serine/threonine protein phosphatase 7long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)	
Solyc02g082740.1	**1.94E+00**	**2.00E-03**	1.46E+00	1.55E-02	1.10E+00	6.24E-02	-4.28E-01	4.55E-01	WT N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4BAE4_SOLLC)	
Solyc12g098900.2	**1.94E+00**	**6.50E-04**	8.63E-02	8.64E-01	-1.06E+00	4.33E-02	8.14E-01	1.16E-01	WT N 14 dpi	STR	Late embryogenesis abundant protein (AHRD V3.3 *** J7F2C7_CAMSI)	
Solyc04g014875.1	**1.94E+00**	**1.06E-03**	1.24E+00	2.60E-02	4.61E-02	9.31E-01	5.95E-01	2.67E-01	WT N 14 dpi	2M	Chalcone--flavonone isomerase (AHRD V3.3 --* CFI_ORYSJ)	
Solyc02g077040.4	**1.93E+00**	**7.66E-03**	6.60E-01	3.31E-01	1.40E-01	8.35E-01	-1.31E+00	5.95E-02	WT N 14 dpi	D	phytophthora-inhibited protease 1	
Solyc06g060680.2	**1.91E+00**	**8.13E-03**	1.32E+00	5.76E-02	7.52E-01	2.69E-01	5.83E-02	9.31E-01	WT N 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9GPM5_POPTR)	GO:0004672|GO:0005524|GO:0006468
Solyc04g077170.3	**1.91E+00**	**3.86E-03**	8.74E-01	1.57E-01	-3.35E-01	5.82E-01	1.06E+00	9.01E-02	WT N 14 dpi	G	EPIDERMAL PATTERNING FACTOR-like protein (AHRD V3.3 *** AT4G37810.1),Pfam:PF17181	
Solyc06g066490.1	**1.90E+00**	**1.46E-03**	1.25E+00	2.70E-02	-5.46E-01	3.14E-01	-2.72E+00	2.56E-05	WT N 14 dpi	D	Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *-* G7II06_MEDTR)	
Solyc07g049530.3	**1.89E+00**	**2.56E-04**	1.22E+00	1.11E-02	9.82E-01	3.71E-02	9.66E-01	4.00E-02	WT N 14 dpi	H	1-aminocyclopropane-1-carboxylate oxidase 1	GO:0016491|GO:0055114
Solyc02g082410.3	**1.82E+00**	**3.07E-03**	1.49E+00	1.30E-02	3.73E-01	5.09E-01	1.41E-01	8.03E-01	WT N 14 dpi	TR	Tonoplast monosaccharide transporter 3	GO:0005215|GO:0016021|GO:0055085|GO:0016020|GO:0022891|GO:0055085|GO:0016020|GO:0022891|GO:0055085
Solyc07g054140.3	**1.80E+00**	**4.12E-05**	8.89E-01	2.19E-02	1.07E-02	9.77E-01	4.94E-01	1.87E-01	WT N 14 dpi	D	Syntaxin, putative (AHRD V3.3 *** B9SLK9_RICCO)	GO:0005484|GO:0006886|GO:0016020|GO:0005515|GO:0005515
Solyc07g005150.2	**1.80E+00**	**2.02E-03**	7.47E-01	1.65E-01	3.76E-01	4.79E-01	2.83E-01	5.93E-01	WT N 14 dpi	PMI	Leucine-rich repeat receptor-like proteinkinase family protein (AHRD V3.3 *** AT4G08850.1)	GO:0005515
Solyc08g067960.3	**1.77E+00**	**1.33E-09**	5.72E-01	6.48E-03	2.09E-01	2.89E-01	9.87E-01	2.55E-05	WT N 14 dpi	DNA	RING finger and CHY zinc finger protein (AHRD V3.3 *** G7JNA1_MEDTR)	GO:0005515|GO:0008270|GO:0008270|GO:0008270
Solyc09g009560.2	**1.77E+00**	**2.37E-05**	9.61E-01	9.61E-03	-3.00E-01	3.90E-01	-8.67E-01	1.81E-02	WT N 14 dpi	G	Terminal flower 1 (AHRD V3.3 *** A0A172JD62_FRAAN)	GO:0003712|GO:0009910

Solyc04g082730.2	**1.75E+00**	**5.24E-04**	1.11E+00	1.86E-02	-1.98E-01	6.58E-01	-1.07E+00	2.29E-02	WT N 14 dpi	STR	HSP20-like chaperones superfamily protein (AHRD V3.3 --* AT1G54850.1)	
Solyc02g065220.3	**1.68E+00**	**7.62E-04**	1.01E+00	2.96E-02	-3.08E+00	2.13E-07	-1.85E+00	2.75E-04	WT N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***A0A103Y530_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc11g068680.2	**1.67E+00**	**4.48E-03**	1.26E+00	2.67E-02	8.56E-01	1.23E-01	-7.74E-01	1.62E-01	WT N 14 dpi	E	ATP synthase protein I (AHRD V3.3 *** A0A1D1ZEB6_9ARAE)	
Solyc08g079960.1	**1.66E+00**	**2.96E-05**	8.44E-01	1.64E-02	-9.27E-01	9.15E-03	4.75E-01	1.61E-01	WT N 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *-* Q9LWA3_SOLLC)	GO:0004252|GO:0006508
Solyc00g014830.3	**1.66E+00**	**3.68E-04**	6.12E-01	1.43E-01	5.87E-01	1.59E-01	9.99E-01	2.08E-02	WT N 14 dpi	E	NADH dehydrogenase subunit 7 (AHRD V3.3 *** A0A0C5B9X5_9SOLA)	GO:0016651|GO:0048038|GO:0051287|GO:0055114
Solyc10g007103.1	**1.64E+00**	**4.23E-03**	2.78E-01	6.01E-01	-3.26E-01	5.39E-01	6.94E-01	1.97E-01	WT N 14 dpi	DNA	Homeobox-leucine zipper protein family (AHRD V3.3 *-* AT1G69780.1)	GO:0003677|GO:0006355|GO:0043565|GO:0006355|GO:0043565
Solyc02g068445.1	**1.64E+00**	**8.98E-03**	9.42E-01	1.17E-01	5.80E-01	3.28E-01	-2.34E-01	6.90E-01	WT N 14 dpi	P	F-box family protein (AHRD V3.3 --* AT3G19890.1)	
Solyc04g018120.1	**1.62E+00**	**8.74E-03**	4.66E-01	4.22E-01	-1.05E-01	8.55E-01	1.81E-01	7.54E-01	WT N 14 dpi	S	LOW QUALITY:Pattern formation proteinEMB30 (AHRD V3.3 --* A0A0B2S8Q4_GLYSO)	
Solyc02g089860.1	**1.60E+00**	**1.12E-03**	7.94E-01	8.08E-02	9.96E-01	3.12E-02	-1.84E-03	9.97E-01	WT N 14 dpi	NA	GNS1/SUR4 membrane protein (AHRD V3.3 *** A0A124SFB5_CYNCS)	GO:0016021
Solyc08g080270.3	**1.59E+00**	**3.52E-03**	9.47E-01	6.72E-02	-3.19E-01	5.25E-01	-7.59E-01	1.38E-01	WT N 14 dpi	TR	UDP-galactose transporter (AHRD V3.3 *** M4QC22_PRUPE)	GO:0055085
Solyc01g066520.3	**1.57E+00**	**9.64E-09**	4.04E-01	4.29E-02	5.80E-02	7.62E-01	7.63E-01	4.50E-04	WT N 14 dpi	C	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (AHRD V3.3 *** K4AWQ5_SOLLC)	GO:0008152|GO:0016746
Solyc01g006020.3	**1.57E+00**	**1.39E-13**	9.43E-01	7.07E-09	1.05E-01	3.56E-01	9.91E-01	2.66E-09	WT N 14 dpi	2M	6,7-dimethyl-8-ribityllumazine synthase (AHRD V3.3 *** AT3G32930.2)	
Solyc04g049677.1	**1.55E+00**	**9.98E-07**	8.62E-01	1.57E-03	2.18E-01	3.80E-01	2.73E-01	2.74E-01	WT N 14 dpi	T	Pseudo-response regulator (AHRD V3.3 *-* X5I0R0_IPONI)	
Solyc06g076850.3	**1.55E+00**	**5.07E-09**	7.62E-01	2.58E-04	4.44E-01	2.05E-02	-1.39E-01	4.46E-01	WT N 14 dpi	H	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT2G29670.2)	GO:0005515
Solyc06g076250.3	**1.54E+00**	**4.74E-11**	2.26E-01	1.26E-01	7.65E-02	5.97E-01	5.02E-01	1.64E-03	WT N 14 dpi	E	PGR5-like protein 1B, chloroplastic (AHRD V3.3 *** A0A0B0MIW0_GOSAR)	
Solyc12g011320.2	**1.51E+00**	**3.49E-08**	5.29E-01	1.20E-02	2.37E-01	2.37E-01	8.87E-01	1.17E-04	WT N 14 dpi	STR	Glutathione S-transferase (AHRD V3.3 *** D3Y4H6_BRUGY)	GO:0005515
Solyc07g055040.1	**1.51E+00**	**1.06E-03**	7.71E-01	7.20E-02	4.36E-01	2.98E-01	-1.44E-01	7.29E-01	WT N 14 dpi	RNA	LOW QUALITY:Agenet-like domain-containing protein (AHRD V3.3 ***A0A103YGJ9_CYNCS)	
Solyc01g059950.1	**1.51E+00**	**7.64E-03**	5.97E-01	2.64E-01	-4.39E-02	9.34E-01	9.74E-02	8.54E-01	WT N 14 dpi	H	LOW QUALITY:GAI-like protein 1	
Solyc01g109660.2	**1.50E+00**	**7.55E-10**	5.43E-01	2.06E-03	3.85E-02	8.10E-01	7.54E-01	6.56E-05	WT N 14 dpi	D	meloidogyne-induced giant cell protein DB275	GO:0000166|GO:0003676|GO:0003676
Solyc07g061820.1	**1.50E+00**	**6.12E-03**	1.39E+00	1.03E-02	-2.82E+00	6.72E-06	-4.46E-01	3.83E-01	WT N 14 dpi	DNA	LOW QUALITY:Replication factor-A protein1-like protein (AHRD V3.3 --* AT4G19130.2)	
Solyc09g060070.2	**1.50E+00**	**5.94E-03**	4.82E-01	3.42E-01	6.49E-01	2.04E-01	4.35E-01	3.91E-01	WT N 14 dpi	NA	RAP release 2, galactose-binding-likedomain protein, putative (DUF1997) (AHRD V3.3 --* AT5G04440.2)	
Solyc09g055940.3	**1.49E+00**	**4.48E-07**	9.06E-01	4.10E-04	6.99E-01	4.31E-03	7.18E-01	3.49E-03	WT N 14 dpi	NA	Sodium Bile acid symporter family (AHRD V3.3 *** AT3G25410.1)	GO:0016020
Solyc10g049870.1	**1.49E+00**	**4.42E-05**	8.47E-01	9.83E-03	-5.06E-01	1.08E-01	-9.65E-02	7.53E-01	WT N 14 dpi	DNA	Zinc finger protein, putative (AHRD V3.3 *** B9SNA3_RICCO)	GO:0046872
Solyc05g013480.3	**1.48E+00**	**2.49E-10**	8.06E-01	1.13E-05	6.11E-02	6.84E-01	5.94E-01	4.81E-04	WT N 14 dpi	H	Tetratricopeptide repeat-like superfamilyprotein (AHRD V3.3 *** A0A061E7M0_THECC)	GO:0005515

Solyc04g014900.3	**1.48E+00**	**7.23E-05**	7.86E-01	1.87E-02	3.85E-01	2.30E-01	-7.89E-01	1.84E-02	WT N 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* M1A662_SOLTU)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc09g059240.3	**1.45E+00**	**6.28E-03**	5.08E-01	3.07E-01	1.03E+00	4.56E-02	1.21E+00	1.99E-02	WT N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9SYM4_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc08g075020.3	**1.45E+00**	**2.66E-04**	-3.35E-01	3.36E-01	-4.63E-01	1.88E-01	7.01E-01	5.08E-02	WT N 14 dpi	CS	Pectinacetylesterase family protein (AHRD V3.3 *** AT4G19420.2)	GO:0016787
Solyc07g065240.2	**1.44E+00**	**4.09E-04**	9.96E-01	9.63E-03	5.03E-01	1.70E-01	8.94E-01	1.87E-02	WT N 14 dpi	PMI	Leucine-rich repeat protein kinase familyprotein, putative (AHRD V3.3 *** A0A061FCG5_THECC)	GO:0004672|GO:0005524|GO:0006468|GO:0005515|GO:0005515
Solyc01g104620.3	**1.44E+00**	**3.61E-06**	6.12E-01	1.91E-02	2.79E-01	2.65E-01	8.38E-01	2.08E-03	WT N 14 dpi	RNA	Class II aaRS and biotin synthetasessuperfamily protein (AHRD V3.3 --* AT3G62120.3)	
Solyc04g076690.3	**1.43E+00**	**8.72E-04**	7.32E-01	6.44E-02	-1.13E+00	6.24E-03	-1.39E+00	1.13E-03	WT N 14 dpi	NA	Protein with RNI-like/FBD-like domain (AHRD V3.3 --* AT3G26930.1)	
Solyc06g064500.2	**1.43E+00**	**5.73E-07**	1.97E-01	3.70E-01	3.07E-01	1.67E-01	5.70E-01	1.40E-02	WT N 14 dpi	P	O-methyltransferase (AHRD V3.3 *** F6M2M1_VITPS)	GO:0008168|GO:0008171|GO:0008171
Solyc00g026160.3	**1.43E+00**	**9.11E-03**	3.26E-01	5.25E-01	-8.36E-01	1.10E-01	4.03E-01	4.32E-01	WT N 14 dpi	TR	Ferric reductase oxidase (AHRD V3.3 ***V9HYU8_MANES)	GO:0016020|GO:0016491|GO:0055114|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc03g116670.3	**1.42E+00**	**1.42E-09**	5.25E-01	2.31E-03	2.67E-01	9.82E-02	8.63E-01	8.11E-06	WT N 14 dpi	H	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G80130.1)	GO:0005515
Solyc02g082420.3	**1.41E+00**	**2.81E-11**	5.92E-01	8.45E-05	1.37E-01	2.92E-01	8.87E-01	2.17E-07	WT N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT1G20823.1)	GO:0005515|GO:0008270
Solyc06g075790.3	**1.41E+00**	**7.26E-15**	8.35E-01	6.88E-10	1.82E-01	4.82E-02	4.01E-01	1.11E-04	WT N 14 dpi	DNA	DNA-binding protein (AHRD V3.3 *** AT5G59830.3)	
Solyc11g069290.2	**1.39E+00**	**1.97E-08**	9.62E-01	8.88E-06	6.66E-01	7.55E-04	6.87E-01	5.51E-04	WT N 14 dpi	2M	Pyridoxal biosynthesis protein PDX2 (AHRD V3.3 *** A0A151SGI6_CAJCA)	GO:0004359|GO:0042819|GO:0042823
Solyc07g066010.3	**1.39E+00**	**7.25E-12**	8.32E-01	1.71E-07	-1.92E-01	1.14E-01	-1.92E-01	1.14E-01	WT N 14 dpi	AM	Amino acid transporter, putative (AHRD V3.3 *** B9T659_RICCO)	
Solyc02g083190.1	**1.39E+00**	**7.30E-07**	9.64E-01	1.22E-04	4.90E-01	2.98E-02	1.74E-01	4.22E-01	WT N 14 dpi	P	LOW QUALITY:F-box family protein(AHRD V3.3 *** B9MX84_POPTR)	GO:0005515
Solyc08g006770.3	**1.39E+00**	**2.73E-11**	9.53E-01	4.63E-08	1.02E-01	4.22E-01	9.42E-02	4.58E-01	WT N 14 dpi	E	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061E128_THECC)	GO:0016491|GO:0055114
Solyc10g079590.1	**1.38E+00**	**4.38E-03**	1.21E+00	1.14E-02	7.41E-01	1.07E-01	7.04E-01	1.24E-01	WT N 14 dpi	RNA	LOW QUALITY:histidine-tRNA ligase(AHRD V3.3 *** AT3G10250.5)	
Solyc11g008020.2	**1.37E+00**	**2.23E-06**	6.02E-01	1.34E-02	-2.01E-01	3.85E-01	-3.73E-01	1.12E-01	WT N 14 dpi	S	GTP-binding family protein (AHRD V3.3 *** A9P9Z6_POPTR)	GO:0005525|GO:0005525|GO:0007264|GO:0005525|GO:0007264
Solyc04g077120.3	**1.36E+00**	**1.76E-08**	3.69E-01	3.91E-02	-6.27E-01	1.04E-03	6.83E-01	4.43E-04	WT N 14 dpi	S	Inositol-tetrakisphosphate 1-kinase (AHRDV3.3 *** K4BUE9_SOLLC)	GO:0000287|GO:0005524|GO:0005622|GO:0032957|GO:0047325|GO:0052725|GO:0052726
Solyc03g115500.3	**1.36E+00**	**2.39E-08**	7.54E-01	1.69E-04	2.20E-01	2.12E-01	6.83E-01	5.03E-04	WT N 14 dpi	CS	Heparanase 1-like protein (AHRD V3.3 *** T2D261_TOBAC)	GO:0016020|GO:0016798
Solyc10g049210.2	**1.36E+00**	**6.34E-10**	7.29E-01	2.51E-05	6.27E-01	1.63E-04	1.70E-01	2.42E-01	WT N 14 dpi	STR	Serine carboxypeptidase, putative (AHRDV3.3 *** B9S819_RICCO)	GO:0004185|GO:0006508
Solyc01g094120.3	**1.35E+00**	**1.21E-08**	7.80E-01	6.90E-05	-1.46E+00	2.67E-09	-2.24E-01	1.86E-01	WT N 14 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** A0A061DTZ5_THECC)	GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc08g062370.3	**1.35E+00**	**5.59E-04**	6.62E-01	6.44E-02	6.15E-02	8.59E-01	-3.13E-01	3.69E-01	WT N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependentoxygenase superfamily protein (AHRD V3.3 *** AT1G78550.1)	GO:0016491|GO:0055114
Solyc01g010700.3	**1.35E+00**	**1.04E-04**	4.74E-01	1.20E-01	5.53E-01	7.18E-02	8.94E-01	5.45E-03	WT N 14 dpi	C	SNF1-related kinase regulatory subunitgamma 1 (AHRD V3.3 *** G7KB20_MEDTR)	GO:0003824

Solyc02g071820.3	**1.35E+00**	**1.27E-05**	9.59E-01	7.27E-04	-3.03E-02	9.05E-01	8.60E-01	2.00E-03	WT N 14 dpi	S	Receptor-like protein kinase (AHRD V3.3 *** B9I1R1_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g061970.3	**1.34E+00**	**2.00E-10**	7.47E-01	7.11E-06	5.53E-01	3.23E-04	-1.03E-01	4.46E-01	WT N 14 dpi	N	putative spermine synthase	GO:0003824
Solyc08g079280.3	**1.34E+00**	**4.75E-06**	5.49E-01	2.61E-02	2.43E-01	3.06E-01	9.87E-02	6.75E-01	WT N 14 dpi	CYTP450	Cytochrome P450 family protein (AHRDV3.3 *** U5GNW2_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc03g082540.3	**1.33E+00**	**1.14E-09**	8.24E-01	5.14E-06	5.99E-03	9.67E-01	-7.15E-03	9.61E-01	WT N 14 dpi	TR	Triose phosphate/phosphate translocator,chloroplastic (AHRD V3.3 --* A0A1D1YFA4_9ARAE)	
Solyc02g092290.3	**1.33E+00**	**6.43E-08**	9.43E-01	1.53E-05	-2.64E-02	8.83E-01	1.33E-01	4.61E-01	WT N 14 dpi	P	F-box family protein (AHRD V3.3 ***B9GFH4_POPTR)	GO:0005515
Solyc09g055765.1	**1.33E+00**	**7.43E-03**	1.14E+00	1.92E-02	-2.34E-01	6.13E-01	2.79E-01	5.47E-01	WT N 14 dpi	T	Transcription factor, putative (AHRD V3.3 *** B9TBR8_RICCO)	GO:0046983
Solyc08g075280.3	**1.31E+00**	**2.33E-07**	9.11E-01	5.17E-05	1.47E-01	4.42E-01	1.76E-02	9.26E-01	WT N 14 dpi	R	Structural constituent of ribosome protein(AHRD V3.3 *** A0A072UL21_MEDTR)	
Solyc08g083010.3	**1.30E+00**	**6.84E-03**	6.08E-01	1.82E-01	6.02E-01	1.86E-01	6.26E-01	1.70E-01	WT N 14 dpi	NA	Homer (AHRD V3.3 *** A0A0B0PVA4_GOSAR)	
Solyc03g114970.3	**1.30E+00**	**3.58E-12**	7.78E-01	1.11E-07	2.98E-01	9.87E-03	3.27E-01	5.24E-03	WT N 14 dpi	CS	SPIRAL1-like1 (AHRD V3.3 ***AT1G26355.1)	
Solyc06g074620.3	**1.30E+00**	**5.85E-05**	9.23E-01	2.23E-03	7.17E-01	1.39E-02	7.56E-01	1.00E-02	WT N 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-bindingsuperfamily protein (AHRD V3.3 --* AT4G29930.2)	
Solyc01g098570.2	**1.30E+00**	**1.19E-03**	6.62E-01	7.59E-02	-6.09E-01	1.01E-01	-7.52E-01	4.55E-02	WT N 14 dpi	G	LOW QUALITY:FANTASTIC four-like protein (DUF3049) (AHRD V3.3 *-*AT1G54740.1)	
Solyc10g005020.3	**1.30E+00**	**3.52E-08**	8.74E-01	1.94E-05	3.93E-01	2.70E-02	3.77E-03	9.82E-01	WT N 14 dpi	NA	DUF4228 domain protein (AHRD V3.3 *** G7LHF9_MEDTR)	
Solyc04g025880.3	**1.29E+00**	**1.44E-12**	1.00E+00	3.64E-10	9.16E-02	3.77E-01	3.66E-01	1.38E-03	WT N 14 dpi	TR	Potassium transporter (AHRD V3.3 *** M0ZY66_SOLTU)	GO:0015079|GO:0016020|GO:0071805
Solyc08g074280.3	**1.29E+00**	**1.95E-10**	9.34E-01	9.87E-08	3.28E-01	1.64E-02	1.87E-01	1.56E-01	WT N 14 dpi	TR	ABC1 family protein (AHRD V3.3 *** AT5G24810.1)	
Solyc06g069710.3	**1.28E+00**	**4.05E-06**	9.59E-01	1.83E-04	-8.51E-01	6.64E-04	1.04E-02	9.63E-01	WT N 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061FWI7_THECC)	GO:0003677|GO:0006355
Solyc03g025600.3	**1.28E+00**	**4.94E-09**	5.33E-01	1.40E-03	-5.42E-01	1.20E-03	5.34E-01	1.38E-03	WT N 14 dpi	CS	Pectinacetylesterase family protein (AHRD V3.3 *** AT5G23870.3)	GO:0016787
Solyc00g025290.1	**1.27E+00**	**7.65E-03**	1.21E+00	1.06E-02	6.54E-01	1.49E-01	8.27E-01	7.14E-02	WT N 14 dpi	C	Alpha-1,4 glucan phosphorylase L-2isozyme (AHRD V3.3 *-* W9S278_9ROSA)	
Solyc06g062430.3	**1.27E+00**	**1.85E-05**	8.40E-01	1.89E-03	4.40E-01	8.15E-02	6.25E-01	1.61E-02	WT N 14 dpi	S	Myo-inositol oxygenase (AHRD V3.3 *** K7VPE5_SOLTU)	GO:0005506|GO:0005737|GO:0019310|GO:0050113|GO:0055114
Solyc01g091870.3	**1.27E+00**	**6.68E-04**	2.10E-01	5.28E-01	-2.74E-01	4.12E-01	3.02E-01	3.66E-01	WT N 14 dpi	STR	SPX domain-containing family protein (AHRD V3.3 *** B9GW54_POPTR)	GO:0016021|GO:0055085
Solyc12g099200.2	**1.27E+00**	**2.62E-06**	8.91E-01	2.74E-04	5.07E-01	2.42E-02	9.40E-01	1.50E-04	WT N 14 dpi	C	Invertase inhibitor (AHRD V3.3 *** I1VR17_SOLTU)	GO:0004857|GO:0004857|GO:0043086|GO:0004857|GO:0043086
Solyc12g014140.2	**1.27E+00**	**7.85E-04**	6.34E-01	6.85E-02	-9.30E-01	9.83E-03	-1.50E+00	1.33E-04	WT N 14 dpi	T	SITCP3	
Solyc03g031600.3	**1.27E+00**	**1.63E-12**	8.09E-01	1.71E-08	6.19E-02	5.44E-01	5.16E-01	2.47E-05	WT N 14 dpi	OX	Peroxisomal membrane protein PMP22 (AHRD V3.3 *** A0A0B0NRG7_GOSAR)	GO:0016021
Solyc06g054313.1	**1.27E+00**	**5.96E-05**	7.15E-01	1.19E-02	4.89E-01	7.55E-02	1.22E-01	6.47E-01	WT N 14 dpi	G	WUSCHEL related homeobox 2 (AHRD V3.3 --* AT5G59340.1)	
Solyc12g009010.2	**1.26E+00**	**8.12E-03**	7.52E-01	9.91E-02	-2.89E-01	5.17E-01	-9.48E-01	4.04E-02	WT N 14 dpi	K	Kinase family protein (AHRD V3.3 ***B9HDX0_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g112320.3	**1.26E+00**	**5.00E-07**	8.98E-01	6.78E-05	-1.01E-01	5.97E-01	5.11E-01	1.20E-02	WT N 14 dpi	TR	Ferric reduction oxidase 8 (AHRD V3.3 ***W9RI94_9ROSA)	GO:0016020|GO:0016491|GO:0055114|GO:0016491|GO:0055114|GO:0016491|GO:0055114

Solyc02g084240.3	**1.25E+00**	**1.20E-04**	-3.79E-02	8.92E-01	-4.87E-01	9.10E-02	8.05E-01	7.45E-03	WT N 14 dpi	DNA	H1 histone-like protein	GO:0000786|GO:0003677|GO:0005634|GO:0006334|GO:0000786|GO:0003677|GO:0006334|GO:0000786|GO:0003677|GO:0006334
Solyc03g007710.3	**1.25E+00**	**4.40E-03**	8.43E-01	4.51E-02	1.24E-01	7.58E-01	-8.12E-02	8.41E-01	WT N 14 dpi	S	Membrane-associated kinase regulator, putative (AHRD V3.3 *** G7IDX6_MEDTR)	
Solyc08g068230.3	**1.24E+00**	**6.13E-04**	6.58E-01	4.95E-02	1.24E-01	7.00E-01	6.47E-01	5.30E-02	WT N 14 dpi	RNA	Pentatricopeptide repeat-containing protein GO:0005515(AHRD V3.3 *** A0A0B2SBT0_GLYSO)	
Solyc09g090350.3	**1.24E+00**	**1.20E-04**	9.36E-01	2.09E-03	2.94E-01	2.93E-01	8.17E-02	7.68E-01	WT N 14 dpi	L	Long-chain-alcohol oxidase (AHRD V3.3 *** K4CW61_SOLLC)	GO:0016491|GO:0055114|GO:0016614|GO:0050660|GO:0055114|GO:0016614|GO:0050660|GO:0055114
Solyc06g069820.3	**1.24E+00**	**1.10E-08**	7.72E-01	2.34E-05	9.90E-01	5.61E-07	3.90E-01	1.51E-02	WT N 14 dpi	NA	DUF674 family protein (AHRD V3.3 *** A0A072TP22_MEDTR)	
Solyc06g009630.1	**1.23E+00**	**1.17E-07**	6.90E-01	4.18E-04	1.76E-01	3.12E-01	8.68E-01	2.71E-05	WT N 14 dpi	E	CP12 (AHRD V3.3 *** O24136_TOBAC)	
Solyc02g092770.3	**1.23E+00**	**9.06E-09**	9.32E-01	1.14E-06	-3.34E-01	3.21E-02	-5.05E-01	2.07E-03	WT N 14 dpi	G	Sigma factor sigb regulation protein rsbq, putative (AHRD V3.3 *** B9SG47_RICCO)	GO:0010223|GO:1901601
Solyc06g005220.2	**1.23E+00**	**2.56E-03**	2.81E-01	4.51E-01	-1.12E-01	7.62E-01	-8.70E-01	2.56E-02	WT N 14 dpi	RNA	LOW QUALITY:Pentatricopeptide repeatprotein (AHRD V3.3 *** A0A1B3IPW0_CAPAN)	GO:0005515
Solyc03g044050.2	**1.21E+00**	**3.35E-03**	3.35E-01	3.81E-01	2.19E-01	5.65E-01	2.15E-01	5.72E-01	WT N 14 dpi	TR	alpha-soluble NSF attachment protein 2 (AHRD V3.3 --* AT3G56190.2)	GO:0003735|GO:0005840|GO:0006412
Solyc01g106830.3	**1.21E+00**	**2.33E-03**	7.74E-01	4.04E-02	5.75E-01	1.21E-01	5.38E-01	1.46E-01	WT N 14 dpi	G	Phytosulfokines 3 (AHRD V3.3 *** W9QZQ5_9ROSA)	GO:0005576|GO:0008083|GO:0008283
Solyc02g088600.3	**1.21E+00**	**2.77E-10**	5.01E-01	3.61E-04	2.08E-01	1.01E-01	4.23E-01	1.86E-03	WT N 14 dpi	RNA	Pentatricopeptide repeat-containing-like protein (AHRD V3.3 *** A0A0B0P8M8_GOSAR)	GO:0005515
Solyc08g045850.3	**1.21E+00**	**1.04E-10**	8.74E-01	5.99E-08	-4.21E-02	7.20E-01	4.46E-01	7.24E-04	WT N 14 dpi	RNA	pentatricopeptide repeat-containing protein GO:0005515	
Solyc02g082767.1	**1.20E+00**	**2.52E-06**	7.70E-01	7.00E-04	7.00E-01	1.71E-03	-5.60E-03	9.78E-01	WT N 14 dpi	STR	ARM repeat superfamily protein (AHRD V3.3 --* AT3G60740.3)	
Solyc05g046300.3	**1.19E+00**	**2.09E-13**	6.33E-01	9.66E-08	-2.32E-01	1.26E-02	4.01E-01	8.79E-05	WT N 14 dpi	STR	Ethanolamine-phosphate cytidylyltransferase (AHRD V3.3 *** A0A0B2NXA1_GLYSO)	GO:0003824|GO:0009058
Solyc01g079360.3	**1.19E+00**	**8.06E-06**	1.91E-01	3.79E-01	4.31E-01	5.45E-02	3.78E-01	8.94E-02	WT N 14 dpi	T	WRKY transcription factor 37	GO:0003700|GO:0006355|GO:0043565
Solyc03g005030.3	**1.19E+00**	**2.42E-08**	5.26E-01	1.70E-03	4.43E-01	6.66E-03	6.33E-01	2.69E-04	WT N 14 dpi	NA	DSR6 (AHRD V3.3 *** A0A076V4W1_CAPAN)	
Solyc11g010590.2	**1.18E+00**	**2.79E-03**	6.09E-01	1.01E-01	-4.13E-01	2.60E-01	2.14E-01	5.55E-01	WT N 14 dpi	L	Very-long-chain (3R)-3-hydroxyacyl-CoAdehydratase (AHRD V3.3 *** A0A068TZ66_COFCA)	
Solyc07g063530.3	**1.18E+00**	**1.26E-08**	7.08E-01	4.58E-05	1.25E-01	3.96E-01	5.11E-01	1.57E-03	WT N 14 dpi	NA	U3 small nucleolar RNA-associated protein14 B isoform 3 (AHRD V3.3 *** A0A061FEA7_THECC)	
Solyc01g067680.3	**1.18E+00**	**2.43E-11**	9.00E-01	6.01E-09	2.27E-01	4.12E-02	7.51E-01	1.62E-07	WT N 14 dpi	P	Tubby-like F-box protein (AHRD V3.3 *** M1APZ0_SOLTU)	GO:0005515
Solyc12g089180.2	**1.18E+00**	**6.51E-10**	8.48E-01	2.97E-07	-2.60E-01	4.51E-02	8.87E-02	4.80E-01	WT N 14 dpi	TR	Sugar facilitator protein 6	GO:0005215|GO:0016021|GO:0055085|GO:0016020|GO:0022891|GO:0055085|GO:0016020|GO:0022891|GO:0055085
Solyc06g068690.3	**1.17E+00**	**2.76E-04**	2.72E-01	3.37E-01	-3.12E-01	2.73E-01	5.88E-01	4.47E-02	WT N 14 dpi	RNA	Glutamyl-tRNA(Gln) amidotransferasesubunit A (AHRD V3.3 *** A0A151S2E8_CAJCA)	GO:0004040
Solyc06g035480.3	**1.17E+00**	**1.25E-03**	6.25E-01	6.40E-02	-9.93E-01	4.91E-03	-7.57E-01	2.70E-02	WT N 14 dpi	K	Serine/threonine protein phosphatase 7long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)	
Solyc12g094550.2	**1.17E+00**	**1.21E-07**	7.23E-01	1.41E-04	3.26E-01	5.50E-02	5.07E-01	4.29E-03	WT N 14 dpi	NA	At1g76250 (AHRD V3.3 *** Q8GX25_ARATH)	

Solyc10g083400.1	**1.17E+00**	**8.40E-07**	3.34E-01	7.74E-02	-2.54E-01 1.74E-01	4.22E-01	2.80E-02	WT N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9T5M5_RICCO)	GO:0005506|GO:0016705|GO:0020037|G O:0055114
Solyc12g010745.1	**1.16E+00**	**5.80E-08**	-1.03E-02	9.47E-01	-1.46E-01 3.54E-01	4.56E-01	6.68E-03	WT N 14 dpi	PMI	LRR receptor-like kinase (AHRD V3.3 ***A7UE73_SOLTU)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g067840.3	**1.16E+00**	**1.76E-04**	3.16E-01	2.44E-01	3.05E-01 2.61E-01	2.77E-01	3.05E-01	WT N 14 dpi	E	Photosystem II reaction center PsbP familyprotein (AHRD V3.3 *** A0A0F7GYP2_9ROSI)	GO:0005509|GO:0009523|GO:0009654|G O:0015979|GO:0019898
Solyc08g076080.3	**1.16E+00**	**8.04E-03**	6.61E-01	1.13E-01	1.09E-01 7.89E-01	-6.05E-01	1.46E-01	WT N 14 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRDV3.3 *** K4CMX5_SOLLC)	GO:0004553|GO:0005975|GO:0005618|GO:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc01g096970.3	**1.15E+00**	**2.04E-03**	8.36E-01	1.95E-02	-1.51E-01 6.56E-01	-7.74E-01	2.94E-02	WT N 14 dpi	G	Vacuolar protein sorting-associated protein9A (AHRD V3.3 --* A0A199ULJ0_ANACO)	
Solyc06g050170.3	**1.15E+00**	**2.81E-08**	3.52E-01	2.38E-02	7.42E-01 2.91E-05	9.85E-01	4.16E-07	WT N 14 dpi	TR	Potassium transporter (AHRD V3.3 *** W8NQ93_OLEEU)	GO:0015079|GO:0016020|GO:0071805
Solyc04g007980.3	**1.15E+00**	**3.35E-11**	6.03E-01	4.59E-06	3.65E-01 1.74E-03	8.97E-01	4.95E-09	WT N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependentoxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)	GO:0016491|GO:0055114
Solyc03g097410.1	**1.15E+00**	**6.38E-10**	7.96E-01	5.31E-07	2.77E-01 2.98E-02	-1.93E-01	1.20E-01	WT N 14 dpi	S	Inositol-tetrakisphosphate 1-kinase (AHRDV3.3 *** K4BJF8_SOLLC)	GO:0000287|GO:0005524|GO:0005622|GO:0032957|GO:0047325|GO:0052725|GO:0052726
Solyc01g010230.2	**1.15E+00**	**1.41E-06**	8.93E-01	4.98E-05	2.10E-01 2.64E-01	-6.16E-02	7.40E-01	WT N 14 dpi	NA	LOW QUALITY:Acanthoscurrin-2 (AHRDV3.3 --* B6TLS9_MAIZE)	
Solyc04g015480.3	**1.14E+00**	**1.06E-08**	7.96E-01	5.04E-06	3.36E-01 2.26E-02	3.77E-01	1.15E-02	WT N 14 dpi	T	BTB/POZ domain-containing proteinTNFAIP1 isoform 2 (AHRD V3.3 *** A0A061DKW6_THECC)	
Solyc03g025850.3	**1.14E+00**	**1.41E-14**	9.92E-01	3.49E-13	-5.91E-01 1.69E-08	2.37E-01	3.44E-03	WT N 14 dpi	PMI	remorin 1	
Solyc03g019650.3	**1.14E+00**	**9.87E-07**	5.11E-01	8.10E-03	9.08E-02 6.14E-01	-3.32E-04	9.99E-01	WT N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT5G14120.1)	
Solyc12g015970.2	**1.13E+00**	**2.14E-07**	9.02E-01	7.82E-06	2.21E-01 1.83E-01	2.73E-01	1.04E-01	WT N 14 dpi	G	GPI-anchored protein LORELEI (AHRD V3.3 *-* A0A151SVS2_CAJCA)	
Solyc03g116460.3	**1.13E+00**	**2.64E-09**	6.84E-01	1.32E-05	-3.66E-01 8.08E-03	8.27E-01	7.44E-07	WT N 14 dpi	AM	Aspartate racemase (AHRD V3.3 *** A0A0B2QLV5_GLYSO)	GO:0006520|GO:0016855|GO:0006807|GO:0036361|GO:0006807|GO:0036361
Solyc05g012510.3	**1.13E+00**	**2.85E-04**	9.44E-01	1.70E-03	-3.41E-01 2.17E-01	-1.67E-01	5.41E-01	WT N 14 dpi	C	Alpha-1,4 glucan phosphorylase (AHRDV3.3 *** K4BXX3_SOLLC)	GO:0004645|GO:0005975|GO:0030170|GO:0005975|GO:0008184|GO:0005975|GO:0008184
Solyc05g054190.3	**1.13E+00**	**1.50E-07**	7.87E-01	3.64E-05	1.15E-01 4.72E-01	-9.66E-02	5.46E-01	WT N 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4C298_SOLLC)	
Solyc05g055430.3	**1.13E+00**	**1.18E-04**	8.34E-01	2.48E-03	-1.86E-01 4.60E-01	4.43E-01	8.65E-02	WT N 14 dpi	NA	RAP release 2%2C galactose-binding-likedomain protein%2C putative (DUF1997) (AHRD V3.3 *** AT5G04440.1)	
Solyc11g006060.1	**1.13E+00**	**7.72E-08**	6.97E-01	1.03E-04	4.63E-01 5.27E-03	6.32E-01	3.14E-04	WT N 14 dpi	E	Rubisco accumulation factor 1.1,chloroplastic (AHRD V3.3 *** RAF1_ARATH)	
Solyc01g010150.3	**1.12E+00**	**2.75E-09**	7.39E-01	4.08E-06	-2.96E-02 8.17E-01	-1.30E-01	3.16E-01	WT N 14 dpi	CS	ACT domain-containing protein (AHRD V3.3 *** A0A118JXJ7_CYNCS)	GO:0008152|GO:0016597
Solyc04g007990.1	**1.12E+00**	**4.42E-04**	1.85E-01	5.13E-01	8.49E-02 7.63E-01	3.38E-01	2.36E-01	WT N 14 dpi	E	LOW QUALITY:ATP synthase subunit beta, chloroplastic (AHRD V3.3 --*ATPB_CALFL)	
Solyc03g120560.3	**1.12E+00**	**1.54E-08**	5.63E-01	3.86E-04	6.57E-01 6.40E-05	1.90E-01	1.79E-01	WT N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)	GO:0005215|GO:0006810|GO:0016020|GO:0005215|GO:0006857|GO:0016020|GO:0005215|GO:0006857|GO:0016020
Solyc09g065870.3	**1.11E+00**	**2.41E-09**	9.83E-01	2.56E-08	1.90E-01 1.41E-01	3.61E-01	7.58E-03	WT N 14 dpi	RNA	E3 ubiquitin-protein ligase RGLG2-likeprotein (AHRD V3.3 *** A0A072V0P7_MEDTR)	

Solyc03g111730.3	**1.11E+00**	**4.89E-03**	8.12E-01	3.35E-02	1.00E+00	1.03E-02	7.65E-01	4.39E-02	WT N 14 dpi	D	KDEL-tailed cysteine endopeptidase	GO:0006508|GO:0008234|GO:0008234|GO:0008234
Solyc12g089000.2	**1.11E+00**	**4.41E-09**	5.89E-01	1.05E-04	4.21E-01	3.03E-03	4.59E-01	1.45E-03	WT N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT4G34370.1)	GO:0004842|GO:0016567|GO:0005515|GO:0008270|GO:0005515|GO:0008270
Solyc01g106175.1	**1.11E+00**	**4.35E-10**	3.96E-01	1.89E-03	1.78E-01	1.33E-01	7.74E-01	3.78E-07	WT N 14 dpi	T	myb domain protein 115 (AHRD V3.3 --* AT5G40360.1)	
Solyc04g077110.3	**1.11E+00**	**4.35E-04**	7.63E-01	1.03E-02	-9.69E-01	1.65E-03	7.36E-01	1.30E-02	WT N 14 dpi	E	Succinate dehydrogenase assembly factor 1, mitochondrial (AHRD V3.3 *-* A0A0B0PRI9_GOSAR)	
Solyc11g066740.2	**1.11E+00**	**1.89E-06**	7.57E-01	3.02E-04	2.11E-01	2.54E-01	-1.50E-01	4.17E-01	WT N 14 dpi	G	reticulata-like protein, putative (DUF3411) (AHRD V3.3 *** AT2G37860.4)	
Solyc09g008830.3	**1.11E+00**	**2.30E-05**	8.70E-01	4.22E-04	-4.21E-01	6.09E-02	-1.86E-01	3.96E-01	WT N 14 dpi	T	Transcription factor, putative (AHRD V3.3 *** B9RIA5_RICCO)	
Solyc03g117300.3	**1.11E+00**	**5.89E-10**	9.44E-01	1.34E-08	2.32E-01	5.57E-02	6.31E-01	1.07E-05	WT N 14 dpi	PMI	Nodulin-like / Major Facilitator Superfamilyprotein (AHRD V3.3 *** A0A0K9Q4D1_ZOSMR)	
Solyc01g066620.3	**1.11E+00**	**1.46E-04**	8.85E-01	1.47E-03	6.91E-01	1.01E-02	6.83E-01	1.09E-02	WT N 14 dpi	L	Fatty acid beta-oxidation multifunctionalprotein (AHRD V3.3 *** A0A077DAS1_9ERIC)	GO:0003824|GO:0008152|GO:0003857|GO:0006631|GO:0016491|GO:0055114|GO:0003857|GO:0006631|GO:0016491|GO:0055114
Solyc01g081293.1	**1.11E+00**	**2.72E-03**	-2.26E-01	5.04E-01	-1.46E+00	1.79E-04	-5.97E-01	8.56E-02	WT N 14 dpi	NA	Redox-regulatory protein FAM213A-likeprotein (AHRD V3.3 *** A0A0B2R8Q7_GLYSO)	GO:0055114
Solyc03g005070.1	**1.11E+00**	**1.05E-05**	6.17E-01	5.32E-03	3.27E-01	1.18E-01	9.20E-01	1.16E-04	WT N 14 dpi	STR	ubiquitin-specific protease 16 (AHRD V3.3 -* AT4G24560.1)	
Solyc06g048820.1	**1.10E+00**	**2.40E-08**	3.80E-01	1.14E-02	2.43E-01	9.26E-02	5.41E-01	6.46E-04	WT N 14 dpi	D	Wound-induced protein 1 (AHRD V3.3 *** WUN1_SOLTU)	
Solyc03g114310.3	**1.10E+00**	**8.91E-06**	7.73E-01	6.48E-04	-7.07E-01	1.53E-03	-1.07E+00	1.28E-05	WT N 14 dpi	K	MAP kinase kinase kinase 28	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g094130.2	**1.10E+00**	**6.75E-06**	5.47E-01	9.58E-03	-9.54E-01	4.78E-05	-4.18E-01	4.20E-02	WT N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9RDF6_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO: 0016705|GO:0055114
Solyc07g065980.3	**1.10E+00**	**1.13E-05**	9.35E-01	9.59E-05	1.58E-01	4.41E-01	6.03E-01	6.29E-03	WT N 14 dpi	C	alkaline alpha-galactosidase seed imbibition protein	GO:0003824
Solyc12g044240.2	**1.10E+00**	**1.81E-04**	9.24E-01	1.10E-03	-2.83E-01	2.70E-01	1.20E-01	6.36E-01	WT N 14 dpi	CS	Dynein light chain family protein (AHRD B9GXB1_POPTR)	GO:0007017|GO:0030286 V3.3 ***
Solyc03g096840.3	**1.10E+00**	**9.90E-07**	7.15E-01	3.10E-04	-5.65E-01	2.92E-03	2.12E-01	2.27E-01	WT N 14 dpi	OX	LOW QUALITY:Hydrogen peroxide-induced 1 (AHRD V3.3 *** B8Y3H9_TOBAC)	
Solyc03g114150.3	**1.09E+00**	**1.31E-11**	5.19E-01	1.09E-05	2.31E-01	2.29E-02	5.53E-01	4.28E-06	WT N 14 dpi	STR	aldehyde dehydrogenase family 2 member B7a	GO:0008152|GO:0016491|GO:0016620|GO:0055114|GO:0008152|GO:0016491|GO:0055114|GO:0008152|GO:0016491|GO:0055114
Solyc08g078140.3	**1.09E+00**	**1.66E-03**	8.83E-01	8.66E-03	6.85E-01	3.65E-02	1.63E-02	9.59E-01	WT N 14 dpi	P	Ubiquitin carboxyl-terminal hydrolase (AHRD V3.3 *** K4CNH3_SOLLC)	GO:0004843|GO:0005622|GO:0006511
Solyc01g006680.3	**1.09E+00**	**4.76E-07**	9.66E-02	5.59E-01	-2.79E-01	9.92E-02	4.35E-01	1.31E-02	WT N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependentoxygenase superfamily protein (AHRD V3.3 *** AT3G20810.5)	
Solyc01g007220.3	**1.09E+00**	**3.02E-07**	9.74E-01	1.83E-06	5.90E-01	9.81E-04	4.04E-01	1.73E-02	WT N 14 dpi	D	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family(AHRD V3.3 *** AT3G52470.1)	
Solyc03g118870.3	**1.08E+00**	**8.45E-03**	1.58E-01	6.81E-01	-1.71E+00	1.28E-04	-2.05E-01	5.94E-01	WT N 14 dpi	K	Octicosapeptide/Phox/Bem1p familyprotein, putative (AHRD V3.3 *** A0A061FV54_THECC)	GO:0005515
Solyc01g005930.3	**1.08E+00**	**8.65E-05**	3.41E-01	1.54E-01	3.77E-01	1.17E-01	7.23E-01	4.56E-03	WT N 14 dpi	L	Lipase/lipooxygenase, PLAT/LH2 (AHRD V3.3 *** A0A118JU91_CYNCS)	GO:0005515

Solyc02g092670.1	**1.08E+00**	**1.56E-06**	9.73E-01	7.68E-06	1.28E-01	4.70E-01	2.68E-01	1.37E-01	WT N 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 ***A9XG40_TOBAC)	GO:0004252|GO:0006508
Solyc11g071560.2	**1.08E+00**	**1.43E-03**	8.62E-01	8.42E-03	2.43E-01	4.28E-01	3.35E-01	2.77E-01	WT N 14 dpi	STR	Hsp20/alpha crystallin family protein (AHRD V3.3 *** Q94GC7_SOLDE)	
Solyc11g065340.2	**1.08E+00**	**5.59E-09**	7.71E-01	1.95E-06	-3.31E-01	1.45E-02	-2.76E-02	8.28E-01	WT N 14 dpi	C	Magnesium-chelatase subunit H (AHRDV3.3 *** A0A0B0N4Q7_GOSAR)	
Solyc12g007090.2	**1.08E+00**	**3.90E-10**	8.62E-01	2.96E-08	3.98E-01	1.31E-03	9.04E-01	1.22E-08	WT N 14 dpi	NA	Tyrosine-protein phosphatase non-receptor type 6 (AHRD V3.3 *** A0A1D1XLX7_9ARAE)	
Solyc08g005420.3	**1.08E+00**	**3.08E-03**	7.97E-01	2.31E-02	9.50E-01	7.87E-03	5.49E-01	1.08E-01	WT N 14 dpi	P	WD40 repeat-containing protein (AHRDV3.3 *** A0A103YEC3_CYNCS)	GO:0005515|GO:0010997|GO:0097027|GO:1904668|GO:0010997|GO:0097027|GO:1904668
Solyc02g086350.3	**1.08E+00**	**4.43E-03**	4.30E-01	2.24E-01	-1.15E+00	2.57E-03	2.47E-01	4.81E-01	WT N 14 dpi	H	Protein PLASTID MOVEMENT IMPAIRED2 (AHRD V3.3 *** W9S0V7_9ROSA)	
Solyc10g076250.2	**1.08E+00**	**1.06E-04**	6.38E-01	1.18E-02	2.79E-01	2.46E-01	6.15E-01	1.48E-02	WT N 14 dpi	N	Alanine-glyoxylate aminotransferase, putative (AHRD V3.3 *** B9SZ94_RICCO)	GO:0003824|GO:0008483|GO:0030170|GO:0008483|GO:0030170
Solyc07g066320.3	**1.07E+00**	**7.45E-09**	8.20E-01	8.58E-07	1.36E-01	2.94E-01	3.11E-01	2.20E-02	WT N 14 dpi	DNA	DNA repair protein recA (AHRD V3.3 ***U5GXJ6_POPTR)	GO:0003677|GO:0005524|GO:0006259|GO:0008094|GO:0003677|GO:0005524|GO:0006281|GO:0008094|GO:0003677|GO:0005524|GO:0006281|GO:0008094
Solyc08g065260.3	**1.07E+00**	**6.51E-06**	4.90E-01	1.59E-02	3.85E-01	5.30E-02	9.06E-01	6.32E-05	WT N 14 dpi	STR	ATP-dependent Clp protease proteolyticsubunit (AHRD V3.3 --* CLPP_GOSBA)	
Solyc02g063220.3	**1.07E+00**	**3.89E-07**	2.95E-01	7.37E-02	-3.97E-02	8.04E-01	4.79E-01	5.58E-03	WT N 14 dpi	C	Mannose-6-phosphate isomerase (AHRDV3.3 *** K4B6K7_SOLLC)	GO:0004476|GO:0004476|GO:0005975|GO:0008270|GO:0004476|GO:0005975|GO:0008270
Solyc01g081270.2	**1.07E+00**	**2.64E-10**	6.96E-01	7.36E-07	1.81E-01	1.04E-01	5.23E-01	4.73E-05	WT N 14 dpi	STR	Glutathione s-transferase, putative (AHRDV3.3 *** B9SPC9_RICCO)	GO:0005515
Solyc11g071620.3	**1.07E+00**	**1.64E-07**	7.98E-01	1.54E-05	-1.94E-01	2.08E-01	1.42E-01	3.52E-01	WT N 14 dpi	OX	aldehyde oxidase	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114
Solyc09g011380.3	**1.06E+00**	**9.28E-04**	4.75E-01	1.07E-01	-5.88E-01	4.88E-02	3.67E-01	2.09E-01	WT N 14 dpi	T	BEL1-like homeodomain protein (AHRD V3.3 *** G7L5K2_MEDTR)	GO:0003677|GO:0003677|GO:0006355|GO:0003677|GO:0006355
Solyc02g068160.1	**1.06E+00**	**9.61E-03**	5.55E-01	1.55E-01	-8.87E-01	2.74E-02	-9.97E-01	1.42E-02	WT N 14 dpi	NA	LOW QUALITY:transmembrane protein,putative (DUF 3339) (AHRD V3.3 *** AT5G63500.1)	
Solyc06g073190.3	**1.06E+00**	**5.86E-11**	5.33E-01	1.29E-05	5.68E-01	5.13E-06	6.49E-01	6.41E-07	WT N 14 dpi	C	fructokinase 2	GO:0004747|GO:0006014|GO:0016773|GO:0016773
Solyc09g008760.1	**1.06E+00**	**5.23E-05**	-1.29E-01	5.60E-01	-3.60E-01	1.11E-01	2.93E-01	1.92E-01	WT N 14 dpi	G	VQ motif-containing protein (AHRD V3.3 *-* AT4G37710.2)	
Solyc09g089580.3	**1.06E+00**	**1.01E-05**	7.88E-01	3.88E-04	-2.71E-01	1.72E-01	3.66E-01	6.91E-02	WT N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependentoxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)	GO:0016491|GO:0055114
Solyc07g064140.1	**1.06E+00**	**6.03E-03**	1.82E-01	6.11E-01	-3.26E-01	3.64E-01	1.26E-01	7.23E-01	WT N 14 dpi	N	Ammonium transporter 1 member 1 (AHRD V3.3 --* AMT11_ARATH)	
Solyc02g082770.3	**1.06E+00**	**1.38E-06**	6.72E-01	5.05E-04	5.08E-01	5.84E-03	4.98E-01	6.75E-03	WT N 14 dpi	L	Phosphoinositide phosphatase family protein (AHRD V3.3 *-* AT3G51460.1)	
Solyc06g083220.3	**1.05E+00**	**1.82E-06**	6.11E-01	1.47E-03	4.28E-01	1.92E-02	4.75E-01	1.03E-02	WT N 14 dpi	P	P-loop containing nucleoside triphosphatehydrolases superfamily protein, putative (AHRD V3.3 *** A0A061DLY3_THECC)	
Solyc05g007080.3	**1.05E+00**	**1.03E-07**	1.32E-02	9.27E-01	1.35E-02	9.26E-01	6.12E-01	2.32E-04	WT N 14 dpi	CS	Alpha-amylase (AHRD V3.3 ***K4BWN3_SOLLC)	GO:0003824|GO:0005975|GO:0003824|GO:0005975|GO:0043169|GO:0003824|GO:0005975|GO:0043169
Solyc01g108450.3	**1.04E+00**	**1.97E-03**	2.63E-01	3.93E-01	6.54E-01	4.06E-02	8.19E-01	1.20E-02	WT N 14 dpi	STR	Carboxypeptidase (AHRD V3.3 *** K4B360_SOLLC)	GO:0004185|GO:0006508

Solyc10g084080.2	**1.04E+00**	**1.66E-04**	4.56E-02	8.49E-01	3.65E-01	1.35E-01	9.90E-01	2.94E-04	WT N 14 dpi	RNA	Pentatricopeptide repeat superfamilyprotein, putative (AHRD V3.3 *** A0A061F037_THECC)	GO:0005515
Solyc03g098480.1	**1.04E+00**	**8.16E-05**	8.36E-01	8.91E-04	-7.47E-01	2.47E-03	-1.25E-01	5.80E-01	WT N 14 dpi	NA	LOW QUALITY:cotton fiber (DUF761) (AHRD V3.3 --* AT1G61260.1)	
Solyc07g005420.2	**1.04E+00**	**2.46E-10**	8.14E-01	2.96E-08	-7.18E-01	2.74E-07	-2.74E-01	1.41E-02	WT N 14 dpi	2M	Thiamin diphosphate-binding fold (THDP- binding) superfamily protein (AHRD V3.3 -- * AT1G21400.5)	
Solyc06g051360.3	**1.04E+00**	**2.22E-08**	5.89E-01	1.30E-04	2.49E-01	6.90E-02	6.53E-01	3.58E-05	WT N 14 dpi	H	Gibberellin 2-beta-dioxygenase 1-likeprotein (AHRD V3.3 *** A0A0B0PL18_GOSAR)	
Solyc04g005470.3	**1.04E+00**	**4.08E-03**	8.94E-01	1.18E-02	-1.99E-01	5.52E-01	-5.02E-01	1.40E-01	WT N 14 dpi	PMI	Remorin family protein (AHRD V3.3 *-* AT1G13920.4)	
Solyc08g068200.3	**1.04E+00**	**1.60E-08**	8.34E-01	7.24E-07	3.86E-01	5.76E-03	4.48E-01	1.75E-03	WT N 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein	GO:0005525
Solyc04g077000.3	**1.03E+00**	**5.22E-07**	7.88E-01	3.01E-05	2.89E-01	7.48E-02	5.55E-01	1.47E-03	WT N 14 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GE38_THECC)	GO:0004842|GO:0016567|GO:0005515|GO:0008270|GO:0005515|GO:0008270
Solyc12g042770.2	**1.03E+00**	**1.70E-05**	4.10E-01	4.61E-02	-2.02E-01	3.12E-01	1.20E-01	5.46E-01	WT N 14 dpi	NA	post-illumination chlorophyll fluorescence increase (AHRD V3.3 *** AT3G15840.1)	
Solyc01g111600.3	**1.03E+00**	**3.55E-10**	6.94E-01	5.34E-07	-1.44E-01	1.81E-01	7.36E-02	4.89E-01	WT N 14 dpi	TR	Heavy metal transport/detoxificationsuperfamily protein (AHRD V3.3 *** AT4G35060.1)	GO:0030001|GO:0046872
Solyc07g048085.1	**1.03E+00**	**2.64E-03**	8.41E-01	1.13E-02	-3.32E-01	2.91E-01	-9.89E-01	3.56E-03	WT N 14 dpi	PMI	Fasciclin-like arabinogalactan protein (AHRD V3.3 *-* G7K503_MEDTR)	
Solyc05g010720.3	**1.02E+00**	**2.65E-05**	8.39E-01	2.92E-04	3.39E-02	8.67E-01	5.87E-01	7.06E-03	WT N 14 dpi	NA	Enoyl-CoA hydratase/isomerase family protein (AHRD V3.3 *** B9HTL0_POPTR)	GO:0003824|GO:0008152
Solyc04g078410.3	**1.02E+00**	**1.86E-05**	2.84E-01	1.55E-01	2.02E-02	9.18E-01	4.37E-01	3.32E-02	WT N 14 dpi	K	Serine/threonine-protein kinase (AHRDV3.3 *** M0ZUR7_SOLTU)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g054690.3	**1.01E+00**	**2.84E-03**	9.58E-01	4.43E-03	3.30E-02	9.15E-01	-9.65E-02	7.56E-01	WT N 14 dpi	2M	ascorbate oxidase	GO:0005507|GO:0005507|GO:0005576|GO:0005507|GO:0005576
Solyc08g075230.1	**1.01E+00**	**3.45E-05**	6.57E-01	3.24E-03	3.02E-01	1.48E-01	1.68E-01	4.15E-01	WT N 14 dpi	D	LOW QUALITY:Late embryogenesisabundant (LEA)hydroxyproline-rich glycoprotein family (AHRD V3.3 *** A0A0K9PHY0_ZOSMR)	
Solyc03g007850.1	**1.01E+00**	**2.14E-03**	2.93E-01	3.32E-01	-8.08E-01	1.13E-02	-2.79E-01	3.55E-01	WT N 14 dpi	RNA	Crooked neck protein, putative (AHRDV3.3 *** B9RCP3_RICCO)	GO:0005515|GO:0006396|GO:0006396
Solyc10g085210.2	**1.01E+00**	**1.28E-03**	4.71E-01	1.04E-01	-2.48E-01	3.84E-01	-3.10E-01	2.77E-01	WT N 14 dpi	T	transcription factor-like protein (AHRD V3.3 *** AT1G58330.1)	GO:0006351|GO:0043565
Solyc05g006340.3	**1.01E+00**	**3.97E-04**	3.01E-01	2.37E-01	7.93E-01	3.71E-03	3.28E-01	1.98E-01	WT N 14 dpi	G	Transducin/WD40 repeat-like superfamilyprotein (AHRD V3.3 *** A0A061FTT2_THECC)	GO:0005515
Solyc09g008940.3	**1.01E+00**	**3.20E-10**	5.83E-01	5.63E-06	4.67E-01	1.07E-04	8.69E-01	6.24E-09	WT N 14 dpi	DNA	AT hook motif DNA-binding family protein (AHRD V3.3 *** G7I9B1_MEDTR)	GO:0003677
Solyc06g083330.2	**1.01E+00**	**5.00E-06**	7.81E-01	1.47E-04	-1.17E-01	5.13E-01	4.27E-01	2.23E-02	WT N 14 dpi	D	LOW QUALITY:acidic leucine-rich nuclear phosphoprotein 32 family B protein (AHRDV3.3 *-* AT3G25130.1)	
Solyc04g009790.3	**1.01E+00**	**1.12E-04**	6.02E-01	1.15E-02	-8.00E-01	1.28E-03	1.84E-01	4.14E-01	WT N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *-* K4BPD4_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc09g065020.3	**1.01E+00**	**8.02E-08**	7.58E-01	7.72E-06	-8.93E-02	5.17E-01	4.70E-01	1.93E-03	WT N 14 dpi	P	F-box family protein (AHRD V3.3 ***A0A061DRU1_THECC)	GO:0005515
Solyc09g074250.3	**1.01E+00**	**2.62E-07**	5.47E-02	7.10E-01	1.74E-01	2.43E-01	-2.23E-01	1.38E-01	WT N 14 dpi	K	Protein kinase family protein (AHRD V3.3 *** AT5G35960.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g091350.3	**1.00E+00**	**2.73E-07**	3.44E-01	2.60E-02	1.10E-01	4.58E-01	5.20E-01	1.45E-03	WT N 14 dpi	C	Glycosyltransferase (AHRD V3.3 ***K4BCT3_SOLLC)	GO:0008152|GO:0016758

Solyc04g082480.3	**1.00E+00**	**2.56E-10**	9.89E-01	3.33E-10	-6.52E-01	7.39E-07	-3.30E-02	7.45E-01	WT N 14 dpi	DNA	Plant regulator RWP-RK family protein,putative (AHRD V3.3 *** A0A061FD78_THECC)	GO:0005515
Solyc10g081340.1	**1.00E+00**	**9.00E-03**	7.82E-01	3.61E-02	1.53E-01	6.69E-01	5.72E-01	1.18E-01	WT N 14 dpi	G	LOW QUALITY:Phytochrome kinase substrate 4, putative (AHRD V3.3 *** A0A061F5H7_THECC)	
Solyc03g093380.2	**-1.00E+00**	**7.69E-06**	-8.07E-01	1.31E-04	-4.27E-01	2.50E-02	-4.02E-01	3.38E-02	WT N 14 dpi	K	protein kinase family protein (AHRD V3.3 *** AT1G51870.2)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc10g008020.3	**-1.00E+00**	**6.18E-04**	-8.51E-01	2.79E-03	-4.78E-01	7.44E-02	-9.92E-01	6.89E-04	WT N 14 dpi	D	CMV 1a interacting protein 1 (AHRD V3.3 *** Q5DT22_TOBAC)	GO:0008152|GO:0008168
Solyc03g083560.1	**-1.00E+00**	**7.51E-05**	2.52E-01	2.48E-01	4.91E-01	2.99E-02	-2.87E-01	1.90E-01	WT N 14 dpi	STR	Phosphate-responsive 1 family protein (AHRD V3.3 *** G7JP91_MEDTR)	
Solyc09g010230.2	**-1.00E+00**	**9.32E-04**	-9.56E-01	1.48E-03	-9.00E-01	2.51E-03	5.65E-01	4.53E-02	WT N 14 dpi	DNA	B3 domain-containing protein family (AHRD V3.3 *** A0A151U3H1_CAJCA)	GO:0003677
Solyc02g032480.2	**-1.01E+00**	**5.43E-03**	-7.40E-01	3.44E-02	-6.05E-01	7.92E-02	-2.72E-01	4.19E-01	WT N 14 dpi	RNA	Nuclear pore complex protein Nup214 (AHRD V3.3 *-* W6JJ76_NICBE)	GO:0005515
Solyc04g015220.3	**-1.01E+00**	**1.74E-06**	-5.98E-01	1.15E-03	-6.82E-01	3.04E-04	-2.33E-01	1.66E-01	WT N 14 dpi	D	Disease resistance protein (AHRD V3.3 *** GO:0043531A0A103XDQ0_CYNCS)	
Solyc08g078810.1	**-1.01E+00**	**1.02E-03**	-4.44E-01	1.15E-01	-9.24E-01	2.23E-03	-6.90E-01	1.77E-02	WT N 14 dpi	G	indeterminate(ID)-domain 16 (AHRD V3.3 -* AT1G25250.3)	
Solyc11g008850.2	**-1.01E+00**	**5.57E-07**	-6.04E-01	5.27E-04	3.80E-01	1.97E-02	-2.36E-01	1.34E-01	WT N 14 dpi	E	Protease Do-like 10 (AHRD V3.3 ***W9SEX8_9ROSA)	GO:0004252|GO:0006508|GO:0005515|GO:0005515
Solyc04g081080.1	**-1.01E+00**	**7.92E-03**	-1.48E-01	6.76E-01	6.51E-01	7.47E-02	-2.89E-01	4.17E-01	WT N 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BVI7_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc05g055840.3	**-1.01E+00**	**5.71E-05**	-2.79E-01	1.95E-01	-5.88E-01	9.55E-03	-2.65E-01	2.18E-01	WT N 14 dpi	C	Glycosyltransferase (AHRD V3.3 ***B6EWY8_LYCBA)	GO:0008152|GO:0016758
Solyc10g049580.2	**-1.01E+00**	**5.75E-03**	2.89E-01	3.98E-01	-9.86E-02	7.72E-01	-7.06E-01	4.56E-02	WT N 14 dpi	CS	Arabinogalactan protein (AHRD V3.3 --* Q9FUL8_NICAL)	
Solyc07g009333.1	**-1.02E+00**	**7.26E-03**	-2.65E-01	4.53E-01	8.57E-02	8.08E-01	3.32E-01	3.50E-01	WT N 14 dpi	P	60S acidic ribosomal protein P3 (AHRDV3.3 *** B9HPG0_POPTR)	
Solyc09g014250.3	**-1.02E+00**	**2.64E-09**	-7.02E-01	1.83E-06	-2.21E-01	6.44E-02	-8.60E-01	6.18E-08	WT N 14 dpi	T	MYB transcription factor (AHRD V3.3 *** Q66RN1_HEVBR)	GO:0003677
Solyc01g109860.3	**-1.02E+00**	**7.27E-03**	-8.02E-01	3.00E-02	-5.41E-01	1.33E-01	-5.68E-01	1.16E-01	WT N 14 dpi	S	Sec14p-like phosphatidylinositol transferfamily protein (AHRD V3.3 *** AT2G18180.2)	GO:0005215|GO:0005622|GO:0006810
Solyc05g011850.1	**-1.02E+00**	**1.27E-03**	1.91E-02	9.46E-01	1.37E-01	6.30E-01	-6.64E-01	2.62E-02	WT N 14 dpi	TR	Sulfotransferase (AHRD V3.3 *** K4BXQ8_SOLLC)	GO:0008146
Solyc02g080040.3	**-1.02E+00**	**1.31E-03**	-5.00E-01	8.83E-02	6.61E-01	2.74E-02	6.39E-01	3.23E-02	WT N 14 dpi	S	Receptor-like kinase (AHRD V3.3 ***G8A106_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc06g066090.3	**-1.02E+00**	**8.49E-10**	-7.92E-01	9.96E-08	-6.08E-02	5.80E-01	-6.50E-01	2.61E-06	WT N 14 dpi	NA	Lactation elevated protein 1 (AHRD V3.3 *** A0A0B0NJ47_GOSAR)	GO:0005524
Solyc03g083590.3	**-1.02E+00**	**3.98E-03**	-6.01E-01	7.38E-02	4.08E-02	9.00E-01	2.70E-01	4.10E-01	WT N 14 dpi	K	Kinase, putative (AHRD V3.3 ***B9R9Q3_RICCO)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc05g015700.1	**-1.02E+00**	**6.57E-03**	-2.34E-01	5.05E-01	-5.42E-01	1.30E-01	-6.46E-01	7.37E-02	WT N 14 dpi	NA	LOW QUALITY:transmembrane protein, putative (DUF 3339) (AHRD V3.3 ***AT3G48660.1)	
Solyc12g011360.2	**-1.03E+00**	**1.35E-03**	-9.95E-01	1.78E-03	6.55E-02	8.20E-01	3.40E-02	9.06E-01	WT N 14 dpi	H	Interactor of constitutive active ROPsprotein, putative (AHRD V3.3 *** A0A072V8T5_MEDTR)	
Solyc01g088520.3	**-1.03E+00**	**7.50E-03**	-5.28E-01	1.47E-01	-3.55E-02	9.21E-01	-1.50E-01	6.76E-01	WT N 14 dpi	TR	Dynamin (AHRD V3.3 *-* A0A118JT45_CYNCS)	
Solyc05g014130.3	**-1.03E+00**	**4.46E-09**	-6.40E-01	1.31E-05	-7.39E-02	5.40E-01	-5.16E-01	1.99E-04	WT N 14 dpi	H	COP1-interacting protein 4 (AHRD V3.3 *-* AT5G37190.3)	

Solyc09g075790.3	**-1.03E+00**	**2.95E-03**	1.69E-01	5.93E-01	-7.95E-01	1.76E-02	-6.08E-01	6.33E-02	WT N 14 dpi	L	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *** A0A0R5QM74_SALMI)	GO:0003824|GO:0008152
Solyc07g056530.3	**-1.03E+00**	**1.75E-03**	5.37E-02	8.57E-01	-2.83E-01	3.47E-01	-6.46E-01	3.82E-02	WT N 14 dpi	TR	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT3G14410.1)	
Solyc05g012230.3	**-1.03E+00**	**1.17E-03**	-6.10E-01	4.08E-02	-1.04E-01	7.17E-01	-6.68E-01	2.61E-02	WT N 14 dpi	CS	Protein POLAR LOCALIZATION DURINGASYMMETRIC DIVISION AND REDISTRIBUTION (AHRD V3.3 --* A0A199UMI0_ANACO)	
Solyc06g082500.3	**-1.03E+00**	**6.38E-04**	-1.61E-01	5.51E-01	2.30E-01	3.95E-01	-4.69E-01	8.99E-02	WT N 14 dpi	TR	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT2G30460.2)	
Solyc07g015800.1	**-1.04E+00**	**3.93E-08**	-9.96E-01	8.17E-08	-4.95E-01	1.10E-03	2.19E-02	8.72E-01	WT N 14 dpi	P	F-box family protein, putative (AHRD V3.3 *** A0A061F027_THECC)	GO:0005515
Solyc11g066160.1	**-1.04E+00**	**5.32E-04**	-4.23E-01	1.20E-01	3.16E-01	2.39E-01	1.71E-01	5.21E-01	WT N 14 dpi	DNA	histone H4 (AHRD V3.3 *** AT2G28740.1)	GO:0000786|GO:0003677|GO:0005634|GO:0000786|GO:0003677|GO:0005634|GO:0006334|GO:0000786|GO:0003677|GO:0005634|GO:0006334
Solyc01g091630.3	**-1.04E+00**	**1.50E-05**	-8.46E-01	2.01E-04	-5.65E-01	7.69E-03	-4.06E-01	4.79E-02	WT N 14 dpi	G	cutin deficient 2	GO:0003677|GO:0006355|GO:0043565|GO:0006355|GO:0043565
Solyc02g062610.3	**-1.04E+00**	**1.35E-05**	-1.83E-01	3.54E-01	-3.80E-01	6.13E-02	-6.31E-01	3.22E-03	WT N 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G36530.2)	
Solyc03g119870.3	**-1.04E+00**	**4.36E-03**	-8.26E-01	2.02E-02	-1.84E-01	5.86E-01	-7.63E-01	3.05E-02	WT N 14 dpi	DNA	C3HC zinc finger-like protein (AHRD V3.3 *** AT1G48950.1)	GO:0005634|GO:0008270
Solyc08g006100.3	**-1.04E+00**	**7.50E-06**	-8.07E-01	2.07E-04	-9.72E-02	6.07E-01	3.13E-02	8.68E-01	WT N 14 dpi	NA	plant/protein (Protein of unknown function, DUF599) (AHRD V3.3 *** AT5G10580.3)	
Solyc05g009460.3	**-1.04E+00**	**1.09E-03**	-6.82E-01	2.38E-02	-5.64E-01	5.79E-02	-8.66E-01	5.25E-03	WT N 14 dpi	NA	Conserved peptide upstream open readingframe 53 (AHRD V3.3 --* B3H7G6_ARATH)	
Solyc02g084450.3	**-1.05E+00**	**4.67E-04**	-6.20E-01	2.59E-02	-3.14E-01	2.42E-01	-5.17E-01	5.94E-02	WT N 14 dpi	D	Disease resistance protein (AHRD V3.3 *** A0A124SFK9_CYNCS)	GO:0005515|GO:0043531|GO:0043531
Solyc03g097940.3	**-1.05E+00**	**3.76E-06**	-5.52E-01	5.00E-03	-6.36E-01	1.56E-03	-9.09E-01	3.01E-05	WT N 14 dpi	TR	Potassium channel (AHRD V3.3 *** H2DPY4_9ROSA)	GO:0005216|GO:0006811|GO:0016020|GO:0055085|GO:0005515|GO:0005515
Solyc06g071920.3	**-1.05E+00**	**8.43E-11**	-8.50E-01	6.35E-09	1.45E-01	1.60E-01	-4.84E-01	5.43E-05	WT N 14 dpi	C	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** C9DRQ8_SOLCH)	GO:0006006|GO:0016620|GO:0050661|GO:0051287|GO:0055114|GO:0016620|GO:0055114|GO:0016620|GO:0055114
Solyc09g007260.3	**-1.06E+00**	**5.68E-03**	-9.03E-01	1.64E-02	1.01E+00	7.92E-03	4.06E-01	2.59E-01	WT N 14 dpi	H	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** G7IU38_MEDTR)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc01g097070.3	**-1.06E+00**	**7.20E-03**	2.31E-01	5.31E-01	3.90E-01	2.94E-01	3.89E-02	9.16E-01	WT N 14 dpi	DNA	DNA topoisomerase (AHRD V3.3 ***K4B095_SOLLC)	GO:0003676|GO:0008270|GO:0003677|GO:0003917|GO:0006265|GO:0003677|GO:0003917|GO:0006265
Solyc01g107050.3	**-1.06E+00**	**3.08E-05**	-2.60E-01	2.28E-01	-2.45E-01	2.55E-01	-2.44E-01	2.56E-01	WT N 14 dpi	S	HXXXD-type acyl-transferase family protein GO:0016747 (AHRD V3.3 *-* AT5G67150.1)	
Solyc07g065120.3	**-1.06E+00**	**3.45E-07**	-4.49E-01	8.06E-03	-5.91E-01	8.34E-04	-8.57E-01	9.90E-06	WT N 14 dpi	L	Glycerophosphoryl diester phosphodiesterase, putative (AHRD V3.3 *** B9SSQ8_RICCO)	GO:0006629|GO:0008081
Solyc06g062883.1	**-1.06E+00**	**1.89E-03**	-9.52E-01	4.69E-03	-4.10E-01	1.94E-01	-9.42E-01	5.07E-03	WT N 14 dpi	H	Ethylene-responsive transcription factor 1B (AHRD V3.3 --* W9SHC2_9ROSA)	
Solyc11g017100.1	**-1.07E+00**	**9.00E-03**	-5.96E-01	1.27E-01	1.76E+00	8.55E-05	9.03E-01	2.45E-02	WT N 14 dpi	T	LOW QUALITY:GRAS family transcription factor	
Solyc02g032460.2	**-1.07E+00**	**9.99E-03**	-6.75E-01	9.15E-02	-3.99E-01	3.09E-01	-9.46E-01	2.10E-02	WT N 14 dpi	RNA	Nuclear pore complex protein Nup214 (AHRD V3.3 *-* W6JJ76_NICBE)	
Solyc02g082150.1	**-1.07E+00**	**7.93E-03**	-6.15E-01	1.11E-01	-6.90E-01	7.54E-02	-8.87E-01	2.49E-02	WT N 14 dpi	E	LOW QUALITY:root hair specific 4 (AHRD V3.3 *-* AT1G30850.1)	
Solyc02g061760.3	**-1.07E+00**	**6.07E-03**	-2.18E-01	5.49E-01	-3.57E-01	3.30E-01	-7.62E-01	4.38E-02	WT N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4B666_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc10g007300.2	**-1.08E+00**	**9.24E-04**	-8.13E-01	9.07E-03	-4.11E-01	1.65E-01	-2.48E-01	3.97E-01	WT N 14 dpi	E	succinate dehydrogenase 2-1 (AHRD V3.3 --* AT3G27380.2)	
Solyc06g036770.1	**-1.08E+00**	**7.52E-03**	-5.28E-02	8.88E-01	3.71E-01	3.29E-01	-2.07E-01	5.84E-01	WT N 14 dpi	CS	LOW QUALITY:CASP-like protein (AHRD V3.3 --* A0A0L9UWM4_PHAAN)	

Solyc04g082220.2	**-1.08E+00**	**2.71E-04**	-3.44E-01	1.93E-01	2.07E-01	4.29E-01	-1.95E-01	4.54E-01	WT N 14 dpi	AM	Amino acid transporter, putative (AHRD V3.3 *** B9R8J4_RICCO)	
Solyc04g074130.3	**-1.09E+00**	**2.51E-04**	-1.95E-01	4.52E-01	1.33E-01	6.08E-01	-4.62E-01	8.25E-02	WT N 14 dpi	TR	Mitochondrial substrate carrier family protein (AHRD V3.3 *** AT5G64970.1)	GO:0055085
Solyc08g066320.3	**-1.09E+00**	**7.98E-03**	-1.47E-01	7.01E-01	-6.62E-01	9.15E-02	-9.98E-01	1.38E-02	WT N 14 dpi	D	kinase family with leucine-rich repeat domain-containing protein (AHRD V3.3 *** AT5G25930.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g076880.3	**-1.09E+00**	**1.90E-05**	-4.36E-01	4.61E-02	1.72E+00	1.06E-08	-1.92E-01	3.65E-01	WT N 14 dpi	TR	Nodulin26-like intrinsic protein 31 (AHRD V3.3 --* K4C978_SOLLC)	
Solyc09g065570.3	**-1.09E+00**	**8.59E-04**	-3.70E-01	2.12E-01	4.51E-01	1.31E-01	1.59E-03	9.96E-01	WT N 14 dpi	K	Kinase family protein (AHRD V3.3 ***B9GSJ9_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g093300.3	**-1.09E+00**	**9.68E-04**	1.17E-01	6.95E-01	1.82E-01	5.41E-01	-6.12E-01	4.74E-02	WT N 14 dpi	DNA	DNA polymerase (AHRD V3.3 ***H9E8V2_SOLLC)	GO:0000166|GO:0003676|GO:0003887|GO:0000166|GO:0003677|GO:0000166|GO:0003677
Solyc04g071600.3	**-1.09E+00**	**1.45E-03**	-3.89E-01	2.17E-01	9.72E-01	3.95E-03	1.20E+00	5.95E-04	WT N 14 dpi	STR	Abscisic acid stress ripening 5	GO:0006950
Solyc07g041750.3	**-1.10E+00**	**2.27E-11**	-9.73E-01	3.06E-10	1.27E-01	2.08E-01	-1.45E-01	1.52E-01	WT N 14 dpi	C	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G35570.1)	
Solyc11g044960.2	**-1.10E+00**	**7.48E-03**	-9.35E-01	2.07E-02	-5.43E-01	1.64E-01	-5.92E-01	1.31E-01	WT N 14 dpi	K	Protein kinase family protein GCN2 (AHRD GO:0005515 V3.3 *-* A0A0N7AH70_TOBAC)	
Solyc09g082820.3	**-1.11E+00**	**2.75E-03**	-7.45E-01	3.45E-02	2.05E-01	5.45E-01	6.41E-01	6.60E-02	WT N 14 dpi	CYTP450	cytochrome P450, family 71, subfamily A,polypeptide 19 (AHRD V3.3 --* AT4G13290.1)	
Solyc02g088630.3	**-1.11E+00**	**9.09E-05**	-7.16E-01	6.04E-03	-6.65E-01	1.00E-02	-9.76E-01	3.86E-04	WT N 14 dpi	P	Hexosyltransferase (AHRD V3.3 *** K4BC18_SOLLC)	GO:0016757|GO:0047262|GO:0047262
Solyc06g035760.3	**-1.11E+00**	**1.08E-03**	-2.84E-01	3.55E-01	1.03E+00	2.20E-03	-6.59E-01	3.83E-02	WT N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***R4R2I7_9SOLA)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc06g072580.3	**-1.12E+00**	**2.95E-12**	-9.28E-01	1.56E-10	6.28E-02	4.96E-01	1.75E-01	6.53E-02	WT N 14 dpi	C	Pyruvate dehydrogenase E1 componentsubunit beta (AHRD V3.3 *** B6T6H3_MAIZE)	GO:0003824|GO:0008152|GO:0004739|GO:0006086|GO:0004739|GO:0006086
Solyc02g084370.1	**-1.12E+00**	**6.03E-03**	-7.59E-01	5.28E-02	-2.37E-01	5.31E-01	-5.77E-01	1.35E-01	WT N 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BAV3_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc12g010320.2	**-1.12E+00**	**8.75E-09**	-4.97E-01	1.05E-03	-5.26E-01	6.11E-04	-9.43E-01	2.09E-07	WT N 14 dpi	L	temperature-induced lipocalin	GO:0005215
Solyc07g043330.2	**-1.13E+00**	**2.51E-05**	-4.45E-01	5.35E-02	-5.37E-02	8.09E-01	-4.54E-01	4.91E-02	WT N 14 dpi	G	Transcription factor GRAS (AHRD V3.3 *** A0A103XVP0_CYNCS)	
Solyc02g080210.3	**-1.13E+00**	**8.73E-03**	-5.05E-01	2.16E-01	3.26E-01	4.19E-01	-1.05E+00	1.42E-02	WT N 14 dpi	CS	Pectinesterase (AHRD V3.3 *** G K4B9P2_SOLLC)	GO:0004857|GO:0005618|GO:0030599|GO:0042545|GO:0005618|GO:0030599|GO:0042545
Solyc11g011050.2	**-1.13E+00**	**2.90E-06**	-1.45E-01	4.52E-01	-9.15E-01	5.61E-05	-7.67E-01	4.31E-04	WT N 14 dpi	G	R2R3MYB transcription factor 43	GO:0003677
Solyc08g008610.3	**-1.13E+00**	**3.50E-03**	-7.91E-01	3.36E-02	1.45E+00	3.64E-04	1.22E+00	1.87E-03	WT N 14 dpi	L	Alpha/beta-Hydrolases superfamily protein(AHRD V3.3 *** A0A061G3V4_THECC)	
Solyc06g075580.3	**-1.13E+00**	**6.93E-04**	-4.69E-01	1.23E-01	-4.19E-01	1.66E-01	-6.11E-01	4.82E-02	WT N 14 dpi	TR	Kinesin-like protein (AHRD V3.3 ***A0A0V0IXV7_SOLCH)	GO:0003777|GO:0005524|GO:0007018|GO:0003777|GO:0005524|GO:0007018|GO:0008017|GO:0003777|GO:0005524|GO:0007018|GO:0008017
Solyc07g017980.1	**-1.14E+00**	**3.99E-03**	-6.05E-01	1.04E-01	1.41E+00	5.99E-04	1.23E+00	2.02E-03	WT N 14 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 ***I3S1U4_MEDTR)	
Solyc03g082470.3	**-1.14E+00**	**1.29E-03**	-6.97E-01	3.65E-02	-8.26E-01	1.47E-02	-9.32E-01	6.68E-03	WT N 14 dpi	S	Receptor-like protein kinase (AHRD V3.3 *** M8BN66_AEGTA)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc05g054680.1	**-1.14E+00**	**8.09E-05**	-8.50E-01	1.82E-03	-7.42E-01	5.46E-03	-5.39E-01	3.65E-02	WT N 14 dpi	K	protein kinase family protein (AHRD V3.3 *** AT5G54380.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468

Solyc03g080120.1	**-1.14E+00**	**2.25E-03**	1.99E-01	5.61E-01	1.16E+00	2.04E-03	9.07E-01	1.24E-02	WT N 14 dpi	NA	LOW QUALITY:holocarboxylasesynthetase 2 (AHRD V3.3 --* AT1G37150.8)	
Solyc10g085670.2	**-1.15E+00**	**2.15E-03**	-3.64E-02	9.15E-01	-1.03E-01	7.63E-01	-8.37E-03	9.80E-01	WT N 14 dpi	K	MAP kinase kinase kinase 79	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g051150.3	**-1.15E+00**	**2.38E-03**	-8.03E-01	2.63E-02	-3.13E-01	3.66E-01	-3.40E-01	3.28E-01	WT N 14 dpi	G	UDP-glucose:sterol glucosyltransferase(AHRD V3.3 *** O22678_AVESA)	GO:0005975|GO:0016758|GO:0030259|GO:0008152|GO:0016758|GO:0008152|GO:0016758
Solyc01g106470.3	**-1.15E+00**	**9.53E-08**	-5.80E-01	1.03E-03	-4.27E-01	1.15E-02	-6.64E-01	2.54E-04	WT N 14 dpi	D	Tunicamycin induced 1 (AHRD V3.3 *** A0A097PPU7_SOLLC)	
Solyc01g067125.1	**-1.15E+00**	**5.99E-03**	-1.84E-01	6.37E-01	-9.89E-01	1.63E-02	-1.98E-01	6.11E-01	WT N 14 dpi	P	Cullin 1, putative (AHRD V3.3 *-* A0A061EP85_THECC)	
Solyc04g016260.3	**-1.15E+00**	**7.61E-06**	-6.79E-01	2.97E-03	4.35E-02	8.35E-01	-4.66E-01	3.29E-02	WT N 14 dpi	TR	Calcium-transporting ATPase (AHRD V3.3 *** M1AYJ8_SOLTU)	GO:0000166|GO:0000166|GO:0046872|GO:0000166|GO:0046872
Solyc01g066870.3	**-1.16E+00**	**1.89E-09**	-7.15E-01	7.50E-06	-4.89E-01	7.56E-04	-2.91E-01	3.15E-02	WT N 14 dpi	K	Protein phosphatase 2C family protein (AHRD V3.3 *** AT3G16560.4)	GO:0003824|GO:0004722|GO:0006470|GO:0004722|GO:0006470
Solyc08g079150.1	**-1.16E+00**	**8.59E-03**	-3.72E-01	3.68E-01	1.11E+00	1.14E-02	-3.58E-01	3.86E-01	WT N 14 dpi	H	SAUR-like auxin-responsive protein family (AHRD V3.3 *** AT4G22620.1)	GO:0009733
Solyc06g074850.3	**-1.16E+00**	**1.67E-03**	4.17E-01	2.17E-01	3.30E-01	3.25E-01	-4.78E-01	1.59E-01	WT N 14 dpi	STR	Carboxypeptidase (AHRD V3.3 *** K4C9K1_SOLLC)	GO:0004185|GO:0006508
Solyc12g007010.2	**-1.16E+00**	**7.99E-06**	-9.84E-01	7.17E-05	-5.02E-01	2.33E-02	-9.24E-01	1.51E-04	WT N 14 dpi	NA	fe-S cluster assembly factor HCF101	GO:0005524
Solyc07g048000.3	**-1.16E+00**	**1.34E-03**	-6.42E-01	5.73E-02	1.57E+00	4.74E-05	3.25E-01	3.23E-01	WT N 14 dpi	G	Phototropic-responsive NPH3	GO:0005515
Solyc08g077880.3	**-1.17E+00**	**6.44E-13**	-9.97E-01	2.23E-11	3.65E-01	3.69E-04	-9.94E-02	2.75E-01	WT N 14 dpi	NA	High molecular mass early light-inducibleHV58, chloroplastic (AHRD V3.3 *** A0A0B0NUU8_GOSAR)	
Solyc08g069010.3	**-1.17E+00**	**1.90E-03**	2.40E-01	4.86E-01	2.93E-03	9.93E-01	-6.60E-01	6.24E-02	WT N 14 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9RNM2_RICCO)	
Solyc08g013940.3	**-1.17E+00**	**8.95E-04**	1.17E-01	7.11E-01	5.23E-02	8.68E-01	-3.54E-01	2.67E-01	WT N 14 dpi	K	Serine/Threonine kinase family protein(AHRD V3.3 *** G7ISK8_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g111880.3	**-1.17E+00**	**2.71E-06**	-8.32E-01	2.53E-04	3.20E-01	1.15E-01	-6.17E-01	4.14E-03	WT N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9RAS2_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc02g079360.2	**-1.17E+00**	**6.17E-10**	-5.06E-01	3.54E-04	6.01E-01	4.61E-05	7.74E-01	1.22E-06	WT N 14 dpi	K	Octicosapeptide/Phox/Bem1p family protein (AHRD V3.3 *** AT4G05150.1)	GO:0005515
Solyc05g056300.3	**-1.17E+00**	**2.72E-06**	-9.70E-01	4.06E-05	1.72E-01	3.88E-01	-4.64E-03	9.81E-01	WT N 14 dpi	OX	Thioredoxin (AHRD V3.3 *** A0A103YEZ4_CYNCS)	GO:0006662|GO:0015035|GO:0045454|GO:0045454|GO:0045454
Solyc09g015450.3	**-1.18E+00**	**1.72E-03**	-2.96E-01	3.87E-01	-5.27E-01	1.30E-01	-3.54E-01	3.02E-01	WT N 14 dpi	T	DNA-directed RNA polymerase subunit beta' (AHRD V3.3 --* RPOC1_BARVE)	
Solyc06g074820.3	**-1.18E+00**	**3.94E-06**	-3.90E-01	6.55E-02	-6.08E-01	5.98E-03	-9.54E-01	7.54E-05	WT N 14 dpi	TR	tonoplast intrinsic protein 1.1	GO:0005215|GO:0006810|GO:0016020
Solyc03g097500.3	**-1.19E+00**	**5.94E-03**	-9.19E-01	2.84E-02	1.20E+00	5.59E-03	7.37E-01	7.39E-02	WT N 14 dpi	CS	Feruloyl transferase (AHRD V3.3 *** D5FPG8_SOLTU)	GO:0016747
Solyc04g072920.3	**-1.19E+00**	**1.12E-06**	-7.03E-01	9.10E-04	1.52E-01	4.26E-01	-1.32E-01	4.87E-01	WT N 14 dpi	K	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** K4BTS9_SOLLC)	GO:0003824|GO:0005992
Solyc09g097865.1	**-1.19E+00**	**3.63E-03**	-4.06E-02	9.14E-01	5.84E-02	8.76E-01	-3.44E-01	3.63E-01	WT N 14 dpi	TR	Kinesin-like protein (AHRD V3.3 *** A0A0D2U096_GOSRA)	
Solyc07g022830.3	**-1.19E+00**	**1.43E-06**	-9.42E-01	4.25E-05	7.08E-01	1.02E-03	9.87E-01	2.28E-05	WT N 14 dpi	CS	EXS family protein (AHRD V3.3 *** B9MXW8_POPTR)	GO:0016021
Solyc01g067210.3	**-1.19E+00**	**8.03E-03**	-1.03E+00	1.95E-02	-8.79E-01	4.39E-02	-4.01E-01	3.43E-01	WT N 14 dpi	P	cullin 1 (AHRD V3.3 *** AT4G02570.4)	GO:0006511|GO:0031461|GO:0031625|GO:0006511|GO:0031625|GO:0006511|GO:0031625
Solyc12g070080.2	**-1.20E+00**	**1.15E-05**	-1.42E-01	5.30E-01	-8.82E-01	5.12E-04	-4.48E-01	5.44E-02	WT N 14 dpi	L	Fatty acid amide hydrolase (AHRD V3.3 *** GO:0004040 A0A172CJD2_POPTO)	

Solyc08g079180.3	**-1.21E+00**	**5.31E-08**	-6.76E-01	2.53E-04	-2.93E-01	7.74E-02	-9.90E-01	1.53E-06	WT N 14 dpi	P	Elongation factor G, chloroplastic (AHRDV3.3 *** K4CNS6_SOLLC)	GO:0003746|GO:0005525|GO:0005622|GO:0006414|GO:0003746|GO:0006414|GO:0009507|GO:0003746|GO:0006414|GO:0009507
Solyc01g107780.3	**-1.21E+00**	**1.91E-05**	-8.25E-01	1.44E-03	3.76E-01	1.16E-01	1.08E+00	8.26E-05	WT N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4B2Z4_SOLLC)	GO:0008152|GO:0016758
Solyc09g011990.1	**-1.21E+00**	**4.77E-05**	4.38E-01	8.90E-02	1.49E-01	5.53E-01	5.00E-01	5.41E-02	WT N 14 dpi	PMI	Clade IV lectin receptor kinase (AHRDV3.3 *** K4CRM4_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc09g065660.3	**-1.21E+00**	**8.16E-03**	-1.03E+00	2.18E-02	-5.62E-01	1.95E-01	-9.88E-01	2.73E-02	WT N 14 dpi	T	SolycHsfA7	GO:0003700|GO:0005634|GO:0006355|GO:0043565
Solyc05g026240.2	**-1.22E+00**	**5.96E-06**	-8.01E-02	7.12E-01	2.05E-01	3.48E-01	-6.69E-01	4.40E-03	WT N 14 dpi	PMI	Leucine-rich repeat receptor-like proteinkinase family (AHRD V3.3 *** A0A0K9Q1P6_ZOSMR)	GO:0005515
Solyc07g007560.3	**-1.22E+00**	**6.43E-06**	-6.44E-01	6.14E-03	1.78E-02	9.35E-01	-4.75E-01	3.71E-02	WT N 14 dpi	TR	phosphate transporter 4-5 (AHRD V3.3 *** AT5G20380.2)	GO:0016021|GO:0055085
Solyc11g040330.2	**-1.22E+00**	**2.37E-10**	-6.29E-01	2.27E-05	1.48E-01	2.37E-01	-3.31E-01	1.17E-02	WT N 14 dpi	CS	Endo-1,4-beta-xylanase A (AHRD V3.3 *** W9QKK9_9ROSA)	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc03g116530.3	**-1.22E+00**	**5.87E-11**	-4.45E-01	6.11E-04	-1.30E-01	2.64E-01	-4.12E-01	1.30E-03	WT N 14 dpi	STR	Lactoylglutathione lyase / glyoxalase Ifamily protein (AHRD V3.3 *** AT1G80160.3)	
Solyc08g014000.3	**-1.22E+00**	**6.57E-05**	-6.99E-01	1.17E-02	2.77E+00	5.29E-11	2.54E+00	3.15E-10	WT N 14 dpi	L	lipoxygenase A	GO:0005515|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc04g070980.3	**-1.23E+00**	**2.33E-03**	-5.85E-01	1.19E-01	4.90E-01	1.89E-01	-3.59E-01	3.32E-01	WT N 14 dpi	L	cycloartenol synthase 1	
Solyc01g006720.3	**-1.23E+00**	**1.74E-04**	2.45E-01	3.88E-01	1.23E+00	1.68E-04	-7.44E-01	1.32E-02	WT N 14 dpi	TR	ABC transporter family protein (AHRD V3.3 *** B9IIG9_POPTR)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc01g096660.3	**-1.23E+00**	**1.80E-07**	-5.12E-01	6.68E-03	6.03E-01	1.85E-03	-4.43E-01	1.70E-02	WT N 14 dpi	E	PSII-associated proline-rich protein	
Solyc12g044380.2	**-1.23E+00**	**7.94E-05**	1.47E-01	5.81E-01	1.21E-01	6.49E-01	-1.50E-01	5.72E-01	WT N 14 dpi	E	Cytochrome c oxidase assembly COX19 (AHRD V3.3 *** A0A0B0NX67_GOSAR)	
Solyc11g006730.1	**-1.23E+00**	**2.66E-03**	-5.29E-01	1.64E-01	5.64E-01	1.40E-01	1.41E+00	7.76E-04	WT N 14 dpi	STR	Germin-like protein 1 (AHRD V3.3 *** B9HVV6_POPTR)	GO:0030145|GO:0045735|GO:0045735
Solyc10g083310.2	**-1.23E+00**	**1.50E-03**	-7.73E-02	8.26E-01	-1.63E-01	6.44E-01	-4.37E-01	2.20E-01	WT N 14 dpi	TR	Kinesin-related protein (AHRD V3.3 ***A0A0B0NF68_GOSAR)	GO:0003777|GO:0005524|GO:0007018|GO:0003777|GO:0005524|GO:0007018|GO:0008017|GO:0003777|GO:0005524|GO:0007018|GO:0008017
Solyc03g006810.3	**-1.24E+00**	**6.42E-05**	-1.72E-01	5.14E-01	-3.46E-01	1.95E-01	1.24E-02	9.62E-01	WT N 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4BEA4_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc02g071570.3	**-1.24E+00**	**6.37E-03**	-1.20E-01	7.76E-01	-6.04E-01	1.60E-01	2.26E-02	9.57E-01	WT N 14 dpi	RNA	Pentatricopeptide repeat superfamilyprotein (AHRD V3.3 *** A0A061GEM0_THECC)	
Solyc03g019760.3	**-1.24E+00**	**1.67E-03**	-9.40E-01	1.34E-02	1.14E+00	3.36E-03	3.39E-01	3.47E-01	WT N 14 dpi	TR	ABC transporter G family member (AHRD V3.3 *** A0A0K9NYG1_ZOSMR)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc12g008610.2	**-1.24E+00**	**6.03E-03**	-5.80E-01	1.74E-01	1.20E-01	7.75E-01	-6.37E-01	1.37E-01	WT N 14 dpi	NA	transmembrane protein (AHRD V3.3 --* AT5G27440.1)	
Solyc07g005090.3	**-1.24E+00**	**9.25E-09**	-3.57E-01	2.46E-02	8.56E-01	5.22E-06	6.76E-01	1.21E-04	WT N 14 dpi	D	Chitinase, putative (AHRD V3.3 *** B9SC02_RICCO)	GO:0004553|GO:0005975|GO:0004568|GO:0006032|GO:0004568|GO:0006032
Solyc02g086230.2	**-1.25E+00**	**2.30E-04**	-8.19E-01	9.26E-03	-6.90E-01	2.56E-02	-4.79E-01	1.12E-01	WT N 14 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9T3G5_RICCO)	GO:0005515
Solyc07g064625.1	**-1.25E+00**	**2.39E-03**	-6.36E-01	9.83E-02	-3.63E-01	3.37E-01	-9.30E-01	1.88E-02	WT N 14 dpi	RNA	Pentatricopeptide repeat-containing protein GO:0005515(AHRD V3.3 *** D7MDP3_ARALL)	
Solyc05g006570.1	**-1.25E+00**	**4.28E-03**	3.70E-01	3.63E-01	-3.18E-01	4.32E-01	-1.47E-01	7.16E-01	WT N 14 dpi	S	Receptor-like kinase (AHRD V3.3 ***A0A0K9P790_ZOSMR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004

											672|GO: 0006468
Solyc07g063170.1	**-1.25E+00**	**2.35E-03**	-6.07E-01	1.15E-01	7.27E-01	6.14E-02	-2.08E-01	5.81E-01	WT N 14 dpi	TR	Sodium/calcium exchanger family protein (AHRD V3.3 --* AT5G17850.2)	
Solyc02g077120.3	**-1.26E+00**	**4.73E-04**	-8.49E-01	1.19E-02	8.59E-02	7.86E-01	-4.85E-01	1.35E-01	WT N 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A199UWQ2_ANACO)	GO:0016788
Solyc07g047850.3	**-1.26E+00**	**3.28E-03**	-8.79E-01	3.24E-02	-2.12E-01	5.90E-01	5.27E-02	8.93E-01	WT N 14 dpi	E	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 ***CB23_ORYSI)	GO:0009765|GO:0016020
Solyc07g009430.1	**-1.26E+00**	**9.18E-04**	-6.97E-01	4.84E-02	-6.42E-03	9.85E-01	1.23E+00	1.15E-03	WT N 14 dpi	P	LOW QUALITY:F-box family protein (AHRD V3.3 *** AT1G19160.1)	GO:0005515
Solyc12g013970.2	**-1.26E+00**	**2.58E-03**	1.94E-01	6.13E-01	-3.18E-01	4.07E-01	-6.84E-01	8.20E-02	WT N 14 dpi	K	Protein kinase, putative (AHRD V3.3 *-* B9SRD1_RICCO),Pfam:PF14381	
Solyc06g062610.2	**-1.27E+00**	**2.49E-03**	-1.41E-01	7.11E-01	-3.85E-01	3.17E-01	-7.84E-01	4.82E-02	WT N 14 dpi	RNA	Pentatricopeptide repeat-containing protein(AHRD V3.3 *** A0A103YL18_CYNCS)	
Solyc06g076830.2	**-1.27E+00**	**5.11E-03**	-2.21E-01	5.98E-01	-7.60E-01	7.80E-02	6.94E-02	8.68E-01	WT N 14 dpi	C	GDP-mannose transporter, putative (AHRD V3.3 *** B9SHZ3_RICCO)	
Solyc12g098753.1	**-1.27E+00**	**5.38E-04**	-1.26E-01	6.98E-01	-3.74E-01	2.57E-01	-6.42E-01	5.71E-02	WT N 14 dpi	G	Pollen protein Ole E I-like protein (AHRD V3.3 *-* A0A072VSY6_MEDTR)	
Solyc09g075680.1	**-1.28E+00**	**6.40E-06**	-6.49E-01	8.01E-03	1.19E+00	1.76E-05	-5.68E-01	1.85E-02	WT N 14 dpi	L	Alpha/beta-Hydrolases superfamily protein(AHRD V3.3 *** A0A061EKQ6_THECC)	GO:0008152|GO:0016787
Solyc05g015980.3	**-1.28E+00**	**5.77E-05**	-6.38E-01	2.40E-02	-7.66E-01	7.91E-03	-4.80E-01	8.27E-02	WT N 14 dpi	S	Gap junction beta-4 protein isoform 1 (AHRD V3.3 *** A0A061E410_THECC)	
Solyc06g069565.1	**-1.28E+00**	**4.44E-03**	-4.98E-01	2.36E-01	1.32E-01	7.50E-01	-1.63E-01	6.95E-01	WT N 14 dpi	NA	staurosporin and temperature sensitive 3- like A (AHRD V3.3 --* AT5G19690.1)	
Solyc02g093680.3	**-1.28E+00**	**2.82E-03**	-7.66E-02	8.45E-01	7.92E-02	8.40E-01	6.41E-02	8.70E-01	WT N 14 dpi	E	succinate dehydrogenase	GO:0006099|GO:0016491|GO:0055114|GO:0009055|GO:0051536|GO:0009055|GO:0051536
Solyc06g048935.1	**-1.28E+00**	**4.92E-03**	-7.48E-01	8.43E-02	-8.91E-01	4.19E-02	-1.04E+00	1.88E-02	WT N 14 dpi	TR	Ferritin (AHRD V3.3 --* F6GXT8_VITVI)	
Solyc06g010030.3	**-1.29E+00**	**8.90E-03**	2.50E-01	5.86E-01	4.12E-01	3.73E-01	8.16E-01	8.43E-02	WT N 14 dpi	D	MLO-like protein (AHRD V3.3 *-* K4C430_SOLLC)	GO:0006952|GO:0016021
Solyc08g007770.3	**-1.29E+00**	**4.66E-03**	-8.91E-01	4.24E-02	-9.56E-01	3.03E-02	-5.44E-01	2.04E-01	WT N 14 dpi	CS	Expansin-like protein (AHRD V3.3 *-* Q0WT83_ARATH)	GO:0005576|GO:0009664|GO:0009664
Solyc01g086650.3	**-1.30E+00**	**1.87E-07**	-7.66E-01	3.23E-04	4.65E-02	8.03E-01	-7.67E-02	6.81E-01	WT N 14 dpi	2M	Siroheme synthase (AHRD V3.3 ***W8SGE9_TOBAC)	GO:0006779|GO:0008168|GO:0055114|GO:0008152|GO:0008168|GO:0008152|GO:0008168
Solyc01g107060.2	**-1.30E+00**	**1.17E-07**	-5.09E-01	8.84E-03	-1.56E-01	3.93E-01	-1.96E-01	2.87E-01	WT N 14 dpi	L	LOW QUALITY:3beta-hydroxysteroid- dehydrogenase/decarboxylase isoform 2 (AHRD V3.3 --* HSDD2_ARATH)	
Solyc04g016060.1	**-1.31E+00**	**5.62E-08**	-7.33E-01	2.59E-04	6.66E-01	7.11E-04	-9.39E-01	1.15E-05	WT N 14 dpi	E	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT2G41660.1)	
Solyc11g067040.2	**-1.31E+00**	**4.29E-03**	-1.15E+00	1.05E-02	-4.79E-01	2.62E-01	-1.48E-01	7.26E-01	WT N 14 dpi	H	Cytoplasmic tRNA 2-thiolation protein 1 (AHRD V3.3 --* A0A059BW08_EUCGR)	GO:0000166|GO:0005524|GO:0005737|GO:0008033|GO:0016879
Solyc05g053690.2	**-1.31E+00**	**3.75E-04**	-4.98E-01	1.33E-01	1.77E-01	5.85E-01	-1.48E-01	6.49E-01	WT N 14 dpi	P	Ubiquitin carboxyl-terminal hydrolase 2 (AHRD V3.3 *** A0A0B2QQX6_GLYSO)	GO:0006511|GO:0036459|GO:0008270|GO:0008270
Solyc01g100600.3	**-1.32E+00**	**8.24E-03**	2.44E-01	6.00E-01	-1.20E-01	7.96E-01	1.55E-01	7.38E-01	WT N 14 dpi	E	Kelch repeat protein, putative (AHRD V3.3 *** B9RFJ9_RICCO)	GO:0005515
Solyc05g012910.3	**-1.32E+00**	**4.02E-04**	-8.13E-01	1.87E-02	-5.56E-01	9.80E-02	-4.80E-01	1.51E-01	WT N 14 dpi	D	NBS-LRR resistance protein-like protein(AHRD V3.3 *-* A1Y9Q6_9SOLN)	GO:0043531
Solyc02g077950.2	**-1.32E+00**	**6.36E-09**	-7.95E-01	2.52E-05	-5.14E-01	2.77E-03	-9.93E-01	9.56E-07	WT N 14 dpi	DNA	Dof zinc finger protein5	GO:0003677|GO:0006355

Solyc02g084280.3	**-1.32E+00**	**8.38E-03**	-5.67E-01	2.31E-01	9.84E-02	8.33E-01	-3.90E-01	4.07E-01	WT N 14 dpi	RNA	Nuclear pore complex protein Nup98b(AHRD V3.3 *-* W6JLG1_NICBE)	
Solyc10g005030.3	**-1.32E+00**	**9.59E-07**	4.98E-01	2.37E-02	2.65E-01	2.12E-01	-2.39E-01	2.59E-01	WT N 14 dpi	T	Pseudo-response regulator 9 (AHRD V3.3 *** D0PPG9_CASSA)	GO:0000160|GO:0005515|GO:0005515
Solyc02g079510.3	**-1.32E+00**	**1.45E-09**	-7.76E-01	1.34E-05	2.90E-01	5.61E-02	-9.35E-01	8.10E-07	WT N 14 dpi	OX	Peroxidase (AHRD V1 **** Q50LG4_TOBAC)%3B contains Interpro domain(s) IPR019793 Peroxidases heam-ligand binding site IPR019794 Peroxidase%2C active site IPR002016 Haem peroxidase%2C plant/fungal/bacterial	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO: 0004601|GO:0042744
Solyc02g005280.1	**-1.33E+00**	**9.77E-04**	-6.83E-01	6.61E-02	2.01E-01	5.78E-01	-3.10E-01	3.92E-01	WT N 14 dpi	RNA	Pentatricopeptide repeat superfamilyprotein, putative (AHRD V3.3 *** A0A061E854_THECC)	
Solyc09g007765.1	**-1.33E+00**	**3.00E-03**	-8.15E-01	5.47E-02	7.32E-01	8.23E-02	-9.02E-01	3.50E-02	WT N 14 dpi	TR	Aquaporin-like protein (AHRD V3.3 *-*A0A103XNC2_CYNCS)	GO:0005215|GO:0006810|GO:0016020
Solyc01g096410.3	**-1.33E+00**	**1.16E-04**	-9.60E-01	3.10E-03	4.28E-02	8.85E-01	-7.62E-01	1.55E-02	WT N 14 dpi	S	Phosphatidylinositol-4-phosphate 5-kinase (AHRD V3.3 *** J7K3W0_TOBAC)	GO:0005524|GO:0016308|GO:0016307|GO:0046488|GO:0016307|GO:0046488
Solyc06g064610.1	**-1.34E+00**	**4.99E-08**	-1.87E-01	2.98E-01	-7.23E-01	3.55E-04	-8.45E-01	5.77E-05	WT N 14 dpi	CS	LOW QUALITY:Glucan endo-1,3-beta-glucosidase (AHRD V3.3 -** A0A0B0PK92_GOSAR)	
Solyc08g066310.2	**-1.34E+00**	**5.06E-08**	-2.23E-01	2.17E-01	-7.80E-02	6.62E-01	-8.89E-01	3.08E-05	WT N 14 dpi	S	Receptor-like protein kinase (AHRD V3.3 *** A0A0K9PZN1_ZOSMR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc11g007803.1	**-1.34E+00**	**5.30E-03**	-7.33E-01	1.07E-01	2.41E-01	5.88E-01	-3.30E-01	4.59E-01	WT N 14 dpi	RNA	Ribonucleases P/MRP protein subunitPOP1, putative (AHRD V3.3 *-* A0A061DRG1_THECC)	
Solyc09g059950.3	**-1.34E+00**	**2.17E-03**	-1.06E-02	9.79E-01	6.50E-01	1.10E-01	6.47E-01	1.12E-01	WT N 14 dpi	AM	Amino acid--[acyl-carrier-protein] ligase (AHRD V3.3 *** A0A0B0MIR3_GOSAR)	
Solyc07g026710.2	**-1.34E+00**	**2.26E-03**	-8.69E-01	3.68E-02	1.97E-01	6.22E-01	-2.22E-01	5.79E-01	WT N 14 dpi	DNA	Transposon protein, putative, Mutator sub-class (AHRD V3.3 *-* Q7XE42_ORYSJ)	
Solyc06g083230.3	**-1.34E+00**	**4.63E-07**	-8.38E-01	3.09E-04	-5.62E-02	7.82E-01	2.19E-02	9.14E-01	WT N 14 dpi	2M	GTP cyclohydrolase 1	GO:0003934|GO:0005737|GO:0046654
Solyc05g054870.3	**-1.35E+00**	**4.77E-03**	-8.77E-01	5.53E-02	1.72E-01	6.97E-01	-3.53E-01	4.26E-01	WT N 14 dpi	RNA	U4/U6 small nuclear Prp3-like ribonucleoprotein (AHRD V3.3 *-*G7IF06_MEDTR)	
Solyc04g078470.3	**-1.35E+00**	**1.28E-04**	2.02E-01	5.07E-01	1.08E+00	1.40E-03	-1.38E-01	6.51E-01	WT N 14 dpi	G	D-type cyclin-3	GO:0005634
Solyc12g036140.2	**-1.35E+00**	**6.46E-03**	-6.26E-01	1.82E-01	-2.42E-01	6.00E-01	-4.05E-01	3.83E-01	WT N 14 dpi	TR	Multidrug resistance protein ABC transporter family protein (AHRD V3.3 *-*A0A072V4E0_MEDTR)	
Solyc04g078500.1	**-1.36E+00**	**2.66E-04**	-4.11E-01	2.12E-01	-5.76E-01	8.47E-02	5.62E-01	9.22E-02	WT N 14 dpi	G	cyclinJ18	
Solyc10g008655.1	**-1.36E+00**	**8.65E-05**	-8.78E-01	5.76E-03	-9.74E-01	2.57E-03	-6.83E-01	2.72E-02	WT N 14 dpi	2M	Anthocyanin 5-aromatic acyltransferase (AHRD V3.3 *-* A0A0B2SWD3_GLYSO)	GO:0016747
Solyc10g084095.1	**-1.36E+00**	**6.96E-03**	-1.23E+00	1.31E-02	-2.87E-01	5.41E-01	1.19E-02	9.80E-01	WT N 14 dpi	K	Kinase-like protein (AHRD V3.3 --* A8BLL9_PRUAV)	
Solyc08g007160.3	**-1.36E+00**	**4.17E-07**	-9.95E-01	4.27E-05	2.89E-02	8.88E-01	-4.71E-02	8.18E-01	WT N 14 dpi	S	Calcineurin B-like protein (AHRD V3.3 ***A1XCM9_POPEU)	GO:0005509|GO:0005515|GO:0005515
Solyc10g084380.1	**-1.36E+00**	**1.16E-03**	-1.66E-01	6.59E-01	4.47E-01	2.41E-01	-7.66E-02	8.39E-01	WT N 14 dpi	T	WRKY transcription factor 44	GO:0003700|GO:0006355|GO:0043565
Solyc10g086430.2	**-1.36E+00**	**1.33E-04**	-2.50E-01	4.18E-01	-8.50E-02	7.82E-01	-3.37E-01	2.77E-01	WT N 14 dpi	H	Transducin/WD-like repeat-protein (AHRDV3.3 *** G7L3F0_MEDTR)	GO:0005515
Solyc12g098757.1	**-1.37E+00**	**1.16E-03**	-1.96E-01	6.05E-01	-7.82E-01	4.65E-02	-3.20E-01	4.00E-01	WT N 14 dpi	CS	Extensin-like protein (AHRD V3.3 *-* Q7DLZ6_VIGUN)	GO:0005199|GO:0009664
Solyc01g068560.3	**-1.37E+00**	**9.84E-06**	-7.63E-01	5.10E-03	-1.05E-01	6.78E-01	-6.94E-01	9.90E-03	WT N 14 dpi	NA	Agglutinin-like protein ALA1, putativeisoform 3 (AHRD V3.3 --* A0A061FRH3_THECC)	

Solyc01g109970.3	**-1.37E+00**	**9.76E-03**	-1.19E+00	2.21E-02	-3.85E-01	4.39E-01	5.69E-01	2.56E-01	WT N 14 dpi	G	SNF2 domain-containing protein / helicasedomain-containing protein (AHRD V3.3 *** AT2G16390.2)	GO:0005524
Solyc09g011170.3	**-1.37E+00**	**5.47E-03**	-2.13E-01	6.41E-01	5.24E-01	2.56E-01	-3.41E-01	4.56E-01	WT N 14 dpi	NA	Prf interactor 30137	GO:0046983
Solyc12g008530.2	**-1.37E+00**	**3.80E-08**	-8.81E-01	3.85E-05	-1.34E-01	4.58E-01	-4.92E-01	1.02E-02	WT N 14 dpi	CS	Pectinesterase (AHRD V3.3 *** K4DBU1_SOLLC)	GO:0005618|GO:0030599|GO:0042545
Solyc04g010135.1	**-1.38E+00**	**3.82E-05**	-8.53E-01	4.91E-03	-3.46E-01	2.23E-01	-6.31E-01	3.14E-02	WT N 14 dpi	H	myo-inositol polyphosphate 5-phosphatase2 (AHRD V3.3 -- * AT4G18010.2)	
Solyc08g006750.3	**-1.38E+00**	**3.12E-07**	-8.12E-01	4.50E-04	1.04E+00	2.27E-05	5.48E-01	1.17E-02	WT N 14 dpi	AM	Aromatic amino acid decarboxylase 2 (AHRD V3.3 *** Q1KSC4_SOLLC)	GO:0003824|GO:0016831|GO:0016831
Solyc06g064550.3	**-1.38E+00**	**4.80E-05**	-4.37E-01	1.35E-01	5.35E-01	7.04E-02	-1.43E-01	6.19E-01	WT N 14 dpi	AM	Aspartokinase-homoserine dehydrogenase (AHRD V3.3 *** O63067_SOYBN)	GO:0004072|GO:0008652|GO:0006520|GO:0055114|GO:0006520|GO:0055114
Solyc04g010200.1	**-1.38E+00**	**9.69E-03**	-1.14E+00	2.95E-02	1.06E+00	4.16E-02	8.23E-01	1.09E-01	WT N 14 dpi	TR	ABC transporter G family member (AHRD V3.3 *** A0A0K9NPK2_ZOSMR)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc04g011600.3	**-1.39E+00**	**1.02E-03**	-7.43E-01	5.79E-02	1.25E+00	2.51E-03	9.25E-01	2.04E-02	WT N 14 dpi	CS	Glycerol-3-phosphate acyltransferase(AHRD V3.3 *** G7KGS4_MEDTR)	GO:0008152|GO:0016746
Solyc05g009420.1	**-1.39E+00**	**1.10E-06**	-3.07E-01	1.74E-01	9.33E-02	6.75E-01	3.61E-01	1.13E-01	WT N 14 dpi	NA	Transmembrane protein, putative (AHRD V3.3 *** G7K1J5_MEDTR)	
Solyc09g018550.1	**-1.40E+00**	**2.16E-03**	-7.65E-01	7.32E-02	4.51E-01	2.81E-01	4.42E-01	2.91E-01	WT N 14 dpi	RNA	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein(AHRD V3.3 --* AT5G46870.2)	
Solyc02g021430.1	**-1.40E+00**	**2.21E-04**	-5.38E-01	1.11E-01	-9.03E-01	1.03E-02	1.60E-01	6.27E-01	WT N 14 dpi	T	Mitochondrial transcription terminationfactor family protein (AHRD V3.3 *** AT2G34620.1)	GO:0003690|GO:0006355
Solyc01g079410.3	**-1.41E+00**	**1.74E-05**	-4.90E-01	7.92E-02	9.60E-01	1.41E-03	-1.43E-01	5.99E-01	WT N 14 dpi	G	Calcium-dependent phosphotriesterasesuperfamily protein (AHRD V3.3 *** A0A061DRE0_THECC)	
Solyc06g072710.3	**-1.42E+00**	**9.37E-06**	-2.05E-01	4.34E-01	-1.96E-01	4.55E-01	-5.32E-01	4.98E-02	WT N 14 dpi	T	Sigma factor (AHRD V3.3 *** Q9SLX3_TOBAC)	GO:0003677|GO:0003700|GO:0006352|GO:0006355|GO:0016987
Solyc07g052680.1	**-1.43E+00**	**4.80E-04**	-6.55E-02	8.56E-01	-1.41E-01	6.97E-01	-6.53E-01	7.89E-02	WT N 14 dpi	TR	ATP binding microtubule motor family protein (AHRD V3.3 --* AT3G51150.4)	
Solyc02g092450.3	**-1.43E+00**	**8.89E-04**	1.07E+00	9.40E-03	6.72E-01	8.85E-02	-5.09E-02	8.94E-01	WT N 14 dpi	TR	Calcium-transporting ATPase (AHRD V3.3 *** M1BXI4_SOLTU)	GO:0000166|GO:0000166|GO:0046872|GO:0000166|GO:0046872
Solyc05g056330.3	**-1.43E+00**	**8.87E-05**	-4.35E-01	1.70E-01	2.72E-01	3.86E-01	-3.28E-01	2.98E-01	WT N 14 dpi	DNA	Transposon protein, putative, CACTA,En/Spm sub-class (AHRD V3.3 *-* Q2QRE9_ORYSJ)	
Solyc01g091700.3	**-1.43E+00**	**5.29E-07**	-8.01E-01	1.01E-03	-2.47E-02	9.10E-01	1.53E+00	1.69E-07	WT N 14 dpi	P	F-box family protein (AHRD V3.3 *** B9IC61_POPTR)	GO:0005515
Solyc05g007290.2	**-1.43E+00**	**9.03E-08**	-6.15E-01	4.09E-03	5.56E-03	9.77E-01	-7.73E-01	5.28E-04	WT N 14 dpi	DNA	Regulator of chromosome condensation(RCC1) family protein (AHRD V3.3 *** G7K368_MEDTR)	GO:0046872
Solyc09g092480.1	**-1.44E+00**	**2.83E-04**	-5.26E-01	1.36E-01	-3.92E-01	2.63E-01	-9.45E-01	1.05E-02	WT N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CWS4_SOLLC)	GO:0008152|GO:0016758
Solyc01g094600.2	**-1.44E+00**	**2.58E-03**	-1.90E-01	6.63E-01	-6.08E-01	1.70E-01	-9.38E-01	3.87E-02	WT N 14 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9RDS2_RICCO)	GO:0005515
Solyc02g089160.3	**-1.44E+00**	**5.47E-03**	-4.36E-01	3.67E-01	-2.06E-01	6.68E-01	-2.27E-01	6.36E-01	WT N 14 dpi	2M	dwarf	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc12g007210.2	**-1.45E+00**	**9.66E-05**	-3.99E-01	2.16E-01	5.90E-01	7.22E-02	2.07E-01	5.16E-01	WT N 14 dpi	CS	Rac-like GTP binding protein (AHRD V3.3 *** O65062_PICMA)	GO:0005525|GO:0005525|GO:0007264|GO:0005525|GO:0007264
Solyc06g068215.1	**-1.45E+00**	**6.92E-03**	-1.34E+00	1.21E-02	-7.71E-01	1.31E-01	-9.44E-01	6.75E-02	WT N 14 dpi	TR	Myosin heavy chain-like protein (AHRD V3.3 --* A0A072UED1_MEDTR)	

Solyc04g058160.2	**-1.47E+00**	**1.03E-07**	-5.46E-01	1.16E-02	-5.98E-01	6.30E-03	1.02E+00	2.73E-05	WT N 14 dpi	NA	Calcium-binding protein (AHRD V3.3 *** A0A1B0WUT3_SOLHA)	GO:0005509
Solyc07g054560.1	**-1.47E+00**	**7.72E-04**	3.28E-02	9.33E-01	5.34E-01	1.77E-01	-4.76E-02	9.02E-01	WT N 14 dpi	NA	LOW QUALITY:CK25 (AHRD V3.3 *** Q1W1G0_TOBAC)	
Solyc01g079100.3	**-1.47E+00**	**9.59E-03**	1.24E-01	8.15E-01	7.04E-01	1.92E-01	5.54E-01	3.02E-01	WT N 14 dpi	P	S-acyltransferase (AHRD V3.3 *** K4AXF6_SOLLC)	
Solyc02g078400.3	**-1.47E+00**	**3.56E-03**	2.47E-01	5.95E-01	2.50E-01	5.91E-01	-9.83E-01	4.20E-02	WT N 14 dpi	N	allantoinase (AHRD V3.3 *** AT4G04955.1)	GO:0000256|GO:0004038|GO:0008270|GO:0050897|GO:0016787|GO:0016787
Solyc07g064820.1	**-1.49E+00**	**4.20E-04**	-7.85E-01	4.23E-02	7.41E-02	8.42E-01	-2.53E-01	4.97E-01	WT N 14 dpi	K	LOW QUALITY:MAP kinase kinase kinase59	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc09g097930.3	**-1.49E+00**	**1.72E-03**	-1.81E-01	6.74E-01	-7.97E-01	7.29E-02	-7.72E-01	8.17E-02	WT N 14 dpi	DNA	dCTP pyrophosphatase 1 (AHRD V3.3 *** A0A0B0PZH5_GOSAR)	GO:0047429
Solyc01g005860.2	**-1.49E+00**	**8.46E-03**	-5.69E-01	2.87E-01	-1.41E+00	1.22E-02	-4.32E-01	4.17E-01	WT N 14 dpi	P	LOW QUALITY:WD repeat protein (AHRDV3.3 --* Q84VB4_ORYSJ)	
Solyc01g079570.3	**-1.50E+00**	**1.62E-06**	-3.33E-01	1.81E-01	-7.55E-01	4.51E-03	-9.62E-01	5.22E-04	WT N 14 dpi	CS	Beta-D-xylosidase family protein (AHRD V3.3 *** B9HWX2_POPTR)	GO:0004553|GO:0005975
Solyc02g079550.2	**-1.50E+00**	**8.36E-04**	-7.67E-01	6.47E-02	5.27E-01	1.97E-01	-3.93E-01	3.32E-01	WT N 14 dpi	K	Serine/threonine-protein kinase (AHRDV3.3 *** B9H1U5_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc02g021270.3	**-1.51E+00**	**3.45E-03**	-1.24E-01	7.94E-01	-7.60E-02	8.72E-01	-4.03E-01	3.99E-01	WT N 14 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9RY36_RICCO)	GO:0005515
Solyc12g008400.2	**-1.51E+00**	**3.15E-03**	-5.73E-01	2.28E-01	-3.26E-01	4.89E-01	2.53E-02	9.57E-01	WT N 14 dpi	S	Receptor-kinase, putative (AHRD V3.3 *-*B9RVA8_RICCO)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc07g006850.2	**-1.51E+00**	**1.83E-07**	-8.82E-01	3.52E-04	-3.61E-01	1.04E-01	-7.13E-01	2.64E-03	WT N 14 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRDV3.3 *-* K4CBF6_SOLLC)	GO:0004553|GO:0005975|GO:0005618|GO:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc08g076610.3	**-1.52E+00**	**1.60E-04**	1.62E-01	6.41E-01	9.81E-01	8.47E-03	7.01E-01	5.18E-02	WT N 14 dpi	DNA	Cell cycle checkpoint protein RAD1 (AHRD GO:0005634V3.3 *-* W9RDU4_9ROSA)	
Solyc08g082130.3	**-1.53E+00**	**4.04E-04**	-2.68E-01	4.83E-01	-3.79E-01	3.22E-01	-4.68E-01	2.24E-01	WT N 14 dpi	T	DNA-directed RNA polymerase subunit beta' (AHRD V3.3 --* RPOC1_CUCSA)	
Solyc01g007895.1	**-1.53E+00**	**2.66E-11**	-9.16E-01	4.83E-07	-8.22E-02	5.55E-01	-5.06E-01	1.08E-03	WT N 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-bindingsuperfamily protein (AHRD V3.3 *-* AT1G31050.6)	GO:0046983
Solyc03g026040.3	**-1.53E+00**	**3.18E-04**	-8.44E-01	3.05E-02	7.93E-01	4.10E-02	2.61E-01	4.85E-01	WT N 14 dpi	PMI	LRR receptor-like kinase family protein (AHRD V3.3 *** A0A072VNY9_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc01g108570.3	**-1.53E+00**	**1.79E-04**	-5.24E-01	1.47E-01	3.96E-01	2.69E-01	-5.33E-01	1.41E-01	WT N 14 dpi	H	Gibberellin receptor GID1L2 IPR013094Alpha_beta hydrolase fold-3	GO:0008152|GO:0016787
Solyc10g081780.2	**-1.55E+00**	**5.12E-03**	-3.62E-01	4.80E-01	-3.81E-01	4.58E-01	4.72E-01	3.60E-01	WT N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT2G35910.1)	GO:0005515|GO:0008270
Solyc02g038690.1	**-1.55E+00**	**6.21E-04**	-6.55E-01	1.12E-01	6.35E-01	1.23E-01	5.12E-01	2.10E-01	WT N 14 dpi	DNA	Histone H2B (AHRD V3.3 ***K4B5W3_SOLLC)	GO:0000786|GO:0003677|GO:0003677|G O:0003677
Solyc02g014460.3	**-1.55E+00**	**1.88E-08**	-9.70E-01	3.47E-05	-4.66E-02	8.12E-01	-7.93E-01	3.80E-04	WT N 14 dpi	P	WD40 repeat-containing protein (AHRD V3.3 *** A0A103XDG9_CYNCS)	GO:0005515|GO:0006974|GO:0006974
Solyc03g097170.3	**-1.55E+00**	**2.53E-05**	-6.15E-01	5.34E-02	8.28E-01	1.13E-02	4.71E-01	1.33E-01	WT N 14 dpi	D	Cinnamoyl-CoA reductase, putative(AHRD V3.3 *** B9S247_RICCO)	GO:0003854|GO:0006694|GO:0016616|G O:0055114

Solyc12g099580.2	**-1.56E+00**	**9.25E-08**	-8.11E-01	7.50E-04	2.98E-01	1.71E-01	-9.24E-01	1.87E-04	WT N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4DHX9_SOLLC)	GO:0016020|GO:0016021|GO:0016021|G O:0022857|GO:0016021|GO:0022857
Solyc09g074430.3	**-1.56E+00**	**2.38E-06**	-8.18E-01	3.94E-03	-5.50E-01	4.30E-02	-9.26E-01	1.37E-03	WT N 14 dpi	OX	SI Monooxygenase	GO:0004499|GO:0050660|GO:0050661|G O:0055114|GO:0016491|GO:0055114|GO: 0016491|GO:0055114
Solyc01g007170.3	**-1.57E+00**	**6.91E-03**	-4.16E-01	4.42E-01	-6.98E-02	8.97E-01	-3.27E-01	5.45E-01	WT N 14 dpi	H	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT3G03680.1)	GO:0005515
Solyc02g077600.3	**-1.57E+00**	**2.42E-04**	-8.95E-01	2.22E-02	-3.61E-01	3.36E-01	-6.29E-01	9.94E-02	WT N 14 dpi	E	Guanylate-binding family protein (AHRD V3.3 *** AT5G46070.1)	GO:0003924|GO:0005525|GO:0005525|G O:0005525
Solyc08g076290.3	**-1.57E+00**	**1.65E-05**	-3.67E-01	2.27E-01	-3.61E-01	2.35E-01	-6.64E-01	3.43E-02	WT N 14 dpi	NA	Inner membrane yohK (AHRD V3.3 *** A0A0B0N2P7_GOSAR)	
Solyc06g053480.3	**-1.58E+00**	**2.24E-13**	-8.89E-01	3.63E-08	-5.99E-01	2.02E-05	-8.54E-01	7.46E-08	WT N 14 dpi	L	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A0V0I9I2_SOLCH)	GO:0006631|GO:0045300|GO:0055114|G O:0006633|GO:0016491|GO:0055114|GO: 0006633|GO:0016491|GO:0055114
Solyc09g008840.3	**-1.58E+00**	**3.89E-04**	-5.05E-01	2.05E-01	-5.27E-01	1.87E-01	-6.44E-01	1.10E-01	WT N 14 dpi	C	Pyruvate kinase family protein (AHRD V3.3 *** AT3G52990.1)	GO:0000287|GO:0004743|GO:0006096|G O:0030955|GO:0003824|GO:0003824
Solyc01g105770.2	**-1.60E+00**	**2.44E-03**	-7.86E-01	1.10E-01	1.09E+00	2.99E-02	4.90E-01	3.12E-01	WT N 14 dpi	0	LOW QUALITY:Leguminosin group485secreted peptide (AHRD V3.3 *** A0A072UVS4_MEDTR)	
Solyc03g019890.3	**-1.61E+00**	**2.53E-03**	-1.03E-01	8.31E-01	-9.93E-02	8.38E-01	8.41E-02	8.62E-01	WT N 14 dpi	C	beta-galactosidase 7	GO:0004553|GO:0005975|GO:0005975|G O:0005975
Solyc09g064170.1	**-1.61E+00**	**2.12E-08**	-9.19E-01	1.16E-04	-5.23E-01	1.59E-02	-3.29E-02	8.72E-01	WT N 14 dpi	RNA	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein(AHRD V3.3 --* AT1G22910.3)	
Solyc05g051610.2	**-1.62E+00**	**1.70E-03**	-1.13E+00	2.15E-02	-1.04E+00	3.26E-02	-1.20E-01	7.97E-01	WT N 14 dpi	K	Kinase family protein (AHRD V3.3 ***D7MGJ0_ARALL)	GO:0004672|GO:0005524|GO:0006468|G O:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc04g071590.3	**-1.62E+00**	**5.58E-05**	-6.41E-01	6.84E-02	1.72E+00	2.66E-05	1.29E+00	7.69E-04	WT N 14 dpi	STR	Abscisic acid stress ripening 3%2C ASR3	GO:0006950
Solyc12g049150.1	**-1.63E+00**	**7.62E-03**	-5.55E-01	3.33E-01	-2.58E-01	6.50E-01	-5.10E-01	3.73E-01	WT N 14 dpi	CS	Extensin-like protein Ext1 (AHRD V3.3 *** Q8VWM5_SOLLC)	
Solyc10g081260.2	**-1.63E+00**	**2.43E-10**	-7.99E-01	4.58E-05	-5.06E-01	4.71E-03	-8.04E-01	4.26E-05	WT N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 ***K4D313_SOLLC)	GO:0006855|GO:0015238|GO:0015297|G O:0016020|GO:0055085
Solyc12g017970.1	**-1.64E+00**	**4.55E-05**	-2.28E-01	5.01E-01	-4.46E-01	1.93E-01	-4.62E-01	1.78E-01	WT N 14 dpi	NA	LOW QUALITY:GPI-anchored adhesin-likeprotein (AHRD V3.3 *** AT2G43990.1)	
Solyc02g067970.3	**-1.64E+00**	**5.90E-03**	4.03E-01	4.67E-01	-8.00E-01	1.55E-01	-4.76E-01	3.91E-01	WT N 14 dpi	DNA	Zinc finger family protein, putative (AHRDV3.3 *** A0A061EDJ4_THECC)	GO:0005515|GO:0008270
Solyc03g083440.3	**-1.65E+00**	**2.01E-08**	-9.90E-01	5.86E-05	-3.08E-01	1.48E-01	-5.56E-01	1.23E-02	WT N 14 dpi	N	Glutamate synthase, putative (AHRD V3.3 *** B9RII5_RICCO)	GO:0003824|GO:0005506|GO:0006537|G O:0010181|GO:0016040|GO:0045181|GO: 0050660|GO:0055114|GO:0005506|GO:0 006537|GO:0010181|GO:0016040|GO:00 45181|GO:0050660|GO:0055114
Solyc12g098780.2	**-1.65E+00**	**1.32E-03**	-3.23E-01	4.88E-01	-1.27E+00	1.04E-02	-1.08E+00	2.69E-02	WT N 14 dpi	0	#REF!	GO:0005199|GO:0009664
Solyc12g017350.2	**-1.66E+00**	**6.17E-03**	-1.51E+00	1.16E-02	-1.41E+00	1.76E-02	-1.36E+00	2.20E-02	WT N 14 dpi	TR	Cation diffusion facilitator 9	GO:0006812|GO:0008324|GO:0016021|G O:0055085

Solyc09g065420.3	**-1.66E+00**	**1.33E-03**	-1.25E+00	1.18E-02	1.47E+00	3.78E-03	1.19E+00	1.61E-02	WT N 14 dpi	L	Lipid transfer protein (AHRD V3.3 ***G7K520_MEDTR)	GO:0006869|GO:0008289
Solyc10g005330.3	**-1.67E+00**	**5.65E-03**	-1.11E-01	8.42E-01	-7.76E-01	1.73E-01	-7.26E-02	8.97E-01	WT N 14 dpi	DNA	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9GU68_POPTR)	GO:0003677|GO:0008289|GO:0008289
Solyc06g008510.3	**-1.68E+00**	**1.98E-03**	2.68E-01	5.87E-01	1.64E-01	7.39E-01	-2.65E-01	5.91E-01	WT N 14 dpi	CS	CDT1-like protein a, chloroplastic (AHRDV3.3 *** A0A0B0P9Z8_GOSAR)	
Solyc11g007190.1	**-1.68E+00**	**9.64E-08**	-6.32E-01	1.06E-02	-7.39E-01	3.43E-03	8.75E-02	7.06E-01	WT N 14 dpi	STR	ARM repeat superfamily protein (AHRD V3.3 --* AT3G03970.6)	
Solyc01g066850.3	**-1.68E+00**	**1.50E-04**	-1.33E-01	7.29E-01	2.08E-01	5.87E-01	2.63E-01	4.93E-01	WT N 14 dpi	H	WAT1-related protein (AHRD V3.3 ***K4AWT5_SOLLC)	GO:0016020|GO:0016021|GO:0016021|G O:0022857|GO:0016021|GO:0022857
Solyc01g099870.2	**-1.70E+00**	**1.44E-04**	-3.97E-01	3.07E-01	1.16E-01	7.64E-01	-7.42E-01	6.23E-02	WT N 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *-* M1CB29_SOLTU)	GO:0016021
Solyc06g054030.2	**-1.70E+00**	**5.38E-03**	1.79E-01	7.51E-01	1.11E+00	5.71E-02	5.40E-01	3.43E-01	WT N 14 dpi	NA	LOW QUALITY:Protease inhibitor/seed storage/lipid transfer family protein (AHRDV3.3 *** B9NBN8_POPTR)	
Solyc03g005460.3	**-1.70E+00**	**6.92E-04**	-1.10E-01	8.06E-01	5.96E-02	8.94E-01	-6.33E-01	1.64E-01	WT N 14 dpi	DNA	Helicase protein with RING/U-box domain-containing protein (AHRD V3.3 *** AT5G43530.1)	GO:0003676|GO:0008270|GO:0016818|G O:0005515|GO:0008270|GO:0005515|GO:0008270
Solyc03g117050.3	**-1.71E+00**	**2.87E-11**	-3.07E-01	5.72E-02	-2.70E-03	9.86E-01	-8.87E-01	4.84E-06	WT N 14 dpi	TR	NOD26-like intrinsic protein 6.1	GO:0005215|GO:0006810|GO:0016020
Solyc05g055690.2	**-1.72E+00**	**8.67E-03**	2.64E-01	6.66E-01	5.56E-01	3.66E-01	-6.01E-01	3.29E-01	WT N 14 dpi	TR	Protein transport protein Sec24-like family(AHRD V3.3 *** A0A151TQ51_CAJCA)	GO:0006886|GO:0006888|GO:0008270|G O:0030127|GO:0006886|GO:0006888|GO:0030127|GO:0006886|GO:0006888|GO:0030127
Solyc12g014360.2	**-1.74E+00**	**1.63E-06**	-5.86E-02	8.37E-01	-1.48E-01	6.04E-01	-4.56E-01	1.18E-01	WT N 14 dpi	CS	protein trichome birefringence-like 41	
Solyc12g007250.1	**-1.75E+00**	**7.20E-03**	-9.03E-01	1.44E-01	-1.05E+00	9.28E-02	-1.68E-01	7.82E-01	WT N 14 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRDV3.3 *** K4DBR2_SOLLC)	GO:0004553|GO:0005975|GO:0005618|G O:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc04g011870.1	**-1.75E+00**	**1.78E-03**	-9.03E-01	8.40E-02	-1.06E-01	8.34E-01	1.84E-01	7.18E-01	WT N 14 dpi	OX	Glutaredoxin family protein (AHRD V3.3 *** B9I9V9_POPTR)	GO:0009055|GO:0015035|GO:0045454
Solyc08g068710.1	**-1.75E+00**	**1.74E-04**	-8.92E-01	3.45E-02	4.81E-01	2.40E-01	1.20E+00	6.02E-03	WT N 14 dpi	STR	Tyramine n-hydroxycinnamoyl transferase (AHRD V3.3 *** Q5D8C0_CAPAN)	GO:0008080
Solyc12g009840.2	**-1.76E+00**	**4.42E-03**	-4.29E-01	4.53E-01	-4.83E-01	3.99E-01	-9.87E-01	9.13E-02	WT N 14 dpi	E	Pyrophosphate-energized vacuolar membrane proton pump (AHRD V3.3 *** AVP_VIGRR)	GO:0004427|GO:0009678|GO:0015992|G O:0016020
Solyc10g006720.3	**-1.77E+00**	**5.24E-05**	-8.30E-01	3.21E-02	9.56E-01	1.49E-02	-6.60E-02	8.58E-01	WT N 14 dpi	K	Serine/threonine-protein kinase (AHRDV3.3 *** M1CC72_SOLTU)	GO:0004672|GO:0005524|GO:0006468|G O:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g084780.3	**-1.78E+00**	**6.25E-03**	6.81E-01	2.64E-01	2.85E-01	6.37E-01	-4.82E-02	9.36E-01	WT N 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4BAZ3_SOLLC)	GO:0004601|GO:0006979|GO:0020037|G O:0055114|GO:0004601|GO:0042744|GO: 0004601|GO:0042744
Solyc08g013670.3	**-1.78E+00**	**6.03E-03**	-1.34E+00	3.30E-02	-7.20E-01	2.37E-01	3.93E-01	5.14E-01	WT N 14 dpi	E	photosystem I reaction center subunit	GO:0009522|GO:0015979
Solyc02g084315.1	**-1.78E+00**	**1.03E-03**	-9.62E-01	5.64E-02	-1.00E+00	4.77E-02	-6.50E-01	1.89E-01	WT N 14 dpi	G	embryo defective 2410 (AHRD V3.3 --* AT2G25660.4)	
Solyc04g014310.1	**-1.80E+00**	**2.73E-03**	-7.47E-01	1.81E-01	1.35E+00	2.01E-02	7.92E-01	1.57E-01	WT N 14 dpi	STR	LOW QUALITY:Proteasome subunit alphatype-4 (AHRD V3.3 --* PSA4_SPIOL)	

Solyc04g079460.1	**-1.81E+00**	**6.27E-03**	-1.33E+00	3.75E-02	-7.11E-01	2.52E-01	-4.66E-01	4.50E-01	WT N 14 dpi	P	Serpin-like protein (AHRD V3.3 *-* Q8GT65_CITPA)	GO:0005615
Solyc01g006530.1	**-1.81E+00**	**1.98E-03**	6.90E-01	2.01E-01	2.22E+00	2.73E-04	2.78E+00	1.68E-05	WT N 14 dpi	K	Serine/threonine-protein kinase (AHRDV3.3 *** K4ASL9_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc07g062470.3	**-1.82E+00**	**1.36E-04**	-1.36E-01	7.40E-01	2.22E-01	5.89E-01	-9.59E-01	2.61E-02	WT N 14 dpi	G	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640)(AHRD V3.3 *** AT2G42610.2)	
Solyc09g092710.3	**-1.83E+00**	**2.41E-03**	-1.23E+00	3.29E-02	-1.32E+00	2.23E-02	-5.07E-01	3.61E-01	WT N 14 dpi	D	Glycine-rich protein (AHRD V3.3 *** D2K2T8_TOBAC)	
Solyc02g077930.2	**-1.83E+00**	**7.82E-03**	-6.00E-01	3.54E-01	3.78E-01	5.57E-01	1.13E-01	8.61E-01	WT N 14 dpi	S	LOW QUALITY:Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRDV3.3 --* AT3G07960.4)	
Solyc01g005850.2	**-1.84E+00**	**1.79E-03**	-8.21E-01	1.31E-01	-9.62E-01	7.95E-02	-1.66E-01	7.55E-01	WT N 14 dpi	CS	LOW QUALITY:Extensin-like protein Dif54 (AHRD V3.3 *** Q43505_SOLLC)	
Solyc07g006630.3	**-1.84E+00**	**7.07E-10**	1.81E-01	3.58E-01	3.26E-01	1.05E-01	-4.13E-02	8.33E-01	WT N 14 dpi	G	CONSTANS-like protein (AHRD V3.3 *** B2MW87_SOLLC)	GO:0005515|GO:0005622|GO:0008270|GO:0005622|GO:0008270
Solyc01g094890.3	**-1.84E+00**	**2.14E-08**	-4.87E-01	4.52E-02	4.53E-01	6.12E-02	-7.52E-01	3.21E-03	WT N 14 dpi	TR	Ferric reductase oxidase (AHRD V3.3 *** V9HYU6_MANES)	GO:0016491|GO:0055114
Solyc12g042170.2	**-1.84E+00**	**1.18E-03**	-3.42E-01	5.04E-01	7.43E-02	8.84E-01	-1.04E+00	4.84E-02	WT N 14 dpi	TR	ADP-ribosylation factor GTPase-activatingprotein (AHRD V3.3 *-* G5DWI4_SILLA)	GO:0005096|GO:0005515|GO:0005515
Solyc11g012230.2	**-1.84E+00**	**6.66E-03**	4.76E-01	4.53E-01	1.64E+00	1.43E-02	5.57E-01	3.81E-01	WT N 14 dpi	G	QWRF motif protein (DUF566) (AHRD V3.3 --* AT2G20815.4)	
Solyc10g083670.2	**-1.85E+00**	**2.97E-03**	5.98E-01	2.98E-01	-5.88E-03	9.92E-01	-1.34E+00	2.49E-02	WT N 14 dpi	CS	Cellulose synthase-like protein (AHRD V3.3 *** L0ASI8_POPTO)	
Solyc08g005640.3	**-1.87E+00**	**2.18E-03**	7.29E-01	1.95E-01	1.32E+00	2.39E-02	-7.80E-01	1.67E-01	WT N 14 dpi	2M	Terpene synthase (AHRD V3.3 ***G5CV51_SOLLC)	GO:0000287|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829
Solyc03g032240.3	**-1.87E+00**	**5.42E-04**	-8.74E-01	7.65E-02	5.86E-02	9.03E-01	-6.16E-01	2.05E-01	WT N 14 dpi	TR	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NYV5_ZOSMR)	GO:0006812|GO:0015299|GO:0016021|GO:0055085
Solyc11g010180.2	**-1.87E+00**	**2.18E-04**	-3.19E-01	4.71E-01	-4.11E-01	3.55E-01	4.88E-01	2.74E-01	WT N 14 dpi	R	Mitochondrial ribosomal protein L37 (AHRD V3.3 *** AT5G14290.1)	
Solyc09g012000.1	**-1.88E+00**	**3.55E-03**	-9.05E-01	1.35E-01	-3.58E-05	1.00E+00	4.62E-02	9.38E-01	WT N 14 dpi	PMI	Clade IV lectin receptor kinase (AHRDV3.3 *** K4CRM5_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc02g072500.3	**-1.88E+00**	**7.89E-03**	4.83E-01	4.67E-01	3.45E-01	6.02E-01	-5.55E-01	4.04E-01	WT N 14 dpi	TR	Nucleobase-ascorbate transporter-like protein (AHRD V3.3 *** G7LJF6_MEDTR)	GO:0005215|GO:0006810|GO:0016020|G O:0055085
Solyc02g083490.3	**-1.90E+00**	**1.91E-03**	-2.92E-01	5.98E-01	-3.54E-01	5.24E-01	1.90E-01	7.32E-01	WT N 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4BAL7_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc03g082790.3	**-1.92E+00**	**6.14E-03**	-1.09E+00	1.04E-01	-1.66E+00	1.59E-02	1.92E-01	7.68E-01	WT N 14 dpi	CS	LOW QUALITY:extensin-like 54	
Solyc12g019620.2	**-1.93E+00**	**2.14E-03**	-1.53E+00	1.21E-02	-2.85E-01	6.19E-01	8.30E-01	1.55E-01	WT N 14 dpi	TR	Pleiotropic drug resistance ABC transporter (AHRD V3.3 ***W0TUG3_ACAMN)	GO:0005524|GO:0016887|GO:0016020|G O:0016020
Solyc02g070940.1	**-1.96E+00**	**1.28E-04**	-8.21E-02	8.52E-01	1.86E-01	6.74E-01	6.57E-01	1.44E-01	WT N 14 dpi	E	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 ***Q41422_SOLTU)	GO:0009765|GO:0016020
Solyc03g033470.3	**-1.96E+00**	**1.28E-03**	3.32E-01	5.46E-01	1.38E-01	8.01E-01	-1.31E+00	2.33E-02	WT N 14 dpi	CS	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G35987.1)	

Solyc02g030220.1	**-1.96E+00**	**1.25E-04**	-9.81E-01	3.29E-02	-1.06E+00	2.20E-02	-6.59E-01	1.42E-01	WT N 14 dpi	CS	LOW QUALITY:Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)	
Solyc08g008660.3	**-1.96E+00**	**1.53E-03**	5.08E-01	3.68E-01	8.92E-01	1.20E-01	8.20E-01	1.51E-01	WT N 14 dpi	T	NAC domain-containing protein, putative (AHRD V3.3 *** A0A061G3T7_THECC)	GO:0003677|GO:0006355
Solyc12g098220.2	**-1.97E+00**	**6.42E-05**	-9.40E-01	3.17E-02	1.87E-02	9.64E-01	-5.32E-02	8.99E-01	WT N 14 dpi	RNA	RNA-binding protein (AHRD V3.3 *-* AT4G13690.1)	
Solyc11g073180.2	**-1.99E+00**	**1.43E-04**	-5.50E-01	2.28E-01	8.73E-01	6.11E-02	4.44E-01	3.28E-01	WT N 14 dpi	RNA	TOX high mobility group box protein,putative (DUF1635) (AHRD V3.3 *** AT2G28690.1)	
Solyc01g020378.1	**-2.00E+00**	**3.28E-03**	-8.98E-01	1.58E-01	-6.15E-01	3.29E-01	2.77E-01	6.58E-01	WT N 14 dpi	D	LOW QUALITY:Calcium-binding EF-hand family protein, putative (AHRD V3.3 ***A0A061FAV4_THECC)	GO:0005509
Solyc03g116790.3	**-2.01E+00**	**2.71E-08**	-9.05E-01	1.55E-03	7.59E-01	6.43E-03	-2.02E-01	4.38E-01	WT N 14 dpi	T	Chaperone protein dnaJ (AHRD V3.3 ***A0A151SPS5_CAJCA)	GO:0005515|GO:0005524|GO:0006457|GO:0009408|GO:0051082|GO:0005524|GO:0006457|GO:0009408|GO:0051082
Solyc07g006090.2	**-2.01E+00**	**4.25E-03**	-4.59E-01	4.81E-01	1.09E+00	1.02E-01	1.50E+00	2.76E-02	WT N 14 dpi	N	Class I glutamine amidotransferase (AHRD V3.3 *-* G7JV26_MEDTR)	
Solyc05g009340.1	**-2.02E+00**	**9.83E-04**	-8.02E-01	1.52E-01	1.19E+00	3.86E-02	1.28E+00	2.62E-02	WT N 14 dpi	NA	LOW QUALITY:BnaC02g18280D protein (AHRD V3.3 *-* A0A078CZZ8_BRANA)	
Solyc04g008570.3	**-2.02E+00**	**7.68E-04**	-1.37E+00	1.56E-02	-8.66E-01	1.15E-01	-3.27E-01	5.43E-01	WT N 14 dpi	RNA	Pentatricopeptide repeat superfamilyprotein, putative (AHRD V3.3 *** A0A061GUB4_THECC)	GO:0005515
Solyc06g064600.1	**-2.03E+00**	**7.08E-03**	-4.41E-01	5.30E-01	2.61E-01	7.10E-01	-8.49E-01	2.32E-01	WT N 14 dpi	RNA	Pentatricopeptide repeat-containing family protein (AHRD V3.3 *** B9I6N6_POPTR)	GO:0005515|GO:0008270|GO:0008270
Solyc05g010800.3	**-2.03E+00**	**6.09E-03**	4.62E-01	5.03E-01	7.77E-01	2.64E-01	1.77E-01	7.96E-01	WT N 14 dpi	DNA	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9RLG1_RICCO)	GO:0003824|GO:0006281|GO:0006284|GO:0008725|GO:0006284|GO:0008725
Solyc11g011000.2	**-2.04E+00**	**4.33E-03**	1.67E-01	7.99E-01	-2.32E-01	7.24E-01	-1.08E+00	1.11E-01	WT N 14 dpi	S	Cysteine-rich repeat secretory protein 60 (AHRD V3.3 *** A0A061EEI8_THECC)	
Solyc02g063360.3	**-2.04E+00**	**3.61E-04**	-9.47E-01	6.82E-02	9.73E-01	6.14E-02	6.01E-01	2.38E-01	WT N 14 dpi	STR	Calcium-dependent lipid-binding domain-containing protein (AHRD V3.3 *** F4K8L6_ARATH)	GO:0005515
Solyc02g078665.1	**-2.05E+00**	**1.48E-03**	-4.38E-01	4.53E-01	7.07E-01	2.30E-01	1.15E+00	5.73E-02	WT N 14 dpi	G	Hydroxyproline-rich glycoprotein familyprotein, putative (AHRD V3.3 --* A0A072UP10_MEDTR)	
Solyc05g055400.3	**-2.06E+00**	**3.44E-03**	1.35E+00	4.43E-02	5.76E-02	9.29E-01	8.77E-01	1.82E-01	WT N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***D9MWM1_SOLTO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc10g076830.2	**-2.06E+00**	**5.37E-03**	6.56E-01	3.43E-01	4.94E-01	4.73E-01	9.12E-01	1.91E-01	WT N 14 dpi	PMI	Laccase (AHRD V3.3 *** P93366_TOBAC)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc03g112060.3	**-2.07E+00**	**2.03E-05**	-4.12E-01	3.09E-01	1.78E+00	1.30E-04	6.89E-01	9.46E-02	WT N 14 dpi	E	Quinolinate synthase A (AHRD V3.3 *** W9RJG8_9ROSA)	GO:0008987|GO:0009435|GO:0051539
Solyc11g018850.1	**-2.07E+00**	**9.98E-04**	-6.07E-01	2.86E-01	2.87E-01	6.11E-01	8.67E-01	1.32E-01	WT N 14 dpi	DNA	Histone-lysine N-methyltransferase ASHR2(AHRD V3.3 --* ASHR2_ARATH)	
Solyc03g111680.3	**-2.08E+00**	**2.10E-03**	-4.99E-01	4.20E-01	1.61E-01	7.94E-01	-3.20E-01	6.03E-01	WT N 14 dpi	DNA	DNA polymerase III subunit gamma/tau (AHRD V3.3 *** A0A0B0NH82_GOSAR)	GO:0003677|GO:0006260|GO:0003887|GO:0005524|GO:0006260|GO:0009360|GO:0003887|GO:0005524|GO:0006260|GO:0009360

Solyc11g006450.2	**-2.08E+00**	**2.42E-03**	-2.69E-01	6.68E-01	3.33E-01	5.95E-01	5.33E-01	3.98E-01	WT N 14 dpi	D	RING/U-box superfamily protein (AHRDV3.3 *** A0A061FQW5_THECC)	GO:0005515|GO:0008270
Solyc06g053380.3	**-2.08E+00**	**8.42E-03**	6.94E-02	9.25E-01	7.04E-01	3.44E-01	3.10E-01	6.75E-01	WT N 14 dpi	D	Chitinase (AHRD V3.3 ***A0A1B1HY32_9APIA)	GO:0004568|GO:0005975|GO:0004568|GO:0006032|GO:0016998|GO:0004568|GO:0006032|GO:0016998
Solyc12g088520.2	**-2.09E+00**	**1.25E-03**	-5.33E-02	9.27E-01	4.45E-01	4.48E-01	2.56E-01	6.61E-01	WT N 14 dpi	G	cyclin A3_3	GO:0005634
Solyc08g015770.3	**-2.10E+00**	**2.65E-05**	-6.85E-01	1.07E-01	-4.73E-01	2.60E-01	-6.50E-01	1.26E-01	WT N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT1G53490.1)	GO:0005515|GO:0008270
Solyc02g077720.3	**-2.10E+00**	**5.39E-03**	-4.03E-01	5.65E-01	1.29E+00	7.35E-02	1.05E+00	1.41E-01	WT N 14 dpi	NA	Transmembrane protein, putative (AHRDV3.3 *** G7ISF1_MEDTR)	
Solyc07g062790.1	**-2.10E+00**	**1.76E-03**	2.38E-01	6.97E-01	-2.75E-01	6.52E-01	1.36E+00	3.25E-02	WT N 14 dpi	DNA	Homeobox-leucine zipper protein family (AHRD V3.3 *-* AT1G69780.1)	GO:0003677|GO:0006355|GO:0043565|GO:0006355|GO:0043565
Solyc10g085080.2	**-2.11E+00**	**1.57E-03**	-2.93E-01	6.29E-01	2.01E-01	7.40E-01	-1.35E+00	3.29E-02	WT N 14 dpi	AM	8-amino-7-oxononanoate synthase (AHRDV3.3 *** AT3G09050.1)	
Solyc02g092630.2	**-2.12E+00**	**2.64E-03**	-1.55E+00	2.19E-02	-2.75E-02	9.66E-01	4.83E-01	4.55E-01	WT N 14 dpi	RNA	LOW QUALITY:Maturase K (AHRD V3.3 -- * MATK_LIRMU)	
Solyc06g073800.3	**-2.13E+00**	**4.55E-03**	1.78E-01	7.97E-01	7.22E-01	3.01E-01	-9.90E-03	9.89E-01	WT N 14 dpi	R	40s ribosomal protein S11 (AHRD V3.3 ***K7XKQ3_SOLTU)	GO:0003735|GO:0005622|GO:0005840|G O:0006412
Solyc02g065430.1	**-2.13E+00**	**8.65E-04**	6.43E-01	2.65E-01	-2.92E-02	9.59E-01	-2.73E-01	6.33E-01	WT N 14 dpi	NA	LOW QUALITY:DUF4228 domain protein (AHRD V3.3 *** G7K9H8_MEDTR)	
Solyc07g007270.3	**-2.14E+00**	**4.93E-03**	3.55E-01	6.14E-01	1.98E+00	8.57E-03	2.95E-01	6.75E-01	WT N 14 dpi	G	root meristem growth factor (AHRD V3.3 -- * AT5G64770.1)	
Solyc03g043720.3	**-2.17E+00**	**7.43E-03**	5.17E-01	4.95E-01	-2.30E-01	7.60E-01	6.14E-01	4.18E-01	WT N 14 dpi	NA	Protein BRICK 1 (AHRD V3.3 *** BRK1_ARATH)	GO:0007015|GO:0031209|GO:0032403
Solyc06g060900.1	**-2.18E+00**	**1.56E-04**	-6.59E-01	1.92E-01	-5.25E-01	2.96E-01	3.66E-02	9.41E-01	WT N 14 dpi	P	LOW QUALITY:PRLI-interacting factor(AHRD V3.3 -- * AT5G19900.5)	
Solyc04g014280.1	**-2.19E+00**	**8.98E-03**	-2.04E+00	1.42E-02	1.64E+00	4.40E-02	-7.75E-01	3.25E-01	WT N 14 dpi	G	LOW QUALITY:hydroxyproline-rich glycoprotein family protein (AHRD V3.3 ***AT5G09520.1)	
Solyc04g007320.2	**-2.19E+00**	**2.11E-03**	-1.82E-01	7.79E-01	-4.44E-01	4.95E-01	-1.31E+00	5.14E-02	WT N 14 dpi	D	Disease resistance protein (TIR-NBS-LRRclass), putative (AHRD V3.3 *** Q2HUD1_MEDTR)	GO:0005515|GO:0007165|GO:0043531|G O:0043531
Solyc06g076790.1	**-2.23E+00**	**1.52E-03**	-5.80E-01	3.66E-01	8.85E-01	1.72E-01	1.16E-01	8.55E-01	WT N 14 dpi	E	LOW QUALITY:Thylakoid soluble phosphoprotein (AHRD V3.3 *** Q8GT36_SPIOL)	
Solyc12g006630.2	**-2.25E+00**	**4.25E-06**	-8.83E-01	3.14E-02	-4.43E-01	2.64E-01	-2.28E-01	5.61E-01	WT N 14 dpi	CS	Dynein light chain-like protein (AHRD V3.3 *-* Q8RV44_ORYSJ)	GO:0007017|GO:0030286
Solyc05g024377.1	**-2.26E+00**	**9.11E-04**	3.32E-01	5.87E-01	1.44E-01	8.13E-01	7.35E-01	2.34E-01	WT N 14 dpi	D	Disease resistance protein (TIR-NBS-LRRclass) (AHRD V3.3 *-* A0A072UXW1_MEDTR)	GO:0005515|GO:0007165
Solyc07g052410.3	**-2.29E+00**	**7.76E-03**	-1.72E+00	3.97E-02	-7.56E-01	3.49E-01	-9.79E-01	2.28E-01	WT N 14 dpi	S	Ras-related small GTP-binding family protein (AHRD V3.3 *** AT5G54840.2)	
Solyc04g008850.1	**-2.30E+00**	**1.06E-04**	-4.56E-01	3.72E-01	6.37E-01	2.16E-01	-3.03E-01	5.52E-01	WT N 14 dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G20015.1)	GO:0004190|GO:0006508
Solyc01g066910.3	**-2.30E+00**	**7.49E-08**	2.73E-01	3.86E-01	1.01E+00	2.99E-03	1.96E-01	5.33E-01	WT N 14 dpi	NA	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MM18_ARALL)	
Solyc07g053375.1	**-2.33E+00**	**3.21E-03**	3.27E-01	6.53E-01	1.54E-01	8.31E-01	9.36E-01	2.03E-01	WT N 14 dpi	AM	methionine synthase 2 (AHRD V3.3 --* AT3G03780.3)	
Solyc09g013160.3	**-2.34E+00**	**1.30E-03**	-3.67E-01	5.75E-01	4.76E-01	4.68E-01	-9.93E-01	1.37E-01	WT N 14 dpi	G	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G09080.3)	GO:0005515
Solyc12g036310.1	**-2.34E+00**	**9.52E-05**	4.12E-01	4.23E-01	9.02E-02	8.60E-01	-8.08E-01	1.23E-01	WT N 14 dpi	E	LOW QUALITY:NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic(AHRD V3.3 --* NU5C_CHLSC)	

Solyc03g098650.3	**-2.35E+00**	**3.03E-04**	1.97E-01	7.29E-01	1.86E-01	7.43E-01	-8.63E-01	1.37E-01	WT N 14 dpi	TR	Heavy metal transport/detoxification superfamily protein, putative (AHRD V3.3 *** A0A061EMU1_THECC)	GO:0030001|GO:0046872
Solyc02g071670.3	**-2.36E+00**	**5.17E-03**	-1.10E+00	1.64E-01	-1.83E+00	2.54E-02	-1.10E+00	1.65E-01	WT N 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 --* AT2G18370.1)	
Solyc03g007940.3	**-2.36E+00**	**3.45E-03**	-1.23E-01	8.68E-01	1.33E+00	8.17E-02	-8.69E-01	2.47E-01	WT N 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT4G23500.1)	GO:0004650|GO:0005975
Solyc08g005090.1	**-2.36E+00**	**1.86E-05**	-6.43E-01	1.66E-01	4.07E-01	3.76E-01	-9.39E-01	4.75E-02	WT N 14 dpi	NA	LOW QUALITY:DUF740 family protein (AHRD V3.3 *-* G7KDT4_MEDTR)	
Solyc05g015656.1	**-2.39E+00**	**5.25E-04**	-8.67E-01	1.63E-01	-8.43E-01	1.74E-01	-1.33E+00	3.70E-02	WT N 14 dpi	K	Serine/threonine protein phosphatase 7long form isogeny (AHRD V3.3 *-* A0A151SDM1_CAJCA)	
Solyc08g077810.2	**-2.41E+00**	**1.28E-03**	-6.42E-01	3.44E-01	-5.25E-01	4.38E-01	-1.58E+00	2.55E-02	WT N 14 dpi	AM	Cationic amino acid transporter, putative (AHRD V3.3 *-* A0A061G4V0_THECC)	
Solyc07g052360.2	**-2.42E+00**	**1.92E-03**	1.91E-01	7.87E-01	-8.35E-01	2.45E-01	-1.44E-01	8.39E-01	WT N 14 dpi	G	GPI-anchored protein (AHRD V3.3 *** AT2G30700.2)	
Solyc11g067110.2	**-2.42E+00**	**5.95E-03**	-5.28E-01	5.20E-01	2.24E-01	7.84E-01	1.96E-01	8.10E-01	WT N 14 dpi	DNA	DNA polymerase epsilon catalytic subunit(AHRD V3.3 *-* AT1G08260.2)	GO:0003676|GO:0003677|GO:0003887|GO:0006260|GO:0006281|GO:0008622|GO:0003677|GO:0003887|GO:0006260|GO:0006281|GO:0008622
Solyc11g018777.1	**-2.45E+00**	**9.10E-03**	-1.33E+00	1.37E-01	-1.17E+00	1.88E-01	-4.09E-01	6.41E-01	WT N 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4D6T3_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc05g052370.3	**-2.45E+00**	**1.31E-03**	-6.67E-01	3.36E-01	1.63E+00	2.44E-02	5.79E-01	4.03E-01	WT N 14 dpi	PMI	Laccase (AHRD V3.3 ***M1CL08_SOLTU)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc06g005390.1	**-2.51E+00**	**6.20E-03**	-6.97E-01	4.15E-01	-3.01E-01	7.23E-01	-1.58E+00	7.13E-02	WT N 14 dpi	DNA	Histone H2B (AHRD V3.3 *** K4C323_SOLLC)	GO:0000786|GO:0003677|GO:0003677|GO:0003677
Solyc06g008990.1	**-2.51E+00**	**4.60E-04**	-1.74E+00	1.01E-02	-6.40E-01	3.16E-01	1.21E+00	6.44E-02	WT N 14 dpi	G	LOW QUALITY:Fantastic four-like protein (AHRD V3.3 *-* G7IE53_MEDTR)	
Solyc09g090320.2	**-2.53E+00**	**5.37E-03**	-8.04E-01	3.44E-01	-1.90E-01	8.22E-01	-2.20E+00	1.40E-02	WT N 14 dpi	TR	Kinesin, motor domain-containing protein (AHRD V3.3 *** A0A103XI34_CYNCS)	GO:0003777|GO:0005524|GO:0007018|GO:0008017
Solyc01g006820.2	**-2.54E+00**	**8.50E-03**	-1.49E+00	1.06E-01	1.36E-01	8.80E-01	-2.16E+00	2.31E-02	WT N 14 dpi	DNA	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein(AHRD V3.3 --* AT5G57150.5)	
Solyc04g080040.3	**-2.54E+00**	**7.75E-03**	-9.23E-01	3.04E-01	-2.22E+00	1.80E-02	-1.19E+00	1.87E-01	WT N 14 dpi	STR	Heat shock protein binding protein, putative (AHRD V3.3 *** B9R7Q9_RICCO)	
Solyc09g075690.1	**-2.55E+00**	**2.97E-04**	-1.14E+00	7.18E-02	-3.01E-01	6.25E-01	5.02E-01	4.18E-01	WT N 14 dpi	L	Alpha/beta-Hydrolases superfamily protein(AHRD V3.3 *** A0A061EKQ6_THECC)	GO:0008152|GO:0016787
Solyc03g112510.2	**-2.56E+00**	**7.97E-04**	-3.58E-01	5.99E-01	-3.46E-01	6.12E-01	-4.00E-01	5.58E-01	WT N 14 dpi	DNA	D111/G-patch domain-containing family protein (AHRD V3.3 *** B9GSH2_POPTR)	GO:0003676
Solyc08g007500.3	**-2.59E+00**	**6.31E-05**	-1.44E+00	1.37E-02	4.59E-01	4.06E-01	-9.88E-01	8.07E-02	WT N 14 dpi	T	PPR containing protein (AHRD V3.3 *** AT4G22758.1)	
Solyc00g006805.1	**-2.62E+00**	**2.57E-03**	-1.74E+00	3.55E-02	-5.10E-01	5.22E-01	-2.85E-01	7.20E-01	WT N 14 dpi	2M	AMP-dependent synthetase and ligasefamily protein (AHRD V3.3 --* AT4G05160.1)	
Solyc04g007470.3	**-2.62E+00**	**5.71E-05**	-2.09E-01	7.05E-01	9.48E-01	9.40E-02	6.39E-01	2.52E-01	WT N 14 dpi	STR	Drought responsive Zinc finger protein	GO:0005622|GO:0008270
Solyc01g095080.3	**-2.65E+00**	**2.61E-03**	-7.48E-01	3.56E-01	2.06E+00	1.55E-02	2.41E+00	5.58E-03	WT N 14 dpi	H	1-aminocyclopropane-1-carboxylic acidsynthase-2	GO:0003824|GO:0003824|GO:0009058|GO:0030170|GO:0003824|GO:0009058|GO:0030170
Solyc05g052650.2	**-2.67E+00**	**4.48E-05**	2.08E-01	7.05E-01	3.35E-01	5.44E-01	6.98E-01	2.11E-01	WT N 14 dpi	S	LOW QUALITY:HXXXD-type acyl- transferase family protein (AHRD V3.3 *-* V5PZN5_9CARY)	GO:0016747

Solyc12g036470.2	**-2.68E+00**	**1.16E-03**	-1.10E+00	1.44E-01	-1.59E+00	3.98E-02	-2.04E+00	1.00E-02	WT N 14 dpi	T	bHLH transcription factor 071	GO:0046983
Solyc07g063165.1	**-2.70E+00**	**4.74E-03**	-1.81E+00	4.85E-02	-6.04E-01	4.95E-01	-8.39E-01	3.46E-01	WT N 14 dpi	CS	3-deoxy-manno-octulosonate cytidylyltransferase (AHRD V3.3 *-* A0A0B2RRY9_GLYSO)	
Solyc06g009770.1	**-2.70E+00**	**4.26E-03**	1.28E+00	1.50E-01	7.78E-01	3.75E-01	-5.14E-01	5.57E-01	WT N 14 dpi	NA	Flagellar biosynthesis protein flhA (AHRDV3.3 *-* A0A1D1YQS8_9ARAE)	
Solyc07g063720.1	**-2.71E+00**	**1.86E-03**	-9.50E-01	2.36E-01	-6.00E-01	4.50E-01	-1.09E+00	1.77E-01	WT N 14 dpi	K	Serine/threonine-protein kinase (AHRDV3.3 *** M1CC72_SOLTU)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g089350.3	**-2.73E+00**	**5.72E-03**	-2.18E+00	2.37E-02	-9.69E-01	2.95E-01	-1.99E-02	9.83E-01	WT N 14 dpi	H	Gibberellin-regulated family protein (AHRDV3.3 *** A0A061EVH9_THECC)	
Solyc09g007480.3	**-2.74E+00**	**1.10E-04**	2.15E-02	9.72E-01	-2.22E-01	7.15E-01	-7.95E-01	1.96E-01	WT N 14 dpi	C	Fructose-bisphosphate aldolase, cytoplasmic isozyme (AHRD V3.3 --* ALF_MAIZE)	
Solyc11g039890.2	**-2.82E+00**	**7.61E-03**	-1.45E+00	1.49E-01	-5.99E-01	5.44E-01	-1.37E-01	8.89E-01	WT N 14 dpi	RNA	Nuclear pore complex protein Nup188a(AHRD V3.3 *-* W6JJC0_NICBE)	GO:0005643
Solyc05g051650.1	**-2.83E+00**	**8.70E-03**	-1.58E+00	1.26E-01	-1.03E+00	3.10E-01	1.12E+00	2.72E-01	WT N 14 dpi	G	QWRF motif protein (DUF566) (AHRD V3.3 *** AT4G25190.1)	
Solyc08g067730.2	**-2.86E+00**	**7.44E-04**	-9.59E-01	2.12E-01	1.11E+00	1.51E-01	4.28E-01	5.72E-01	WT N 14 dpi	D	RING/U-box superfamily protein (AHRDV3.3 --* AT1G30860.1)	
Solyc12g049250.2	**-2.97E+00**	**1.53E-04**	-1.02E+00	1.41E-01	3.59E-01	5.96E-01	-1.47E+00	3.68E-02	WT N 14 dpi	G	alpha-L-arabinofuranosidase 1 (AHRD V3.3 --* AT3G10740.4)	
Solyc03g082770.1	**-2.97E+00**	**3.27E-03**	-8.41E-01	3.66E-01	-2.35E+00	1.64E-02	-2.07E+00	3.23E-02	WT N 14 dpi	CS	LOW QUALITY:Extensin-like protein Dif10(AHRD V3.3 *** Q43504_SOLLC)	
Solyc04g080530.3	**-3.00E+00**	**1.03E-04**	2.08E-01	7.53E-01	7.25E-01	2.78E-01	4.80E-02	9.42E-01	WT N 14 dpi	CS	Pectinesterase (AHRD V3.3 *** K4BVD2_SOLLC)	GO:0005618|GO:0030599|GO:0042545
Solyc01g097930.3	**-3.06E+00**	**2.77E-04**	-7.55E-01	3.08E-01	-1.05E+00	1.60E-01	-1.60E+00	3.68E-02	WT N 14 dpi	AM	Cysteine synthase (AHRD V3.3 ***K4B0I0_SOLLC)	GO:0004124|GO:0006535|GO:0006535|GO:0006535
Solyc05g007480.1	**-3.11E+00**	**5.45E-04**	-1.80E+00	3.09E-02	1.92E-01	8.10E-01	3.94E-01	6.21E-01	WT N 14 dpi	G	LOW QUALITY:Phytochrome kinase substrate protein, putative (AHRD V3.3 ***G7KDX6_MEDTR)	
Solyc02g062340.3	**-3.12E+00**	**3.61E-03**	-1.89E+00	6.40E-02	-7.96E-01	4.21E-01	-5.06E-01	6.08E-01	WT N 14 dpi	C	Fructose-bisphosphate aldolase (AHRDV3.3 *** K4B6C3_SOLLC)	GO:0003824|GO:0004332|GO:0006096|GO:0004332|GO:0006096
Solyc02g087790.2	**-3.13E+00**	**5.43E-05**	-1.78E-01	7.86E-01	8.13E-01	2.21E-01	-2.24E-01	7.32E-01	WT N 14 dpi	C	Aldose 1-epimerase (AHRD V3.3 ***K4BBT5_SOLLC)	GO:0003824|GO:0005975|GO:0030246|GO:0005975|GO:0016853|GO:0005975|GO:0016853
Solyc11g061960.2	**-3.17E+00**	**1.86E-06**	-3.61E-01	4.92E-01	4.70E-01	3.73E-01	-6.32E-01	2.34E-01	WT N 14 dpi	K	Kinase family protein (AHRD V3.3 ***D7KZX4_ARALL)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc11g020760.2	**-3.18E+00**	**4.90E-04**	-1.44E+00	8.30E-02	2.65E-01	7.42E-01	-9.09E-01	2.65E-01	WT N 14 dpi	RNA	DEAD/DEAH box RNA helicase family protein (AHRD V3.3 *-* AT1G35530.3)	GO:0003677|GO:0005524|GO:0016787
Solyc12g038240.2	**-3.20E+00**	**1.75E-04**	-6.88E-02	9.26E-01	-1.42E+00	6.16E-02	-1.07E+00	1.56E-01	WT N 14 dpi	G	LOW QUALITY:hydroxyproline-rich glycoprotein family protein (AHRD V3.3 --*AT5G09530.1)	
Solyc09g010990.3	**-3.20E+00**	**2.70E-03**	-3.18E-01	7.44E-01	7.90E-01	4.20E-01	9.85E-01	3.17E-01	WT N 14 dpi	PMI	Laccase (AHRD V3.3 ***M1AHK0_SOLTU)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc11g012240.1	**-3.25E+00**	**3.25E-05**	-7.32E-01	2.69E-01	7.70E-01	2.45E-01	5.10E-01	4.38E-01	WT N 14 dpi	P	MBOAT (membrane bound O-acyl transferase) family protein (AHRD V3.3 *** AT5G55350.1)	GO:0008374
Solyc09g008750.1	**-3.26E+00**	**6.02E-05**	-1.48E+00	3.92E-02	-4.11E-01	5.52E-01	3.55E-01	6.07E-01	WT N 14 dpi	G	VQ motif-containing protein, putative (AHRD V3.3 *** A0A061DH87_THECC)	
Solyc01g110360.3	**-3.28E+00**	**1.72E-05**	-1.02E+00	1.15E-01	-1.21E+00	6.42E-02	-7.49E-01	2.41E-01	WT N 14 dpi	C	Fructose-bisphosphate aldolase (AHRD V3.3 *** K4B3P9_SOLLC)	GO:0003824|GO:0004332|GO:0006096|GO:0004332|GO:0006096

Solyc07g008300.2	**-3.30E+00**	**4.34E-03**	2.93E-01	7.83E-01	2.39E-01	8.22E-01	-9.17E-01	3.93E-01	WT N 14 dpi	AM	Choline monooxygenase (AHRD V3.3 ***D2DEK9_LYCBA)	GO:0005506|GO:0006725|GO:0051537|GO:0055114|GO:0005506|GO:0016708|GO:0019439|GO:0051537|GO:0055114|GO:0005506|GO:0016708|GO:0019439|GO:0051537|GO:0055114
Solyc06g008050.3	**-3.34E+00**	**2.66E-03**	-1.60E+00	1.23E-01	-2.67E+00	1.32E-02	-1.64E+00	1.15E-01	WT N 14 dpi	OX	Flavin-containing monooxygenase (AHRDV3.3 *** D2IGV3_SOLLC)	GO:0004499|GO:0050660|GO:0050661|GO:0055114|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc04g012050.3	**-3.43E+00**	**6.34E-04**	-6.75E-01	4.51E-01	1.07E+00	2.35E-01	9.03E-01	3.15E-01	WT N 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9RA19_9ROSA)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc02g090720.3	**-3.46E+00**	**5.50E-04**	-4.49E-01	6.12E-01	-1.13E-01	8.98E-01	-3.10E-01	7.26E-01	WT N 14 dpi	NA	BEST plant protein match is: (TAIR:plant.1)protein, putative (AHRD V3.3 *** G7K7Z5_MEDTR)	
Solyc02g083480.3	**-3.49E+00**	**1.85E-03**	4.22E-01	6.78E-01	-8.61E-01	3.99E-01	1.05E+00	3.08E-01	WT N 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4BAL6_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc10g074540.1	**-3.50E+00**	**1.35E-04**	-1.22E+00	1.30E-01	-9.81E-01	2.21E-01	-1.41E+00	8.35E-02	WT N 14 dpi	STR	Phosphate-responsive 1 family protein(AHRD V3.3 *** D7L8T1_ARALL)	
Solyc12g019230.2	**-3.51E+00**	**9.58E-07**	-4.47E-01	4.22E-01	1.25E+00	3.13E-02	1.16E-03	9.98E-01	WT N 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT3G59850.2)	GO:0004650|GO:0005975
Solyc02g085880.2	**-3.51E+00**	**3.90E-04**	-2.17E+00	1.84E-02	3.26E+00	8.38E-04	1.88E+00	3.85E-02	WT N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9RSK4_RICCO)	GO:0005506|GO:0016705|GO:0020037|G O:0055114
Solyc12g098540.2	**-3.62E+00**	**5.85E-03**	-1.57E+00	2.03E-01	2.97E+00	2.06E-02	3.02E-01	8.04E-01	WT N 14 dpi	K	Apyrase (AHRD V3.3 *** APY_SOLTU)	GO:0016787
Solyc05g013470.3	**-3.63E+00**	**5.62E-04**	-2.48E-01	7.90E-01	-4.68E-01	6.17E-01	4.90E-01	6.01E-01	WT N 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 ***K4BY68_SOLLC)	GO:0006855|GO:0015238|GO:0015297|G O:0016020|GO:0055085
Solyc05g052300.3	**-3.70E+00**	**5.69E-06**	-6.29E-01	3.43E-01	8.15E-02	9.01E-01	-7.24E-01	2.76E-01	WT N 14 dpi	AM	Amino acid transporter family protein (AHRD V3.3 *** B9HYI5_POPTR)	
Solyc03g032245.1	**-3.94E+00**	**8.45E-06**	1.44E-01	8.41E-01	-1.29E+00	8.19E-02	-1.73E-03	9.98E-01	WT N 14 dpi	STR	LOW QUALITY:IQ domain-containingprotein (AHRD V3.3 *-* A0A0K9P301_ZOSMR)	GO:0005515
Solyc08g007840.2	**-4.47E+00**	**1.70E-03**	-3.17E+00	1.99E-02	4.22E-01	7.43E-01	1.49E+00	2.55E-01	WT N 14 dpi	STR	Dehydration-responsive element binding factor (AHRD V3.3 *** X2JR99_POPNI)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc08g007570.3	**-5.02E+00**	**9.53E-04**	-2.64E+00	6.02E-02	-2.20E+00	1.14E-01	-1.87E-01	8.90E-01	WT N 14 dpi	DNA	Homeobox-leucine zipper protein HOX9,putative (AHRD V3.3 *** A0A061DUZ5_THECC)	
Solyc01g087440.3	**-5.47E+00**	**7.26E-07**	-1.34E+00	1.22E-01	-1.09E+00	2.08E-01	-1.27E+00	1.44E-01	WT N 14 dpi	NA	Protein EFR3 like B (AHRD V3.3 *-* A0A0B2PVI4_GLYSO)	
Solyc03g078500.3	5.53E+00	2.56E-06	6.96E+00	5.38E-08	**-3.79E+00**	**3.51E-04**	-2.26E+00	2.10E-02	WT NoN 14 dpi	2M	UDP-glucuronosyltransferase	GO:0008152|GO:0016758
Solyc03g097870.3	4.59E+00	2.44E-06	5.31E+00	2.29E-07	**-2.78E+00**	**1.21E-03**	-1.18E-01	8.79E-01	WT NoN 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJK4_SOLLC)	GO:0016021
Solyc11g069750.2	3.70E+00	4.73E-16	3.84E+00	2.02E-16	**-1.88E+00**	**1.52E-09**	1.26E-01	5.48E-01	WT NoN 14 dpi	N	High-affinity nitrate transporter (AHRD V3.3 *** Q76IJ7_PRUPE)	GO:0016021|GO:0055085
Solyc07g054790.1	3.11E+00	6.74E-08	3.52E+00	6.86E-09	**-1.30E+00**	**4.44E-03**	-4.22E-01	3.21E-01	WT NoN 14 dpi	D	Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)	
Solyc06g050870.3	2.80E+00	3.18E-02	4.93E+00	4.92E-04	**-5.20E+00**	**2.73E-04**	1.67E+00	1.88E-01	WT NoN 14 dpi	E	Hypoxia-responsive family protein (AHRDV3.3 *** A0A061FYY0_THECC)	
Solyc12g006570.2	2.66E+00	3.01E-02	1.69E+00	1.56E-01	**3.68E+00**	**3.84E-03**	-4.98E-01	6.71E-01	WT NoN 14 dpi	2M	Sesquiterpene synthase (AHRD V3.3 ***G5CV52_SOLLC)	GO:0000287|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829
Solyc05g008150.3	2.56E+00	1.02E-01	2.27E+00	1.46E-01	**4.42E+00**	**7.10E-03**	8.33E-01	5.86E-01	WT NoN 14 dpi	STR	Metallocarboxypeptidase inhibitor (AHRDV3.3 *** O24373_SOLTU)	
Solyc08g062220.3	2.54E+00	2.23E-02	2.43E+00	2.81E-02	**3.65E+00**	**1.72E-03**	2.58E+00	2.03E-02	WT NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CL11_SOLLC)	GO:0008152|GO:0016758
Solyc10g050990.1	2.33E+00	6.92E-02	4.44E+00	1.26E-03	**-4.70E+00**	**7.43E-04**	-8.07E-01	5.17E-01	WT NoN 14 dpi	C	Pyruvate kinase (AHRD V3.3 --*A9TZX1_PHYPA)	
Solyc07g026650.3	2.21E+00	4.69E-05	2.48E+00	1.02E-05	**-2.64E+00**	**3.94E-06**	1.72E+00	8.04E-04	WT NoN 14 dpi	H	1-aminocyclopropane-1-carboxylate oxidase 5	GO:0016491|GO:0055114

Solyc07g017370.2	2.10E+00	5.27E-02	2.33E+00	3.30E-02	**3.30E+00**	**3.72E-03**	4.47E-01	6.69E-01	WT NoN 14 dpi	2M	AMP-dependent synthetase and ligasefamily protein (AHRD V3.3 --* AT2G47240.4)	
Solyc02g069810.2	1.96E+00	1.06E-04	9.88E-01	2.97E-02	**-1.24E+00**	**7.95E-03**	1.15E+00	1.29E-02	WT NoN 14 dpi	T	Bromo-adjacent-like (BAH) domain protein(AHRD V3.3 *-* A0A072VCT6_MEDTR)	GO:0003682
Solyc04g082180.4	1.85E+00	1.84E-04	1.68E+00	5.26E-04	**-1.54E+00**	**1.20E-03**	-9.23E-01	3.83E-02	WT NoN 14 dpi	2M	alcohol dehydrogenase	
Solyc12g005700.2	1.81E+00	1.98E-02	1.09E+00	1.46E-01	**3.04E+00**	**3.05E-04**	1.80E+00	2.05E-02	WT NoN 14 dpi	NA	transmembrane protein, putative (DUF1218) (AHRD V3.3 *** AT4G21310.1)	
Solyc12g010940.1	1.77E+00	2.68E-09	2.18E+00	3.63E-11	**-1.15E+00**	**4.42E-06**	-5.66E-01	8.70E-03	WT NoN 14 dpi	NA	LOW QUALITY:DUF1685 family protein(AHRD V3.3 *** A0A072V475_MEDTR)	
Solyc12g044983.1	1.59E+00	1.19E-01	2.94E-01	7.69E-01	**3.60E+00**	**1.20E-03**	1.46E+00	1.52E-01	WT NoN 14 dpi	CYTP450	Cytochrome P450 family protein (AHRDV3.3 *** B9HFV6_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc01g096720.3	1.51E+00	1.48E-01	1.77E+00	9.23E-02	**3.31E+00**	**3.13E-03**	1.99E+00	6.10E-02	WT NoN 14 dpi	TR	zinc induced facilitator-like 1 (AHRD V3.3 *** AT5G13750.1)	GO:0016021|GO:0055085
Solyc07g061820.1	1.50E+00	6.12E-03	1.39E+00	1.03E-02	**-2.82E+00**	**6.72E-06**	-4.46E-01	3.83E-01	WT NoN 14 dpi	DNA	LOW QUALITY:Replication factor-A protein1-like protein (AHRD V3.3 --* AT4G19130.2)	
Solyc01g099620.3	1.43E+00	4.18E-07	1.28E+00	2.50E-06	**-1.05E+00**	**4.08E-05**	-2.19E-01	3.13E-01	WT NoN 14 dpi	OX	Respiratory burst oxidase, putative (AHRDV3.3 *** B9RFA3_RICCO)	GO:0004601|GO:0050664|GO:0055114|GO:0005509|GO:0005509
Solyc12g088130.2	1.42E+00	1.31E-01	2.50E+00	1.07E-02	**-4.40E+00**	**5.18E-05**	-1.09E+00	2.43E-01	WT NoN 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-bindingsuperfamily protein (AHRD V3.3 *** AT5G10570.1)	GO:0046983
Solyc12g098170.1	1.41E+00	1.45E-03	2.00E+00	2.95E-05	**-2.28E+00**	**4.84E-06**	-4.02E-01	3.20E-01	WT NoN 14 dpi	P	LOW QUALITY:F-box family protein, putative (AHRD V3.3 *** S1RTT0_THECC)	
Solyc08g078695.1	1.40E+00	1.01E-02	1.04E+00	4.98E-02	**1.65E+00**	**3.00E-03**	1.39E+00	1.05E-02	WT NoN 14 dpi	STR	Heat-shock protein, putative (AHRD V3.3 *** B9SSG1_RICCO)	
Solyc03g082950.3	1.37E+00	6.90E-02	1.93E+00	1.30E-02	**2.19E+00**	**5.67E-03**	3.84E-01	6.01E-01	WT NoN 14 dpi	NA	BSD domain-containing protein (AHRDV3.3 --* AT2G10950.3)	
Solyc10g008050.2	1.37E+00	1.36E-01	1.48E+00	1.09E-01	**2.64E+00**	**6.54E-03**	1.19E+00	1.93E-01	WT NoN 14 dpi	NA	Transmembrane protein, putative (AHRD V3.3 *** G7JV20_MEDTR)	
Solyc01g094120.3	1.35E+00	1.21E-08	7.80E-01	6.90E-05	**-1.46E+00**	**2.67E-09**	-2.24E-01	1.86E-01	WT NoN 14 dpi	CYTP450	Cytochrome P450 family protein (AHRDV3.3 *** A0A061DTZ5_THECC)	GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc10g085500.2	1.34E+00	3.79E-03	1.98E+00	7.25E-05	**-2.10E+00**	**3.52E-05**	-8.36E-01	5.72E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9SRM6_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc09g008670.3	1.30E+00	2.50E-01	1.87E+00	1.03E-01	**3.34E+00**	**5.60E-03**	2.84E+00	1.64E-02	WT NoN 14 dpi	D	threonine deaminase	GO:0004794|GO:0009097|GO:0006520|GO:0030170|GO:0006520|GO:0030170
Solyc07g007760.3	1.25E+00	1.03E-01	2.96E-01	6.92E-01	**2.39E+00**	**3.32E-03**	7.26E-01	3.35E-01	WT NoN 14 dpi	D	defensin-like protein	GO:0006952
Solyc02g087090.3	1.23E+00	2.11E-07	1.70E+00	4.68E-10	**-1.89E+00**	**4.83E-11**	8.68E-02	6.25E-01	WT NoN 14 dpi	OX	alpha-DOX2	GO:0004601|GO:0006979|GO:0020037|GO:0055114
Solyc09g015230.1	1.21E+00	1.65E-01	1.72E+00	5.34E-02	**-4.00E+00**	**7.46E-05**	-1.07E+00	2.20E-01	WT NoN 14 dpi	K	Protein kinase family protein (AHRD V3.3 *** AT3G25490.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g005530.1	1.17E+00	1.41E-01	1.18E+00	1.36E-01	**-2.82E+00**	**1.10E-03**	-2.28E-01	7.69E-01	WT NoN 14 dpi	TR	Phosphate transporter (AHRD V3.3 ***Q9AYT2_TOBAC)	GO:0005315|GO:0006817|GO:0016021|GO:0016021|GO:0022857|GO:0055085|GO:0016021|GO:0022857|GO:0055085
Solyc04g081630.2	1.17E+00	1.50E-02	1.92E+00	2.15E-04	**-2.01E+00**	**1.27E-04**	-7.69E-01	9.73E-02	WT NoN 14 dpi	STR	Heat shock protein 90 (AHRD V3.3 *-* Q9MB32_ORYSA)	GO:0005524|GO:0006457|GO:0006950|GO:0051082
Solyc04g007760.3	1.13E+00	9.65E-02	1.39E+00	4.48E-02	**2.17E+00**	**2.82E-03**	1.07E-01	8.72E-01	WT NoN 14 dpi	D	Sn-1 protein (AHRD V3.3 ***Q42393_CAPAN)	GO:0006952|GO:0009607
Solyc03g115910.2	1.13E+00	8.71E-02	9.02E-01	1.69E-01	**2.57E+00**	**4.28E-04**	6.68E-01	3.04E-01	WT NoN 14 dpi	T	Transcription factor, MADS-box (AHRD V3.3 *** A0A118JYM5_CYNCS)	GO:0003677|GO:0046983
Solyc04g082120.3	1.12E+00	1.38E-01	1.73E+00	2.57E-02	**2.24E+00**	**5.03E-03**	1.18E+00	1.20E-01	WT NoN 14 dpi	P	Prolyl oligopeptidase family protein (AHRDV3.3 *** AT1G76140.1)	GO:0004252|GO:0006508|GO:0004252|GO:0070008|GO:0004252|GO:0070008

Solyc01g081293.1	1.11E+00	2.72E-03	-2.26E-01	5.04E-01	**-1.46E+00**	**1.79E-04**	-5.97E-01	8.56E-02	WT NoN 14 dpi	NA	Redox-regulatory protein FAM213A-likeprotein (AHRD V3.3 *** A0A0B2R8Q7_GLYSO)	GO:0055114
Solyc10g008900.3	1.10E+00	8.52E-02	1.86E+00	5.42E-03	**-1.92E+00**	**4.36E-03**	8.93E-01	1.58E-01	WT NoN 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4CY66_SOLLC)	
Solyc09g091000.3	1.10E+00	1.86E-01	-1.22E-01	8.81E-01	**2.57E+00**	**3.73E-03**	1.67E+00	4.85E-02	WT NoN 14 dpi	D	Major allergen d 1 (AHRD V3.3 *** Q8L6K9_MALDO)	GO:0006952|GO:0009607
Solyc01g091260.3	1.08E+00	2.25E-02	1.00E+00	3.37E-02	**2.15E+00**	**5.75E-05**	2.71E-01	5.50E-01	WT NoN 14 dpi	NA	Myeloid leukemia factor 1 (AHRD V3.3 *** A0A0B0Q1A9_GOSAR)	
Solyc03g118870.3	1.08E+00	8.45E-03	1.58E-01	6.81E-01	**-1.71E+00**	**1.28E-04**	-2.05E-01	5.94E-01	WT NoN 14 dpi	K	Octicosapeptide/Phox/Bem1p familyprotein, putative (AHRD V3.3 *** A0A061FV54_THECC)	GO:0005515
Solyc02g086350.3	1.08E+00	4.43E-03	4.30E-01	2.24E-01	**-1.15E+00**	**2.57E-03**	2.47E-01	4.81E-01	WT NoN 14 dpi	H	Protein PLASTID MOVEMENT IMPAIRED2 (AHRD V3.3 *** W9S0V7_9ROSA)	
Solyc02g082920.3	1.07E+00	9.86E-02	9.41E-01	1.43E-01	**2.80E+00**	**1.31E-04**	1.65E+00	1.37E-02	WT NoN 14 dpi	D	acidic extracellular 26 kD chitinase	GO:0004568|GO:0005975|GO:0004568|GO:0006032|GO:0016998|GO:0004568|GO:0006032|GO:0016998
Solyc08g062360.3	1.05E+00	5.55E-02	1.26E+00	2.44E-02	**1.55E+00**	**6.62E-03**	8.36E-01	1.24E-01	WT NoN 14 dpi	P	Ankyrin repeat family protein (AHRD V3.3 *** F8WLA0_CITUN)	GO:0005515
Solyc01g108800.3	1.02E+00	8.62E-02	-5.47E-01	3.50E-01	**-2.10E+00**	**1.14E-03**	-1.28E+00	3.42E-02	WT NoN 14 dpi	CS	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** A0A072TKX0_MEDTR)	GO:0003860
Solyc08g078845.1	9.96E-01	6.43E-03	9.94E-01	6.56E-03	**1.33E+00**	**5.30E-04**	7.11E-01	4.41E-02	WT NoN 14 dpi	RNA	YbaK/aminoacyl-tRNA synthetase- associated domain-containing protein (AHRD V3.3 *-* AT4G16510.2)	
Solyc05g041420.3	9.83E-01	5.19E-04	4.63E-01	7.30E-02	**1.65E+00**	**4.81E-07**	7.65E-01	4.79E-03	WT NoN 14 dpi	K	MAP kinase kinase kinase 36	GO:0004672|GO:0005524|GO:0006468
Solyc12g044630.2	9.65E-01	4.83E-03	3.21E-01	3.14E-01	**1.41E+00**	**1.24E-04**	-3.02E-01	3.43E-01	WT NoN 14 dpi	CS	Profilin (AHRD V3.3 *** M1CJS2_SOLTU)	GO:0003779
Solyc01g010480.3	9.52E-01	2.72E-02	-1.37E-01	7.40E-01	**1.36E+00**	**2.51E-03**	1.49E-01	7.16E-01	WT NoN 14 dpi	G	LOV/LOV protein (AHRD V3.3 *** E3WH16_SOLLC)	GO:0000155|GO:0000160
Solyc07g009020.2	9.51E-01	1.87E-05	1.36E+00	6.47E-08	**-1.15E+00**	**1.09E-06**	-1.22E-01	5.06E-01	WT NoN 14 dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952
Solyc12g005800.2	9.50E-01	3.06E-04	1.57E+00	2.78E-07	**-1.16E+00**	**2.60E-05**	-7.67E-01	2.40E-03	WT NoN 14 dpi	T	Myb transcription factor (AHRD V3.3 *** A0A072UKM9_MEDTR)	GO:0003677
Solyc02g082170.2	9.47E-01	3.05E-06	3.93E-01	2.10E-02	**1.04E+00**	**6.56E-07**	2.55E-01	1.22E-01	WT NoN 14 dpi	TR	Purine permease-related family protein (AHRD V3.3 *** B9GYR4_POPTR)	GO:0005215|GO:0016021
Solyc06g072530.3	9.33E-01	1.21E-01	1.48E+00	1.75E-02	**-1.66E+00**	**8.35E-03**	-1.43E+00	2.11E-02	WT NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4C8X3_SOLLC)	
Solyc08g067620.2	9.30E-01	2.04E-02	1.65E+00	1.74E-04	**-1.11E+00**	**6.89E-03**	-1.01E+00	1.23E-02	WT NoN 14 dpi	TR	Pleiotropic drug resistance ABCtransporter (AHRD V3.3 *** W0TUG3_ACAMN)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc01g103140.3	9.20E-01	2.68E-02	1.04E+00	1.32E-02	**1.33E+00**	**2.20E-03**	3.54E-01	3.75E-01	WT NoN 14 dpi	TR	Chloride channel protein (AHRD V3.3 ***Q40485_TOBAC)	GO:0005216|GO:0055085|GO:0005247|GO:0006821|GO:0016020|GO:0005247|GO:0006821|GO:0016020
Solyc07g009030.3	8.89E-01	5.00E-05	9.05E-01	4.01E-05	**-1.91E+00**	**1.03E-10**	-3.24E-01	8.87E-02	WT NoN 14 dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952
Solyc10g084040.2	8.84E-01	1.68E-04	9.19E-01	1.08E-04	**1.28E+00**	**1.04E-06**	9.91E-02	6.26E-01	WT NoN 14 dpi	E	Thylakoid lumenal 15.0 kDa protein 2,chloroplastic (AHRD V3.3 *** TL15B_ARATH)	
Solyc03g121550.3	8.84E-01	1.25E-02	-6.15E-02	8.53E-01	**1.55E+00**	**7.33E-05**	3.17E-01	3.45E-01	WT NoN 14 dpi	RNA	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT4G18750.1)	
Solyc09g007270.3	8.81E-01	1.13E-05	8.14E-01	3.34E-05	**1.49E+00**	**1.33E-09**	2.62E-01	1.19E-01	WT NoN 14 dpi	OX	Ascorbate peroxidase (AHRD V3.3 ***B9VRH6_CITMA)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0055114|GO:0004601|GO:0055114
Solyc03g007380.2	8.76E-01	2.80E-02	9.50E-01	1.80E-02	**1.19E+00**	**4.08E-03**	8.39E-01	3.47E-02	WT NoN 14 dpi	T	WRKY transcription factor 52	GO:0003700|GO:0006355|GO:0043565

Solyc06g059990.3	8.73E-01	1.26E-02	1.33E-01	6.87E-01	**1.34E+00**	**3.52E-04**	4.86E-01	1.48E-01	WT NoN 14 dpi	DNA	Alkyl transferase (AHRD V3.3 *** K7W9N9_SOLLC)	GO:0016765
Solyc03g032230.1	8.70E-01	2.03E-01	4.65E-01	4.92E-01	**-2.18E+00**	**3.09E-03**	-8.80E-01	1.99E-01	WT NoN 14 dpi	NA	LOW QUALITY:DUF241 domain protein (AHRD V3.3 *** G7LA86_MEDTR)	
Solyc03g120990.3	8.66E-01	2.10E-01	7.09E-01	3.02E-01	**2.77E+00**	**3.51E-04**	4.95E-01	4.69E-01	WT NoN 14 dpi	C	Malic enzyme (AHRD V3.3 ***M0ZRW2_SOLTU)	GO:0004470|GO:0004471|GO:0006108|GO:0055114|GO:0004471|GO:0051287|GO:0055114|GO:0004471|GO:0051287|GO:0055114
Solyc06g074230.3	8.66E-01	1.41E-03	1.64E+00	3.78E-07	**-1.41E+00**	**4.11E-06**	-5.58E-01	2.95E-02	WT NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 ***K4C9E1_SOLLC)	
Solyc01g081630.3	8.60E-01	7.01E-05	9.85E-01	1.16E-05	**-1.19E+00**	**6.52E-07**	-7.34E-01	4.33E-04	WT NoN 14 dpi	G	UPSTREAM OF FLC protein (DUF966) (AHRD V3.3 *** AT1G05577.1)	
Solyc03g006870.3	8.60E-01	7.87E-06	7.25E-01	7.72E-05	**1.34E+00**	**4.24E-09**	3.49E-01	3.27E-02	WT NoN 14 dpi	C	phosphoglucomutase (AHRD V3.3 ***AT5G51820.1)	GO:0000287|GO:0005975|GO:0005975
Solyc05g052420.2	8.55E-01	4.61E-04	8.89E-01	3.04E-04	**-1.20E+00**	**6.69E-06**	2.66E-02	9.02E-01	WT NoN 14 dpi	H	Abscisic acid receptor (AHRD V3.3 *** G7JKP6_MEDTR)	
Solyc06g072865.1	8.41E-01	3.45E-01	7.57E-01	3.95E-01	**3.09E+00**	**1.57E-03**	2.16E+00	2.04E-02	WT NoN 14 dpi	K	Protein phosphatase 2C family protein(AHRD V3.3 --* AT2G46920.4)	
Solyc07g009050.3	8.39E-01	3.62E-04	1.07E+00	1.83E-05	**-2.30E+00**	**2.08E-11**	-7.00E-01	2.07E-03	WT NoN 14 dpi	D	Defensin-like protein, putative (AHRD V3.3 *** A0A061E6R0_THECC)	GO:0006952
Solyc11g005180.1	8.33E-01	6.87E-03	9.26E-01	3.07E-03	**-1.40E+00**	**4.20E-05**	6.40E-01	3.27E-02	WT NoN 14 dpi	G	LOW QUALITY:Protein SENSITIVITY TO RED LIGHT REDUCED 1 (AHRD V3.3 *-*SRR1_ARATH)	GO:0003676
Solyc04g056620.2	8.30E-01	2.53E-01	1.45E+00	5.15E-02	**-2.56E+00**	**1.33E-03**	6.41E-01	3.75E-01	WT NoN 14 dpi	H	Auxin Efflux Facilitator 10	GO:0016021|GO:0055085
Solyc01g108740.3	8.26E-01	1.19E-04	1.11E+00	2.17E-06	**-1.75E+00**	**5.25E-10**	-2.36E-01	2.06E-01	WT NoN 14 dpi	H	Methyl esterase (AHRD V3.3 ***A0A072UEL6_MEDTR)	
Solyc11g012250.1	8.02E-01	5.36E-03	1.25E+00	6.98E-05	**-1.43E+00**	**1.20E-05**	5.31E-01	5.47E-02	WT NoN 14 dpi	P	MBOAT (Membrane bound O-acyl transferase) family protein, putative (AHRDV3.3 *** Q2HT39_MEDTR)	GO:0008374
Solyc09g009490.3	7.99E-01	1.41E-02	1.91E-01	5.34E-01	**-1.39E+00**	**1.10E-04**	-5.82E-01	6.65E-02	WT NoN 14 dpi	H	Abscisic acid insensitive (AHRD V3.3 ***B3U2B5_CUCSA)	GO:0003700|GO:0005634|GO:0009737|GO:0045893|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565
Solyc08g068120.2	7.93E-01	2.56E-02	3.84E-01	2.61E-01	**1.44E+00**	**2.21E-04**	-2.83E-01	4.06E-01	WT NoN 14 dpi	DNA	DNA polymerase theta (AHRD V3.3 *** A0A0B2Q221_GLYSO)	GO:0003676|GO:0003676|GO:0005524|GO:0003676|GO:0005524
Solyc07g042100.3	7.85E-01	1.72E-01	1.36E+00	2.22E-02	**-3.93E+00**	**1.91E-07**	-4.23E-01	4.56E-01	WT NoN 14 dpi	H	Early auxin response protein (AHRD V3.3 *** Q69P88_ORYSJ)	
Solyc01g091030.3	7.83E-01	1.09E-03	2.42E-01	2.66E-01	**-1.70E+00**	**2.10E-08**	-7.07E-01	2.71E-03	WT NoN 14 dpi	H	Small auxin up-regulated RNA1	GO:0009733
Solyc06g083120.1	7.81E-01	1.49E-02	4.29E-01	1.64E-01	**1.34E+00**	**1.44E-04**	9.23E-01	4.86E-03	WT NoN 14 dpi	DNA	LOW QUALITY:ARGONAUTE 3 (AHRDV3.3 --* AT1G31290.3)	
Solyc12g042230.2	7.76E-01	4.32E-02	5.56E-01	1.40E-01	**1.26E+00**	**1.88E-03**	7.91E-01	3.97E-02	WT NoN 14 dpi	E	ATP synthase subunit beta, chloroplastic (AHRD V3.3 *** ATPB_SOLBU)	GO:0015986
Solyc07g045000.3	7.74E-01	1.72E-02	3.41E-01	2.72E-01	**1.10E+00**	**1.30E-03**	-6.35E-02	8.36E-01	WT NoN 14 dpi	E	Homeodomain-like superfamily protein(AHRD V3.3 *-* AT2G02060.2)	GO:0003677
Solyc06g051830.2	7.69E-01	5.30E-02	1.35E-01	7.25E-01	**-2.53E+00**	**4.84E-07**	-5.99E-01	1.26E-01	WT NoN 14 dpi	TR	Potassium transporter (AHRD V3.3 *** K4C5X2_SOLLC)	GO:0015079|GO:0016020|GO:0071805
Solyc07g063480.3	7.67E-01	4.04E-02	8.52E-01	2.41E-02	**-1.41E+00**	**5.23E-04**	3.50E-01	3.34E-01	WT NoN 14 dpi	K	protein kinase family protein (AHRD V3.3 *-* AT5G54380.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g091000.1	7.65E-01	2.52E-01	1.30E+00	5.77E-02	**-2.81E+00**	**2.12E-04**	-3.44E-01	6.03E-01	WT NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12520.1)	
Solyc04g005260.2	7.60E-01	4.29E-01	2.59E+00	1.10E-02	**-2.76E+00**	**7.28E-03**	-2.18E+00	2.92E-02	WT NoN 14 dpi	DNA	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** B9RLG1_RICCO)	GO:0003824|GO:0006281|GO:0006284|GO:0008725|GO:0006284|GO:0008725
Solyc07g039410.3	7.58E-01	1.54E-01	1.57E+00	5.28E-03	**-1.78E+00**	**1.98E-03**	-7.89E-01	1.38E-01	WT NoN 14 dpi	D	EDNR2GH3 protein (AHRD V3.3 *** E0Y3V4_9SOLN)	GO:0043531

Solyc06g050130.3	7.52E-01	7.07E-05	9.79E-01	1.74E-06	**1.27E+00**	**2.09E-08**	6.59E-01	3.28E-04	WT NoN 14 dpi	C	Alpha-galactosidase (AHRD V3.3 ***K4C5G0_SOLLC)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc03g006080.3	7.50E-01	2.81E-02	4.00E-01	2.25E-01	**1.10E+00**	**2.10E-03**	2.69E-01	4.10E-01	WT NoN 14 dpi	PMI	LRR receptor-like kinase (AHRD V3.3 ***A0A072V4N4_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g039850.1	7.48E-01	4.54E-02	9.71E-01	1.13E-02	**1.36E+00**	**7.51E-04**	1.12E-01	7.56E-01	WT NoN 14 dpi	E	LOW QUALITY:ATP synthase subunit beta (AHRD V3.3 *-* ATCG00480.1)	GO:0005524
Solyc02g065230.3	7.43E-01	2.21E-01	1.26E+00	4.36E-02	**-1.89E+00**	**3.71E-03**	-1.53E+00	1.60E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***Q8H0I6_PETHY)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc04g049240.1	7.38E-01	9.01E-02	7.59E-01	8.19E-02	**1.51E+00**	**1.34E-03**	6.93E-01	1.10E-01	WT NoN 14 dpi	E	Photosystem II protein D1 (AHRD V3.3 --* PSBA_CRYJA)	
Solyc03g097380.3	7.37E-01	1.25E-04	-2.28E-01	1.75E-01	**-1.36E+00**	**9.75E-09**	4.70E-01	7.91E-03	WT NoN 14 dpi	TR	Heavy metal transport/detoxificationsuperfamily protein (AHRD V3.3 *** AT5G50740.5)	GO:0030001|GO:0046872
Solyc06g007600.3	7.35E-01	2.79E-02	3.79E-01	2.40E-01	**1.18E+00**	**8.97E-04**	7.27E-01	2.94E-02	WT NoN 14 dpi	RNA	serine-rich protein-like protein (AHRD V3.3 -* AT3G56500.1)	
Solyc04g080500.3	7.33E-01	2.52E-01	1.16E+00	7.58E-02	**-2.27E+00**	**1.24E-03**	-6.70E-01	2.94E-01	WT NoN 14 dpi	T	Myb family transcription factor family protein (AHRD V3.3 *** B9H0R6_POPTR)	GO:0003677
Solyc02g091700.3	7.29E-01	5.15E-03	2.56E-01	2.93E-01	**-1.36E+00**	**5.31E-06**	-8.84E-01	1.00E-03	WT NoN 14 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)	
Solyc05g052680.1	7.25E-01	1.25E-02	1.14E+00	2.57E-04	**-1.07E+00**	**5.29E-04**	-6.48E-01	2.38E-02	WT NoN 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 ***AT2G39980.1)	GO:0016747
Solyc05g050960.3	7.23E-01	2.03E-02	6.74E-01	2.93E-02	**1.47E+00**	**3.05E-05**	8.03E-01	1.08E-02	WT NoN 14 dpi	DNA	DNA repair RAD51-like protein (AHRDV3.3 *** A0A0B0M9S0_GOSAR)	GO:0003677|GO:0003677|GO:0005524|GO:0006281|GO:0008094|GO:0003677|GO:0005524|GO:0006281|GO:0008094
Solyc02g069040.3	7.22E-01	8.08E-02	5.82E-01	1.55E-01	**-1.13E+00**	**8.37E-03**	8.62E-02	8.30E-01	WT NoN 14 dpi	NA	transmembrane protein, putative (DUF594) (AHRD V3.3 *-* AT5G45540.1)	
Solyc11g069240.2	7.05E-01	1.01E-02	6.47E-01	1.71E-02	**1.02E+00**	**4.40E-04**	8.03E-01	4.01E-03	WT NoN 14 dpi	DNA	Zinc finger family protein (AHRD V3.3 *** S8C619_9LAMI)	GO:0003676|GO:0046872|GO:0046872
Solyc01g095500.3	7.05E-01	1.60E-01	2.84E-01	5.64E-01	**2.68E+00**	**9.37E-06**	1.32E+00	1.15E-02	WT NoN 14 dpi	S	SI Cytokinin Response Factor 5	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc10g047170.2	7.00E-01	6.04E-06	5.30E-01	2.19E-04	**-1.44E+00**	**9.65E-12**	5.49E-01	1.46E-04	WT NoN 14 dpi	TR	sulfate transporter 1	GO:0005886|GO:0008272|GO:0015116|GO:0008271|GO:0008272|GO:0008271|GO:0008272
Solyc03g025585.1	6.90E-01	9.54E-03	-2.02E-01	4.19E-01	**-1.04E+00**	**2.56E-04**	-1.32E-01	5.98E-01	WT NoN 14 dpi	P	Tripeptidyl-peptidase 2 (AHRD V3.3 *-* A0A0B0NVF8_GOSAR)	
Solyc09g066270.3	6.75E-01	1.01E-01	8.83E-01	3.51E-02	**1.45E+00**	**1.15E-03**	-3.99E-01	3.23E-01	WT NoN 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9T847_RICCO)	
Solyc03g121200.3	6.75E-01	4.24E-04	8.72E-01	1.92E-05	**-1.32E+00**	**2.40E-08**	5.23E-02	7.56E-01	WT NoN 14 dpi	2M	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 --* A0A151QNQ1_CAJCA)	
Solyc12g044930.2	6.63E-01	3.12E-03	6.03E-01	6.39E-03	**1.07E+00**	**1.77E-05**	8.26E-01	4.00E-04	WT NoN 14 dpi	P	F-box family protein (AHRD V3.3 *** AT2G02240.1)	GO:0005515
Solyc01g095320.3	6.61E-01	2.03E-01	4.49E-01	3.84E-01	**2.63E+00**	**2.08E-05**	1.09E+00	4.16E-02	WT NoN 14 dpi	P	BAG family molecular chaperone regulator6 (AHRD V3.3 *** A0A0B2R655_GLYSO)	GO:0005515|GO:0051087|GO:0051087
Solyc07g006145.1	6.57E-01	7.40E-02	3.74E-01	2.99E-01	**1.33E+00**	**8.45E-04**	1.80E-01	6.15E-01	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***A9ZT56_COPJA)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc02g083500.3	6.50E-01	7.77E-02	2.35E-01	5.12E-01	**1.52E+00**	**2.15E-04**	9.65E-01	1.13E-02	WT NoN 14 dpi	CS	cell wall integrity/stress response component (AHRD V3.3 *** AT5G66090.1)	GO:0006950
Solyc02g068400.3	6.43E-01	8.34E-02	6.81E-01	6.77E-02	**1.20E+00**	**2.49E-03**	4.72E-01	1.98E-01	WT NoN 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT4G20050.5)	
Solyc04g015400.3	6.42E-01	1.48E-01	4.51E-01	3.04E-01	**1.33E+00**	**4.88E-03**	7.45E-01	9.52E-02	WT NoN 14 dpi	L	GDSL esterase/lipase EXL3, putative (AHRD V3.3 *** A0A061GMX5_THECC)	

Solyc05g046000.3	6.38E-01	6.52E-05	8.82E-01	5.97E-07	**-2.01E+00**	**3.19E-14**	-5.41E-01	4.32E-04	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4C0T3_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc04g005070.3	6.22E-01	5.21E-03	5.78E-01	8.78E-03	**1.33E+00**	**6.66E-07**	-4.23E-01	4.82E-02	WT NoN 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)	GO:0005215|GO:0006810|GO:0016020
Solyc12g088380.1	6.21E-01	3.84E-01	1.46E+00	4.71E-02	**-3.11E+00**	**1.51E-04**	-6.92E-01	3.33E-01	WT NoN 14 dpi	DNA	LOW QUALITY:basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT2G14760.1)	
Solyc00g100880.3	6.14E-01	1.55E-01	3.02E-01	4.77E-01	**-1.58E+00**	**8.51E-04**	1.49E+00	1.49E-03	WT NoN 14 dpi	D	LURP-one-like protein (AHRD V3.3 *** AT1G53875.1)	
Solyc11g056640.2	6.08E-01	6.83E-02	2.35E-01	4.69E-01	**1.15E+00**	**1.37E-03**	1.98E-01	5.41E-01	WT NoN 14 dpi	NA	Inactive rhomboid 1 (AHRD V3.3 *** A0A0B0MQ80_GOSAR)	
Solyc11g065720.2	6.07E-01	1.50E-01	1.04E+00	1.72E-02	**1.52E+00**	**1.01E-03**	-5.77E-02	8.89E-01	WT NoN 14 dpi	TR	ABC transporter-like family-protein (AHRDV3.3 *** A0A072VNR4_MEDTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO:0016887|GO:0005524|GO:0016887
Solyc01g103920.3	6.06E-01	5.02E-01	1.73E-01	8.47E-01	**4.06E+00**	**1.09E-04**	5.07E-01	5.73E-01	WT NoN 14 dpi	E	Ferredoxin (AHRD V3.3 ***A0A0K0PY61_NICBE)	GO:0009055|GO:0022900|GO:0051537|GO:0009055|GO:0051536|GO:0009055|GO:0051536
Solyc10g055190.1	6.03E-01	5.90E-02	1.44E+00	7.33E-05	**-1.74E+00**	**5.57E-06**	-2.11E-01	4.95E-01	WT NoN 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4D1B2_SOLLC)	
Solyc07g009040.3	5.98E-01	9.13E-03	6.31E-01	6.29E-03	**-1.69E+00**	**2.05E-08**	-9.64E-01	1.14E-04	WT NoN 14 dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952
Solyc02g065150.2	5.98E-01	1.91E-01	1.13E+00	1.75E-02	**1.97E+00**	**1.55E-04**	4.60E-01	3.11E-01	WT NoN 14 dpi	G	LOB domain-containing 36-like protein (AHRD V3.3 *** A0A0B0PS92_GOSAR)	
Solyc03g118900.2	5.96E-01	3.37E-01	8.77E-01	1.62E-01	**-3.49E+00**	**5.36E-06**	-1.25E+00	5.02E-02	WT NoN 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4BM39_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc06g072403.1	5.95E-01	6.47E-03	2.17E-01	2.90E-01	**-1.06E+00**	**1.73E-05**	-8.59E-01	2.27E-04	WT NoN 14 dpi	S	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 (AHRD V3.3 *-* A0A0B2RAB0_GLYSO)	
Solyc12g097095.1	5.85E-01	8.08E-02	1.49E+00	9.47E-05	**-1.74E+00**	**1.22E-05**	-7.83E-01	2.24E-02	WT NoN 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4DHI2_SOLLC)	
Solyc06g073590.3	5.82E-01	1.20E-01	9.50E-01	1.44E-02	**-1.28E+00**	**1.59E-03**	-4.17E-01	2.60E-01	WT NoN 14 dpi	TR	Nodulin26-like intrinsic protein 31 (AHRD V3.3 *** K4C978_SOLLC)	GO:0005215|GO:0006810|GO:0016020
Solyc02g087450.3	5.82E-01	1.03E-01	3.61E-01	3.03E-01	**1.29E+00**	**8.89E-04**	2.44E-01	4.84E-01	WT NoN 14 dpi	G	Nuclear mitotic apparatus 1 (AHRD V3.3 *-* A0A0B0NXR3_GOSAR)	
Solyc02g077420.3	5.82E-01	1.31E-01	8.28E-01	3.54E-02	**2.77E+00**	**7.35E-08**	7.58E-02	8.40E-01	WT NoN 14 dpi	L	Phospholipase A1 (AHRD V3.3 *** A5YW95_CAPAN)	GO:0006629|GO:0008970|GO:0008970
Solyc04g010270.1	5.71E-01	3.57E-02	1.45E+00	6.44E-06	**-1.32E+00**	**2.55E-05**	-4.36E-01	1.03E-01	WT NoN 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4BPI1_SOLLC)	
Solyc04g081130.1	5.67E-01	6.65E-01	9.90E-02	9.40E-01	**-3.87E+00**	**6.15E-03**	-2.66E+00	5.03E-02	WT NoN 14 dpi	NA	LOW QUALITY:glyoxal oxidase-related protein (AHRD V3.3 *** AT1G19900.1)	
Solyc01g087820.2	5.57E-01	5.48E-03	2.44E-01	1.96E-01	**1.10E+00**	**2.49E-06**	6.09E-01	2.71E-03	WT NoN 14 dpi	STR	subtilisin-like protease 4B	GO:0004252|GO:0006508
Solyc12g089360.1	5.52E-01	8.06E-02	1.54E+00	2.89E-05	**-2.89E+00**	**6.64E-10**	-8.52E-01	9.46E-03	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4DH07_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc04g011760.3	5.51E-01	2.89E-02	1.32E+00	8.30E-06	**-2.96E+00**	**2.22E-12**	-7.90E-01	2.71E-03	WT NoN 14 dpi	2M	Geraniol 8-hydroxylase (AHRD V3.3 --* C76B6_CATRO)	
Solyc09g097980.3	5.42E-01	1.78E-02	6.76E-01	4.06E-03	**1.12E+00**	**1.88E-05**	5.92E-01	1.04E-02	WT NoN 14 dpi	E	NAD(P)-linked oxidoreductase superfamilyprotein (AHRD V3.3 *** AT1G60710.1)	
Solyc03g082620.3	5.36E-01	1.82E-02	5.05E-01	2.53E-02	**1.77E+00**	**8.72E-09**	2.47E-01	2.55E-01	WT NoN 14 dpi	TR	Yellow stripe 1A transporter (AHRD V3.3 *** A0A0K9P9K5_ZOSMR)	GO:0055085
Solyc03g095980.3	5.29E-01	4.05E-01	2.28E-02	9.71E-01	**-3.73E+00**	**2.79E-06**	-5.99E-01	3.46E-01	WT NoN 14 dpi	T	bHLH transcription factor 021	GO:0046983
Solyc01g066760.2	5.22E-01	1.73E-01	1.45E-01	7.01E-01	**1.51E+00**	**4.27E-04**	1.35E-01	7.21E-01	WT NoN 14 dpi	T	DNA-directed RNA polymerase subunit beta' (AHRD V3.3 --* RPOC1_LOLPR)	
Solyc10g080920.2	5.17E-01	3.39E-01	-7.52E-01	1.69E-01	**-4.16E+00**	**2.79E-08**	-1.30E+00	2.15E-02	WT NoN 14 dpi	T	Myb family transcription factor family protein (AHRD V3.3 *** B9GRM8_POPTR)	GO:0003677

Solyc04g076440.1	5.13E-01	3.58E-01	7.91E-01	1.61E-01	**2.25E+00**	**3.57E-04**	1.45E+00	1.37E-02	WT NoN 14 dpi	H	LOW QUALITY:Tetratricopeptide repeat-like superfamily protein (AHRD V3.3 *-* A0A061FLU3_THECC)	
Solyc08g076300.3	5.08E-01	1.57E-02	8.41E-01	2.26E-04	**1.04E+00**	**1.69E-05**	-1.39E-01	4.86E-01	WT NoN 14 dpi	2M	4-coumarate--CoA ligase family protein (AHRD V3.3 *** B9GZT7_POPTR)	GO:0003824|GO:0008152
Solyc02g094340.1	5.03E-01	6.97E-02	-4.26E-02	8.74E-01	**-1.76E+00**	**5.35E-07**	-2.20E-01	4.16E-01	WT NoN 14 dpi	T	GRAS family transcription factor (AHRD V3.3 *** A0A061ECZ9_THECC)	
Solyc06g072400.2	5.02E-01	2.41E-02	2.25E-01	2.92E-01	**-1.04E+00**	**4.03E-05**	-7.34E-01	1.69E-03	WT NoN 14 dpi	T	TBP-associated factor 2 (AHRD V3.3 --* AT1G73960.2)	
Solyc11g072930.2	4.98E-01	1.74E-01	1.42E+00	4.88E-04	**-1.97E+00**	**8.84E-06**	-2.59E-01	4.74E-01	WT NoN 14 dpi	PMI	Leucine-rich repeat transmembrane protein kinase protein, putative (AHRD V3.3 *** A0A061GWK2_THECC)	GO:0005515
Solyc01g097470.3	4.91E-01	2.41E-01	2.18E-01	5.99E-01	**2.18E+00**	**1.54E-05**	5.82E-01	1.67E-01	WT NoN 14 dpi	NA	Neurogenic locus notch-like protein (AHRD V3.3 *** A0A072VSF9_MEDTR)	
Solyc05g050510.3	4.91E-01	4.62E-02	1.56E-01	5.10E-01	**-1.12E+00**	**6.44E-05**	9.69E-01	3.35E-04	WT NoN 14 dpi	NA	Protein yippee-like (AHRD V3.3 *** K4C183_SOLLC)	
Solyc03g120620.3	4.86E-01	8.93E-02	7.27E-01	1.39E-02	**-1.25E+00**	**1.21E-04**	-7.35E-01	1.30E-02	WT NoN 14 dpi	DNA	Homeobox leucine zipper protein (AHRD V3.3 *** G7IUR3_MEDTR)	GO:0003677|GO:0006355|GO:0043565|GO:0006355|GO:0043565
Solyc12g089370.2	4.86E-01	7.82E-02	1.40E+00	1.58E-05	**-1.32E+00**	**3.60E-05**	-3.80E-01	1.63E-01	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4DH08_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc03g007290.3	4.82E-01	3.79E-03	8.92E-01	3.42E-06	**1.14E+00**	**5.77E-08**	2.24E-01	1.51E-01	WT NoN 14 dpi	K	Trehalose 6-phosphate phosphatase (AHRD V3.3 *** K4BEF2_SOLLC)	GO:0003824|GO:0005992
Solyc08g067030.3	4.80E-01	5.02E-01	1.14E+00	1.18E-01	**2.31E+00**	**2.99E-03**	6.18E-01	3.89E-01	WT NoN 14 dpi	NA	transmembrane protein, putative (Proteinof unknown function, DUF642) (AHRD V3.3 *** AT5G11420.1)	
Solyc01g067540.1	4.77E-01	5.41E-01	1.30E+00	1.04E-01	**3.67E+00**	**6.42E-05**	8.25E-02	9.15E-01	WT NoN 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *** W9R6V3_9ROSA)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc10g084910.2	4.76E-01	6.60E-02	2.19E-01	3.85E-01	**1.91E+00**	**3.86E-08**	8.64E-01	1.78E-03	WT NoN 14 dpi	DNA	C2H2 zinc finger protein (AHRD V3.3 *-* A5JUQ4_SOYBN)	GO:0003676|GO:0007275|GO:0007275
Solyc02g082330.1	4.72E-01	3.05E-01	-5.07E-01	2.71E-01	**-1.60E+00**	**1.51E-03**	7.12E-01	1.27E-01	WT NoN 14 dpi	P	LOW QUALITY:P-loop containing nucleoside triphosphate hydrolasessuperfamily protein (AHRD V3.3 --* AT1G12770.2)	
Solyc02g076710.3	4.66E-01	2.50E-01	6.70E-01	1.03E-01	**1.41E+00**	**1.54E-03**	3.98E-01	3.25E-01	WT NoN 14 dpi	G	Cysteine protease (AHRD V3.3 *** Q7XYU8_ANTAD)	GO:0006508|GO:0008234|GO:0008234|GO:0008234
Solyc12g096110.2	4.65E-01	3.72E-01	-1.53E-01	7.68E-01	**1.88E+00**	**1.10E-03**	2.04E-01	6.94E-01	WT NoN 14 dpi	H	BREVIS RADIX	
Solyc08g005620.3	4.65E-01	5.44E-01	1.07E+00	1.71E-01	**-5.31E+00**	**2.03E-07**	-1.89E+00	1.94E-02	WT NoN 14 dpi	H	Gibberellin-regulated protein (AHRD V3.3 *** K0E174_POPTO)	
Solyc09g011620.1	4.64E-01	4.79E-01	1.29E+00	5.70E-02	**2.74E+00**	**2.57E-04**	1.53E+00	2.55E-02	WT NoN 14 dpi	STR	Glutathione S-transferase (AHRD V3.3 *** C0LF68_CAPAN)	GO:0005515
Solyc01g109480.3	4.63E-01	2.65E-02	1.28E-01	5.21E-01	**-1.34E+00**	**3.51E-07**	1.75E-02	9.30E-01	WT NoN 14 dpi	STR	LOW QUALITY:BURP domain protein RD22 (AHRD V3.3 --* RD22_ARATH)	
Solyc06g050440.3	4.58E-01	3.89E-01	-6.31E-02	9.05E-01	**2.25E+00**	**2.19E-04**	4.93E-01	3.54E-01	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4C5I8_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc08g082470.1	4.58E-01	5.90E-02	7.90E-01	2.15E-03	**1.33E+00**	**5.17E-06**	4.09E-01	8.92E-02	WT NoN 14 dpi	D	LOW QUALITY:Late embryogenesisabundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT4G23930.1)	
Solyc01g086670.3	4.55E-01	3.10E-01	1.13E+00	1.62E-02	**2.08E+00**	**7.03E-05**	3.67E-01	4.12E-01	WT NoN 14 dpi	NA	LOW QUALITY:Expressed protein-RZ53 (AHRD V3.3 --* E0CW61_9ORYZ)	
Solyc07g007250.3	4.52E-01	6.48E-01	-2.38E+00	2.22E-02	**4.58E+00**	**7.96E-05**	1.70E+00	9.39E-02	WT NoN 14 dpi	STR	Metallocarboxypeptidase inhibitor (AHRD V3.3 *** MCPI_SOLLC)	GO:0004866
Solyc11g073040.1	4.51E-01	3.85E-01	1.49E+00	7.10E-03	**-1.77E+00**	**1.82E-03**	-8.05E-02	8.76E-01	WT NoN 14 dpi	CS	Dirigent protein (AHRD V3.3 *-* M1B9I8_SOLTU)	

Solyc03g079880.3	4.48E-01	1.04E-02	1.27E-01	4.40E-01	**1.15E+00**	**1.55E-07**	6.70E-01	3.32E-04	WT NoN 14 dpi	NA	Protease inhibitor/seed storage/lipid transfer family protein (AHRD V3.3 *** B9HHI8_POPTR)	
Solyc09g008380.3	4.45E-01	2.78E-01	9.24E-01	2.97E-02	**1.49E+00**	**1.02E-03**	2.20E-01	5.88E-01	WT NoN 14 dpi	CS	Pectate lyase (AHRD V3.3 *** K4CQM6_SOLLC)	
Solyc12g089270.1	4.36E-01	5.81E-01	-1.21E+00	1.33E-01	**-4.47E+00**	**5.05E-06**	-1.57E+00	5.39E-02	WT NoN 14 dpi	H	Auxin responsive SAUR protein (AHRD V3.3 *** A0A103XGS0_CYNCS)	GO:0009733
Solyc06g048410.3	4.33E-01	1.16E-02	1.79E-01	2.72E-01	**1.72E+00**	**5.11E-11**	9.81E-01	1.73E-06	WT NoN 14 dpi	OX	iron superoxide dismutase	GO:0004784|GO:0006801|GO:0046872|GO:0055114
Solyc04g072320.2	4.30E-01	3.25E-01	3.03E-01	4.86E-01	**-2.24E+00**	**1.96E-05**	1.38E+00	3.56E-03	WT NoN 14 dpi	RNA	RNA polymerase I subunit 43 (AHRD V3.3 -* AT1G60620.2)	
Solyc07g052540.3	4.28E-01	6.44E-01	1.30E+00	1.66E-01	**-4.68E+00**	**2.55E-05**	-1.85E+00	5.39E-02	WT NoN 14 dpi	OX	Peroxidase (AHRD V1 ****Q07445_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc01g096340.3	4.16E-01	7.79E-02	5.43E-01	2.42E-02	**-1.28E+00**	**6.65E-06**	-8.85E-01	6.09E-04	WT NoN 14 dpi	H	Small auxin up-regulated RNA2	GO:0009733
Solyc11g010350.2	4.14E-01	1.99E-02	1.65E-01	3.31E-01	**-1.01E+00**	**2.20E-06**	-8.46E-01	2.93E-05	WT NoN 14 dpi	CS	Glucan 1,3-beta-glucosidase (AHRD V3.3 *** A0A151U914_CAJCA)	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc03g034206.1	4.09E-01	2.29E-01	5.13E-01	1.34E-01	**1.04E+00**	**4.36E-03**	4.88E-01	1.54E-01	WT NoN 14 dpi	T	BZIP domain class transcription factor(AHRD V3.3 --* D9ZIP9_MALDO)	
Solyc02g090220.3	4.07E-01	3.58E-01	8.81E-01	5.32E-02	**1.94E+00**	**1.47E-04**	-1.66E-01	7.05E-01	WT NoN 14 dpi	DNA	Zinc finger, Dof-type (AHRD V3.3 *** A0A124SC40_CYNCS)	GO:0003677|GO:0006355
Solyc02g083070.2	4.07E-01	4.70E-01	3.48E-01	5.36E-01	**-2.24E+00**	**4.27E-04**	-6.68E-01	2.40E-01	WT NoN 14 dpi	NA	LOW QUALITY:DUF241 domain protein(AHRD V3.3 *** G7LA86_MEDTR)	
Solyc02g005310.2	4.06E-01	1.02E-01	-2.58E-01	2.90E-01	**-1.16E+00**	**5.28E-05**	3.31E-02	8.91E-01	WT NoN 14 dpi	DNA	DNA glycosylase (AHRD V3.3 *** A0A103X5G9_CYNCS)	GO:0003824|GO:0006281|GO:0006284|GO:0006284
Solyc10g074830.1	4.06E-01	5.55E-01	4.68E-01	4.96E-01	**-2.76E+00**	**4.00E-04**	-4.74E-01	4.91E-01	WT NoN 14 dpi	E	LOW QUALITY:ER-based factor for assembly of V-ATPase (AHRD V3.3 *-*AT5G52980.1)	
Solyc06g051090.2	4.02E-01	1.41E-01	5.78E-01	3.82E-02	**-1.36E+00**	**2.47E-05**	-5.52E-01	4.70E-02	WT NoN 14 dpi	P	U-box domain-containing protein 13 (AHRD V3.3 *** W9RRI9_9ROSA)	GO:0004842|GO:0016567|GO:0005488|GO:0005488
Solyc01g009715.1	4.01E-01	2.07E-01	8.74E-01	9.10E-03	**-1.02E+00**	**2.81E-03**	-3.47E-01	2.73E-01	WT NoN 14 dpi	DNA	RING finger protein, putative (AHRD V3.3 *** A0A061E508_THECC)	
Solyc06g076300.3	3.98E-01	3.96E-01	8.78E-01	6.80E-02	**1.64E+00**	**1.45E-03**	1.04E+00	3.35E-02	WT NoN 14 dpi	K	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** G7JUV7_MEDTR)	GO:0008152|GO:0016787
Solyc02g089470.1	3.94E-01	6.94E-01	1.32E+00	1.95E-01	**5.06E+00**	**2.58E-05**	2.69E+00	1.16E-02	WT NoN 14 dpi	AM	Glutamine dumper, putative (AHRD V3.3 -** G7I7K5_MEDTR)	
Solyc05g012730.1	3.88E-01	5.52E-02	8.92E-01	9.39E-05	**-1.65E+00**	**5.80E-09**	-6.08E-01	4.09E-03	WT NoN 14 dpi	P	Exostosin family protein (AHRD V3.3 *** AT5G61840.1)	
Solyc01g104720.3	3.85E-01	1.78E-01	8.56E-01	4.92E-03	**-1.36E+00**	**4.90E-05**	-1.22E-01	6.66E-01	WT NoN 14 dpi	D	thionin-like protein (AHRD V3.3 -**AT1G25275.1)	
Solyc06g050800.3	3.85E-01	3.77E-01	1.68E-01	6.99E-01	**1.28E+00**	**6.16E-03**	4.31E-01	3.25E-01	WT NoN 14 dpi	AM	Amino acid transporter family protein (AHRD V3.3 *** B9HYI5_POPTR)	
Solyc06g061230.3	3.80E-01	6.37E-02	5.99E-01	5.16E-03	**1.03E+00**	**1.67E-05**	5.94E-01	5.52E-03	WT NoN 14 dpi	STR	Metallocarboxypeptidase inhibitor (AHRDV3.3 -** M1D4V9_SOLTU)	
Solyc09g066260.3	3.79E-01	6.02E-01	-1.32E-01	8.55E-01	**3.84E+00**	**1.36E-05**	1.52E+00	4.33E-02	WT NoN 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9S4L6_RICCO)	
Solyc06g081980.1	3.79E-01	3.66E-02	5.63E-01	3.00E-03	**1.15E+00**	**4.29E-07**	4.58E-01	1.32E-02	WT NoN 14 dpi	2M	Pyridoxal biosynthesis protein PDX1-like protein (AHRD V3.3 *** T2DNB9_PHAVU)	GO:0003824|GO:0003824|GO:0008152|G O:0003824|GO:0008152
Solyc03g122190.3	3.78E-01	3.36E-01	9.38E-02	8.09E-01	**1.37E+00**	**1.48E-03**	5.04E-01	2.02E-01	WT NoN 14 dpi	H	Jasmonate zim-domain protein (AHRD V3.3 *** G7IIQ4_MEDTR)	
Solyc09g091210.3	3.76E-01	1.13E-01	8.08E-01	1.63E-03	**-1.24E+00**	**1.17E-05**	-2.38E-01	3.09E-01	WT NoN 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4CWE7_SOLLC)	
Solyc01g010520.3	3.70E-01	3.24E-01	6.59E-01	8.50E-02	**1.32E+00**	**1.39E-03**	3.02E-01	4.20E-01	WT NoN 14 dpi	DNA	helicase with zinc finger protein (AHRD V3.3 *** AT2G46420.3)	

Solyc06g069030.3	3.65E-01	3.65E-01	-1.68E-01	6.74E-01	**1.16E+00**	**7.03E-03**	8.44E-01	4.26E-02	WT NoN 14 dpi	NA	PAP fibrillin domain protein,expressed protein (AHRD V3.3 *** G7LD88_MEDTR)	
Solyc01g099880.3	3.60E-01	6.15E-01	-2.35E-01	7.43E-01	**3.12E+00**	**1.68E-04**	1.03E+00	1.58E-01	WT NoN 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4B122_SOLLC)	GO:0016021
Solyc12g095750.2	3.60E-01	6.55E-01	7.01E-01	3.87E-01	**3.55E+00**	**1.44E-04**	-2.09E-01	7.95E-01	WT NoN 14 dpi	H	Auxin efflux carrier family protein, putative(AHRD V3.3 *** A0A061FMX0_THECC)	GO:0016021|GO:0055085
Solyc10g052490.2	3.60E-01	5.95E-01	1.64E+00	2.15E-02	**3.06E+00**	**1.07E-04**	2.36E-01	7.27E-01	WT NoN 14 dpi	OX	Isoflavone reductase homolog (AHRD V3.3 *** IFRH_SOLTU)	
Solyc02g086180.3	3.60E-01	6.27E-02	7.28E-01	5.62E-04	**1.69E+00**	**1.45E-09**	7.62E-01	3.48E-04	WT NoN 14 dpi	L	Delta(7)-sterol-C5(6)-desaturase (AHRD V3.3 *** SC5D_TOBAC)	GO:0005506|GO:0006633|GO:0016491|GO:0055114
Solyc02g077430.3	3.59E-01	4.88E-01	-5.35E-01	3.04E-01	**1.78E+00**	**1.72E-03**	1.06E+00	4.71E-02	WT NoN 14 dpi	L	Phospholipase A1 (AHRD V3.3 *** A5YW95_CAPAN)	GO:0006629|GO:0008970|GO:0008970
Solyc02g069030.3	3.56E-01	1.65E-01	3.27E-01	2.01E-01	**-1.04E+00**	**3.09E-04**	-2.98E-01	2.42E-01	WT NoN 14 dpi	D	PHLOEM protein 2-like protein (AHRDV3.3 *** M1JV45_GOSHI)	
Solyc01g058100.2	3.51E-01	4.66E-01	3.08E-01	5.21E-01	**1.85E+00**	**6.00E-04**	8.42E-01	8.73E-02	WT NoN 14 dpi	E	NAD(P)H-quinone oxidoreductase subunitK, chloroplastic (AHRD V3.3 --* NDHK_ANTFO)	
Solyc09g009600.2	3.50E-01	6.00E-01	9.86E-01	1.46E-01	**-3.61E+00**	**9.69E-06**	-1.74E+00	1.39E-02	WT NoN 14 dpi	G	Purple acid phosphatase (AHRD V3.3 ***K4CQY9_SOLLC)	GO:0003993|GO:0046872|GO:0016787|G O:0016787
Solyc01g081000.3	3.44E-01	3.00E-01	5.90E-01	8.14E-02	**1.15E+00**	**1.60E-03**	2.55E-01	4.40E-01	WT NoN 14 dpi	K	Phosphatase 2C family protein, putative (AHRD V3.3 *** A0A061GDE7_THECC)	GO:0003824
Solyc06g048860.2	3.39E-01	5.56E-01	-6.71E-01	2.49E-01	**1.82E+00**	**3.58E-03**	1.50E+00	1.39E-02	WT NoN 14 dpi	PMI	Laccase (AHRD V3.3 ***A0A022PYV8_ERYGU)	GO:0005507|GO:0005507|GO:0016491|G O:0055114|GO:0005507|GO:0016491|GO: 0055114
Solyc02g069025.1	3.34E-01	6.87E-01	5.78E-01	4.87E-01	**-2.76E+00**	**2.40E-03**	-1.74E-01	8.34E-01	WT NoN 14 dpi	D	Phloem protein 2-like protein (AHRD V3.3 *** A0A103Y5W1_CYNCS)	
Solyc11g066120.2	3.34E-01	2.23E-01	5.41E-01	5.38E-02	**1.05E+00**	**5.91E-04**	3.67E-01	1.82E-01	WT NoN 14 dpi	G	CLAVATA3/ESR (CLE)-related protein 46(AHRD V3.3 --* CLE46_ARATH)	
Solyc11g067080.2	3.31E-01	6.42E-02	7.19E-01	2.88E-04	**1.06E+00**	**1.70E-06**	1.62E-01	3.55E-01	WT NoN 14 dpi	K	Protein kinase like protein (AHRD V3.3 ***Q0WN21_ARATH)	GO:0004672|GO:0005524|GO:0006468|G O:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc10g009130.3	3.17E-01	1.51E-01	1.48E-01	4.95E-01	**1.20E+00**	**7.28E-06**	5.96E-01	9.94E-03	WT NoN 14 dpi	G	nuclear fusion defective 6 (AHRD V3.3 *-*AT2G20585.5)	
Solyc04g081860.3	3.14E-01	7.54E-01	1.21E+00	2.32E-01	**-6.43E+00**	**7.54E-07**	-2.66E+00	1.26E-02	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4BVR5_SOLLC)	GO:0004601|GO:0006979|GO:0020037|G O:0055114|GO:0004601|GO:0042744|GO: 0004601|GO:0042744
Solyc05g051380.3	3.04E-01	4.35E-01	4.03E-01	3.03E-01	**1.45E+00**	**8.72E-04**	3.07E-01	4.30E-01	WT NoN 14 dpi	H	AP2-like ethylene-responsive transcriptionfactor (AHRD V3.3 *** G7JWC7_MEDTR)	GO:0003677|GO:0003700|GO:0006355|G O:0003700|GO:0006355
Solyc04g071490.3	3.02E-01	4.74E-01	2.32E-01	5.81E-01	**-1.20E+00**	**7.82E-03**	-7.10E-01	9.93E-02	WT NoN 14 dpi	STR	Heat shock family protein (AHRD V3.3 *-* B9GTI4_POPTR)	
Solyc01g079260.3	2.98E-01	2.64E-01	8.50E-01	3.16E-03	**1.41E+00**	**1.18E-05**	2.73E-01	3.05E-01	WT NoN 14 dpi	T	WRKY transcription factor 23	GO:0003700|GO:0006355|GO:0043565
Solyc04g009420.3	2.96E-01	5.89E-01	1.29E+00	2.42E-02	**1.90E+00**	**1.67E-03**	1.09E+00	5.36E-02	WT NoN 14 dpi	E	PsbP domain protein (AHRD V3.3 *** G7JC63_MEDTR)	GO:0005509|GO:0009523|GO:0009654|G O:0015979|GO:0019898
Solyc06g083930.2	2.91E-01	7.34E-01	-1.03E+00	2.35E-01	**3.10E+00**	**1.17E-03**	1.62E-01	8.50E-01	WT NoN 14 dpi	G	LOB domain-containing protein, putative(AHRD V3.3 *** B9S4L6_RICCO)	
Solyc09g018070.1	2.91E-01	6.11E-01	1.44E+00	1.75E-02	**-1.93E+00**	**2.11E-03**	-4.49E-01	4.34E-01	WT NoN 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4CS74_SOLLC)	GO:0006855|GO:0015238|GO:0015297|G O:0016020|GO:0055085

Solyc08g065190.3	2.88E-01	1.52E-02	1.18E-01	2.96E-01	**1.22E+00**	**3.09E-11**	2.75E-01	1.97E-02	WT NoN 14 dpi	TR	zinc transporter (AHRD V3.3 ***AT1G10970.2)	GO:0005385|GO:0016021|GO:0071577|GO:0016020|GO:0030001|GO:0046873|GO:0055085|GO:0016020|GO:0030001|GO:0046873|GO:0055085
Solyc12g096430.1	2.86E-01	3.45E-01	-5.98E-03	9.84E-01	**1.04E+00**	**1.81E-03**	2.66E-01	3.80E-01	WT NoN 14 dpi	P	LOW QUALITY:Ubiquitin carboxyl-terminalhydrolase family protein (AHRD V3.3 *** D7MB42_ARALL)	GO:0016579|GO:0036459
Solyc08g078920.2	2.86E-01	6.32E-01	1.28E+00	3.95E-02	**-2.59E+00**	**1.73E-04**	-9.60E-01	1.15E-01	WT NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 ***A0A061DW53_THECC)	
Solyc05g021390.3	2.86E-01	3.42E-01	3.89E-01	2.00E-01	**1.26E+00**	**2.49E-04**	4.62E-01	1.30E-01	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***A0A161ABB0_OCIBA)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc12g045020.2	2.85E-01	2.15E-01	3.80E-02	8.67E-01	**1.24E+00**	**8.70E-06**	6.06E-01	1.20E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 family protein (AHRDV3.3 *** B9HFW5_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO: 0016705|GO:0055114
Solyc03g122080.3	2.83E-01	4.85E-01	1.05E+00	1.40E-02	**1.30E+00**	**3.15E-03**	9.37E-01	2.71E-02	WT NoN 14 dpi	NA	DUF936 family protein (AHRD V3.3 *** A0A072THZ7_MEDTR)	
Solyc10g078440.1	2.77E-01	5.25E-01	-8.13E-01	7.01E-02	**-1.41E+00**	**2.96E-03**	-1.77E-02	9.67E-01	WT NoN 14 dpi	G	LOW QUALITY:VQ motif family protein (AHRD V3.3 *-* B6TQH0_MAIZE)	
Solyc07g007990.3	2.69E-01	3.79E-01	8.81E-01	6.94E-03	**1.30E+00**	**1.99E-04**	1.69E-01	5.78E-01	WT NoN 14 dpi	TR	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT4G32272.1)	
Solyc04g050790.3	2.68E-01	3.90E-01	1.96E-01	5.28E-01	**1.19E+00**	**6.68E-04**	7.75E-01	1.80E-02	WT NoN 14 dpi	D	Pathogenic type III effector avirulence factor Avr cleavage site-containing protein(AHRD V3.3 *** A0A118JW76_CYNCS)	
Solyc10g007890.3	2.67E-01	1.63E-01	4.71E-01	1.78E-02	**1.20E+00**	**7.65E-07**	7.17E-01	6.85E-04	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***A9ZT56_COPJA)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc09g010840.1	2.66E-01	5.78E-01	6.56E-01	1.77E-01	**1.37E+00**	**7.66E-03**	-6.19E-01	2.02E-01	WT NoN 14 dpi	D	phantastica	GO:0003677|GO:0005634|GO:0006351|GO:0010338|GO:0005634|GO:0006351|GO: 0010338
Solyc08g075610.2	2.64E-01	5.48E-01	-4.52E-01	3.07E-01	**1.27E+00**	**6.97E-03**	1.19E+00	1.12E-02	WT NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CMS8_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc12g009220.2	2.61E-01	7.26E-01	-3.33E-01	6.55E-01	**2.08E+00**	**9.11E-03**	6.14E-01	4.12E-01	WT NoN 14 dpi	H	jasmonate ZIM-domain protein 1	
Solyc05g047590.3	2.61E-01	6.52E-01	6.16E-02	9.15E-01	**-1.90E+00**	**2.67E-03**	-1.33E+00	2.83E-02	WT NoN 14 dpi	CS	SI Pectinesterase	GO:0004857|GO:0005618|GO:0030599|GO:0042545|GO:0005618|GO:0030599|GO:0042545
Solyc12g010730.2	2.59E-01	2.51E-01	8.11E-02	7.16E-01	**1.42E+00**	**8.57E-07**	6.73E-01	5.29E-03	WT NoN 14 dpi	NA	Plant/F9H3-4 protein (AHRD V3.3 *** A0A072VLR0_MEDTR)	
Solyc11g065470.2	2.54E-01	1.98E-01	7.54E-01	5.74E-04	**-1.06E+00**	**8.26E-06**	-2.19E-01	2.65E-01	WT NoN 14 dpi	C	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)	
Solyc08g068140.3	2.51E-01	6.69E-01	2.57E-01	6.62E-01	**3.14E+00**	**1.21E-05**	-2.24E-01	7.04E-01	WT NoN 14 dpi	STR	BURP domain protein RD22 (AHRD V3.3 -- * RD22_ARATH)	
Solyc06g076760.2	2.43E-01	6.16E-01	8.00E-02	8.69E-01	**1.69E+00**	**1.55E-03**	1.15E+00	2.35E-02	WT NoN 14 dpi	PMI	Laccase 1a	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:

											0055114
Solyc02g082870.3	2.33E-01	6.15E-01	7.83E-01	9.82E-02	**-1.51E+00**	**2.74E-03**	-4.37E-01	3.48E-01	WT NoN 14 dpi	2M	AMP-dependent synthetase and ligasefamily protein (AHRD V3.3 *** AT2G17650.1)	GO:0003824|GO:0008152
Solyc08g079190.1	2.32E-01	8.31E-01	1.43E+00	1.94E-01	**-4.31E+00**	**4.52E-04**	-1.18E+00	2.80E-01	WT NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12490.1)	
Solyc10g075100.2	2.28E-01	6.69E-01	2.49E-01	6.41E-01	**1.83E+00**	**1.86E-03**	1.37E+00	1.50E-02	WT NoN 14 dpi	L	Non-specific lipid-transfer protein (AHRDV3.3 *** Q4A1N1_SOLLC)	GO:0006869|GO:0008289
Solyc01g091110.2	2.25E-01	6.33E-01	1.20E+00	1.63E-02	**-1.99E+00**	**2.31E-04**	-1.05E+00	3.35E-02	WT NoN 14 dpi	CS	LOW QUALITY:Plant invertase/pectin methylesterase inhibitor (AHRD V3.3 *** G7IYJ3_MEDTR)	GO:0004857
Solyc07g052530.3	2.21E-01	7.35E-01	9.81E-01	1.42E-01	**-4.25E+00**	**6.29E-07**	-1.53E+00	2.57E-02	WT NoN 14 dpi	OX	Peroxidase (AHRD V1 ****Q07445_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO: 0004601|GO:0042744
Solyc04g076720.2	2.21E-01	6.37E-01	7.93E-01	9.90E-02	**1.61E+00**	**1.81E-03**	1.10E+00	2.56E-02	WT NoN 14 dpi	STR	WD repeat domain phosphoinositide-interacting 3 (AHRD V3.3 *-* A0A0B0P0U0_GOSAR)	
Solyc06g069640.3	2.21E-01	5.16E-01	-3.20E-01	3.49E-01	**-1.28E+00**	**7.72E-04**	2.04E-01	5.48E-01	WT NoN 14 dpi	DNA	dCTP pyrophosphatase 1 (AHRD V3.3 ***A0A151SL49_CAJCA)	GO:0047429
Solyc08g074480.1	2.17E-01	6.45E-01	1.28E+00	1.11E-02	**1.64E+00**	**1.67E-03**	7.66E-01	1.13E-01	WT NoN 14 dpi	CS	14 kDa proline-rich protein DC2.15 (AHRD V3.3 *** A0A0B2P545_GLYSO)	
Solyc06g083170.3	2.08E-01	5.13E-01	6.18E-01	5.98E-02	**1.10E+00**	**1.74E-03**	1.34E-01	6.73E-01	WT NoN 14 dpi	T	bHLH transcription factor 049	GO:0046983
Solyc05g013660.3	2.07E-01	2.63E-01	7.98E-01	1.60E-04	**-1.08E+00**	**2.57E-06**	-7.34E-01	4.01E-04	WT NoN 14 dpi	AM	lysine ketoglutarate reductase trans- splicing protein (DUF707) (AHRD V3.3 *** AT1G67850.7)	
Solyc02g070080.3	2.03E-01	5.03E-01	2.55E-01	4.01E-01	**-1.64E+00**	**9.74E-06**	-3.49E-01	2.53E-01	WT NoN 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G10500.1)	GO:0016491|GO:0055114
Solyc02g065590.3	2.02E-01	4.63E-01	5.72E-02	8.34E-01	**1.04E+00**	**7.04E-04**	4.03E-01	1.50E-01	WT NoN 14 dpi	H	Carboxylic ester hydrolase (AHRD V3.3 *** A0A087H6F2_ARAAL)	
Solyc06g008760.1	2.02E-01	4.02E-01	2.60E-01	2.82E-01	**-1.44E+00**	**2.12E-06**	-6.56E-01	1.02E-02	WT NoN 14 dpi	OX	Glutaredoxin (AHRD V3.3 *** B3F8F2_SOLTU)	GO:0009055|GO:0015035|GO:0045454
Solyc06g008590.3	2.00E-01	5.30E-01	-3.62E-01	2.59E-01	**1.54E+00**	**4.43E-05**	9.18E-01	7.08E-03	WT NoN 14 dpi	H	auxin-regulated IAA17	GO:0005515|GO:0005634|GO:0006355|GO:0005634|GO:0006355
Solyc01g103250.3	2.00E-01	7.01E-01	-3.63E-01	4.87E-01	**-1.55E+00**	**5.82E-03**	-1.32E+00	1.63E-02	WT NoN 14 dpi	DNA	Zinc finger CCCH domain-containingprotein 44 (AHRD V3.3 *** W9SKR1_9ROSA)	GO:0003677|GO:0005515|GO:0005515
Solyc12g007080.2	1.99E-01	7.50E-01	1.30E+00	4.54E-02	**2.15E+00**	**1.78E-03**	-2.68E+00	1.95E-04	WT NoN 14 dpi	DNA	Plant regulator RWP-RK family protein (AHRD V3.3 --* AT2G17150.6)	
Solyc07g063880.3	1.98E-01	5.92E-01	-1.80E-01	6.25E-01	**-1.73E+00**	**6.43E-05**	-3.02E-01	4.13E-01	WT NoN 14 dpi	C	Beta-glucosidase, putative (AHRD V3.3 *** B9SY45_RICCO)	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc04g008090.3	1.96E-01	5.51E-01	8.26E-01	1.71E-02	**1.60E+00**	**4.12E-05**	6.52E-02	8.42E-01	WT NoN 14 dpi	T	PLATZ transcription factor family protein,putative (AHRD V3.3 *** A0A061EGB3_THECC)	GO:0005622|GO:0008270
Solyc02g062780.3	1.91E-01	2.87E-01	6.47E-01	1.09E-03	**1.16E+00**	**6.20E-07**	4.01E-01	3.11E-02	WT NoN 14 dpi	DNA	chromatin remodeling 1 (AHRD V3.3 ***AT5G66750.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc05g012805.1	1.87E-01	5.79E-01	-1.92E-01	5.69E-01	**-1.02E+00**	**4.99E-03**	8.04E-01	2.30E-02	WT NoN 14 dpi	NA	transmembrane protein (AHRD V3.3 *** AT3G11810.1)	
Solyc01g103060.3	1.83E-01	5.81E-01	8.35E-01	1.68E-02	**1.19E+00**	**1.17E-03**	9.59E-01	6.89E-03	WT NoN 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** A0A072UG85_MEDTR)	GO:0006869|GO:0008289

Solyc04g007530.3	1.81E-01	6.35E-01	8.92E-01	2.60E-02	**2.02E+00**	**1.38E-05**	2.82E-01	4.63E-01	WT NoN 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4BNR0_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc02g068320.2	1.70E-01	2.36E-01	5.72E-01	3.87E-04	**1.09E+00**	**3.05E-08**	2.86E-02	8.40E-01	WT NoN 14 dpi	E	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** A0A061DTA0_THECC)	GO:0016491|GO:0055114
Solyc01g091320.3	1.69E-01	4.45E-01	9.52E-01	1.85E-04	**1.24E+00**	**6.15E-06**	-2.92E-01	1.92E-01	WT NoN 14 dpi	L	sterol C4-methyl oxidase 1-2 (AHRD V3.3 *** AT4G22756.1)	GO:0005506|GO:0006633|GO:0016491|GO:0055114
Solyc03g034375.1	1.67E-01	2.94E-01	1.21E-01	4.43E-01	**1.36E+00**	**3.60E-09**	8.64E-01	8.33E-06	WT NoN 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** S4TID2_GOSHI)	GO:0006869
Solyc04g054257.1	1.65E-01	5.93E-01	-2.41E-01	4.38E-01	**1.13E+00**	**1.00E-03**	7.61E-01	1.96E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 family protein (AHRDV3.3 *** B9HFW5_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc05g055990.3	1.60E-01	4.63E-01	4.68E-01	3.80E-02	**-1.04E+00**	**4.85E-05**	1.03E+00	5.59E-05	WT NoN 14 dpi	TR	plasma membrane intrinsic protein 2.12	GO:0005215|GO:0006810|GO:0016020
Solyc12g095810.2	1.57E-01	3.95E-01	3.39E-01	7.34E-02	**1.07E+00**	**3.32E-06**	1.21E-01	5.09E-01	WT NoN 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)	GO:0005215|GO:0006810|GO:0016020
Solyc02g014830.3	1.57E-01	6.47E-01	1.09E+00	3.41E-03	**-1.20E+00**	**1.56E-03**	-1.68E-02	9.61E-01	WT NoN 14 dpi	STR	Carboxypeptidase (AHRD V3.3 *** K4B4T2_SOLLC)	GO:0004185|GO:0006508
Solyc03g095780.2	1.55E-01	2.07E-01	9.55E-02	4.34E-01	**-1.40E+00**	**8.67E-12**	4.57E-02	7.07E-01	WT NoN 14 dpi	H	Abscisic acid receptor (AHRD V3.3 *** G7JKP6_MEDTR)	
Solyc12g043150.2	1.54E-01	5.25E-01	-4.40E-01	7.70E-02	**-1.24E+00**	**2.10E-05**	2.46E-02	9.19E-01	WT NoN 14 dpi	TR	Regulator of Vps4 activity in the MVB pathway protein, putative (AHRD V3.3 *** A0A061GBK3_THECC)	GO:0015031
Solyc03g007775.1	1.53E-01	7.09E-01	7.01E-01	9.61E-02	**1.24E+00**	**5.07E-03**	-1.48E-01	7.18E-01	WT NoN 14 dpi	E	NAD(P)H-quinone oxidoreductase subunit5, chloroplastic (AHRD V3.3 --* NU5C_SORBI)	
Solyc08g081630.2	1.49E-01	7.44E-01	-6.18E-01	1.84E-01	**1.51E+00**	**2.52E-03**	1.14E+00	1.85E-02	WT NoN 14 dpi	T	WRKY transcription factor 56	GO:0003700|GO:0006355|GO:0043565
Solyc05g052860.3	1.49E-01	7.24E-01	4.92E-01	2.48E-01	**-1.39E+00**	**2.55E-03**	-8.62E-01	4.85E-02	WT NoN 14 dpi	L	Lipase (AHRD V3.3 *** G7JAK3_MEDTR)	
Solyc06g076060.1	1.47E-01	7.18E-01	1.53E+00	7.90E-04	**-1.20E+00**	**6.26E-03**	-8.07E-01	5.60E-02	WT NoN 14 dpi	DNA	LOW QUALITY:Cyclin-dependent proteinkinase inhibitor SMR3 (AHRD V3.3 *-* M5W251_PRUPE)	
Solyc02g092490.3	1.47E-01	7.57E-01	6.20E-01	1.99E-01	**3.58E+00**	**4.95E-08**	8.99E-01	6.74E-02	WT NoN 14 dpi	H	Acyl-CoA N-acyltransferases (NAT)superfamily protein (AHRD V3.3 *** AT2G23060.1)	GO:0008080
Solyc04g039920.1	1.43E-01	8.51E-01	1.89E+00	1.90E-02	**-3.23E+00**	**2.29E-04**	4.93E-01	5.19E-01	WT NoN 14 dpi	STR	12-oxophytodienoate reductase-like protein (AHRD V3.3 *-* OPRL_SOLLC)	GO:0003824|GO:0010181|GO:0016491|GO:0055114|GO:0010181|GO:0016491|GO:0055114
Solyc08g076850.3	1.43E-01	6.48E-01	8.35E-01	1.21E-02	**1.78E+00**	**4.60E-06**	-2.94E-01	3.50E-01	WT NoN 14 dpi	G	Tetraspanin family protein (AHRD V3.3 *** AT5G46700.1)	GO:0016021
Solyc09g092230.2	1.39E-01	7.07E-01	5.65E-01	1.34E-01	**1.80E+00**	**4.22E-05**	-3.45E-01	3.54E-01	WT NoN 14 dpi	E	LOW QUALITY:Chlorophyll a-b bindingprotein of LHCII type I, chloroplastic (AHRD V3.3 --* CB2_DUNSA)	
Solyc04g016250.3	1.39E-01	6.31E-01	6.65E-01	2.81E-02	**1.12E+00**	**6.07E-04**	3.96E-01	1.77E-01	WT NoN 14 dpi	E	Mitochondrial glycoprotein family protein (AHRD V3.3 *** AT2G41600.7)	GO:0005759
Solyc05g053180.3	1.35E-01	7.68E-01	-9.21E-02	8.40E-01	**-1.57E+00**	**1.86E-03**	6.32E-01	1.74E-01	WT NoN 14 dpi	TR	ABC-2 and Plant PDR ABC-type transporter family protein (AHRD V3.3 --*AT4G15233.6)	
Solyc08g066590.3	1.33E-01	8.55E-01	1.34E+00	7.39E-02	**-2.65E+00**	**1.08E-03**	5.08E-01	4.87E-01	WT NoN 14 dpi	H	Root cap protein 3	
Solyc12g088820.2	1.32E-01	6.52E-01	2.12E-01	4.70E-01	**-1.49E+00**	**2.32E-05**	-7.96E-01	1.07E-02	WT NoN 14 dpi	K	Protein kinase family protein (AHRD V3.3 *** AT5G09890.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468

Solyc01g104110.3	1.30E-01	4.76E-01	7.79E-01	2.03E-04	**-1.14E+00**	**1.13E-06**	-1.96E-01	2.85E-01	WT NoN 14 dpi	G	11S globulin seed storage protein 2 (AHRD V3.3 *** A0A0B2RJF9_GLYSO)	GO:0045735
Solyc07g020800.3	1.28E-01	5.61E-01	5.78E-01	1.33E-02	**1.49E+00**	**2.97E-07**	1.61E-01	4.66E-01	WT NoN 14 dpi	CS	Rac-like GTP binding protein (AHRD V3.3 *** O65062_PICMA)	GO:0005525|GO:0005525|GO:0007264|G O:0005525|GO:0007264
Solyc08g048525.1	1.27E-01	6.37E-01	-6.39E-02	8.12E-01	**-1.21E+00**	**1.18E-04**	-9.82E-01	1.09E-03	WT NoN 14 dpi	K	protein phosphatase 2A subunit A3 (AHRD V3.3 --* AT1G13320.3)	
Solyc01g104710.3	1.24E-01	8.28E-01	6.96E-01	2.27E-01	**-2.89E+00**	**2.43E-05**	-1.13E+00	5.46E-02	WT NoN 14 dpi	D	thionin-like protein (AHRD V3.3 -**AT1G25275.2)	
Solyc09g014720.2	1.21E-01	8.78E-01	6.31E-01	4.26E-01	**-2.47E+00**	**4.02E-03**	-1.48E-03	9.99E-01	WT NoN 14 dpi	K	Kinase, putative (AHRD V3.3 ***B9RE26_RICCO)	GO:0004672|GO:0005524|GO:0006468|G O:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc02g090930.3	1.17E-01	5.54E-01	1.22E-01	5.35E-01	**1.21E+00**	**1.50E-06**	3.40E-01	9.24E-02	WT NoN 14 dpi	L	Lipase (AHRD V3.3 *** A0A0B2PU23_GLYSO)	GO:0006629
Solyc02g083870.3	1.16E-01	8.39E-01	7.30E-01	2.08E-01	**-2.52E+00**	**1.43E-04**	-6.33E-01	2.72E-01	WT NoN 14 dpi	H	Gibberellin-regulated protein 2, putative (AHRD V3.3 *** B9SLF4_RICCO)	
Solyc04g049090.3	1.11E-01	3.89E-01	1.86E-02	8.85E-01	**-1.04E+00**	**1.27E-08**	-2.04E-01	1.19E-01	WT NoN 14 dpi	D	SlMlo1	GO:0006952|GO:0016021
Solyc12g040640.2	1.07E-01	8.56E-01	1.57E+00	1.29E-02	**2.04E+00**	**1.85E-03**	4.12E-01	4.89E-01	WT NoN 14 dpi	C	Beta-glucosidase, putative (AHRD V3.3 *** B9T4F7_RICCO)	GO:0004553|GO:0005975|GO:0005975|G O:0005975
Solyc10g086320.2	9.63E-02	5.88E-01	4.62E-01	1.43E-02	**1.24E+00**	**1.71E-07**	9.51E-01	1.18E-05	WT NoN 14 dpi	S	Phosphatidylinositol-4-phosphate 5-kinasefamily protein (AHRD V3.3 *** A0A072VJC1_MEDTR)	GO:0016307|GO:0046488
Solyc01g099210.3	9.58E-02	7.22E-01	4.89E-01	7.81E-02	**-2.21E+00**	**1.04E-08**	-5.65E-01	4.40E-02	WT NoN 14 dpi	L	Lipoxygenase (AHRD V3.3 *** A8W7J7_CAMSI)	GO:0005515|GO:0016491|GO:0055114|G O:0016491|GO:0055114
Solyc03g120440.2	9.52E-02	7.38E-01	-3.70E-01	2.00E-01	**1.52E+00**	**1.22E-05**	6.99E-01	1.99E-02	WT NoN 14 dpi	G	cyclin A2_1	GO:0005634
Solyc02g071060.3	9.47E-02	7.56E-01	8.21E-01	1.13E-02	**1.31E+00**	**1.84E-04**	-3.41E-02	9.11E-01	WT NoN 14 dpi	TR	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)	GO:0005215|GO:0016021
Solyc02g086260.1	9.29E-02	6.97E-01	2.10E-01	3.83E-01	**1.37E+00**	**4.37E-06**	6.37E-01	1.23E-02	WT NoN 14 dpi	R	LOW QUALITY:50S ribosomal protein-related, putative (AHRD V3.3 *** A0A061EGK7_THECC)	
Solyc08g067700.1	9.19E-02	6.73E-01	8.20E-01	7.77E-04	**-1.36E+00**	**1.14E-06**	-5.60E-01	1.51E-02	WT NoN 14 dpi	K	LOW QUALITY:Serine/threonine protein kinase, putative isoform 1 (AHRD V3.3 --* A0A061GQI4_THECC)	
Solyc05g015300.3	8.94E-02	7.59E-01	9.36E-01	3.22E-03	**-1.85E+00**	**9.16E-07**	-3.57E-01	2.27E-01	WT NoN 14 dpi	STR	BURP domain protein RD22 (AHRD V3.3 *** RD22_ARATH)	
Solyc12g014580.2	8.94E-02	9.02E-01	5.90E-01	4.18E-01	**-2.03E+00**	**8.73E-03**	-9.33E-01	2.04E-01	WT NoN 14 dpi	G	Pollen allergen Ole e 6-like protein (AHRD V3.3 *** A0A075WG86_CAPAN)	
Solyc03g117500.1	8.90E-02	7.56E-01	8.18E-01	7.81E-03	**1.44E+00**	**2.91E-05**	2.24E-01	4.36E-01	WT NoN 14 dpi	G	VQ motif-containing protein (AHRD V3.3 *** AT1G80450.1)	
Solyc03g116720.2	8.66E-02	9.10E-01	1.65E-01	8.29E-01	**2.44E+00**	**3.48E-03**	-6.25E-01	4.17E-01	WT NoN 14 dpi	S	Histidine-containing phosphotransferprotein, putative (AHRD V3.3 *** B9RV70_RICCO)	GO:0000160|GO:0004871
Solyc03g121230.3	8.25E-02	5.98E-01	6.04E-02	6.99E-01	**-2.37E+00**	**1.98E-14**	-8.63E-01	7.53E-06	WT NoN 14 dpi	K	protein kinase family protein (AHRD V3.3 *** AT1G51870.2)	GO:0004672|GO:0005524|GO:0006468|G O:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc01g088620.3	7.79E-02	7.83E-01	8.56E-01	5.10E-03	**1.17E+00**	**2.82E-04**	-1.37E-01	6.28E-01	WT NoN 14 dpi	E	Ferredoxin-related (AHRD V3.3 *** A0A061E2R5_THECC)	
Solyc06g068620.3	7.77E-02	8.47E-01	8.82E-01	3.59E-02	**1.67E+00**	**2.95E-04**	3.86E-01	3.41E-01	WT NoN 14 dpi	NA	Negative regulator of sporulation MDS3 (AHRD V3.3 *-* A0A0B0N6H6_GOSAR)	
Solyc08g074740.3	7.47E-02	7.06E-01	8.32E-01	2.45E-04	**1.14E+00**	**4.25E-06**	1.99E-01	3.19E-01	WT NoN 14 dpi	DNA	Poly [ADP-ribose] polymerase (AHRD V3.3 *** K4CMJ2_SOLLC)	GO:0003950|GO:0003950|GO:0006471|G O:0003950|GO:0006471
Solyc07g054400.2	6.58E-02	8.01E-01	6.02E-01	2.81E-02	**1.05E+00**	**3.86E-04**	6.76E-01	1.47E-02	WT NoN 14 dpi	G	Centromere protein S (AHRD V3.3 *-*W9S2H7_9ROSA)	GO:0046982|GO:0071821|GO:0071821
Solyc06g064760.1	6.42E-02	8.72E-01	-7.01E-02	8.60E-01	**-1.16E+00**	**6.79E-03**	3.74E-01	3.51E-01	WT NoN 14 dpi	D	NBS-LRR resistance protein-like protein (AHRD V3.3 *** A1Y9R1_SOLLC)	GO:0043531

Solyc06g074500.2	6.13E-02	6.97E-01	4.14E-01	1.32E-02	**-1.00E+00**	**8.36E-07**	-3.70E-01	2.50E-02	WT NoN 14 dpi	NA	DUF868 family protein (AHRD V3.3 ***G7JKY7_MEDTR)	
Solyc04g051680.3	5.92E-02	8.89E-01	2.38E-01	5.77E-01	**-1.78E+00**	**2.62E-04**	-5.21E-01	2.27E-01	WT NoN 14 dpi	S	Rab family GTPase (AHRD V3.3 *** D8RRT7_SELML)	GO:0005525|GO:0005525|GO:0007264|GO:0005525|GO:0007264
Solyc02g085360.3	5.91E-02	8.25E-01	-6.42E-03	9.81E-01	**1.16E+00**	**1.81E-04**	-8.11E-01	5.10E-03	WT NoN 14 dpi	H	CYP90B3 mRNA for cytochrome P450	GO:0004497|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc02g084800.3	5.21E-02	8.22E-01	8.00E-01	1.72E-03	**1.30E+00**	**6.02E-06**	7.52E-01	2.90E-03	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***A0A0D9X2X2_9ORYZ)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc05g025620.2	3.76E-02	9.12E-01	-6.74E-01	5.53E-02	**-1.27E+00**	**8.60E-04**	-1.64E-01	6.28E-01	WT NoN 14 dpi	L	alpha/beta-Hydrolases superfamily protein(AHRD V3.3 *-* AT3G47560.4)	
Solyc01g111330.3	3.74E-02	9.09E-01	2.84E-01	3.90E-01	**1.31E+00**	**4.34E-04**	1.56E-01	6.36E-01	WT NoN 14 dpi	D	Pathogenesis-related thaumatin familyprotein (AHRD V3.3 *** A0A072UXB7_MEDTR)	
Solyc09g018200.1	3.66E-02	9.06E-01	-8.30E-01	1.24E-02	**-1.03E+00**	**2.54E-03**	9.83E-01	3.74E-03	WT NoN 14 dpi	G	LOW QUALITY:ovate family protein 17	GO:0003677
Solyc06g074390.3	3.59E-02	9.34E-01	-5.99E-01	1.78E-01	**1.71E+00**	**5.37E-04**	1.18E+00	1.10E-02	WT NoN 14 dpi	CS	Fatty acyl-CoA reductase (AHRD V3.3 *** K4C9F7_SOLLC)	GO:0080019
Solyc01g095440.2	3.49E-02	9.26E-01	3.46E-01	3.60E-01	**-1.08E+00**	**7.57E-03**	-6.81E-01	7.83E-02	WT NoN 14 dpi	NA	LOW QUALITY:transmembrane protein,putative (DUF1191) (AHRD V3.3 *** AT4G01140.1)	
Solyc03g093060.1	3.35E-02	9.73E-01	2.44E-01	8.05E-01	**-4.34E+00**	**1.48E-04**	-1.35E+00	1.79E-01	WT NoN 14 dpi	G	Cortical cell-delineating protein	
Solyc09g091030.3	2.99E-02	8.61E-01	2.36E-01	1.75E-01	**1.01E+00**	**2.93E-06**	2.68E-01	1.26E-01	WT NoN 14 dpi	CS	Beta-amylase 1	GO:0000272|GO:0016161|GO:0005975|G O:0005975
Solyc06g074420.1	2.70E-02	9.34E-01	7.97E-01	2.09E-02	**-1.29E+00**	**5.04E-04**	-6.15E-01	6.91E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** B9HQW0_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc03g005015.1	2.55E-02	9.49E-01	-2.62E-01	5.13E-01	**1.19E+00**	**5.62E-03**	1.77E-02	9.65E-01	WT NoN 14 dpi	P	Peptidase family M48 family protein (AHRDV3.3 *-* AT3G27110.2)	
Solyc06g075630.3	1.96E-02	9.29E-01	6.57E-01	5.58E-03	**-1.51E+00**	**2.39E-07**	-4.68E-01	4.07E-02	WT NoN 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4C9S8_SOLLC)	
Solyc11g072670.1	1.75E-02	9.71E-01	2.78E-02	9.54E-01	**-1.36E+00**	**8.34E-03**	-7.13E-01	1.45E-01	WT NoN 14 dpi	RNA	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein(AHRD V3.3 --* AT4G00830.6)	
Solyc05g010060.3	1.72E-02	9.55E-01	-2.91E-01	3.45E-01	**1.15E+00**	**8.10E-04**	-6.03E-02	8.43E-01	WT NoN 14 dpi	STR	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A072TS35_MEDTR)	
Solyc04g005720.3	1.44E-02	9.74E-01	2.99E-01	4.96E-01	**-2.15E+00**	**3.70E-05**	-7.88E-01	8.03E-02	WT NoN 14 dpi	OX	Caleosin-related family protein (AHRDV3.3 *** AT1G70680.1)	
Solyc10g008330.3	1.09E-02	9.68E-01	5.59E-01	4.99E-02	**-1.28E+00**	**7.21E-05**	-7.05E-01	1.53E-02	WT NoN 14 dpi	H	MLP protein (AHRD V3.3 *** A0A0B0N0M0_GOSAR)	GO:0006952|GO:0009607
Solyc10g086490.2	9.37E-03	9.52E-01	2.05E-01	1.93E-01	**-1.45E+00**	**8.16E-10**	5.83E-02	7.08E-01	WT NoN 14 dpi	K	Protein phosphatase 2c, putative (AHRDV3.3 *** B9T262_RICCO)	GO:0003824|GO:0004722|GO:0006470|G O:0004722|GO:0006470
Solyc01g100630.2	5.08E-03	9.90E-01	4.09E-04	9.99E-01	**-1.37E+00**	**2.01E-03**	-8.56E-01	4.16E-02	WT NoN 14 dpi	OX	Catalase (AHRD V3.3 *-* CATA_SOLAP)	GO:0004096|GO:0006979|GO:0020037|GO:0055114|GO:0004096|GO:0020037|GO:0055114|GO:0004096|GO:0020037|GO:0055114
Solyc03g112755.1	2.19E-03	9.94E-01	8.53E-01	6.75E-03	**1.14E+00**	**5.81E-04**	-4.18E-01	1.61E-01	WT NoN 14 dpi	H	Tornado 1 (AHRD V3.3 *-* A0A061F576_THECC)	
Solyc11g065990.2	7.85E-04	9.99E-01	6.91E-01	1.53E-01	**-1.32E+00**	**9.11E-03**	-5.29E-01	2.69E-01	WT NoN 14 dpi	CS	Actin (AHRD V3.3 *** ACT_GOSHI)	
Solyc07g017540.3	-3.37E-03	9.88E-01	4.40E-01	6.49E-02	**1.21E+00**	**1.64E-05**	9.33E-01	3.76E-04	WT NoN 14 dpi	DNA	LEU22441 LeRAD51	GO:0000166|GO:0003677|GO:00036

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Solyc02g065560.1	-4.40E-03	9.88E-01	-8.56E-01	6.92E-03	**1.17E+00**	**4.72E-04**	-4.44E-01	1.40E-01	WT NoN 14 dpi	RNA	Pentatricopeptide repeat-containingprotein, putative (AHRD V3.3 *** B9R8H7_RICCO)	GO:0005515
Solyc08g013930.3	-5.38E-03	9.94E-01	5.70E-01	4.11E-01	**-2.80E+00**	**3.63E-04**	-2.17E-01	7.53E-01	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4CJ27_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc07g056570.1	-8.47E-03	9.90E-01	2.77E-01	6.80E-01	**1.88E+00**	**9.07E-03**	9.87E-01	1.50E-01	WT NoN 14 dpi	H	notabilis	GO:0016702|GO:0055114
Solyc12g056730.1	-9.89E-03	9.83E-01	4.20E-02	9.28E-01	**1.57E+00**	**2.29E-03**	8.09E-01	9.25E-02	WT NoN 14 dpi	PMI	LRR receptor-like kinase (AHRD V3.3 ***A0A072VNN3_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc09g098610.2	-1.52E-02	9.67E-01	-3.25E-01	3.85E-01	**1.30E+00**	**1.51E-03**	8.02E-01	3.83E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***Q8H0I6_PETHY)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc10g079980.1	-1.79E-02	9.46E-01	8.03E-01	5.04E-03	**-1.42E+00**	**1.16E-05**	-1.23E-01	6.43E-01	WT NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4D2N9_SOLLC)	GO:0008152|GO:0016758
Solyc06g050860.3	-1.92E-02	9.00E-01	7.10E-01	7.59E-05	**-1.07E+00**	**1.77E-07**	-9.28E-02	5.44E-01	WT NoN 14 dpi	T	BTB/POZ domain-containing protein (AHRD V3.3 *** AT3G56230.1)	GO:0005515
Solyc07g063490.3	-1.93E-02	9.65E-01	2.86E-01	5.19E-01	**-1.41E+00**	**3.36E-03**	4.34E-01	3.30E-01	WT NoN 14 dpi	G	Root cap/late embryogenesis-like protein (AHRD V3.3 *** A0A072VAI7_MEDTR)	
Solyc04g016330.3	-1.96E-02	9.29E-01	4.93E-01	3.25E-02	**1.50E+00**	**2.85E-07**	8.84E-01	4.19E-04	WT NoN 14 dpi	C	Glycerol-3-phosphate dehydrogenase[NAD(+)] (AHRD V3.3 *** K4BQD3_SOLLC)	GO:0004367|GO:0005975|GO:0055114|GO:0004367|GO:0006072|GO:0009331|GO:0055114|GO:0004367|GO:0006072|GO:0009331|GO:0055114
Solyc07g042170.3	-2.00E-02	9.58E-01	-1.17E-01	7.59E-01	**1.39E+00**	**1.15E-03**	2.39E-02	9.50E-01	WT NoN 14 dpi	H	Jasmonate-zim-domain protein (AHRD V3.3 *** A0A167V6B7_CAMSI)	
Solyc01g106943.1	-2.28E-02	9.37E-01	-4.85E-01	1.03E-01	**-1.01E+00**	**1.66E-03**	-9.56E-01	2.63E-03	WT NoN 14 dpi	TR	Myosin heavy chain-like protein (AHRD V3.3 *-* G7JZT3_MEDTR)	
Solyc03g112210.1	-2.40E-02	9.48E-01	-2.62E-01	4.82E-01	**-1.20E+00**	**3.07E-03**	8.27E-01	3.29E-02	WT NoN 14 dpi	NA	LOW QUALITY:Phloem specific protein (AHRD V3.3 -** G7J4R7_MEDTR)	
Solyc06g073760.3	-2.40E-02	9.58E-01	5.29E-01	2.49E-01	**1.92E+00**	**2.38E-04**	5.03E-01	2.72E-01	WT NoN 14 dpi	C	Beta-glucosidase (AHRD V3.3 *** A0A0B4PJM3_SOYBN)	GO:0004553|GO:0005975
Solyc07g056140.3	-2.42E-02	8.88E-01	9.94E-02	5.66E-01	**1.02E+00**	**2.75E-06**	-9.80E-01	5.12E-06	WT NoN 14 dpi	C	ADP-glucose pyrophosphorylase small subunit	GO:0005978|GO:0008878|GO:0009058|GO:0016779|GO:0009058|GO:0016779
Solyc02g077540.3	-2.46E-02	9.72E-01	5.62E-01	4.24E-01	**-2.07E+00**	**6.09E-03**	-1.65E+00	2.48E-02	WT NoN 14 dpi	NA	transmembrane protein%2C putative(Protein of unknown function%2C DUF599) (AHRD V3.3 *** AT3G18215.1)	
Solyc01g105800.3	-2.65E-02	9.46E-01	1.32E+00	1.96E-03	**-1.46E+00**	**7.97E-04**	-7.08E-01	7.63E-02	WT NoN 14 dpi	T	MADS box transcription factor (AHRD V1 **-- Q2NNB9_ELAGV)%3B containsInterpro domain(s) IPR002100 Transcription factor%2C MADS-box	GO:0000165|GO:0000977|GO:0045944|GO:0003677|GO:0046983|GO:0003677|GO: 0046983
Solyc06g071220.1	-2.65E-02	9.60E-01	-1.15E-01	8.29E-01	**-1.70E+00**	**3.47E-03**	9.21E-01	9.24E-02	WT NoN 14 dpi	STR	LOW QUALITY:Peptidase S41 family protein (AHRD V3.3 --* AT5G46390.2)	
Solyc12g037950.2	-3.26E-02	9.02E-01	8.79E-01	2.45E-03	**-2.44E+00**	**9.80E-10**	-7.35E-01	9.37E-03	WT NoN 14 dpi	OX	Protein PLANT CADMIUM RESISTANCE2 (AHRD V3.3 *** A0A1D1Y359_9ARAE)	
Solyc06g009610.1	-3.57E-02	9.35E-01	1.11E-01	8.01E-01	**-2.32E+00**	**1.50E-05**	-1.19E+00	1.15E-02	WT NoN 14 dpi	T	LOW QUALITY:GRAS family transcriptionfactor, putative (AHRD V3.3 *** A0A061EWU1_THECC)	
Solyc05g055540.2	-3.70E-02	9.40E-01	-1.47E-02	9.76E-01	**-1.56E+00**	**3.69E-03**	7.67E-01	1.29E-01	WT NoN 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT2G39210.1)	GO:0016021|GO:0055085

Solyc08g066150.1	-3.74E-02	9.21E-01	-4.51E-01	2.36E-01	**-1.41E+00**	**8.26E-04**	2.29E-01	5.42E-01	WT NoN 14 dpi	D	LOW QUALITY:Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 -- * AT3G44480.5)	
Solyc07g009500.2	-4.19E-02	9.60E-01	-2.06E+00	1.97E-02	**3.09E+00**	**9.42E-04**	1.82E+00	3.71E-02	WT NoN 14 dpi	D	Chitinase (AHRD V3.3 *-* Q9SQF7_BRAJU)	GO:0008061
Solyc02g087610.1	-4.21E-02	8.74E-01	1.46E-01	5.85E-01	**1.14E+00**	**2.06E-04**	4.23E-01	1.21E-01	WT NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein(AHRD V3.3 *** D7LM18_ARALL)	
Solyc04g071540.3	-4.84E-02	8.75E-01	1.81E-01	5.57E-01	**-1.01E+00**	**2.76E-03**	-7.36E-01	2.30E-02	WT NoN 14 dpi	CS	Sterol glucosyltransferase (AHRD V3.3 ***Q2I015_9SOLA)	GO:0005975|GO:0016758|GO:0030259|GO:0008152|GO:0016758|GO:0008152|GO:0016758
Solyc05g050730.1	-4.91E-02	9.47E-01	5.95E-01	4.21E-01	**-3.03E+00**	**3.09E-04**	-4.02E-01	5.86E-01	WT NoN 14 dpi	G	Stigma-specific protein Stig1 (AHRD V3.3 *** A0A103Y3M1_CYNCS)	
Solyc08g078910.1	-5.92E-02	9.19E-01	9.49E-01	1.12E-01	**-2.26E+00**	**5.84E-04**	-7.62E-01	1.99E-01	WT NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12520.1)	
Solyc07g055560.3	-6.50E-02	7.92E-01	1.29E-01	6.02E-01	**1.70E+00**	**2.33E-07**	6.21E-01	1.73E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***A0A124SAX2_CYNCS)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc06g071240.2	-6.84E-02	8.86E-01	3.41E-01	4.77E-01	**1.95E+00**	**3.28E-04**	9.50E-01	5.45E-02	WT NoN 14 dpi	N	Glutamine-dependent NAD(+) synthetase (AHRD V3.3 *-* NADE_ARATH)	
Solyc06g009670.3	-7.50E-02	8.32E-01	3.58E-01	3.17E-01	**-1.30E+00**	**9.97E-04**	-6.10E-01	9.36E-02	WT NoN 14 dpi	STR	DNAJ heat shock N-terminal domain- containing family protein (AHRD V3.3 *** B9GSH4_POPTR)	GO:0005515
Solyc11g010260.2	-7.60E-02	7.82E-01	2.46E-01	3.73E-01	**1.11E+00**	**3.83E-04**	2.43E-01	3.78E-01	WT NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein GO:0005515(AHRD V3.3 *** A0A103XU85_CYNCS)	
Solyc01g104400.3	-9.17E-02	7.69E-01	9.42E-01	5.23E-03	**1.69E+00**	**1.02E-05**	9.29E-01	5.79E-03	WT NoN 14 dpi	G	Basic blue protein (AHRD V3.3 *** A0A151R520_CAJCA)	GO:0009055
Solyc12g089380.2	-9.54E-02	8.82E-01	4.38E-02	9.46E-01	**-3.15E+00**	**4.10E-05**	-1.35E+00	4.37E-02	WT NoN 14 dpi	CS	expansin 8	GO:0005576|GO:0009664|GO:0009664
Solyc08g079317.1	-9.75E-02	7.73E-01	-3.02E-01	3.76E-01	**-1.19E+00**	**1.46E-03**	-6.07E-01	8.12E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 family protein (AHRDV3.3 *** U5GNW2_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc10g017490.2	-1.02E-01	7.16E-01	-1.94E-02	9.45E-01	**-1.19E+00**	**2.23E-04**	-8.22E-01	6.37E-03	WT NoN 14 dpi	K	MAP kinase kinase kinase 74	GO:0004672|GO:0005524|GO:0006468|GO:0005515|GO:0005515
Solyc12g017460.1	-1.03E-01	7.68E-01	6.76E-02	8.47E-01	**-1.25E+00**	**1.27E-03**	-5.56E-01	1.21E-01	WT NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A199UFA2_ANACO)	GO:0016788
Solyc06g005610.1	-1.08E-01	8.64E-01	-6.61E-01	2.99E-01	**-2.85E+00**	**1.06E-04**	-9.28E-01	1.49E-01	WT NoN 14 dpi	NA	LOW QUALITY:RTL5-like protein (AHRD V3.3 *** F5C0G8_SOLCH)	
Solyc10g076410.1	-1.11E-01	4.44E-01	-2.26E-01	1.26E-01	**-1.12E+00**	**2.67E-08**	-2.76E-01	6.40E-02	WT NoN 14 dpi	H	Abscisic acid receptor (AHRD V3.3 *** G7KT83_MEDTR)	
Solyc07g063110.3	-1.14E-01	3.41E-01	2.06E-01	9.33E-02	**-1.17E+00**	**2.82E-10**	7.85E-03	9.47E-01	WT NoN 14 dpi	P	Core-2/I-branching beta-1,6-N- acetylglucosaminyltransferase family protein (AHRD V3.3 *** F4JIW2_ARATH)	GO:0008375|GO:0016020
Solyc02g071690.2	-1.18E-01	8.73E-01	4.03E-01	5.87E-01	**-2.19E+00**	**6.13E-03**	-7.03E-01	3.46E-01	WT NoN 14 dpi	L	Lipase, GDSL (AHRD V3.3 *** A0A124S9Z4_CYNCS)	GO:0016788
Solyc12g098870.2	-1.19E-01	8.46E-01	-2.80E-01	6.48E-01	**-2.21E+00**	**1.20E-03**	-9.00E-01	1.50E-01	WT NoN 14 dpi	TR	ABC transporter B family protein (AHRDV3.3 *** G7IBR0_MEDTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO:0016887|GO:0005524|GO:0016887
Solyc04g082170.3	-1.22E-01	4.33E-01	4.72E-01	4.70E-03	**-1.96E+00**	**1.12E-12**	-4.22E-01	1.05E-02	WT NoN 14 dpi	2M	alcohol dehydrogenase	GO:0008270|GO:0016491|GO:0055114|G

											O:0055114|GO:0055114
Solyc02g063420.3	-1.23E-01	4.96E-01	-3.01E-01	1.02E-01	**-1.11E+00**	**1.39E-06**	-6.73E-01	8.26E-04	WT NoN 14 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)	
Solyc04g073990.3	-1.26E-01	4.24E-01	-3.56E-01	2.98E-02	**1.18E+00**	**4.34E-08**	6.95E-01	1.33E-04	WT NoN 14 dpi	TR	annexin p34	GO:0005509|GO:0005544
Solyc12g042600.2	-1.27E-01	8.62E-01	1.49E+00	4.96E-02	**2.96E+00**	**3.61E-04**	1.93E+00	1.28E-02	WT NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DF51_SOLLC)	GO:0008152|GO:0016758
Solyc07g009435.1	-1.30E-01	4.42E-01	-6.01E-01	1.29E-03	**-1.14E+00**	**3.16E-07**	8.79E-01	1.65E-05	WT NoN 14 dpi	D	Proteinase inhibitor (AHRD V3.3 --* A0A0R4WFE9_TOBAC)	
Solyc04g077050.3	-1.34E-01	4.65E-01	4.25E-01	2.67E-02	**1.22E+00**	**3.96E-07**	1.02E-01	5.79E-01	WT NoN 14 dpi	AM	Amino acid transporter (AHRD V3.3 *** P93561_SOLTU)	
Solyc03g093070.1	-1.40E-01	8.35E-01	5.20E-01	4.41E-01	**-3.72E+00**	**7.34E-06**	-1.44E+00	3.93E-02	WT NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12520.1)	
Solyc04g079730.1	-1.41E-01	7.17E-01	-6.58E-01	9.93E-02	**1.16E+00**	**5.78E-03**	-6.98E-02	8.57E-01	WT NoN 14 dpi	D	allene oxide synthase	GO:0004497|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc01g079460.2	-1.56E-01	6.21E-01	4.81E-01	1.34E-01	**-1.54E+00**	**3.76E-05**	-2.47E-01	4.33E-01	WT NoN 14 dpi	NA	LOW QUALITY:BnaC09g16130D protein (AHRD V3.3 *** A0A078E278_BRANA)	
Solyc10g084230.2	-1.57E-01	8.38E-01	-2.53E-01	7.42E-01	**-2.89E+00**	**8.21E-04**	-1.77E+00	2.81E-02	WT NoN 14 dpi	NA	DUF1685 family protein (AHRD V3.3 ***G7LJH7_MEDTR)	
Solyc05g013930.2	-1.57E-01	7.14E-01	-4.97E-02	9.08E-01	**2.39E+00**	**6.45E-06**	2.71E-01	5.28E-01	WT NoN 14 dpi	RNA	RNA-binding family protein (AHRD V3.3 *** B9HLD5_POPTR)	GO:0000166|GO:0003676|GO:0003676
Solyc06g051130.1	-1.58E-01	4.54E-01	-4.72E-01	3.19E-02	**-1.17E+00**	**6.77E-06**	-5.76E-01	1.03E-02	WT NoN 14 dpi	NA	LOW QUALITY:Transferase family protein(AHRD V3.3 *** B9HSL5_POPTR)	GO:0016747
Solyc01g006790.2	-1.58E-01	4.63E-01	5.23E-01	2.10E-02	**-1.04E+00**	**4.60E-05**	-1.81E-01	4.01E-01	WT NoN 14 dpi	NA	BnaAnng41820D protein (AHRD V3.3 *** A0A078K412_BRANA)	
Solyc01g109390.3	-1.63E-01	6.64E-01	1.08E+00	7.29E-03	**-1.74E+00**	**7.66E-05**	3.95E-02	9.16E-01	WT NoN 14 dpi	NA	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MM18_ARALL)	
Solyc09g082480.2	-1.68E-01	8.86E-01	8.22E-01	4.84E-01	**3.83E+00**	**2.79E-03**	1.12E+00	3.42E-01	WT NoN 14 dpi	DNA	RNA-directed DNA methylation protein (AHRD V3.3 *** G7K3Q7_MEDTR)	GO:0005634|GO:0044030
Solyc03g118940.3	-1.68E-01	8.14E-01	-7.63E-01	2.90E-01	**2.35E+00**	**2.63E-03**	-1.36E+00	6.43E-02	WT NoN 14 dpi	C	Glycosyltransferase, putative (AHRD V3.3 *** B9S2Z4_RICCO)	GO:0016757
Solyc12g010980.2	-1.68E-01	9.01E-01	7.01E-01	6.05E-01	**4.40E+00**	**2.95E-03**	2.61E+00	6.22E-02	WT NoN 14 dpi	S	HXXXD-type acyl-transferase family protein GO:0016747 (AHRD V3.3 *** AT3G26040.1)	
Solyc06g007230.1	-1.68E-01	8.39E-01	1.56E+00	6.80E-02	**2.54E+00**	**4.69E-03**	2.11E+00	1.63E-02	WT NoN 14 dpi	D	RING/U-box superfamily protein (AHRDV3.3 *** AT2G42360.1)	GO:0005515|GO:0008270
Solyc07g055010.3	-1.70E-01	7.68E-01	1.29E-01	8.22E-01	**-2.73E+00**	**6.27E-05**	-7.82E-01	1.83E-01	WT NoN 14 dpi	TR	Heavy metal transport/detoxificationsuperfamily protein (AHRD V3.3 *** A0A061GX23_THECC)	GO:0030001|GO:0046872
Solyc01g006840.3	-1.73E-01	4.24E-01	2.18E-01	3.15E-01	**-1.35E+00**	**1.12E-06**	-6.27E-01	6.75E-03	WT NoN 14 dpi	S	Calcium-dependent protein kinase, putative (AHRD V3.3 *** B9RL17_RICCO)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc01g104850.3	-1.75E-01	8.41E-01	8.02E-01	3.64E-01	**-2.53E+00**	**7.26E-03**	-2.35E+00	1.20E-02	WT NoN 14 dpi	STR	Carboxypeptidase (AHRD V3.3 *** K4B257_SOLLC)	GO:0004185|GO:0006508
Solyc01g088490.3	-1.77E-01	6.19E-01	6.68E-01	6.99E-02	**1.31E+00**	**9.70E-04**	7.11E-01	5.46E-02	WT NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein(AHRD V3.3 *** A0A103XV88_CYNCS)	

Solyc03g119660.2	-1.84E-01	4.38E-01	1.01E+00	2.01E-04	**-3.08E+00**	**6.52E-13**	-8.65E-01	1.05E-03	WT NoN 14 dpi	OX	Plant cadmium resistance 2 (AHRD V3.3 *-* A0A0K9PLA8_ZOSMR)	
Solyc11g066140.2	-1.93E-01	4.23E-01	-2.54E-01	2.92E-01	**-1.16E+00**	**4.52E-05**	-4.33E-01	7.87E-02	WT NoN 14 dpi	TR	P-hydroxybenzoic acid efflux pump subunitaaeB (AHRD V3.3 *** A0A061GW63_THECC)	
Solyc06g005320.1	-1.98E-01	6.00E-01	-5.71E-01	1.37E-01	**-2.70E+00**	**1.11E-07**	-4.28E-01	2.60E-01	WT NoN 14 dpi	T	MYB-related transcription factor (AHRD V3.3 *-* A0A059PRS8_SALMI)	GO:0003677
Solyc07g065320.3	-1.98E-01	2.45E-01	-2.29E-02	8.92E-01	**1.51E+00**	**1.82E-09**	9.89E-01	2.99E-06	WT NoN 14 dpi	TR	ABC subfamily C transporter (AHRD V3.3 *** A0A0D3RBU8_WHEAT)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO:0016887|GO:0005524|GO:0016887
Solyc05g014290.3	-2.00E-01	8.01E-01	3.18E-01	6.90E-01	**-3.78E+00**	**6.05E-05**	-2.00E+00	1.75E-02	WT NoN 14 dpi	G	R2R3MYB transcription factor 40	GO:0003677
Solyc07g062630.1	-2.03E-01	6.95E-01	-5.56E-02	9.14E-01	**1.48E+00**	**7.73E-03**	1.03E+00	5.56E-02	WT NoN 14 dpi	TR	ABC transporter family protein (AHRD V3.3 *** B9I1V7_POPTR)	GO:0005524|GO:0016887|GO:0016020|G O:0016020
Solyc05g053400.2	-2.03E-01	4.76E-01	2.24E-01	4.34E-01	**1.03E+00**	**1.10E-03**	-3.60E-01	2.12E-01	WT NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** A0A0A1WC49_NICAT)	GO:0008152|GO:0016758
Solyc07g043670.1	-2.09E-01	5.96E-01	3.78E-01	3.41E-01	**-2.66E+00**	**3.23E-07**	-1.05E+00	1.19E-02	WT NoN 14 dpi	S	LOW QUALITY:HXXXD-type acyl- transferase family protein (AHRD V3.3 *** AT4G15390.2)	GO:0016747
Solyc04g056550.1	-2.09E-01	7.62E-01	1.98E+00	7.61E-03	**-2.59E+00**	**8.05E-04**	-1.34E+00	6.10E-02	WT NoN 14 dpi	T	LOW QUALITY:MADS-box transcriptionfactor family protein (AHRD V3.3 *** AT4G36590.1)	GO:0003677|GO:0046983
Solyc04g081460.2	-2.11E-01	4.80E-01	-3.28E-01	2.76E-01	**-1.20E+00**	**3.91E-04**	-6.63E-01	3.31E-02	WT NoN 14 dpi	S	calcineurin B-like protein 10 (AHRD V3.3 -- * AT4G33000.6)	
Solyc09g075750.1	-2.15E-01	6.31E-01	2.87E-01	5.21E-01	**-1.26E+00**	**8.72E-03**	1.10E-01	8.05E-01	WT NoN 14 dpi	S	membrane-associated kinase regulator (AHRD V3.3 *** AT5G26230.1)	
Solyc07g054145.1	-2.20E-01	2.88E-01	-1.04E-01	6.13E-01	**-1.08E+00**	**1.49E-05**	-4.58E-01	3.22E-02	WT NoN 14 dpi	P	CAAX amino terminal protease family protein (AHRD V3.3 *** AT2G20725.1)	GO:0016020
Solyc03g070430.1	-2.24E-01	3.41E-01	-4.49E-01	6.32E-02	**1.21E+00**	**1.82E-05**	6.15E-01	1.33E-02	WT NoN 14 dpi	RNA	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT4G14170.2)	
Solyc07g006610.3	-2.34E-01	2.37E-01	-4.92E-01	1.72E-02	**-1.02E+00**	**1.58E-05**	-2.76E-01	1.65E-01	WT NoN 14 dpi	K	Tyrosine kinase family protein (AHRD V3.3 *** G7JD53_MEDTR)	GO:0004672|GO:0005524|GO:0006468|G O:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc02g024060.2	-2.35E-01	6.85E-01	-1.54E+00	1.26E-02	**-2.38E+00**	**3.12E-04**	1.33E-01	8.18E-01	WT NoN 14 dpi	PMI	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *-* Q8GY50_ARATH)	
Solyc08g074683.1	-2.37E-01	6.21E-01	-4.41E-02	9.27E-01	**1.70E+00**	**1.42E-03**	-5.98E-01	2.18E-01	WT NoN 14 dpi	2M	polyphenol oxidase precursor	GO:0004097|GO:0046148|GO:0055114|G O:0004097|GO:0055114|GO:0004097|GO: 0055114
Solyc11g072040.2	-2.39E-01	4.10E-01	-1.75E-01	5.45E-01	**1.28E+00**	**1.40E-04**	-3.21E-02	9.11E-01	WT NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** W9RH15_9ROSA)	GO:0016788
Solyc07g052240.3	-2.41E-01	5.66E-01	-5.00E-01	2.38E-01	**-1.77E+00**	**2.27E-04**	-1.09E+00	1.45E-02	WT NoN 14 dpi	D	L-ascorbate oxidase-like protein (AHRDV3.3 *** A2Q4H7_MEDTR)	GO:0005507|GO:0005507|GO:0016491|G O:0055114|GO:0005507|GO:0016491|GO: 0055114
Solyc01g108680.3	-2.41E-01	5.05E-01	4.46E-01	2.21E-01	**-1.38E+00**	**6.63E-04**	3.49E-02	9.23E-01	WT NoN 14 dpi	H	Methyl esterase (AHRD V3.3 *** A0A072UEL6_MEDTR)	
Solyc01g106200.2	-2.43E-01	5.67E-01	1.92E-01	6.50E-01	**-1.37E+00**	**3.00E-03**	3.38E-01	4.26E-01	WT NoN 14 dpi	TR	Oligopeptide transporter, putative (AHRDV3.3 *** B9RX59_RICCO)	GO:0055085
Solyc10g047810.2	-2.43E-01	2.53E-01	-2.77E-01	1.94E-01	**-1.21E+00**	**3.99E-06**	-6.20E-01	6.22E-03	WT NoN 14 dpi	PMI	Clade XVII lectin receptor kinase (AHRDV3.3 *** K4D043_SOLLC)	GO:0004672|GO:0005524|GO:0006468|G O:0004672|GO:0006468|GO:0004672|GO: 0006468

Solyc08g076640.1	-2.47E-01	7.27E-01	1.91E-01	7.87E-01	**-2.02E+00**	**7.80E-03**	-2.54E-01	7.19E-01	WT NoN 14 dpi	P	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 ***AT1G03230.1)	GO:0004190|GO:0006508
Solyc06g059880.3	-2.49E-01	6.78E-01	4.14E-01	4.91E-01	**-6.72E+00**	**1.73E-11**	-1.31E+00	3.58E-02	WT NoN 14 dpi	AM	Acetolactate synthase	GO:0000287|GO:0003984|GO:0009082|GO:0030976|GO:0050660|GO:0000287|GO:0030976|GO:0000287|GO:0030976
Solyc07g005900.3	-2.56E-01	5.19E-01	5.81E-01	1.51E-01	**1.26E+00**	**3.43E-03**	1.27E-01	7.49E-01	WT NoN 14 dpi	D	Calcium-binding EF-hand family protein (AHRD V3.3 *** A0A061GQP8_THECC)	GO:0005509
Solyc05g010330.3	-2.71E-01	5.09E-01	-4.60E-01	2.66E-01	**1.42E+00**	**1.68E-03**	1.11E+00	1.12E-02	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4BXK6_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc06g005310.3	-2.75E-01	3.35E-01	-4.90E-01	9.13E-02	**-2.26E+00**	**1.60E-08**	-2.66E-01	3.51E-01	WT NoN 14 dpi	T	MYB transcription factor	GO:0003677
Solyc12g019440.2	-2.77E-01	6.40E-01	8.65E-02	8.84E-01	**-2.14E+00**	**1.13E-03**	-5.45E-01	3.60E-01	WT NoN 14 dpi	CS	Pectinacetylesterase family protein (AHRD V3.3 *** AT4G19420.2)	GO:0016787
Solyc02g083040.1	-2.79E-01	6.47E-01	-4.65E-02	9.39E-01	**-1.89E+00**	**4.21E-03**	-1.66E+00	1.09E-02	WT NoN 14 dpi	NA	LOW QUALITY:DUF241 domain protein(AHRD V3.3 *** G7LA86_MEDTR)	
Solyc07g061880.2	-2.82E-01	2.02E-01	-2.43E-01	2.71E-01	**-1.43E+00**	**5.40E-07**	-9.35E-01	2.00E-04	WT NoN 14 dpi	NA	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151TAX5_CAJCA)	
Solyc07g053450.3	-2.84E-01	5.66E-01	3.82E-01	4.42E-01	**-2.49E+00**	**2.75E-05**	-9.58E-01	6.12E-02	WT NoN 14 dpi	T	BZIP family transcription factor (AHRDV3.3 *** A0A072VB17_MEDTR)	GO:0003700|GO:0006355|GO:0043565
Solyc03g120060.2	-2.87E-01	6.03E-01	8.14E-01	1.48E-01	**1.98E+00**	**1.21E-03**	6.86E-01	2.20E-01	WT NoN 14 dpi	H	castasterone 26-hydroxylase	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc06g064770.1	-2.91E-01	7.22E-01	-5.80E-01	4.80E-01	**-2.31E+00**	**8.28E-03**	-1.49E+00	7.75E-02	WT NoN 14 dpi	2M	LOW QUALITY:UDP-Glycosyltransferasesuperfamily protein (AHRD V3.3 --* AT2G28080.1)	
Solyc06g054280.1	-2.96E-01	6.39E-01	-5.57E-01	3.80E-01	**-2.92E+00**	**8.01E-05**	-1.34E+00	4.03E-02	WT NoN 14 dpi	P	LOW QUALITY:E3 UFM1-protein ligase 1 homolog (AHRD V3.3 --* UFL1_ARATH)	
Solyc01g080380.3	-3.02E-01	4.73E-01	9.04E-01	3.85E-02	**1.26E+00**	**5.53E-03**	5.37E-01	2.06E-01	WT NoN 14 dpi	N	S-adenosylmethionine decarboxylaseproenzyme (AHRD V3.3 *** A0A068TRL8_COFCA)	GO:0004014|GO:0004014|GO:0006597|GO:0008295|GO:0004014|GO:0006597|GO:0008295
Solyc03g112980.1	-3.05E-01	3.37E-01	1.06E-01	7.36E-01	**1.14E+00**	**1.11E-03**	7.26E-01	2.78E-02	WT NoN 14 dpi	P	translation initiation factor 3 subunit I (AHRD V3.3 --* AT1G54680.4)	
Solyc05g008290.3	-3.06E-01	4.52E-02	8.83E-02	5.48E-01	**1.46E+00**	**2.23E-10**	4.29E-01	6.57E-03	WT NoN 14 dpi	E	Cupredoxin superfamily protein (AHRDV3.3 *** AT1G23010.1)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO: 0055114
Solyc10g052600.1	-3.07E-01	5.15E-01	2.29E-01	6.26E-01	**-1.44E+00**	**4.64E-03**	1.93E-01	6.81E-01	WT NoN 14 dpi	CS	LOW QUALITY:S-adenosyl-L-methionine- dependent methyltransferases superfamilyprotein (AHRD V3.3 *** A0A061GFE0_THECC)	GO:0008168
Solyc00g215560.2	-3.08E-01	4.99E-01	-1.25E+00	1.00E-02	**-1.42E+00**	**3.89E-03**	7.18E-01	1.21E-01	WT NoN 14 dpi	C	glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containingprotein (AHRD V3.3 -- * AT1G10050.3)	
Solyc04g055130.1	-3.09E-01	3.65E-01	-9.83E-01	6.93E-03	**-1.68E+00**	**3.27E-05**	5.81E-01	9.46E-02	WT NoN 14 dpi	H	LOW QUALITY:C2 domain protein (AHRD V3.3 *** A0A072UZT9_MEDTR)	
Solyc11g065930.2	-3.10E-01	9.63E-02	-1.65E-01	3.67E-01	**1.06E+00**	**3.16E-06**	-2.00E-01	2.75E-01	WT NoN 14 dpi	N	Xanthine dehydrogenase (AHRD V3.3 ***H6UJ41_CAMSI)	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114

Solyc10g005140.1	-3.10E-01	6.34E-01	-1.44E-01	8.24E-01	**-2.06E+00**	**3.64E-03**	-1.79E-01	7.82E-01	WT NoN 14 dpi	K	Protein kinase superfamily protein (AHRDV3.3 *** AT2G46850.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g058100.3	-3.13E-01	5.90E-02	-6.42E-01	4.09E-04	**-1.58E+00**	**2.62E-10**	7.80E-01	4.16E-05	WT NoN 14 dpi	NA	Metallothionein-like protein type 2 (AHRD V3.3 *** MT2X_SOLLC)	GO:0046872
Solyc08g005493.1	-3.19E-01	2.30E-01	-1.26E-01	6.30E-01	**-1.02E+00**	**5.78E-04**	2.97E-01	2.64E-01	WT NoN 14 dpi	G	Phototropic-responsive NPH3 family protein (AHRD V3.3 --* AT3G26490.4)	
Solyc01g080580.3	-3.20E-01	6.19E-02	3.58E-01	3.83E-02	**-1.21E+00**	**7.97E-08**	-5.88E-01	1.39E-03	WT NoN 14 dpi	DNA	inosine-uridine preferring nucleoside hydrolase family protein (AHRD V3.3 *** AT5G18860.2)	
Solyc01g073810.2	-3.23E-01	2.51E-01	-8.18E-02	7.68E-01	**-1.67E+00**	**2.18E-06**	1.30E+00	7.02E-05	WT NoN 14 dpi	S	LOW QUALITY:Cysteine/Histidine-rich C1domain family protein (AHRD V3.3 *** AT2G44380.1)	GO:0005515|GO:0008270
Solyc05g031600.2	-3.26E-01	6.55E-01	-1.67E+00	2.87E-02	**-2.67E+00**	**1.03E-03**	-1.86E+00	1.61E-02	WT NoN 14 dpi	H	tryptophan aminotransferase related 2 (AHRD V3.3 *** AT4G24670.2)	GO:0003824|GO:0016846|GO:0016846
Solyc07g006900.2	-3.30E-01	5.67E-01	-4.71E-01	4.15E-01	**-2.33E+00**	**3.74E-04**	-1.47E+00	1.57E-02	WT NoN 14 dpi	H	SlPIN2	GO:0010315|GO:0010329|GO:0016021|GO:0016021|GO:0055085|GO:0016021|GO:0055085
Solyc11g066680.1	-3.32E-01	1.90E-01	5.52E-01	3.41E-02	**1.31E+00**	**1.54E-05**	5.29E-01	4.18E-02	WT NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4D9S5_SOLLC)	GO:0008152|GO:0016758
Solyc09g075670.1	-3.32E-01	3.94E-01	-5.97E-01	1.32E-01	**1.42E+00**	**1.05E-03**	8.25E-01	4.11E-02	WT NoN 14 dpi	L	Alpha/beta-Hydrolases superfamily protein(AHRD V3.3 *** A0A061EKQ6_THECC)	GO:0008152|GO:0016787
Solyc10g076820.2	-3.35E-01	2.93E-01	2.51E-01	4.28E-01	**-1.43E+00**	**1.02E-04**	-6.59E-01	4.50E-02	WT NoN 14 dpi	T	Myb family transcription factor family protein (AHRD V3.3 *** B9HCK2_POPTR)	GO:0003677
Solyc11g028310.2	-3.37E-01	3.40E-01	-7.93E-01	3.08E-02	**-1.83E+00**	**1.64E-05**	-4.21E-01	2.35E-01	WT NoN 14 dpi	DNA	DNA topoisomerase 6 subunit B (AHRD V3.3 *-* A0A0V0IMM5_SOLCH)	GO:0003677|GO:0003918|GO:0005524|GO:0006265
Solyc10g085380.2	-3.42E-01	4.63E-01	6.11E-01	1.94E-01	**-2.11E+00**	**9.72E-05**	-7.79E-01	1.01E-01	WT NoN 14 dpi	D	Short-chain dehydrogenase/reductase family protein (AHRD V3.3 *** B9HD90_POPTR),Pfam:PF13561	
Solyc04g009180.2	-3.44E-01	2.74E-02	-1.58E-01	2.93E-01	**-1.12E+00**	**5.13E-08**	-8.91E-01	2.22E-06	WT NoN 14 dpi	T	TCP transcription factor 14	
Solyc01g079160.3	-3.46E-01	3.58E-01	8.28E-01	3.41E-02	**2.26E+00**	**1.96E-06**	7.73E-01	4.67E-02	WT NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** W9R6R2_9ROSA)	GO:0016788
Solyc10g054440.2	-3.49E-01	2.58E-01	-3.00E-01	3.31E-01	**1.43E+00**	**6.96E-05**	9.91E-01	3.00E-03	WT NoN 14 dpi	N	arginine decarboxylase 1	GO:0003824|GO:0006527|GO:0008295|GO:0008792|GO:0006527|GO:0008295|GO:0008792
Solyc09g014710.3	-3.54E-01	9.80E-02	-5.42E-01	1.43E-02	**-1.28E+00**	**1.46E-06**	-4.84E-01	2.70E-02	WT NoN 14 dpi	K	Kinase, putative (AHRD V3.3 ***B9RE26_RICCO)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g007955.1	-3.56E-01	1.12E-01	-1.47E-01	5.03E-01	**1.15E+00**	**1.51E-05**	8.04E-01	9.83E-04	WT NoN 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT1G10740.4)	
Solyc05g009660.3	-3.56E-01	3.61E-01	-9.05E-01	2.58E-02	**-1.18E+00**	**4.82E-03**	-2.97E-01	4.44E-01	WT NoN 14 dpi	G	Transcription factor PERIANTHIA-likeprotein (AHRD V3.3 *** A0A0B0NQX8_GOSAR)	GO:0003700|GO:0006355|GO:0043565|GO:0006351|GO:0043565|GO:0006351|GO:0043565
Solyc10g076660.2	-3.57E-01	5.46E-01	2.73E-01	6.44E-01	**1.70E+00**	**7.37E-03**	1.31E+00	3.36E-02	WT NoN 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependentoxygenase superfamily protein (AHRD V3.3 *** AT5G05600.1)	GO:0016491|GO:0055114
Solyc01g102310.3	-3.59E-01	1.35E-03	-3.23E-01	3.32E-03	**-1.31E+00**	**6.62E-13**	-6.23E-01	1.39E-06	WT NoN 14 dpi	P	GRIP and coiled-coil domain-containingprotein, putative (AHRD V3.3 *-* B9RFR9_RICCO)	

Solyc07g017880.3	-3.64E-01	5.77E-01	5.80E-01	3.76E-01	**-3.39E+00**	**1.73E-05**	-1.37E+00	4.29E-02	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4CCK2_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc01g079980.3	-3.64E-01	2.48E-01	-2.70E-01	3.88E-01	**-1.69E+00**	**9.22E-06**	-5.11E-01	1.09E-01	WT NoN 14 dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03220.1)	GO:0004190|GO:0006508
Solyc04g076970.3	-3.65E-01	4.57E-01	-3.18E-01	5.16E-01	**2.25E+00**	**8.44E-05**	8.22E-01	1.01E-01	WT NoN 14 dpi	T	transcription factor-like protein (AHRD V3.3 *** AT1G58330.1)	GO:0006351|GO:0043565
Solyc02g090350.3	-3.75E-01	5.94E-01	-4.16E-01	5.55E-01	**3.02E+00**	**1.91E-04**	1.17E+00	1.04E-01	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***A0A103Y530_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc09g005400.3	-3.77E-01	7.49E-01	3.55E-01	7.63E-01	**6.84E+00**	**3.65E-06**	2.91E+00	1.92E-02	WT NoN 14 dpi	H	MLP (AHRD V3.3 *** G8DRV9_GOSBA)	GO:0006952|GO:0009607
Solyc07g040750.2	-3.79E-01	5.77E-01	4.59E-01	5.00E-01	**2.42E+00**	**1.33E-03**	1.67E+00	1.99E-02	WT NoN 14 dpi	RNA	RNA helicase DEAD21	GO:0003676|GO:0005524
Solyc07g053890.3	-3.81E-01	2.51E-01	-6.74E-01	4.79E-02	**1.01E+00**	**4.55E-03**	3.99E-01	2.30E-01	WT NoN 14 dpi	L	O-acyltransferase WSD1 (AHRD V3.3 *** A0A151TQI5_CAJCA)	GO:0004144|GO:0004144|GO:0045017|GO:0004144|GO:0045017
Solyc06g062390.3	-3.84E-01	2.04E-01	-5.10E-01	9.48E-02	**1.36E+00**	**9.45E-05**	3.90E-02	8.96E-01	WT NoN 14 dpi	S	Acid phosphatase-like protein 1 (AHRD V3.3 *** V9MHL3_9ROSA)	GO:0003993
Solyc10g078580.1	-3.85E-01	4.28E-01	1.94E-01	6.88E-01	**-2.10E+00**	**1.67E-04**	-1.32E+00	1.05E-02	WT NoN 14 dpi	CS	Arabinogalactan peptide 14 (AHRD V3.3 *** AGP14_ARATH)	
Solyc05g046030.3	-3.93E-01	4.50E-01	2.91E-01	5.75E-01	**-2.78E+00**	**1.15E-05**	-1.04E+00	5.18E-02	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4C0T6_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc06g019170.3	-4.00E-01	2.12E-02	-9.42E-02	5.68E-01	**1.14E+00**	**2.14E-07**	-5.12E-02	7.56E-01	WT NoN 14 dpi	STR	Delta-1-pyrroline-5-carboxylate synthetase(AHRD V3.3 *** G3M3X3_SOLTO)	GO:0003824|GO:0006561|GO:0055114|GO:0004349|GO:0006561|GO:0004349|GO:0006561
Solyc01g102380.4	-4.01E-01	1.40E-02	-1.42E-01	3.59E-01	**-2.01E+00**	**5.66E-13**	4.14E-01	1.14E-02	WT NoN 14 dpi	STR	germin	
Solyc08g006250.1	-4.02E-01	3.11E-01	-6.30E-01	1.18E-01	**-1.23E+00**	**3.99E-03**	5.12E-01	2.00E-01	WT NoN 14 dpi	TR	Copper transporter, putative (AHRD V3.3 *** A0A061GWU0_THECC)	GO:0005375|GO:0016021|GO:0035434
Solyc12g005710.2	-4.05E-01	3.53E-01	6.90E-01	1.19E-01	**-1.91E+00**	**1.45E-04**	-7.93E-01	7.55E-02	WT NoN 14 dpi	E	Blue copper protein (AHRD V3.3 *** W9S2S3_9ROSA)	GO:0009055
Solyc02g067600.1	-4.07E-01	4.12E-01	1.97E-01	6.89E-01	**-1.45E+00**	**6.32E-03**	6.86E-01	1.72E-01	WT NoN 14 dpi	STR	Dehydrin family protein (AHRD V3.3 --* AT1G20450.2)	
Solyc09g091400.3	-4.08E-01	1.48E-01	2.35E-01	3.98E-01	**1.39E+00**	**2.90E-05**	-1.11E-01	6.88E-01	WT NoN 14 dpi	S	Receptor protein kinase (AHRD V3.3 ***Q9FEU2_PINSY)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g111700.2	-4.08E-01	3.39E-01	-4.13E-01	3.34E-01	**1.36E+00**	**3.17E-03**	-1.62E-01	7.02E-01	WT NoN 14 dpi	STR	26S proteasome non-ATPase regulatorysubunit 3 (AHRD V3.3 *** G7J5U6_MEDTR)	GO:0000502|GO:0030234|GO:0042176|G O:0005515|GO:0005515
Solyc06g005330.3	-4.16E-01	1.30E-01	-7.71E-01	7.65E-03	**-1.73E+00**	**7.18E-07**	2.27E-01	4.01E-01	WT NoN 14 dpi	G	R2R3MYB transcription factor 59	GO:0003677
Solyc11g066250.2	-4.20E-01	1.05E-01	-2.41E-01	3.43E-01	**1.39E+00**	**8.12E-06**	3.33E-01	1.95E-01	WT NoN 14 dpi	STR	Carboxypeptidase (AHRD V3.3 *** K4D9N3_SOLLC)	GO:0004185|GO:0006508
Solyc06g082020.3	-4.22E-01	1.95E-01	-9.09E-02	7.77E-01	**-1.36E+00**	**2.22E-04**	-6.86E-02	8.31E-01	WT NoN 14 dpi	E	Alternative NAD(P)H dehydrogenase 1 (AHRD V3.3 --* A0A061GX18_THECC)	
Solyc07g055990.3	-4.23E-01	3.57E-01	2.19E-01	6.31E-01	**-2.02E+00**	**1.35E-04**	-1.12E+00	1.96E-02	WT NoN 14 dpi	CS	Xyloglucan endotransglucosylase/hydrolase 7 (AHRDV1 **** C0IRG6_ACTDE)	GO:0004553|GO:0005975|GO:0005618|GO:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc12g006680.2	-4.26E-01	7.86E-01	7.32E-01	6.41E-01	**-4.74E+00**	**5.18E-03**	3.76E-01	8.10E-01	WT NoN 14 dpi	PMI	Early nodulin 93 protein (AHRD V3.3 *** A3FGC9_9ROSI)	

Solyc07g042440.3	-4.29E-01	5.40E-01	-3.84E-02	9.56E-01	**2.31E+00**	**2.55E-03**	7.12E-01	3.12E-01	WT NoN 14 dpi	OX	Peroxiredoxin (AHRD V3.3 *** A0A0B4SWQ5_9ROSI)	GO:0016209|GO:0016491|GO:0055114|GO:0045454|GO:0045454
Solyc06g066650.3	-4.29E-01	2.02E-01	1.18E-01	7.21E-01	**-1.57E+00**	**6.20E-05**	-7.06E-01	4.06E-02	WT NoN 14 dpi	DNA	rop guanine nucleotide exchange factor- like protein (AHRD V3.3 *** AT1G52240.1)	GO:0005089
Solyc08g079920.2	-4.31E-01	4.29E-02	3.59E-01	8.81E-02	**-1.88E+00**	**1.13E-09**	-5.94E-01	7.00E-03	WT NoN 14 dpi	P	P69f protein	GO:0004252|GO:0006508
Solyc07g042490.1	-4.36E-01	1.24E-01	-1.11E-01	6.88E-01	**-1.68E+00**	**1.87E-06**	-5.31E-01	6.40E-02	WT NoN 14 dpi	H	LOW QUALITY:Auxin responsive SAURprotein (AHRD V3.3 *** A0A118K7G8_CYNCS)	GO:0009733
Solyc11g040140.2	-4.38E-01	6.69E-01	-5.12E-02	9.60E-01	**-3.76E+00**	**9.94E-04**	-2.21E+00	3.82E-02	WT NoN 14 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRDV3.3 *** K4D7Y8_SOLLC)	GO:0004553|GO:0005975|GO:0005618|GO:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc12g088870.1	-4.40E-01	1.11E-01	-3.88E-01	1.58E-01	**1.31E+00**	**4.38E-05**	7.52E-01	9.16E-03	WT NoN 14 dpi	T	PHD finger transcription factor (AHRD V3.3 --* AT5G58610.9)	
Solyc11g012130.2	-4.42E-01	1.37E-01	-4.84E-01	1.05E-01	**1.69E+00**	**3.53E-06**	2.23E-01	4.46E-01	WT NoN 14 dpi	E	Blue copper protein (AHRD V3.3 *** A0A0B2RLQ3_GLYSO)	GO:0009055
Solyc03g120600.3	-4.43E-01	1.70E-01	4.87E-01	1.32E-01	**-1.86E+00**	**3.09E-06**	1.99E-02	9.50E-01	WT NoN 14 dpi	OX	Plant cadmium resistance 2 (AHRD V3.3 *** A0A0K9NVT8_ZOSMR)	
Solyc09g065700.3	-4.43E-01	1.82E-02	-5.46E-01	4.59E-03	**-1.16E+00**	**5.93E-07**	-3.91E-01	3.52E-02	WT NoN 14 dpi	G	BEACH-DOMAIN HOMOLOG A1 (AHRD V3.3 *** AT1G03060.2)	GO:0005488|GO:0005515|GO:0005515
Solyc04g063390.2	-4.44E-01	5.31E-02	-4.13E-02	8.52E-01	**-1.05E+00**	**5.95E-05**	-5.81E-01	1.36E-02	WT NoN 14 dpi	P	Chaperone protein dnaJ, putative (AHRD V3.3 *** B9S2N8_RICCO)	
Solyc01g087560.3	-4.47E-01	2.37E-02	-6.18E-02	7.42E-01	**-1.09E+00**	**3.59E-06**	-4.06E-01	3.81E-02	WT NoN 14 dpi	NA	Methyltransferase (AHRD V3.3 *** K4AYE6_SOLLC)	GO:0006694|GO:0008168|GO:0008152|GO:0008168|GO:0008152|GO:0008168
Solyc05g008550.3	-4.52E-01	4.43E-01	7.31E-01	2.19E-01	**-1.79E+00**	**4.84E-03**	-8.70E-01	1.46E-01	WT NoN 14 dpi	STR	LOW QUALITY:Metallocarboxypeptidase inhibitor (AHRD V3.3 -** O24639_SOLTU)	
Solyc06g007610.2	-4.52E-01	3.40E-01	-1.06E-01	8.21E-01	**1.36E+00**	**7.35E-03**	1.21E+00	1.56E-02	WT NoN 14 dpi	STR	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** A0A061DM50_THECC)	
Solyc11g007730.2	-4.54E-01	1.50E-01	-2.29E-01	4.60E-01	**1.72E+00**	**7.04E-06**	9.79E-01	3.63E-03	WT NoN 14 dpi	N	Bark storage protein A (AHRD V3.3 *** W9SCI4_9ROSA)	GO:0003824|GO:0009116
Solyc08g078020.1	-4.56E-01	1.29E-01	4.35E-01	1.47E-01	**-1.15E+00**	**5.34E-04**	-8.10E-01	9.90E-03	WT NoN 14 dpi	PMI	LOW QUALITY:Methionine rich arabinogalactan (AHRD V3.3 *** Q52QJ6_SOLLC)	
Solyc10g079700.2	-4.66E-01	9.44E-02	-3.79E-01	1.70E-01	**-1.38E+00**	**2.38E-05**	-9.86E-02	7.17E-01	WT NoN 14 dpi	S	Two-component response regulator (AHRD V3.3 *** A0A059T9P7_ROSCN)	GO:0000160
Solyc02g085630.3	-4.67E-01	2.81E-01	2.32E-01	5.89E-01	**1.74E+00**	**3.52E-04**	2.39E-01	5.78E-01	WT NoN 14 dpi	DNA	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9MXR7_POPTR)	GO:0003677|GO:0006355|GO:0043565|GO:0006355|GO:0043565
Solyc07g043710.3	-4.68E-01	2.97E-01	-8.63E-02	8.46E-01	**-2.36E+00**	**1.34E-05**	-9.82E-01	3.44E-02	WT NoN 14 dpi	S	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)	GO:0016747
Solyc05g014085.1	-4.69E-01	1.94E-01	-9.31E-01	1.36E-02	**-1.21E+00**	**2.00E-03**	-6.17E-01	9.13E-02	WT NoN 14 dpi	P	F-box family protein (AHRD V3.3 *-* B9HK48_POPTR)	
Solyc05g008880.1	-4.70E-01	2.98E-01	-3.40E-01	4.50E-01	**-1.79E+00**	**4.17E-04**	1.04E+00	2.72E-02	WT NoN 14 dpi	AM	LOW QUALITY:proline transporter 2 (AHRD V3.3 --* AT3G55740.3)	
Solyc03g123590.3	-4.73E-01	1.68E-02	-2.22E-01	2.40E-01	**1.29E+00**	**2.35E-07**	5.16E-01	9.91E-03	WT NoN 14 dpi	PMI	Remorin family protein (AHRD V3.3 *** B9N7I2_POPTR)	
Solyc04g071075.1	-4.80E-01	2.94E-01	4.67E-01	3.07E-01	**1.58E+00**	**1.64E-03**	7.87E-01	9.08E-02	WT NoN 14 dpi	H	Auxin efflux carrier family protein (AHRD V3.3 --* AT1G76530.3)	
Solyc02g072160.3	-4.83E-01	5.15E-02	2.30E-01	3.39E-01	**1.23E+00**	**2.14E-05**	7.60E-01	3.52E-03	WT NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT4G18810.1)	

Solyc01g067120.3	-4.85E-01	4.61E-02	3.59E-01	1.33E-01	**-1.20E+00**	**2.03E-05**	-7.80E-01	2.37E-03	WT NoN 14 dpi	P	Cullin 1, putative (AHRD V3.3 ***A0A061EP85_THECC)	GO:0006511|GO:0031625
Solyc01g096320.3	-5.00E-01	6.80E-02	5.67E-01	4.04E-02	**1.03E+00**	**5.64E-04**	-1.04E-01	6.95E-01	WT NoN 14 dpi	DNA	Homeobox-leucine zipper protein (AHRDV3.3 *** M4W1Z7_TOBAC)	GO:0003677|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565
Solyc04g049920.3	-5.00E-01	3.17E-01	4.36E-02	9.30E-01	**-2.15E+00**	**1.72E-04**	-1.21E+00	2.07E-02	WT NoN 14 dpi	RNA	RNA-binding region-containing protein, putative (AHRD V3.3 *** B9SD37_RICCO)	GO:0000166|GO:0003676|GO:0003676
Solyc10g049420.2	-5.01E-01	2.90E-01	-7.06E-01	1.40E-01	**-1.31E+00**	**8.89E-03**	-1.03E+00	3.57E-02	WT NoN 14 dpi	S	TRAF-like superfamily protein (AHRD V3.3 -* AT5G52330.4)	
Solyc09g065760.3	-5.03E-01	1.86E-01	-5.31E-01	1.64E-01	**1.66E+00**	**1.32E-04**	4.48E-01	2.37E-01	WT NoN 14 dpi	NA	DUF506 family protein (AHRD V3.3 ***G7ICN8_MEDTR)	
Solyc04g008230.3	-5.05E-01	2.29E-01	-3.61E-01	3.87E-01	**-1.52E+00**	**1.01E-03**	-3.87E-01	3.54E-01	WT NoN 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G48100.1)	GO:0004650|GO:0005975
Solyc12g005440.1	-5.05E-01	1.78E-01	-6.74E-01	7.62E-02	**1.90E+00**	**2.02E-05**	8.44E-01	2.90E-02	WT NoN 14 dpi	S	LOW QUALITY:HXXXD-type acyl- transferase family protein, putative (AHRDV3.3 *** A0A061E8Z9_THECC)	GO:0016747
Solyc12g098790.1	-5.08E-01	2.02E-01	1.22E-01	7.56E-01	**-2.40E+00**	**1.56E-06**	3.72E-02	9.24E-01	WT NoN 14 dpi	D	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT5G24870.3)	
Solyc07g052460.3	-5.11E-01	4.19E-02	-2.56E-01	2.93E-01	**-1.09E+00**	**1.09E-04**	-6.24E-01	1.47E-02	WT NoN 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-bindingsuperfamily protein (AHRD V3.3 --* AT1G31050.7)	
Solyc01g096280.2	-5.14E-01	4.63E-02	2.43E-01	3.31E-01	**-1.13E+00**	**9.53E-05**	-5.65E-01	2.96E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***F4YF83_9APIA)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc02g078040.3	-5.14E-01	5.53E-02	3.18E-01	2.25E-01	**1.50E+00**	**3.82E-06**	3.46E-01	1.88E-01	WT NoN 14 dpi	G	Pollen Ole e 1 allergen and extensin familyprotein (AHRD V3.3 *** AT2G34700.1)	GO:0005199
Solyc04g071270.1	-5.17E-01	3.74E-01	1.18E+00	4.87E-02	**-1.88E+00**	**2.92E-03**	-1.24E+00	3.90E-02	WT NoN 14 dpi	P	LOW QUALITY:F-box family protein, putative (AHRD V3.3 ***A0A061FZW6_THECC)	GO:0005515
Solyc02g078100.3	-5.17E-01	3.67E-01	3.37E-01	5.55E-01	**-1.65E+00**	**6.94E-03**	3.16E-01	5.80E-01	WT NoN 14 dpi	G	Pollen Ole e 1 allergen/extensin (AHRDV3.3 *-* A0A124SHL8_CYNCS)	GO:0005199
Solyc02g091070.3	-5.20E-01	1.73E-01	5.06E-01	1.85E-01	**1.25E+00**	**2.34E-03**	4.32E-01	2.55E-01	WT NoN 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4BCQ6_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc05g007650.1	-5.22E-01	3.83E-01	-7.01E-01	2.44E-01	**-2.09E+00**	**1.47E-03**	-2.08E-01	7.27E-01	WT NoN 14 dpi	NA	LOW QUALITY:Clavata3/ESR (CLE) genefamily member MtCLE24 (AHRD V3.3 --* G7KF79_MEDTR)	
Solyc04g007200.3	-5.22E-01	1.15E-01	-7.37E-01	2.96E-02	**-1.81E+00**	**5.99E-06**	-7.63E-01	2.46E-02	WT NoN 14 dpi	D	methylketone synthase IIb	
Solyc08g005120.3	-5.40E-01	3.38E-02	-8.90E-01	1.05E-03	**-1.03E+00**	**2.35E-04**	1.17E+00	5.14E-05	WT NoN 14 dpi	D	Cinnamoyl-CoA reductase-like protein(AHRD V3.3 *** G7KDR3_MEDTR)	
Solyc09g075870.2	-5.41E-01	6.22E-03	-2.20E-01	2.36E-01	**-1.18E+00**	**7.54E-07**	6.65E-01	1.14E-03	WT NoN 14 dpi	L	Lipoxygenase (AHRD V3.3 *** A0A0V0IV70_SOLCH)	GO:0005515|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc04g057830.1	-5.41E-01	1.53E-01	3.60E-01	3.36E-01	**1.04E+00**	**8.79E-03**	7.64E-02	8.37E-01	WT NoN 14 dpi	NA	LOW QUALITY:DUF4228 domain protein(AHRD V3.3 *** G7K362_MEDTR)	
Solyc04g051280.3	-5.44E-01	5.12E-01	6.83E-01	4.11E-01	**3.14E+00**	**7.11E-04**	1.13E+00	1.78E-01	WT NoN 14 dpi	NA	Transmembrane protein, putative (AHRD V3.3 *-* A0A072VMC3_MEDTR)	
Solyc05g018310.1	-5.52E-01	4.56E-02	3.64E-01	1.78E-01	**-1.24E+00**	**7.52E-05**	2.95E-02	9.12E-01	WT NoN 14 dpi	D	RING/U-box superfamily protein, putative(AHRD V3.3 *** A0A061GMH2_THECC)	GO:0005515|GO:0008270
Solyc01g091420.2	-5.55E-01	1.33E-01	1.77E-01	6.26E-01	**1.34E+00**	**9.18E-04**	2.28E-01	5.29E-01	WT NoN 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9RDE1_RICCO)	
Solyc12g049190.2	-5.59E-01	6.74E-02	8.92E-01	5.28E-03	**1.45E+00**	**3.99E-05**	6.13E-01	4.63E-02	WT NoN 14 dpi	PMI	Leucine-rich repeat receptor-like proteinkinase family protein (AHRD V3.3 *-* AT4G08850.1)	GO:0005515

Solyc01g094340.3	-5.66E-01	3.83E-02	-9.51E-01	1.11E-03	**-1.20E+00**	**9.22E-05**	7.20E-01	1.00E-02	WT NoN 14 dpi	L	Carboxyltransferase alpha Subunit (AHRD V3.3 *** A0A0G2SJ78_SALMI)	GO:0003989|GO:0006633|GO:0009317|GO:0016874|GO:0016874
Solyc04g082030.1	-5.66E-01	1.01E-02	3.63E-03	9.86E-01	**2.08E+00**	**1.64E-10**	3.33E-01	1.15E-01	WT NoN 14 dpi	N	ornithine decarboxylase	GO:0003824|GO:0006596|GO:0006596
Solyc06g065670.3	-5.67E-01	1.56E-01	-9.72E-01	1.89E-02	**1.16E+00**	**6.20E-03**	6.68E-01	9.71E-02	WT NoN 14 dpi	TR	Pleiotropic drug resistance ABCtransporter (AHRD V3.3 *** W0TUG3_ACAMN)	GO:0005524|GO:0016887|GO:0016020|G O:0016020
Solyc06g007280.2	-5.68E-01	7.00E-02	-5.57E-01	7.55E-02	**-1.08E+00**	**1.34E-03**	-8.02E-01	1.31E-02	WT NoN 14 dpi	RNA	Pentatricopeptide repeat protein (AHRD V3.3 *-* A0A1B3IPW0_CAPAN)	GO:0005515
Solyc03g093650.3	-5.71E-01	2.50E-03	-1.80E-01	3.00E-01	**1.40E+00**	**1.19E-08**	-2.39E-01	1.72E-01	WT NoN 14 dpi	TR	ABC transporter B family protein (AHRDV3.3 *** A0A072UBK0_MEDTR)	GO:0005524|GO:0006810|GO:0016021|G O:0042626|GO:0055085|GO:0005524|GO:0016887|GO:0005524|GO:0016887
Solyc05g008300.2	-5.75E-01	1.36E-01	2.13E-01	5.72E-01	**1.44E+00**	**6.95E-04**	-6.48E-01	9.44E-02	WT NoN 14 dpi	TR	Heavy metal transport/detoxificationsuperfamily protein (AHRD V3.3 *-* AT1G23000.2)	GO:0030001|GO:0046872
Solyc11g066640.1	-5.76E-01	4.59E-01	4.82E-02	9.50E-01	**-3.82E+00**	**3.56E-05**	-6.07E-01	4.36E-01	WT NoN 14 dpi	2M	Hydroxycinnamoyl CoA quinatetransferase 2 (AHRD V3.3 *** D8L7F0_CYNCS)	GO:0016747
Solyc05g056170.3	-5.77E-01	3.72E-04	5.98E-01	2.51E-04	**-1.03E+00**	**9.90E-08**	-5.10E-01	1.27E-03	WT NoN 14 dpi	D	phenylalanine ammonia-lyase 2	GO:0003824|GO:0005737|GO:0006559|GO:0016841|GO:0005737|GO:0006559|GO:0016841
Solyc09g065430.3	-5.89E-01	6.65E-02	4.78E-01	1.32E-01	**1.36E+00**	**1.61E-04**	7.39E-01	2.37E-02	WT NoN 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)	GO:0006869|GO:0008289
Solyc10g078370.2	-5.90E-01	4.48E-03	-1.73E-01	3.71E-01	**1.26E+00**	**4.83E-07**	-8.06E-01	2.43E-04	WT NoN 14 dpi	H	Auxin Efflux Facilitator 9	GO:0016021|GO:0055085
Solyc02g079500.4	-5.93E-01	3.72E-01	-6.19E-01	3.52E-01	**2.46E+00**	**8.59E-04**	1.76E+00	1.23E-02	WT NoN 14 dpi	OX	Peroxidase (AHRD V1 **** Q50LG4_TOBAC)%3B contains Interpro domain(s) IPR019793 Peroxidases heam-ligand binding site IPR019794 Peroxidase%2C active site IPR002016 Haem peroxidase%2C plant/fungal/bacterial	
Solyc03g114625.1	-5.93E-01	8.03E-02	-7.94E-01	2.21E-02	**-1.36E+00**	**3.06E-04**	8.48E-02	7.97E-01	WT NoN 14 dpi	C	Carbohydrate-binding-like fold (AHRD V3.3 --* AT5G01260.2)	
Solyc11g071990.2	-5.96E-01	9.61E-04	-4.09E-01	1.68E-02	**-1.03E+00**	**9.02E-07**	-7.99E-01	3.54E-05	WT NoN 14 dpi	D	Apoptosis-inducing factor, putative (AHRD V3.3 *** B9SD10_RICCO)	GO:0016491|GO:0055114
Solyc01g107830.3	-6.01E-01	3.94E-01	-1.36E+00	6.11E-02	**1.97E+00**	**8.68E-03**	4.87E-01	4.88E-01	WT NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4B2Z9_SOLLC)	GO:0008152|GO:0016758
Solyc02g068795.1	-6.01E-01	6.35E-02	-1.08E-01	7.31E-01	**-1.09E+00**	**1.67E-03**	-2.10E-01	5.04E-01	WT NoN 14 dpi	S	Rho GTPase activation protein (RhoGAP)with PH domain-containing protein (AHRD V3.3 --* AT5G12150.2)	
Solyc01g102420.1	-6.05E-01	1.63E-01	-3.61E-01	3.99E-01	**-1.20E+00**	**8.79E-03**	-6.14E-01	1.57E-01	WT NoN 14 dpi	NA	LOW QUALITY:LisH domain and HEATrepeat-containing protein KIAA1468 (AHRD V3.3 --* A0A1D1YW69_9ARAE)	
Solyc09g005970.1	-6.06E-01	7.84E-02	-5.75E-01	9.36E-02	**1.29E+00**	**6.15E-04**	5.55E-01	1.05E-01	WT NoN 14 dpi	TR	ABC transporter family protein (AHRD V3.3 *** B9ICA5_POPTR)	GO:0005524|GO:0016887|GO:0016020|G O:0016020
Solyc04g009910.3	-6.09E-01	2.06E-03	-2.60E-01	1.55E-01	**1.71E+00**	**5.50E-10**	8.86E-01	3.59E-05	WT NoN 14 dpi	K	phosphoenolpyruvate carboxylase kinase1	GO:0004672|GO:0005524|GO:0006468|G O:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g074730.1	-6.13E-01	2.94E-02	-1.36E-01	6.12E-01	**-1.24E+00**	**8.26E-05**	-9.61E-01	1.28E-03	WT NoN 14 dpi	CS	Arabinogalactan-protein (AHRD V3.3 *** Q40380_NICAL)	
Solyc10g007290.3	-6.15E-01	1.46E-03	1.40E-01	4.26E-01	**1.41E+00**	**1.25E-08**	-1.36E-01	4.39E-01	WT NoN 14 dpi	C	Phosphoenolpyruvate carboxylase (AHRDV3.3 *** CAPP_TOBAC)	GO:0003824|GO:0006099|GO:0008964|G O:0015977|GO:0006099|GO:0008964|GO:

											0015977
Solyc12g098880.2	-6.27E-01	4.87E-01	9.25E-01	3.08E-01	**-2.63E+00**	**6.61E-03**	-1.94E-01	8.29E-01	WT NoN 14 dpi	S	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein (AHRDV3.3 --* AT1G45010.4)	
Solyc08g079250.3	-6.28E-01	2.39E-01	2.38E-01	6.52E-01	**-2.55E+00**	**4.46E-05**	-7.82E-01	1.45E-01	WT NoN 14 dpi	NA	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** C0KHK1_9CARY)	
Solyc12g005370.2	-6.28E-01	4.17E-01	4.30E-01	5.77E-01	**-3.40E+00**	**1.39E-04**	-1.03E+00	1.88E-01	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4DB75_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc02g065555.1	-6.31E-01	1.07E-02	-8.64E-01	8.61E-04	**1.33E+00**	**4.23E-06**	9.48E-01	3.32E-04	WT NoN 14 dpi	TR	Calcium uniporter, mitochondrial (AHRD V3.3 *** A0A0B0PJN2_GOSAR)	
Solyc01g108700.3	-6.35E-01	2.89E-01	-4.85E-02	9.35E-01	**-1.92E+00**	**3.02E-03**	-3.97E-01	5.04E-01	WT NoN 14 dpi	T	LOW QUALITY:transcription initiation factor TFIID subunit 1b-like protein (AHRD V3.3 -** AT3G19030.1)	
Solyc03g114820.3	-6.35E-01	1.04E-01	-6.84E-01	8.10E-02	**-2.17E+00**	**4.86E-06**	-8.38E-01	3.51E-02	WT NoN 14 dpi	DNA	Adenine nucleotide alpha hydrolases-likesuperfamily protein, putative (AHRD V3.3 *** A0A061FX93_THECC)	GO:0006950
Solyc03g025490.3	-6.36E-01	1.61E-01	-2.09E-01	6.39E-01	**-2.41E+00**	**1.04E-05**	-1.16E+00	1.42E-02	WT NoN 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependentoxygenase superfamily protein (AHRD V3.3 *** AT4G23340.1)	GO:0016491|GO:0055114
Solyc02g082940.3	-6.38E-01	1.94E-01	-3.43E-01	4.80E-01	**-2.93E+00**	**1.94E-06**	-8.26E-01	9.66E-02	WT NoN 14 dpi	CS	Trichome birefringence-like protein (AHRD V3.3 *** G7JKP3_MEDTR)	
Solyc09g082290.3	-6.42E-01	3.50E-01	-2.80E-01	6.82E-01	**2.00E+00**	**6.42E-03**	1.74E+00	1.62E-02	WT NoN 14 dpi	NA	Protease inhibitor/seed storage/lipid transfer family protein (AHRD V3.3 *** B9NBN8_POPTR)	
Solyc08g080745.1	-6.44E-01	1.11E-02	-4.20E-01	8.60E-02	**-1.57E+00**	**4.55E-07**	1.92E+00	1.38E-08	WT NoN 14 dpi	NA	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT2G44210.1)	
Solyc12g100230.1	-6.49E-01	2.49E-01	-2.16E-02	9.69E-01	**-2.43E+00**	**1.57E-04**	-1.38E+00	1.85E-02	WT NoN 14 dpi	2M	Fatty acid desaturase (AHRD V3.3 *** E5D7U7_9GENT)	GO:0006629|GO:0016717|GO:0055114|GO:0016717|GO:0055114
Solyc08g005960.2	-6.50E-01	4.24E-01	5.83E-01	4.73E-01	**-2.37E+00**	**6.57E-03**	-1.80E+00	3.35E-02	WT NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT2G45180.1)	
Solyc01g112175.1	-6.51E-01	1.09E-01	-5.67E-01	1.61E-01	**-1.63E+00**	**3.17E-04**	-9.24E-01	2.66E-02	WT NoN 14 dpi	RNA	RNA polymerase II transcriptionalcoactivator (AHRD V3.3 --* G7JC59_MEDTR)	GO:0003677|GO:0006355
Solyc07g006590.1	-6.53E-01	5.42E-03	-6.13E-01	8.44E-03	**-1.19E+00**	**8.01E-06**	-8.50E-01	5.30E-04	WT NoN 14 dpi	K	LOW QUALITY:kinase superfamily with octicosapeptide/Phox/Bem1p domain- containing protein (AHRD V3.3 --* AT3G24715.3)	
Solyc01g107140.2	-6.54E-01	3.46E-01	5.98E-01	3.88E-01	**-3.78E+00**	**8.17E-06**	-1.32E+00	6.42E-02	WT NoN 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-*AT2G14760.1)	GO:0046983
Solyc01g079270.1	-6.58E-01	3.71E-01	-1.05E+00	1.59E-01	**-3.37E+00**	**8.45E-05**	-1.85E+00	1.64E-02	WT NoN 14 dpi	T	Transcription factor, putative (AHRD V3.3 *- GO:0046983 * B9RNB4_RICCO)	
Solyc01g081340.3	-6.63E-01	2.25E-01	-9.11E-01	9.92E-02	**1.67E+00**	**4.24E-03**	2.87E-01	5.94E-01	WT NoN 14 dpi	H	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase 1 (AHRD V3.3 *** B5TVE1_TOBAC)	GO:0008168
Solyc03g119070.2	-6.71E-01	6.56E-02	4.44E-01	2.14E-01	**1.13E+00**	**3.25E-03**	1.03E-01	7.71E-01	WT NoN 14 dpi	DNA	LOW QUALITY:Flap endonuclease 1 (AHRD V3.3 *** A0A0K9P479_ZOSMR)	GO:0003677|GO:0003824|GO:0004518|GO:0004518
Solyc03g114180.3	-6.76E-01	6.27E-03	-9.08E-01	4.78E-04	**-1.25E+00**	**8.93E-06**	1.80E-01	4.35E-01	WT NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BKS0_SOLLC)	GO:0008152|GO:0016758

Solyc02g088390.3	-6.79E-01	2.77E-02	6.23E-02	8.32E-01	**-1.04E+00**	**1.44E-03**	-8.40E-01	7.76E-03	WT NoN 14 dpi	E	Blue copper protein, putative (AHRD V3.3 *** B9T3T7_RICCO)	GO:0009055
Solyc03g115960.3	-6.85E-01	1.59E-01	-4.29E-02	9.28E-01	**1.32E+00**	**9.80E-03**	9.08E-01	6.53E-02	WT NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2P2I1_GLYSO)	GO:0016788
Solyc09g005410.2	-6.86E-01	4.49E-01	9.88E-01	2.78E-01	**5.34E+00**	**2.69E-06**	1.84E-01	8.38E-01	WT NoN 14 dpi	D	Major latex-like protein (AHRD V3.3 *** B5THI3_PANGI)	GO:0006952|GO:0009607
Solyc06g033920.1	-6.95E-01	5.61E-02	-6.05E-01	9.36E-02	**1.12E+00**	**3.47E-03**	-2.79E-01	4.29E-01	WT NoN 14 dpi	PMI	Leucine-rich repeat receptor-like proteinkinase family protein (AHRD V3.3 *** AT3G24240.1)	GO:0005515
Solyc09g066410.2	-6.96E-01	5.04E-01	-7.63E-01	4.65E-01	**3.10E+00**	**5.67E-03**	2.04E-01	8.45E-01	WT NoN 14 dpi	STR	Phosphate transporter (AHRD V3.3 ***A0A0B5GK48_SOLLC)	GO:0005315|GO:0006817|GO:0016021|GO:0016021|GO:0022857|GO:0055085|GO:0016021|GO:0022857|GO:0055085
Solyc01g104730.2	-6.96E-01	5.07E-01	-3.55E-01	7.34E-01	**2.99E+00**	**7.85E-03**	1.77E+00	1.00E-01	WT NoN 14 dpi	TR	organic solute transporter ostalpha protein (DUF300) (AHRD V3.3 *-* AT1G11200.1)	
Solyc02g082930.3	-7.18E-01	7.23E-02	-2.29E-02	9.53E-01	**1.56E+00**	**3.83E-04**	8.15E-01	4.33E-02	WT NoN 14 dpi	D	acidic extracellular 27 kD chitinase	GO:0004568|GO:0005975|GO:0004568|GO:0006032|GO:0016998|GO:0004568|GO:0006032|GO:0016998
Solyc12g017850.2	-7.23E-01	4.90E-02	5.38E-02	8.79E-01	**1.36E+00**	**6.47E-04**	8.25E-01	2.61E-02	WT NoN 14 dpi	G	senescence-associated family protein,putative (DUF581) (AHRD V3.3 *** AT5G20700.1)	
Solyc09g063010.3	-7.23E-01	2.18E-02	-7.50E-01	1.77E-02	**-1.79E+00**	**2.25E-06**	-4.38E-01	1.51E-01	WT NoN 14 dpi	T	bHLH transcription factor 058	
Solyc01g110684.1	-7.34E-01	3.14E-01	-1.57E+00	3.76E-02	**-2.13E+00**	**6.31E-03**	-1.28E+00	8.60E-02	WT NoN 14 dpi	RNA	K-box region and MADS-box transcriptionfactor family protein (AHRD V3.3 --* AT5G65070.6)	
Solyc04g072000.3	-7.38E-01	1.77E-03	-6.53E-01	4.80E-03	**1.01E+00**	**5.88E-05**	8.06E-01	7.73E-04	WT NoN 14 dpi	D	Chitinase (AHRD V3.3 ***A0A1B1HY32_9APIA)	GO:0004568|GO:0005975|GO:0004568|GO:0006032|GO:0016998|GO:0004568|GO: 0006032|GO:0016998
Solyc04g014290.1	-7.49E-01	9.67E-02	-2.75E-01	5.33E-01	**1.53E+00**	**1.65E-03**	1.17E+00	1.23E-02	WT NoN 14 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** A0A072V4P7_MEDTR)	
Solyc09g008590.3	-7.51E-01	1.98E-01	-1.37E-01	8.11E-01	**-2.43E+00**	**2.31E-04**	-7.19E-01	2.17E-01	WT NoN 14 dpi	G	Pollen Ole e 1 allergen and extensin familyprotein (AHRD V3.3 *** AT3G09925.1),Pfam:PF01190	
Solyc03g096290.3	-7.55E-01	5.48E-03	5.92E-01	2.52E-02	**1.29E+00**	**2.14E-05**	7.03E-01	9.05E-03	WT NoN 14 dpi	TR	plasma membrane intrinsic protein 1.7	GO:0005215|GO:0006810|GO:0016020
Solyc02g084910.3	-7.57E-01	8.44E-02	-1.32E+00	4.25E-03	**1.64E+00**	**6.38E-04**	7.09E-01	1.05E-01	WT NoN 14 dpi	P	P-loop containing nucleoside triphosphate GO:0005524hydrolases superfamily protein (AHRD V3.3 *** AT5G17760.1)	
Solyc07g053630.3	-7.64E-01	6.91E-04	-7.57E-01	7.62E-04	**-1.45E+00**	**9.76E-08**	-2.88E-01	1.58E-01	WT NoN 14 dpi	S	Two-component response regulator-likeAPRR2 (AHRD V3.3 *** A0A151SET7_CAJCA)	GO:0003677
Solyc05g008020.3	-7.65E-01	1.94E-01	-6.54E-01	2.64E-01	**-1.69E+00**	**6.67E-03**	-6.19E-02	9.15E-01	WT NoN 14 dpi	K	mitogen-activated protein kinase 15	GO:0004672|GO:0005524|GO:0006468|GO:0004707|GO:0005524|GO:0006468|GO:0004707|GO:0005524|GO:0006468
Solyc12g096620.1	-7.67E-01	4.13E-01	-1.16E+00	2.18E-01	**-6.55E+00**	**1.62E-07**	-1.02E+00	2.80E-01	WT NoN 14 dpi	L	GDSL esterase	GO:0016788
Solyc06g076560.2	-7.72E-01	4.99E-02	2.76E-01	4.68E-01	**1.33E+00**	**1.51E-03**	2.56E-01	5.00E-01	WT NoN 14 dpi	STR	17.6 kD class I small heat shock protein	
Solyc01g068420.3	-7.75E-01	3.77E-01	-1.16E+00	1.91E-01	**-4.21E+00**	**4.67E-05**	-2.21E+00	1.66E-02	WT NoN 14 dpi	CS	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)	
Solyc00g009090.3	-7.79E-01	1.86E-02	2.13E-02	9.46E-01	**1.66E+00**	**1.43E-05**	1.96E-01	5.33E-01	WT NoN 14 dpi	PMI	LRR receptor-like kinase (AHRD V3.3 ***A0A072VNN3_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468

Solyc08g080930.1	-7.79E-01	1.17E-01	-9.77E-01	5.23E-02	**-1.51E+00**	**4.23E-03**	-2.77E-01	5.69E-01	WT NoN 14 dpi	CS	Xyloglucan galactosyltransferaseKATAMARI1 (AHRD V3.3 *** W9R3A3_9ROSA)	
Solyc02g071875.1	-7.80E-01	2.09E-02	-9.35E-01	6.67E-03	**-1.03E+00**	**3.28E-03**	-7.62E-01	2.37E-02	WT NoN 14 dpi	PMI	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** C0LGF2_ARATH)	
Solyc03g043715.1	-7.81E-01	5.24E-02	-1.56E-01	6.88E-01	**1.20E+00**	**4.27E-03**	1.00E+00	1.48E-02	WT NoN 14 dpi	NA	Protein BRICK 1 (AHRD V3.3 *** BRK1_ARATH)	GO:0007015|GO:0031209|GO:0032403
Solyc08g078940.1	-7.87E-01	2.02E-01	3.91E-02	9.49E-01	**-2.47E+00**	**3.54E-04**	3.02E-01	6.19E-01	WT NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT1G12100.1)	
Solyc01g100750.2	-7.93E-01	3.52E-01	3.22E-01	7.04E-01	**2.69E+00**	**3.52E-03**	2.13E-01	8.02E-01	WT NoN 14 dpi	NA	LOW QUALITY:plant/protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT1G56580.1)	
Solyc08g078030.3	-8.04E-01	8.84E-02	2.20E-02	9.62E-01	**1.31E+00**	**7.86E-03**	6.05E-01	1.94E-01	WT NoN 14 dpi	NA	Transferase, putative (AHRD V3.3 *** B9T0L5_RICCO)	GO:0016747
Solyc01g096260.3	-8.05E-01	1.32E-01	8.75E-01	1.02E-01	**-1.67E+00**	**3.29E-03**	3.11E-01	5.52E-01	WT NoN 14 dpi	DNA	NAD-dependent protein deacetylase HST1-like protein (AHRD V3.3 *** AT2G46640.2)	
Solyc06g008560.2	-8.17E-01	1.02E-01	1.01E-01	8.36E-01	**-2.02E+00**	**2.87E-04**	-8.33E-01	9.51E-02	WT NoN 14 dpi	NA	ternary complex factor MIP1 leucine-zipperprotein (Protein of unknown function, DUF547) (AHRD V3.3 *** AT2G39690.1)	
Solyc11g007500.2	-8.19E-01	1.94E-01	-5.14E-01	4.10E-01	**2.06E+00**	**2.52E-03**	9.33E-01	1.41E-01	WT NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** M1BPV9_SOLTU)	GO:0008152|GO:0016758
Solyc04g014350.1	-8.24E-01	8.35E-02	-4.22E-01	3.65E-01	**1.86E+00**	**3.98E-04**	1.21E+00	1.39E-02	WT NoN 14 dpi	H	LOW QUALITY:Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT1G69350.1)	
Solyc06g009510.1	-8.26E-01	1.46E-01	-3.95E-01	4.80E-01	**-3.11E+00**	**6.38E-06**	-1.36E+00	2.02E-02	WT NoN 14 dpi	T	Transcription factor, putative (AHRD V3.3 GO:0046983 *** B9RNB4_RICCO)	
Solyc07g006020.3	-8.27E-01	2.82E-02	-4.03E-01	2.67E-01	**-1.09E+00**	**5.21E-03**	-7.07E-01	5.76E-02	WT NoN 14 dpi	H	ADIPOR-like receptor (AHRD V3.3 ***W9QY38_9ROSA)	GO:0016021
Solyc06g062450.3	-8.32E-01	6.97E-06	-3.99E-01	1.22E-02	**-1.01E+00**	**3.40E-07**	-1.97E-01	1.95E-01	WT NoN 14 dpi	PMI	Leucine-rich repeat protein kinase familyprotein, putative (AHRD V3.3 *** A0A061GIV3_THECC)	
Solyc09g075930.2	-8.33E-01	7.36E-02	-2.94E-01	5.16E-01	**-1.61E+00**	**1.32E-03**	-8.61E-01	6.52E-02	WT NoN 14 dpi	AM	Amine oxidase (AHRD V3.3 ***K4CVH0_SOLLC)	GO:0005507|GO:0008131|GO:0009308|G O:0048038|GO:0055114
Solyc03g093050.1	-8.37E-01	3.18E-01	-8.19E-01	3.28E-01	**-3.51E+00**	**2.34E-04**	-1.78E+00	4.01E-02	WT NoN 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12520.1)	
Solyc06g053520.3	-8.37E-01	6.80E-02	-8.28E-01	7.07E-02	**1.30E+00**	**6.61E-03**	2.40E-01	5.89E-01	WT NoN 14 dpi	N	spermidine synthase (AHRD V3.3 ***AT1G23820.1)	GO:0003824
Solyc09g015000.3	-8.37E-01	9.72E-02	-2.69E-01	5.85E-01	**1.42E+00**	**7.31E-03**	-1.31E-02	9.79E-01	WT NoN 14 dpi	STR	Heat-shock protein, putative (AHRD V3.3 *** B9S3B2_RICCO)	
Solyc03g005190.3	-8.58E-01	2.96E-02	-8.88E-01	2.48E-02	**-1.49E+00**	**4.80E-04**	-8.45E-01	3.19E-02	WT NoN 14 dpi	L	Phosphoinositide phosphatase family protein (AHRD V3.3 --* AT3G43220.3)	
Solyc09g097850.1	-8.60E-01	1.37E-03	-2.62E-01	2.84E-01	**1.31E+00**	**1.00E-05**	1.39E-01	5.67E-01	WT NoN 14 dpi	G	Cysteine proteinase inhibitor (AHRD V3.3 GO:0004869 *** K4CWV7_SOLLC)	
Solyc10g009240.3	-8.66E-01	2.52E-02	-9.71E-01	1.31E-02	**1.17E+00**	**3.49E-03**	8.33E-01	3.08E-02	WT NoN 14 dpi	L	3-ketoacyl-CoA synthase (AHRD V3.3 ***B9GRP8_POPTR)	GO:0003824|GO:0008152|GO:0006633|G O:0016020|GO:0016747|GO:0006633|GO: 0016020|GO:0016747
Solyc10g079900.2	-8.71E-01	3.61E-01	-3.96E-01	6.76E-01	**2.98E+00**	**3.81E-03**	1.82E+00	6.32E-02	WT NoN 14 dpi	DNA	Rho termination factor (AHRD V3.3 --* AT4G18740.4)	

Solyc02g080450.1	-8.72E-01	1.02E-03	4.52E-01	6.58E-02	**1.41E+00**	**2.71E-06**	1.71E-01	4.75E-01	WT NoN 14 dpi	CS	LOW QUALITY:CELLULOSE SYNTHASEINTERACTIVE 3 (AHRD V3.3 --* AT1G77460.4)	
Solyc03g114240.3	-8.81E-01	7.63E-02	-4.37E-01	3.68E-01	**-1.61E+00**	**2.29E-03**	-9.69E-01	5.26E-02	WT NoN 14 dpi	CS	Polygalacturonase non-catalytic protein (AHRD V3.3 *** G7K1D9_MEDTR)	
Solyc12g094660.2	-8.99E-01	4.22E-02	-2.65E-01	5.34E-01	**1.18E+00**	**9.49E-03**	6.99E-01	1.09E-01	WT NoN 14 dpi	D	Disease resistance protein (AHRD V3.3 *** GO:0043531A0A103YE14_CYNCS)	
Solyc03g114620.1	-9.07E-01	3.04E-01	-1.21E+00	1.72E-01	**-2.98E+00**	**1.96E-03**	1.60E+00	7.62E-02	WT NoN 14 dpi	N	LOW QUALITY:Glutamine dumper 2,putative (AHRD V3.3 *** A0A061ENI6_THECC)	
Solyc02g088080.2	-9.22E-01	1.94E-01	2.95E-01	6.74E-01	**-2.27E+00**	**2.93E-03**	-1.05E+00	1.41E-01	WT NoN 14 dpi	OX	Thioredoxin superfamily protein (AHRDV3.3 --* AT3G56420.3)	
Solyc06g051840.1	-9.26E-01	3.02E-02	-4.19E-01	3.08E-01	**1.68E+00**	**3.14E-04**	8.70E-01	4.07E-02	WT NoN 14 dpi	T	Solanum lycopersicum Cytokinin Response Factor 6	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc00g170200.1	-9.35E-01	7.04E-05	1.64E-01	4.14E-01	**-2.47E+00**	**2.10E-12**	-8.70E-01	1.66E-04	WT NoN 14 dpi	H	LOW QUALITY:Sigma factor sigB regulation protein rsbQ (AHRD V3.3 ***A0A0B2Q4V2_GLYSO)	
Solyc06g084820.2	-9.38E-01	1.59E-05	-4.45E-01	1.85E-02	**-1.10E+00**	**1.44E-06**	-1.33E-01	4.58E-01	WT NoN 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** A0A061G7Z4_THECC)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO: 0016705|GO:0055114
Solyc01g107730.3	-9.38E-01	1.24E-03	-7.08E-02	7.86E-01	**1.16E+00**	**1.30E-04**	-1.22E-01	6.40E-01	WT NoN 14 dpi	G	D-type cyclin-2	GO:0005634
Solyc12g040470.2	-9.39E-01	3.11E-01	3.47E-01	7.06E-01	**3.43E+00**	**8.66E-04**	-2.58E+00	8.71E-03	WT NoN 14 dpi	L	non-specific phospholipase C2 (AHRD V3.3 --* AT2G26870.1)	
Solyc11g067180.2	-9.42E-01	3.50E-01	1.19E+00	2.41E-01	**2.87E+00**	**7.57E-03**	2.08E+00	4.56E-02	WT NoN 14 dpi	CS	Fatty acyl-CoA reductase (AHRD V3.3 *** K4D9X5_SOLLC)	GO:0080019
Solyc09g091810.1	-9.48E-01	1.65E-01	5.06E-01	4.53E-01	**2.99E+00**	**1.26E-04**	-1.23E-01	8.54E-01	WT NoN 14 dpi	NA	LOW QUALITY:CLAVATA3/ESR-related protein (AHRD V3.3 --* A0A0A0LNB8_CUCSA)	
Solyc06g067910.3	-9.54E-01	3.93E-02	-4.60E-01	3.05E-01	**-1.63E+00**	**1.01E-03**	-1.06E+00	2.30E-02	WT NoN 14 dpi	NA	transmembrane protein, putative (Proteinof unknown function, DUF642) (AHRD V3.3 *** AT5G11420.1)	
Solyc06g035980.3	-9.54E-01	3.77E-01	-4.23E-01	6.94E-01	**-3.30E+00**	**4.56E-03**	-1.18E+00	2.77E-01	WT NoN 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT3G11620.9)	
Solyc05g006510.1	-9.56E-01	4.36E-03	-7.24E-01	2.57E-02	**-1.35E+00**	**1.58E-04**	-6.87E-01	3.36E-02	WT NoN 14 dpi	P	Hexosyltransferase (AHRD V3.3 ***K4BWH7_SOLLC)	GO:0016757
Solyc01g009410.3	-9.58E-01	2.09E-01	-5.18E-01	4.92E-01	**-2.15E+00**	**7.76E-03**	-1.58E+00	4.28E-02	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4ATD7_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO: 0004601|GO:0042744
Solyc12g049110.1	-9.77E-01	2.47E-01	-4.56E-01	5.85E-01	**-3.92E+00**	**6.69E-05**	-2.21E+00	1.27E-02	WT NoN 14 dpi	P	LOW QUALITY:Patatin group A-3 (AHRDV3.3 --* PATA3_SOLTU)	
Solyc09g014530.3	-9.84E-01	9.28E-02	2.19E-01	7.01E-01	**2.49E+00**	**1.56E-04**	3.10E-01	5.87E-01	WT NoN 14 dpi	H	MLP (AHRD V3.3 *** G8DRV9_GOSBA)	GO:0006952|GO:0009607
Solyc02g078620.1	-9.87E-01	5.57E-02	-1.03E+00	4.73E-02	**1.58E+00**	**3.52E-03**	2.72E-01	5.86E-01	WT NoN 14 dpi	DNA	Dof zinc finger protein (AHRD V3.3 ***W9RD26_9ROSA)	GO:0003677|GO:0006355
Solyc12g062250.2	-1.00E+00	1.43E-02	-2.12E-01	5.83E-01	**1.28E+00**	**2.50E-03**	1.05E-01	7.84E-01	WT NoN 14 dpi	C	like SEX4 1 (AHRD V3.3 *** AT3G01510.1)	GO:0005515|GO:0005983|GO:0005983
Solyc04g014320.1	-1.01E+00	3.02E-02	-1.63E-01	7.15E-01	**1.33E+00**	**5.54E-03**	9.02E-01	5.11E-02	WT NoN 14 dpi	0	LOW QUALITY:Leguminosin group485secreted peptide (AHRD V3.3 *** G7KAG0_MEDTR)	
Solyc08g005720.3	-1.03E+00	1.56E-02	-2.25E-01	5.76E-01	**-1.19E+00**	**5.93E-03**	-7.42E-01	7.28E-02	WT NoN 14 dpi	2M	Terpene synthase 18 (AHRD V3.3 *-* R9R6F3_SOLLC)	GO:0000287|GO:0010333|GO:0016829|GO:0003824|GO:0003824
Solyc03g059080.2	-1.04E+00	2.15E-01	-8.59E-01	3.03E-01	**-4.09E+00**	**3.45E-05**	-2.13E+00	1.48E-02	WT NoN 14 dpi	K	Kinase family protein (AHRD V3.3 ***B9HA11_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468

Solyc04g014330.1	-1.05E+00	2.07E-02	-2.60E-01	5.46E-01	**1.46E+00**	**2.04E-03**	9.90E-01	2.78E-02	WT NoN 14 dpi	0	LOW QUALITY:Leguminosin group485 secreted peptide (AHRD V3.3 *** G7KAF8_MEDTR)	
Solyc02g014730.3	-1.05E+00	1.39E-02	-1.12E+00	9.26E-03	**1.58E+00**	**5.40E-04**	1.00E+00	1.87E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***A0A103YA00_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO: 0016705|GO:0055114
Solyc06g083700.3	-1.06E+00	2.12E-01	-1.61E-02	9.85E-01	**-3.82E+00**	**8.97E-05**	-1.47E+00	8.72E-02	WT NoN 14 dpi	OX	Flavin-containing monooxygenase (AHRDV3.3 *** D2IGV4_SOLLC)	GO:0004499|GO:0050660|GO:0050661|GO:0055114|GO:0016491|GO:0055114|GO: 0016491|GO:0055114
Solyc09g007260.3	-1.06E+00	5.68E-03	-9.03E-01	1.64E-02	**1.01E+00**	**7.92E-03**	4.06E-01	2.59E-01	WT NoN 14 dpi	H	AP2-like ethylene-responsive transcriptionfactor (AHRD V3.3 *** G7IU38_MEDTR)	GO:0003677|GO:0003700|GO:0006355|G O:0003700|GO:0006355
Solyc11g017100.1	-1.07E+00	9.00E-03	-5.96E-01	1.27E-01	**1.76E+00**	**8.55E-05**	9.03E-01	2.45E-02	WT NoN 14 dpi	T	LOW QUALITY:GRAS family transcription factor	
Solyc02g080670.3	-1.07E+00	8.21E-02	-5.94E-01	3.24E-01	**-2.40E+00**	**4.11E-04**	-1.40E+00	2.60E-02	WT NoN 14 dpi	D	L-ascorbate oxidase (AHRD V3.3 ***A0A0B0MPT8_GOSAR)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO: 0055114
Solyc09g061890.3	-1.08E+00	1.17E-01	-1.93E-01	7.74E-01	**-2.46E+00**	**1.06E-03**	-1.32E+00	5.83E-02	WT NoN 14 dpi	CS	Pectate lyase (AHRD V3.3 *** M1BAL5_SOLTU)	
Solyc08g076880.3	-1.09E+00	1.90E-05	-4.36E-01	4.61E-02	**1.72E+00**	**1.06E-08**	-1.92E-01	3.65E-01	WT NoN 14 dpi	TR	Nodulin26-like intrinsic protein 31 (AHRDV3.3 --* K4C978_SOLLC)	
Solyc07g052660.1	-1.10E+00	8.04E-02	-1.36E-01	8.24E-01	**-3.46E+00**	**5.30E-06**	-1.21E+00	5.63E-02	WT NoN 14 dpi	E	Blue copper protein (AHRD V3.3 *** W9S2S3_9ROSA)	GO:0009055
Solyc09g084460.3	-1.10E+00	3.97E-01	-3.96E-01	7.60E-01	**5.28E+00**	**3.48E-04**	8.09E-01	5.34E-01	WT NoN 14 dpi	D	Proteinase inhibitor I (AHRD V3.3 ***Q43648_SOLTU)	GO:0004867|GO:0009611
Solyc02g065740.3	-1.10E+00	3.42E-01	-1.55E+00	1.87E-01	**-3.54E+00**	**4.64E-03**	-4.39E-02	9.70E-01	WT NoN 14 dpi	CS	Alpha-1,4-glucan-protein synthase [UDP-forming] (AHRD V3.3 *** UPTG_PEA)	GO:0016866|GO:0030244
Solyc06g035760.3	-1.11E+00	1.08E-03	-2.84E-01	3.55E-01	**1.03E+00**	**2.20E-03**	-6.59E-01	3.83E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 ***R4R2I7_9SOLA)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO: 0016705|GO:0055114
Solyc06g050530.3	-1.11E+00	9.92E-03	-1.15E+00	7.84E-03	**1.39E+00**	**1.85E-03**	8.86E-01	3.59E-02	WT NoN 14 dpi	PMI	Laccase (AHRD V3.3 ***I1M7Q3_SOYBN)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO: 0055114
Solyc08g079090.3	-1.13E+00	1.87E-02	-5.39E-01	2.42E-01	**-1.67E+00**	**1.03E-03**	-9.77E-01	3.97E-02	WT NoN 14 dpi	G	Monocopper oxidase-like protein SKU5(AHRD V3.3 *** SKU5_ARATH)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO: 0055114
Solyc02g093070.3	-1.13E+00	1.37E-01	-7.23E-01	3.36E-01	**-4.18E+00**	**6.07E-06**	-1.92E+00	1.53E-02	WT NoN 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependentoxygenase superfamily protein (AHRD V3.3 *** AT3G50210.4)	GO:0016491|GO:0055114
Solyc06g075570.2	-1.13E+00	2.64E-02	-7.29E-01	1.42E-01	**-2.50E+00**	**2.14E-05**	-1.25E+00	1.57E-02	WT NoN 14 dpi	OX	Respiratory burst oxidase-like protein (AHRD V3.3 *** G7L3G1_MEDTR)	GO:0004601|GO:0050664|GO:0055114|GO:0005509|GO:0005509
Solyc03g080120.1	-1.14E+00	2.25E-03	1.99E-01	5.61E-01	**1.16E+00**	**2.04E-03**	9.07E-01	1.24E-02	WT NoN 14 dpi	NA	LOW QUALITY:holocarboxylasesynthetase 2 (AHRD V3.3 --* AT1G37150.8)	
Solyc01g096940.3	-1.15E+00	1.71E-02	7.71E-01	9.93E-02	**1.30E+00**	**7.96E-03**	-1.48E-01	7.45E-01	WT NoN 14 dpi	S	Receptor-like kinase 17 (AHRD V3.3 ***A5A0Y6_SOLCH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO: 0006468
Solyc07g053600.3	-1.15E+00	2.42E-02	2.08E-01	6.69E-01	**1.74E+00**	**1.25E-03**	8.98E-01	7.33E-02	WT NoN 14 dpi	S	Receptor-like protein kinase HSL1 (AHRDV3.3 *** HSL1_ARATH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:

											0006468
Solyc01g110580.2	-1.15E+00	1.45E-01	-7.92E-01	3.12E-01	**-3.00E+00**	**6.00E-04**	-1.20E+00	1.29E-01	WT NoN 14 dpi	H	Small auxin up-regulated RNA5	GO:0009733
Solyc07g048000.3	-1.16E+00	1.34E-03	-6.42E-01	5.73E-02	**1.57E+00**	**4.74E-05**	3.25E-01	3.23E-01	WT NoN 14 dpi	G	Phototropic-responsive NPH3	GO:0005515
Solyc10g045240.2	-1.16E+00	2.02E-02	2.54E-01	5.93E-01	**2.46E+00**	**1.88E-05**	6.69E-01	1.66E-01	WT NoN 14 dpi	C	Beta-glucosidase (AHRD V3.3 *** L0ASF2_POPTO)	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc03g097500.3	-1.19E+00	5.94E-03	-9.19E-01	2.84E-02	**1.20E+00**	**5.59E-03**	7.37E-01	7.39E-02	WT NoN 14 dpi	CS	Feruloyl transferase (AHRD V3.3 *** D5FPG8_SOLTU)	GO:0016747
Solyc03g115750.1	-1.19E+00	1.02E-01	-1.25E+00	8.49E-02	**-2.59E+00**	**1.05E-03**	-9.22E-01	1.99E-01	WT NoN 14 dpi	CS	Xyloglucan galactosyltransferase KATAMARI1 (AHRD V3.3 *** W9RU56_9ROSA)	
Solyc12g006050.2	-1.19E+00	3.55E-02	-9.06E-01	1.04E-01	**1.70E+00**	**4.04E-03**	-3.70E-01	4.97E-01	WT NoN 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT3G21670.1)	GO:0005215|GO:0006810|GO:0016020
Solyc05g012735.1	-1.21E+00	3.32E-02	-8.39E-01	1.29E-01	**-1.58E+00**	**6.62E-03**	-1.25E+00	2.83E-02	WT NoN 14 dpi	D	Disease resistance protein R1 (AHRD V3.3 *-* H2KMC8_SOLTU)	
Solyc02g082090.3	-1.21E+00	4.16E-02	-8.93E-01	1.24E-01	**-1.96E+00**	**1.74E-03**	-1.13E+00	5.52E-02	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4BA79_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO: 0004601|GO:0042744
Solyc06g009280.1	-1.22E+00	2.72E-02	-4.89E-01	3.57E-01	**-2.22E+00**	**2.41E-04**	-1.26E+00	2.27E-02	WT NoN 14 dpi	TR	ABC transporter B family protein (AHRDV3.3 *** G7IBR0_MEDTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO: 0016887|GO:0005524|GO:0016887
Solyc01g006720.3	-1.23E+00	1.74E-04	2.45E-01	3.88E-01	**1.23E+00**	**1.68E-04**	-7.44E-01	1.32E-02	WT NoN 14 dpi	TR	ABC transporter family protein (AHRD V3.3 *** B9IIG9_POPTR)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc03g019760.3	-1.24E+00	1.67E-03	-9.40E-01	1.34E-02	**1.14E+00**	**3.36E-03**	3.39E-01	3.47E-01	WT NoN 14 dpi	TR	ABC transporter G family member (AHRD V3.3 *** A0A0K9NYG1_ZOSMR)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc11g011110.2	-1.26E+00	1.06E-02	-6.81E-01	1.48E-01	**1.79E+00**	**5.91E-04**	1.17E+00	1.66E-02	WT NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** W9S179_9ROSA)	GO:0016788
Solyc09g075680.1	-1.28E+00	6.40E-06	-6.49E-01	8.01E-03	**1.19E+00**	**1.76E-05**	-5.68E-01	1.85E-02	WT NoN 14 dpi	L	Alpha/beta-Hydrolases superfamily protein(AHRD V3.3 *** A0A061EKQ6_THECC)	GO:0008152|GO:0016787
Solyc08g080060.3	-1.30E+00	1.86E-01	-9.15E-01	3.50E-01	**-3.62E+00**	**8.67E-04**	-1.92E+00	5.63E-02	WT NoN 14 dpi	CS	Expansin-like protein (AHRD V3.3 *** Q0WT83_ARATH)	GO:0005576|GO:0009664|GO:0009664
Solyc11g009100.2	-1.31E+00	7.13E-02	-2.00E+00	8.11E-03	**1.99E+00**	**8.30E-03**	1.09E+00	1.30E-01	WT NoN 14 dpi	TR	ABC transporter G family member (AHRD V3.3 *** A0A0K9NWI5_ZOSMR)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc07g016210.1	-1.32E+00	2.33E-01	-3.31E-01	7.62E-01	**4.23E+00**	**6.03E-04**	1.79E+00	1.10E-01	WT NoN 14 dpi	NA	Specific tissue protein (AHRD V3.3 *** G7IZL4_MEDTR)	
Solyc01g100770.2	-1.32E+00	1.14E-01	6.81E-01	4.06E-01	**2.48E+00**	**5.00E-03**	1.42E+00	8.95E-02	WT NoN 14 dpi	NA	LOW QUALITY:plant/protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT1G56580.1)	
Solyc12g089350.2	-1.32E+00	1.76E-02	-1.11E+00	4.22E-02	**2.10E+00**	**4.36E-04**	1.18E+00	3.28E-02	WT NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2SN40_GLYSO)	GO:0016788
Solyc10g082040.2	-1.33E+00	4.84E-02	-1.18E+00	7.70E-02	**-2.29E+00**	**1.44E-03**	3.72E-02	9.54E-01	WT NoN 14 dpi	H	HVA22-like protein (AHRD V3.3 *** K4D390_SOLLC)	
Solyc04g078470.3	-1.35E+00	1.28E-04	2.02E-01	5.07E-01	**1.08E+00**	**1.40E-03**	-1.38E-01	6.51E-01	WT NoN 14 dpi	G	D-type cyclin-3	GO:0005634
Solyc01g080230.3	-1.38E+00	4.42E-06	-1.27E+00	1.37E-05	**1.16E+00**	**4.86E-05**	9.26E-02	7.00E-01	WT NoN 14 dpi	CS	Endo-1,3-1,4-beta-d-glucanase, putative(AHRD V3.3 *** B9RSS4_RICCO)	GO:0016787
Solyc08g006750.3	-1.38E+00	3.12E-07	-8.12E-01	4.50E-04	**1.04E+00**	**2.27E-05**	5.48E-01	1.17E-02	WT NoN 14 dpi	AM	Aromatic amino acid decarboxylase 2 (AHRD V3.3 *** Q1KSC4_SOLLC)	GO:0003824|GO:0016831|GO:0016831
Solyc12g011280.2	-1.38E+00	8.33E-02	-5.26E-01	4.99E-01	**-2.84E+00**	**1.01E-03**	-1.95E-01	8.01E-01	WT NoN 14 dpi	E	Chlorophyll a-b binding protein,chloroplastic (AHRD V3.3 *** K4DCL4_SOLLC)	GO:0009765|GO:0016020
Solyc02g093650.3	-1.38E+00	1.04E-02	-1.19E+00	2.54E-02	**2.37E+00**	**6.98E-05**	1.16E+00	2.90E-02	WT NoN 14 dpi	PMI	Early nodulin-like protein (AHRD V3.3 *** A0A072U7R7_MEDTR)	GO:0009055

Solyc04g011600.3	-1.39E+00	1.02E-03	-7.43E-01	5.79E-02	**1.25E+00**	**2.51E-03**	9.25E-01	2.04E-02	WT NoN 14 dpi	CS	Glycerol-3-phosphate acyltransferase(AHRD V3.3 *** G7KGS4_MEDTR)	GO:0008152|GO:0016746
Solyc01g108210.3	-1.39E+00	3.73E-02	-1.78E+00	9.40E-03	**1.83E+00**	**7.71E-03**	-2.37E+00	9.49E-04	WT NoN 14 dpi	CYTP450	Cytochrome P450 family ABA 8'-hydroxylase (AHRD V3.3 *** G7JL85_MEDTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc12g006000.1	-1.40E+00	7.48E-02	-1.38E+00	7.93E-02	**-2.66E+00**	**1.60E-03**	-8.43E-01	2.73E-01	WT NoN 14 dpi	TR	ENTH/ANTH/VHS superfamily protein(AHRD V3.3 *** AT1G05020.1)	GO:0005543|GO:0005545|GO:0030136|GO:0030276|GO:0048268|GO:0005545|GO:0030136|GO:0030276|GO:0048268
Solyc02g069420.3	-1.40E+00	8.84E-02	-1.39E+00	9.18E-02	**-2.35E+00**	**6.48E-03**	-7.36E-01	3.62E-01	WT NoN 14 dpi	L	Phospholipid-transporting ATPase (AHRD V3.3 *** M1BWN2_SOLTU)	GO:0000166|GO:0000166|GO:0046872|GO:0000166|GO:0046872
Solyc05g006190.1	-1.43E+00	6.60E-02	-4.91E-01	5.14E-01	**-2.61E+00**	**1.66E-03**	-1.46E+00	6.07E-02	WT NoN 14 dpi	L	LOW QUALITY:O-acyltransferase (AHRDV3.3 --* T2HV99_EUPLA)	
Solyc08g079080.4	-1.44E+00	1.42E-01	-1.68E+00	9.01E-02	**-3.70E+00**	**6.36E-04**	-2.57E+00	1.22E-02	WT NoN 14 dpi	NA	symbol=lin9	
Solyc05g043360.2	-1.45E+00	1.77E-01	2.00E-01	8.50E-01	**-4.20E+00**	**4.39E-04**	-2.45E+00	2.64E-02	WT NoN 14 dpi	PMI	Laccase (AHRD V3.3 ***A0A067JKU4_JATCU)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO: 0055114
Solyc01g097720.1	-1.46E+00	1.02E-02	-4.84E-01	3.66E-01	**-1.85E+00**	**1.67E-03**	-4.88E-01	3.63E-01	WT NoN 14 dpi	CS	Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)	
Solyc06g066110.1	-1.47E+00	2.67E-02	4.07E-01	5.20E-01	**2.00E+00**	**3.59E-03**	1.53E+00	2.14E-02	WT NoN 14 dpi	NA	LOW QUALITY:DUF1677 family protein (DUF1677) (AHRD V3.3 *** AT1G72510.2)	
Solyc11g006290.2	-1.53E+00	4.10E-02	1.31E+00	7.53E-02	**-3.46E+00**	**4.68E-05**	-1.91E+00	1.23E-02	WT NoN 14 dpi	L	3-oxo-5-alpha-steroid 4-dehydrogenasefamily protein (AHRD V3.3 *** AT5G16010.1)	GO:0005737|GO:0006629|GO:0016021|G O:0016627
Solyc05g006220.3	-1.58E+00	8.33E-02	1.04E-01	9.07E-01	**2.79E+00**	**3.82E-03**	1.38E+00	1.30E-01	WT NoN 14 dpi	H	IAA-amino acid hydrolase ILR1, putative(AHRD V3.3 *** B9S2J7_RICCO)	GO:0008152|GO:0016787|GO:0016787|G O:0016787
Solyc12g017340.1	-1.60E+00	8.97E-02	-1.25E+00	1.81E-01	**-3.05E+00**	**2.41E-03**	-1.96E+00	4.02E-02	WT NoN 14 dpi	TR	LOW QUALITY:Cation efflux family protein(AHRD V3.3 --* A0A061FA80_THECC)	
Solyc03g118930.2	-1.60E+00	4.32E-02	-9.19E-01	2.34E-01	**-3.54E+00**	**7.60E-05**	-1.20E+00	1.23E-01	WT NoN 14 dpi	C	LOW QUALITY:Glycosyltransferase, putative (AHRD V3.3 *** B9S2Z4_RICCO)	GO:0016757
Solyc09g082080.1	-1.61E+00	8.85E-02	1.94E+00	4.16E-02	**2.85E+00**	**4.14E-03**	1.60E+00	8.91E-02	WT NoN 14 dpi	G	LOW QUALITY:ovate family protein 19	
Solyc05g055320.3	-1.64E+00	3.43E-02	-1.17E+00	1.24E-01	**-5.20E+00**	**1.66E-07**	-1.22E+00	1.09E-01	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4C2K8_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO: 0004601|GO:0042744
Solyc09g065420.3	-1.66E+00	1.33E-03	-1.25E+00	1.18E-02	**1.47E+00**	**3.78E-03**	1.19E+00	1.61E-02	WT NoN 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)	GO:0006869|GO:0008289
Solyc10g018330.2	-1.67E+00	1.64E-02	-2.06E-01	7.54E-01	**-2.31E+00**	**1.50E-03**	-1.21E+00	7.34E-02	WT NoN 14 dpi	NA	Retrovirus-related Pol polyprotein fromtransposon TNT 1-94 (AHRD V3.3 *-* A0A151TG49_CAJCA)	GO:0004857
Solyc10g084000.2	-1.74E+00	3.19E-02	-9.48E-01	2.27E-01	**2.76E+00**	**1.32E-03**	2.03E+00	1.38E-02	WT NoN 14 dpi	TR	Heavy metal transport/detoxificationsuperfamily protein (AHRD V3.3 *** AT2G36950.1)	GO:0030001|GO:0046872
Solyc03g098060.2	-1.76E+00	3.40E-02	-1.70E+00	3.97E-02	**-2.90E+00**	**1.07E-03**	-1.35E+00	9.89E-02	WT NoN 14 dpi	G	ZF-HD homeobox protein (AHRD V3.3 ***A0A061FW93_THECC)	GO:0003677
Solyc06g073480.3	-1.82E+00	2.51E-02	-1.99E+00	1.56E-02	**-2.21E+00**	**8.03E-03**	-6.12E-01	4.32E-01	WT NoN 14 dpi	G	Phototropic-responsive NPH3 familyprotein, putative (AHRD V3.3 *** A0A061EZT3_THECC)	GO:0005515
Solyc11g007210.2	-1.84E+00	6.66E-02	-6.49E-01	5.05E-01	**-3.98E+00**	**3.27E-04**	-7.28E-01	4.55E-01	WT NoN 14 dpi	OX	Peroxidase (AHRD V3.3 ***K4D4Y2_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:

											0004601|GO:0042744
Solyc04g007630.2	-1.88E+00	1.77E-02	-1.44E+00	6.28E-02	**2.29E+00**	**4.74E-03**	-1.26E+00	1.02E-01	WT NoN 14 dpi	TR	Heavy metal transport/detoxificationsuperfamily protein (AHRD V3.3 *** AT1G71050.1)	GO:0030001|GO:0046872
Solyc12g038680.1	-1.99E+00	2.43E-02	-3.76E-01	6.54E-01	**-3.77E+00**	**1.16E-04**	-9.40E-01	2.68E-01	WT NoN 14 dpi	S	LOW QUALITY:Cysteine/Histidine-rich C1domain family protein (AHRD V3.3 *** AT2G44380.1)	
Solyc06g063330.3	-1.99E+00	1.05E-01	-2.89E+00	2.20E-02	**-4.05E+00**	**2.07E-03**	-1.69E+00	1.66E-01	WT NoN 14 dpi	E	vacuolar ATP synthase subunit A (AHRDV3.3 *** AT1G78900.2)	GO:0005524|GO:0015991|GO:0033180|G O:0046961|GO:0015991|GO:0033180|GO: 0046961
Solyc09g074570.1	-2.03E+00	1.21E-02	5.07E-01	5.07E-01	**-2.23E+00**	**6.53E-03**	-2.08E+00	1.06E-02	WT NoN 14 dpi	OX	Glutaredoxin (AHRD V3.3 *** B3F8F2_SOLTU)	GO:0009055|GO:0015035|GO:0045454
Solyc11g013810.2	-2.06E+00	8.70E-07	-1.72E+00	1.35E-05	**1.29E+00**	**4.58E-04**	4.01E-01	2.23E-01	WT NoN 14 dpi	N	Nitrate reductase (AHRD V3.3 ***K4D6I5_SOLLC)	GO:0006809|GO:0042128|GO:0050464|G O:0016491|GO:0030151|GO:0055114|GO: 0016491|GO:0030151|GO:0055114
Solyc03g112060.3	-2.07E+00	2.03E-05	-4.12E-01	3.09E-01	**1.78E+00**	**1.30E-04**	6.89E-01	9.46E-02	WT NoN 14 dpi	E	Quinolinate synthase A (AHRD V3.3 *** W9RJG8_9ROSA)	GO:0008987|GO:0009435|GO:0051539
Solyc10g005190.1	-2.09E+00	2.84E-02	-1.31E+00	1.57E-01	**-3.18E+00**	**1.57E-03**	-1.94E+00	4.07E-02	WT NoN 14 dpi	E	LOW QUALITY:root hair specific 4 (AHRD V3.3 *** AT1G30850.1)	
Solyc01g005880.1	-2.09E+00	2.73E-02	-1.11E+00	2.26E-01	**-3.43E+00**	**7.23E-04**	-1.36E+00	1.41E-01	WT NoN 14 dpi	CS	LOW QUALITY:Extensin-like protein Dif10 (AHRD V3.3 *** Q43504_SOLLC)	
Solyc07g007270.3	-2.14E+00	4.93E-03	3.55E-01	6.14E-01	**1.98E+00**	**8.57E-03**	2.95E-01	6.75E-01	WT NoN 14 dpi	G	root meristem growth factor (AHRD V3.3 -- * AT5G64770.1)	
Solyc00g071180.3	-2.20E+00	3.19E-01	4.86E-02	9.82E-01	**6.47E+00**	**6.17E-03**	2.25E+00	3.09E-01	WT NoN 14 dpi	AM	multicystatin	GO:0004869
Solyc01g066910.3	-2.30E+00	7.49E-08	2.73E-01	3.86E-01	**1.01E+00**	**2.99E-03**	1.96E-01	5.33E-01	WT NoN 14 dpi	NA	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MM18_ARALL)	
Solyc01g080870.3	-2.69E+00	1.14E-02	7.25E-01	4.69E-01	**4.42E+00**	**1.33E-04**	2.29E+00	2.83E-02	WT NoN 14 dpi	TR	Peptide transporter, putative (AHRD V3.3 *** B9SKJ1_RICCO)	GO:0005215|GO:0006810|GO:0016020
Solyc08g068990.2	-2.71E+00	1.32E-02	-1.07E+00	3.00E-01	**-3.42E+00**	**2.42E-03**	-2.32E-01	8.21E-01	WT NoN 14 dpi	D	Pathogenesis-related protein 1 (AHRD V3.3 *** A0MZ69_MUSAC)	GO:0005576
Solyc06g050760.1	-3.08E+00	1.69E-15	-2.44E+00	3.55E-13	**2.04E+00**	**1.98E-11**	5.22E-01	7.79E-03	WT NoN 14 dpi	D	Wound-induced protein 1 (AHRD V3.3 *** WUN1_SOLTU)	
Solyc02g085880.2	-3.51E+00	3.90E-04	-2.17E+00	1.84E-02	**3.26E+00**	**8.38E-04**	1.88E+00	3.85E-02	WT NoN 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9RSK4_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114

Table S 8. List of differentially expressed genes (DEGs) identified in tomato roots 1 day post inoculation (dpi) with Gluconacetobacter diazotrophicus nifD- strain. *Fold change values of DEGs identified in tomato roots with G. diazotrophicus nifD- strain as compared to uninoculated plants (Control) in modified Hoagland in the absence (nifD- NoN) or presence of 2 mM KNO3 (nifD- N) in hydroponic systems at 1dpi. Tomato gene identifier (ITAG3.2 release), Log2-transformed fold change values and P values calculated for each pairwise comparison between bacterium-inoculated and uninoculated samples are reported. Clustering results of the DEGs, classified as genes significantly modulated (in bold, P ≤ 0.01 and Log2(fold change) ≥ 1 or ≤ -1) by nifD- in either N or NoN condition. Protein description and abbreviation codes of functional classes were assigned on the basis of the protein description and function. Gene ontology (GO) terms were based on the ITAG3.2 release (https://solgenomics.net/organism/Solanum_lycopersicum/genome).*

Gene ID	WT N	P.Value	*nifD*- N	P. Value	WT NoN	P. Value	*nifD*- NoN	P.Value	Cluster	Functional Class	Gene Description	GO
Solyc03g005770.3	5,01E-01	4,21E-01	**3,22E+00**	**1,79E-05**	-1,25E+00	5,18E-02	5,09E-01	4,14E-01	*nifD*- N 1 dpi	E	chlorophyll a/b-binding protein	GO:0009765|GO:0016020
Solyc01g094250.3	2,36E+00	2,14E-02	**3,13E+00**	**3,19E-03**	2,95E-01	7,62E-01	6,50E-01	5,05E-01	*nifD*- N 1 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G61220.1)	
Solyc09g015230.1	2,82E-01	7,42E-01	**2,86E+00**	**2,40E-03**	1,61E+00	6,97E-02	9,40E-01	2,79E-01	*nifD*- N 1 dpi	K	Protein kinase family protein (AHRD V3.3 *** AT3G25490.1)	GO:0004672|GO:0005524|GO:0006468
Solyc10g079900.2	1,34E+00	1,65E-01	**2,85E+00**	**5,41E-03**	-9,25E-02	9,22E-01	-3,12E-01	7,42E-01	*nifD*- N 1 dpi	DNA	Rho termination factor (AHRD V3.3 --* AT4G18740.4)	
Solyc03g025190.4	2,52E+00	1,29E-02	**2,66E+00**	**8,97E-03**	-4,16E-01	6,62E-01	-3,41E-01	7,20E-01	*nifD*- N 1 dpi	TR	anthocyanin permease	
Solyc04g079510.2	1,34E+00	1,18E-01	**2,43E+00**	**7,00E-03**	-3,74E+00	1,22E-04	-2,20E+00	1,32E-02	*nifD*- N 1 dpi	TR	Peptide transporter	GO:0005215|GO:0006810|GO:0016020
Solyc12g049350.2	6,90E-01	3,95E-01	**2,40E+00**	**5,78E-03**	-2,82E+00	1,54E-03	-1,56E+00	6,08E-02	*nifD*- N 1 dpi	T	R2R3MYB transcription factor 11	GO:0003677
Solyc07g056570.1	-1,67E-01	8,04E-01	**2,19E+00**	**2,85E-03**	-2,05E-01	7,60E-01	1,12E-01	8,67E-01	*nifD*- N 1 dpi	H	notabilis	GO:0016702|GO:0055114
Solyc09g015240.1	1,38E+00	4,21E-02	**2,11E+00**	**3,11E-03**	-4,46E-01	4,97E-01	5,09E-02	9,38E-01	*nifD*- N 1 dpi	K	Protein kinase family protein (AHRD V3.3 *** B5RHV5_MUSBA)	GO:0004672|GO:0005524|GO:0006468
Solyc10g018390.2	3,19E-01	6,65E-01	**2,07E+00**	**8,87E-03**	6,18E-01	4,05E-01	8,71E-01	2,43E-01	*nifD*- N 1 dpi	AM	Tryptophan synthase (AHRD V3.3 *** K4CYW3_SOLLC)	GO:0000162|GO:0004834
Solyc09g066450.2	7,50E-01	7,13E-02	**1,99E+00**	**3,58E-05**	5,01E-01	2,20E-01	-2,54E-01	5,30E-01	*nifD*- N 1 dpi	T	GRAS family transcription factor (AHRD V3.3 *** A0A061DWK6_THECC)	
Solyc01g104915.1	1,04E+00	6,37E-02	**1,96E+00**	**1,17E-03**	1,11E+00	4,96E-02	-2,68E-01	6,22E-01	*nifD*- N 1 dpi	TR	Two pore calcium channel protein 1 (AHRD V3.3 --* TPC1_WHEAT)	
Solyc03g044028.1	9,62E-01	1,25E-01	**1,95E+00**	**3,55E-03**	-1,29E+00	4,29E-02	-2,94E-01	6,32E-01	*nifD*- N 1 dpi	E	Oxygen-evolving enhancer protein 2-2, chloroplastic (AHRD V3.3 --* PSBP2_TOBAC)	
Solyc07g018190.3	9,23E-01	7,53E-02	**1,92E+00**	**7,01E-04**	-1,41E-01	7,79E-01	-1,76E-01	7,26E-01	*nifD*- N 1 dpi	S	Receptor-kinase, putative (AHRD V3.3 *** B9SUC9_RICCO)	GO:0004672|GO:0005524|GO:0006468
Solyc06g008990.1	5,11E-01	4,22E-01	**1,91E+00**	**5,33E-03**	-1,58E+00	1,82E-02	-2,86E-01	6,52E-01	*nifD*- N 1 dpi	G	LOW QUALITY:Fantastic four-like protein (AHRD V3.3 *-* G7IE53_MEDTR)	
Solyc09g092470.2	9,10E-01	1,24E-01	**1,80E+00**	**4,06E-03**	1,00E+00	9,23E-02	2,59E-01	6,54E-01	*nifD*- N 1 dpi	2M	sesquiterpene synthase 14	GO:0000287|GO:0010333|GO:0016829
Solyc07g039410.3	1,15E+00	3,43E-02	**1,73E+00**	**2,43E-03**	-8,92E-02	8,64E-01	-1,41E-01	7,87E-01	*nifD*- N 1 dpi	D	EDNR2GH3 protein (AHRD V3.3 *** E0Y3V4_9SOLN)	GO:0043531
Solyc08g079300.3	1,00E+00	1,20E-01	**1,73E+00**	**9,97E-03**	-2,66E+00	2,36E-04	-1,36E+00	3,78E-02	*nifD*- N 1 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** U5GNW2_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc06g053520.3	9,42E-01	4,17E-02	**1,61E+00**	**1,12E-03**	2,24E-01	6,14E-01	3,81E-01	3,94E-01	*nifD*- N 1 dpi	N	spermidine synthase (AHRD V3.3 *** AT1G23820.1)	GO:0003824
Solyc08g006025.1	9,27E-01	3,81E-02	**1,56E+00**	**1,07E-03**	-2,15E-01	6,16E-01	3,76E-01	3,83E-01	*nifD*- N 1 dpi	T	NAC domain-containing protein (AHRD V3.3 *-* I6YR01_9CARY)	GO:0003677|GO:0006355

Solyc10g008400.1	1,15E+00	1,32E-02	**1,48E+00**	**2,10E-03**	8,79E-01	5,20E-02	-2,62E-02	9,52E-01	*nifD*- N 1 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G74990.1)	GO:0005515|GO:0008270
Solyc05g005670.1	2,02E-01	6,28E-01	**1,47E+00**	**1,47E-03**	5,85E-01	1,68E-01	-1,13E-01	7,85E-01	*nifD*- N 1 dpi	P	U-box domain-containing protein 18 (AHRD V3.3 *** W9RKZ7_9ROSA)	GO:0004842|GO:0016567
Solyc02g062230.1	6,73E-01	4,41E-02	**1,45E+00**	**1,08E-04**	3,71E-01	2,54E-01	3,58E-01	2,71E-01	*nifD*- N 1 dpi	H	Small auxin up-regulated RNA32	GO:0009733
Solyc06g068620.3	1,53E-01	7,05E-01	**1,42E+00**	**1,48E-03**	1,09E+00	1,08E-02	4,02E-01	3,22E-01	*nifD*- N 1 dpi	NA	Negative regulator of sporulation MDS3 (AHRD V3.3 *-* A0A0B0N6H6_GOSAR)	
Solyc08g079140.1	7,70E-01	8,69E-02	**1,41E+00**	**3,18E-03**	-8,06E-02	8,54E-01	4,95E-01	2,64E-01	*nifD*- N 1 dpi	H	Small auxin up-regulated RNA67	GO:0009733
Solyc01g067850.2	5,75E-01	1,39E-01	**1,38E+00**	**1,16E-03**	5,22E-01	1,78E-01	2,30E-01	5,47E-01	*nifD*- N 1 dpi	OX	Peroxidase (AHRD V3.3 *** K4AX33_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114
Solyc01g095820.2	4,75E-01	3,69E-02	**1,34E+00**	**1,43E-06**	-1,29E-01	5,55E-01	-1,41E-01	5,20E-01	*nifD*- N 1 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *-* AT2G25410.1)	GO:0005515|GO:0008270
Solyc03g119510.3	1,06E+00	1,72E-02	**1,24E+00**	**6,37E-03**	-2,08E-01	6,23E-01	-1,91E-01	6,50E-01	*nifD*- N 1 dpi	E	ATP synthase subunit B (AHRD V3.3 --* AT5G10320.6)	
Solyc01g073910.3	3,00E-01	3,47E-01	**1,16E+00**	**1,07E-03**	9,66E-01	4,86E-03	6,13E-01	6,17E-02	*nifD*- N 1 dpi	DNA	homeobox leucine zipper protein (AHRD V3.3 *** AT5G06710.1)	GO:0003677
Solyc01g095810.3	3,01E-01	1,23E-01	**1,16E+00**	**1,92E-06**	1,48E-01	4,39E-01	1,77E-01	3,56E-01	*nifD*- N 1 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061DTM6_THECC)	GO:0005515|GO:0008270
Solyc01g068630.3	5,27E-01	1,86E-01	**1,15E+00**	**6,34E-03**	1,96E-02	9,60E-01	2,78E-01	4,80E-01	*nifD*- N 1 dpi	K	Haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *** B9I993_POPTR)	GO:0008152|GO:0016787
Solyc10g080690.2	8,09E-01	3,49E-03	**1,13E+00**	**1,32E-04**	4,81E-01	6,70E-02	-2,14E-01	4,04E-01	*nifD*- N 1 dpi	P	Patatin (AHRD V3.3 *** K4D2V9_SOLLC)	GO:0006629
Solyc04g078640.2	5,29E-01	2,63E-02	**1,12E+00**	**3,55E-05**	4,01E-01	8,54E-02	5,04E-01	3,35E-02	*nifD*- N 1 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *-* A0A0K9P1G2_ZOSMR)	GO:0003677
Solyc03g115870.3	9,74E-01	7,66E-05	**1,11E+00**	**1,46E-05**	9,46E-01	1,09E-04	8,44E-02	6,87E-01	*nifD*- N 1 dpi	OX	Thioredoxin (AHRD V3.3 *** A0A072UTZ5_MEDTR)	GO:0045454
Solyc07g053890.3	2,27E-01	4,91E-01	**1,10E+00**	**2,32E-03**	-2,15E-01	5,13E-01	1,32E-01	6,88E-01	*nifD*- N 1 dpi	L	O-acyltransferase WSD1 (AHRD V3.3 *** A0A151TQI5_CAJCA)	GO:0004144
Solyc01g110920.3	8,46E-01	1,93E-02	**1,06E+00**	**4,33E-03**	5,52E-01	1,16E-01	5,17E-01	1,40E-01	*nifD*- N 1 dpi	H	Small auxin up-regulated RNA26	GO:0009733
Solyc02g091930.3	7,31E-01	1,29E-04	**1,05E+00**	**7,97E-07**	7,54E-01	8,91E-05	4,61E-01	8,72E-03	*nifD*- N 1 dpi	DNA	Homeobox-leucine zipper protein family (AHRD V3.3 *** AT4G37790.1)	GO:0003677
Solyc12g055970.2	7,35E-01	6,45E-03	**1,05E+00**	**2,64E-04**	4,02E-01	1,17E-01	1,48E-01	5,57E-01	*nifD*- N 1 dpi	CS	Endoglucanase (AHRD V3.3 *** Q93WY9_TOBAC)	GO:0003824
Solyc01g100910.3	7,62E-01	3,50E-02	**1,05E+00**	**5,07E-03**	-3,67E-01	2,93E-01	-8,61E-02	8,03E-01	*nifD*- N 1 dpi	H	WAT1-related protein (AHRD V3.3 *** K4B1C2_SOLLC)	GO:0016020|GO:0016021
Solyc04g012010.3	5,11E-01	6,79E-02	**1,03E+00**	**6,95E-04**	4,40E-01	1,13E-01	1,75E-01	5,19E-01	*nifD*- N 1 dpi	D	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G38350.1)	GO:0043531
Solyc01g102900.3	9,22E-01	6,96E-03	**1,03E+00**	**2,99E-03**	-1,16E-01	7,14E-01	-7,60E-01	2,29E-02	*nifD*- N 1 dpi	STR	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)	GO:0030145
Solyc07g009060.3	9,29E-01	6,05E-05	**1,03E+00**	**1,62E-05**	4,09E-01	4,52E-02	9,33E-01	5,77E-05	*nifD*- N 1 dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952
Solyc05g009460.3	-3,81E-02	8,94E-01	**-1,01E+00**	**1,43E-03**	5,26E-02	8,54E-01	-5,01E-02	8,61E-01	*nifD*- N 1 dpi	NA	Conserved peptide upstream open reading frame 53 (AHRD V3.3 --* B3H7G6_ARATH)	
Solyc00g005040.3	-5,06E-01	1,01E-01	**-1,08E+00**	**1,18E-03**	-6,65E-01	3,43E-02	-8,40E-01	9,03E-03	*nifD*- N 1 dpi	TR	Potassium channel (AHRD V3.3 *-* D0EM91_9ROSI)	
Solyc07g039440.1	7,97E-02	8,23E-01	**-1,12E+00**	**3,68E-03**	-1,74E-01	6,24E-01	4,81E-01	1,84E-01	*nifD*- N 1 dpi	D	LOW QUALITY:Disease resistance protein (AHRD V3.3 *-* D1GEE0_BRARP)	GO:0043531
Solyc02g067320.2	-4,89E-01	1,64E-01	**-1,20E+00**	**1,71E-03**	-1,61E-01	6,42E-01	-8,32E-02	8,09E-01	*nifD*- N 1 dpi	G	ZF-HD homeobox protein (AHRD V3.3 *** Q9ARE3_FLABI)	GO:0003677

Solyc06g066520.1	-5,49E-01	1,13E-01	**-1,25E+00**	**9,19E-04**	-7,03E-01	4,57E-02	2,65E-01	4,35E-01	*nifD*- N 1 dpi	D	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein 146 (AHRD V3.3 *** Q9FQZ6_TOBAC)	
Solyc00g010525.1	-2,29E-01	6,01E-01	**-1,29E+00**	**6,37E-03**	9,61E-01	3,56E-02	1,22E+00	9,27E-03	*nifD*- N 1 dpi	H	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT5G46400.3)	
Solyc08g083110.3	-1,20E+00	1,20E-02	**-1,36E+00**	**5,04E-03**	4,13E-01	3,60E-01	5,31E-01	2,42E-01	*nifD*- N 1 dpi	AM	Cystathionine gamma-synthase, putative (AHRD V3.3 *-* B9RYU1_RICCO)	GO:0003824
Solyc02g068250.3	-3,86E-01	3,30E-01	**-1,39E+00**	**1,41E-03**	3,20E-01	4,19E-01	1,97E-01	6,17E-01	*nifD*- N 1 dpi	G	microspore-specific promoter 2 (AHRD V3.3 *-* AT5G46795.1)	
Solyc06g069070.1	-7,94E-01	8,31E-02	**-1,57E+00**	**1,43E-03**	4,06E-01	3,65E-01	3,98E-01	3,74E-01	*nifD*- N 1 dpi	L	Lipid transfer protein (AHRD V3.3 *** S4TID2_GOSHI)	GO:0006869
Solyc10g084070.1	2,27E-01	6,41E-01	**-1,59E+00**	**2,84E-03**	-6,18E-01	2,11E-01	-2,09E-02	9,66E-01	*nifD*- N 1 dpi	CS	LOW QUALITY:Endoglucanase (AHRD V3.3 --* A0A022RID5_ERYGU)	
Solyc05g007770.3	-8,83E-01	1,05E-01	**-1,60E+00**	**5,40E-03**	2,40E-01	6,52E-01	4,84E-02	9,27E-01	*nifD*- N 1 dpi	T	NAC domain TF	GO:0003677|GO:0006355
Solyc12g098610.2	-1,07E-01	8,56E-01	**-1,64E+00**	**9,73E-03**	-7,06E-01	2,41E-01	-7,98E-02	8,93E-01	*nifD*- N 1 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4DHN4_SOLLC)	GO:0004553|GO:0005975
Solyc12g038605.1	6,34E-01	2,92E-01	**-1,70E+00**	**7,71E-03**	6,89E-01	2,53E-01	5,19E-01	3,86E-01	*nifD*- N 1 dpi	NA	LINE-1 reverse transcriptase (AHRD V3.3 --* A0A1D1ZAL7_9ARAE)	
Solyc02g092120.3	-1,21E+00	7,76E-02	**-1,86E+00**	**9,09E-03**	-5,75E-02	9,31E-01	1,87E-01	7,79E-01	*nifD*- N 1 dpi	G	Phytosulfokines 3 family protein (AHRD V3.3 *** B9IBM1_POPTR)	GO:0005576|GO:0008083|GO:0008283
Solyc01g099590.3	-2,03E+00	3,69E-02	**-3,30E+00**	**1,40E-03**	-1,26E+00	1,85E-01	-4,81E-01	6,07E-01	*nifD*- N 1 dpi	P	glutathione-S-transferase	GO:0005515
Solyc10g051120.2	-1,43E+00	9,95E-02	**-3,47E+00**	**3,13E-04**	-1,10E+00	2,01E-01	5,86E-01	4,89E-01	nifD- N 1 dpi	C	Mitochondrial pyruvate carrier (AHRD V3.3 *-* M1AEY6_SOLTU)	GO:0005743|GO:0006850
Solyc08g075190.1	8,52E-01	1,04E-01	1,11E+00	5,14E-03	7,87E-01	1,31E-01	**1,54E+00**	**5,14E-03**	*nifD*- NoN 1 dpi	H	LOW QUALITY:C2 and GRAM domain-containing protein At1g03370 (AHRD V3.3 --* C2GR1_ARATH)	
Solyc07g005630.3	8,11E-01	3,43E-01	1,02E+00	3,04E-03	1,36E+00	1,17E-01	**2,75E+00**	**3,04E-03**	*nifD*- NoN 1 dpi	D	LOW QUALITY:Defensin (AHRD V3.3 -** W8S9R7_ECLPR)	GO:0006952
Solyc12g089190.1	7,47E-01	1,25E-02	9,28E-01	3,35E-05	-4,95E-01	8,70E-02	**-1,39E+00**	**3,35E-05**	*nifD*- NoN 1 dpi	T	Myb family transcription factor family protein (AHRD V3.3 *** B9H0R6_POPTR)	GO:0003677
Solyc01g079910.1	1,13E+00	8,57E-02	9,15E-01	3,40E-03	1,70E+00	1,24E-02	**2,04E+00**	**3,40E-03**	*nifD*- NoN 1 dpi	CS	LOW QUALITY:Xyloglucan-specific endoglucanase inhibitor protein 2 (AHRD V3.3 *-* F1DHN5_SOLTU)	GO:0004190|GO:0006508
Solyc08g068140.3	2,96E-01	6,14E-01	8,74E-01	4,84E-03	-3,20E-01	5,87E-01	**-1,79E+00**	**4,84E-03**	*nifD*- NoN 1 dpi	STR	BURP domain protein RD22 (AHRD V3.3 --* RD22_ARATH)	
Solyc01g005040.3	1,79E+00	1,46E-01	8,41E-01	2,28E-03	2,34E+00	6,08E-02	**4,03E+00**	**2,28E-03**	*nifD*- NoN 1 dpi	CS	CASP-like protein (AHRD V3.3 *** K4AS71_SOLLC)	
Solyc04g016020.1	1,15E+00	1,25E-01	7,18E-01	2,14E-03	1,82E+00	1,85E-02	**2,47E+00**	**2,14E-03**	*nifD*- NoN 1 dpi	NA	LOW QUALITY:transmembrane protein, putative (DUF247) (AHRD V3.3 *-* AT2G44930.1)	
Solyc03g096430.1	5,40E-01	3,26E-02	6,97E-01	2,79E-04	8,21E-01	2,02E-03	**1,00E+00**	**2,79E-04**	*nifD*- NoN 1 dpi	CS	LOW QUALITY:CLIP-associating protein 1 (AHRD V3.3 --* A0A0B2NZ56_GLYSO)	
Solyc09g066260.3	5,87E-01	4,21E-01	6,85E-01	8,90E-03	1,92E+00	1,27E-02	**2,03E+00**	**8,90E-03**	*nifD*- NoN 1 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9S4L6_RICCO)	
Solyc07g008600.1	9,27E-01	3,74E-03	6,74E-01	1,27E-03	4,99E-01	9,82E-02	**1,05E+00**	**1,27E-03**	*nifD*- NoN 1 dpi	PMI	LOW QUALITY:Leucine-rich receptor-like kinase family protein (AHRD V3.3 *** A0A072UGF0_MEDTR)	GO:0005515
Solyc12g044200.2	1,35E+00	3,42E-03	6,62E-01	6,26E-03	-6,22E-01	1,50E-01	**-1,25E+00**	**6,26E-03**	*nifD*- NoN 1 dpi	D	Disease resistance protein (CC-NBS-LRR class) family protein (AHRD V3.3 *** A0A072VNI6_MEDTR)	GO:0043531
Solyc10g086520.2	-6,92E-02	8,78E-01	5,90E-01	1,34E-03	8,98E-01	5,50E-02	**1,61E+00**	**1,34E-03**	*nifD*- NoN 1 dpi	CS	expansin 6	GO:0005576
Solyc09g075330.3	8,67E-01	5,15E-04	5,71E-01	5,56E-05	5,10E-01	2,76E-02	**1,05E+00**	**5,56E-05**	*nifD*- NoN 1 dpi	CS	Pectinesterase (AHRD V3.3 *** K4CVB0_SOLLC)	GO:0004857

Solyc01g094380.2	5,15E-01	2,37E-01	5,36E-01	6,15E-03	8,26E-01	6,30E-02	**1,27E+00**	**6,15E-03**	*nifD*- NoN 1 dpi	P	LOW QUALITY:Protein O-glucosyltransferase 1 (AHRD V3.3 *** A0A0B2PAD6_GLYSO)	
Solyc03g120600.3	7,42E-01	2,58E-02	5,28E-01	3,66E-04	7,35E-01	2,70E-02	**1,28E+00**	**3,66E-04**	*nifD*- NoN 1 dpi	OX	Plant cadmium resistance 2 (AHRD V3.3 *** A0A0K9NVT8_ZOSMR)	
Solyc02g079440.2	6,00E-01	1,13E-01	5,23E-01	3,95E-03	7,40E-01	5,37E-02	**1,16E+00**	**3,95E-03**	*nifD*- NoN 1 dpi	E	FAD-binding Berberine family protein (AHRD V3.3 *** AT4G20860.1)	GO:0003824|GO:0016614|GO:0050660|GO:0055114
Solyc12g040740.2	-2,63E-01	7,13E-01	5,19E-01	1,22E-03	1,31E+00	7,52E-02	**2,57E+00**	**1,22E-03**	*nifD*- NoN 1 dpi	PMI	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-* AT4G08850.1)	GO:0005515
Solyc10g007103.1	8,16E-01	1,32E-01	5,07E-01	7,06E-03	1,30E+00	2,00E-02	**1,53E+00**	**7,06E-03**	*nifD*- NoN 1 dpi	DNA	Homeobox-leucine zipper protein family (AHRD V3.3 *-* AT1G69780.1)	GO:0003677
Solyc12g056855.1	3,41E-01	5,01E-01	3,86E-01	7,04E-03	-3,62E-01	4,75E-01	**-1,46E+00**	**7,04E-03**	*nifD*- NoN 1 dpi	STR	2OG-Fe(II) oxygenase (AHRD V3.3 *-* Q2HV29_MEDTR)	
Solyc02g031790.2	4,52E-01	4,67E-01	3,86E-01	2,38E-03	1,02E+00	1,09E-01	**2,06E+00**	**2,38E-03**	*nifD*- NoN 1 dpi	S	Receptor-like protein kinase (AHRD V3.3 *** RPK1_IPONI)	GO:0004672|GO:0005524|GO:0006468
Solyc12g100350.2	8,10E-01	1,69E-01	3,82E-01	7,33E-04	9,75E-01	1,01E-01	**-2,19E+00**	**7,33E-04**	*nifD*- NoN 1 dpi	G	calpain-type cysteine protease family (AHRD V3.3 *-* AT1G55350.6)	
Solyc09g074620.3	3,98E-01	2,92E-01	3,66E-01	7,49E-03	-3,65E-01	3,33E-01	**-1,08E+00**	**7,49E-03**	*nifD*- NoN 1 dpi	NA	Zinc metalloproteinase aureolysin (AHRD V3.3 *** A0A0B0PSB0_GOSAR)	
Solyc03g031590.3	-4,12E-01	3,39E-01	3,66E-01	7,89E-04	9,72E-01	2,99E-02	**1,61E+00**	**7,89E-04**	*nifD*- NoN 1 dpi	TR	S-type anion channel SLAH1 (AHRD V3.3 *** SLAH1_ARATH)	GO:0006873|GO:0008308|GO:0016021
Solyc02g086467.1	5,91E-01	2,83E-01	3,48E-01	3,08E-03	1,41E+00	1,49E-02	**1,76E+00**	**3,08E-03**	*nifD*- NoN 1 dpi	DNA	Histone H4 (AHRD V3.3 --* A0A0D3DSU9_BRAOL)	
Solyc03g019750.3	-6,80E-01	2,30E-01	3,23E-01	2,92E-03	1,10E+00	5,64E-02	**1,82E+00**	**2,92E-03**	*nifD*- NoN 1 dpi	CS	Alpha-1,4-glucan-protein synthase [UDP-forming] (AHRD V3.3 *** UPTG_PEA)	GO:0016866|GO:0030244
Solyc01g073840.1	5,18E-01	2,77E-01	2,81E-01	1,67E-03	9,49E-01	5,23E-02	**1,64E+00**	**1,67E-03**	*nifD*- NoN 1 dpi	S	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)	GO:0005515|GO:0008270
Solyc10g018200.2	1,59E-01	7,88E-01	2,75E-01	9,22E-03	1,57E+00	1,23E-02	**1,64E+00**	**9,22E-03**	*nifD*- NoN 1 dpi	NA	DUF1442 family protein (AHRD V3.3 *** G7KG71_MEDTR)	
Solyc01g112130.3	-2,38E-01	6,73E-01	2,53E-01	6,87E-03	-1,11E+00	5,63E-02	**-1,64E+00**	**6,87E-03**	*nifD*- NoN 1 dpi	OX	Flavin-containing monooxygenase (AHRD V3.3 *** M1B691_SOLTU)	GO:0004499|GO:0050660|GO:0050661|GO:0055114
Solyc03g115255.1	-4,55E-01	2,46E-01	1,03E-01	9,56E-03	1,03E+00	1,24E-02	**1,07E+00**	**9,56E-03**	*nifD*- NoN 1 dpi	N	Nodule-inception protein (AHRD V3.3 -** A0A1B1XWN4_ARAHY)	
Solyc04g054745.1	-4,95E-01	3,82E-01	9,99E-02	1,96E-03	-1,52E+00	1,14E-02	**-1,92E+00**	**1,96E-03**	*nifD*- NoN 1 dpi	T	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 --* AT5G64360.7)	
Solyc06g073760.3	-4,63E-01	3,12E-01	8,26E-02	1,48E-03	8,60E-01	6,67E-02	**1,60E+00**	**1,48E-03**	*nifD*- NoN 1 dpi	C	Beta-glucosidase (AHRD V3.3 *** A0A0B4PJM3_SOYBN)	GO:0004553|GO:0005975
Solyc01g105070.3	5,06E-01	1,96E-01	8,10E-02	6,20E-03	-6,16E-02	8,73E-01	**1,14E+00**	**6,20E-03**	*nifD*- NoN 1 dpi	OX	LECEVI16G peroxidase precursor	GO:0004601|GO:0006979|GO:0020037|GO:0055114
Solyc01g067107.1	4,90E-01	3,04E-01	7,02E-02	5,15E-03	-2,61E-02	9,56E-01	**-1,43E+00**	**5,15E-03**	*nifD*- NoN 1 dpi	G	ARABIDILLO-1 (AHRD V3.3 --* AT2G44900.2)	
Solyc09g014230.2	2,82E-01	5,82E-01	6,66E-02	1,12E-03	-1,10E+00	3,99E-02	**-1,86E+00**	**1,12E-03**	*nifD*- NoN 1 dpi	TR	Peptide transporter, putative (AHRD V3.3 *** B9T6M4_RICCO)	GO:0005215|GO:0006810|GO:0016020
Solyc11g010180.2	-2,77E-01	5,30E-01	5,53E-02	4,63E-04	7,65E-01	9,12E-02	**1,75E+00**	**4,63E-04**	*nifD*- NoN 1 dpi	R	Mitochondrial ribosomal protein L37 (AHRD V3.3 *** AT5G14290.1)	
Solyc05g050130.3	2,47E-01	3,82E-01	4,60E-02	3,26E-05	4,11E-01	1,50E-01	**1,39E+00**	**3,26E-05**	*nifD*- NoN 1 dpi	D	Acidic endochitinase (AHRD V3.3 *** CHIA_TOBAC)	GO:0004553|GO:0005975
Solyc11g072330.2	-2,86E-01	4,68E-01	3,92E-02	2,70E-03	7,06E-01	8,01E-02	**1,29E+00**	**2,70E-03**	*nifD*- NoN 1 dpi	S	Two-component response regulator (AHRD V3.3 *-* W9QMB4_9ROSA)	GO:0000160
Solyc10g005860.3	4,42E-01	2,58E-01	-7,52E-03	3,58E-03	-2,77E-03	9,94E-01	**-1,23E+00**	**3,58E-03**	*nifD*- NoN 1 dpi	P	WW domain-containing protein, putative isoform 4 (AHRD V3.3 *-* A0A061FBS1_THECC)	
Solyc00g174340.2	2,10E+00	7,35E-02	-2,99E-02	7,09E-03	9,80E-01	3,92E-01	**3,30E+00**	**7,09E-03**	*nifD*- NoN 1 dpi	D	Pathogenesis-related protein 1 (AHRD V3.3 *** Q75QH2_CAPCH)	GO:0005576

Solyc02g091700.3	6,40E-01	1,25E-02	-4,84E-02	1,10E-06	7,55E-01	3,94E-03	**1,51E+00**	**1,10E-06**	*nifD*- NoN 1 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)	
Solyc02g084315.1	3,32E-01	4,97E-01	-9,64E-02	4,55E-03	-7,02E-01	1,57E-01	**-1,50E+00**	**4,55E-03**	*nifD*- NoN 1 dpi	G	embryo defective 2410 (AHRD V3.3 --* AT2G25660.4)	
Solyc09g059675.1	-2,34E-01	4,75E-01	-1,23E-01	4,04E-03	8,72E-01	1,19E-02	**1,02E+00**	**4,04E-03**	*nifD*- NoN 1 dpi	L	alpha/beta hydrolase family protein (AHRD V3.3 *** AT1G15060.2)	
Solyc11g027630.1	6,62E-01	1,05E-01	-1,35E-01	9,17E-04	8,39E-01	4,28E-02	**1,47E+00**	**9,17E-04**	*nifD*- NoN 1 dpi	C	LOW QUALITY:glycosyl hydrolase 9A3 (AHRD V3.3 --* AT4G24260.1)	
Solyc10g080330.2	1,51E-01	6,78E-01	-1,54E-01	6,83E-03	6,65E-01	7,70E-02	**1,06E+00**	**6,83E-03**	*nifD*- NoN 1 dpi	RNA	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9S1X9_RICCO)	GO:0005515
Solyc12g006530.2	-2,01E-01	7,08E-01	-1,80E-01	1,81E-03	9,28E-01	9,19E-02	**1,84E+00**	**1,81E-03**	*nifD*- NoN 1 dpi	2M	Terpene cyclase/mutase family member (AHRD V3.3 *** M1BMW3_SOLTU)	GO:0016866
Solyc08g076400.3	5,37E-02	8,83E-01	-2,07E-01	4,97E-03	1,10E-02	9,76E-01	**1,12E+00**	**4,97E-03**	*nifD*- NoN 1 dpi	T	Myb family transcription factor family protein (AHRD V3.3 *** U5GMY7_POPTR)	GO:0003677
Solyc03g083005.1	3,36E-01	5,62E-01	-2,42E-01	9,52E-03	-1,15E+00	5,56E-02	**-1,60E+00**	**9,52E-03**	*nifD*- NoN 1 dpi	D	RING/U-box superfamily protein (AHRD V3.3 --* AT5G10650.3)	
Solyc12g040470.2	4,71E-01	6,09E-01	-2,72E-01	2,43E-03	-1,31E+00	1,63E-01	**-3,06E+00**	**2,43E-03**	*nifD*- NoN 1 dpi	L	non-specific phospholipase C2 (AHRD V3.3 --* AT2G26870.1)	
Solyc01g099880.3	-6,53E-01	3,65E-01	-3,41E-01	2,30E-03	-2,30E-01	7,48E-01	**2,40E+00**	**2,30E-03**	*nifD*- NoN 1 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4B122_SOLLC)	GO:0016021
Solyc11g027710.1	6,38E-02	8,46E-01	-3,58E-01	2,46E-03	7,41E-01	3,12E-02	**1,09E+00**	**2,46E-03**	*nifD*- NoN 1 dpi	T	WRKY DNA-binding protein 55 (AHRD V3.3 --* AT2G40740.3)	
Solyc01g044240.3	-9,89E-02	8,03E-01	-3,75E-01	4,53E-03	6,55E-01	1,06E-01	**1,22E+00**	**4,53E-03**	*nifD*- NoN 1 dpi	C	Soluble inorganic pyrophosphatase 1 (AHRD V3.3 --* IPYR1_ARATH)	
Solyc08g076000.3	-6,44E-01	1,11E-01	-3,97E-01	8,19E-03	1,03E+00	1,44E-02	**1,12E+00**	**8,19E-03**	*nifD*- NoN 1 dpi	D	NBS-LRR resistance protein (AHRD V3.3 *** B6E013_SOLBU)	GO:0005515
Solyc04g072070.3	-1,97E+00	1,71E-02	-3,99E-01	5,12E-03	-1,27E+00	1,11E-01	**-2,36E+00**	**5,12E-03**	*nifD*- NoN 1 dpi	STR	WRKY transcription factor 55	GO:0003700|GO:0006355|GO:0043565
Solyc09g098080.3	1,34E+00	1,68E-02	-4,62E-01	9,01E-04	1,41E-01	7,89E-01	**1,96E+00**	**9,01E-04**	*nifD*- NoN 1 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CWX9_SOLLC)	GO:0008152|GO:0016758
Solyc01g005900.2	-2,37E-01	7,45E-01	-6,04E-01	1,73E-03	2,75E-01	7,06E-01	**2,52E+00**	**1,73E-03**	*nifD*- NoN 1 dpi	S	HXXXD-type acyl-transferase family protein (AHRD V3.3 *-* AT1G28680.1)	GO:0016747
Solyc12g088140.2	-1,43E+00	3,55E-04	-6,60E-01	5,58E-04	1,07E-01	7,60E-01	**1,37E+00**	**5,58E-04**	*nifD*- NoN 1 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)	
Solyc00g010525.1	-2,29E-01	6,01E-01	-1,29E+00	9,27E-03	9,61E-01	3,56E-02	**1,22E+00**	**9,27E-03**	*nifD*- NoN 1 dpi	H	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 --* AT5G46400.3)	

Table S 9. Table S9. List of differentially expressed genes (DEGs) identified in tomato roots 14 days post inoculation (dpi) with Gluconacetobacter diazotrophicus nifD- strain. *Fold change values of DEGs identified in tomato roots with G. diazotrophicus nifD- strain as compared to uninoculated plants (Control) in modified Hoagland in the absence (nifD- NoN) or presence of 2 mM KNO3 (nifD- N) in hydroponic systems at 14dpi. Tomato gene identifier (ITAG3.2 release), Log2-transformed fold change values and P values calculated for each pairwise comparison between bacterium-inoculated and uninoculated samples are reported. Clustering results of the DEGs, classified as genes significantly modulated (in bold, P ≤ 0.01 and Log2(fold change) ≥ 1 or ≤ -1) by nifD- in either N or NoN condition. Protein description and abbreviation codes of functional classes were assigned on the basis of the protein description and function. Gene ontology (GO) terms were based on the ITAG3.2 release (https://solgenomics.net/organism/Solanum_lycopersicum/genome).*

Gene ID	WT N	P.Value	*nifD*- N	P. Value	WT NoN	P. Value	*nifD*- NoN	P.Value	Cluster	Functional Class	Gene Description	GO
Solyc02g084850.3	3,27E+00	2,62E-02	**6,22E+00**	**1,33E-04**	1,66E+00	2,43E-01	-9,85E-01	4,84E-01	*nifD*- N 14 dpi	H	Abscisic acid and environmental stress-inducible protein TAS14 (AHRD V3.3 *** TAS14_SOLLC)	GO:0006950|GO:0009415

Solyc10g075070.2	1,99E+00	2,43E-02	**5,66E+00**	**3,33E-07**	-8,07E-01	3,40E-01	-7,11E-01	4,00E-01	*nifD*- N 14 dpi	L	Non-specific lipid-transfer protein (AHRD V3.3 *** K4D1U9_SOLLC)	GO:0006869|GO:0008289
Solyc02g077020.3	3,78E+00	2,10E-02	**5,32E+00**	**1,89E-03**	1,37E+00	3,82E-01	-2,05E+00	1,93E-01	*nifD*- N 14 dpi	L	Phospholipase A1 (AHRD V3.3 *** A5YW95_CAPAN)	GO:0006629|GO:0008970|GO:0008970
Solyc06g050870.3	2,80E+00	3,18E-02	**4,93E+00**	**4,92E-04**	-5,20E+00	2,73E-04	1,67E+00	1,88E-01	*nifD*- N 14 dpi	E	Hypoxia-responsive family protein (AHRD V3.3 *** A0A061FYY0_THECC)	
Solyc10g050990.1	2,33E+00	6,92E-02	**4,44E+00**	**1,26E-03**	-4,70E+00	7,43E-04	-8,07E-01	5,17E-01	*nifD*- N 14 dpi	C	Pyruvate kinase (AHRD V3.3 --* A9TZX1_PHYPA)	
Solyc09g098420.2	1,34E+00	1,95E-01	**4,12E+00**	**3,69E-04**	1,27E+00	2,20E-01	-5,28E-01	6,04E-01	*nifD*- N 14 dpi	PMI	Leucine-rich repeat receptor protein kinase EXS (AHRD V3.3 *** A0A1D1XPP4_9ARAE)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc05g053170.3	8,89E-01	4,45E-01	**3,98E+00**	**1,86E-03**	1,80E+00	1,28E-01	-5,25E-01	6,51E-01	*nifD*- N 14 dpi	2M	Chalcone synthase (AHRD V3.3 *** CHSY_PERFR)	GO:0003824|GO:0008152|GO:0009058|GO:0016746|GO:0009058|GO:0016746
Solyc11g012210.1	2,46E+00	1,20E-02	**3,93E+00**	**2,13E-04**	1,34E+00	1,53E-01	2,03E+00	3,49E-02	*nifD*- N 14 dpi	P	MBOAT (membrane bound O-acyl transferase) family protein (AHRD V3.3 *** AT5G55340.1)	GO:0008374
Solyc09g064820.1	3,24E+00	1,54E-02	**3,90E+00**	**4,33E-03**	2,64E+00	4,42E-02	7,23E-01	5,68E-01	*nifD*- N 14 dpi	P	EID1-like F-box protein 2 (AHRD V3.3 *** A0A0B2NUB4_GLYSO)	
Solyc10g050730.2	1,92E+00	2,42E-02	**3,87E+00**	**5,50E-05**	1,37E+00	9,99E-02	1,54E+00	6,64E-02	*nifD*- N 14 dpi	E	Plastocyanin-like domain protein (AHRD V3.3 *** G7JMH1_MEDTR)	GO:0009055
Solyc04g054960.1	1,42E+00	8,06E-02	**3,79E+00**	**4,89E-05**	1,93E+00	2,00E-02	-8,25E-01	3,00E-01	*nifD*- N 14 dpi	D	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT5G21130.1)	
Solyc09g090630.2	3,21E+00	1,32E-02	**3,79E+00**	**4,22E-03**	1,95E+00	1,18E-01	1,18E+00	3,36E-01	*nifD*- N 14 dpi	DNA	Histone-lysine N-methyltransferase (AHRD V3.3 *** W9RT47_9ROSA)	GO:0005515|GO:0005634|GO:0008270|GO:0018024|GO:0034968|GO:0005634|GO:0008270|GO:0018024|GO:0034968
Solyc06g051940.3	1,82E+00	1,16E-01	**3,74E+00**	**2,64E-03**	8,78E-01	4,41E-01	-3,27E+00	7,38E-03	*nifD*- N 14 dpi	K	Protein phosphatase 2c, putative (AHRD V3.3 *** B9RIK1_RICCO)	GO:0003824|GO:0004722|GO:0006470|GO:0004722|GO:0006470
Solyc05g006860.3	1,25E+00	9,14E-02	**3,59E+00**	**3,11E-05**	4,77E-01	5,09E-01	-1,41E+00	5,87E-02	*nifD*- N 14 dpi	OX	Thioredoxin family protein (AHRD V3.3 *** B9IJS4_POPTR)	GO:0006662|GO:0015035|GO:0045454|GO:0045454|GO:0045454
Solyc07g006620.3	2,23E+00	1,89E-02	**3,47E+00**	**6,27E-04**	-6,48E-01	4,74E-01	-8,00E-01	3,78E-01	*nifD*- N 14 dpi	S	Receptor-like kinase (AHRD V3.3 *** G7JD52_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g091250.3	6,43E-01	2,99E-01	**3,43E+00**	**6,25E-06**	1,44E+00	2,54E-02	3,81E-02	9,50E-01	*nifD*- N 14 dpi	NA	DUF1442 family protein (AHRD V3.3 *** G7J167_MEDTR)	
Solyc10g017990.2	1,82E+00	6,57E-02	**3,40E+00**	**1,39E-03**	-1,32E+00	1,75E-01	-7,97E-01	4,09E-01	*nifD*- N 14 dpi	H	Cytokinin oxidase/dehydrogenase-like (AHRD V3.3 *** I0IUQ9_SOLLC)	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0003824|GO:0050660
Solyc04g079760.3	2,74E+00	1,92E-02	**3,37E+00**	**5,03E-03**	8,80E-01	4,30E-01	-1,04E+00	3,53E-01	*nifD*- N 14 dpi	R	Structural constituent of ribosome, putative (AHRD V3.3 *** A0A061EZC6_THECC)	
Solyc03g121900.1	1,53E+00	7,51E-02	**3,29E+00**	**4,99E-04**	8,57E-01	3,10E-01	1,80E+00	3,88E-02	*nifD*- N 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT5G48490.1)	
Solyc11g021230.1	2,38E+00	5,11E-02	**3,28E+00**	**9,08E-03**	3,04E+00	1,46E-02	2,38E+00	5,05E-02	*nifD*- N 14 dpi	E	NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic (AHRD V3.3 *** NU1C_LACSA)	GO:0016020|GO:0055114
Solyc08g063130.3	1,23E+00	2,14E-01	**3,23E+00**	**2,56E-03**	-1,32E-01	8,92E-01	-1,46E+00	1,43E-01	*nifD*- N 14 dpi	E	FAD/NAD(P)-binding oxidoreductase family protein (AHRD V3.3 *** AT5G05320.1)	GO:0016491|GO:0055114|GO:0071949|GO:0071949
Solyc02g011815.1	1,86E+00	6,65E-02	**3,17E+00**	**3,15E-03**	1,39E+00	1,64E-01	8,31E-01	4,01E-01	*nifD*- N 14 dpi	P	30S ribosomal protein S15, chloroplastic (AHRD V3.3 *-* RR15_SOLLC)	GO:0003735|GO:0005622|GO:0005840|GO:0006412|GO:0003735|GO:0005840|GO:0006412|GO:0003735|GO:0005840|GO:0006412
Solyc08g014030.1	1,72E+00	1,07E-02	**3,16E+00**	**2,94E-05**	-1,56E+00	1,90E-02	-1,54E+00	2,07E-02	*nifD*- N 14 dpi	T	GRAS family transcription factor (AHRD V3.3 *** A0A061EK79_THECC)	
Solyc06g064960.3	2,41E+00	2,07E-02	**3,12E+00**	**3,78E-03**	-1,12E+00	2,65E-01	-3,36E+00	2,04E-03	*nifD*- N 14 dpi	L	Lipase, GDSL (AHRD V3.3 *** A0A124SDS7_CYNCS)	GO:0016788
Solyc07g052170.1	1,55E+00	6,99E-02	**3,08E+00**	**9,18E-04**	-1,68E-01	8,40E-01	1,86E-01	8,23E-01	*nifD*- N 14 dpi	D	LOW QUALITY:Dirigent protein (AHRD V3.3 *** K4CFB6_SOLLC)	
Solyc11g069640.2	1,47E+00	9,02E-02	**3,05E+00**	**1,18E-03**	1,37E+00	1,13E-01	1,50E+00	8,42E-02	*nifD*- N 14 dpi	C	Carbonic anhydrase, putative (AHRD V3.3 *** B9STU9_RICCO)	GO:0004089|GO:0006730|GO:0008270
Solyc05g013890.2	1,07E+00	2,08E-01	**3,05E+00**	**1,06E-03**	-4,16E-01	6,18E-01	-1,30E+00	1,27E-01	*nifD*- N 14 dpi	TR	ABC transporter B family protein (AHRD V3.3 *** G7JF16_MEDTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO:0016887|GO:0005524|GO:0016887

Solyc01g009480.3	1,76E+00	3,76E-02	**3,04E+00**	**8,34E-04**	9,48E-01	2,48E-01	-4,90E-02	9,52E-01	*nifD*- N 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G44510.2)	
Solyc07g041680.2	1,37E+00	3,21E-02	**3,03E+00**	**3,43E-05**	1,32E+00	3,80E-02	7,59E-01	2,21E-01	*nifD*- N 14 dpi	TR	LOW QUALITY:Ycf1 (AHRD V3.3 *-* A0A0N7CFU2_SOLTU)	
Solyc01g098740.3	-3,78E-02	9,72E-01	**3,01E+00**	**8,41E-03**	9,00E-01	4,01E-01	-6,15E-02	9,54E-01	*nifD*- N 14 dpi	K	Protein kinase (AHRD V3.3 *** C6ZRT6_SOYBN)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g087970.1	1,35E+00	1,03E-01	**2,99E+00**	**9,06E-04**	-3,34E-02	9,67E-01	-6,67E-01	4,10E-01	*nifD*- N 14 dpi	DNA	Mini zinc finger protein (AHRD V3.3 *** A0ZXL1_SOLLC)	
Solyc11g006250.2	-2,52E-01	7,42E-01	**2,91E+00**	**7,20E-04**	-1,95E-01	7,99E-01	-2,36E+00	4,39E-03	*nifD*- N 14 dpi	L	GDSL-motif lipase/hydrolase family protein 2	GO:0016788
Solyc08g078180.1	1,10E+00	2,35E-01	**2,89E+00**	**3,80E-03**	2,56E-01	7,80E-01	8,75E-01	3,44E-01	*nifD*- N 14 dpi	H	Ethylene Response Factor A.1	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc02g067490.3	8,52E-01	2,52E-01	**2,89E+00**	**5,04E-04**	4,25E-01	5,63E-01	-5,61E-01	4,47E-01	*nifD*- N 14 dpi	CS	Actin cross-linking protein, putative (AHRD V3.3 *** A0A061E7B5_THECC)	
Solyc04g014730.3	1,13E+00	2,19E-01	**2,89E+00**	**3,55E-03**	1,46E+00	1,18E-01	-5,84E-01	5,22E-01	*nifD*- N 14 dpi	AM	fumarylacetoacetase (AHRD V3.3 *** AT1G12050.1)	GO:0003824|GO:0008152|GO:0004334|GO:0009072|GO:0004334|GO:0009072
Solyc02g071350.3	2,19E+00	3,02E-02	**2,88E+00**	**5,65E-03**	1,84E+00	6,54E-02	-1,63E+00	1,01E-01	*nifD*- N 14 dpi	TR	ABC transporter B family protein (AHRD V3.3 *** G7ILW7_MEDTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085|GO:0005524|GO:0016887|GO:0005524|GO:0016887
Solyc04g008470.3	2,37E+00	2,05E-02	**2,84E+00**	**6,54E-03**	1,49E+00	1,33E-01	-1,61E+00	1,05E-01	*nifD*- N 14 dpi	D	Defensin (AHRD V3.3 *** C1K3M7_VIGUN)	GO:0006952
Solyc01g105870.3	-5,75E-01	4,14E-01	**2,83E+00**	**3,82E-04**	3,16E-01	6,53E-01	-4,22E-01	5,48E-01	*nifD*- N 14 dpi	2M	(E)-beta-ocimene synthase (AHRD V1 **** Q5CD81_CITUN)%3B contains Interpro domain(s) IPR005630 Terpene synthase%2C metal-binding domain	GO:0000287|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829
Solyc08g013740.3	1,66E+00	5,59E-02	**2,81E+00**	**2,26E-03**	2,16E+00	1,52E-02	9,84E-01	2,47E-01	*nifD*- N 14 dpi	CS	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G10440.1)	GO:0008168
Solyc02g077110.3	3,60E-01	6,00E-01	**2,80E+00**	**3,41E-04**	1,08E+00	1,25E-01	6,99E-01	3,13E-01	*nifD*- N 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G18550.2)	GO:0006629|GO:0008970|GO:0008970
Solyc03g070390.3	6,42E-01	4,87E-01	**2,79E+00**	**5,12E-03**	1,71E+00	7,16E-02	-9,22E-01	3,21E-01	*nifD*- N 14 dpi	CS	Alpha-1,4-glucan-protein synthase [UDP-forming] 1 (AHRD V3.3 *** UPTG1_SOLTU)	GO:0016866|GO:0030244
Solyc10g008180.2	1,66E+00	3,30E-02	**2,77E+00**	**9,05E-04**	1,47E+00	5,74E-02	1,21E+00	1,12E-01	*nifD*- N 14 dpi	STR	26S proteasome regulatory subunit (AHRD V3.3 *** I0YWJ7_COCSC)	GO:0000502|GO:0030234|GO:0042176|GO:0005488|GO:0005488
Solyc01g108560.4	3,02E-01	6,93E-01	**2,74E+00**	**1,25E-03**	9,33E-01	2,29E-01	-3,47E-01	6,50E-01	*nifD*- N 14 dpi	P	Acetyl esterase IPR013094 Alpha_beta hydrolase fold-3	
Solyc02g091040.3	1,51E+00	4,55E-02	**2,65E+00**	**1,07E-03**	1,17E+00	1,17E-01	-4,76E-01	5,14E-01	*nifD*- N 14 dpi	T	myb domain protein 76 (AHRD V3.3 --* AT5G07700.2)	
Solyc11g072110.2	1,53E+00	2,08E-02	**2,59E+00**	**3,19E-04**	1,14E+00	7,91E-02	8,47E-01	1,85E-01	*nifD*- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G55290.1)	GO:0016491|GO:0055114
Solyc10g080840.1	7,96E-01	3,67E-01	**2,47E+00**	**8,57E-03**	1,48E-01	8,66E-01	5,53E-01	5,30E-01	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A2PZD4_IPONI)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc03g117310.1	-7,15E-02	9,06E-01	**2,47E+00**	**3,60E-04**	3,60E-01	5,54E-01	-6,94E-01	2,58E-01	*nifD*- N 14 dpi	DNA	LOW QUALITY:Sterile alpha motif (SAM) domain-containing protein (AHRD V3.3 *** AT1G80520.1)	
Solyc01g057260.3	1,77E+00	4,01E-02	**2,47E+00**	**5,80E-03**	7,25E-01	3,84E-01	1,36E-04	1,00E+00	*nifD*- N 14 dpi	NA	transmembrane protein, putative (DUF247) (AHRD V3.3 *-* AT3G50140.2)	
Solyc08g078900.1	5,63E-01	1,38E-01	**2,46E+00**	**4,53E-07**	-4,11E-01	2,75E-01	-6,44E-01	9,22E-02	*nifD*- N 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12490.1)	
Solyc05g051010.3	1,42E+00	1,01E-01	**2,46E+00**	**6,51E-03**	6,00E-01	4,77E-01	-1,35E+00	1,16E-01	*nifD*- N 14 dpi	2M	Dihydroflavonol 4-reductase-like protein (AHRD V3.3 *** G7JDF6_MEDTR)	GO:0003854|GO:0006694|GO:0016616|GO:0055114
Solyc05g021090.3	4,37E-01	6,22E-01	**2,44E+00**	**9,91E-03**	5,02E-01	5,72E-01	-2,67E-01	7,63E-01	*nifD*- N 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061FA31_THECC)	GO:0003677|GO:0006355
Solyc03g079980.2	6,66E-01	2,79E-01	**2,44E+00**	**4,13E-04**	1,29E+00	4,20E-02	-8,55E-01	1,68E-01	*nifD*- N 14 dpi	NA	transmembrane protein, putative (Protein of unknown function, DUF599) (AHRD V3.3 *** AT3G18215.1)	

Solyc01g080990.3	1,33E+00	2,58E-02	**2,42E+00**	**2,15E-04**	7,44E-01	1,98E-01	-5,76E-01	3,16E-01	*nifD*- N 14 dpi	H	Carboxyl methyltransferase (AHRD V3.3 *** Q70T29_BIXOR)	GO:0008168
Solyc10g081550.2	7,96E-01	1,58E-01	**2,39E+00**	**1,82E-04**	6,93E-01	2,17E-01	-1,40E+00	1,72E-02	*nifD*- N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9SYM5_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc01g005760.3	1,89E+00	3,59E-02	**2,39E+00**	**9,50E-03**	3,38E-01	6,95E-01	-3,96E-01	6,46E-01	*nifD*- N 14 dpi	PMI	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** AT4G26540.1)	GO:0005515
Solyc10g007510.2	1,36E+00	2,83E-02	**2,38E+00**	**3,86E-04**	1,01E+00	9,57E-02	1,53E+00	1,45E-02	*nifD*- N 14 dpi	CS	Glucan endo-1,3-beta-glucosidase (AHRD V3.3 *** A0A0B0NBZ5_GOSAR)	
Solyc05g005170.3	-3,70E-01	6,01E-01	**2,36E+00**	**2,32E-03**	8,33E-01	2,45E-01	2,42E-01	7,32E-01	*nifD*- N 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** A0A061E6B2_THECC)	GO:0004650|GO:0005975
Solyc06g052020.2	1,58E+00	3,34E-02	**2,36E+00**	**2,49E-03**	-3,03E-01	6,70E-01	-1,98E-01	7,81E-01	*nifD*- N 14 dpi	NA	Transmembrane protein, putative (AHRD V3.3 -** A0A072V1A4_MEDTR)	
Solyc04g007590.2	1,42E+00	7,60E-02	**2,35E+00**	**5,10E-03**	-2,39E+00	4,52E-03	-5,58E+00	1,13E-07	*nifD*- N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4BNR6_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc04g028460.1	7,27E-01	2,62E-01	**2,34E+00**	**1,05E-03**	7,35E-01	2,57E-01	7,96E-01	2,20E-01	*nifD*- N 14 dpi	RNA	LOW QUALITY:RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT4G00830.6)	
Solyc05g005540.3	2,63E-01	6,28E-01	**2,34E+00**	**1,83E-04**	1,04E+00	6,28E-02	-1,98E+00	1,06E-03	*nifD*- N 14 dpi	CS	Polygalacturonase non-catalytic subunit AroGP3 (AHRD V3.3 *** GP3_SOLLC)	
Solyc03g033410.3	-1,03E+00	1,24E-01	**2,34E+00**	**1,32E-03**	-3,49E-01	5,96E-01	-7,48E-01	2,60E-01	*nifD*- N 14 dpi	S	Ubiquitin-conjugating enzyme E2 (AHRD V3.3 *** A0A172S1R1_NICBE)	
Solyc05g052100.3	1,08E+00	1,37E-01	**2,30E+00**	**3,01E-03**	1,93E+00	1,08E-02	-1,96E-01	7,82E-01	*nifD*- N 14 dpi	N	Glutamate dehydrogenase (AHRD V3.3 *** K4C1P1_SOLLC)	GO:0004352|GO:0006520|GO:0016491|GO:0055114|GO:0006520|GO:0016491|GO:0055114
Solyc11g071350.1	3,60E-01	6,50E-01	**2,28E+00**	**7,37E-03**	1,71E+00	3,80E-02	6,59E-01	4,08E-01	*nifD*- N 14 dpi	G	aluminum activated malate transporter family protein (AHRD V3.3 *** AT1G08440.1)	GO:0015743
Solyc04g010320.1	1,47E+00	6,83E-02	**2,27E+00**	**7,06E-03**	3,86E-01	6,22E-01	-1,62E+00	4,60E-02	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q1AGW1_CAPAN)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc01g105590.2	9,06E-01	1,21E-01	**2,25E+00**	**5,05E-04**	3,31E-01	5,64E-01	5,68E-02	9,21E-01	*nifD*- N 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC)	GO:0016747
Solyc02g081510.2	1,13E+00	1,19E-01	**2,24E+00**	**3,81E-03**	1,20E+00	1,00E-01	9,78E-01	1,76E-01	*nifD*- N 14 dpi	S	Receptor-like kinase (AHRD V3.3 *** G7I978_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g123410.1	-2,32E-01	6,35E-01	**2,23E+00**	**9,30E-05**	-8,96E-01	7,47E-02	2,00E-01	6,82E-01	*nifD*- N 14 dpi	STR	Germin-like protein (AHRD V3.3 *** Q0PWM4_CAPCH)	GO:0030145|GO:0045735|GO:0045735
Solyc10g037880.2	8,11E-01	4,66E-02	**2,23E+00**	**4,90E-06**	-4,79E-01	2,28E-01	-1,15E+00	6,32E-03	*nifD*- N 14 dpi	E	Blue copper (AHRD V3.3 *** A0A0B0MZW4_GOSAR)	GO:0009055
Solyc08g014310.3	5,78E-01	4,66E-01	**2,23E+00**	**8,40E-03**	1,09E+00	1,74E-01	-1,28E+00	1,14E-01	*nifD*- N 14 dpi	N	spermidine synthase (AHRD V3.3 *** AT1G23820.1)	GO:0003824|GO:0030750|GO:0030750
Solyc10g045775.1	-6,11E-01	4,42E-01	**2,23E+00**	**8,47E-03**	-4,29E-01	5,88E-01	-1,58E+00	5,40E-02	*nifD*- N 14 dpi	STR	HSP20-like chaperones superfamily protein (AHRD V3.3 --* AT4G02450.2)	
Solyc07g052250.3	8,89E-01	1,91E-01	**2,22E+00**	**2,46E-03**	3,62E-01	5,89E-01	-1,38E+00	4,76E-02	*nifD*- N 14 dpi	NA	Unknown protein (AHRD V3.3)	
Solyc05g024370.1	1,62E-01	8,39E-01	**2,21E+00**	**9,63E-03**	5,65E-01	4,81E-01	-2,75E-01	7,31E-01	*nifD*- N 14 dpi	D	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT5G17680.2)	GO:0043531
Solyc03g095650.3	2,00E+00	1,16E-02	**2,20E+00**	**6,10E-03**	8,92E-01	2,37E-01	-5,08E-02	9,46E-01	*nifD*- N 14 dpi	D	MLO-like protein (AHRD V3.3 *** K4BIY8_SOLLC)	GO:0006952|GO:0016021
Solyc10g006800.3	1,50E+00	1,34E-02	**2,19E+00**	**6,31E-04**	-5,59E-01	3,30E-01	-2,06E-01	7,18E-01	*nifD*- N 14 dpi	S	Cyclic nucleotide-gated ion channel, putative (AHRD V3.3 *** B9SIE1_RICCO)	GO:0005216|GO:0006811|GO:0016020|GO:0055085
Solyc07g055065.1	1,14E+00	8,01E-02	**2,18E+00**	**1,75E-03**	6,79E-01	2,87E-01	2,75E-01	6,64E-01	*nifD*- N 14 dpi	G	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *-* AT2G42610.2)	
Solyc06g076910.2	4,09E-01	3,62E-01	**2,16E+00**	**4,50E-05**	6,95E-01	1,27E-01	6,90E-01	1,29E-01	*nifD*- N 14 dpi	S	Receptor-kinase, putative (AHRD V3.3 *** B9SUC9_RICCO)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g006700.1	7,01E-01	2,57E-01	**2,15E+00**	**1,50E-03**	4,27E-01	4,87E-01	6,34E-02	9,17E-01	*nifD*- N 14 dpi	D	Pathogenesis-related family protein (AHRD V3.3 *** B9IM28_POPTR)	GO:0005576

Solyc12g009270.1	3,08E-01	3,43E-01	**2,11E+00**	**5,17E-07**	1,93E-01	5,49E-01	-1,07E+00	2,40E-03	*nifD*- N 14 dpi	CS	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** A0A061GSW0_THECC)	GO:0004857
Solyc12g096980.2	6,82E-01	2,10E-01	**2,11E+00**	**4,99E-04**	1,33E+00	1,88E-02	-8,43E-01	1,24E-01	*nifD*- N 14 dpi	H	auxin-regulated IAA11	GO:0005515|GO:0005634|GO:0006355|GO:0005634|GO:0006355
Solyc12g011300.2	-1,47E-01	7,80E-01	**2,10E+00**	**4,51E-04**	1,09E+00	4,75E-02	-6,51E-01	2,23E-01	*nifD*- N 14 dpi	STR	Glutathione s-transferase, putative (AHRD V3.3 *** B9T3K4_RICCO)	GO:0005515
Solyc12g049320.2	1,10E+00	9,89E-02	**2,09E+00**	**3,16E-03**	3,39E-01	6,03E-01	-1,49E+00	2,87E-02	*nifD*- N 14 dpi	PMI	Nodulation signaling pathway 1-like protein (AHRD V3.3 *** A0MSK8_NICBE)	
Solyc01g096690.2	3,60E-01	5,56E-01	**2,06E+00**	**2,20E-03**	-8,44E-01	1,74E-01	3,35E-01	5,85E-01	*nifD*- N 14 dpi	K	Kinase family protein (AHRD V3.3 *-* A0A0K9PUI0_ZOSMR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc06g060580.2	1,54E+00	1,16E-02	**2,05E+00**	**1,22E-03**	-1,30E+00	2,93E-02	-1,11E+00	6,07E-02	*nifD*- N 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4C6N8_SOLLC)	GO:0016021
Solyc12g013570.2	1,60E+00	1,09E-02	**2,05E+00**	**1,63E-03**	9,45E-01	1,17E-01	1,01E+00	9,32E-02	*nifD*- N 14 dpi	OX	Plant cadmium resistance 2, putative (AHRD V3.3 *** A0A061E1P7_THECC)	
Solyc01g110160.3	6,91E-01	2,51E-01	**2,03E+00**	**1,95E-03**	3,97E-01	5,06E-01	4,31E-01	4,71E-01	*nifD*- N 14 dpi	R	Ribosomal RNA small subunit methyltransferase H (AHRD V3.3 *** A0A1D1Y2V6_9ARAE)	
Solyc02g080060.1	1,28E+00	4,67E-02	**2,01E+00**	**3,00E-03**	-1,19E+00	6,35E-02	-5,04E-01	4,19E-01	*nifD*- N 14 dpi	D	Cysteine-rich receptor-kinase-like protein (AHRD V3.3 *** A0A072VRC1_MEDTR)	
Solyc01g057465.1	1,48E+00	3,56E-02	**2,01E+00**	**5,68E-03**	4,63E-01	4,93E-01	1,83E-01	7,85E-01	*nifD*- N 14 dpi	TR	Metal tolerance protein (AHRD V3.3 --* E5GC92_CUCME)	
Solyc02g076910.3	1,57E+00	3,65E-02	**2,01E+00**	**9,25E-03**	6,45E-01	3,74E-01	-1,25E+00	9,25E-02	*nifD*- N 14 dpi	G	Cysteine protease (AHRD V3.3 *** E7D4U5_TOBAC)	GO:0006508|GO:0008234|GO:0008234|GO:0008234
Solyc09g007470.1	1,16E+00	1,11E-02	**2,00E+00**	**6,91E-05**	-6,89E-01	1,15E-01	4,29E-01	3,20E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:Protamine P1 family protein (AHRD V3.3 *** G7L1S0_MEDTR)	
Solyc08g014110.1	-9,42E-01	1,43E-01	**1,99E+00**	**3,61E-03**	1,73E+00	1,01E-02	-2,61E-01	6,79E-01	*nifD*- N 14 dpi	DNA	LOW QUALITY:B3 domain-containing protein REM13 (AHRD V3.3 --* AT2G24650.7)	
Solyc03g113420.3	8,52E-01	1,08E-02	**1,99E+00**	**9,05E-07**	3,22E-01	3,08E-01	-2,25E-01	4,75E-01	*nifD*- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT5G62680.1)	GO:0005215|GO:0006810|GO:0016020
Solyc04g056550.1	-2,09E-01	7,62E-01	**1,98E+00**	**7,61E-03**	-2,59E+00	8,05E-04	-1,34E+00	6,10E-02	*nifD*- N 14 dpi	T	LOW QUALITY:MADS-box transcription factor family protein (AHRD V3.3 *** AT4G36590.1)	GO:0003677|GO:0046983
Solyc06g074070.3	-9,94E-02	8,36E-01	**1,98E+00**	**3,16E-04**	2,32E-01	6,29E-01	-1,11E+00	2,72E-02	*nifD*- N 14 dpi	S	Receptor-kinase-like protein (AHRD V3.3 *** A0A072U3D4_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g071085.1	7,20E-01	1,29E-02	**1,97E+00**	**1,03E-07**	-2,46E-01	3,69E-01	-1,47E-01	5,91E-01	*nifD*- N 14 dpi	G	Hydroxyproline-rich glycoprotein (AHRD V3.3 *** Q8H9E0_SOLTU)	GO:0005199|GO:0009664
Solyc07g008520.3	7,96E-01	9,19E-02	**1,95E+00**	**2,22E-04**	1,11E-01	8,09E-01	-3,34E-01	4,69E-01	*nifD*- N 14 dpi	TR	Peptide transporter (AHRD V3.3 *** W9RPK3_9ROSA)	GO:0005215|GO:0006810|GO:0016020|GO:0005215|GO:0006857|GO:0016020|GO:0005215|GO:0006857|GO:0016020
Solyc02g030260.2	1,19E+00	8,84E-02	**1,95E+00**	**7,69E-03**	8,94E-02	8,96E-01	9,18E-01	1,86E-01	*nifD*- N 14 dpi	D	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 --* AT5G38350.1)	
Solyc04g012190.2	9,25E-01	1,55E-01	**1,93E+00**	**5,24E-03**	4,80E-01	4,54E-01	-9,37E-01	1,50E-01	*nifD*- N 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* M1A662_SOLTU)	GO:0005524
Solyc04g081630.2	1,17E+00	1,50E-02	**1,92E+00**	**2,15E-04**	-2,01E+00	1,27E-04	-7,69E-01	9,73E-02	*nifD*- N 14 dpi	STR	Heat shock protein 90 (AHRD V3.3 *-* Q9MB32_ORYSA)	GO:0005524|GO:0006457|GO:0006950|GO:0051082
Solyc11g042820.2	6,21E-01	6,17E-04	**1,91E+00**	**4,80E-12**	8,80E-01	8,80E-06	-4,13E-01	1,55E-02	*nifD*- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT1G59740.1)	GO:0005215|GO:0006810|GO:0016020
Solyc00g009050.2	7,56E-01	2,13E-01	**1,91E+00**	**3,38E-03**	1,05E-01	8,61E-01	-6,18E-01	3,06E-01	*nifD*- N 14 dpi	NA	UPF0544 protein C5orf45 isogeny (AHRD V3.3 *** A0A151T4T7_CAJCA)	
Solyc09g015870.3	1,18E+00	7,89E-02	**1,91E+00**	**6,43E-03**	9,04E-01	1,71E-01	9,49E-01	1,52E-01	*nifD*- N 14 dpi	E	Cytochrome c oxidase subunit 2 (AHRD V3.3 *-* J7MFY4_MALDO)	GO:0004129|GO:0005507|GO:0016020|GO:0016021|GO:0022900|GO:0016021|GO:0022900
Solyc08g066720.2	4,44E-01	4,91E-01	**1,90E+00**	**6,07E-03**	-9,19E-01	1,60E-01	-1,04E+00	1,14E-01	*nifD*- N 14 dpi	2M	Carotenoid cleavage dioxygenase (AHRD V3.3 *** B6UEM5_MAIZE)	GO:0016702|GO:0055114
Solyc04g064620.3	1,35E-01	8,41E-01	**1,89E+00**	**8,94E-03**	-1,27E+00	6,83E-02	-7,86E-01	2,51E-01	*nifD*- N 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BT53_SOLLC)	GO:0016021

Solyc00g136565.1	1,48E+00	1,38E-02	**1,89E+00**	**2,30E-03**	1,24E+00	3,53E-02	6,09E-01	2,86E-01	*nifD*- N 14 dpi	E	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)	GO:0016491|GO:0055114
Solyc01g090340.2	9,62E-01	3,20E-03	**1,87E+00**	**1,12E-06**	4,34E-01	1,55E-01	-1,17E+00	5,56E-04	*nifD*- N 14 dpi	H	Ethylene-responsive transcription factor, putative (AHRD V3.3 *** B9RD03_RICCO)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc10g008900.3	1,10E+00	8,52E-02	**1,86E+00**	**5,42E-03**	-1,92E+00	4,36E-03	8,93E-01	1,58E-01	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4CY66_SOLLC)	
Solyc04g079570.1	-2,29E-01	7,17E-01	**1,83E+00**	**7,01E-03**	1,26E+00	5,53E-02	-1,05E+00	1,05E-01	*nifD*- N 14 dpi	DNA	LOW QUALITY:Dof zinc finger protein (AHRD V3.3 *** W9QMS6_9ROSA)	GO:0003677|GO:0006355
Solyc02g087660.3	1,49E+00	2,21E-02	**1,83E+00**	**6,16E-03**	2,78E-01	6,54E-01	1,44E-01	8,16E-01	*nifD*- N 14 dpi	H	SlPIN8	GO:0016021|GO:0055085
Solyc06g074000.1	1,41E+00	1,27E-02	**1,83E+00**	**1,92E-03**	-1,16E+00	3,75E-02	-1,15E+00	3,86E-02	*nifD*- N 14 dpi	P	LOW QUALITY:Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G52500.1)	GO:0004190|GO:0006508
Solyc05g010030.3	2,57E-01	4,17E-01	**1,82E+00**	**3,91E-06**	5,22E-01	1,07E-01	-2,75E-01	3,86E-01	*nifD*- N 14 dpi	E	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT3G25640.2)	
Solyc12g056600.3	1,19E+00	1,98E-02	**1,82E+00**	**8,37E-04**	8,37E-01	9,31E-02	3,95E-02	9,35E-01	*nifD*- N 14 dpi	D	short-chain dehydrogenase-reductase,Pfam:PF13561	
Solyc09g011270.3	1,04E+00	2,30E-02	**1,81E+00**	**2,64E-04**	-1,91E+00	1,43E-04	-1,98E+00	9,15E-05	*nifD*- N 14 dpi	S	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G37820.1)	
Solyc07g005110.3	5,98E-01	9,45E-03	**1,80E+00**	**7,02E-09**	-1,71E-02	9,37E-01	-4,20E-02	8,45E-01	*nifD*- N 14 dpi	K	Receptor-like kinase CHRK1 (AHRD V3.3 *** Q9SWX8_TOBAC)	GO:0004553|GO:0005975|GO:0004568|GO:0006032|GO:0004568|GO:0006032
Solyc06g048750.3	9,62E-01	1,77E-02	**1,80E+00**	**6,90E-05**	-7,31E-01	6,54E-02	-1,71E+00	1,31E-04	*nifD*- N 14 dpi	NA	Unknown protein (AHRD V3.3)	
Solyc03g006830.3	7,87E-01	1,22E-01	**1,77E+00**	**1,38E-03**	4,56E-01	3,63E-01	-9,93E-01	5,44E-02	*nifD*- N 14 dpi	T	MADS-box transcription factor FYFL (AHRD V3.3 *** W5S185_SOLLC)	GO:0000165|GO:0000977|GO:0045944|GO:0003677|GO:0046983|GO:0003677|GO:0046983
Solyc12g087940.2	-5,72E-01	2,63E-01	**1,76E+00**	**1,60E-03**	7,29E-01	1,57E-01	6,02E-02	9,05E-01	*nifD*- N 14 dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061FET5_THECC)	GO:0004190|GO:0006508
Solyc07g008107.1	8,54E-01	3,41E-03	**1,76E+00**	**5,01E-07**	2,54E-01	3,46E-01	-1,41E-01	5,98E-01	*nifD*- N 14 dpi	E	Blue copper protein (AHRD V3.3 *-* A0A151SLU0_CAJCA)	GO:0009055
Solyc09g098000.3	1,08E+00	8,55E-02	**1,75E+00**	**7,52E-03**	1,51E+00	1,93E-02	-6,81E-01	2,69E-01	*nifD*- N 14 dpi	E	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** AT1G60690.1)	
Solyc06g068770.3	1,35E+00	1,21E-02	**1,74E+00**	**1,82E-03**	-3,19E-01	5,29E-01	-1,18E+00	2,68E-02	*nifD*- N 14 dpi	NA	DB279	
Solyc04g007670.1	6,62E-01	9,10E-03	**1,74E+00**	**7,60E-08**	-1,57E-01	5,08E-01	8,11E-02	7,32E-01	*nifD*- N 14 dpi	G	LOW QUALITY:CheY-like two-component responsive regulator family protein (AHRD V3.3 --* AT4G18020.9)	
Solyc01g103360.3	5,34E-01	3,35E-01	**1,74E+00**	**3,69E-03**	-2,34E-01	6,71E-01	2,09E-01	7,04E-01	*nifD*- N 14 dpi	CS	glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT1G09610.1)	GO:0045492
Solyc06g068440.3	9,90E-01	1,88E-08	**1,72E+00**	**1,70E-13**	1,95E-01	1,26E-01	-6,69E-01	1,19E-05	*nifD*- N 14 dpi	D	cinnamoyl-CoA reductase	GO:0003824|GO:0050662
Solyc09g005110.3	-1,17E+00	4,46E-02	**1,72E+00**	**4,71E-03**	3,58E-02	9,49E-01	-2,50E-01	6,56E-01	*nifD*- N 14 dpi	C	Pyruvate decarboxylase (AHRD V3.3 *** Q8H9C6_SOLTU)	GO:0000287|GO:0030976|GO:0003824|GO:0030976|GO:0003824|GO:0030976
Solyc06g051250.1	-1,26E+00	3,72E-02	**1,72E+00**	**6,19E-03**	6,01E-01	3,06E-01	-1,89E-01	7,45E-01	*nifD*- N 14 dpi	D	LOW QUALITY:RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FKY9_THECC)	GO:0005515|GO:0008270
Solyc03g033710.3	6,48E-01	1,00E-02	**1,70E+00**	**1,01E-07**	-4,41E-01	6,97E-02	-7,56E-01	3,27E-03	*nifD*- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4BFP3_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc01g091465.1	7,62E-01	1,76E-01	**1,70E+00**	**4,63E-03**	-9,69E-03	9,86E-01	-8,38E-01	1,38E-01	*nifD*- N 14 dpi	D	Calcium-binding EF-hand (AHRD V3.3 *** A0A103XUP9_CYNCS)	GO:0005509
Solyc06g005130.3	8,96E-01	4,25E-02	**1,70E+00**	**4,31E-04**	-1,42E-02	9,73E-01	-1,20E+00	8,56E-03	*nifD*- N 14 dpi	DNA	Dof zinc finger protein (AHRD V3.3 *** W9RMR9_9ROSA)	GO:0003677|GO:0006355
Solyc08g042010.3	9,27E-01	7,93E-02	**1,69E+00**	**2,62E-03**	-1,90E-01	7,11E-01	-2,29E+00	1,25E-04	*nifD*- N 14 dpi	P	Exostosin family protein (AHRD V3.3 *** A0A061GIR4_THECC)	
Solyc09g014940.2	-7,93E-01	1,56E-01	**1,68E+00**	**4,79E-03**	-1,53E+00	9,35E-03	-4,25E+00	2,86E-08	*nifD*- N 14 dpi	D	Wound-induced protein 1 (AHRD V3.3 *** A0A0B2R5F9_GLYSO)	

Solyc02g093230.3	7,42E-01	3,52E-03	**1,67E+00**	**1,20E-07**	-1,16E+00	3,25E-05	-1,79E+00	3,62E-08	*nifD*- N 14 dpi	2M	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** CAMT_SOLTU)	GO:0008171
Solyc04g011340.3	9,99E-01	1,04E-02	**1,66E+00**	**1,01E-04**	-8,46E-01	2,73E-02	-1,04E+00	8,22E-03	*nifD*- N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4BPI9_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc12g007160.2	6,43E-01	2,02E-01	**1,66E+00**	**2,39E-03**	2,71E-01	5,86E-01	-1,48E-01	7,65E-01	*nifD*- N 14 dpi	H	ABIL1-like protein (AHRD V3.3 *** B7FL53_MEDTR)	
Solyc08g067620.2	9,30E-01	2,04E-02	**1,65E+00**	**1,74E-04**	-1,11E+00	6,89E-03	-1,01E+00	1,23E-02	*nifD*- N 14 dpi	TR	Pleiotropic drug resistance ABC transporter (AHRD V3.3 *** W0TUG3_ACAMN)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc12g057070.2	6,40E-01	7,17E-02	**1,65E+00**	**5,33E-05**	-4,92E-01	1,61E-01	-5,48E-01	1,20E-01	*nifD*- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** Q589Y2_TOBAC)	GO:0008152|GO:0016758
Solyc06g074230.3	8,66E-01	1,41E-03	**1,64E+00**	**3,78E-07**	-1,41E+00	4,11E-06	-5,58E-01	2,95E-02	*nifD*- N 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4C9E1_SOLLC)	
Solyc02g076890.1	6,42E-01	2,38E-01	**1,64E+00**	**4,88E-03**	-1,31E+00	2,10E-02	-7,67E-01	1,61E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:DUF538 family protein (Protein of unknown function, DUF538) (AHRD V3.3 *** AT4G24130.1)	
Solyc12g098490.2	6,10E-01	2,05E-03	**1,63E+00**	**1,32E-09**	-8,65E-01	4,91E-05	-1,18E+00	5,20E-07	*nifD*- N 14 dpi	AM	Serine hydroxymethyltransferase (AHRD V3.3 *** M1A0B7_SOLTU)	GO:0003824|GO:0004372|GO:0006544|GO:0006563|GO:0030170|GO:0004372|GO:0006544|GO:0006563|GO:0030170
Solyc02g093250.3	6,84E-01	1,60E-03	**1,63E+00**	**7,20E-09**	-9,53E-01	4,29E-05	-1,33E+00	2,98E-07	*nifD*- N 14 dpi	2M	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** CAMT_SOLTU)	GO:0008171
Solyc05g007790.3	7,16E-01	9,82E-03	**1,63E+00**	**1,07E-06**	-2,29E+00	2,39E-09	-1,06E+00	3,37E-04	*nifD*- N 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4BWV4_SOLLC)	
Solyc08g014490.1	6,17E-02	9,12E-01	**1,62E+00**	**7,11E-03**	9,24E-01	1,08E-01	-1,04E+00	7,28E-02	*nifD*- N 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)	GO:0016747
Solyc10g011940.1	-2,00E-01	7,32E-01	**1,62E+00**	**9,39E-03**	3,64E-01	5,33E-01	-3,02E-01	6,04E-01	*nifD*- N 14 dpi	DNA	chromatin remodeling factor (AHRD V3.3 *-* AT4G31900.3)	
Solyc04g058150.3	4,49E-01	7,03E-02	**1,62E+00**	**3,41E-07**	-5,99E-01	1,83E-02	-1,70E-01	4,81E-01	*nifD*- N 14 dpi	NA	Metallothionein-like protein (AHRD V3.3 *** A8DUB1_SOLLC)	GO:0046872
Solyc06g074630.3	6,96E-01	1,21E-03	**1,61E+00**	**7,00E-09**	3,16E-01	1,10E-01	-8,73E-01	1,08E-04	*nifD*- N 14 dpi	CS	Cellulose synthase-like protein (AHRD V3.3 *** L0ATP8_POPTO)	
Solyc06g075500.3	-3,57E-01	5,11E-01	**1,61E+00**	**6,00E-03**	-2,51E-01	6,43E-01	-3,78E-02	9,44E-01	*nifD*- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT3G45710.1)	GO:0005215|GO:0006810|GO:0016020|GO:0005215|GO:0006857|GO:0016020|GO:0005215|GO:0006857|GO:0016020
Solyc10g083210.2	8,65E-01	3,98E-03	**1,60E+00**	**3,63E-06**	5,26E-02	8,49E-01	5,78E-01	4,42E-02	*nifD*- N 14 dpi	DNA	B3 domain-containing protein family (AHRD V3.3 *** A0A151U3H1_CAJCA)	GO:0003677
Solyc05g056450.3	2,80E-01	2,10E-01	**1,60E+00**	**8,66E-08**	5,23E-01	2,38E-02	7,26E-02	7,41E-01	*nifD*- N 14 dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT2G03200.1)	GO:0004190|GO:0006508
Solyc01g087540.3	-7,71E-01	1,38E-01	**1,60E+00**	**3,89E-03**	1,16E+00	2,98E-02	-2,78E-01	5,86E-01	*nifD*- N 14 dpi	NA	imidazolonepropionase (Protein of unknown function, DUF642) (AHRD V3.3 *** AT2G41810.1)	
Solyc01g100210.3	9,98E-01	6,50E-06	**1,59E+00**	**2,04E-09**	-3,76E-01	4,36E-02	4,17E-02	8,16E-01	*nifD*- N 14 dpi	P	Hexosyltransferase (AHRD V3.3 *** K4B155_SOLLC)	GO:0016757
Solyc12g005720.1	9,58E-01	1,01E-03	**1,59E+00**	**1,77E-06**	1,43E-01	5,85E-01	4,20E-01	1,16E-01	*nifD*- N 14 dpi	PMI	Cysteine-rich RLK (Receptor-like kinase) protein (AHRD V3.3 *** G7IKM1_MEDTR)	
Solyc03g119880.3	-5,71E-01	1,94E-01	**1,59E+00**	**1,02E-03**	9,23E-01	4,07E-02	3,78E-01	3,86E-01	*nifD*- N 14 dpi	PMI	Early nodulin-like protein (AHRD V3.3 *** G7JR03_MEDTR)	GO:0009055
Solyc10g005060.3	8,93E-01	3,61E-06	**1,59E+00**	**1,01E-10**	-2,87E-02	8,52E-01	-1,20E-01	4,38E-01	*nifD*- N 14 dpi	CS	Caffeic acid O-methyltransferase (AHRD V3.3 *** A0A072TEU0_MEDTR)	GO:0008168|GO:0008171|GO:0008171
Solyc07g039410.3	7,58E-01	1,54E-01	**1,57E+00**	**5,28E-03**	-1,78E+00	1,98E-03	-7,89E-01	1,38E-01	*nifD*- N 14 dpi	D	EDNR2GH3 protein (AHRD V3.3 *** E0Y3V4_9SOLN)	GO:0043531
Solyc12g005800.2	9,50E-01	3,06E-04	**1,57E+00**	**2,78E-07**	-1,16E+00	2,60E-05	-7,67E-01	2,40E-03	*nifD*- N 14 dpi	T	Myb transcription factor (AHRD V3.3 *** A0A072UKM9_MEDTR)	GO:0003677
Solyc09g010200.3	5,83E-01	4,98E-02	**1,56E+00**	**8,85E-06**	-1,93E+00	3,16E-07	-1,06E+00	8,79E-04	*nifD*- N 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4CR48_SOLLC)	
Solyc01g104915.1	2,76E-01	6,11E-01	**1,56E+00**	**7,54E-03**	-1,37E+00	1,73E-02	-1,27E+00	2,55E-02	*nifD*- N 14 dpi	TR	Two pore calcium channel protein 1 (AHRD V3.3 --* TPC1_WHEAT)	

Solyc10g045500.2	6,55E-01	2,52E-01	**1,55E+00**	**9,98E-03**	-6,66E-02	9,06E-01	5,26E-01	3,55E-01	*nifD*- N 14 dpi	G	Calcium-dependent phospholipid-binding Copine family protein (AHRD V3.3 *-* AT1G08860.1)	GO:0005544|GO:0060548
Solyc04g016070.2	8,73E-01	1,07E-04	**1,55E+00**	**1,47E-08**	-5,60E-02	7,72E-01	3,58E-01	7,24E-02	*nifD*- N 14 dpi	T	LOW QUALITY:MADS-box transcription factor (AHRD V3.3 *** A0A023JBP0_9ROSI)	GO:0003700|GO:0005634|GO:0006355
Solyc03g078100.3	-2,67E-01	5,63E-01	**1,55E+00**	**2,20E-03**	1,45E-02	9,75E-01	-7,06E-01	1,33E-01	*nifD*- N 14 dpi	CS	Pectinesterase (AHRD V3.3 *** K4BHP0_SOLLC)	GO:0004857|GO:0005618|GO:0030599|GO:0042545|GO:0005618|GO:0030599|GO:0042545
Solyc05g046010.3	5,91E-01	3,74E-02	**1,55E+00**	**4,97E-06**	3,20E-01	2,46E-01	1,23E-01	6,52E-01	*nifD*- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4C0T4_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc02g093090.1	6,61E-01	4,70E-05	**1,54E+00**	**1,47E-11**	-4,12E-01	5,27E-03	-2,80E-01	4,89E-02	*nifD*- N 14 dpi	CS	glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT1G71690.1)	GO:0045492
Solyc09g098160.3	7,67E-01	1,57E-05	**1,54E+00**	**6,23E-11**	-7,85E-01	1,13E-05	-2,53E-01	9,21E-02	*nifD*- N 14 dpi	D	pirin	
Solyc01g068130.3	5,32E-01	1,22E-02	**1,54E+00**	**3,01E-08**	1,53E-01	4,45E-01	-6,94E-01	1,64E-03	*nifD*- N 14 dpi	K	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase (AHRD V3.3 *** AT2G47010.2)	
Solyc10g083250.2	7,49E-01	7,40E-03	**1,54E+00**	**2,71E-06**	-7,25E-01	9,17E-03	-1,04E-01	6,91E-01	*nifD*- N 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4D3B2_SOLLC)	
Solyc12g089360.1	5,52E-01	8,06E-02	**1,54E+00**	**2,89E-05**	-2,89E+00	6,64E-10	-8,52E-01	9,46E-03	*nifD*- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4DH07_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc09g065590.3	4,19E-01	1,61E-01	**1,54E+00**	**1,60E-05**	9,33E-01	3,49E-03	-5,12E-01	8,92E-02	*nifD*- N 14 dpi	H	auxin canalization protein (DUF828) (AHRD V3.3 *** AT3G22810.1)	
Solyc06g076060.1	1,47E-01	7,18E-01	**1,53E+00**	**7,90E-04**	-1,20E+00	6,26E-03	-8,07E-01	5,60E-02	*nifD*- N 14 dpi	DNA	LOW QUALITY:Cyclin-dependent protein kinase inhibitor SMR3 (AHRD V3.3 *-* M5W251_PRUPE)	
Solyc06g005560.3	6,87E-01	1,31E-01	**1,53E+00**	**1,80E-03**	9,96E-01	3,21E-02	-5,43E-01	2,28E-01	*nifD*- N 14 dpi	CS	expansin9	GO:0005576|GO:0009664|GO:0009664
Solyc02g084790.3	8,71E-01	9,50E-03	**1,52E+00**	**4,57E-05**	3,09E-01	3,29E-01	3,78E-01	2,35E-01	*nifD*- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4BAZ4_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc01g094990.2	7,25E-01	9,80E-02	**1,52E+00**	**1,33E-03**	8,48E-01	5,51E-02	2,55E-01	5,51E-01	*nifD*- N 14 dpi	C	LOW QUALITY:transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)	
Solyc10g076400.2	8,80E-01	3,63E-04	**1,52E+00**	**1,73E-07**	-9,70E-01	1,21E-04	-9,49E-01	1,57E-04	*nifD*- N 14 dpi	CS	Trichome birefringence-like protein (AHRD V3.3 *** G7JKP3_MEDTR)	
Solyc03g116370.3	8,76E-01	2,04E-02	**1,51E+00**	**2,37E-04**	-2,68E+00	5,40E-08	-1,73E+00	4,90E-05	*nifD*- N 14 dpi	G	RP/EB family microtubule-associated protein (AHRD V3.3 *** A0A072TJV8_MEDTR)	GO:0005515|GO:0008017|GO:0008017
Solyc06g005280.1	-5,71E-01	2,17E-01	**1,51E+00**	**2,53E-03**	1,41E-01	7,57E-01	-1,07E+00	2,52E-02	*nifD*- N 14 dpi	TR	LOW QUALITY:Exocyst subunit exo70 family protein (AHRD V3.3 *** G7IUA9_MEDTR)	GO:0000145|GO:0006887
Solyc08g075990.3	9,71E-01	4,44E-02	**1,50E+00**	**3,06E-03**	7,47E-01	1,16E-01	2,39E-01	6,07E-01	*nifD*- N 14 dpi	E	LOW PSII ACCUMULATION protein (DUF1995) (AHRD V3.3 *** AT5G48790.1)	
Solyc01g044420.3	-5,64E-02	9,04E-01	**1,50E+00**	**3,26E-03**	-6,17E-01	1,93E-01	-8,53E-01	7,61E-02	*nifD*- N 14 dpi	DNA	calmodulin-binding family protein (AHRD V3.3 *** AT3G13600.2)	
Solyc01g008790.3	6,56E-01	1,58E-01	**1,49E+00**	**2,75E-03**	1,11E+00	2,08E-02	-5,02E-01	2,76E-01	*nifD*- N 14 dpi	L	Non specific phospholipase C (AHRD V3.3 *** A0A0K9P3E0_ZOSMR)	GO:0003824|GO:0008152|GO:0016788|GO:0016788
Solyc11g073040.1	4,51E-01	3,85E-01	**1,49E+00**	**7,10E-03**	-1,77E+00	1,82E-03	-8,05E-02	8,76E-01	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *-* M1B9I8_SOLTU)	
Solyc12g097095.1	5,85E-01	8,08E-02	**1,49E+00**	**9,47E-05**	-1,74E+00	1,22E-05	-7,83E-01	2,24E-02	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4DHI2_SOLLC)	
Solyc11g012705.1	7,96E-01	3,93E-03	**1,48E+00**	**3,47E-06**	9,39E-01	9,31E-04	5,99E-01	2,47E-02	*nifD*- N 14 dpi	G	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** AT5G47635.1)	
Solyc07g066250.1	7,32E-01	1,14E-01	**1,48E+00**	**2,87E-03**	1,74E-01	7,00E-01	-1,77E+00	5,47E-04	*nifD*- N 14 dpi	T	GRAS family transcription factor (AHRD V3.3 *** A0A061F3B6_THECC)	GO:0005634|GO:0010223
Solyc06g060910.2	1,14E+00	1,53E-02	**1,47E+00**	**2,55E-03**	1,72E-01	7,00E-01	-4,69E-01	2,97E-01	*nifD*- N 14 dpi	TR	Glycerol-3-phosphate transporter, putative (AHRD V3.3 *** B9T0L8_RICCO)	GO:0005215|GO:0006810|GO:0016021|GO:0016021|GO:0055085|GO:0016021|GO:0055085
Solyc02g071410.3	8,93E-01	8,30E-02	**1,46E+00**	**6,57E-03**	-2,44E-01	6,26E-01	4,14E-02	9,34E-01	*nifD*- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT4G25300.1)	GO:0016491|GO:0055114

Solyc11g069540.2	6,63E-01	7,50E-04	**1,46E+00**	**6,96E-09**	-4,97E-01	8,10E-03	-6,28E-01	1,25E-03	*nifD*- N 14 dpi	TR	Nucleotide/sugar transporter family protein (AHRD V3.3 *** AT2G28315.1)	
Solyc04g010270.1	5,71E-01	3,57E-02	**1,45E+00**	**6,44E-06**	-1,32E+00	2,55E-05	-4,36E-01	1,03E-01	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4BPI1_SOLLC)	
Solyc02g066980.1	-4,74E-01	3,00E-01	**1,45E+00**	**3,23E-03**	-4,16E-01	3,61E-01	-5,44E-01	2,35E-01	*nifD*- N 14 dpi	K	LOW QUALITY:TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT5G15510.1)	GO:0005819|GO:0005874|GO:0032147|GO:0060236
Solyc08g077060.3	9,73E-01	4,44E-03	**1,45E+00**	**8,65E-05**	8,79E-01	9,14E-03	9,17E-01	6,85E-03	*nifD*- N 14 dpi	DNA	Zinc finger, LSD1-type (AHRD V3.3 *** A0A103XQX8_CYNCS)	
Solyc07g047740.3	8,58E-01	1,58E-03	**1,45E+00**	**2,80E-06**	-2,15E+00	2,82E-09	-1,04E+00	2,36E-04	*nifD*- N 14 dpi	OX	TOMTPX2A peroxidase	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc07g043070.3	5,29E-01	2,82E-01	**1,45E+00**	**5,76E-03**	2,65E-01	5,86E-01	-9,94E-02	8,38E-01	*nifD*- N 14 dpi	S	Rab3 GTPase-activating protein catalytic subunit (AHRD V3.3 --* AT5G55060.3)	
Solyc09g007420.3	4,56E-01	1,45E-02	**1,45E+00**	**9,24E-09**	-5,51E-01	3,89E-03	-8,72E-01	3,32E-05	*nifD*- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** I1Z1X6_TOBAC)	GO:0015018|GO:0016020
Solyc04g054950.3	1,15E+00	2,65E-02	**1,44E+00**	**6,77E-03**	1,15E+00	2,67E-02	1,07E+00	3,74E-02	*nifD*- N 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561	GO:0016491
Solyc04g072780.3	7,18E-01	3,22E-03	**1,44E+00**	**7,04E-07**	1,81E-01	4,20E-01	-4,42E-01	5,59E-02	*nifD*- N 14 dpi	G	senescence-associated family protein (DUF581) (AHRD V3.3 *** AT1G22160.1)	
Solyc10g055190.1	6,03E-01	5,90E-02	**1,44E+00**	**7,33E-05**	-1,74E+00	5,57E-06	-2,11E-01	4,95E-01	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4D1B2_SOLLC)	
Solyc12g087855.1	-1,54E-01	7,68E-01	**1,44E+00**	**9,94E-03**	1,19E+00	2,98E-02	-5,45E-01	3,02E-01	*nifD*- N 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G22490.1)	GO:0046983
Solyc06g065530.3	7,11E-01	2,41E-02	**1,43E+00**	**5,29E-05**	3,24E-01	2,85E-01	5,34E-01	8,37E-02	*nifD*- N 14 dpi	L	GDSL-like lipase/acylhydrolase superfamily protein	GO:0016788
Solyc03g005760.1	-6,35E-01	6,39E-02	**1,43E+00**	**1,87E-04**	-1,34E-01	6,86E-01	-6,58E-02	8,43E-01	*nifD*- N 14 dpi	E	chlorophyll a/b-binding protein	GO:0009765|GO:0016020
Solyc03g005630.3	2,84E-01	4,70E-01	**1,43E+00**	**1,05E-03**	3,97E-01	3,15E-01	-1,37E-01	7,27E-01	*nifD*- N 14 dpi	NA	Mammalian uncoordinated homology 13, domain 2 (AHRD V3.3 *** A0A103Y0Q9_CYNCS)	
Solyc02g062510.3	5,16E-01	6,62E-02	**1,43E+00**	**1,53E-05**	-9,52E-01	1,56E-03	-2,25E-01	4,11E-01	*nifD*- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4B6D9_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc02g077360.1	5,62E-02	8,85E-01	**1,43E+00**	**1,02E-03**	5,86E-02	8,80E-01	8,87E-01	2,99E-02	*nifD*- N 14 dpi	H	Ethylene Response Factor B.2	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc10g083410.1	4,88E-01	6,98E-02	**1,43E+00**	**8,74E-06**	-2,24E-01	3,93E-01	-1,46E-01	5,77E-01	*nifD*- N 14 dpi	D	LOW QUALITY:Peptidoglycan-binding LysM domain protein (AHRD V3.3 *** A0A072VJR4_MEDTR)	
Solyc05g054470.3	9,45E-01	8,82E-03	**1,42E+00**	**2,36E-04**	-2,55E-01	4,51E-01	-1,45E+00	1,88E-04	*nifD*- N 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G28290.6)	
Solyc02g062230.1	9,77E-01	4,99E-03	**1,42E+00**	**1,40E-04**	6,38E-01	5,55E-02	3,91E-01	2,30E-01	*nifD*- N 14 dpi	H	Small auxin up-regulated RNA32	GO:0009733
Solyc11g072930.2	4,98E-01	1,74E-01	**1,42E+00**	**4,88E-04**	-1,97E+00	8,84E-06	-2,59E-01	4,74E-01	*nifD*- N 14 dpi	PMI	Leucine-rich repeat transmembrane protein kinase protein, putative (AHRD V3.3 *** A0A061GWK2_THECC)	GO:0005515
Solyc04g025040.1	1,86E-01	3,59E-01	**1,42E+00**	**1,61E-07**	-6,01E-01	5,74E-03	-4,40E-01	3,66E-02	*nifD*- N 14 dpi	RNA	Pre-mRNA splicing Prp18-interacting factor (AHRD V3.3 --* AT3G45950.1)	
Solyc12g036325.1	8,87E-01	3,07E-08	**1,42E+00**	**2,21E-12**	1,11E-01	3,38E-01	-2,58E-01	3,22E-02	*nifD*- N 14 dpi	K	Protein kinase family protein (AHRD V3.3 *** AT5G38210.3)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc10g076510.2	8,94E-02	6,31E-01	**1,41E+00**	**4,41E-08**	5,93E-02	7,50E-01	-2,55E-01	1,78E-01	*nifD*- N 14 dpi	C	Pyruvate decarboxylase (AHRD V3.3 *** Q8H9C6_SOLTU)	GO:0000287|GO:0030976|GO:0003824|GO:0030976|GO:0003824|GO:0030976
Solyc09g059473.1	4,86E-01	1,93E-02	**1,41E+00**	**1,23E-07**	-2,35E+00	4,29E-12	-1,99E+00	1,53E-10	*nifD*- N 14 dpi	D	S-norcoclaurine synthase 1 (AHRD V3.3 *** A0A061FEF4_THECC)	GO:0006952|GO:0009607
Solyc07g065390.3	7,29E-01	6,39E-02	**1,40E+00**	**9,55E-04**	6,26E-01	1,09E-01	5,03E-01	1,93E-01	*nifD*- N 14 dpi	DNA	rop guanine nucleotide exchange factor-like protein (AHRD V3.3 --* AT1G52240.1)	
Solyc12g089370.2	4,86E-01	7,82E-02	**1,40E+00**	**1,58E-05**	-1,32E+00	3,60E-05	-3,80E-01	1,63E-01	*nifD*- N 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4DH08_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744

Solyc04g074900.3	7,00E-01	1,32E-02	**1,40E+00**	**1,43E-05**	4,35E-01	1,11E-01	2,31E-03	9,93E-01	*nifD*- N 14 dpi	R	40S ribosomal protein S21 (AHRD V3.3 *** K4BU28_SOLLC)	GO:0003735|GO:0005622|GO:0005840|GO:0006412
Solyc03g093280.2	-4,37E-01	3,63E-01	**1,39E+00**	**6,66E-03**	7,99E-01	1,03E-01	8,35E-01	8,86E-02	*nifD*- N 14 dpi	2M	Aldo/keto reductase family oxidoreductase (AHRD V3.3 *** A0A072UK59_MEDTR)	GO:0016491|GO:0055114
Solyc03g111510.3	4,66E-01	9,50E-02	**1,39E+00**	**2,23E-05**	5,90E-01	3,73E-02	3,67E-01	1,84E-01	*nifD*- N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT1G13195.1)	GO:0005515|GO:0008270
Solyc01g098500.3	-3,75E-01	3,90E-01	**1,39E+00**	**3,37E-03**	-2,17E-01	6,17E-01	-9,54E-01	3,52E-02	*nifD*- N 14 dpi	TR	Sugar facilitator protein 5	GO:0005215|GO:0016021|GO:0055085|GO:0016020|GO:0022891|GO:0055085|GO:0016020|GO:0022891|GO:0055085
Solyc12g005880.2	8,13E-01	9,62E-04	**1,38E+00**	**1,07E-06**	-3,81E-01	9,25E-02	-5,56E-01	1,72E-02	*nifD*- N 14 dpi	P	Hexosyltransferase (AHRD V3.3 *** K4DBC6_SOLLC)	GO:0006486|GO:0008378|GO:0016020
Solyc06g006090.1	6,06E-01	8,68E-02	**1,38E+00**	**4,02E-04**	-2,42E-03	9,94E-01	-2,41E-01	4,86E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:JOSEPHIN-like protein, putative (AHRD V3.3 *-* A0A061GWC4_THECC)	
Solyc03g079960.3	1,10E+00	1,10E-02	**1,38E+00**	**2,01E-03**	1,40E-02	9,72E-01	-4,33E-03	9,91E-01	*nifD*- N 14 dpi	D	Pathogenesis-related thaumatin superfamily protein (AHRD V3.3 *** AT5G24620.3)	
Solyc12g006110.2	8,66E-01	1,15E-04	**1,38E+00**	**1,18E-07**	-7,25E-01	7,97E-04	-8,15E-01	2,34E-04	*nifD*- N 14 dpi	PMI	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7K0M1_MEDTR)	
Solyc06g061280.3	2,52E-01	5,50E-01	**1,38E+00**	**2,79E-03**	5,00E-01	2,41E-01	-7,88E-01	7,00E-02	*nifD*- N 14 dpi	D	Cinnamoyl-CoA reductase, putative (AHRD V3.3 *** B9S247_RICCO)	GO:0003824|GO:0050662
Solyc01g099925.1	6,17E-01	4,68E-02	**1,38E+00**	**8,52E-05**	1,42E-01	6,34E-01	-5,27E-03	9,86E-01	*nifD*- N 14 dpi	DNA	zinc finger protein 6 (AHRD V3.3 --* AT1G67030.1)	
Solyc04g078140.3	8,92E-01	1,62E-02	**1,38E+00**	**5,13E-04**	3,43E-01	3,32E-01	-4,65E-01	1,91E-01	*nifD*- N 14 dpi	E	Cytochrome B5 (AHRD V3.3 *** Q9ZSP7_PETHY)	GO:0020037
Solyc01g090120.3	5,10E-01	8,95E-04	**1,37E+00**	**1,92E-10**	-1,75E-01	2,10E-01	-2,27E-01	1,08E-01	*nifD*- N 14 dpi	E	Blue copper (AHRD V3.3 *-* A0A0B0MZW4_GOSAR)	GO:0009055
Solyc05g011970.3	8,89E-01	8,16E-07	**1,37E+00**	**2,55E-10**	-2,23E-01	1,18E-01	-6,31E-01	1,04E-04	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103XV52_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc01g098310.2	7,06E-01	1,64E-01	**1,37E+00**	**9,86E-03**	-1,36E+00	1,06E-02	-2,05E+00	3,18E-04	*nifD*- N 14 dpi	STR	DNAJ heat shock N-terminal domain-containing protein, putative (AHRD V3.3 *-* A0A061F0P5_THECC)	
Solyc04g078040.3	9,55E-01	3,85E-02	**1,37E+00**	**4,27E-03**	-1,29E-01	7,71E-01	-1,72E-01	6,98E-01	*nifD*- N 14 dpi	OX	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein (AHRD V3.3 *** AT5G43140.1)	GO:0016021
Solyc02g081445.1	9,20E-01	2,00E-03	**1,37E+00**	**2,55E-05**	-7,59E-02	7,79E-01	-2,25E-01	4,07E-01	*nifD*- N 14 dpi	CS	Cellulose synthase (AHRD V3.3 --* A0A151RTU1_CAJCA)	
Solyc00g013140.2	1,12E+00	1,86E-02	**1,37E+00**	**4,91E-03**	6,28E-01	1,69E-01	6,41E-01	1,61E-01	*nifD*- N 14 dpi	E	NADH-ubiquinone oxidoreductase chain 5 (AHRD V3.3 *** NU5M_WHEAT)	GO:0008137|GO:0042773|GO:0055114
Solyc05g005470.3	2,30E-01	3,17E-01	**1,36E+00**	**2,29E-06**	-5,43E-01	2,34E-02	-4,39E-01	6,27E-02	*nifD*- N 14 dpi	G	Nucleoredoxin 1	GO:0045454
Solyc07g009020.2	9,51E-01	1,87E-05	**1,36E+00**	**6,47E-08**	-1,15E+00	1,09E-06	-1,22E-01	5,06E-01	*nifD*- N 14 dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952
Solyc07g065940.1	6,88E-01	3,85E-02	**1,36E+00**	**2,15E-04**	-3,77E-01	2,43E-01	-2,55E-01	4,26E-01	*nifD*- N 14 dpi	NA	Transmembrane protein, putative (AHRD V3.3 *** G7K4U4_MEDTR)	
Solyc07g062100.3	2,56E-01	5,83E-01	**1,36E+00**	**6,78E-03**	4,16E-01	3,75E-01	-1,53E-01	7,42E-01	*nifD*- N 14 dpi	DNA	PHD-zinc-finger-like domain protein (AHRD V3.3 *** G7ZV42_MEDTR)	GO:0005515|GO:0005515|GO:0008270|GO:0005515|GO:0008270
Solyc11g007030.2	3,76E-01	2,02E-01	**1,35E+00**	**7,41E-05**	7,38E-01	1,64E-02	-3,19E-01	2,77E-01	*nifD*- N 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G36290.1)	
Solyc06g074360.3	9,50E-01	4,56E-03	**1,35E+00**	**1,59E-04**	7,08E-01	2,88E-02	1,50E-02	9,61E-01	*nifD*- N 14 dpi	T	TRANSPARENT TESTA 1 protein, putative (AHRD V3.3 *** B9SCR9_RICCO)	GO:0003676|GO:0046872|GO:0046872
Solyc08g066270.2	4,66E-02	9,16E-01	**1,35E+00**	**5,01E-03**	-7,54E-01	9,83E-02	-1,64E+00	9,81E-04	*nifD*- N 14 dpi	D	kinase family with leucine-rich repeat domain-containing protein (AHRD V3.3 *** AT5G25930.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g008140.3	6,81E-01	2,25E-05	**1,35E+00**	**1,55E-10**	-1,52E-01	2,59E-01	-5,89E-02	6,59E-01	*nifD*- N 14 dpi	E	Blue copper protein (AHRD V3.3 *-* A0A151SLU0_CAJCA)	GO:0009055
Solyc02g061850.3	-3,50E-02	9,23E-01	**1,34E+00**	**9,03E-04**	1,29E-01	7,21E-01	-1,04E+00	7,34E-03	*nifD*- N 14 dpi	L	Phospholipase D (AHRD V3.3 *** K4B675_SOLLC)	GO:0003824|GO:0004630|GO:0005509|GO:0016020|GO:0046470|GO:0004630|GO:0005509|GO:0016020|GO:0046470

Solyc08g007690.1	5,70E-01	2,12E-01	**1,34E+00**	**5,84E-03**	-2,65E-02	9,53E-01	-8,14E-01	7,95E-02	*nifD*- N 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)	GO:0004252|GO:0006508
Solyc03g112090.3	4,87E-01	3,05E-01	**1,34E+00**	**8,05E-03**	1,63E-01	7,29E-01	1,74E-01	7,12E-01	*nifD*- N 14 dpi	N	high-affinity nitrate transporter-like protein (AHRD V3.3 *-* AT4G24715.1)	GO:0010167|GO:0015706
Solyc11g007940.2	9,99E-01	1,14E-02	**1,33E+00**	**1,26E-03**	5,72E-01	1,31E-01	-8,91E-01	2,24E-02	*nifD*- N 14 dpi	NA	RNA-binding protein Nova-1 (AHRD V3.3 *** A0A151T0U1_CAJCA)	GO:0003676|GO:0003723|GO:0003723
Solyc07g054230.3	6,53E-01	3,17E-03	**1,33E+00**	**5,42E-07**	6,90E-01	2,00E-03	4,42E-01	3,67E-02	*nifD*- N 14 dpi	TR	Regulator of Vps4 activity in the MVB pathway protein, putative (AHRD V3.3 *** A0A061E4V2_THECC)	GO:0015031
Solyc01g105880.4	-3,29E-01	4,78E-01	**1,33E+00**	**7,48E-03**	1,05E+00	2,93E-02	-6,17E-01	1,88E-01	*nifD*- N 14 dpi	2M	Monoterpenoid synthase 2	
Solyc08g075210.2	4,59E-01	1,08E-01	**1,32E+00**	**5,80E-05**	2,93E-01	2,98E-01	-8,68E-02	7,55E-01	*nifD*- N 14 dpi	S	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G30280.1)	GO:0016747
Solyc01g105800.3	-2,65E-02	9,46E-01	**1,32E+00**	**1,96E-03**	-1,46E+00	7,97E-04	-7,08E-01	7,63E-02	*nifD*- N 14 dpi	T	MADS box transcription factor (AHRD V1 **-- Q2NNB9_ELAGV)%3B contains Interpro domain(s) IPR002100 Transcription factor%2C MADS-box	GO:0000165|GO:0000977|GO:0045944|GO:0003677|GO:0046983|GO:0003677|GO:0046983
Solyc11g056500.2	9,17E-01	3,85E-02	**1,32E+00**	**4,17E-03**	8,17E-01	6,31E-02	5,93E-01	1,70E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:OR338 (AHRD V3.3 *-* R4IUB8_VICFA)	
Solyc09g009550.3	2,04E-01	5,45E-01	**1,32E+00**	**5,13E-04**	3,05E-01	3,68E-01	-8,22E-01	2,04E-02	*nifD*- N 14 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061ETT5_THECC)	
Solyc04g011760.3	5,51E-01	2,89E-02	**1,32E+00**	**8,30E-06**	-2,96E+00	2,22E-12	-7,90E-01	2,71E-03	*nifD*- N 14 dpi	2M	Geraniol 8-hydroxylase (AHRD V3.3 --* C76B6_CATRO)	
Solyc09g075820.3	7,27E-01	4,94E-03	**1,32E+00**	**7,57E-06**	4,68E-01	5,86E-02	-2,47E-01	3,06E-01	*nifD*- N 14 dpi	TR	Sugar transporter protein 2	GO:0005215|GO:0016021|GO:0055085|GO:0016020|GO:0022891|GO:0055085|GO:0016020|GO:0022891|GO:0055085
Solyc05g006790.2	-1,41E-01	7,22E-01	**1,32E+00**	**2,40E-03**	3,59E-01	3,66E-01	3,73E-01	3,48E-01	*nifD*- N 14 dpi	CS	Actin cross-linking protein, putative (AHRD V3.3 *** A0A061E7B5_THECC)	
Solyc10g079750.2	9,24E-01	2,42E-02	**1,31E+00**	**2,16E-03**	6,51E-01	1,03E-01	2,69E-01	4,91E-01	*nifD*- N 14 dpi	T	BTB/POZ ankyrin repeat protein (AHRD V3.3 *** G8GTN4_MEDTR)	GO:0005515
Solyc03g033770.1	1,42E-01	7,03E-01	**1,31E+00**	**1,45E-03**	5,76E-02	8,77E-01	4,47E-01	2,35E-01	*nifD*- N 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT3G50940.1)	
Solyc12g100260.1	1,01E+00	1,17E-02	**1,31E+00**	**1,56E-03**	3,81E-01	3,13E-01	-2,49E-01	5,07E-01	*nifD*- N 14 dpi	2M	Fatty acid desaturase (AHRD V3.3 *-* B3SP99_CAPAN)	
Solyc03g114800.1	5,48E-01	7,39E-02	**1,31E+00**	**1,49E-04**	5,83E-01	5,85E-02	-1,04E+00	1,59E-03	*nifD*- N 14 dpi	TR	Sulfotransferase (AHRD V3.3 *** K4BKY2_SOLLC)	GO:0008146
Solyc02g092050.3	7,00E-01	7,05E-02	**1,31E+00**	**1,62E-03**	2,87E-01	4,47E-01	-1,28E+00	1,92E-03	*nifD*- N 14 dpi	H	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** A0A072VCJ1_MEDTR)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc08g078730.3	4,92E-01	1,26E-02	**1,31E+00**	**1,57E-07**	-1,90E-01	3,10E-01	4,92E-01	1,26E-02	*nifD*- N 14 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT2G35730.1)	GO:0030001|GO:0046872
Solyc11g008630.2	6,17E-01	4,13E-02	**1,30E+00**	**1,15E-04**	-1,47E+00	2,63E-05	-1,02E+00	1,56E-03	*nifD*- N 14 dpi	S	HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT1G65450.1)	GO:0016747
Solyc11g012420.2	3,43E-01	9,84E-02	**1,30E+00**	**7,04E-07**	1,73E-01	3,94E-01	1,30E-01	5,20E-01	*nifD*- N 14 dpi	H	Auxin induced-like protein (AHRD V3.3 *** A0A0K9NX81_ZOSMR)	
Solyc08g005250.3	5,61E-01	1,93E-03	**1,30E+00**	**1,94E-08**	-9,27E-01	5,46E-06	-7,47E-01	9,85E-05	*nifD*- N 14 dpi	DNA	Lysine-specific demethylase REF6 (AHRD V3.3 *-* W9R3C0_9ROSA)	
Solyc10g083180.2	5,03E-01	4,80E-03	**1,30E+00**	**2,06E-08**	-9,38E-01	4,74E-06	-8,23E-01	3,00E-05	*nifD*- N 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061EUQ7_THECC),Pfam:PF13561	GO:0016491
Solyc02g091690.3	-1,07E-01	7,67E-01	**1,29E+00**	**1,24E-03**	9,92E-01	1,00E-02	-4,38E-01	2,31E-01	*nifD*- N 14 dpi	T	bHLH transcription factor 081	GO:0046983
Solyc11g010780.1	3,46E-01	1,33E-02	**1,29E+00**	**2,77E-10**	-6,11E-02	6,43E-01	-6,53E-01	3,28E-05	*nifD*- N 14 dpi	C	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XS50_DAUCA)	GO:0008152|GO:0016758
Solyc08g075120.3	5,91E-02	8,52E-01	**1,29E+00**	**3,56E-04**	7,86E-01	1,89E-02	-4,53E-01	1,60E-01	*nifD*- N 14 dpi	DNA	Rop guanine nucleotide exchange factor, putative (AHRD V3.3 *** B9S1Q7_RICCO)	GO:0005089
Solyc12g037930.2	7,86E-01	1,19E-02	**1,28E+00**	**1,57E-04**	-4,06E-01	1,74E-01	-1,17E+00	4,49E-04	*nifD*- N 14 dpi	DNA	zinc finger (Ran-binding) family protein (AHRD V3.3 --* AT5G17790.1)	

Solyc00g005000.3	9,00E-01	2,60E-05	**1,28E+00**	**1,02E-07**	9,05E-01	2,42E-05	-7,83E-01	1,49E-04	*nifD*- N 14 dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT3G20015.1)	GO:0004190|GO:0006508
Solyc01g080770.3	6,70E-01	6,36E-04	**1,28E+00**	**7,85E-08**	4,58E-01	1,33E-02	-5,10E-01	6,58E-03	*nifD*- N 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4AXX0_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g117960.3	7,67E-01	2,34E-02	**1,28E+00**	**4,66E-04**	4,75E-01	1,48E-01	3,13E-01	3,34E-01	*nifD*- N 14 dpi	DNA	forkhead-associated domain-containing protein / FHA domain-containing protein (AHRD V3.3 *** AT5G07400.1)	GO:0003676|GO:0008270|GO:0016818|GO:0005515|GO:0005515
Solyc05g051350.2	5,59E-01	1,83E-01	**1,27E+00**	**4,40E-03**	-2,49E-01	5,47E-01	-1,53E-01	7,12E-01	*nifD*- N 14 dpi	CS	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT1G09910.1)	GO:0003824|GO:0005975|GO:0030246|GO:0030246|GO:0030246
Solyc12g011370.2	8,82E-01	2,06E-04	**1,27E+00**	**1,41E-06**	2,03E-01	3,28E-01	-3,82E-01	7,29E-02	*nifD*- N 14 dpi	AM	Cationic amino acid transporter, putative (AHRD V3.3 *** B9RY28_RICCO)	GO:0003333|GO:0015171|GO:0016020
Solyc02g091300.3	4,99E-01	2,39E-02	**1,27E+00**	**1,91E-06**	5,34E-01	1,64E-02	9,64E-03	9,63E-01	*nifD*- N 14 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A061EH84_THECC)	GO:0030001|GO:0046872
Solyc09g005690.3	8,60E-01	3,75E-04	**1,27E+00**	**2,34E-06**	-1,07E-01	6,16E-01	5,64E-02	7,91E-01	*nifD*- N 14 dpi	S	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2-like protein (AHRD V3.3 *** A0A0B0NZB0_GOSAR)	GO:0046856
Solyc10g055200.1	3,71E-01	5,70E-02	**1,27E+00**	**3,26E-07**	3,59E-01	6,46E-02	-6,72E-01	1,29E-03	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4D1B3_SOLLC)	
Solyc11g010420.2	8,29E-01	9,36E-04	**1,27E+00**	**5,36E-06**	2,11E-01	3,51E-01	-1,73E-01	4,42E-01	*nifD*- N 14 dpi	2M	Dihydrofolate reductase-like protein (AHRD V3.3 *** G7JXR7_MEDTR)	
Solyc11g011970.2	5,68E-01	4,90E-05	**1,27E+00**	**4,26E-11**	-1,14E-02	9,23E-01	-1,44E-01	2,29E-01	*nifD*- N 14 dpi	K	Tyrosine-protein phosphatase (AHRD V3.3 *** R9Q9C6_FRAVE)	GO:0004725|GO:0004725|GO:0016311|GO:0016791|GO:0004725|GO:0016311|GO:0016791
Solyc11g007150.2	9,93E-01	1,73E-04	**1,27E+00**	**7,43E-06**	-3,51E-01	1,34E-01	-3,05E-02	8,94E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:Unknown protein (AHRD V3.3)	
Solyc01g065500.3	6,41E-01	8,37E-05	**1,27E+00**	**1,28E-09**	4,89E-01	1,49E-03	-3,88E-01	9,09E-03	*nifD*- N 14 dpi	H	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein (AHRD V3.3 *** AT5G17980.1)	GO:0005515
Solyc08g066660.1	6,00E-01	4,51E-03	**1,26E+00**	**6,38E-07**	-1,45E+00	6,00E-08	-1,56E+00	1,56E-08	*nifD*- N 14 dpi	H	Ethylene-responsive transcription factor TINY (AHRD V3.3 *** TINY_ARATH)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc09g011770.3	1,28E-02	9,37E-01	**1,25E+00**	**3,23E-08**	-3,24E-01	5,45E-02	-8,44E-01	1,83E-05	*nifD*- N 14 dpi	P	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** A0A061EYJ3_THECC)	GO:0008270
Solyc04g009860.3	9,96E-01	2,51E-08	**1,25E+00**	**2,83E-10**	3,77E-01	6,10E-03	-1,15E-01	3,69E-01	*nifD*- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)	GO:0016491|GO:0055114
Solyc11g012250.1	8,02E-01	5,36E-03	**1,25E+00**	**6,98E-05**	-1,43E+00	1,20E-05	5,31E-01	5,47E-02	*nifD*- N 14 dpi	P	MBOAT (Membrane bound O-acyl transferase) family protein, putative (AHRD V3.3 *** Q2HT39_MEDTR)	GO:0008374
Solyc04g009870.1	4,69E-01	1,02E-01	**1,25E+00**	**1,26E-04**	-5,06E-01	7,88E-02	-3,67E-01	1,96E-01	*nifD*- N 14 dpi	2M	Beta-carotene hydroxylase 2, chloroplastic (AHRD V3.3 --* BCH2_CAPAN)	
Solyc12g096320.2	9,93E-01	6,87E-04	**1,25E+00**	**5,21E-05**	-5,12E-01	5,76E-02	5,51E-01	4,18E-02	*nifD*- N 14 dpi	AM	Gamma-glutamylcyclotransferase (AHRD V3.3 *** K4DHA5_SOLLC)	GO:0003839|GO:0006751
Solyc08g082990.3	8,06E-01	1,09E-06	**1,25E+00**	**3,73E-10**	-2,83E-01	3,53E-02	-3,69E-01	7,53E-03	*nifD*- N 14 dpi	TR	Oligopeptide transporter, putative (AHRD V3.3 *** B9RYS3_RICCO)	GO:0055085
Solyc08g077110.3	2,17E-01	5,84E-01	**1,24E+00**	**3,86E-03**	3,96E-01	3,22E-01	-6,31E-01	1,19E-01	*nifD*- N 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061GAH7_THECC)	GO:0003677|GO:0006355
Solyc06g071390.3	6,28E-01	1,49E-02	**1,24E+00**	**2,25E-05**	7,63E-01	3,92E-03	1,71E-01	4,85E-01	*nifD*- N 14 dpi	NA	Deleted in split hand/splt foot protein 1 (AHRD V3.3 *** D2XQ35_IPOBA)	GO:0006406|GO:0008541|GO:0043248
Solyc07g041770.1	-1,43E-01	6,22E-01	**1,24E+00**	**1,89E-04**	6,43E-01	3,30E-02	-2,66E-01	3,59E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:Membrane lipoprotein (AHRD V3.3 *** A0A061GT32_THECC)	
Solyc04g015120.3	5,33E-01	8,44E-02	**1,24E+00**	**2,98E-04**	1,78E-01	5,54E-01	2,13E-02	9,43E-01	*nifD*- N 14 dpi	P	U-box domain-containing protein 33 (AHRD V3.3 *** W9RCI3_9ROSA)	
Solyc06g075220.1	-1,59E-01	7,21E-01	**1,24E+00**	**9,30E-03**	-3,34E-01	4,56E-01	2,67E-01	5,50E-01	*nifD*- N 14 dpi	PMI	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7L2R9_MEDTR)	
Solyc11g012910.2	7,64E-01	2,51E-06	**1,24E+00**	**4,03E-10**	5,95E-01	8,08E-05	7,47E-01	3,57E-06	*nifD*- N 14 dpi	AM	Gamma-glutamylcyclotransferase (AHRD V3.3 *** K4D695_SOLLC)	GO:0003839|GO:0006751
Solyc09g072790.3	8,44E-01	3,20E-02	**1,24E+00**	**2,67E-03**	6,49E-01	9,32E-02	-8,34E-02	8,24E-01	*nifD*- N 14 dpi	G	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 *-* AT5G55550.6)	GO:0000166|GO:0003676|GO:0003676

Solyc01g008640.3	7,10E-01	5,47E-03	**1,24E+00**	**1,68E-05**	8,26E-01	1,59E-03	5,40E-01	2,93E-02	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q9AVQ2_SOLTU)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc03g096030.3	4,44E-01	1,09E-02	**1,24E+00**	**4,43E-08**	-6,79E-01	2,80E-04	-5,32E-01	2,90E-03	*nifD*- N 14 dpi	CS	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT3G55990.1)	GO:0050826
Solyc05g009470.3	3,69E-01	3,33E-01	**1,23E+00**	**2,88E-03**	-7,55E-02	8,42E-01	-9,83E-01	1,45E-02	*nifD*- N 14 dpi	C	Alpha-glucosidase (AHRD V3.3 *** Q9LEC9_SOLTU)	GO:0003824|GO:0005975|GO:0030246|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc03g094120.3	2,79E-01	4,10E-01	**1,23E+00**	**1,04E-03**	4,38E-02	8,96E-01	6,08E-01	7,96E-02	*nifD*- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** A0A164WZ41_DAUCA)	
Solyc03g025410.3	5,76E-01	2,04E-01	**1,23E+00**	**9,93E-03**	8,34E-01	7,04E-02	9,25E-01	4,64E-02	*nifD*- N 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *-* AT4G23430.2)	
Solyc02g083120.2	7,22E-01	4,01E-02	**1,23E+00**	**1,11E-03**	1,65E-01	6,25E-01	-4,73E-02	8,88E-01	*nifD*- N 14 dpi	NA	DUF241 domain protein (AHRD V3.3 *** G7LA88_MEDTR)	
Solyc01g103470.2	7,30E-01	3,41E-02	**1,23E+00**	**8,80E-04**	-9,48E-01	7,41E-03	-2,94E-01	3,75E-01	*nifD*- N 14 dpi	NA	Cytosolic Fe-S cluster assembly factor nar-1 (AHRD V3.3 *** A0A1D1Z971_9ARAE)	
Solyc04g080550.3	-1,02E-01	7,78E-01	**1,23E+00**	**2,09E-03**	6,73E-01	7,19E-02	8,34E-01	2,81E-02	*nifD*- N 14 dpi	OX	Isoflavone reductase-like protein (AHRD V3.3 *** ALL12_OLEEU)	
Solyc11g065760.2	6,93E-01	1,54E-03	**1,22E+00**	**1,31E-06**	9,61E-01	4,32E-05	5,39E-01	1,06E-02	*nifD*- N 14 dpi	K	TK1-like deoxyribonucleoside kinase	GO:0004797|GO:0005524
Solyc01g105520.3	-5,19E-02	8,89E-01	**1,22E+00**	**2,77E-03**	8,35E-01	3,24E-02	-2,65E-02	9,43E-01	*nifD*- N 14 dpi	DNA	DNA helicase (AHRD V3.3 *** I1Q0P7_ORYGL)	GO:0003677|GO:0005524|GO:0006260
Solyc05g051310.1	2,22E-01	4,30E-01	**1,22E+00**	**1,65E-04**	1,17E-01	6,77E-01	-1,40E+00	3,04E-05	*nifD*- N 14 dpi	H	LOW QUALITY:Ethylene-responsive transcription factor 5 (AHRD V3.3 *-* ERF5_NICSY)	
Solyc03g033270.3	8,60E-01	1,52E-02	**1,22E+00**	**1,08E-03**	3,76E-02	9,10E-01	6,68E-02	8,41E-01	*nifD*- N 14 dpi	C	Maltose excess protein 1-like protein (AHRD V3.3 *** S8DX10_9LAMI)	
Solyc10g083300.2	7,91E-01	2,23E-02	**1,22E+00**	**9,21E-04**	2,87E-01	3,85E-01	7,90E-01	2,23E-02	*nifD*- N 14 dpi	CS	cell-wall invertase	GO:0004553|GO:0005975
Solyc09g082270.3	6,46E-01	4,99E-04	**1,21E+00**	**6,98E-08**	4,49E-01	1,03E-02	1,24E-01	4,52E-01	*nifD*- N 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)	GO:0006869|GO:0008289
Solyc01g021600.3	6,63E-01	1,68E-02	**1,21E+00**	**8,33E-05**	5,43E-01	4,63E-02	-5,61E-01	3,99E-02	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4AV41_SOLLC)	
Solyc01g097550.3	6,44E-01	2,33E-02	**1,20E+00**	**1,30E-04**	-2,53E-01	3,51E-01	-4,57E-02	8,65E-01	*nifD*- N 14 dpi	TR	annexin 6	GO:0005509|GO:0005544
Solyc07g062220.3	3,64E-01	2,65E-01	**1,20E+00**	**8,94E-04**	-9,32E-01	7,23E-03	1,88E-01	5,60E-01	*nifD*- N 14 dpi	CS	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)	
Solyc11g012040.2	6,95E-01	8,75E-02	**1,20E+00**	**5,07E-03**	1,47E-01	7,10E-01	-1,61E-01	6,85E-01	*nifD*- N 14 dpi	P	Ubiquitin-specific protease family C19-related protein (AHRD V3.3 *** AT4G22290.1)	
Solyc06g063210.3	1,63E-01	4,54E-01	**1,20E+00**	**7,53E-06**	1,77E-01	4,17E-01	-7,14E-01	2,67E-03	*nifD*- N 14 dpi	N	glutamate receptor-like 2.5	GO:0004970|GO:0016020
Solyc01g111230.3	5,17E-01	2,41E-04	**1,20E+00**	**3,13E-10**	-4,44E-01	1,13E-03	-3,72E-01	5,05E-03	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4B3Y5_SOLLC)	
Solyc12g009820.2	6,27E-01	1,15E-01	**1,20E+00**	**4,48E-03**	-1,97E+00	2,56E-05	-2,67E+00	2,39E-07	*nifD*- N 14 dpi	G	Monogalactosyldiacylglycerol synthase (AHRD V3.3 *** G7JGJ5_MEDTR)	GO:0009247|GO:0016758|GO:0016758|GO:0016758
Solyc01g097390.3	-1,75E-02	9,60E-01	**1,20E+00**	**2,05E-03**	5,62E-01	1,19E-01	-4,46E-01	2,13E-01	*nifD*- N 14 dpi	E	NAD(P)-linked oxidoreductase superfamily protein (AHRD V3.3 *** A0A061F182_THECC)	
Solyc08g078870.2	4,98E-01	1,56E-02	**1,19E+00**	**1,59E-06**	2,87E-01	1,47E-01	7,72E-01	4,60E-04	*nifD*- N 14 dpi	CS	14 kDa proline-rich protein DC2.15, putative (AHRD V3.3 *** B9RD76_RICCO)	
Solyc01g110340.3	7,91E-01	1,07E-02	**1,19E+00**	**3,28E-04**	1,57E-01	5,89E-01	-3,74E-01	2,04E-01	*nifD*- N 14 dpi	CS	Endoglucanase (AHRD V3.3 *** M0ZU30_SOLTU)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc12g009930.2	5,34E-01	2,05E-02	**1,19E+00**	**9,46E-06**	9,21E-01	2,44E-04	-1,13E+00	1,84E-05	*nifD*- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DC81_SOLLC)	GO:0008152|GO:0016758
Solyc10g038080.2	2,67E-01	9,15E-02	**1,19E+00**	**3,06E-08**	-5,27E-01	1,90E-03	-4,18E-01	1,09E-02	*nifD*- N 14 dpi	C	Shikimate dehydrogenase, 3-dehydroquinate dehydratase (AHRD V3.3 *** A0A0K9PLS3_ZOSMR)	GO:0003824|GO:0003855|GO:0003855

Solyc04g076660.3	5,19E-01	9,49E-02	**1,19E+00**	**5,20E-04**	1,10E-02	9,71E-01	-2,16E-01	4,78E-01	*nifD*- N 14 dpi	CS	Rhamnogalacturonate lyase family protein (AHRD V3.3 *** AT1G09910.1)	GO:0003824|GO:0005975|GO:0030246|GO:0030246|GO:0030246
Solyc01g104770.3	6,44E-01	6,96E-02	**1,19E+00**	**1,78E-03**	9,05E-01	1,32E-02	6,37E-01	7,23E-02	*nifD*- N 14 dpi	T	transcription factor (AHRD V3.3 *** AT1G76870.3)	
Solyc11g007620.1	5,24E-01	2,14E-01	**1,18E+00**	**7,92E-03**	4,71E-01	2,62E-01	8,95E-01	3,86E-02	*nifD*- N 14 dpi	P	F-box family protein (AHRD V3.3 *** D7L723_ARALL)	GO:0005515
Solyc04g079830.2	7,90E-01	1,46E-05	**1,18E+00**	**2,04E-08**	-3,77E-01	1,72E-02	-4,02E-01	1,17E-02	*nifD*- N 14 dpi	T	BEL1-like homeodomain protein 2 (AHRD V3.3 *** A0A0B2SBB1_GLYSO)	GO:0003677|GO:0003677|GO:0006355|GO:0003677|GO:0006355
Solyc01g006060.3	-7,04E-02	8,10E-01	**1,18E+00**	**4,03E-04**	2,72E-01	3,57E-01	-3,70E-01	2,14E-01	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4ASH2_SOLLC)	
Solyc02g078570.3	6,48E-01	4,07E-06	**1,18E+00**	**7,51E-11**	-4,22E-02	7,08E-01	-2,09E-01	7,16E-02	*nifD*- N 14 dpi	CS	Epoxide hydrolase (AHRD V3.3 *** I3SWK6_MEDTR)	GO:0003824
Solyc01g110060.3	2,93E-01	2,01E-01	**1,18E+00**	**1,76E-05**	2,85E-01	2,14E-01	4,12E-01	7,67E-02	*nifD*- N 14 dpi	G	Purple acid phosphatase (AHRD V3.3 *** A0A0V0IAA9_SOLCH)	GO:0003993|GO:0046872|GO:0016787|GO:0016787
Solyc02g069250.3	1,07E+00	1,06E-02	**1,17E+00**	**5,46E-03**	5,01E-01	2,07E-01	-4,97E-01	2,10E-01	*nifD*- N 14 dpi	CS	Cinnamyl alcohol dehydrogenase (AHRD V3.3 *** A0A1B0YY99_DAUCA)	GO:0008270|GO:0016491|GO:0055114|GO:0016491|GO:0016491
Solyc06g072060.1	4,29E-01	2,81E-01	**1,17E+00**	**5,69E-03**	-8,73E-01	3,37E-02	-3,27E-01	4,08E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:transmembrane protein, putative (DUF 3339) (AHRD V3.3 *** AT5G08391.1)	
Solyc03g115890.3	-1,14E-01	6,62E-01	**1,17E+00**	**1,16E-04**	-3,21E-01	2,24E-01	-1,56E+00	2,32E-06	*nifD*- N 14 dpi	CS	expansin 10	GO:0005576|GO:0009664|GO:0009664
Solyc07g008590.1	6,19E-01	9,85E-02	**1,17E+00**	**3,27E-03**	8,90E-01	2,07E-02	2,42E-01	5,09E-01	*nifD*- N 14 dpi	PMI	LOW QUALITY:Leucine-rich receptor-like kinase family protein (AHRD V3.3 *** G7K7L1_MEDTR)	GO:0005515
Solyc12g100270.2	9,90E-01	1,05E-04	**1,17E+00**	**1,23E-05**	5,53E-01	1,68E-02	-1,55E-01	4,81E-01	*nifD*- N 14 dpi	L	Fatty acid hydroxylase superfamily (AHRD V3.3 *** AT1G02205.2)	GO:0005506|GO:0006633|GO:0016491|GO:0055114
Solyc09g011670.3	8,05E-01	8,34E-04	**1,16E+00**	**9,99E-06**	1,51E-01	4,85E-01	5,55E-01	1,49E-02	*nifD*- N 14 dpi	DNA	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G53990.1)	GO:0006950
Solyc06g036430.3	6,08E-01	3,49E-04	**1,16E+00**	**2,56E-08**	5,68E-01	7,09E-04	6,91E-01	8,10E-05	*nifD*- N 14 dpi	D	Reticulon-like protein (AHRD V3.3 *** K4C509_SOLLC)	
Solyc09g090550.3	5,21E-01	1,26E-01	**1,16E+00**	**1,63E-03**	1,06E-01	7,50E-01	4,52E-01	1,82E-01	*nifD*- N 14 dpi	NA	Actin-related protein 2/3 complex subunit 2 (AHRD V3.3 *** A0A061EMV9_THECC)	GO:0005885|GO:0015629|GO:0030833|GO:0034314
Solyc02g067190.3	4,05E-01	3,01E-01	**1,16E+00**	**5,72E-03**	-2,28E+00	2,96E-06	-1,37E+00	1,41E-03	*nifD*- N 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4B751_SOLLC)	
Solyc01g109880.3	4,23E-01	6,78E-02	**1,16E+00**	**1,97E-05**	1,72E-01	4,46E-01	-1,34E+00	2,38E-06	*nifD*- N 14 dpi	T	BZIP transcription factor (AHRD V3.3 *** C0KYN1_SOLLC)	GO:0003700|GO:0006355|GO:0043565
Solyc08g077840.3	9,08E-01	2,75E-05	**1,16E+00**	**7,51E-07**	3,04E-01	1,01E-01	-2,49E-01	1,75E-01	*nifD*- N 14 dpi	N	ureidoglycine aminohydrolase (AHRD V3.3 *** AT4G17050.1)	
Solyc11g007330.2	2,30E-01	4,74E-01	**1,16E+00**	**1,18E-03**	-4,50E-01	1,68E-01	-1,90E-01	5,54E-01	*nifD*- N 14 dpi	S	RAB6-interacting golgin (DUF662) (AHRD V3.3 *** AT2G27740.1)	
Solyc11g012320.2	7,46E-01	9,50E-08	**1,16E+00**	**1,68E-11**	5,78E-01	5,89E-06	5,91E-01	4,26E-06	*nifD*- N 14 dpi	P	SKP1-like 12 (AHRD V3.3 --* AT4G34470.1)	
Solyc07g055080.3	5,40E-01	1,42E-04	**1,15E+00**	**6,25E-10**	4,90E-01	4,20E-04	-9,45E-02	4,42E-01	*nifD*- N 14 dpi	STR	Proteasome subunit alpha type (AHRD V3.3 *** K4CG47_SOLLC)	GO:0004175|GO:0006511|GO:0019773|GO:0004298|GO:0004298
Solyc10g047540.2	7,97E-01	3,99E-02	**1,15E+00**	**4,30E-03**	-1,52E-01	6,83E-01	8,25E-01	3,38E-02	*nifD*- N 14 dpi	DNA	Basic helix loop helix protein, putative (AHRD V3.3 *-* A0A072TTF3_MEDTR)	
Solyc06g073610.3	2,69E-01	3,04E-01	**1,15E+00**	**1,33E-04**	1,21E-01	6,40E-01	-2,81E-01	2,83E-01	*nifD*- N 14 dpi	G	cyclin B1	GO:0005634
Solyc08g074682.1	9,40E-01	1,83E-02	**1,15E+00**	**4,86E-03**	-5,90E-02	8,76E-01	6,40E-01	9,81E-02	*nifD*- N 14 dpi	2M	polyphenol oxidase precursor	GO:0004097|GO:0046148|GO:0055114|GO:0004097|GO:0055114|GO:0004097|GO:0055114
Solyc04g074740.3	7,15E-02	6,20E-01	**1,15E+00**	**1,70E-08**	-4,85E-01	2,20E-03	-8,84E-01	1,55E-06	*nifD*- N 14 dpi	E	Blue copper protein, putative (AHRD V3.3 *** B9RJR1_RICCO)	GO:0009055
Solyc01g097340.3	3,93E-01	7,36E-02	**1,15E+00**	**1,12E-05**	-2,04E-01	3,42E-01	-1,19E+00	6,73E-06	*nifD*- N 14 dpi	2M	GDP-mannose 3',5'-epimerase (AHRD V3.3 *** C6K2K9_SOLLC)	GO:0003824|GO:0050662|GO:0047918|GO:0051287|GO:0047918|GO:0051287
Solyc08g021820.3	2,53E-01	5,09E-01	**1,14E+00**	**5,47E-03**	1,02E+00	1,22E-02	-6,87E-01	8,02E-02	*nifD*- N 14 dpi	H	auxin-regulated IAA29	GO:0005515|GO:0005634|GO:0006355|GO:0005634|GO:0006355

Solyc04g074390.3	5,43E-01	9,89E-02	**1,14E+00**	**1,32E-03**	-3,88E-01	2,32E-01	-8,97E-01	8,97E-03	*nifD*- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** M1D1E1_SOLTU)	GO:0008152|GO:0016758
Solyc10g008890.3	6,12E-01	2,52E-02	**1,14E+00**	**1,51E-04**	5,80E-01	3,30E-02	3,64E-01	1,69E-01	*nifD*- N 14 dpi	NA	Optic atrophy 3 protein (OPA3) (AHRD V3.3 *** AT1G28510.1)	
Solyc04g079990.3	-7,64E-01	2,02E-02	**1,14E+00**	**1,02E-03**	6,62E-01	4,16E-02	-6,16E-01	5,65E-02	*nifD*- N 14 dpi	DNA	DNA-3-methyladenine glycosylase, putative (AHRD V3.3 *** A0A061FDE4_THECC)	GO:0003824|GO:0006281|GO:0006284|GO:0008725|GO:0006284|GO:0008725
Solyc05g007450.3	4,64E-01	2,54E-01	**1,14E+00**	**7,94E-03**	5,50E-01	1,78E-01	-1,72E-03	9,97E-01	*nifD*- N 14 dpi	DNA	Origin recognition complex, subunit 6 (AHRD V3.3 *** A0A118K386_CYNCS)	GO:0003677|GO:0005664|GO:0006260|GO:0005664|GO:0006260|GO:0005664|GO:0006260
Solyc05g052680.1	7,25E-01	1,25E-02	**1,14E+00**	**2,57E-04**	-1,07E+00	5,29E-04	-6,48E-01	2,38E-02	*nifD*- N 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT2G39980.1)	GO:0016747
Solyc05g054430.3	-2,10E-01	5,53E-01	**1,14E+00**	**3,18E-03**	7,91E-01	3,25E-02	-7,73E-02	8,27E-01	*nifD*- N 14 dpi	DNA	DNA replication complex GINS protein PSF2 (AHRD V3.3 *** K4C2C1_SOLLC)	GO:0005634|GO:0006260
Solyc02g076740.2	6,01E-01	5,40E-02	**1,13E+00**	**7,79E-04**	4,00E-01	1,91E-01	-6,37E-01	4,22E-02	*nifD*- N 14 dpi	STR	Late embryogenesis abundant protein (LEA) family protein (AHRD V3.3 --* AT5G44310.2)	
Solyc10g044880.1	5,45E-01	1,28E-01	**1,13E+00**	**3,07E-03**	-1,70E-01	6,28E-01	-8,46E-02	8,09E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:oxidoreductase/transition metal ion-binding protein (AHRD V3.3 *** AT2G31940.1)	
Solyc07g065400.3	9,66E-01	1,62E-02	**1,13E+00**	**5,67E-03**	3,00E-01	4,31E-01	6,82E-01	8,09E-02	*nifD*- N 14 dpi	TR	Mitochondrial import inner membrane translocase subunit TIM50-C (AHRD V1 *-*- D3TQJ3_GLOMM)	
Solyc04g078620.3	7,52E-01	3,49E-07	**1,13E+00**	**1,55E-10**	4,34E-01	5,86E-04	-6,15E-02	5,83E-01	*nifD*- N 14 dpi	S	Ubiquitin-conjugating enzyme family protein (AHRD V3.3 *** A9PAA6_POPTR)	
Solyc01g073670.3	3,34E-01	1,52E-01	**1,13E+00**	**3,52E-05**	3,90E-01	9,63E-02	-6,57E-01	7,41E-03	*nifD*- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT3G60070.5),Pfam:PF13347	
Solyc10g005950.3	5,81E-01	1,16E-02	**1,13E+00**	**1,68E-05**	7,40E-01	1,88E-03	-2,70E-02	9,00E-01	*nifD*- N 14 dpi	DNA	Nudix hydrolase (AHRD V3.3 *** A0A061F5Q1_THECC)	GO:0016787
Solyc04g040180.3	5,58E-01	1,17E-03	**1,13E+00**	**8,62E-08**	8,36E-01	1,00E-05	8,07E-01	1,66E-05	*nifD*- N 14 dpi	H	S-adenosylmethionine-dependent methyltransferase, putative (AHRD V3.3 *** B9SZS6_RICCO)	GO:0008152|GO:0008168
Solyc02g062463.1	1,11E-01	5,93E-01	**1,12E+00**	**1,06E-05**	5,96E-01	7,58E-03	-1,12E-02	9,57E-01	*nifD*- N 14 dpi	E	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)	GO:0016491|GO:0055114
Solyc10g080970.2	9,55E-01	8,37E-12	**1,12E+00**	**2,32E-13**	1,86E-01	3,13E-02	2,08E-01	1,69E-02	*nifD*- N 14 dpi	STR	Methylenetetrahydrofolate dehydrogenase, putative (AHRD V3.3 *** B9T0V4_RICCO)	GO:0003824|GO:0004488|GO:0009396|GO:0055114|GO:0003824|GO:0009396|GO:0055114|GO:0003824|GO:0009396|GO:0055114
Solyc04g072450.3	9,85E-01	1,21E-10	**1,12E+00**	**7,41E-12**	3,80E-02	6,93E-01	-1,41E-01	1,51E-01	*nifD*- N 14 dpi	DNA	Zinc finger CCCH domain-containing protein 54 (AHRD V3.3 --* C3H54_ORYSJ)	
Solyc04g014510.3	-8,40E-02	7,77E-01	**1,12E+00**	**7,66E-04**	5,26E-01	8,53E-02	1,65E-01	5,79E-01	*nifD*- N 14 dpi	N	glutamine synthase	GO:0003824|GO:0004356|GO:0006542|GO:0006807|GO:0004356|GO:0006542|GO:0006807
Solyc02g079010.3	4,08E-01	1,05E-01	**1,12E+00**	**9,78E-05**	-3,99E-01	1,13E-01	-2,35E-01	3,42E-01	*nifD*- N 14 dpi	NA	Cotton fiber expressed protein (AHRD V3.3 *** A0A109Y892_GOSBA)	
Solyc08g078300.3	6,40E-01	1,70E-03	**1,12E+00**	**1,96E-06**	3,24E-01	8,80E-02	-1,32E+00	1,16E-07	*nifD*- N 14 dpi	DNA	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9MUS1_POPTR)	GO:0003677|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565
Solyc07g005910.3	6,80E-01	4,21E-02	**1,12E+00**	**1,68E-03**	2,58E-01	4,24E-01	5,18E-02	8,72E-01	*nifD*- N 14 dpi	NA	zein-binding protein (Protein of unknown function, DUF593) (AHRD V3.3 *** AT5G57830.1)	
Solyc03g119210.1	3,46E-01	3,73E-02	**1,11E+00**	**1,85E-07**	5,48E-01	1,81E-03	9,37E-02	5,57E-01	*nifD*- N 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** S4TID2_GOSHI)	GO:0006869
Solyc01g108740.3	8,26E-01	1,19E-04	**1,11E+00**	**2,17E-06**	-1,75E+00	5,25E-10	-2,36E-01	2,06E-01	*nifD*- N 14 dpi	H	Methyl esterase (AHRD V3.3 *** A0A072UEL6_MEDTR)	
Solyc06g054290.2	-6,26E-01	1,01E-01	**1,11E+00**	**5,83E-03**	-1,41E+00	7,07E-04	-1,05E+00	8,10E-03	*nifD*- N 14 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EKQ6_THECC)	GO:0008152|GO:0016787
Solyc01g109610.3	7,87E-01	4,10E-03	**1,10E+00**	**1,63E-04**	7,16E-01	8,17E-03	-4,07E-01	1,16E-01	*nifD*- N 14 dpi	2M	Erythronate-4-phosphate dehydrogenase family protein (AHRD V3.3 *** G7JG61_MEDTR)	
Solyc04g078660.1	3,68E-01	2,63E-03	**1,10E+00**	**2,60E-10**	-1,45E+00	6,47E-13	-1,29E+00	8,46E-12	*nifD*- N 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT5G42830.1)	GO:0016747
Solyc06g007960.3	9,38E-01	3,03E-03	**1,10E+00**	**7,21E-04**	-3,47E-01	2,36E-01	-1,25E+00	1,82E-04	*nifD*- N 14 dpi	2M	Caffeic O-methyltransferase (AHRD V3.3 *** A0A068FLE8_PUNGR)	GO:0008168|GO:0008171|GO:0008171

Solyc08g078930.1	2,05E-01	2,34E-01	**1,10E+00**	**6,63E-07**	-1,22E+00	1,11E-07	-1,05E+00	1,48E-06	*nifD*- N 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT4G12520.1)	
Solyc08g081400.3	5,72E-01	9,69E-03	**1,10E+00**	**1,35E-05**	-1,80E-02	9,31E-01	-4,27E-01	4,71E-02	*nifD*- N 14 dpi	T	Homeobox protein BEL1 like (AHRD V3.3 *-* A0A0B2QVN2_GLYSO)	
Solyc09g083400.3	3,59E-01	1,59E-02	**1,10E+00**	**2,57E-08**	-9,13E-01	6,25E-07	-1,03E+00	8,29E-08	*nifD*- N 14 dpi	CS	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT3G23090.4)	
Solyc03g033730.1	4,83E-01	3,95E-02	**1,10E+00**	**4,21E-05**	-1,77E-01	4,34E-01	-1,14E-01	6,12E-01	*nifD*- N 14 dpi	T	LOW QUALITY:BZIP transcription factor (AHRD V3.3 *** C0KYN1_SOLLC)	GO:0003700|GO:0006355|GO:0043565
Solyc07g052910.3	8,51E-01	7,18E-03	**1,09E+00**	**8,88E-04**	-1,13E-01	7,02E-01	1,64E-01	5,79E-01	*nifD*- N 14 dpi	NA	transmembrane protein, putative (DUF1218) (AHRD V3.3 *** AT4G21310.1)	
Solyc02g014830.3	1,57E-01	6,47E-01	**1,09E+00**	**3,41E-03**	-1,20E+00	1,56E-03	-1,68E-02	9,61E-01	*nifD*- N 14 dpi	STR	Carboxypeptidase (AHRD V3.3 *** K4B4T2_SOLLC)	GO:0004185|GO:0006508
Solyc07g065090.2	4,55E-01	3,62E-02	**1,09E+00**	**1,51E-05**	6,95E-01	2,33E-03	6,36E-01	4,71E-03	*nifD*- N 14 dpi	D	polygalacturonase inhibitor protein	GO:0005515
Solyc05g007940.3	3,96E-01	1,50E-01	**1,09E+00**	**3,75E-04**	-1,63E-01	5,47E-01	3,28E-02	9,03E-01	*nifD*- N 14 dpi	RNA	LERNALX L.esculentum ribonuclease lx	GO:0003723|GO:0033897
Solyc01g007130.3	4,65E-01	1,89E-02	**1,09E+00**	**3,44E-06**	6,45E-03	9,73E-01	-1,02E+00	9,21E-06	*nifD*- N 14 dpi	S	Receptor-like protein kinase (AHRD V3.3 *** Q58JF6_SOLPI)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g114750.3	3,86E-01	2,96E-03	**1,09E+00**	**1,15E-09**	-1,67E+00	1,19E-13	-1,24E+00	8,04E-11	*nifD*- N 14 dpi	CS	18S pre-ribosomal assembly protein gar2-like protein (AHRD V3.3 *-* AT2G03810.7)	
Solyc09g089890.1	8,88E-02	7,00E-01	**1,09E+00**	**6,08E-05**	-2,93E-02	8,99E-01	-5,74E-01	1,82E-02	*nifD*- N 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** A0A061EMD3_THECC)	GO:0005515|GO:0008270
Solyc04g026030.3	4,04E-01	6,54E-02	**1,09E+00**	**2,13E-05**	-1,61E-01	4,51E-01	-7,56E-01	1,32E-03	*nifD*- N 14 dpi	N	Spermidine synthase (AHRD V3.3 *** SPDE_NICSY)	GO:0003824|GO:0006595|GO:0006595
Solyc04g048900.3	7,61E-01	4,48E-05	**1,09E+00**	**2,08E-07**	1,96E-01	2,19E-01	-6,03E-01	6,45E-04	*nifD*- N 14 dpi	P	Calreticulin (AHRD V3.3 *** G7KRL3_MEDTR)	GO:0005509|GO:0005509|GO:0005515|GO:0005509|GO:0005515
Solyc10g076940.2	4,02E-01	2,13E-01	**1,09E+00**	**1,95E-03**	8,03E-01	1,70E-02	-2,51E-01	4,31E-01	*nifD*- N 14 dpi	NA	Protein zinc induced facilitator-like 1 (AHRD V3.3 *** A0A0B0NBA1_GOSAR)	GO:0016021|GO:0055085
Solyc11g012710.2	9,23E-01	1,53E-06	**1,08E+00**	**1,03E-07**	4,80E-01	3,44E-03	-2,05E-01	1,80E-01	*nifD*- N 14 dpi	C	SNF1-related protein kinase regulatory subunit beta-2 (AHRD V3.3 *** AT4G16360.1)	GO:0005515|GO:0009744|GO:0043562|GO:0009744|GO:0043562
Solyc12g015920.2	3,53E-01	1,05E-01	**1,08E+00**	**2,24E-05**	-9,86E-01	7,73E-05	2,06E-01	3,35E-01	*nifD*- N 14 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-* AT5G48290.1)	
Solyc09g091430.3	8,26E-02	7,59E-01	**1,08E+00**	**4,00E-04**	2,02E-02	9,40E-01	-8,82E-01	2,74E-03	*nifD*- N 14 dpi	CS	Pectate lyase (AHRD V3.3 *** M1CWG5_SOLTU)	
Solyc01g109390.3	-1,63E-01	6,64E-01	**1,08E+00**	**7,29E-03**	-1,74E+00	7,66E-05	3,95E-02	9,16E-01	*nifD*- N 14 dpi	NA	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MM18_ARALL)	
Solyc02g070540.3	1,19E-01	5,82E-01	**1,08E+00**	**3,07E-05**	7,90E-01	1,05E-03	-4,39E-01	5,06E-02	*nifD*- N 14 dpi	P	carbohydrate binding domain-containing protein	
Solyc10g006500.3	2,56E-01	4,88E-01	**1,08E+00**	**6,37E-03**	6,84E-01	7,12E-02	8,88E-01	2,18E-02	*nifD*- N 14 dpi	P	Hexosyltransferase (AHRD V3.3 *** K4CXI1_SOLLC)	GO:0016757|GO:0047262|GO:0047262
Solyc11g069390.1	-4,08E-01	2,94E-01	**1,08E+00**	**8,80E-03**	-6,40E-01	1,05E-01	3,76E-02	9,22E-01	*nifD*- N 14 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT3G45230.1)	
Solyc03g005200.3	1,68E-02	9,46E-01	**1,08E+00**	**1,57E-04**	-4,30E-01	8,99E-02	1,92E-01	4,39E-01	*nifD*- N 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)	GO:0006869|GO:0008289
Solyc02g030170.3	8,01E-01	1,90E-09	**1,08E+00**	**3,79E-12**	-3,89E-01	1,75E-04	1,88E-01	4,40E-02	*nifD*- N 14 dpi	2M	DWARF1/DIMINUTO	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0016491|GO:0050660|GO:0055114|GO:0016491|GO:0050660|GO:0055114
Solyc04g006960.3	3,68E-01	1,45E-01	**1,08E+00**	**1,70E-04**	3,47E-01	1,69E-01	-1,28E+00	1,87E-05	*nifD*- N 14 dpi	TR	ABC transporter family protein (AHRD V3.3 *** A0A097P9T3_HEVBR)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc05g008620.3	6,83E-02	8,15E-01	**1,08E+00**	**9,62E-04**	9,06E-01	4,29E-03	5,61E-01	6,35E-02	*nifD*- N 14 dpi	DNA	DNA replication complex GINS protein psf3 (AHRD V3.3 *** A0A061FM87_THECC)	
Solyc03g115660.3	-1,94E-02	9,33E-01	**1,08E+00**	**7,05E-05**	-3,69E-02	8,73E-01	-6,35E-01	9,80E-03	*nifD*- N 14 dpi	K	Protein kinase superfamily protein (AHRD V3.3 *** AT1G18670.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468

Solyc03g019790.3	4,77E-01	1,23E-02	**1,07E+00**	**2,23E-06**	-1,45E-01	4,22E-01	-3,92E-01	3,61E-02	*nifD*- N 14 dpi	C	alpha-galactosidase	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc10g078470.2	3,52E-01	1,32E-01	**1,07E+00**	**6,90E-05**	-6,77E-02	7,67E-01	-7,22E-02	7,52E-01	*nifD*- N 14 dpi	AM	Tryptophan/tyrosine permease (AHRD V3.3 *** AT2G33260.2)	GO:0003333|GO:0005887|GO:0015173|GO:0015801|GO:0005887|GO:0015173|GO:0015801
Solyc03g114760.3	9,11E-01	5,14E-04	**1,07E+00**	**8,18E-05**	-8,40E-01	1,14E-03	-9,76E-01	2,45E-04	*nifD*- N 14 dpi	D	movement protein binding protein 2C (AHRD V3.3 *** AT5G08120.1)	
Solyc07g009050.3	8,39E-01	3,62E-04	**1,07E+00**	**1,83E-05**	-2,30E+00	2,08E-11	-7,00E-01	2,07E-03	*nifD*- N 14 dpi	D	Defensin-like protein, putative (AHRD V3.3 *** A0A061E6R0_THECC)	GO:0006952
Solyc04g081990.3	8,54E-01	3,73E-06	**1,07E+00**	**9,23E-08**	4,94E-01	2,26E-03	-3,13E-01	4,17E-02	*nifD*- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT5G42210.1)	GO:0005215|GO:0016021|GO:0055085|GO:0016021|GO:0055085
Solyc01g005000.3	7,78E-01	3,61E-02	**1,07E+00**	**5,35E-03**	-7,05E-01	5,56E-02	-8,71E-01	2,02E-02	*nifD*- N 14 dpi	N	Glutamate decarboxylase (AHRD V3.3 *** B1Q3F2_SOLLC)	GO:0003824|GO:0004351|GO:0006536|GO:0030170|GO:0004351|GO:0006536|GO:0030170
Solyc06g054070.3	5,65E-01	1,56E-02	**1,07E+00**	**4,60E-05**	4,94E-01	3,22E-02	4,66E-01	4,20E-02	*nifD*- N 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** G7K520_MEDTR)	
Solyc02g079170.3	7,75E-01	2,11E-04	**1,07E+00**	**3,11E-06**	1,74E-01	3,41E-01	5,52E-02	7,61E-01	*nifD*- N 14 dpi	E	External alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial (AHRD V3.3 *** NDB2_ARATH)	GO:0005509|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc02g092450.3	-1,43E+00	8,89E-04	**1,07E+00**	**9,40E-03**	6,72E-01	8,85E-02	-5,09E-02	8,94E-01	*nifD*- N 14 dpi	TR	Calcium-transporting ATPase (AHRD V3.3 *** M1BXI4_SOLTU)	GO:0000166|GO:0000166|GO:0046872|GO:0000166|GO:0046872
Solyc03g097650.3	7,47E-01	4,60E-03	**1,07E+00**	**1,57E-04**	1,81E-01	4,58E-01	-9,35E-01	6,43E-04	*nifD*- N 14 dpi	T	NAC domain protein (AHRD V3.3 *** B2ZGQ7_SOYBN)	GO:0003677|GO:0006355
Solyc01g100370.3	7,05E-01	9,49E-04	**1,06E+00**	**6,78E-06**	-4,35E-01	2,95E-02	5,04E-01	1,30E-02	*nifD*- N 14 dpi	DNA	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G62550.1)	GO:0006950
Solyc05g005080.3	5,99E-01	2,67E-04	**1,06E+00**	**6,65E-08**	-5,61E-01	5,43E-04	-7,54E-01	1,53E-05	*nifD*- N 14 dpi	CS	Endo-1,4-beta-glucanase	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc05g051660.1	9,27E-01	3,18E-06	**1,06E+00**	**3,74E-07**	3,56E-01	3,15E-02	-2,94E-01	7,21E-02	*nifD*- N 14 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061EKQ6_THECC)	GO:0008152|GO:0016787
Solyc02g089250.3	-3,24E-01	2,96E-01	**1,06E+00**	**1,79E-03**	3,59E-02	9,07E-01	-5,44E-01	8,48E-02	*nifD*- N 14 dpi	G	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *** A0A061EFL6_THECC)	
Solyc10g081770.2	7,08E-01	2,84E-02	**1,06E+00**	**1,89E-03**	4,75E-01	1,32E-01	3,66E-01	2,42E-01	*nifD*- N 14 dpi	TR	polyketide cyclase/dehydrase/lipid transport superfamily protein (AHRD V3.3 *** AT5G06440.3)	
Solyc11g042420.2	6,67E-01	1,82E-02	**1,06E+00**	**4,85E-04**	1,35E-01	6,15E-01	2,14E-01	4,25E-01	*nifD*- N 14 dpi	E	Cytochrome c (AHRD V3.3 *** CYC_SOLTU)	GO:0009055|GO:0020037
Solyc02g063160.3	9,68E-01	1,25E-07	**1,05E+00**	**2,70E-08**	1,26E-01	3,58E-01	4,49E-01	2,53E-03	*nifD*- N 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT5G16120.4)	
Solyc12g005030.2	9,17E-01	2,36E-03	**1,05E+00**	**6,55E-04**	-5,89E-01	3,97E-02	-8,95E-01	2,88E-03	*nifD*- N 14 dpi	K	Protein kinase (AHRD V3.3 *** Q9AR92_MEDSA)	GO:0004672|GO:0005524|GO:0006468|GO:0005524|GO:0005524
Solyc10g017570.3	3,97E-01	9,71E-03	**1,05E+00**	**7,76E-08**	3,10E-01	3,83E-02	6,10E-01	2,22E-04	*nifD*- N 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G61220.1)	
Solyc08g074690.3	2,93E-01	4,44E-01	**1,05E+00**	**9,78E-03**	-9,04E-01	2,40E-02	9,24E-01	2,14E-02	*nifD*- N 14 dpi	2M	Polyphenol oxidase (AHRD V3.3 *** J7ES67_NICBE)	GO:0004097|GO:0046148|GO:0055114|GO:0004097|GO:0055114|GO:0004097|GO:0055114
Solyc02g069260.3	3,86E-01	3,72E-02	**1,05E+00**	**2,75E-06**	8,16E-01	8,86E-05	3,16E-02	8,59E-01	*nifD*- N 14 dpi	RNA	Argonaute2a	GO:0003676|GO:0005515|GO:0005515
Solyc02g032030.1	-2,69E-03	9,86E-01	**1,05E+00**	**2,12E-07**	-1,34E+00	2,39E-09	-1,12E+00	6,52E-08	*nifD*- N 14 dpi	CS	Dirigent protein (AHRD V3.3 *** K4B5E9_SOLLC)	
Solyc11g005840.2	4,40E-01	1,90E-03	**1,05E+00**	**1,11E-08**	2,64E-01	4,81E-02	-1,18E-01	3,63E-01	*nifD*- N 14 dpi	AM	Cysteine desulfurase (AHRD V3.3 *** A0A0K9Q199_ZOSMR)	GO:0003824
Solyc02g089480.1	2,06E-01	5,43E-01	**1,05E+00**	**4,34E-03**	-3,69E-01	2,80E-01	-3,73E-01	2,76E-01	*nifD*- N 14 dpi	AM	Glutamine dumper 2, putative (AHRD V3.3 *** A0A061ENI6_THECC)	
Solyc01g080910.2	1,66E-01	5,48E-01	**1,05E+00**	**7,35E-04**	3,73E-01	1,84E-01	-4,16E-01	1,40E-01	*nifD*- N 14 dpi	RNA	LOW QUALITY:polyadenylate-binding protein 1-B-binding protein (AHRD V3.3 *** AT4G19950.1)	
Solyc04g074820.2	5,03E-01	9,69E-02	**1,04E+00**	**1,41E-03**	-3,53E-01	2,37E-01	-9,88E-01	2,29E-03	*nifD*- N 14 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061FLH6_THECC)	GO:0005515|GO:0008270

Solyc03g112840.2	1,32E-01	6,54E-01	**1,04E+00**	**1,43E-03**	-9,29E-01	3,67E-03	-4,74E-01	1,15E-01	*nifD*- N 14 dpi	NA	Transmembrane protein, putative (AHRD V3.3 *** G7J5E4_MEDTR)	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
Solyc04g008730.3	7,93E-01	8,19E-05	**1,04E+00**	**1,93E-06**	1,57E-01	3,63E-01	-4,51E-01	1,34E-02	*nifD*- N 14 dpi	C	Alpha-galactosidase (AHRD V3.3 *** K4BP29_SOLLC)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc01g073680.3	1,09E-02	9,56E-01	**1,04E+00**	**1,35E-05**	7,20E-01	9,77E-04	-3,11E-01	1,21E-01	*nifD*- N 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** A0A072TPI6_MEDTR)	
Solyc02g036300.3	8,94E-01	1,63E-03	**1,04E+00**	**3,88E-04**	-7,60E-01	6,04E-03	-3,42E-01	1,90E-01	*nifD*- N 14 dpi	L	malonyl-CoA decarboxylase family protein (AHRD V3.3 *-* AT4G04320.2)	GO:0006633|GO:0050080
Solyc02g087580.3	4,14E-01	1,32E-01	**1,04E+00**	**6,23E-04**	-9,10E-01	2,09E-03	-5,66E-01	4,31E-02	*nifD*- N 14 dpi	CS	Actin cross-linking (AHRD V3.3 *** A0A103Y4S4_CYNCS)	
Solyc09g030450.3	5,26E-01	9,66E-05	**1,04E+00**	**1,74E-09**	2,81E-01	2,11E-02	-4,88E-02	6,73E-01	*nifD*- N 14 dpi	S	Receptor-like kinase (AHRD V3.3 *** G7K0V8_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g009090.3	7,79E-01	2,57E-02	**1,03E+00**	**4,22E-03**	-1,39E+00	2,65E-04	-1,53E+00	8,96E-05	*nifD*- N 14 dpi	D	defensin-like protein (AHRD V3.3 *** AT1G19610.1)	GO:0006952
Solyc12g007140.2	9,56E-01	9,92E-07	**1,03E+00**	**2,79E-07**	-1,84E-01	2,31E-01	-6,02E-01	4,56E-04	*nifD*- N 14 dpi	CS	Actin-binding LIM 3 (AHRD V3.3 *** A0A0B0MT11_GOSAR)	
Solyc11g066820.2	5,40E-01	1,12E-02	**1,03E+00**	**1,90E-05**	-4,28E-01	3,95E-02	-1,37E+00	2,59E-07	*nifD*- N 14 dpi	CS	Cellulose synthase-like protein (AHRD V3.3 *** L0ATP8_POPTO)	
Solyc01g107650.3	1,60E-01	4,58E-01	**1,03E+00**	**4,96E-05**	-2,15E-01	3,21E-01	-5,97E-01	9,31E-03	*nifD*- N 14 dpi	K	Ovary receptor kinase 1 (AHRD V3.3 *** S4WIP5_SOLCH)	GO:0004672|GO:0005524|GO:0006468
Solyc05g005180.3	2,04E-01	5,67E-01	**1,03E+00**	**7,06E-03**	3,65E-01	3,10E-01	4,11E-01	2,55E-01	*nifD*- N 14 dpi	NA	enoyl-CoA hydratase/isomerase D (AHRD V3.3 *** AT1G60550.1)	GO:0003824|GO:0008152|GO:0008935|GO:0009234|GO:0008935|GO:0009234
Solyc10g007310.1	4,43E-01	8,18E-02	**1,03E+00**	**2,72E-04**	2,56E-01	3,04E-01	-1,28E-01	6,05E-01	*nifD*- N 14 dpi	G	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT2G42610.2)	
Solyc10g076780.1	5,54E-01	1,68E-02	**1,03E+00**	**6,93E-05**	6,88E-02	7,53E-01	2,94E-01	1,87E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:Alpha 1,4-glycosyltransferase family protein (AHRD V3.3 *** A0A061EQG3_THECC)	
Solyc04g072850.3	4,13E-01	2,48E-01	**1,03E+00**	**6,86E-03**	-3,04E-01	3,93E-01	1,16E-01	7,42E-01	*nifD*- N 14 dpi	CS	Beta-D-xylosidase (AHRD V3.3 *** H1AC33_SOLLC)	GO:0004553|GO:0005975
Solyc01g105320.3	4,19E-01	4,77E-02	**1,03E+00**	**2,77E-05**	6,41E-02	7,53E-01	-9,72E-02	6,34E-01	*nifD*- N 14 dpi	P	Metacaspase 1, putative (AHRD V3.3 *** A0A061E359_THECC),Pfam:PF00656	
Solyc04g011767.1	3,81E-01	2,62E-01	**1,02E+00**	**4,84E-03**	4,07E-01	2,32E-01	6,64E-02	8,43E-01	*nifD*- N 14 dpi	RNA	Pentatricopeptide repeat-containing protein At5g14770, mitochondrial (AHRD V3.3 --* PP381_ARATH)	
Solyc09g075960.1	9,76E-01	1,07E-02	**1,02E+00**	**7,72E-03**	4,98E-02	8,89E-01	-5,18E-01	1,56E-01	*nifD*- N 14 dpi	NA	Plant/T24G3-80 protein (AHRD V3.3 *** G7I6W7_MEDTR)	
Solyc02g091290.3	7,21E-01	2,74E-04	**1,02E+00**	**2,70E-06**	3,90E-01	3,14E-02	9,29E-02	5,92E-01	*nifD*- N 14 dpi	2M	Protein pigment defective 194 (AHRD V3.3 *** A0A0G2T576_9ROSI)	GO:0003824|GO:0004479|GO:0071951|GO:0004479|GO:0071951
Solyc10g039210.3	2,73E-01	2,66E-01	**1,02E+00**	**2,42E-04**	2,24E-01	3,60E-01	-4,05E-01	1,04E-01	*nifD*- N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9SYM5_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc07g065530.1	3,08E-01	2,82E-01	**1,02E+00**	**1,19E-03**	3,92E-01	1,74E-01	-2,45E-01	3,90E-01	*nifD*- N 14 dpi	DNA	LOW QUALITY:Transducin family protein / WD-40 repeat family protein (AHRD V3.3 --* AT1G15750.4)	
Solyc03g112100.3	4,53E-01	4,02E-03	**1,02E+00**	**1,64E-07**	-2,10E-01	1,55E-01	6,27E-02	6,66E-01	*nifD*- N 14 dpi	N	high-affinity nitrate transporter-like protein (AHRD V3.3 *** AT4G24715.1)	GO:0010167|GO:0015706
Solyc06g082210.1	4,39E-01	1,96E-02	**1,02E+00**	**4,65E-06**	3,33E-01	6,99E-02	-2,20E-01	2,24E-01	*nifD*- N 14 dpi	G	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT1G07090.1)	
Solyc07g008920.3	5,24E-01	2,54E-03	**1,02E+00**	**7,53E-07**	-9,40E-02	5,54E-01	-3,02E-02	8,49E-01	*nifD*- N 14 dpi	TR	Oxysterol-binding protein-like (AHRD V3.3 *** A0A0K9NXU5_ZOSMR)	
Solyc07g043230.3	5,37E-01	3,40E-02	**1,02E+00**	**2,58E-04**	-6,30E-02	7,95E-01	-3,94E-01	1,13E-01	*nifD*- N 14 dpi	TR	Zinc transporter protein (AHRD V3.3 *** D5LMF9_9FABA)	GO:0005385|GO:0016021|GO:0071577|GO:0016020|GO:0030001|GO:0046873|GO:0055085|GO:0016020|GO:0030001|GO:0046873|GO:0055085
Solyc02g085910.3	9,31E-01	3,03E-03	**1,02E+00**	**1,43E-03**	4,52E-01	1,24E-01	7,82E-01	1,08E-02	*nifD*- N 14 dpi	G	LOB domain-containing protein (AHRD V3.3 *** A0A0K9PUI8_ZOSMR)	
Solyc12g040790.2	1,87E-01	4,61E-01	**1,02E+00**	**4,15E-04**	-1,87E-02	9,41E-01	-7,40E-01	6,63E-03	*nifD*- N 14 dpi	AM	Phosphoethanolamine N-methyltransferase (AHRD V3.3 *** A0A075BJJ7_LYCBA)	GO:0000234|GO:0006656|GO:0008152|GO:0008168|GO:0008152|GO:0008168

Solyc11g006030.1	4,33E-03	9,89E-01	**1,02E+00**	**3,52E-03**	5,01E-01	1,25E-01	8,02E-01	1,76E-02	*nifD*- N 14 dpi	P	U-box domain-containing family protein (AHRD V3.3 *** U5FLQ4_POPTR)	GO:0004842|GO:0016567|GO:0005488|GO:0005488
Solyc03g119660.2	-1,84E-01	4,38E-01	**1,01E+00**	**2,01E-04**	-3,08E+00	6,52E-13	-8,65E-01	1,05E-03	*nifD*- N 14 dpi	OX	Plant cadmium resistance 2 (AHRD V3.3 *-* A0A0K9PLA8_ZOSMR)	
Solyc08g005550.3	6,28E-01	7,59E-03	**1,01E+00**	**8,05E-05**	2,38E-01	2,82E-01	8,18E-02	7,09E-01	*nifD*- N 14 dpi	D	alternative oxidase 1c	GO:0009916|GO:0055114
Solyc07g005130.3	5,62E-01	7,01E-05	**1,01E+00**	**5,79E-09**	-9,48E-02	4,32E-01	2,08E-01	9,22E-02	*nifD*- N 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT4G31020.2)	
Solyc03g034057.1	5,17E-01	4,90E-03	**1,01E+00**	**2,48E-06**	-1,91E+00	1,57E-11	-1,24E+00	8,37E-08	*nifD*- N 14 dpi	D	Disease resistance protein (TIR-NBS-LRR class) family (AHRD V3.3 --* AT4G08450.2)	
Solyc06g008820.3	8,98E-01	2,05E-05	**1,01E+00**	**3,75E-06**	7,08E-01	3,66E-04	1,61E-01	3,60E-01	*nifD*- N 14 dpi	TR	Na+/H+ antiporter 1	GO:0005774|GO:0005886|GO:0006814|GO:0009651|GO:0055075|GO:0006812|GO:0015299|GO:0016021|GO:0006812|GO:0015299|GO:0016021
Solyc02g063300.3	9,22E-01	2,72E-04	**1,01E+00**	**9,48E-05**	2,20E-02	9,21E-01	-8,24E-02	7,09E-01	*nifD*- N 14 dpi	STR	carboxypeptidase (AHRD V3.3 *** AT5G38060.1)	
Solyc07g005760.3	8,43E-01	1,24E-04	**1,01E+00**	**1,18E-05**	-1,40E-02	9,41E-01	3,24E-02	8,64E-01	*nifD*- N 14 dpi	2M	hydroxycinnamoyl CoA quinate transferase	GO:0016747
Solyc08g075320.3	9,19E-01	4,27E-05	**1,01E+00**	**1,19E-05**	-1,49E+00	2,07E-08	-1,36E+00	9,97E-08	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 family ABA 8'-hydroxylase (AHRD V3.3 *** G7L7U3_MEDTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc09g010480.1	3,09E-01	7,07E-02	**1,01E+00**	**1,72E-06**	3,01E-01	7,79E-02	2,30E-02	8,89E-01	*nifD*- N 14 dpi	D	LOW QUALITY:forkhead box protein G1 (AHRD V3.3 *** AT2G37530.1)	
Solyc07g054690.1	3,20E-01	3,35E-01	**1,01E+00**	**4,69E-03**	1,30E-01	6,93E-01	-3,51E-01	2,92E-01	*nifD*- N 14 dpi	NA	LOW QUALITY:BnaA01g17000D protein (AHRD V3.3 *** A0A078DPQ5_BRANA)	
Solyc11g044940.1	-2,88E-01	3,42E-01	**1,01E+00**	**2,21E-03**	5,06E-02	8,66E-01	-1,04E-01	7,28E-01	*nifD*- N 14 dpi	K	Kinase family protein (AHRD V3.3 *** A0A0K9P5Z4_ZOSMR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g081600.3	9,74E-01	8,89E-03	**1,01E+00**	**7,01E-03**	-2,31E-01	5,09E-01	-1,16E+00	2,34E-03	*nifD*- N 14 dpi	TR	Zinc transporter protein (AHRD V3.3 *** A5BDR3_VITVI)	GO:0005385|GO:0016021|GO:0071577|GO:0016020|GO:0030001|GO:0046873|GO:0055085|GO:0016020|GO:0030001|GO:0046873|GO:0055085
Solyc10g083290.4	4,04E-01	2,39E-01	**1,00E+00**	**5,96E-03**	-2,66E-01	4,34E-01	7,55E-01	3,30E-02	*nifD*- N 14 dpi	NA	symbol=Lin6	
Solyc06g036440.2	1,77E-01	4,90E-01	**1,00E+00**	**5,21E-04**	-8,37E-01	2,82E-03	4,87E-02	8,49E-01	*nifD*- N 14 dpi	STR	S-type anion channel (AHRD V3.3 *** A0A098GMQ9_9ROSI)	GO:0006873|GO:0008308|GO:0016021|GO:0016021|GO:0055085|GO:0016021|GO:0055085
Solyc07g042190.3	4,45E-01	5,65E-02	**1,00E+00**	**1,26E-04**	-5,12E-01	3,00E-02	-7,40E-01	2,69E-03	*nifD*- N 14 dpi	NA	DUF581 family protein (AHRD V3.3 *** B7FN07_MEDTR)	
Solyc12g055920.2	3,07E-01	6,72E-02	**1,00E+00**	**1,37E-06**	-9,66E-01	2,50E-06	-1,23E+00	4,62E-08	*nifD*- N 14 dpi	S	Calcineurin B, putative (AHRD V3.3 *** B9RCU6_RICCO)	GO:0005509
Solyc01g105630.3	-3,96E-02	8,99E-01	**1,00E+00**	**3,31E-03**	4,00E-01	2,08E-01	2,24E-01	4,75E-01	*nifD*- N 14 dpi	DNA	Calmodulin, putative (AHRD V3.3 *** B9S4P7_RICCO)	GO:0005509
Solyc01g096440.3	4,78E-02	8,87E-01	**-1,00E+00**	**5,79E-03**	-7,43E-01	3,43E-02	-2,23E-01	5,08E-01	*nifD*- N 14 dpi	RNA	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061EFM5_THECC)	GO:0005515|GO:0008270|GO:0008270
Solyc01g087730.3	-2,91E-01	2,28E-02	**-1,00E+00**	**9,20E-09**	-5,37E-02	6,59E-01	5,59E-01	8,63E-05	*nifD*- N 14 dpi	R	Ribosomal protein (AHRD V3.3 *** K4AYG3_SOLLC)	GO:0003723|GO:0003723|GO:0003735|GO:0006412|GO:0015934|GO:0003723|GO:0003735|GO:0006412|GO:0015934
Solyc04g049380.3	-6,14E-01	1,64E-03	**-1,00E+00**	**5,09E-06**	-8,75E-02	6,21E-01	-1,24E-01	4,82E-01	*nifD*- N 14 dpi	K	Protein kinase superfamily protein (AHRD V3.3 *** AT2G39190.2)	GO:0004672|GO:0005524|GO:0006468
Solyc06g048890.3	-9,21E-01	1,59E-02	**-1,00E+00**	**9,37E-03**	1,94E-01	5,91E-01	-8,67E-01	2,23E-02	*nifD*- N 14 dpi	K	Protein kinase (AHRD V3.3 *-* A0A0K9NZM3_ZOSMR)	
Solyc08g044280.1	-6,16E-01	8,59E-02	**-1,00E+00**	**7,42E-03**	-3,74E-01	2,89E-01	-7,42E-01	4,12E-02	*nifD*- N 14 dpi	DNA	LOW QUALITY:Adenine nucleotide alpha hydrolase-like domain kinase (AHRD V3.3 --* A0A072V3K5_MEDTR)	
Solyc05g026420.1	-5,24E-01	1,38E-02	**-1,00E+00**	**2,90E-05**	-1,17E-02	9,53E-01	2,63E-01	1,95E-01	*nifD*- N 14 dpi	TR	Ferritin-2, chloroplastic (AHRD V3.3 --* FRI2_SOYBN)	
Solyc05g055120.3	-4,57E-01	1,16E-02	**-1,01E+00**	**2,70E-06**	-1,91E-01	2,67E-01	2,55E-01	1,42E-01	*nifD*- N 14 dpi	S	Phosphatidylinositol-4-phosphate 5-kinase family protein (AHRD V3.3 --* AT1G10900.3)	
Solyc02g067350.3	-3,72E-01	1,09E-01	**-1,01E+00**	**1,27E-04**	-1,11E-01	6,25E-01	2,45E-01	2,84E-01	*nifD*- N 14 dpi	NA	DUF1666 family protein (AHRD V3.3 *** Q2HVS4_MEDTR)	GO:0003735|GO:0005622|GO:0005840|GO:0006412

Solyc10g024370.2	-4,76E-02	8,96E-01	**-1,01E+00**	**9,64E-03**	-3,88E-01	2,93E-01	7,51E-01	4,76E-02	*nifD*- N 14 dpi	L	Phospholipase D (AHRD V3.3 *** K4CZ56_SOLLC)	GO:0003824|GO:0004630|GO:0005509|GO:0016020|GO:0046470|GO:0004630|GO:0005509|GO:0016020|GO:0046470
Solyc09g018170.3	-8,98E-01	1,00E-08	**-1,01E+00**	**1,00E-09**	-4,98E-01	1,02E-04	1,75E-01	1,20E-01	*nifD*- N 14 dpi	K	MAP kinase kinase kinase 70	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc12g056550.1	-6,52E-01	1,85E-03	**-1,01E+00**	**1,26E-05**	-4,89E-01	1,52E-02	-4,09E-01	3,89E-02	*nifD*- N 14 dpi	NA	LOW QUALITY:Plant/F1M20-13 protein (AHRD V3.3 *** G7IBZ7_MEDTR)	
Solyc01g086895.1	-5,58E-01	9,47E-02	**-1,01E+00**	**4,11E-03**	-5,78E-01	8,42E-02	-8,29E-01	1,60E-02	*nifD*- N 14 dpi	TR	Potassium transporter (AHRD V3.3 --* A0A0D3GJS3_9ORYZ)	
Solyc07g065290.3	1,31E-01	6,86E-01	**-1,01E+00**	**4,09E-03**	4,98E-01	1,34E-01	9,84E-01	5,07E-03	*nifD*- N 14 dpi	T	Zinc finger transcription factor 51	GO:0000166|GO:0003676|GO:0003676
Solyc08g066730.3	-2,71E-01	1,41E-01	**-1,01E+00**	**5,73E-06**	2,29E-01	2,10E-01	4,02E-01	3,29E-02	*nifD*- N 14 dpi	RNA	N6-adenosine-methyltransferase MT-A70-like protein (AHRD V3.3 *** W9QTM1_9ROSA)	GO:0006139|GO:0008168
Solyc04g053080.3	-4,74E-01	1,82E-03	**-1,02E+00**	**7,00E-08**	-5,83E-01	2,29E-04	1,97E-02	8,86E-01	*nifD*- N 14 dpi	P	OTU-like cysteine protease family protein (AHRD V3.3 *** B9I9W0_POPTR)	
Solyc01g067600.3	-6,75E-01	2,64E-02	**-1,02E+00**	**1,51E-03**	-8,10E-01	8,94E-03	-6,85E-01	2,43E-02	*nifD*- N 14 dpi	DNA	Zinc finger, CW-type (AHRD V3.3 *** A0A103XJ19_CYNCS)	GO:0008270
Solyc01g103540.3	-5,06E-01	3,00E-04	**-1,02E+00**	**7,43E-09**	-5,96E-01	4,24E-05	-5,77E-02	6,38E-01	*nifD*- N 14 dpi	RNA	evolutionarily conserved C-terminal region 2 (AHRD V3.3 *-* AT3G13460.4)	GO:0003723
Solyc06g054220.2	-1,78E-01	2,94E-01	**-1,02E+00**	**1,76E-06**	-2,27E-01	1,82E-01	2,81E-01	1,02E-01	*nifD*- N 14 dpi	E	Photosystem II reaction center PsbP family protein (AHRD V3.3 --* AT4G15510.1)	
Solyc03g112350.3	-7,02E-01	1,05E-02	**-1,02E+00**	**4,51E-04**	-4,06E-01	1,23E-01	-2,43E-01	3,48E-01	*nifD*- N 14 dpi	RNA	RNA helicase DEAD12	GO:0003676|GO:0005524
Solyc04g045660.3	-1,64E-01	4,28E-01	**-1,02E+00**	**3,34E-05**	-2,76E-01	1,88E-01	-4,88E-01	2,43E-02	*nifD*- N 14 dpi	DNA	MLH1	GO:0005524|GO:0006298|GO:0030983
Solyc08g066060.2	-9,54E-01	5,29E-03	**-1,03E+00**	**2,98E-03**	-2,36E-01	4,58E-01	1,01E-01	7,49E-01	*nifD*- N 14 dpi	DNA	LOW QUALITY:chromatin remodeling factor CHD3 (PICKLE) (AHRD V3.3 --* AT2G25170.4)	
Solyc12g035130.2	-5,35E-01	2,36E-04	**-1,03E+00**	**1,21E-08**	-7,13E-01	5,74E-06	-3,85E-02	7,61E-01	*nifD*- N 14 dpi	RNA	RNA helicase DEAD36	GO:0003676|GO:0005524|GO:0005515|GO:0005515
Solyc06g069370.3	-8,03E-01	3,44E-07	**-1,03E+00**	**3,82E-09**	-1,67E-01	1,70E-01	-4,37E-01	1,03E-03	*nifD*- N 14 dpi	T	bHLH transcription factor 046	
Solyc02g080010.2	-2,28E-01	5,32E-01	**-1,03E+00**	**8,09E-03**	-4,59E-01	2,13E-01	1,15E-01	7,51E-01	*nifD*- N 14 dpi	S	Receptor-like protein kinase (AHRD V3.3 *** C6ZRS0_SOYBN)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g079540.2	4,65E-01	1,92E-01	**-1,03E+00**	**6,37E-03**	-1,23E-01	7,25E-01	-5,50E-03	9,87E-01	*nifD*- N 14 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** E5D7E5_TOBAC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc10g044670.2	-7,00E-01	2,26E-08	**-1,03E+00**	**8,71E-12**	-4,65E-01	1,70E-05	2,25E-02	8,01E-01	*nifD*- N 14 dpi	S	phytochrome A	GO:0000155|GO:0000160|GO:0000155|GO:0007165|GO:0000155|GO:0007165
Solyc02g077190.2	-5,17E-01	2,64E-02	**-1,03E+00**	**7,44E-05**	1,81E-01	4,17E-01	-1,60E-01	4,74E-01	*nifD*- N 14 dpi	DNA	chromatin remodeling factor18 (AHRD V3.3 --* AT1G48310.2)	
Solyc10g083760.2	-5,19E-01	1,17E-04	**-1,04E+00**	**1,74E-09**	1,54E-01	1,91E-01	2,92E-01	1,70E-02	*nifD*- N 14 dpi	AM	chloroplast threonine deaminase 1 precursor	GO:0004794|GO:0009097|GO:0006520|GO:0030170|GO:0006520|GO:0030170
Solyc12g035420.2	-4,71E-01	1,65E-01	**-1,04E+00**	**4,11E-03**	-3,47E-02	9,17E-01	7,08E-02	8,32E-01	*nifD*- N 14 dpi	G	Developmentally regulated GTP-binding protein, putative (AHRD V3.3 *-* B9S5S3_RICCO)	
Solyc10g083690.3	-6,62E-01	4,23E-05	**-1,04E+00**	**3,68E-08**	9,46E-02	4,88E-01	1,50E+00	2,32E-11	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q8H0I7_PETHY)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc02g083670.3	-7,38E-01	3,56E-05	**-1,04E+00**	**1,92E-07**	-2,15E-01	1,58E-01	-1,75E-02	9,07E-01	*nifD*- N 14 dpi	H	histidine kinase 1 (AHRD V3.3 *** AT2G17820.1)	GO:0000155|GO:0007165|GO:0000160|GO:0000160
Solyc03g113970.3	-4,21E-01	2,28E-03	**-1,05E+00**	**6,94E-09**	-4,23E-01	2,20E-03	4,21E-01	2,30E-03	*nifD*- N 14 dpi	DNA	Calmodulin-binding protein (AHRD V3.3 *-* AT5G57580.1)	GO:0005516|GO:0006950
Solyc05g017785.1	-8,60E-01	1,69E-03	**-1,05E+00**	**2,25E-04**	-3,61E-01	1,53E-01	-1,68E-02	9,46E-01	*nifD*- N 14 dpi	G	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein (AHRD V3.3 --* AT1G11100.5)	
Solyc03g043660.3	-6,95E-01	1,77E-06	**-1,05E+00**	**1,07E-09**	-2,49E-01	3,71E-02	2,01E-01	8,77E-02	*nifD*- N 14 dpi	E	Protease Do-like 7 (AHRD V3.3 *** DEGP7_ARATH)	GO:0004252|GO:0006508|GO:0005515|GO:0005515

Solyc09g010630.3	-8,30E-01	1,43E-09	**-1,05E+00**	**1,02E-11**	-6,59E-01	1,07E-07	-1,25E-01	1,80E-01	*nifD*- N 14 dpi	STR	HSC2-like	
Solyc05g005750.3	-6,45E-01	8,06E-05	**-1,05E+00**	**4,50E-08**	-1,70E-01	2,28E-01	1,02E+00	8,56E-08	*nifD*- N 14 dpi	C	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *** B9S4L7_RICCO)	GO:0003824|GO:0005992
Solyc01g006650.2	-8,13E-01	1,28E-02	**-1,06E+00**	**1,82E-03**	-7,68E-01	1,80E-02	-6,67E-01	3,74E-02	*nifD*- N 14 dpi	H	ETHYLENE INSENSITIVE 3-like 3 protein (AHRD V3.3 *** A0A0B2RCL4_GLYSO)	GO:0003700|GO:0005634
Solyc06g053450.3	-5,19E-01	2,69E-03	**-1,06E+00**	**3,71E-07**	7,36E-02	6,42E-01	7,96E-01	2,72E-05	*nifD*- N 14 dpi	G	SUN-like protein 17	GO:0005515
Solyc07g056540.3	-3,01E-01	4,28E-02	**-1,06E+00**	**6,05E-08**	-7,53E-02	5,98E-01	7,11E-01	3,18E-05	*nifD*- N 14 dpi	D	glycolate oxidase X92888	GO:0003824|GO:0010181|GO:0016491|GO:0055114|GO:0010181|GO:0016491|GO:0055114
Solyc03g117710.2	-9,04E-01	2,15E-02	**-1,06E+00**	**7,93E-03**	-3,95E-01	2,94E-01	3,39E-02	9,27E-01	*nifD*- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *-* AT1G79710.2)	GO:0006810|GO:0016021
Solyc11g008220.2	-9,82E-01	1,46E-02	**-1,07E+00**	**8,62E-03**	-4,76E-01	2,16E-01	3,11E-01	4,14E-01	*nifD*- N 14 dpi	RNA	Glycine-rich RNA-binding protein, putative (AHRD V3.3 *-* B9T555_RICCO)	GO:0000166|GO:0003676|GO:0003676
Solyc07g055320.3	-9,73E-01	2,00E-08	**-1,07E+00**	**3,34E-09**	-5,38E-01	1,61E-04	-1,89E-01	1,32E-01	*nifD*- N 14 dpi	E	ATP-dependent zinc metalloprotease FTSH protein (AHRD V3.3 *** A0A072UQU8_MEDTR)	GO:0004222|GO:0005524|GO:0006508|GO:0004222|GO:0016020|GO:0004222|GO:0016020
Solyc09g010970.3	-9,47E-01	1,10E-07	**-1,07E+00**	**1,21E-08**	-4,06E-02	7,58E-01	-6,06E-01	8,69E-05	*nifD*- N 14 dpi	C	Carbonic anhydrase (AHRD V3.3 *** K4CRC3_SOLLC)	GO:0004089|GO:0008270|GO:0004089|GO:0008270|GO:0015976|GO:0004089|GO:0008270|GO:0015976
Solyc07g047940.3	-7,48E-01	1,25E-03	**-1,07E+00**	**2,11E-05**	-4,36E-01	4,48E-02	1,12E+00	1,20E-05	*nifD*- N 14 dpi	T	Zinc finger transcription factor 49	GO:0000166|GO:0003676|GO:0003676
Solyc11g050890.2	-8,52E-01	1,19E-02	**-1,08E+00**	**2,11E-03**	1,59E-01	6,18E-01	5,87E-02	8,53E-01	*nifD*- N 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT3G49650.1)	
Solyc06g082880.2	-8,28E-01	2,15E-02	**-1,08E+00**	**3,64E-03**	5,19E-01	1,37E-01	2,39E-01	4,85E-01	*nifD*- N 14 dpi	RNA	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9T5G9_RICCO)	GO:0005515|GO:0008270|GO:0008270
Solyc11g068895.1	-7,99E-01	7,66E-03	**-1,08E+00**	**5,82E-04**	-4,49E-01	1,16E-01	-9,97E-01	1,30E-03	*nifD*- N 14 dpi	D	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT2G27260.1)	
Solyc06g074720.3	-5,45E-01	1,18E-03	**-1,09E+00**	**1,12E-07**	-3,57E-01	2,45E-02	3,50E-02	8,17E-01	*nifD*- N 14 dpi	RNA	RNA binding protein-like protein (AHRD V3.3 *** Q2VCH8_SOLTU)	GO:0000166|GO:0003676|GO:0003676
Solyc11g008215.1	-6,55E-01	1,21E-02	**-1,09E+00**	**1,36E-04**	-6,96E-01	8,11E-03	-6,08E-01	1,88E-02	*nifD*- N 14 dpi	R	Mitochondrial ribosomal protein L37 (AHRD V3.3 --* AT5G14290.1)	
Solyc02g082613.1	-6,77E-01	8,02E-02	**-1,09E+00**	**7,04E-03**	-1,90E-01	6,12E-01	-1,56E-01	6,77E-01	*nifD*- N 14 dpi	G	Phototropic-responsive NPH3 family protein (AHRD V3.3 --* AT1G03010.3)	
Solyc01g110680.3	-7,97E-01	6,56E-05	**-1,09E+00**	**7,29E-07**	3,70E-02	8,27E-01	3,92E-01	2,72E-02	*nifD*- N 14 dpi	H	Small auxin up-regulated RNA12	GO:0009733
Solyc04g071080.1	-1,06E+00	1,05E-02	**-1,09E+00**	**8,93E-03**	6,42E-01	1,08E-01	8,03E-03	9,84E-01	*nifD*- N 14 dpi	CS	Extensin (AHRD V3.3 *** Q06446_SOLTU)	GO:0005199|GO:0009664
Solyc06g066080.1	-1,92E-01	5,79E-01	**-1,09E+00**	**3,71E-03**	5,23E-01	1,39E-01	1,25E-01	7,19E-01	*nifD*- N 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XZP2_CYNCS)	GO:0005515|GO:0008270|GO:0008270
Solyc03g116270.3	-9,78E-01	3,25E-07	**-1,09E+00**	**4,72E-08**	-5,15E-01	1,35E-03	-4,40E-01	4,99E-03	*nifD*- N 14 dpi	E	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061FWB6_THECC)	GO:0016491|GO:0055114
Solyc05g056325.1	-7,34E-01	2,19E-02	**-1,10E+00**	**1,17E-03**	-5,59E-01	7,43E-02	-2,83E-01	3,56E-01	*nifD*- N 14 dpi	RNA	Tyrosyl-tRNA synthetase, class Ib, bacterial/mitochondrial (AHRD V3.3 --* AT3G02660.2)	
Solyc01g087003.1	-8,04E-01	3,54E-02	**-1,10E+00**	**5,37E-03**	7,94E-02	8,28E-01	-1,78E-01	6,27E-01	*nifD*- N 14 dpi	RNA	Pentatricopeptide repeat protein (AHRD V3.3 *-* A0A1B3IPW0_CAPAN)	
Solyc01g100920.3	-5,13E-01	6,65E-02	**-1,10E+00**	**3,51E-04**	3,93E-01	1,55E-01	-2,15E-01	4,29E-01	*nifD*- N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4B1C3_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc02g083850.3	-8,65E-01	2,93E-07	**-1,10E+00**	**3,42E-09**	4,36E-01	1,91E-03	8,01E-01	1,04E-06	*nifD*- N 14 dpi	S	Calcium-dependent protein kinase (AHRD V3.3 *** C6KGT3_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc09g056135.1	-7,07E-01	1,09E-02	**-1,11E+00**	**2,20E-04**	-3,79E-01	1,53E-01	-4,08E-01	1,26E-01	*nifD*- N 14 dpi	R	Ribosomal protein L15 (AHRD V3.3 *** K4CTA8_SOLLC)	GO:0003735|GO:0005622|GO:0005840|GO:0006412|GO:0003735|GO:0005840|GO:0003735|GO:0005840
Solyc06g084615.1	-2,14E-02	9,57E-01	**-1,11E+00**	**8,63E-03**	5,47E-02	8,90E-01	-2,05E-02	9,59E-01	*nifD*- N 14 dpi	2M	beta-carotene isomerase D27 (AHRD V3.3 *** AT4G01995.1)	

Solyc06g065040.3	-6,50E-01	4,21E-04	**-1,12E+00**	**2,40E-07**	-4,13E-01	1,63E-02	1,03E-01	5,25E-01	*nifD*- N 14 dpi	T	bHLH transcription factor 086	GO:0046983
Solyc11g006750.1	-4,96E-01	1,74E-01	**-1,12E+00**	**4,01E-03**	1,37E-01	7,02E-01	1,33E-01	7,11E-01	*nifD*- N 14 dpi	NA	F1F0-ATPase inhibitor protein (AHRD V3.3 *** AT5G04750.1)	GO:0005739|GO:0032780|GO:0042030
Solyc02g014730.3	-1,05E+00	1,39E-02	**-1,12E+00**	**9,26E-03**	1,58E+00	5,40E-04	1,00E+00	1,87E-02	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103YA00_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc02g037590.2	-2,03E-01	4,36E-01	**-1,13E+00**	**1,74E-04**	-5,58E-01	3,92E-02	4,80E-02	8,53E-01	*nifD*- N 14 dpi	D	LOW QUALITY:Mannose-binding lectin superfamily protein (AHRD V3.3 --* AT1G60110.3)	
Solyc03g063220.2	-8,30E-01	2,52E-02	**-1,13E+00**	**3,39E-03**	-9,59E-01	1,08E-02	-7,08E-01	5,31E-02	*nifD*- N 14 dpi	RNA	RNA helicase DEAH-box8	GO:0005524
Solyc03g044330.1	-6,45E-01	7,40E-05	**-1,13E+00**	**1,01E-08**	3,49E-01	1,72E-02	3,39E-01	2,00E-02	*nifD*- N 14 dpi	AM	Acetolactate synthase (AHRD V3.3 *** A0A0V0IYE7_SOLCH)	GO:0000287|GO:0003984|GO:0009082|GO:0030976|GO:0050660|GO:0000287|GO:0030976|GO:0000287|GO:0030976
Solyc01g096370.3	-8,12E-01	7,92E-05	**-1,13E+00**	**6,56E-07**	1,94E-01	2,74E-01	-7,02E-01	4,13E-04	*nifD*- N 14 dpi	DNA	Basic helix loop helix (BHLH) family transcription factor (AHRD V3.3 *** A0A072TYH1_MEDTR)	GO:0046983
Solyc01g060170.3	-6,00E-01	2,28E-02	**-1,14E+00**	**1,05E-04**	-5,62E-01	3,20E-02	-2,41E-01	3,41E-01	*nifD*- N 14 dpi	T	calmodulin-binding transcription activator (AHRD V3.3 *-* AT3G16940.2)	GO:0003677|GO:0005634
Solyc01g007980.3	-6,39E-01	1,25E-03	**-1,14E+00**	**8,45E-07**	-3,31E-01	7,22E-02	-5,94E-01	2,37E-03	*nifD*- N 14 dpi	K	Protein kinase family protein (AHRD V3.3 *** C6ZRU6_SOYBN)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g116843.1	9,88E-02	7,85E-01	**-1,14E+00**	**3,82E-03**	-8,65E-02	8,11E-01	-1,74E-01	6,32E-01	*nifD*- N 14 dpi	RNA	Pentatricopeptide repeat superfamily protein (AHRD V3.3 *** A0A061GFS6_THECC)	GO:0005515|GO:0008270|GO:0008270
Solyc02g089610.2	-9,13E-01	1,41E-02	**-1,14E+00**	**2,91E-03**	5,24E-01	1,42E-01	1,81E-01	6,06E-01	*nifD*- N 14 dpi	N	S-adenosylmethionine decarboxylase 2	GO:0004014|GO:0004014|GO:0006597|GO:0008295|GO:0004014|GO:0006597|GO:0008295
Solyc01g100100.3	-9,44E-01	3,80E-03	**-1,14E+00**	**7,14E-04**	1,14E+00	7,18E-04	1,42E+00	6,29E-05	*nifD*- N 14 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061E1W0_THECC)	GO:0005515|GO:0008270
Solyc12g096720.2	-3,12E-01	3,26E-01	**-1,15E+00**	**1,12E-03**	5,45E-01	9,30E-02	1,64E-01	6,05E-01	*nifD*- N 14 dpi	S	Receptor-like kinase (AHRD V3.3 *-* D4QD70_DIACA)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc09g075360.3	-7,86E-01	2,86E-02	**-1,15E+00**	**2,20E-03**	-5,57E-01	1,12E-01	-7,06E-01	4,74E-02	*nifD*- N 14 dpi	CS	endo-1,4-beta-glucanase precursor	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc01g105497.1	-5,31E-01	1,47E-01	**-1,16E+00**	**3,05E-03**	-3,64E-01	3,15E-01	9,93E-02	7,82E-01	*nifD*- N 14 dpi	N	ureide permease 2 (AHRD V3.3 --* AT2G03530.5)	
Solyc08g007060.3	-8,87E-01	2,58E-04	**-1,16E+00**	**8,33E-06**	-9,17E-01	1,78E-04	-2,28E-01	2,86E-01	*nifD*- N 14 dpi	TR	Peptide transporter, putative (AHRD V3.3 *** B9S1I2_RICCO)	GO:0005215|GO:0006810|GO:0016020
Solyc08g016588.1	-7,84E-01	4,85E-02	**-1,17E+00**	**4,81E-03**	-1,84E-01	6,31E-01	-5,12E-01	1,88E-01	*nifD*- N 14 dpi	DNA	Zinc finger CCCH domain-containing protein 54 (AHRD V3.3 --* C3H54_ORYSJ)	
Solyc07g045030.3	-8,23E-01	9,30E-03	**-1,17E+00**	**4,74E-04**	2,13E-01	4,73E-01	-2,83E-01	3,42E-01	*nifD*- N 14 dpi	T	NAC domain-containing protein, putative (AHRD V3.3 *** B9RI29_RICCO)	GO:0003677|GO:0006355
Solyc04g054770.1	-2,78E-01	2,64E-01	**-1,18E+00**	**5,41E-05**	-4,88E-01	5,58E-02	-2,94E-01	2,38E-01	*nifD*- N 14 dpi	P	LOW QUALITY:Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 --* AT5G45790.2)	
Solyc01g028860.3	-7,82E-01	9,86E-08	**-1,19E+00**	**2,62E-11**	-2,70E-01	1,80E-02	-4,03E-04	9,97E-01	*nifD*- N 14 dpi	RNA	evolutionarily conserved C-terminal region 2 (AHRD V3.3 *** AT3G13460.1)	GO:0003723
Solyc11g007990.2	-2,94E-01	4,05E-01	**-1,19E+00**	**1,99E-03**	1,43E-01	6,82E-01	1,23E+00	1,54E-03	*nifD*- N 14 dpi	C	chloroplast malate dehydrogenase (mdh)	GO:0003824|GO:0005975|GO:0016616|GO:0055114|GO:0006108|GO:0016615|GO:0055114|GO:0006108|GO:0016615|GO:0055114
Solyc01g104470.3	-6,19E-01	6,49E-04	**-1,20E+00**	**6,05E-08**	4,34E-02	7,88E-01	1,89E-01	2,48E-01	*nifD*- N 14 dpi	R	Acidic ribosomal protein P0 (AHRD V3.3 *** B9I0W5_POPTR)	GO:0000027|GO:0005622|GO:0042254|GO:0005622|GO:0042254
Solyc10g054480.2	-2,66E-01	3,00E-01	**-1,20E+00**	**6,10E-05**	3,19E-01	2,15E-01	3,84E-01	1,38E-01	*nifD*- N 14 dpi	E	FAD-binding Berberine family protein, putative (AHRD V3.3 *** A0A061G791_THECC)	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114
Solyc10g049800.2	-4,46E-01	2,75E-01	**-1,21E+00**	**5,61E-03**	-4,78E-03	9,91E-01	3,77E-01	3,55E-01	*nifD*- N 14 dpi	NA	DUF936 family protein (AHRD V3.3 *-* A0A072VCI3_MEDTR)	
Solyc08g005970.3	-9,39E-01	2,43E-09	**-1,21E+00**	**1,30E-11**	-2,88E-01	1,11E-02	-1,62E-01	1,37E-01	*nifD*- N 14 dpi	DNA	Protein arginine N-methyltransferase (AHRD V3.3 *** K4CI86_SOLLC)	GO:0006479|GO:0008168|GO:0006479|GO:0008168|GO:0035246|GO:0006479|GO:0008168|GO:0035246
Solyc05g048810.3	-4,68E-01	6,72E-03	**-1,21E+00**	**4,71E-08**	-2,55E-01	1,20E-01	2,21E-01	1,77E-01	*nifD*- N 14 dpi	DNA	Adenosine-deaminase family protein (AHRD V3.3 *** B9I8G9_POPTR)	GO:0003723|GO:0004000|GO:0006396

Solyc01g107270.3	-8,52E-01	6,37E-05	**-1,21E+00**	**3,60E-07**	6,14E-03	9,73E-01	-7,54E-01	2,66E-04	*nifD*- N 14 dpi	R	40S ribosomal protein S24 (AHRD V3.3 *-* A0A0D3F2R2_9ORYZ)	
Solyc02g005140.3	-9,76E-01	6,12E-05	**-1,21E+00**	**3,03E-06**	-3,89E-01	6,77E-02	-2,06E-01	3,22E-01	*nifD*- N 14 dpi	NA	GPI-anchored adhesin-like protein, putative (Protein of unknown function, DUF547) (AHRD V3.3 --* AT1G16750.1)	
Solyc03g120110.3	-3,83E-01	1,33E-01	**-1,21E+00**	**4,34E-05**	5,93E-01	2,38E-02	2,48E-01	3,23E-01	*nifD*- N 14 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** A0A178VFP7_ARATH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc10g055720.2	-8,44E-01	6,78E-06	**-1,21E+00**	**1,58E-08**	5,79E-02	7,03E-01	5,64E-01	8,91E-04	*nifD*- N 14 dpi	K	MAP kinase kinase kinase 75	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g065590.3	-3,74E-01	2,83E-01	**-1,21E+00**	**1,46E-03**	2,23E+00	6,23E-07	2,00E+00	3,58E-06	*nifD*- N 14 dpi	E	Nicotinamide-nucleotide adenylyltransferase (AHRD V3.3 *** K4CHN7_SOLLC)	GO:0003824|GO:0009058|GO:0009435|GO:0016779|GO:0009435|GO:0016779
Solyc06g051380.2	-6,72E-01	1,27E-01	**-1,22E+00**	**8,46E-03**	-3,21E-01	4,57E-01	-1,97E-01	6,47E-01	*nifD*- N 14 dpi	G	transducin family protein / WD-40 repeat family protein (AHRD V3.3 *-* AT5G05570.2)	GO:0005515
Solyc07g065840.2	-8,85E-01	2,75E-08	**-1,22E+00**	**4,99E-11**	-6,46E-01	5,26E-06	-1,48E-01	2,00E-01	*nifD*- N 14 dpi	STR	molecular chaperone Hsp90-2	GO:0005524|GO:0006457|GO:0006950|GO:0051082
Solyc12g096730.3	-2,56E-01	4,38E-01	**-1,22E+00**	**9,09E-04**	3,39E-01	3,07E-01	2,32E-01	4,81E-01	*nifD*- N 14 dpi	CS	polygalacturonase TPG6	GO:0004650|GO:0005975
Solyc12g056560.2	-6,77E-01	2,61E-03	**-1,22E+00**	**2,52E-06**	-8,55E-01	2,75E-04	-3,73E-01	7,78E-02	*nifD*- N 14 dpi	STR	Heat shock family protein (AHRD V3.3 *-* B9GTI4_POPTR)	
Solyc09g075580.1	-1,08E+00	1,82E-02	**-1,22E+00**	**8,38E-03**	-6,97E-01	1,16E-01	-1,74E-01	6,89E-01	*nifD*- N 14 dpi	G	LOW QUALITY:CheY-like two-component responsive regulator family protein (AHRD V3.3 --* AT4G18020.9)	
Solyc11g006465.1	-7,18E-01	2,33E-05	**-1,23E+00**	**3,15E-09**	-5,43E-01	6,13E-04	-4,70E-02	7,38E-01	*nifD*- N 14 dpi	STR	DnaJ-like protein (AHRD V3.3 *-* Q9M7M2_SOLLC)	
Solyc03g115650.3	-4,42E-01	4,10E-02	**-1,23E+00**	**2,80E-06**	3,58E-01	9,34E-02	7,39E-01	1,35E-03	*nifD*- N 14 dpi	P	eukaryotic translation initiation factor 5A-1	GO:0003723|GO:0003746|GO:0006452|GO:0043022|GO:0045901|GO:0045905|GO:0003723|GO:0003746|GO:0043022|GO:0045901|GO:0003723|GO:0003746|GO:0043022|GO:0045901
Solyc07g025490.2	-8,63E-01	2,54E-03	**-1,23E+00**	**6,31E-05**	-8,11E-01	4,18E-03	-7,64E-01	6,52E-03	*nifD*- N 14 dpi	TR	OSBP(oxysterol binding protein)-related protein 4B (AHRD V3.3 --* AT4G25850.3)	
Solyc09g007343.1	3,51E-01	4,00E-01	**-1,23E+00**	**5,74E-03**	-6,56E-02	8,74E-01	-2,99E-01	4,71E-01	*nifD*- N 14 dpi	P	LOW QUALITY:F-box protein (AHRD V3.3 --* G7IWM2_MEDTR)	
Solyc07g055470.3	-7,05E-02	8,39E-01	**-1,24E+00**	**1,32E-03**	-9,44E-01	1,08E-02	9,54E-01	1,00E-02	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc05g047540.3	-8,49E-01	1,58E-02	**-1,24E+00**	**8,66E-04**	-1,11E-01	7,39E-01	4,01E-01	2,33E-01	*nifD*- N 14 dpi	RNA	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061GYI5_THECC)	
Solyc01g110735.1	-9,44E-01	2,02E-02	**-1,24E+00**	**3,10E-03**	-2,88E-01	4,56E-01	-5,64E-01	1,51E-01	*nifD*- N 14 dpi	H	SAUR-like auxin-responsive protein family (AHRD V3.3 *-* AT5G18030.1)	GO:0009733
Solyc10g079780.1	-5,42E-01	1,68E-01	**-1,25E+00**	**3,06E-03**	1,15E-02	9,76E-01	6,22E-01	1,15E-01	*nifD*- N 14 dpi	P	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 (AHRD V3.3 -** DAD1_ORYSI)	
Solyc08g067200.2	-6,37E-01	1,62E-01	**-1,25E+00**	**9,07E-03**	-3,84E-01	3,93E-01	-6,60E-03	9,88E-01	*nifD*- N 14 dpi	RNA	Dicer-like protein 3 (AHRD V3.3 *-* X4Y6L7_SOLLC)	GO:0003676|GO:0005524
Solyc12g098850.2	-8,23E-01	2,24E-05	**-1,25E+00**	**2,71E-08**	-4,89E-01	4,99E-03	4,49E-01	9,18E-03	*nifD*- N 14 dpi	H	ethylene-forming enzyme	
Solyc03g113340.3	-5,59E-01	5,53E-02	**-1,25E+00**	**1,31E-04**	-5,82E-01	4,66E-02	1,70E+00	2,06E-06	*nifD*- N 14 dpi	PMI	Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** AT1G74780.1)	
Solyc02g089400.3	-8,94E-01	6,01E-03	**-1,26E+00**	**2,77E-04**	-2,28E-02	9,40E-01	-1,19E-01	6,94E-01	*nifD*- N 14 dpi	AM	Amino acid transporter, putative (AHRD V3.3 *** B9T738_RICCO)	
Solyc02g091655.1	-5,39E-01	1,06E-02	**-1,27E+00**	**7,59E-07**	-1,61E-01	4,18E-01	8,34E-02	6,73E-01	*nifD*- N 14 dpi	DNA	Telomerase activating protein Est1 (AHRD V3.3 --* AT1G28260.2)	
Solyc06g036230.3	-8,85E-01	5,53E-02	**-1,27E+00**	**7,79E-03**	-8,83E-01	5,56E-02	3,89E-01	3,85E-01	*nifD*- N 14 dpi	NA	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *-* D7LUP2_ARALL)	
Solyc03g115220.3	-9,02E-01	1,29E-05	**-1,27E+00**	**5,11E-08**	9,87E-02	5,61E-01	7,60E-01	1,19E-04	*nifD*- N 14 dpi	2M	Flavonoid 3'-hydroxylase (AHRD V3.3 *** A0A0N6XG41_LYCBA)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114

Solyc02g083690.2	-1,32E-01	7,45E-01	**-1,28E+00**	**3,89E-03**	1,42E+00	1,58E-03	2,57E+00	9,77E-07	*nifD*- N 14 dpi	STR	LOW QUALITY:Senescence/dehydration-associated protein-like protein (AHRD V3.3 *** AT2G17840.1)	
Solyc04g050220.2	-8,95E-01	4,34E-03	**-1,28E+00**	**1,41E-04**	-5,01E-01	9,18E-02	2,48E-01	3,93E-01	*nifD*- N 14 dpi	P	F-box and associated interaction domains-containing protein (AHRD V3.3 --* AT3G25460.1)	
Solyc07g055640.1	-8,18E-01	8,74E-02	**-1,28E+00**	**9,76E-03**	-2,25E-01	6,29E-01	6,10E-01	1,96E-01	*nifD*- N 14 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A0D4BTD1_SOLPN)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc09g065155.1	-5,77E-01	1,11E-01	**-1,30E+00**	**9,51E-04**	-2,27E-01	5,22E-01	-6,59E-03	9,85E-01	*nifD*- N 14 dpi	P	FZO-like (AHRD V3.3 *-* A0A061DQU9_THECC)	GO:0003824
Solyc11g010220.2	-4,56E-02	9,16E-01	**-1,31E+00**	**4,89E-03**	7,72E-01	8,16E-02	4,18E-01	3,35E-01	*nifD*- N 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118I7L5_CYNCS)	GO:0005515
Solyc03g117380.3	-6,39E-01	1,03E-03	**-1,31E+00**	**4,95E-08**	-3,01E-01	9,35E-02	-1,91E-01	2,79E-01	*nifD*- N 14 dpi	H	Protein TOPLESS (AHRD V3.3 *-* TPL_ARATH)	GO:0006355
Solyc10g086410.3	-5,56E-01	2,10E-05	**-1,31E+00**	**3,08E-12**	-1,02E-01	3,53E-01	1,49E-02	8,91E-01	*nifD*- N 14 dpi	STR	LEHSC270 hsc-2heat shock protein cognate 70	
Solyc02g084910.3	-7,57E-01	8,44E-02	**-1,32E+00**	**4,25E-03**	1,64E+00	6,38E-04	7,09E-01	1,05E-01	*nifD*- N 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT5G17760.1)	GO:0005524
Solyc10g078720.2	-7,99E-01	5,24E-05	**-1,33E+00**	**1,70E-08**	-4,73E-01	8,18E-03	7,58E-01	1,00E-04	*nifD*- N 14 dpi	T	Myb family transcription factor family protein (AHRD V3.3 *** B9HAD3_POPTR)	GO:0003677
Solyc03g121510.3	-9,04E-01	3,27E-03	**-1,33E+00**	**6,32E-05**	-3,84E-01	1,80E-01	-2,09E-02	9,41E-01	*nifD*- N 14 dpi	CYTP450	Cytochrome P450, putative (AHRD V3.3 *** B9SN45_RICCO)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc12g017515.1	3,65E-01	4,01E-01	**-1,34E+00**	**4,18E-03**	-7,59E-02	8,60E-01	-7,17E-01	1,05E-01	*nifD*- N 14 dpi	STR	Late embryogenesis abundant protein Lea14 (AHRD V3.3 *** A0A0K9PIU3_ZOSMR)	GO:0009269
Solyc07g008740.2	1,49E-02	9,70E-01	**-1,34E+00**	**1,80E-03**	-8,10E-01	4,56E-02	-5,71E-01	1,51E-01	*nifD*- N 14 dpi	K	Kinase family protein (AHRD V3.3 *-* D7LXZ8_ARALL)	GO:0004672|GO:0005524|GO:0006468
Solyc07g017670.2	-1,01E+00	2,64E-02	**-1,35E+00**	**3,99E-03**	-1,20E-01	7,82E-01	-9,87E-03	9,82E-01	*nifD*- N 14 dpi	AM	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (AHRD V3.3 *-* A0A072V2T5_MEDTR)	
Solyc03g020040.3	1,07E+00	2,47E-02	**-1,36E+00**	**5,67E-03**	8,36E-01	7,42E-02	7,96E-01	8,83E-02	*nifD*- N 14 dpi	D	Pin-II type proteinase inhibitor 69 (AHRD V3.3 *** A0A097J9C9_CAPAN)	GO:0004867
Solyc06g068270.3	-2,98E-01	5,38E-01	**-1,36E+00**	**8,62E-03**	-8,64E-01	8,17E-02	1,49E+00	4,36E-03	*nifD*- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G49390.1)	GO:0016491|GO:0055114
Solyc01g100095.1	-9,02E-01	1,97E-03	**-1,37E+00**	**1,88E-05**	1,92E-01	4,70E-01	9,84E-01	8,89E-04	*nifD*- N 14 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061E1W0_THECC)	GO:0005515|GO:0008270
Solyc02g089615.1	-1,01E+00	3,33E-02	**-1,37E+00**	**5,33E-03**	6,09E-01	1,88E-01	-4,11E-02	9,28E-01	*nifD*- N 14 dpi	N	S-adenosylmethionine decarboxylase uORF (AHRD V3.3 *-* Q6RUQ6_DAUCA)	
Solyc03g095370.3	-4,83E-01	9,51E-02	**-1,38E+00**	**4,02E-05**	-6,05E-01	3,95E-02	2,21E-01	4,35E-01	*nifD*- N 14 dpi	STR	CLP protease regulatory subunit CLPX1, mitochondrial (AHRD V3.3 --* CLPX1_ARATH)	
Solyc05g055110.3	-8,25E-01	2,17E-03	**-1,38E+00**	**5,47E-06**	-1,22E-01	6,20E-01	1,72E-01	4,84E-01	*nifD*- N 14 dpi	RNA	Nuclear pore complex protein Nup136d (AHRD V3.3 *** W6JJ82_NICBE)	
Solyc06g010240.2	-1,21E+00	1,61E-02	**-1,39E+00**	**6,63E-03**	-2,18E-01	6,47E-01	-3,65E-01	4,45E-01	*nifD*- N 14 dpi	DNA	Helicase protein MOM1 (AHRD V3.3 *-* A0A0B2QJF7_GLYSO)	
Solyc08g067870.2	-9,69E-01	5,57E-02	**-1,39E+00**	**7,94E-03**	-7,29E-01	1,43E-01	-1,10E+00	3,15E-02	*nifD*- N 14 dpi	G	embryo defective 2410 (AHRD V3.3 *** AT2G25660.3)	
Solyc06g008265.1	-6,24E-01	1,70E-01	**-1,39E+00**	**4,10E-03**	1,14E+00	1,59E-02	5,08E-01	2,61E-01	*nifD*- N 14 dpi	PMI	Leucine-rich repeat receptor-like protein kinase family protein, putative (AHRD V3.3 *** A0A061GI31_THECC)	GO:0005515
Solyc08g006025.1	-3,98E-01	3,56E-01	**-1,39E+00**	**2,97E-03**	1,04E+00	2,09E-02	3,57E-01	4,08E-01	*nifD*- N 14 dpi	T	NAC domain-containing protein (AHRD V3.3 *-* I6YR01_9CARY)	GO:0003677|GO:0006355
Solyc12g017430.2	-6,56E-01	6,62E-02	**-1,39E+00**	**3,86E-04**	-7,59E-01	3,54E-02	-8,06E-01	2,61E-02	*nifD*- N 14 dpi	TR	ENTH/ANTH/VHS superfamily protein (AHRD V3.3 *-* AT2G01600.1)	GO:0005543
Solyc03g119930.1	-7,84E-01	9,06E-04	**-1,40E+00**	**4,39E-07**	8,75E-01	2,92E-04	1,05E+00	3,12E-05	*nifD*- N 14 dpi	TR	Sulfate transporter, putative (AHRD V3.3 *** B9RUY1_RICCO)	GO:0015098|GO:0015689|GO:0015098|GO:0015689|GO:0016021|GO:0015098|GO:0015689|GO:0016021
Solyc01g006310.3	-8,50E-01	2,96E-02	**-1,40E+00**	**8,13E-04**	9,51E-01	1,61E-02	1,45E+00	5,87E-04	*nifD*- N 14 dpi	OX	SlPeroxidase	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744

Solyc09g005880.1	-2,59E-01	6,06E-01	**-1,42E+00**	**8,21E-03**	-9,01E-01	8,13E-02	-8,91E-01	8,47E-02	*nifD*- N 14 dpi	K	LOW QUALITY:Membrane-associated kinase regulator-like protein, putative (AHRD V3.3 *** A0A072VS60_MEDTR)	
Solyc11g011740.1	-1,17E+00	1,73E-02	**-1,43E+00**	**4,67E-03**	-1,09E-01	8,14E-01	-4,73E-01	3,14E-01	*nifD*- N 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *** F2Y9E9_COFAR)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc01g110688.1	-1,25E+00	1,09E-02	**-1,43E+00**	**4,12E-03**	-8,06E-01	8,84E-02	-1,65E-01	7,21E-01	*nifD*- N 14 dpi	DNA	CTP synthase (AHRD V3.3 --* A0A068U755_COFCA)	
Solyc10g085850.1	-9,07E-01	6,61E-03	**-1,44E+00**	**7,78E-05**	1,18E+00	7,01E-04	1,43E+00	8,14E-05	*nifD*- N 14 dpi	PMI	LOW QUALITY:S-locus lectin protein kinase family protein (AHRD V3.3 --* AT1G61360.1)	
Solyc09g057900.2	-8,02E-01	1,47E-02	**-1,44E+00**	**7,46E-05**	-3,38E-01	2,80E-01	-9,22E-01	5,85E-03	*nifD*- N 14 dpi	RNA	evolutionarily conserved C-terminal region 4 (AHRD V3.3 --* AT1G55500.6)	
Solyc08g067280.1	-5,47E-01	1,76E-01	**-1,45E+00**	**1,03E-03**	-9,44E-01	2,38E-02	-1,06E+00	1,23E-02	*nifD*- N 14 dpi	G	squamosa promoter binding protein-like 7 (AHRD V3.3 --* AT5G18830.3)	
Solyc02g089497.1	-1,07E+00	4,93E-02	**-1,47E+00**	**8,51E-03**	1,44E-01	7,83E-01	4,69E-01	3,73E-01	*nifD*- N 14 dpi	DNA	Minichromosome maintenance (MCM2/3/5) family protein (AHRD V3.3 --* AT5G46280.4)	
Solyc01g006050.2	-1,47E-01	6,03E-01	**-1,48E+00**	**1,62E-05**	5,77E-01	4,90E-02	2,09E+00	6,27E-08	*nifD*- N 14 dpi	NA	LOW QUALITY:Transmembrane protein 45B (AHRD V3.3 *** A0A151U0K4_CAJCA)	
Solyc07g061940.3	-7,25E-01	2,44E-05	**-1,48E+00**	**9,34E-11**	-1,22E-01	3,95E-01	1,83E-01	2,06E-01	*nifD*- N 14 dpi	AM	Acetolactate synthase (AHRD V3.3 *** A0A0V0IYE7_SOLCH)	GO:0000287|GO:0003984|GO:0009082|GO:0030976|GO:0050660|GO:0000287|GO:0030976|GO:0000287|GO:0030976
Solyc02g086300.3	-9,13E-01	3,66E-02	**-1,49E+00**	**1,36E-03**	3,10E+00	6,45E-08	4,05E+00	3,80E-10	*nifD*- N 14 dpi	N	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *** AT5G38200.1)	GO:0006541|GO:0016787
Solyc11g006740.2	-6,30E-01	1,72E-01	**-1,49E+00**	**2,64E-03**	2,72E+00	2,13E-06	2,17E+00	5,09E-05	*nifD*- N 14 dpi	P	F-box protein PP2 (AHRD V3.3 *** A0A059PC27_CICAR)	GO:0005515
Solyc10g086090.2	-6,33E-01	4,05E-02	**-1,50E+00**	**2,47E-05**	1,68E+00	5,27E-06	2,17E+00	8,24E-08	*nifD*- N 14 dpi	D	Trypsin inhibitor 1 (AHRD V3.3 *** ITR1_NICSY)	GO:0004867|GO:0009611
Solyc10g018310.1	1,14E-01	7,73E-01	**-1,50E+00**	**6,77E-04**	-3,11E-01	4,32E-01	7,80E-02	8,43E-01	*nifD*- N 14 dpi	H	LOW QUALITY:regulatory components of ABA receptor 3 (AHRD V3.3 --* AT5G53160.2)	
Solyc09g092720.3	-7,91E-01	1,11E-01	**-1,50E+00**	**4,26E-03**	3,91E-01	4,22E-01	7,28E-01	1,42E-01	*nifD*- N 14 dpi	D	Glycine-rich protein (AHRD V3.3 *** D2K2T8_TOBAC)	
Solyc10g052650.2	-8,62E-01	8,18E-04	**-1,51E+00**	**5,16E-07**	-2,17E-01	3,48E-01	3,37E-01	1,51E-01	*nifD*- N 14 dpi	P	F-box protein (AHRD V3.3 *-* A0A0B2RZB4_GLYSO)	
Solyc08g006930.3	-7,35E-01	1,47E-01	**-1,51E+00**	**4,90E-03**	-5,99E-01	2,35E-01	7,81E-01	1,25E-01	*nifD*- N 14 dpi	E	Photosystem I reaction center subunit psaK (AHRD V3.3 *** W9SCM1_9ROSA)	GO:0009522|GO:0015979|GO:0016020|GO:0009522|GO:0015979|GO:0016168|GO:0009522|GO:0015979|GO:0016168
Solyc01g110970.3	-6,98E-01	1,53E-01	**-1,52E+00**	**3,62E-03**	4,98E-01	3,04E-01	-4,43E-01	3,59E-01	*nifD*- N 14 dpi	H	Auxin responsive SAUR protein (AHRD V3.3 *-* A0A103Y0W3_CYNCS)	GO:0009733
Solyc08g061520.3	-1,15E+00	1,59E-02	**-1,53E+00**	**1,95E-03**	-4,09E-01	3,66E-01	-3,49E-01	4,39E-01	*nifD*- N 14 dpi	TR	myosin (AHRD V3.3 *-* AT4G33200.3)	GO:0003774|GO:0005524|GO:0016459
Solyc05g046130.3	-9,31E-01	2,10E-04	**-1,54E+00**	**1,54E-07**	-6,51E-01	5,71E-03	7,72E-01	1,42E-03	*nifD*- N 14 dpi	NA	transmembrane protein, putative (DUF1218) (AHRD V3.3 *** AT4G21310.1)	
Solyc03g111425.1	-5,58E-01	1,82E-01	**-1,55E+00**	**7,47E-04**	-2,19E-01	5,95E-01	2,92E-01	4,78E-01	*nifD*- N 14 dpi	STR	DnaJ heat shock amino-terminal domain protein (AHRD V3.3 --* AT5G53150.6)	
Solyc04g079680.3	-5,52E-01	1,43E-02	**-1,63E+00**	**3,48E-08**	-8,95E-01	2,42E-04	2,24E-02	9,16E-01	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103YCJ3_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc03g046275.1	-6,06E-01	2,02E-01	**-1,64E+00**	**1,55E-03**	1,04E-01	8,25E-01	-1,35E-01	7,74E-01	*nifD*- N 14 dpi	T	DNA-directed RNA polymerase subunit (AHRD V3.3 --* A0A068TZY7_COFCA)	
Solyc02g085005.1	-6,67E-01	1,92E-01	**-1,65E+00**	**2,69E-03**	-6,57E-02	8,96E-01	-4,19E-01	4,08E-01	*nifD*- N 14 dpi	NA	BnaC08g22290D protein (AHRD V3.3 *** A0A078CC33_BRANA)	
Solyc05g044630.3	-1,25E+00	2,47E-02	**-1,70E+00**	**3,35E-03**	-1,95E-01	7,14E-01	-2,65E-01	6,18E-01	*nifD*- N 14 dpi	E	NifU-like protein 3 (AHRD V3.3 *-* W9RHZ6_9ROSA)	GO:0005506|GO:0016226|GO:0051536
Solyc07g005895.1	-4,34E-01	4,25E-01	**-1,70E+00**	**3,78E-03**	-1,26E+00	2,68E-02	-2,30E-01	6,70E-01	*nifD*- N 14 dpi	P	galactosyltransferase family protein (AHRD V3.3 *-* AT1G30260.1)	
Solyc01g066270.3	-1,33E+00	3,63E-02	**-1,78E+00**	**6,45E-03**	4,91E-01	4,22E-01	1,72E+00	8,38E-03	*nifD*- N 14 dpi	DNA	LOW QUALITY:AT-hook motif nuclear-localized protein 1 (AHRD V3.3 --* AT4G12080.1)	

Solyc01g097280.2	-3,81E-01	5,32E-01	**-1,79E+00**	**6,29E-03**	1,34E+00	3,48E-02	2,06E+00	2,09E-03	*nifD*- N 14 dpi	D	Pathogenesis-related protein PR-4 (AHRD V3.3 *** PR4_PRUPE)	GO:0008061|GO:0042742|GO:0050832|GO:0042742|GO:0050832
Solyc04g016177.1	-7,71E-01	2,99E-02	**-1,79E+00**	**1,42E-05**	-2,51E-01	4,61E-01	-2,05E-01	5,47E-01	*nifD*- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** M1CLQ4_SOLTU)	GO:0008152|GO:0016758
Solyc02g085190.2	-1,13E+00	9,08E-02	**-1,80E+00**	**9,53E-03**	-1,09E+00	1,03E-01	-1,01E+00	1,28E-01	*nifD*- N 14 dpi	T	GATA transcription factor, putative (AHRD V3.3 *** B9S6H2_RICCO)	GO:0003700|GO:0006355|GO:0008270|GO:0043565|GO:0006355|GO:0008270|GO:0006355|GO:0008270
Solyc00g136560.3	1,60E-02	9,77E-01	**-1,80E+00**	**2,53E-03**	5,53E-01	3,13E-01	2,66E+00	3,90E-05	*nifD*- N 14 dpi	DNA	Alkyl transferase (AHRD V3.3 *** K7X479_SOLLC)	GO:0016765
Solyc12g100350.2	-1,13E+00	6,00E-02	**-1,81E+00**	**4,06E-03**	-7,22E-01	2,19E-01	1,18E-01	8,38E-01	*nifD*- N 14 dpi	G	calpain-type cysteine protease family (AHRD V3.3 *-* AT1G55350.6)	
Solyc08g006410.3	-9,13E-01	9,69E-02	**-1,83E+00**	**1,94E-03**	3,15E-01	5,57E-01	2,80E-01	6,01E-01	*nifD*- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CIC9_SOLLC)	GO:0008152|GO:0016758
Solyc09g072770.1	-7,18E-01	1,07E-01	**-1,84E+00**	**2,26E-04**	1,01E+00	2,61E-02	7,96E-01	7,53E-02	*nifD*- N 14 dpi	G	Pollen Ole e 1 allergen and extensin family protein (AHRD V3.3 *-* AT2G41400.1)	
Solyc04g009020.3	-1,65E+00	1,36E-02	**-1,88E+00**	**5,57E-03**	-1,13E+00	8,08E-02	-3,71E-01	5,56E-01	*nifD*- N 14 dpi	RNA	PsbB mRNA maturation factor Mbb1 (AHRD V3.3 *** W9RTZ1_9ROSA)	GO:0005515|GO:0006396|GO:0006396
Solyc04g011800.1	5,22E-01	2,16E-01	**-1,90E+00**	**9,53E-05**	-1,06E-01	7,98E-01	1,84E-01	6,59E-01	*nifD*- N 14 dpi	OX	Glutaredoxin family protein (AHRD V3.3 *** B9I9V9_POPTR)	GO:0009055|GO:0015035|GO:0045454
Solyc01g102910.3	-7,85E-01	1,52E-01	**-1,90E+00**	**1,43E-03**	8,80E-01	1,10E-01	-1,14E+00	4,16E-02	*nifD*- N 14 dpi	STR	Germin family protein (AHRD V3.3 *** G7I5N4_MEDTR)	GO:0030145|GO:0045735|GO:0045735
Solyc07g007860.1	-9,37E-01	1,24E-01	**-1,98E+00**	**2,42E-03**	-5,11E-01	3,94E-01	-4,19E-01	4,84E-01	*nifD*- N 14 dpi	G	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *-* AT2G10940.2)	
Solyc10g050670.1	-1,29E+00	3,68E-02	**-1,99E+00**	**2,20E-03**	5,98E-01	3,15E-01	-2,47E-01	6,76E-01	*nifD*- N 14 dpi	G	LOW QUALITY:LOB domain-containing protein 7 (AHRD V3.3 --* AT1G72980.1)	
Solyc03g096660.2	-6,27E-01	3,04E-01	**-2,00E+00**	**2,57E-03**	1,34E+00	3,37E-02	-6,99E-02	9,08E-01	*nifD*- N 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561	GO:0016491
Solyc11g009100.2	-1,31E+00	7,13E-02	**-2,00E+00**	**8,11E-03**	1,99E+00	8,30E-03	1,09E+00	1,30E-01	*nifD*- N 14 dpi	TR	ABC transporter G family member (AHRD V3.3 *** A0A0K9NWI5_ZOSMR)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc09g089760.1	-1,85E+00	1,16E-02	**-2,00E+00**	**6,95E-03**	-1,59E+00	2,74E-02	-8,96E-01	2,00E-01	*nifD*- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)	GO:0016491|GO:0055114
Solyc05g050810.3	-1,12E+00	3,09E-02	**-2,01E+00**	**3,56E-04**	-5,47E-01	2,73E-01	-5,82E-01	2,44E-01	*nifD*- N 14 dpi	STR	DnaJ protein (AHRD V3.3 *-* A0A199V3N0_ANACO)	GO:0006457|GO:0051082|GO:0031072|GO:0051082|GO:0031072|GO:0051082
Solyc10g007420.4	-8,16E-01	4,12E-03	**-2,02E+00**	**3,21E-08**	-1,25E-02	9,62E-01	9,62E-01	9,99E-04	*nifD*- N 14 dpi	AM	gamma-glutamylhydrolase	
Solyc03g114700.2	-8,57E-01	1,70E-01	**-2,03E+00**	**2,54E-03**	1,27E+00	4,71E-02	-5,10E-01	4,09E-01	*nifD*- N 14 dpi	CS	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT5G57300.4)	
Solyc05g009620.3	-8,70E-01	4,68E-02	**-2,03E+00**	**4,73E-05**	1,83E+00	1,74E-04	2,39E+00	5,01E-06	*nifD*- N 14 dpi	OX	Protein PLANT CADMIUM RESISTANCE 2 (AHRD V3.3 *** A0A1D1Y359_9ARAE)	
Solyc07g052750.1	-4,52E-01	3,24E-01	**-2,05E+00**	**1,09E-04**	-1,14E+00	1,77E-02	2,56E-01	5,73E-01	*nifD*- N 14 dpi	T	STOREKEEPER protein (AHRD V3.3 *-* STK_SOLTU)	
Solyc06g082300.3	-1,00E+00	1,15E-01	**-2,13E+00**	**1,89E-03**	-1,16E+00	6,95E-02	-8,73E-01	1,67E-01	*nifD*- N 14 dpi	C	UDP-glycosyltransferase (AHRD V3.3 *** A0A067XTI9_CICAR)	GO:0008152|GO:0016758
Solyc10g039390.1	-1,01E+00	3,21E-02	**-2,21E+00**	**4,16E-05**	1,40E+00	4,43E-03	1,26E+00	9,06E-03	*nifD*- N 14 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** AT1G29000.2)	GO:0030001|GO:0046872
Solyc11g065600.2	-6,82E-02	9,26E-01	**-2,25E+00**	**4,47E-03**	-5,30E-01	4,70E-01	1,57E-01	8,30E-01	*nifD*- N 14 dpi	CS	xyloglucan endotransglucosylase-hydrolase 4	GO:0004553|GO:0005975|GO:0005618|GO:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc05g006610.3	-5,97E-01	2,26E-01	**-2,33E+00**	**5,32E-05**	-7,17E-01	1,48E-01	-5,51E-01	2,62E-01	*nifD*- N 14 dpi	G	CLAVATA3/ESR (CLE)-related 25-like protein (AHRD V3.3 *** A0A0B0NFL0_GOSAR)	
Solyc07g005630.3	-1,06E+00	2,18E-01	**-2,45E+00**	**7,28E-03**	2,45E-01	7,72E-01	-6,22E-02	9,41E-01	*nifD*- N 14 dpi	D	LOW QUALITY:Defensin (AHRD V3.3 -** W8S9R7_ECLPR)	GO:0006952
Solyc09g092760.2	4,74E-02	9,39E-01	**-2,47E+00**	**4,77E-04**	3,78E-01	5,46E-01	3,58E-01	5,67E-01	*nifD*- N 14 dpi	G	RNA-binding (RRM/RBD/RNP motifs) family protein (AHRD V3.3 --* AT2G41060.3)	

Solyc11g005480.2	-1,28E-02	9,82E-01	**-2,49E+00**	**1,22E-04**	1,31E+00	2,51E-02	1,51E+00	1,09E-02	*nifD*- N 14 dpi	NA	Citrate binding protein (AHRD V3.3 *** Q8H9C1_SOLTU)	
Solyc11g069880.1	-5,70E-02	9,43E-01	**-2,51E+00**	**3,73E-03**	1,71E+00	3,99E-02	2,16E+00	1,10E-02	*nifD*- N 14 dpi	D	Kiwellin (AHRD V3.3 *** A0A061GX31_THECC)	
Solyc02g063410.3	-1,44E+00	1,10E-01	**-2,56E+00**	**6,64E-03**	-1,94E+00	3,47E-02	6,84E-01	4,38E-01	*nifD*- N 14 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT5G65660.1)	
Solyc10g074440.2	2,73E-02	9,70E-01	**-2,62E+00**	**1,16E-03**	1,60E+00	3,50E-02	2,14E+00	6,09E-03	*nifD*- N 14 dpi	D	Chitinase (AHRD V3.3 *** B9VRK7_CAPAN)	GO:0004568|GO:0005975|GO:0004568|GO:0006032|GO:0016998|GO:0004568|GO:0006032|GO:0016998
Solyc03g096300.3	-8,05E-01	2,49E-01	**-2,66E+00**	**6,10E-04**	1,58E+00	2,85E-02	1,11E-02	9,87E-01	*nifD*- N 14 dpi	G	WUSCHEL-related homeobox protein (AHRD V3.3 *** A0A097I3L1_ROSCN)	GO:0003677
Solyc01g005900.2	-1,95E+00	1,20E-02	**-2,69E+00**	**9,50E-04**	-1,45E+00	5,50E-02	-6,85E-01	3,50E-01	*nifD*- N 14 dpi	S	HXXXD-type acyl-transferase family protein (AHRD V3.3 *-* AT1G28680.1)	GO:0016747
Solyc09g089720.2	-1,37E+00	9,80E-02	**-2,69E+00**	**2,43E-03**	1,82E-01	8,21E-01	7,30E-01	3,69E-01	*nifD*- N 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.1)	GO:0016491|GO:0055114
Solyc10g080817.1	-9,58E-01	2,90E-01	**-2,70E+00**	**5,34E-03**	8,01E-01	3,75E-01	1,60E+00	8,22E-02	*nifD*- N 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A2PZD4_IPONI)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc12g096200.2	-2,08E+00	1,14E-02	**-2,72E+00**	**1,44E-03**	2,37E-01	7,58E-01	-5,29E-01	4,93E-01	*nifD*- N 14 dpi	G	R2R3MYB transcription factor 6	GO:0003677
Solyc12g042960.2	-2,24E+00	1,14E-02	**-2,72E+00**	**2,82E-03**	-1,90E-01	8,19E-01	8,26E-01	3,25E-01	*nifD*- N 14 dpi	N	LOW QUALITY:PII, uridylyltransferase (DUF2921) (AHRD V3.3 *** AT1G52780.1)	
Solyc12g100150.2	-1,60E+00	2,88E-02	**-2,72E+00**	**5,44E-04**	4,24E-01	5,44E-01	-1,27E+00	7,64E-02	*nifD*- N 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9RI26_RICCO)	
Solyc02g085660.1	-7,26E-01	4,65E-01	**-2,73E+00**	**9,72E-03**	1,28E+00	2,03E-01	1,87E+00	6,74E-02	*nifD*- N 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BB77_SOLLC)	GO:0008152|GO:0016758
Solyc06g060340.3	-2,16E+00	1,12E-02	**-2,76E+00**	**1,77E-03**	3,53E-01	6,59E-01	-5,90E-01	4,62E-01	*nifD*- N 14 dpi	E	photosystem II subunit S	
Solyc08g074883.1	-2,03E+00	2,81E-02	**-2,98E+00**	**2,13E-03**	-4,14E-01	6,39E-01	-1,50E+00	9,76E-02	*nifD*- N 14 dpi	E	CURVATURE THYLAKOID protein (AHRD V3.3 --* AT1G52220.2)	
Solyc02g077575.1	5,45E-02	9,48E-01	**-2,98E+00**	**1,41E-03**	1,21E+00	1,59E-01	-2,13E-01	8,01E-01	*nifD*- N 14 dpi	D	MLO-like protein (AHRD V3.3 *** G9BBX3_CAPAN)	GO:0006952|GO:0016021
Solyc07g026930.2	-2,07E+00	1,39E-02	**-3,03E+00**	**6,68E-04**	-1,21E+00	1,35E-01	-9,96E-01	2,14E-01	*nifD*- N 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT5G42210.1)	GO:0005215|GO:0016021|GO:0055085|GO:0016021|GO:0055085
Solyc12g088970.1	-2,64E+00	1,19E-02	**-3,03E+00**	**4,59E-03**	-1,41E+00	1,62E-01	-2,17E+00	3,55E-02	*nifD*- N 14 dpi	CYTP450	CytochromeP450	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc06g072455.1	-1,04E+00	2,79E-01	**-3,07E+00**	**3,12E-03**	8,16E-01	3,94E-01	-3,45E-01	7,17E-01	*nifD*- N 14 dpi	RNA	LOW QUALITY:Agenet-like domain-containing protein (AHRD V3.3 *** A0A103YGJ9_CYNCS)	
Solyc03g080075.1	-2,73E+00	1,02E-02	**-3,15E+00**	**3,65E-03**	-7,55E-01	4,50E-01	-1,16E+00	2,51E-01	*nifD*- N 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4BHY3_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc02g091820.2	-1,85E+00	3,64E-02	**-3,16E+00**	**8,83E-04**	6,55E-01	4,42E-01	1,39E+00	1,10E-01	*nifD*- N 14 dpi	T	bHLH transcription factor 016	GO:0046983
Solyc12g005730.2	-7,29E-01	2,75E-01	**-3,18E+00**	**4,90E-05**	4,30E-01	5,17E-01	-1,44E+00	3,71E-02	*nifD*- N 14 dpi	C	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)	
Solyc10g084960.2	-1,03E+00	2,80E-01	**-3,44E+00**	**1,06E-03**	-2,03E-01	8,29E-01	5,56E-01	5,56E-01	*nifD*- N 14 dpi	STR	Glutathione S-transferase-like protein (AHRD V3.3 *** K7VK72_SOLTU)	GO:0005515
Solyc06g083560.3	-2,32E+00	4,96E-02	**-3,44E+00**	**5,14E-03**	-2,41E+00	4,16E-02	-6,58E-01	5,63E-01	*nifD*- N 14 dpi	G	transducin family protein / WD-40 repeat family protein (AHRD V3.3 --* AT5G08560.3)	
Solyc03g114530.3	-6,17E-03	9,94E-01	**-3,65E+00**	**1,52E-04**	1,53E+00	7,36E-02	2,57E+00	4,32E-03	*nifD*- N 14 dpi	2M	Strictosidine synthase-like protein, putative (AHRD V3.3 *** G7JT39_MEDTR)	GO:0009058|GO:0016844
Solyc08g068860.3	-2,12E+00	2,33E-02	**-3,65E+00**	**3,20E-04**	3,75E-01	6,73E-01	-1,39E-01	8,75E-01	*nifD*- N 14 dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** A0A061GIP5_THECC)	GO:0004190|GO:0006508
Solyc12g006810.2	-2,13E+00	1,33E-02	**-3,78E+00**	**7,18E-05**	-1,67E+00	4,74E-02	-9,69E-01	2,37E-01	*nifD*- N 14 dpi	S	SOUL heme-binding family protein (AHRD V3.3 *** AT5G20140.1)	

Solyc12g009065.1	-2,28E+00	1,65E-02	**-3,88E+00**	**1,85E-04**	-8,80E-01	3,31E-01	9,18E-01	3,12E-01	*nifD*- N 14 dpi	D	RING/U-box superfamily protein, putative (AHRD V3.3 *** A0A061GT61_THECC)	GO:0005515|GO:0008270
Solyc01g087180.3	-8,93E-01	4,74E-01	**-3,97E+00**	**3,38E-03**	-7,56E-01	5,44E-01	-1,33E+00	2,90E-01	*nifD*- N 14 dpi	G	Microspore-specific promoter 2, putative (AHRD V3.3 --* A0A061G480_THECC)	
Solyc05g050590.3	-3,45E+00	7,12E-02	**-5,97E+00**	**3,15E-03**	-4,36E+00	2,52E-02	-4,42E+00	2,33E-02	*nifD*- N 14 dpi	S	Phosphatidylinositol 3-and 4-kinase family protein (AHRD V3.3 *** D7LEK1_ARALL)	GO:0005515|GO:0016301|GO:0016301
Solyc09g097760.3	-3,10E+00	7,01E-02	**-6,72E+00**	**3,65E-04**	-2,20E+00	1,92E-01	-5,43E-01	7,43E-01	nifD- N 14 dpi	D	Glycine rich protein (AHRD V3.3 *-* Q94CG1_TOBAC)	
Solyc09g082550.3	3,25E+00	5,33E-06	4,56E+00	1,86E-08	7,86E-01	1,79E-01	**-2,00E+00**	**1,66E-03**	*nifD*- NoN 14 dpi	TR	Sulfate transporter (AHRD V3.3 *** D7LTZ8_ARALL)	GO:0008271|GO:0008272|GO:0008271|GO:0008272|GO:0016020|GO:0055085|GO:0008271|GO:0008272|GO:0016020|GO:0055085
Solyc02g070070.1	2,14E+00	9,44E-03	3,88E+00	2,78E-05	-6,47E-02	9,33E-01	**-2,39E+00**	**4,27E-03**	*nifD*- NoN 14 dpi	E	FAD-binding Berberine family protein (AHRD V3.3 *** AT2G34790.1)	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114|GO:0003824|GO:0050660|GO:0055114
Solyc04g079260.3	2,71E+00	5,58E-02	3,75E+00	1,02E-02	1,20E+00	3,82E-01	**3,84E+00**	**8,77E-03**	*nifD*- NoN 14 dpi	P	Patatin (AHRD V3.3 *** K4BV10_SOLLC)	GO:0006629|GO:0008152|GO:0008152
Solyc06g051940.3	1,82E+00	1,16E-01	3,74E+00	2,64E-03	8,78E-01	4,41E-01	**-3,27E+00**	**7,38E-03**	*nifD*- NoN 14 dpi	K	Protein phosphatase 2c, putative (AHRD V3.3 *** B9RIK1_RICCO)	GO:0003824|GO:0004722|GO:0006470|GO:0004722|GO:0006470
Solyc08g062970.1	2,52E+00	1,70E-09	3,54E+00	1,22E-12	-1,44E-01	6,07E-01	**-1,09E+00**	**5,73E-04**	*nifD*- NoN 14 dpi	OX	Glutaredoxin (AHRD V3.3 *** A0A118JSL8_CYNCS)	GO:0009055|GO:0015035|GO:0045454
Solyc03g096770.1	2,73E+00	1,15E-04	3,52E+00	3,70E-06	-1,19E+00	5,87E-02	**-1,86E+00**	**4,73E-03**	*nifD*- NoN 14 dpi	STR	Response to low sulfur protein, putative (AHRD V3.3 *** G7J9Q1_MEDTR)	
Solyc04g064900.1	2,48E+00	1,19E-03	3,48E+00	2,49E-05	-1,05E+00	1,34E-01	**-2,22E+00**	**3,05E-03**	*nifD*- NoN 14 dpi	CS	Endoglucanase (AHRD V3.3 *-* A0A067LEU1_JATCU)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc06g064960.3	2,41E+00	2,07E-02	3,12E+00	3,78E-03	-1,12E+00	2,65E-01	**-3,36E+00**	**2,04E-03**	*nifD*- NoN 14 dpi	L	Lipase, GDSL (AHRD V3.3 *** A0A124SDS7_CYNCS)	GO:0016788
Solyc06g048780.1	2,83E+00	1,65E-02	2,94E+00	1,30E-02	2,00E+00	8,09E-02	**3,43E+00**	**4,49E-03**	*nifD*- NoN 14 dpi	2M	LOW QUALITY:PLAC8 family protein (AHRD V3.3 *-* AT3G10980.1)	
Solyc11g006250.2	-2,52E-01	7,42E-01	2,91E+00	7,20E-04	-1,95E-01	7,99E-01	**-2,36E+00**	**4,39E-03**	*nifD*- NoN 14 dpi	L	GDSL-motif lipase/hydrolase family protein 2	GO:0016788
Solyc03g096780.1	2,06E+00	1,10E-05	2,86E+00	5,51E-08	-9,84E-01	1,53E-02	**-1,27E+00**	**2,47E-03**	*nifD*- NoN 14 dpi	STR	Response to low sulfur protein, putative (AHRD V3.3 *** G7J9Q1_MEDTR)	
Solyc12g008380.1	2,00E+00	2,80E-04	2,73E+00	5,29E-06	-7,36E-01	1,35E-01	**-1,48E+00**	**4,48E-03**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** I3SWH2_MEDTR)	
Solyc07g045460.3	1,78E+00	3,89E-05	2,58E+00	1,33E-07	-2,68E-01	4,63E-01	**-1,00E+00**	**9,58E-03**	*nifD*- NoN 14 dpi	C	SNF1-related protein kinase regulatory subunit beta-2 (AHRD V3.3 *** AT4G16360.1)	GO:0005515|GO:0009744|GO:0043562|GO:0009744|GO:0043562
Solyc05g009590.3	1,79E+00	7,65E-08	2,46E+00	1,56E-10	-4,41E-01	7,93E-02	**-1,20E+00**	**3,61E-05**	*nifD*- NoN 14 dpi	G	aluminum activated malate transporter family protein (AHRD V3.3 *** AT1G18420.1)	GO:0015743
Solyc05g005540.3	2,63E-01	6,28E-01	2,34E+00	1,83E-04	1,04E+00	6,28E-02	**-1,98E+00**	**1,06E-03**	*nifD*- NoN 14 dpi	CS	Polygalacturonase non-catalytic subunit AroGP3 (AHRD V3.3 *** GP3_SOLLC)	
Solyc06g072350.3	2,59E+00	4,07E-02	2,31E+00	6,54E-02	6,68E-01	5,83E-01	**5,15E+00**	**2,27E-04**	*nifD*- NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4C8V5_SOLLC)	
Solyc10g037880.2	8,11E-01	4,66E-02	2,23E+00	4,90E-06	-4,79E-01	2,28E-01	**-1,15E+00**	**6,32E-03**	*nifD*- NoN 14 dpi	E	Blue copper (AHRD V3.3 *** A0A0B0MZW4_GOSAR)	GO:0009055
Solyc12g009270.1	3,08E-01	3,43E-01	2,11E+00	5,17E-07	1,93E-01	5,49E-01	**-1,07E+00**	**2,40E-03**	*nifD*- NoN 14 dpi	CS	Plant invertase/pectin methylesterase inhibitor superfamily protein (AHRD V3.3 *** A0A061GSW0_THECC)	GO:0004857
Solyc12g095740.2	2,61E+00	1,45E-02	2,08E+00	4,73E-02	2,74E+00	1,06E-02	**3,13E+00**	**4,22E-03**	*nifD*- NoN 14 dpi	DNA	ARID/BRIGHT DNA-binding domain-containing protein (AHRD V3.3 *-* AT1G76510.4)	
Solyc07g064870.3	1,29E+00	4,44E-06	2,07E+00	1,12E-09	-9,99E-01	1,38E-04	**-1,51E+00**	**3,87E-07**	*nifD*- NoN 14 dpi	CS	Endoglucanase (AHRD V3.3 *** M1C0J8_SOLTU)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc03g020050.3	1,30E+00	1,59E-01	2,00E+00	3,38E-02	6,66E-01	4,62E-01	**5,13E+00**	**4,97E-06**	*nifD*- NoN 14 dpi	D	VIROID-INDUCIBLE PROTEINASE INHIBITOR II	GO:0004867
Solyc08g066650.3	1,19E+00	2,03E-06	2,00E+00	1,52E-10	1,49E-01	4,53E-01	**-1,41E+00**	**1,32E-07**	*nifD*- NoN 14 dpi	2M	Carotenoid Cleavage Dioxygenase 8	GO:0016702|GO:0055114

Solyc09g018430.3	1,43E+00	9,33E-03	1,98E+00	6,13E-04	-5,68E-01	2,73E-01	**-1,54E+00**	**5,55E-03**	*nifD*- NoN 14 dpi	NA	Gamma-interferon-inducible lysosomal thiol reductase (AHRD V3.3 *-* A0A151RU75_CAJCA)	
Solyc01g100900.3	1,53E+00	5,91E-06	1,90E+00	1,88E-07	-7,22E-02	7,92E-01	**-1,08E+00**	**4,66E-04**	*nifD*- NoN 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4B1C1_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc04g074330.3	1,09E+00	1,36E-05	1,88E+00	1,24E-09	-3,71E-01	8,07E-02	**-1,26E+00**	**1,69E-06**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BTX1_SOLLC)	GO:0008152|GO:0016758
Solyc02g079350.3	1,37E+00	1,01E-04	1,88E+00	1,15E-06	-7,10E-01	2,49E-02	**-1,64E+00**	**9,42E-06**	*nifD*- NoN 14 dpi	DNA	Equilibrative nucleoside transporter family protein (AHRD V3.3 *** B9H1Z9_POPTR)	GO:0005337|GO:0006810|GO:0016021
Solyc01g090340.2	9,62E-01	3,20E-03	1,87E+00	1,12E-06	4,34E-01	1,55E-01	**-1,17E+00**	**5,56E-04**	*nifD*- NoN 14 dpi	H	Ethylene-responsive transcription factor, putative (AHRD V3.3 *** B9RD03_RICCO)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc09g008320.3	1,85E+00	2,97E-05	1,86E+00	2,87E-05	-9,13E-01	1,96E-02	**-1,43E+00**	**6,07E-04**	*nifD*- NoN 14 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4CQM0_SOLLC)	GO:0004553|GO:0005975|GO:0005618|GO:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc06g066830.3	1,64E+00	4,52E-09	1,83E+00	4,91E-10	-2,20E-01	2,58E-01	**-1,37E+00**	**1,18E-07**	*nifD*- NoN 14 dpi	E	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)	GO:0016491|GO:0055114
Solyc06g048750.3	9,62E-01	1,77E-02	1,80E+00	6,90E-05	-7,31E-01	6,54E-02	**-1,71E+00**	**1,31E-04**	*nifD*- NoN 14 dpi	NA	Unknown protein (AHRD V3.3)	
Solyc02g085400.3	1,15E+00	1,83E-01	1,80E+00	4,24E-02	-1,97E+00	2,71E-02	**-3,06E+00**	**1,22E-03**	*nifD*- NoN 14 dpi	P	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT2G25737.1)	GO:0016021
Solyc05g050240.3	1,68E+00	8,32E-03	1,80E+00	5,22E-03	-1,10E-01	8,53E-01	**-2,06E+00**	**1,70E-03**	*nifD*- NoN 14 dpi	E	Plastid division protein PDV1 (AHRD V3.3 *-* A0A199W2F8_ANACO)	
Solyc04g072030.1	1,75E+00	9,71E-09	1,78E+00	6,77E-09	4,62E-01	3,75E-02	**-1,33E+00**	**1,19E-06**	*nifD*- NoN 14 dpi	TR	Dynamin-related protein (AHRD V3.3 *** A0A1B0UTC3_TOBAC)	GO:0003924|GO:0005525|GO:0005525|GO:0005525
Solyc02g079980.3	2,19E+00	7,45E-03	1,75E+00	2,81E-02	-1,72E+00	3,08E-02	**-2,19E+00**	**7,44E-03**	*nifD*- NoN 14 dpi	P	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT1G61740.1)	GO:0016021
Solyc11g010340.2	1,15E+00	2,46E-03	1,74E+00	2,89E-05	-7,43E-01	4,01E-02	**-2,50E+00**	**1,07E-07**	*nifD*- NoN 14 dpi	T	bHLH transcription factor 069	GO:0046983
Solyc02g080080.3	1,49E+00	1,11E-01	1,70E+00	6,95E-02	2,21E+00	2,10E-02	**2,86E+00**	**3,83E-03**	*nifD*- NoN 14 dpi	S	Receptor-like protein kinase (AHRD V3.3 *** C6ZRS0_SOYBN)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc06g005130.3	8,96E-01	4,25E-02	1,70E+00	4,31E-04	-1,42E-02	9,73E-01	**-1,20E+00**	**8,56E-03**	*nifD*- NoN 14 dpi	DNA	Dof zinc finger protein (AHRD V3.3 *** W9RMR9_9ROSA)	GO:0003677|GO:0006355
Solyc03g031910.3	9,34E-01	2,72E-01	1,69E+00	5,27E-02	-1,20E+00	1,60E-01	**-3,51E+00**	**2,72E-04**	*nifD*- NoN 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061EY56_THECC)	
Solyc08g042010.3	9,27E-01	7,93E-02	1,69E+00	2,62E-03	-1,90E-01	7,11E-01	**-2,29E+00**	**1,25E-04**	*nifD*- NoN 14 dpi	P	Exostosin family protein (AHRD V3.3 *** A0A061GIR4_THECC)	
Solyc04g011340.3	9,99E-01	1,04E-02	1,66E+00	1,01E-04	-8,46E-01	2,73E-02	**-1,04E+00**	**8,22E-03**	*nifD*- NoN 14 dpi	H	WAT1-related protein (AHRD V3.3 *** K4BPI9_SOLLC)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc05g056440.2	1,24E+00	2,00E-04	1,64E+00	5,08E-06	-5,74E-01	5,58E-02	**-1,06E+00**	**1,05E-03**	*nifD*- NoN 14 dpi	H	Small auxin up-regulated RNA57	GO:0009733
Solyc12g098490.2	6,10E-01	2,05E-03	1,63E+00	1,32E-09	-8,65E-01	4,91E-05	**-1,18E+00**	**5,20E-07**	*nifD*- NoN 14 dpi	AM	Serine hydroxymethyltransferase (AHRD V3.3 *** M1A0B7_SOLTU)	GO:0003824|GO:0004372|GO:0006544|GO:0006563|GO:0030170|GO:0004372|GO:0006544|GO:0006563|GO:0030170
Solyc02g093250.3	6,84E-01	1,60E-03	1,63E+00	7,20E-09	-9,53E-01	4,29E-05	**-1,33E+00**	**2,98E-07**	*nifD*- NoN 14 dpi	2M	Caffeoyl-CoA O-methyltransferase (AHRD V3.3 *** CAMT_SOLTU)	GO:0008171
Solyc01g079130.2	1,02E+00	1,20E-04	1,63E+00	1,15E-07	-5,30E-01	2,60E-02	**-1,13E+00**	**3,30E-05**	*nifD*- NoN 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G02460.1)	GO:0004650|GO:0005975
Solyc11g042940.2	8,21E-01	2,08E-01	1,62E+00	1,76E-02	7,42E-01	2,54E-01	**-2,57E+00**	**4,23E-04**	*nifD*- NoN 14 dpi	C	Xylulose kinase, putative (AHRD V3.3 *** B9RHB4_RICCO)	GO:0005975|GO:0016773
Solyc03g025870.3	1,23E+00	7,09E-05	1,61E+00	1,60E-06	-7,98E-01	5,06E-03	**-1,06E+00**	**3,87E-04**	*nifD*- NoN 14 dpi	G	R2R3MYB transcription factor 19	GO:0003677
Solyc02g085020.3	1,51E+00	2,00E-01	1,60E+00	1,78E-01	4,21E-01	7,18E-01	**-4,40E+00**	**7,46E-04**	*nifD*- NoN 14 dpi	2M	dihydroflavonol 4-reductase	GO:0003824|GO:0050662
Solyc05g008050.2	7,30E-01	3,97E-01	1,57E+00	7,49E-02	9,06E-01	2,94E-01	**-2,75E+00**	**3,22E-03**	*nifD*- NoN 14 dpi	DNA	Homeobox associated leucine zipper protein (AHRD V3.3 *** I3SMB9_MEDTR)	GO:0003677|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565

Solyc03g114705.1	1,37E+00	3,13E-03	1,56E+00	1,01E-03	-9,27E-01	3,63E-02	**-1,52E+00**	**1,25E-03**	*nifD*- NoN 14 dpi	H	DELLA protein (AHRD V3.3 --* Q0HA73_MALDO)	
Solyc03g097580.3	3,60E-01	7,09E-01	1,55E+00	1,17E-01	-6,85E-01	4,80E-01	**-4,11E+00**	**2,17E-04**	*nifD*- NoN 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJH5_SOLLC)	GO:0016021
Solyc01g079910.1	1,13E+00	8,51E-02	1,52E+00	2,39E-02	-1,44E+00	3,09E-02	**2,17E+00**	**2,08E-03**	*nifD*- NoN 14 dpi	CS	LOW QUALITY:Xyloglucan-specific endoglucanase inhibitor protein 2 (AHRD V3.3 *-* F1DHN5_SOLTU)	GO:0004190|GO:0006508
Solyc04g071615.1	1,32E+00	3,96E-02	1,50E+00	2,05E-02	-5,24E-01	3,98E-01	**-2,05E+00**	**2,44E-03**	*nifD*- NoN 14 dpi	H	ASR4 (AHRD V3.3 *** Q2QJT5_SOLLC)	GO:0006950
Solyc06g054500.1	1,42E+00	2,39E-01	1,50E+00	2,13E-01	-2,92E+00	1,97E-02	**-4,31E+00**	**1,11E-03**	*nifD*- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4C6D6_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc12g006260.1	9,45E-01	1,75E-01	1,48E+00	3,82E-02	-6,35E-01	3,58E-01	**4,19E+00**	**1,66E-06**	*nifD*- NoN 14 dpi	CS	L-fucokinase/GDP-L-fucose pyrophosphorylase (AHRD V3.3 --* AT1G01220.7)	
Solyc07g066250.1	7,32E-01	1,14E-01	1,48E+00	2,87E-03	1,74E-01	7,00E-01	**-1,77E+00**	**5,47E-04**	*nifD*- NoN 14 dpi	T	GRAS family transcription factor (AHRD V3.3 *** A0A061F3B6_THECC)	GO:0005634|GO:0010223
Solyc01g101190.3	2,12E+00	1,40E-01	1,48E+00	3,00E-01	3,53E+00	1,79E-02	**5,51E+00**	**5,36E-04**	*nifD*- NoN 14 dpi	2M	Alpha-humulene/(-)-(E)-beta-caryophyllene synthase (AHRD V1 **** HUMS_ARATH)%3B contains Interpro domain(s) IPR005630 Terpene synthase%2C metal-binding domain	GO:0000287|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829
Solyc04g080990.2	1,63E+00	1,44E-04	1,47E+00	4,38E-04	1,30E-01	7,24E-01	**-1,23E+00**	**2,38E-03**	*nifD*- NoN 14 dpi	TR	S-type anion channel SLAH1 (AHRD V3.3 *** SLAH1_ARATH)	GO:0006873|GO:0008308|GO:0016021|GO:0016021|GO:0055085|GO:0016021|GO:0055085
Solyc05g054470.3	9,45E-01	8,82E-03	1,42E+00	2,36E-04	-2,55E-01	4,51E-01	**-1,45E+00**	**1,88E-04**	*nifD*- NoN 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 --* AT2G28290.6)	
Solyc04g014550.3	8,47E-02	9,13E-01	1,40E+00	8,08E-02	4,38E-01	5,74E-01	**2,42E+00**	**4,20E-03**	*nifD*- NoN 14 dpi	CS	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT5G37478.1)	GO:0005819|GO:0005874|GO:0032147|GO:0060236
Solyc04g074120.3	1,07E+00	4,85E-03	1,39E+00	4,62E-04	-7,31E-01	4,43E-02	**-1,01E+00**	**7,11E-03**	*nifD*- NoN 14 dpi	DNA	Synaptonemal complex protein 1 (AHRD V3.3 *** A0A151TZS6_CAJCA)	
Solyc01g098310.2	7,06E-01	1,64E-01	1,37E+00	9,86E-03	-1,36E+00	1,06E-02	**-2,05E+00**	**3,18E-04**	*nifD*- NoN 14 dpi	STR	DNAJ heat shock N-terminal domain-containing protein, putative (AHRD V3.3 *-* A0A061F0P5_THECC)	
Solyc08g066270.2	4,66E-02	9,16E-01	1,35E+00	5,01E-03	-7,54E-01	9,83E-02	**-1,64E+00**	**9,81E-04**	*nifD*- NoN 14 dpi	D	kinase family with leucine-rich repeat domain-containing protein (AHRD V3.3 *** AT5G25930.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g061850.3	-3,50E-02	9,23E-01	1,34E+00	9,03E-04	1,29E-01	7,21E-01	**-1,04E+00**	**7,34E-03**	*nifD*- NoN 14 dpi	L	Phospholipase D (AHRD V3.3 *** K4B675_SOLLC)	GO:0003824|GO:0004630|GO:0005509|GO:0016020|GO:0046470|GO:0004630|GO:0005509|GO:0016020|GO:0046470
Solyc03g114800.1	5,48E-01	7,39E-02	1,31E+00	1,49E-04	5,83E-01	5,85E-02	**-1,04E+00**	**1,59E-03**	*nifD*- NoN 14 dpi	TR	Sulfotransferase (AHRD V3.3 *** K4BKY2_SOLLC)	GO:0008146
Solyc02g092050.3	7,00E-01	7,05E-02	1,31E+00	1,62E-03	2,87E-01	4,47E-01	**-1,28E+00**	**1,92E-03**	*nifD*- NoN 14 dpi	H	AP2-like ethylene-responsive transcription factor (AHRD V3.3 *** A0A072VCJ1_MEDTR)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc04g074380.3	1,23E+00	3,35E-03	1,30E+00	2,10E-03	-7,04E-01	7,58E-02	**-1,81E+00**	**6,58E-05**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *-* M1D1E1_SOLTU)	GO:0008152|GO:0016758
Solyc12g007080.2	1,99E-01	7,50E-01	1,30E+00	4,54E-02	2,15E+00	1,78E-03	**-2,68E+00**	**1,95E-04**	*nifD*- NoN 14 dpi	DNA	Plant regulator RWP-RK family protein (AHRD V3.3 --* AT2G17150.6)	
Solyc00g203660.2	1,11E+00	8,08E-02	1,29E+00	4,34E-02	1,62E+00	1,30E-02	**1,81E+00**	**6,18E-03**	*nifD*- NoN 14 dpi	E	Ribulose bisphosphate carboxylase large chain (AHRD V3.3 *-* RBL_SOLBU)	GO:0000287
Solyc10g050210.2	2,18E+00	2,29E-05	1,29E+00	5,35E-03	-1,16E-02	9,78E-01	**-1,71E+00**	**4,28E-04**	*nifD*- NoN 14 dpi	H	Abscisic acid responsive element-binding factor 1 family protein (AHRD V3.3 *** U5GLH1_POPTR)	GO:0003700|GO:0006355|GO:0043565
Solyc12g037930.2	7,86E-01	1,19E-02	1,28E+00	1,57E-04	-4,06E-01	1,74E-01	**-1,17E+00**	**4,49E-04**	*nifD*- NoN 14 dpi	DNA	zinc finger (Ran-binding) family protein (AHRD V3.3 --* AT5G17790.1)	
Solyc05g009580.3	1,45E+00	5,61E-02	1,27E+00	9,07E-02	8,49E-01	2,52E-01	**2,43E+00**	**2,47E-03**	*nifD*- NoN 14 dpi	G	aluminum activated malate transporter family protein (AHRD V3.3 *** AT1G68600.1)	GO:0015743
Solyc07g066560.1	1,50E+00	1,68E-03	1,27E+00	6,14E-03	-5,83E-01	1,83E-01	**-1,26E+00**	**6,57E-03**	*nifD*- NoN 14 dpi	H	Small auxin up-regulated RNA65	GO:0009733
Solyc06g066490.1	1,90E+00	1,46E-03	1,25E+00	2,70E-02	-5,46E-01	3,14E-01	**-2,72E+00**	**2,56E-05**	*nifD*- NoN 14 dpi	D	Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *-* G7II06_MEDTR)	

Solyc05g024410.3	-4,22E-01	6,03E-01	1,24E+00	1,34E-01	2,43E-01	7,64E-01	**-3,40E+00**	**2,51E-04**	*nifD*- NoN 14 dpi	TR	Na+/H+ exchanger 8 (AHRD V3.3 --* AT1G14660.2)	
Solyc01g105350.2	5,93E-01	3,78E-01	1,23E+00	7,53E-02	1,45E-01	8,28E-01	**-3,76E+00**	**5,67E-06**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4B2A5_SOLLC)	GO:0008152|GO:0016758
Solyc05g051310.1	2,22E-01	4,30E-01	1,22E+00	1,65E-04	1,17E-01	6,77E-01	**-1,40E+00**	**3,04E-05**	*nifD*- NoN 14 dpi	H	LOW QUALITY:Ethylene-responsive transcription factor 5 (AHRD V3.3 *-* ERF5_NICSY)	
Solyc12g009930.2	5,34E-01	2,05E-02	1,19E+00	9,46E-06	9,21E-01	2,44E-04	**-1,13E+00**	**1,84E-05**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DC81_SOLLC)	GO:0008152|GO:0016758
Solyc01g091760.2	-6,56E-01	4,67E-01	1,17E+00	1,98E-01	-1,22E+00	1,83E-01	**-2,97E+00**	**2,59E-03**	*nifD*- NoN 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *** W9R099_9ROSA)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc03g115890.3	-1,14E-01	6,62E-01	1,17E+00	1,16E-04	-3,21E-01	2,24E-01	**-1,56E+00**	**2,32E-06**	*nifD*- NoN 14 dpi	CS	expansin 10	GO:0005576|GO:0009664|GO:0009664
Solyc04g040120.1	8,72E-01	5,68E-02	1,16E+00	1,36E-02	1,03E+00	2,65E-02	**-1,56E+00**	**1,44E-03**	*nifD*- NoN 14 dpi	2M	Fatty acid desaturase (AHRD V3.3 *** I3RV99_9ERIC)	GO:0006629|GO:0016717|GO:0055114|GO:0016717|GO:0055114
Solyc01g109880.3	4,23E-01	6,78E-02	1,16E+00	1,97E-05	1,72E-01	4,46E-01	**-1,34E+00**	**2,38E-06**	*nifD*- NoN 14 dpi	T	BZIP transcription factor (AHRD V3.3 *** C0KYN1_SOLLC)	GO:0003700|GO:0006355|GO:0043565
Solyc12g008850.2	1,42E+00	1,17E-01	1,16E+00	1,97E-01	-9,61E-01	2,81E-01	**2,49E+00**	**8,47E-03**	*nifD*- NoN 14 dpi	DNA	Lysine-specific histone demethylase 1 homolog 1 (AHRD V3.3 *** LDL1_ARATH)	GO:0016491|GO:0055114
Solyc01g097340.3	3,93E-01	7,36E-02	1,15E+00	1,12E-05	-2,04E-01	3,42E-01	**-1,19E+00**	**6,73E-06**	*nifD*- NoN 14 dpi	2M	GDP-mannose 3',5'-epimerase (AHRD V3.3 *** C6K2K9_SOLLC)	GO:0003824|GO:0050662|GO:0047918|GO:0051287|GO:0047918|GO:0051287
Solyc08g078300.3	6,40E-01	1,70E-03	1,12E+00	1,96E-06	3,24E-01	8,80E-02	**-1,32E+00**	**1,16E-07**	*nifD*- NoN 14 dpi	DNA	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9MUS1_POPTR)	GO:0003677|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565
Solyc06g007960.3	9,38E-01	3,03E-03	1,10E+00	7,21E-04	-3,47E-01	2,36E-01	**-1,25E+00**	**1,82E-04**	*nifD*- NoN 14 dpi	2M	Caffeic O-methyltransferase (AHRD V3.3 *** A0A068FLE8_PUNGR)	GO:0008168|GO:0008171|GO:0008171
Solyc03g094010.3	7,20E-01	2,06E-01	1,10E+00	5,92E-02	5,73E-01	3,12E-01	**-1,90E+00**	**2,11E-03**	*nifD*- NoN 14 dpi	N	glutamate dehydrogenase	GO:0004352|GO:0006520|GO:0016491|GO:0055114|GO:0006520|GO:0016491|GO:0055114
Solyc09g083400.3	3,59E-01	1,59E-02	1,10E+00	2,57E-08	-9,13E-01	6,25E-07	**-1,03E+00**	**8,29E-08**	*nifD*- NoN 14 dpi	CS	TPX2 (targeting protein for Xklp2) protein family (AHRD V3.3 *** AT3G23090.4)	
Solyc01g007130.3	4,65E-01	1,89E-02	1,09E+00	3,44E-06	6,45E-03	9,73E-01	**-1,02E+00**	**9,21E-06**	*nifD*- NoN 14 dpi	S	Receptor-like protein kinase (AHRD V3.3 *** Q58JF6_SOLPI)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g006960.3	3,68E-01	1,45E-01	1,08E+00	1,70E-04	3,47E-01	1,69E-01	**-1,28E+00**	**1,87E-05**	*nifD*- NoN 14 dpi	TR	ABC transporter family protein (AHRD V3.3 *** A0A097P9T3_HEVBR)	GO:0005524|GO:0016887|GO:0016020|GO:0016020
Solyc02g065060.3	-5,43E-02	9,61E-01	1,08E+00	3,38E-01	2,55E+00	2,87E-02	**3,51E+00**	**3,76E-03**	*nifD*- NoN 14 dpi	L	3-ketodihydrosphingosine reductase (AHRD V3.3 *** A0A0B0PNI7_GOSAR)	
Solyc11g066820.2	5,40E-01	1,12E-02	1,03E+00	1,90E-05	-4,28E-01	3,95E-02	**-1,37E+00**	**2,59E-07**	*nifD*- NoN 14 dpi	CS	Cellulose synthase-like protein (AHRD V3.3 *** L0ATP8_POPTO)	
Solyc08g068540.3	1,42E+00	2,11E-02	1,03E+00	8,66E-02	2,53E-01	6,66E-01	**1,88E+00**	**3,17E-03**	*nifD*- NoN 14 dpi	DNA	B3 domain-containing protein (AHRD V3.3 *** W9QJE4_9ROSA)	GO:0003677
Solyc03g113950.3	1,66E+00	1,40E-02	1,02E+00	1,17E-01	1,33E+00	4,48E-02	**2,16E+00**	**2,07E-03**	*nifD*- NoN 14 dpi	DNA	Calmodulin-binding protein (AHRD V3.3 *-* AT5G57580.1)	GO:0005516|GO:0006950
Solyc02g081600.3	9,74E-01	8,89E-03	1,01E+00	7,01E-03	-2,31E-01	5,09E-01	**-1,16E+00**	**2,34E-03**	*nifD*- NoN 14 dpi	TR	Zinc transporter protein (AHRD V3.3 *** A5BDR3_VITVI)	GO:0005385|GO:0016021|GO:0071577|GO:0016020|GO:0030001|GO:0046873|GO:0055085|GO:0016020|GO:0030001|GO:0046873|GO:0055085
Solyc06g072430.2	1,27E+00	1,20E-03	1,00E+00	7,72E-03	-3,26E-01	3,56E-01	**-1,01E+00**	**7,24E-03**	*nifD*- NoN 14 dpi	P	BAG family molecular chaperone regulator 5 (AHRD V3.3 *-* W9QTU5_9ROSA)	GO:0005515|GO:0051087|GO:0051087
Solyc12g055920.2	3,07E-01	6,72E-02	1,00E+00	1,37E-06	-9,66E-01	2,50E-06	**-1,23E+00**	**4,62E-08**	*nifD*- NoN 14 dpi	S	Calcineurin B, putative (AHRD V3.3 *** B9RCU6_RICCO)	GO:0005509
Solyc09g018280.1	9,01E-01	3,31E-04	9,98E-01	1,03E-04	-1,56E-01	4,79E-01	**-1,00E+00**	**9,86E-05**	*nifD*- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4CS94_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g106600.2	3,31E-01	6,95E-01	9,89E-01	2,48E-01	9,69E-01	2,58E-01	**3,35E+00**	**4,66E-04**	*nifD*- NoN 14 dpi	D	Pathogenesis-related protein 1 (AHRD V3.3 *** E2GEU1_9ROSI)	GO:0005576
Solyc06g051800.3	3,60E-01	4,07E-01	9,89E-01	2,90E-02	-2,45E-01	5,71E-01	**-1,35E+00**	**4,00E-03**	*nifD*- NoN 14 dpi	CS	expansin 1	GO:0005576|GO:0009664|GO:0009664

Solyc01g110843.1	6,76E-01	3,25E-01	9,88E-01	1,54E-01	-1,49E+00	3,58E-02	**-1,94E+00**	**7,77E-03**	*nifD*- NoN 14 dpi	H	SAUR-like auxin-responsive protein family (AHRD V3.3 *** A0A061DYL9_THECC)	GO:0009733
Solyc01g095360.2	7,16E-01	7,17E-02	9,86E-01	1,58E-02	2,39E-01	5,36E-01	**-1,40E+00**	**1,10E-03**	*nifD*- NoN 14 dpi	S	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT4G01200.1)	GO:0005515
Solyc01g104290.2	-1,43E-01	6,55E-01	9,84E-01	4,46E-03	-9,09E-01	7,96E-03	**-1,36E+00**	**2,14E-04**	*nifD*- NoN 14 dpi	D	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** G7K8X4_MEDTR)	
Solyc01g100000.3	1,96E+00	2,25E-02	9,79E-01	2,35E-01	1,96E+00	2,21E-02	**4,45E+00**	**8,96E-06**	*nifD*- NoN 14 dpi	P	F-box protein (AHRD V3.3 *** W9RMP6_9ROSA)	GO:0005515
Solyc10g085800.2	3,52E-01	2,18E-01	9,76E-01	1,68E-03	-6,19E-01	3,50E-02	**-1,61E+00**	**4,52E-06**	*nifD*- NoN 14 dpi	T	PLATZ transcription factor family protein (AHRD V3.3 *** G7IA73_MEDTR)	
Solyc02g091910.2	3,52E-01	5,99E-01	9,74E-01	1,53E-01	7,34E-01	2,77E-01	**-3,10E+00**	**7,63E-05**	*nifD*- NoN 14 dpi	G	Epidermal patterning factor-like protein (AHRD V3.3 *** G7K151_MEDTR),Pfam:PF17181	
Solyc08g080640.2	6,11E-01	2,46E-02	9,67E-01	8,37E-04	9,99E-01	6,06E-04	**2,54E+00**	**2,88E-10**	*nifD*- NoN 14 dpi	D	Osmotin-like protein (Fragment) IPR017949 Thaumatin, conserved site IPR001938	
Solyc04g014530.1	6,41E-02	8,53E-01	9,54E-01	9,91E-03	3,09E-01	3,75E-01	**2,07E+00**	**2,31E-06**	*nifD*- NoN 14 dpi	H	Ethylene Response Factor C.2	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc01g006580.3	8,96E-01	1,66E-05	9,53E-01	6,85E-06	5,31E-01	4,30E-03	**1,19E+00**	**2,04E-07**	*nifD*- NoN 14 dpi	E	2-oxoglutarate-dependent dioxygenase-related family protein (AHRD V3.3 *** B9GL08_POPTR)	GO:0016491|GO:0055114
Solyc12g011170.2	6,38E-01	9,33E-02	9,27E-01	1,79E-02	-8,02E-01	3,79E-02	**-1,04E+00**	**8,95E-03**	*nifD*- NoN 14 dpi	L	Phospholipase D (AHRD V3.3 *** M1AD93_SOLTU)	GO:0003824|GO:0004630|GO:0005509|GO:0016020|GO:0046470|GO:0004630|GO:0005509|GO:0016020|GO:0046470
Solyc03g025190.4	1,43E-01	8,80E-01	9,19E-01	3,38E-01	2,26E-01	8,12E-01	**-2,67E+00**	**8,69E-03**	*nifD*- NoN 14 dpi	TR	anthocyanin permease	
Solyc02g091140.3	1,09E-01	5,58E-01	9,14E-01	3,81E-05	-8,71E-01	7,02E-05	**-1,42E+00**	**3,81E-08**	*nifD*- NoN 14 dpi	H	S-adenosyl-L-methionine:carboxyl methyltransferase family protein (AHRD V3.3 *** B9HJH9_POPTR)	GO:0008168
Solyc03g093330.3	-8,87E-02	6,62E-01	9,12E-01	1,13E-04	-4,80E-01	2,43E-02	**-1,34E+00**	**4,66E-07**	*nifD*- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C1J5_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g110890.1	6,81E-02	8,49E-01	9,06E-01	1,70E-02	-1,16E-01	7,46E-01	**-1,36E+00**	**7,18E-04**	*nifD*- NoN 14 dpi	CS	LOW QUALITY:glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT4G24910.1)	GO:0045492
Solyc02g090120.1	9,53E-01	9,92E-05	9,04E-01	1,83E-04	3,44E-02	8,69E-01	**1,20E+00**	**4,54E-06**	*nifD*- NoN 14 dpi	G	LOW QUALITY:Inositol 1,4,5-trisphosphate receptor-interacting protein-like 2 (AHRD V3.3 -** A0A1D1XL30_9ARAE)	
Solyc01g109790.3	4,42E-01	1,49E-02	8,99E-01	1,55E-05	3,00E-01	8,80E-02	**-2,60E+00**	**1,90E-14**	*nifD*- NoN 14 dpi	C	ADP-glucose pyrophosphorylase large subunit 1	GO:0005978|GO:0008878|GO:0009058|GO:0016779|GO:0009058|GO:0016779
Solyc01g081620.3	4,69E-01	2,37E-01	8,88E-01	3,03E-02	-8,05E-01	4,78E-02	**-1,93E+00**	**3,59E-05**	*nifD*- NoN 14 dpi	G	Vacuolar protein sorting-associated protein 62 (AHRD V3.3 *** A0A103Y146_CYNCS)	
Solyc04g014520.1	-8,77E-01	2,63E-01	8,83E-01	2,59E-01	-3,42E-01	6,59E-01	**-2,40E+00**	**4,24E-03**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:Transmembrane protein 45B (AHRD V3.3 *** A0A151U0K4_CAJCA)	
Solyc03g118820.3	9,66E-01	5,74E-04	8,79E-01	1,43E-03	3,52E-01	1,65E-01	**1,05E+00**	**2,30E-04**	*nifD*- NoN 14 dpi	S	RAB GTPase A6A (AHRD V3.3 *** A0A061FW42_THECC)	GO:0005525|GO:0005525|GO:0007264|GO:0005525|GO:0007264
Solyc04g007250.1	9,05E-01	1,95E-02	8,78E-01	2,30E-02	4,18E-01	2,60E-01	**2,96E+00**	**1,39E-08**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** G7K1J5_MEDTR)	
Solyc06g054150.1	9,26E-01	1,69E-04	8,77E-01	3,12E-04	8,18E-01	6,46E-04	**1,08E+00**	**2,59E-05**	*nifD*- NoN 14 dpi	STR	LOW QUALITY:17.6 kDa class II heat shock protein (AHRD V3.3 *** A0A061EM62_THECC)	
Solyc01g067700.3	8,08E-02	8,32E-01	8,75E-01	2,87E-02	1,82E-01	6,35E-01	**-1,19E+00**	**4,20E-03**	*nifD*- NoN 14 dpi	DNA	SAGA-associated factor 11 (AHRD V3.3 *-* J3NDX3_ORYBR)	
Solyc05g051270.3	8,71E-01	1,43E-01	8,74E-01	1,41E-01	-7,17E-01	2,24E-01	**-4,25E+00**	**8,28E-08**	*nifD*- NoN 14 dpi	S	Cysteine-rich repeat secretory protein 60 (AHRD V3.3 *** A0A061EEI8_THECC)	
Solyc07g052230.3	7,11E-01	4,61E-03	8,74E-01	7,73E-04	-8,56E-01	9,47E-04	**-1,74E+00**	**4,99E-08**	*nifD*- NoN 14 dpi	D	L-ascorbate oxidase like (AHRD V3.3 *** A0A0B2S927_GLYSO)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc05g056430.2	4,46E-01	4,05E-01	8,69E-01	1,11E-01	-1,39E+00	1,36E-02	**-1,95E+00**	**1,01E-03**	*nifD*- NoN 14 dpi	H	Small auxin up-regulated RNA56	GO:0009733
Solyc07g049670.3	3,84E-01	7,32E-02	8,69E-01	2,66E-04	-2,09E-01	3,19E-01	**-1,14E+00**	**8,91E-06**	*nifD*- NoN 14 dpi	2M	Benzyl alcohol O-benzoyltransferase (AHRD V3.3 *** BEBT_TOBAC)	GO:0016747

Solyc01g109150.4	7,44E-01	8,86E-05	8,67E-01	1,18E-05	-2,05E-01	2,11E-01	**1,19E+00**	**7,49E-08**	*nifD*- NoN 14 dpi	CYTP450	cytochrome P450 CYP74C4	
Solyc09g063060.3	4,81E-01	5,73E-01	8,66E-01	3,14E-01	9,54E-01	2,69E-01	**2,77E+00**	**2,98E-03**	*nifD*- NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A0B2RSX5_GLYSO)	GO:0016788
Solyc05g051870.3	2,26E-01	4,44E-01	8,66E-01	6,15E-03	-1,98E-01	5,00E-01	**-1,03E+00**	**1,46E-03**	*nifD*- NoN 14 dpi	G	Pollen Ole e 1 allergen/extensin (AHRD V3.3 *** A0A103XBC9_CYNCS),Pfam:PF01190	
Solyc11g071940.1	-1,68E-01	8,65E-01	8,56E-01	3,90E-01	-1,91E+00	6,19E-02	**-3,54E+00**	**1,28E-03**	*nifD*- NoN 14 dpi	G	FANTASTIC four-like protein (DUF3049) (AHRD V3.3 *-* AT5G19260.1)	
Solyc09g062970.1	-1,09E+00	1,77E-01	8,56E-01	2,86E-01	-2,18E+00	1,01E-02	**-3,29E+00**	**2,92E-04**	*nifD*- NoN 14 dpi	L	GDSL-like Lipase/Acylhydrolase superfamily protein (AHRD V3.3 --* AT3G53100.1)	
Solyc01g059965.1	-2,34E-01	8,16E-01	8,53E-01	4,00E-01	9,50E-01	3,49E-01	**4,54E+00**	**1,10E-04**	*nifD*- NoN 14 dpi	CS	Beta-1,3-glucanase (AHRD V3.3 *** G9G7S0_HEVBR)	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc09g072640.3	-3,98E-02	9,19E-01	8,51E-01	3,68E-02	1,87E-01	6,32E-01	**-1,10E+00**	**8,39E-03**	*nifD*- NoN 14 dpi	H	ROP-interactive CRIB motif protein (AHRD V3.3 *-* A0A072U2K9_MEDTR)	
Solyc05g007510.3	8,44E-01	8,42E-03	8,49E-01	8,08E-03	-4,52E-01	1,39E-01	**-1,36E+00**	**9,84E-05**	*nifD*- NoN 14 dpi	RNA	RNA-directed RNA polymerase	GO:0000166|GO:0003676|GO:0003676
Solyc05g054480.3	-1,84E-01	5,86E-01	8,48E-01	1,78E-02	-4,51E-01	1,89E-01	**-1,69E+00**	**3,01E-05**	*nifD*- NoN 14 dpi	CS	Actin (AHRD V3.3 *** ACT1_TOBAC)	
Solyc08g082440.3	7,05E-01	1,60E-02	8,48E-01	4,63E-03	9,32E-02	7,36E-01	**1,29E+00**	**7,50E-05**	*nifD*- NoN 14 dpi	C	UDP-glucose 4-epimerase (AHRD V3.3 *** Q6XZA0_SOLTU)	GO:0003978|GO:0006012|GO:0005975|GO:0016857|GO:0005975|GO:0016857
Solyc06g035720.3	2,26E-01	5,45E-02	8,44E-01	5,79E-08	-4,88E-01	1,90E-04	**-1,06E+00**	**6,87E-10**	*nifD*- NoN 14 dpi	P	BAG family molecular chaperone regulator 2 (AHRD V3.3 *** BAG2_ARATH)	GO:0005515|GO:0051087|GO:0051087
Solyc08g014330.3	5,02E-01	1,93E-01	8,40E-01	3,39E-02	-2,13E-01	5,74E-01	**-1,09E+00**	**7,23E-03**	*nifD*- NoN 14 dpi	AM	Amine oxidase (AHRD V3.3 *** K4CJ66_SOLLC)	GO:0005507|GO:0008131|GO:0009308|GO:0048038|GO:0055114
Solyc06g071070.1	4,05E-01	5,73E-02	8,39E-01	3,46E-04	9,77E-01	5,86E-05	**1,37E+00**	**4,26E-07**	*nifD*- NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT3G03980.1),Pfam:PF13561	GO:0016491
Solyc01g099450.3	3,72E-01	3,31E-01	8,38E-01	3,42E-02	-4,63E-01	2,28E-01	**-1,21E+00**	**3,44E-03**	*nifD*- NoN 14 dpi	DNA	ATP-dependent DNA helicase Q-like SIM (AHRD V3.3 *-* W9S050_9ROSA)	
Solyc03g078780.2	8,29E-01	7,32E-02	8,37E-01	7,08E-02	-1,27E-01	7,77E-01	**-1,92E+00**	**2,02E-04**	*nifD*- NoN 14 dpi	C	UDP-glycosyltransferase (AHRD V3.3 *** A0A164TMY6_DAUCA)	GO:0008152|GO:0016758
Solyc02g090310.1	-7,70E-03	9,74E-01	8,36E-01	1,51E-03	-1,16E-01	6,28E-01	**-1,28E+00**	**1,08E-05**	*nifD*- NoN 14 dpi	DNA	Dof zinc finger protein (AHRD V3.3 *-* W9QGW0_9ROSA)	GO:0003677|GO:0006355
Solyc07g049660.3	1,60E-01	5,68E-01	8,30E-01	5,92E-03	5,65E-02	8,40E-01	**-1,25E+00**	**1,19E-04**	*nifD*- NoN 14 dpi	2M	Benzyl alcohol O-benzoyltransferase (AHRD V3.3 *-* BEBT_TOBAC)	GO:0016747
Solyc07g053640.1	-4,05E-01	1,81E-01	8,27E-01	9,33E-03	2,32E-01	4,37E-01	**-1,27E+00**	**2,15E-04**	*nifD*- NoN 14 dpi	CS	LOW QUALITY:Arabinogalactan-protein (AHRD V3.3 *-* Q41256_NICAL)	
Solyc05g009990.3	-4,18E-01	4,34E-01	8,24E-01	1,30E-01	4,66E-01	3,85E-01	**1,60E+00**	**5,30E-03**	*nifD*- NoN 14 dpi	PMI	Leucine-rich repeat family protein (AHRD V3.3 *** A0A061ECS2_THECC)	GO:0005515
Solyc01g101170.3	8,89E-01	5,47E-01	8,22E-01	5,77E-01	3,55E+00	2,19E-02	**5,94E+00**	**3,90E-04**	*nifD*- NoN 14 dpi	2M	Viridiflorene synthase (AHRD V3.3 *** TPS31_SOLLC)	GO:0000287|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829
Solyc12g005820.2	8,30E-01	6,21E-05	8,14E-01	7,83E-05	4,02E-01	2,88E-02	**1,18E+00**	**3,45E-07**	*nifD*- NoN 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G27660.1)	
Solyc03g007760.3	3,48E-01	1,05E-02	8,04E-01	9,79E-07	-4,34E-01	1,98E-03	**-1,53E+00**	**3,78E-12**	*nifD*- NoN 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT4G28000.1)	GO:0005524
Solyc06g084420.1	2,01E-02	9,58E-01	8,03E-01	4,11E-02	-8,76E-01	2,70E-02	**-1,08E+00**	**7,57E-03**	*nifD*- NoN 14 dpi	PMI	Leucine-rich repeat receptor-like kinase (AHRD V3.3 *** A0A0K9PKL2_ZOSMR)	GO:0005515
Solyc06g065340.1	4,45E-01	1,36E-01	8,01E-01	1,02E-02	-4,54E-01	1,29E-01	**-1,53E+00**	**1,68E-05**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Ca(2+)-dependent nuclease family protein (AHRD V3.3 --* AT2G40410.2)	
Solyc07g055720.3	2,74E-01	6,82E-01	7,98E-01	2,38E-01	1,40E+00	4,41E-02	**2,09E+00**	**3,92E-03**	*nifD*- NoN 14 dpi	STR	Heat shock protein, putative (AHRD V3.3 *** Q8LD91_ARATH)	
Solyc10g078920.2	4,11E-01	6,92E-01	7,98E-01	4,44E-01	1,82E+00	8,81E-02	**3,63E+00**	**1,56E-03**	*nifD*- NoN 14 dpi	OX	Thioredoxin (AHRD V3.3 *** G7KVF9_MEDTR)	GO:0006662|GO:0015035|GO:0045454|GO:0045454|GO:0045454

Solyc03g120930.1	-1,31E-01	5,54E-01	7,97E-01	1,21E-03	-3,39E-01	1,34E-01	**-1,80E+00**	**1,17E-08**	*nifD*- NoN 14 dpi	D	Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** G7LFZ0_MEDTR)	
Solyc03g112300.3	1,38E+00	1,56E-02	7,93E-01	1,49E-01	3,01E-01	5,77E-01	**2,88E+00**	**1,20E-05**	*nifD*- NoN 14 dpi	K	Octicosapeptide/Phox/Bem1p domain-containing protein kinase (AHRD V3.3 *-* A0A0K9NT10_ZOSMR)	GO:0005515
Solyc10g055810.2	3,53E-01	1,45E-01	7,89E-01	2,44E-03	2,61E-01	2,77E-01	**2,21E+00**	**8,04E-10**	*nifD*- NoN 14 dpi	D	chitinase Z15140	GO:0004568|GO:0005975|GO:0004568|GO:0006032|GO:0016998|GO:0004568|GO:0006032|GO:0016998
Solyc05g008270.3	6,45E-01	5,06E-02	7,86E-01	1,92E-02	1,53E-01	6,30E-01	**-1,31E+00**	**3,00E-04**	*nifD*- NoN 14 dpi	NA	DUF3326 family protein (AHRD V3.3 *** A0A072VFG1_MEDTR)	
Solyc11g072030.2	2,77E-01	3,06E-01	7,79E-01	6,89E-03	4,15E-01	1,30E-01	**1,14E+00**	**2,10E-04**	*nifD*- NoN 14 dpi	L	Lipid transfer protein (AHRD V3.3 *** B7FFE5_MEDTR)	
Solyc08g078550.1	7,36E-02	7,08E-01	7,78E-01	4,78E-04	2,79E-01	1,63E-01	**1,22E+00**	**1,36E-06**	*nifD*- NoN 14 dpi	STR	Metalloendoproteinase 1, putative (AHRD V3.3 *** B9T8P6_RICCO)	GO:0004222|GO:0006508|GO:0008270|GO:0031012|GO:0006508|GO:0008237|GO:0008270|GO:0006508|GO:0008237|GO:0008270
Solyc03g114310.3	1,10E+00	8,91E-06	7,73E-01	6,48E-04	-7,07E-01	1,53E-03	**-1,07E+00**	**1,28E-05**	*nifD*- NoN 14 dpi	K	MAP kinase kinase kinase 28	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g067620.3	4,02E-01	5,91E-03	7,73E-01	4,62E-06	5,74E-01	2,27E-04	**-1,37E+00**	**1,61E-10**	*nifD*- NoN 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT3G21420.1)	GO:0016491|GO:0055114
Solyc04g080260.3	3,00E-01	5,33E-02	7,67E-01	2,17E-05	-2,09E-01	1,71E-01	**-1,37E+00**	**1,19E-09**	*nifD*- NoN 14 dpi	CS	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9R7T0_RICCO)	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc04g077230.1	2,34E-01	3,19E-01	7,67E-01	2,60E-03	9,80E-01	2,41E-04	**1,01E+00**	**1,79E-04**	*nifD*- NoN 14 dpi	H	Indole-3-acetaldehyde oxidase (AHRD V3.3 --* ALDO1_MAIZE)	
Solyc06g051350.3	-3,54E-02	8,52E-01	7,59E-01	4,11E-04	-3,82E-01	5,15E-02	**-1,38E+00**	**8,22E-08**	*nifD*- NoN 14 dpi	CS	trichome birefringence-like protein (DUF828) (AHRD V3.3 *** AT3G55990.1)	GO:0050826
Solyc07g053080.3	-6,27E-01	5,23E-02	7,48E-01	2,25E-02	2,37E-02	9,39E-01	**-1,16E+00**	**8,74E-04**	*nifD*- NoN 14 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *-* K4CFK6_SOLLC)	GO:0004672|GO:0006468
Solyc08g078470.3	1,34E-01	5,50E-01	7,45E-01	2,38E-03	4,60E-01	4,78E-02	**1,12E+00**	**2,91E-05**	*nifD*- NoN 14 dpi	G	FHA domain-containing protein (AHRD V3.3 *-* W9R6B4_9ROSA)	GO:0005515
Solyc08g082860.3	1,66E-01	1,83E-01	7,45E-01	1,73E-06	3,75E-01	4,61E-03	**-1,18E+00**	**3,97E-10**	*nifD*- NoN 14 dpi	C	Trehalase (AHRD V3.3 *** K4CPT2_SOLLC)	GO:0003824|GO:0004555|GO:0005991|GO:0004555|GO:0005991
Solyc05g005920.3	5,89E-01	9,49E-04	7,44E-01	7,45E-05	-3,50E-01	3,58E-02	**-1,09E+00**	**2,71E-07**	*nifD*- NoN 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)	GO:0005215|GO:0006810|GO:0016020
Solyc05g053200.2	3,51E-01	1,94E-01	7,40E-01	9,39E-03	6,98E-01	1,36E-02	**-1,01E+00**	**6,99E-04**	*nifD*- NoN 14 dpi	NA	Mutator-like transposase-like protein (AHRD V3.3 *** Q9FI74_ARATH)	GO:0005515|GO:0008270|GO:0008270
Solyc03g059270.3	-2,85E-01	5,57E-01	7,36E-01	1,37E-01	-2,30E-01	6,36E-01	**-1,91E+00**	**4,89E-04**	*nifD*- NoN 14 dpi	DNA	Protein TRANSPARENT TESTA 1 (AHRD V3.3 *** A0A0B2PI42_GLYSO)	GO:0003676|GO:0046872|GO:0046872
Solyc05g053520.3	-3,95E-01	5,20E-01	7,35E-01	2,36E-01	3,81E-01	5,34E-01	**-2,37E+00**	**6,02E-04**	*nifD*- NoN 14 dpi	DNA	DNA polymerase delta subunit 4 family (AHRD V3.3 *** D7KJU8_ARALL)	GO:0005634|GO:0006260
Solyc08g066370.2	1,94E+00	1,83E-03	7,32E-01	2,02E-01	-1,31E+00	2,72E-02	**-3,38E+00**	**2,34E-06**	*nifD*- NoN 14 dpi	K	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151SE46_CAJCA)	
Solyc07g045440.1	3,09E-01	9,75E-02	7,31E-01	4,02E-04	-4,76E-01	1,38E-02	**-1,15E+00**	**9,75E-07**	*nifD*- NoN 14 dpi	PMI	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** G7K0M1_MEDTR)	
Solyc01g079940.3	-4,70E-02	8,71E-01	7,27E-01	1,81E-02	6,84E-01	2,53E-02	**2,02E+00**	**2,07E-07**	*nifD*- NoN 14 dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03220.1)	GO:0004190|GO:0006508
Solyc03g006010.3	-1,71E-01	5,47E-01	7,26E-01	1,57E-02	-8,72E-01	4,57E-03	**-1,33E+00**	**6,79E-05**	*nifD*- NoN 14 dpi	K	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase (AHRD V3.3 *** AT2G47010.2)	
Solyc04g005060.3	1,77E-01	7,25E-01	7,25E-01	1,58E-01	-2,99E-01	5,53E-01	**-3,07E+00**	**1,74E-06**	*nifD*- NoN 14 dpi	CS	TPX2 (Targeting protein for Xklp2) family protein, putative (AHRD V3.3 *** G7K5M5_MEDTR)	
Solyc02g094400.3	6,71E-01	6,93E-03	7,24E-01	3,95E-03	7,58E-01	2,73E-03	**3,44E+00**	**2,98E-14**	*nifD*- NoN 14 dpi	L	Glycerophosphodiester phosphodiesterase, putative (AHRD V3.3 *** B9RH28_RICCO)	GO:0006629|GO:0008081
Solyc07g006680.1	-6,96E-01	3,10E-02	7,24E-01	2,53E-02	-4,29E-01	1,72E-01	**-1,40E+00**	**1,03E-04**	*nifD*- NoN 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT3G26040.1)	GO:0016747
Solyc11g008720.2	7,34E-01	2,95E-06	7,17E-01	4,24E-06	3,82E-01	4,70E-03	**1,05E+00**	**6,37E-09**	*nifD*- NoN 14 dpi	C	Beta-glucosidase (AHRD V3.3 *** K4D5D2_SOLLC)	GO:0004553|GO:0005975|GO:0005975|GO:0005975

Solyc03g044090.3	7,20E-01	1,49E-02	7,16E-01	1,54E-02	1,13E-01	6,85E-01	**-1,17E+00**	**2,47E-04**	*nifD*- NoN 14 dpi	G	Phototropic-responsive NPH3 family protein	
Solyc01g005590.2	-1,11E-01	5,72E-01	7,11E-01	1,10E-03	-7,48E-01	6,69E-04	**-1,11E+00**	**5,01E-06**	*nifD*- NoN 14 dpi	CS	Arabinogalactan peptide 14 (AHRD V3.3 *** A0A151TQT2_CAJCA)	
Solyc01g105300.3	1,08E-02	9,79E-01	7,11E-01	8,98E-02	8,90E-01	3,65E-02	**1,15E+00**	**8,49E-03**	*nifD*- NoN 14 dpi	P	Metacaspase-1 (AHRD V3.3 *-* A0A0B2R4L3_GLYSO)	
Solyc07g062810.3	4,94E-01	1,23E-03	7,04E-01	2,18E-05	1,72E-01	2,16E-01	**-1,22E+00**	**2,17E-09**	*nifD*- NoN 14 dpi	AM	Branched-chain-amino-acid aminotransferase-like protein (AHRD V3.3 *** I3SQ86_MEDTR)	GO:0003824|GO:0008152|GO:0008696|GO:0030170|GO:0046656|GO:0008696|GO:0030170|GO:0046656
Solyc07g052550.2	1,38E+00	1,24E-01	7,01E-01	4,27E-01	-6,20E-01	4,81E-01	**-3,04E+00**	**1,69E-03**	*nifD*- NoN 14 dpi	OX	Peroxidase (AHRD V1 **** Q07445_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc10g085460.2	5,13E-01	6,50E-03	7,01E-01	4,20E-04	-2,76E-01	1,24E-01	**-1,29E+00**	**6,63E-08**	*nifD*- NoN 14 dpi	D	Nbs-lrr resistance protein, putative (AHRD V3.3 *** A0A061FEU3_THECC)	GO:0043531
Solyc06g063110.2	-5,37E-01	4,40E-02	6,97E-01	1,08E-02	8,71E-01	2,04E-03	**1,08E+00**	**2,39E-04**	*nifD*- NoN 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT1G72310.1)	GO:0005515|GO:0008270
Solyc04g080705.1	9,69E-01	1,16E-10	6,94E-01	7,49E-08	2,54E-01	1,16E-02	**1,23E+00**	**6,39E-13**	*nifD*- NoN 14 dpi	D	Bifunctional nuclease 1 (AHRD V3.3 *** BBD1_ARATH)	
Solyc02g081070.3	1,87E-01	3,20E-01	6,94E-01	9,04E-04	-3,15E-01	1,01E-01	**-1,04E+00**	**6,68E-06**	*nifD*- NoN 14 dpi	K	Kinase (AHRD V3.3 *** D7ME76_ARALL)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g063000.3	1,03E-01	6,36E-01	6,94E-01	3,53E-03	-5,60E-01	1,55E-02	**-1,19E+00**	**9,53E-06**	*nifD*- NoN 14 dpi	DNA	Nucleosome assembly protein 1-like 1 (AHRD V3.3 *** A0A0B2RMX0_GLYSO)	GO:0005634|GO:0006334
Solyc02g069670.3	-1,35E-01	4,83E-01	6,93E-01	1,19E-03	1,27E-01	5,11E-01	**-1,31E+00**	**2,70E-07**	*nifD*- NoN 14 dpi	C	Alpha-glucosidase (AHRD V3.3 *** AGLU_SPIOL)	GO:0003824|GO:0005975|GO:0030246|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc07g054170.3	4,09E-01	3,22E-01	6,86E-01	1,02E-01	3,27E-01	4,26E-01	**-1,28E+00**	**3,90E-03**	*nifD*- NoN 14 dpi	CS	expansin B3 (AHRD V3.3 *** AT4G28250.1)	GO:0005576|GO:0005576|GO:0019953|GO:0005576|GO:0019953
Solyc10g081720.2	3,64E-02	8,23E-01	6,83E-01	2,46E-04	-4,01E-01	1,93E-02	**-1,12E+00**	**2,41E-07**	*nifD*- NoN 14 dpi	PMI	fasciclin superfamily protein	
Solyc08g080770.3	8,26E-01	2,72E-01	6,82E-01	3,62E-01	-9,23E-02	9,01E-01	**-2,84E+00**	**6,70E-04**	*nifD*- NoN 14 dpi	D	LURP-one-like protein (AHRD V3.3 *** AT1G53875.1)	
Solyc02g070420.2	2,33E-02	9,46E-01	6,80E-01	5,83E-02	-4,36E-01	2,15E-01	**-1,17E+00**	**2,10E-03**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:transmembrane protein (AHRD V3.3 *-* AT2G34530.4)	
Solyc10g084600.2	6,11E-01	2,91E-02	6,80E-01	1,63E-02	5,42E-01	5,05E-02	**1,45E+00**	**1,02E-05**	*nifD*- NoN 14 dpi	NA	Plant protein 1589 of unknown function (AHRD V3.3 *** AT3G55240.1)	
Solyc02g071950.1	9,13E-01	1,23E-05	6,74E-01	4,94E-04	3,94E-01	2,79E-02	**1,08E+00**	**9,36E-07**	*nifD*- NoN 14 dpi	AM	LOW QUALITY:asparagine synthetase 2 (AHRD V3.3 --* AT5G65010.1)	
Solyc09g008060.3	-1,15E-01	4,73E-01	6,74E-01	2,40E-04	-3,05E-01	6,50E-02	**-1,27E+00**	**1,73E-08**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CQJ5_SOLLC)	GO:0008152|GO:0016758
Solyc06g005620.3	7,85E-01	2,59E-04	6,72E-01	1,26E-03	7,30E-01	5,60E-04	**1,56E+00**	**7,59E-09**	*nifD*- NoN 14 dpi	TR	zinc transporter	GO:0016020|GO:0030001|GO:0046873|GO:0055085
Solyc07g063600.3	1,60E+00	1,05E-02	6,71E-01	2,59E-01	2,05E-01	7,27E-01	**2,21E+00**	**7,78E-04**	*nifD*- NoN 14 dpi	E	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** M1BNX7_SOLTU)	GO:0009765|GO:0016020
Solyc02g093210.3	-1,14E+00	4,22E-02	6,67E-01	2,23E-01	2,62E-01	6,28E-01	**-2,04E+00**	**7,58E-04**	*nifD*- NoN 14 dpi	L	PI-PLC X domain-containing protein (AHRD V3.3 *** W9SGY7_9ROSA)	GO:0006629|GO:0008081
Solyc09g014160.2	-1,32E-01	6,01E-01	6,65E-01	1,29E-02	-1,47E-01	5,60E-01	**-1,39E+00**	**7,68E-06**	*nifD*- NoN 14 dpi	NA	UPF0503 protein, chloroplastic (AHRD V3.3 *** A0A199UN58_ANACO)	
Solyc08g006000.3	9,19E-01	5,19E-13	6,65E-01	5,46E-10	1,24E-01	8,49E-02	**1,01E+00**	**6,07E-14**	*nifD*- NoN 14 dpi	NA	keratin-associated protein (DUF1218) (AHRD V3.3 *** AT4G31130.1)	
Solyc01g079960.2	2,07E-01	2,17E-01	6,63E-01	4,06E-04	3,25E-01	5,73E-02	**1,07E+00**	**6,47E-07**	*nifD*- NoN 14 dpi	P	Eukaryotic aspartyl protease family protein (AHRD V3.3 *** AT1G03220.1)	GO:0004190|GO:0006508
Solyc02g065800.2	6,69E-01	1,90E-01	6,56E-01	1,98E-01	2,29E-01	6,48E-01	**1,61E+00**	**3,26E-03**	*nifD*- NoN 14 dpi	T	TCP transcription factor 28	
Solyc09g014480.2	-4,49E-01	2,85E-01	6,51E-01	1,26E-01	6,93E-01	1,05E-01	**1,74E+00**	**2,69E-04**	*nifD*- NoN 14 dpi	D	Polygalacturonase inhibitor protein (AHRD V3.3 *** Q40160_SOLLC)	GO:0005515
Solyc08g082250.3	-4,68E-01	1,87E-01	6,48E-01	7,23E-02	7,61E-02	8,28E-01	**-1,04E+00**	**5,92E-03**	*nifD*- NoN 14 dpi	CS	endo-beta-1,4-D-glucanase (Cel8)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975

Solyc01g107800.3	2,24E-01	2,14E-01	6,47E-01	1,11E-03	1,46E-01	4,16E-01	**-1,31E+00**	**6,97E-08**	*nifD*- NoN 14 dpi	CS	glucuronoxylan 4-O-methyltransferase-like protein (DUF579) (AHRD V3.3 *** AT1G71690.1)	GO:0045492
Solyc05g046110.3	-4,68E-02	9,45E-01	6,46E-01	3,41E-01	6,57E-01	3,33E-01	**2,49E+00**	**9,50E-04**	*nifD*- NoN 14 dpi	C	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)	
Solyc09g091550.3	-2,83E-01	7,28E-01	6,45E-01	4,30E-01	-2,14E+00	1,33E-02	**-2,83E+00**	**1,63E-03**	*nifD*- NoN 14 dpi	H	S-adenosyl-L-methionine: salicylic acid carboxyl methyltransferase (AHRD V3.3 *** D2Y3T9_SOLLC)	GO:0008168
Solyc10g076500.2	-8,56E-02	7,36E-01	6,38E-01	1,74E-02	-4,86E-01	6,38E-02	**-1,28E+00**	**2,70E-05**	*nifD*- NoN 14 dpi	PMI	Leucine-rich-repeat receptor-like protein (AHRD V3.3 *** A0A0D4WVW2_GOSBA)	GO:0005515
Solyc12g014140.2	1,27E+00	7,85E-04	6,34E-01	6,85E-02	-9,30E-01	9,83E-03	**-1,50E+00**	**1,33E-04**	*nifD*- NoN 14 dpi	T	SITCP3	
Solyc09g059470.3	-5,90E-01	1,13E-01	6,32E-01	9,06E-02	-6,00E-01	1,07E-01	**-1,20E+00**	**2,51E-03**	*nifD*- NoN 14 dpi	P	Trypsin-like cysteine/serine peptidase domain-containing protein (AHRD V3.3 *** A0A103YNC2_CYNCS)	
Solyc06g050350.3	-8,04E-02	8,20E-01	6,29E-01	8,42E-02	3,04E-01	3,93E-01	**-1,62E+00**	**9,28E-05**	*nifD*- NoN 14 dpi	G	weak chloroplast movement under blue light protein (DUF827) (AHRD V3.3 *** AT2G38370.2)	
Solyc12g042840.2	8,80E-01	9,63E-04	6,29E-01	1,32E-02	9,23E-02	6,99E-01	**1,48E+00**	**1,27E-06**	*nifD*- NoN 14 dpi	STR	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** AT1G80160.3)	
Solyc04g007000.1	1,14E+00	1,25E-02	6,28E-01	1,50E-01	-2,42E-01	5,72E-01	**3,40E+00**	**1,79E-08**	*nifD*- NoN 14 dpi	T	AP2/B3 transcription factor family protein (AHRD V3.3 *** AT1G25560.1)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc02g072030.1	8,07E-01	2,07E-01	6,26E-01	3,24E-01	-1,89E-02	9,76E-01	**-1,88E+00**	**5,55E-03**	*nifD*- NoN 14 dpi	G	LOW QUALITY:ovate family protein 5	
Solyc03g083320.3	3,62E-01	3,88E-02	6,26E-01	8,56E-04	-7,27E-01	1,76E-04	**-1,43E+00**	**4,66E-09**	*nifD*- NoN 14 dpi	S	calcium sensor calcineurin B	GO:0005509
Solyc01g091180.3	-1,39E+00	7,09E-02	6,21E-01	4,07E-01	-9,74E-02	8,96E-01	**-3,37E+00**	**1,05E-04**	*nifD*- NoN 14 dpi	TR	peptide transporter 1 (AHRD V3.3 *** AT3G54140.2)	GO:0005215|GO:0006810|GO:0016020
Solyc10g047240.2	3,43E-01	2,73E-02	6,21E-01	2,54E-04	-7,76E-01	1,56E-05	**-1,13E+00**	**3,45E-08**	*nifD*- NoN 14 dpi	TR	annexin 9	GO:0005509|GO:0005544
Solyc12g008550.2	6,75E-01	3,00E-04	6,14E-01	7,97E-04	7,19E-01	1,47E-04	**2,30E+00**	**1,13E-13**	*nifD*- NoN 14 dpi	P	Peptidase M28 family protein (AHRD V3.3 *-* AT5G19740.1)	
Solyc02g087070.3	6,81E-01	2,05E-03	6,12E-01	4,83E-03	1,01E-01	6,16E-01	**1,04E+00**	**1,96E-05**	*nifD*- NoN 14 dpi	OX	alpha-DOX1	GO:0004601|GO:0006979|GO:0020037|GO:0055114
Solyc02g088180.3	5,83E-01	1,12E-03	6,11E-01	7,10E-04	-4,31E-01	1,17E-02	**1,29E+00**	**1,37E-08**	*nifD*- NoN 14 dpi	T	NAC domain-containing protein (AHRD V3.3 *** A0A060A652_BOENI)	GO:0003677|GO:0006355
Solyc10g076710.2	3,00E-01	2,00E-01	6,10E-01	1,28E-02	-1,06E-01	6,45E-01	**-2,05E+00**	**2,05E-09**	*nifD*- NoN 14 dpi	L	Phosphoinositide phospholipase C (AHRD V3.3 *** A0A067L8K5_JATCU)	GO:0004435|GO:0006629|GO:0007165|GO:0035556|GO:0005515|GO:0005515
Solyc05g006450.2	-1,66E-01	6,16E-01	6,09E-01	7,44E-02	-8,55E-02	7,96E-01	**-1,18E+00**	**1,35E-03**	*nifD*- NoN 14 dpi	STR	Carboxypeptidase (AHRD V3.3 *-* K4BWH2_SOLLC)	GO:0004185|GO:0006508
Solyc10g086250.2	-1,59E+00	7,35E-02	6,09E-01	4,80E-01	-1,64E+00	6,46E-02	**-2,95E+00**	**1,85E-03**	*nifD*- NoN 14 dpi	G	R2R3MYB transcription factor 75	GO:0003677
Solyc01g111250.3	-1,76E-01	5,00E-01	6,04E-01	2,73E-02	-1,05E-02	9,68E-01	**-1,23E+00**	**6,39E-05**	*nifD*- NoN 14 dpi	L	1-phosphatidylinositol phosphodiesterase-related family protein (AHRD V3.3 *** B9H168_POPTR)	GO:0006629|GO:0008081
Solyc09g009280.1	6,89E-01	7,83E-03	6,03E-01	1,83E-02	1,31E-01	5,88E-01	**1,01E+00**	**2,77E-04**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:DUF868 family protein (AHRD V3.3 *** G7L506_MEDTR)	
Solyc03g096350.3	-6,65E-02	7,38E-01	5,98E-01	5,41E-03	-8,53E-01	1,99E-04	**-1,01E+00**	**2,34E-05**	*nifD*- NoN 14 dpi	T	Myb family transcription factor family protein (AHRD V3.3 *** B9HT09_POPTR)	GO:0003677
Solyc02g090410.3	5,63E-01	1,81E-02	5,97E-01	1,28E-02	6,12E-01	1,09E-02	**1,46E+00**	**6,22E-07**	*nifD*- NoN 14 dpi	G	ASYMMETRIC LEAVES 2-like 1 (AHRD V3.3 *** A0A061DMY0_THECC)	
Solyc11g064840.1	-2,45E-02	9,46E-01	5,90E-01	1,09E-01	6,88E-01	6,38E-02	**-1,04E+00**	**7,16E-03**	*nifD*- NoN 14 dpi	S	LOW QUALITY:Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** G7K355_MEDTR)	GO:0005515
Solyc09g090670.3	-3,18E-01	1,82E-01	5,88E-01	1,77E-02	-9,81E-01	2,59E-04	**-1,58E+00**	**3,23E-07**	*nifD*- NoN 14 dpi	OX	Oxidation resistance 1 (AHRD V3.3 *** A0A0B0PUF7_GOSAR)	
Solyc02g078650.3	1,76E-01	5,55E-01	5,87E-01	5,65E-02	4,42E-01	1,45E-01	**1,60E+00**	**1,04E-05**	*nifD*- NoN 14 dpi	2M	Polyphenol oxidase (AHRD V3.3 *** A0A118JXA6_CYNCS)	GO:0004097|GO:0046148|GO:0055114|GO:0004097|GO:0055114|GO:0004097|GO:0055114

Solyc02g082830.2	-2,08E-01	2,49E-01	5,80E-01	2,92E-03	-4,64E-01	1,42E-02	**-1,27E+00**	**1,22E-07**	*nifD*- NoN 14 dpi	AM	Phosphoserine aminotransferase (AHRD V3.3 *** K4BAF3_SOLLC)	GO:0003824|GO:0004648|GO:0006564|GO:0004648|GO:0006564
Solyc01g086720.3	3,61E-01	2,93E-01	5,80E-01	9,66E-02	-4,29E-01	2,13E-01	**-1,45E+00**	**2,07E-04**	*nifD*- NoN 14 dpi	DNA	C2 domain-containing family protein (AHRD V3.3 *** B9GFS0_POPTR)	GO:0005515
Solyc02g021410.3	2,11E-01	6,55E-01	5,78E-01	2,27E-01	1,19E+00	1,72E-02	**2,04E+00**	**1,77E-04**	*nifD*- NoN 14 dpi	TR	Cation/H(+) antiporter (AHRD V3.3 *** A0A0K9NPK0_ZOSMR)	GO:0006812|GO:0015299|GO:0016021|GO:0055085
Solyc05g054850.1	6,60E-02	8,55E-01	5,77E-01	1,19E-01	6,02E-01	1,05E-01	**-1,53E+00**	**2,23E-04**	*nifD*- NoN 14 dpi	S	membrane-associated kinase regulator (AHRD V3.3 *** AT2G39370.1)	
Solyc10g050980.1	-9,42E-01	3,59E-01	5,76E-01	5,73E-01	-1,06E-01	9,17E-01	**2,86E+00**	**8,85E-03**	*nifD*- NoN 14 dpi	RNA	PAB-dependent poly(A)-specific ribonuclease subunit PAN2 (AHRD V3.3 -** A0A1D1XPR6_9ARAE)	
Solyc09g065890.3	7,78E-01	1,93E-05	5,76E-01	6,74E-04	1,10E-01	4,67E-01	**1,32E+00**	**2,76E-09**	*nifD*- NoN 14 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061DP20_THECC)	GO:0006629
Solyc01g091660.3	-5,09E-01	6,65E-02	5,73E-01	4,07E-02	-2,80E-01	3,01E-01	**-1,00E+00**	**8,66E-04**	*nifD*- NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G47140.1),Pfam:PF13561	
Solyc12g007070.2	8,32E-01	5,73E-07	5,72E-01	1,16E-04	3,14E-01	1,97E-02	**1,22E+00**	**4,62E-10**	*nifD*- NoN 14 dpi	T	SolycHsfC1	GO:0003700|GO:0005634|GO:0006355|GO:0043565
Solyc04g008080.1	5,92E-01	4,13E-03	5,72E-01	5,36E-03	1,91E-02	9,20E-01	**1,06E+00**	**6,65E-06**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Dirigent protein (AHRD V3.3 *** K4BNW4_SOLLC)	
Solyc12g006460.2	-4,12E-01	2,13E-01	5,71E-01	8,88E-02	7,96E-01	2,07E-02	**-1,26E+00**	**6,33E-04**	*nifD*- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A124SDJ5_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc03g078640.1	1,49E-01	4,31E-01	5,70E-01	5,20E-03	1,60E-02	9,32E-01	**-1,21E+00**	**7,73E-07**	*nifD*- NoN 14 dpi	RNA	LOW QUALITY:Mediator of RNA polymerase II transcription subunit 26, putative (AHRD V3.3 *** A0A061DI33_THECC)	
Solyc06g008930.3	2,99E-01	2,88E-01	5,70E-01	4,91E-02	5,57E-01	5,42E-02	**1,21E+00**	**1,71E-04**	*nifD*- NoN 14 dpi	H	MLP-like protein 31 (AHRD V3.3 -** A0A151QPB6_CAJCA)	
Solyc02g080900.3	-1,25E-01	6,44E-01	5,68E-01	4,34E-02	-3,28E-02	9,03E-01	**-1,19E+00**	**1,39E-04**	*nifD*- NoN 14 dpi	D	Wall-associated receptor kinase 3-like protein (AHRD V3.3 *** A0A0B0PL73_GOSAR)	GO:0030247
Solyc09g075260.3	7,99E-01	2,26E-04	5,67E-01	5,34E-03	6,98E-01	9,15E-04	**1,08E+00**	**4,12E-06**	*nifD*- NoN 14 dpi	CS	pectinesterase (Protein of unknown function, DUF538) (AHRD V3.3 *** AT1G02816.1)	
Solyc07g044960.1	4,56E-01	2,82E-02	5,67E-01	7,65E-03	-4,73E-01	2,32E-02	**-1,05E+00**	**1,43E-05**	*nifD*- NoN 14 dpi	CS	Xyloglucan galactosyltransferase KATAMARI1, putative (AHRD V3.3 *** B9R9L8_RICCO)	
Solyc09g009420.1	-1,94E+00	3,41E-02	5,62E-01	5,22E-01	-4,85E-01	5,80E-01	**-2,49E+00**	**8,08E-03**	*nifD*- NoN 14 dpi	P	LOW QUALITY:AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT2G47240.4)	
Solyc06g043113.1	3,40E-01	6,29E-01	5,60E-01	4,27E-01	-8,00E-02	9,09E-01	**-2,43E+00**	**1,74E-03**	*nifD*- NoN 14 dpi	K	Serine/threonine protein phosphatase 7 long form isogeny (AHRD V3.3 *-* A0A151R878_CAJCA)	
Solyc10g006880.3	9,60E-01	2,24E-01	5,53E-01	4,80E-01	1,46E+00	6,95E-02	**3,17E+00**	**3,53E-04**	*nifD*- NoN 14 dpi	T	NAC domain protein (AHRD V3.3 *** Q56UP7_SOLLC)	GO:0003677|GO:0006355
Solyc10g083970.1	-2,05E-01	2,01E-01	5,50E-01	1,69E-03	-4,57E-01	7,28E-03	**-1,08E+00**	**2,56E-07**	*nifD*- NoN 14 dpi	H	S-adenosylmethionine synthase (AHRD V3.3 *** A0A0V0IPC3_SOLCH)	GO:0004478|GO:0005524|GO:0006556|GO:0004478|GO:0006556|GO:0004478|GO:0006556
Solyc03g082840.3	5,84E-01	5,82E-04	5,43E-01	1,18E-03	-3,71E-01	1,93E-02	**-1,34E+00**	**2,12E-09**	*nifD*- NoN 14 dpi	DNA	Dof zinc finger protein (AHRD V3.3 *** A0A068PXR9_TOBAC)	GO:0003677|GO:0006355
Solyc10g054280.2	-1,54E-02	9,51E-01	5,42E-01	3,78E-02	1,22E-01	6,27E-01	**-1,40E+00**	**6,29E-06**	*nifD*- NoN 14 dpi	K	Haloacid dehalogenase-like hydrolase (AHRD V3.3 *** G7JVF5_MEDTR)	GO:0008152|GO:0016787
Solyc06g006020.2	-1,36E+00	5,85E-02	5,41E-01	4,37E-01	2,86E-01	6,79E-01	**-2,20E+00**	**3,56E-03**	*nifD*- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1ANR5_SOLTU)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g006100.3	-9,24E-02	7,74E-01	5,40E-01	1,02E-01	4,72E-01	1,51E-01	**-1,13E+00**	**1,54E-03**	*nifD*- NoN 14 dpi	G	cytosine-5 DNA methyltransferase1L	GO:0003682|GO:0008168|GO:0008168
Solyc03g005770.3	-1,68E-01	7,86E-01	5,39E-01	3,87E-01	-6,35E-01	3,10E-01	**3,25E+00**	**1,58E-05**	*nifD*- NoN 14 dpi	E	chlorophyll a/b-binding protein	GO:0009765|GO:0016020
Solyc12g088170.2	3,60E-01	7,40E-01	5,39E-01	6,19E-01	-9,44E-01	3,87E-01	**-5,18E+00**	**5,40E-05**	*nifD*- NoN 14 dpi	S	HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC)	GO:0016747
Solyc11g069925.1	-2,83E-01	2,18E-01	5,36E-01	2,42E-02	-2,42E-01	2,90E-01	**-1,21E+00**	**1,15E-05**	*nifD*- NoN 14 dpi	D	Disease resistance protein (AHRD V3.3 *** A0A068EUA9_SOLLC)	GO:0043531

Solyc10g084780.2	7,73E-02	9,30E-01	5,34E-01	5,46E-01	-1,40E+00	1,22E-01	**-2,47E+00**	**8,78E-03**	*nifD*- NoN 14 dpi	CS	Expansin (AHRD V3.3 *** A0A075EYP6_TOBAC)	GO:0005576|GO:0009664|GO:0009664
Solyc02g076850.2	9,52E-01	4,50E-04	5,32E-01	3,36E-02	6,71E-01	8,89E-03	**1,57E+00**	**5,07E-07**	*nifD*- NoN 14 dpi	DNA	Dof zinc finger protein4	GO:0003677|GO:0006355
Solyc05g005930.2	-1,84E-03	9,95E-01	5,32E-01	8,87E-02	-1,82E-01	5,50E-01	**-1,29E+00**	**2,20E-04**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BWC0_SOLLC)	GO:0008152|GO:0016758
Solyc08g078460.3	5,20E-01	1,43E-02	5,32E-01	1,25E-02	-1,63E-02	9,35E-01	**1,68E+00**	**6,62E-09**	*nifD*- NoN 14 dpi	NA	Oxidoreductase family protein (AHRD V3.3 *** AT4G17370.1)	GO:0008152|GO:0016491|GO:0055114|GO:0016491|GO:0016491
Solyc08g076257.1	-3,63E-01	1,77E-01	5,28E-01	5,36E-02	-1,67E-01	5,29E-01	**-1,58E+00**	**2,38E-06**	*nifD*- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *-* A0A103XWG4_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc04g015540.1	9,74E-01	1,29E-01	5,27E-01	4,04E-01	5,69E-01	3,69E-01	**-2,53E+00**	**3,96E-04**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:Transmembrane protein, putative (AHRD V3.3 *** A0A072UCS3_MEDTR)	
Solyc06g073530.2	1,83E+00	4,04E-02	5,27E-01	5,39E-01	1,48E+00	9,29E-02	**4,01E+00**	**7,08E-05**	*nifD*- NoN 14 dpi	RNA	Argonaute4c	GO:0003676|GO:0005515|GO:0005515
Solyc08g068160.2	2,14E-01	4,05E-01	5,26E-01	4,75E-02	-5,68E-01	3,34E-02	**-1,62E+00**	**9,44E-07**	*nifD*- NoN 14 dpi	OX	Flavin-containing monooxygenase (AHRD V3.3 *** K4CM40_SOLLC)	GO:0004499|GO:0050660|GO:0050661|GO:0055114|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc03g019870.3	-3,15E-01	3,70E-01	5,24E-01	1,41E-01	-5,79E-01	1,06E-01	**-1,22E+00**	**1,60E-03**	*nifD*- NoN 14 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** U5FM31_POPTR)	GO:0004497|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc03g058910.3	-1,24E+00	1,37E-01	5,24E-01	5,22E-01	7,81E-01	3,43E-01	**-2,91E+00**	**1,33E-03**	*nifD*- NoN 14 dpi	CS	Pectate lyase (AHRD V3.3 *** M1A3P9_SOLTU)	
Solyc03g116975.1	5,08E-01	4,39E-01	5,19E-01	4,30E-01	4,76E-01	4,69E-01	**-2,02E+00**	**4,34E-03**	*nifD*- NoN 14 dpi	G	SNARE-interacting KEULE-like protein (AHRD V3.3 --* A0A0B0MFS4_GOSAR)	
Solyc07g006300.3	1,99E-01	5,36E-01	5,09E-01	1,20E-01	6,54E-01	4,90E-02	**-1,07E+00**	**2,37E-03**	*nifD*- NoN 14 dpi	L	Fatty acid hydroxylase superfamily (AHRD V3.3 *** AT5G57800.1)	GO:0005506|GO:0006633|GO:0016491|GO:0055114
Solyc02g085290.3	2,96E-01	2,98E-01	5,08E-01	7,99E-02	-5,35E-01	6,61E-02	**-1,17E+00**	**2,74E-04**	*nifD*- NoN 14 dpi	NA	Maf protein, putative (AHRD V3.3 *** B9SNZ2_RICCO)	GO:0047429
Solyc07g041830.3	9,12E-01	1,33E-04	5,03E-01	2,03E-02	2,16E-01	2,97E-01	**1,77E+00**	**3,97E-09**	*nifD*- NoN 14 dpi	DNA	Damaged dna-binding 2, putative isoform 1 (AHRD V3.3 *** A0A061GM96_THECC)	
Solyc01g107690.3	-5,03E-01	4,77E-01	4,99E-01	4,81E-01	-2,34E-01	7,40E-01	**-2,59E+00**	**9,86E-04**	*nifD*- NoN 14 dpi	P	ATP-dependent Clp protease ATP-binding subunit ClpX (AHRD V3.3 *-* A0A1D1XQW5_9ARAE)	GO:0005524|GO:0005524|GO:0006457|GO:0051082|GO:0005524|GO:0006457|GO:0051082
Solyc05g051220.3	3,45E-01	2,90E-02	4,98E-01	2,58E-03	5,94E-01	5,02E-04	**1,39E+00**	**1,09E-09**	*nifD*- NoN 14 dpi	TR	Potassium channel TORK1 (AHRD V3.3 *** Q5NT78_TOBAC)	GO:0005216|GO:0006811|GO:0016020|GO:0055085|GO:0005249|GO:0006813|GO:0016020|GO:0005249|GO:0006813|GO:0016020
Solyc07g042460.2	-1,26E-01	3,42E-01	4,98E-01	7,28E-04	-9,22E-01	1,64E-07	**-1,07E+00**	**1,15E-08**	*nifD*- NoN 14 dpi	OX	Respiratory burst oxidase, putative (AHRD V3.3 *** B9RR53_RICCO)	GO:0004601|GO:0050664|GO:0055114|GO:0005509|GO:0005509
Solyc12g009470.2	5,69E-01	1,34E-07	4,97E-01	1,30E-06	-1,34E-01	1,03E-01	**1,07E+00**	**3,41E-13**	*nifD*- NoN 14 dpi	P	yellow-green-2	GO:0004392|GO:0006788|GO:0055114
Solyc03g082900.3	5,20E-01	7,37E-02	4,96E-01	8,73E-02	2,21E-02	9,38E-01	**1,54E+00**	**9,31E-06**	*nifD*- NoN 14 dpi	CS	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9SJT3_RICCO)	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc08g075630.3	-2,64E-01	6,70E-01	4,95E-01	4,27E-01	1,37E+00	3,45E-02	**2,18E+00**	**1,52E-03**	*nifD*- NoN 14 dpi	D	NBS-LRR resistance protein (AHRD V3.3 *** B6E013_SOLBU)	GO:0005515|GO:0043531|GO:0043531
Solyc07g065610.1	3,81E-01	2,95E-01	4,93E-01	1,78E-01	-3,06E-01	3,98E-01	**-1,34E+00**	**8,75E-04**	*nifD*- NoN 14 dpi	PMI	Clade XIV lectin receptor kinase (AHRD V3.3 *** K4CHN9_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g112297.1	1,17E+00	2,51E-02	4,90E-01	3,27E-01	4,06E-01	4,16E-01	**2,59E+00**	**1,62E-05**	*nifD*- NoN 14 dpi	K	Octicosapeptide/Phox/Bem1p domain-containing protein kinase (AHRD V3.3 *-* A0A0K9NT10_ZOSMR)	GO:0005515
Solyc10g086190.2	-4,40E-01	7,71E-03	4,89E-01	3,51E-03	-8,37E-01	9,27E-06	**-1,13E+00**	**7,92E-08**	*nifD*- NoN 14 dpi	K	Adenosine kinase, putative (AHRD V3.3 *** B9T0A9_RICCO)	GO:0004001|GO:0006166|GO:0016773|GO:0016773
Solyc09g089930.2	-1,17E-01	7,50E-01	4,84E-01	1,96E-01	3,87E-01	2,99E-01	**1,14E+00**	**4,54E-03**	*nifD*- NoN 14 dpi	H	ethylene responsive factor E.2	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc12g019740.2	9,79E-01	1,29E-08	4,84E-01	4,27E-04	4,15E-01	1,86E-03	**1,43E+00**	**5,41E-12**	*nifD*- NoN 14 dpi	OX	Thioredoxin, putative (AHRD V3.3 *** B9SHJ2_RICCO)	GO:0045454
Solyc09g057630.3	-5,82E-01	7,26E-02	4,83E-01	1,32E-01	-5,16E-01	1,09E-01	**-1,00E+00**	**3,37E-03**	*nifD*- NoN 14 dpi	CS	Glucan endo-1,3-beta-glucosidase-like protein (AHRD V3.3 *** A0A072TYH8_MEDTR)	GO:0004553|GO:0005975|GO:0005975|GO:0005975

Solyc04g076130.3	9,41E-01	2,72E-03	4,83E-01	1,01E-01	9,26E-01	3,10E-03	**1,65E+00**	**4,29E-06**	*nifD*- NoN 14 dpi	STR	Serine carboxypeptidase, putative (AHRD V3.3 *-* B9R6Y4_RICCO)	GO:0004185|GO:0006508
Solyc12g008680.2	4,52E-01	4,66E-01	4,81E-01	4,38E-01	-1,56E+00	1,66E-02	**-2,90E+00**	**6,77E-05**	*nifD*- NoN 14 dpi	RNA	RNA-binding CRS1 / YhbY (CRM) domain protein (AHRD V3.3 --* AT3G27550.3)	
Solyc12g096480.1	-7,29E-03	9,84E-01	4,80E-01	1,85E-01	-2,38E-01	5,05E-01	**-1,21E+00**	**1,99E-03**	*nifD*- NoN 14 dpi	AM	Glutamine dumper 4, putative (AHRD V3.3 *** A0A061GHE4_THECC)	
Solyc02g094060.3	8,62E-01	1,12E-01	4,78E-01	3,71E-01	-1,41E-01	7,91E-01	**1,73E+00**	**2,76E-03**	*nifD*- NoN 14 dpi	TR	Chloride channel protein (AHRD V3.3 *** Q9XF71_TOBAC)	GO:0005216|GO:0055085|GO:0005247|GO:0006821|GO:0016020|GO:0005247|GO:0006821|GO:0016020
Solyc05g010710.2	6,61E-03	9,75E-01	4,75E-01	3,21E-02	2,82E-01	1,90E-01	**-1,36E+00**	**7,18E-07**	*nifD*- NoN 14 dpi	C	UDP-glycosyltransferase (AHRD V3.3 *** A0A165XX62_DAUCA)	GO:0008152|GO:0016758
Solyc04g007780.3	1,21E-01	8,95E-01	4,73E-01	6,07E-01	-1,39E+00	1,38E-01	**-3,12E+00**	**1,99E-03**	*nifD*- NoN 14 dpi	H	MLP (AHRD V3.3 *** G8DRV9_GOSBA)	GO:0006952|GO:0009607
Solyc05g055990.3	1,60E-01	4,63E-01	4,68E-01	3,80E-02	-1,04E+00	4,85E-05	**1,03E+00**	**5,59E-05**	*nifD*- NoN 14 dpi	TR	plasma membrane intrinsic protein 2.12	GO:0005215|GO:0006810|GO:0016020
Solyc05g009880.3	-7,33E-01	2,75E-03	4,67E-01	4,47E-02	-1,56E-03	9,94E-01	**-1,53E+00**	**2,54E-07**	*nifD*- NoN 14 dpi	T	bHLH transcription factor 038	GO:0046983
Solyc07g021700.3	3,02E-01	3,50E-02	4,65E-01	2,05E-03	-7,26E-01	1,36E-05	**-1,01E+00**	**7,24E-08**	*nifD*- NoN 14 dpi	G	Pollen-specific SF21-like protein (AHRD V3.3 *** G7LJK8_MEDTR)	
Solyc02g083290.3	4,74E-01	6,20E-03	4,56E-01	8,05E-03	-1,05E-01	5,15E-01	**1,02E+00**	**9,07E-07**	*nifD*- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9N912_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc11g008010.2	7,36E-01	3,01E-08	4,54E-01	5,58E-05	5,53E-01	3,58E-06	**1,10E+00**	**8,50E-12**	*nifD*- NoN 14 dpi	T	NAC domain protein, (AHRD V3.3 *** A0A061FQ99_THECC)	GO:0003677|GO:0006355
Solyc04g016590.3	1,06E+00	1,43E-01	4,52E-01	5,26E-01	-2,30E-01	7,46E-01	**-2,62E+00**	**9,66E-04**	*nifD*- NoN 14 dpi	T	global transcription factor C (AHRD V3.3 --* AT4G10710.2)	
Solyc02g036260.3	1,13E-01	6,85E-01	4,47E-01	1,16E-01	-6,70E-01	2,20E-02	**-1,19E+00**	**2,05E-04**	*nifD*- NoN 14 dpi	STR	ERD (early-responsive to dehydration stress) family protein (AHRD V3.3 *** AT4G22120.6)	GO:0016020
Solyc02g083310.3	7,22E-01	1,25E-05	4,45E-01	2,70E-03	1,34E-01	3,28E-01	**1,17E+00**	**3,61E-09**	*nifD*- NoN 14 dpi	D	Wound-responsive family protein, putative (AHRD V3.3 *** A0A061DF47_THECC)	GO:0004518
Solyc03g005820.3	6,83E-01	9,15E-06	4,45E-01	1,39E-03	7,03E-02	5,76E-01	**1,33E+00**	**5,75E-11**	*nifD*- NoN 14 dpi	TR	Purine permease (AHRD V3.3 *** A0A072UW47_MEDTR)	GO:0005215|GO:0016021
Solyc06g053700.1	-2,29E-02	9,24E-01	4,42E-01	7,32E-02	5,78E-01	2,17E-02	**1,00E+00**	**2,56E-04**	*nifD*- NoN 14 dpi	NA	ATBET12, putative (AHRD V3.3 *** B9STJ3_RICCO)	
Solyc04g025530.3	3,12E-01	4,84E-01	4,41E-01	3,24E-01	1,13E+00	1,58E-02	**1,57E+00**	**1,38E-03**	*nifD*- NoN 14 dpi	N	glutamate decarboxylase (AHRD V3.3 *** AT5G17330.1)	GO:0003824|GO:0004351|GO:0006536|GO:0030170|GO:0004351|GO:0006536|GO:0030170
Solyc11g006270.2	5,50E-01	3,94E-02	4,41E-01	9,42E-02	8,36E-01	2,86E-03	**1,83E+00**	**1,20E-07**	*nifD*- NoN 14 dpi	L	3-oxo-5-alpha-steroid 4-dehydrogenase family protein (AHRD V3.3 *** A0A072UJC1_MEDTR)	GO:0005737|GO:0006629|GO:0016021|GO:0016627
Solyc03g117430.3	9,75E-01	8,66E-11	4,38E-01	7,19E-05	2,27E-01	2,17E-02	**1,04E+00**	**2,36E-11**	*nifD*- NoN 14 dpi	NA	COBW domain-containing protein 1 (AHRD V3.3 *** A0A0B2RY32_GLYSO)	
Solyc12g088330.1	-2,81E-01	2,79E-01	4,38E-01	9,65E-02	7,75E-01	5,18E-03	**1,76E+00**	**2,35E-07**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:ZCF37, putative (AHRD V3.3 *** A0A061F7D6_THECC)	
Solyc06g051460.3	-3,77E-01	1,00E-01	4,35E-01	6,02E-02	-2,86E-01	2,08E-01	**-1,30E+00**	**3,60E-06**	*nifD*- NoN 14 dpi	P	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061FKC4_THECC)	GO:0005524|GO:0019538|GO:0019538
Solyc01g081190.3	7,93E-01	1,48E-03	4,32E-01	6,37E-02	3,14E-01	1,71E-01	**1,08E+00**	**4,93E-05**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Calcium-binding EF hand family protein (AHRD V3.3 *** AT1G64850.1)	GO:0005509
Solyc09g018750.3	5,10E-01	1,97E-05	4,22E-01	2,10E-04	-2,78E-01	8,75E-03	**1,10E+00**	**2,03E-11**	*nifD*- NoN 14 dpi	NA	CBS domain-containing protein (AHRD V3.3 *** A0T1V6_PLESU)	
Solyc10g086100.2	6,46E-01	2,96E-03	4,21E-01	4,21E-02	4,12E-01	4,62E-02	**1,65E+00**	**8,27E-09**	*nifD*- NoN 14 dpi	D	Proteinase inhibitor (AHRD V3.3 *** A0A0R4WSF0_TOBAC)	GO:0004867|GO:0009611
Solyc00g136260.1	7,35E-01	3,00E-02	4,20E-01	2,01E-01	-2,17E-01	5,04E-01	**1,61E+00**	**3,05E-05**	*nifD*- NoN 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** A0A061FKT7_THECC)	GO:0005515|GO:0008270
Solyc07g007420.3	4,72E-01	3,55E-01	4,17E-01	4,13E-01	9,93E-01	5,84E-02	**1,75E+00**	**1,76E-03**	*nifD*- NoN 14 dpi	PMI	F-box/LRR-repeat protein, putative (AHRD V3.3 *-* B9RVD1_RICCO)	

Solyc07g061920.3	-2,13E-03	9,90E-01	4,13E-01	2,29E-02	-1,78E-01	3,05E-01	**-1,54E+00**	**1,97E-09**	*nifD*- NoN 14 dpi	CS	glucan synthase-like 4 (AHRD V3.3 *** AT3G14570.1)	GO:0000148|GO:0003843|GO:0006075|GO:0016020
Solyc01g088250.3	1,66E-01	5,70E-01	4,12E-01	1,64E-01	-1,27E-01	6,64E-01	**-1,50E+00**	**1,95E-05**	*nifD*- NoN 14 dpi	G	SUN domain protein3	GO:0005515
Solyc02g092840.1	1,41E-02	9,46E-01	4,08E-01	5,81E-02	-2,82E-01	1,83E-01	**-1,34E+00**	**7,25E-07**	*nifD*- NoN 14 dpi	CS	Xyloglucan galactosyltransferase KATAMARI1, putative (AHRD V3.3 *** B9R9L8_RICCO)	
Solyc08g078540.3	-9,90E-02	7,71E-01	4,08E-01	2,37E-01	3,87E-02	9,10E-01	**-1,14E+00**	**2,36E-03**	*nifD*- NoN 14 dpi	C	O-fucosyltransferase family protein (AHRD V3.3 *** AT4G16650.2)	
Solyc09g011140.3	-2,34E-01	8,07E-02	4,08E-01	3,86E-03	-5,94E-01	9,34E-05	**-1,05E+00**	**1,30E-08**	*nifD*- NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT5G06060.1),Pfam:PF13561	GO:0016491
Solyc11g005560.2	-7,23E-01	1,10E-02	4,05E-01	1,37E-01	-9,46E-02	7,23E-01	**-1,02E+00**	**6,45E-04**	*nifD*- NoN 14 dpi	CS	Cellulose synthase (AHRD V3.3 *** M0ZXJ5_SOLTU)	GO:0005515|GO:0008270|GO:0016020|GO:0016760|GO:0030244|GO:0016020|GO:0016760|GO:0030244
Solyc07g065220.2	8,94E-01	1,08E-05	4,05E-01	2,07E-02	6,25E-01	7,87E-04	**1,10E+00**	**4,36E-07**	*nifD*- NoN 14 dpi	STR	Calcium-dependent lipid-binding domain-containing protein (AHRD V3.3 *** G5DXN7_SILLA)	GO:0005515
Solyc12g014490.2	-9,80E-01	3,09E-04	4,03E-01	9,92E-02	1,01E-01	6,71E-01	**-1,01E+00**	**2,29E-04**	*nifD*- NoN 14 dpi	G	Microtubule associated family protein (AHRD V3.3 *** B9GJD5_POPTR)	GO:0000226|GO:0000910|GO:0008017
Solyc01g088780.3	-1,06E+00	1,20E-01	4,01E-01	5,46E-01	-1,65E-02	9,80E-01	**-2,05E+00**	**4,42E-03**	*nifD*- NoN 14 dpi	CS	Rac-like GTP binding protein (AHRD V3.3 *** O65062_PICMA)	GO:0005525|GO:0005525|GO:0007264|GO:0005525|GO:0007264
Solyc08g066840.3	-4,94E-01	3,56E-02	4,01E-01	8,34E-02	-3,85E-01	9,56E-02	**-1,24E+00**	**8,08E-06**	*nifD*- NoN 14 dpi	TR	tonoplast intrinsic protein 4.1	GO:0005215|GO:0006810|GO:0016020
Solyc02g092215.1	-3,27E-01	2,33E-01	3,98E-01	1,49E-01	8,27E-01	4,79E-03	**-1,53E+00**	**5,61E-06**	*nifD*- NoN 14 dpi	P	Galactosyl transferase GMA12/MNN10 family protein (AHRD V3.3 *** AT2G22900.1)	GO:0016021|GO:0016757
Solyc01g097570.2	6,50E-01	7,25E-03	3,98E-01	8,58E-02	-3,96E-01	8,70E-02	**1,09E+00**	**4,52E-05**	*nifD*- NoN 14 dpi	K	LOW QUALITY:kinase-like protein (AHRD V3.3 --* AT1G66940.4)	
Solyc04g014650.3	-5,78E-01	2,07E-01	3,97E-01	3,82E-01	4,85E-01	2,88E-01	**-1,34E+00**	**5,92E-03**	*nifD*- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *-* M1A662_SOLTU)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g014470.3	-4,62E-01	3,50E-01	3,97E-01	4,21E-01	-8,13E-01	1,06E-01	**-1,44E+00**	**6,43E-03**	*nifD*- NoN 14 dpi	L	Alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** A0A061GF41_THECC)	GO:0006629|GO:0008970|GO:0008970
Solyc12g044920.2	-1,29E-01	5,83E-01	3,95E-01	1,01E-01	1,29E-01	5,84E-01	**-1,27E+00**	**1,04E-05**	*nifD*- NoN 14 dpi	L	Phospholipid-transporting ATPase (AHRD V3.3 *** A0A0V0IZF4_SOLCH)	GO:0000166|GO:0000166|GO:0046872|GO:0000166|GO:0046872
Solyc01g090700.3	8,11E-01	9,65E-07	3,92E-01	4,82E-03	3,14E-01	2,05E-02	**1,24E+00**	**3,73E-10**	*nifD*- NoN 14 dpi	CS	3-hydroxyisobutyryl-CoA hydrolase-like protein (AHRD V3.3 *** A0A0K9Q5H5_ZOSMR)	GO:0003860
Solyc04g016470.3	1,18E+00	2,82E-01	3,90E-01	7,18E-01	6,57E-01	5,44E-01	**3,50E+00**	**3,04E-03**	*nifD*- NoN 14 dpi	CS	LEQA L.esculentum TomQ'a beta(1,3)glucanase	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc08g007230.2	3,07E-01	5,46E-01	3,90E-01	4,43E-01	1,35E+00	1,20E-02	**2,52E+00**	**3,20E-05**	*nifD*- NoN 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *** A0A024CAT9_BRAJU)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc01g079150.3	-6,04E-01	1,69E-02	3,86E-01	1,14E-01	4,98E-01	4,49E-02	**-1,86E+00**	**2,62E-08**	*nifD*- NoN 14 dpi	TR	Boron transporter (AHRD V3.3 *** B6V758_VITVI)	GO:0005452|GO:0006820|GO:0016020|GO:0006820|GO:0016021|GO:0006820|GO:0016021
Solyc03g115640.3	-5,72E-01	2,49E-01	3,85E-01	4,35E-01	-1,22E+00	1,81E-02	**-1,67E+00**	**1,93E-03**	*nifD*- NoN 14 dpi	NA	DUF538 family protein (Protein of unknown function%2C DUF538) (AHRD V3.3 *** AT2G03350.1)	
Solyc06g082860.3	-3,79E-01	1,21E-01	3,85E-01	1,16E-01	-7,88E-01	2,61E-03	**-1,16E+00**	**4,64E-05**	*nifD*- NoN 14 dpi	OX	Cytochrome b561/ferric reductase transmembrane with DOMON related domain-containing protein (AHRD V3.3 *** AT3G07570.1)	
Solyc01g096190.3	-2,49E-01	1,77E-01	3,82E-01	4,23E-02	-2,98E-01	1,07E-01	**-1,00E+00**	**7,05E-06**	*nifD*- NoN 14 dpi	E	Ca2+-ATPase	GO:0000166|GO:0000166|GO:0046872|GO:0000166|GO:0046872
Solyc03g114210.3	9,05E-01	1,29E-04	3,80E-01	7,00E-02	-3,10E-01	1,36E-01	**2,18E+00**	**4,58E-11**	*nifD*- NoN 14 dpi	K	Protein kinase (AHRD V3.3 *** Q9FGB1_ARATH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g012030.3	2,04E-02	9,26E-01	3,79E-01	9,39E-02	-3,85E-01	8,89E-02	**-1,08E+00**	**3,71E-05**	*nifD*- NoN 14 dpi	STR	DHHC-type zinc finger family protein	
Solyc01g080680.3	9,37E-01	1,44E-02	3,78E-01	2,99E-01	-7,47E-01	4,65E-02	**1,27E+00**	**1,49E-03**	*nifD*- NoN 14 dpi	TR	Sugar facilitator protein 3	GO:0005215|GO:0016021|GO:0055085|GO:0016020|GO:0022891|GO:0055085|GO:0016020|GO:0022891|GO:0055085
Solyc01g091610.1	1,68E-01	6,42E-01	3,78E-01	2,99E-01	-5,61E-01	1,27E-01	**-1,31E+00**	**1,09E-03**	*nifD*- NoN 14 dpi	RNA	LOW QUALITY:Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151TBJ2_CAJCA)	GO:0005515|GO:0008270|GO:0008270

Solyc02g082050.3	-5,48E-02	9,30E-01	3,75E-01	5,50E-01	1,29E-01	8,37E-01	**-2,28E+00**	**1,07E-03**	*nifD*- NoN 14 dpi	D	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.2)	GO:0005515|GO:0007165|GO:0043531|GO:0043531
Solyc12g009600.2	2,84E-01	6,97E-01	3,75E-01	6,08E-01	4,23E-01	5,63E-01	**2,22E+00**	**4,99E-03**	*nifD*- NoN 14 dpi	E	Thylakoid lumenal 16.5 kDa protein (AHRD V3.3 *** A0A061GNW6_THECC)	
Solyc08g080630.3	9,68E-01	1,67E-03	3,74E-01	1,86E-01	3,42E-01	2,25E-01	**2,27E+00**	**1,11E-08**	*nifD*- NoN 14 dpi	H	Ethylene-responsive proteinase inhibitor 1 (AHRD V3.3 *** IER1_SOLLC)	GO:0004867|GO:0009611
Solyc08g067000.3	-3,21E-01	4,09E-01	3,74E-01	3,38E-01	-4,43E-02	9,09E-01	**-1,68E+00**	**1,80E-04**	*nifD*- NoN 14 dpi	RNA	Serine/arginine repetitive matrix protein 2 isoform 1 (AHRD V3.3 --* A0A061DPI3_THECC)	
Solyc08g068800.3	-2,39E-01	5,49E-01	3,72E-01	3,54E-01	-3,39E-02	9,32E-01	**-1,51E+00**	**7,46E-04**	*nifD*- NoN 14 dpi	OX	Glutathione peroxidase (AHRD V3.3 *** A0A068UHC8_COFCA)	GO:0004602|GO:0006979|GO:0055114
Solyc06g071370.1	7,78E-01	1,61E-04	3,72E-01	4,46E-02	-1,16E-02	9,48E-01	**1,05E+00**	**2,67E-06**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:NHL domain-containing protein, putative (AHRD V3.3 *-* A0A061EBN2_THECC)	
Solyc12g089290.2	-4,17E-01	1,12E-01	3,70E-01	1,57E-01	6,15E-01	2,27E-02	**1,44E+00**	**6,20E-06**	*nifD*- NoN 14 dpi	H	HVA22-like protein (AHRD V3.3 *** K4DH00_SOLLC)	
Solyc08g065420.3	2,41E-01	4,70E-01	3,68E-01	2,73E-01	-6,27E-02	8,50E-01	**-2,14E+00**	**6,97E-07**	*nifD*- NoN 14 dpi	T	bell-like homeodomain protein 4	GO:0003677|GO:0003677|GO:0006355|GO:0003677|GO:0006355
Solyc02g089690.3	-1,45E-01	5,70E-01	3,64E-01	1,61E-01	3,89E-01	1,35E-01	**-1,26E+00**	**3,60E-05**	*nifD*- NoN 14 dpi	CS	Trichome birefringence-like 19 (AHRD V3.3 *** A0A061EH35_THECC)	
Solyc03g097640.3	7,68E-01	3,07E-06	3,63E-01	9,52E-03	5,49E-01	2,56E-04	**1,03E+00**	**2,31E-08**	*nifD*- NoN 14 dpi	TR	Mitochondrial import inner membrane translocase subunit (AHRD V3.3 *** S8CMW8_9LAMI)	
Solyc01g112260.3	-2,58E-01	1,21E-01	3,61E-01	3,43E-02	-9,78E-01	2,17E-06	**-1,21E+00**	**6,28E-08**	*nifD*- NoN 14 dpi	C	Phosphoenolpyruvate carboxylase (AHRD V3.3 --* A7DX51_9POAL)	
Solyc07g056610.2	1,88E-01	7,04E-01	3,59E-01	4,71E-01	1,09E+00	3,46E-02	**1,53E+00**	**4,50E-03**	*nifD*- NoN 14 dpi	NA	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT2G44210.1)	
Solyc03g111670.3	-8,34E-01	1,51E-03	3,52E-01	1,46E-01	-4,36E-01	7,47E-02	**-1,15E+00**	**4,46E-05**	*nifD*- NoN 14 dpi	K	Protein kinase (AHRD V3.3 *** D6N3G3_MALDO)	GO:0004672|GO:0005524|GO:0006468|GO:0005515|GO:0005515
Solyc05g012110.3	9,00E-01	2,05E-06	3,52E-01	2,48E-02	1,88E-02	9,00E-01	**1,49E+00**	**1,93E-10**	*nifD*- NoN 14 dpi	C	6-phosphogluconolactonase, putative (AHRD V3.3 *** B9REC3_RICCO)	GO:0005975|GO:0005975|GO:0006098|GO:0017057|GO:0005975|GO:0006098|GO:0017057
Solyc12g009070.1	-1,97E+00	5,33E-02	3,48E-01	7,23E-01	-6,35E-01	5,19E-01	**2,89E+00**	**6,26E-03**	*nifD*- NoN 14 dpi	DNA	Replication protein A 70 kDa DNA-binding subunit (AHRD V3.3 --* A0A151SSR0_CAJCA)	
Solyc12g040470.2	-9,39E-01	3,11E-01	3,47E-01	7,06E-01	3,43E+00	8,66E-04	**-2,58E+00**	**8,71E-03**	*nifD*- NoN 14 dpi	L	non-specific phospholipase C2 (AHRD V3.3 --* AT2G26870.1)	
Solyc10g081430.2	-5,32E-01	9,25E-04	3,46E-01	2,22E-02	-3,83E-01	1,22E-02	**-1,15E+00**	**1,56E-08**	*nifD*- NoN 14 dpi	P	exostosin family protein (AHRD V3.3 *** AT3G45400.1)	
Solyc03g006700.3	1,45E-01	2,57E-01	3,46E-01	1,04E-02	9,65E-01	3,75E-08	**1,02E+00**	**1,42E-08**	*nifD*- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4BE93_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc10g049970.2	4,10E-01	2,89E-02	3,45E-01	6,20E-02	8,84E-01	3,51E-05	**1,37E+00**	**3,45E-08**	*nifD*- NoN 14 dpi	AM	Kynurenine formamidase (AHRD V3.3 *** A0A151RRB2_CAJCA)	GO:0004061|GO:0019441
Solyc04g063380.3	6,31E-01	4,35E-07	3,45E-01	1,11E-03	3,92E-01	3,05E-04	**1,18E+00**	**1,80E-12**	*nifD*- NoN 14 dpi	P	F-box family protein (AHRD V3.3 *** B9H7L8_POPTR)	GO:0005515
Solyc02g083280.3	9,67E-01	6,71E-03	3,45E-01	3,02E-01	4,93E-01	1,45E-01	**2,15E+00**	**6,41E-07**	*nifD*- NoN 14 dpi	P	Rhodanese-related sulfurtransferase (AHRD V3.3 *** B7FGV4_MEDTR)	
Solyc12g088220.2	-2,83E-01	5,66E-01	3,45E-01	4,86E-01	1,98E-01	6,88E-01	**-1,42E+00**	**7,25E-03**	*nifD*- NoN 14 dpi	NA	SlBCAT1	GO:0003824|GO:0008152|GO:0004084|GO:0009081|GO:0004084|GO:0009081
Solyc04g082450.3	4,72E-01	9,88E-02	3,43E-01	2,25E-01	7,88E-01	8,37E-03	**1,28E+00**	**8,81E-05**	*nifD*- NoN 14 dpi	NA	integral membrane hemolysin-III-like protein (AHRD V3.3 *-* AT2G45250.1)	GO:0006351|GO:0007049|GO:0070176
Solyc08g082720.3	-1,25E-01	7,23E-01	3,42E-01	3,38E-01	1,25E-01	7,24E-01	**-1,07E+00**	**5,01E-03**	*nifD*- NoN 14 dpi	DNA	DDE family endonuclease (AHRD V3.3 *-* AT4G10890.3)	
Solyc07g062960.1	2,45E-01	3,93E-01	3,41E-01	2,38E-01	6,82E-01	2,32E-02	**1,14E+00**	**4,48E-04**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:polypyrimidine tract-binding protein 2 (AHRD V3.3 --* AT5G53180.6)	
Solyc06g005420.1	3,87E-01	6,18E-03	3,41E-01	1,44E-02	2,73E-01	4,50E-02	**1,23E+00**	**7,29E-10**	*nifD*- NoN 14 dpi	DNA	histone H4 (AHRD V3.3 *** AT2G28740.1)	GO:0000786|GO:0003677|GO:0005634|GO:0000786|GO:0003677|GO:0005634|GO:0006334|GO:0000786|GO:0003677|GO:0005634|GO:0006334

Solyc10g050200.1	4,41E-01	4,18E-01	3,37E-01	5,34E-01	6,09E-01	2,66E-01	**-1,67E+00**	**4,42E-03**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:transmembrane protein, putative (DUF679 domain membrane protein 2) (AHRD V3.3 *** AT3G21550.1)	
Solyc03g083490.3	8,15E-01	3,37E-01	3,36E-01	6,90E-01	-1,51E+00	8,09E-02	**-3,83E+00**	**9,78E-05**	*nifD*- NoN 14 dpi	NA	DUF1442 family protein (AHRD V3.3 *** B7FH79_MEDTR)	
Solyc06g084155.1	-5,52E-03	9,80E-01	3,33E-01	1,40E-01	-1,73E-01	4,38E-01	**1,03E+00**	**7,18E-05**	*nifD*- NoN 14 dpi	TR	Sulfate transporter, putative (AHRD V3.3 *-* B9SFG4_RICCO)	GO:0008271|GO:0008272|GO:0016020|GO:0055085|GO:0008272|GO:0009507|GO:0015116|GO:0008272|GO:0009507|GO:0015116
Solyc03g043920.3	-7,86E-02	6,54E-01	3,32E-01	6,71E-02	-8,02E-01	9,29E-05	**-1,78E+00**	**1,36E-10**	*nifD*- NoN 14 dpi	CS	Xyloglucan alpha-1,6-xylosyltransferase (AHRD V3.3 *** X2CZ83_PINRA)	GO:0016021|GO:0016757
Solyc05g052750.3	7,82E-01	3,38E-05	3,28E-01	4,58E-02	-1,75E-01	2,74E-01	**1,15E+00**	**8,58E-08**	*nifD*- NoN 14 dpi	L	Alpha/beta hydrolase related protein (AHRD V3.3 *** A0A061FLN1_THECC)	
Solyc03g123710.3	8,35E-01	2,21E-01	3,27E-01	6,28E-01	7,38E-01	2,78E-01	**-2,15E+00**	**3,37E-03**	*nifD*- NoN 14 dpi	G	purple acid phosphatase 17 (AHRD V3.3 --* AT3G17790.1)	
Solyc01g103120.3	-1,78E-01	7,22E-01	3,27E-01	5,15E-01	-4,80E-01	3,41E-01	**-1,39E+00**	**9,45E-03**	*nifD*- NoN 14 dpi	TR	Dynamin family protein (AHRD V3.3 *-* B9N0H6_POPTR)	GO:0003924|GO:0005525
Solyc01g091050.3	1,12E+00	5,80E-02	3,27E-01	5,66E-01	1,47E+00	1,45E-02	**3,71E+00**	**5,58E-07**	*nifD*- NoN 14 dpi	CS	Pectinesterase (AHRD V3.3 *** K4AZ45_SOLLC)	GO:0004857|GO:0005618|GO:0030599|GO:0042545|GO:0005618|GO:0030599|GO:0042545
Solyc11g072750.2	-2,73E-01	7,50E-01	3,26E-01	7,03E-01	-1,84E+00	3,91E-02	**-2,76E+00**	**3,12E-03**	*nifD*- NoN 14 dpi	D	Chitinase (AHRD V3.3 *** G7KL79_MEDTR)	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc01g006825.1	-5,16E-01	2,21E-02	3,25E-01	1,37E-01	-4,88E-01	2,94E-02	**-1,19E+00**	**7,29E-06**	*nifD*- NoN 14 dpi	PMI	Fasciclin-like arabinogalactan protein 17 (AHRD V3.3 *** FLA17_ARATH)	
Solyc05g013860.3	-1,93E-01	6,65E-01	3,23E-01	4,71E-01	-2,96E-01	5,08E-01	**-1,91E+00**	**1,96E-04**	*nifD*- NoN 14 dpi	G	sieve element occlusion protein (AHRD V3.3 *** AT1G67790.1)	
Solyc03g112580.3	-2,66E-01	3,45E-01	3,23E-01	2,53E-01	-3,08E-01	2,74E-01	**-1,47E+00**	**1,43E-05**	*nifD*- NoN 14 dpi	S	Receptor protein kinase, putative (AHRD V3.3 *** B9RAX9_RICCO)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g007330.1	8,26E-01	3,11E-04	3,21E-01	1,18E-01	-6,37E-03	9,75E-01	**1,29E+00**	**7,49E-07**	*nifD*- NoN 14 dpi	D	Serine-rich protein-related (AHRD V3.3 *** A0A061GN42_THECC)	
Solyc09g089880.3	7,49E-01	4,44E-04	3,19E-01	9,87E-02	4,91E-01	1,39E-02	**1,63E+00**	**3,41E-09**	*nifD*- NoN 14 dpi	E	Electron transfer flavoprotein beta-subunit, putative (AHRD V3.3 *** B9STH5_RICCO)	GO:0009055
Solyc03g112330.3	6,68E-01	3,89E-04	3,13E-01	6,76E-02	3,73E-01	3,14E-02	**1,01E+00**	**1,78E-06**	*nifD*- NoN 14 dpi	P	U-box domain-containing protein kinase family protein (AHRD V3.3 *-* AT2G19410.2)	GO:0006950
Solyc03g082740.3	5,93E-01	6,83E-04	3,12E-01	5,29E-02	4,59E-01	6,17E-03	**1,10E+00**	**1,47E-07**	*nifD*- NoN 14 dpi	NA	Protein yippee-like (AHRD V3.3 *** A0A0V0HBB0_SOLCH)	
Solyc12g096090.2	4,42E-01	2,49E-02	3,11E-01	1,06E-01	3,78E-01	5,20E-02	**1,06E+00**	**5,81E-06**	*nifD*- NoN 14 dpi	NA	Cadmium induced protein AS8 (AHRD V3.3 *** A9PH05_POPTR)	
Solyc08g081420.3	1,75E-02	9,25E-01	3,10E-01	1,03E-01	2,06E-01	2,72E-01	**-1,30E+00**	**1,84E-07**	*nifD*- NoN 14 dpi	C	transferring glycosyl group transferase (DUF604) (AHRD V3.3 *** AT5G41460.1)	
Solyc02g065070.3	5,22E-01	1,59E-05	3,10E-01	4,13E-03	1,96E-01	5,71E-02	**1,02E+00**	**1,08E-10**	*nifD*- NoN 14 dpi	K	CDPK-related kinase (AHRD V3.3 *** AT3G50530.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc09g061930.3	-2,90E-01	3,09E-02	3,08E-01	2,25E-02	2,93E-01	2,95E-02	**-1,16E+00**	**1,42E-09**	*nifD*- NoN 14 dpi	K	Ovary receptor kinase 7 (AHRD V3.3 *** S4WHD2_SOLCH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g005300.1	6,12E-01	1,60E-02	3,07E-01	2,07E-01	-6,26E-01	1,39E-02	**1,33E+00**	**6,94E-06**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:RING-finger, DEAD-like helicase, PHD and SNF2 domain-containing protein (AHRD V3.3 --* AT2G40770.3)	
Solyc02g080580.1	6,91E-01	3,05E-01	3,06E-01	6,47E-01	1,42E+00	4,10E-02	**2,65E+00**	**4,69E-04**	*nifD*- NoN 14 dpi	G	LOW QUALITY:senescence regulator (Protein of unknown function, DUF584) (AHRD V3.3 *** AT4G04630.1)	
Solyc10g081120.2	8,95E-01	4,32E-06	3,04E-01	5,99E-02	4,33E-01	9,46E-03	**1,78E+00**	**1,17E-11**	*nifD*- NoN 14 dpi	G	alpha-L-arabinofuranosidase	GO:0046373|GO:0046556
Solyc04g072320.2	4,30E-01	3,25E-01	3,03E-01	4,86E-01	-2,24E+00	1,96E-05	**1,38E+00**	**3,56E-03**	*nifD*- NoN 14 dpi	RNA	RNA polymerase I subunit 43 (AHRD V3.3 --* AT1G60620.2)	
Solyc00g100880.3	6,14E-01	1,55E-01	3,02E-01	4,77E-01	-1,58E+00	8,51E-04	**1,49E+00**	**1,49E-03**	*nifD*- NoN 14 dpi	D	LURP-one-like protein (AHRD V3.3 *** AT1G53875.1)	
Solyc09g074620.3	2,94E-01	4,34E-01	3,02E-01	4,23E-01	1,60E-01	6,69E-01	**1,04E+00**	**9,53E-03**	*nifD*- NoN 14 dpi	NA	Zinc metalloproteinase aureolysin (AHRD V3.3 *** A0A0B0PSB0_GOSAR)	

Solyc04g078690.3	5,35E-01	2,74E-02	3,00E-01	2,01E-01	4,90E-01	4,21E-02	**2,23E+00**	**4,26E-10**	*nifD*- NoN 14 dpi	T	bHLH transcription factor 035	GO:0046983
Solyc02g077880.3	7,29E-01	9,00E-04	2,97E-01	1,38E-01	3,05E-02	8,76E-01	**1,31E+00**	**3,95E-07**	*nifD*- NoN 14 dpi	H	auxin repressed/dormancy associated protein	
Solyc09g011750.3	-6,16E-01	2,68E-02	2,97E-01	2,67E-01	-2,75E-01	3,04E-01	**-1,18E+00**	**1,31E-04**	*nifD*- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9IG10_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc02g078500.2	-1,49E-04	1,00E+00	2,96E-01	3,91E-01	7,43E-01	3,79E-02	**3,90E+00**	**1,27E-11**	*nifD*- NoN 14 dpi	NA	Stem-specific protein TSJT1, putative (AHRD V3.3 *** B9RZ68_RICCO)	
Solyc03g058370.2	3,60E-01	6,48E-01	2,94E-01	7,09E-01	8,02E-01	3,13E-01	**-3,03E+00**	**6,42E-04**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4AWL3_SOLLC)	GO:0008152|GO:0016758
Solyc11g072850.2	-5,56E-01	2,77E-01	2,93E-01	5,63E-01	1,19E+00	2,48E-02	**-1,40E+00**	**9,78E-03**	*nifD*- NoN 14 dpi	T	CCT motif family protein (AHRD V3.3 *** A0A061GWL0_THECC)	GO:0005515
Solyc03g112460.3	-6,63E-01	1,09E-01	2,92E-01	4,72E-01	-4,31E-01	2,90E-01	**-2,14E+00**	**1,38E-05**	*nifD*- NoN 14 dpi	H	Tryptophan aminotransferase related 2, putative (AHRD V3.3 *** A0A061FUE1_THECC)	GO:0003824|GO:0016846|GO:0016846
Solyc07g043500.1	5,11E-01	1,57E-01	2,89E-01	4,18E-01	4,74E-01	1,89E-01	**-1,44E+00**	**3,64E-04**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4CEK8_SOLLC)	GO:0008152|GO:0016758
Solyc01g096560.2	-6,42E-01	1,24E-01	2,88E-01	4,82E-01	-1,09E+00	1,18E-02	**-1,77E+00**	**1,77E-04**	*nifD*- NoN 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** A0A0B2PRM9_GLYSO)	GO:0004252|GO:0006508
Solyc02g093330.3	-1,83E+00	1,28E-02	2,87E-01	6,79E-01	-1,04E+00	1,40E-01	**-3,40E+00**	**3,80E-05**	*nifD*- NoN 14 dpi	RNA	Nuclear pore complex Nup98-Nup96 (AHRD V3.3 *-* A0A0B0NED3_GOSAR)	
Solyc01g108000.3	3,78E-03	9,87E-01	2,86E-01	2,21E-01	-7,24E-01	3,88E-03	**-1,53E+00**	**4,47E-07**	*nifD*- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *** D7L9X7_ARALL)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc10g006030.3	4,81E-01	1,43E-03	2,86E-01	4,39E-02	4,54E-01	2,40E-03	**1,10E+00**	**1,44E-08**	*nifD*- NoN 14 dpi	R	Ribosomal protein S10 (AHRD V3.3 *** A0A103Y4F5_CYNCS)	GO:0003723|GO:0003735|GO:0005622|GO:0005840|GO:0006412|GO:0003735|GO:0005840|GO:0006412|GO:0003735|GO:0005840|GO:0006412
Solyc05g013680.3	-5,35E-01	4,02E-03	2,85E-01	1,05E-01	8,45E-02	6,22E-01	**-1,29E+00**	**4,90E-08**	*nifD*- NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** W9RN10_9ROSA)	GO:0016788
Solyc03g071533.1	-2,80E-01	7,05E-01	2,85E-01	7,01E-01	4,21E-01	5,71E-01	**-2,35E+00**	**3,55E-03**	*nifD*- NoN 14 dpi	OX	catalase 3 (AHRD V3.3 --* AT1G20620.6)	
Solyc08g007660.2	4,40E-01	3,44E-01	2,83E-01	5,41E-01	6,26E-01	1,83E-01	**-1,27E+00**	**9,86E-03**	*nifD*- NoN 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** Q9LWA3_SOLLC)	GO:0004252|GO:0006508
Solyc08g079870.3	-2,57E-01	7,60E-01	2,81E-01	7,39E-01	1,47E+00	8,87E-02	**2,35E+00**	**9,01E-03**	*nifD*- NoN 14 dpi	P	subtilisin	GO:0004252|GO:0006508
Solyc03g095820.3	-3,48E-02	9,67E-01	2,79E-01	7,38E-01	-1,90E-01	8,20E-01	**-2,72E+00**	**2,87E-03**	*nifD*- NoN 14 dpi	CS	Trichome birefringence-like protein (AHRD V3.3 *** G7K771_MEDTR)	
Solyc08g048545.1	-4,28E-01	4,03E-01	2,78E-01	5,86E-01	-3,36E-01	5,11E-01	**-1,80E+00**	**1,45E-03**	*nifD*- NoN 14 dpi	E	NADH-ubiquinone oxidoreductase chain 4 (AHRD V3.3 --* A0A199VVJ6_ANACO)	
Solyc11g066720.2	-3,57E-01	1,81E-02	2,76E-01	6,16E-02	-3,30E-01	2,79E-02	**-1,20E+00**	**5,92E-09**	*nifD*- NoN 14 dpi	CS	UDP-apiose/xylose synthase (AHRD V3.3 *** Q2I2N3_SOLTU)	GO:0003824|GO:0050662
Solyc04g076303.1	6,85E-01	1,98E-03	2,75E-01	1,79E-01	-1,34E-01	5,06E-01	**1,67E+00**	**7,82E-09**	*nifD*- NoN 14 dpi	TR	Mechanosensitive ion channel-like protein (AHRD V3.3 *** G7J535_MEDTR)	GO:0016020|GO:0055085
Solyc09g091970.3	-2,28E-01	7,43E-01	2,75E-01	6,93E-01	1,61E+00	2,74E-02	**-1,99E+00**	**7,74E-03**	*nifD*- NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** AT2G21280.2)	GO:0003824|GO:0050662
Solyc06g082950.3	1,37E+00	4,34E-02	2,74E-01	6,74E-01	6,17E-01	3,47E-01	**1,91E+00**	**6,50E-03**	*nifD*- NoN 14 dpi	E	Photosystem I reaction center subunit XI (AHRD V3.3 *** A0A061DNS9_THECC)	GO:0009522|GO:0009538|GO:0015979
Solyc03g117490.3	5,25E-01	1,44E-06	2,73E-01	3,28E-03	4,15E-02	6,27E-01	**1,12E+00**	**5,63E-13**	*nifD*- NoN 14 dpi	C	Glycerol kinase (AHRD V3.3 *** GLPK_ARATH)	GO:0004370|GO:0006072|GO:0005975|GO:0016773|GO:0005975|GO:0016773
Solyc05g055020.3	1,51E-01	5,41E-01	2,72E-01	2,76E-01	-9,80E-01	4,61E-04	**-1,13E+00**	**8,84E-05**	*nifD*- NoN 14 dpi	G	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640) (AHRD V3.3 *** AT5G28490.1)	
Solyc10g080430.1	-1,19E-01	8,37E-01	2,71E-01	6,40E-01	-1,17E+00	5,07E-02	**-1,62E+00**	**8,79E-03**	*nifD*- NoN 14 dpi	H	C2 calcium/lipid-binding and GRAM domain protein (AHRD V3.3 *** A0A072TGP1_MEDTR)	GO:0005515
Solyc01g094020.3	5,75E-02	7,88E-01	2,65E-01	2,21E-01	-1,57E-02	9,41E-01	**-1,02E+00**	**5,68E-05**	*nifD*- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9IC34_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468

Solyc09g015520.3	-2,13E-01	1,21E-01	2,65E-01	5,63E-02	7,12E-02	5,96E-01	**-1,18E+00**	**2,33E-09**	*nifD*- NoN 14 dpi	PMI	Leucine-rich receptor-like protein kinase family protein (AHRD V3.3 *** A0A061EHU9_THECC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc06g066360.2	4,65E-01	1,95E-01	2,65E-01	4,55E-01	6,50E-01	7,40E-02	**1,99E+00**	**5,71E-06**	*nifD*- NoN 14 dpi	DNA	RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-* G7IWF3_MEDTR)	
Solyc04g054340.1	3,55E-01	1,85E-01	2,65E-01	3,19E-01	7,03E-01	1,22E-02	**3,46E+00**	**5,35E-13**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:transmembrane protein (AHRD V3.3 --* AT5G65440.9)	
Solyc06g053210.3	9,75E-01	2,18E-04	2,63E-01	2,57E-01	8,41E-01	1,01E-03	**1,26E+00**	**7,93E-06**	*nifD*- NoN 14 dpi	P	Ubiquitin (AHRD V3.3 *** J7G5B5_ROSRU)	GO:0003735|GO:0005840|GO:0006412|GO:0005515|GO:0005515
Solyc06g073165.1	9,39E-01	8,57E-03	2,61E-01	4,36E-01	-4,17E-01	2,18E-01	**1,48E+00**	**1,38E-04**	*nifD*- NoN 14 dpi	STR	LOW QUALITY:BURP domain-containing protein (AHRD V3.3 *-* AT1G23760.1)	
Solyc02g081770.1	-1,18E+00	1,07E-01	2,61E-01	7,14E-01	-1,69E+00	2,40E-02	**-2,43E+00**	**1,93E-03**	*nifD*- NoN 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein, putative (AHRD V3.3 *** A0A061E8Z9_THECC)	GO:0016747
Solyc07g065880.3	-3,48E-01	3,39E-02	2,60E-01	1,06E-01	-1,64E-01	3,02E-01	**-1,28E+00**	**1,10E-08**	*nifD*- NoN 14 dpi	TR	Kinesin motor family protein (AHRD V3.3 *** B9N5N8_POPTR)	GO:0003777|GO:0005524|GO:0007018|GO:0008017|GO:0005515|GO:0005515
Solyc08g013845.1	-5,81E-01	3,82E-01	2,59E-01	6,95E-01	-2,16E-02	9,74E-01	**-1,87E+00**	**8,24E-03**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** M1BVJ8_SOLTU)	GO:0008152|GO:0016758
Solyc01g096360.3	-2,77E-01	3,36E-01	2,59E-01	3,68E-01	-3,57E-01	2,17E-01	**-1,22E+00**	**2,09E-04**	*nifD*- NoN 14 dpi	S	Rho GTPase activating protein 2	GO:0007165
Solyc11g011860.1	-2,89E-01	4,42E-01	2,51E-01	5,04E-01	-2,85E-01	4,48E-01	**-1,26E+00**	**2,22E-03**	*nifD*- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151RGT3_CAJCA)	GO:0005515|GO:0008270|GO:0008270
Solyc04g071120.3	7,92E-01	1,64E-05	2,50E-01	1,07E-01	-3,72E-01	1,99E-02	**1,22E+00**	**1,44E-08**	*nifD*- NoN 14 dpi	K	Protein kinase, putative (AHRD V3.3 *** B9T446_RICCO)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g087810.2	1,36E-01	8,58E-01	2,50E-01	7,44E-01	1,17E+00	1,35E-01	**4,05E+00**	**1,38E-05**	*nifD*- NoN 14 dpi	STR	subtilisin-like serine protease family protein	GO:0004252|GO:0006508
Solyc02g088400.3	4,81E-01	5,40E-01	2,49E-01	7,51E-01	-3,12E-01	6,91E-01	**-2,28E+00**	**6,90E-03**	*nifD*- NoN 14 dpi	DNA	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 --* A0A0X7YCF6_SOLTU)	
Solyc07g061730.3	5,96E-01	3,85E-01	2,47E-01	7,17E-01	-5,83E-01	3,96E-01	**2,64E+00**	**5,87E-04**	*nifD*- NoN 14 dpi	H	gibberellin 2-oxidase 5	GO:0016491|GO:0055114
Solyc03g115870.3	4,04E-01	6,22E-02	2,46E-01	2,46E-01	6,92E-01	2,58E-03	**2,45E+00**	**7,29E-12**	*nifD*- NoN 14 dpi	OX	Thioredoxin (AHRD V3.3 *** A0A072UTZ5_MEDTR)	GO:0045454
Solyc08g065870.3	5,46E-01	5,13E-05	2,44E-01	4,00E-02	1,67E-01	1,50E-01	**1,22E+00**	**4,71E-11**	*nifD*- NoN 14 dpi	G	EARLY FLOWERING 3 (AHRD V3.3 *** A0A088PY80_9ROSI)	
Solyc01g108190.3	2,42E-01	4,74E-01	2,43E-01	4,72E-01	-3,73E-01	2,73E-01	**1,08E+00**	**3,25E-03**	*nifD*- NoN 14 dpi	D	Calcium-binding EF-hand (AHRD V3.3 *** A0A118JV88_CYNCS)	GO:0005509
Solyc12g006490.2	7,01E-03	9,67E-01	2,43E-01	1,56E-01	-1,98E-01	2,44E-01	**-1,29E+00**	**3,33E-08**	*nifD*- NoN 14 dpi	P	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein (AHRD V3.3 *** A0A061GNR0_THECC)	GO:0008375|GO:0016020
Solyc10g084325.1	-2,42E-01	3,39E-01	2,40E-01	3,43E-01	-9,87E-02	6,95E-01	**-1,04E+00**	**2,94E-04**	*nifD*- NoN 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *** O82777_SOLLC)	GO:0004252|GO:0006508
Solyc12g040320.2	1,63E-01	5,44E-01	2,40E-01	3,75E-01	-2,61E-01	3,35E-01	**-1,03E+00**	**6,41E-04**	*nifD*- NoN 14 dpi	PMI	Leucine-rich repeat (LRR) family protein (AHRD V3.3 *** AT5G07910.1)	GO:0005515
Solyc04g080940.3	8,64E-02	5,26E-01	2,39E-01	8,72E-02	-1,08E-01	4,30E-01	**-1,04E+00**	**3,85E-08**	*nifD*- NoN 14 dpi	H	WAT1-related protein (AHRD V3.3 *** M0ZWN9_SOLTU)	GO:0016020|GO:0016021|GO:0016021|GO:0022857|GO:0016021|GO:0022857
Solyc06g009783.1	-3,32E-01	1,45E-01	2,37E-01	2,92E-01	-7,94E-01	1,33E-03	**-1,61E+00**	**1,03E-07**	*nifD*- NoN 14 dpi	TR	Kinesin-like protein (AHRD V3.3 *-* F8UN41_TOBAC)	GO:0003777|GO:0005524|GO:0007018|GO:0008017
Solyc06g082910.3	4,15E-03	9,86E-01	2,36E-01	3,24E-01	-2,31E-02	9,22E-01	**-1,38E+00**	**3,55E-06**	*nifD*- NoN 14 dpi	CS	Formin-like protein (AHRD V3.3 *** K4CAE6_SOLLC)	
Solyc06g069150.1	-2,92E-01	4,98E-01	2,36E-01	5,83E-01	-5,16E-01	2,35E-01	**-1,55E+00**	**1,19E-03**	*nifD*- NoN 14 dpi	G	LOW QUALITY:Zinc finger BED domain-containing protein DAYSLEEPER (AHRD V3.3 --* DSLE_ARATH)	
Solyc03g120380.3	1,75E-01	8,41E-01	2,34E-01	7,89E-01	-8,05E-01	3,61E-01	**-2,95E+00**	**2,15E-03**	*nifD*- NoN 14 dpi	H	auxin-regulated IAA19	GO:0005515|GO:0005634|GO:0006355|GO:0005634|GO:0006355
Solyc02g081050.3	-5,49E-02	7,40E-01	2,33E-01	1,66E-01	-8,27E-01	3,02E-05	**-1,23E+00**	**6,11E-08**	*nifD*- NoN 14 dpi	S	Receptor protein kinase, putative (AHRD V3.3 *** B9RXG1_RICCO)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468

Solyc09g011200.2	-9,79E-01	2,49E-02	2,33E-01	5,76E-01	1,10E+00	1,29E-02	**1,51E+00**	**1,11E-03**	*nifD*- NoN 14 dpi	K	Protein kinase family protein (AHRD V3.3 *** AT5G02070.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g114730.3	-2,69E-01	1,38E-01	2,33E-01	1,98E-01	-6,94E-01	5,56E-04	**-1,27E+00**	**1,18E-07**	*nifD*- NoN 14 dpi	C	O-fucosyltransferase family protein (AHRD V3.3 *** AT5G15740.1)	
Solyc09g075140.3	5,81E-01	6,97E-04	2,32E-01	1,36E-01	4,04E-01	1,27E-02	**1,10E+00**	**1,03E-07**	*nifD*- NoN 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT3G62860.1)	
Solyc05g056540.3	5,29E-01	5,88E-05	2,32E-01	4,51E-02	3,03E-02	7,86E-01	**1,28E+00**	**9,91E-12**	*nifD*- NoN 14 dpi	2M	Alcohol dehydrogenase (AHRD V3.3 *** M8AF04_TRIUA)	GO:0055114
Solyc10g084980.2	-5,37E-01	2,12E-01	2,31E-01	5,87E-01	-1,13E+00	1,23E-02	**-1,50E+00**	**1,41E-03**	*nifD*- NoN 14 dpi	TR	Copper transporter, putative (AHRD V3.3 *** A0A061ER83_THECC)	GO:0005375|GO:0016021|GO:0035434
Solyc02g088230.3	-9,77E-01	1,38E-02	2,28E-01	5,43E-01	1,90E-01	6,12E-01	**-1,49E+00**	**4,35E-04**	*nifD*- NoN 14 dpi	STR	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A0B0MVV1_GOSAR)	GO:0016021
Solyc10g083460.1	4,21E-01	7,62E-03	2,27E-01	1,31E-01	6,79E-01	8,32E-05	**1,75E+00**	**4,69E-12**	*nifD*- NoN 14 dpi	STR	Zinc finger A20 and AN1 domain-containing stress-associated protein (AHRD V3.3 *** V5PZR5_9CARY)	GO:0003677|GO:0008270|GO:0008270|GO:0008270
Solyc02g077770.3	9,86E-01	1,26E-02	2,27E-01	5,42E-01	3,51E-01	3,48E-01	**2,25E+00**	**1,91E-06**	*nifD*- NoN 14 dpi	AM	bidirectional amino acid transporter 1 (AHRD V3.3 --* AT2G01170.2)	
Solyc05g007770.3	9,99E-01	6,87E-02	2,26E-01	6,70E-01	-1,14E-01	8,30E-01	**2,40E+00**	**1,10E-04**	*nifD*- NoN 14 dpi	T	NAC domain TF	GO:0003677|GO:0006355
Solyc03g114100.1	5,35E-03	9,77E-01	2,25E-01	2,41E-01	-1,35E-01	4,78E-01	**1,96E+00**	**9,56E-11**	*nifD*- NoN 14 dpi	CS	4-coumarate:CoA ligase 1 (AHRD V3.3 --* AT1G51680.3)	
Solyc02g065770.3	-2,73E-01	6,66E-02	2,25E-01	1,26E-01	-3,76E-01	1,38E-02	**-1,12E+00**	**2,44E-08**	*nifD*- NoN 14 dpi	CS	COBRA protein (AHRD V3.3 *** K4B708_SOLLC)	GO:0010215|GO:0016049|GO:0031225
Solyc04g009640.3	-9,42E-01	2,48E-01	2,25E-01	7,80E-01	6,18E-01	4,45E-01	**-3,20E+00**	**4,65E-04**	*nifD*- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1A662_SOLTU)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc09g092290.1	1,87E-01	6,09E-01	2,23E-01	5,42E-01	-3,37E-01	3,59E-01	**-1,85E+00**	**2,42E-05**	*nifD*- NoN 14 dpi	D	Ph-3 resistance protein (AHRD V3.3 *** A0A060D304_SOLPI)	GO:0043531
Solyc02g093335.1	-5,79E-01	1,68E-02	2,22E-01	3,36E-01	-6,59E-01	7,38E-03	**-1,36E+00**	**2,57E-06**	*nifD*- NoN 14 dpi	RNA	Nuclear pore complex Nup98-Nup96 (AHRD V3.3 *** A0A0B0NED3_GOSAR)	GO:0005643|GO:0006810
Solyc03g006880.3	-4,90E-01	5,50E-01	2,21E-01	7,86E-01	-2,12E+00	1,45E-02	**-2,53E+00**	**4,31E-03**	*nifD*- NoN 14 dpi	H	gibberellin 20-oxidase-1	GO:0016491|GO:0055114
Solyc02g090490.3	1,08E+00	1,92E-02	2,21E-01	6,14E-01	7,11E-01	1,13E-01	**1,33E+00**	**5,02E-03**	*nifD*- NoN 14 dpi	P	Patatin (AHRD V3.3 *** K4BCJ8_SOLLC)	GO:0006629|GO:0008152|GO:0008152
Solyc01g007780.3	4,52E-01	4,24E-03	2,18E-01	1,43E-01	7,86E-01	1,05E-05	**1,33E+00**	**1,32E-09**	*nifD*- NoN 14 dpi	H	HVA22-like protein (AHRD V3.3 *** M1BCP5_SOLTU)	
Solyc01g106205.1	6,48E-01	2,54E-01	2,18E-01	6,98E-01	-8,65E-01	1,31E-01	**-3,83E+00**	**2,66E-07**	*nifD*- NoN 14 dpi	STR	myosin-M heavy protein (AHRD V3.3 --* AT3G54060.2)	
Solyc06g069300.1	-7,54E-01	3,07E-02	2,17E-01	5,16E-01	-1,22E-01	7,14E-01	**-1,87E+00**	**5,88E-06**	*nifD*- NoN 14 dpi	E	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617) (AHRD V3.3 *** AT5G23100.1)	
Solyc01g090800.3	-2,88E-02	9,38E-01	2,16E-01	5,62E-01	-7,20E-01	6,11E-02	**-2,39E+00**	**7,39E-07**	*nifD*- NoN 14 dpi	G	cyclinU2_1	GO:0000079|GO:0019901
Solyc00g217960.1	4,73E-01	1,03E-01	2,15E-01	4,49E-01	6,64E-01	2,55E-02	**2,12E+00**	**5,26E-08**	*nifD*- NoN 14 dpi	D	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT1G49200.1)	GO:0005515|GO:0008270
Solyc04g080600.3	1,72E-01	1,63E-01	2,15E-01	8,41E-02	-6,58E-01	9,70E-06	**-1,02E+00**	**5,78E-09**	*nifD*- NoN 14 dpi	STR	DnaJ domain-containing protein (AHRD V3.3 *-* A0A103XYN8_CYNCS)	
Solyc08g077170.3	-1,67E+00	5,14E-02	2,15E-01	7,95E-01	-7,32E-01	3,80E-01	**-5,17E+00**	**1,17E-06**	*nifD*- NoN 14 dpi	TR	Peptide transporter, putative (AHRD V3.3 *** B9S1I2_RICCO)	GO:0005215|GO:0006810|GO:0016020
Solyc12g017380.2	-1,25E+00	1,84E-02	2,14E-01	6,69E-01	7,71E-01	1,32E-01	**-1,39E+00**	**9,71E-03**	*nifD*- NoN 14 dpi	TR	Organic cation/carnitine transporter (AHRD V3.3 *** A0A072TPM4_MEDTR)	GO:0016021|GO:0022857|GO:0055085
Solyc04g015470.3	-2,31E-01	2,67E-01	2,13E-01	3,03E-01	-1,70E-01	4,11E-01	**-1,32E+00**	**6,81E-07**	*nifD*- NoN 14 dpi	S	Phosphatidylinositol-4-phosphate 5-kinase, putative (AHRD V3.3 *** B9RJA3_RICCO)	GO:0016307|GO:0046488
Solyc05g006210.3	-1,87E-01	5,49E-01	2,12E-01	4,99E-01	5,71E-01	7,59E-02	**1,03E+00**	**2,68E-03**	*nifD*- NoN 14 dpi	CS	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** B9RPA4_RICCO)	GO:0004553|GO:0005975|GO:0005975|GO:0005975

Solyc12g056960.2	2,37E-01	1,57E-01	2,11E-01	2,04E-01	-5,38E-02	7,43E-01	**1,14E+00**	**2,04E-07**	*nifD*- NoN 14 dpi	CS	Glucan 1,3-beta-glucosidase (AHRD V3.3 *** A0A151TZN5_CAJCA)	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc09g065910.2	5,06E-01	2,52E-01	2,11E-01	6,29E-01	-1,88E-01	6,66E-01	**1,36E+00**	**4,01E-03**	*nifD*- NoN 14 dpi	E	photosystem II reaction center W (AHRD V3.3 *** AT2G30570.1)	GO:0009507|GO:0009523|GO:0015979
Solyc10g005200.3	-2,68E-01	1,94E-01	2,11E-01	3,04E-01	-9,79E-01	4,90E-05	**-1,88E+00**	**9,84E-10**	*nifD*- NoN 14 dpi	C	glycosyltransferase family protein (DUF23) (AHRD V3.3 *** AT5G44670.1)	
Solyc10g005090.3	5,31E-01	4,02E-02	2,07E-01	4,06E-01	4,37E-01	8,74E-02	**1,02E+00**	**3,25E-04**	*nifD*- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7M1C9_ARALL)	GO:0005515
Solyc11g007860.1	4,46E-01	9,18E-04	2,01E-01	1,03E-01	1,78E-01	1,46E-01	**1,15E+00**	**5,24E-10**	*nifD*- NoN 14 dpi	DNA	LOW QUALITY:Cyclin-dependent protein kinase inhibitor Siamese (AHRD V3.3 *** M4M6N3_GOSAR)	
Solyc02g078810.3	6,64E-01	2,83E-02	1,97E-01	4,97E-01	8,31E-01	7,36E-03	**1,05E+00**	**1,05E-03**	*nifD*- NoN 14 dpi	DNA	Bromodomain 4, putative (AHRD V3.3 *** A0A061GG17_THECC)	GO:0003677|GO:0005515|GO:0005515
Solyc02g080100.1	3,38E-01	4,78E-01	1,97E-01	6,79E-01	-4,64E-01	3,32E-01	**-1,35E+00**	**8,00E-03**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT4G05220.1)	
Solyc01g111830.3	-3,70E-01	1,57E-01	1,95E-01	4,50E-01	-7,63E-01	5,80E-03	**-1,06E+00**	**2,90E-04**	*nifD*- NoN 14 dpi	NA	Methyltransferase (AHRD V3.3 *** K4B445_SOLLC)	GO:0006694|GO:0008168|GO:0008152|GO:0008168|GO:0008152|GO:0008168
Solyc03g120170.1	2,51E-01	3,14E-01	1,93E-01	4,35E-01	7,88E-01	3,35E-03	**1,47E+00**	**2,45E-06**	*nifD*- NoN 14 dpi	NA	NHL domain-containing protein, putative (AHRD V3.3 --* A0A061EBN2_THECC)	
Solyc04g081530.1	4,11E-01	3,33E-01	1,91E-01	6,50E-01	9,23E-01	3,56E-02	**3,05E+00**	**9,59E-08**	*nifD*- NoN 14 dpi	STR	DNAJ-like protein (AHRD V3.3 *** A2TJX6_SOLLC)	
Solyc07g039505.1	-7,02E-02	8,45E-01	1,91E-01	5,95E-01	-4,16E-02	9,08E-01	**-1,07E+00**	**5,85E-03**	*nifD*- NoN 14 dpi	C	Beta-glucosidase 3 (AHRD V3.3 --* BGL03_ORYSJ)	
Solyc06g083750.3	-3,91E-01	1,80E-02	1,90E-01	2,32E-01	-6,18E-02	6,93E-01	**-1,34E+00**	**4,43E-09**	*nifD*- NoN 14 dpi	S	Cysteine-rich repeat secretory protein (AHRD V3.3 *** A0A0K9P487_ZOSMR)	
Solyc02g077230.3	-1,80E-01	4,52E-01	1,89E-01	4,30E-01	-3,40E-01	1,61E-01	**1,15E+00**	**4,94E-05**	*nifD*- NoN 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 --* AT2G03140.9)	
Solyc05g052890.3	6,81E-01	1,23E-01	1,87E-01	6,65E-01	-7,57E-01	8,81E-02	**1,51E+00**	**1,58E-03**	*nifD*- NoN 14 dpi	E	Cytochrome f (AHRD V3.3 --* CYF_PINTH)	
Solyc03g121920.3	3,61E-01	6,86E-02	1,86E-01	3,37E-01	3,03E-01	1,23E-01	**1,44E+00**	**5,30E-08**	*nifD*- NoN 14 dpi	TR	Mitochondrial carrier protein (AHRD V3.3 *** F8WLA3_CITUN)	GO:0055085
Solyc01g010220.3	4,14E-01	4,43E-02	1,83E-01	3,58E-01	-2,38E-01	2,35E-01	**-1,05E+00**	**1,32E-05**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151RZV3_CAJCA)	
Solyc02g084400.3	-7,95E-01	2,58E-02	1,82E-01	5,92E-01	-3,99E-01	2,45E-01	**-1,10E+00**	**2,97E-03**	*nifD*- NoN 14 dpi	K	Protein kinase-like (AHRD V3.3 *** Q2HTV1_MEDTR)	
Solyc01g090560.3	-1,79E-01	5,90E-01	1,82E-01	5,83E-01	1,34E-01	6,86E-01	**-1,14E+00**	**1,70E-03**	*nifD*- NoN 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *-* W9R3T6_9ROSA)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc03g111310.3	5,96E-01	6,20E-05	1,79E-01	1,62E-01	-9,36E-02	4,60E-01	**1,34E+00**	**5,23E-11**	*nifD*- NoN 14 dpi	C	SNF1-related protein kinase regulatory subunit gamma 1 (AHRD V3.3 *** A0A061G5Z8_THECC)	GO:0003824
Solyc11g069620.2	-6,73E-01	7,36E-03	1,78E-01	4,47E-01	-6,00E-02	7,97E-01	**-1,39E+00**	**2,48E-06**	*nifD*- NoN 14 dpi	D	Disease resistance protein (AHRD V3.3 *** A0A068EUA9_SOLLC)	GO:0043531
Solyc10g024360.2	-3,62E-01	2,22E-01	1,78E-01	5,43E-01	-7,61E-01	1,42E-02	**-1,07E+00**	**1,00E-03**	*nifD*- NoN 14 dpi	TR	Potassium channel (AHRD V3.3 *** Q9SSV3_NICPA)	GO:0005216|GO:0006811|GO:0016020|GO:0055085|GO:0005249|GO:0006813|GO:0016020|GO:0005249|GO:0006813|GO:0016020
Solyc01g109120.3	8,58E-02	7,36E-01	1,75E-01	4,93E-01	9,26E-01	1,09E-03	**1,38E+00**	**1,03E-05**	*nifD*- NoN 14 dpi	G	Transducin/WD40 repeat-like superfamily protein (AHRD V3.3 *** AT3G18950.1)	GO:0005515
Solyc12g096830.2	5,25E-01	6,71E-04	1,75E-01	2,10E-01	3,10E-01	3,10E-02	**1,47E+00**	**4,66E-11**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DHF6_SOLLC)	GO:0008152|GO:0016758
Solyc01g101120.3	7,50E-01	3,25E-04	1,70E-01	3,57E-01	2,20E-01	2,36E-01	**1,33E+00**	**9,29E-08**	*nifD*- NoN 14 dpi	CS	Glucan endo-1,3-beta-glucosidase (AHRD V3.3 *** A0A0B0PV84_GOSAR)	
Solyc09g092420.2	7,66E-01	7,64E-04	1,69E-01	4,07E-01	-1,42E-01	4,86E-01	**1,06E+00**	**1,68E-05**	*nifD*- NoN 14 dpi	AM	Amino acid permease family protein (AHRD V3.3 *** AT1G31830.1)	GO:0003333|GO:0015171|GO:0016020
Solyc03g082890.3	4,81E-01	3,34E-02	1,65E-01	4,48E-01	7,04E-01	2,92E-03	**1,71E+00**	**1,96E-08**	*nifD*- NoN 14 dpi	NA	Thylakoid lumenal 17.4 kDa protein (AHRD V3.3 *** B7FHD5_MEDTR)	

Solyc06g075510.3	-7,91E-01	3,55E-06	1,64E-01	2,35E-01	-4,30E-01	3,67E-03	**-1,40E+00**	**1,14E-10**	*nifD*- NoN 14 dpi	G	APETALA2e	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc07g054730.1	5,32E-01	7,27E-04	1,62E-01	2,55E-01	6,81E-01	4,37E-05	**1,76E+00**	**1,52E-12**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Wound-responsive family protein, putative (AHRD V3.3 *** A0A061E4N2_THECC)	
Solyc01g105180.3	-2,19E-01	3,37E-02	1,60E-01	1,13E-01	-4,70E-01	5,49E-05	**-1,20E+00**	**2,55E-12**	*nifD*- NoN 14 dpi	DNA	Protein DA1-related 1 (AHRD V3.3 *** A0A199UXH9_ANACO)	
Solyc11g072580.2	-6,41E-01	3,64E-04	1,60E-01	3,15E-01	-7,86E-01	3,21E-05	**-1,65E+00**	**7,62E-11**	*nifD*- NoN 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT3G45660.3)	GO:0005215|GO:0006810|GO:0016020
Solyc12g089210.2	5,80E-01	2,12E-04	1,59E-01	2,48E-01	2,27E-01	1,04E-01	**1,16E+00**	**4,62E-09**	*nifD*- NoN 14 dpi	N	Ornithine carbamoyltransferase (AHRD V3.3 *** K4BVE0_SOLLC)	GO:0004585|GO:0006591|GO:0006520|GO:0016597|GO:0016743|GO:0006520|GO:0016597|GO:0016743
Solyc11g011610.2	4,32E-01	1,25E-02	1,57E-01	3,39E-01	7,75E-01	5,60E-05	**1,27E+00**	**2,52E-08**	*nifD*- NoN 14 dpi	NA	UPF0678 fatty acid-binding protein-like protein family (AHRD V3.3 *** A0A151RPZ2_CAJCA)	
Solyc02g070910.3	-6,12E-01	1,49E-01	1,51E-01	7,16E-01	-5,87E-01	1,66E-01	**-1,68E+00**	**3,70E-04**	*nifD*- NoN 14 dpi	NA	Ontology_term=GO:0004675	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g071690.3	1,95E-01	3,48E-01	1,48E-01	4,75E-01	-5,47E-01	1,27E-02	**1,18E+00**	**4,31E-06**	*nifD*- NoN 14 dpi	DNA	Alba DNA/RNA-binding protein (AHRD V3.3 *-* AT1G76010.2)	GO:0003676
Solyc11g012260.2	4,67E-01	1,93E-03	1,46E-01	2,91E-01	1,40E-01	3,11E-01	**1,15E+00**	**6,54E-09**	*nifD*- NoN 14 dpi	P	MBOAT (Membrane bound O-acyl transferase) family protein, putative (AHRD V3.3 *** Q2HT39_MEDTR)	
Solyc01g109430.3	-2,71E-01	3,94E-01	1,44E-01	6,48E-01	-8,89E-01	8,63E-03	**-1,02E+00**	**3,00E-03**	*nifD*- NoN 14 dpi	P	PPPDE putative thiol peptidase family protein	
Solyc08g014610.3	1,69E-01	6,06E-01	1,44E-01	6,59E-01	8,51E-01	1,41E-02	**1,02E+00**	**4,01E-03**	*nifD*- NoN 14 dpi	AM	Aminotransferase (AHRD V3.3 *** D2KZ08_WHEAT)	GO:0003824|GO:0008483|GO:0030170|GO:0008483|GO:0030170
Solyc04g011440.4	5,63E-01	2,83E-03	1,43E-01	4,09E-01	-1,18E-01	4,94E-01	**-1,00E+00**	**3,57E-06**	*nifD*- NoN 14 dpi	H	ethylene-responsive heat shock protein cognate 70	
Solyc01g098640.3	1,90E-01	3,82E-01	1,39E-01	5,21E-01	8,53E-01	4,74E-04	**1,47E+00**	**2,80E-07**	*nifD*- NoN 14 dpi	E	Thylakoid lumen 18.3 kDa protein (AHRD V3.3 *** A0A061F263_THECC)	
Solyc02g089620.3	-2,56E-01	1,28E-01	1,36E-01	4,12E-01	-7,12E-01	1,78E-04	**-1,31E+00**	**1,61E-08**	*nifD*- NoN 14 dpi	AM	proline dehydrogenase	GO:0004657|GO:0006562
Solyc05g050540.3	-1,41E-01	7,56E-01	1,34E-01	7,68E-01	-2,69E-01	5,55E-01	**-1,76E+00**	**5,98E-04**	*nifD*- NoN 14 dpi	PMI	Laccase (AHRD V3.3 *** B9SBE5_RICCO)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc07g007020.3	-7,97E-01	3,28E-06	1,34E-01	3,30E-01	4,50E-01	2,57E-03	**-1,06E+00**	**2,68E-08**	*nifD*- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *** B9GLQ0_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g081260.3	-8,26E-01	7,14E-06	1,31E-01	3,80E-01	-8,55E-01	4,29E-06	**-1,21E+00**	**1,16E-08**	*nifD*- NoN 14 dpi	NA	Filament-plant-like protein (AHRD V3.3 *** A0A072VFI4_MEDTR)	
Solyc11g069630.1	-3,52E-01	1,84E-01	1,30E-01	6,18E-01	-3,57E-01	1,79E-01	**-1,26E+00**	**4,72E-05**	*nifD*- NoN 14 dpi	PMI	LOW QUALITY:LysM type receptor kinase (AHRD V3.3 *** D3KU02_LOTJA)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc07g007325.1	4,58E-01	2,50E-01	1,30E-01	7,42E-01	4,32E-01	2,77E-01	**1,33E+00**	**2,11E-03**	*nifD*- NoN 14 dpi	D	Serine-rich protein-related (AHRD V3.3 *-* A0A061GN42_THECC)	
Solyc05g049990.3	-7,22E-01	7,58E-04	1,29E-01	5,01E-01	-4,02E-01	4,31E-02	**-1,36E+00**	**1,31E-07**	*nifD*- NoN 14 dpi	TR	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** A0A072TW71_MEDTR)	
Solyc05g052880.3	1,18E+00	1,12E-02	1,27E-01	7,73E-01	2,02E-01	6,45E-01	**2,47E+00**	**5,81E-06**	*nifD*- NoN 14 dpi	NA	Plant/T7H20-70 protein (AHRD V3.3 *** A0A072U1L2_MEDTR)	
Solyc10g079640.2	-6,44E-01	1,38E-01	1,25E-01	7,69E-01	1,70E-01	6,89E-01	**-1,63E+00**	**6,74E-04**	*nifD*- NoN 14 dpi	H	IAA-amino acid hydrolase ILR1, putative (AHRD V3.3 *** B9RJ28_RICCO)	GO:0008152|GO:0016787|GO:0016787|GO:0016787
Solyc01g090660.3	-6,96E-01	4,35E-01	1,25E-01	8,88E-01	-1,17E-01	8,95E-01	**-2,87E+00**	**3,06E-03**	*nifD*- NoN 14 dpi	2M	carotenoid cleavage dioxygenase7	GO:0016702|GO:0055114
Solyc05g013180.3	-2,49E-01	2,99E-01	1,25E-01	6,00E-01	4,88E-01	4,83E-02	**1,71E+00**	**1,13E-07**	*nifD*- NoN 14 dpi	STR	Phosphate transporter PHO1-like protein (AHRD V3.3 *** A0A193CD86_9ERIC)	GO:0016021
Solyc00g112930.3	-4,32E-01	5,69E-02	1,24E-01	5,71E-01	-3,47E-01	1,22E-01	**-1,70E+00**	**2,84E-08**	*nifD*- NoN 14 dpi	G	Alpha-n-acetylglucosaminidase, putative (AHRD V3.3 *-* B9R8Y6_RICCO)	
Solyc07g018070.3	-3,27E-01	1,62E-02	1,22E-01	3,48E-01	3,40E-01	1,28E-02	**-1,04E+00**	**1,24E-08**	*nifD*- NoN 14 dpi	P	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein, putative (AHRD V3.3 *** A0A061GSB6_THECC)	GO:0019538

Solyc06g053840.3	5,97E-01	1,12E-03	1,21E-01	4,65E-01	2,41E-02	8,84E-01	**1,52E+00**	**1,01E-09**	*nifD*- NoN 14 dpi	H	auxin-regulated IAA4	GO:0005515|GO:0005634|GO:0006355|GO:0005634|GO:0006355
Solyc08g007270.3	-7,53E-01	2,38E-03	1,17E-01	6,04E-01	2,27E-01	3,18E-01	**-1,87E+00**	**7,94E-09**	*nifD*- NoN 14 dpi	DNA	Homeobox-leucine zipper family protein (AHRD V3.3 *** B9GYL8_POPTR)	GO:0003677|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565
Solyc11g072470.2	-1,53E+00	1,39E-02	1,13E-01	8,47E-01	1,12E-01	8,48E-01	**-2,30E+00**	**5,07E-04**	*nifD*- NoN 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9SK21_RICCO)	
Solyc04g016480.3	-1,98E-02	9,40E-01	1,12E-01	6,71E-01	-9,51E-01	1,21E-03	**-1,24E+00**	**6,99E-05**	*nifD*- NoN 14 dpi	G	SUN-like protein 12	GO:0005515
Solyc11g068370.2	5,49E-01	1,42E-04	1,12E-01	3,72E-01	5,05E-01	3,62E-04	**1,24E+00**	**2,09E-10**	*nifD*- NoN 14 dpi	T	bZIP transcription factor family protein (AHRD V3.3 *** AT1G08320.4)	GO:0003700|GO:0006355|GO:0043565|GO:0006351|GO:0043565|GO:0006351|GO:0043565
Solyc06g076470.3	2,91E-01	5,62E-02	1,10E-01	4,59E-01	9,01E-01	1,58E-06	**1,46E+00**	**2,10E-10**	*nifD*- NoN 14 dpi	NA	Plant/T7H20-70 protein (AHRD V3.3 *** G7L5L0_MEDTR)	
Solyc09g065540.3	7,40E-01	1,64E-04	1,07E-01	5,28E-01	2,00E-01	2,45E-01	**1,91E+00**	**1,63E-11**	*nifD*- NoN 14 dpi	L	biotin-binding protein	GO:0003824|GO:0005524|GO:0004075|GO:0005524|GO:0004075|GO:0005524
Solyc06g063060.3	8,28E-01	2,35E-02	1,07E-01	7,58E-01	-2,87E-01	4,12E-01	**2,06E+00**	**2,58E-06**	*nifD*- NoN 14 dpi	H	Auxin-repressed protein-like protein (AHRD V3.3 *** Q84KS0_TOBAC)	
Solyc03g119470.2	-3,78E-01	3,30E-01	1,06E-01	7,83E-01	-1,83E-01	6,35E-01	**-1,35E+00**	**1,51E-03**	*nifD*- NoN 14 dpi	NA	DUF1666 family protein (AHRD V3.3 *** G7KN40_MEDTR)	GO:0003735|GO:0005622|GO:0005840|GO:0006412
Solyc03g005600.3	-6,78E-01	8,32E-03	1,03E-01	6,67E-01	-7,96E-01	2,47E-03	**-1,25E+00**	**1,79E-05**	*nifD*- NoN 14 dpi	CS	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G04430.3)	GO:0008168
Solyc05g025900.3	4,37E-01	1,70E-02	1,00E-01	5,65E-01	4,50E-01	1,44E-02	**1,66E+00**	**4,74E-10**	*nifD*- NoN 14 dpi	DNA	Damaged dna-binding 2, putative isoform 1 (AHRD V3.3 *** A0A061GKJ3_THECC)	
Solyc12g055930.2	-1,45E-01	5,10E-01	9,60E-02	6,62E-01	-9,56E-01	1,64E-04	**-1,11E+00**	**2,62E-05**	*nifD*- NoN 14 dpi	C	UDP-glucose 4-epimerase (AHRD V3.3 *** Q6XZA0_SOLTU)	GO:0003978|GO:0006012
Solyc03g122310.3	8,95E-01	2,89E-05	9,58E-02	5,92E-01	9,13E-01	2,23E-05	**1,18E+00**	**4,93E-07**	*nifD*- NoN 14 dpi	STR	Aldehyde dehydrogenase (AHRD V3.3 *** Q9FPK6_ORYSA)	GO:0008152|GO:0016491|GO:0016620|GO:0055114|GO:0008152|GO:0016491|GO:0055114|GO:0008152|GO:0016491|GO:0055114
Solyc03g007180.1	-4,04E-01	2,11E-02	9,52E-02	5,67E-01	-3,69E-01	3,36E-02	**-1,45E+00**	**3,15E-09**	*nifD*- NoN 14 dpi	NA	F5O11.10, putative isoform 1 (AHRD V3.3 *** A0A061G0M8_THECC)	GO:0003676
Solyc06g069410.3	6,41E-01	2,16E-05	9,44E-02	4,53E-01	1,19E-01	3,47E-01	**1,10E+00**	**2,65E-09**	*nifD*- NoN 14 dpi	TR	ADP,ATP carrier protein, mitochondrial (AHRD V3.3 *** ADT_ORYSJ)	GO:0005215|GO:0005743|GO:0006810|GO:0055085|GO:0055085|GO:0055085
Solyc02g038740.3	2,52E-01	4,19E-01	9,20E-02	7,67E-01	4,00E-01	2,04E-01	**1,37E+00**	**1,47E-04**	*nifD*- NoN 14 dpi	L	3-hydroxy-3-methylglutaryl coenzyme A reductase (AHRD V3.3 *** K4B5W7_SOLLC)	GO:0004420|GO:0008299|GO:0016021|GO:0050661|GO:0055114|GO:0004420|GO:0015936|GO:0050662|GO:0055114|GO:0004420|GO:0015936|GO:0050662|GO:0055114
Solyc03g116510.1	7,58E-01	3,68E-02	9,15E-02	7,92E-01	7,16E-03	9,84E-01	**2,03E+00**	**3,40E-06**	*nifD*- NoN 14 dpi	NA	cotton fiber protein (AHRD V3.3 *** AT1G15385.1)	
Solyc05g014690.2	-4,11E-02	9,01E-01	9,02E-02	7,84E-01	-3,67E-02	9,11E-01	**-1,31E+00**	**4,44E-04**	*nifD*- NoN 14 dpi	RNA	RNA helicase DEAH-box14	GO:0003676|GO:0005524|GO:0003676|GO:0005524|GO:0008026|GO:0003676|GO:0005524|GO:0008026
Solyc03g093250.2	-4,57E-01	2,49E-01	8,71E-02	8,24E-01	8,63E-02	8,25E-01	**-1,35E+00**	**1,79E-03**	*nifD*- NoN 14 dpi	DNA	Structural maintenance of chromosomes protein (AHRD V3.3 *** A0A068V0V7_COFCA)	GO:0005515|GO:0005524|GO:0005694|GO:0051276
Solyc09g089865.1	2,64E-01	2,29E-01	8,50E-02	6,95E-01	1,98E-01	3,66E-01	**1,16E+00**	**1,18E-05**	*nifD*- NoN 14 dpi	D	DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein (AHRD V3.3 --* AT1G31880.2)	
Solyc08g007630.1	-3,29E-01	2,20E-01	8,30E-02	7,54E-01	-4,49E-01	9,87E-02	**-1,83E+00**	**2,12E-07**	*nifD*- NoN 14 dpi	D	Disease resistance protein (AHRD V3.3 *** A0A068EX87_SOLHA)	GO:0005515|GO:0043531|GO:0043531
Solyc12g077370.2	8,56E-02	6,86E-01	8,17E-02	7,00E-01	2,82E-02	8,94E-01	**1,91E+00**	**1,62E-09**	*nifD*- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** M1BPG2_SOLTU)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g025380.3	5,06E-01	2,62E-01	8,03E-02	8,57E-01	8,87E-02	8,42E-01	**1,43E+00**	**3,24E-03**	*nifD*- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4BF11_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc07g062280.3	4,54E-01	1,29E-01	7,98E-02	7,85E-01	8,71E-01	5,79E-03	**1,36E+00**	**7,64E-05**	*nifD*- NoN 14 dpi	N	Gamma-glutamyl hydrolase (AHRD V3.3 *** X5HY53_IPONI)	GO:0003824|GO:0006541|GO:0008242|GO:0006541|GO:0016787|GO:0006541|GO:0016787
Solyc11g066880.2	-8,63E-01	6,11E-05	7,70E-02	6,73E-01	-4,07E-02	8,23E-01	**-1,22E+00**	**3,89E-07**	*nifD*- NoN 14 dpi	G	Phytosulfokine 3, putative (AHRD V3.3 *** A0A061ESV9_THECC)	GO:0005576|GO:0008083|GO:0008283
Solyc01g094230.3	1,87E-01	8,35E-01	7,64E-02	9,32E-01	-8,44E-01	3,49E-01	**-3,05E+00**	**1,97E-03**	*nifD*- NoN 14 dpi	E	ATP synthase subunit c, chloroplastic (AHRD V3.3 -* ATPH_CHAGL)	GO:0004722|GO:0006470

Solyc04g009000.1	-7,98E-01	1,34E-02	7,47E-02	8,06E-01	-2,26E-01	4,58E-01	**-1,20E+00**	**4,89E-04**	*nifD*- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XCD9_CYNCS)	GO:0005515|GO:0008270|GO:0008270
Solyc05g056070.3	-4,41E-01	4,42E-01	7,04E-02	9,02E-01	8,14E-01	1,62E-01	**1,79E+00**	**3,98E-03**	*nifD*- NoN 14 dpi	E	photosystem 1 protein	GO:0009765|GO:0016020
Solyc01g109140.3	3,60E-01	1,53E-01	6,99E-02	7,77E-01	-3,42E-01	1,74E-01	**1,15E+00**	**7,53E-05**	*nifD*- NoN 14 dpi	L	divinyl ether synthase	GO:0004497|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc04g078610.3	-5,56E-01	1,18E-01	6,65E-02	8,48E-01	-7,20E-01	4,62E-02	**-1,07E+00**	**4,39E-03**	*nifD*- NoN 14 dpi	TR	Kinesin-like protein (AHRD V3.3 *** A0A0V0IYA4_SOLCH)	GO:0003777|GO:0005524|GO:0007018|GO:0003777|GO:0005524|GO:0007018|GO:0008017|GO:0003777|GO:0005524|GO:0007018|GO:0008017
Solyc03g117420.3	6,48E-01	1,96E-04	6,64E-02	6,60E-01	-3,18E-02	8,33E-01	**1,36E+00**	**1,62E-09**	*nifD*- NoN 14 dpi	PMI	F-box/LRR-repeat protein (AHRD V3.3 *** A0A0K9PK37_ZOSMR)	GO:0005515
Solyc09g008030.1	2,07E-01	1,54E-01	6,35E-02	6,56E-01	4,91E-01	1,81E-03	**1,22E+00**	**4,50E-09**	*nifD*- NoN 14 dpi	T	TCP transcription factor 19	
Solyc10g078230.2	4,28E-01	6,28E-01	6,34E-02	9,43E-01	2,45E-01	7,81E-01	**3,22E+00**	**1,05E-03**	*nifD*- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** A0A103VZI8_CYNCS)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc11g065910.1	-5,14E-01	2,02E-01	6,33E-02	8,73E-01	-3,73E-01	3,51E-01	**-1,17E+00**	**6,29E-03**	*nifD*- NoN 14 dpi	D	Aspartic protease inhibitor 9 (AHRD V3.3 --* API9_SOLTU)	
Solyc07g064470.3	5,77E-01	2,00E-01	5,56E-02	9,00E-01	8,75E-01	5,67E-02	**1,30E+00**	**6,59E-03**	*nifD*- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *-* A0A061FD55_THECC)	GO:0005506|GO:0016705|GO:0020037|GO:0055114
Solyc04g063230.3	-5,78E-01	2,99E-04	5,45E-02	6,97E-01	-5,16E-01	9,51E-04	**-1,02E+00**	**8,46E-08**	*nifD*- NoN 14 dpi	CS	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT5G64030.1)	GO:0008168
Solyc05g007470.3	-6,93E-01	5,51E-05	5,43E-02	7,08E-01	-5,52E-01	7,07E-04	**-1,85E+00**	**1,09E-12**	*nifD*- NoN 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT3G28580.1)	GO:0005524
Solyc02g072520.3	-2,87E-01	7,90E-02	5,29E-02	7,38E-01	-2,48E-01	1,26E-01	**-1,17E+00**	**7,23E-08**	*nifD*- NoN 14 dpi	S	Receptor kinase, putative (AHRD V3.3 *** A0A061GFM9_THECC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc05g008390.3	4,26E-01	5,81E-04	4,95E-02	6,52E-01	4,05E-02	7,13E-01	**1,53E+00**	**1,44E-13**	*nifD*- NoN 14 dpi	P	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** A0A061EGA0_THECC)	GO:0008270
Solyc11g069820.2	-1,03E-01	7,87E-01	4,82E-02	8,99E-01	-1,86E-01	6,26E-01	**-1,96E+00**	**2,10E-05**	*nifD*- NoN 14 dpi	TR	ABC transporter G family-like protein (AHRD V3.3 *** A0A072UJT7_MEDTR)	GO:0005524|GO:0016887
Solyc06g010010.2	5,37E-01	2,64E-01	4,81E-02	9,19E-01	9,89E-01	4,52E-02	**1,34E+00**	**8,38E-03**	*nifD*- NoN 14 dpi	D	MLO-like protein (AHRD V3.3 *-* K4C428_SOLLC)	GO:0006952|GO:0016021
Solyc02g088690.3	-2,80E-01	1,87E-01	4,69E-02	8,23E-01	-5,37E-01	1,53E-02	**-1,17E+00**	**5,89E-06**	*nifD*- NoN 14 dpi	CS	UDP-glucose 6-dehydrogenase family protein (AHRD V3.3 *** AT3G29360.2)	GO:0003979|GO:0016616|GO:0051287|GO:0055114|GO:0016616|GO:0051287|GO:0055114
Solyc01g096880.3	6,43E-01	4,01E-02	4,55E-02	8,80E-01	7,26E-01	2,19E-02	**1,07E+00**	**1,37E-03**	*nifD*- NoN 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT2G26690.1)	GO:0005215|GO:0006810|GO:0016020|GO:0005215|GO:0006857|GO:0016020|GO:0005215|GO:0006857|GO:0016020
Solyc04g076220.3	6,10E-01	6,59E-03	4,28E-02	8,37E-01	2,63E-01	2,14E-01	**1,10E+00**	**1,51E-05**	*nifD*- NoN 14 dpi	DNA	AT hook motif DNA-binding family protein (AHRD V3.3 *** G7J554_MEDTR)	
Solyc09g082110.3	3,95E-01	4,83E-02	4,14E-02	8,30E-01	3,95E-01	4,85E-02	**1,06E+00**	**7,93E-06**	*nifD*- NoN 14 dpi	STR	Seed maturation protein/ Late embryogenesis abundant protein (AHRD V3.3 *** A0A0K9PC32_ZOSMR)	
Solyc08g014440.3	2,95E-01	2,71E-02	4,14E-02	7,45E-01	4,97E-01	5,47E-04	**1,08E+00**	**5,02E-09**	*nifD*- NoN 14 dpi	T	BTB/POZ and TAZ domain protein (AHRD V3.3 *** G7K3T4_MEDTR)	GO:0003712|GO:0004402|GO:0005634|GO:0006355|GO:0008270|GO:0005515|GO:0005515
Solyc03g116860.3	-7,95E-01	4,67E-05	3,98E-02	8,09E-01	-9,06E-01	7,94E-06	**-1,24E+00**	**4,69E-08**	*nifD*- NoN 14 dpi	H	Acyl-CoA N-acyltransferases superfamily protein (AHRD V3.3 *** A0A061G857_THECC)	GO:0008080
Solyc12g014100.2	6,65E-01	5,41E-05	3,65E-02	7,93E-01	3,06E-02	8,26E-01	**1,32E+00**	**5,81E-10**	*nifD*- NoN 14 dpi	AM	homogentisate 1,2-dioxygenase	GO:0004411|GO:0006559|GO:0006570|GO:0055114
Solyc03g112390.3	4,81E-04	9,98E-01	3,63E-02	8,71E-01	-2,86E-01	2,09E-01	**-1,14E+00**	**2,39E-05**	*nifD*- NoN 14 dpi	G	R2R3MYB transcription factor 86	GO:0003677
Solyc08g079020.3	7,38E-01	9,96E-04	3,43E-02	8,64E-01	-3,28E-01	1,11E-01	**1,46E+00**	**8,75E-08**	*nifD*- NoN 14 dpi	P	Adenine phosphoribosyltransferase-like protein (AHRD V3.3 *** G7JW03_MEDTR)	GO:0003999|GO:0005737|GO:0006168|GO:0009116|GO:0009116
Solyc03g078650.3	-3,03E-01	1,72E-01	3,29E-02	8,80E-01	-5,27E-01	2,16E-02	**-1,63E+00**	**5,22E-08**	*nifD*- NoN 14 dpi	L	Lipase (AHRD V3.3 *** G7JAK3_MEDTR)	

Solyc03g033610.1	-8,58E-01	5,55E-03	3,19E-02	9,11E-01	-5,71E-01	5,43E-02	**-1,00E+00**	**1,59E-03**	*nifD*- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4BFN3_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc06g068500.3	4,43E-01	1,42E-02	3,10E-02	8,55E-01	1,52E-01	3,74E-01	**1,30E+00**	**3,53E-08**	*nifD*- NoN 14 dpi	T	Chaperone DnaJ domain protein (AHRD V3.3 *** B7FGF7_MEDTR)	
Solyc12g010420.1	3,21E-01	4,19E-01	2,86E-02	9,42E-01	-3,71E-01	3,51E-01	**1,60E+00**	**3,67E-04**	*nifD*- NoN 14 dpi	P	LOW QUALITY:NHL domain protein (AHRD V3.3 --* AT5G14895.1)	
Solyc05g008780.3	-6,34E-01	3,67E-03	2,78E-02	8,90E-01	-6,19E-01	4,41E-03	**-1,05E+00**	**1,52E-05**	*nifD*- NoN 14 dpi	TR	PROTON PUMP INTERACTOR 1 family protein (AHRD V3.3 *-* U5GXF2_POPTR)	
Solyc05g056545.1	3,91E-01	6,27E-03	2,44E-02	8,54E-01	1,43E-01	2,87E-01	**1,11E+00**	**7,23E-09**	*nifD*- NoN 14 dpi	2M	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9RHN6_RICCO)	GO:0008270|GO:0016491|GO:0055114|GO:0055114|GO:0055114
Solyc06g009795.1	-4,39E-01	2,07E-01	2,21E-02	9,48E-01	-3,34E-01	3,34E-01	**-1,53E+00**	**1,24E-04**	*nifD*- NoN 14 dpi	CS	Pectin lyase-like superfamily protein (AHRD V3.3 *-* AT3G16850.1)	
Solyc12g008510.2	5,56E-01	7,23E-04	2,12E-02	8,85E-01	-5,33E-01	1,10E-03	**1,08E+00**	**7,25E-08**	*nifD*- NoN 14 dpi	C	Phosphotransferase (AHRD V3.3 *** K4DBT9_SOLLC)	GO:0001678|GO:0004396|GO:0005524|GO:0005536|GO:0005975|GO:0046835|GO:0005524|GO:0005975|GO:0016773|GO:0005524|GO:0005975|GO:0016773
Solyc02g069540.2	-1,09E-01	7,94E-01	2,06E-02	9,61E-01	-4,44E-01	2,94E-01	**-1,48E+00**	**1,46E-03**	*nifD*- NoN 14 dpi	CS	Protein POLAR LOCALIZATION DURING ASYMMETRIC DIVISION AND REDISTRIBUTION (AHRD V3.3 *** A0A199UWZ9_ANACO)	
Solyc00g110870.3	-3,93E-01	2,69E-02	2,05E-02	9,03E-01	-4,69E-01	9,49E-03	**-1,13E+00**	**4,19E-07**	*nifD*- NoN 14 dpi	PMI	Leucine-rich repeat receptor-like protein kinase (AHRD V3.3 *** C0LGR2_ARATH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g006220.3	1,91E-01	3,32E-01	1,97E-02	9,20E-01	-1,03E-01	6,00E-01	**-1,31E+00**	**3,93E-07**	*nifD*- NoN 14 dpi	CS	Trichome birefringence-like protein (AHRD V3.3 *** G7IKB9_MEDTR)	
Solyc10g074820.1	-5,75E-01	3,01E-02	1,90E-02	9,40E-01	-5,23E-01	4,66E-02	**-1,02E+00**	**3,80E-04**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:transmembrane protein, putative (DUF1191) (AHRD V3.3 *** AT3G08600.1)	
Solyc01g007930.3	5,26E-01	4,59E-04	1,52E-02	9,08E-01	4,72E-01	1,33E-03	**1,15E+00**	**3,11E-09**	*nifD*- NoN 14 dpi	P	F-box family protein (AHRD V3.3 *** AT1G70590.1)	GO:0005515
Solyc09g082370.3	1,16E-02	9,70E-01	1,48E-02	9,61E-01	-1,74E-01	5,68E-01	**-1,03E+00**	**1,98E-03**	*nifD*- NoN 14 dpi	S	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 (AHRD V3.3 *** W9RZ96_9ROSA)	GO:0046856
Solyc12g096400.2	1,94E-02	9,22E-01	1,48E-02	9,40E-01	3,22E-02	8,70E-01	**1,09E+00**	**8,26E-06**	*nifD*- NoN 14 dpi	DNA	Calmodulin-binding family protein (AHRD V3.3 *** B9NA01_POPTR)	GO:0005516
Solyc04g007075.1	-3,58E-01	2,87E-01	8,41E-03	9,80E-01	-5,43E-01	1,11E-01	**-1,43E+00**	**1,93E-04**	*nifD*- NoN 14 dpi	D	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *-* AT1G69550.1)	
Solyc03g044480.3	6,25E-01	1,02E-02	7,98E-03	9,72E-01	5,66E-01	1,85E-02	**1,16E+00**	**2,38E-05**	*nifD*- NoN 14 dpi	G	Cyclin-dependent kinase inhibitor family protein (AHRD V3.3 *-* AT2G23430.1)	GO:0004861|GO:0005634|GO:0007050
Solyc04g082910.1	7,02E-01	1,89E-03	6,48E-03	9,75E-01	4,36E-01	4,09E-02	**1,11E+00**	**1,02E-05**	*nifD*- NoN 14 dpi	E	CP12 domain-containing family protein (AHRD V3.3 *-* B9GPM1_POPTR)	
Solyc09g092130.3	5,39E-01	3,98E-01	6,30E-03	9,92E-01	7,48E-01	2,44E-01	**3,18E+00**	**2,85E-05**	*nifD*- NoN 14 dpi	C	Sucrose-phosphate synthase (AHRD V3.3 *** A0A0U1ZVB4_LYCBA)	GO:0005985|GO:0016157|GO:0005985|GO:0046524|GO:0005985|GO:0046524
Solyc05g012010.3	3,52E-01	1,60E-02	3,01E-03	9,83E-01	5,94E-02	6,67E-01	**1,65E+00**	**4,28E-12**	*nifD*- NoN 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT5G15790.5)	GO:0005515|GO:0008270|GO:0008270|GO:0008270
Solyc02g072540.3	-1,03E+00	2,74E-01	2,93E-03	9,97E-01	-2,27E+00	2,09E-02	**-2,79E+00**	**5,58E-03**	*nifD*- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** A0A0V0IFU0_SOLCH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g007180.3	1,10E-01	5,74E-01	2,48E-03	9,90E-01	5,39E-01	9,56E-03	**1,14E+00**	**3,18E-06**	*nifD*- NoN 14 dpi	CS	Gamma-tubulin complex component (AHRD V3.3 *** K4AST4_SOLLC)	GO:0000226|GO:0000922|GO:0005815|GO:0007020|GO:0043015
Solyc05g055550.3	7,72E-01	5,92E-02	2,37E-03	9,95E-01	3,01E-01	4,49E-01	**3,10E+00**	**2,26E-08**	*nifD*- NoN 14 dpi	NA	TSA: Wollemia nobilis Ref_Wollemi_Transcript_5463_1093 transcribed RNA sequence (AHRD V3.3 *** A0A0C9RPH1_9SPER)	
Solyc03g032210.3	1,47E-01	3,28E-01	3,91E-04	9,98E-01	3,78E-01	1,67E-02	**2,15E+00**	**6,45E-14**	*nifD*- NoN 14 dpi	2M	AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** AT2G17650.1)	GO:0003824|GO:0008152
Solyc06g074190.3	2,25E-01	5,42E-01	-6,57E-05	1,00E+00	8,27E-01	3,17E-02	**-1,13E+00**	**4,45E-03**	*nifD*- NoN 14 dpi	NA	Plant/F24K9-26 protein (AHRD V3.3 *** A0A072UED0_MEDTR)	
Solyc10g008570.3	-4,74E-01	1,75E-01	-1,07E-03	9,97E-01	2,86E-01	4,08E-01	**-1,13E+00**	**2,65E-03**	*nifD*- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A124SD53_CYNCS)	GO:0005484|GO:0006886|GO:0016020|GO:0005515|GO:0005515
Solyc08g008080.1	7,40E-01	1,23E-01	-2,29E-03	9,96E-01	-5,75E-01	2,26E-01	**1,55E+00**	**2,53E-03**	*nifD*- NoN 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *** AT1G63840.1)	GO:0005515|GO:0008270

Solyc10g005960.1	-5,19E-01	4,94E-02	-3,16E-03	9,90E-01	-4,97E-01	5,91E-02	**-1,30E+00**	**2,30E-05**	*nifD*- NoN 14 dpi	PMI	Fasciclin-like arabinogalactan protein (AHRD V3.3 *** A0A072UY96_MEDTR)	
Solyc01g100220.3	-4,97E-01	9,37E-02	-3,33E-03	9,91E-01	-1,85E-01	5,24E-01	**-1,08E+00**	**8,41E-04**	*nifD*- NoN 14 dpi	T	GATA transcription factor, putative (AHRD V3.3 *** B9RZK8_RICCO)	GO:0003700|GO:0006355|GO:0008270|GO:0043565|GO:0006355|GO:0008270|GO:0006355|GO:0008270
Solyc08g014080.3	-6,62E-02	6,15E-01	-4,32E-03	9,74E-01	9,69E-01	6,84E-08	**1,01E+00**	**3,04E-08**	*nifD*- NoN 14 dpi	P	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** A0A061EJY7_THECC)	GO:0008270
Solyc02g092790.3	-5,57E-01	2,52E-02	-7,74E-03	9,74E-01	-8,99E-01	7,28E-04	**-1,12E+00**	**6,53E-05**	*nifD*- NoN 14 dpi	CS	Arabinogalactan 1	
Solyc10g086760.2	-7,74E-01	3,63E-04	-9,76E-03	9,59E-01	-9,92E-03	9,58E-01	**-1,11E+00**	**3,46E-06**	*nifD*- NoN 14 dpi	CS	Tubulin beta chain (AHRD V3.3 *** A0A103XQ61_CYNCS)	GO:0003924|GO:0005200|GO:0005525|GO:0005874|GO:0007017|GO:0005200|GO:0005525|GO:0005874|GO:0007017
Solyc07g053585.1	3,87E-01	9,50E-02	-1,42E-02	9,50E-01	6,00E-01	1,25E-02	**1,06E+00**	**6,72E-05**	*nifD*- NoN 14 dpi	RNA	Peptidyl-tRNA hydrolase II (PTH2) family protein (AHRD V3.3 --* AT5G16870.1)	
Solyc07g049300.3	-7,20E-01	4,72E-02	-1,44E-02	9,67E-01	3,68E-01	2,97E-01	**-1,29E+00**	**9,38E-04**	*nifD*- NoN 14 dpi	CS	Endoglucanase (AHRD V3.3 *** M0ZJ27_SOLTU)	GO:0003824|GO:0004553|GO:0005975|GO:0004553|GO:0005975
Solyc10g008400.1	3,88E-01	3,77E-01	-2,01E-02	9,63E-01	1,04E+00	2,37E-02	**2,52E+00**	**3,90E-06**	*nifD*- NoN 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G74990.1)	GO:0005515|GO:0008270|GO:0046872|GO:0046872
Solyc12g010430.1	1,31E-01	4,21E-01	-2,17E-02	8,94E-01	1,17E-01	4,74E-01	**1,76E+00**	**3,80E-11**	*nifD*- NoN 14 dpi	P	LOW QUALITY:NHL domain protein (AHRD V3.3 --* AT3G01430.1)	
Solyc10g005300.3	2,49E-01	2,33E-01	-2,32E-02	9,10E-01	2,23E-01	2,86E-01	**1,21E+00**	**3,06E-06**	*nifD*- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *** U5GUL9_POPTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g008960.3	-4,87E-01	6,63E-02	-2,66E-02	9,17E-01	-3,62E-01	1,65E-01	**1,00E+00**	**5,31E-04**	*nifD*- NoN 14 dpi	H	GRAM domain-containing protein / ABA-responsive protein-like protein (AHRD V3.3 *** AT5G23370.1)	
Solyc03g120160.1	6,41E-02	7,66E-01	-2,95E-02	8,91E-01	-4,25E-01	5,71E-02	**1,07E+00**	**3,49E-05**	*nifD*- NoN 14 dpi	RNA	serine-rich protein-like protein (AHRD V3.3 --* AT5G55980.1)	
Solyc02g090580.3	-2,73E-01	2,36E-01	-3,14E-02	8,90E-01	-2,70E-01	2,42E-01	**-1,01E+00**	**1,41E-04**	*nifD*- NoN 14 dpi	NA	ternary complex factor MIP1 leucine-zipper protein (Protein of unknown function, DUF547) (AHRD V3.3 *** AT4G37080.3)	
Solyc02g071700.3	-6,44E-01	4,92E-02	-3,63E-02	9,08E-01	5,84E-01	7,26E-02	**-1,63E+00**	**1,97E-05**	*nifD*- NoN 14 dpi	L	Lipase, GDSL (AHRD V3.3 *** A0A103XTV4_CYNCS)	GO:0016788
Solyc04g082210.3	3,00E-01	1,20E-01	-3,80E-02	8,41E-01	5,11E-01	1,13E-02	**1,02E+00**	**1,03E-05**	*nifD*- NoN 14 dpi	E	NADH-ubiquinone oxidoreductase chain (AHRD V3.3 *** AT1G20460.1)	
Solyc02g080230.3	4,12E-01	3,20E-01	-4,18E-02	9,19E-01	-4,54E-01	2,74E-01	**-1,36E+00**	**2,53E-03**	*nifD*- NoN 14 dpi	H	ROP-interactive CRIB motif-containing protein 10 (AHRD V3.3 *-* A0A061GGE1_THECC)	
Solyc06g067870.3	-2,50E-01	1,30E-01	-4,19E-02	7,96E-01	-4,50E-01	9,29E-03	**-1,96E+00**	**3,36E-12**	*nifD*- NoN 14 dpi	E	2-oxoglutarate-dependent dioxygenase (AHRD V3.3 *** H9AY17_SALMI)	GO:0016491|GO:0055114
Solyc07g054080.2	3,56E-01	3,26E-02	-4,25E-02	7,89E-01	8,89E-02	5,77E-01	**1,46E+00**	**1,13E-09**	*nifD*- NoN 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G19310.1)	GO:0005515|GO:0008270|GO:0046872|GO:0046872
Solyc03g083030.3	-4,46E-01	7,80E-03	-4,72E-02	7,62E-01	2,70E-01	9,25E-02	**-1,02E+00**	**5,53E-07**	*nifD*- NoN 14 dpi	NA	ABL interactor-like protein 3 (AHRD V3.3 *** AT5G24310.1)	
Solyc11g066100.2	-4,92E-01	1,23E-01	-4,88E-02	8,76E-01	1,81E-01	5,63E-01	**-1,66E+00**	**1,24E-05**	*nifD*- NoN 14 dpi	STR	heat shock protein 70 (AHRD V3.3 *** AT3G12580.1)	
Solyc12g044420.1	6,34E-03	9,82E-01	-5,30E-02	8,54E-01	-5,40E-01	7,00E-02	**-1,37E+00**	**6,14E-05**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** G7LFZ0_MEDTR)	
Solyc12g014590.2	2,67E-01	1,30E-01	-5,41E-02	7,54E-01	2,83E-01	1,09E-01	**1,08E+00**	**1,17E-06**	*nifD*- NoN 14 dpi	D	Pirin-like protein family (AHRD V3.3 *** A0A151SXI4_CAJCA)	
Solyc05g051900.3	7,49E-01	5,32E-03	-6,05E-02	8,08E-01	8,63E-01	1,68E-03	**3,56E+00**	**7,47E-14**	*nifD*- NoN 14 dpi	TR	Major facilitator superfamily transporter (AHRD V3.3 *** A0A0K0KFR2_CARHR)	GO:0016021|GO:0055085
Solyc12g008490.2	-6,08E-01	2,66E-02	-6,50E-02	8,03E-01	-8,98E-01	1,84E-03	**-1,20E+00**	**9,32E-05**	*nifD*- NoN 14 dpi	NA	Nucleotide-diphospho-sugar transferase domain protein (AHRD V3.3 *** G7L7F4_MEDTR)	GO:0016757
Solyc11g005440.2	-4,15E-01	1,17E-01	-6,55E-02	8,00E-01	9,51E-02	7,13E-01	**-1,27E+00**	**3,60E-05**	*nifD*- NoN 14 dpi	DNA	Endonuclease or glycosyl hydrolase, putative isoform 1 (AHRD V3.3 *** A0A061DIG3_THECC)	GO:0005777|GO:0010468
Solyc01g010050.3	6,35E-01	1,67E-04	-6,69E-02	6,47E-01	-6,28E-02	6,67E-01	**1,10E+00**	**4,80E-08**	*nifD*- NoN 14 dpi	N	S-adenosylmethionine decarboxylase proenzyme (AHRD V3.3 *** K4ATK0_SOLLC)	GO:0004014|GO:0004014|GO:0006597|GO:0008295|GO:0004014|GO:0006597|GO:0008295

Solyc06g083210.3	1,23E-01	2,03E-01	-6,72E-02	4,83E-01	2,19E-01	2,85E-02	**1,02E+00**	**4,78E-11**	*nifD*- NoN 14 dpi	K	Protein kinase superfamily protein (AHRD V3.3 *** AT4G13020.1)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc01g068020.3	1,41E-01	4,43E-01	-6,94E-02	7,05E-01	5,27E-01	7,34E-03	**1,12E+00**	**1,63E-06**	*nifD*- NoN 14 dpi	TR	Polyketide cyclase / dehydrase and lipid transport protein (AHRD V3.3 *** AT4G01883.1)	
Solyc01g109160.4	3,51E-01	7,49E-01	-7,11E-02	9,48E-01	1,51E+00	1,76E-01	**4,54E+00**	**2,87E-04**	*nifD*- NoN 14 dpi	2M	CYP74C4	
Solyc06g083660.3	-7,70E-01	2,28E-06	-7,56E-02	5,58E-01	-4,76E-01	9,26E-04	**-1,02E+00**	**1,91E-08**	*nifD*- NoN 14 dpi	NA	methyl-coenzyme M reductase II subunit gamma, putative (DUF3741) (AHRD V3.3 *** AT4G28760.2)	
Solyc09g064630.3	-3,96E-01	1,58E-03	-7,59E-02	5,04E-01	-6,82E-02	5,49E-01	**-1,06E+00**	**8,22E-10**	*nifD*- NoN 14 dpi	H	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *-* AT4G17940.1)	GO:0005515
Solyc01g091200.3	-3,10E-01	1,39E-01	-7,71E-02	7,07E-01	-8,08E-01	4,97E-04	**-1,13E+00**	**7,85E-06**	*nifD*- NoN 14 dpi	C	UDP-glucuronate 4-epimerase 4 (AHRD V3.3 *** GAE4_ARATH)	GO:0003824|GO:0050662|GO:0005975|GO:0016857|GO:0005975|GO:0016857
Solyc08g061800.3	-5,98E-02	8,60E-01	-7,98E-02	8,14E-01	5,90E-01	9,13E-02	**1,33E+00**	**5,51E-04**	*nifD*- NoN 14 dpi	NA	BnaC08g32970D protein (AHRD V3.3 *-* A0A078CHK0_BRANA)	
Solyc07g007680.3	-3,55E-01	8,98E-04	-8,08E-02	4,01E-01	-4,11E-01	1,92E-04	**-1,01E+00**	**5,76E-11**	*nifD*- NoN 14 dpi	STR	Calcium-dependent lipid-binding (CaLB domain) family protein (AHRD V3.3 *** AT1G05500.1)	GO:0005515|GO:0008289|GO:0008289
Solyc01g073810.2	-3,23E-01	2,51E-01	-8,18E-02	7,68E-01	-1,67E+00	2,18E-06	**1,30E+00**	**7,02E-05**	*nifD*- NoN 14 dpi	S	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)	GO:0005515|GO:0008270
Solyc04g071755.1	3,36E-01	8,82E-03	-8,44E-02	4,84E-01	4,40E-01	1,02E-03	**1,03E+00**	**4,18E-09**	*nifD*- NoN 14 dpi	P	Tubby-like F-box protein (AHRD V3.3 *** K4BTG5_SOLLC)	
Solyc06g073990.2	4,10E-01	1,77E-01	-8,44E-02	7,77E-01	7,64E-01	1,57E-02	**1,38E+00**	**8,37E-05**	*nifD*- NoN 14 dpi	NA	Gb:AAF02129.1, putative (AHRD V3.3 *** A0A061GVZ4_THECC)	
Solyc02g090470.3	2,59E-01	3,59E-01	-8,48E-02	7,62E-01	-5,50E-01	5,85E-02	**2,00E+00**	**1,26E-07**	*nifD*- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *** K4BCJ6_SOLLC)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc03g123830.3	-3,66E-01	1,11E-02	-9,03E-02	5,05E-01	-5,71E-01	2,32E-04	**-1,10E+00**	**1,18E-08**	*nifD*- NoN 14 dpi	AM	D-3-phosphoglycerate dehydrogenase (AHRD V3.3 *** K4BN81_SOLLC)	GO:0004617|GO:0006564|GO:0008152|GO:0016597|GO:0008152|GO:0016597
Solyc09g011110.1	9,72E-01	1,46E-05	-9,19E-02	6,19E-01	4,43E-01	2,26E-02	**1,08E+00**	**3,12E-06**	*nifD*- NoN 14 dpi	DNA	LOW QUALITY:Zinc finger, C2H2 (AHRD V3.3 *** A0A118K1X3_CYNCS)	GO:0003676|GO:0007275|GO:0007275
Solyc02g065400.3	2,59E-01	3,70E-01	-9,35E-02	7,45E-01	-6,16E-02	8,30E-01	**2,15E+00**	**5,24E-08**	*nifD*- NoN 14 dpi	E	33kDa precursor protein of oxygen-evolving complex	GO:0005509|GO:0009523|GO:0009654|GO:0015979|GO:0019898|GO:0042549|GO:0016021|GO:0016021
Solyc02g080615.1	-5,07E-01	7,47E-02	-9,35E-02	7,35E-01	3,51E-01	2,10E-01	**-1,01E+00**	**1,02E-03**	*nifD*- NoN 14 dpi	P	Ankyrin repeat family protein (AHRD V3.3 *** AT1G62050.1)	GO:0005515
Solyc02g078690.2	3,91E-01	5,12E-01	-9,38E-02	8,75E-01	-8,84E-01	1,45E-01	**1,78E+00**	**5,50E-03**	*nifD*- NoN 14 dpi	STR	Carboxypeptidase (AHRD V3.3 *** K4B993_SOLLC)	GO:0004185|GO:0006508
Solyc08g080080.3	-4,85E-01	1,18E-02	-9,39E-02	6,05E-01	-8,31E-01	9,00E-05	**-1,11E+00**	**1,61E-06**	*nifD*- NoN 14 dpi	P	WD40 repeat-containing protein (AHRD V3.3 *** A0A103XFY3_CYNCS)	GO:0005515|GO:0010997|GO:0097027|GO:1904668|GO:0010997|GO:0097027|GO:1904668
Solyc01g087040.2	6,71E-02	7,26E-01	-9,63E-02	6,16E-01	2,33E-01	2,30E-01	**1,97E+00**	**1,15E-10**	*nifD*- NoN 14 dpi	E	PsbP-like (AHRD V3.3 *** A0A0U9HL69_KLEFL)	GO:0005509|GO:0009523|GO:0009654|GO:0015979|GO:0019898
Solyc09g063130.3	6,57E-01	3,63E-02	-9,70E-02	7,47E-01	-1,32E-01	6,62E-01	**1,33E+00**	**1,42E-04**	*nifD*- NoN 14 dpi	E	Photosystem I reaction center subunit IV (AHRD V3.3 *** A0A0K9P6J8_ZOSMR)	GO:0009522|GO:0009538|GO:0015979
Solyc02g091370.2	4,68E-01	3,67E-03	-9,80E-02	5,09E-01	7,00E-01	6,11E-05	**2,01E+00**	**2,38E-13**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4BCT5_SOLLC)	GO:0008152|GO:0016758
Solyc11g066320.2	9,38E-02	3,66E-01	-9,89E-02	3,41E-01	-1,06E-01	3,09E-01	**1,10E+00**	**5,09E-11**	*nifD*- NoN 14 dpi	P	Exostosin family protein (AHRD V3.3 *** AT2G28110.1)	
Solyc10g006120.2	3,62E-01	3,22E-01	-9,93E-02	7,84E-01	6,12E-02	8,66E-01	**-1,10E+00**	**4,89E-03**	*nifD*- NoN 14 dpi	TR	extracellular ligand-gated ion channel protein (DUF3537) (AHRD V3.3 *** AT3G20300.1)	
Solyc03g005960.3	-4,83E-01	1,43E-01	-9,95E-02	7,58E-01	6,89E-01	4,04E-02	**-1,48E+00**	**8,77E-05**	*nifD*- NoN 14 dpi	K	protein kinase LESK1	GO:0004672|GO:0005524|GO:0006468|GO:0005515|GO:0005515
Solyc12g096870.1	-7,10E-01	5,12E-06	-1,00E-01	4,26E-01	-5,26E-01	2,49E-04	**-1,13E+00**	**1,43E-09**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** Q0PI14_VITLA)	GO:0008152|GO:0016758
Solyc02g084720.3	-7,16E-01	4,02E-03	-1,01E-01	6,58E-01	-6,25E-01	1,05E-02	**-1,43E+00**	**1,13E-06**	*nifD*- NoN 14 dpi	C	beta-galactosidase 6	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc08g076253.1	-4,91E-01	1,73E-01	-1,02E-01	7,73E-01	-1,68E-01	6,35E-01	**-1,18E+00**	**2,43E-03**	*nifD*- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *-* Q9M7M3_CAPAN)	GO:0005506|GO:0016705|GO:0020037|GO:0055114

Solyc03g113300.3	-4,85E-01	2,04E-01	-1,02E-01	7,85E-01	-4,17E-01	2,73E-01	**-1,05E+00**	**8,85E-03**	*nifD*- NoN 14 dpi	E	NAD(P)-binding Rossmann-fold superfamily protein (AHRD V3.3 *** A0A061G3Y5_THECC),Pfam:PF13561	GO:0016491
Solyc05g050110.3	6,01E-01	1,77E-01	-1,03E-01	8,14E-01	-1,12E-01	7,99E-01	**1,97E+00**	**1,12E-04**	*nifD*- NoN 14 dpi	NA	DUF2358 family protein (DUF2358) (AHRD V3.3 *** AT2G46220.1)	
Solyc06g067860.3	-2,37E-01	1,33E-01	-1,05E-01	4,98E-01	-5,64E-01	1,04E-03	**-1,35E+00**	**2,97E-09**	*nifD*- NoN 14 dpi	E	2-oxoglutarate-dependent dioxygenase (AHRD V3.3 *** A0A061G9S7_THECC)	GO:0016491|GO:0055114
Solyc07g018010.3	-3,88E-01	1,30E-02	-1,09E-01	4,61E-01	2,29E-01	1,27E-01	**-1,15E+00**	**2,36E-08**	*nifD*- NoN 14 dpi	T	bHLH transcription factor139	GO:0046983
Solyc09g089770.3	-3,77E-01	1,48E-01	-1,09E-01	6,71E-01	-9,06E-01	1,40E-03	**-1,07E+00**	**2,53E-04**	*nifD*- NoN 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G06620.2)	GO:0016491|GO:0055114
Solyc11g069180.2	6,83E-01	4,91E-05	-1,10E-01	4,39E-01	3,33E-01	2,55E-02	**1,24E+00**	**3,09E-09**	*nifD*- NoN 14 dpi	H	Acyl-CoA dehydrogenase (AHRD V3.3 *** G7JQF7_MEDTR)	GO:0003995|GO:0003995|GO:0055114|GO:0003995|GO:0055114
Solyc12g095980.2	8,23E-02	8,85E-01	-1,11E-01	8,45E-01	-7,63E-01	1,88E-01	**-2,40E+00**	**2,39E-04**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT1G17620.1)	
Solyc10g079960.1	-3,86E-01	1,44E-01	-1,11E-01	6,67E-01	-7,41E-01	7,67E-03	**-1,04E+00**	**3,89E-04**	*nifD*- NoN 14 dpi	D	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase (AHRD V3.3 *-* A0A151RD44_CAJCA)	
Solyc07g052690.3	-4,55E-02	9,30E-01	-1,13E-01	8,28E-01	-9,77E-01	6,82E-02	**-2,15E+00**	**2,93E-04**	*nifD*- NoN 14 dpi	CS	Beta-amylase (AHRD V3.3 *-* K4CFG8_SOLLC)	GO:0000272|GO:0016161|GO:0005975|GO:0005975
Solyc08g082630.3	2,02E-02	9,42E-01	-1,13E-01	6,84E-01	-7,75E-02	7,80E-01	**-1,37E+00**	**3,69E-05**	*nifD*- NoN 14 dpi	H	Auxin Response Factor 9A	GO:0003677|GO:0003677|GO:0005634|GO:0006355|GO:0009725|GO:0003677|GO:0005634|GO:0006355|GO:0009725
Solyc06g050140.1	2,29E-01	4,14E-01	-1,13E-01	6,86E-01	-4,28E-01	1,34E-01	**1,23E+00**	**1,49E-04**	*nifD*- NoN 14 dpi	DNA	LOW QUALITY:Plant regulator RWP-RK family protein (AHRD V3.3 --* AT2G17150.6)	
Solyc12g095780.2	-3,05E-01	1,55E-01	-1,24E-01	5,57E-01	-3,24E-01	1,32E-01	**-1,02E+00**	**4,47E-05**	*nifD*- NoN 14 dpi	G	hydroxyproline-rich glycoprotein family protein (AHRD V3.3 *** AT1G76660.1)	
Solyc03g077950.2	1,14E-01	7,38E-01	-1,24E-01	7,17E-01	-4,39E-01	2,04E-01	**-1,21E+00**	**1,34E-03**	*nifD*- NoN 14 dpi	C	O-fucosyltransferase family protein (AHRD V3.3 *** AT2G01480.1)	
Solyc06g036460.3	1,91E-02	9,63E-01	-1,28E-01	7,58E-01	-4,47E-01	2,86E-01	**-1,19E+00**	**7,52E-03**	*nifD*- NoN 14 dpi	S	Membrane-associated kinase regulator-like protein, putative (AHRD V3.3 *** A0A072U8P3_MEDTR)	
Solyc12g043005.1	-8,37E-01	1,84E-01	-1,28E-01	8,36E-01	-7,89E-01	2,10E-01	**-1,86E+00**	**5,41E-03**	*nifD*- NoN 14 dpi	P	Coatomer subunit beta-like protein (AHRD V3.3 *-* A0A072UH84_MEDTR)	GO:0005515
Solyc05g005010.3	-3,11E-01	5,15E-02	-1,28E-01	4,06E-01	8,50E-02	5,81E-01	**-1,06E+00**	**2,26E-07**	*nifD*- NoN 14 dpi	NA	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT5G18460.1)	
Solyc09g074270.3	-3,62E-01	9,37E-03	-1,31E-01	3,18E-01	-1,23E-01	3,50E-01	**-1,18E+00**	**1,34E-09**	*nifD*- NoN 14 dpi	H	Gid1-like gibberellin receptor (AHRD V3.3 *** M9N8R2_NICAT)	GO:0008152|GO:0016787
Solyc03g119740.3	-4,05E-01	2,88E-01	-1,34E-01	7,22E-01	-2,62E-01	4,89E-01	**-1,20E+00**	**3,62E-03**	*nifD*- NoN 14 dpi	T	MYB-like transcription factor family protein (AHRD V3.3 *** A0A072USM0_MEDTR)	GO:0003677
Solyc06g066540.1	8,05E-01	1,66E-01	-1,37E-01	8,10E-01	-2,75E-01	6,30E-01	**-2,70E+00**	**6,14E-05**	*nifD*- NoN 14 dpi	H	Ethylene-responsive transcription factor TINY (AHRD V3.3 *** TINY_ARATH)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc03g119990.3	-9,23E-01	8,96E-04	-1,41E-01	5,71E-01	-3,15E-01	2,12E-01	**-1,51E+00**	**1,71E-06**	*nifD*- NoN 14 dpi	L	Alpha/beta hydrolase-like (AHRD V3.3 *** A0A0K9P0U5_ZOSMR)	
Solyc02g081980.3	-9,96E-01	1,12E-03	-1,42E-01	6,05E-01	2,27E-01	4,12E-01	**1,29E+00**	**6,41E-05**	*nifD*- NoN 14 dpi	K	Apyrase (AHRD V3.3 *** APY_SOLTU)	GO:0016787
Solyc01g104810.2	-1,14E+00	1,93E-02	-1,44E-01	7,55E-01	-1,00E-01	8,28E-01	**-1,43E+00**	**4,17E-03**	*nifD*- NoN 14 dpi	TR	Vacuolar iron transporter family protein (AHRD V3.3 *** A0A061FJ80_THECC)	
Solyc12g088360.2	6,87E-01	1,35E-03	-1,47E-01	4,50E-01	2,21E-01	2,58E-01	**1,13E+00**	**3,04E-06**	*nifD*- NoN 14 dpi	P	U-box domain-containing protein (AHRD V3.3 *** A0A0K9PK99_ZOSMR)	GO:0005488|GO:0005515|GO:0005515
Solyc07g062070.3	7,70E-02	4,70E-01	-1,47E-01	1,73E-01	3,05E-01	7,38E-03	**1,45E+00**	**2,09E-13**	*nifD*- NoN 14 dpi	R	Ribokinase (AHRD V3.3 *** M1AA65_SOLTU)	GO:0004747|GO:0006014|GO:0016773|GO:0016773
Solyc02g086915.1	-6,37E-01	2,46E-03	-1,48E-01	4,44E-01	-9,51E-03	9,60E-01	**1,31E+00**	**2,78E-07**	*nifD*- NoN 14 dpi	P	Peptidyl-prolyl cis-trans isomerase CYP38 (AHRD V3.3 *** W9SGV3_9ROSA)	
Solyc09g008860.3	-1,07E+00	1,02E-02	-1,53E-01	6,95E-01	-1,38E-01	7,24E-01	**-1,60E+00**	**3,24E-04**	*nifD*- NoN 14 dpi	K	Ovary receptor kinase 14 (AHRD V3.3 *** S4WME3_SOLCH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468

Solyc07g056040.3	8,75E-02	7,28E-01	-1,54E-01	5,42E-01	6,11E-01	2,11E-02	**1,37E+00**	**9,45E-06**	*nifD*- NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4CGD7_SOLLC)	
Solyc11g011330.2	-8,33E-01	8,69E-06	-1,54E-01	3,16E-01	1,13E-02	9,41E-01	**-1,00E+00**	**4,99E-07**	*nifD*- NoN 14 dpi	2M	Alcohol dehydrogenase, putative (AHRD V3.3 *** B9T7R7_RICCO)	GO:0008270|GO:0016491|GO:0055114|GO:0016491|GO:0016491
Solyc02g024000.3	-3,71E-01	4,59E-02	-1,56E-01	3,85E-01	-4,21E-01	2,49E-02	**-1,02E+00**	**5,06E-06**	*nifD*- NoN 14 dpi	P	WPP domain-associated protein (AHRD V3.3 *** WAP_SOLLC)	
Solyc07g041340.2	5,31E-01	1,55E-03	-1,57E-01	3,06E-01	4,06E-02	7,89E-01	**1,23E+00**	**1,31E-08**	*nifD*- NoN 14 dpi	G	Protein ELF4-LIKE 4 (AHRD V3.3 *** A0A0B2QCK9_GLYSO)	
Solyc01g108030.3	5,97E-01	2,01E-02	-1,62E-01	5,08E-01	6,50E-01	1,21E-02	**2,77E+00**	**1,22E-11**	*nifD*- NoN 14 dpi	AM	3-methylcrotonyl-CoA carboxylase (AHRD V3.3 *** AT4G34030.1)	GO:0016874
Solyc03g116470.2	1,37E-01	5,80E-01	-1,62E-01	5,15E-01	-4,92E-01	5,53E-02	**1,83E+00**	**6,91E-08**	*nifD*- NoN 14 dpi	NA	transmembrane protein (AHRD V3.3 *** AT1G80200.3)	
Solyc03g118510.3	-9,72E-01	2,44E-04	-1,63E-01	4,82E-01	-4,48E-01	6,05E-02	**-1,27E+00**	**7,84E-06**	*nifD*- NoN 14 dpi	K	Ovary receptor kinase 27 (AHRD V3.3 *** S4WIQ7_SOLCH)	GO:0004672|GO:0005524|GO:0006468|GO:0005515|GO:0005515
Solyc11g017290.1	-1,05E+00	3,88E-02	-1,65E-01	7,35E-01	-1,80E-01	7,12E-01	**-1,93E+00**	**4,56E-04**	*nifD*- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JW06_CYNCS)	GO:0005515
Solyc06g075480.3	-1,87E+00	6,34E-02	-1,67E-01	8,64E-01	3,98E-01	6,83E-01	**-2,78E+00**	**7,63E-03**	*nifD*- NoN 14 dpi	TR	Major facilitator superfamily protein (AHRD V3.3 *** AT3G45700.1)	GO:0005215|GO:0006810|GO:0016020
Solyc11g005690.2	-3,72E-01	2,59E-01	-1,69E-01	6,04E-01	-1,32E-01	6,85E-01	**-1,43E+00**	**1,56E-04**	*nifD*- NoN 14 dpi	G	TONSOKU protein (AHRD V3.3 *** Q4W7J1_TOBAC)	GO:0005515
Solyc04g054890.3	1,56E-01	2,58E-01	-1,72E-01	2,12E-01	2,57E-01	6,74E-02	**1,28E+00**	**7,02E-10**	*nifD*- NoN 14 dpi	H	Acyl-coenzyme A oxidase (AHRD V3.3 *** K4BSN7_SOLLC)	GO:0003995|GO:0055114|GO:0003997|GO:0005777|GO:0006631|GO:0050660|GO:0055114|GO:0003997|GO:0005777|GO:0006631|GO:0050660|GO:0055114
Solyc07g006130.2	2,54E-01	1,71E-01	-1,75E-01	3,41E-01	7,24E-01	4,56E-04	**1,16E+00**	**8,48E-07**	*nifD*- NoN 14 dpi	P	Eukaryotic peptide chain release factor subunit 1-1 (AHRD V3.3 *** ERF1X_ARATH)	GO:0005737|GO:0006415|GO:0016149
Solyc02g086360.3	4,30E-01	3,01E-02	-1,77E-01	3,54E-01	-3,93E-01	4,57E-02	**1,12E+00**	**2,52E-06**	*nifD*- NoN 14 dpi	K	Phox/Bem1p (AHRD V3.3 *** A0A124SEH3_CYNCS)	GO:0005515
Solyc04g082290.3	-4,00E-01	1,93E-01	-1,77E-01	5,59E-01	9,38E-02	7,56E-01	**2,60E+00**	**3,93E-09**	*nifD*- NoN 14 dpi	NA	At1g76250 (AHRD V3.3 *-* Q8GX25_ARATH)	
Solyc03g120690.3	-4,05E-02	9,26E-01	-1,77E-01	6,84E-01	-6,16E-01	1,65E-01	**1,55E+00**	**1,30E-03**	*nifD*- NoN 14 dpi	CS	Dynein light chain family protein (AHRD V3.3 *** B9GXB1_POPTR)	GO:0007017|GO:0030286
Solyc01g011430.3	-5,56E-01	3,18E-04	-1,79E-01	1,93E-01	-7,61E-01	5,68E-06	**-1,21E+00**	**1,87E-09**	*nifD*- NoN 14 dpi	L	O-acyltransferase WSD1-like protein (AHRD V3.3 *** A0A0B0PTU2_GOSAR)	GO:0004144|GO:0004144|GO:0045017|GO:0004144|GO:0045017
Solyc02g079960.3	3,24E-01	1,11E-01	-1,80E-01	3,69E-01	-2,70E-01	1,82E-01	**1,45E+00**	**8,23E-08**	*nifD*- NoN 14 dpi	OX	Thioredoxin (AHRD V3.3 *** A0A061F6X0_THECC)	GO:0006662|GO:0015035|GO:0045454|GO:0045454|GO:0045454
Solyc09g065390.1	7,59E-01	4,44E-02	-1,81E-01	6,19E-01	3,07E-01	4,00E-01	**1,77E+00**	**4,14E-05**	*nifD*- NoN 14 dpi	RNA	LOW QUALITY:Pre-mRNA cleavage complex 2 protein Pcf11, putative isoform 2 (AHRD V3.3 *-* A0A061GBF7_THECC)	
Solyc02g033060.3	5,78E-01	9,74E-02	-1,82E-01	5,94E-01	-1,98E-01	5,62E-01	**1,66E+00**	**4,05E-05**	*nifD*- NoN 14 dpi	NA	TSA: Wollemia nobilis Ref_Wollemi_Transcript_5463_1093 transcribed RNA sequence (AHRD V3.3 *** A0A0C9RPH1_9SPER)	
Solyc11g065630.2	-3,85E-01	3,68E-01	-1,84E-01	6,66E-01	6,22E-01	1,51E-01	**1,30E+00**	**4,90E-03**	*nifD*- NoN 14 dpi	TR	Myosin-related family protein (AHRD V3.3 *** B9HNX7_POPTR)	
Solyc09g014870.1	1,86E-01	4,55E-01	-1,85E-01	4,56E-01	-2,76E-01	2,70E-01	**1,56E+00**	**1,05E-06**	*nifD*- NoN 14 dpi	TR	Copper transporter family protein (AHRD V3.3 *** B9HPB1_POPTR)	GO:0005375|GO:0016021|GO:0035434
Solyc03g097240.3	4,22E-01	3,55E-02	-1,86E-01	3,38E-01	-3,82E-02	8,42E-01	**1,08E+00**	**6,11E-06**	*nifD*- NoN 14 dpi	STR	DnAJ-like protein (AHRD V3.3 *-* W9QKC5_9ROSA)	
Solyc11g065195.1	-7,83E-01	2,67E-01	-1,86E-01	7,90E-01	2,77E-03	9,97E-01	**-1,97E+00**	**8,30E-03**	*nifD*- NoN 14 dpi	NA	Laminin subunit beta-1 (AHRD V3.3 *-* A0A0B0N352_GOSAR)	
Solyc08g083100.2	7,00E-01	9,62E-03	-1,86E-01	4,63E-01	9,79E-01	6,00E-04	**1,15E+00**	**1,05E-04**	*nifD*- NoN 14 dpi	G	Embryogenesis-associated EMB8 (AHRD V3.3 *-* A0A0B0P518_GOSAR)	
Solyc01g091300.3	-5,87E-01	1,29E-01	-1,87E-01	6,21E-01	-7,25E-01	6,33E-02	**-1,35E+00**	**1,26E-03**	*nifD*- NoN 14 dpi	G	SNARE-interacting protein KEULE (AHRD V3.3 *** A0A1D1XCK2_9ARAE)	GO:0006904|GO:0016192
Solyc06g069230.3	-9,62E-01	2,65E-04	-1,90E-01	4,12E-01	-3,71E-01	1,15E-01	**-1,33E+00**	**3,83E-06**	*nifD*- NoN 14 dpi	DNA	DNA mismatch repair protein (AHRD V3.3 *** Q6DQL7_PETHY)	GO:0003677|GO:0005524|GO:0006298|GO:0032300|GO:0005524|GO:0006298|GO:0030983|GO:0005524|GO:0006298|GO:0030983

Solyc07g017610.3	6,23E-01	1,10E-04	-1,92E-01	1,73E-01	3,52E-01	1,61E-02	**1,06E+00**	**3,53E-08**	*nifD*- NoN 14 dpi	AM	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (AHRD V3.3 *** G7JS28_MEDTR)	GO:0016491|GO:0055114
Solyc08g080570.3	4,95E-01	2,12E-01	-1,93E-01	6,22E-01	1,61E-01	6,80E-01	**2,70E+00**	**2,17E-07**	*nifD*- NoN 14 dpi	C	UDP-glucose 4-epimerase (AHRD V3.3 *** GALE1_PEA)	GO:0003978|GO:0006012
Solyc03g120180.2	3,33E-01	6,07E-01	-1,95E-01	7,63E-01	1,18E+00	7,79E-02	**2,76E+00**	**2,07E-04**	*nifD*- NoN 14 dpi	NA	Transmembrane protein, putative (AHRD V3.3 *** G7JJB2_MEDTR)	
Solyc06g070900.3	-8,94E-01	7,55E-04	-1,96E-01	4,10E-01	-8,18E-02	7,29E-01	**-2,02E+00**	**4,61E-09**	*nifD*- NoN 14 dpi	T	TCP transcription factor 17	
Solyc10g052880.1	-3,03E-01	3,93E-01	-2,00E-01	5,70E-01	8,91E-01	1,67E-02	**1,32E+00**	**8,34E-04**	*nifD*- NoN 14 dpi	PMI	LOW QUALITY:Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** A0A061DFG6_THECC)	GO:0005515
Solyc04g076700.3	3,74E-01	3,48E-03	-2,01E-01	9,53E-02	7,00E-01	2,42E-06	**1,01E+00**	**4,21E-09**	*nifD*- NoN 14 dpi	T	MADS-box transcription factor (AHRD V3.3 *** G7IS85_MEDTR)	GO:0000165|GO:0000977|GO:0045944|GO:0003677|GO:0046983|GO:0003677|GO:0046983
Solyc07g052370.3	9,62E-01	3,71E-01	-2,03E-01	8,49E-01	1,39E+00	1,99E-01	**3,38E+00**	**3,62E-03**	*nifD*- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q9M7M3_CAPAN)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc07g006650.3	5,92E-02	6,63E-01	-2,05E-01	1,39E-01	4,12E-01	4,99E-03	**2,25E+00**	**2,47E-15**	*nifD*- NoN 14 dpi	C	Xylose isomerase (AHRD V3.3 *** A0A0V0IEZ8_SOLCH)	GO:0005975|GO:0009045|GO:0009045|GO:0009045
Solyc07g026675.1	7,05E-01	5,07E-02	-2,06E-01	5,55E-01	-1,68E-01	6,30E-01	**2,02E+00**	**3,55E-06**	*nifD*- NoN 14 dpi	T	myb-like transcription factor family protein (AHRD V3.3 *-* AT5G56840.1)	GO:0003677
Solyc08g029000.3	9,06E-02	6,71E-01	-2,06E-01	3,39E-01	-6,10E-01	7,72E-03	**1,11E+00**	**1,67E-05**	*nifD*- NoN 14 dpi	L	Lipoxygenase (AHRD V3.3 *** Q43800_TOBAC)	GO:0005515|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc04g077470.3	-5,95E-01	2,32E-03	-2,08E-01	2,49E-01	-7,34E-01	3,03E-04	**-1,48E+00**	**7,28E-09**	*nifD*- NoN 14 dpi	CS	Cellulose synthase-like protein (AHRD V3.3 *** L0ASJ1_POPTO)	
Solyc01g079530.3	2,51E-01	5,56E-01	-2,10E-01	6,22E-01	-4,08E-01	3,41E-01	**1,44E+00**	**2,09E-03**	*nifD*- NoN 14 dpi	P	RING/FYVE/PHD zinc finger superfamily protein (AHRD V3.3 *** AT1G02610.1)	GO:0008270
Solyc01g080460.3	-1,25E-01	7,10E-01	-2,12E-01	5,31E-01	-8,79E-01	1,41E-02	**-1,18E+00**	**1,63E-03**	*nifD*- NoN 14 dpi	C	pyruvate orthophosphate dikinase (AHRD V3.3 *** AT4G15530.6)	GO:0003824|GO:0003824|GO:0005524|GO:0003824|GO:0005524
Solyc04g074860.4	-5,97E-01	3,27E-05	-2,14E-01	8,34E-02	-3,37E-01	8,78E-03	**-1,09E+00**	**1,31E-09**	*nifD*- NoN 14 dpi	TR	Mate efflux family protein (AHRD V1 **--D7MN36_ARALY)	
Solyc08g062610.3	3,21E-01	7,84E-02	-2,17E-01	2,26E-01	2,71E-02	8,78E-01	**1,54E+00**	**3,21E-09**	*nifD*- NoN 14 dpi	2M	(S)-coclaurine N-methyltransferase (AHRD V3.3 *** W9QPZ2_9ROSA)	
Solyc02g090500.3	-8,32E-01	1,84E-01	-2,18E-01	7,23E-01	-5,99E-01	3,34E-01	**-3,72E+00**	**1,92E-06**	*nifD*- NoN 14 dpi	D	Phenylalanine ammonia-lyase (AHRD V3.3 --* D3K195_9ROSA)	
Solyc07g065970.1	-4,20E-02	8,76E-01	-2,19E-01	4,17E-01	3,40E-01	2,13E-01	**1,34E+00**	**3,03E-05**	*nifD*- NoN 14 dpi	P	Chaperone protein DNAj, putative (AHRD V3.3 *** B9SXA3_RICCO)	
Solyc04g024430.3	2,85E-01	1,17E-01	-2,19E-01	2,24E-01	2,22E-01	2,19E-01	**1,40E+00**	**2,09E-08**	*nifD*- NoN 14 dpi	DNA	DNA polymerase epsilon catalytic subunit (AHRD V3.3 --* AT1G08260.1)	
Solyc02g081530.1	-5,72E-01	3,64E-02	-2,20E-01	4,04E-01	-3,56E-01	1,81E-01	**-1,08E+00**	**3,14E-04**	*nifD*- NoN 14 dpi	P	Ubiquitin carboxyl-terminal hydrolase family protein (AHRD V3.3 *** AT1G06440.1)	
Solyc03g122320.1	-4,83E-01	3,44E-01	-2,20E-01	6,64E-01	-1,17E+00	2,77E-02	**1,82E+00**	**1,26E-03**	*nifD*- NoN 14 dpi	P	LOW QUALITY:P-loop nucleoside triphosphate hydrolase superfamily protein (AHRD V3.3 --* G7I3Y4_MEDTR)	
Solyc10g008650.2	-7,42E-01	1,17E-01	-2,20E-01	6,34E-01	-1,07E+00	2,72E-02	**-1,75E+00**	**7,26E-04**	*nifD*- NoN 14 dpi	2M	LOW QUALITY:Anthocyanin 5-aromatic acyltransferase (AHRD V3.3 *-* A0A0B2REP2_GLYSO)	
Solyc04g076120.3	1,97E-01	3,44E-01	-2,22E-01	2,87E-01	9,52E-01	8,42E-05	**1,28E+00**	**1,24E-06**	*nifD*- NoN 14 dpi	STR	Serine carboxypeptidase, putative (AHRD V3.3 *-* B9R6Y4_RICCO)	GO:0004185|GO:0006508
Solyc04g025940.3	1,97E-01	7,39E-02	-2,25E-01	4,29E-02	1,77E-02	8,68E-01	**1,19E+00**	**1,84E-11**	*nifD*- NoN 14 dpi	C	Trehalose-6-phosphate synthase-6 (AHRD V3.3 *** A0A0S2A6P6_HEVBR)	GO:0003824|GO:0005992
Solyc05g052670.1	-5,14E-01	5,37E-01	-2,26E-01	7,85E-01	9,29E-01	2,68E-01	**2,54E+00**	**4,74E-03**	*nifD*- NoN 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT2G39980.1)	GO:0016747
Solyc04g011490.3	-5,51E-02	8,37E-01	-2,28E-01	3,98E-01	-5,84E-01	3,65E-02	**1,28E+00**	**5,49E-05**	*nifD*- NoN 14 dpi	CS	CASP-like protein (AHRD V3.3 *** K4BPK2_SOLLC)	
Solyc01g103590.3	1,42E-02	9,43E-01	-2,29E-01	2,54E-01	-8,96E-02	6,52E-01	**1,03E+00**	**1,79E-05**	*nifD*- NoN 14 dpi	STR	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** A0A061DWL3_THECC)	

Solyc12g013700.2	2,59E-01	4,86E-01	-2,30E-01	5,35E-01	3,17E-01	3,94E-01	**2,37E+00**	**7,44E-07**	*nifD*- NoN 14 dpi	NA	Stem-specific protein tsjt1, putative (AHRD V3.3 *** D6BRF0_JATCU)	
Solyc12g049520.2	-1,62E-01	8,45E-01	-2,31E-01	7,81E-01	-1,24E+00	1,46E-01	**-2,38E+00**	**7,70E-03**	*nifD*- NoN 14 dpi	H	COP1-interacting-like protein (AHRD V3.3 *-* G7L8C6_MEDTR)	
Solyc06g048950.3	-8,29E-01	5,22E-06	-2,33E-01	1,20E-01	-2,12E-01	1,56E-01	**-1,10E+00**	**4,87E-08**	*nifD*- NoN 14 dpi	PMI	Leucine-rich receptor-like kinase family protein (AHRD V3.3 *** A0A072V1G8_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc05g053120.1	1,32E+00	1,61E-01	-2,35E-01	7,99E-01	1,12E+00	2,30E-01	**3,16E+00**	**1,85E-03**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** A0A0A1WC49_NICAT)	GO:0008152|GO:0016758
Solyc12g098590.2	3,60E-01	5,90E-01	-2,35E-01	7,26E-01	-7,25E-01	2,83E-01	**-6,20E+00**	**9,00E-10**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4DHN2_SOLLC)	GO:0008152|GO:0016758
Solyc02g090610.1	3,60E-01	4,77E-01	-2,35E-01	6,42E-01	4,11E-01	4,18E-01	**-3,94E+00**	**2,47E-08**	*nifD*- NoN 14 dpi	G	LOW QUALITY:Cyclin-dependent kinase D-1 (AHRD V3.3 --* CDKD1_ORYSI)	GO:0048364
Solyc09g008360.2	3,60E-01	6,41E-01	-2,35E-01	7,61E-01	3,02E-01	6,95E-01	**-3,96E+00**	**2,12E-05**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:Heparan-alpha-glucosaminide N-acetyltransferase (AHRD V3.3 *** A0A0B2STS8_GLYSO)	
Solyc01g006640.1	3,60E-01	6,67E-01	-2,35E-01	7,79E-01	-4,85E-01	5,63E-01	**-2,40E+00**	**7,56E-03**	*nifD*- NoN 14 dpi	P	LOW QUALITY:AMP-dependent synthetase and ligase family protein (AHRD V3.3 *** A0A061GTM3_THECC)	GO:0003824|GO:0008152|GO:0004096|GO:0020037|GO:0055114|GO:0004096|GO:0020037|GO:0055114
Solyc07g008210.3	3,60E-01	4,83E-01	-2,35E-01	6,47E-01	9,53E-01	7,12E-02	**-2,55E+00**	**3,14E-05**	*nifD*- NoN 14 dpi	H	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *-* AT1G80130.1)	GO:0005515
Solyc05g010080.3	-7,71E-02	8,37E-01	-2,36E-01	5,30E-01	5,48E-02	8,83E-01	**-1,35E+00**	**1,15E-03**	*nifD*- NoN 14 dpi	T	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 --* AT1G62970.1)	
Solyc03g116480.1	2,75E-01	4,29E-01	-2,40E-01	4,90E-01	-1,71E-01	6,21E-01	**2,38E+00**	**2,42E-07**	*nifD*- NoN 14 dpi	H	LOW QUALITY:F-box only protein 6 (AHRD V3.3 *** A0A0B2SU90_GLYSO)	GO:0005515
Solyc07g065165.1	-3,88E-01	3,13E-01	-2,41E-01	5,29E-01	-4,52E-02	9,06E-01	**-1,27E+00**	**2,45E-03**	*nifD*- NoN 14 dpi	D	Pirin-like protein (AHRD V3.3 *** A0A0B2SAS7_GLYSO)	
Solyc10g011730.3	-1,08E+00	4,30E-02	-2,43E-01	6,34E-01	-1,35E+00	1,32E-02	**-1,88E+00**	**9,57E-04**	*nifD*- NoN 14 dpi	CS	Arabinogalactan peptide 20 (AHRD V3.3 *** AGP20_ARATH)	
Solyc10g006900.3	4,26E-01	3,39E-01	-2,44E-01	5,81E-01	4,43E-01	3,20E-01	**1,32E+00**	**5,71E-03**	*nifD*- NoN 14 dpi	E	light dependent NADH:protochlorophyllide oxidoreductase 3 s2	GO:0016630|GO:0055114
Solyc01g044240.3	4,68E-01	2,43E-01	-2,46E-01	5,35E-01	7,56E-01	6,48E-02	**1,10E+00**	**9,20E-03**	*nifD*- NoN 14 dpi	C	Soluble inorganic pyrophosphatase 1 (AHRD V3.3 --* IPYR1_ARATH)	
Solyc04g077030.3	5,29E-01	3,70E-03	-2,47E-01	1,48E-01	-1,71E-01	3,12E-01	**1,03E+00**	**1,54E-06**	*nifD*- NoN 14 dpi	C	Xylulose kinase, putative (AHRD V3.3 *** A0A061FE36_THECC)	GO:0005975|GO:0016773
Solyc09g091580.3	-4,70E-01	7,53E-02	-2,48E-01	3,36E-01	1,90E-01	4,60E-01	**-1,03E+00**	**3,87E-04**	*nifD*- NoN 14 dpi	K	ABC1 protein kinase 6 (AHRD V3.3 *** Q9LRN0_ARATH)	GO:0004672|GO:0005524|GO:0006468
Solyc03g121540.3	6,37E-01	5,11E-02	-2,49E-01	4,30E-01	5,72E-01	7,77E-02	**3,13E+00**	**2,08E-10**	*nifD*- NoN 14 dpi	C	beta-galactosidase 3	GO:0004553|GO:0005975|GO:0005975|GO:0005975
Solyc05g053100.3	8,05E-01	1,21E-01	-2,51E-01	6,22E-01	-1,65E-01	7,45E-01	**2,37E+00**	**7,35E-05**	*nifD*- NoN 14 dpi	E	Dihydrolipoyl dehydrogenase (AHRD V3.3 *** W9QVW5_9ROSA)	GO:0016491|GO:0050660|GO:0055114|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc02g087840.3	-5,02E-01	1,56E-01	-2,51E-01	4,73E-01	-7,05E-01	5,08E-02	**-1,24E+00**	**1,36E-03**	*nifD*- NoN 14 dpi	DNA	Homeobox associated leucine zipper protein (AHRD V3.3 *** A0A072U5Q1_MEDTR)	GO:0003677|GO:0003700|GO:0006355|GO:0043565|GO:0003700|GO:0006355|GO:0043565
Solyc09g065550.3	-6,31E-01	3,29E-02	-2,51E-01	3,78E-01	-6,89E-01	2,08E-02	**-1,05E+00**	**9,28E-04**	*nifD*- NoN 14 dpi	K	Kinase interacting (KIP1-like) family protein, putative (AHRD V3.3 *** A0A061DQM7_THECC)	GO:0003779
Solyc06g068570.3	3,98E-01	2,33E-01	-2,53E-01	4,46E-01	-3,46E-01	2,99E-01	**1,03E+00**	**4,17E-03**	*nifD*- NoN 14 dpi	H	AP2-like ethylene-responsive transcription factor	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc10g008440.3	-3,66E-01	7,12E-01	-2,54E-01	7,98E-01	-2,62E+00	1,29E-02	**-3,71E+00**	**8,27E-04**	*nifD*- NoN 14 dpi	CS	expansin B3 (AHRD V3.3 *** AT4G28250.1)	GO:0005576|GO:0005576|GO:0019953|GO:0005576|GO:0019953
Solyc03g078710.2	-3,91E-01	2,62E-02	-2,55E-01	1,36E-01	-3,52E-01	4,31E-02	**-1,06E+00**	**8,77E-07**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** M1C4J3_SOLTU)	GO:0008152|GO:0016758
Solyc07g026680.2	7,33E-01	1,87E-02	-2,56E-01	3,89E-01	-2,94E-02	9,21E-01	**2,01E+00**	**2,86E-07**	*nifD*- NoN 14 dpi	T	Myb-like transcription factor family protein, putative (AHRD V3.3 *** A0A061GMU9_THECC)	GO:0003677
Solyc09g011560.2	-8,75E-01	4,36E-03	-2,59E-01	3,63E-01	-6,73E-01	2,38E-02	**-1,01E+00**	**1,31E-03**	*nifD*- NoN 14 dpi	STR	Glutathione S-transferase (AHRD V3.3 *** C0LF68_CAPAN)	GO:0005515

Solyc05g023830.1	-3,48E-01	3,74E-01	-2,65E-01	4,97E-01	2,75E-01	4,81E-01	**1,19E+00**	**4,61E-03**	*nifD*- NoN 14 dpi	T	LOW QUALITY:Malate dehydrogenase [NADP], chloroplastic (AHRD V3.3 --* MDHP_MAIZE)	
Solyc12g099970.2	3,27E-01	1,41E-02	-2,68E-01	4,06E-02	1,62E-02	8,97E-01	**1,76E+00**	**1,23E-13**	*nifD*- NoN 14 dpi	K	SNF1 kinase complex anchoring protein	GO:0005515|GO:0009744|GO:0043562|GO:0009744|GO:0043562
Solyc01g080170.3	3,19E-01	3,41E-02	-2,70E-01	6,94E-02	1,90E-01	1,93E-01	**1,17E+00**	**1,15E-08**	*nifD*- NoN 14 dpi	2M	Hydroxymethylglutaryl-CoA lyase (AHRD V3.3 *** W9QRW1_9ROSA)	GO:0003824
Solyc03g098010.3	-8,42E-01	3,16E-01	-2,70E-01	7,45E-01	-6,95E-01	4,06E-01	**-3,11E+00**	**8,37E-04**	*nifD*- NoN 14 dpi	STR	phosphate starvation inducible gene TPSI1	GO:0003993|GO:0016787|GO:0016787
Solyc06g066730.3	-7,06E-01	1,47E-03	-2,71E-01	1,83E-01	-7,49E-01	8,50E-04	**-1,28E+00**	**7,85E-07**	*nifD*- NoN 14 dpi	P	Coatomer beta subunit, putative (AHRD V3.3 *** B9SQC0_RICCO)	GO:0005198|GO:0006886|GO:0016192|GO:0030117|GO:0005515|GO:0005515
Solyc04g009280.1	-4,40E-01	2,02E-01	-2,72E-01	4,26E-01	-4,75E-02	8,89E-01	**-1,11E+00**	**2,86E-03**	*nifD*- NoN 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *-* AT3G57180.1)	
Solyc10g080610.1	3,39E-01	1,68E-01	-2,75E-01	2,60E-01	2,58E-01	2,90E-01	**1,72E+00**	**1,31E-07**	*nifD*- NoN 14 dpi	P	F-box/kelch-repeat protein (AHRD V3.3 *** A0A172MAC1_VITPS)	GO:0005515
Solyc07g062490.1	-7,87E-01	6,40E-02	-2,75E-01	5,04E-01	7,17E-01	8,96E-02	**1,64E+00**	**4,23E-04**	*nifD*- NoN 14 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *-* A0A067JEE7_JATCU)	
Solyc04g071523.1	4,56E-01	2,77E-01	-2,76E-01	5,07E-01	-1,00E+00	2,20E-02	**1,43E+00**	**1,77E-03**	*nifD*- NoN 14 dpi	NA	UPF0496 protein (AHRD V3.3 *** A0A0B2QAE4_GLYSO)	
Solyc01g103500.3	9,95E-02	8,52E-01	-2,85E-01	5,94E-01	5,75E-02	9,14E-01	**-1,47E+00**	**9,86E-03**	*nifD*- NoN 14 dpi	TR	Multidrug resistance 3 (AHRD V3.3 *** A0A0B0MAA3_GOSAR)	
Solyc06g065100.3	1,30E-02	9,19E-01	-2,86E-01	3,32E-02	4,72E-02	7,13E-01	**1,21E+00**	**6,24E-10**	*nifD*- NoN 14 dpi	G	R2R3MYB transcription factor 3	GO:0003677
Solyc05g007060.3	5,59E-01	1,87E-02	-2,87E-01	2,09E-01	3,95E-01	8,76E-02	**1,51E+00**	**3,62E-07**	*nifD*- NoN 14 dpi	NA	Plant/T7N9-9 protein (AHRD V3.3 *** G7K9S8_MEDTR)	
Solyc02g005200.3	5,00E-01	4,07E-02	-2,90E-01	2,22E-01	5,56E-01	2,41E-02	**1,66E+00**	**1,47E-07**	*nifD*- NoN 14 dpi	RNA	RNA binding protein (AHRD V3.3 *** AT3G08010.1)	
Solyc02g036280.3	2,42E-01	4,49E-01	-2,94E-01	3,59E-01	-2,27E-01	4,77E-01	**-1,07E+00**	**2,23E-03**	*nifD*- NoN 14 dpi	D	Pvr4 (AHRD V3.3 *-* A0A1D5AHY8_CAPAN)	
Solyc01g073840.1	-9,20E-01	5,94E-02	-2,98E-01	5,29E-01	8,50E-01	8,01E-02	**2,23E+00**	**6,34E-05**	*nifD*- NoN 14 dpi	S	LOW QUALITY:Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)	GO:0005515|GO:0008270
Solyc06g066640.3	-1,60E+00	1,06E-01	-3,00E-01	7,57E-01	1,53E+00	1,21E-01	**4,51E+00**	**7,57E-05**	*nifD*- NoN 14 dpi	E	Photosystem I reaction center subunit VI (AHRD V3.3 *** B7FN63_MEDTR)	GO:0009522|GO:0009538|GO:0015979
Solyc01g095100.3	-8,09E-02	5,93E-01	-3,01E-01	5,43E-02	-8,87E-02	5,58E-01	**1,39E+00**	**1,03E-09**	*nifD*- NoN 14 dpi	T	WRKY transcription factor 22	GO:0003700|GO:0006355|GO:0043565
Solyc04g079110.1	-9,06E-01	1,38E-03	-3,05E-01	2,39E-01	-5,73E-01	3,19E-02	**-1,58E+00**	**1,34E-06**	*nifD*- NoN 14 dpi	K	LOW QUALITY:BRI1 kinase inhibitor 1 (AHRD V3.3 *** A0A061FJ36_THECC)	
Solyc12g099940.2	9,49E-02	4,47E-01	-3,09E-01	1,85E-02	-1,73E-02	8,89E-01	**1,16E+00**	**7,25E-10**	*nifD*- NoN 14 dpi	H	Acyl-CoA N-acyltransferase (AHRD V3.3 *** A0A103YFJ4_CYNCS)	GO:0008080
Solyc10g081000.1	1,39E-01	3,72E-01	-3,10E-01	5,40E-02	4,98E-01	3,20E-03	**1,03E+00**	**3,95E-07**	*nifD*- NoN 14 dpi	G	LOW QUALITY:sequence-specific DNA binding transcription factor ATNDX (AHRD V3.3 --* AT4G03090.5)	
Solyc01g073860.3	-9,02E-01	3,68E-03	-3,10E-01	2,82E-01	-2,92E-01	3,10E-01	**1,34E+00**	**6,71E-05**	*nifD*- NoN 14 dpi	S	Cysteine/Histidine-rich C1 domain family protein (AHRD V3.3 *** AT2G44380.1)	
Solyc03g113845.1	-5,38E-01	1,01E-01	-3,11E-01	3,35E-01	-8,19E-01	1,55E-02	**-1,03E+00**	**3,21E-03**	*nifD*- NoN 14 dpi	G	Alpha-N-acetylglucosaminidase family protein (AHRD V3.3 *-* A0A072UZT3_MEDTR)	
Solyc12g099650.2	5,20E-01	5,36E-01	-3,17E-01	7,06E-01	1,07E+00	2,10E-01	**2,64E+00**	**3,82E-03**	*nifD*- NoN 14 dpi	E	Photosystem II 5 kDa protein (AHRD V3.3 *** K7WNW4_SOLTU)	
Solyc03g117580.3	2,46E-01	3,63E-01	-3,19E-01	2,41E-01	1,93E-01	4,76E-01	**2,12E+00**	**2,16E-08**	*nifD*- NoN 14 dpi	NA	GAG1At protein (AHRD V3.3 *** AT1G16000.1)	
Solyc02g066950.3	-8,54E-01	6,69E-03	-3,22E-01	2,77E-01	-6,51E-01	3,34E-02	**-1,68E+00**	**4,11E-06**	*nifD*- NoN 14 dpi	CS	Alpha-amylase, putative (AHRD V3.3 *** B9SJF1_RICCO)	
Solyc00g098560.3	5,32E-02	7,84E-01	-3,24E-01	1,03E-01	1,88E-01	3,37E-01	**1,30E+00**	**3,54E-07**	*nifD*- NoN 14 dpi	L	GDSL esterase/lipase (AHRD V3.3 *** A0A199UQJ3_ANACO)	GO:0016788

Solyc02g072480.3	-6,15E-01	1,19E-02	-3,30E-01	1,59E-01	-4,40E-01	6,38E-02	**-1,03E+00**	**1,18E-04**	*nifD*- NoN 14 dpi	PMI	LRR receptor-like kinase (AHRD V3.3 *** A0A072V4N4_MEDTR)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g007790.3	2,01E-01	2,02E-01	-3,32E-01	4,07E-02	5,58E-01	1,25E-03	**1,00E+00**	**7,12E-07**	*nifD*- NoN 14 dpi	L	3-hydroxy-3-methylglutaryl coenzyme A synthase	GO:0003824|GO:0008152|GO:0004421|GO:0008299|GO:0004421|GO:0008299
Solyc02g090450.3	-4,82E-01	1,54E-02	-3,32E-01	8,57E-02	-7,07E-01	7,90E-04	**1,99E+00**	**5,93E-11**	*nifD*- NoN 14 dpi	OX	Sl Peroxidase	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc09g008430.3	-2,14E-02	9,39E-01	-3,36E-01	2,38E-01	7,35E-01	1,39E-02	**1,43E+00**	**2,46E-05**	*nifD*- NoN 14 dpi	DNA	CHY zinc finger family protein, expressed (AHRD V3.3 *** Q337P1_ORYSJ)	GO:0005515|GO:0008270
Solyc02g084630.3	6,43E-02	6,40E-01	-3,37E-01	2,01E-02	3,35E-01	2,07E-02	**1,10E+00**	**1,61E-08**	*nifD*- NoN 14 dpi	T	TDR6 transcription factor	GO:0000165|GO:0000977|GO:0045944|GO:0003677|GO:0046983|GO:0003677|GO:0046983
Solyc01g100660.3	-2,30E-01	1,31E-01	-3,39E-01	2,99E-02	9,50E-02	5,25E-01	**1,35E+00**	**1,48E-09**	*nifD*- NoN 14 dpi	T	Basic helix-loop-helix transcription factor (AHRD V3.3 *** A0A0S3TVX2_CITUN)	GO:0046983
Solyc04g082420.3	1,90E-01	1,73E-01	-3,40E-01	1,91E-02	-3,29E-01	2,26E-02	**1,22E+00**	**2,04E-09**	*nifD*- NoN 14 dpi	T	BTB/POZ domain-containing protein (AHRD V3.3 *** AT2G30600.6)	GO:0005515
Solyc05g015840.3	-7,11E-01	1,44E-02	-3,50E-01	2,09E-01	-1,78E-01	5,17E-01	**-1,14E+00**	**2,81E-04**	*nifD*- NoN 14 dpi	G	Squamosa promoter binding protein 13	GO:0003677|GO:0005634
Solyc01g098140.3	3,10E-01	2,85E-02	-3,50E-01	1,47E-02	-1,45E-01	2,87E-01	**1,23E+00**	**1,34E-09**	*nifD*- NoN 14 dpi	L	alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *** AT2G45600.1)	GO:0008152|GO:0016787
Solyc09g090430.3	4,96E-02	7,34E-01	-3,52E-01	2,20E-02	2,58E-01	8,62E-02	**1,03E+00**	**1,45E-07**	*nifD*- NoN 14 dpi	N	Cyanate hydratase (AHRD V3.3 *** M1BFS5_SOLTU)	GO:0003677|GO:0008824|GO:0009439|GO:0008824|GO:0009439
Solyc02g089890.3	-2,13E-01	2,29E-01	-3,53E-01	5,10E-02	-4,24E-01	2,10E-02	**-1,29E+00**	**6,64E-08**	*nifD*- NoN 14 dpi	TR	PQ-loop repeat family protein / transmembrane family protein (AHRD V3.3 *** AT4G36850.1)	
Solyc02g085315.1	-2,30E-01	1,61E-01	-3,55E-01	3,52E-02	2,85E-01	8,62E-02	**1,02E+00**	**1,01E-06**	*nifD*- NoN 14 dpi	S	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 --* A0A061DH70_THECC)	
Solyc08g069110.3	-1,99E-01	5,42E-01	-3,58E-01	2,76E-01	1,37E-01	6,75E-01	**1,18E+00**	**1,13E-03**	*nifD*- NoN 14 dpi	C	NAD-dependent epimerase/dehydratase family protein (AHRD V3.3 *** AT1G53500.1)	
Solyc04g008455.1	-7,98E-01	1,10E-01	-3,59E-01	4,63E-01	-3,11E-01	5,25E-01	**-1,45E+00**	**5,83E-03**	*nifD*- NoN 14 dpi	TR	Potassium transporter (AHRD V3.3 *** K4BP01_SOLLC)	GO:0015079|GO:0016020|GO:0071805
Solyc12g010900.1	2,33E-01	1,99E-01	-3,62E-01	5,08E-02	4,17E-01	2,60E-02	**1,12E+00**	**1,14E-06**	*nifD*- NoN 14 dpi	P	F-box protein (AHRD V3.3 *** T1RVG4_STRHE)	
Solyc10g086570.3	4,91E-01	5,43E-01	-3,64E-01	6,52E-01	1,57E+00	5,91E-02	**5,93E+00**	**6,98E-08**	*nifD*- NoN 14 dpi	T	Chaperone DnaJ (AHRD V3.3 *** A0A0B0NPS3_GOSAR)	GO:0031072|GO:0051082
Solyc08g068960.3	-9,41E-01	1,71E-05	-3,67E-01	5,00E-02	-5,99E-01	2,47E-03	**-1,35E+00**	**5,68E-08**	*nifD*- NoN 14 dpi	H	Histidine kinase 5 (AHRD V3.3 *** W9RFB6_9ROSA)	GO:0000155|GO:0007165|GO:0000160|GO:0000160
Solyc10g017960.2	6,98E-02	7,99E-01	-3,68E-01	1,88E-01	-5,23E-02	8,49E-01	**2,01E+00**	**8,29E-08**	*nifD*- NoN 14 dpi	P	F-box protein PP2-A13 (AHRD V3.3 *** P2A13_ARATH)	GO:0005515
Solyc03g026020.3	3,45E-01	6,34E-03	-3,69E-01	3,86E-03	3,84E-01	2,81E-03	**1,07E+00**	**1,20E-09**	*nifD*- NoN 14 dpi	STR	SolycHsfB2a	GO:0003700|GO:0005634|GO:0006355|GO:0043565
Solyc04g081560.3	-2,46E-01	4,22E-01	-3,70E-01	2,31E-01	4,64E-01	1,36E-01	**2,83E+00**	**8,38E-10**	*nifD*- NoN 14 dpi	D	Pathogenesis-related thaumatin family protein (AHRD V3.3 *** A0A072UXB7_MEDTR)	
Solyc03g083240.3	-6,81E-01	1,11E-02	-3,72E-01	1,48E-01	-6,52E-01	1,47E-02	**-1,19E+00**	**6,08E-05**	*nifD*- NoN 14 dpi	D	Transcription factor jumonji domain-containing protein, putative isoform 2 (AHRD V3.3 --* A0A061G2X9_THECC)	GO:0003677
Solyc05g052900.3	3,75E-01	2,90E-01	-3,73E-01	2,93E-01	-1,41E-01	6,89E-01	**1,27E+00**	**1,16E-03**	*nifD*- NoN 14 dpi	NA	Ras-related protein, expressed (AHRD V3.3 *** D8L9F8_WHEAT)	GO:0005525|GO:0005525|GO:0007264|GO:0005525|GO:0007264
Solyc06g008810.3	-7,99E-01	2,69E-01	-3,75E-01	6,00E-01	-1,16E+00	1,14E-01	**-2,44E+00**	**1,96E-03**	*nifD*- NoN 14 dpi	TR	Transport inhibitor response 1 (AHRD V3.3 *-* C7E4R3_TOBAC)	
Solyc10g011750.3	-7,63E-01	2,79E-02	-3,77E-01	2,60E-01	-3,43E-01	3,04E-01	**-1,15E+00**	**1,60E-03**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (AHRD V3.3 *** AT2G46300.1)	
Solyc04g078640.2	2,24E-01	3,28E-01	-3,77E-01	1,05E-01	5,61E-01	1,92E-02	**1,76E+00**	**2,85E-08**	*nifD*- NoN 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *-* A0A0K9P1G2_ZOSMR)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc08g075870.3	-3,74E-01	1,00E-01	-3,78E-01	9,68E-02	-9,80E-01	1,39E-04	**-1,34E+00**	**1,84E-06**	*nifD*- NoN 14 dpi	CS	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT4G19120.2)	GO:0008168

Solyc10g018530.2	1,29E-01	5,51E-01	-3,78E-01	8,70E-02	-1,23E-01	5,68E-01	**-1,02E+00**	**5,80E-05**	*nifD*- NoN 14 dpi	DNA	DNA mismatch repair protein MutS (AHRD V3.3 *** G7K3K2_MEDTR)	GO:0005524|GO:0006298|GO:0030983
Solyc01g081420.2	-2,68E-01	6,15E-01	-3,79E-01	4,78E-01	-1,07E+00	5,29E-02	**-1,56E+00**	**6,35E-03**	*nifD*- NoN 14 dpi	RNA	Serrate RNA effector molecule (AHRD V3.3 *-* A0A1D1Y9V9_9ARAE)	
Solyc11g020610.3	1,89E-01	7,80E-02	-3,79E-01	1,06E-03	3,87E-01	8,66E-04	**1,83E+00**	**5,85E-16**	*nifD*- NoN 14 dpi	G	cytosolic neutral/alkaline invertase D	GO:0003824|GO:0033926|GO:0033926
Solyc07g063410.3	5,22E-01	1,23E-01	-3,79E-01	2,57E-01	-2,94E-01	3,78E-01	**1,68E+00**	**2,52E-05**	*nifD*- NoN 14 dpi	H	JA2-like	GO:0003677|GO:0006355
Solyc12g099440.2	6,54E-01	9,06E-07	-3,85E-01	8,48E-04	2,16E-01	4,40E-02	**1,26E+00**	**2,70E-12**	*nifD*- NoN 14 dpi	L	Fatty acid beta-oxidation multifunctional protein (AHRD V3.3 *** A0A077DAS1_9ERIC)	GO:0003824|GO:0008152|GO:0003857|GO:0006631|GO:0016491|GO:0055114|GO:0003857|GO:0006631|GO:0016491|GO:0055114
Solyc06g075345.1	1,33E-01	7,84E-01	-3,87E-01	4,28E-01	3,17E-01	5,15E-01	**-1,55E+00**	**3,34E-03**	*nifD*- NoN 14 dpi	NA	Unknown protein (AHRD V3.3)	
Solyc04g071600.3	-1,09E+00	1,45E-03	-3,89E-01	2,17E-01	9,72E-01	3,95E-03	**1,20E+00**	**5,95E-04**	*nifD*- NoN 14 dpi	STR	Abscisic acid stress ripening 5	GO:0006950
Solyc11g069450.1	-2,46E-01	1,86E-01	-3,91E-01	4,00E-02	5,09E-01	9,27E-03	**1,38E+00**	**4,63E-08**	*nifD*- NoN 14 dpi	G	LOW QUALITY:Senescence regulator (AHRD V3.3 *** A0A103XHC6_CYNCS)	
Solyc07g062605.1	-4,60E-01	9,15E-02	-3,94E-01	1,45E-01	-5,26E-01	5,57E-02	**-1,18E+00**	**1,30E-04**	*nifD*- NoN 14 dpi	H	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein (AHRD V3.3 *-* AT3G14980.6)	
Solyc03g007460.2	-1,84E-02	9,42E-01	-3,96E-01	1,29E-01	-2,76E-01	2,84E-01	**-1,11E+00**	**1,68E-04**	*nifD*- NoN 14 dpi	T	Solanum lycopersicum Cytokinin Response Factor 4	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc10g079770.2	-1,38E-03	9,93E-01	-3,97E-01	1,76E-02	-1,45E-02	9,27E-01	**1,44E+00**	**1,36E-09**	*nifD*- NoN 14 dpi	CS	Triacylglycerol lipase SDP1 (AHRD V3.3 *** W9RS42_9ROSA)	GO:0004806|GO:0006629|GO:0006629|GO:0006629
Solyc04g074850.3	1,53E-01	4,65E-01	-3,97E-01	6,58E-02	5,36E-01	1,54E-02	**1,05E+00**	**2,89E-05**	*nifD*- NoN 14 dpi	D	ripening regulated protein DDTFR18	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc04g007050.3	-7,38E-01	3,26E-04	-3,97E-01	3,48E-02	-7,52E-01	2,67E-04	**-1,15E+00**	**8,09E-07**	*nifD*- NoN 14 dpi	D	Disease resistance protein (AHRD V3.3 *** A0A103XDQ0_CYNCS)	GO:0043531
Solyc02g085620.3	-4,16E-01	6,25E-01	-3,98E-01	6,40E-01	-1,72E+00	5,22E-02	**-2,74E+00**	**3,19E-03**	*nifD*- NoN 14 dpi	K	Protein kinase (AHRD V3.3 *** A0A087GEP9_ARAAL)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g117675.1	1,92E-01	5,08E-01	-3,99E-01	1,75E-01	4,52E-02	8,76E-01	**1,83E+00**	**9,34E-07**	*nifD*- NoN 14 dpi	DNA	ATP-dependent DNA helicase (AHRD V3.3 *** AT2G24100.1)	
Solyc03g034010.3	-6,83E-01	5,22E-02	-3,99E-01	2,46E-01	-7,26E-01	4,01E-02	**-1,49E+00**	**1,53E-04**	*nifD*- NoN 14 dpi	P	U-box domain-containing family protein (AHRD V3.3 *-* U5GHQ7_POPTR)	
Solyc01g109580.3	-1,06E+00	1,85E-02	-4,04E-01	3,45E-01	-1,03E+00	2,13E-02	**-1,37E+00**	**3,21E-03**	*nifD*- NoN 14 dpi	CS	Adenylyl cyclase-associated protein (AHRD V3.3 *** K4B3H1_SOLLC)	GO:0000902|GO:0003779|GO:0007010|GO:0003779|GO:0007010
Solyc01g008930.4	-3,64E-01	9,11E-03	-4,05E-01	4,23E-03	-1,86E-01	1,62E-01	**-1,02E+00**	**2,39E-08**	*nifD*- NoN 14 dpi	S	AUREA phytochromobilin synthase	
Solyc06g069880.1	-1,52E-01	5,60E-01	-4,08E-01	1,26E-01	-1,13E-01	6,64E-01	**-1,16E+00**	**1,25E-04**	*nifD*- NoN 14 dpi	G	LOW QUALITY:Phytochrome kinase substrate-related family protein (AHRD V3.3 *** B9N4C0_POPTR)	
Solyc10g006440.3	4,73E-01	1,87E-01	-4,15E-01	2,45E-01	-5,71E-01	1,14E-01	**1,18E+00**	**2,37E-03**	*nifD*- NoN 14 dpi	TR	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT4G27100.2)	
Solyc03g026050.3	-9,14E-01	1,74E-01	-4,16E-01	5,30E-01	-1,74E+00	1,31E-02	**-1,84E+00**	**9,21E-03**	*nifD*- NoN 14 dpi	G	Terminal flower 1 (AHRD V3.3 *** G7ZV36_MEDTR)	
Solyc01g010460.3	-3,44E-01	2,59E-01	-4,18E-01	1,73E-01	-1,22E-01	6,85E-01	**-1,03E+00**	**1,86E-03**	*nifD*- NoN 14 dpi	S	5'-AMP-activated protein kinase-like protein (AHRD V3.3 *** AT1G27070.1)	
Solyc07g006500.3	4,47E-01	1,64E-01	-4,19E-01	1,91E-01	3,99E-01	2,12E-01	**2,49E+00**	**1,97E-08**	*nifD*- NoN 14 dpi	C	trehalose-6-phosphate synthase 1	GO:0003824|GO:0005992
Solyc04g015360.3	-2,01E-02	9,71E-01	-4,19E-01	4,43E-01	-9,53E-01	8,87E-02	**-1,69E+00**	**4,23E-03**	*nifD*- NoN 14 dpi	T	GATA transcription factor (AHRD V3.3 *** K4BQ39_SOLLC)	GO:0003677|GO:0005634|GO:0045893|GO:0003700|GO:0006355|GO:0008270|GO:0043565|GO:0003700|GO:0006355|GO:0008270|GO:0043565
Solyc05g025580.1	9,23E-02	7,61E-01	-4,20E-01	1,74E-01	1,68E-01	5,81E-01	**1,29E+00**	**2,30E-04**	*nifD*- NoN 14 dpi	OX	LOW QUALITY:N-glycosylase/DNA lyase OGG1 (AHRD V3.3 --* OGG1_ARATH)	
Solyc03g093930.3	-1,27E+00	9,42E-02	-4,20E-01	5,72E-01	-2,89E-01	6,96E-01	**-2,29E+00**	**4,39E-03**	*nifD*- NoN 14 dpi	T	MYB family protein (AHRD V3.3 *-* A0A067JDM6_JATCU)	GO:0003677

Solyc08g080745.1	-6,44E-01	1,11E-02	-4,20E-01	8,60E-02	-1,57E+00	4,55E-07	**1,92E+00**	**1,38E-08**	*nifD*- NoN 14 dpi	NA	carboxyl-terminal peptidase (DUF239) (AHRD V3.3 *** AT2G44210.1)	
Solyc01g081330.3	-2,95E-01	2,68E-01	-4,21E-01	1,19E-01	-3,36E-01	2,09E-01	**-1,12E+00**	**2,28E-04**	*nifD*- NoN 14 dpi	P	Chaperone protein DNAj, putative (AHRD V3.3 *** B9RJS6_RICCO)	GO:0005524|GO:0006457|GO:0009408|GO:0051082|GO:0006457|GO:0051082|GO:0006457|GO:0051082
Solyc11g007790.1	-8,21E-01	3,06E-01	-4,22E-01	5,96E-01	-1,12E+00	1,66E-01	**-2,66E+00**	**2,30E-03**	*nifD*- NoN 14 dpi	D	LOW QUALITY:Nbs-lrr resistance protein (AHRD V3.3 *** A0A061F8I5_THECC)	GO:0005515|GO:0043531|GO:0043531
Solyc01g108490.3	-4,28E-02	8,83E-01	-4,23E-01	1,54E-01	6,35E-01	3,69E-02	**1,70E+00**	**3,39E-06**	*nifD*- NoN 14 dpi	STR	Carboxypeptidase (AHRD V3.3 *** K4B364_SOLLC)	GO:0004185|GO:0006508
Solyc11g006630.1	-1,98E-01	1,91E-01	-4,24E-01	8,04E-03	-6,94E-01	7,49E-05	**-1,13E+00**	**4,09E-08**	*nifD*- NoN 14 dpi	D	Disease resistance protein (AHRD V3.3 *** A0A103Y7R3_CYNCS)	GO:0043531
Solyc01g097260.3	-9,08E-02	8,14E-01	-4,24E-01	2,78E-01	-1,99E-01	6,07E-01	**1,10E+00**	**8,07E-03**	*nifD*- NoN 14 dpi	STR	Zn-dependent exopeptidases superfamily protein (AHRD V3.3 --* AT1G67420.6)	
Solyc02g073571.1	2,15E-01	6,50E-01	-4,25E-01	3,73E-01	3,62E-01	4,47E-01	**1,94E+00**	**3,26E-04**	*nifD*- NoN 14 dpi	NA	UPF0183 protein family (AHRD V3.3 *-* A0A151TIL6_CAJCA)	
Solyc07g007290.1	-1,30E+00	1,59E-01	-4,30E-01	6,34E-01	-1,81E+00	5,27E-02	**-2,56E+00**	**8,22E-03**	*nifD*- NoN 14 dpi	OX	LOW QUALITY:Flavin-containing monooxygenase (AHRD V3.3 *** A0A022R7T6_ERYGU)	GO:0004499|GO:0050660|GO:0050661|GO:0055114|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc01g057770.3	-5,45E-01	1,29E-01	-4,32E-01	2,25E-01	-6,02E-01	9,52E-02	**-1,08E+00**	**4,66E-03**	*nifD*- NoN 14 dpi	TR	Boron transporter (AHRD V3.3 *** B6V758_VITVI)	GO:0005452|GO:0006820|GO:0016020|GO:0006820|GO:0016021|GO:0006820|GO:0016021
Solyc03g031530.3	-7,33E-01	3,96E-03	-4,33E-01	7,28E-02	-2,81E-04	9,99E-01	**1,33E+00**	**4,75E-06**	*nifD*- NoN 14 dpi	P	Sulfite exporter TauE/SafE family protein (AHRD V3.3 *** AT1G61740.1)	GO:0016021
Solyc01g010770.3	1,52E-01	4,91E-01	-4,34E-01	5,68E-02	-2,10E-01	3,43E-01	**1,52E+00**	**2,16E-07**	*nifD*- NoN 14 dpi	D	Hypersensitive-induced response protein (AHRD V3.3 *** Q6UNT3_CUCSA)	
Solyc04g025477.1	-1,57E-01	7,23E-01	-4,38E-01	3,28E-01	-3,36E-01	4,50E-01	**-1,45E+00**	**2,79E-03**	*nifD*- NoN 14 dpi	K	CDPK-related kinase (AHRD V3.3 *-* AT3G50530.2)	GO:0004672|GO:0005524|GO:0006468
Solyc02g031980.3	-4,52E-02	6,16E-01	-4,39E-01	4,19E-05	5,32E-02	5,56E-01	**1,06E+00**	**6,19E-12**	*nifD*- NoN 14 dpi	N	urease accessory protein D	GO:0006807|GO:0016151
Solyc11g027840.2	5,55E-01	1,56E-01	-4,42E-01	2,55E-01	3,35E-01	3,85E-01	**2,95E+00**	**3,28E-08**	*nifD*- NoN 14 dpi	CS	1,4-beta-D-glucanase (AHRD V3.3 *** B4FHX7_MAIZE)	GO:0016787
Solyc09g083380.3	-1,81E-01	1,30E-01	-4,42E-01	7,76E-04	-3,22E-01	1,01E-02	**1,46E+00**	**1,68E-12**	*nifD*- NoN 14 dpi	DNA	Histone H1 (AHRD V3.3 *-* H1_MAIZE)	GO:0000786|GO:0003677|GO:0005634|GO:0006334|GO:0000786|GO:0003677|GO:0006334|GO:0000786|GO:0003677|GO:0006334
Solyc09g091945.1	-1,03E+00	1,22E-02	-4,47E-01	2,52E-01	-1,00E+00	1,41E-02	**-1,49E+00**	**6,21E-04**	*nifD*- NoN 14 dpi	NA	4F5 family protein (AHRD V3.3 *-* G7LFV3_MEDTR)	
Solyc06g060180.2	-3,27E-02	9,49E-01	-4,50E-01	3,84E-01	-1,37E-02	9,79E-01	**1,53E+00**	**5,84E-03**	*nifD*- NoN 14 dpi	2M	Terpene synthase (AHRD V3.3 *** G5CV42_SOLLC)	GO:0000287|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829|GO:0008152|GO:0010333|GO:0016829
Solyc04g056440.2	-5,01E-01	4,52E-01	-4,51E-01	4,98E-01	3,14E-01	6,36E-01	**-2,35E+00**	**1,40E-03**	*nifD*- NoN 14 dpi	L	Cyclopropane-fatty-acyl-phospholipid synthase (AHRD V3.3 *-* AT3G23530.1)	GO:0016491|GO:0055114
Solyc00g247300.3	4,61E-01	3,40E-02	-4,55E-01	3,64E-02	4,29E-01	4,75E-02	**1,38E+00**	**4,31E-07**	*nifD*- NoN 14 dpi	CYTP450	Cytochrome P450 family protein (AHRD V3.3 *** B9HFW6_POPTR)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc07g054060.3	6,59E-02	8,83E-01	-4,55E-01	3,14E-01	1,07E+00	2,33E-02	**2,84E+00**	**9,42E-07**	*nifD*- NoN 14 dpi	NA	Phospho-N-acetylmuramoyl-pentapeptide-transferase, putative (AHRD V3.3 *-* A0A061EAV9_THECC)	
Solyc06g008195.1	-8,32E-01	6,60E-02	-4,55E-01	3,03E-01	-1,86E-01	6,71E-01	**-1,75E+00**	**4,38E-04**	*nifD*- NoN 14 dpi	L	3-ketoacyl-CoA synthase 7 (AHRD V3.3 --* AT1G71160.1)	
Solyc06g007440.3	-2,63E-01	3,04E-01	-4,59E-01	7,92E-02	4,68E-01	7,37E-02	**2,23E+00**	**2,66E-09**	*nifD*- NoN 14 dpi	K	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4C3C6_SOLLC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc09g091460.3	-1,04E+00	1,14E-02	-4,61E-01	2,39E-01	-6,16E-02	8,73E-01	**-1,11E+00**	**7,57E-03**	*nifD*- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *-* D7KE69_ARALL)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc04g082010.1	1,39E-02	9,73E-01	-4,64E-01	2,60E-01	1,83E-01	6,53E-01	**1,56E+00**	**6,67E-04**	*nifD*- NoN 14 dpi	E	pre-plastocyanin	GO:0005507|GO:0009055
Solyc11g011160.1	5,94E-02	6,33E-01	-4,65E-01	8,46E-04	-5,30E-01	2,16E-04	**1,05E+00**	**5,27E-09**	*nifD*- NoN 14 dpi	DNA	HMG-Y-related A (AHRD V3.3 *** A0A0B0M969_GOSAR)	GO:0000785|GO:0003677|GO:0005634|GO:0006355|GO:0000786|GO:0003677|GO:0005634|GO:0006334|GO:0000786|GO:0003677|GO:0005634|GO:0006334
Solyc03g005810.3	2,09E-01	5,41E-01	-4,67E-01	1,78E-01	3,72E-01	2,81E-01	**1,33E+00**	**5,45E-04**	*nifD*- NoN 14 dpi	TR	Purine permease family protein (AHRD V3.3 *** D7MCV2_ARALL)	GO:0005215|GO:0016021

Solyc10g006430.2	1,06E-01	6,99E-01	-4,68E-01	9,51E-02	5,20E-01	6,55E-02	**1,61E+00**	**2,92E-06**	*nifD*- NoN 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 --* AT1G61660.7)	
Solyc11g071600.2	-9,80E-02	4,44E-01	-4,71E-01	9,35E-04	2,56E-01	5,24E-02	**1,47E+00**	**8,65E-12**	*nifD*- NoN 14 dpi	OX	aldehyde oxidase	GO:0003824|GO:0016614|GO:0050660|GO:0055114|GO:0005506|GO:0016491|GO:0055114|GO:0005506|GO:0016491|GO:0055114
Solyc08g081740.3	-7,58E-02	7,85E-01	-4,74E-01	9,62E-02	-7,12E-01	1,55E-02	**-1,08E+00**	**5,58E-04**	*nifD*- NoN 14 dpi	P	P-loop containing nucleoside triphosphate hydrolases superfamily protein (AHRD V3.3 *** AT1G64110.5)	GO:0005524
Solyc08g007480.2	1,91E-02	9,45E-01	-4,77E-01	9,18E-02	5,75E-01	4,47E-02	**2,18E+00**	**1,94E-08**	*nifD*- NoN 14 dpi	NA	DUF1442 family protein (AHRD V3.3 *** G7KG69_MEDTR)	
Solyc02g032950.3	2,11E-01	4,61E-01	-4,83E-01	9,93E-02	8,05E-01	8,48E-03	**1,09E+00**	**6,85E-04**	*nifD*- NoN 14 dpi	T	WRKY transcription factor 16	GO:0003700|GO:0006355|GO:0043565
Solyc04g077860.3	-5,46E-01	4,34E-02	-4,83E-01	7,13E-02	-6,45E-01	1,86E-02	**1,48E+00**	**4,87E-06**	*nifD*- NoN 14 dpi	G	Sigma factor sigb regulation protein rsbq, putative (AHRD V3.3 *** B9R708_RICCO)	GO:0010223|GO:1901601
Solyc07g065670.1	3,09E-01	5,39E-01	-4,84E-01	3,38E-01	8,47E-01	1,00E-01	**2,22E+00**	**1,41E-04**	*nifD*- NoN 14 dpi	D	RING/U-box superfamily protein (AHRD V3.3 --* AT5G03180.4)	
Solyc07g063560.3	-1,34E-01	6,72E-01	-4,88E-01	1,31E-01	1,92E-01	5,45E-01	**1,26E+00**	**4,35E-04**	*nifD*- NoN 14 dpi	NA	Cotton fiber expressed protein (AHRD V3.3 *** A0A109Y892_GOSBA)	
Solyc02g089720.2	-5,49E-01	6,45E-03	-4,89E-01	1,39E-02	6,62E-01	1,41E-03	**1,01E+00**	**9,93E-06**	*nifD*- NoN 14 dpi	C	Glycoside hydrolase, family 81 (AHRD V3.3 *** A0A103YH72_CYNCS)	GO:0052861
Solyc06g054540.3	1,90E-01	3,88E-01	-4,94E-01	3,14E-02	-2,91E-01	1,91E-01	**2,01E+00**	**1,15E-09**	*nifD*- NoN 14 dpi	P	CHY-type/CTCHY-type/RING-type Zinc finger protein (AHRD V3.3 *** AT5G18650.1)	GO:0005515|GO:0008270|GO:0008270|GO:0008270
Solyc01g005090.3	-6,11E-01	2,41E-05	-4,94E-01	3,18E-04	-9,86E-01	9,89E-09	**-1,16E+00**	**3,78E-10**	*nifD*- NoN 14 dpi	S	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 (AHRD V3.3 *** A0A0B2RAB0_GLYSO)	GO:0046856
Solyc05g050500.1	-5,97E-02	6,38E-01	-4,95E-01	5,44E-04	-2,34E-01	7,31E-02	**1,11E+00**	**2,98E-09**	*nifD*- NoN 14 dpi	E	LOW QUALITY:ATP synthase delta chain, putative (AHRD V3.3 *** B9SBC4_RICCO)	GO:0015986|GO:0046933
Solyc08g075420.3	1,62E-01	2,53E-01	-4,98E-01	1,34E-03	1,44E-01	3,08E-01	**1,01E+00**	**9,48E-08**	*nifD*- NoN 14 dpi	R	Ribosomal protein L2 (AHRD V3.3 *-* Q8VZZ7_SOLLC)	GO:0003735|GO:0005840|GO:0006412
Solyc07g042810.2	1,42E-01	6,30E-01	-4,98E-01	9,77E-02	-5,20E-01	8,46E-02	**-1,01E+00**	**1,76E-03**	*nifD*- NoN 14 dpi	TR	Chloroplast envelope membrane protein, CemA (AHRD V3.3 *** A0A118K0H5_CYNCS)	GO:0016021
Solyc07g017680.2	-3,71E-01	1,39E-01	-5,02E-01	4,87E-02	-5,81E-01	2,43E-02	**-1,27E+00**	**1,89E-05**	*nifD*- NoN 14 dpi	AM	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (AHRD V3.3 *-* A0A072V2T5_MEDTR)	
Solyc08g007650.1	5,95E-01	4,40E-01	-5,05E-01	5,12E-01	1,04E+00	1,84E-01	**-3,35E+00**	**1,59E-04**	*nifD*- NoN 14 dpi	STR	Subtilisin-like protease (AHRD V3.3 *-* Q9LWA3_SOLLC)	GO:0004252|GO:0006508
Solyc04g081060.3	1,97E-01	6,70E-01	-5,07E-01	2,77E-01	4,40E-01	3,44E-01	**-2,03E+00**	**1,47E-04**	*nifD*- NoN 14 dpi	TR	Kinesin-like protein (AHRD V3.3 *** A0A068UGU8_COFCA)	GO:0003777|GO:0005524|GO:0007018|GO:0008017
Solyc01g094460.3	1,37E-01	6,24E-01	-5,13E-01	7,45E-02	-5,13E-01	7,47E-02	**1,26E+00**	**1,10E-04**	*nifD*- NoN 14 dpi	DNA	AT hook motif DNA-binding family protein (AHRD V3.3 *** A0A072TNY7_MEDTR)	
Solyc03g006800.1	-6,89E-01	1,14E-02	-5,16E-01	5,13E-02	4,15E-01	1,12E-01	**1,16E+00**	**9,72E-05**	*nifD*- NoN 14 dpi	T	TCP transcription factor 21	
Solyc12g098520.2	3,38E-02	7,70E-01	-5,27E-01	9,61E-05	3,79E-01	2,72E-03	**1,19E+00**	**1,12E-10**	*nifD*- NoN 14 dpi	STR	SolycHsfA5	GO:0003700|GO:0005634|GO:0006355|GO:0043565
Solyc11g006730.1	-1,23E+00	2,66E-03	-5,29E-01	1,64E-01	5,64E-01	1,40E-01	**1,41E+00**	**7,76E-04**	*nifD*- NoN 14 dpi	STR	Germin-like protein 1 (AHRD V3.3 *** B9HVV6_POPTR)	GO:0030145|GO:0045735|GO:0045735
Solyc01g009230.3	-1,63E-01	8,45E-01	-5,32E-01	5,26E-01	-1,23E+00	1,51E-01	**-2,37E+00**	**8,37E-03**	*nifD*- NoN 14 dpi	H	sitiens	
Solyc08g079480.3	2,30E-01	3,03E-01	-5,36E-01	2,15E-02	-3,57E-01	1,16E-01	**1,38E+00**	**1,21E-06**	*nifD*- NoN 14 dpi	NA	DUF1442 family protein (AHRD V3.3 *** G7KG71_MEDTR)	
Solyc08g006230.3	-4,18E-01	3,80E-02	-5,37E-01	9,35E-03	-9,69E-01	2,84E-05	**-1,13E+00**	**3,20E-06**	*nifD*- NoN 14 dpi	T	Transcriptional factor B3 family protein (AHRD V3.3 *-* AT4G00260.1)	GO:0003677
Solyc01g108300.3	1,24E-01	6,07E-01	-5,39E-01	3,29E-02	8,10E-01	2,25E-03	**1,65E+00**	**2,53E-07**	*nifD*- NoN 14 dpi	T	Myb family transcription factor	GO:0003677
Solyc11g011670.1	-4,23E-01	5,61E-01	-5,40E-01	4,58E-01	-1,03E+00	1,63E-01	**2,09E+00**	**7,20E-03**	*nifD*- NoN 14 dpi	H	SAUR-like auxin-responsive protein family, putative (AHRD V3.3 *** A0A061E5G9_THECC)	GO:0009733

Solyc11g069580.2	-7,53E-01	5,84E-05	-5,43E-01	1,90E-03	-7,04E-01	1,32E-04	**-1,15E+00**	**9,25E-08**	*nifD*- NoN 14 dpi	S	Cyclic nucleotide-gated channel (AHRD V3.3 *** A0A0K9PRG4_ZOSMR)	GO:0005216|GO:0006811|GO:0016020|GO:0055085
Solyc12g035475.1	-6,76E-01	1,63E-01	-5,45E-01	2,58E-01	3,01E-01	5,29E-01	**-1,58E+00**	**2,45E-03**	*nifD*- NoN 14 dpi	NA	Endoplasmic reticulum metallopeptidase 1 (AHRD V3.3 *-* W9S320_9ROSA)	
Solyc09g075540.1	-1,83E-01	5,00E-01	-5,45E-01	5,16E-02	-8,26E-01	4,73E-03	**-1,12E+00**	**2,78E-04**	*nifD*- NoN 14 dpi	CS	Protein COBRA, putative (AHRD V3.3 *** B9RZK6_RICCO)	GO:0010215|GO:0016049|GO:0031225
Solyc08g074255.1	-2,97E-01	2,85E-01	-5,45E-01	5,54E-02	-8,52E-03	9,75E-01	**1,12E+00**	**3,53E-04**	*nifD*- NoN 14 dpi	D	LOW QUALITY:NBS/LRR resistance protein-like protein (AHRD V3.3 *** Q8LKJ0_CAPAN)	GO:0043531
Solyc04g058160.2	-1,47E+00	1,03E-07	-5,46E-01	1,16E-02	-5,98E-01	6,30E-03	**1,02E+00**	**2,73E-05**	*nifD*- NoN 14 dpi	NA	Calcium-binding protein (AHRD V3.3 *** A0A1B0WUT3_SOLHA)	GO:0005509
Solyc03g031450.3	1,58E-01	5,47E-01	-5,52E-01	4,32E-02	-3,88E-01	1,47E-01	**2,09E+00**	**1,75E-08**	*nifD*- NoN 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *-* AT1G61660.7)	GO:0046983
Solyc03g031890.3	3,18E-01	2,74E-01	-5,52E-01	6,26E-02	3,67E-01	2,07E-01	**3,12E+00**	**3,37E-11**	*nifD*- NoN 14 dpi	OX	Oxidative stress 3, putative isoform 2 (AHRD V3.3 *** A0A061GIQ6_THECC)	
Solyc12g056050.1	-2,62E-01	2,88E-01	-5,54E-01	2,99E-02	-4,10E-01	1,01E-01	**1,03E+00**	**2,24E-04**	*nifD*- NoN 14 dpi	C	LOW QUALITY:Starch synthase 1, chloroplastic/amyloplastic (AHRD V3.3 --* SSY1_WHEAT)	
Solyc03g118790.2	-7,42E-01	3,19E-02	-5,55E-01	1,02E-01	-5,45E-01	1,08E-01	**-1,13E+00**	**1,88E-03**	*nifD*- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9SU85_RICCO)	
Solyc05g007020.3	-2,37E-01	7,30E-02	-5,56E-01	1,79E-04	9,44E-02	4,64E-01	**1,25E+00**	**3,12E-10**	*nifD*- NoN 14 dpi	G	LOV/LOV protein (AHRD V3.3 *** E3WH16_SOLLC)	GO:0000155|GO:0000160
Solyc12g098800.2	-1,83E+00	8,49E-02	-5,58E-01	5,89E-01	-2,40E+00	2,67E-02	**-3,34E+00**	**3,01E-03**	*nifD*- NoN 14 dpi	CS	LOW QUALITY:Extensin (AHRD V3.3 --* Q9FSG0_NICSY)	GO:0005199|GO:0009664
Solyc06g068230.3	-1,13E+00	1,10E-02	-5,58E-01	1,88E-01	1,41E-01	7,35E-01	**-1,74E+00**	**2,70E-04**	*nifD*- NoN 14 dpi	H	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT1G15290.1)	GO:0005515
Solyc03g121240.1	-8,84E-01	9,48E-02	-5,60E-01	2,82E-01	1,39E-01	7,87E-01	**2,17E+00**	**2,43E-04**	*nifD*- NoN 14 dpi	DNA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein (AHRD V3.3 *** AT3G21330.1)	GO:0046983
Solyc06g074800.1	-7,48E-01	9,72E-06	-5,74E-01	2,73E-04	-3,41E-01	1,89E-02	**1,02E+00**	**7,08E-08**	*nifD*- NoN 14 dpi	DNA	LOW QUALITY:Zinc finger family protein (AHRD V3.3 *** B9HQP7_POPTR)	GO:0046872
Solyc12g011410.1	-8,96E-01	2,19E-02	-5,77E-01	1,28E-01	-8,13E-01	3,58E-02	**-1,32E+00**	**1,38E-03**	*nifD*- NoN 14 dpi	RNA	LOW QUALITY:tRNA-splicing ligase (DUF239) (AHRD V3.3 --* AT5G56530.2)	
Solyc02g088983.1	1,26E-01	8,48E-01	-5,79E-01	3,83E-01	-2,89E-01	6,61E-01	**-2,10E+00**	**3,50E-03**	*nifD*- NoN 14 dpi	DNA	LOW QUALITY:Arginine/serine-rich splicing factor, putative (AHRD V3.3 --* B9RNP5_RICCO)	GO:0003676|GO:0008270
Solyc11g006720.2	-5,80E-01	6,34E-02	-5,79E-01	6,37E-02	1,59E-01	6,00E-01	**2,05E+00**	**3,10E-07**	*nifD*- NoN 14 dpi	T	MYB-like transcription factor family protein (AHRD V3.3 *** G7ZYT0_MEDTR)	GO:0003677
Solyc01g107120.3	2,01E-01	6,55E-01	-5,80E-01	2,05E-01	9,44E-01	4,41E-02	**1,67E+00**	**8,95E-04**	*nifD*- NoN 14 dpi	NA	DUF936 family protein (AHRD V3.3 *** G7JEV5_MEDTR)	
Solyc11g012360.2	2,65E-01	3,09E-01	-5,84E-01	3,04E-02	3,33E-01	2,03E-01	**1,99E+00**	**2,99E-08**	*nifD*- NoN 14 dpi	TR	Tonoplast dicarboxylate transporter (AHRD V3.3 *** K4D641_SOLLC)	GO:0005215|GO:0006814|GO:0016020|GO:0055085
Solyc10g081880.2	-6,89E-01	1,06E-01	-5,85E-01	1,67E-01	-4,48E-01	2,87E-01	**-1,17E+00**	**8,85E-03**	*nifD*- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A118JSG8_CYNCS)	GO:0005515
Solyc05g055860.3	-6,84E-01	1,68E-01	-5,92E-01	2,31E-01	-1,13E+00	2,75E-02	**-2,48E+00**	**2,36E-05**	*nifD*- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *** D7L628_ARALL)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g080750.3	-3,42E-01	2,07E-01	-5,93E-01	3,40E-02	4,42E-01	1,08E-01	**1,72E+00**	**7,62E-07**	*nifD*- NoN 14 dpi	D	LURP-one-like protein (AHRD V3.3 *** AT1G53875.1)	
Solyc03g119590.1	5,25E-01	3,84E-01	-5,97E-01	3,24E-01	-2,08E-01	7,28E-01	**-2,30E+00**	**6,67E-04**	*nifD*- NoN 14 dpi	D	LOW QUALITY:NIMIN2c protein (AHRD V3.3 *** A0FJY4_TOBAC)	
Solyc07g055620.2	-4,04E-02	9,38E-01	-6,00E-01	2,52E-01	2,56E-01	6,21E-01	**-1,55E+00**	**5,65E-03**	*nifD*- NoN 14 dpi	D	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 *-* AT5G38350.1)	
Solyc06g075170.1	-5,29E-01	2,00E-01	-6,01E-01	1,48E-01	3,85E-01	3,48E-01	**1,53E+00**	**8,11E-04**	*nifD*- NoN 14 dpi	G	Senescence regulator (AHRD V3.3 *** A0A103XHC6_CYNCS)	
Solyc06g068890.1	-4,61E-01	2,36E-01	-6,04E-01	1,24E-01	6,23E-01	1,14E-01	**1,34E+00**	**1,58E-03**	*nifD*- NoN 14 dpi	D	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 --* AT5G63760.4)	

Solyc02g079280.3	-7,65E-01	2,03E-01	-6,07E-01	3,10E-01	-6,88E-01	2,51E-01	**-1,76E+00**	**5,97E-03**	*nifD*- NoN 14 dpi	T	MYB transcription factor (AHRD V3.3 *** A0A0U3IU11_MESCR)	GO:0003677
Solyc01g106820.3	1,02E-01	7,67E-01	-6,09E-01	8,66E-02	-2,44E-01	4,81E-01	**1,14E+00**	**2,68E-03**	*nifD*- NoN 14 dpi	DNA	Sterol regulatory element-binding protein site 2 protease, putative (AHRD V3.3 *** B9S7Z4_RICCO)	
Solyc01g109600.3	9,01E-02	5,31E-01	-6,14E-01	2,06E-04	5,29E-02	7,13E-01	**1,13E+00**	**2,25E-08**	*nifD*- NoN 14 dpi	T	BTB/POZ domain-containing protein (AHRD V3.3 *** A0A1D1XPT6_9ARAE)	
Solyc03g114350.1	-2,08E-03	9,92E-01	-6,17E-01	4,84E-03	3,71E-02	8,55E-01	**1,34E+00**	**4,63E-07**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:DUF1645 family protein (AHRD V3.3 *** G7J5G5_MEDTR)	
Solyc06g007580.1	-2,36E-01	5,73E-01	-6,18E-01	1,46E-01	1,09E+00	1,40E-02	**2,88E+00**	**2,12E-07**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:DUF506 family protein (AHRD V3.3 *** G7LF52_MEDTR)	
Solyc01g009560.1	5,07E-01	6,83E-01	-6,27E-01	6,14E-01	3,27E-01	7,92E-01	**-3,55E+00**	**7,79E-03**	*nifD*- NoN 14 dpi	G	Terminal flower 1-like protein (AHRD V3.3 *** A0A0S1LKM5_CHRMO)	
Solyc01g111950.3	6,43E-01	4,55E-01	-6,29E-01	4,65E-01	6,28E-02	9,42E-01	**-2,64E+00**	**4,56E-03**	*nifD*- NoN 14 dpi	PMI	Proline-rich receptor-like protein kinase PERK1 (AHRD V3.3 *** W9RKU6_9ROSA)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc08g077530.3	-5,40E-01	1,70E-01	-6,39E-01	1,07E-01	-1,54E-01	6,90E-01	**2,05E+00**	**1,32E-05**	*nifD*- NoN 14 dpi	CS	Beta-amylase (AHRD V3.3 *** K4CNB2_SOLLC)	GO:0000272|GO:0016161|GO:0005975|GO:0005975
Solyc09g056130.3	-1,67E-01	6,57E-01	-6,40E-01	9,77E-02	-6,48E-01	9,39E-02	**-1,63E+00**	**1,72E-04**	*nifD*- NoN 14 dpi	NA	Cellular retinaldehyde-binding/triple function, C-terminal (AHRD V3.3 *-* Q2HW59_MEDTR)	
Solyc04g072280.3	-5,75E-01	6,41E-01	-6,42E-01	6,03E-01	1,65E+00	1,87E-01	**3,82E+00**	**4,24E-03**	*nifD*- NoN 14 dpi	PMI	Laccase (AHRD V3.3 *** A0A022Q9N6_ERYGU)	GO:0005507|GO:0005507|GO:0016491|GO:0055114|GO:0005507|GO:0016491|GO:0055114
Solyc08g061060.2	1,06E-02	9,79E-01	-6,44E-01	1,19E-01	-8,82E-01	3,66E-02	**1,43E+00**	**1,42E-03**	*nifD*- NoN 14 dpi	D	Barwin-like endoglucanase (AHRD V3.3 *** A0A103XZL4_CYNCS)	
Solyc02g078510.3	-1,61E-01	6,54E-01	-6,51E-01	7,84E-02	2,71E-01	4,53E-01	**2,30E+00**	**7,76E-07**	*nifD*- NoN 14 dpi	C	Acylsugar acyltransferase 3 (AHRD V3.3 *-* A0A0B5JC18_SOLHA)	GO:0016747
Solyc01g109270.3	3,32E-02	9,73E-01	-6,54E-01	5,02E-01	-2,01E+00	4,64E-02	**-2,90E+00**	**5,62E-03**	*nifD*- NoN 14 dpi	E	electron transporter, putative (Protein of unknown function, DUF547) (AHRD V3.3 *** AT5G66600.9)	
Solyc06g066680.3	3,69E-01	5,22E-01	-6,58E-01	2,58E-01	1,55E-01	7,87E-01	**2,78E+00**	**4,49E-05**	*nifD*- NoN 14 dpi	TR	Mitochondrial carrier protein (AHRD V3.3 *** A0A0K9PC13_ZOSMR)	GO:0055085
Solyc06g082450.1	-1,04E+00	1,63E-02	-6,58E-01	1,17E-01	-7,99E-01	5,99E-02	**-1,41E+00**	**1,86E-03**	*nifD*- NoN 14 dpi	G	LOW QUALITY:ovate family protein	
Solyc07g053010.2	-6,10E-01	2,80E-02	-6,66E-01	1,74E-02	-8,36E-01	3,74E-03	**-1,10E+00**	**2,71E-04**	*nifD*- NoN 14 dpi	D	NBS-LRR type disease resistance protein (AHRD V3.3 *** Q19PJ0_POPTR)	GO:0043531
Solyc03g082520.1	9,47E-01	5,68E-02	-6,71E-01	1,70E-01	1,32E+00	1,03E-02	**2,49E+00**	**1,88E-05**	*nifD*- NoN 14 dpi	H	Small auxin up-regulated RNA36	GO:0009733
Solyc11g073270.1	-7,06E-01	1,75E-02	-6,71E-01	2,33E-02	-8,06E-02	7,74E-01	**-1,24E+00**	**1,50E-04**	*nifD*- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** A0A103XPT2_CYNCS)	GO:0005515
Solyc02g083835.1	-2,06E-01	3,65E-01	-6,72E-01	5,78E-03	1,83E-01	4,19E-01	**1,73E+00**	**3,43E-08**	*nifD*- NoN 14 dpi	T	Chaperone DnaJ-like protein (AHRD V3.3 *** A0A1C6ZYA6_MEDSA)	
Solyc09g090220.3	-9,24E-01	7,70E-03	-6,76E-01	4,41E-02	-7,88E-01	2,06E-02	**-1,02E+00**	**3,63E-03**	*nifD*- NoN 14 dpi	RNA	Pentatricopeptide repeat-containing protein (AHRD V3.3 *** D7L3A6_ARALL)	GO:0005515|GO:0008270|GO:0008270
Solyc09g007720.3	-6,78E-01	9,10E-02	-6,76E-01	9,19E-02	4,15E-01	2,93E-01	**1,49E+00**	**6,85E-04**	*nifD*- NoN 14 dpi	R	Ribosomal protein S7, mitochondrial (AHRD V3.3 --* RT07_BETVU)	
Solyc04g009290.1	-8,97E-01	9,03E-07	-6,78E-01	5,13E-05	-4,17E-01	6,17E-03	**-1,55E+00**	**2,85E-11**	*nifD*- NoN 14 dpi	D	Nbs-lrr resistance protein (AHRD V3.3 *** A0A061FZT5_THECC)	GO:0043531
Solyc03g115780.2	-1,77E+00	1,59E-02	-6,79E-01	3,30E-01	-9,06E-01	1,97E-01	**-2,27E+00**	**2,73E-03**	*nifD*- NoN 14 dpi	NA	APOLLO (AHRD V3.3 *** U5U5R8_9BRAS)	GO:0003676
Solyc06g072230.1	-6,25E-01	1,85E-02	-6,81E-01	1,10E-02	6,14E-01	2,04E-02	**1,30E+00**	**1,98E-05**	*nifD*- NoN 14 dpi	D	Kunitz trypsin inhibitor (AHRD V3.3 *** B8Y888_TOBAC)	GO:0004866
Solyc05g021535.1	-8,35E-01	2,18E-03	-6,82E-01	1,00E-02	-4,45E-01	8,10E-02	**-1,18E+00**	**5,91E-05**	*nifD*- NoN 14 dpi	T	calmodulin-binding transcription activator (AHRD V3.3 --* AT3G16940.3)	GO:0003677|GO:0005634
Solyc07g006880.1	5,62E-01	2,79E-01	-6,85E-01	1,89E-01	9,99E-01	6,02E-02	**2,04E+00**	**4,67E-04**	*nifD*- NoN 14 dpi	DNA	Zinc finger protein, putative (AHRD V3.3 *** B9T768_RICCO)	GO:0046872
Solyc09g008080.3	-3,32E-01	2,72E-01	-6,96E-01	2,63E-02	-2,00E-01	5,04E-01	**2,01E+00**	**3,34E-07**	*nifD*- NoN 14 dpi	R	Ribosomal protein S5/Elongation factor G/III/V family protein (AHRD V3.3 --* AT1G56070.3)	GO:0005515

Solyc06g082970.3	-7,51E-01	7,51E-02	-6,97E-01	9,73E-02	-3,79E-01	3,58E-01	**-1,14E+00**	**9,46E-03**	*nifD*- NoN 14 dpi	T	Chaperone DnaJ-domain superfamily protein (AHRD V3.3 *** A0A0F7H181_9ROSI)	
Solyc07g009430.1	-1,26E+00	9,18E-04	-6,97E-01	4,84E-02	-6,42E-03	9,85E-01	**1,23E+00**	**1,15E-03**	*nifD*- NoN 14 dpi	P	LOW QUALITY:F-box family protein (AHRD V3.3 *** AT1G19160.1)	GO:0005515
Solyc01g066290.2	-5,87E-01	7,58E-02	-6,99E-01	3,66E-02	-3,11E-01	3,35E-01	**1,01E+00**	**3,84E-03**	*nifD*- NoN 14 dpi	STR	LOW QUALITY:Xaa-Pro aminopeptidase 1 (AHRD V3.3 --* A0A199W6F4_ANACO)	
Solyc01g087800.2	1,12E+00	3,24E-01	-7,06E-01	5,33E-01	4,22E-01	7,09E-01	**4,51E+00**	**4,33E-04**	*nifD*- NoN 14 dpi	P	LOW QUALITY:Subtilisin-like protease (AHRD V3.3 *** O82777_SOLLC)	GO:0004252|GO:0006508
Solyc05g041200.3	8,23E-01	2,99E-01	-7,11E-01	3,68E-01	1,50E+00	6,38E-02	**3,19E+00**	**3,60E-04**	*nifD*- NoN 14 dpi	2M	4-hydroxyphenylpyruvate dioxygenase (AHRD V3.3 *** K4C0A1_SOLLC)	GO:0003868|GO:0009072|GO:0016701|GO:0055114
Solyc10g075150.2	2,42E+00	1,17E-01	-7,13E-01	6,37E-01	2,16E-01	8,86E-01	**4,43E+00**	**6,41E-03**	*nifD*- NoN 14 dpi	L	Non-specific lipid-transfer protein (AHRD V3.3 *** M1AVB3_SOLTU)	GO:0006869|GO:0008289
Solyc03g071570.3	-1,00E-01	8,82E-01	-7,21E-01	2,89E-01	-1,27E+00	6,72E-02	**-3,23E+00**	**5,22E-05**	*nifD*- NoN 14 dpi	CS	Pectate lyase (AHRD V3.3 *** K4BHI7_SOLLC)	
Solyc02g082450.3	4,45E-01	4,30E-01	-7,22E-01	2,05E-01	9,95E-01	8,46E-02	**2,10E+00**	**8,26E-04**	*nifD*- NoN 14 dpi	H	Auxin efflux carrier family protein (AHRD V3.3 *** AT2G17500.4)	GO:0016021|GO:0055085
Solyc07g063770.3	-2,22E+00	1,35E-02	-7,33E-01	3,90E-01	-6,51E-01	4,44E-01	**-2,77E+00**	**2,78E-03**	*nifD*- NoN 14 dpi	K	Serine/threonine-protein kinase (AHRD V3.3 *** A0A0V0IT75_SOLCH)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g071555.1	-8,51E-01	2,52E-02	-7,34E-01	5,07E-02	-8,82E-01	2,08E-02	**-1,51E+00**	**2,60E-04**	*nifD*- NoN 14 dpi	RNA	RNA binding protein (AHRD V3.3 --* A0A0K9NY52_ZOSMR)	GO:0000166|GO:0003676|GO:0003676
Solyc03g113240.3	2,80E-01	3,79E-01	-7,34E-01	2,68E-02	5,07E-01	1,17E-01	**1,45E+00**	**8,90E-05**	*nifD*- NoN 14 dpi	NA	transmembrane protein, putative (DUF1118) (AHRD V3.3 *** AT1G74730.1)	
Solyc12g019550.2	1,96E-01	7,05E-01	-7,38E-01	1,61E-01	-9,46E-01	7,57E-02	**2,95E+00**	**4,56E-06**	*nifD*- NoN 14 dpi	L	Lipase maturation factor 2 (AHRD V3.3 *** A0A1D1ZBR5_9ARAE)	
Solyc03g116290.2	7,09E-02	7,02E-01	-7,43E-01	4,16E-04	1,20E-01	5,18E-01	**1,98E+00**	**4,86E-11**	*nifD*- NoN 14 dpi	E	2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein, putative (AHRD V3.3 *** A0A061FWB6_THECC)	GO:0016491|GO:0055114
Solyc01g008800.2	-1,13E+00	2,09E-02	-7,44E-01	1,16E-01	-2,46E-01	5,94E-01	**-1,35E+00**	**6,46E-03**	*nifD*- NoN 14 dpi	D	disease resistance protein (TIR-NBS-LRR class) (AHRD V3.3 *** AT5G17680.1)	GO:0005515|GO:0005515|GO:0007165|GO:0005515|GO:0007165
Solyc06g005470.3	1,94E-01	3,10E-01	-7,45E-01	4,89E-04	6,32E-01	2,30E-03	**1,37E+00**	**9,89E-08**	*nifD*- NoN 14 dpi	NA	Metallothionein-like protein type 2 (AHRD V3.3 *** MT2Z_SOLLC)	GO:0046872
Solyc01g100460.3	1,20E-01	8,39E-01	-7,47E-01	2,13E-01	1,23E+00	4,60E-02	**4,01E+00**	**3,00E-07**	*nifD*- NoN 14 dpi	T	BZIP transcription factor family protein (AHRD V3.3 *** B9GSS6_POPTR)	GO:0003700|GO:0006355|GO:0043565
Solyc01g095080.3	-2,65E+00	2,61E-03	-7,48E-01	3,56E-01	2,06E+00	1,55E-02	**2,41E+00**	**5,58E-03**	*nifD*- NoN 14 dpi	H	1-aminocyclopropane-1-carboxylic acid synthase-2	GO:0003824|GO:0003824|GO:0009058|GO:0030170|GO:0003824|GO:0009058|GO:0030170
Solyc02g093160.3	-1,20E+00	1,25E-01	-7,49E-01	3,33E-01	-8,26E-01	2,86E-01	**-2,57E+00**	**2,24E-03**	*nifD*- NoN 14 dpi	NA	Filament-like plant protein (AHRD V3.3 *** A0A072UQ33_MEDTR)	
Solyc07g054880.3	-7,24E-01	3,40E-03	-7,50E-01	2,54E-03	-6,34E-01	9,03E-03	**1,04E+00**	**8,67E-05**	*nifD*- NoN 14 dpi	D	methylketone synthase Ie	
Solyc05g015850.3	2,94E-01	5,55E-01	-7,51E-01	1,40E-01	1,37E+00	1,00E-02	**2,16E+00**	**1,77E-04**	*nifD*- NoN 14 dpi	T	WRKY transcription factor 75	GO:0003700|GO:0006355|GO:0043565
Solyc02g030215.1	-1,40E+00	6,06E-02	-7,51E-01	3,01E-01	-7,09E-01	3,29E-01	**-2,23E+00**	**4,24E-03**	*nifD*- NoN 14 dpi	DNA	INO80 complex subunit D-like protein (AHRD V3.3 --* AT2G31600.6)	
Solyc01g110920.3	-5,79E-01	9,98E-02	-7,53E-01	3,56E-02	5,76E-02	8,66E-01	**1,13E+00**	**2,67E-03**	*nifD*- NoN 14 dpi	H	Small auxin up-regulated RNA26	GO:0009733
Solyc05g008440.2	-1,60E-01	2,38E-01	-7,54E-01	5,90E-06	2,05E-01	1,35E-01	**1,01E+00**	**4,88E-08**	*nifD*- NoN 14 dpi	NA	Sarcoplasmic reticulum histidine-rich calcium-binding protein (AHRD V3.3 *-* B6TJG2_MAIZE)	
Solyc10g084070.1	1,63E-01	7,37E-01	-7,57E-01	1,28E-01	8,00E-01	1,09E-01	**1,65E+00**	**2,11E-03**	*nifD*- NoN 14 dpi	CS	LOW QUALITY:Endoglucanase (AHRD V3.3 --* A0A022RID5_ERYGU)	
Solyc03g044580.1	-1,68E-01	7,64E-01	-7,63E-01	1,81E-01	-1,53E+00	1,05E-02	**-2,70E+00**	**4,78E-05**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:transmembrane protein (AHRD V3.3 -** AT2G23440.1)	GO:0048364
Solyc11g044910.2	1,06E+00	9,60E-02	-7,64E-01	2,24E-01	1,56E+00	1,74E-02	**3,02E+00**	**4,34E-05**	*nifD*- NoN 14 dpi	CS	Beta-D-xylosidase family protein (AHRD V3.3 *** B9HWX2_POPTR)	GO:0004553|GO:0005975

Solyc04g063350.3	1,83E+00	5,02E-02	-7,79E-01	3,89E-01	1,66E+00	7,36E-02	**3,07E+00**	**1,96E-03**	*nifD*- NoN 14 dpi	C	Pyruvate dehydrogenase E1 component subunit alpha (AHRD V3.3 *** A0A178WNY2_ARATH)	GO:0008152|GO:0016624
Solyc09g014280.1	-3,38E-01	2,70E-02	-7,87E-01	1,03E-05	-1,30E-01	3,75E-01	**1,18E+00**	**1,24E-08**	*nifD*- NoN 14 dpi	S	LOW QUALITY:HXXXD-type acyl-transferase family protein (AHRD V3.3 *** AT5G01210.1)	GO:0016747
Solyc01g108630.3	-1,46E+00	1,13E-02	-7,87E-01	1,54E-01	-1,05E+00	6,08E-02	**-1,93E+00**	**1,32E-03**	*nifD*- NoN 14 dpi	N	nii1 nitrite reductase	GO:0016491|GO:0020037|GO:0051536|GO:0055114|GO:0016491|GO:0055114|GO:0016491|GO:0055114
Solyc10g050220.2	-3,46E-02	9,02E-01	-7,88E-01	8,74E-03	5,37E-01	6,43E-02	**1,04E+00**	**8,86E-04**	*nifD*- NoN 14 dpi	G	cold regulated protein 27 (AHRD V3.3 *** AT5G42900.2)	
Solyc09g055320.1	-6,13E-01	1,12E-01	-7,88E-01	4,38E-02	-5,92E-01	1,24E-01	**-1,17E+00**	**4,12E-03**	*nifD*- NoN 14 dpi	E	LOW QUALITY:Oxygen-evolving enhancer protein 2, chloroplastic (AHRD V3.3 --* PSBP_HELAN)	
Solyc07g062670.1	-6,45E-01	3,36E-01	-7,94E-01	2,38E-01	-7,58E-01	2,59E-01	**3,75E+00**	**5,44E-06**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:Clavata3/ESR (CLE) gene family member (AHRD V3.3 --* A0A072TRR8_MEDTR)	
Solyc05g046290.3	6,61E-02	9,09E-01	-7,99E-01	1,75E-01	3,02E-01	6,03E-01	**1,84E+00**	**3,50E-03**	*nifD*- NoN 14 dpi	CS	Xyloglucan endotransglucosylase/hydrolase (AHRD V3.3 *** K4C0W2_SOLLC)	GO:0004553|GO:0005975|GO:0005618|GO:0006073|GO:0016762|GO:0048046|GO:0005618|GO:0006073|GO:0016762|GO:0048046
Solyc01g091700.3	-1,43E+00	5,29E-07	-8,01E-01	1,01E-03	-2,47E-02	9,10E-01	**1,53E+00**	**1,69E-07**	*nifD*- NoN 14 dpi	P	F-box family protein (AHRD V3.3 *** B9IC61_POPTR)	GO:0005515
Solyc04g071770.3	1,67E-01	7,68E-01	-8,05E-01	1,64E-01	2,08E-01	7,14E-01	**2,27E+00**	**4,24E-04**	*nifD*- NoN 14 dpi	H	Ethylene-responsive transcription factor (AHRD V3.3 *** W9RA19_9ROSA)	GO:0003677|GO:0003700|GO:0006355|GO:0003700|GO:0006355
Solyc06g054327.1	7,30E-01	1,32E-01	-8,06E-01	9,78E-02	6,51E-01	1,77E-01	**1,42E+00**	**5,56E-03**	*nifD*- NoN 14 dpi	RNA	maturase K (AHRD V3.3 --* ATCG00040.1)	
Solyc02g030464.1	5,66E-02	9,07E-01	-8,07E-01	1,04E-01	1,15E+00	2,36E-02	**1,40E+00**	**7,16E-03**	*nifD*- NoN 14 dpi	CS	Glucan endo-1,3-beta-glucosidase 8 (AHRD V3.3 --* E138_ARATH)	
Solyc02g081340.3	5,33E-01	5,39E-01	-8,12E-01	3,52E-01	6,36E-02	9,41E-01	**-2,93E+00**	**2,12E-03**	*nifD*- NoN 14 dpi	STR	Glutathione S-transferase (AHRD V3.3 *** E1AWJ7_CAPAN)	GO:0005515
Solyc02g072150.3	-6,87E-01	7,83E-03	-8,18E-01	2,02E-03	-4,25E-01	8,60E-02	**1,01E+00**	**2,60E-04**	*nifD*- NoN 14 dpi	C	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *** B9S8D6_RICCO)	GO:0003824|GO:0005992
Solyc07g053360.3	-6,94E-01	2,95E-01	-8,19E-01	2,19E-01	1,01E+00	1,33E-01	**1,98E+00**	**5,30E-03**	*nifD*- NoN 14 dpi	STR	Late embryogenesis abundant domain-containing family protein (AHRD V3.3 *** B9IQP9_POPTR)	
Solyc11g007807.1	-1,16E+00	3,21E-02	-8,24E-01	1,19E-01	-2,94E-01	5,70E-01	**-1,61E+00**	**4,06E-03**	*nifD*- NoN 14 dpi	RNA	Ribonucleases P/MRP protein subunit POP1 (AHRD V3.3 *-* A0A0B2R1D7_GLYSO)	GO:0001682|GO:0004526
Solyc04g078910.3	-1,77E-02	9,56E-01	-8,24E-01	1,48E-02	9,97E-01	4,01E-03	**1,38E+00**	**1,76E-04**	*nifD*- NoN 14 dpi	OX	Thioredoxin, putative (AHRD V3.3 *** B9R7C2_RICCO)	GO:0006662|GO:0015035|GO:0045454|GO:0045454|GO:0045454
Solyc01g107780.3	-1,21E+00	1,91E-05	-8,25E-01	1,44E-03	3,76E-01	1,16E-01	**1,08E+00**	**8,26E-05**	*nifD*- NoN 14 dpi	C	Glycosyltransferase (AHRD V3.3 *** K4B2Z4_SOLLC)	GO:0008152|GO:0016758
Solyc04g080720.3	-9,65E-01	9,01E-05	-8,35E-01	4,61E-04	9,17E-01	1,64E-04	**1,57E+00**	**5,57E-08**	*nifD*- NoN 14 dpi	NA	Transferase family protein (AHRD V3.3 *-* B9H4E9_POPTR)	GO:0016747
Solyc10g076220.2	-8,83E-01	3,59E-04	-8,35E-01	6,35E-04	-4,86E-01	3,23E-02	**-1,28E+00**	**3,02E-06**	*nifD*- NoN 14 dpi	OX	Peroxidase (AHRD V3.3 *** A0A0D9X2X2_9ORYZ)	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc03g111620.1	-6,79E-01	1,58E-01	-8,36E-01	8,53E-02	1,26E-01	7,89E-01	**1,42E+00**	**5,39E-03**	*nifD*- NoN 14 dpi	CS	LOW QUALITY:S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 *** AT1G24480.1)	GO:0008152|GO:0008168
Solyc07g053790.2	-2,52E-01	7,43E-01	-8,47E-01	2,75E-01	-9,17E-01	2,37E-01	**-2,99E+00**	**5,59E-04**	*nifD*- NoN 14 dpi	K	targeting protein for XKLP2 (AHRD V3.3 *** AT1G03780.2)	GO:0005819|GO:0005874|GO:0032147|GO:0060236
Solyc02g014187.1	-1,22E+00	1,52E-02	-8,53E-01	8,03E-02	-4,52E-01	3,44E-01	**-1,35E+00**	**8,00E-03**	*nifD*- NoN 14 dpi	NA	Sacsin (AHRD V3.3 *-* A0A0B0NEN2_GOSAR)	
Solyc06g068910.3	-9,19E-01	2,71E-03	-8,55E-01	4,82E-03	-3,25E-01	2,52E-01	**-1,00E+00**	**1,28E-03**	*nifD*- NoN 14 dpi	S	receptor-like kinase 1 (AHRD V3.3 *** AT1G48480.1)	GO:0004672|GO:0005524|GO:0006468|GO:0005515|GO:0005515
Solyc05g016380.3	-6,62E-01	3,00E-01	-8,55E-01	1,84E-01	-7,80E-01	2,24E-01	**-2,04E+00**	**3,12E-03**	*nifD*- NoN 14 dpi	P	Rhomboid-like protein (AHRD V3.3 *-* I3SPB7_MEDTR)	
Solyc06g083710.2	-1,64E+00	2,77E-02	-8,55E-01	2,36E-01	-2,52E-01	7,24E-01	**-2,30E+00**	**3,07E-03**	*nifD*- NoN 14 dpi	NA	DENN domain-containing protein 5B (AHRD V3.3 *** A0A0B2PJ42_GLYSO)	
Solyc05g010775.1	-7,84E-01	3,65E-03	-8,56E-01	1,76E-03	-5,25E-01	4,20E-02	**-1,22E+00**	**3,60E-05**	*nifD*- NoN 14 dpi	K	CDK-activating kinase 1AT (AHRD V3.3 --* AT4G28980.3)	

Solyc03g025180.2	-7,62E-01	5,09E-02	-8,59E-01	2,93E-02	-2,10E-01	5,78E-01	**1,11E+00**	**6,11E-03**	*nifD*- NoN 14 dpi	2M	LOW QUALITY:Isoflavone-7-O-methyltransferase 8 (AHRD V3.3 --* 7OMT8_MEDSA)	
Solyc01g095030.3	-8,41E-01	3,01E-07	-8,62E-01	1,98E-07	-7,61E-01	1,54E-06	**-1,02E+00**	**8,64E-09**	*nifD*- NoN 14 dpi	T	Myb family transcription factor family protein (AHRD V3.3 *** B9I8P3_POPTR)	GO:0003677
Solyc07g052960.2	-2,45E-02	9,55E-01	-8,67E-01	5,27E-02	-4,38E-01	3,14E-01	**-2,61E+00**	**1,87E-06**	*nifD*- NoN 14 dpi	T	GRAS family TF	
Solyc12g005280.2	-7,95E-02	8,90E-01	-8,77E-01	1,37E-01	1,96E-01	7,35E-01	**-2,58E+00**	**1,24E-04**	*nifD*- NoN 14 dpi	RNA	tRNA (guanine(37)-N1)-methyltransferase (AHRD V3.3 *** K4DB66_SOLLC)	GO:0009019|GO:0030488
Solyc10g079300.2	-1,01E+00	3,40E-02	-8,83E-01	6,17E-02	-1,24E+00	1,07E-02	**-1,41E+00**	**4,49E-03**	*nifD*- NoN 14 dpi	TR	Calcium-transporting ATPase (AHRD V3.3 *** M1AEH1_SOLTU)	GO:0000166|GO:0000166|GO:0046872|GO:0000166|GO:0046872
Solyc08g005120.3	-5,40E-01	3,38E-02	-8,90E-01	1,05E-03	-1,03E+00	2,35E-04	**1,17E+00**	**5,14E-05**	*nifD*- NoN 14 dpi	D	Cinnamoyl-CoA reductase-like protein (AHRD V3.3 *** G7KDR3_MEDTR)	
Solyc08g068710.1	-1,75E+00	1,74E-04	-8,92E-01	3,45E-02	4,81E-01	2,40E-01	**1,20E+00**	**6,02E-03**	*nifD*- NoN 14 dpi	STR	Tyramine n-hydroxycinnamoyl transferase (AHRD V3.3 *** Q5D8C0_CAPAN)	GO:0008080
Solyc04g071140.3	-2,78E-01	1,58E-01	-9,04E-01	7,23E-05	-1,67E-01	3,91E-01	**1,00E+00**	**1,92E-05**	*nifD*- NoN 14 dpi	AM	Serine decarboxylase (AHRD V3.3 *** SDC1_ARATH)	GO:0003824|GO:0016831|GO:0016831
Solyc09g010240.2	-1,50E-01	5,78E-01	-9,07E-01	2,16E-03	-6,27E-01	2,62E-02	**1,41E+00**	**1,50E-05**	*nifD*- NoN 14 dpi	G	Embryo defective 2735 (AHRD V3.3 *-* U5U071_PHAVU)	
Solyc09g014520.3	-9,66E-01	1,55E-02	-9,10E-01	2,17E-02	5,08E-01	1,84E-01	**1,20E+00**	**3,46E-03**	*nifD*- NoN 14 dpi	E	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** K4CRS9_SOLLC)	GO:0009765|GO:0016020
Solyc07g005520.1	-1,44E-01	4,82E-01	-9,45E-01	8,02E-05	-2,57E-03	9,90E-01	**1,05E+00**	**1,96E-05**	*nifD*- NoN 14 dpi	T	BTB/POZ domain-containing protein (AHRD V3.3 *** W9QLB4_9ROSA)	GO:0005515|GO:0051260|GO:0051260
Solyc00g007160.2	-9,17E-01	1,15E-01	-9,51E-01	1,02E-01	-6,24E-01	2,76E-01	**-2,46E+00**	**1,74E-04**	*nifD*- NoN 14 dpi	NA	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-* A0A151SHE2_CAJCA)	
Solyc06g068985.1	-1,05E+00	2,04E-02	-9,53E-01	3,41E-02	-8,75E-01	5,01E-02	**-1,31E+00**	**4,92E-03**	*nifD*- NoN 14 dpi	K	Kinase family protein (AHRD V3.3 *-* B9IEA9_POPTR)	
Solyc04g050520.3	-1,16E+00	3,68E-02	-9,99E-01	6,81E-02	-9,86E-01	7,16E-02	**-1,54E+00**	**6,84E-03**	*nifD*- NoN 14 dpi	P	Translational activator GCN1-like protein (AHRD V3.3 *** A0A072U5F0_MEDTR)	GO:0005488|GO:0006417|GO:0019887|GO:0019901|GO:0033554|GO:0033674|GO:0043022|GO:0006417|GO:0019887|GO:0019901|GO:0033554|GO:0033674|GO:0043022
Solyc04g072605.1	-2,47E-01	6,83E-01	-1,00E+00	1,06E-01	-5,09E-01	4,02E-01	**-2,42E+00**	**4,22E-04**	*nifD*- NoN 14 dpi	C	ATP-dependent 6-phosphofructokinase (AHRD V3.3 *** K4BTP5_SOLLC)	GO:0003872|GO:0006002|GO:0006096|GO:0003872|GO:0006096|GO:0003872|GO:0006096
Solyc03g097570.3	-4,14E-01	4,78E-01	-1,01E+00	9,10E-02	-5,12E-01	3,81E-01	**-2,77E+00**	**5,42E-05**	*nifD*- NoN 14 dpi	TR	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJH4_SOLLC)	GO:0016021
Solyc03g111140.3	7,24E-01	3,32E-01	-1,02E+00	1,78E-01	1,55E+00	4,42E-02	**3,80E+00**	**2,15E-05**	*nifD*- NoN 14 dpi	C	Malate synthase (AHRD V3.3 *** K4BJX7_SOLLC)	GO:0003824|GO:0004474|GO:0006097|GO:0004474|GO:0006097
Solyc03g083190.2	-8,90E-01	3,73E-02	-1,03E+00	1,73E-02	-9,84E-01	2,24E-02	**-1,18E+00**	**7,16E-03**	*nifD*- NoN 14 dpi	DNA	gamma-irradiation and mitomycin c induced 1 (AHRD V3.3 *-* AT5G24280.3)	
Solyc09g082870.2	-1,86E+00	1,08E-01	-1,03E+00	3,63E-01	-1,98E+00	8,84E-02	**-3,22E+00**	**7,81E-03**	*nifD*- NoN 14 dpi	TR	Calcium-transporting ATPase (AHRD V3.3 *** M1DTS0_SOLTU)	GO:0000166|GO:0000166|GO:0046872|GO:0000166|GO:0046872
Solyc10g083690.3	-6,62E-01	4,23E-05	-1,04E+00	3,68E-08	9,46E-02	4,88E-01	**1,50E+00**	**2,32E-11**	*nifD*- NoN 14 dpi	CYTP450	Cytochrome P450 (AHRD V3.3 *** Q8H0I7_PETHY)	GO:0005506|GO:0016705|GO:0020037|GO:0055114|GO:0016705|GO:0055114|GO:0016705|GO:0055114
Solyc09g091510.3	-1,22E+00	1,64E-01	-1,05E+00	2,32E-01	-1,09E-01	9,00E-01	**-3,33E+00**	**6,16E-04**	*nifD*- NoN 14 dpi	2M	chalcone synthase 1	GO:0003824|GO:0008152|GO:0009058|GO:0016746|GO:0009058|GO:0016746
Solyc05g005750.3	-6,45E-01	8,06E-05	-1,05E+00	4,50E-08	-1,70E-01	2,28E-01	**1,02E+00**	**8,56E-08**	*nifD*- NoN 14 dpi	C	Trehalose-6-phosphate synthase, putative (AHRD V3.3 *** B9S4L7_RICCO)	GO:0003824|GO:0005992
Solyc12g044330.2	-1,10E+00	3,31E-05	-1,06E+00	4,85E-05	-4,63E-01	4,40E-02	**2,09E+00**	**5,89E-10**	*nifD*- NoN 14 dpi	TR	tonoplast intrinsic protein 2.1	GO:0005215|GO:0006810|GO:0016020
Solyc07g047940.3	-7,48E-01	1,25E-03	-1,07E+00	2,11E-05	-4,36E-01	4,48E-02	**1,12E+00**	**1,20E-05**	*nifD*- NoN 14 dpi	T	Zinc finger transcription factor 49	GO:0000166|GO:0003676|GO:0003676
Solyc02g084130.3	-1,15E+00	3,78E-02	-1,08E+00	4,88E-02	7,12E-01	1,85E-01	**2,09E+00**	**4,89E-04**	*nifD*- NoN 14 dpi	DNA	uridine kinase-like 5 (AHRD V3.3 --* AT3G27440.3)	
Solyc12g096840.2	-1,80E+00	7,36E-02	-1,08E+00	2,73E-01	1,24E+00	2,12E-01	**4,04E+00**	**2,99E-04**	*nifD*- NoN 14 dpi	STR	Tyramine N-feruloyltransferase 4/11, putative (AHRD V3.3 *** B9T0B8_RICCO)	GO:0008080

Solyc01g094050.1	-1,72E+00	3,26E-02	-1,09E+00	1,63E-01	-1,24E+00	1,14E-01	**-2,18E+00**	**7,98E-03**	*nifD*- NoN 14 dpi	D	beige/BEACH domain protein (AHRD V3.3 *-* AT3G60920.2)	
Solyc03g097050.3	-9,69E-01	9,97E-02	-1,12E+00	5,93E-02	-1,20E+00	4,39E-02	**-2,00E+00**	**1,63E-03**	*nifD*- NoN 14 dpi	CS	Cellulose synthase-like protein (AHRD V3.3 *** L0ATQ4_POPTO)	GO:0016020|GO:0016760|GO:0030244
Solyc10g079660.2	-7,21E-01	3,31E-01	-1,12E+00	1,34E-01	-1,57E+00	4,05E-02	**-2,03E+00**	**9,78E-03**	*nifD*- NoN 14 dpi	STR	bHLH transcription factor 067	GO:0003677|GO:0005488|GO:0005488
Solyc03g059090.1	-1,22E+00	9,12E-02	-1,14E+00	1,15E-01	-9,20E-01	1,99E-01	**-2,25E+00**	**3,46E-03**	*nifD*- NoN 14 dpi	R	Ribosomal protein L32e (AHRD V3.3 -** AT5G46430.2)	
Solyc12g096500.2	-1,28E+00	3,31E-09	-1,14E+00	2,69E-08	-2,61E-01	8,47E-02	**1,26E+00**	**4,12E-09**	*nifD*- NoN 14 dpi	G	CONSTANS-like protein (AHRD V3.3 *** Q0MQL9_SOLTU)	GO:0005515|GO:0005622|GO:0008270|GO:0005622|GO:0008270
Solyc10g085140.1	4,58E-01	5,66E-01	-1,17E+00	1,50E-01	1,78E-01	8,23E-01	**2,60E+00**	**2,80E-03**	*nifD*- NoN 14 dpi	DNA	Alkyl transferase (AHRD V3.3 *-* K7X479_SOLLC)	GO:0016765
Solyc11g007990.2	-2,94E-01	4,05E-01	-1,19E+00	1,99E-03	1,43E-01	6,82E-01	**1,23E+00**	**1,54E-03**	*nifD*- NoN 14 dpi	C	chloroplast malate dehydrogenase (mdh)	GO:0003824|GO:0005975|GO:0016616|GO:0055114|GO:0006108|GO:0016615|GO:0055114|GO:0006108|GO:0016615|GO:0055114
Solyc06g069660.2	-6,20E-01	3,62E-01	-1,20E+00	8,45E-02	-9,30E-01	1,76E-01	**-1,99E+00**	**6,20E-03**	*nifD*- NoN 14 dpi	CS	Formin-like protein (AHRD V3.3 *-* A0A068VCP1_COFCA)	GO:0005515
Solyc02g092517.1	-1,16E+00	8,97E-02	-1,20E+00	7,88E-02	-1,60E+00	2,21E-02	**-2,23E+00**	**2,25E-03**	*nifD*- NoN 14 dpi	DNA	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A151THR9_CAJCA)	
Solyc02g085745.1	-3,66E-01	3,06E-01	-1,20E+00	2,03E-03	-1,55E+00	1,59E-04	**1,36E+00**	**6,45E-04**	*nifD*- NoN 14 dpi	P	Rhomboid-like protein (AHRD V3.3 *** K4BB87_SOLLC)	GO:0004252|GO:0016021
Solyc12g013620.2	-1,81E+00	9,45E-07	-1,21E+00	2,23E-04	2,61E-01	3,63E-01	**1,51E+00**	**1,36E-05**	*nifD*- NoN 14 dpi	H	jasmonic acid 2	GO:0003677|GO:0006355
Solyc03g098680.3	9,29E-01	3,92E-01	-1,22E+00	2,63E-01	2,44E+00	3,08E-02	**4,02E+00**	**8,67E-04**	*nifD*- NoN 14 dpi	D	Kunitz trypsin inhibitor (AHRD V3.3 *** Q4W181_POPTN)	GO:0004866
Solyc03g083870.3	-1,36E+00	8,61E-02	-1,23E+00	1,18E-01	3,38E-01	6,61E-01	**2,12E+00**	**9,76E-03**	*nifD*- NoN 14 dpi	CS	Pectinesterase (AHRD V3.3 *** K4BIG2_SOLLC)	GO:0004857|GO:0005618|GO:0030599|GO:0042545|GO:0005618|GO:0030599|GO:0042545
Solyc03g118410.3	-1,00E+00	2,25E-04	-1,25E+00	1,41E-05	-9,81E-01	2,89E-04	**1,24E+00**	**1,53E-05**	*nifD*- NoN 14 dpi	L	Acyl carrier protein (AHRD V3.3 *** Q672Q9_SOLLC)	GO:0006633
Solyc03g113340.3	-5,59E-01	5,53E-02	-1,25E+00	1,31E-04	-5,82E-01	4,66E-02	**1,70E+00**	**2,06E-06**	*nifD*- NoN 14 dpi	PMI	Nodulin-like / Major Facilitator Superfamily protein (AHRD V3.3 *** AT1G74780.1)	
Solyc02g067280.1	-1,19E+00	6,72E-02	-1,26E+00	5,32E-02	-3,32E-01	5,98E-01	**-2,48E+00**	**4,84E-04**	*nifD*- NoN 14 dpi	D	LOW QUALITY:RING/U-box superfamily protein (AHRD V3.3 *-* AT3G61180.1)	GO:0005515|GO:0008270
Solyc08g068280.1	-6,96E-01	3,22E-01	-1,29E+00	7,24E-02	9,67E-01	1,73E-01	**-1,96E+00**	**8,47E-03**	*nifD*- NoN 14 dpi	STR	Tyramine N-feruloyltransferase 4/11, putative (AHRD V3.3 *** B9T0B8_RICCO)	GO:0008080
Solyc01g104413.1	-1,54E+00	3,28E-02	-1,30E+00	6,94E-02	-2,98E-01	6,67E-01	**-2,45E+00**	**1,39E-03**	*nifD*- NoN 14 dpi	RNA	Pre-mRNA-processing-splicing factor (AHRD V3.3 --* AT1G80070.1)	
Solyc02g090600.1	-1,54E+00	9,17E-02	-1,30E+00	1,52E-01	-2,50E-01	7,79E-01	**-3,02E+00**	**2,04E-03**	*nifD*- NoN 14 dpi	T	DNA-directed RNA polymerase II subunit RPB1-like protein (AHRD V3.3 --* AT3G50610.2)	GO:0048364
Solyc06g068270.3	-2,98E-01	5,38E-01	-1,36E+00	8,62E-03	-8,64E-01	8,17E-02	**1,49E+00**	**4,36E-03**	*nifD*- NoN 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G49390.1)	GO:0016491|GO:0055114
Solyc05g053550.3	-1,79E+00	5,71E-02	-1,36E+00	1,41E-01	-5,40E-01	5,53E-01	**-5,40E+00**	**2,49E-06**	*nifD*- NoN 14 dpi	2M	chalcone synthase 2	GO:0003824|GO:0008152|GO:0009058|GO:0016746|GO:0009058|GO:0016746
Solyc03g119930.1	-7,84E-01	9,06E-04	-1,40E+00	4,39E-07	8,75E-01	2,92E-04	**1,05E+00**	**3,12E-05**	*nifD*- NoN 14 dpi	TR	Sulfate transporter, putative (AHRD V3.3 *** B9RUY1_RICCO)	GO:0015098|GO:0015689|GO:0015098|GO:0015689|GO:0016021|GO:0015098|GO:0015689|GO:0016021
Solyc01g006310.3	-8,50E-01	2,96E-02	-1,40E+00	8,13E-04	9,51E-01	1,61E-02	**1,45E+00**	**5,87E-04**	*nifD*- NoN 14 dpi	OX	SlPeroxidase	GO:0004601|GO:0006979|GO:0020037|GO:0055114|GO:0004601|GO:0042744|GO:0004601|GO:0042744
Solyc01g006050.2	-1,47E-01	6,03E-01	-1,48E+00	1,62E-05	5,77E-01	4,90E-02	**2,09E+00**	**6,27E-08**	*nifD*- NoN 14 dpi	NA	LOW QUALITY:Transmembrane protein 45B (AHRD V3.3 *** A0A151U0K4_CAJCA)	
Solyc04g051540.3	-5,12E-01	4,34E-01	-1,48E+00	3,01E-02	-1,07E-01	8,69E-01	**-2,20E+00**	**2,13E-03**	*nifD*- NoN 14 dpi	T	WRKY transcription factor 13	GO:0003700|GO:0006355|GO:0043565
Solyc07g062903.1	-7,15E-01	1,95E-01	-1,49E+00	1,03E-02	-5,66E-01	3,02E-01	**-1,55E+00**	**7,68E-03**	*nifD*- NoN 14 dpi	NA	Protein yippee-like (AHRD V3.3 --* A0A0V0H400_SOLCH)	

Solyc11g006710.2	-1,29E+00	1,95E-03	-1,59E+00	2,45E-04	3,08E-01	4,18E-01	**1,07E+00**	**8,04E-03**	*nifD*- NoN 14 dpi	AM	Cationic amino acid transporter, putative (AHRD V3.3 *** B9RPW6_RICCO)	GO:0003333|GO:0015171|GO:0016020
Solyc01g099580.2	-1,83E+00	4,04E-02	-1,69E+00	5,63E-02	1,86E+00	3,76E-02	**2,47E+00**	**7,20E-03**	*nifD*- NoN 14 dpi	S	Cysteine/Histidine-rich C1 domain family protein, putative (AHRD V3.3 *-* A0A061EYK7_THECC)	
Solyc02g092550.3	-1,44E+00	1,48E-04	-1,71E+00	1,71E-05	9,28E-01	8,34E-03	**1,23E+00**	**7,94E-04**	*nifD*- NoN 14 dpi	G	LOB domain-containing protein, putative (AHRD V3.3 *** B9SGY6_RICCO)	
Solyc04g005180.3	-1,73E+00	3,90E-02	-1,77E+00	3,55E-02	-1,82E+00	3,07E-02	**-2,82E+00**	**1,54E-03**	*nifD*- NoN 14 dpi	AM	Isochorismate synthase, chloroplastic (AHRD V3.3 *-* ICS_CATRO)	
Solyc08g007805.1	-8,10E-01	4,63E-01	-1,78E+00	1,14E-01	-9,89E-01	3,71E-01	**-3,30E+00**	**5,52E-03**	*nifD*- NoN 14 dpi	E	NADH dehydrogenase 1 alpha subcomplex subunit 8 (AHRD V3.3 *-* A0A0K9PKB1_ZOSMR)	
Solyc01g066270.3	-1,33E+00	3,63E-02	-1,78E+00	6,45E-03	4,91E-01	4,22E-01	**1,72E+00**	**8,38E-03**	*nifD*- NoN 14 dpi	DNA	LOW QUALITY:AT-hook motif nuclear-localized protein 1 (AHRD V3.3 --* AT4G12080.1)	
Solyc01g097280.2	-3,81E-01	5,32E-01	-1,79E+00	6,29E-03	1,34E+00	3,48E-02	**2,06E+00**	**2,09E-03**	*nifD*- NoN 14 dpi	D	Pathogenesis-related protein PR-4 (AHRD V3.3 *** PR4_PRUPE)	GO:0008061|GO:0042742|GO:0050832|GO:0042742|GO:0050832
Solyc00g136560.3	1,60E-02	9,77E-01	-1,80E+00	2,53E-03	5,53E-01	3,13E-01	**2,66E+00**	**3,90E-05**	*nifD*- NoN 14 dpi	DNA	Alkyl transferase (AHRD V3.3 *** K7X479_SOLLC)	GO:0016765
Solyc03g114080.2	-1,09E+00	1,51E-01	-1,92E+00	1,52E-02	-2,55E-01	7,32E-01	**-2,30E+00**	**4,45E-03**	*nifD*- NoN 14 dpi	PMI	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** A0A061G0X7_THECC)	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc10g018190.2	-6,91E-01	4,19E-01	-1,98E+00	2,67E-02	-7,31E-01	3,93E-01	**-3,21E+00**	**7,68E-04**	*nifD*- NoN 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT5G24530.1)	GO:0016491|GO:0055114
Solyc02g071430.3	-1,19E-01	8,81E-01	-2,14E+00	1,18E-02	2,12E+00	1,22E-02	**2,47E+00**	**4,28E-03**	*nifD*- NoN 14 dpi	H	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein (AHRD V3.3 *** AT1G17010.1)	GO:0016491|GO:0055114
Solyc05g009720.3	-1,59E+00	2,85E-04	-2,15E+00	5,73E-06	4,03E-01	2,97E-01	**1,30E+00**	**2,08E-03**	*nifD*- NoN 14 dpi	S	Two-component response regulator (AHRD V3.3 *** W9RG69_9ROSA)	GO:0003677
Solyc10g050510.1	-1,79E+00	5,78E-03	-2,21E+00	9,64E-04	-1,13E+00	6,73E-02	**1,98E+00**	**2,62E-03**	*nifD*- NoN 14 dpi	T	LOW QUALITY:transcription initiation factor TFIID subunit 1b-like protein (AHRD V3.3 -** AT3G19030.1)	
Solyc01g111880.3	-1,41E+00	8,42E-07	-2,26E+00	1,26E-10	9,10E-01	3,19E-04	**2,02E+00**	**1,25E-09**	*nifD*- NoN 14 dpi	K	MAP kinase kinase kinase 11	GO:0004672|GO:0005524|GO:0006468|GO:0004672|GO:0006468|GO:0004672|GO:0006468
Solyc03g111710.3	-1,62E+00	1,51E-07	-2,43E+00	5,72E-11	6,59E-01	7,37E-03	**2,81E+00**	**2,45E-12**	*nifD*- NoN 14 dpi	T	BTB/POZ and TAZ domain protein (AHRD V3.3 *** G7JMM8_MEDTR)	GO:0003712|GO:0004402|GO:0005634|GO:0006355|GO:0008270|GO:0005515|GO:0005515
Solyc03g026230.1	-1,64E+00	1,73E-04	-2,45E+00	6,36E-07	5,49E-01	1,55E-01	**1,23E+00**	**2,97E-03**	*nifD*- NoN 14 dpi	STR	Protein DETOXIFICATION (AHRD V3.3 *** K4BF96_SOLLC)	GO:0006855|GO:0015238|GO:0015297|GO:0016020|GO:0055085
Solyc05g008910.3	-1,86E+00	7,22E-02	-2,54E+00	1,68E-02	1,08E+00	2,89E-01	**2,93E+00**	**6,75E-03**	*nifD*- NoN 14 dpi	N	Class I glutamine amidotransferase-like superfamily protein (AHRD V3.3 *-* AT5G38200.1)	GO:0006541|GO:0016787
Solyc10g074440.2	2,73E-02	9,70E-01	-2,62E+00	1,16E-03	1,60E+00	3,50E-02	**2,14E+00**	**6,09E-03**	*nifD*- NoN 14 dpi	D	Chitinase (AHRD V3.3 *** B9VRK7_CAPAN)	GO:0004568|GO:0005975|GO:0004568|GO:0006032|GO:0016998|GO:0004568|GO:0006032|GO:0016998
Solyc03g114530.3	-6,17E-03	9,94E-01	-3,65E+00	1,52E-04	1,53E+00	7,36E-02	**2,57E+00**	**4,32E-03**	*nifD*- NoN 14 dpi	2M	Strictosidine synthase-like protein, putative (AHRD V3.3 *** G7JT39_MEDTR)	GO:0009058|GO:0016844
Solyc08g006860.3	-3,66E+00	1,32E-04	-5,17E+00	1,09E-06	1,50E+00	7,82E-02	**2,91E+00**	**1,44E-03**	*nifD*- NoN 14 dpi	P	Patatin (AHRD V3.3 *** K4CIH4_SOLLC)	GO:0006629|GO:0008152|GO:0008152