AGRICULTURAL UNIVERSITY OF ATHENS
DEPARTMENT OF CROP SCIENCE
LABORATORY OF VEGETABLE PRODUCTION

Impact of grafting on growth, yield, quality, and physiological characteristics of tomato grown under sub-optimal temperature conditions

Georgia Ntatsi, B.Sc., M.Sc.
Ph.D. Dissertation

Athens, 2013

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Athens, 2013

Στους γονείς μου Νικόλαο και Κασσιανή

(To my parents Nikolao and Kassiani)

“Δός μοι πᾷ στῶ καὶ τὰν γᾶν κινήσω”

(Give me but one firm place on which to stand, and I will move the earth)

Archimedes

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ABSTRACT

Increased tomato (*Solanum lycopersicum* L.) tolerance to sub-optimal temperature (T) through grafting onto cold-tolerant rootstocks could extend the growing period in the field and in unheated greenhouses, and reduce energy costs in heated greenhouses. Phytohormones seem to be involved in the tolerance of tomato to sub-optimal T stress. Hence, the selection of rootstock/scion combinations with enhanced tolerance to sub-optimal T requires a better understanding of the root-to-shoot interactions with respect to hormonal transport and signaling. To attain this goal, six trials were conducted employing reciprocal grafting of standard tomato cultivars and mutants that are deficient in the biosynthesis/catabolism of abscisic acid (ABA), cytokinin (CK) or salicylic acid (SA), or exhibit low sensitivity to ethylene (ET) or auxin (IAA). The exposure of tomato to sub-optimal day/night T (17/14 °C) decreased drastically the rates of shoot elongation and leaf area expansion in all trials in comparison with optimal day/night T levels (22/18 °C). With respect to the genetic combination of rootstock and scion genotypes, it was found that ABA produced in both plant parts exerts a protective role on tomato shoot growth under sub-optimal T stress, while the contribution of ABA was only partially reflected by leaf ABA levels. The use of an ET-insensitive genotype either as rootstock or as scion also improved sub-optimal T tolerance. Sufficient IAA sensitivity in tomato shoot seems to be positively related to shoot elongation rates under sub-optimal T conditions. The use of a mutant with enhanced CK catabolism either as rootstock or as scion restricted leaf expansion at optimal T but had no impact on leaf expansion under sub-optimal T conditions. Impaired SA biosynthesis in the shoot was associated with a higher susceptibility to sub-optimal T in terms of shoot elongation, whereas leaf expansion was similarly affected by SA biosynthesis at both T regimes. In conclusion, ABA seems to enhance tomato tolerance to sub-optimal T and indirectly control endogenous ET levels, while increased levels of IAA and SA in the shoot promote shoot elongation in tomato plants grown under sub-optimal T conditions.

To further elucidate the role of abscisic acid (ABA) in tomato responses to sub-optimal root temperature (T), a near-isogenic line carrying the ‘notabilis’ null mutation in the ABA biosynthesis gene *LeNCED1* was reciprocally grafted with its parental cultivar Ailsa Craig. Exposure of tomato to sub-optimal root T (15°C) decreased leaf

area expansion, shoot elongation and plant biomass in comparison with optimal root T (25 ^{o}C). Both sub-optimal root T and null mutation of the *LeNCED1* gene in the root and shoot reduced leaf area and total plant biomass, but these two factors did not interact. Transpiration rates and stomatal conductance decreased, while net CO_2 assimilation was not influenced by root exposure to sub-optimal T. However, 'notabilis' scions exhibited higher net assimilation rates, stomatal conductance and transpiration rates than 'Ailsa Craig' scions. Moreover, 'notabilis' plants invested much more biomass in the root than 'Ailsa Craig' self-grafts, thereby improving their water uptake capacity. Lipid peroxidation as well as polyamines and guaiacol-peroxidase (G-POD), which are considered to possess antioxidant properties, increased in the leaves of all grafting combinations of tomato when exposed to sub-optimal root T. All grafting combinations showed an increase in shoot ABA levels when exposed to sub-optimal root T. However, the levels of ABA in the shoot of 'notabilis' did not differ significantly from those found in 'Ailsa Craig', indicating that inactivation of *LeNCED1* did not impair ABA accumulation in the leaves at low root-zone T. The genes *LeNCED2* and *LeNCED6* were not up-regulated at low root-zone T and were therefore not responsible for ABA biosynthesis in 'notabilis'. Increased ABA levels in tomato exposed to sub-optimal root T were associated with elevated levels of the polyamine putrescine which contributes to ABA biosynthesis. In conclusion, the introgression in 'Ailsa Craig' that contains the mutation resulting from inactivation of the *LeNCED1* gene includes further genetic differences that influence responses to sub-optimal root-zone T, such as plant growth restriction and ROS scavenging modification.

The accession 'LA 1777' of *Solanum habrochaites* S. Knapp and D.M. Spooner, a wild relative species of tomato, is of particular interest as a potential germplasm source to widen the genetic variation of the cultivated tomato in low temperature tolerance. However, the hypothesis that 'LA 1777' is able to alleviate low-temperature stress when grafted onto different scions is based only on vegetative growth data obtained from short-term experiments, while data from long-term experiments indicating a positive relationship between grafting onto 'LA 1777' and tomato fruit yield have not been reported so far. Thus, a third experiment was designed to test the hypothesis that using wild relatives of *S. lycopersicon* as rootstocks, characterized by a vigorous root system and tolerance to sub-optimal T, may minimize yield losses in elite cultivars of grafted tomato when exposed to sub-optimal T. In particular, tomato (*Solanum lycopersicum* L. cv. Kommeet) plants were either self-grafted, grafted onto the cold-sensitive hybrid ‘Moneymaker’ or onto ‘LA 1777’, a cold-tolerant accession of *Solanum habrochaites*. The plants were grown at three different air/root-zone temperatures (T): optimal (19.4 ^{o}C), intermediate (17 ^{o}C) or low (14.6 ^{o}C) both the latter considered being different degrees of sub-optimal temperature. Grafting tomato cv. ‘Kommeet’ onto ‘LA 1777’ increased shoot growth at intermediate and optimal T, and root growth at low or intermediate T in comparison with self-grafting or grafting onto ‘Moneymaker’. Reducing T significantly suppressed fruit yield due to a reduction in the number of fruit per plant, without interacting with the grafting treatments. Grafting ‘Kommeet’ onto ‘LA 1777’ remarkably restricted fresh and dry fruit mass in comparison with self-grafting of ‘Kommeet’, due to a reduction in the fruit number per plant while not influencing flower number per plant and mean fruit mass, regardless of T regime. The negative effect of ‘LA 1777’ on fruit set when used as tomato rootstock points to the impairment of pollen fertility through signals originating from the root. At sub-optimal T, the plants grafted onto ‘LA 1777’ were capable of increasing soluble carbohydrates, total amino acids (TAAC), and guaiacol peroxidase (GPOD) activity in the roots to higher levels than those grafted onto *S. lycopersicum* rootstocks, while maintaining an appreciably lower malondialdehyde content. These differences point to a much weaker oxidative stress in the roots of plants grafted onto ‘LA 1777’ than in those grafted onto *S. lycopersicum* when exposed to sub-optimal T. Furthermore, the plants grafted onto ‘LA 1777’ exhibited significantly higher levels of soluble carbohydrates, TAAC, and GPOD activity in leaves, and fruit and SOD in fruit at sub-optimal T, which indicates that ‘LA 1777’ is capable of improving the levels of antioxidant compounds in the shoot of tomato, thereby improving its adaptation to lower T than optimal.

An alternative strategy to increase tomato tolerance to sub-optimal T is to develop tolerant rootstocks and graft elite cultivars onto them. To attain this goal, a better understanding of adaptive mechanisms to sub-optimal T, associated with root functions and root-to-shoot signaling through hormonal messengers, is needed. Taking the above into consideration, in a heated glasshouse at the Leibniz-Institute of Vegetable and Ornamental Crops, Großbeeren, Germany, the commercial tomato cultivar ‘Kommeet’ was grafted onto the tomato cv. Moneymaker (sensitive) or onto the line accession ‘LA 1777’ of the wild tomato species S. *habrochaites* (tolerant). Self-grafted tomato plants were used as controls. Grafting was performed when seedlings had developed 3-4 true leaves. Grafted tomato plants were grown in an NFT system with re-circulating nutrient solution differing in root temperature (T), which was either optimal (day and night 25±0.6 °C) or sub-optimal (day and night 15±0.4 °C) while the air the air T was optimal (day and night 25±0.6 °C) throughout the experiment. After 30 days, leaf and root samples were collected and the differences in growth, physiology and global gene expression in the roots and leaves of all grafting combinations under both sub- and optimal root T were further investigated. Comparative transcriptome analysis identified no genes in the leaves of ‘Kommeet’ grafted onto ‘LA 1777’, while in the leaves of ‘Kommeet’ grafted onto ‘Moneymaker’ 361 differentially expressed genes were annotated. On the other hand 1509 and 2036 sub-optimal root T-responsive genes were identified in the roots of ‘LA 1777’ and ‘Moneymaker’ rootstocks, respectively. In the present study the up-regulation of many genes associated with cell wall synthesis in the tolerant genotype were related to the increased root:shoot ratio and the upward transport capacity of water and nutrients. In addition, changes in root phytohormone production due to sub-optimal root T affected root-to-shoot hormone signaling only in the sensitive genotype by causing hormonal imbalances in the scion. These results provide new insights into the molecular mechanisms of sub-optimal T tolerance of tomato by evaluating genes controlling biochemical pathways and physiological procedures that are related to ‘LA 1777’. The knowledge acquired through the research conducted in this thesis could be utilized to establish biomarkers to screen not only wild tomato genotypes serving as rootstocks, but also rootstock/scion combinations potentially tolerant to sub-optimal T.

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ΠΕΡΙΛΗΨΗ

Στις Μεσογειακές χώρες όπως η Ελλάδα, τα περισσότερα θερμοκήπια με κηπευτικά δεν θερμαίνονται τον χειμώνα, με αποτέλεσμα φυτά όπως η τομάτα να καλλιεργούνται σε θερμοκρασίες κυμαινόμενες μεταξύ των δυο ορίων, χαμηλής (≥12 °C) και αρίστης (≤20 °C). Οι επιδράσεις της έκθεσης της τομάτας σε αυτά τα οριακά χαμηλά επίπεδα θερμοκρασιών (13 – 19 ^{o}C) είναι ιδιαίτερα δυσμενείς στην ανάπτυξη και την παραγωγή των φυτών. Ωστόσο, το εύρος της μείωσης της ανάπτυξης και της παραγωγής εξαρτάται από την γονοτυπική ανοχή των φυτών στην έκθεση τους στις συγκεκριμένες συνθήκες. Είναι προφανές ότι η καλλιέργεια γονοτύπων υψηλής παραγωγικότητας με αυξημένη ανοχή σε οριακά χαμηλά επίπεδα θερμοκρασιών δύναται να οδηγήσει τόσο στη μείωση του κόστους των καυσίμων στα θερμοκήπια, με αντίστοιχη εξοικονόμηση ενέργειας, όσο και στην επιμήκυνση της καλλιεργητικής περιόδου και στην πρωϊμιση της παραγωγής στις υπαίθριες καλλιέργειες.

Η δημιουργία νέων ποικιλιών ή υβριδίων τομάτας με ανοχή σε οριακά χαμηλές θερμοκρασίες δεν είναι αντικειμενικά εφικτή, λόγω της χαμηλής γενετικής ποικιλομορφίας των υπαρχόντων γενοτύπων σε αυτό το γενετικό χαρακτηριστικό. Ωστόσο, μια εναλλακτική και φιλική προς το περιβάλλον τεχνική, αυτή του εμβολιασμού, θα μπορούσε να οδηγήσει στην επιθυμητή διεύρυνση των ορίων ανοχής των φυτών σε συνθήκες οριακά χαμηλών θερμοκρασιών. Αυτό μπορεί να επιτευχθεί αν καταστεί δυνατή η επιλογή ή δημιουργία συμβατών υποκειμένων με αυξημένη ανοχή σε οριακά χαμηλές θερμοκρασίες, τα οποία προφανώς ως αυτόρριζα φυτά δεν χρειάζεται να δίνουν υψηλή παραγωγή και ποιότητα καρπών. Για να καταστεί όμως δυνατή σε σύντομο χρόνο η επιλογή ή η δημιουργία μέσω γενετικής βελτίωσης υποκειμένων εμβολιασμού με αυξημένη ανοχή σε οριακά χαμηλές θερμοκρασίες, απαιτείται η κατανόηση των μηχανισμών που υπεισέρχονται στην ανοχή των φυτών σε αυτές τις συνθήκες, καθώς και του τρόπου με τον οποίο σχετίζονται αυτοί οι μηχανισμοί με την ανάπτυξή τους. Ένας από τους σημαντικότερους μηχανισμούς με τον οποίο το υποκείμενο ασκεί επιρροή στο εκάστοτε εμβόλιο, καθορίζοντας με αυτόν τον τρόπο τα επίπεδα ανοχής του τελευταίου σε διάφορους παράγοντες καταπόνησης, αποτελεί η επαγωγή διαφοροποίησης στην ακροπεταλική και βασιπεταλική μεταφορά μεταβολιτών μέσω ορμονικών αγγελιοφόρων. Η καλύτερη κατανόηση του μηχανισμού αυτού μπορεί να οδηγήσει στην επιλογή του καταλλήλου συνδυασμού

υποκειμένου/εμβολίου που δύναται να προσδώσει αυξημένη ανοχή σε συνθήκες χαμηλών θερμοκρασιών.

Προκειμένου λοιπόν να μελετηθεί αυτός ο μηχανισμός, αρχικά διεξήχθησαν έξι παράλληλα επιμέρους πειράματα στο πλαίσιο μίας ενιαίας πειραματικής εργασίας. Στην πρώτη αυτή πειραματική εργασία χρησιμοποιήθηκαν φυτά από τέσσερις διαφορετικές ποικιλίες τομάτας, καθεμία από τις οποίες εμβολιάστηκε στην αντίστοιχη μεταλλαγμένη (ισογονιδιακή) της ποικιλία και αντίστροφα, ενώ παράλληλα πραγματοποιήθηκε και αυτοεμβολιασμός των εκάστοτε ζευγών ποικιλιών (κανονικής και μεταλλαγμένης). Για τις δύο από τις τέσσερις ποικιλίες τομάτας υπήρχαν δύο διαφορετικά μεταλλαγμένες ποικιλίες και συνεπώς συνολικά δοκιμάσθηκαν έξι μεταλλαγμένες ποικιλίες και ειδικότερα μία σε καθένα από τα έξι επιμέρους πειράματα. Το ιδιαίτερο χαρακτηριστικό που διαφοροποιούσε τις έξι συνολικά μεταλλαγμένες ποικιλίες συνίστατο είτε στην αδυναμία αυτών να βιοσυνθέσουν/καταβολίσουν αμπσισικό οξύ (ABA) ή κυτοκινίνη (CK) ή σαλικυλικό οξύ (SA), είτε στην μειωμένη ευαισθησία τους στο αιθυλένιο (ET) ή την αυξίνη (IAA), με αποτέλεσμα την παραγωγή χαμηλών ενδογενών επιπέδων της εκάστοτε ορμόνης ή την χαμηλή ανταπόκριση στην παρουσία της. Για το ABA υπήρχαν δύο διαφορετικές μεταλλαγές που κατέστειλαν την βιοσύνθεσή του. Όλα τα πειράματα έδειξαν ότι η έκθεση της τομάτας σε χαμηλές θερμοκρασίες ημέρας/νύχτας T (17/14 °C), μειώνει δραστικά τον ρυθμό επιμήκυνσης των βλαστών, συγκρινόμενη με τον αντίστοιχο ρυθμό σε κανονικές συνθήκες θερμοκρασίας ημέρας/νύχτας (22/18 °C). Η μελέτη των επιπτώσεων των διαφορετικών γενετικών συνδυασμών ρίζας και υποκειμένου έδειξε ότι η παραγωγή ABA τόσο στα φύλλα όσο και στις ρίζες ασκεί προστατευτικό ρόλο στην ανάπτυξη των φυτών κάτω από συνθήκες καταπόνησης χαμηλών θερμοκρασιών, παρά το γεγονός ότι η συμβολή αυτή του ABA στην συγκεκριμένη καταπόνηση αντικατοπτρίζεται εν μέρει μόνο από τα επίπεδα του ABA στα φύλλα. Επιπλέον, η χρήση του γονότυπου με κανονική ευαισθησία στην παραγωγή ενδογενούς αιθυλενίου είτε ως υποκειμένου είτε ως εμβολίου αύξησε επίσης την ανοχή στην καταπόνηση σε οριακά χαμηλές θερμοκρασίες σε σύγκριση με την μεταλλαγμένη ποικιλία με μειωμένη ευαισθησία στο ET. Επαρκής ποσότητα ενδογενούς αυξίνης στο υπέργειο μέρος φυτών τομάτας φαίνεται ότι συσχετίζεται θετικά με το ρυθμό ανάπτυξης αυτού σε συνθήκες καταπόνησης λόγω οριακά χαμηλών θερμοκρασιών. Η χρήση της μεταλλαγμένης ποικιλίας που παρουσιάζει αυξημένο καταβολισμό κυτοκινίνης, είτε ως εμβόλιο είτε ως υποκείμενο, περιόρισε την επιμήκυνση των φύλλων υπό κανονικές συνθήκες ανάπτυξης, ενώ η επίδραση αυτή ήταν μηδαμινή όταν η θερμοκρασία ήταν χαμηλή. Μειωμένη βιοσύνθεση σαλικυλικού οξέως στο βλαστικό μέρος των φυτών που αναπτυχτήκαν σε συνθήκες οριακά χαμηλών θερμοκρασιών οδήγησε σε μειωμένο ρυθμό επιμήκυνσης των βλαστών, ενώ ο ρυθμός επιμήκυνσης των φύλλων μειώθηκε το ίδιο και στις δυο θερμοκρασίες ανάπτυξης (κανονική και χαμηλή). Συμπερασματικά, από την παραπάνω πειραματική εργασία προέκυψε ότι η παραγωγή ενδογενούς ABA ενισχύει την ανοχή της τομάτας σε οριακά χαμηλές θερμοκρασίες και έμμεσα ελέγχει τα ενδογενή επίπεδα του αιθυλενίου, ενώ η ανύψωση των ενδογενών επιπέδων της αυξίνης και του σαλικυλικού οξέως στο βλαστό ενισχύει την επιμήκυνση του στις συνθήκες αυτές.

Λαμβάνοντας υπόψη τα παραπάνω πειραματικά δεδομένα, τα οποία έδειξαν ότι η ορμόνη που συμβάλλει στην διατήρηση της ανάπτυξης των φυτών υπό συνθήκες έκθεσης σε οριακά χαμηλές θερμοκρασίες είναι κυρίως το ABA, αποφασίσθηκε να πραγματοποιηθεί ένα νέο πείραμα με στόχο την περαιτέρω διερεύνηση του θέματος. Ειδικότερα, ο σκοπός του πειράματος αυτού ήταν η συσχέτιση των ενδογενών επιπέδων του ABA με την ανοχή των φυτών σε συνθήκες έκθεσης σε οριακά χαμηλές θερμοκρασίες στο περιβάλλον της ρίζας.

Προκειμένου λοιπόν να μελετηθεί ο ρόλος του ενδογενούς ABA στην ανοχή της τομάτας στις οριακά χαμηλές θερμοκρασίες, φυτά τομάτας της ποικιλίας ‘Ailsa Craig’ εμβολιαστήκαν στην ισογονιδιακή ποικιλία τομάτας ‘notabilis’ που παρουσιάζεται ως μετάλλαξη της ‘Ailsa Craig’ στερούμενη ABA. Παράλληλα πραγματοποιήθηκε και ο αντίστροφος εμβολιασμός (‘notabilis’ σε ‘Ailsa Craig’) ενώ επιπλέον πραγματοποιήθηκε και αυτοεμβολιασμός των δυο ποικιλιών. Εφαρμοστήκαν δυο επίπεδα θερμοκρασίας ρίζας (15 και 25 ^{o}C), ενώ η θερμοκρασία αέρα διατηρήθηκε σταθερή στους 25 ^{o}C καθ’ όλη τη διάρκεια του πειράματος. Τα αποτελέσματα έδειξαν ότι τόσο η χαμηλή θερμοκρασία ρίζας όσο και η έλλειψη του *LeNCED1* γονιδίου που είναι υπεύθυνο για την παραγωγή ABA τόσο στα φύλλα όσο και στις ρίζες μείωσε την φυλλική επιφάνεια, το ύψος και την ξηρή ουσία των φυτών χωρίς όμως σημαντική αλληλεπίδραση μεταξύ των δύο αυτών παραγόντων. Ο ρυθμός διαπνοής και η στοματική αγωγιμότητα μειώθηκαν, ενώ η αφομοίωση του CO_2 δεν επηρεάστηκε από την έκθεση της ρίζας σε χαμηλές θερμοκρασίες. Ωστόσο, τα φύλλα της ισογονιδιακής ποικιλίας ‘notabilis’ παρουσίασαν υψηλότερους ρυθμούς καθαρής αφομοίωσης CO_2, στοματικής αγωγιμότητας και διαπνοής σε σύγκριση με αυτά της ποικιλίας ‘Ailsa Craig’. Παράλληλα, τα φυτά ‘notabilis’ συσσώρευσαν πολύ περισσότερη βιομάζα στη ρίζα σε σύγκριση με αυτά της ποικιλίας ‘Ailsa Craig’ βελτιώνοντας έτσι την ικανότητα πρόσληψης ύδατος. Η υπεροξείδωση των λιπιδίων καθώς και οι πολυαμίνες και η υπεροξειδάση της γκουαϊακόλης (G-POD), οι οποίες θεωρούνται ότι διαθέτουν αντιοξειδωτικές ιδιότητες, παρουσίασαν αύξηση στα φύλλα όλων των συνδυασμών εμβολιασμένων φυτών τομάτας όταν αυτά εκτέθηκαν σε χαμηλές θερμοκρασίες στο περιβάλλον της ρίζας. Ὁλοι οι συνδυασμοί εμβολιασμένων φυτών παρουσίασαν αυξημένα επίπεδα ABA στα φύλλα σε συνθήκες καταπόνησης εξαιτίας της έκθεσης τους σε οριακά χαμηλές θερμοκρασίες. Ωστόσο, τα επίπεδα του ABA στο φύλλα του ‘notabilis’ δεν διέφεραν σημαντικά από εκείνα της ποικιλίας ‘Ailsa Craig’, γεγονός που καταδεικνύει ότι η απουσία του *LeNCED1* γονιδίου δεν οδηγεί σε μείωση των ενδογενών επιπέδων του ABA στα φύλλα σε χαμηλές θερμοκρασίες ρίζας. Αυτό έρχεται σε αντίθεση με τα ως τώρα δεδομένα που παρουσιάζουν την ποικιλία ‘notabilis’ ως μετάλλαξη στερούμενη ABA. Παράλληλα η επικράτηση των χαμηλών αυτών θερμοκρασιών δεν οδήγησε στην υπερ-έκφραση των γονίδιων *LeNCED*2 και *LeNCED6* και ως εκ τούτου διαπιστώθηκε ότι δεν είναι αυτά υπεύθυνα για τη βιοσύνθεση ABA που παρατηρήθηκε στην ισογονιδιακή ποικιλία ‘notabilis’. Τα αυξημένα επίπεδα του ABA σχετίστηκαν με αυξημένα επίπεδα της πολυαμίνης πουτρεσκίνης η οποία συμβάλλει στην βιοσύνθεση αυτού. Συμπερασματικά, η ισογονιδιακή ποικιλία ‘notabilis’, η οποία περιέχει μετάλλαξη που οδηγεί στην απενεργοποίηση του υπευθύνου για την παραγωγή ABA γονιδίου *LeNCED1*, χρήζει περαιτέρω γενετικής διερεύνησης. Και αυτό διότι επάγει επιπλέον αλλαγές πέραν της βιοσύνθεσης ABA σε γενετικό επίπεδο, οι οποίες είναι ικανές να επηρεάσουν την αντίδραση του στην καταπόνηση λόγω επικράτησης χαμηλών θερμοκρασιών στο περιβάλλον της ρίζας. Οι αλλαγές αυτές δύνανται να οδηγήσουν στον περιορισμό της ανάπτυξης των φυτών και την καταστολή της δράσης μηχανισμών που εξουδετερώνουν τις ελεύθερες ρίζες οξυγόνου (ROS).

Σε ένα επόμενο πείραμα, χρησιμοποιήθηκε η καθαρή σειρά ‘LA 1777’ του συγγενούς με την καλλιεργούμενη τομάτα είδους *Solanum habrochaites*, το οποίο κατάγεται από το Περού, από περιοχές με υψόμετρο 3200 μ. Χαρακτηριστικά γνωρίσματα αυτού του είδους αγριοτομάτας, αποτελούν τόσο το πλούσιο ριζικό του σύστημα όσο και η αυξημένη ανοχή του σε χαμηλές θερμοκρασίες ανάπτυξης. Για το λόγο αυτό, το συγκεκριμένο είδος χρησιμοποιήθηκε ως πιθανή πηγή γενετικού υλικού για την διεύρυνση της γενετικής παραλλακτικότητας της καλλιεργούμενης τομάτας με στόχο την δημιουργία υποκειμένων εμβολιασμού που αυξάνουν την ανεκτικότητα των εμβολιασμένων φυτών σε οριακά χαμηλές θερμοκρασίες. Ωστόσο, η υπόθεση ότι το *S.*

habrochaites και ειδικότερα το ‘LA 1777’ δύναται να αυξήσει την ανοχή σε οριακά χαμηλές θερμοκρασίες όταν χρησιμοποιείται ως υποκείμενο εμβολιασμού, βασίζεται σε δεδομένα βλαστικής ανάπτυξης που παρθήκαν από πειράματα μικρής καλλιεργητικής διάρκειας. Αντίθετα, δεδομένα που να συσχετίζουν την παραγωγή καρπών σε εμβολιασμένα φυτά με την χρήση του ‘LA 1777’ ως υποκειμένου, δεν έχουν αναφερθεί μέχρι σήμερα. Η ύπαρξη επομένως συσχέτισης μεταξύ παραγωγής καρπών κάτω από συνθήκες οριακά χαμηλών θερμοκρασιών και χρήσης του ‘LA 1777’ ως υποκειμένου, απαιτεί διερεύνηση. Προκειμένου λοιπόν να μελετηθεί η συσχέτιση αυτή, ένα τρίτο πείραμα σχεδιάστηκε στα πλαίσια της παρούσας διδακτορικής διατριβής. Στόχοι αυτού του πειράματος ήταν: α) να μελετηθεί η επίδραση του *S. habrochaites* και ειδικότερα της καθαρής σειράς ‘LA 1777’ ως υποκειμένου εμβολιασμού παραγωγικών υβριδίων τομάτας στην βλαστική ανάπτυξη και την παραγωγή καρπών σε συνθήκες οριακά χαμηλών θερμοκρασιών και β) να διερευνηθεί η ύπαρξη φυσιολογικών μηχανισμών ανοχής του εμβολιασμένου φυτού στις χαμηλές θερμοκρασίες οι οποίες επάγονται από το συγκεκριμένο υποκείμενο. Ειδικότερα, η εμπορική ποικιλία τομάτας ‘Kommeet’ εμβολιάστηκε τόσο στις δικές της ρίζες (αυτοεμβολιασμός) όσο και σε δυο υποκείμενα με διαφορετική ανοχή στο κρύο, ένα ευαίσθητο (‘Moneymaker’) και ένα ανθεκτικό (‘LA 1777’). Τα εμβολιασμένα φυτά αναπτύχθηκαν σε τρεις διαφορετικές θερμοκρασίες περιβάλλοντος, μια βέλτιστη (19,4 ^{o}C) και δύο εντός του εύρους των οριακά χαμηλών τιμών και ειδικότερα μια ενδιάμεση (17 ^{o}C) και μια χαμηλή (14,6 ^{o}C). Ο εμβολιασμός της ποικιλίας ‘Kommeet’ στο υποκείμενο ‘LA 1777’ οδήγησε σε αύξηση της βλαστικής ανάπτυξης τόσο στην ενδιάμεση όσο και στην βέλτιστη θερμοκρασία καλλιέργειας και σε αυξημένη παραγωγή ριζικής βιομάζας στην χαμηλή και στην ενδιάμεση θερμοκρασία σε σύγκριση με τον αυτοεμβολιασμό και τον εμβολιασμό στο υποκείμενο ‘Moneymaker’. Η μείωση της θερμοκρασίας οδήγησε σε αισθητή μείωση της παραγωγής η οποία προήλθε από μείωση του αριθμού των καρπών ανά φυτό, χωρίς ωστόσο οι δύο αυτοί παράγοντες (θερμοκρασία ανάπτυξης και εμβολιασμός) να αλληλεπιδρούν. Ο εμβολιασμός της ποικιλίας ‘Kommeet’ στο υποκείμενο ‘LA 1777’ οδήγησε σε αισθητή μείωση του συνολικού νωπού και ξηρού βάρους καρπών ανά φυτό σε σύγκριση με τον αυτοεμβολιασμό, λόγω της μείωσης του αριθμού των καρπών ανά φυτό. Τόσο όμως ο αριθμός των ανθέων ανά φυτό όσο και το μέσο βάρος του καρπού δεν παρουσίασαν καμία μείωση οφειλόμενη στον εμβολιασμό στο ‘LA 1777’, ανεξαρτήτως της θερμοκρασίας στην οποία αναπτύχθηκαν τα φυτά. Από τα δεδομένα αυτά προκύπτει σαφώς ότι ο εμβολιασμός της ‘Kommeet’ στο ‘LA

1777’ περιορίζει σημαντικά την καρπόδεση. Η αρνητική αυτή επίπτωση της χρήσης του υποκειμένου ‘LA 1777’ στην καρπόδεση των φυτών τομάτας ποικιλίας ‘Kommeet’, υποδηλώνει την ύπαρξη ερεθισμάτων προερχομένων από την ρίζα, τα οποία επιδρούν δυσμενώς στην γονιμότητα της παραγόμενης γύρης. Σε συνθήκες χαμηλών θερμοκρασιών, η χρήση του ‘LA 1777’ ως υποκειμένου αύξησε τα επίπεδα των διαλυτών σακχάρων, τα ολικά αμινοξέα (TAAC), και την δραστηριότητα της υπεροξειδάσης της γκουαϊακόλης (G-POD) στις ρίζες σε σύγκριση με την χρήση των δύο ποικιλιών καλλιεργούμενης τομάτας (*S. lycopesricum*) ως υποκειμένων, διατηρώντας παράλληλα σε αισθητά χαμηλότερα επίπεδα την περιεκτικότητα της μηλονοδιαλδεΰδης (MDA), η παρουσία της οποίας υποδηλώνει οξειδωτική καταπόνηση. Οι διαφορές αυτές καταδεικνύουν μια ασθενέστερη οξειδωτική καταπόνηση στις ρίζες των φυτών ‘LA 1777’ συγκριτικά με τις ρίζες των δύο ποικιλιών *S. lycopersicum* (‘Kommeet’ και ‘Moneymaker’) όταν αυτές εκτίθενται σε οριακά χαμηλές θερμοκρασίες. Επιπρόσθετα, τα εμβολιασμένα φυτά σε ‘LA 1777’ παρουσίασαν σημαντικά υψηλότερα επίπεδα διαλυτών υδατανθράκων, TAAC και δραστηριότητας της G-POD στα φύλλα και στους καρπούς και της SOD στους καρπούς υπό συνθήκες χαμηλών θερμοκρασιών. Τα αποτελέσματα αυτά καταδεικνύουν ότι η χρήση του ‘LA 1777’ ως υποκείμενου, δύναται να τροποποιήσει τα επίπεδα ουσιών που ελέγχουν την οξειδωτική καταπόνηση στους βλαστούς της τομάτας, βελτιώνοντας έτσι την προσαρμογή της σε συνθήκες οριακά χαμηλών θερμοκρασιών (13 – 18 ^{o}C).

Μια άλλη εναλλακτική μέθοδος βελτίωσης της ανεκτικότητας της τομάτας σε οριακά χαμηλές θερμοκρασίες είναι η δημιουργία διειδικών υβριδίων της καλλιεργούμενης τομάτας με είδη άγριας τομάτας που είναι ανεκτικά στις οριακά χαμηλές θερμοκρασίες, με στόχο τη χρήση τους ως υποκειμένων εμβολιασμού. Η χρήση της εναλλακτικής αυτής μεθόδου υπαγορεύεται και από το γεγονός ότι η δημιουργία υψηλοαποδοτικών ποικιλιών ή υβριδίων τομάτας με ανεκτικότητα στις χαμηλές θερμοκρασίες έχει αποτύχει μέχρι σήμερα. Η αποτυχία αυτή οφείλεται στη μειωμένη γενετική ποικιλομορφία εντός του είδους *S. lycopersicum* όσον αφορά την ανεκτικότητα σε χαμηλές θερμοκρασίες, σε συνδυασμό με την μειωμένη γονιμότητα της γύρης στα υβρίδια του *S. lycopersicum* με ανεκτικούς στο κρύο γονότυπους του *S. habrochaites*. Για την δημιουργία όμως υποκειμένων με ανεκτικότητα σε χαμηλές θερμοκρασίες, είναι αναγκαία η καλύτερη κατανόηση των μηχανισμών προσαρμογής που σχετίζονται με λειτουργίες της ρίζας και ιδιαίτερα με την δράση ουσιών (πχ. φυτορμονών, αντιοξειδωτικών ενζύμων, υδατανθράκων κ.ά.) που παράγονται στην ρίζα και δρουν ως διαβιβαστές μηνυμάτων, επηρεάζοντας το υπέργειο μέρος του φυτού.

Λαμβάνοντας υπόψη τα παραπάνω, σε θερμοκήπιο του Leibniz-Institute of Vegetable and Ornamental Crops, στο Großbeeren της Γερμανίας πραγματοποιήθηκε ένα πείραμα με φυτά τομάτας ποικιλίας ‘Kommeet’ εμβολιασμένα σε δύο υποκείμενα με διαφορετική ανοχή σε οριακά χαμηλές θερμοκρασίες, το ‘Moneymaker’ (ευαίσθητο) και το ‘LA1777’ (ανεκτικό). Τα φυτά καλλιεργήθηκαν σε υδροπονικό σύστημα NFT με θερμοκρασίες ρίζας 15 ^{o}C ή 25 ^{o}C και θερμοκρασία αέρα 25 ^{o}C σε όλη τη διάρκεια του πειράματος. Μετά από έκθεση των φυτών για ένα μήνα στις προαναφερθείσες θερμοκρασίες, συλλέχθηκαν δείγματα ρίζας και φύλλων για την μελέτη της επίδρασης της θερμοκρασίας ρίζας τόσο στην ανάπτυξη και την φυσιολογία όσο στην συνολική γονιδιακή τους έκφραση, χρησιμοποιώντας c-DNA μικροσυστοιχίες. Η μελέτη όλων αυτών των παραγόντων πραγματοποιήθηκε και στα δυο μέρη του φυτού (φύλλα και ρίζες), καθώς και στις δυο διαφορετικές συνθήκες ανάπτυξης από άποψη θερμοκρασίας ρίζας.

Η συγκριτική μεταγραφική ανάλυση εντόπισε μηδενική αλλαγή στην έκφραση των γονιδίων στα φύλλα της ποικιλίας ‘Kommeet’ που εμβολιαστήκαν στο ανεκτικό στο ψύχος υποκείμενο, όταν οι ρίζες των φυτών εκτέθηκαν σε οριακά χαμηλές θερμοκρασίες. Αντιθέτως, στα φύλλα των φυτών ποικιλίας ‘Kommeet’ που εμβολιαστήκαν στο ευαίσθητο στο ψύχος υποκείμενο (‘Moneymaker’), 361 γονίδια παρουσίασαν αλλαγή στην γονιδιακή τους έκφραση, όταν οι ρίζες τους εκτέθηκαν σε οριακά χαμηλές θερμοκρασίες. Όσον αναφορά τα δύο διαφορετικά υποκείμενα, ‘LA 1777’ και ‘Moneymaker’, 1506 και 2036 γονίδια αντίστοιχα εμφάνισαν σημαντική διαφοροποίηση στην έκφραση τους (υπερ-έκφραση ή υπο-έκφραση) στις ρίζες όταν αυτές εκτέθηκαν σε οριακά χαμηλές θερμοκρασίες Στην παρούσα μελέτη διαπιστώθηκε υπερ-έκφραση πολλών γονιδίων που σχετίζονται με τη σύνθεση του κυτταρικού τοιχώματος στις ρίζες του ανεκτικού στο ψύχος γονότυπου, η οποία οδηγεί σε αύξηση της αναλογίας μεταξύ ρίζας και βλαστού, συμβάλλοντας θετικά στην ανοδική μεταφορά νερού και θρεπτικών συστατικών από τις ρίζες προς τον βλαστό. Επιπλέον, οι αλλαγές στην παραγωγή των φυτορμονών στην ρίζα λόγω της καταπόνησης από χαμηλές θερμοκρασίες στο περιβάλλον αυτής, επηρέασαν σημαντικά την διαβίβαση ερεθισμάτων μεταξύ ριζών και υπέργειου μέρους των φυτών. Η επιρροή αυτή όμως παρατηρήθηκε μόνο στα φύλλα της ποικιλίας ‘Kommeet’ που εμβολιάστηκε στο ευαίσθητο στο ψύχος υποκείμενο, με αποτέλεσμα να προκληθεί ανισορροπία στο ορμονικό ισοζύγιο του εμβολίου σε αυτή την περίπτωση.

Τα αποτελέσματα της αξιολόγησης των γονιδίων του υποκειμένου 'LA 1777', τα οποία ελέγχουν βιοχημικά μονοπάτια και φυσιολογικές διαδικασίες σχετιζόμενες με ανοχή σε οριακά χαμηλές θερμοκρασίες είναι χρήσιμα για την κατανόηση των μοριακών μηχανισμών ανεκτικότητας της τομάτας σε χαμηλές θερμοκρασίες. Οι γνώσεις που αποκτήθηκαν από την έρευνα που διεξήχθη κατά την εκπόνηση της συγκεκριμένης διδακτορικής διατριβής θα μπορούσαν να αξιοποιηθούν για την συγκριτική αξιολόγηση της ανεκτικότητας διαφόρων γονοτύπων και συνδυασμών υποκειμένων/εμβολίων σε χαμηλές θερμοκρασίες. Τέλος, τα δεδομένα που προέκυψαν υποδεικνύουν γονίδια πού μπορούν να χρησιμοποιηθούν ως δείκτες σε προγράμματα γενετικής βελτίωσης, με στόχο την δημιουργία υποκειμένων εμβολιασμού τομάτας με ανεκτικότητα στις χαμηλές θερμοκρασίες.

CHAPTER 1. INTRODUCTION-LITERATURE REVIEW

Tomato (*Solanum lycopersicum* L.) is a major horticultural crop with an estimated global production of over 120 million metric tons and enormous economical importance. It is believed to originate from the coastal tropical and sub-tropical regions of South America and is adapted to warm climates (Jones, 1999). Its current economic optimum temperature (T) for greenhouse cultivation is 19-20 ^{o}C (Van der Ploeg and Heuvelink, 2005), whereas growth and development of agriculturally used cultivars are inhibited at temperatures below 12 °C (Criddle et al., 1997). Tomatoes are produced in the open field during summer and under cover throughout the year (Venema et al., 2008).Tomato plants grown for commercial purposes may be subjected to different types of stress during the cropping period. The main reasons for cultivating tomatoes under unfavorable soil and environmental conditions (Schwarz et al., 2010) is the limited availability of arable land and the high market demand for this commodity around the world.

A form of abiotic stress that is commonly encountered by vegetables and restricts their yield potential is exposure to sub-optimal temperatures (T), which range between two thresholds, a minimum (8-12 °C) and an optimum (18-27 °C) for tomato crops cultivated in greenhouses (Criddle et al., 1997; Schwarz et al., 2010). This threshold is defined as the threshold for optimal biochemical/physiological activity or morphological development and the threshold at which the plant can successfully complete its life cycle (Greaves, 1996). In the range above this threshold (approx. 25–30 °C), metabolic rates increase exponentially with temperature. Sub-optimal temperatures down to 10-12 °C adversely affect tomato growth and development through shortening of the internodes (which restricts plant height), retarded leaf expansion, reduced leaf number and total leaf fresh weight, while increasing the dry matter content and thickness of leaves as a result of increased starch storage (Venema et al., 1999). These effects are ascribed to the fact that when T falls below 12 ^{o}C growth is inhibited due to irreversible alterations and dysfunctions at the cellular level, particularly in species originating from warm-climates (Kodama et al., 1995). Indeed, profound alterations occur in several cellular processes, such as ion transport, photosynthesis, carbohydrate and lipid metabolism, protein synthesis, osmotic homeostasis and gene expression (Rosa et al., 2009a). As reported by Schwarz et al. (2010), each aspect of growth, development and/or fruit formation has its own temperature optimum, which varies among and within species as well with plant age. However, the most vulnerable stage in the growth cycle of higher plants is the reproductive phase (Nishiyama, 2005), and specifically the formation of reproductive organs such as flowers, fruits and seeds, the development of which depends on the interactions between plant morphology, physiology and growth conditions (Van der Ploeg and Heuvelink, 2005). According to these authors, the optimal T for fruit set is between 18ºC and 20°C. Temperatures below this level may lead to the suppression of yield due to decreased fruit set owing to a reduction in both pollen quantity and quality (Dominguez et al., 2005) and retardation of truss appearance (Van der Ploeg and Heuvelink, 2005), leading to a reduction in the number of fruit per plant which may, however, during long-term exposure result in larger fruits due to less inter-fruit competition (Van der Ploeg and Heuvelink, 2005). Additionally, at a cellular level temperatures below optimum impair cell membrane fluidity and permeability, thereby resulting in ion leakage (Abbas et al., 2012), whereas intra- and extracellular water and nutrient movements are inhibited (Salinas 2002; Mahajan and Tuteja, 2005), reactive oxygen species are generated (Gill and Tuteja, 2010), photosynthesis may be restricted (Theocharis et al., 2012) and yield reduced. Further alterations in physiological processes that are associated with increased sensitivity to sub-optimal T levels include changes in root phytohormone biosynthesis (Schwarz et al., 2010), which has an impact on root-to-shoot hormone signaling resulting in a tremendous reduction in plant productivity.

To avoid yield losses due to sub-optimal T, indoor production of this economically important crop is crucial. However, off-season cultivation entails high-energy inputs for heating during the cold season of the year, especially in North European countries. Indeed, Elings et al., (2005) calculated that a reduction of 2 ^{o}C in the mean T maintained inside the greenhouse leads to a saving of 16% in energy costs. Therefore, due to increasing energy prices and public concern about environmental problems related to CO_2 emissions from the combustion of fossil fuel, the greenhouse industry is forced to improve its energy-efficiency, defined as the amount of fruits produced per unit energy input (kg MJ^{-1}).

The high-energy costs required for greenhouse heating stress the need to seek alternative approaches for enhancing the tolerance of tomato to sub-optimal T stress, such as the introduction of new cultivars that are more tolerant to sub-optimal T (Ntatsi et al., 2014). An increase in the tolerance of tomato to sub-optimal T could extend the growing period in field-grown crops as well as in unheated greenhouses, which are very common in Mediterranean countries. Unfortunately, the very low genetic diversity of existing cultivars (Venema et al., 2008), which did not allow the identification of genes conferring tolerance to sub-optimal T (Schwarz et al., 2010), in combination with limitations in breeding methodology has caused this approach to fail to date. Nevertheless, the variation in low-temperature tolerance between wild tomato species (*Solanum* sp.), specifically those originating from high altitudes with large diurnal variations in day/night T, is much larger (Tachibana, 1982 and Venema et al., 2005). Thus, an alternative strategy to enhance the tolerance of common tomato cultivars or hybrids to sub-optimal T is to graft them onto wild tomato species that are compatible with the cultivated species and tolerant to sub-optimal T.

A promising tool to achieve this goal is grafting onto rootstocks that are known to affect canopy development, disease resistance or cold hardiness (Schwarz et al., 2010). The production of fruit vegetables using grafted seedlings started more than 50 years ago and has currently become a common practice in many parts of the world. Worldwide, a high percentage of fruit vegetables under intensive, commercial production are already grafted (Lee et al., 2010). The main objectives of using rootstocks to graft vegetables are: i) reduced incidence of soil borne diseases, ii) enhancement of tolerance to abiotic stress, iii) increased plant vitality and nutrient uptake, and iv) maintaining or even enhancing yield potential (Davis et al., 2008; Flores et al., 2010). Even though graft compatibility often limits rootstocks to a few closely related species, it has been found that interspecific hybrids often render high quality rootstocks which greatly increase the genetic diversity of the rootstock

Grafting does not automatically improve tolerance to sub-optimal T stress (Schwarz et al., 2010). Indeed, as reported by Khah et al. (2006), several scion/rootstock combinations of tomato did not respond positively in terms of growth and fruit yield under low T. Although the number of possible rootstock/scion combinations is theoretically unlimited, the response of each combination to low T stress depends on other environmental parameters as well (Schwarz et al., 2010). Hence, to reduce the lower threshold of optimal T for elite tomato cultivars by grafting, a better understanding of the mechanisms and signaling pathways governing the contribution of the root genotype to the stress tolerance of the scion is needed.

Previous research has indicated that the performance of a rootstock depends not only on its genotype but also on the scion genotype and *vice versa*, which means that the response of a grafted plant is specific for each rootstock/scion combination. In other words, a rootstock that is tolerant to sub-optimal T, may express this trait or not, depending on the genotype of the scion. This is because the tolerance to sub-optimal T is a complex secondary trait depending on many primary traits (e.g. root and leaf morphology characteristics, plant hormones, ROS scavenging compounds, etc.), which operate both in the root and the shoot. Thus, a change in any of these traits in the shoot when a different tomato hybrid is used as scion, may alter the interactions with other traits, thereby accentuating or attenuating the tolerance of the specific grafting combination to sub-optimal T. According to Jensen et al. (2003), acropetal and basipetal metabolite transport is modified by hormonal messengers under low T conditions. Hence grafting, which results in two different genotypes in the root and shoot, is an excellent tool to investigate interactions of metabolite transport with sub-optimal T. For example, Zhou et al. (2007) demonstrated that some signals (i.e. ABA/CK) originating from chilling-resistant cucumber rootstocks contributed to the protection of leaf photosynthesis in a chilling-sensitive scion. Nevertheless, the underlying signaling pathways are poorly understood.

The Solanaceae family includes many wild relatives of the cultivated tomato species *S. lycopersicum*, with different degrees of tolerances to abiotic and biotic stress. Because *S. lycopersicon* is characterized by low genotype diversity with respect to cold stress responses (Schwarz et al., 2010), the use of other Solana-species or of intraspecific breeds as rootstocks might be a useful alternative. For example, increased tolerance to cooling/sub-optimal temperature of the root zone might be achieved through the use of *S. habrochaites* 'LA1777' as a rootstock (Venema et al., 2008). According to (Venema et al., 2005, 2008), accessions of *Solanum habrochaites*, synonym *Lycopersicon hirsutum* Dunal (Spooner et al., 2005), are of particular interest as potential germplasm sources to widen the genetic variation in the low T tolerance of cultivated tomato. This wild tomato species originates from an altitude of 3,200 m (Rick 1994) where an adaptation to sub-optimal T stress can be expected (Patterson et al., 1978). The superiority of *S. habrochaites* in terms of cold adaptability is attributed to adaptive mechanisms that alleviate cell damage and preserve its reproduction ability under sub-optimal T conditions (Venema et al., 2008).

Comparative analyses of many physiological responses to cold stress conducted during recent decades resulted in several hypotheses that could provide explanations for the tolerance or sensitivity to chilling in plants, using S. *habrochaites* as a model

(Venema et al., 2005). Several studies on the genetic basis which elucidate the underlying key-molecular and physiological mechanisms of cold tolerance in S. *habrochaites* led to the identification of QTLs important for controlling shoot wilting under root chilling and for the plastochron index, as reviewed by Schwarz et al. (2010).

Recent studies indicate that moderately sub-optimal T has no adverse impact on the root growth of high-altitude accessions of *S. habrochaites* (Venema et al., 2008). Therefore, a reduction in the upward transport capacity of water and nutrients is not expected when this *S. habrochaites* accession line is exposed to sub-optimal T (Venema et al., 2008). Similarly, imbalances in the supply rate of root-deprived phytohormones to the scion caused by exposure to sub-optimal T are also not expected for *S. habrochaites*. This hypothesis is further strengthened by findings indicating that the use of rootstocks with a vigorous root system results in increased nutrient and water uptake, thereby enhancing the growth rate and yield performance of the whole plant (Lee, 1994).

Under specific environmental situations, such as sub-optimal T, or in specific plant genotypes an imbalance between root water uptake and leaf transpiration occurs. A mechanism to avoid stress-induced growth retardation is the modification of root water uptake capacity compared with stomata closure (Matsuo et al., 2009). According to Aroca et al., (2001) chilling sensitivity differences among genotypes are ascribed to different responses of root water uptake rate. Indeed, when the temperature falls below optimum, root water uptake decreases due to the decrease in vapor pressure difference between the leaf surface and the area (Aroca et al., 2003), while water viscosity increases (Bloom et al., 2004). According to the same authors, although transpiration decreases, the stomata of the sensitive genotypes remain open while those of the tolerant ones close rapidly, indicating an adaptive mechanism to sub-optimal T. Besides its functioning, low temperature affect root growth, size and architecture (Nagel et al., 2009). Changes in root morphology may be interpreted as adaptation of nutrient acquisition mechanisms to low T, aimed at extending the absorbing surface area per unit root weight or length (Macduff et al., 1986). Thus, the formation of a more extensive root system by the T-tolerant rootstocks of grafted tomato plants and the concomitant increase in root:shoot ratio as T falls,, provides an advantage in terms of nutrient and water uptake to these plants when exposed to sub-optimal T. An increase in root:shoot ratio has been interpreted by Equiza et al. (2001) as an adaptation aimed at overcoming restrictions in water absorption which, in the case of low T, might be related to increased water viscosity and root resistance to water transport. A putative osmosensor localized at the cell membrane was suggested for sensing the osmotic change in *Arabidopsis* cells (Urao et al., 1999). Cellulose, which constitutes the major part of plant cell walls and contributes to cell shape and plant morphology, is synthesized by cellulose synthase complexes localized on the plasma membrane (Doblin et al., 2002). An increase in the genes associated with this osmoprotectant in T-tolerant genotypes could explain why sub-optimal T has no adverse impact on the root growth of genotypes of increased tolerance, such as the high-altitude accessions of *S. habrochaites* (Venema et al., 2008), and therefore, why a reduction in upward transport capacity of water and nutrients is not expected when these accessions are exposed to sub-optimal T, as already reported by Bloom et al., (1998, 2004) who suggested that the uptake of some nutrients and water are strongly affected by reducing root T in non-grafted *S. lycopersicum* but not in *S. habrochaites*.

Plant metabolism is modulated due to an interaction of stress- and sugar-signaling pathways under abiotic stress conditions (Gupta and Knaur, 2005). During cold stress, sucrose accumulation in leaves leads to a feed-back inhibition of photosynthesis (Chiou and Bush, 1998; Ruelland et al., 2009). Thus, cellular components and structures are modified due to sub-optimal T exposure resulting, for example, in mitochondria swelling and disruption of protein-lipid accumulation and protein denaturation and stability (Kratsch and Wise, 2000; Siddiqui and Caviocchioli, 2006). Moreover, cellular dehydration caused by sub-optimal T stress is attributed to the reduced uptake of water by roots (Yadav, 2010) and the inhibition of stomatal closure. According to Chinnusammy et al., (2007), sub-optimal T reduces not only water but also nutrient uptake, thereby causing osmotic stress. In addition, sub-optimal T causes peroxidation of unsaturated membrane lipids (Theocharis et al., 2012) thereby increasing membrane permeability to nutrients and ions, resulting in ion leakage (Gao et al., 2008). Such modifications are capable of disorganizing the entire plastid leading to growth reduction, with an indirect yield loss. Furthermore, at sub-optimal T, the reactions of the Calvin cycle are down-regulated, and this may lead to over-reduction of the photosynthetic light reactions and generation of reactive oxygen species (ROS) (Ensminger et al., 2006).

ROS are generated in plant cells even during normal metabolic process, such as photosynthesis and respiration (Apel and Hirt, 2004). Under optimal growth conditions, the damaging effect of ROS is prevented through the scavenging activity of antioxidants, such as superoxide dismutase (SOD, EC 1.12.1.1) and guaiacol peroxidase

(GPOD, EC 1.11.1.7) (Sundar et al., 2004). ROS-scavenging capacity can be enhanced by hormones (e.g. cytokinins), as reported by Zhou et al. (2007). However, when the balance between the scavenging activity of antioxidants and ROS formation is disturbed due to sub-optimal T stress, oxidative damage results.

As reported by Zhou et al. (2007), some signals originating from the roots of a chilling-resistant cucumber rootstock (i.e. ABA and cytokinins) protected leaf photosynthesis in shoots of a chilling-sensitive scion. Under stress conditions, such as low temperature, the reactions of the Calvin cycle are down-regulated, and this may lead to over-reduction of the photosynthetic light reactions and the generation of reactive oxygen species (ROS) (Ensminger et al., 2006). Zhou et al. (2009) demonstrated that increased ABA concentration in xylem sap could enhance the activity of antioxidants and induce stomata closure, which could lead to decreased CO_2 fixation and increased ROS generation. The accumulated sugars may act as osmolytes or substrates for cellular respiration (Gupta and Knaur, 2005) or as antioxidative agents (Bogdanovic et al., 2008) that scavenge ROS (Noctor and Foyer, 1998).

The polyamines putrescine (Put), spermidine (Spd) and spermine (Spm) can also protect cells from oxidative damage by acting as ROS scavengers (Alcazar et al., 2010; Rhee et al., 2007; Zhao and Yang, 2008) or by stimulating non-photochemical quenching (Ioannidis and Kotzabasis, 2007). Put levels increase during cold stress in many plant species (Kushad and Yelenosky 1987; Lee et al., 2012; Shen et al., 2000) and may affect ABA biosynthesis through the activation of the *Arabidopsis AtNCED3* gene (Cuevas et al., 2008). Regulation of ABA homeostasis is an important process during plant adaptation to abiotic stress and involves changes in ABA biosynthesis, catabolism, transport and conjugation in a tissue-specific manner (Baron et al., 2012; Nambara and Marion-Poll 2005). ABA biosynthesis is controlled by the genes encoding 9-*cis*-epoxycarotenoid dioxygenases (*NCED*), which use substrates of the xanthophyll-cycle to produce xanthoxin, a precursor of ABA (Seo and Koshiba, 2002). Since at least two *NCED*s (*NCED1* and *NCED2*) play an important role in ABA biosynthesis, the use of mutants with impaired function of *NCED*s provide a useful tool to elucidate the involvement of ABA homeostasis in stress tolerance (Taylor et al., 2005). Focusing on tolerance to sub-optimal T in the root zone, the comparison of rootstock/scion combinations with different tolerance to sub-optimal T should provide a better understanding of the root to shoot interactions with respect to hormonal transport and signaling.

Plants have evolved adaptive mechanisms to alleviate cell damage and retain their ability to reproduce under sub-optimal T conditions. One of the mechanisms by which the rootstock may influence the stress tolerance of the scion is the induction of alterations in acropetal and basipetal metabolite transport through hormonal messengers (Jensen et al., 2003). With respect to the role of phytohormones, ABA seems to play a key role in sustaining root growth rates under drought stress conditions (Sharp and Le Noble, 2002 and Spollen et al., 2000). Furthermore, sub-optimal T conditions were found to slow down the upward transport of cytokinins arising from the roots, and this seems to restrict shoot biomass accumulation (Ali et al., 1996). On the other hand, Veselova et al. (2005) reported that the levels of indole-3-acetic acid (IAA) were raised in the shoot of wheat when the roots were cooled at 6 °C. Rayle and Cleland (1992) found that the retardation of root elongation imposed by sub-optimal T in cold-sensitive tomato cultivars is attributed to hormonal signals arising from the shoot, such as auxin, which affect the activity of H^+-ATPases and concomitantly apoplastic pH and the process of wall loosening. Nevertheless, cell elongation in roots is influenced by many other endogenous growth regulators, such as ethylene, abscisic acid, and cytokinin (Schwarz et al., 2010). With respect to the role of ethylene in the responses of tomato to low T, Huang and Lin (2003) found that ethylene production tends to increase in tomato seedlings treated with cold water and this leads to shoot growth inhibition. Further alterations in physiological processes that are associated with increased sensitivity to sub-optimal T levels include reductions in the hydraulic conductance of the roots, which restrict water and nutrient uptake (Tindall et al., 1990 and Aroca et al., 2001), insufficient stomata closure resulting in increased photoinhibition at low T (Venema et al., 2005), and changes in root phytohormone biosynthesis which also affect root-to-shoot hormone signalling (Schwarz et al., 2010).

As indicated above, another adaptive mechanism is stomata closure. The stomata of chilling-susceptible tomato plants did not close at 5 °C until a water loss equivalent to 20% of the fresh weight was reached (Bloom et al., 2004), while transpiration of cold-adapted plants was more responsive to reduced water status at that T (Guye and Wilson, 1987). This was associated with a higher ABA content in cold-acclimated plants (Daie and Campbell, 1981). Oswald et al. (2001) suggest an interaction between photosynthetic electron transport and ABA-derived regulatory mechanisms which modulate the expression of genes linked to photosynthesis in response to demand. As stated by Hetherington and Davis (1998), ABA triggers stomatal closure, which limits water loss through transpiration. However, according to Holbrook et al., (2002), xylem ABA and the ability of roots to produce ABA is not related to stomata closure, and the signal from the roots that triggers ABA production is unknown. ABA also triggers the activation of freezing tolerance mechanisms (COR genes), through secondary messengers such as H_2O_2 and Ca^{2+} (Xiong et al., 2001). Moreover, many cold-regulated genes of *Arabidopsis* were found to be inducible by ABA as well as by cold. According to Atkin et al., (1973), low root temperatures lead to an increase in the upward transport of abscisic acid, inducing accumulation of ABA in the shoot. ABA is also a stress signal, which moves from the roots to the aerial part of the plant via the xylem. ABA accumulated in root tissues is released into the xylem vessels and transported to the shoot where stomata and meristematic activities are regulated to enable the plant to cope with the stress situation. Endogenous ABA can also be synthesized in the shoots and transferred through the phloem to the roots. Thus, ABA is a plant hormone that can be produced in both root and shoot, and transported acropetally through the xylem and basipetally through the phloem, respectively (Taiz and Zeiger, 2007), making signal transduction *via* ABA possible in both directions. The recirculation of ABA between xylem and phloem implies that xylem ABA concentration in grafted plants depends on the genotype of both rootstock and scion. ABA may function as a growth promoter under stress conditions, such as soil compaction (Mulholland et al., 1996, 1999) and drought (Sharp and LeNoble, 2002), but may also reduce shoot growth in plants exposed to water stress (Creelman et al., 1990; Saab et al., 1990; Zhang and Davies, 1990). Moreover, as reported by Bloom et al. (2004), several other signals such as cytokinins and nitric oxide appear to be associated with ABA in promoting stomatal closure. It is clear, therefore, that ABA produced under low temperatures plays an important role in the tolerance of plants to T stress. However, little is known about the role of ABA in tomato responses to sub-optimal T.

The use of grafted tomato plants with distinctly different root and shoot genotypes regarding the biosynthesis of and/or sensitivity to specific plant hormones might be an efficient tool to elucidate the role of these hormones in plant tolerance to sub-optimal T. Indeed, several mutants lacking or overproducing specific plant hormones, such as ABA ethylene, etc. are available for research purposes (Rodriguez et al., 2010, Ntatsi et al., 2012, 2013). Using this approach, it is possible to relate specific physiological characteristics (e.g. hormone levels and mobility in root and shoot, gas exchange, indicators of oxidative stress, nutrient uptake efficiency, antioxidant enzymes activity, and carbohydrate accumulation) to plant tolerance to sub-optimal T and yield performance.

To elucidate the crucial physiological and molecular mechanisms that underline the positive impact of ‘LA 1777’ rootstocks on tomato scion performance at sub-optimal temperatures and therefore relate specific physiological characteristics (e.g. hormone levels and mobility in root and shoot, gas exchange, indicators of oxidative stress, antioxidant enzymes activity, and carbohydrate accumulation) to this tolerance and concomitant yield performance, microarray analysis is required. Gene expression profiling using cDNA microarrays is a novel approach for identifying even more transcripts and pathways related to tolerance mechanisms. Abiotic-stress transcriptome profiling in model species, such as *Arabidopsis*, has revealed several new stress-related pathways in addition to the previously well-described CBF pathway (Chinnusamy et al., 2007; Zhou et al., 2011). In tomato, transcriptome analysis has been used to compare patterns of gene expression under salt or drought stress (Gong et al., 2010; Sun et al., 2010). However, to the best of our knowledge, comparative transcriptome analysis of cold-tolerant and cold-sensitive tomato under sub-optimal T stress has yet to be reported.

Following this approach, it is possible to identify and evaluate genes controlling biochemical reaction chains and physiological procedures that are related to sub-optimal T tolerance. The knowledge obtained could be subsequently utilized to establish biomarkers that might be used to screen not only wild tomato genotypes serving as rootstocks, but also rootstock/scion combinations that are likely to be tolerant to sub-optimal T.

From the foregoing it is apparent that the use of grafting as a tool to alleviate the adverse effect of sub-optimal T stress on tomato crop performance is a multi-complex phenomenon. Thus, its investigation requires approaches at different levels, namely agronomical, physiological, biochemical and molecular. As already reported, rootstocks may affect canopy development, disease incidence and cold hardiness. Interactions between rootstocks and scions originate from alterations in the exchange of metabolites initiated through hormonal messengers (Jensen et al., 2003). Thus, at least some plant hormones are directly or indirectly involved in the responses of plants to sub-optimal T. Therefore the first experiment of this thesis was designed so as to provide an insight into the contribution of phytohormones in alleviating the impact of sub-optimal temperature stress on grafted tomato. The use of grafted tomato plants with distinctly different root and shoot genotypes regarding the biosynthesis of or sensitivity to specific plant hormones might be an efficient tool to elucidate the role of these hormones in plant tolerance to sub-optimal T. A similar approach was recently applied by Albacete et al. (2008, 2009) and Perez-Alfocea et al. (2010) to elucidate the role of phytohormones in salt tolerance of tomato. The research presented in this paper was designed to provide a better understanding of the contribution of auxin (IAA), ethylene (ET), ABA, cytokinin (CK) and salicylic acid (SA) to the response of tomato to sub-optimal T stress. We investigated genetic combinations of mutants deficient in biosynthesis/metabolism of ABA, CK or SA or less sensitive to IAA or ET, self-grafted or grafted with their wild-type counterparts. A clear conclusion of this study was that hormonal signaling aimed at plant adaptation to stress conditions seemed to be an important factor in regulating plant growth under sub-optimal T conditions. ABA, auxin and SA appeared to be the key-hormones involved and may therefore be considered those on which plant breeders have to focus in relevant breeding programs for tomato response to sub-optimal T. Consequently, the research presented in the second experiment of this thesis aimed at obtaining a better understanding of the implications of ABA biosynthesis and homeostasis in the responses of tomato to sub-optimal T stress in the root zone. To distinguish between the functions of root- and shoot-synthesized ABA, self- and reciprocal- grafting of the tomato mutant ‘notabilis’, which carries a null mutation in the ABA biosynthesis gene *LeNCED1* (Burbidge et al., 1999), and its near-isogenic wild-type counterpart ‘Ailsa Craig’, was performed. Links between ABA, sugar, and polyamine metabolism were studied under both control/optimal and sub-optimal T in the root zone. The results clearly indicated that further research was needed to elucidate root to shoot interactions with respect to hormonal transport and signaling under sub-optimal T in the root zone and that root-delivered physiological and molecular mechanisms were involved in optimizing rootstock-scion interaction and scion performance.

As already reported, *Solanum habrochaites* is of particular interest as a potential germplasm source to widen the genetic variation of the cultivated tomato for low temperature tolerance. However, all the experiments that support the hypothesis that ‘LA 1777’ is able to alleviate low-temperature stress for different scions were tested on a relative short-term basis. No production data were available for long-term grafting experiments. Thus a third experiment was designed to test the hypothesis that using wild relatives of *S. lycopersicon* as rootstocks, characterized by a vigorous root system and tolerance to sub-optimal T, may minimize yield losses in elite cultivars of grafted tomato when exposed to sub-optimal T. In particular, the following genotypes were used as rootstocks: a) the cold tolerant *S. habrochaites* accession 'LA 1777' (Venema et al., 2008) and b) the elite cultivar Moneymaker which, according to Venema et al., (2008), appears to be cold-sensitive. The two tested rootstocks were grafted onto scions of the same commercial tomato cultivar, 'Kommeet'. Moreover, a control treatment with self-grafted 'Kommeet' plants was applied, to avoid confounding any effects imposed by the grafting incision with those arising from the rootstock genotype. The impact of the rootstock genotype on plant growth and yield under conditions of sub-optimal (intermediate or low) T was assessed by measuring characteristics of shoot and root growth, fruit set, yield, and fruit quality. To elucidate the physiological mechanisms underlying the observed effects on growth and yield, carbohydrate accumulation, C:N ratio, oxidation characteristics, and antioxidant enzyme activities were also measured. The results of this experiment indicated that the use of cold-tolerant accessions of *S. habrochaites* as tomato rootstocks can enhance the tolerance of grafted plants to sub-optimal T. However, protection conferred by S. *habrochaites* against cold-induced stress may be not beneficial in terms of yield under sub-optimal T conditions because this wild tomato may impair scion pollen fertility even when used as a tomato rootstock. To elucidate the crucial physiological and molecular mechanisms that underline the positive impact of *S. habrochaites* accession LA 1777 rootstocks on tomato scion performance at sub-optimal temperatures and therefore relate specific physiological characteristics (e.g. hormone levels and mobility in root and shoot, gas exchange, indicators of oxidative stress, antioxidant enzyme activity, and carbohydrate accumulation) to this tolerance and concomitant yield performance, a fourth experiment was performed using microarray analysis. To the best of our knowledge, comparative transcriptome analysis of cold-tolerant and -sensitive tomato genotypes under sub-optimal T stress has yet to be reported. Therefore, gene expression between the wild tomato S. *habrochaites* accession LA1777 and the *S. lycopersicon* cultivar Moneymaker were analyzed comparatively. The results presented here provide new insights into the molecular mechanisms underlying sub-optimal T tolerance of the wild tomato S. *habrochaites*. The knowledge obtained could then be utilized to establish biomarkers that might be used to screen not only wild tomato genotypes serving as rootstocks, but also rootstock/scion combinations that are likely to be tolerant to sub-optimal temperature. Thus, the introgression of desirable genes related to sub-optimal temperature tolerance into appropriate rootstock genotypes could be made more efficient by Marker Assisted Selection (Schwarz et al., 2010).

CHAPTER 2. MATERIALS AND METHODS

2.1. Plant material and growth conditions

2.1.1. Contribution of phytohormones in alleviating the impact of sub-optimal temperature stress on grafted tomato

Six parallel experiments with reciprocal genetic combinations of tomato mutants and their wild-type counterparts were conducted from 07 April to 26 May 2010. The experiments were conducted in a heated greenhouse at the Leibniz-Institute of Vegetable and Ornamental Crops, Großbeeren, Germany (latitude 52° 20′ N, longitude 13° 18′ E, altitude 40 m). The phytohormone mutants used were: (a) the ABA deficient (−ABA) tomato mutant ‘notabilis’ which is believed to be a null mutation in the gene LeNCED1, which encodes the biosynthesis of a 9-cis-epoxycarotenoid dioxygenase involved in ABA biosynthesis, and is a recessive mutation of the parental variety ‘Ailsa Craig’ (Thompson et al., 2004; A.J. Thompson, Univ. of Cranfield, UK); (b) the −ABA mutant ‘sitiens’ which is considered to contain a mutation in an aldehyde-oxidase (AO) gene specific for ABA biosynthesis (Harrison et al., 2011 and Seo and Koshiba, 2002), a recessive mutation of the parental variety ‘Moneymaker’ (M. Koornneef, Max Plank Institute for Plant Breeding Research, Köln, Germany); (c) the ‘Never-ripe’ (Nr) tomato mutant present in ‘Ailsa Craig’, which is ethylene-insensitive (−ETsens) and unable to perceive ethylene due to a mutation in the Never-ripe (Nr) ethylene-binding domain (Lanahan et al., 1994; T. Wills, Tomato Genetics Resource Centre, U.C. Davis, USA); (d) ‘diageotropica’ (dgt), which is a low auxin-sensitivity mutant (−IAAsens) that arose from a spontaneous, single gene, a recessive mutation of the parental variety ‘VFN-8’ (Muday et al., 1995; T. Wills Tomato Genetics Resource Centre, U.C. Davis, USA); (e) the transgenic line dgt-‘CKX2’ × ‘Moneymaker’ (equivalent to ‘CKX2’ × ‘Moneymaker’) generated by overexpressing the cytokinin oxidase from ‘Micro-Tom’ × ‘Moneymaker’, which results in plants with low endogenous cytokinin levels (−CK) (L.E.P. Perez, Univ. Sao Paulo, Brazil); and (f) ‘nahG’, a transgenic tomato expressing the salicylate hydroxylase-encoding gene nahG, which prevents the accumulation of SA (−SA) by converting it to catechol (Shah et al., 1997), a recessive mutation of the parental variety ‘Moneymaker’ (J. Jones, Sainsbury Lab. John Innes Centre Norwich, UK). The use of the two ABA mutants was aimed at testing whether mutants originating from different wild-type cultivars with reduced biosynthesis of the same plant hormone, respond differently to sub-optimal temperature stress. The wild-type cultivars used were: (a) ‘Ailsa Craig’ as a standard ABA-producing and ETsens cultivar, (b) ‘Moneymaker’ as a standard ABA- and SA-producing cultivar, (c) ‘VFN-8’ as a standard IAAsens cultivar, and (d) ‘Micro-Tom’ as a standard cytokinin-producing cultivar.

Tomato seeds of the mutants and cultivars mentioned above were germinated and grown in vermiculite for about 20 days. Grafting was performed when seedlings had developed 3–4 true leaves manually by the technicians at the IGZ Grossbeeren using the tube method. The tomato mutants were self-grafted and reciprocally grafted in combination with their parental wild-type cultivars. The genetic combinations were transferred into gullies (8 m × 0.2 m × 0.07 m) with a recirculating nutrient solution (de Kreij et al., 1997) and grown hydroponically. The rootstock/scion combinations with respect to standard (+) or deficient (−) in hormone biosynthesis/catabolism or in hormone sensitivity (sens), specifically abscisic acid (ABA), ethylene (ET), auxin (IAA), cytokinin (CK), and salicylic acid (SA), were as follows: +/+, +/−, −/+ and −/−. Due to technical reasons, the −CK/−CK genetic combination was unsuccessful and, therefore, a treatment with low CK in both, rootstock and scion, was not tested. Prior to transplanting, the roots of the young seedlings were carefully washed in tap water to remove adhering vermiculite. The gullies were supplied continuously with nutrient solution at a flow rate of 2 l min^{-1} which was pumped from a 150 l supply tank. During the growing period of 49 days (from planting until harvest), the nutrient solution consumed was replaced with replenishment solution from a storage tanks when necessary. The pH of the solutions was adjusted daily to 5.6 by adding appropriate amounts of 1N HNO_3 stock solution. Each gully contained 12 plants and the plant density was approximately 2 plants m^{-2}. Four plants per treatment were used. After transplanting and during the initial 14 days (optimal period), plants were cultivated at a mean temperature of 19.8±2.4 °C (day/night T = 21.8 °C/17.9 °C). Subsequently, the plants were exposed to a moderately low temperature (sub-optimal T period) for 14 days at 15.1 ± 3.1 °C (day/night 17.3 °C/13.8 °C). During the experiment, the mean relative humidity was 87%, the CO_2 concentration was 400 µmol mol^{-1}, and the mean daily photosynthetic active radiation was 21 ± 7.2 mol m^{-2} d^{-1} inside the greenhouse with a maximum PAR of 2000 µmol m^{-2} s^{-1}.

2.1.2. A study on ABA involvement in the response of tomato to sub-optimal root temperature using reciprocal grafts with ‘notabilis’, a null mutant in the ABA-biosynthesis gene *LeNCED1*

The ‘notabilis’ mutant is a near-isogenic line derived from repeated backcrossing to the cultivar Ailsa Craig which carries to a function the wild-type *LeNCED1* gene (Maxon-Smith and Ritchie, 1983). Self- and reciprocal grafting of the mutant and ‘Ailsa Craig’ was conducted in a heated glasshouse at the Leibniz-Institute of Vegetable and Ornamental Crops, Großbeeren, Germany (latitude 52° 20' N, longitude 13° 18' E, altitude 40 m). Seeds were germinated in vermiculite for about 20 days. Splice grafting (Savvas et al., 2011) was performed when seedlings had developed 3-4 true leaves. The rootstock/scion combinations, using conventional tomato genetics notation, were +/+, +/*not*, *not*/+ and *not*/*not*, where *not* represents the ‘notabilis’ genotype and “+” the wild-type functional allele. In October 2010, grafted tomato plants were transferred to gullies (8 m×0.2 m×0.07 m) in which a standard nutrient solution for tomato (de Kreij et al., 1997) re-circulated. Prior to transplanting, the roots of the young seedlings were carefully washed in tap water to remove aggregates of the growing medium. The gullies were continuously supplied with nutrient solution which was pumped from a 150 l supply tank at a flow rate of 2 l min^{-1}. Twelve plants were accommodated in each gully with a plant density of approximately 2 plants m^{-2}. During the growth period of 30 days (from planting until harvest), the nutrient solution was replenished on a daily basis. The pH in the re-circulating nutrient solutions was adjusted daily to 5.6-5.7 by adding appropriate amounts of 1N HNO_3 stock solution. The experimental installation consisted of two groups of channels differing in the temperature (T) of the re-circulating nutrient solution, which was either optimal (day and night 25±0.6 °C) or sub-optimal (day and night 15±0.4 °C). The target solution temperatures were accurately maintained by cooling and heating pipe systems which were connected to the respective solution tanks. The mean daily air T in both treatments was 25±0.8 °C with a maximum and minimum of 22.4 and 25.2 °C, respectively. The mean relative humidity was 70%, the CO_2 concentration 400 µmol mol^{-1} and the mean daily photosynthetically active radiation 15 mol m^{-2} d^{-1}.

2.1.3. Growth, yield, and metabolic responses of temperature-stressed tomato to grafting onto rootstocks differing in cold tolerance

At the Leibniz Institute of Vegetable and Ornamental Crops, Großbeeren, Germany (latitude 52° 20' N, longitude 13° 18' E, altitude 40 m), the commercial tomato cultivar Kommeet was cultivated following self-grafting or grafting onto the tomato cultivar ‘Moneymaker’ or onto the line accession ‘LA 1777’ (S. *habrochaites*). Seeds of ‘LA 1777’ were sown in coarse sand on 20 June 2011; the two other cultivars were sown one week later. Grafting was performed one month afterwards, when seedlings had developed 3-4 true leaves.

Grafted plants were transplanted on 11 Aug 2011 into six 60 m^2 greenhouse cabins and cultivated at a heating set point of 16/18 °C for night/day, respectively. Gable peak ventilation was used once air temperatures reached 27 °C for both day and night. At a relative humidity above 80 % the gable vents were opened for exchange with outside air to reduce relative humidity. Pure carbon dioxide (CO_2) was supplied in order to keep CO_2 concentration in all cabins at ambient levels matching the outside environment.

Grafted plants were transferred into gullies (8 m×0.2 m×0.07 m) where they were grown in nutrient film technique. A standard nutrient solution (de Kreij at al. 1997) for tomato was prepared by mixing stock solutions and rain water (de Kreij at al. 1997) and was supplied to the gullies every 10 min for 20 sec. The composition of the nutrient solution was measured periodically in the laboratory and corrected when necessary.

Once the second truss was flowering, on 9 September, set points for heating by night/day were shifted within three days to 18/20, 14/16 and 9/11 °C in each of the two greenhouse cabins related. Different set points for heating in combination with global radiation and outside temperature (T) resulted in mean cabin T during the treatments of 19.4 °C (optimal), 17 °C (intermediate) and 14.6 °C (low).

Differences in the mean T resulted mainly from the differences during the night phase, while during the daytime and more specifically the middle of the day T differences between treatments were slight due to solar radiation and equal set points for ventilation. Towards the end of the experiment, however, daytime solar radiation could not compensate for lower heating set points in the low T treatments resulting in mean average T in the low T treatment of only 11 °C. Treatments had minimum/maximum T as follows: optimal 14.1/30.0, intermediate 12.7/30.7, and low 9.2/30.1 °C.

Mean daily photosynthetically active radiation (PAR) at the canopy top decreased from 13.7 mol m^{-2} during the first four weeks after planting to 2.5 mol m^{-2} during the last four weeks of the experiment. Mean daily integral of PAR over the entire treatment period was 7.4 mol m^{-2} d^{-1}. Experiment was terminated on 15 Dec 2011.

2.1.4. Expression profiling of tolerant and sensitive tomato rootstock genotypes under sub-optimal temperature stress

In a heated glasshouse at the Leibniz-Institute of Vegetable and Ornamental Crops, Großbeeren, Germany (latitude 52° 20' N, longitude 13° 18' E, altitude 40 m) the commercial tomato cultivar ‘Kommeet’ was grafted onto the tomato cv. ‘Moneymaker’ or onto the line accession ‘LA 1777’ of the wild tomato species S. *habrochaites*. Seeds of these two tomato genotypes were germinated in vermiculite for about 20 days. Splice grafting (Savvas et al., 2011) was performed when seedlings had developed 3-4 true leaves. In December, grafted tomato plants were transferred into gullies (8 m×0.2 m×0.07 m) in which a standard nutrient solution for tomato (de Kreij at al., 1997) was re-circulated. Prior to transplanting, the roots of the young seedlings were carefully washed in tap water to remove aggregates of the growing medium. The gullies were continuously supplied with nutrient solution which was pumped from a 150 l supply tank at a flow rate of 2 l min^{-1}. Twelve plants were accommodated in each gully with a plant density of approximately 2 plants m^{-2}. During the growth period of 30 days (from planting until harvest), the nutrient solution was replenished on a daily basis. The pH in the re-circulating nutrient solution was adjusted daily to 5.6-5.7 by adding appropriate amounts of 1N HNO_3 stock solution. The experimental installation consisted of two groups of channels differing in the temperature (T) of the re-circulating nutrient solution, which was either optimal (day and night 25±0.6 °C) or suboptimal (day and night 15±0.4 °C). The target solution temperatures were accurately maintained by cooling and heating pipe systems which were connected to the respective solution tanks. The mean daily air T in both treatments was 25±0.8 °C, with a maximum and minimum of 22.4 and 25.2 °C, respectively. The mean relative humidity was 70%, the CO_2 concentration 400 µmol mol^{-1} and the mean daily photosynthetically active radiation 15 mol m^{-2} d^{-1}.

2.2. Growth measurements

In the 1st experiment biomass could not be measured during the different temperature periods since the plants could not be destroyed or taken out from the cultivation system. Therefore, at the beginning and end of each period, leaf width (*w*, cm) was measured, and leaf area of each leaf (*All*, dm^2) and of the whole plant (*Alp*, m^2) were calculated as described by Schwarz and Kläring (2001). The values obtained were used to calculate the relative growth rate of *Alp* (RLA). Shoot length of four plants per treatment was measured at the same time and relative growth rate of shoot length (RSL) was calculated. Since the specific leaf area calculated at the end of the experiment did not differ between treatments, we assumed leaf area was suitable trait to characterize biomass.

At the end of the 2nd and 3rd experiments, leaf width (*w*), shoot length and number of leaves were measured for two plants per experimental unit. Leaf area (A_{lp}, m^2 $plant^{-1}$) was calculated on the basis of leaf width, as described by Schwarz and Kläring (2001) in the 2nd and 3rd experiment. In the 3rd experiment at four dates, 20, 34, 59, and 95 days after treatment start, the total number of flowers and fruits were counted at each truss beginning with the third until the eights. Leaf area was calculated as a mean of five fully expanded leaves. Therefore we measured the width of leaf 11 to 15 counted from the shoot tip at the four dates 20, 34, 59, and 95 days after treatment start (Schwarz and Kläring, 2001). From all the experiments harvested plants were divided into stems, leaves and roots. Additionally, in the 3rd experiment, fruits were recorded, weighed fresh (F_{rp}, g $plant^{-1}$), then dried separately at 70 °C to constant mass, the weight of which was measured. Root samples of about 1 g fresh weight were taken to measure the specific length of the roots (*Lrw*, m g^{-1}) and their mean diameter (2*Rr*, mm) using an image analysis system (WinRhizo, Regents Instruments, Quebec, Canada). Total root length ($RL = Lrw \times Frp$, m $plant^{-1}$), root surface area ($Arw = RL \times Rr \times 2\pi$, m^2 $plant^{-1}$), and the specific root area related to fresh weight were estimated ($SRA = A_{rw} \times F_{rp}^{-1}$, cm^2 g^{-1}) (Ntatsi et al., 2013).

2.3. Yield

In the 3rd experiment with 6 heated glasshouse rooms, harvesting commenced on 26 October and terminated on 15 December 2011. The number of harvested fruit per plant and the total fruit yield per plant were recorded up to the 6th truss. Moreover, the total number of flowers and fruit on each plant were measured until the end of the experiment (from the 3rd up to the 8th truss) in order to estimate the impact of the treatments on fruit set.

2.4. Gas exchange, chlorophyll fluorescence and chlorophyll measurements

At the end of each T period (optimal and sub-optimal) in the first experiment and one day before the termination in the second and fourth experiments, four plants from each grafting treatment were used for leaf gas exchange measurements. The most recent fully expanded leaf was used in an open gas exchange system (Li-6400, Li-Cor, Inc., Lincoln, NE, USA). Net CO_2 assimilation (A, μmol m^{-2} s^{-1}), stomatal conductance (g_s, mmol m^{-2} s^{-1}), intercellular CO_2 concentration (c_i) and transpiration rate (E, mmol m^{-2} s^{-1}) were determined between 9:00 and 12:00 hrs at a photosynthetic photon flux density (PPFD) of 1000 μmol m^{-2} s^{-1}. The relative humidity was maintained at 70% and the leaf T in the leaf chamber was adjusted to 28±0.5 °C. Water use efficiency (WUE, μmol $mmol^{-1}$) was calculated as A/E. Chlorophyll fluorescence was measured on the same leaves used for gas exchange measurements after light- or dark-adaptation by employing a pulse amplitude modulated leaf chamber fluorometer (Li-6400, Li-Cor, Inc., Lincoln, NE, USA). Minimal fluorescence values in the dark-adapted state (F_o) were obtained by application of a low-intensity red measuring light source (630 nm), whereas maximal fluorescence values (F_m) were measured after applying a saturating light pulse of 8,000 μmol m^{-2} s^{-1}, and thus maximum/effective quantum yield of PSII for Fv/Fm in the dark-adapted state was calculated as $F_v/F_m = (F_m - F_o)/F_m$. The leaf area assayed was dark-adapted for at least 30 min prior to F_v/F_m measurements. Minimum (F'_o) and maximum (F'_m) values of fluorescence in the light-adapted state at 800 μmol m^{-2} s^{-1} were also obtained. After leaves were continuously illuminated with actinic light for 6 min, the steady-state fluorescence (F_s) was recorded. Using these parameters, the following ratios were calculated: maximum/effective quantum yield of

PSII for F'v/F'm in the light-adapted state as $F'_{v}/F'_{m}=(F'_{m}-F'_{o})/F'_{m}$, effective quantum yield as $\Phi_{PSII}=(F'_{m}-F_{s})/F'_{m}$, photochemical quenching as $q_{P}=(F'_{m}-F_{s})/F'_{m}-F'_{o}$, and non-photochemical quenching as $NPQ=(F_{m}-F'_{m})/F'_{m}$.

At the end of each *T* period (optimal and sub-optimal) in the first experiment, chlorophyll measurements were conducted using the Minolta SPAD-502 Chlorophyll Meter (Spectrum Technologies, Plainfield III) and the calibration equation between readings of the instrument and leaf chlorophyll content was used as described by Kapotis et al. (2003).

2.5. ABA measurements

Extraction, clean-up and analysis of ABA were performed only in the 1st and 2nd experiments and carried out according to a modified protocol described by Müller et al. (2002). Shock-frozen plant material of about 100 mg fresh mass was extracted using 10 µl of internal standard (1.03 pmol/µl $(^{2}H)_{6}$-ABA). For the clean-up, solid phase extraction columns (Chromabond NH_2 shorty 10 mg, Macherey-Nagel GmbH & Co. KG, Düren, Germany) were used in the following sequence: Equilibration with 200 µl diethyl ether; application of the dissolved sample; washing (a) twice with 200 µl diethyl ether, (b) three times with 200 µl of a mixture of chloroform/2-propanol (2:1, v/v), (c) three times with 200 µl chloroform and (d) with 100 µl diethyl ether; elution of analytes with three flushes of 200 µl diethyl ether containing 4% acetic acid. Combined eluates were reduced to dryness in a stream of nitrogen, methylated and further treated and analysed by GC–MS/MS (Müller et al., 2002), using a Varian Saturn 2200 ion-trap mass spectrometer connected to a CP-3800 gas chromatograph fitted with a CombiPal autoinjector (Agilent, Santa Clara, California, USA).

2.6. Analytical determinations

In the 2nd, 3rd and 4th experiments, soluble sugars were measured according to Geigenberger and Stitt (1993), starch according to Sonnewald (1992), and total amino acids according to Moore and Stein (1948) using a Synergy HT 96-position microplate spectrophotometer (BioTek instruments GmbH, Winooski, VT, USA).

Carotenoids (lutein and ß-carotene) and chlorophyll a and b were determined by HPLC according to Krumbein (1996). The analyses were carried out in the 2nd experiment as double estimations of four replications of four leaves per replicate from each grafting and temperature combination.

Hydrogen peroxide (H_2O_2) was determined according to Mukherjee and Choudhuri (1983) and electrolyte leakage as described by Lutts et al. (1995). Lipid peroxidation was determined in terms of the concentration of thiobarbituric acid-reactive substances (TBARS) and quantified on its product, malondialdehye (MDA) according to the method described by He et al. (2009) and Hodges et al. (1998). No MDA could be detected in fruit of the 3rd experiment and therefore no data are presented.

For enzyme analysis, 0.1 g of each pulverized, frozen sample (leaf, root or fruit) was homogenized with ice-cold 25 mM HEPES buffer (pH 7.8) including 0.2 mM EDTA, 2 mM ascorbate and 2% (w/v) polyvinylpyrrolidon (PVP). The homogenate was centrifuged at 4 °C and 14,000 rpm for 5 min. The supernatants were used for enzyme analysis. All steps in the preparation of the enzyme extracts were carried out at 4 ^{o}C.

Protein content was determined as described by Bradford (1976) with bovine serum albumin as the standard.

Ascorbate peroxidase (APX) activity was determined according to Nakano and Asada (1981) as the decrease in absorbance at 290 nm due to ascorbate oxidation (E = 2.8 mM^{-1} cm^{-1}) and the reaction was initiated by adding hydrogen peroxide.

Catalase (CAT) activity was measured according to Cakmak and Marshner (1992), as modified by Ogweno et al. (2009). Briefly, 200 µl of reaction mixture containing 25 mM potassium phosphate buffer (pH 7.0), 0.1 mM EDTA, 10 mM H_2O_2 and 10 µl plant extract were used. The decline in absorbance at 240 nm due to H_2O_2 decomposition was measured for five minutes (E = 39.4 mM^{-1} cm^{-1}).

Guaiacol peroxidase (G-POD) activity was determined according to Cakmak and Marshner (1992) as modified by Egley et al. (1983). Increase in absorbance at 510 nm caused by guaiacol oxidation (E = 26.6 mM^{-1} cm^{-1}) was measured over 50 min.

Glutathione reductase (GR) activity was assayed according to Rao et al. (1996), with some modifications. Briefly, the reaction mixture in a total volume of 200 µl consisted of 25 mM potassium phosphate buffer (pH 7.0), 0.1 mM EDTA, 0.5 mM oxidized glutathione, 0.12 mM NADPH and 10 µl plant sample. GR activity was measured at 340 nm by following the decrease in absorbance of oxidized glutathione (GSSG) (E = 6.2 mM^{-1} cm^{-1}).

Superoxide dismutase (SOD) activity was determined using the method of Rao and Sresty (2000). One unit of enzyme activity was defined as the amount of enzyme required to result in a 50% inhibition in the rate of nitro blue tetrazolium reduction measured at 560 nm.

In the second experiment polyamines (putrescine, spermidine and spermine) were determined according to Lee et al. (2012).

Total C and total N were determined only in the 3rd experiment and measured in powdered oven-dried leaf, root and fruit samples by applying Dumas combustion using a C-N analyzer (LECO CHN-1000).

2.7. Gene expression

In the 2nd experiment, gene expression was determined according to Schaarschmidt et al. (2006), with some modifications. The RNA extraction was performed by the RNAeasy® Plant Mini Kit (Qiagen GmbH, Hilden, Germany) while the concentration was estimated using a spectrophotometer (NanoDrop ND-1000, PeqLab Biotechnologie GmbH, Erlangen, Germany). To avoid genomic DNA contamination, samples were treated with TURBO DNase (Ambion Inc. Austin, TX, USA) following the manufacturer´s instructions. Prior to cDNA synthesis, an aliquot of the samples was checked for genomic DNA contamination by quantitative PCR with intron-specific primers. For cDNA synthesis SuperScriptII reverse transcriptase (Invitrogen Inc., Carslbad, CA, USA) was used according to the manufacturer´s instructions. cDNA quality was checked a 1.2 % agarose gel. The efficiency of cDNA synthesis was estimated by quantitative real-time polymerase chain reaction (qRT-PCR) using two primer pairs amplifying the 5´and 3´regions of glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (AB110609, forward 5´-GATATCCCATGGGGTGAAGC-3´ and reverse 5´-CACAACCTTCTTGGCACCAC-3´and forward 5´-GGCTGCAATCAAGGAGGAAT-3´ and reverse 5´-CAGCCTTGGCATCAAAAATG-3´). The expression of the genes *LeNCED2* (Zhang et al., 2009; EU912387) (forward TCCATGGTCATTCTGGAATTGC and reverse CATTAGCAACTCCAGTCCCATG), NCED3 (GQ222384.1) (forward

TTCGCGATCACTGAGAAATACG and reverse GTTCTTGTCATAGATCACCGGC), LeNCED6 (XM_004240167) (forward ATCATCACCGTCACAATCATCG and reverse TTCTAGCATGTCCAAAGCACTG), LeCCD1A (AY576001.1) (forward AGCAGCGTTATGTGTATGGAAC and reverse AACATTCCCTCCAACTTCAAGC) and LeCCD1B (AY576002.2) (forward AATTTGATTTGCATGCCGAACC and reverse CAAATCTTCCAGGTCCAAGGTC) from *Solanum lycopersicum* was tested with qRT-PCR. For *LeNCED2, NCED3, LeNCED6, LeCCD1A, and LeCCD1B* the expression analyses were conducted for three biological replicates containing pooled samples of three roots of one grafting treatment, fold differences were derived by comparison with two housekeeping genes, ubiquitin (TC115896) and cyclophilin (TC115937) (Rohrmann et al., 2011), and calculated using the ΔΔCt quantification algorithm (Maloney et al., 2010). Amplification conditions were as follows: 2 min at 50°C; 10 min at 95°C; 40 cycles each of 15 s at 95°C followed by 1 min at 60°C; 15 s at 95°C; 20 s at 60°C; 15 s at 95°C. Primer specificity was confirmed with melting curve analysis on a Fast Real-Time PCR system 7900 HT (Applied Biosystems, Carlsbad, CA, USA) using the Power SYBR Green PCR Master Mix (Applied Biosystems Inc., Carlsbad, CA, USA). The Software SDS 2.4 was used for analysis of the data.

2.8. Microarray Analysis

For microarray analysis, leaf and root samples from ‘LA 1777’ and ‘Moneymaker’ genotypes were collected 30 days after employing sub-optimal T stress and immediately frozen in liquid nitrogen and stored at −80°C until use. Twelve independent biological samples for each treatment were harvested, and each of the three replicates used contained 4 plants all of which were used for total RNA isolation.

Microarrays were performed using the Agilents’ 022270 tomato microarray (http://www.genomics.agilent.com/article.jsp?pageId=1508). All experiments analyzing RNA expression levels were performed using three independent replicates of leaf and root materials, obtained from the 3rd and 4th leaf and roots from ‘Kommeet’ scions grafted onto either ‘LA 1777’ or ‘Moneymaker’ under optimal or sub-optimal root T conditions. Leaf and root material were homogenized using a ball mill (Retsch). Immediately afterwards, RNA was extracted from the homogenized leaf or root material. The RNA extraction was performed by the RNAeasy® Plant Mini Kit (Qiagen GmbH, Hilden, Germany) while the RNA concentration was estimated using a spectrophotometer (NanoDrop ND-1000, PeqLab Biotechnologie GmbH, Erlangen, Germany). After quality control using an Agilent Bioanalyzer, at least 10 µg of total RNA was sent to imaGenes Berlin (http://www.lifesciences.sourcebioscience.com/genomic-services/gene-expression-.aspx) for microarray analysis. At the service provider, cDNA synthesis, biotinylation, and microarray hybridization were performed exactly as specified by Agilent as described in (http://www.chem.agilent.com/library/usermanuals/public/g4140-90041_one-color_tecan.pdf).

The raw microarray data were processed using the Robin application (Lohse et al., 2010) to check the hybridization quality and identify significantly differentially expressed genes. Four samples (one of every control treatment for each plant part, namely leaves or roots and from each grafting combination, namely 'Kommeet' onto 'LA 1777' or onto 'Moneymaker') were excluded from downstream analysis because they showed strong outlier behavior during quality checks. Statistical assessment of differential gene expression was performed using default settings in Robin. Briefly, raw chip data were normalized by applying the Robust Multichip Average method (Irizarry et. al., 2003), and subsequently, differentially expressed genes were identified using the limma R package (Smyth, 2004). Genes showing an absolute log2-fold change greater than 1 and a corrected P value (using the method developed by Benjamini and Hochberg, 1995) less than 0.05 were accepted as significantly differentially expressed.

Assignment of the different genes represented by identifiers to respective bins and visualization of data sets were realized using MapMan software (Thimm et al., 2004). MapMan files were constructed from resulting analysis log2-fold change values, where any poor-quality spots created during the experimental process were down-weighted. Moreover, only spots that had detectable signals in both channels over all arrays were averaged for display in MapMan. For each identifier, the gene with the highest homology was provided with an identifier and description.

The significantly changed genes were divided into up-regulated and down-regulated genes and the differences in gene expression were visualized using MapMan (Thimm et al., 2004; Usadel et al., 2005) and PageMan (Usadel et al., 2006). Enrichments of functional categories of the MapMan annotation in the significantly differentially expressed genes were tested for significance by applying Fisher tests with a Bonferroni correction for multiple tests using Mefisto Version 0.23beta (http://www.usadellab.org). The average log signal values under control and sub-optimal root T stress conditions in the roots of both genotypes are presented as heatmaps generated by Microsoft Office Excel Software 2007.

The probe sequences of differentially expressed genes were retrieved manually by using NCBI’s GenBank accession numbers as described in Agilents’ source ID. To determine the Unigene Identification and gi numbers we performed BLAST searches using as query sequences those obtained from NCBI against SGN tomato DB contained in the SGN whole genome database (http://solgenomics.net).

The microarrays data of this study will be submitted in MIAME-compliant (for minimum information about a microarray experiment) format to the Gene Expression Omnibus database (http://www.ncbi.nlm.nih.gov/geo/) and will be assigned an accession number. For a complete description of the experimental design of the microarray experiment and the submission details, readers are referred to this accession number.

The microarray data from this article will be found in the National Center for Biotechnology Information Gene Expression Omnibus database (http://www.ncbi.nlm.nih.gov/geo/) under an accession number to be given after the assignment of the data.

2.9. Statistical analysis

2.9.1. Contribution of phytohormones in alleviating the impact of sub-optimal temperature stress on grafted tomato

The data on ABA, RSL, RLA, total chlorophyll content and gas exchange were statistically analysed by applying 2-factorial ANOVA, with two *T* and four genetic combinations as experimental factors and levels, respectively, (2 × 4). However, the ABA and root growth data (RL, SRA) were subjected to one-way ANOVA to assess merely the responses of the genetic combinations to sub-optimal *T*. Significance of the main factors and interactions was assessed at three confidence levels (0.05, 0.01 and 0.001, denoted by *, ** and *** in the relevant tables, respectively). When the genetic combination or the interaction was significant, means were separated by applying Duncan's multiple range test ($p \leq 0.05$). The STATISTICA software package

(STATISTICA for Windows 8.0, Tulsa, OK, USA) was used to perform statistical analysis.

2.9.2. A study on ABA involvement in the response of tomato to sub-optimal root temperature using reciprocal grafts with ‘notabilis’, a null mutant in the ABA-biosynthesis gene *LeNCED1*

The two temperature treatments were combined with the four grafting combinations in a 2-factorial experimental design with four replications per treatment and three plants per replication (experimental unit). Initially, the data were subjected to factorial analysis of variance. When the root temperature and/or the grafting combination had a significant impact but the interaction between them was insignificant, the means between the two tested T levels and/or the four grafting combinations, respectively, were separated using Duncan’s Multiple Range Test ($P < 0.05$). The same test was used to separate the means of all eight treatments when the interaction was significant. All statistical analyses were carried out using the STATISTICA software package, version 9.0.

2.9.3. Growth, yield, and metabolic responses of temperature-stressed tomato to grafting onto rootstocks differing in cold tolerance

The three temperature treatments were combined with the three grafting combinations in a 2-factorial experimental design with two replications per temperature and five per grafting combinations except Moneymaker that we had only one plant per replication per temperature. Initially, the data were subjected to factorial analysis of variance. When the temperature and/or the grafting combination had a significant impact but the interaction between them was insignificant, the means between the three tested T levels and/or the three grafting combinations, respectively, were separated using Duncan’s Multiple Range Test ($P < 0.05$). The same test was used to separate the means of all nine treatments when the interaction was significant. All statistical analyses were carried out using the STATISTICA software package, version 9.0.

2.9.4. Expression profiling of tolerant and sensitive tomato rootstock genotypes under sub-optimal temperature stress

The two temperature treatments were combined with the two grafting combinations in a 2-factorial experimental design with four replications per treatment and three plants per replication (experimental unit). Initially, the data were subjected to factorial analysis of variance. When the root temperature and/or the grafting combination had a significant impact but the interaction between them was insignificant, the means between the two tested T levels and/or the two grafting combinations, respectively, were separated using Duncan's Multiple Range Test ($P < 0.05$). The same test was used to separate the means of all four treatments when the interaction was significant. All statistical analyses were carried out using the STATISTICA software package, version 9.0.

CHAPTER 3. RESULTS

3.1. Contribution of phytohormones in alleviating the impact of sub-optimal temperature stress on grafted tomato

The induction of sub-optimal T stress had no significant impact on the levels of ABA in the leaves of grafted tomato, regardless of the root and scion genotype (data not shown). The ABA concentration in the leaves of tomato was significantly lower when the scion was one of the ABA-deficient mutants, specifically ‘notabilis’ or ‘sitiens’, in comparison with ‘Ailsa Craig’ or ‘Moneymaker’, respectively (Table 1). The genotype of the rootstock had no additional impact on the leaf ABA status when the scion was ‘Ailsa Craig’. However, the levels of ABA in the leaves of plants with ‘Moneymaker’ as scion were lower when the rootstock genotype was the ABA-deficient mutant ‘sitiens’ than when both the rootstock and the scion were ‘Moneymaker’.

Table 1. Abscisic acid concentration in the leaves of grafted tomato plants obtained by using as rootstock and scion a standard elite hybrid (+ABA) and an ABA-deficient mutant (-ABA) in all rootstock/scion (R/S) combinations. The standard hybrid and the ABA-deficient counterpart were, respectively, either ‘Ailsa Craig’ (+ABA) and ‘notabilis’ (-ABA), or ‘Moneymaker’ (+ABA) and ‘sitiens’ (-ABA). Different letters indicate significant differences between the means of four replications.

Grafting treatment (R/S)	**ABA (pmol g^{-1} FW)**	
	‘Ailsa Craig’ and ‘notabilis’	‘Moneymaker’ and ‘sitiens’
+ABA/+ABA	341 a	477 a
+ABA/-ABA	194 b	72 c
-ABA/+ABA	310 a	299 b
-ABA/-ABA	192 b	93 c

The exposure of tomato plants obtained from the genetic combinations of the ABA-deficient mutant ‘sitiens’ and its wild-type counterpart ‘Moneymaker’ to sub-optimal T stress restricted significantly their relative shoot length (RSL) and their relative leaf area (RLA), irrespective of the genetic combinations (Table 2). A similar impact of sub-optimal T on RSL and RLA was observed also in the trial with ‘notabilis’ as ABA-deficient mutant and ‘Ailsa Craig’ as its wild-type counterpart (data not shown). In the genetic combinations of ‘Moneymaker’ and ‘sitiens’, the rootstock and scion genotypes had no impact on RSL and RLA when the root and air *T* was optimal. However, under sub-optimal T levels, the plants with the ABA-deficient mutant ‘sitiens’ as either scion or rootstock or both exhibited significantly lower levels of RSL and RLA than the self-grafted ‘Moneymaker’ plants (Table 2). Comparing RSL and RLA under sub-optimal T (Table 2) with the ABA levels determined in the leaves of the different rootstock/scion combinations of ‘Moneymaker’ (Table 1), the highest shoot growth correlated with highest ABA levels whereas the strongest reduction in shoot growth for the −ABA/−ABA combination was associated with the lowest ABA levels. However, the intermediate reduction of RSL and RLA, when the −ABA genotype ‘sitiens’ was singly used either as rootstock or as scion, was associated with a moderate reduction of ABA levels when ‘sitiens’ was used as rootstock but with very low ABA levels when the same mutant was used as scion. In fact, the +ABA/−ABA combination had similarly low ABA level in leaves as the −ABA/−ABA combination (Table 1) but nevertheless produced a significantly higher RLA (Table 2).

The leaf chlorophyll content was slightly higher in the period of sub-optimal temperature stress than in the optimal T period, but was not influenced by the genetic combination (‘Moneymaker’ or ‘sitiens’). The root length (RL) and the specific root area (SRA), which were measured only during the period of sub-optimal T stress, exhibited either no (RL) or only a weak and inconsistent response (SRA) to the genetic combinations when these were either ‘Moneymaker’ or ‘sitiens’ (Table 2). In the trial with self- and reciprocal-grafting of the ABA-deficient mutant ‘notabilis’ and its wild-type counterpart ‘Ailsa Craig’, the genetic combination had no impact on either of the measured shoot and root growth parameters and the leaf chlorophyll content (data not shown).

Table 2. Effects of transient exposure of grafted tomato to sub-optimal day/night temperature (T) on relative shoot length (RSL), relative leaf area (RLA), total chlorophyll content (Chl), root length (RL), and root specific area (RSA). Grafted plants were obtained using 'Moneymaker' (+ABA) and 'sitiens' (-ABA) in all rootstock/scion (R/S) combinations. Different letters indicate significant differences between means of four replications.

Air/root T	**(R/S)**	**RSL**	**RLA**	**Chl (mg g^{-1} FW)**	**RL (mm)**	**RSA (cm^2 g^{-1} FW)**
Optimal	+ABA/+ABA	0.066 a	0.083 a	229 c	—	—
	+ABA/-ABA	0.068 a	0.084 a	224 c	—	—
	-ABA/+ABA	0.070 a	0.098 a	231 bc	—	—
	-ABA/-ABA	0.069 a	0.082 a	248 a	—	—
Sub-optimal	+ABA/+ABA	0.030 b	0.043 b	248 a	549	1729
	+ABA/-ABA	0.019 cd	0.021 c	251 a	984	2382
	-ABA/+ABA	0.022 c	0.010 cd	222 c	887	2103
	-ABA/-ABA	0.018 d	0.006 d	241 ab	668	2065
Main effects						
Air/root T	Optimal	0.068	0.087	233	—	—
	Sub-optimal	0.022	0.020	241	772	2070
Grafting	+ABA/+ABA	0.048	0.063	239	549	1729 b
	+ABA/-ABA	0.044	0.053	238	984	2382 a
	-ABA/+ABA	0.046	0.054	227	887	2103 ab
	-ABA/-ABA	0.044	0.044	245	668	2065 ab
Statistical significance						
Air/root T		***	***	**	—	—
Grafting		*	***	NS	NS	*
Air/root T × grafting		*	***	*	—	—

The effects of the ABA-deficient mutant 'notabilis' on gas exchange and water use efficiency were similar with those of 'sitiens' but the differences in the trial with 'notabilis' were smaller. Therefore, in this paper only the gas exchange data from the trial with ‘Moneymaker’ as wild-type cultivar and ‘sitiens’ as ABA-deficient mutant will be presented. In the latter, the net photosynthetic rates (*A*) and the water use efficiency (WUE) were reduced when the plants were exposed to sub-optimal *T*, without any interaction with the genetic combinations (Table 3). However, the stomatal conductance (*gs*), the intercellular CO_2 concentration (*ci*), and the transpiration rates (*E*) were not influenced by the exposure of the genetic combinations to sub-optimal *T* stress in comparison with the optimal *T* period, regardless of the genetic treatment. With respect to the genetic treatments, the plants with ‘sitiens’ as scion exhibited significantly higher levels of *A*, *gs*, *ci*, and*E*, and significantly reduced WUE than those with ‘Moneymaker’ as scion, regardless of the rootstock genotype and the applied *T* regime, and this was associated with significantly lower leaf ABA levels.

Table 3. Effects of transient exposure of grafted tomato to sub-optimal day/night temperature (T) on leaf net CO_2 assimilation rate (*A*), stomatal conductance (g_s), intercellular CO_2 concentration (c_i), transpiration rate (*E*), and water use efficiency (WUE). Grafted plants were obtained using ‘Moneymaker’ (+ABA) and ‘sitiens’ (-ABA) in all rootstock/scion (R/S) combinations. Different letters indicate significant differences between means of four replications.

Air/root T	**(R/S)**	***A* (µmol CO_2 m^{-2} s^{-1})**	**g_s (mmol H_2O m^{-2} s^{-1})**	***E* (mmol H_2O m^{-2} s^{-1})**	**c_i (µl l^{-1})**	**WUE (µmol CO_2 $mmol^{-1}$ H_2O)**
Air/root T	Optimal	15.57a	0.399	2.90	276	6.84 a
	Sub-optimal	12.69b	0.386	3.07	264	4.82 b
Grafting	+ABA/+ABA	8.98 b	0.141 b	1.71 b	227 b	7.39 a
	+ABA/-ABA	17.22 a	0.607 a	4.22 a	319 a	4.41 b
	-ABA/+ABA	11.37 b	0.080 b	1.18 b	217 b	5.15 ab
	-ABA/-ABA	19.85 a	0.657 a	4.30 a	311 a	4.73 b
Statistical significance						
Air/root T		*	NS	NS	NS	*
Grafting		***	***	***	***	*
Air/root T × grafting		NS	NS	NS	NS	NS

In the trial with the cultivar ‘Ailsa Craig’ and the ‘Never-ripe’ tomato mutant, the RSL and the RLA were lower during the period of sub-optimal T stress in comparison with the optimal T period, regardless of the genetic combination (Table 4). However, while the RSL was not influenced by the genetic treatments, the RLA was significantly lower in self-grafted ‘Never-ripe’ tomato mutants in comparison with self-grafted ‘Ailsa Craig’ plants. Under normal T conditions, the RLA was lower in plants obtained by grafting the ET-insensitive ‘Nr’ mutant onto ‘Ailsa Craig’ in comparison with that found in self-grafted ‘Ailsa Craig’ plants. However, under sub-optimal T conditions, the highest RLA was measured in plants with ‘Ailsa Craig’ as rootstock and ‘Nr’ as scion followed by ‘Nr’/‘Ailsa Craig’ plants, in comparison with the self-grafted ‘Ailsa Craig’ and ‘Nr’ plants, which exhibited the lowest RSL.

The leaf chlorophyll content increased in the period of sub-optimal T stress in comparison with the optimal T period. With respect to the genetic combination, the highest leaf chlorophyll content was found in plants with the ET-insensitive tomato mutant ‘Never-ripe’ as scion but the difference was significant only in comparison with that measured in the self-grafted ‘Ailsa Craig’ tomato plants. Nevertheless, no interaction between T and genetic treatment was found. The root length and the specific root area were not influenced either by the T or by the genetic treatment (data not shown).

With respect to the gas exchange parameters, only the net photosynthesis was reduced by the exposure of the genetic combinations to sub-optimal temperature. However, the levels of *gs*, *ci*, *E*, and WUE were not influenced either by T or by the genetic combinations when these were either the cultivar ‘Ailsa Craig’ or the ET-insensitive tomato mutant ‘Never-ripe’ (data not shown).

Table 4. Effects of transient exposure of grafted tomato to sub-optimal day/night temperature (T) on relative shoot length (RSL), relative leaf area (RLA), total chlorophyll content (Chl) and leaf net CO_2 assimilation rate (*A*). Grafted plants were obtained using 'Ailsa Craig' (+ETsens) and 'Never-ripe (Nr)' (-ETsens) in all rootstock/scion (R/S) combinations. Different letters indicate significant differences between means of four replications.

Air/root Temperature (^{o}C)	**Grafting treatment (R/S)**	**RSL**	**RLA**	**Chl (mg g^{-1} FW)**	***A*** **(µmol CO_2 m^{-2} s^{-1})**
Optimal	+ETsens/+ETsens	0.076	0.100 a	271	13.47
	+ETsens/-ETsens	0.075	0.097 b	336	17.83
	-ETsens/+ETsens	0.075	0.101 a	293	14.08
	-ETsens/-ETsens	0.074	0.097 b	309	15.70
Sub-optimal	+ETsens/+ETsens	0.019	0.009 e	311	14.50
	+ETsens/-ETsens	0.021	0.024 c	362	10.45
	-ETsens/+ETsens	0.020	0.017 d	350	12.35
	-ETsens/-ETsens	0.027	0.010 e	389	10.61
Main effects					
Air/root T	Optimal	0.075 a	0.099	302 b	15.27 a
	Sub-optimal	0.022 b	0.015	353 a	11.97 b
Grafting	+ETsens/+ETsens	0.048 b	0.055	291 b	13.98
	+ETsens/-ETsens	0.048 b	0.060	349 a	14.14
	-ETsens/+ETsens	0.048 b	0.059	321ab	13.21
	-ETsens/-ETsens	0.051 a	0.053	349 a	13.15
Statistical significance					
Air/root T		***	***	***	*
Grafting		*	***	**	NS
Air/root T × grafting		NS	***	NS	NS

In the trial with the genetic combinations of the cultivar ‘VFN-8’ and the IAA-reduced sensitivity mutant ‘dgt’, both the RSL and the RLA were reduced in the period of sub-optimal *T* stress in comparison with the optimal T period (Table 5). In contrast, the leaf chlorophyll content increased when the plants were exposed to sub-optimal *T* stress in comparison with the optimal T period, regardless of the genetic combinations. The self-grafted tomato plants ‘VFN-8’ exhibited significantly higher RSL rates than the self-grafted ‘dgt’ mutants that are characterized by reduced sensitivity to IAA, while the ‘VFN-8’ plants grafted onto ‘dgt’ exhibited similar RSL rates with the ‘dgt’ plants grafted onto ‘VFN-8’, regardless of the T regime. The RLA was significantly higher in the plants with ‘VFN-8’ as scion, in comparison with that found in plants with ‘dgt’ as scion, although under sub-optimal temperature conditions the differences were insignificant. The total leaf chlorophyll content was higher in the self-grafted ‘dgt’ plants than in plants in which either the rootstock or the scion or both were ‘VFN-8’, regardless of the T regime. Furthermore, the self-grafted ‘VFN-8’ plants exhibited higher values of RL and SRA than the self-grafted ‘dgt’ plants during their exposure to sub-optimal temperature stress. However, the highest RL was found in ‘VFN-8’ plants grafted onto ‘dgt’, while the highest SRA was found in the self-grafted ‘VFN-8’ plants.

Table 5. Effects of transient exposure of grafted tomato to sub-optimal day/night temperature (T) on relative shoot length (RSL), relative leaf area (RLA), total chlorophyll content (Chl), root length (RL), and root specific area (RSA). Grafted plants were obtained using ‘VFN-8’ (+IAAsens) and ‘dgt’ (-IAAsens) in all rootstock/scion (R/S) combinations. Different letters indicate significant differences between means of four replications.

Air/root T	**(R/S)**	**RSL**	**RLA**	**Chl (mg g^{-1} FW)**	**RL (mm)**	**RSA (cm^{2} g^{-1} FW)**
Optimal	+IAAsens/+IAAsens	0.068 a	0.094 a	354	—	—
	+IAAsens/-IAAsens	0.065 a	0.076 b	332	—	—
	-IAAsens/+IAAsens	0.064 a	0.092a	334	—	—

	-IAAsens/-IAAsens	0.057 b	0.068 c	474	—	—
Sub-optimal	+IAAsens/+IAAsens	0.039 c	0.006 d	359	737	2459
	+IAAsens/-IAAsens	0.029 d	0.004 d	432	588	1572
	-IAAsens/+IAAsens	0.025 de	0.004 d	411	1045	1520
	-IAAsens/-IAAsens	0.021 e	0.003 d	476	519	1013
Main effects						
Air/root T	Optimal	0.064	0.083	373 b	—	—
	Sub-optimal	0.022	0.004	419 a	722	1641
Grafting	+IAAsens/+IAAsens	0.043	0.050	356 b	737 ab	2459 a
	+IAAsens/-IAAsens	0.047	0.040	382 b	588 bc	1572 b
	-IAAsens/+IAAsens	0.043	0.048	372 b	1045 a	1520 b
	-IAAsens/-IAAsens	0.039	0.036	475 a	519 c	1013 c
Statistical significance						
Air/root T		***	***	*	—	—
Grafting		*	***	**	**	**
Air/root T × grafting		***	***	NS	—	—

The gas exchange parameters *A*, *gs*, *ci*, and *E* did not respond to exposure to sub-optimal T stress in tomato plants obtained by genetic combinations of the standard cultivar ‘VFN-8’ and the ‘dgt’ mutant that is characterized by reduced sensitivity to IAA (Table 6). However, the WUE was significantly reduced by the exposure to sub-optimal T, regardless of the genetic combinations (‘VFN-8’ and ‘dgt’). When ‘dgt’ was used as scion, the net photosynthetic and transpiration rates as well as the stomatal conductance were appreciably reduced in comparison with those measured in plants with ‘VFN-8’ as scion, regardless of the rootstock genotype and the T regime. Nevertheless, the intercellular CO_2 concentration and the WUE were not influenced by the genetic combinations, when these were either ‘VFN-8’ or ‘dgt’.

Table 6. Effects of transient exposure of grafted tomato to sub-optimal day/night temperature (T) on leaf net CO_2 assimilation rate (*A*), stomatal conductance (g_s), intercellular CO_2 concentration (c_i), transpiration rate (*E*), and water use efficiency (WUE). Grafted plants were obtained using 'VFN-8' (+IAAsens) and 'dgt' (-IAAsens) in all rootstock/scion (R/S) combinations. Different letters indicate significant differences between means of four replications.

Air/root T	**(R/S)**	***A*** **(μmol CO_2 m^{-2} s^{-1})**	**g_s (mmol H_2O m^{-2} s^{-1})**	***E*** **(mmol H_2O m^{-2} s^{-1})**	**c_i (μl l^{-1})**	**WUE (μmol CO_2 $mmol^{-1}$ H_2O)**
Air/root T	Optimal	13.52	0.190	1.82	217	9.47 a
	Sub-optimal	10.87	0.128	1.37	228	4.20 b
Grafting	+IAAsens/+IAAsens	17.30 a	0.331 a	2.73 a	276	6.68
	+IAAsens/-IAAsens	8.24 b	0.053 b	0.67 b	237	8.49
	-IAAsens/+IAAsens	15.07 a	0.285 a	2.92 a	241	4.60
	-IAAsens/-IAAsens	7.74 b	0.042 b	0.72 b	164	7.69
		Statistical significance				
Air/root T		NS	NS	NS	NS	*
Grafting		***	***	***	NS	NS
Air/root T × grafting		NS	NS	NS	NS	NS

In the genetic combinations of the standard cytokinin-producing cultivar 'Micro-Tom' and the transgenic line dgt-'CKX2' × 'Moneymaker' with enhanced cytokinin catabolism, the sub-optimal T reduced both the RL and the SRA (Table 7). The use of the CK-deficient transgenic line either as rootstock or as scion increased the RSL of tomato in the period of plant exposure to sub-optimal T stress while the reverse was the case when the CK-deficient transgenic line was used either as rootstock or as scion under optimal T. In contrast, the RLA was not influenced by the rootstock/scion genotype when the grafted plants were exposed to sub-optimal T stress, although it was restricted by the use of the CK-deficient transgenic line either as rootstock or as scion under optimal T conditions. With respect to the root growth, the use of a CK-deficient transgenic line as rootstock enhanced appreciably the L_{rp} of tomato in comparison with that measured in plants with the standard CK-producing cultivar 'Micro-Tom' as rootstock, regardless of the scion genotype. However, the specific root area was not influenced by the genetic combination, when this was either 'Micro-Tom' or its CK-deficient counterpart. The leaf chlorophyll level was not influenced by the temperature regime, but was reduced when the CK-deficient transgenic line was used either as rootstock or as scion, in comparison with that found in self-grafted 'Micro-Tom' plants. With respect to the gas exchange parameters, the net photosynthesis and the intercellular CO_2 concentration were not influenced either by sub-optimal T stress or by the genetic combinations (data not shown). Nevertheless, the stomatal conductance and the transpiration rates were reduced under sub-optimal temperature conditions, regardless of the genetic combination.

Table 7. Effects of transient exposure of grafted tomato to sub-optimal day/night temperature (T) on relative shoot length (RSL), relative leaf area (RLA), total chlorophyll content (Chl), root length (RL), stomatal conductance (g_s) and transpiration rate (*E*). Grafted plants were obtained using 'Micro-Tom' (+CK) and 'dgt-CKX2' (-CK) in all rootstock/scion (R/S) combinations. Different letters indicate significant differences between means of four replications.

Air/root T	**(R/S)**	**RSL**	**RLA**	**RL (mm)**	**Chl (mg g^{-1} FW)**	**g_s (mmol H_2O m^{-2} s^{-1})**	***E* (mmol H_2O m^{-2} s^{-1})**
Optimal	+CK/+CK	0.072 a	0.101 a	—	301	0.186	1.81
	+CK/-CK	0.062 c	0.080 c	—	174	0.178	1.69
	-CK/+CK	0.067 b	0.091 b	—	194	0.157	1.47
Sub-optimal	+CK/+CK	0.021 f	0.025 d	806	304	0.297	2.67
	+CK/-CK	0.037 d	0.023 d	560	255	0.292	3.15
	-CK/+CK	0.032 e	0.023 d	2038	249	0.225	2.46
Main effects							

Air/root T	Optimal	0.067	0.091	──	223	0.173 b	1.66 b
	Sub-optimal	0.030	0.024	1134	270	0.271 a	2.76 a
Grafting	+CK/+CK	0.046	0.063	806 b	303 a	0.242	2.24
	+CK/-CK	0.050	0.051	560 b	214 b	0.235	2.42
	-CK/+CK	0.050	0.057	2038 a	222 b	0.191	1.96
Statistical significance							
Air/root T		***	***	──	NS	**	***
Grafting		*	***	**	*	NS	NS
Air/root T × grafting		***	***	──	NS	NS	NS

In the genetic combination of the standard tomato cultivar ‘Moneymaker’ and the transgenic tomato ‘nahG’, which prevents the accumulation of SA by converting it to catechol, both the RSL and RLA were lower in the period of sub-optimal T stress than in the optimal T period (Table 8). In contrast, the leaf chlorophyll content was similar under the two different T regimes. With respect to the genetic combinations, the RSL was not influenced under optimal T conditions but was higher in self-grafted ‘Moneymaker’ plants than in those obtained using the SA-deficient transgenic cultivar ‘nahG’ as scion under sub-optimal temperature conditions. However, the RLA was higher in self-grafted ‘Moneymaker’ plants than in those obtained using the SA-deficient transgenic cultivar ‘nahG’ as scion, without any interaction with the temperature regime. The leaf chlorophyll content was depending only on the scion genotype. In particular, the plants with ‘nahG’ as scion exhibited significantly lower levels of leaf chlorophyll than those with ‘Moneymaker’ as scion, regardless of the rootstock genotype. The rates of net photosynthesis and transpiration, as well as the stomatal conductance, tended to decrease in the period of sub-optimal T stress in comparison with the optimal T period but the differences were statistically insignificant. Overall, self-grafted ‘nahG’ plants exhibited significantly lower rates of net photosynthesis and transpiration, as well as stomatal conductance, in comparison with plants with ‘Moneymaker’ as scion, regardless of the rootstock genotype. The root growth parameters (RL and SRA), the intercellular CO_2 concentration and the WUE were not influenced either by T or by the genetic combinations of ‘Moneymaker’ and ‘nahG’.

Table 8. Effects of transient exposure of grafted tomato to sub-optimal day/night temperature (T) on relative shoot length (RSL), relative leaf area (RLA), total chlorophyll content (Chl), leaf net CO_2 assimilation rate (A), stomatal conductance (g_s) and transpiration rate (E). Grafted plants were obtained using 'Moneymaker' (+SA) and 'nahG' (-SA) in all rootstock/scion (R/S) combinations. Different letters indicate significant differences between means of four replications.

Air/root T	**(R/S)**	**RSL**	**RLA**	**Chl (mg g^{-1} FW)**	**A (µmol CO_2 m^{-2} s^{-1})**	**g_s (mmol H_2O m^{-2} s^{-1})**	**E (mmol H_2O m^{-2} s^{-1})**
Optimal	+SA /+ SA	0.066 a	0.087	229 b	11.06	0.122	1.290
	+SA /-SA	0.067 a	0.070	210 b	4.87	0.043	0.471
	-SA /+SA	0.069 a	0.085	315 a	11.56	0.111	1.343
	-SA /-SA	0.069 a	0.070	221 b	3.17	0.029	0.453
Sub-optimal	+SA /+ SA	0.030 b	0.022	365 a	8.90	0.160	2.123
	+SA /-SA	0.018 c	0.012	122 c	3.20	0.031	0.360
	-SA /+SA	0.021 bc	0.004	379 a	8.45	0.066	0.909
	-SA /-SA	0.017 c	0.005	175 bc	7.80	0.069	0.322
Main effects							
Air/root T	Optimal	0.068	0.078 a	244	7.66	0.080	0.918
	Sub-optimal	0.021	0.011 b	262	7.09	0.083	0.929
Grafting	+SA /+ SA	0.048	0.055 a	297	9.98 a	0.141 a	1.707 a
	+SA /-SA	0.042	0.041 b	172	4.15 b	0.037 b	0.415 b
	-SA /+SA	0.045	0.044ab	343	10.01 a	0.092 a	1.157 a
	-SA /-SA	0.043	0.037 b	198	5.49 b	0.052 b	0.387 b
Statistical significance							
Air/root T		***	***	NS	NS	NS	NS
Grafting		*	*	***	*	*	*
Air/root T × grafting		*	NS	***	NS	NS	NS

3.2.A study on ABA involvement in the response of tomato to sub-optimal root temperature using reciprocal grafts with ‘notabilis’, a null mutant in the ABA-biosynthesis gene *LeNCED1*

Sub-optimal root T reduced leaf area (A_{lp}), root dry mass (D_{rp}) and total plant dry mass (D_{pp}) but had no impact on shoot length (L_{sp}) and root specific area (A_{rw}) of tomato, regardless of genotype (Table 1). Self-grafting of ‘notabilis’ (*not*/*not*) was associated with reduced A_{lp}, L_{sp} and D_{pp} in comparison with all other grafting combinations. However, the number of leaves per plant was not influenced either by the root T or by the grafting combination (data not shown). Furthermore, the D_{rp} was not influenced by genotype (Table 9). The L_{sp} was maximized in the wild-type self-graft combination (+/+), followed by the grafting combination in which the wild-type gene was present only in the shoot (*not*/+). The +/*not* combination further reduced L_{sp}, while the *not*/*not* combination minimized L_{sp}. In contrast, the A_{rw} was maximized when this gene was present in both root and shoot but minimized when this gene was present in the shoot only (*not*/+; +/+).

Table 9. Effect of 30 days exposure of grafted tomato to sub-optimal (day and night 15±0.4 °C) root temperature (T) on total leaf area (TA_{lp}), shoot length (L_{sp}), root specific area (A_{rw}), root dry mass (D_{rp}), and total plant dry mass (D_{pp}). The rootstock/scion combinations are, using conventional tomato genetics notation, +/+, +/*not*, *not*/+ and *not*/*not*, where *not* represents the ‘notabilis’ genotype and “+” the ‘Ailsa Craig’ wild-type functional allele. Different letters within the same column indicate significant differences between means of four replications according to the Duncan’s Multiple Range Test ($p \leq 0.05$).

Treatments		**TA_{lp} (cm^2)**	**L_{sp} (cm)**	**A_{rw} (cm^2* g^{-1} DW)**	**D_{rp} (g)**	**D_{pp} (g)**
Root T	Sub-optimal	11694 b	72.40	17.86	0.53 b	9.03 b
	Optimal	16925 a	76.55	18.70	0.72 a	12.53 a
R/S combination	*not*/*not*	7508 b	52.60 d	25.19a	0.53	8.66 b
	not/+	16697 a	81.78 b	12.96b	0.68	11.78 a

	+/*not*	14322 a	68.13 c	21.64ab	0.73	12.70 a
	+/+	18710 a	95.40 a	13.33b	0.57	9.98 a
Statistical significance						
Root T		**	NS	NS	***	***
R/S combination		***	***	*	NS	*
Root T × R/S combination		NS	NS	NS	NS	NS

The rate of net CO_2 assimilation (A) did not respond to exposure of the roots of tomato plants to sub-optimal T, regardless of the grafting combination (Table 10). Moreover, chlorophyll fluorescence measurements of light-adapted and dark-adapted leaves were not influenced either by the root T or by the grafting combination (data not shown). However, stomatal conductance (g_s) and transpiration rate (E) were significantly reduced, while water use efficiency (WUE) was significantly increased by the exposure of the roots to sub-optimal T, regardless of the grafting combination. In *not*/+ plants, A was reduced in comparison with the *not*/*not* and +/*not* grafting combinations. Furthermore, this combination increased g_s and E, regardless of the T regime in the root. WUE was lowest in the *not*/*not* graft combination and greatest in +/+, regardless of root T.

Table 10. Effect of 30-days exposure of grafted tomato to sub-optimal (day and night 15±0.4 °C) root temperature (T) on leaf net CO2 assimilation rate (A), stomatal conductance (gs), transpiration rate (E), and water use efficiency (WUE). The rootstock/scion combinations are, using conventional tomato genetics notation, +/+, +/not, not/+ and not/not, where not represents the ‘notabilis’ genotype and “+” the ‘Ailsa Craig’ wild-type functional allele. Different letters within the same column indicate significant differences between means of four replications according to the Duncan’s Multiple Range Test ($p \leq 0.05$).

Treatments	***A*** **(μmol CO_2 m^{-2} s^{-1})**	**g_s (mmol m^{-2} s^{-1})**	***E*** **(mmol H_2O m^{-2} s^{-1})**	**WUE (μmol CO_2 $mmol^{-1}$ H_2O)**

Root T	Sub-optimal	11.21	0.237 b	4.22 b	2.79 a
	Optimal	11.47	0.320 a	5.31 a	2.21 b
R/S combination	*not*/*not*	12.42 a	0.340 a	5.79 a	2.17 b
	not/+	9.39 b	0.221 b	3.76 b	2.58 b
	+/*not*	12.50 a	0.328 a	5.54 a	2.35 b
	+/+	10.08 b	0.216 b	3.84 b	3.22 a
Statistical significance					
Root T		NS	**	**	**
R/S combination		*	***	***	*
Root T × R/S combination		NS	NS	NS	NS

The exposure of tomato to sub-optimal root T increased significantly the concentration of sucrose in the leaves and decreased the starch contents in the roots, regardless of the grafting combination (Table 11). In contrast, the concentrations of fructose and starch in the leaves were similar under the two different T regimes. However, in roots a significant effect of temperature was only found for fructose contents. In particular, fructose amounted to 6.40 µmol g^{-1} FW in plants grown at 25 °C but decreased to 4.17 µmol g^{-1} FW in plants grown at 15 °C. The *not*/*not* grafting combination restricted the concentrations of fructose and starch while increasing that of sucrose in the leaves in comparison with those found when this gene was present in the shoot (*not*/+, +/+; Table 11). When roots were wild-type (+/*not* or +/+), the leaf fructose levels were similar to those found in *not*/*not*, without any interaction with root T. In contrast, leaf starch levels were differently influenced by the grafting combination at the two root T levels. At sub-optimal root T, wild-type scions (*not*/+, +/+) resulted in significantly higher leaf starch levels than mutant scions (*not*/*not*, +/*not*). However, under optimal root T levels, the highest leaf starch levels were found when the mutation was only present in the shoot (+/*not*).

Table 11. Effect of a 30-days exposure of grafted tomato to sub-optimal (day and night 15±0.4 °C) root temperature (T) on fructose and sucrose in leaves and starch in leaves and roots. The rootstock/scion combinations are, using conventional tomato genetics notation, +/+, +/*not*, *not*/+ and *not*/*not*, where *not* represents the 'notabilis' genotype and "+" the 'Ailsa Craig' wild-type functional allele. Different letters within the same column indicate significant differences between means of four replications according to the Duncan's Multiple Range Test (p ≤ 0.05).

Treatments		**Fructose**	**Sucrose**	**Starch**	
		µmol mg^{-1} FW		**µmol g^{-1} FW**	
		Leaves		Leaves	Roots
Sub-optimal Root T	*not*/*not*	6.82	11.34	13.19 b	0.535
	not/+	8.36	6.66	25.17 a	0.504
	+/*not*	6.40	9.68	13.02 b	0.334
	+/+	5.80	8.09	23.12 a	0.335
Optimal Root T	*not*/*not*	5.52	8.45	16.79 ab	0.588
	not/+	7.81	5.77	17.30 ab	0.697
	+/*not*	7.50	8.11	24.00 a	0.590
	+/+	5.82	6.32	22.53 a	0.629
Main effects					
Root T	Sub-optimal	6.85	8.94 a	18.63	0.427b
	Optimal	6.66	7.16 b	20.15	0.626a
R/S combination	*not*/*not*	6.17 b	9.89 a	14.99 b	0.562
	not/+	8.08 a	6.21 b	21.23 a	0.601
	+/*not*	6.95 ab	8.89 ab	18.51 a	0.462
	+/+	5.81 b	7.21 b	22.83 a	0.482
Statistical significance					
Root T		NS	*	NS	**
R/S combination		***	**	*	NS
Root T × R/S combination		NS	NS	*	NS

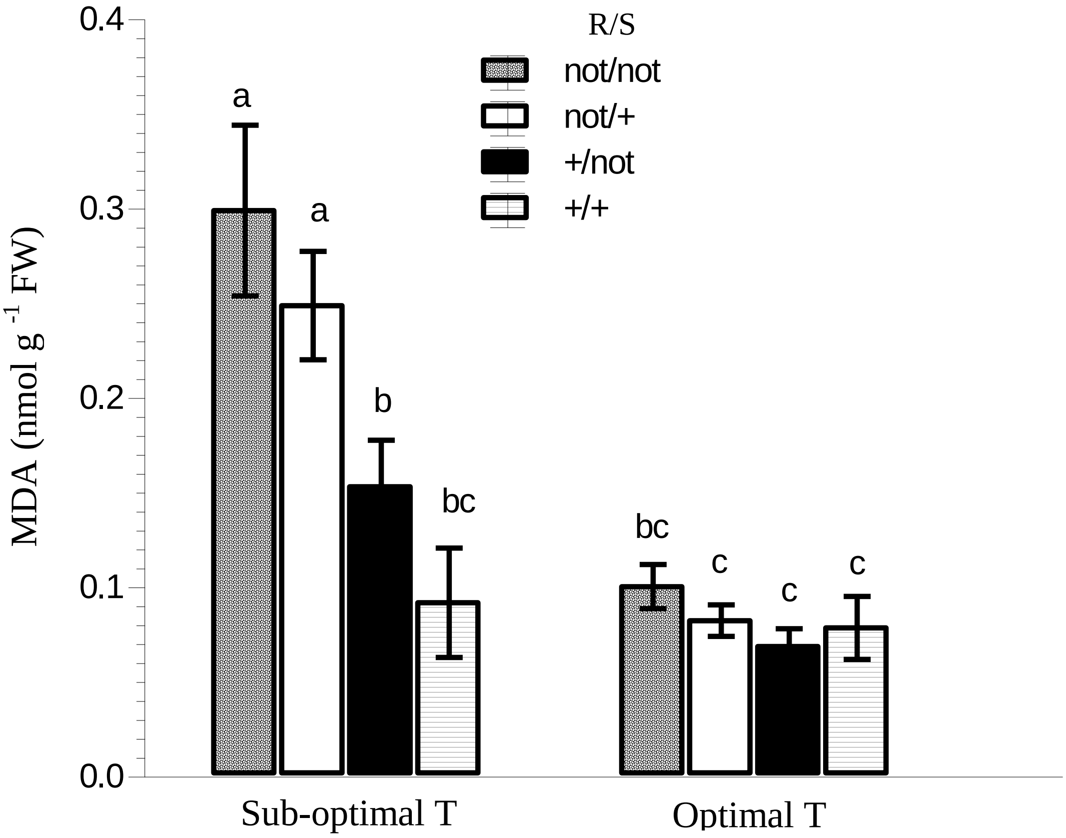
The exposure of tomato plants to sub-optimal root T increased the total amino acid contents in roots and leaves significantly but had no impact on the levels of chlorophyll a and b (data not shown) and lutein contents in the leaf and total proteins in the roots (Table 12). Both leaf chlorophyll a and lutein were significantly higher in +/+ plants in comparison with all other grafting combinations. In contrast, the total amino acids in leaves were significantly higher in *not*/*not* plants in comparison with all other grafting combinations. The levels of total amino acids in the root were not influenced by the grafting combination, while root protein was maximized in the wild- type self-graft (+/+) and minimized in *not*/*not*. The total protein levels in leaves were not influenced either by the root T or by the grafting combination (data not shown).

Table 12. Effect of 30-days exposure of grafted tomato to sub-optimal (day and night 15±0.4 °C) root temperature (T) on chlorophyll a content (Chl a), lutein content, total amino acids in leaves and roots and proteins in roots. The rootstock/scion combinations are, using conventional tomato genetics notation, +/+, +/*not*, *not*/+ and *not*/*not*, where *not* represents the 'notabilis' genotype and "+" the 'Ailsa Craig' wild-type functional allele. Different letters within the same column indicate significant differences between means of four replications according to the Duncan's Multiple Range Test ($p \leq 0.05$).

Treatments		**Chl a (mg g^{-1} FW)**	**Lutein (mg g^{-1} FW)**	**Total amino acids (µmol*mg^{-1} FW)**		**Root protein (mg g^{-1} FW)**
		Leaves	Leaves	Leaves	Roots	Roots
Root T	Sub-optimal	815.6	292.8	1209 a	371 a	10.61
	Optimal	764.8	272.6	982 b	292 b	10.59
R/S combination	*not*/*not*	767.9 b	275.1 b	1500 a	355	9.46 b
	not/+	795.4 b	262.4 b	932 b	318	10.98 ab
	+/*not*	734.7 b	259.5 b	1107 b	331	10.60 ab
	+/+	862.8 a	311.9 a	842 b	322	11.36 a
Statistical significance						
Root T		NS	NS	*	**	NS
R/S combination		*	**	***	NS	*
Root T × R/S combination		NS	NS	NS	NS	NS

The exposure of tomato to sub-optimal root T increased significantly the malondialdehyde (MDA) content in leaves (Fig. 1). The grafting combination had no impact on MDA content in leaves when the root T was optimal. However, at sub-optimal root T, the plants grafted onto the *LeNCED1* mutant (*not*/+, *not*/*not*) exhibited significantly higher leaf MDA levels than the plants with wild-type roots.

Fig. 1. Effect of 30-days exposure of grafted tomato to sub-optimal (day and night 15±0.4 °C) root temperature (T) on MDA (malondialdehyde) content of leaves. The rootstock/scion combinations are, using conventional tomato genetics notation, +/+, +/*not*, *not*/+ and *not*/*not*, where *not* represents the 'notabilis' genotype and "+" the 'Ailsa Craig' wild-type functional allele. Different lower-case letters on the bars indicate significant differences between means ± standard errors of four replications according to the Duncan's Multiple Range Test ($p \leq 0.05$).



The activity of catalase (CAT) in the leaves of tomato was reduced while that of guaiacol peroxidase (G-POD) in the roots was elevated when the roots were subjected to sub-optimal T stress, regardless of grafting combination (Table 13). In contrast, the exposure of tomato roots to sub-optimal T had no impact on electrolyte leakage and H_2O_2 contents in the leaves or superoxide dismutase (SOD) activity in the roots. The activities of G-POD and SOD in the roots of tomato were not influenced by either the root T or the grafting combination (data not shown). In mutant self-grafts (*not*/*not*), electrolyte leakage from the leaves and the activity of G-POD in the roots were significantly higher in comparison with the other three combinations. The H_2O_2 level was significantly lower when the scion was mutant (*not*/*not*, +/*not*) in comparison with wild-type scion (*not*/+, +/+). CAT activity in leaves was not influenced by the root/shoot genotype. The SOD activity in the root of *not*/*not* plants was significantly higher than in +/+ plants, while the values measured in the reciprocal grafts did not differ significantly from those found in self-grafted plants.

Table 13. Effect of 30-days exposure of grafted tomato to sub-optimal (day and night 15±0.4 °C) root temperature (T) on electrolyte leakage (%), H_2O_2 and CAT in leaves, and G-POD and SOD in roots. The rootstock/scion combinations are, using conventional tomato genetics notation, +/+, +/*not*, *not*/+ and *not*/*not*, where *not* represents the 'notabilis' genotype and "+" the 'Ailsa Craig' wild-type functional allele. Different letters within the same column indicate significant differences between means of four replications according to the Duncan's Multiple Range Test ($p \leq 0.05$).

Treatments		**Electrolyte leakage %**	**H_2O_2 (µmol g^{-1} FW)**	**CAT (µmol H_2O_2 mg^{-1} FW min^{-1})**	**G-POD (µmol TG mg^{-1} FW min^{-1})**	**SOD (units g^{-1} FW)**
		Leaves			Roots	
Root T	Sub-optimal	20.87	6.68	1.37 b	6.27 a	97
	Optimal	20.14	8.60	2.73 a	4.90 b	96
R/S combination	*not*/*not*	25.83 a	7.24 b	2.54	7.25 a	109 a
	not/+	18.50 b	8.91 a	1.62	5.52 b	96 ab

+/*not*	20.42 b	8.14 b	2.80	5.01 b	97 ab
+/+	17.27 b	9.85 a	1.24	4.57 b	83 b
Statistical significance					
Root T	NS	NS	*	*	NS
R/S combination	*	**	NS	*	*
Root T × R/S combination	NS	NS	NS	NS	NS

Both sub-optimal root T and grafting combination had no impact on leaf putrescine (Put) (Table 14). The root Put was also not influenced by the grafting combination. In contrast, the root Put increased in response to sub-optimal root T. At optimal root T, the self-grafted ‘notabilis’ plants exhibited reduced leaf spermidine (Spd) levels, while the +/*not* plants exhibited the highest values. However, at sub-optimal root T, the leaf Spd levels were significantly lower also when the mutant was used only as scion or rootstock. Similarly to Put, the root Spd increased significantly at sub-optimal root T. The root Spd levels differed only between the two self-grafted combinations (+/+, *not*/*not*), with +/+ giving the lowest and *not*/*not* the highest values, without any interaction with root T. The highest leaf spermine (Spm) levels were measured in +/+ plants at sub-optimal root T, while the lowest values were measured in mutant self-grafts (*not*/*not*) at optimal root T. The root Spm was significantly reduced by sub-optimal root T, but was not influenced by the root/shoot genotype.

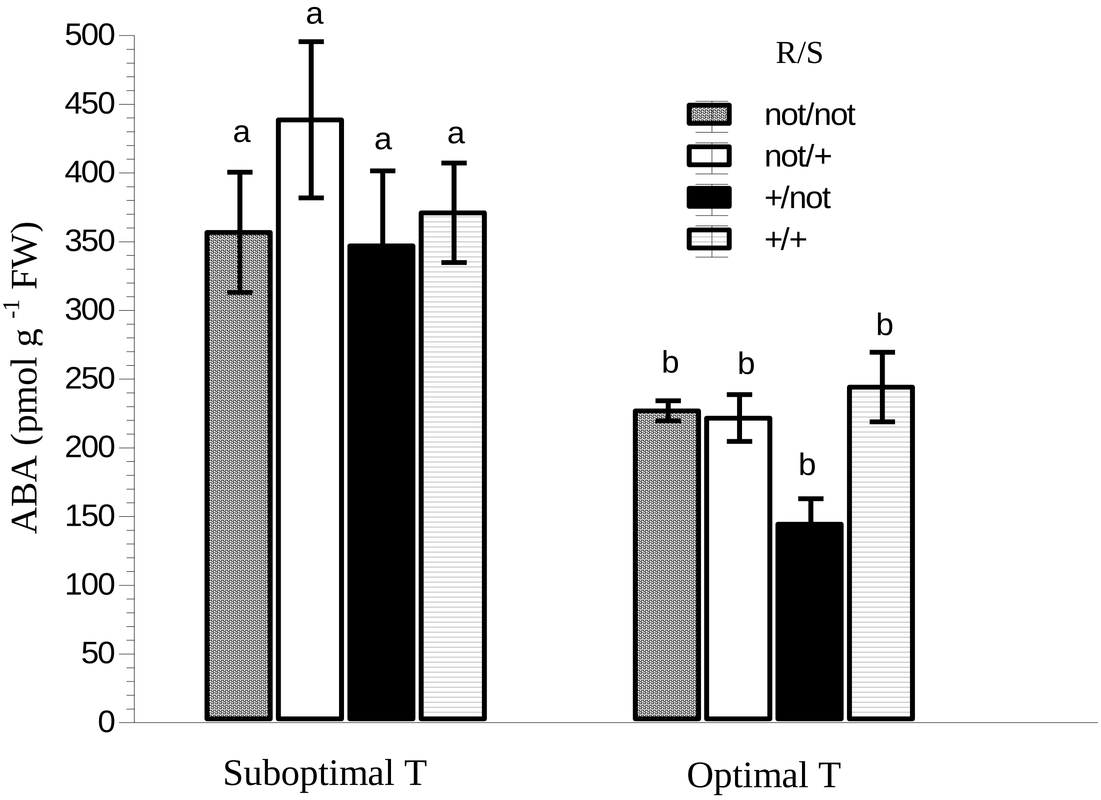
Table 14. Effect of 30-days exposure of grafted tomato to sub-optimal (day and night 15±0.4 °C) root temperature (T) on putrescine (Put), spermidine (Spd) and spermine (Spm). The rootstock/scion combinations are, using conventional tomato genetics notation, +/+, +/not, not/+ and not/not, where not represents the ‘notabilis’ genotype and “+” the ‘Ailsa Craig’ wild-type functional allele. Different letters within the same column indicate significant differences between means of four replications according to the Duncan’s Multiple Range Test (p ≤ 0.05).

Treatments	**Put**		**Spd**		**Spm**	
	(nmol g^{-1} FW)					
	Leaves	Roots	Leaves	Roots	Leaves	Roots

Sub-optimal Root T	*not*/*not*	219.7	51.66	321.2 cd	132.9	89.09 bc	16.65
	not/+	200.8	49.65	318.3 d	122.8	98.61 b	14.22
	+/*not*	219.4	44.15	369.5 cd	124.9	96.41 b	14.49
	+/+	229.4	50.95	442.5 b	129.9	123.1 a	14.65
Optimal Root T	*not*/*not*	219.7	26.06	318.6 d	115.1	71.94 c	23.47
	not/+	206.3	29.50	410.3 ab	92.74	102.3 b	22.36
	+/*not*	249.4	28.06	475.6 a	80.94	91.71 b	21.00
	+/+	214.8	27.42	406.2 ab	69.39	94.20 b	19.74
Main Effects							
Root T	Sub-optimal	217.2	49.10 a	365.6	127.6 a	102.6	15.00 b
	Optimal	222.6	27.76 b	402.7	89.55 b	90.03	21.64 a
R/S combination	*not*/*not*	219.7	38.86	319.7	124.0 a	79.29	20.06
	not/+	203.6	39.58	364.3	107.8 ab	100.5	18.29
	+/*not*	234.4	36.11	422.6	102.9 ab	94.06	17.75
	+/+	222.1	39.18	424.3	99.62 b	108.6	17.19
Statistical significance							
Root T		NS	***	NS	***	*	***
R/S combination		NS	NS	**	*	**	NS
Root T × R/S combination		NS	NS	*	NS	*	NS

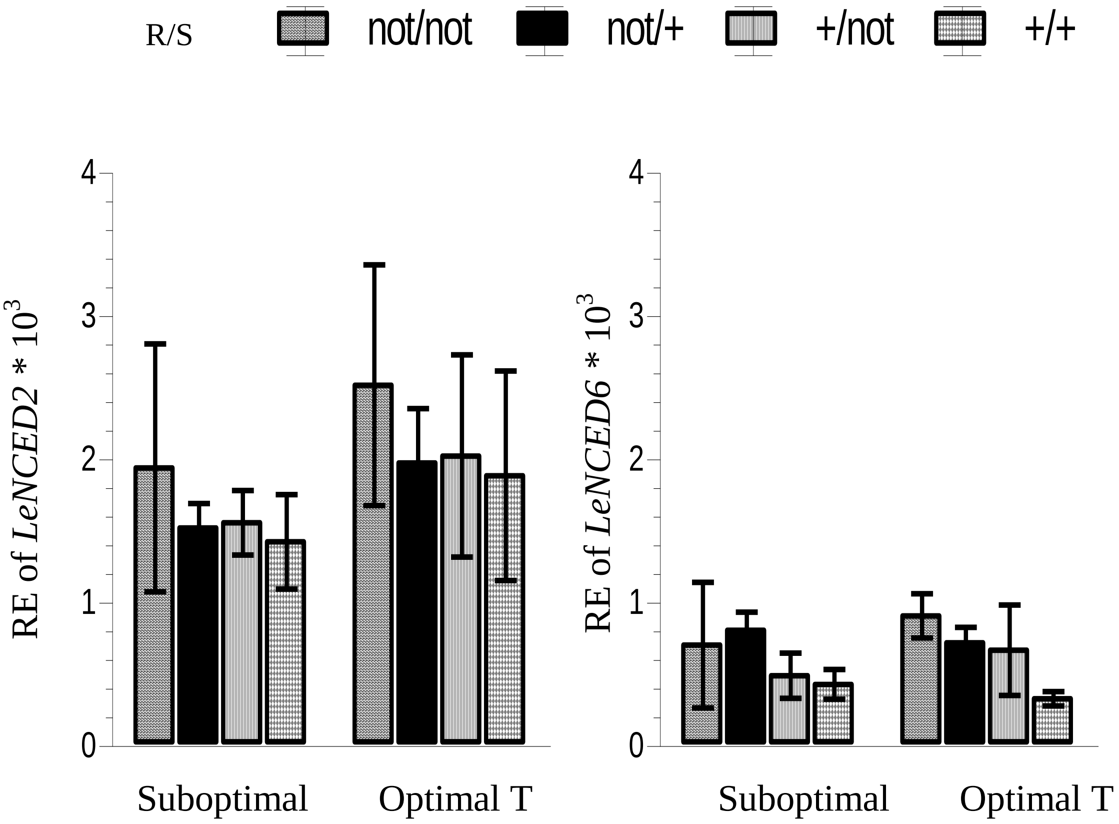
The levels of abscisic acid (ABA) in the leaves of grafted tomato increased under sub-optimal T regardless of the grafting combination (Fig. 2). However, the graft combination had no impact on the level of endogenous ABA in the leaves of tomato, irrespective of the root T.

Fig. 2 Effect of 30-days exposure of grafted tomato to sub-optimal (day and night 15±0.4 °C) root temperature (T) on ABA (abscisic acid) content of leaves. The rootstock/scion combinations are, using conventional tomato genetics notation, +/+, +/*not*, *not*/+ and *not*/*not*, where *not* represents the 'notabilis' genotype and "+" the 'Ailsa Craig' wild-type functional allele. Different lower-case letters on the bars indicate significant differences between means ± standard errors of four replications according to the Duncan's Multiple Range Test ($p \leq 0.05$).



To test if the gene expression of other members of the *NCED* family might have affected ABA biosynthesis, the expression of *LeNCED2* and *LeNCED6* was measured by qRT-PCR (Fig. 3). The expression of both genes was very low and not influenced either by the 'notabilis' mutation or by sub-optimal T. As a control, the expression of two genes of the same gene family of carotenoid cleavage dioxygenases (CCDs, *LeCCD1A* and *LeCCD1B*, participating in the biosynthesis of carotenoids, see Simkin et al., 2004 and Walter and Strack, 2011) was measured. The expression was found to be higher than expression of *LeNCED2* and *LeNCED6* (data not shown) confirming the very low expression of *LeNCED2* and *LeNCED6* under the conditions of the present investigation. Additionally, the expression of *NCED3* was analyzed with primers designed for the NCBI sequence (GQ222384.1). Gene expression of *NCED3* could not be confidently confirmed due to very low expression signals. Due to a 99% similarity between tomato and *Diospyros kaki* on the nucleotide level as found in the NCBI database we cannot exclude the possibility that the *NCED3* sequence derived from *Diospyros kaki*.

Fig. 3. Effect of 30-days exposure of grafted tomato to sub-optimal (day and night 15±0.4 °C) root temperature (T) on the relative expression (RE) of *LeNCED2* and *LeNCED6* gene in roots. The rootstock/scion combinations are, using conventional tomato genetics notation, +/+, +/*not*, *not*/+ and *not*/*not*, where *not* represents the 'notabilis' genotype and "+" the 'Ailsa Craig' wild-type functional allele. Means ± standard errors of four replications did not differ significantly according to the Duncan's Multiple Range Test ($p \leq 0.05$).

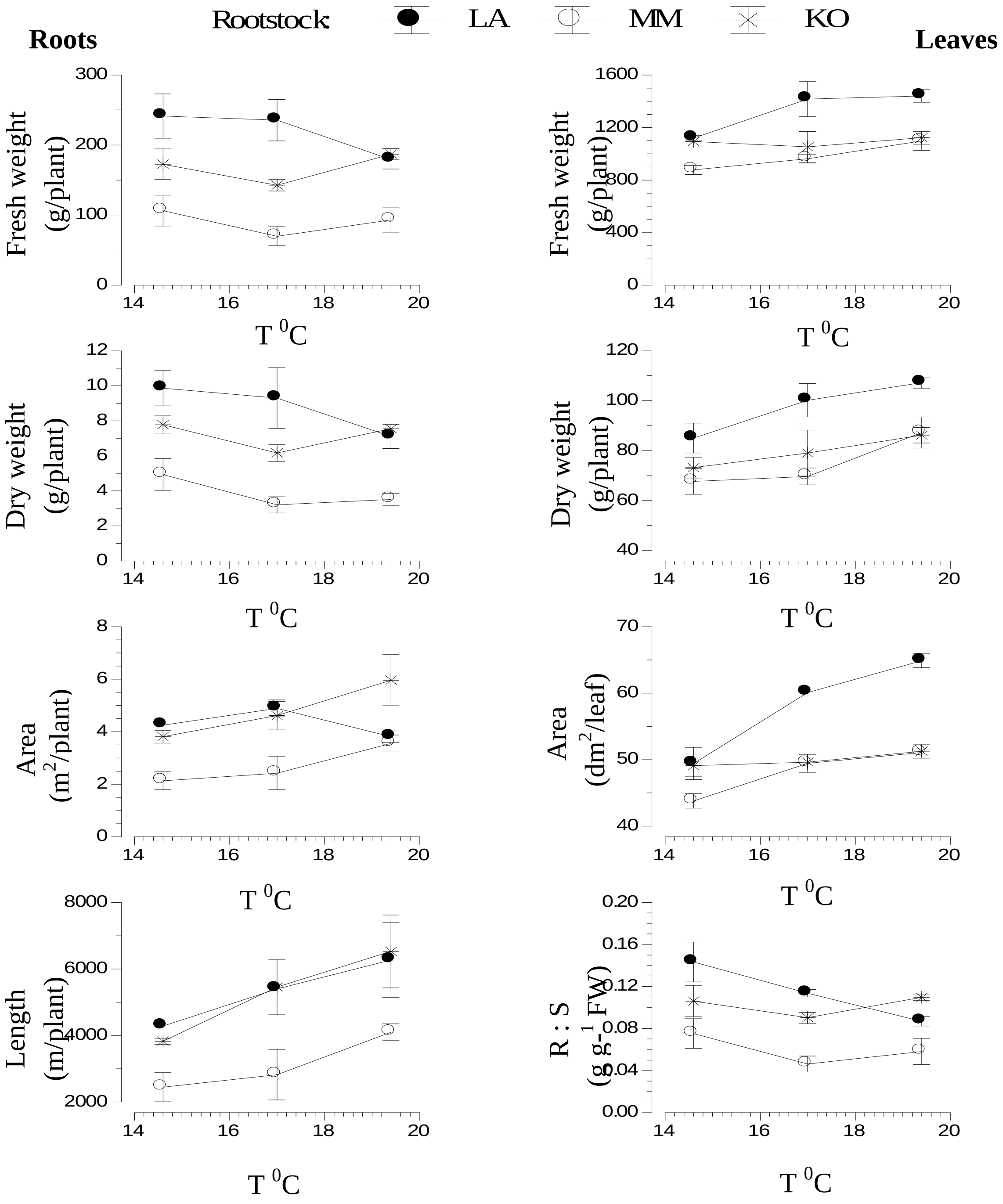


3.3. Growth, yield, and metabolic responses of temperature-stressed tomato to grafting onto rootstocks differing in cold tolerance.

Root fresh and dry weight of plants grafted onto ‘LA 1777’ were significantly higher than in self-grafted ‘Kommeet’ plants at low (14.6 °C) and intermediate T (17 °C) (Fig. 4), but at optimum T (19.4 °C) tended to decrease. In self-grafted ‘Kommeet’ root fresh and dry weight remained unchanged and thus no significant difference was found between them. Plants grafted onto ‘Moneymaker’ exhibited consistently lower root fresh and dry weight than those grafted onto the other two rootstocks at all T levels. Total root area and total root length were higher in self-grafted ‘Kommeet’ and those grafted onto ‘LA 1777’ than in plants grafted onto ‘Moneymaker’ at 14.6 and 17 °C, while at 19.4 °C total root area of plants grafted onto ‘LA 1777’ was reduced to similar levels with those found in plants grafted onto ‘Moneymaker’.

Grafting cv. ‘Kommeet’ onto *S. habrochaites,* accession LA 1777, increased both fresh and dry leaf mass and total leaf area at optimal or intermediate T, in comparison with self-grafting of ‘Kommeet’, or grafting onto the cold-sensitive tomato cultivar ‘Moneymaker’ (Fig. 4). However, at low T, leaf fresh and dry weight and total leaf area of plants grafted onto ‘LA 1777’ decreased to similar levels with those measured in self-grafted ‘Kommeet’. Nevertheless, leaf fresh and dry weight and total leaf area measured in ‘Kommeet’ grafted onto ‘Moneymaker’ were also reduced at 14.6 °C, and thus they remained at significantly lower levels than in plants grafted onto ‘LA 1777’. Depending on the differences reported above and their extent at 14.6 and 17 °C, root/shoot ratio was significantly higher in ‘Kommeet’ grafted onto ‘LA 1777’ than in the other two treatments. However, at 19.4 °C the self-grafted “Kommeet” exhibited a significantly higher root/shoot ratio than those grafted onto ‘LA 1777’.

Fig. 4. Effects of three different temperatures (T) and rootstock genotype of tomato cv. 'Kommeet' (KO), self-grafted or grafted onto the rootstocks 'LA1777' (LA) or 'Moneymaker' (MO), on root fresh and dry weight, mean area per a fully expanded leaf and length (left), leaf fresh weight, dry weight and area and root:shoot ratio (R:S) (right). The values are means ± standard errors of four replications.



Total fresh and dry weight of fruits per plant, and fresh weight of marketable fruits were strongly reduced when plants were exposed to low T (14.6 °C) in comparison with intermediate (17 °C) or optimal T (19.4 °C), regardless of grafting treatment (Table 15). Decrease in T from 19.4 to 17 °C reduced only fresh and marketable fruit weight but had no significant impact on fruit dry weight. In contrast, fruit size (i.e. the mean fresh weight per fruit) was enhanced by the reduction of T from 19.4 to 17 or 14.6 °C, regardless of grafting treatment. Remarkably, the intermediate T significantly reduced the amount of fruit fresh weight affected by blossom-end rot (BER), while at 14.6 °C no fruit with BER were recorded. No interaction was observed between T and rootstock genotype.

The total fresh and marketable weight of ‘Kommeet’ grafted onto ‘LA 1777’ were significantly lower than that of self-grafted ‘Kommeet’ (Table 15). Yield of plants grafted onto ‘Moneymaker’ appeared to be lower than that of self-grafted ‘Kommeet’ and higher than that of plants grafted onto ‘LA 1777’ but the differences were insignificant. However, the fruit dry weight of plants grafted onto ‘Moneymaker’ was significantly lower than that measured in self-grafted ‘Kommeet’. Plants grafted onto ‘LA 1777’ produced significantly fewer fruits with BER in comparison with those grafted onto ‘Moneymaker’ or self-grafted. Rootstock genotype had no impact on mean fruit weight. .

Table 15. Effects of three different temperatures (T) and rootstock genotype of tomato cv. ‘Kommeet’ (KO) self-grafted or grafted onto the rootstocks ‘LA 1777’ (LA) or ‘Moneymaker’ (MO) on fruit fresh, dry and marketable weight per plant, mean fruit size and the incidence of blossom-end rot (BER). Different letters within the same column indicate significant differences between the means of four replications separately for T and rootstock according to Duncan’s Multiple Range Test ($p \leq 0.05$). NS, *, ** and *** indicate not significant (NS) or significant differences at $p \leq 0.05$, $p \leq 0.01$ and $p \leq 0.001$, respectively.

		Weight				
Treatments		**Fresh** (g/plant)	**Dry** (g/plant)	**Mean** (g/fruit)	**Marketable** (g/plant)	**BER** (g/plant)
T	Low	819 c	25.80 b	172 a	807 c	0.00 b
	Intermediate	2589 b	84.25 a	142 b	2546 b	11.38 b

	Optimal	3261 a	93.08 a	104 c	2974 a	103.08 a
R /S	LA/KO	1891 b	62.61 b	140	1806 b	8.07 b
	MM/KO	2160 ab	52.92 b	137	2053 ab	51.15 a
	KO/KO	2619 a	87.60 a	137	2467 a	55.24 a
Statistical significance						
T		***	***	***	***	**
R/S combination		*	*	NS	*	*
T × R/S combination		NS	NS	NS	NS	NS

The number of fruits per plant and fruit/flower ratio were reduced when tomato was exposed to low T in comparison with intermediate or optimal T, regardless of grafting treatment (Table 16). Decrease in T from 19.4 to 17 °C reduced only fruit number and fruit/flower ratio but had no significant impact on flower number. Grafting ‘Kommeet’ onto ‘LA 1777’ had no impact on flower number in comparison with self-grafting of ‘Kommeet’. However, it significantly reduced fruit numbers due to reduced fruit setting as indicated by a decrease in the fruit/flower ratio. The ratio recorded in plants grafted onto ‘LA 1777’ was significantly lower compared with that estimated for plants grafted onto ‘Moneymaker’. Grafting ‘Kommeet’ onto ‘LA 1777’ or ‘Moneymaker’ resulted in similar fruit numbers without any significant interaction with T treatment. ‘Kommeet’ grafted onto ‘Moneymaker’ set less fruits, as indicated by the fruit/flower ratio compared with self-grafted ‘Kommeet’.

Table 16. Effects of three different temperatures (T) and rootstock genotype of tomato cv. ‘Kommeet’ (KO), self-grafted or grafted onto the rootstocks ‘LA 1777’ (LA) or ‘Moneymaker’ (MO) on fruit and flower number and fruit:flower ratio (FR:FL) from 3rd up to 8th truss. Different letters within the same column indicate significant differences between the means of four replications for T and rootstock separately according to Duncan’s Multiple Range Test ($p \leq 0.05$). NS, *, ** and *** indicate not significant (NS) or significant differences at $p \leq 0.05$, $p \leq 0.01$ and $p \leq 0.001$, respectively.

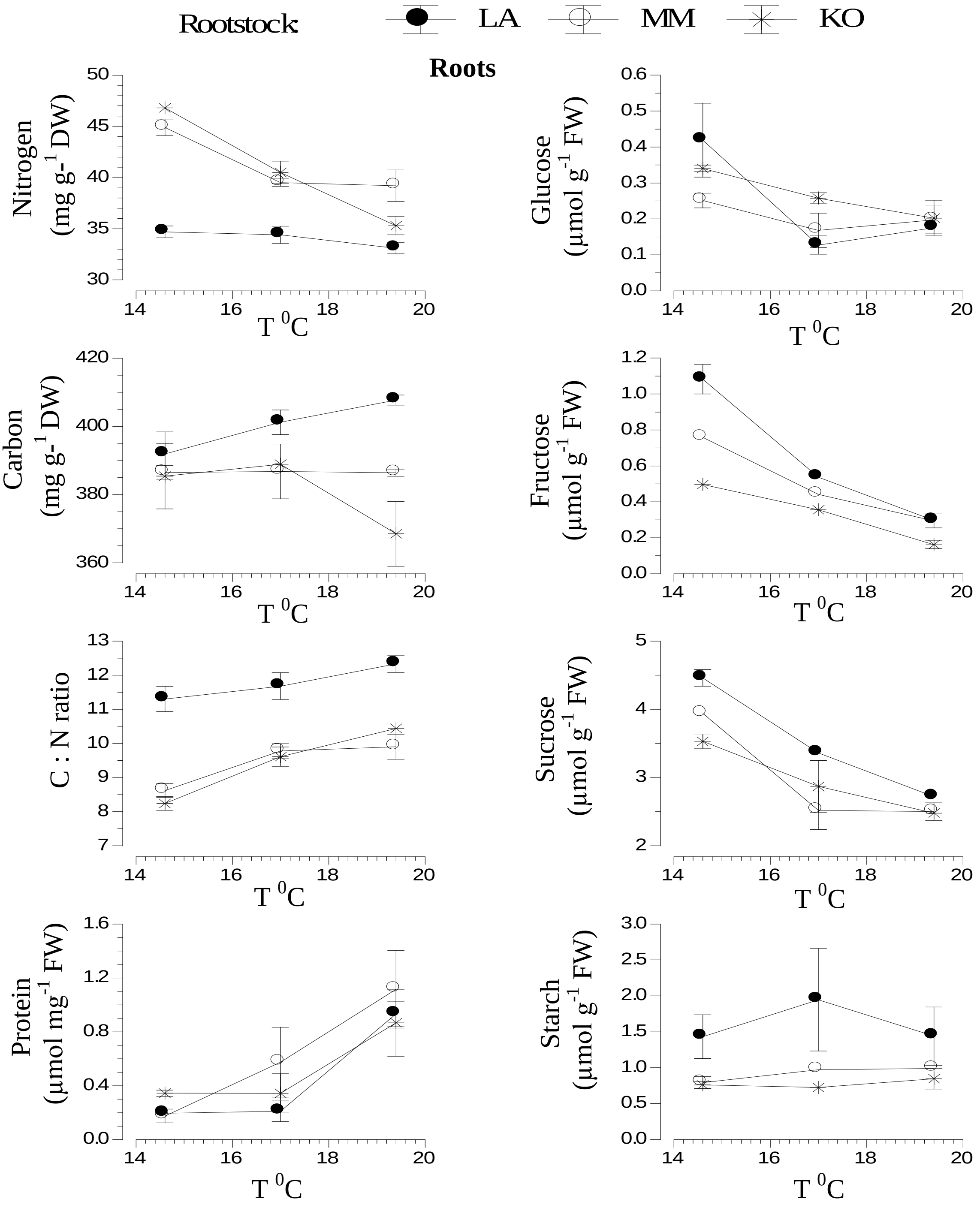
Treatments	**Fruit (No/plant)**	**Flowers (No/plant)**	**FR:FL (No/No)**

T	Low	8.4 c	50.21	0.17 c
	Intermediate	15.44 b	54.00	0.29 b
	Optimal	19.46 a	52.89	0.36 a
R / S	LA/KO	10.13 b	52.71	0.19 c
	MM/KO	13.83 b	50.67	0.27 b
	KO/KO	19.34 a	53.73	0.36 a
		Statistical significance		
T		**	NS	**
R/S combination		*	NS	*
T × R/S combination		NS	NS	NS

In roots, ‘Kommeet’ grafted onto ‘LA 1777’ exhibited significantly lower total-N concentrations at low (14.6 °C) and intermediate T (17 °C), and significantly higher total C concentrations at intermediate and optimal T (19.4 °C), in comparison with the other two grafting treatments (Fig. 5). At optimal T, total N in roots of ‘LA 1777’ was significantly lower only in comparison with ‘Moneymaker’ grafted plants. Decrease of T from 19.4 to 17 and 14.6 °C increased total N level in roots of ‘Kommeet’ or ‘Moneymaker’ but had no impact on that measured in ‘LA 1777’. In contrast, T decrease from 19.4 to 14.6 ^{o}C increased total C concentration in the roots of ‘LA 1777’, while not influencing total C in the other two rootstocks.

Root C:N ratio decreased with decreasing T in all grafting treatments, while the highest C:N ratio in roots was measured in ‘LA 1777’ at all T. Reduction of T from 19.4 to 14.6 °C in the greenhouse environment reduced the total protein content of roots, regardless of rootstock genotype without any significant differences between grafting treatments (Fig. 5). Exposure of tomato plants to 14.6 °C increased the glucose, fructose and sucrose concentration of roots when compared with 17 and 19.4 °C but had no impact on starch. Root glucose concentrations were not affected by the rootstock. However, fructose, sucrose and starch levels in roots of ‘LA 1777’ were significantly higher at 14.6 °C than those measured in ‘Kommeet’ or ‘Moneymaker’. Furthermore, at 17 °C, starch levels were significantly higher in roots of ‘LA 1777’ than in the other two rootstocks.

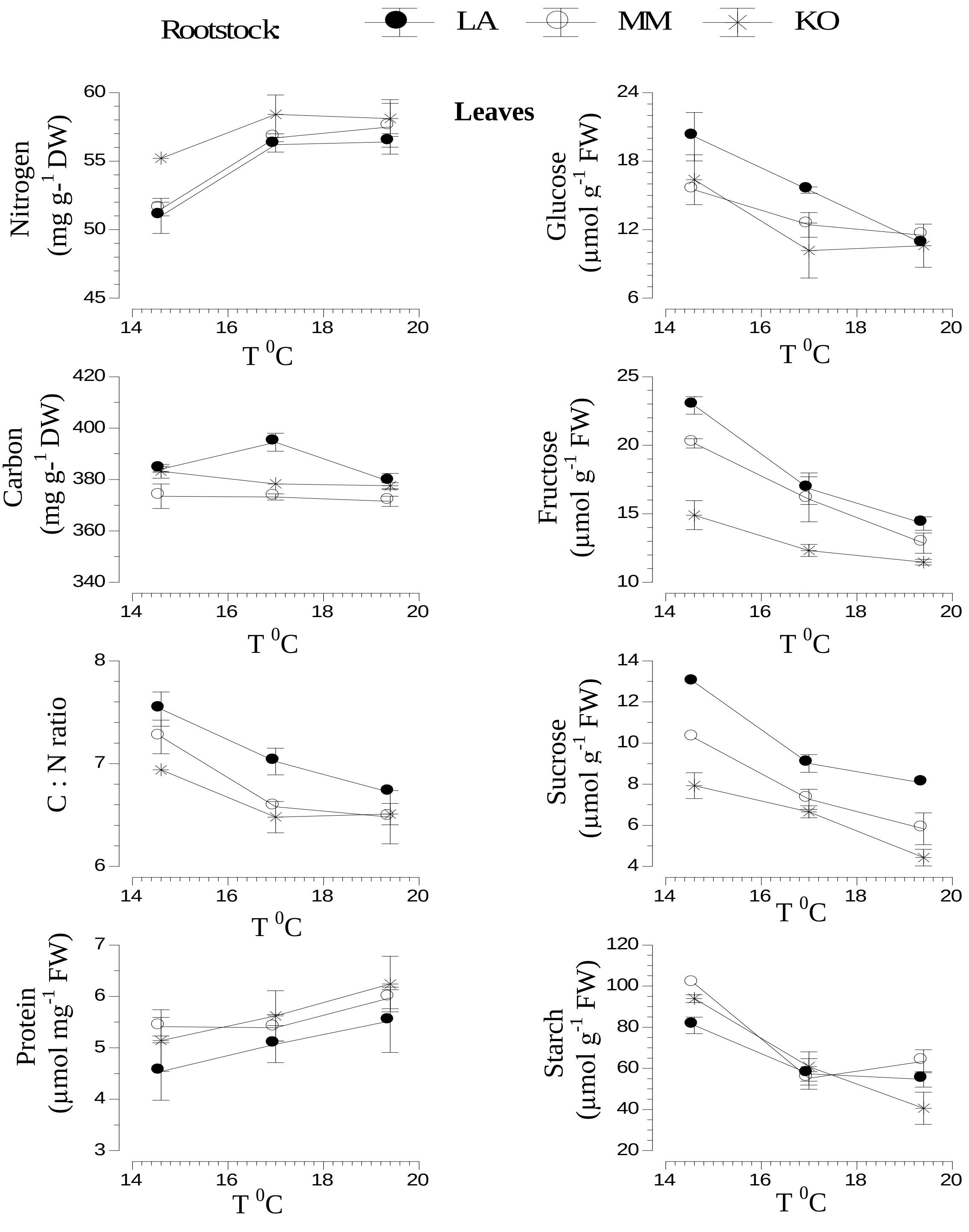
Fig. 5. Effects of three different temperatures (T) and rootstock genotype of tomato cv. ‘Kommeet’ (KO), self-grafted or grafted onto the rootstocks ‘LA1777’ (LA) or ‘Moneymaker’ (MO), on total nitrogen (N), total carbon (C) and total ratio of carbon to nitrogen (C:N), total protein, glucose, fructose, sucrose and starch content of roots. The values are means ± standard errors of four replications.



Decrease of T to 14.6 °C in the greenhouse environment reduced total N in leaves, regardless of the rootstock genotype (Fig. 6). However, the reduction was larger in plants grafted onto ‘LA 1777’ and ‘Moneymaker’, than in self-grafted ‘Kommeet’. Leaf carbon concentration increased slightly in self-grafted ‘Kommeet’ as T decreased from 19.4 to 14.6 °C, while in plants with ‘LA 1777’ rootstocks, leaf C increased strongly as T decreased from 19.4 to 17 °C but dropped to similar levels as in self-grafted ‘Kommeet’ at 14.6 °C. Leaf C concentration in plants grafted onto ‘Moneymaker’ was significantly lower than in the other two grafting treatments at all T levels. As a result of these variations in leaf C and N, leaf C:N ratio tended to increase as T decreased, while highest C:N values were found in plants grafted onto ‘LA 1777’. On the other hand, the total protein content of leaves declined with decreasing T, without any significant difference between grafting treatments.

Exposure of tomato plants to 14.6 °C increased the glucose, fructose, sucrose and starch concentration of leaves when compared with 17 and 19.4 °C (Fig. 6). At sub-optimal T, leaf glucose, fructose and sucrose concentrations were significantly higher in ‘Kommeet” grafted onto ‘LA 1777’ than in self-grafted and plants grafted onto ‘Moneymaker’, with the exception of fructose at 17 °C, which was similar in the hetero-grafted plants. On the other hand, grafting onto ‘LA1777’ reduced starch concentrations in the leaves of plants growing at 14.6 °C. Furthermore, at 14.6 °C, fructose and sucrose concentrations in leaves of plants grafted onto ‘Moneymaker’ were significantly higher than in self-grafted plants.

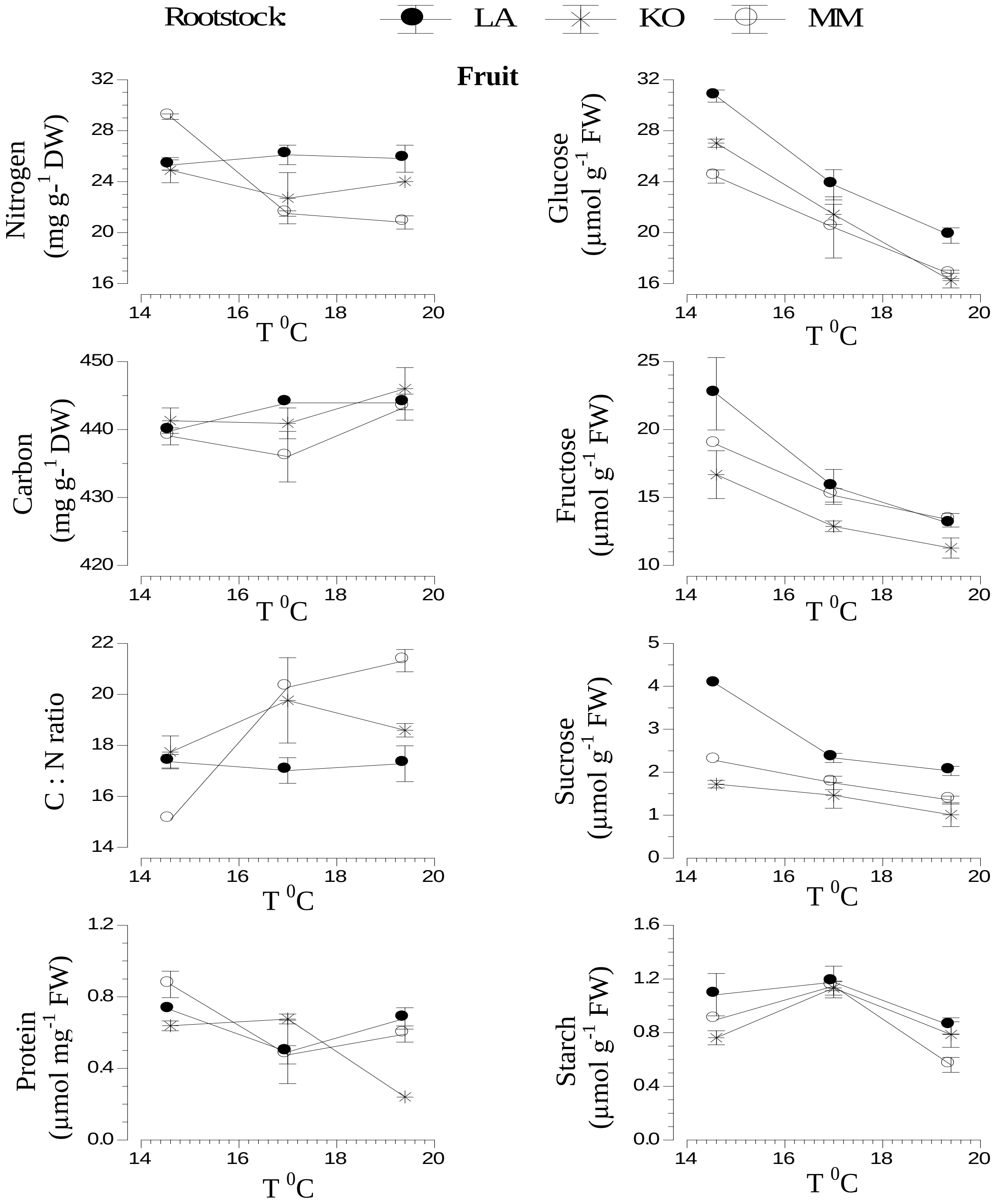
Fig. 6. Effects of three different temperatures (T) and rootstock genotype of tomato cv. 'Kommeet' (KO), self-grafted or grafted onto the rootstocks 'LA1777' (LA) or 'Moneymaker' (MO), on total nitrogen (N), total carbon (C) and total ratio of carbon to nitrogen (C:N), total protein, glucose, fructose, sucrose and starch content of leaves. The values are means ± standard errors of four replications.



Total N in fruits of plants grafted onto ‘Moneymaker’ was low at 19.4 and 17 °C, but increased appreciably at 14.6 °C, thereby reaching higher levels than in the other two grafting treatments (Fig. 7). Total C in fruits decreased as T was reduced from 19.4 to 14.6 °C, without significant differences between grafting treatments. Reduction of T decreased the C:N ratio in fruits of plants grafted onto ‘Moneymaker’, but had no impact on C:N ratio in fruits of self-grafted or plants grafted onto ‘LA 1777’; the latter, however, exhibited significantly lower fruit C:N ratios at 17 and 19.4 °C than self-grafted ‘Kommeet’ or plants grafted onto ‘Moneymaker’. When T was reduced from 19.4 to 14.6 °C, total protein concentration increased in fruits from plants grafted onto ‘Moneymaker’ and self-grafted ‘Kommeet’ while in the latter an increase was also observed at 17 °C (Fig. 7). In contrast, fruit protein concentration was not influenced by T in plants grafted onto ‘LA 1777’.

At optimal T, self-grafted ‘Kommeet’ exhibited the lowest fruit protein concentration in comparison with the hetero-grafted plants, but this difference was reversed at intermediate T. Concentrations of glucose, fructose, and sucrose in fruits increased significantly with decreasing T in all grafting treatments. Fruit glucose, fructose, and sucrose concentrations in plants grafted onto ‘LA 1777’ were significantly higher than in the other two grafting treatments at all T levels, except fructose at intermediate and optimal T, which was similar in the hetero-grafted plants. At optimal T, plants grafted onto ‘Moneymaker’ exhibited lower fruit starch levels than self-grafted ‘Kommeet’ and plants grafted onto ‘Moneymaker’. When T was reduced from 19.4 to 17 °C, fruit starch concentration increased to similar levels in all grafting treatments. However, at 14.6 °C, starch concentration decreased to lower levels than at 17 °C in fruits of self-grafted or plants grafted onto ‘Moneymaker’ (Fig.7).

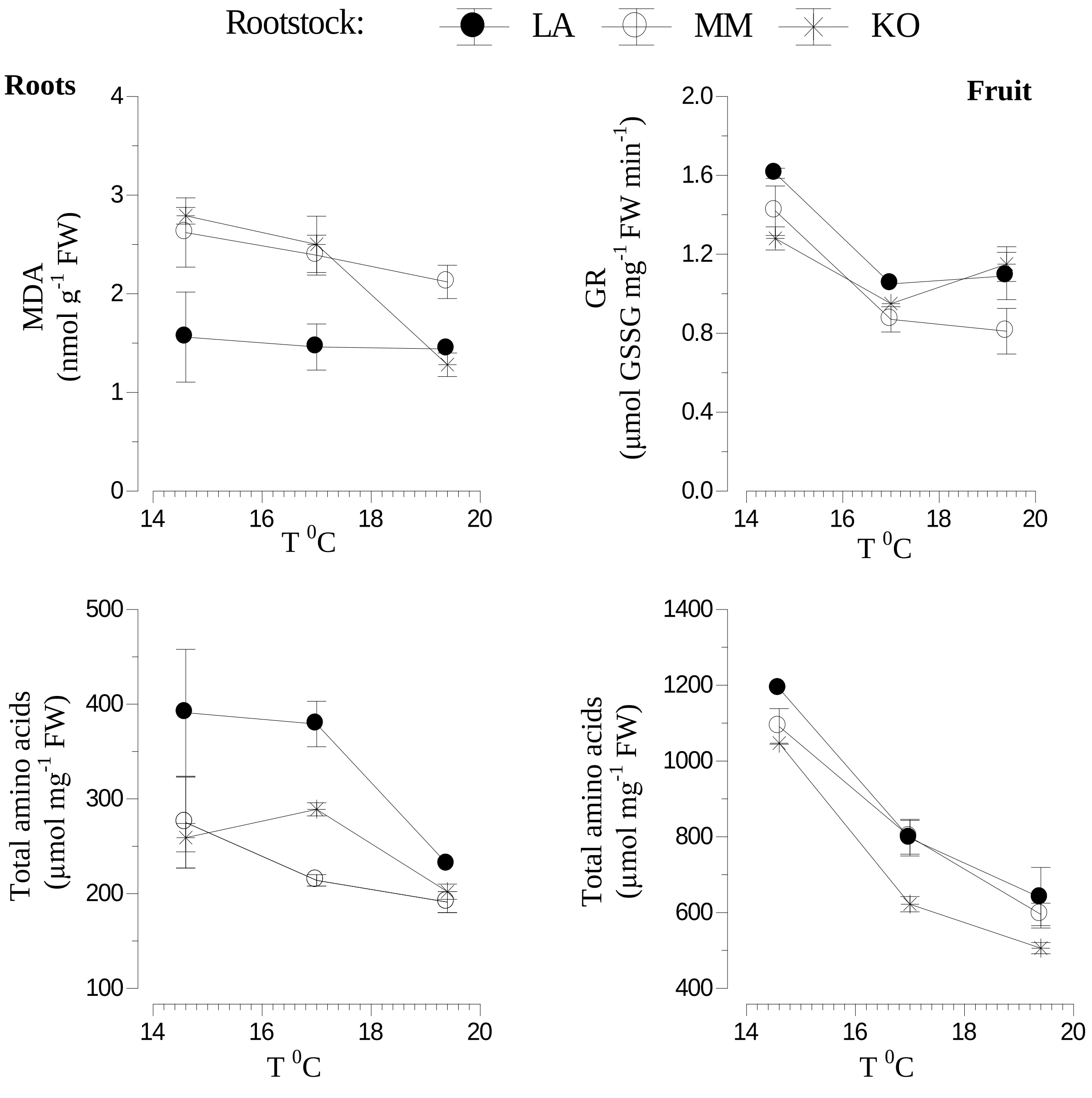
Fig. 7. Effects of three different temperatures (T) and rootstock genotype of tomato cv. ‘Kommeet’ (KO), self-grafted or grafted onto the rootstocks ‘LA1777’ (LA) or ‘Moneymaker’ (MO), on total nitrogen (N), total carbon (C) and total ratio of carbon to nitrogen (C:N), total protein, glucose, fructose, sucrose and starch content of fruit. The values are means ± standard errors of four replications.



Decreasing T increased root malondialdehyde (MDA) concentration when ‘Kommeet’ was either self-grafted or grafted onto ‘Moneymaker’ but had no significant impact when plants were grafted onto ‘LA 1777’ (Fig. 8). As a result, at sub-optimal T root MDA was significantly lower in plants grafted onto ‘LA 1777’ than in self-grafted plants or those grafted onto ‘Moneymaker’. In contrast, the MDA concentration in leaves was not influenced either by T or by the rootstock genotype (data not shown). Glutathione reductase (GR) activity in roots and leaves was not influenced by T or rootstock genotype (data not shown). In fruits, GR activity at 19.4 °C was significantly lower in plants grafted onto ‘Moneymaker’ than in the other two grafting treatments, while it was not influenced by a T decrease from 19.4 to 17 °C. However, at 14.6 °C, GR activity in fruits increased in all grafting treatments, the increase being significantly higher in plants grafted onto ‘LA 1777’.

Total amino-acid concentration in the roots tended to increase with decreasing T. This increase was greater in plants grafted onto ‘LA 1777’ than in self-grafted plants and those grafted onto ‘Moneymaker’ and this resulted in significantly higher total amino acid concentrations in the first compared with the latter two grafting treatments. At intermediate T, total amino-acid concentration in the roots of plants grafted onto ‘Moneymaker’ was significantly lower than in those of self-grafted ‘Kommeet’. Total amino acid concentration in leaves was not influenced either by T or by the rootstock genotype (data not shown). Fruit total amino acid concentration increased in all grafting treatments with decreasing T, the increase being more profound as T was reduced from 17 to 14.6 °C (Fig. 8). At intermediate and optimal T, the lowest total amino acid concentration in fruits was measured in self-grafted ‘Kommeet’, while at 14.6 °C the fruit total amino acid concentration was significantly higher in plants grafted onto ‘LA 1777’ than in those grafted onto *S. lycopersicum* rootstocks.

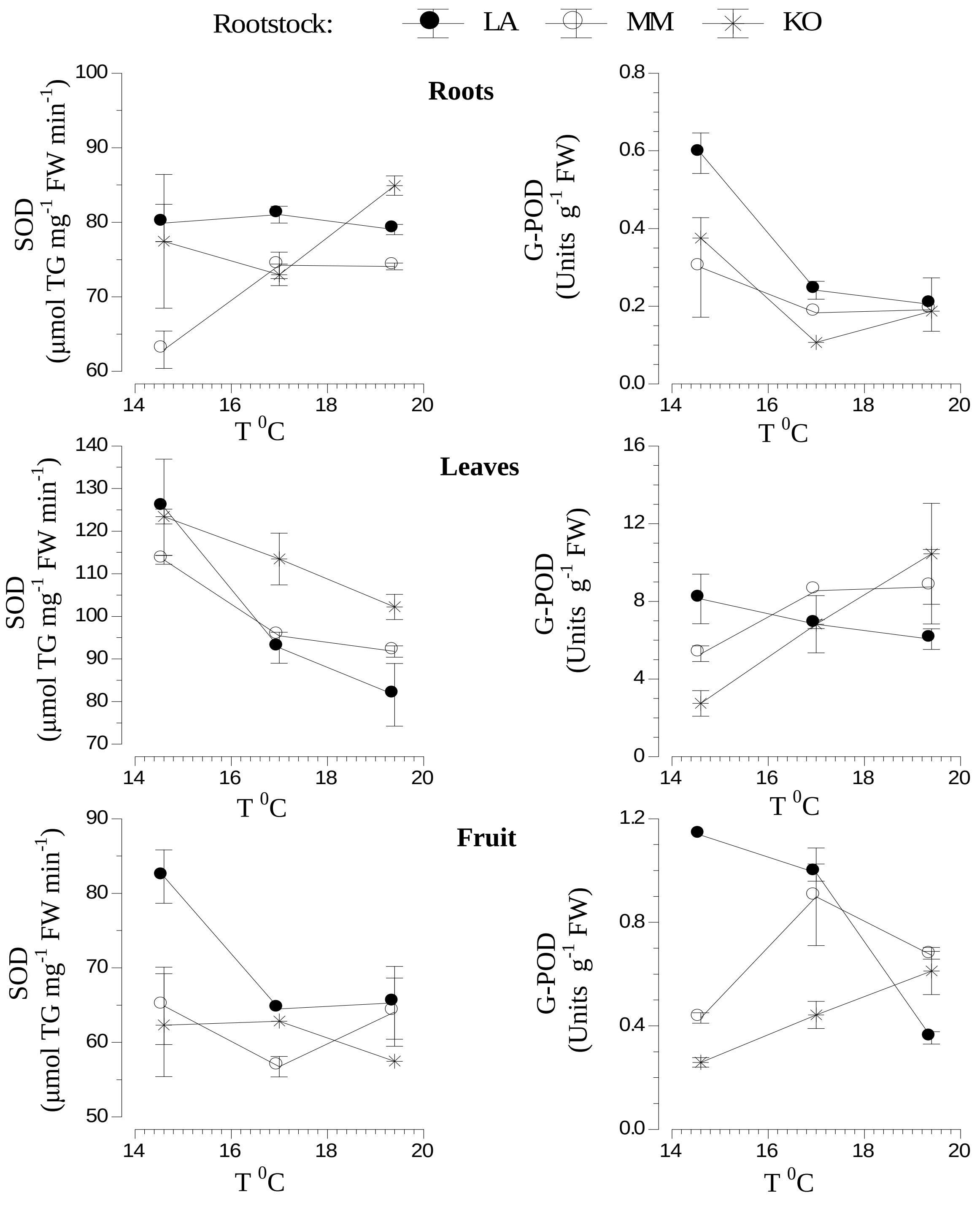
Fig. 8. Effects of three different temperatures (T) and rootstock genotype of tomato cv. ‘Kommeet’ (KO), self-grafted or grafted onto the rootstocks ‘LA1777’ (LA) or ‘Moneymaker’ (MO), on malondialdehyde (MDA) content and total amino acids of roots (left) and glutathione reductase (GR) activity and total amino acids of fruit (right). The values are means ± standard errors of four replications.



Superoxide dismutase (SOD) activity in roots of plants grafted onto 'LA1777' was similar at all T levels (Fig. 9). However, SOD activity in roots decreased as T was reduced from 19.4 to 17 °C in self-grafted 'Kommeet' and from 19.4 to 14.6 °C in plants grafted onto 'Moneymaker'. Highest SOD activity in roots was recorded in self-grafted 'Kommeet' at optimal T and in plants grafted onto 'LA 1777' at intermediate T, while at low T no significant difference was found between these two grafting treatments. SOD activity was significantly higher in leaves of self-grafted 'Kommeet' than in those of hetero-grafted plants at 19.4 and 17 °C. However, at 14.6 ^{o}C, leaf SOD activity was similar in all grafting treatments. SOD activity in fruits was not influenced by a T decrease from 19.4 to 17 °C or by grafting treatment at 19.4 °C, but was significantly reduced by grafting onto 'Moneymaker' at 17 °C. At 14.6 °C, fruit SOD activity increased in plants grafted onto 'LA1777', while it was not influenced by T in the other two grafting treatments.

Root GPOD activity in self-grafted plants and plants grafted onto 'LA 1777' increased at low T, in comparison with intermediate or optimal T, the increase being more profound when the root genotype was 'LA 1777'. In contrast, T had no impact on root guaiacol peroxidase (GPOD) activity in plants grafted onto 'Moneymaker'. Low T reduced GPOD activity in the leaves of 'Kommeet' grafted onto *S. lycopersicum* rootstocks, but not in those grafted onto 'LA 1777', which exhibited the highest GPOD levels at low T (Fig. 9). Lowest GPOD activity at 19.4 °C was measured in fruits from plants grafted onto 'LA 1777'. However, at 17 °C, fruit GPOD activity increased in plants grafted onto 'LA 1777' to similar levels as in plants grafted onto 'Moneymaker', while the values measured in self-grafted 'Kommeet' were significantly lower than in the other two grafting treatments. The further T decrease from 17 to 14.6 °C reduced GPOD activity in fruits from plants grafted onto 'Moneymaker' and self-grafted plants, but increased fruit GPOD activity in plants grafted onto 'LA 1777'.

Fig. 9. Effects of three different temperatures (T) and rootstock genotype of tomato cv. ‘Kommeet’ (KO), self-grafted or grafted onto the rootstocks ‘LA1777’ (LA) or ‘Moneymaker’ (MO), on guaiacol peroxidase (GPOD) and superoxide dismutase (SOD) activity of roots (top), leaves (middle) and fruit (bottom). The values are the means ± standard errors of four replications.



3.4. Expression profiling of tolerant and sensitive tomato rootstock genotypes under sub-optimal temperature stress

3.4.1. Differences in growth and physiological parameters between sub-optimal temperature tolerant and sensitive tomato genotypes

Sub-optimal root T reduced shoot fresh and dry mass and total leaf area (Table 17). Grafting onto ‘LA 1777’ was associated with reduced shoot fresh dry mass and total leaf area. However, the dry matter content of the shoot was not influenced either by the root T or by the rootstock/scion combination (Table 23). The fresh and dry mass of roots and the % dry matter were significantly reduced when exposed to sub-optimal root T. The impact of sub-optimal T on roots was also influenced by the grafting combination, as indicated by the significant interaction between these two experimental factors. Specifically, under optimal root T the use of ‘Moneymaker’ as rootstock was associated with significantly higher levels of root fresh and dry mass in comparison with ‘LA 1777’, whereas the exposure of tomato plants to sub-optimal root T showed no significant difference between the two rootstocks tested (Table 17).

Table 17. Effects of transient exposure of grafted tomato to sub-optimal root temperature (T) on fresh and dry mass of shoot, total leaf area (TLA), fresh (FW), dry weight (DW) and dry matter content (DC) of roots. Grafted plants were obtained using ‘Moneymaker’ (MO) and ‘LA 1777’ (LA) as rootstocks and ‘Kommeet’ (KO) as scion in the rootstock/scion (R/S) combinations. Different letters within the same column indicate significant differences between the means of four replications according to Duncan’s Multiple Range Test ($p \leq 0.05$).

Treatment		**Shoot**		**TLA**	**Roots**		**Roots**
		(g FW)	(g DW)	(cm^2)	(g FW)	(g DW)	% DC
Sub-optimal T	LA / KO	63,42	4,77	1558 b	16,08 b	0,65 b	4,82b
	MO / KO	126,32	8,38	2576 b	14,13 b	0,73 b	4,50b
Optimal T	LA / KO	79,45	5,23	1787 b	7,11 b	0,40 b	5,20b
	MO / KO	212,73	14,03	4887 a	28,32a	1,26a	6,64a
Main effects							
Root T	Sub-optimal	94,87 b	6,58 b	2140 b	15,10	0,69	4,66b

	Optimal	146,09 a	9,63 a	3116 a	17,72	0,83	5,92a
R/S genotype	LA / KO	71,43 b	5,00 b	1689 b	11,60b	0,53b	5,01b
	MO / KO	169,53 a	11,21 a	3567 a	21,22a	0,99a	5,57a
Statistical significance							
Root T		*	*	*	NS	NS	***
R/S genotype		**	**	***	*	*	*
Root T × R/S genotype		NS	NS	*	*	*	**

No other root characteristic (Table 18) was influenced either by the root T or by the rootstock/scion genotypes apart from the mean root diameter which was maximum under the exposure of plants to sub-optimal root T regardless of the rootstock genotype.

Table 18. Effects of transient exposure of grafted tomato to sub-optimal root temperature (T) on root length (RL), root average diameter (RAD), root length (RL) related to fresh (FW) and dry weight (DW) and specific root area (RSA) related to FW and DW of roots. Grafted plants were obtained using ‘Moneymaker’ (MO) and ‘LA 1777’ (LA) as rootstocks and ‘Kommeet’ (KO) as scion in the rootstock/scion (R/S) combinations. Different letters within the same column indicate significant differences between the means of four replications according to Duncan’s Multiple Range Test ($p \leq 0.05$).

Treatment		**RL (mm)**	**RAD (mm)**	**RL (mm / FM)**	**RL (mm / DW)**	**RSA (cm^2 g^{-1}) / FW**	**RSA (cm^2 g^{-1}) / DW**
Root T	Sub-optimal	820	0,34a	1034	695	329	21,89
	Optimal	851	0,28b	1020	599	270	22,91
R/S genotype	LA / KO	866	0,31	842	497	299	23,10
	MO / KO	805	0,31	1212	798	301	21,70
Statistical significance							
Root T		NS	*	NS	NS	NS	NS
R/S genotype		NS	NS	NS	NS	NS	NS
Root T × R/S genotype		NS	NS	NS	NS	NS	NS

The rate of net CO_2 assimilation (*A*) and the transpiration rates (*E*) did not respond to sub-optimal root zone temperature, regardless of the rootstock genotype, i.e. the presence of 'LA 1777' or 'Moneymaker' (Table 19). Moreover, chlorophyll fluorescence measurements of light-adapted and dark-adapted leaves were not influenced either by the root T or by the rootstock/scion genotypes (Table 19). A significant induction of stomatal conductance (g_s) was occurred when plants were subjected to root sub-optimal temperature while this increase was also profound when 'LA 1777' was used as a rootstock even though no interaction with the rootstock/scion genotype occurred. However, water use efficiency (WUE) was significantly increased while intracellular CO_2 (c_i) was significantly reduced by the exposure of the roots to sub-optimal T, regardless of the rootstock genotype.

Table 19. Effects of transient exposure of grafted tomato to sub-optimal root temperature (T) on leaf net CO_2 assimilation rate (*A*), stomatal conductance (g_s), intercellular CO_2 concentration (c_i), transpiration rate (*E*), and water use efficiency (WUE). Grafted plants were obtained using 'Moneymaker' (MO) and 'LA 1777' (LA) as rootstocks and 'Kommeet' (KO) as scion in the rootstock/scion (R/S) combinations. Different letters within the same column indicate significant differences between the means of four replications according to Duncan's Multiple Range Test ($p \leq 0.05$).

Treatments		***A*** **(μmol CO_2 m^{-2} s^{-1})**	**g_s (mmol m^{-2} s^{-1})**	**c_i (μl l^{-1})**	***E*** **(mmol H_2O m^{-2} s^{-1})**	**WUE (μmol CO_2 $mmol^{-1}$ H_2O)**
Root T	Sub-optimal	12,05	0,187 a	273 b	3,51	3,47a
	Optimal	10,50	0,158 b	286 a	3,43	3,06b
R/S genotype	LA / KO	11,38	0,165 b	281	3,50	3,25
	MO / KO	11,13	0,180 a	278	3,43	3,28
Statistical significance						
Root T		NS	*	*	NS	**
R/S genotype		NS	*	NS	NS	NS
Root T × R/S genotype		NS	NS	NS	NS	NS

Moreover, chlorophyll fluorescence measurements of light-adapted and dark-adapted leaves (Table 20) and carbohydrates (Table 21) were not influenced either by the root T or by the rootstock genotype.

Table 20. Effects of transient exposure of grafted tomato to sub-optimal root temperature (T) on maximum quantum use efficiency of PSII in the dark-adapted state (Fv/Fm), effective quantum use efficiency of PSII in the light-adapted state (F′v/F′m), photochemical quenching (qP), effective quantum yield (ΦPSII), non-photochemical quenching (NPQ) and steady-state fluorescence (Fs). Grafted plants were obtained using 'Moneymaker' (MO) and 'LA 1777' (LA) as rootstocks and 'Kommeet' (KO) as scion in the rootstock/scion (R/S) combinations.

Treatments		**Fv/Fm**	**Fv'/Fm'**	**qP**	**ΦPSII**	**NPQ**	**Fs**
Root T	Sub-optimal	0,803	0,474	0,421	0,202	0,593	2013
	Optimal	0,797	0,471	0,372	0,175	0,595	2098
R/S genotype	LA / KO	0,798	0,472	0,395	0,188	0,597	2080
	MO / KO	0,802	0,474	0,396	0,187	0,591	2031
Statistical significance							
Root T		NS	NS	NS	NS	NS	NS
R/S genotype		NS	NS	NS	NS	NS	NS
Root T × R/S genotype		NS	NS	NS	NS	NS	NS

Table 21. Effects of transient exposure of grafted tomato to sub-optimal root temperature (T) on glucose, fructose and sucrose of leaves and roots. Grafted plants were obtained using 'Moneymaker' (MO) and 'LA 1777' (LA) as rootstocks and 'Kommeet' (KO) as scion in the rootstock/scion (R/S) combinations.

Treatments		**Glucose**		**Fructose**		**Sucrose**	
		Leaves	Roots	Leaves	Roots	Leaves	Roots
		(μmol g^{-1} FW)					
Root T	Sub-optimal	7,78	0,68	6,64	0,49	3,33	2,33
	Optimal	8,45	0,63	6,82	0,85	3,08	2,90

R/S genotype	LA / KO	7,36	0,54	5,84	0,74	2,98	2,75
	MO / KO	8,88	0,76	7,61	0,60	3,42	2,48
Statistical significance							
Root T		NS	NS	NS	NS	NS	NS
R/S genotype		NS	NS	NS	NS	NS	NS
Root T × R/S genotype		NS	NS	NS	NS	NS	NS

The activity of guaiacol peroxidase (G-POD) increased in the roots of tomato when subjected to sub-optimal T stress. The activities of G-POD in the leaves and glutathione reductase (GR) and superoxide dismutase SOD in the leaves and roots of tomato were not influenced by either the root T or the rootstock genotype. However, when ‘LA 1777’ was used as a rootstock the activity of G-POD in the roots was significantly higher in comparison with the combination resulting from the grafting of ‘Moneymaker’ and ‘Kommeet’ (Table 22).

Table 22. Effects of transient exposure of grafted tomato to sub-optimal root temperature (T) on guaiacol peroxidase (G-POD), glutathione reductase (GR) and superoxide dismutase (SOD) of leaves and roots. Grafted plants were obtained using ‘Moneymaker’ (MO) and ‘LA 1777’ (LA) as rootstocks and ‘Kommeet’ (KO) as scion in the rootstock/scion (R/S) combinations. Different letters within the same column indicate significant differences between the means of four replications according to Duncan’s Multiple Range Test ($p \leq 0.05$).

Treatments		**G-POD**		**GR**		**SOD**	
		Leaves	Roots	Leaves	Roots	Leaves	Roots
		(µmol TG mg^{-1} FW min^{-1})		(µmol TG mg^{-1} FW min^{-1})		(Units g^{-1} FW)	
Root T	Sub-optimal	2,82	3,32 a	10,92	4,10	114	273
	Optimal	2,91	2,32 b	9,80	5,45	98	440
R/S genotype	LA / KO	2,89	2,27 b	10,14	3,67	106	385
	MO / KO	2,84	3,37 a	10,58	5,89	106	328

Statistical significance						
Root T	NS	*	NS	NS	NS	NS
R/S genotype	NS	*	NS	NS	NS	NS
Root T × R/S genotype	NS	NS	NS	NS	NS	NS

The levels of total amino acids in leaves and roots, the electrolyte leakage (%) and the content of starch in both plant parts were not influenced either by the root T or by the rootstock genotype (Table 23). The same behavior was also profound in the measurements of MDA, H_2O_2 and total protein content in the leaves and roots (Table 24).

Table 23. Effects of transient exposure of grafted tomato to sub-optimal root temperature (T) on dry matter content of shoot, total amino acids in leaves and roots, electrolyte leakage (EL) (%) and the starch content of leaves and roots. Grafted plants were obtained using ‘Moneymaker’ (MO) and ‘LA1777’ (LA) as rootstocks and ‘Kommeet’ (KO) as scion in the rootstock/scion (R/S) combinations.

Treatments		**% DC**	**T AA**		**EL (%)**	**Starch**	
		Shoot	Leaves	Roots		Leaves	Roots
			(μmol*mg^{-1} FW)			(μmol g^{-1} FW)	
Root T	Sub-optimal	7,51	7,02	3,40	16,64	30,43	0,67
	Optimal	7,21	7,51	2,46	14,52	37,90	0,75
R/S genotype	LA / KO	7,41	6,60	3,12	15,49	33,69	0,74
	MO / KO	7,30	7,93	2,82	15,67	35,05	0,69
Statistical significance							
Root T		NS	NS	NS	NS	NS	NS
R/S genotype		NS	NS	NS	NS	NS	NS
Root T × R/S genotype		NS	NS	NS	NS	NS	NS

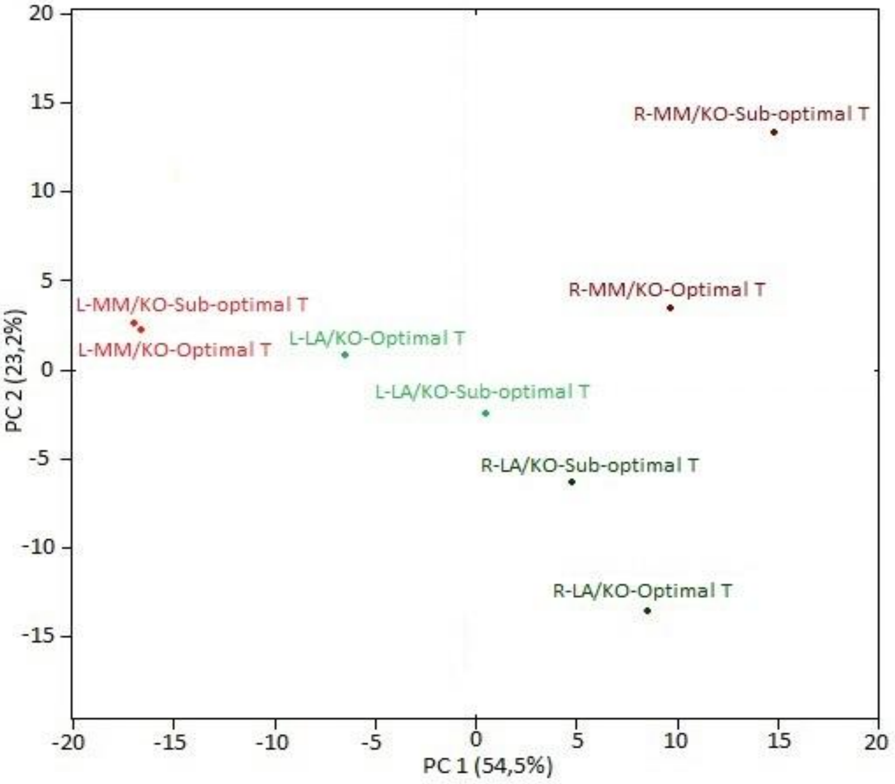
Table 24. Effects of transient exposure of grafted tomato to sub-optimal root temperature (T) on lipid peroxidation (MDA), and the H_2O_2 and protein concentration in leaves and roots. Grafted plants were obtained using 'Moneymaker' (MO) and 'LA 1777' (LA) as rootstocks and 'Kommeet' (KO) as scion in the rootstock/scion (R/S) combinations. Different letters within the same column indicate significant differences between the means of four replications according to Duncan's Multiple Range Test ($p \leq 0.05$).

Treatments		**MDA**		**H_2O_2**		**Protein**	
		Leaves	Roots	Leaves	Roots	Leaves	Roots
		(nmol g^{-1} FW)		(µmol g^{-1} FW)		(mg g^{-1} FW)	
Root T	Sub-optimal	8,81	3,73	19,81	3,28	3,50	0,44
	Optimal	7,25	3,07	18,33	3,66	2,70	1,62
R/S genotype	LA / KO	8,31	4,20	19,73	3,54	3,44	0,52
	MO / KO	7,74	2,61	18,41	3,40	2,76	1,41
Statistical significance							
Root T		NS	NS	NS	NS	NS	NS
R/S genotype		NS	NS	NS	NS	NS	NS
Root T × R/S genotype		NS	NS	NS	NS	*	NS

3.4.2. Differences in gene expression between tolerant and sensitive genotypes under sub-optimal T stress

Principal component analysis (PCA) is used to reduce multivariate data complexity as a method of identifying patterns and expressing data in ways that highlight similarities and differences (Kaplan et al., 2007). In this study, we used PCA to evaluate simultaneous changes in global gene expression patterns in leaves and roots of grafted plants (Fig. 10). The cumulative contribution ratio of the PCA reached 54.5% up to the second principal component (PC2), indicating correct application of PCA to the transcript profiles of the analyzed plant parts and T treatments. Indeed, the second principal component identified discrete responses between leaves and roots, reaching a cumulative contribution ratio of 23.2%, while the first principal component showed a further separation of the rootstock genotypes. All of these PCA components were statistically significant. As far as the leaves are concerned, the first component had a similar trajectory and magnitude in the non sub-optimal T-stressed samples, suggesting the existence of a common transcriptional response. On the other hand, under sub-optimal T stress this response in the leaves of ‘Kommeet’ grafted onto ‘LA 1777’ was clearly separable from that of the leaves of ‘Kommeet’ grafted onto ‘Moneymaker’, indicating that large and coherent transcriptional changes were induced by the shift in root T in the two different grafting combinations. Moreover, the transcript profile of ‘Kommeet’ grafted onto ‘Moneymaker’ (KO/MM) and grown under optimal T conditions was similar to that of sub-optimal root T-exposed KO/MM plants. The PC2 values of the leaves of ‘Kommeet’ grafted onto ‘LA 1777’ or ‘Moneymaker’ subjected either to optimal or sub-optimal root T were nearly zero (Fig. 10). The PC2 value of ‘Moneymaker’ rootstocks subjected to either optimal or sub-optimal root T was positive, but PC2 for ‘LA 1777’ rootstocks, at both root T treatments, was negative. Moreover, the suboptimal T-stressed root samples were clearly separable from their respective control root samples in both genotypes, indicating that large and coherent transcriptional changes were induced by this root T shift of 10 ^{o}C.

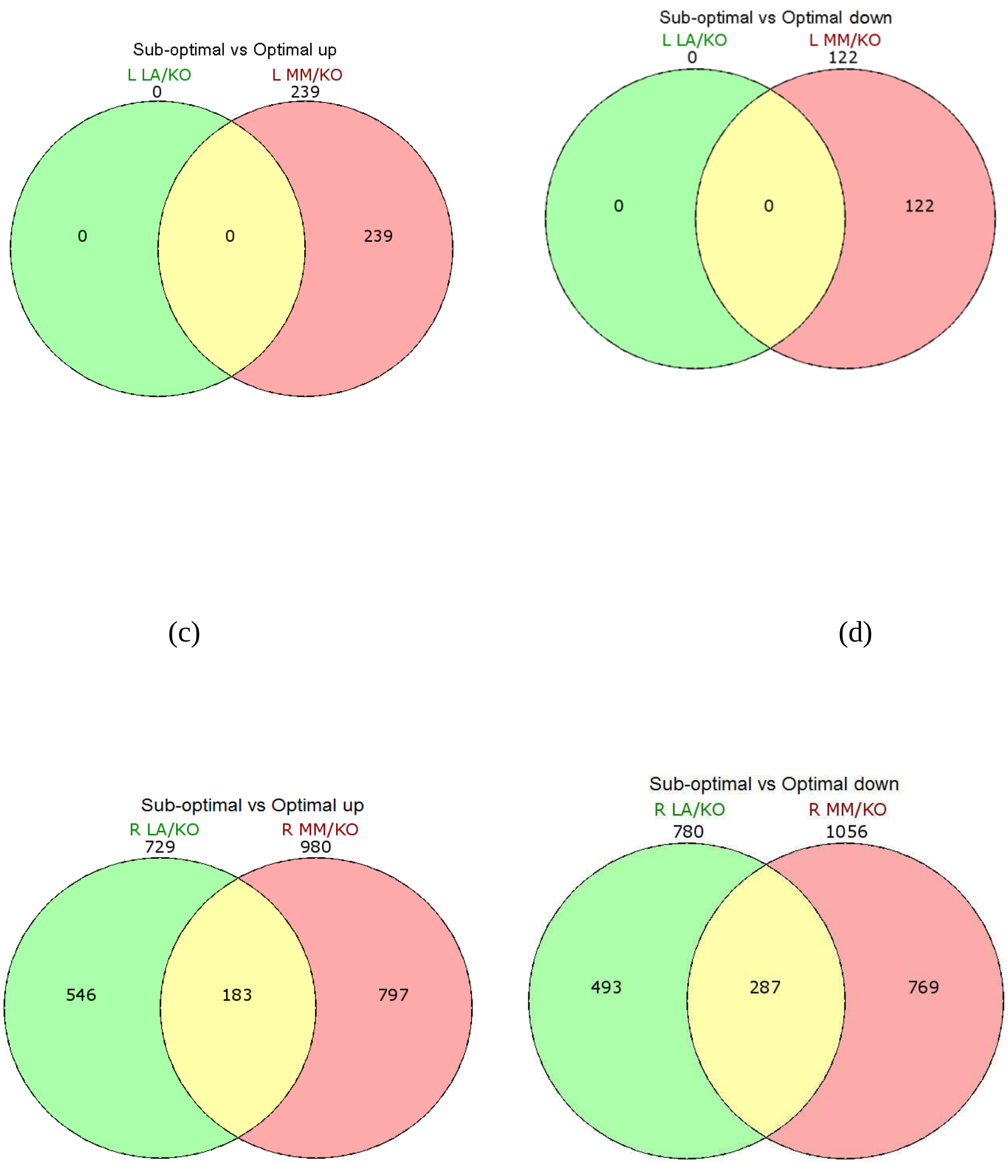
Fig. 10. Principal component analysis (PCA) of transcript profiles of the leaves (L) and the roots (R) of 'Kommeet' (KO) grafted onto 'LA 1777' (LA) (R/S:LA/KO) or 'Moneymaker' (MO) (R/S:MM/KO) and subjected to optimal or sub-optimal root temperatures (T) (sub-optimal/optimal T).



To investigate the differences in gene expression between a tolerant ('LA 1777') and a sensitive ('Moneymaker') tomato genotype in response to sub-optimal root T stress, we performed comparative transcriptome analysis using Agilent microarray. The Venn diagram in Fig. 11a and 11b shows the grouping between genes that were up- or down-regulated in the leaves of 'Kommeet' in only one of the two grafting combinations namely 'Kommeet' onto 'LA 1777' and 'Kommeet' onto 'Moneymaker' or in both grafting combinations. The Venn diagram in Fig. 11c and 11d shows the grouping between genes that were up- or down-regulated in the roots of 'LA 1777' or 'Moneymaker' or in both rootstocks. In order to make the list for each plant part (leaves or roots) and genotype ('Kommeet', 'LA 1777' or 'Moneymaker'), all of the probe sets on the microarray which showed a ≥ twofold change (either up-regulated or down-regulated relative to control) in signal intensity after filtering with a student's t-test at $p \leq 0.05$ were included.

Fig. 11. Venn diagrams showing number and overlap of the differentially expressed genes under sub-optimal T stress in the leaves (L) and roots (R) of ‘Kommeet’ (KO) plants onto ‘LA 1777’ (LA) or ‘Moneymaker’ (MM). (a) Number of up-regulated genes in the leaves (log2 ratio stress/control≥1 and q-value<0.05). (b) Number of down-regulated genes in the leaves (log2 ratio stress/control≤−1 and q-value<0.05). (c) Number of up-regulated genes in the roots (log2 ratio stress/control≥1 and q-value<0.05). (d) Number of down-regulated genes in the roots (log2 ratio stress/control≤−1 and q-value<0.05). The numbers in parenthesis indicate the total number of genes up- or down-regulated by sub-optimal stress in the roots of each genotype.

(a) (b)

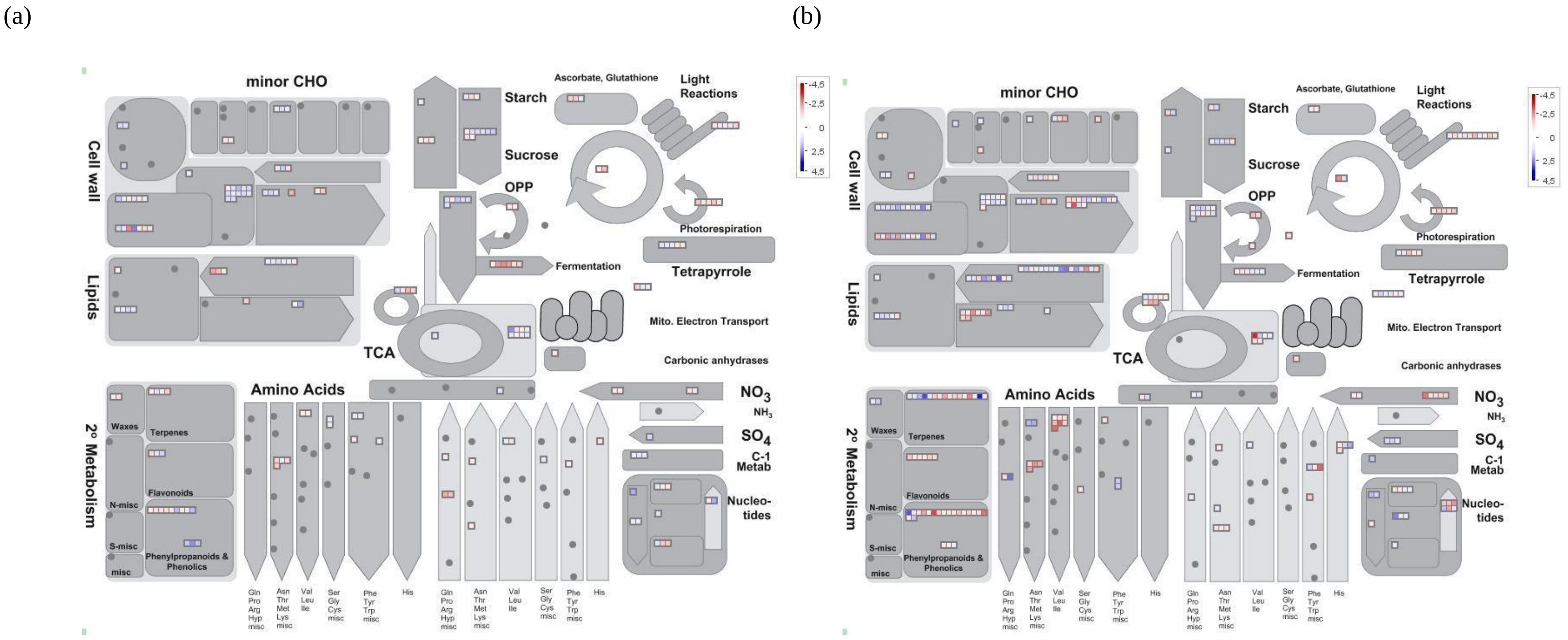


(c) (d)

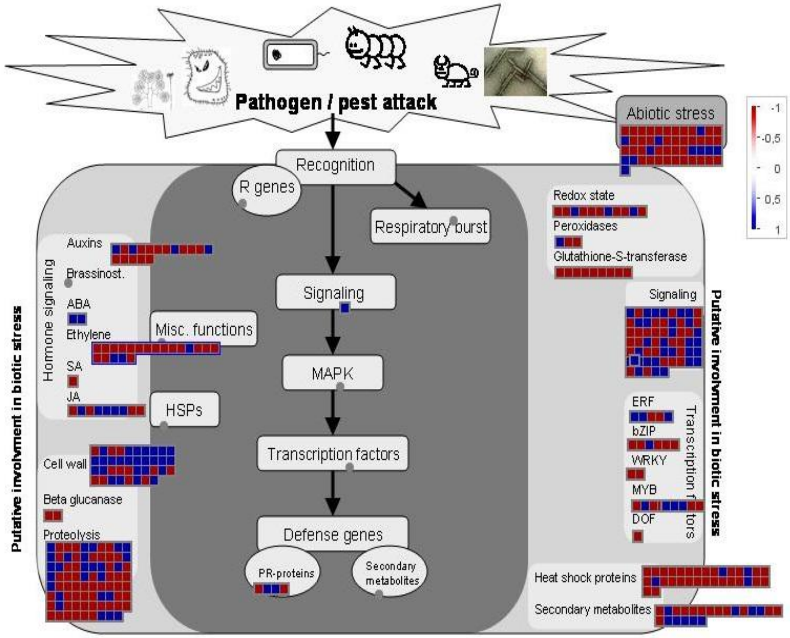
After 30 days of sub-optimal temperature stress, a total of 361 (239 up- and 122 down-regulated) genes were differentially expressed in the leaves of ‘Kommeet’ that was grafted onto ‘Moneymaker’ while in the leaves of ‘Kommeet’ grafted onto ‘LA 1777’ no gene changes were identified (Fig. 11a, 11b). On the other hand in the roots of ‘Moneymaker’ a total of 2036 (980 up- and 1056 down-regulated) genes (q-value<0.5, log2 ratio (sub-optimal T stress/control) above 1 and below -1) and 1509 (729 up- and 780 down-regulated) sub-optimal-responsive genes (q-value<0.5, log2 ratio (sub-optimal T stress/control) above 1 and below -1) were identified in the roots of ‘LA 1777’ (Fig. 11c, 11d). Among them, 1039 cold-responsive genes (546 up- and 493 down-regulated) were exclusively identified in the roots of ‘LA 1777’, whereas 1566 cold-responsive genes (797 up- and 769 down-regulated) were uniquely observed in ‘Moneymaker’. A total of 470 genes (183 up- and 287 down-regulated) were commonly regulated by sub-optimal T stress in the two tomato genotypes (Fig. 11c and 11d).

The general up- or down regulation of gene expression of the roots of both rootstock genotypes (‘LA 1777’ and ‘Moneymaker’) can also been seen in the MapMan images of the functional categories metabolism (Fig. 12a, 12b), stress (Fig. 12c, 12d), large enzyme (Fig. 13a and 13b), cellular response (Fig. 14a and 14b) and regulation (Fig. 15a and 15b).

Fig. 12. Mapman visualisation of the expression of genes from the functional categories metabolism (12a, 12b) and stress (12c, 12d) of sub-optimal-temperature-induced changes to root global transcript levels for the two tested tomato rootstock genotypes, ‘LA 1777’ (12a, 12c) and ‘Moneymaker’ (12b, 12d), respectively. Log2 expression values for individual genes are plotted onto boxes grouped according to their putative functional annotation. Boxes are colored red or blue depending on whether their abundance increased (blue) or decreased (red). Color intensity reflects the extent of change in abundance, with more intense color meaning a larger change in abundance.


(a) (b)

(c)


Pathogen / pest attack
Abiotic stress
-1
-0,5
0
0,5
1
Recognition
R genes
Respiratory burst
Signaling
MAPK
Transcription factors
Defense genes
PR-proteins
Secondary metabolites
Hormone signaling
Auxins
Brassinost.
ABA
Ethylene
SA
JA
Misc. functions
HSPs
Cell wall
Beta glucanase
Proteolysis
Redox state
Peroxidases
Glutathione-S-transferase
Signaling
ERF
bZIP
WRKY
MYB
DOF
Transcription factors
Heat shock proteins
Secondary metabolites
Putative involvment in biotic stress
Putative involvment in biotic stress

(d)

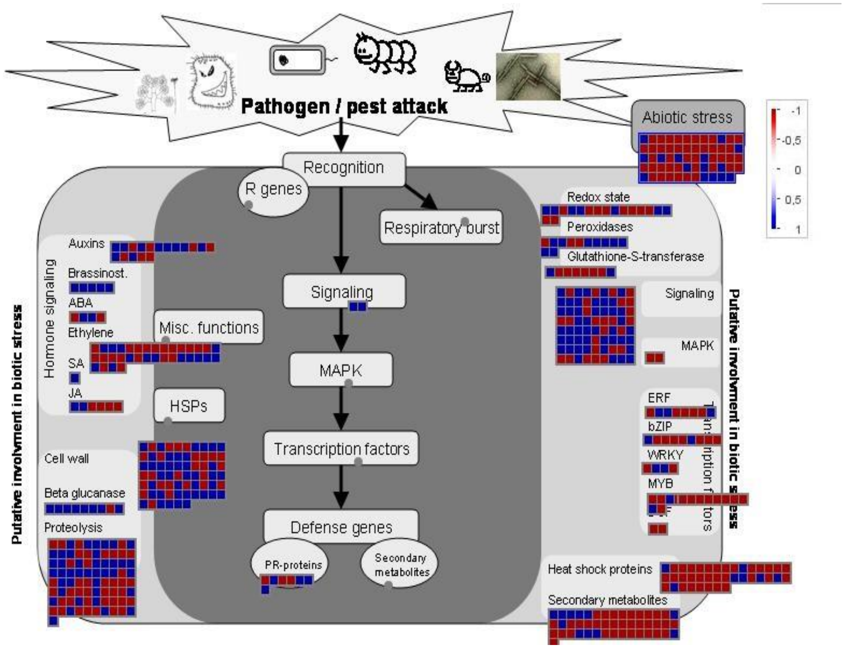
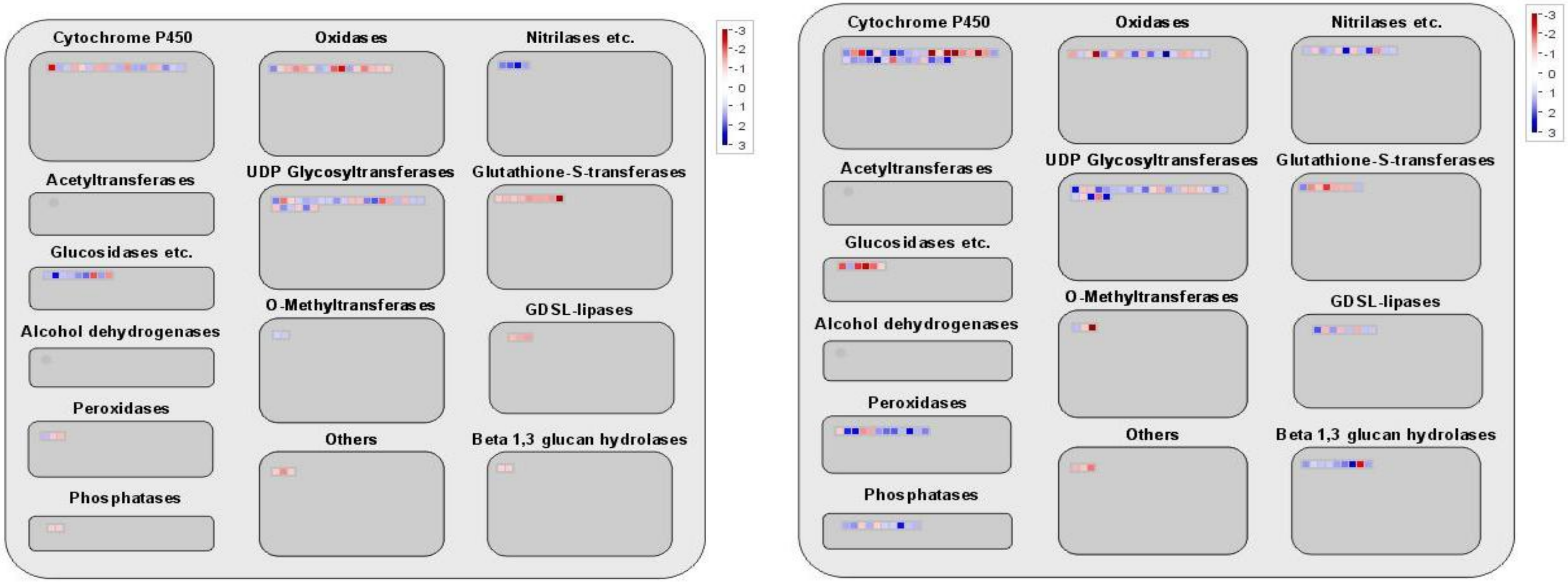
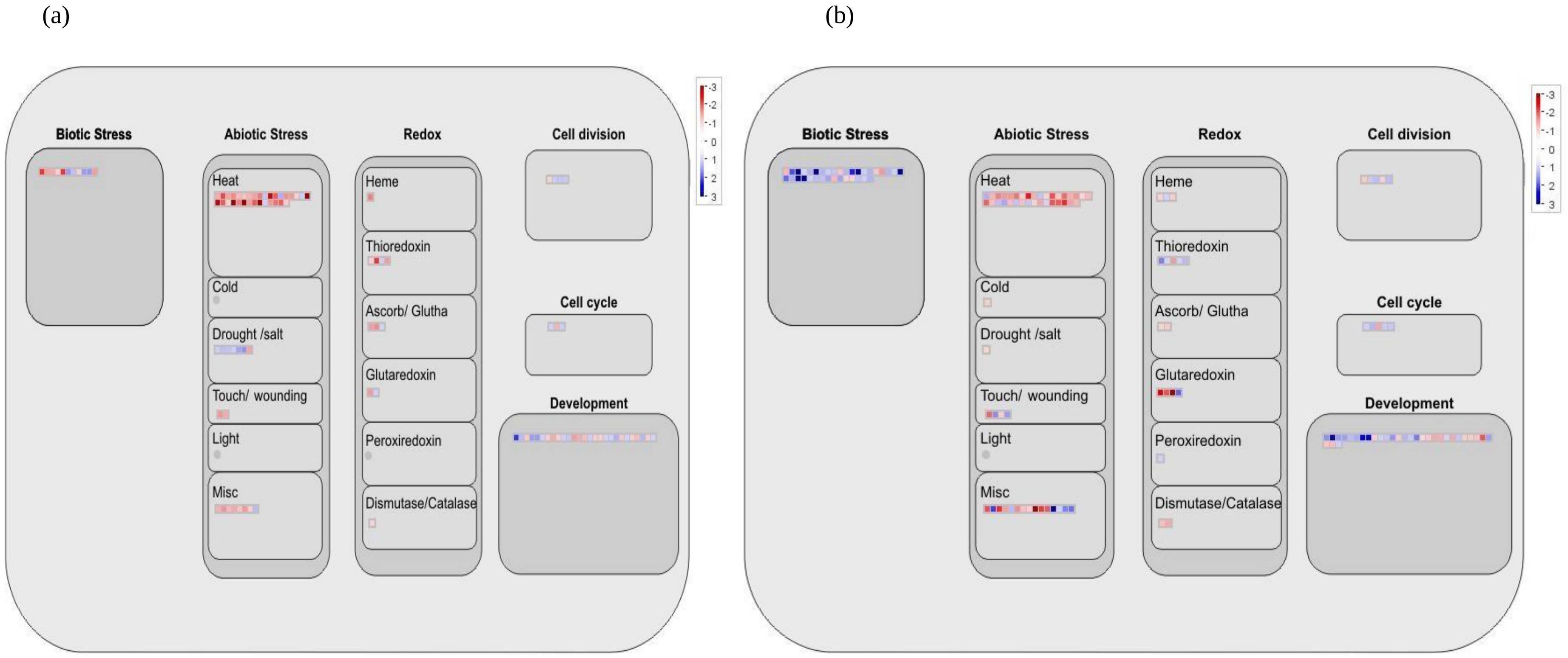

Pathogen / pest attack
Abiotic stress
-1
-0,5
0
0,5
1
Recognition
R genes
Respiratory burst
Signaling
MAPK
Transcription factors
Defense genes
PR-proteins
Secondary metabolites
Hormone signaling
Auxins
Brassinost.
ABA
Ethylene
SA
JA
Misc. functions
HSPs
Cell wall
Beta glucanase
Proteolysis
Redox state
Peroxidases
Glutathione-S-transferase
Signaling
MAPK
ERF
bZIP
WRKY
MYB
Transcription factors
Heat shock proteins
Secondary metabolites
Putative involvment in biotic stress
Putative involvment in biotic stress

Fig. 13. Mapman visualisation of the expression of genes from the functional category **large enzyme families** of sub-optimal-temperature-induced changes to root global transcript levels for the two tested tomato rootstock genotypes, ‘LA 1777’ (a) and ‘Moneymaker’ (b), respectively. Log2 expression values for individual genes are plotted onto boxes grouped according to their putative functional annotation. Boxes are colored red or blue depending on whether their abundance increased (blue) or decreased (red). Color intensity reflects the extent of change in abundance, with more intense color meaning a larger change in abundance



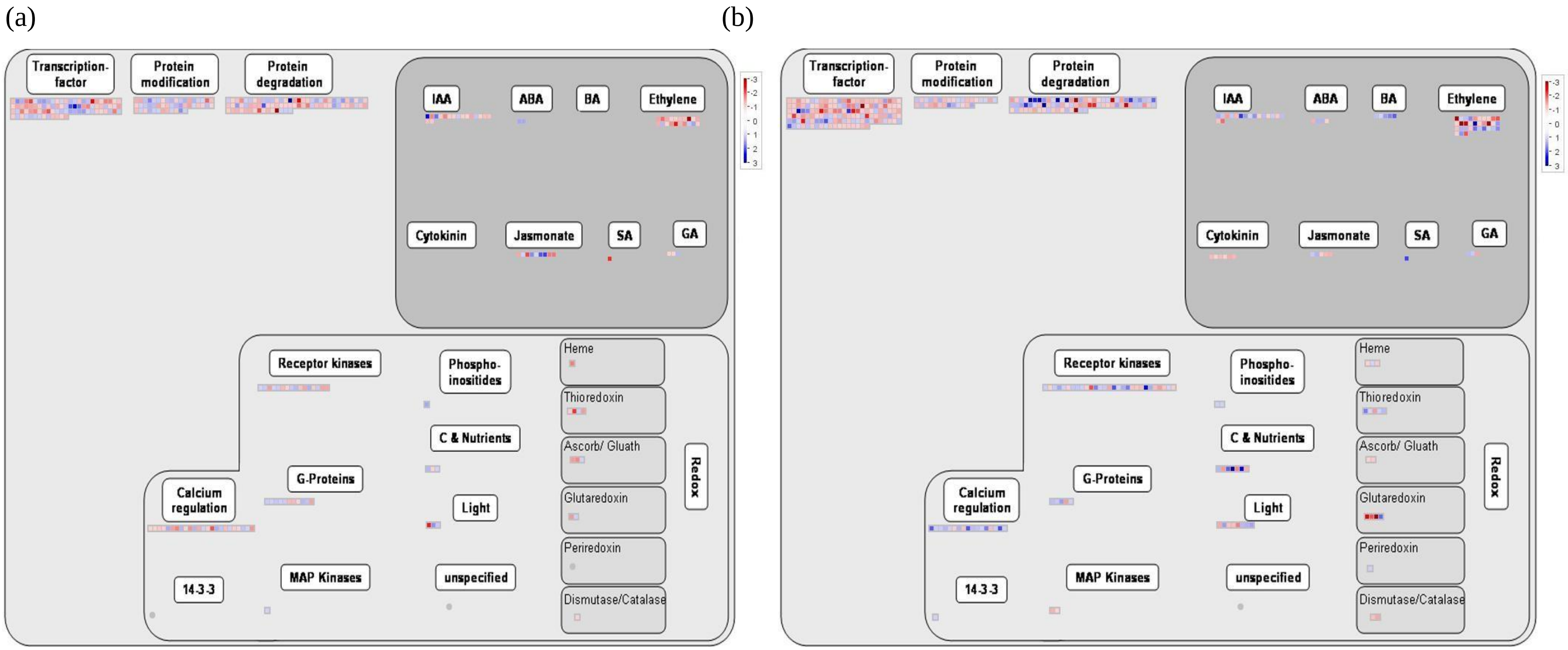
(a) (b)

Fig. 14. Mapman visualisation of the expression of genes from the functional category **cellular response** of sub-optimal-temperature-induced changes to root global transcript levels for the two tested tomato rootstock genotypes, 'LA 1777' (a) and 'Moneymaker' (b), respectively. Log2 expression values for individual genes are plotted onto boxes grouped according to their putative functional annotation. Boxes are colored red or blue depending on whether their abundance increased (blue) or decreased (red). Color intensity reflects the extent of change in abundance, with more intense color meaning a larger change in abundance


(a)

(b)

Fig. 15. Mapman visualisation of the expression of genes from the functional category **regulation** of sub-optimal-temperature-induced changes to root global transcript levels for the two tested tomato rootstock genotypes, ‘LA 1777’ (a) and ‘Moneymaker’ (b), respectively. Log2 expression values for individual genes are plotted onto boxes grouped according to their putative functional annotation. Boxes are colored red or blue depending on whether their abundance increased (blue) or decreased (red). Color intensity reflects the extent of change in abundance, with more intense color meaning a larger change in abundance


(a)

(b)

3.4.3. Identification of sub-optimal-responsive up- or down-stream genes of the leaves of ‘Kommeet’ grafted onto ‘LA 1777’ or ‘Moneymaker’ and of the roots of the two rootstock genotypes

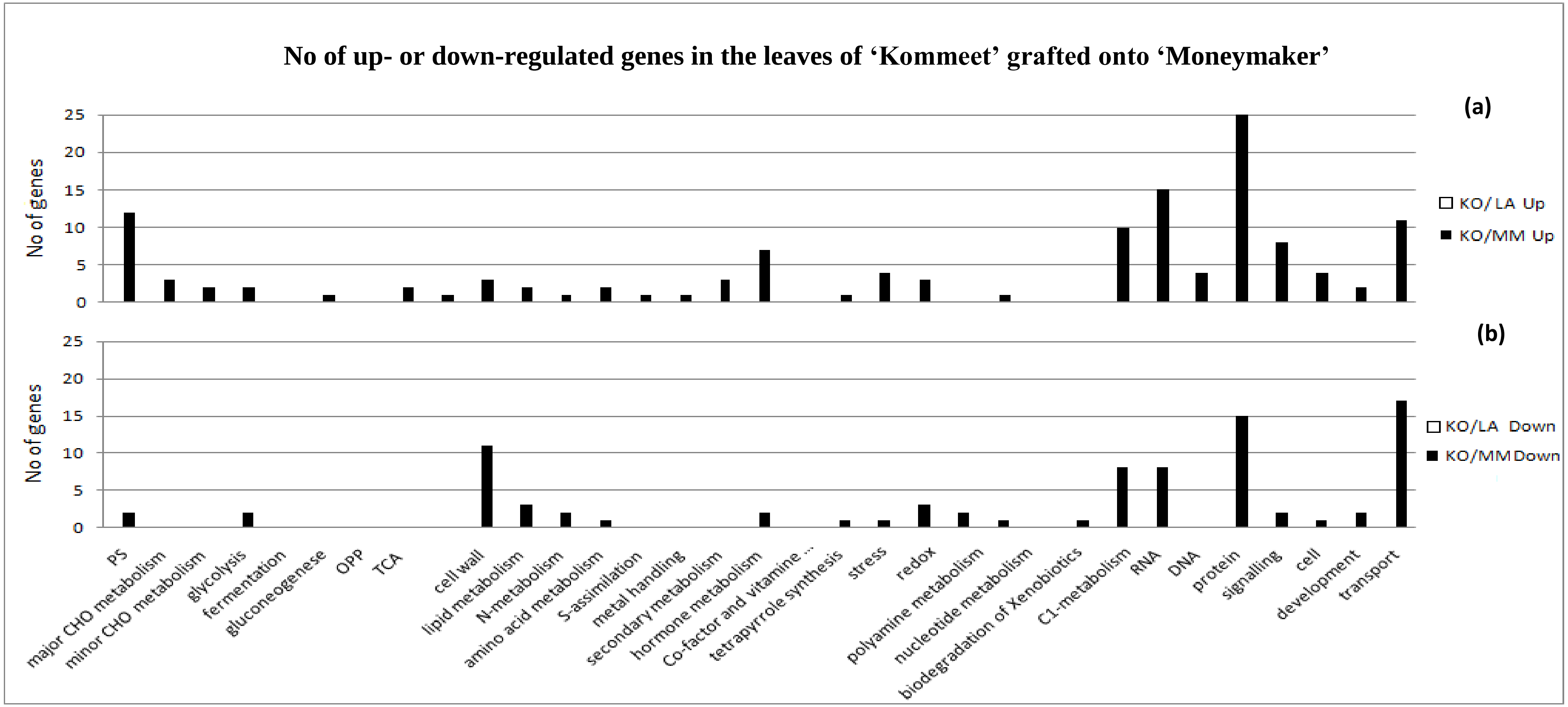
Differentially regulated genes belonged to almost all functional categories of the MapMan annotation. Of the 239 up-regulated genes in ‘Kommeet’ plants grafted onto ‘Moneymaker’, 131 were unknown, while the other gene products included protein synthesis, degradation and post-translational modification (25 genes), RNA regulation of transcription (15 genes), PS light reaction of photosystem I (PSI polypeptide subunits) and the Calvin cyle (rubisco small subunit) (12 genes), transport (11 genes), miscellaneous (10 genes), signaling (8 genes) and hormone metabolism (7 genes) (Fig. 16a, Annex Table 1). All the other categories were present with a number of 2-4genes out of 108 that were up-regulated, namely CHO metabolism, TCA, cell wall, lipid metabolism, amino acid metabolism, stress, secondary metabolism, cell organisation and development. Only one gene of the categories fermentation, gluconeogenesis, mitochondrial electron transport, N-metabolism, S-assimilation, metal handling, tetrapyrrole synthesis, and nucleotide metabolism was up regulated and none in the categories Co-factor and vitamin metabolism, polyamine metabolism and C1-metabolism. Of the 122 down-regulated genes in the leaves of ‘Kommeet’ grafted onto ‘Moneymaker’, 85 were unknown and the other gene products included transport (17 genes), protein synthesis, degradation and postranslational modification (15 genes), cell wall (11 genes), miscellaneous, RNA regulation of transcription (8genes each) (Fig. 16b, Annex Excel Table 2). 2-3 genes of the categories PS, glycolysis, lipid metabolism, N-metabolism, auxin metabolism, redox glutaredoxins, signaling and development were down regulated. On the other hand no genes were down-regulated in the categories CHO metabolism, gluconeogenesis, mitochondrial electron transport, TCA, secondary metabolism, and DNA synthesis.

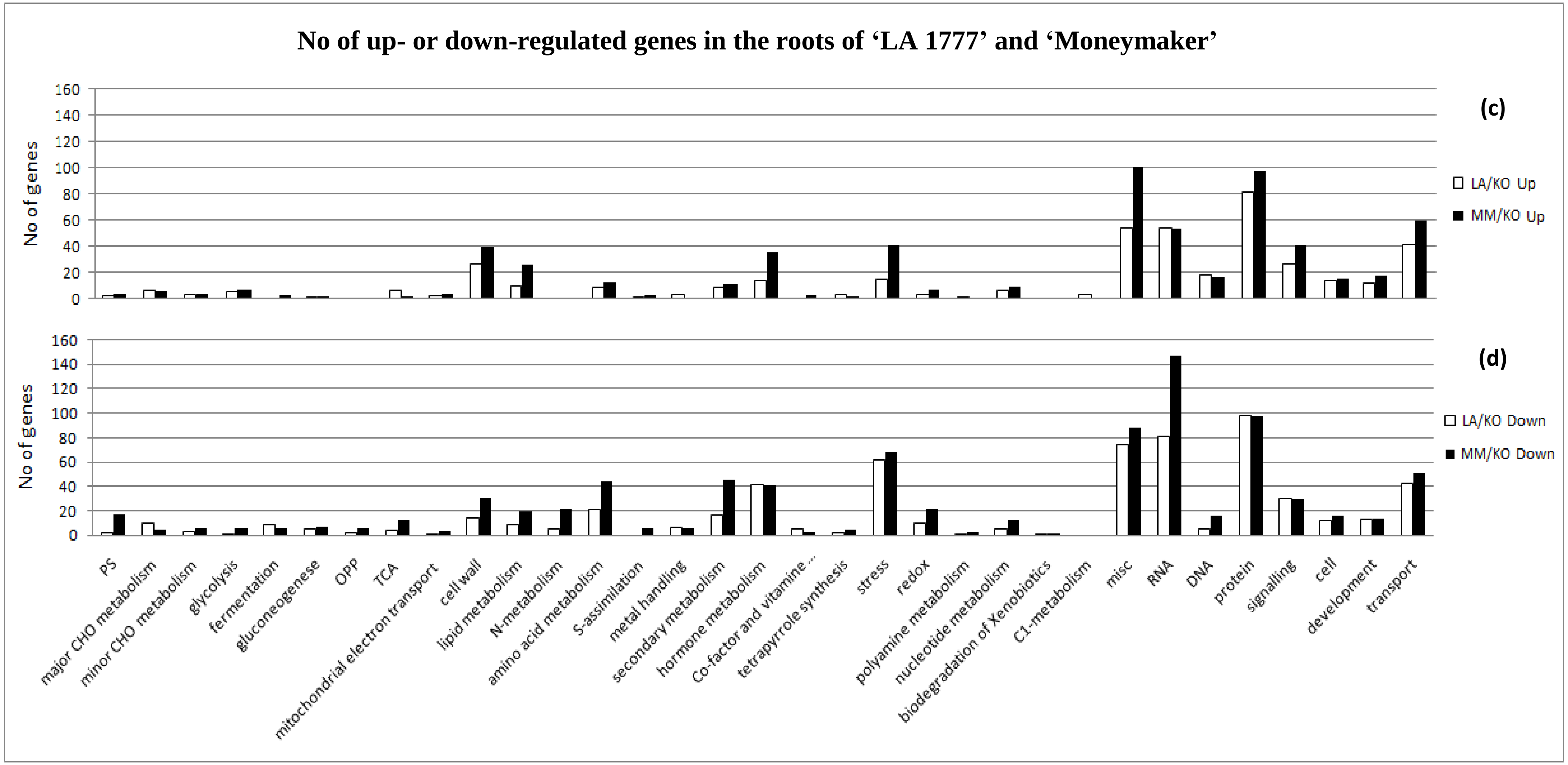
In the roots of ‘LA 1777’ 729 up-regulated genes were identified of which 299 were unknown. The largest proportion belonged to the category protein synthesis, degradation and post-translational modification (81 out of 430 genes with known function), followed by ' miscellaneous, RNA regulation of transcription (54 genes) and transport (Fig. 16c, Annex Table 3 and 4). Signaling (27 genes), cell wall (26 genes), stress (15 genes) and hormone metabolism (14 genes) and amino acid and secondary metabolism (9genes) were also present.

All other categories include 2-6 up-regulated genes while no genes were detected in OPP and N-metabolism. As far as the down-regulated genes are concerned the unknown down-regulated genes in the roots of 'LA 1777'subjected to sub-optimal root T were 184 out of 780. The most abundant categories were protein synthesis, degradation and post-translational modification (98 genes each out of 596 genes with known function), followed by RNA regulation of transcription (81 genes), miscellaneous (74 genes), stress (62 genes), transport (43 genes), hormone metabolism (42 genes) and signaling (27 genes). Categories of secondary metabolism, cell wall, development, cell organization, major CHO metabolism, redox and, lipid metabolism formed a second group representing around 10-17 genes each. In all the other categories only 1-5 genes out of 596 were down-regulated (Fig. 16d, Annex Table 3 and 5).

Of the 980 up-regulated genes in the roots of 'Moneymaker' rootstocks, subjected to sub-optimal root T conditions, 353 were unknown. The most abundant categories were miscellaneous (101 out of 627 genes with known function), protein synthesis, degradation and post-translational modification (98 genes each), followed by transport (60 genes), RNA regulation of transcription (53 genes), signaling and stress (41 genes each), cell wall (40 genes), and lipid metabolism (26 genes) (Fig. 16c, Annex Table 3 and 6). All the other categories, namely hormone metabolism, DNA synthesis, amino acid and secondary metabolism, development and cell organization were also present including around 10-18 up-regulated genes each while no genes were detected in OPP and N-metabolism. All the remaining categories were weakly represented. The down-regulated genes identified in the roots of the same genotype, namely 'Moneymaker', were 1056 of which 211 were unknown. The other gene products included RNA regulation of transcription (148 out of 845 genes with known function), protein synthesis, degradation and post-translational modification (98 genes each), followed by miscellaneous (88 genes), stress (68 genes), transport (51 genes), secondary metabolism (45 genes), amino acid metabolism (44 genes) hormone metabolism (41 genes), cell wall (31 genes), signaling (29 genes) and N-metabolism and stress (21 genes each). All the other categories were weakly represented and only lipid metabolism, cell organization, development and TCA included around 12-16 down-regulated genes each (Fig. 16d, Annex Table 3 and 7).

Fig. 16. Functional classification of the number of genes up- (log2 ratio stress/control≥1 and q-value<0.05) or down-regulated (log2 ratio stress/control≤−1 and q-value<0.05) in the leaves of ‘Kommeet’ grafted onto ‘Moneymaker’ (R/S: KO/MM) (a, b) and in the roots of ‘LA 1777’ and ‘Moneymaker’ (c, d) that were annotated to each MapMan functional category. No diagram is presented for the leaves of ‘Kommeet’ plants grafted onto ‘LA 1777’ (R/S: LA/KO) because no genes were annotated to the MapMan functional categories. Only pathways corresponding to genes with known function, which could be assigned to a MapMan category, were used for these figures.




No of up- or down-regulated genes in the roots of ‘LA 1777’ and ‘Moneymaker’

3.4.4. Enrichment of functional categories of the MapMan annotation in the significantly differentially sub-optimal-responsive up- or down-stream genes of the roots of the two tested rootstock genotypes ‘LA 1777’ or ‘Moneymaker’

Globally the expression changes of genes from a number of functional categories appeared to be different in the roots of the two tested tomato rootstock genotypes. In specific Pageman visualization of MapMan functional categories enriched in the genes differentially expressed in the roots of ‘LA 1777’ and ‘Moneymaker’ subjected to sub-optimal root temperature conditions were PS, Major CHO metabolism, cell wall, lipid metabolism, N-metabolism, amino acid metabolism, secondary metabolism, hormone metabolism, biotic stress, RNA, and regulation of transcription, DNA synthesis, protein synthesis and degradation, calcium signaling development, transport and some miscellaneous categories (Fig. 17).Only the heat stress genes appeared to be common to the two tested genotypes.

The overrepresentation analysis of MapMan function classes among the up- or down-regulated genes of the roots of ‘LA 1777’ or ‘Moneymaker’ under sub-optimal root temperature conditions is presented in the Table 25. The enrichment of functional categories of the MapMan annotation in the significantly differentially expressed genes were tested for significance by applying Fisher tests with a Bonferroni correction for multiple tests using Mefisto Version 0.23beta. As a result the coordinated regulation of genes from various functional categories was identified. The following MapMan functional categories were significantly enriched in the up-regulated genes of a) ‘LA 1777’: cell wall genes associated with cellulose synthesis through cellulose synthase, hormone metabolism and jasmonate synthesis-degradation, allene and not-assigned, and b) ‘Moneymaker’: lipid metabolism genes associated with fatty acids desaturation, genes associated with biotic stress, miscellaneous genes from the functional category cytochrome P450 as well as protein degradation of AAA proteins and not assigned genes (Table 25). The down-regulated genes in the MapMan functional categories that were significantly enriched in both rootstock genotypes were amino acid metabolism genes associated with branched chain group synthesis and the aspartate family (particularly methionine), secondary metabolism of isoprenoids (particularly terpenoids) and phenylpropanoids, hormone metabolism genes associated with ethylene synthesis-degradation, heat stress and protein synthesis. In addition RNA regulation of transcription of the MYB domain transcription factor family was particularly enriched in the down-regulated genes of ‘LA 1777’ together with not-assigned genes, while genes associated with biotic stress, cytokinin metabolism and RNA regulation of transcription were enriched only in the down-regulated genes of ‘Moneymaker’ roots subjected to sub-optimal T (Table 25).

Fig. 17. Pageman visualization of MapMan functional categories enriched in genes differentially expressed in the roots of ‘LA 1777’ (LA) and ‘Moneymaker’ (MM) genotype subjected to sub-optimal root T. The degree of enrichment of functional categories in up- and down-regulated genes is given by shades of blue and red, respectively.

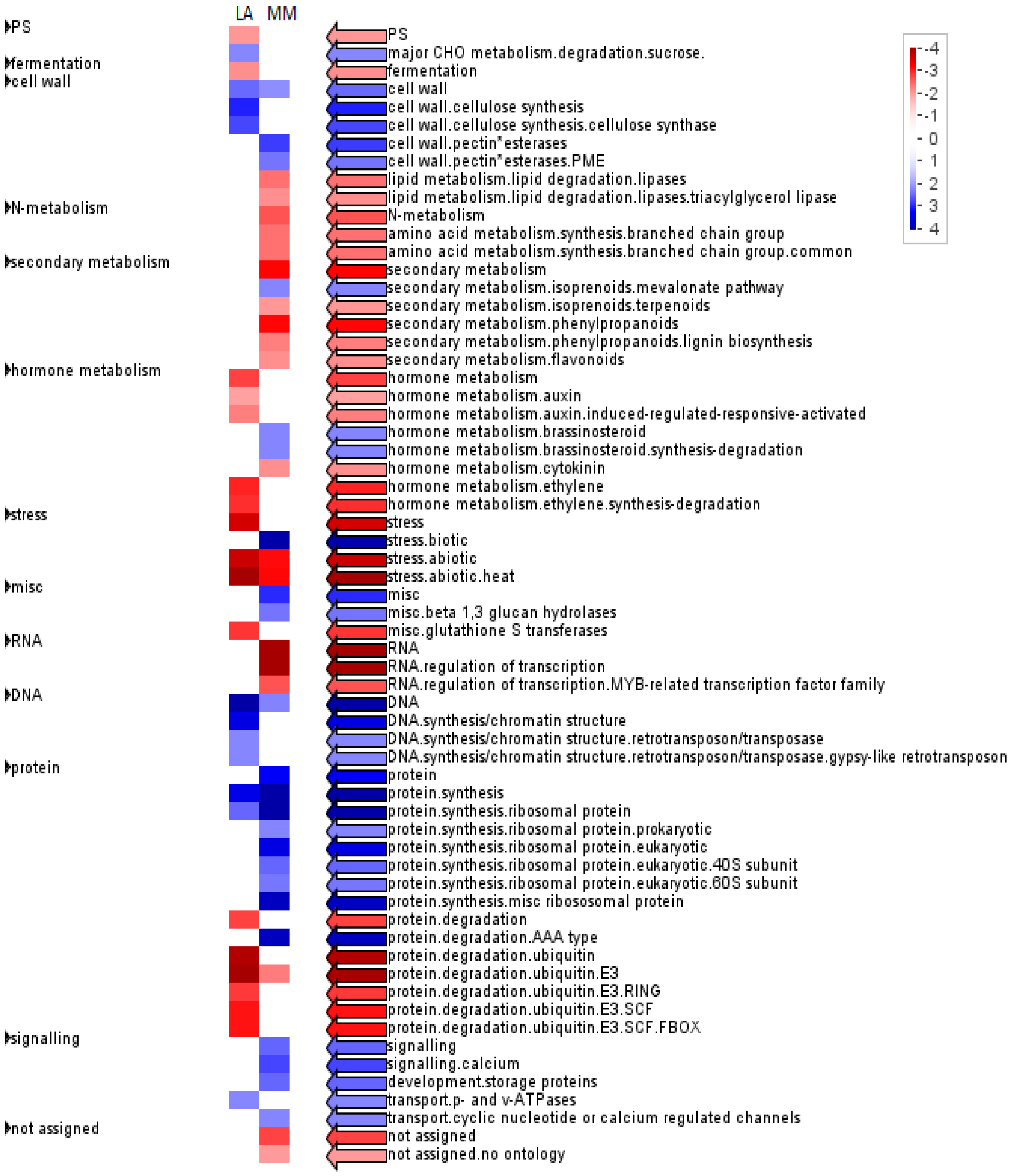


Table 25. Over-representation of MapMan function classes among the up- and down-regulated genes of the roots of 'LA 1777' (LA) and 'Moneymaker' (MM) under sub-optimal root temperature. Enrichments of functional categories of the MapMan annotation in the significantly differentially expressed genes were tested for significance by applying Fisher tests with a Bonferroni correction for multiple tests using Mefisto Version 0.23beta (http://www.usadellab.org). NS indicates the not significantly enriched MapMan function categories ($p<0.05$, FDR as the cut off) among the up-regulated or down-regulated genes in the two rootstock genotypes.

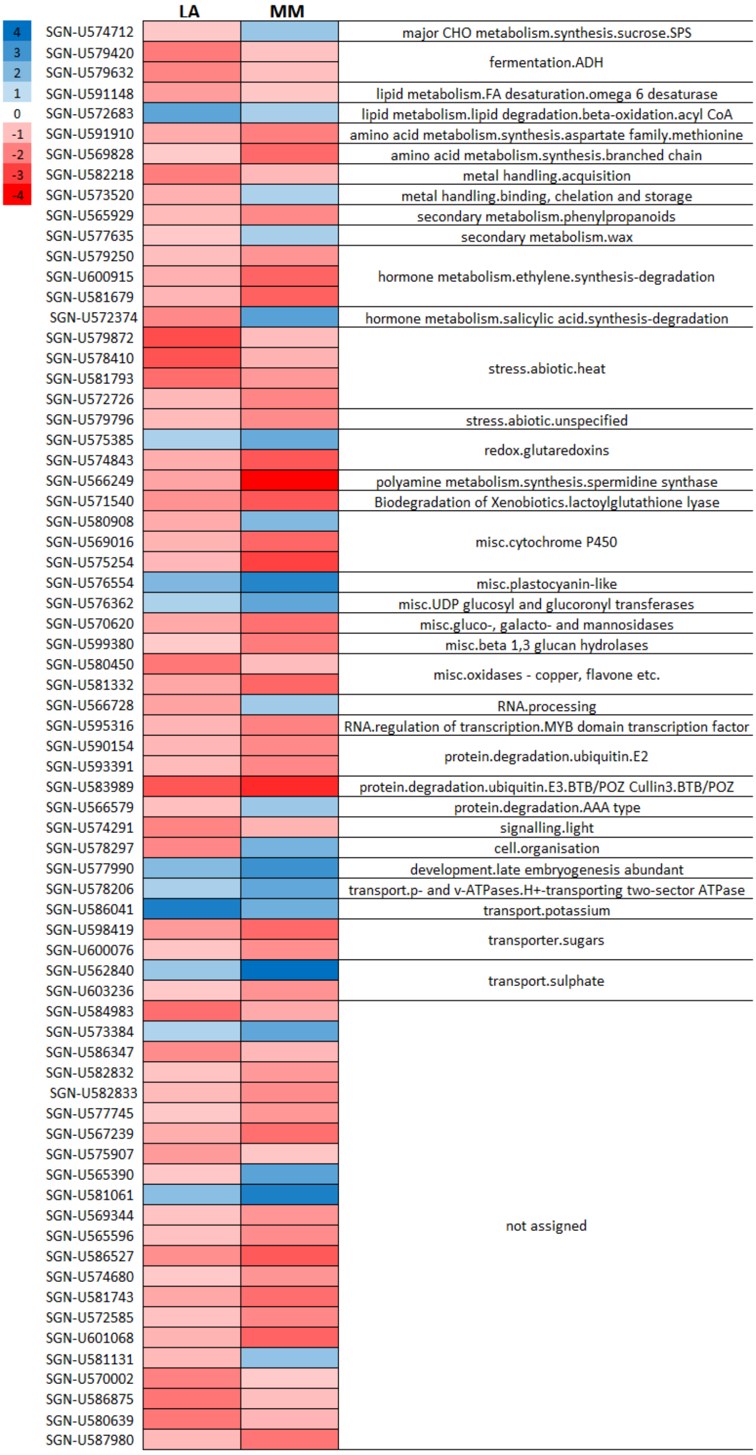
Bin Code	**Bin Name**	**Up**		**Down**	
		LA	**MM**	**LA**	**MM**
10.2	cell wall.cellulose synthesis.cellulose synthase	0.009	NS	NS	NS
11.2	lipid metabolism.FA desaturation	NS	0.003	NS	NS
13.1.4.1	amino acid metabolism.synthesis.branched chain group.common	NS	NS	0.002	0.009
13.1.3.4	amino acid metabolism.synthesis.aspartate family.methionine	NS	NS	0.003	0.011
16.1.5	secondary metabolism.isoprenoids.terpenoids	NS	NS	<0.001	0.004
16.2	secondary metabolism.phenylpropanoids	NS	NS	0.001	<0.001
17.4	hormone metabolism.cytokinin	NS	NS	NS	<0.001
17.5.1	hormone metabolism.ethylene.synthesis-degradation	NS	NS	<0.001	0.002
17.7.1.3	hormone metabolism.jasmonate.synthesis-degradation.allene	0.010	NS	NS	NS
20.1	Stress biotic	NS	<0.001	NS	<0.001
20.2.1	Stress-abiotic heat	NS	NS	<0.001	<0.001
26.1	misc.cytochrome P450	NS	0.011	NS	NS
27.3	RNA.regulation of transcription	NS	NS	NS	<0.001

27.3.26	RNA.regulation of transcription. MYB-related transcription factor family	NS	NS	<0.001	NS
29.2	protein.synthesis	NS	NS	<0.001	0.04
29.5.9	protein.degradation.AAA type	NS	0.001	NS	NS
35	not assigned	0.01	<0.001	0.005	NS

3.4.5. Differentially expressed genes altered between tolerant and sensitive rootstock genotypes under sub-optimal root temperature

Of the 480 genes expressed in the roots of the two tested rootstock genotypes, namely 'LA 1777' and 'Moneymaker', when subjected to sub-optimal root T conditions only ten genes were differentially expressed between the roots of the tolerant and the sensitive rootstock genotypes (Fig. 18, Annex Table 3). These genes were associated with a variety of functional groups, including major CHO metabolism-synthesis, specifically sucrose phosphate synthase (*SGN-U574712*), a heavy metal transport/detoxification protein (*SGN-U573520*), the *CER1* fatty acid hydroxylase gene (*SGN-U577635*), a salicylic acid carboxyl methyltransferase (*SGN-U572374*), the *CYP72A15* Cytochrome P450 gene (*SGN-U580908*), small nuclear ribonucleoprotein D1 (*SGN-U566728*), the *AAA*-ATPase *1* gene (*SGN-U566579*) of the protein degradation functional category, an F-box protein (*SGN-U578297*) from the cell organization functional category and two (*SGN-U565390*; *SGN-U581131*) that were not assigned to one of the MapMan functional categories. From 470 genes that were commonly expressed (up- or down-regulated) under sub-optimal root T conditions in the roots of both rootstock genotypes, only 60 appear to have a very large difference in their $\log_2$ fold change (LA/MM ≥ 1 or ≤ -1).Of them 20 were unknown (Fig. 18; Annex Table 3) while the other 40 were from a variety of functional groups. Specifically, 2 genes were associated with the MapMan functional category fermentation, namely alcohol dehydrogenase 1 (*SGN-U579632*) and alcohol dehydrogenase 2 (*SGN-U579420*), which were more strongly down-regulated in 'LA 1777' in comparison to 'Moneymaker', 2 genes associated with lipid metabolism, an Omega-6 fatty acid desaturase (*SGN-U591148*) more strongly down-regulated in 'LA 1777' than in 'Moneymaker', and an acyl-CoA reductase gene (*SGN-U572683*) more strongly up-regulated in the tolerant genotype in comparison to the sensitive one. Two genes were identified to be strongly down-regulated in 'Moneymaker' in comparison to 'LA 1777', namely the S-adenosylmethionine synthetase gene *SAM1* (*SGN-U591910*) and the branched-chain amino acid aminotransferase gene *SlBCAT1* (*SGN-U569828*), both involved in amino acid metabolism. One gene associated with metal handling acquisition (*ATFRO4/FRO4* (Ferric reduction oxidase 4); *SGN-U582218*) is strongly down-regulated in the roots of the tolerant rootstock genotype when subjected to sub-optimal root T in comparison with the sensitive one. The reverse is the case for a transferase family protein, anthranilate N-hydroxycinnamoyl/benzoyltransferase (*SGN-U565929*). Genes involved in hormone metabolism, specifically ethylene synthesis-degradation, related to an ethylene-forming enzyme (*SGN-U579250*), a flavonol synthase/flavanone 3-hydroxylase gene (*SGN-U600915*) and the 1-aminocyclopropane-1-carboxylate oxidase 1 gene (*SGN-U581679*), all of which were more strongly down-regulated in the sensitive rootstock genotype than in the tolerant one. Another MapMan functional category in which genes of both cultivars were down-regulated was that of heat stress. The four genes that participated in this category were an ethylene-responsive heat shock protein cognate 70, a heat shock protein 90, a small heat shock protein-like (HSP15.7-CI) and (*SGN-U579872; SGN-U578410*; *SGN-U578410*), which all have the same pattern: strongly down-regulated in the tolerant to sub-optimal root T tomato rootstock genotype when compared to the sensitive one, while the reverse is the case for a heat shock protein, Hsp40 (*SGN-U572726*) and an MLP-like protein 28 (*SGN-U575385*) (Annex Table 3). Nine more genes were identified as strongly down-regulated in 'Moneymaker' in comparison to 'LA 1777', namely two glutaredoxins (*SGN-U575385*; *SGN-U574843*), putrescine N-methyltransferase (*SGN-U566249)* involved in polyamine metabolism, glyoxalase (*SGN-U571540*) and *CYP72A14* (*SGN-U569016*), *CYP71A22* (*SGN-U575254*), cell wall hydrolase LEU13054 (*SGN-U570620*), glycosyl hydrolase family protein 17 (*SGN-U599380*) and a NADP-dependent oxidoreductase (*SGN-U581332*) from the miscellaneous functional group of MapMan. On the other hand, two genes that were placed in the same MapMan functional group appeared to be strongly up-regulated in the roots of 'Moneymaker' in comparison with that of 'LA 1777' and two strongly down-regulated in the roots of 'LA 1777'. These genes were a plastocyanin-like domain-containing protein (*SGN-U576554*), *DOGT1*, a UDP glucosyl and glucoronyl transferase (*SGN-U576362*) and an alcohol dehydrogenase zinc-containing (*SGN-U580450*), and a phototropic-responsive NPH3 family protein (*SGN-U574291*). Only one gene from the functional category of RNA regulation of transcription was strongly down-regulated in 'Moneymaker' in comparison with 'LA 1777', namely *MYB111* (*SGN-U595316*) from the MYB domain transcription factor family, and three ubiquitin genes (*SGN-U590154*; *SGN-U593391*; *SGN-U583989*). A *LEA* gene (*SGN-U577990*) was strongly up-regulated in 'Moneymaker' in comparison with 'LA 1777', as well as two genes that belong to the transport functional group (*SGN-U578206*; *SGN-U562840*). The reverse was the case for *HAK5* gene (*SGN-U586041*) involved in potassium transport (Annex Table 3). Last, but not least, 3 genes from the transport functional category appeared to be strongly down-regulated in the sensitive genotype in comparison with the tolerant one: two sugar-associated genes (*SGN-U598419*; *SGN-U600076*) and one sulfate transporter (*SGN-U603236*).

Fig. 18. Heat map of genes significantly differentially expressed (q-value<0.05) between ‘LA 1777’ (LA) and ‘Moneymaker’ (MM) genotypes under sub-optimal root T. Sub-optimal-responsive genes with statistically significant differences (p) in expression between tolerant and sensitive genotypes were clustered using Microsoft Excel 2007. The color intensity represents the gene expression value (log2 ratio sub- /optimal T), as indicated by the color scale.



CHAPTER 4. DISCUSSION

4.1. Contribution of phytohormones in alleviating the impact of sub-optimal temperature stress on grafted tomato

The exposure of tomato to sub-optimal T resulted in profound decreases in the rates of shoot elongation and leaf area expansion in all genetic combinations involving genotypes deficient in biosynthesis/metabolism of or less sensitive to different phytohormones and their wild-type counterparts. Previous studies reported by Venema et al., 1999, 2008 indicated that the reduction in leaf expansion at sub-optimal T is not due to a limited supply of assimilates, since the leaves accumulate large amounts of starch. In the present study, the rates of net assimilation were reduced only in two of the six genetic combinations ('Moneymaker' combined with 'sitiens' and 'Ailsa Craig' combined with 'Nr'), whereas the differences were rather small and not commensurate with the suppressions in shoot growth rates. Hence, the present study is in agreement with the view that other factors than the production and availability of assimilates restrict the shoot growth of tomato under sub-optimal T conditions (Schwarz et al., 2010). However, the gas exchange data presented in this paper indicate that a restriction in carbon assimilation may be an additional though not the major factor limiting the shoot growth of tomato under sub-optimal T conditions, depending on the genotype. As reported by Schwarz et al. (2010), the limitations in shoot growth during the vegetative phase of tomato seem to originate mainly from root hormonal signals associated with water and nutrient uptake in combination with a decreased elasticity of the epidermal cell walls.

Previous research revealed that the low levels of ABA in 'notabilis' in comparison with the parental wild-type tomato are due to an inactive allele of the gene *LeNCED1,* which is involved in ABA biosynthesis (Burbidge et al., 1999). The results shown in Table 1 demonstrate that the genotype of 'notabilis' is much less efficient than that of 'sitiens' in restricting the ABA levels in leaves, in agreement with previous findings (Herde et al., 1999). The modest restriction of ABA production in 'notabilis', despite the presence of an inactive allele of the gene *LeNCED1,* indicates that the role of *LeNCED1* in ABA-biosynthesis can be partially circumvented over alternative paths. This hypothesis needs to be tested in further experiments. The relatively high levels of ABA in leaves of plants with 'notabilis' as scion may explain why the shoot growth parameters did not respond to the genetic combination and the T regime in the corresponding trial. Obviously the ABA levels were still sufficient to support growth under sub-optimal T.

In contrast to 'notabilis', the ABA-deficient mutant 'sitiens' is characterized by appreciably lower tolerance to sub-optimal T stress than its wild-type counterpart 'Moneymaker'. The lower tolerance of 'sitiens' is manifested in the markedly stronger reductions of RSL and RLA in tomato plants with this ABA-deficient mutant as either rootstock or scion or both than in self-grafted 'Moneymaker' plants under sub-optimal T but not under optimal T conditions. The observation that the impairment of growth under sub-optimal T by use of the ABA-deficient scion was associated with lower leaf ABA levels reinforces the notion that ABA contributes to tolerance of tomato to sub-optimal T. However, the contribution of root-produced ABA to shoot growth of tomato under sub-optimal T was not completely reflected by the leaf ABA level. This indicates that root-produced ABA may stimulate protective processes in the root already, which contribute to shoot growth (Sharp and Le Noble, 2002). In addition, root-sourced ABA may enhance ABA levels preferentially in distinct compartments of the leaf (Pastor et al., 1999; Zhang and Outlaw, 2001), which may disappear or appear extenuated in the bulk leaf extract. The lower leaf ABA level, when 'sitiens' was singly used as rootstock compared to the self-grafted wild type which contrasted to the same low ABA levels for both combinations (−/−; +/−), indicate that the transport of root-sourced ABA to the shoot depends on shoot ABA.

Nevertheless, the enhanced susceptibility of tomato to sub-optimal T stress that is associated with reduced endogenous ABA levels seems to be restricted to shoot growth, since the root length was not influenced by the use of the ABA-deficient mutant as either rootstock or scion or both. Some researchers found that ABA may function as a promoter of growth under abiotic stress conditions such as soil compaction (Mulholland et al., 1996, 1999) and drought (Sharp and Le Noble, 2002). However, other researchers found that ABA may negatively affect shoot growth during abiotic stresses (Creelman et al., 1990; Saab et al., 1990; Zhang and Davies, 1990). The results presented in Table 2 indicate that the production of ABA both in shoot and root mitigates the adverse effects of sub-optimal T on shoot growth in tomato but has no impact on root growth. The data of stomatal gas exchange reveals a strong control of stomatal conductance and of CO_2 gas exchange of tomato by ABA particularly in the leaves which is consistent with the current concept of stomatal control (Acharya and Assmann, 2009). Even though the measurement of stomatal gas exchange of both T treatments was conducted under high T, the similar responses to ABA-deficiency for both treatments, cultivated either at optimal or at sub-optimal *T*, do not support a protective role of ABA under T stress conditions via the altered stomata closure and photosynthesis.

Sharp et al. (2000) and Sharp and Le Noble, (2002) ascribed the protective role of ABA under water stress conditions to restriction of ethylene production, which seems to be a widespread function of ABA in plants. Various authors suggest that ABA suppresses ethylene production, specifically its precursor 1-aminocyclopropane-1-carboxylic acid because ABA-deficient mutants exhibit enhanced ethylene levels (Rodriguez et al., 2010; Sharp et al., 2000; Spollen et al., 2000). However, these authors could not find a direct link between these two phytohormones. In *Arabidopsis* it was found that signaling in sugar metabolism closely interacts with signaling pathways of ABA (Arenas-Huertero et al., 2000; Laby et al., 2000; Huijser et al., 2000; Rook et al., 2001; Cheng et al., 2002) and ethylene (Zhou et al., 1998).

If ABA exerts a protective role to tomato under sub-optimal T conditions by controlling the levels of endogenous ethylene, a blockage of ethylene signal perception might enhance plant tolerance to sub-optimal T stress. Indeed, as shown in Table 4, the plants with the 'Never-ripe' (Nr) tomato mutant of 'Ailsa Craig' either as scion or as rootstock exhibited significantly higher rates of leaf area expansion (higher RLA) than the self-grafted wild-type 'Ailsa Craig' plants. A negative relationship between leaf expansion and ethylene evolution rates from leaves of tomato exposed to compacted-soil stress has been reported also by Hussain et al. (2000). However, the present results indicate further that, when both the rootstock and the scion are ethylene-insensitive, the tolerance of tomato to sub-optimal T is not improved. By contrast, some sensitivity to ethylene (+ETsens) in the roots or especially in the shoots seems to be necessary to improve RLA under low T. A similar response is observed also under optimal conditions, where ethylene sensitivity in the shoot seems to be associated with a higher RLA. These results stay in accordance with an ambivalent influence of ethylene on tomato under chilling stress observed by Ciardi et al. (1997). They concluded from their experiments comparing chilling responses of Nr tomato with those of wild-type plants in combination with hardening that ethylene may limit growth caused by an initial chill but at the same time increases the tolerance of plants to subsequent chilling periods. Furthermore, the present results indicate that the role of ABA and ethylene in tomato susceptibility to sub-optimal T is not related to photosynthesis or transpiration, despite the significant differences in leaf chlorophyll between the standard and the 'Nr' genotype of 'Ailsa Craig' (Table 4).

The results on shoot growth (Table 5) reveal that under optimal conditions, the sensitivity of the scion to IAA is related with RLA, but not with RSL, which is in disagreement with the expected role of IAA in cell enlargement and stem growth (Davies, 2004). This positive correlation between IAA sensitivity and leaf relative growth rate was also found by Albacete et al. (2008), who on the other hand found no correlation of leaf IAA with shoot relative growth rate. However, at sub-optimal T, the shoot length seems to be much more severely affected by IAA insensitivity than at optimal T conditions. The role of IAA in promoting cell elongation by imposing wall loosening is well known (Rayle and Cleland, 1992). As reported by Veselova et al. (2005), cooling of the root at 6 °C through the supply of cold water enhances markedly the concentration of IAA in the shoots. Hence, it is likely that the grafted plants with IAA-insensitive scion were more severely affected by sub-optimal T because they were incapable of responding to the presumably high levels of IAA in the shoot. Nevertheless, the rate of leaf growth in tomato decreases by IAA-sensitivity in the shoot but this effect was restricted to the optimal T whereas RLA was generally low with sub-optimal T. The negative effect of auxin sensitivity in the shoot on leaf expansion seems to arise mainly from impairment of net assimilation at chloroplast level rather than stomata closure. Indeed, in contrast to *A* and *gs*, the intercellular level of CO_2 was not affected by IAA-sensitivity in the shoot, a response which, according to Farquhar and Sharkey (1982), indicates a direct impairment of the carbon fixation apparatus. However, auxin may control leaf growth independent of net assimilation. Thus, analysis of spatial distribution and biosynthesis of IAA in *Arabidopsis* during vegetative growth revealed that normal leaf expansion depends on rigorous control of IAA homeostasis (Ljung et al., 2001).

With respect to root growth, the results of the present research indicate that IAA-insensitivity in the roots in combination with standard IAA sensitivity in the shoot enhances the total length of the roots. Moreover, under sub-optimal *T*, the root length increased significantly in the −IAAsens/+IAAsens combination, but without any concomitant effect on the specific root surface. This result is in agreement with the suggestion of Taiz and Zeiger (2002) that roots may require a minimum concentration of auxin to grow, but root growth is strongly inhibited by auxin levels that promote stem elongation. Nevertheless, IAA-insensitivity either in the root or in the shoot of tomato results in thinner roots as indicated by the relevant values of root specific area.

The results on RSL and RLA shown in Table 7 indicate that low CK levels in the root but especially in the shoot restrict the rates of shoot and leaf area expansion under optimal T conditions, which is in agreement with current knowledge (Hare et al., 1997; Taiz and Zeiger, 2002). However, under sub-optimal T conditions, enhanced cytokinin catabolism either in the shoot or in the root did not restrict leaf area growth. Previous research has indicated that exposure of plants to low T results in a sharp decline in CK concentration in shoots due to increased activity of CK-oxidase (Veselova et al., 2005). Reduced cytokinin transport from cooled tomato roots to the shoot has been reported also by Ali et al. (1996). Thus, restriction in transport and stimulation of oxidation of CK under sub-optimal T conditions may have already decreased CK to such a low level in wild-type tomato genotypes that additional oxidation of CK in the −CK scion or −CK rootstock was not effective on leaf growth. In contrast to the leaf area, the shoot length seems to be favored by CK deficiency in the root but especially in the shoot as can be concluded from the relevant data shown in Table 7. Interestingly the elongation growth of hypocotyls of Arabidopsis could be both inhibited but also stimulated by CK, while the direction of response was obviously dependent on auxin transport and the ethylene response pathway (Smets et al., 2005). The increase in the total root length that was observed when wild-type tomato scions were grafted onto the CK-deficient mutant is similar to that caused by the –IAAsens/+IAAsens genetic combination. This is not surprising, since both CK and auxin have a crucial role in the control of root growth, specifically in the rates of cell differentiation and generation of new cells, respectively (Moubayidin et al., 2009). According to the same authors, the role of auxin in the root meristem of *Arabidopsis thaliana* is to sustain root apical meristem activity by promoting cell division while on the other hand CK promotes cell differentiation by repressing both auxin signaling and transport. Nevertheless, the increased root length in plants with CK-deficient root genotype observed in the present study is in agreement with previous findings indicating that application of this plant hormone causes a decrease in root meristem size because of a progressive decrease in meristematic cell number (Dello Ioio et al., 2007). The increases in stomatal conductance and transpiration rates in plants obtained by self- and reciprocal grafting of ‘Micro-Tom’ and ‘dgt-CKX2’ under sub-optimal T conditions, which were independent of CK deficiency in roots and shoot, seem to be related to the specific tomato genotype.

Recent studies indicated that SA may confer tolerance to environmental stress as well, an effect which seems to be associated with a signaling role of this plant hormone (Senaratna et al., 2000). Nevertheless, the results obtained from the present study indicate that SA produced in the roots may mitigate the adverse effects of sub-optimal T stress on shoot length but not on leaf area expansion. On the other hand, SA deficiency in the shoot of tomato decreases similarly the rates of leaf area expansion under optimal and sub-optimal T conditions, as indicated by the relevant RLA measurements (Table 8). The beneficial effect of normal SA biosynthesis in the shoot on leaf area expansion was associated with a positive role of SA in leaf stomatal conductance and concomitantly in net CO_2 assimilation. Raskin (1992) suggested that SA induces rapid stomata closure in several plant species under stress conditions. However, the present study indicates that, in the absence of stress conditions, SA produced in the shoot is essential in maintaining normal stomatal conductance and this function is not reversed under sub-optimal T conditions. The detrimental effects of SA-deficiency in the shoot on leaf growth and gas exchange were not alleviated when SA biosynthesis in the root was normal (−SA/+SA). The absence of any effect of

SA arising from the root on shoot growth is in disagreement with results reported by Janda et al. (1999), which indicated that exogenous supply of SA to the root of maize via hydroponic nutrient solution provided protection against subsequent low-T stress. A likely explanation is that the rate of SA translocation from the root to the shoot is higher when it is exogenously applied to the root system in comparison with that for SA originating from endogenous biosynthesis. Furthermore, the present research revealed a positive impact of normal SA biosynthesis in the shoot on leaf chlorophyll content when tomato is exposed to sub-optimal T stress. This finding is consistent with a previous report of Szepesi et al. (2009) who found that SA promotes pigment biosynthesis under salt stress conditions.

4.2. A study on ABA involvement in the response of tomato to sub-optimal root temperature using reciprocal grafts with ‘notabilis’, a null mutant in the ABA-biosynthesis gene *LeNCED1*

The profound decrease in leaf area, root and total dry mass of tomato plants exposed to sub-optimal root T is in agreement with previous results reported by Venema et al. (2008). The restriction in leaf area was ascribed by Venema et al. (1999, 2008) to lower leaf turgor or inhibition of cell division and not to limited supply of assimilates. In agreement with that consideration, in the present study the rates of net assimilation did not decrease, while the levels of sucrose and total amino acids increased significantly in leaves of plants exposed to sub-optimal root T. An accumulation of amino acids in response to sub-optimal T, originating mainly from up-regulation of the nitrate reductase activity (Tucker and Ort, 2002), has been reported also by Mitchell and Madore (1992). As reported by Cook et al. (2004), Ma et al. (2009), and Zhang et al. (2007), plants subjected to sub-optimal T stress utilize sugars and amino acids as protective compounds. Nevertheless, in the present study, the mechanisms resulting in an accumulation of sugars and amino acids in leaves were presumably associated with a reduced sink activity owing to exposure of the root to sub-optimal T. Indeed, since a reduced sink activity in cold-stressed roots was not accompanied by down-regulation of net photosynthesis, compounds as sugars, starch and amino acids were forced to accumulate.

The restricted leaf area and total plant biomass in self-grafted ‘notabilis’ plants in comparison with all other rootstock/scion combinations indicates that the lack of the *LeNCED1* gene activity in both root and shoot of tomato impairs plant growth. Similar results were obtained by Thompson et al. (2004) in a study in which ‘notabilis’ was compared with ‘Ailsa Craig’. A new finding originating from the current study is that the presence of the wild-type allele of the *LeNCED1* gene in only the root or shoot can compensate for the null mutation of this gene in the other plant part. On the other hand, shoot elongation of tomato seems to respond quantitatively to the presence of the wild-type *LeNCED1* gene, since its mutation only in root or shoot restricted shoot length, but to a lesser extent than complete absence.

The *NCED1* gene encodes a 9-cis-epoxycarotenoid dioxygenase which is involved in ABA biosynthesis and, therefore, 'notabilis' is known to be deficient in ABA biosynthesis induced by water deficit (Thompson et al., 2004). However, it has been repeatedly shown that the lack of ABA biosynthesis in this line is dependent on environmental conditions. Thus, under non-stress conditions differences in leaf ABA levels between 'notabilis' and wild-type plants were rather small, whereas ABA accumulation in response to water deficit, wounding, heat and electric current was strongly attenuated in 'notabilis' (Herde et al., 1999; Parry et al., 1988; Thompson et al., 2004). In the present study, the mutation of the *LeNCED1* gene did not restrict the levels of endogenous ABA in the shoot of tomato under both optimal and sub-optimal root T conditions. Hence, the restriction of plant growth in self-grafted 'notabilis' plants cannot be ascribed to a lasting ABA deficiency. However, since ABA biosynthesis is subject to plant development (Baron et al., 2012) and duration of the cold stress period (Chen et al., 1983; Daie and Campbell, 1981), we cannot exclude that the ABA levels were transiently affected other factors in our study. The response of ABA to low T depends on plant genotype, the level of T and the duration of the stress period (Chen et al., 1983; Daie and Campbell, 1981; Zhou et al., 2007). In a recent experiment reported by Ntatsi et al. (2013), the same rootstock/scion combinations as the ones used in the present study were cultivated for two subsequent periods of 14 days differing in the air temperatures (19.8 and 15.1 °C, respectively).

Leaf ABA levels were similar at the end of both periods and not affected by the genotype of the rootstock but were significantly lower, when 'notabilis' was used as scion. In the present study, the sub-optimal T (15 °C) was restricted to the root zone and this raised leaf ABA compared to a root T of 25 °C, while ABA levels were independent of the rootstock/scion combination. The different ABA responses in the two studies may reflect an influence of either the different air temperatures (19.8 and 15.1 °C versus 15 and 25 °C), or the different time periods of growth and temperature exposure (14 days versus 30 days), or the plant part exposed to sub-optimal temperature (whole plant versus roots). Interestingly it has been shown recently that under non-stress conditions 'notabilis' plants contain similar ABA levels in roots as wild-type plants (Rodriguez et al., 2010). Considering these relationships, we assume that the higher leaf ABA levels in response to low root T reflect enhanced ABA biosynthesis in roots. Because the decrease in general greenhouse temperature to 15 °C did not enhance leaf ABA (Ntatsi et al., 2013), the higher leaf ABA in response to a root T of 15 °C seems to be the consequence of an imbalance between root and air temperature. Since low T also affects water balance of plants, the increase of ABA may partially result from a secondary water deficit as already discussed by Daie and Campbell (1981). Water deficit stress should be stronger when only root T is low compared to whole-plant exposure to low T, because the higher shoot T in the former case enhances water use for transpiration and expansion growth versus a decreased uptake of water.

The *NCED* genes form a gene family with nine members in Arabidopsis (Schwartz et al., 2003, Walter and Strack 2011) and also more than one gene in other species (Nambara and Marion-Poll, 2005; Tan et al., 1997) and five in tomato (www.ncbi.nlm.nih.gov). Thus, if one gene of the family is inactivated, another family member may take over its function (Tan et al., 1997). Such redundancy ensures the functionality of important biosynthetic pathways. However, for tomato only *LeNCED1*, *2* and *6* are known to be involved in the ABA pathway (Zhang et al., 2009) while the other two *NCED* genes, namely *NCED4* (XM_004245956.1), and *NCED7* (NM_001247504.1) encode carotenoid cleavage dioxygenases and therefore regulate carotenoid biosynthesis (Vogel, et al., 2010) which is not related to ABA metabolism.

In the present study, no lasting effect was observed of either root zone T or grafting combination on expression of two other genes of the same family (*LeNCED2* and *LeNCED6*). Moreover, the low expression values of these genes do not support a substantial role of them in substitution of the *LeNCED1* function. It is, however, possible that another gene of the *NCED* gene family performs this function, such as *NCED3*, a key gene in ABA biosynthesis that responds to cold (Cuevas et al., 2008). The transcription of the *NCED3* gene is enhanced by Put (Cuevas et al., 2009). When the root of tomato was exposed to sub-optimal T, the root Put content increased significantly, irrespective of the grafting combination. This may be associated with a higher activity of the *NCED3* gene and concomitantly with higher ABA levels in T-stressed plants. But gene expression of *NCED3* in the different grafts could not be confidently confirmed due to very low expression signals. ABA is known to impose stomatal closure through the activation of non-selective ion channels (Schroeder, 1992). Hence, the significant reduction of stomatal conductance and transpiration rate in plants with roots exposed to sub-optimal T was presumably a result of the increased leaf ABA content.

The restriction of plant growth in plants with a null mutant *LeNCED1* gene in both root and shoot cannot be ascribed to impairment of gas exchange, since stomatal conductance (g_s), net assimilation rate (A) and transpiration rate (E) were significantly higher. Despite the decreased plant biomass, the higher net photosynthetic rates in 'notabilis' scions are indeed ascribed to a decrease in the specific leaf area (thicker leaves) since the restriction in leaf area was much stronger than the reduction in shoot biomass. Moreover, the higher sucrose levels in leaves of plants with 'notabilis' as scion further confirm that the restriction in plant growth imposed by the absence of the *LeNCED1* gene in both root and shoot is not associated with impaired A. On the other hand, the significantly higher levels of A, g_s, and E in plants with 'notabilis' as scion in comparison with those having 'Ailsa Craig' as scion were not associated with the level of ABA in the leaves, since the latter was not influenced by the shoot genotype. Nevertheless, the higher levels of A, g_s, and E in plants with 'notabilis' as scion were due to a difference in ABA biosynthesis because *LeNCED1* only functions in that process. Presumably, the ABA fraction that was measured in the present study is not the perceived fraction, or the ABA levels are different at specific parts of the plant or times of day which were not sampled. Contradictory findings on 'notabilis' leaf ABA (Jones et al., 1987; Thompson et al., 2004) may indicate that under normal growth conditions ABA levels in 'notabilis' are not different than in the wild-type parental genotype, but when mild stress is induced (including the normal diurnal drop in leaf water potential), then ABA in 'notabilis' fails to go up and stomata stay more open. It has been reported that H_2O_2 could also cause stomata closure by affecting pathways that are usually induced by ABA (Neill et al., 2002). H_2O_2 levels were lowest in plants with 'notabilis' as scion. Presumably, the reduced H_2O_2 levels restricted signaling to the guard cells to initiate stomata closure thereby leading to either prolonged stomatal opening or an increased number of open stomata and therefore an increased stomatal conductance.

The reduced plant growth of self-grafted 'notabilis' plants despite the increased net CO_2 assimilation rates indicates that other metabolic pathways are impaired when the *LeNCED1* gene is mutated. Previous research has indicated that the ethylene levels in 'notabilis' are significantly higher than in its wild-type counterpart 'Ailsa Craig' (Hussain et al., 2000; Rodriguez et al., 2010; Sharp et al., 2000). It has been suggested that ABA may restrict ethylene production, but direct evidence for such a link is missing. Thus, it is likely that the increased ethylene levels in 'notabilis' are mediated through other signals, such as sugars (Cheng et al., 2002; Rook et al., 2001).

The decreased shoot elongation when the *LeNCED1* gene is knocked out only in the root or in the shoot of tomato was accompanied by restricted levels of chlorophyll a and lutein in the leaves. A likely explanation is that what function the ABA would normally do have been lost, thereby lowering the production of chlorophylls and carotenoids (Niyogi et al., 1997). The lack of *LeNCED1* activity may trigger a signal that leads to lower production of chlorophylls and lutein and presumably other pigments involved in the two photosystems. This signal may be a substance that can be transported acropetally, probably ABA, because the leaves of ‘Ailsa Craig’ scions grafted onto ‘notabilis’ contained less chlorophyll a and lutein than those of self-grafted ‘Ailsa Craig’ plants. Further studies are needed to elucidate whether signaling molecules like ethylene precursors that are activated in the absence of the *LeNCED1* gene have an impact on chlorophyll and lutein biosynthesis and whether this is associated with lower shoot elongation in ‘notabilis’ plants.

The higher specific root area in *not*/*not* and +/*not*, which indicates thinner roots, in combination with higher stomatal conductance and transpiration in ‘notabilis’ scions, is anticipated to increase water uptake capacity (Lee et al., 2005). Thus, the absence of the *LeNCED1* in the shoot, which induces higher water losses by altering stomatal regulation, is compensated for in the root by an increased water uptake capacity owing to higher specific root area, higher R:S ratio and reduced leaf area to root weight ratio. Indeed, the ratio between root and shoot weight was higher in *not*/*not* (0.065) than in +/+ plants (0.041). Also the ratios between leaf area and total root weight were higher in *not* compared with + plants (in $m^2 \cdot g^{-1}$: *not*/*not* 1.42, *not*/+ 2.46, +/*not* 1.96, and +/+ 3.28). These findings indicate that ‘notabilis’ plants invested much more biomass into the root relatively to +/+ and deployed concomitantly a higher water uptake capacity. This characteristic is considered an adaptive mechanism that can compensate for the decrease in water movement through the roots when these are subjected to sub-optimal temperatures (Bloom et al., 2004; Schwarz et al., 2010).

Under stress conditions more ROS, such as H_2O_2, are produced in plant tissues (Cheeseman, 2007). In the present study, the non-photochemical quenching mechanism was not influenced either by root T, the ‘notabilis’ mutation or both together. Thus, the lower H_2O_2 levels in the leaves of self-grafted ‘notabilis’ plants lead to the conclusion that another reaction is responsible for scavenging H_2O_2. The lower levels of H_2O_2 in leaves of tomato plants with ‘notabilis’ as scion point to either a more effective protection against formation of H_2O_2 arising from the mutation, or an involvement of H_2O_2 in other scavenging reactions such as the glutathione antioxidant system (Taiz and Zeiger, 2007), or in formation of other ROS (Brosché et al., 2010). Since the lower H_2O_2 levels in leaves of self-grafted ‘notabilis’ plants were accompanied by a higher G-POD activity, it can be assumed that G-POD is at least one of the compounds that are responsible for scavenging H_2O_2 (Abassi et al., 1998). Presumably, G-POD takes over the role of CAT in H_2O_2 scavenging when the *LeNCED1* gene is knocked out, even though both enzymes do not operate in the same compartment. Moreover, SOD which is responsible for the conversion of superoxide anions into H_2O_2 and O_2 (Lederer, 2002) appeared to be closely related to the mutation of the *LeNCED1* gene. Thus it is likely, that the increased activity of SOD and G-POD in mutant tissues compensates for the possible impairment of other ROS scavenging systems that are normally activated by ABA produced from activity of *LeNCED1*. Presumably, SOD scavenges superoxide anions and then G-POD scavenges the resulting H_2O_2 (Cheng, 2011). Further research is needed to identify the possible ROS scavenging systems that are activated via *LeNCED1* activity. The 15 ^{o}C root T treatment was sufficient to induce stress responses in the leaves as illustrated by the reductions in chlorophyll a, lutein and SOD activity, and the increase of ABA contents and G-POD activity. However, these responses were unrelated to H_2O_2. This is attributed to the strong increase in lipid peroxidation in plants exposed to sub-optimal root T, as revealed by the profound increase in MDA content in the stressed plants. As a result, H_2O_2 interacts quicker with various enzymes, such as APX, CAT, GR, etc. (Cheng, 2011) and is therefore not detectable anymore. This is more profound in 'notabilis' self-grafted plants where both lipid peroxidation and electrolyte leakage are very high. An increase in MDA content is in accordance with the findings of Latef and Chaoxing (2011), who reported a MDA increase of 85 % in tomato plants exposed to 8 °C for one week, as compared with plants constantly grown at 25 °C. In the present study however, the exposure of plants to sub-optimal root T led to an increase of 240 % in MDA, presumably due to longer exposure to sub-optimal T. This leads to the conclusion that lipid peroxidation occurs at any T below the sub-optimal root T threshold applied in the present study and, if such a threshold is achieved, the duration of the sub-optimal root T affects lipid peroxidation more than the T itself.

Recent studies revealed the protective role of polyamines against sub-optimal T stress by acting as ROS scavengers (Alcazar et al., 2010; Oufir et al., 2008; Rhee et al., 2007; Zhao and Yang, 2008). Spd and Spm are capable of reducing the occurrence of singlet oxygen thereby restricting lipid peroxidation (Zhao and Yang, 2008), while Put, the biosynthetic precursor of Spd and Spm (Alcazar et al., 2010) reduces electrolyte leakage under cold stress (Kim et al., 2002). The elevated Put and Spd levels found in roots exposed to sub-optimal T are in agreement with findings in *Arabidopsis* and the ABA-deficient tomato mutant 'flacca'

(Kasukabe et al., 2004; Kim et al., 2002), where elevated Put and Spd levels were found in the leaves whereas roots were not tested. Furthermore, our results reveal that Put and Spd generated in roots exposed to sub-optimal T are not transported to the shoot. The marked increase of the Spd and Put levels in roots exposed to sub-optimal T is attributed to the decrease of Spm content. Indeed, as reported by Alcazar et al. (2010), the formation of Put, which has an important signaling function under cold stress, results from inter-conversion of Spd to Put via the acetylation mechanism, while Spd is also a derivative of Spm decomposition (Cuevas et al., 2008; Oufir et al., 2008).

4.3. Growth, yield, and metabolic responses of temperature-stressed tomato to grafting onto rootstocks differing in cold tolerance

In contrast to a previous report (Bloom et al., 2004) but in accordance with later results (Venema et al., 2008), ‘LA 1777’ (an accession of *S. habrochaites*), proved to be a compatible rootstock for cultivated tomato (S. *lycopersicum*). Moreover, in the present study the growing period after grafting lasted 21 weeks, including a nine week harvesting period, longer than the five week harvest period used in the study of Venema et al. (2008). Thus, the present study is the first report on the long-term compatibility of ‘LA 1777’ when used as a rootstock for cultivated tomato.

As indicated by the data shown in Fig. 1, vegetative shoot growth of ‘Kommeet’ was not affected by intermediate T (17 °C), while it was affected by long-term exposure to low T (14.6 °C), depending on the rootstock genotype. Mild reductions of vegetative growth of ‘Kommeet’ at low T, when used as scion in grafted tomato, are in contrast to those previously reported (Venema et al., 2008), after short-term exposure (two weeks) of ‘Moneymaker’, self-grafted or grafted onto ‘LA 1777’, to 15 °C in comparison with 25 °C. The first reason for this difference in response of tomato to low T is the genotype of the scion. It seems that ‘Kommeet’ as scion is much more tolerant to sub-optimal T than ‘Moneymaker’, which is considered to be cold-sensitive (Fernández-Muñoz et al., 1995; Domínguez et al., 2005). Genotypic differences in responses of tomato shoot growth to sub-optimal T have also been reported by Paul et al. (1984). An additional reason for the difference in response of grafted tomato to low T (14.6 °C) between our experiment and that of Venema et al. (2008) is the duration of exposure. It seems that short-term low T stress severely impairs vegetative growth of tomato, but in the long term growth can partly recover due to physiological adaptation to stress conditions (Goulas et al., 2006).

Shortening of root length at low T, regardless of rootstock genotype, indicates that low T imposesformation of thicker roots in tomato, as reported by Kasper and Bland (1992). Nevertheless, our knowledge about key-physiological mechanisms underlying the inhibitory effect of sub-optimal root-zone T on the cell cycle and cell elongation in roots is currently insufficient (Walter et al., 2009). Rootstock genotype has a strong impact on root growth when the same cultivar is used as scion, as indicated by huge differences in root biomass between grafting treatments tested even at optimal T. However, the most interesting finding of this study regarding vegetative tomato growth is that ‘Kommeet’ grafted onto ‘LA 1777’ exhibited improved shoot growth at intermediate and optimal T, and root growth at low or intermediate T in comparison with self-grafted plants or ‘Kommeet’ grafted onto ‘Moneymaker’. These findings, in combination with the fact that sub-optimal T did not restrict root length, while enhancing total root area in ‘Kommeet’ grafted onto ‘LA 1777’, indicate that this graft combination provides clear advantages in terms of vegetative tomato growth. Uptake of some nutrients and water are strongly affected by reducing root T in non-grafted *S. lycopersicum* but not in *S. habrochaites* (Bloom et al., 1998, 2004). Change in root morphology may be interpreted as adaptation of nutrient acquisition mechanisms to low T, aimed at extending the absorbing surface area per unit root weight or length (Macduff et al., 1986). Thus, the formation of a more extensive root system by tomato plants grafted onto ‘LA 1777’ as T is reduced, and the concomitant increase in root/shoot ratio, provides an additional advantage to these plants when exposed to sub-optimal T, in terms of nutrient and water uptake. An increase in root/shoot ratio has been interpreted by Equiza et al. (2001) as an adaptation aimed at overcoming restrictions in water absorption which, in the case of low T, might be related to increased water viscosity and root resistance to water transport.

Reductions in fruit yield when tomato is exposed to sub-optimal T have been already reported by several investigators (Aroca et al., 2003; Korkmaz et al., 2002; Van der Ploeg and Heuvelink, 2005). Suppression of yield at sub-optimal T in our study originates from decreased fruit set owing to a reduction in both pollen quantity, quality (Dominguez et al., 2005) and retardation of truss appearance rates (Van der Ploeg and Heuvelink, 2005), which restricts fruit number per plant. Our findings support this hypothesis since sub-optimal T decreased total fruit yield by reducing total fruit number, while average yield rose. Increase of the average fresh fruit weight as T was lowered indicates that low T impairs more severely formation and fecundity of pollen than the availability of assimilates after fruit setting, as also suggested by Adams et al. (2001) and Schwarz et al. (2010).

Another interesting finding of the present study is that reducing ambient T reduced the incidence of the Ca-related physiological disorder blossom-end rot (BER) in fruits. According to Kiegle et al. (2001), low T increases cytosolic Ca^{2+}, while according to Knight et al. (1996) and Tahtiharju et al. (1997), Ca^{2+} could play an essential role in the cold acclimation process. As reported by Ho and White (2005), cytosolic Ca^{2+} coordinates cell expansion by influencing the incorporation of vesicles containing enzymes required for membrane and wall construction into the plasma membrane. Therefore, an increase in fruit Ca due to sub-optimal T may prevent morphological defects, such as membrane permeability that may result in abnormal leakage of solutes from cells and cell death, and concomitantly the occurrence of BER. Significant restriction of BER in fruits by grafting onto 'LA 1777' points to an involvement of Ca^{2+} transport to fruits. Further research is needed to elucidate the mechanisms underlying this relationship.

Grafting 'Kommeet' onto 'LA 1777' significantly restricted total fruit yield in comparison with self-grafting, due to a huge reduction in fruit number per plant. Since the flower number per plant was similar in 'Kommeet' grafted onto 'LA 1777' and self-grafted 'Kommeet', it is concluded that the use of 'LA 1777' as rootstock impairs pollen fertility. Pollen produced by *S. habrochaites* is more cold tolerant than that of *S. lycopersicum* (Dominguez et al. 2005). However, according to the same authors, *S. lycopersicum* × *S. habrochaites* crosses and subsequently segregating generations with *S. lycopersicum* show reduced pollen fertility due to interspecific hybrid sterility. The present study indicates that the combination of *S. habrochaites* and *S. lycopersicum* impairs pollen fertility not only if these relative species are crossed but also if the latter is grafted onto the former. These findings point to a role of plant hormones originating from the roots and transported to the shoot either on pollen viability or on some other function related to pollination and fruit set (Sirova et al., 2011; Garay-Arroyo et al., 2012). Thus, in terms of yield performance, the use of S. *habrochaites* as rootstock may pose similar difficulties with those faced when using this wild tomato species for breeding elite cultivars, i.e. reduced pollen fertility. Further research is needed to confirm this hypothesis.

Previous research has indicated that the exposure of tomato to low T suppresses carbon export from leaves, thereby causing accumulation of soluble carbohydrates in these plant tissues (Strand et al., 2003; Rosa et al., 2009a). Restriction of sugar export from the leaves of cold-stressed plants originates mainly from reduced sink activity due to exposure of roots, fruits and stem apices to low T (Rosa et al., 2009b). Reduced carbon utilization in sink organs stressed by low T slows down the rate of sugar unloading thereby imposing a feed-back retardation of sugar loading in leaf phloem (Ainsworth and Bush, 2011). As a result, soluble carbohydrates may accumulate in both photosynthetically active leaves and sink organs, such as roots and fruits, as was the case in the present study. Nevertheless, the accumulation of soluble sugars in plant tissues stressed by low T may also serve as an adaptive mechanism to stress conditions. Plant metabolism is modulated under abiotic stress conditions and accumulated sugars may act as osmolytes or substrates for cellular respiration (Gupta and Knaur, 2005) or as antioxidative agents (Bogdanovic et al., 2008) that scavenge reactive oxygen species (ROS) (Noctor and Foyer, 1998). Thus, a greater accumulation of soluble sugars in plant tissues exposed to sub-optimal T may indicate a higher adaptability to cold-stress conditions. In agreement with this consideration, in our study soluble carbohydrate levels in the roots of plants grafted onto the cold tolerant rootstock ‘LA 1777’ were higher than in roots of the other grafting combinations under low T (14.6 °C).

Higher soluble sugar levels in leaves and fruits of plants grafted onto ‘LA 1777’ compared with self-grafted plants or those grafted onto ‘Moneymaker’ at 14.6 °C may predominantly reflect the stronger reduction in leaf biomass in the first compared with the latter two treatments when T dropped (Fig. 1). However, higher soluble sugar levels at 17 °C in leaves and fruits of plants grafted onto ‘LA 1777’ compared with the other two grafting treatments were not accompanied by significant reductions in shoot biomass. Thus, it is reasonable to assume that at 17 °C increased levels of glucose and fructose in leaves and fruits of plants grafted onto ‘LA 1777’, compared with those from the other two grafting treatments, served mainly as an adaptive mechanism to sub-optimal T that is triggered by the roots. This consideration is in agreement with previous findings (Cook et al., 2004; Ma et al., 2009; Zhang et al., 2007) indicating that plants subjected to sub-optimal T stress utilize sugars and amino acids as protective compounds. Protection of leaf growth and photosynthesis through hormonal signals originating from cucumber roots under cold stress conditions, such as abscisic acid, has been reported by Zhou et al. (2007). A link between signaling pathways of abscisic acid and sugar metabolism has been reported by several investigators in *Arabidopsis* (Arenas-Huerto et al., 2000; Rook et al., 2001; Cheng et al., 2002).

Striking differences in root N and C between ‘Kommeet’ grafted onto ‘LA 1777’ and plants that were either self-grafted or grafted onto ‘Moneymaker’ presumably reflect anatomical differences related to the allocation of plant biomass into polysaccharides deposited in cell walls and cytosol. Reduced root and leaf protein as T decreased was obviously related to substantial increases in total amino acid concentration in roots and fruits. As reported by Mitchell and Madore (1992) and Zhang et al. (2007), plants subjected to sub-optimal T utilize amino acids, in addition to sugars, as protective compounds. Accumulation of amino acids in plant tissues exposed to sub-optimal T originates mainly from up-regulation of nitrate reductase activity (Tucker and Ort, 2002). Thus, it seems that the stronger increase of total amino acid concentration in the roots of plants grafted onto 'LA 1777' and plants either self- grafted or grafted onto 'Moneymaker' reflects the higher tolerance of 'LA 1777' to sub-optimal T. Nevertheless, the ability of 'LA 1777' to increase total amino acid concentration when exposed to sub-optimal T does not seem to be governed by root/shoot signalling compounds. Indeed, grafting of 'Kommeet' onto 'LA 1777' did not result in a stronger increase in total amino acids in the leaves and fruits in comparison with self-grafting or grafting onto 'Moneymaker'.

Malondialdehyde (MDA) is one of several low-molecular-weight end products arising from the decomposition of various primary and secondary lipid peroxidation compounds (Demiral and Türkan, 2005). Therefore, an increased MDA level in plant tissues is considered to be a definite index of oxidative stress resulting from increased formation of ROS. The contrasting differences in root MDA levels between 'Kommeet' plants grafted onto 'LA 1777' and those grafted onto *S. lycopersicum* rootstocks when exposed to 17 and 14.6 °C, clearly demonstrate the superiority of the former in avoiding oxidative stress caused by sub-optimal T. Nevertheless, use of a cold tolerant rootstock did not reduce the oxidative stress in the leaves of tomato when plants were exposed to sub-optimal T, as indicated by the similar leaf MDA levels in all grafting treatments at 17 and 14.6 °C. Plants are capable of deploying various enzymatic defense systems to minimize the deleterious effects of ROS which include the enzymes glutathione reductase (GR), guaiacol peroxidase (GPOD), and superoxide dismutase (SOD) (Gill and Tuteja, 2010; Tuteja 2009). As reported by Foyer and Noctor (2005), antioxidant capacity increases during cold acclimatization in several plants as an adaptive mechanism to low T, especially in those characterized by enhanced tolerance to sub-optimal or low T. The results of the present study indicate a weak involvement of GPOD, SOD, and GR in defense mechanisms against oxidative stress caused by low T when tomato is grafted onto *S. lycopersicum* rootstocks, which restricted root, leaves, and fruits, respectively. However, plants grafted onto 'LA 1777' were capable of appreciably raising GPOD activity in roots and fruits and SOD activity in leaves and fruits when exposed to low T, thereby increasing their capacity to scavenge ROS induced by low T stress. These results indicate that the activities of some antioxidant enzymes in leaves and fruits of tomato are influenced not only by the shoot but also by the root genotype. Similar results have been reported by Zhang et al., (2010) and Liu et al. (2012). Further research is needed to elucidate the underlying signaling pathways contributing to the protection of leaves and fruits from oxidative stress that are governed by root genotype.

4.4. Expression profiling of tolerant and sensitive tomato rootstock genotypes under sub-optimal temperature stress

In this study, transcript profiling and the growth and physiological responses of a commercial tomato cv. Kommeet grafted onto two rootstocks differing in their tolerance to sub-optimal temperature (T) (Venema et al., 2008) were combined in order to achieve a more comprehensive understanding of the dynamic sequence of events linking gene-to-growth/physiological networks under sub-optimal root T. The present findings complement and extend previous research by others, where the positive impact of the high-altitude accession LA 1777 (*S. habrochaites*) rootstocks on tomato scion performance at sub-optimal T has been demonstrated with regards to growth and physiological responses. This is ascribed to the fact that no study has so far identified and evaluated genes controlling biochemical reaction chains and physiological procedures that are related to the sub-optimal root T tolerance of ‘LA 1777’ (Venema et al., 2005, 2008; Schwarz et al., 2010).

In the present study, PCA identified discrete responses between leaves and roots of grafted plants subjected to sub-optimal root T and enabled a distinct separation of the two tested rootstock genotypes. Indeed, at leaf level ‘Kommeet’ scions showed a similar trajectory and magnitude in the non sub-optimal T-stressed samples, suggesting the existence of a common transcriptional response. However, under sub-optimal root T large and coherent transcriptional changes were induced by a 10 ^{o}C shift in the root T which clearly demonstrates the impact of the rootstock genotype on scion performance under the stress applied. Moreover, the sub-optimal T-stressed root samples were clearly separable from their respective control root samples in both genotypes, indicating that a root T shift of 10 ^{o}C is enough to impose changes at transcript level.

In this study we showed that the exposure of tomato to sub-optimal temperature resulted in a profound decrease in shoot fresh and dry mass of tomato plants exposed to sub-optimal root T, which is in agreement with previous studies (Venema et al. 2008; Ntatsi et al., 2013). As already reported by Venema et al., (2008), grafting tomato onto ‘LA 1777’ was able to improve shoot growth by stimulating leaf area expansion. This is supported by the findings of this study. To identify those genes that may be relevant for the differences in sub-optimal root

T tolerance between grafted plants, we compared the responses of tomato cv. Kommeet grafted either onto ‘LA 1777’ or onto ‘Moneymaker’. The comparative transcriptome profiling of the two plant parts (leaves and roots) and the two different root T of ‘Kommeet’ plants grafted onto ‘LA 1777’ or ‘Moneymaker’ resulted in 261 genes that were differentially expressed in the leaves of ‘Kommeet’ grafted onto the cold sensitive genotype while no gene changes were observed in the leaves of grafted ‘Kommeet’ plants when the rootstock was tolerant. These numbers coincide with the differences in growth obtained in the leaves of the tested plants and reveal that the impact of ‘LA 1777’ on scion performance is independent of the root zone T (Venema et al., 2008). In the present study, at optimal T ‘LA 1777’ rootstocks affected shoot growth, revealing a high impact of grafting on plant development. This is probably due to the fact that root growth of ‘LA 1777’ is inhibited under normal root T. However when plants were subjected to sub-optimal root T, an apparent increase of more than 50% was achieved, even though this increase was not statistically different. At transcript level the number of genes that were significantly up- or down regulated was much higher in the roots of the sensitive genotype. Indeed, the number of the genes exclusively repressed by sub-optimal root T in the sensitive genotype was approximately 50% more than the number of genes exclusively repressed in the tolerant genotype. As reported by Schwarz et al. (2010), under sub-optimal T low temperature tolerant rootstocks maintain higher root growth rates that the sensitive ones. Perhaps the stress applied is not enough to indicate these differences and this is probably the reason why ‘LA 1777’ shows independence to the root zone T (Venema et al., 2008). This independence was also enhanced by the fact that no impact of sub-optimal T on root performance of this high-altitude accession of wild species line (‘LA 1777’) was obtained (Bloom et al., 1998, 2004). Hence, the present study is in agreement with the view that factors other than the production and availability of assimilates restrict shoot growth under sub-optimal T conditions (Ntatsi et al., 2013). Indeed, the supply of assimilates was not limited by the exposure of plants to sub-optimal root T.

In agreement with this consideration, the rates of net assimilation in leaves and the starch content of the leaves and roots were not decreased by the stress applied to the root environment. At transcript level in the leaves of ‘Kommeet’ plants grafted onto ‘Moneymaker’, 11 genes were up-regulated while in the roots the number of the PS-down-regulated genes was higher in the sensitive genotype when compared to the tolerant one (Liu et al., 2012). This explains why the supply of assimilates for the tested grafted plants was not limited by exposure to sub-optimal root T even though the rootstock genotype exhibited different temperature tolerance. It also and clearly demonstrates that air T can help plants overcome possible restrictions at the photosynthetic level imposed by root T stress. However, the gas exchange data presented here indicate that a restriction in carbon assimilation may be an additional, but not major, factor limiting the shoot growth of tomato under sub-optimal root T, depending on the genotype. Indeed plants grafted onto 'Moneymaker' showed higher stomatal conductance in comparison with those grafted onto the high-altitude accession of wild species ('LA 1777'). This difference is associated with the propensity of this wild tomato species to close stomata during chilling, due to a rapid decline in water movement caused by sub-optimal root T that prompts the shoots of the cold-tolerant species to close their stomata, whereas the stomata of tomato sensitive genotypes remain open (Venema et al., 2008; Bloom et al., 2004).

Under specific environmental situations, such as sub-optimal T, or in specific plant genotypes, an imbalance between root water uptake and leaf transpiration occurs. A mechanism to avoid stress-induced growth retardation is the modification of root water uptake capacity due to stomata closure (Matsuo et al., 2009). According to Aroca et al. (2001), chilling sensitivity differences among genotypes are ascribed to different responses of root water uptake rate. Thus, when temperature falls below the optimum, root water uptake decreases due to a decrease in vapor pressure difference between the leaf surface and leaf area (Aroca et al., 2003), while water viscosity increases (Bloom et al., 2004). According to the same authors, although transpiration decreases, the stomata of sensitive genotypes remain open while those of tolerant ones close rapidly, indicating an adaptive mechanism to sub-optimal T. Besides this function, low temperature also affects root growth, size and architecture (Nagel et al., 2009). Changes in root morphology may be interpreted as an adaptation of nutrient acquisition mechanisms to low T, aimed at extending the absorbing surface area per unit root weight or length (Macduff et al., 1986). Thus, the formation of a more extensive root system by tomato plants grafted onto 'LA 1777' as T is reduced, and the concomitant increase in root:shoot ratio, provides an additional advantage to these plants when exposed to sub-optimal T, in terms of nutrient and water uptake. In the present study sub-optimal root T resulted in an approximately 2.5 fold increase in root:shoot ratio when plants were grafted onto 'LA 1777', while no increase was observed in the root:shoot ratio between optimal and sub-optimal root T when 'Moneymaker' was used as a rootstock. An increase in root:shoot ratio has been interpreted by Equiza et al. (2001) as an adaptation aimed at overcoming restrictions in water absorption which, in the case of low T, might be related to increased water viscosity and root resistance to water transport. A putative osmosensor localized at the cell membrane was suggested for sensing the osmotic change in *Arabidopsis* cells (Urao et al., 1999).

Cellulose constitutes the major component of plant cell walls, determining cell shape and plant morphology, and is synthesized by cellulose synthase complexes localized on the plasma membrane (Doblin et al., 2002). In the present study, cell wall MapMan functional category was significantly enriched in the up-regulated genes of the roots of 'LA 1777', suggesting that cellulose synthesis may be one of the main adaptative mechanism of plants to sub-optimal root T. This provides an explanation why sub-optimal T has no adverse impact on root growth of high-altitude accessions of *S. habrochaites* (Venema et al., 2008), and therefore, why a reduction in upward transport capacity of water and nutrients is not expected when this *S. habrochaites* accession line is exposed to sub-optimal T. These results are in agreement with those of Bloom et al. (1998, 2004), who suggested that the uptake of some nutrients and water are strongly affected by reducing root T in non-grafted *S. lycopersicum* but not in *S. habrochaites*. Indeed, a gene encoding potassium transport (*HAK5*, S*GN-U586041*) and one sulfate transporter gene (*SGN-U564643)* are strongly up-regulated in the roots of 'LA 1777' in comparison to 'Moneymaker', while N metabolism was significantly enriched only in the down-regulated genes in the roots of 'Moneymaker'. Moreover, the down-regulation of *ATFRO4/FRO4 (*ferric reduction oxidase 4; *SGN-U582218*) in the tolerant genotype suggests that no iron-limiting stress is observed due to the fact that in iron-efficient plants, iron deficiency responses, such as Fe(III) chelate reduction and the Fe(II) transporter) are obviously enhanced under iron-limiting stress (Bienfait et al. 1983; Fox et al. 1996).

Studies analyzing the effects of low temperature on root-derived phytohormones clearly demonstrate that changes in their production induced by the stress applied have a strong impact on both root growth and root-to-shoot signaling imposing alterations in shoot physiology and thus productivity (Aloni et al., 2010; Schwarz et al., 2010). However, due to intensive hormone cross-talk (positive or negative), individual processes are affected by multiple hormones. Under stress conditions a range of hormones divided into two groups namely "positive growth regulators" (auxin, cytokinins [CKs], and brassinosteroids) and "stress hormones" (abscisic acid [ABA], jasmonic acid [JA], salicylic acid [SA] and ethylene) are regulated. As already reported, sub-optimal T has no adverse impact on root growth of high-altitude accessions of *S. habrochaites* (Venema et al., 2008); thus, imbalances in supply rate of root-deprived phytohormones to the scion caused by exposure to sub-optimal T are also not expected for this genotype, and root-to-shoot communication is unaffected. In agreement with this consideration, no differentially expressed hormone-related genes were found in the shoot of 'Kommeet' plants grafted onto 'LA 1777', while the reverse was the case for those grafted onto 'Moneymaker'. Indeed, in 'Kommeet' scions grafted onto the sensitive genotype six hormone-related genes (three lipoxygenases, two auxin-related, and DWF1) were up-regulated while two auxin related genes were down-regulated. However, at root level the MapMan functional category significantly enriched in the up-regulated genes of the roots of 'LA 1777' was JA-related, suggesting that this hormone imposes a crucial role in sub-optimal root T tolerance. According to (Vankova, 2010), JA governs the response to wounding and necrotroph attack, and is essential for regulating the systemic defense response in tomato (Sun et al., 2011). Previous studies indicated that the expression of pathogenesis-related proteins (PRs) and phenylalanine ammonia lyase (PAL) were induced by JA (Liu et al., 2012). Interestingly, the expression of PR and PAL genes was exclusively altered only in the sensitive genotype. This enhances the hypothesis that JA may act as a positive regulator in response to sub-optimal root T in tomato.

Interestingly, in the present study, CK metabolism functional category was significantly enriched in the down-regulated genes in the root of the sensitive genotype. Previous research has indicated that exposure of plants to low temperature results in a sharp decline in cytokinin concentration in shoots due to increased activity of cytokinin-oxidase (Veselova et al., 2005). In the present study, the down-regulation of two genes encoding a CK oxidase/dehydrogenase, which catalyzes the degradation of CK, resulted in higher CK concentrations in the root zone. According to Ntatsi et al. (2013), increased root length in the absence of CK in the root is in agreement with previous findings which indicate that the application of this plant hormone causes a decrease in root meristem size because of a progressive decrease in meristematic cell number (Dello Ioio et al., 2007). Besides cytokinin, auxin also decelerates root-elongation in a concentration-dependent way (Schwarz et al., 2010). A study by Shibasaki et al. (2009) on cold-induced changes in auxin transport suggested the involvement of auxin in cold stress responses, while recently Ntatsi et al. (2013) reported that reduced production of IAA in the roots in combination with standard IAA biosynthesis in the shoot enhanced the total length of the roots. In the present study the number of down-regulated auxin-responsive genes is higher in the tolerant genotype than in the sensitive one, which is in agreement with the suggestion of Taiz and Zeiger (2007) and Ntatsi et al., (2013) that roots may require a minimum concentration of auxin to grow under sub-optimal T conditions.

Another hormone that is a crucial to plant defence against abiotic stress is ABA (Ntatsi et al., 2014). The protective role of this hormone is attributed to the stabilization of membranes as well as the improvement of water status by elevation of root hydraulic conductivity and stomata closure. However, in the present study we cannot identify the role of ABA since the *NCED3* gene that was up-regulated in the roots of both genotypes (and according to Ntatsi et al, (2014) plays a role in ABA biosynthesis) could not be confidently confirmed due to very low expression signals, whereas *NCED4* that was up-regulated in the leaves of 'Kommeet' grafted onto 'Moneymaker' encodes carotenoid cleavage dioxygenases and therefore regulates carotenoid biosynthesis (Huang et al., 2009; Vogel, et al., 2010), which is not related to ABA metabolism (Ntatsi et al., 2014). Sharp et al., (2000) and Sharp and LeNoble (2002) ascribed the protective role of ABA under water stress conditions to a restriction of ethylene production, which seems to be a widespread function of ABA in plants. Various authors suggest that ABA suppresses ethylene production, specifically its precursor 1-aminocyclopropane-1-carboxylic acid (ACC), because ABA-deficient mutants exhibit enhanced ethylene levels (Rodriguez et al., 2010; Sharp et al., 2000; Spollen et al., 2000). However, these authors could not find a direct link between these two phytohormones. Thus it is possible, that the impact of ABA on the endogenous ethylene levels is mediated through other signals, such as sugars. In *Arabidopsis* it was found that signalling in sugar metabolism closely interacts with signaling pathways of ABA (Arenas-Huerto et al., 2000; Laby et al., 2000; Huijser et al., 2000; Rook et al., 2001; Cheng et al., 2002) and ethylene (Zhou et al., 1998). In the present study both genotypes were significantly enriched by genes that were down regulating ethylene degradation, namely an ethylene-forming enzyme (*SGN-U579250*), a flavonol synthase/flavanone 3-hydroxylase gene (*SGN-U600915*) and 1-aminocyclopropane-1-carboxylate oxidase 1 (*SGN-U581679*). All of them were strongly down-regulated in the sensitive tomato rootstock genotype in comparison with the tolerant one, which supports the hypothesis of Ntatsi et al. (2013) that a blockage of ethylene production might enhance plant tolerance to sub-optimal temperature stress.

As reported by (Cheeseman, 2007), under stress conditions more ROS, such as H_2O_2, are produced in plant tissues. However in this study the plants did not produce any protective compounds against low T stress, such as sugars and amino acids (Cook et al., 2004; Zhang et al., 2007; Ma et al., 2009). This is ascribed to the fact that the sugar transporters are down-regulated in the roots of both genotypes, while the amino acid synthesis MapMan functional category was significantly enriched in the down-regulated genes of the same roots. In addition, two genes were identified as down-regulated in 'LA 1777' and 'Moneymaker' (slightly stronger when compared with ‘LA 1777’), namely S-adenosylmethionine synthetase *SAM1* (*SGN-U591910*) and the branched-chain amino acid aminotransferase *SlBCAT1* (*SGN-U569828*), both involved in amino acid metabolism. All of the foregoing enhances the hypothesis that the stress applied was not enough to disrupt major metabolic processes, such as secondary metabolism, protein synthesis and heat stress which are enriched in the down-regulated genes of both rootstock genotypes. Thus in the present study the non-photochemical quenching mechanism was not influenced either by T or by the rootstock, or both, while a slight but insignificant increase of MDA and H_2O_2 levels in leaves of the tested plants was noted. This supports the hypothesis that another reaction is responsible for scavenging MDA and $H_2O_{2.}$ These results point to an involvement of MDA and H_2O_2 in other scavenging reactions, such as the glutathione antioxidant system (Taiz and Zeiger, 2007). Indeed the increase of G-POD activity under sub-optimal root T indicates the existence of a mechanism against this stress that helps the plant overcome the consequences of exposure to low T by producing more protective compounds (Tuteja, 2009) to scavenge MDA and H_2O_2 (Abassi et al., 1998). Thus, plants grafted onto ‘LA 1777’ exhibited a 2-fold increase in root GPOD in comparison with those grafted onto ‘Moneymaker’, a result which can be ascribed to the fact that in the roots of ‘Moneymaker’ the down-regulated genes of the redox bin category are twice the number of the down-regulated genes in the roots of ‘LA 1777’.

CHAPTER 5. CONCLUSION

In conclusion sub-optimal day/night T (17/14 °C) results in substantial suppression of the shoot growth rates, which is not due to restriction in the rates of net CO_2 assimilation. Hormonal signalling aimed at plant adaptation to stress conditions seems to be an important factor in regulating plant growth under sub-optimal T conditions. In particular, normal ABA biosynthesis particularly in the shoot but also in the root was found to promote the tolerance of tomato to sub-optimal T, presumably by indirectly controlling the levels of endogenous ethylene, which seems to increase tomato susceptibility to sub-optimal T stress. The contribution of ABA to the tolerance of tomato to sub-optimal T stress was only partially reflected by leaf ABA level and is probably not related to its effects on stomatal conductance and gas exchange. Sufficient auxin sensitivity in the shoot of tomato promotes shoot elongation in tomato plants grown under sub-optimal T conditions. CK deficiency either in the root or in the shoot restricts leaf area expansion under optimal T conditions but has no impact on leaf area when the plants are exposed to sub-optimal T. SA deficiency in the shoot of tomato has no impact on shoot elongation under standard T conditions but restricts the shoot length of plants exposed to sub-optimal T. However, the leaf area is equally impaired by insufficient SA biosynthesis at optimal and sub-optimal T regimes, which indicates that SA does not protect leaf growth under sub-optimal T stress. In summary, ABA, auxin and SA appear to be the key-hormones in tomato responses to sub-optimal T conditions on which plant breeders have to focus in relevant breeding programs.

A closer examination on the role of ABA revealed that both sub-optimal root (T) and absence of the *LeNCED1* gene in root and shoot of self-grafted ‘notabilis’ (*not*/*not*) reduced leaf area and total plant biomass, but there was no interaction between these two factors. The lack of the *LeNCED1* gene only in the root or only in the shoot restricted shoot length but was not sufficient to decrease significantly the leaf area and total plant biomass. The absence of the *LeNCED1* gene in *not*/*not* was associated with significantly higher g_s, A, transpiration rates and water uptake capacity than in wild-type ‘Ailsa Craig’ scions. These results indicate that the growth restriction imposed by inactivation of the *LeNCED1* gene is not a result of impaired photosynthesis. Moreover, the absence of the *LeNCED1* in the shoot, which induced higher water losses by altering stomatal regulation, was compensated by an increased water uptake capacity of the root.

In addition, inactivation of the *LeNCED1* gene in ‘notabilis’ did not restrict the levels of endogenous ABA in the shoot of tomato under both optimal and sub-optimal root T conditions, although ‘notabilis’ is known to be deficient in ABA biosynthesis induced by water deficit. Knocking out the *LeNCED1* increases ROS production and restricts ROS scavenging, as indicated by the higher H_2O_2 levels and the increased G-POD activity in *not*/*not* plants, respectively. Gene analysis did not provide indication for substitution of *LeNCED1* function by up-regulation of *LeNCED2* and/or *LeNCED6.* The increase of ABA levels in tomato leaves may have been caused by activation of the *NCED3* gene as shown for Arabidopsis, although the activation of *NCED3* gene expression in tomato could not be confidently confirmed. Further research is needed to identify the possible ROS scavenging systems that are activated via *LeNCED1* and elucidate root to shoot interactions with respect to hormonal transport and signaling under sub-optimal T in the root zone.

The use of wild relatives of *S. lycopersicon* as rootstocks, characterized by a vigorous root system and tolerance to sub-optimal T, to minimize yield losses in elite cultivars of grafted tomato when exposed to sub-optimal T, revealed that the use of cold-tolerant accessions of *S. habrochaites* as tomato rootstocks can indeed enhance the tolerance of grafted plants to sub-optimal T. However, protection conferred by S. *habrochaites* against cold-induced stress may be not be beneficial in terms of yield under sub-optimal T conditions because this wild tomato may impair pollen fertility even when used as a rootstock. Future research using microarray analysis of accessions of *S. habrochaites* as rootstocks in a series of rootstock/scion combinations might elucidate genes controlling root/shoot signaling that influence pollen fertility. Acquired knowledge could be utilized to establish biomarkers to screen not only wild tomato genotypes serving as rootstocks but also to test rootstock/scion combinations potentially tolerant to sub-optimal T.

Grafting tomato cv. ‘Kommeet’ onto the cold-tolerant accession ‘LA 1777’ of the wild relative of tomato, *S. habrochaites*, increases root biomass at low (14.6 ^{o}C) and intermediate (17 ^{o}C) T (both sub-optimal), and leaf biomass at 17 and 19.4 ^{o}C in comparison with self-grafting and grafting onto the cold-sensitive hybrid ‘Moneymaker’. However, grafting onto ‘LA 1777’ significantly restricts fruit yield due to a serious reduction in the number of fruits per plant, while not influencing the number of flowers per plant in comparison with self-grafting, which points to a root-induced restriction of fruit set. These results indicate that *S. habrochaites* impairs pollen fertility not only when used to breed interspecific hybrids with *S. lycopersicum,* but also when used as a rootstock.

The increase in soluble carbohydrates, total amino acids, and guaiacol peroxidase (GPOD) activity in the roots of plants grafted onto ‘LA 1777’ and the low malondialdehyde (MDA) content at sub-optimal (intermediate or low) T point to a much weaker cold-induced oxidative stress in the roots of these plants. Furthermore, the plants grafted onto ‘LA 1777’ exhibited significantly higher levels of soluble carbohydrates, total amino acids, and GPOD activity in leaves and fruit, and SOD in fruit at 14.6 ^{o}C. These results indicate that ‘LA 1777’ is capable of improving the levels of some antioxidant compounds in the shoot of tomato, thereby improving its adaptation to 14.6 ^{o}C.

Taken together, the results of the present study indicate that the use of cold-tolerant accessions of *S. habrochaites* as tomato rootstocks can enhance the tolerance of the grafted plants to sub-optimal T by improving their capacity to scavenge reactive oxygen species. However, the protection conferred by S. *habrochaites* against cold-induced oxidative stress may be not beneficial in terms of fruit yield under sub-optimal T conditions because this wild relative of tomato may impair pollen fertility even when used as a tomato rootstock.

Transcript profiling of comparative transcriptome analysis of leaves and roots of tomato cv. ‘Kommeet’ grafted onto the wild tomato S. *habrochaites* accession ‘LA 1777’ and the *S. lycopersicon* cv. ‘Moneymaker’ and subjected to sub-optimal root T revealed that a root T shift of 10 ^{o}C is enough not only to impose changes at transcript level but clearly indicate the impact of the rootstock genotype on scion performance under sub-optimal root T.

No transcript changes were observed in the leaves of ‘Kommeet’ grafted onto the cold-tolerant rootstock ‘LA 1777’ while the use of the cold-sensitive tomato genotype ‘Moneymaker’ as rootstock resulted in large and coherent transcriptional changes in the leaves of the same scion (‘Kommeet’). These changes were attributed to the differences in gene expression in the roots of both genotypes that control biochemical reaction chains and physiological procedures related to sub-optimal root T.

In the present study, grafting onto ‘LA 1777’ improved shoot growth by stimulating leaf area expansion and resulted in an approximately 2.5 fold increase of the root:shoot ratio. This increase is attributed to modifications in the cell walls suggesting that cellulose synthesis may be one of the main adaptive mechanisms of plants to sub-optimal root T. At a hormonal level the results of this study revealed that JA may act as a positive regulator in response to sub-optimal root T in tomato while the down-regulation of genes related to CK metabolism as well as auxin and ethylene-responsive genes suggests a significant role of these hormones in tolerance to sub-optimal root T.

In conclusion the knowledge acquired in this work could be used to define appropriate criteria for the selection and breeding of vigorous ‘energy-efficient’ tomato rootstocks and subsequently utilized to establish biomarkers that might be used to screen not only wild tomato genotypes serving as rootstocks but also rootstock/scion combinations that are likely to be tolerant to sub-optimal T.

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Education:

1994: High School of Filippiada, Preveza, Grade: 19 (12/14)
1997: Lyceum of Filippiada, Preveza, Grade: 19
2005: Bachelor of Science (BSc) in Agronomy, Agricultural University of Athens, Department of Crop Science, Laboratory of Floriculture and Landscape Architecture, (The program is a five-year curriculum), Grade: 6.93
2008: Master in Science (MSc), Agrochremistry and Biological Cultivations, University of Ioannina, Department of Chemistry, Grade: 9.12
2009: PhD Student, Agricultural University of Athens, Department of Crop Science, Laboratory of Vegetable Production, (in progress)

Professional Experience:

2000: Practical work at Benakeio Phytopothology Institute
2001: Practical work at Agricultural University of Athens, Department of Crop Science, Laboratory of Floriculture and Landscape Architecture
2003: Practical work at fytotechniki : Afoi Xylogianni-Baili, Fytotexniki
2006 (21/8-13/11): Working in the Agricultural Organization of Greece (OPEKEPE) as an Agronomist
2006-7(16/11-15/07): Working in the Agricultural Insurance Organization of Greece as an Agronomist
2007-8(13/11-31/1): Working in the Agricultural Organization of Greece (OPEKEPE) as an Agronomist
2007-8(1/10-24/2): Lecturer at the T.E.I. of Hpeirou
2009-11: Laboratory assistant at the Agricultural University of Athens, Department of Crop Science, Laboratory of Vegetable Production
2010 (7/4-31/12): Research Fellow at Leibniz-Institut für Gemüse- und Zierpflanzenbau Großbeeren/Erfurt, Berlin, Germany
2011 (20/6-20/9): Research Trainee at Leibniz-Institut für Gemüse- und Zierpflanzenbau Großbeeren/Erfurt, Berlin, Germany (ERASMUS Project).
2011-12 (1/10/11-30/6/12): Research Fellow at Leibniz-Institut für Gemüse- und Zierpflanzenbau Großbeeren/Erfurt, Berlin, Germany
2012-13: Laboratory assistant at the Agricultural University of Athens, Department of Crop Science, Laboratory of Vegetable Production
2013 (20/08/13-20/10/13): Research Fellow at Max Planck Institute of Molecular Plant Physiology Potsdam-Golm, Germany

Languages

English

1993: Palso Elementary Certificate in English
1995: Cambridge First Certificate in English
2007: Cambridge Proficiency (CPE) in English,
    Michigan Proficiency in English,
    EDEXEL Proficiency in English

German

2001: Goethe-Institut Zertifikat Deutsch
2003: Goethe-Institut Zentrale Mittelstufenprüfung

Computer Skills

2004: Microsoft Office Specialist MASTER in: Microsoft Access 2000, Microsoft Word 2000, Microsoft PowerPoint 2000, Microsoft Outlook 2000, Microsoft Excel 2000
2004: Microsoft Office Specialist EXPERT in: Microsoft Word 2000, Microsoft Excel 2000
2007: Cambridge International Diploma in It Skills: Microsoft Word, Microsoft Excel and Internet
2008: Cambridge International Diploma in It Skills (PHP Website program language)

Reviewer of Scientific Journals

1. Scientia Horticulturae (I.F. for 2012: 1.396)

Recent research projects:

1. Member of the research team in an INTERREG IIIA GREECE-ITALY research project titled: Development and promotion for organic farming producing systems - Pro.Bio.Sis., I2101029, which was implemented by the Faculty of Agricultural technology of TEI of Epirus. Duration of the project: 01/01/2006 to 12/31/2008.
2. Member of the research team in a Project Based Personnel Exchange Programme with Germany (IKYDA 2007). Title of the project: «Improving salinity tolerance and fruit quality of vegetable products by grafting». Collaborating institution: «Institute for Vegetable and Ornamental Crops, Großbeeren, Germany». Source of funds: State Scholarships Foundation of Greece. Duration of the project: 01/01/2007 to 12/31/2008.
3. Member of the research team of the Agricultural University of Athens in a project titled «New technologies for Greener greenhouses under the supervision of Prof Olympios Christos. Duration:.18/2/2008 – 7/3/2008.
4. Member of the research team of the Agricultural University of Athens in a project titled «Revitalization of urban ecosystems through vascular plants: assessment of technogenic pollution impact (GARDEN CITY) » Under the supervision of Ass. Prof Saitanis Konstantinos. Duration: 4/11/2009 – 4/12/2009.
5. Member of the research team of the Agricultural University of Athens in an FP.7 RTD project. Project acronym: LEGUME FUTURES. Project full title: Legume- supported cropping systems for Europe. Grant agreement no. 245216 CP-FP. Duration of the project: 03/01/2010 to 02/28/2014.
6. External researcher in the research team of the project “Improvement of stress tolerance using rootstocks” (“Erhöhung von Stresstoleranz durch den Einsatz von Unterlagen”) which is funded from the German Federal Ministry of Food, Agriculture, and Consumer Protection and implemented by «Leibniz-Institute for Vegetable and Ornamental Crops Großbeeren und Erfurt». Co-ordinator: Dr. Dietmar Schwarz. Duration of the project: 01/01/2010 – 31/12/2012.

7. Member of the scientific team of the Agricultural University of Athens in a Project titled «Development of good agricultural practices in horticulture in pumice and diffusion of the results in the cultivation practice» and ELKE code 34.0231, funded by LAVA A.E.. Duration: από 01/11/2010 - 31/10/2012.
8. Member of the team of the Agricultural University of Athens in a LEONARDO Project titled: "AGRICOM "Transfer of the Water Competences Model to AGRIcultural COMpetences" within the framework of the Programme «Lifelong Learning Programme Leonardo da Vinci - Transfer of Innovation – Call 2011». Duration: 01/10/2011 to 30/09/2013.
9. Member of the Management Committee and Editor of the COST Action FA1204 "Vegetable Grafting to Improve Yield and Fruit Quality under Biotic and Abiotic Stress Conditions" Duration 01/10/2012 to 30/19/2016 http://www.cost.eu/domains_actions/fa/Actions/FA1204?
10. Member of the team of the Agricultural University of Athens in a LEONARDO Project titled: "GreeNET: Environmental Education through Enquiry and Technology, 527891-LLP-1-2012-1-GR-COMENIUS-CNW" within the framework of the Programme «Lifelong Learning Programme Leonardo da Vinci - Transfer of Innovation». Duration: 01/11/2012 to 31/10/2015.
11. Member of the research team in a Research Project of the action ARCHIMEDES, which was co-funded by the EU and the Greek Ministry of Education and Religions titled: « ½ effect of mycorhizal and other symbiotic microorganisms on plants cultivated in soil and soilless culture systems under biotic and abiotic stress conditions" which is implemented by the Faculty of Agricultural technology of TEI of Epirus Duration of the project: 01/01/2013 to 31/12/2015.

Publications

I. Publications in international refereed journals with impact factor

1. Savvas, D., Papastavrou, D., **Ntatsi, G**., Ropokis, A., Olympios, C., Hartman, H., Schwarz, D., 2009. Interactive effects of grafting and Mn-supply on growth, yield and nutrient uptake by tomato. HortScience 44, 1978-1982.
2. Savvas, D., Savva, A., Ntatsi, G., Ropokis, A., Karapanos, I., Krumbein, A., Olympios, C., 2011. Effects of three commercial rootstocks on mineral nutrition, fruit yield and quality in salinised tomatoes. Journal of Plant Nutrition and Soil Science 174, 154–162
3. **Ntatsi, G.**, Savvas, D., Druege, U., Schwarz, D., 2013. Contribution of phytohormones in alleviating the impact of sub-optimal temperature stress on grafted tomato. Scientia Horticulturae 149, 28-38.
4. Savvas, D., **Ntatsi, G**., Barouchas, P., 2013. Impact of Cd and Ni on cation uptake by cucumber grafted onto four commercial rootstocks. Scientia Horticulturae Special Issue 149, 86-96.
5. **Ntatsi G**., Savvas, D., Huntenburg, K., Druege, U., Hincha, D.K., Zuther E., Schwarz, D., 2014. A study on ABA involvement in the response of tomato to sub-optimal root temperature using reciprocal grafts with notabilis, a null mutant in the ABA-biosynthesis gene *LeNCED1*. Environmental and Experimental Botany, 97, 11-21.
6. Petropoulos S.A., Olympios C., Ropokis A., Vlachou **G., Ntatsi** G., Paraskeuopoulos A., Passam H.C., 2014. Fruit volatile, quality and yield of watermelon as affected by grafting. Journal of Agricultural Science and Technology (in press).
7. **Ntatsi G**., Savvas, D., Klaering H.P., Schwarz, D., 2014. Growth, yield, and metabolic responses of temperature-stressed tomato to grafting onto rootstocks differing in cold

tolerance. Journal of the Americn Society for Horticultural Science, (submitted for publication).

8. **Ntatsi G**., Savvas, D, Papasotiropoulos, V., Katsileros, A., Hincha, D.K., Zuther E., Schwarz, D. (2014) Expression profiling of tolerant and sensitive tomato rootstock genotypes under sub-optimal temperature stress (in prep)
9. Savvas, D., Thompson, A.J., Venema, J.H., Schwarz, D., **Ntatsi, G**., 2014 New insights in responses of fruiting vegetables to sub-optimal temperature stress – a review, Environmental and Experimental Botany (in prep).

II. Publications in international refereed journals without impact factor

1. Savvas, D., **G. Ntatsi**, H.C. Passam, 2008. Plant nutrition and physiological disorders in greenhouse grown tomato, pepper and eggplant. European Journal of Plant Science and Biotechnology 2, 45-61.

III. Publications in Proceedings of International Congresses and Symposia

1. Savvas, D., G. Patakioutas, **G. Ntatsi** and G. Karras, 2008. Application of some systemic pesticides via the root system in substrate grown crops under conditions of complete nutrient solution recycling. Acta Horticulturae 819, 451-458.
2. **Ntatsi, G.,** Savvas, D., Schwarz, D., 2012. Role of abscisic acid in the adaptation of grafted tomato to moderately sub-optimal temperature stress. Acta Horticulturae 952, pp. 295-302.
3. Lycoskoufis I., Mavrogiannopoulos G., Savvas D., **Ntatsi G**. 2012 Impact of salinity due to a high concentration of NaCl or to a high concentration of nutrients on tomato plants. Acta Horticulturae 952, pp. 689-696.
4. Petropoulos S., Olympios C., **Ntatsi G**., Passam C. 2012 Effects of grafting and salinity on agronomic characteristics and ion uptake by cucumber plants grown in a closed hydroponic system. Acta Horticulturae 952, pp. 637-644.
5. Savvas, D., **Ntatsi, G**., Moiras, N., Tsakalidis, A., Ropokis, A., Liopa-Tsakalidi, A. 2012 Impact of grafting and rootstock on the responses of cucumber to heavy metal stress. Acta Horticulturae 960 , pp. 49-56
6. Savvas, D., **Ntatsi, G**., Rodopoulou, M., Goumenaki, F., 2013 Nutrient uptake concentrations in a cucumber crop grown in a closed hydroponic system under Mediterranean climatic conditions as influenced by irrigation schedule, Acta Horticulturae (in press).

IV. Abstracts and Posters in Proceedings of Internationa Congresses and Symposia

1. **Ntatsi, G**., Savvas, D., Schwarz, D., 2011. Impact of root-produced auxin on scion characteristics under sub-optimal temperature conditions using auxin-lacking mutants. International Symposium on Vegetable Grafting, Viterbo-Italy, Book of Abstracts, pp. 87.
2. **Ntatsi, G**., Savvas, D., Huntenburg, K., Druege, U., Hincha, D.K., Zuther, E., Schwarz, D., 2011. Contribution of rootstock ABA to growth, nutrient uptake, gas exchange and antioxidative potential in tomato at sub-optimal temperature. International Symposium on Vegetable Grafting, Viterbo-Italy, Book of Abstracts, pp. 88
3. Savvas D., **Ntatsi, G**., Ropokis, A., 2013. Impact of grafting and rootstock genotype on mineral uptake by fruit vegetables. 1st Meeting of Cost Action FA 1204, 11-12 March, 2013, Athens, Greece, Book of Abstracts, pp. 61

4. Savvas, D., Oztekin, G.B., Tepecik, M., Papanikolaou, A., Katsiki, V., Ropokis, A., **Ntatsi, G.**, 2013. Effects of grafting and rootstock genotype on nutrient uptake by tomato 2nd Meeting of Cost Action FA 1204, 11-14 November, 2013, Murcia, Spain Book of Abstracts.

V. Publications in Proceedings of National Congresses and Symposia

1. Ακουμιανάκη-Ιωαννίδου Α, Παπανικολάου Α ,**Ντάτση Γ**, 2005. Επίδραση του μήκους βλαστού και της συγκέντρωσης της γλυκερίνης στη μεταποίηση φυλλωμάτων *Viburnum fragrans, Buxus sempervirens* και *Ruscus hypoglossum* Πρακτικά Ελληνικής Εταιρείας Επιστήμης Οπωροκηπευτικών, τόμος 12α, σελ. 175.
2. Ακουμιανάκη-Ιωαννίδου Α, Παπανικολάου Α, **Ντάτση Γ**, 2005. Χρήση της γλυκερίνης στη μεταποίηση φυλλωμάτων καλλωπιστικών φυτών. Πρακτικά Ελληνικής Εταιρείας Επιστήμης Οπωροκηπευτικών, τόμος 12β, σελ. 83.
3. Πατακιούτας, Γ., Μ. Αναγνώστου, Β. Λούτσου, Δ. Σάββας, Θ. Σακελλαρίδης, Γ. Ντάτση, 2007. Διερεύνηση της συμπεριφοράς της φυτοπροστατευτικής ουσίας thiacloprid σε καλλιέργεια τομάτας σε κλειστό υδροπονικό σύστημα. 23ο Συνέδριο της Ελληνικής Εταιρείας Επιστήμης Οπωροκηπευτικών, Χανιά, 23-26 Οκτωβρίου 2007. τόμος 13Β, σ. 943-946.
4. **Ντάτση, Γ.**, Σάββας, Δ., Huntenburg, K., Druege, U., Hincha, D.K., Zuther, E., Schwarz, D., 2011. Επίδραση του αμπσισικού οξέως και της θερμοκρασίας ρίζας στη φυσιολογία εμβολιασμένων φυτών τομάτας. 25ο Πανελλήνιο Συνέδριο Ελληνικής Εταιρείας Επιστήμης Οπωροκηπευτικών Λεμεσός, Κύπρος τόμος 15Α, σ. 275-278.
5. Σάββας Δ., **Ντάτση Γ.**, Κοντοπούλου Χ.Κ., Ροπόκης Α., Κότσιρας Α., Δημόπουλος Β., Χανής Δ. 2011. Βελτιστοποίηση της διαχείρισης της άρδευσης σε καλλιέργεια αγγουριάς σε τρεις διαφορετικούς τύπους ελαφρόπετρας. 25ο Πανελλήνιο Συνέδριο Ελληνικής Εταιρείας Επιστήμης Οπωροκηπευτικών Λεμεσός, Κύπρος τόμος 15Α, σ. 250-252.
6. Σάββας, Δ., Oztekin, G.B., Tepecik, M., Παπανικολάου, Α., Κατσίκη, Β., Ροπόκης. Α, **Ντάτση, Γ.**, 2013, Επίδραση του εμβολιασμού στην απορρόφηση θρεπτικών στοιχείων σε καλλιέργεια τομάτας σε κλειστό υδροπονικό σύστημα, 26ο Πανελλήνιο Συνέδριο Ελληνικής Εταιρείας Επιστήμης Οπωροκηπευτικών, Καλαμάτα, 15-18 Οκτωβρίου 2013, Περιλήψεις Ανακοινώσεων.
7. Σάββας, Δ., Πατεράκης, Π., Βουρναδάκη, Π., Ροπόκης. Α, **Ντάτση, Γ.**, 2013, Συγκριτική αξιολόγηση δύο τύπων ελαφρόπετρας, πετροβάμβακα, περλίτη και κόκου σε καλλιέργεια τομάτας. 26ο Πανελλήνιο Συνέδριο Ελληνικής Εταιρείας Επιστήμης Οπωροκηπευτικών, Καλαμάτα, 15-18 Οκτωβρίου 2013, Περιλήψεις Ανακοινώσεων.

V. Abstracts of oral presentations in Proceedings of National Congresses and Symposia

1. **Ντάτση, Γ.**, Σάββας, Δ., Γκίζας, Γ., Μάντζος, Ν., Γκόλια, Ε., 2007. Επίδραση της συγκέντρωσης ασβεστίου στο νερό άρδευσης σε καλλιέργεια τομάτας σε κλειστό υδροπονικό σύστημα. 23ο Συνέδριο της Ελληνικής Εταιρείας Επιστήμης Οπωροκηπευτικών, Χανιά, 23-26 Οκτωβρίου 2007. Περιλήψεις Ανακοινώσεων, σ. 42.
2. Σάββας, Δ., Δ. Παπασταύρου, **Γ. Ντάτση**, Α. Ροπόκης, Χ. Ολύμπιος, 2009. Επιδράσεις υποκειμένου εμβολιασμού τομάτας και μαγγανίου στην ανάπτυξη, την παραγωγή και την απορρόφηση θρεπτικών στοιχείων. 24^{ο} Πανελλήνιο Συνέδριο Ελληνικής Εταιρείας Επιστήμης Οπωροκηπευτικών, Βέροια, 20-23 Οκτωβρίου 2009, Περιλήψεις Ανακοινώσεων, σελ. 83.

AGRICULTURAL UNIVERSITY OF ATHENS
DEPARTMENT OF CROP SCIENCE
LABORATORY OF VEGETABLE PRODUCTION

Impact of grafting on growth, yield, quality, and physiological characteristics of tomato grown under sub-optimal temperature conditions

Georgia Ntatsi, B.Sc., M.Sc.
Ph.D. Dissertation-ANNEX

Athens, 2013

Table 1. List of up-regulated genes genes (log2 ratio sub-/optimal T≥1 and q-value<0.05) deteced only in the leaves of the grafted ‘Kommeet’ plants onto ‘Moneymaker’ (R/S:MM/KO) under sub-optimal root T stress.

Bin Code	BinName	SGN	NCBI	description	MM/KO Log FC	adj.P.Val
35.1	not assigned.no ontology.glycine rich proteins	SGN-U574441	DB700201	glycine-rich protein	2,572	0,010
35.2	not assigned.unknown	SGN-U576950	AK321639	Unknown	2,403	0,010
35.2	not assigned.unknown	SGN-U594880	AK326516	Unknown	2,338	0,012
35.2	not assigned.unknown	SGN-U571899	AK247512	Unknown	2,289	0,014
35.1	not assigned.no ontology.glycine rich proteins	SGN-U576949	TA52683_4081	glycine-rich protein	2,237	0,010
35.2	not assigned.unknown	SGN-U573645	TC232099	Unknown	2,164	0,010
35.2	not assigned.unknown	SGN-U588177	AW625268	Unknown	2,126	0,025
35.3	not assigned.disagreeing hits	SGN-U577961	AW649553	Unknown	2,081	0,022
35.2	not assigned.unknown	SGN-U564787	BI932571	QRT3 | QRT3 (QUARTET 3)	2,028	0,015
35.2	not assigned.unknown	SGN-U590500	BF097871	Unknown	2,012	0,015
35.3	not assigned.disagreeing hits	SGN-U580778	TC245073	tetratricopeptide repeat (TPR)-containing protein	1,922	0,020
35.3	not assigned.disagreeing hits	SGN-U583609		Unknown protein	1,914	0,016
34.99	transport.misc	SGN-U573904	BI928029	Unknown	1,905	0,024
35.2	not assigned.unknown	SGN-U599066	BP895853	Unknown	1,778	0,010
1.1.2.2	PS.lightreaction.photosystem I.PSI polypeptide subunits	SGN-U577591	BG628561	PSAN | PSAN (photosystem I reaction center subunit PSI-N)	1,744	0,028
35.2	not assigned.unknown	SGN-U589504	AK327967	Unknown	1,708	0,012
35.2	not assigned.unknown	SGN-U596305	AJ784685	Unknown	1,695	0,010
10.7	cell wall.modification	SGN-U575872	AB036338	XTH27, ATXTH27, EXGT-A3 | EXGT-A3 (endo-xyloglucan transferase A3)	1,688	0,014
35.2	not assigned.unknown	SGN-U570550	TC217439	Unknown	1,660	0,011
35.3	not assigned.disagreeing hits	SGN-U592671	AI782735	PSBW | PSBW (PHOTOSYSTEM II REACTION CENTER W)	1,639	0,023
35.2	not assigned.unknown	SGN-U597278	CD002185	Unknown	1,634	0,010

35.3	not assigned.disagreeing hits	SGN-U577430	BP895733	stress-inducible protein, putative	1,602	0,042
1.	PS.calvin cyle.rubisco small subunit	SGN-U578204	AW929996	RUB1-conjugating enzyme, putative	1,578	0,037
29.	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L12	SGN-U580444	BP903366	RPL12, RPL12-A | RPL12-A (RIBOSOMAL PROTEIN L12-A)	1,553	0,019
29.	protein.synthesis.misc ribososomal protein	SGN-U567476	BP902045	ribosomal protein L17 family protein	1,542	0,017
6.4	gluconeogenese/ glyoxylate cycle.PEPCK	SGN-U574829	BE463138	PCK2, PEPCK | PCK2/PEPCK (PHOSPHOENOLPYRUVATE CARBOXYKINASE 2)	1,540	0,012
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U588948	AW032412	ATGCN5 | ATGCN5 (Arabidopsis thaliana general control non-repressible 5)	1,531	0,010
35.3	not assigned.disagreeing hits	SGN-U581546	BP903575	Unknown	1,515	0,032
35.2	not assigned.unknown	SGN-U580305	TC241247	Unknown	1,498	0,016
27.	RNA.regulation of transcription.unclassified	SGN-U584863	AW034700	zinc finger (CCCH-type) family protein	1,497	0,017
35.3	not assigned.disagreeing hits	SGN-U579307	AK323682	GST6, ATGSTF5, GSTF8, ATGSTF8 | ATGSTF8 (GLUTATHIONE S-TRANSFERASE 8); glutathione transferase	1,494	0,013
20.2.1	stress.abiotic.heat	SGN-U580107	AW218084	ATHSP90.1, ATHS83, HSP81.1, HSP83, HSP81-1 | HSP81-1 (HEAT SHOCK PROTEIN 81-1)	1,445	0,039
16.2.1.1	secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL	SGN-U581307	BP906065	PAL1 | PAL1 (PHE AMMONIA LYASE 1)	1,437	0,010
35.3	not assigned.disagreeing hits	SGN-U572429	TA36380_4081	VAMP726, ATVAMP726 | ATVAMP726 (VESICLE-ASSOCIATED MEMBRANE PROTEIN)	1,432	0,037
35.3	not assigned.disagreeing hits	SGN-U580941	TA35619_4081	ribulose bisphosphate carboxylase small chain 2B / RuBisCO small subunit 2B (RBCS-2B) (ATS2B)	1,409	0,015

10.7	cell wall.modification	SGN-U562920	TC233683	EXP11, ATEXP11, ATHEXP ALPHA 1.14, ATEXPA11 | ATEXPA11 (ARABIDOPSIS THALIANA EXPANSIN A11)	1,406	0,039
17.	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase	SGN-U572040	NM_001247330	ATLOX2, LOX2 | LOX2 (LIPOXYGENASE 2)	1,403	0,011
35.2	not assigned.unknown	SGN-U602497		Unknown	1,400	0,010
35.1	not assigned.no ontology	SGN-U580270	TA38055_4081	Rubber elongation factor (REF) family protein	1,394	0,012
35.3	not assigned.disagreeing hits	SGN-U577535	NM_001246860	FSD1 | FSD1 (FE SUPEROXIDE DISMUTASE 1); iron superoxide dismutase	1,388	0,014
35.2	not assigned.unknown	SGN-U582285	DB715523	Unknown	1,379	0,010
35.2	not assigned.unknown	SGN-U578765	TA42075_4081	Unknown	1,370	0,037
16.2.1.1	secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL	SGN-U580612	AW035414	PAL2 | PAL2 (phenylalanine ammonia-lyase 2)	1,359	0,011
35.2	not assigned.unknown	SGN-U586010	TA54542_4081	Unknown	1,358	0,010
1.	PS.calvin cyle.rubisco interacting	SGN-U591567	AW615920	RCA | RCA (RUBISCO ACTIVASE)	1,355	0,010
35.2	not assigned.unknown	SGN-U595834	TC217346	Unknown	1,346	0,010
29.	protein.degradation.cysteine protease	SGN-U592087	AI488671	proteinase inhibitor 1 ppi3a4	1,340	0,028
35.3	not assigned.disagreeing hits	SGN-U578438	TA35934_4081	ribulose bisphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B)	1,334	0,033
26.	misc.glutathione S transferases	SGN-U596258	DB711682	ATGSTU8 | ATGSTU8 (Arabidopsis thaliana Glutathione S-transferase (class tau) 8)	1,332	0,010
27.	RNA.regulation of transcription.unclassified	SGN-U588355	AI773423	aspartyl protease family protein	1,332	0,012
29.	protein assembly and cofactor ligation	SGN-U586752	TA56545_4081	YCF2.2 | hypothetical protein	1,332	0,010

17.	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase	SGN-U572041	NM_001246883	ATLOX2, LOX2 | LOX2 (LIPOXYGENASE 2)	1,328	0,011
26.	misc.gluco-, galacto- and mannosidases	SGN-U566590	AK320376	alpha-glucosidase 1 (AGLU1)	1,318	0,013
35.2	not assigned.unknown	SGN-U572647	EG553709	ECT11 | ECT11 (evolutionarily conserved C-terminal region 11)	1,317	0,010
35.3	not assigned.disagreeing hits	SGN-U579906	TC243979	CAB4, LHCA4 | LHCA4 (Photosystem I light harvesting complex gene 4); chlorophyll binding	1,317	0,012
35.2	not assigned.unknown	SGN-U578803	Z29099	Unknown	1,306	0,010
35.1	not assigned.no ontology	SGN-U568129	BG734603	Unknown	1,296	0,023
34.13	transport.peptides and oligopeptides	SGN-U568485	DB719807	ATOPT4 | ATOPT4 (oligopeptide transporter 4)	1,294	0,024
35.2	not assigned.unknown	SGN-U572359	TA55818_4081	Unknown	1,290	0,010
21.	redox.dismutases and catalases	SGN-U590926	AW930492	CAT2 | CAT2 (CATALASE 2)	1,278	0,022
28.1.3	DNA.synthesis/chromatin structure.histone	SGN-U581474	TA39023_4081	HIS1-3 | HIS1-3 (HISTONE H1-3)	1,276	0,016
1.	PS.calvin cyle.rubisco interacting	SGN-U577570	AW624572	RCA | RCA (RUBISCO ACTIVASE)	1,275	0,010
35.2	not assigned.unknown	SGN-U577584	Z29112	Unknown	1,275	0,011
8.3	TCA / org. transformation.carbonic anhydrases	SGN-U577458	BG629415	CA1 | CA1 (CARBONIC ANHYDRASE 1)	1,273	0,020
27.	RNA.regulation of transcription.AtSR Transcription Factor family	SGN-U570269	JN566049	calmodulin-binding protein	1,273	0,010
27.	RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family	SGN-U562847	AK247700	CIA2 | CIA2 (CHLOROPLAST IMPORT APPARATUS 2)	1,270	0,010
27.	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U578683	NM_001247670	EDA29, BLH1 | BLH1 (embryo sac development arrest 29)	1,270	0,010

29.	protein.postranslational modification	SGN-U575600	AK247509	SnRK3.16, CIPK1 | CIPK1 (CBL-INTERACTING PROTEIN KINASE 1)	1,266	0,010
13.2	amino acid metabolism.degradation.serine-glycine-cysteine group.glycine	SGN-U580312	DB710078	ATGLDP1 | ATGLDP1 (ARABIDOPSIS THALIANA GLYCINE DECARBOXYLASE P-PROTEIN 1)	1,264	0,010
35.2	not assigned.unknown	SGN-U583033	BI206277	Unknown	1,261	0,010
2.	major CHO metabolism.synthesis.starch.debranching	SGN-U586477	BP907893	ATISA2, ISA2, DBE1, BE2 | ATISA2/BE2/DBE1/ISA2 (DEBRANCHING ENZYME 1)	1,254	0,010
20.1	stress.biotic	SGN-U582492	BF097276	pathogenesis-related thaumatin family protein	1,252	0,034
1.1.2.2	PS.lightreaction.photosystem II.PSII polypeptide subunits	SGN-U584978	BI211136	PSBD | PSII D2 protein	1,238	0,026
35.2	not assigned.unknown	SGN-U590724	ES891593	putative rox1 - nicotiana tabacum	1,237	0,022
35.2	not assigned.unknown	SGN-U592641	BI928729	Unknown	1,235	0,023
35.2	not assigned.unknown	SGN-U590599	TA36485_4081	Unknown	1,227	0,013
35.3	not assigned.disagreeing hits	SGN-U595018	BG129889	RTL2 | RTL2 (RNASE THREE-LIKE PROTEIN 2); double-stranded RNA binding / ribonuclease III	1,227	0,046
35.2	not assigned.unknown	SGN-U577128	TA54822_4081	Unknown	1,223	0,011
29.	protein assembly and cofactor ligation	SGN-U598585	BI423085	YCF5 | hypothetical protein	1,218	0,012
34.3	transport.amino acids	SGN-U571400	BI934999	AAP7 | AAP7 (amino acid permease 7)	1,216	0,010
35.2	not assigned.unknown	SGN-U580051	TA49476_4081	CTP synthase, putative	1,211	0,014
35.3	not assigned.disagreeing hits	SGN-U593417	TA57020_4081	PSBR | PSBR (photosystem II subunit R)	1,211	0,039

35.3	not assigned.disagreeing hits	SGN-U577791	AK321989	CEO, ATP8, CEO1, RCD1 | RCD1 (RADICAL-INDUCED CELL DEATH1)	1,204	0,010
21.	redox.dismutases and catalases	SGN-U578588	NM_001246860	FSD1 | FSD1 (FE SUPEROXIDE DISMUTASE 1)	1,198	0,034
30.1	signalling.in sugar and nutrient physiology	SGN-U566807	BP909550	GLU1, GLS1, GLUS | GLS1/GLU1/GLUS (FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1)	1,197	0,010
15.	metal handling.binding, chelation and storage	SGN-U580570	AK328771	CCH | CCH (COPPER CHAPERONE)	1,196	0,010
26.	misc.alcohol dehydrogenases	SGN-U579777	BT014401	oxidoreductase, zinc-binding dehydrogenase family protein	1,196	0,010
35.2	not assigned.unknown	SGN-U570636	DB720064	Unknown	1,190	0,010
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U564193	AK247211	Unknown	1,189	0,010
35.2	not assigned.unknown	SGN-U572110	BP908751	Unknown	1,189	0,013
35.2	not assigned.unknown	SGN-U578350	AK325709	Unknown	1,189	0,028
35.2	not assigned.unknown	SGN-U604380	DB716135	Unknown	1,188	0,010
17.	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase	SGN-U572039	AK246936	ATLOX2, LOX2 | LOX2 (LIPOXYGENASE 2)	1,186	0,010
2.	major CHO metabolism.degradation.starch.glucan water dikinase	SGN-U564724	NM_001247476	SOP1, SOP, GWD1, GWD, SEX1 | SEX1 (STARCH EXCESS 1)	1,183	0,010
27.	RNA.regulation of transcription.putative transcription regulator	SGN-U572695	DB723409	ATSIZ1, SIZ1 | ATSIZ1/SIZ1	1,183	0,010
9.	mitochondrial electron transport / ATP synthesis.cytochrome c	SGN-U595393	AW623310	CCB382 | cytochrome c biogenesis orf382	1,178	0,011

2.	major CHO metabolism.degradation.sucrose.invertases.vacuolar	SGN-U578195	BI923413	beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar	1,174	0,011
1.1.2.2	PS.lightreaction.photosystem I.PSI polypeptide subunits	SGN-U581403	AK325834	PSAA | Encodes psaA protein comprising the reaction center for photosystem I along with psaB protein	1,170	0,010
26.	misc.gluco-, galacto- and mannosidases	SGN-U578537	NM_001247383	BGAL8 | BGAL8 (BETA-GALACTOSIDASE 8)	1,169	0,010
35.2	not assigned.unknown	SGN-U581205	AI487335	metallothionein-like protein type 2 a (lemt(a))	1,167	0,013
35.2	not assigned.unknown	SGN-U578456	TA36487_4081	Unknown	1,164	0,010
35.3	not assigned.disagreeing hits	SGN-U593247	BG131298	ATP binding / ATP-dependent helicase	1,164	0,012
35.2	not assigned.unknown	SGN-U577133	AK247788	Unknown	1,163	0,014
35.1	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U582282	AK320215	pentatricopeptide (PPR) repeat-containing protein	1,162	0,010
1.1.1.2	PS.lightreaction.photosystem II.PSII polypeptide subunits	SGN-U590407	BG630939	Unknown	1,160	0,011
27.	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U570921	AK328436	SGR5, ATIDD15 | ATIDD15/SGR5 (ARABIDOPSIS THALIANA INDETERMINATE(ID)-DOMAIN 15, SHOOT GRAVITROPISM 5)	1,159	0,030
27.	RNA.transcription	SGN-U583812	AK321664	SIG5, SIGE | SIGE (RNA polymerase sigma subunit E)	1,158	0,016
35.2	not assigned.unknown	SGN-U592773	BG133640	Unknown	1,154	0,024
1.	PS.lightreaction.cytochrome b6/f	SGN-U585402	TA49289_4081	PETA | Encodes cytochrome f apoprotein	1,152	0,010

29.	protein.aa activation	SGN-U570864	BT013813	ATERS, ERS, OVA3 | ATERS/ERS/OVA3 (OVULE ABORTION 3)	1,152	0,010
27.	RNA.regulation of transcription.unclassified	SGN-U572457	TA44053_4081	SEU | SEU (SEUSS)	1,151	0,012
35.2	not assigned.unknown	SGN-U568578	AK322992	Unknown	1,151	0,032
35.2	not assigned.unknown	SGN-U569379	DB711718	Unknown	1,149	0,018
35.2	not assigned.unknown	SGN-U586478	AK247791	Unknown	1,149	0,010
35.2	not assigned.unknown	SGN-U581689	DB727089	Unknown	1,148	0,031
35.2	not assigned.unknown	SGN-U567758	AK323034	Unknown	1,146	0,012
16.2.1.1	secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL	SGN-U577677	AW031670	PAL1 | PAL1 (PHE AMMONIA LYASE 1)	1,141	0,044
20.2.1	stress.abiotic.heat	SGN-U592593	TA36596_4081	ERD8, HSP81-2 | HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8)	1,139	0,026
3.	minor CHO metabolism.callose	SGN-U601297	AW931535	GSL12, ATGSL12 | ATGSL12 (GLUCAN SYNTHASE-LIKE 12); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups	1,136	0,010
27.	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U593540	NM_001247670	EDA29, BLH1 | BLH1 (embryo sac development arrest 29)	1,134	0,010
1.	PS.lightreaction.cyclic electron flow-chlororespiration	SGN-U573171	TA54086_4081	NDHA | NADH dehydrogenase ND1	1,133	0,010
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U565173	BG130129	ATGCN5 | ATGCN5 (Arabidopsis thaliana general control non-repressible 5)	1,133	0,010
35.2	not assigned.unknown	SGN-U597667	AW929637	Unknown	1,133	0,024

35.2	not assigned.unknown	SGN-U588034	BP875995	Unknown	1,133	0,012
26.	misc.plastocyanin-like	SGN-U578700	DB703596	plastocyanin-like domain-containing protein	1,130	0,013
35.3	not assigned.disagreeing hits	SGN-U590297	AW443738	PSBR | PSBR (photosystem II subunit R)	1,129	0,027
29.	protein assembly and cofactor ligation	SGN-U571569	TA49156_4081	YCF2.2 | hypothetical protein	1,125	0,010
31.3	cell.cycle	SGN-U565671	AK247853	CYCT1;4 | CYCT1;4; cyclin-dependent protein kinase	1,121	0,010
14.3	S-assimilation.sulfite redox	SGN-U577417	JQ341913	SIR | SIR (sulfite reductase)	1,119	0,013
26.	misc.gluco-, galacto- and mannosidases	SGN-U581494	NM_001247388	BGAL3 | BGAL3 (beta-galactosidase 3)	1,119	0,010
34.15	transport.potassium	SGN-U567214	AK324971	potassium channel tetramerisation domain-containing protein	1,119	0,010
35.2	not assigned.unknown	SGN-U603515	CD002358	Unknown	1,119	0,013
26.	misc.peroxidases	SGN-U571827	TA35832_4081	XIPOTL1, PEAMT, NMT1 | NMT1 (N-METHYLTRANSFERASE 1)	1,118	0,045
34.12	transport.metal	SGN-U575796	AK326329	ZIP4 | ZIP4 (ZINC TRANSPORTER 4 PRECURSOR)	1,117	0,029
28.1.3	DNA.synthesis/chromatin structure.histone	SGN-U578037	NM_001247056	histone H1, putative	1,114	0,011
35.1	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U589203	DB710188	binding	1,114	0,010
3.	minor CHO metabolism.myo-inositol.InsP Synthases	SGN-U581270	BT013505	inositol-3-phosphate synthase isozyme 2 / myo-inositol-1-phosphate synthase 2 / MI-1-P synthase 2 / IPS 2	1,110	0,014
20.1.7	stress.biotic.PR-proteins	SGN-U564276	AI483711	disease resistance protein (CC-NBS class), putative	1,109	0,010

29.	protein.degradation.AAA type	SGN-U585950	TA56469_4081	AAA-type ATPase family protein	1,109	0,012
17.	hormone metabolism.abscisic acid.synthesis-degradation	SGN-U570287	BI925021	NCED4 | NCED4 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 4)	1,106	0,010
29.	protein.degradation	SGN-U577971	NM_001246933	cytosol aminopeptidase family protein	1,105	0,018
30.2.11	signalling.receptor kinases.leucine rich repeat XI	SGN-U582105	TA54577_4081	QRP1, ER | ER (ERECTA)	1,105	0,011
29.	protein.degradation.ubiquitin	SGN-U583217	DB711779	UBP23 | UBP23 (UBIQUITIN-SPECIFIC PROTEASE 23)	1,103	0,017
35.2	not assigned.unknown	SGN-U576748	TC243415	Unknown	1,103	0,012
30.11	signalling.light	SGN-U568534	AJ002284	HY3, OOP1, PHYB | PHYB (PHYTOCHROME B); G-protein coupled photoreceptor/ signal transducer	1,102	0,012
13.1	amino acid metabolism.synthesis.central amino acid metabolism.GABA.Glutamate decarboxylase	SGN-U578641	NM_001246893	GAD1, GAD | GAD (Glutamate decarboxylase 1)	1,101	0,013
35.2	not assigned.unknown	SGN-U595365	AW217409	Unknown	1,099	0,010
29.	protein.degradation.ubiquitin.E3.HECT	SGN-U585416	AW929155	UPL1 | UPL1 (UBIQUITIN-PROTEIN LIGASE 1)	1,097	0,010
35.2	not assigned.unknown	SGN-U600718	AK322099	Unknown	1,096	0,010
27.	RNA.processing	SGN-U598320	DB720040	polynucleotide adenylyltransferase family protein	1,094	0,034
35.2	not assigned.unknown	SGN-U579730	BP889596	heat shock protein	1,093	0,010
11.	lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	SGN-U586846	TA50166_4081	acetyl-CoA synthetase, putative / acetate-CoA ligase, putative	1,092	0,010

35.2	not assigned.unknown	SGN-U567279	AK325859	Unknown	1,090	0,011
29.	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S12	SGN-U585674	BI208864	RPSL2 | ribosomal protein L2	1,089	0,010
26.	misc.acid and other phosphatases	SGN-U569473	BT013277	phosphatidic acid phosphatase family protein / PAP2 family protein	1,086	0,020
35.1	not assigned.no ontology	SGN-U595253	BE353524	toprim domain-containing protein	1,084	0,010
35.2	not assigned.unknown	SGN-U568215	BI931971	Unknown	1,084	0,023
29.	protein.postranslational modification	SGN-U586247	GO374069	shaggy-related protein kinase delta / ASK-delta / ASK-dzeta (ASK4)	1,082	0,010
17.	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U581774	BI934113	Unknown	1,081	0,037
27.	RNA.regulation of transcription.SET-domain transcriptional regulator family	SGN-U576415	DB724330	SET domain-containing protein	1,080	0,010
26.	misc.acid and other phosphatases	SGN-U572370	AK323467	ATPAP26, PAP26 | ATPAP26/PAP26 (purple acid phosphatase 26)	1,079	0,012
27.	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	SGN-U564759	AK247076	basic helix-loop-helix (bHLH) family protein	1,079	0,010
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U570680	AK325032	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	1,073	0,010
35.2	not assigned.unknown	SGN-U578798	AK325905	Unknown	1,070	0,010
31.1	cell.organisation	SGN-U572552	BE433030	VLN2 | VLN2 (VILLIN 2)	1,069	0,013
35.3	not assigned.disagreeing hits	SGN-U569795	AK246954	ATHB13 | ATHB13; DNA binding / transcription factor	1,067	0,010
35.2	not assigned.unknown	SGN-U568321	AW036282	Unknown	1,065	0,027

1.	PS.calvin cyle.transketolase	SGN-U577918	DB685806	transketolase, putative	1,063	0,010
30.6	signalling.MAP kinases	SGN-U600372	NM_001247850	MAP3KE1, MAPKKK7 | MAPKKK7 (MAP3K EPSILON PROTEIN KINASE)	1,063	0,010
33.99	development.unspecified	SGN-U576575	DB714870	OCP11, AGO4 | AGO4 (ARGONAUTE 4)	1,062	0,012
27.	RNA.regulation of transcription.ARF, Auxin Response Factor family	SGN-U601907	NM_001247867	ARF16 | ARF16 (AUXIN RESPONSE FACTOR 16)	1,059	0,010
30.6	signalling.MAP kinases	SGN-U585828	BT012818	MPK16 | MPK16 (mitogen-activated protein kinase 16)	1,056	0,010
29.	protein.degradation	SGN-U565971	TA37671_4081	ATPREP1, ATZNMP | ATPREP1/ATZNMP (PRESEQUENCE PROTEASE 1)	1,053	0,010
34.2	transporter.sugars	SGN-U584596	DB684285	sugar transporter, putative	1,053	0,010
35.2	not assigned.unknown	SGN-U582638	AK326747	Unknown	1,052	0,031
29.	protein.aa activation	SGN-U575488	TA42394_4081	EDD, EDD1 | EDD1 (EMBRYO-DEFECTIVE-DEVELOPMENT 1)	1,051	0,010
30.5	signalling.G-proteins	SGN-U575315	AK324564	ATROPGEF14, ROPGEF14 | ATROPGEF14/ROPGEF14 (KINASE PARTNER PROTEIN-LIKE)	1,050	0,028
35.2	not assigned.unknown	SGN-U578752	AK320878	Unknown	1,049	0,016
35.2	not assigned.unknown	SGN-U583088	AK320855	Unknown	1,048	0,010
28.1.3	DNA.synthesis/chromatin structure.histone	SGN-U578275	NM_001247460	HIS1-3 | HIS1-3 (HISTONE H1-3)	1,047	0,024
35.1	not assigned.no ontology.epsin N-terminal homology (ENTH) domain-containing protein	SGN-U586146	BG126244	epsin N-terminal homology (ENTH) domain-containing protein	1,045	0,010
29.	protein.postranslational modification	SGN-U599017	BG126855	protein kinase family protein	1,044	0,010

35.2	not assigned.unknown	SGN-U601405	BP876420	Unknown	1,042	0,018
29.	protein.postranslational modification	SGN-U563240	NM_001247285	NPH1, JK224, RPT1, PHOT1 | PHOT1 (phototropin 1)	1,041	0,010
35.3	not assigned.disagreeing hits	SGN-U575548	BP908868	Unknown	1,040	0,017
35.1	not assigned.no ontology.ABC1 family protein	SGN-U573869	AK326082	ABC1 family protein	1,039	0,010
34.13	transport.peptides and oligopeptides	SGN-U565029	BT012745	YSL3 | YSL3 (YELLOW STRIPE LIKE 3)	1,038	0,036
29.	protein.postranslational modification	SGN-U588657	NM_001247360	NPL1, PHOT2 | PHOT2 (NON PHOTOTROPIC HYPOCOTYL 1-LIKE)	1,037	0,010
35.1	not assigned.no ontology	SGN-U574041	AK247024	dentin sialophosphoprotein-related	1,037	0,012
35.3	not assigned.disagreeing hits	SGN-U590449	BG127002	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,037	0,010
4.	glycolysis.UGPase	SGN-U579867	AK322946	UGP | UGP (UDP-glucose pyrophosphorylase)	1,036	0,010
29.	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S7	SGN-U587845	AW650353	RPS7.1, RPS7 | encodes a chloroplast ribosomal protein S7, a constituent of the small subunit of the ribosomal complex	1,036	0,014
35.2	not assigned.unknown	SGN-U577489	BG626289	Unknown	1,036	0,021
27.	RNA.transcription	SGN-U572563	AW218409	REV1 | REV1 (Reversionless 1); damaged DNA binding / magnesium ion binding / nucleotidyltransferase	1,035	0,010
30.2	signalling.receptor kinases.leucine rich repeat II	SGN-U604395	DB697797	leucine-rich repeat transmembrane protein kinase, putative	1,033	0,012
31.2	cell.division	SGN-U563856	DB721790	EMB2763 | EMB2763 (EMBRYO DEFECTIVE 2763)	1,031	0,010
35.2	not assigned.unknown	SGN-U571188	DB681038	EX1 | EX1 (EXECUTER1)	1,030	0,010

35.2	not assigned.unknown	SGN-U569799	AK324103	Unknown	1,029	0,013
19.10	tetrapyrrole synthesis.magnesium chelatase	SGN-U584293	TA37910_4081	CCH, CHLH, CCH1, GUN5 | GUN5 (GENOMES UNCOUPLED 5)	1,028	0,010
35.2	not assigned.unknown	SGN-U599535	BG123732	Unknown	1,026	0,014
35.2	not assigned.unknown	SGN-U564677	TA51695_4081	Unknown	1,025	0,010
35.2	not assigned.unknown	SGN-U572070	AI895243	drought-responsive family protein	1,025	0,016
28.1	DNA.synthesis/chromatin structure	SGN-U572198	NM_001247866	inositol polyphosphate 5-phosphatase	1,022	0,013
35.1	not assigned.no ontology	SGN-U578189	TA37116_4081	leucine-rich repeat family protein	1,022	0,022
35.3	not assigned.disagreeing hits	SGN-U569012	NM_001247398	scarecrow-like transcription factor 8 (SCL8)	1,021	0,014
17.	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U581437	AK326294	Unknown	1,020	0,011
30.1	signalling.in sugar and nutrient physiology	SGN-U573931	DB713791	GLU1, GLS1, GLUS | GLS1/GLU1/GLUS (FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1)	1,020	0,010
35.2	not assigned.unknown	SGN-U576675	AK327988	Unknown	1,020	0,010
23.	nucleotide metabolism.salvage.phosphoribosyltransferases.aprt	SGN-U580093	TA36378_4081	APT1, ATAPT1, APRT | APT1	1,019	0,022
35.2	not assigned.unknown	SGN-U601464	DB718443	Unknown	1,019	0,035
35.2	not assigned.unknown	SGN-U584633	AK325869	Unknown	1,018	0,018
29.	protein.degradation	SGN-U565394	TA41738_4081	metalloendopeptidase	1,017	0,012

29.	protein.degradation	SGN-U562601	TA37220_4081	peptidase M1 family protein	1,017	0,012
1.	PS.lightreaction.cyclic electron flow-chlororespiration	SGN-U603513	AW647925	NDHE | NADH dehydrogenase ND4L	1,016	0,013
17.	hormone metabolism.brassinosteroid.synthesis-degradation.sterols.DWF1	SGN-U578468		DIM, EVE1, DW1, DIM1, CBB1, DWF1 | DWF1 (DIMINUTO 1)	1,015	0,029
29.	protein.degradation.serine protease	SGN-U583067	TA41865_4081	SCPL10 | SCPL10 (serine carboxypeptidase-like 10)	1,015	0,010
35.1	not assigned.no ontology	SGN-U567593	DB691630	Met-10+ like family protein	1,015	0,011
1.	PS.lightreaction.NADH DH	SGN-U602959	AW033442	NDHG | NADH dehydrogenase ND6	1,013	0,010
35.2	not assigned.unknown	SGN-U564511	DB711248	Unknown	1,013	0,014
35.3	not assigned.disagreeing hits	SGN-U593210	AF123256	17.8 kDa class I heat shock protein (HSP17.8-CI)	1,013	0,044
35.3	not assigned.disagreeing hits	SGN-U577253	AI773247	DRT112 | DRT112 (DNA-damage-repair/toleration protein 112); copper ion binding / electron carrier	1,013	0,023
35.2	not assigned.unknown	SGN-U576132	AK324400	Similar to amine oxidase/ copper ion binding	1,012	0,013
21.	redox.dismutases and catalases	SGN-U578839	NM_001247898	CAT2 | CAT2 (CATALASE 2)	1,011	0,016
34.	transport.p- and v-ATPases	SGN-U574344	DB715393	PMA2, AHA2 | AHA2 (Arabidopsis H(+)-ATPase 2)	1,011	0,010
30.11	signalling.light	SGN-U570880	AK320687	binding / catalytic/ coenzyme binding	1,010	0,011
31.1	cell.organisation	SGN-U570838	BT013746	cytoplasmic linker protein-related	1,010	0,010

34.9	transport.metabolite transporters at the mitochondrial membrane	SGN-U579511	AW030370	mitochondrial substrate carrier family protein	1,008	0,030
35.3	not assigned.disagreeing hits	SGN-U597024	BE450642	polynucleotide adenylyltransferase/ protein binding	1,008	0,017
4.	glycolysis.phosphoglycerate mutase	SGN-U580730	TA36719_4081	2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative	1,007	0,011
35.1	not assigned.no ontology	SGN-U600379	AK327901	hydrolase, alpha/beta fold family protein	1,007	0,016
29.	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S4	SGN-U563384	AJ785218	RPS4 | Chloroplast encoded ribosomal protein S4	1,005	0,010
29.	protein.folding	SGN-U581439	TA35711_4081	Chaperonin, putative	1,004	0,013
33.99	development.unspecified	SGN-U567378	AK327271	senescence-associated family protein	1,004	0,019
35.1	not assigned.no ontology.ABC1 family protein	SGN-U579429	BG130241	ATATH13 | ATATH13 (ABC2 homolog 13)	1,004	0,014
35.2	not assigned.unknown	SGN-U582659	TA49256_4081	HB-6 | homeodomain protein (BELLRINGER)	1,004	0,010
35.3	not assigned.disagreeing hits	SGN-U590306	GO374731	25 kda protein dehydrin	1,004	0,016
35.2	not assigned.unknown	SGN-U572208	BP909791	EMB2754 | EMB2754 (EMBRYO DEFECTIVE 2754)	1,001	0,033
11.	lipid metabolism."exotics" (steroids, squalene etc).sphingolipids.ceramidase	SGN-U569677	AK325960	ceramidase family protein	1,000	0,012
35.2	not assigned.unknown	SGN-U599354	BP886805	EMB2754 | EMB2754 (EMBRYO DEFECTIVE 2754); binding / small GTPase regulator	1,000	0,014

Table 2. List of down-regulated genes genes (log2 sub-/optimal T≤−1and q-value<0.05) deteced only in the leaves of the grafted ‘Kommeet’ plants onto ‘Moneymaker’ (R/S:MM/KO) under sub-optimal root T stress.

Bin Code	BinName	SGN	NCBI	description	MM/KO Log FC	adj.P.Val
21.	redox.glutaredoxins	SGN-U597671	AK320876	glutaredoxin family protein	-2,058	0,010
34.21	transport.calcium	SGN-U564412	AK322020	ATHCX1, CAX1-LIKE, ATCAX3, CAX3 | CAX3 (cation exchanger 3)	-1,843	0,010
35.3	not assigned.disagreeing hits	SGN-U564449	NM_001247444	JAZ3, JAI3, TIFY6B | JAI3/JAZ3/TIFY6B (JASMONATE-ZIM-DOMAIN PROTEIN 3)	-1,811	0,010
10.7	cell wall.modification	SGN-U579445	NM_001247543	XTH23, XTR6 | XTR6 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6)	-1,658	0,016
35.2	not assigned.unknown	SGN-U577683	AK321000	Unknown	-1,656	0,011
27.	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U572081	AK321000	CRF3 | CRF3 (CYTOKININ RESPONSE FACTOR 3)	-1,639	0,011
4.14	glycolysis.PEPCase	SGN-U576252	GO372583	ATPPC1 | ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1)	-1,580	0,013
35.2	not assigned.unknown	SGN-U564446	NM_001247444	JAZ3, JAI3, TIFY6B | JAI3/JAZ3/TIFY6B (JASMONATE-ZIM-DOMAIN PROTEIN 3)	-1,573	0,010
21.	redox.glutaredoxins	SGN-U594589	AK323900	glutaredoxin family protein	-1,570	0,012
1.	PS.calvin cyle.rubisco small subunit	SGN-U578258	AI772989	RBCS1A | RBCS1A; ribulose-bisphosphate carboxylase	-1,516	0,027
29.	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L2	SGN-U581377	NM_001247186	60S ribosomal protein L8 (RPL8C)	-1,421	0,010
34.21	transport.calcium	SGN-U575138	AK322020	ATHCX1, CAX1-LIKE, ATCAX3, CAX3 | CAX3 (cation exchanger 3)	-1,399	0,010
35.2	not assigned.unknown	SGN-U582002	AK326369	Unknown	-1,383	0,010

34.22	transport.cyclic nucleotide or calcium regulated channels	SGN-U575807	AK319969	CNGC4, HLM1, DND2, ATCNGC4 | ATCNGC4 (DEFENSE, NO DEATH 2)	-1,360	0,010
10.7	cell wall.modification	SGN-U579684	NM_001247543	XTH23, XTR6 | XTR6 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6)	-1,349	0,010
27.	RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family	SGN-U566244	TA48654_4081	LBD37 | LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37)	-1,326	0,010
27.	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U576149	NM_001246920	DNA binding / transcription factor	-1,319	0,013
27.	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U572337	DB710333	ZAT12, RHL41 | RHL41 (RESPONSIVE TO HIGH LIGHT 41)	-1,313	0,019
10.7	cell wall.modification	SGN-U587048	AB036338	XTH27, ATXTH27, EXGT-A3 | EXGT-A3 (endo-xyloglucan transferase A3)	-1,309	0,014
35.2	not assigned.unknown	SGN-U564053	TA41825_4081	TMAC2 (TWO OR MORE ABRES-CONTAINING GENE 2)	-1,307	0,010
11.	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U591148	AK326063	FAD2 | FAD2 (FATTY ACID DESATURASE 2)	-1,280	0,010
29.	protein.targeting.secretory pathway.unspecified	SGN-U578714	AK321235	protein transport protein sec61, putative	-1,278	0,010
10.7	cell wall.modification	SGN-U577928	NM_001247549	xyloglucan:xyloglucosyl transferase	-1,270	0,012
35.3	not assigned.disagreeing hits	SGN-U578366	TA36834_4081	BTI1 | BTI1 (VIRB2-INTERACTING PROTEIN 1)	-1,267	0,046
29.	protein.targeting.mitochondria	SGN-U563007	ES895947	UNE3, PGA2, TATC, APG2 | APG2 (ALBINO AND PALE GREEN 2)	-1,252	0,011
35.1	not assigned.no ontology	SGN-U579623	BT012752	endomembrane protein 70, putative	-1,252	0,010

10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U585891	TA38690_4081	CESA3, IXR1, ATCESA3, ATH-B, CEV1 | CESA3 (CELLULOSE SYNTHASE 3)	-1,245	0,012
26.	misc.GDSL-motif lipase	SGN-U585129	AK324959	GDSL-motif lipase/hydrolase family protein	-1,243	0,014
35.3	not assigned.disagreeing hits	SGN-U564186	NM_001247465	PEPCK2, PPCK2 | PPCK2 (PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE 2)	-1,235	0,018
10.7	cell wall.modification	SGN-U580011	GO373736	xyloglucan:xyloglucosyl transferase	-1,230	0,010
10.1	cell wall.precursor synthesis.GMD	SGN-U574104	AK320665	GMD1 | GMD1 (GDP-D-MANNOSE 4,6-DEHYDRATASE 1)	-1,229	0,010
29.	protein.synthesis.elongation	SGN-U580418	NM_001247106	elongation factor 1-alpha / EF-1-alpha	-1,226	0,013
35.2	not assigned.unknown	SGN-U595908	AK326369	Unknown	-1,223	0,012
27.	RNA.regulation of transcription.TCP transcription factor family	SGN-U562794	NM_001247037	TCP family transcription factor, putative	-1,220	0,011
35.2	not assigned.unknown	SGN-U568469	AK327411	Unknown	-1,216	0,010
29.	protein.postranslational modification	SGN-U576520	TA42638_4081	phosphoprotein phosphatase	-1,209	0,010
17.	hormone metabolism.auxin.synthesis-degradation	SGN-U575074	AK322390	ILL6 | ILL6 (IAA-leucine resistant (ILR)-like gene 6)	-1,206	0,029
19.30	tetrapyrrole synthesis.urogen III methylase	SGN-U572308	AK247184	UPM1 | UPM1 (UROPHORPHYRIN METHYLASE 1)	-1,196	0,012
35.1	not assigned.no ontology	SGN-U564290	NM_001247310	CPI1 | CPI1 (CYCLOPROPYL ISOMERASE)	-1,184	0,016
29.	protein.synthesis.elongation	SGN-U578831	BG130184	elongation factor 1-alpha / EF-1-alpha	-1,180	0,013

34.11	transport.NDP-sugars at the ER	SGN-U583061	AK321118	ATUTR3, UTR3 | ATUTR3/UTR3 (UDP-GALACTOSE TRANSPORTER 3)	-1,179	0,010
11.	lipid metabolism."exotics" (steroids, squalene etc).methylsterol monooxygenase	SGN-U572947	AK247484	ATSMO1, ATSMO1-1, SMO1-1 | SMO1-1 (STEROL-4ALPHA-METHYL OXIDASE 1-1)	-1,176	0,047
34.19.4	transport.Major Intrinsic Proteins.TIP	SGN-U581024	NM_001247174	TIP1;1, GAMMA-TIP1, GAMMA-TIP | GAMMA-TIP (Tonoplast intrinsic protein (TIP) gamma)	-1,176	0,010
35.1	not assigned.no ontology	SGN-U571363	AK322844	ACR4 | ACR4 (ACT REPEAT 4)	-1,175	0,014
11.	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U591547	AK326063	FAD2 | FAD2 (FATTY ACID DESATURASE 2)	-1,173	0,013
1.	PS.calvin cycle.TPI	SGN-U581594	AK319602	TIM | TIM (TRIOSEPHOSPHATE ISOMERASE)	-1,172	0,016
35.3	not assigned.disagreeing hits	SGN-U581131	NM_001246846	lipid-associated family protein	-1,171	0,016
34.99	transport.misc	SGN-U579304	AK328220	permease-related	-1,159	0,012
22.	polyamine metabolism.synthesis.spermidine synthase	SGN-U581525	NM_001247478	SPMS, SPDS3 | SPDS3 (SPERMIDINE SYNTHASE 3)	-1,155	0,012
29.	protein.degradation.ubiquitin.proteasom	SGN-U583931	AK327752	26S proteasome regulatory subunit, putative (RPN9)	-1,155	0,014
34.21	transport.calcium	SGN-U564776	DB700370	ATHCX1, CAX1-LIKE, ATCAX3, CAX3 | CAX3 (cation exchanger 3)	-1,154	0,010
35.2	not assigned.unknown	SGN-U575759	AK247685	Unknown	-1,140	0,012
35.3	not assigned.disagreeing hits	SGN-U576855	AK327505	cinnamoyl-CoA reductase-related	-1,127	0,036
20.1	stress.biotic	SGN-U566861	BG130936	acidic endochitinase (CHIB1)	-1,126	0,017
13.1	amino acid metabolism.synthesis.aspartate family.methionine	SGN-U577720	TA36189_4081	ATMETS, ATMS1, ATCIMS | ATCIMS (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)	-1,124	0,014
35.2	not assigned.unknown	SGN-U581731	AK319718	Unknown	-1,121	0,010
10.5.1	cell wall.cell wall proteins.AGPs	SGN-U571367	AK325576	FLA1 | FLA1	-1,117	0,018

35.1	not assigned.no ontology	SGN-U592802	GO375653	Identical to Protein FBL4 (FBL4)	-1,117	0,010
26.	misc.plastocyanin-like	SGN-U586153	GO372726	plastocyanin-like domain-containing protein	-1,116	0,014
29.	protein.synthesis.misc ribososomal protein	SGN-U579674	TA36331_4081	40S ribosomal protein S2 (RPS2D)	-1,111	0,012
27.	RNA.regulation of transcription.WRKY domain transcription factor family	SGN-U564691	AK323971	ATWRKY53, WRKY53 | WRKY53 (WRKY DNA-binding protein 53)	-1,106	0,010
35.1	not assigned.no ontology	SGN-U585005	AK322296	ATHST | ATHST; prenyltransferase	-1,102	0,010
26.	misc.GDSL-motif lipase	SGN-U566206	AK319817	lipase, putative	-1,099	0,011
27.	RNA.processing	SGN-U576432	BW685805	ATFIB2, FIB2 | FIB2 (FIBRILLARIN 2)	-1,097	0,017
26.	misc.GDSL-motif lipase	SGN-U588843	AK324959	GDSL-motif lipase/hydrolase family protein	-1,095	0,014
34.3	transport.amino acids	SGN-U586631	BP896391	ATAVP3, AVP-3, AVP1 | AVP1 (vacuolar-type H+-pumping pyrophosphatase 1)	-1,094	0,015
35.2	not assigned.unknown	SGN-U569014	AK324909	Unknown	-1,093	0,011
34.18	transport.unspecified cations	SGN-U577978	AK326152	sodium symporter-related	-1,091	0,010
29.	protein.synthesis.elongation	SGN-U570252	AK322741	PBS lyase HEAT-like repeat-containing protein	-1,085	0,010
26.	misc.oxidases - copper, flavone etc.	SGN-U573441	GO376156	copper amine oxidase, putative	-1,084	0,024
25	C1-metabolism	SGN-U580665	AK319810	SHM4 | SHM4 (SERINE HYDROXYMETHYLTRANSFERASE 4)	-1,083	0,012
34.3	transport.amino acids	SGN-U583643	AK324639	amino acid transporter family protein	-1,082	0,010
34.3	transport.amino acids	SGN-U580565	NM_001247057	ATPROT2, ProT2 | ProT2 (PROLINE TRANSPORTER 2)	-1,079	0,019
29.	protein.degradation.ubiquitin.E3.RING	SGN-U582422	AW216567	zinc finger (C3HC4-type RING finger) family protein	-1,069	0,016
35.2	not assigned.unknown	SGN-U583850	AW625371	Unknown	-1,068	0,026
22.	Polyaminemetabolism.synthesis.SAM decarboxylase	SGN-U581249	BT013882	adenosylmethionine decarboxylase family protein	-1,064	0,018
35.1	not assigned.no ontology	SGN-U583406	AK328397	nucleolar essential protein-related	-1,063	0,013

35.1	not assigned.no ontology	SGN-U567710	AJ784534	EMB2734 | EMB2734 (EMBRYO DEFECTIVE 2734)	-1,063	0,014
26.	misc.cytochrome P450	SGN-U573215	TA36292_4081	AR2, ATR2 | ATR2 (ARABIDOPSIS P450 REDUCTASE 2)	-1,061	0,026
27.	RNA.regulation of transcription.unclassified	SGN-U584308	BT012902	ATRBP47C | ATRBP47C; RNA binding	-1,060	0,022
12.1.1	N-metabolism.nitrate metabolism.NR	SGN-U579543	TA36941_4081	B29, NIA2-1, CHL3, NR, NR2, NIA2 | NIA2 (NITRATE REDUCTASE 2)	-1,059	0,025
35.2	not assigned.unknown	SGN-U568967	TA55191_4081	!LOW SCORING HIT! SGN-U568967: Tomato 200607#2 [4 ESTs aligned]	-1,058	0,012
35.2	not assigned.unknown	SGN-U574470	TA53116_4081	Unknown	-1,055	0,010
29.	protein.postranslational modification	SGN-U576543	TA53431_4081	MAPKKK21 | MAPKKK21; ATP binding / protein kinase	-1,054	0,040
34.19.4	transport.Major Intrinsic Proteins.PIP	SGN-U590165	HQ684021	PIP3A, PIP2;7, SIMIP, PIP3 | PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3)	-1,054	0,010
35.2	not assigned.unknown	SGN-U594649	TA42932_4081	Unknown	-1,052	0,042
35.1	not assigned.no ontology	SGN-U604003	BP910574	oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1,051	0,013
26.	misc.plastocyanin-like	SGN-U595621	BP901095	plastocyanin-like domain-containing protein	-1,048	0,010
4.13	glycolysis.PK	SGN-U566980	TA38607_4081	transketolase family protein	-1,043	0,011
29.	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S4	SGN-U579513	AI781614	40S ribosomal protein S4 (RPS4D)	-1,041	0,018
34.	transport.p- and v-ATPases	SGN-U572299	AK320905	ATVHA-C, DET3 | DET3 (DE-ETIOLATED 3)	-1,041	0,012
35.2	not assigned.unknown	SGN-U570831	DV104791	Unknown	-1,040	0,010

29.	protein.postranslational modification	SGN-U585750	AK247687	protein phosphatase 2C-related / PP2C-related	-1,039	0,021
10.2	cell wall.precursor synthesis.UGD	SGN-U581969	AI490652	UDP-glucose 6-dehydrogenase, putative	-1,038	0,012
35.2	not assigned.unknown	SGN-U577484	NM_001247630	Unknown	-1,037	0,012
26.	misc.short chain dehydrogenase/reductase (SDR)	SGN-U583958	TA55883_4081	SIS4, GIN1, SDR1, ISI4, SRE1, ATABA2, ABA2 | ABA2 (ABA DEFICIENT 2)	-1,036	0,010
35.3	not assigned.disagreeing hits	SGN-U592107	NM_001247584	UBC9 | UBC9 (UBIQUITIN CONJUGATING ENZYME 9)	-1,031	0,010
35.1	not assigned.no ontology	SGN-U571505	AK320133	RNA recognition motif (RRM)-containing protein	-1,027	0,010
35.3	not assigned.disagreeing hits	SGN-U580639	TA44716_4081	Unknown	-1,026	0,012
12.1.1	N-metabolism.nitrate metabolism.NR	SGN-U583893	TA38880_4081	CBR1, ATCBR | ATCBR (NADH:CYTOCHROME B5 REDUCTASE 1)	-1,023	0,012
33.99	development.unspecified	SGN-U582104	AK326238	transducin family protein / WD-40 repeat family protein	-1,023	0,012
21.	redox.thioredoxin	SGN-U567134	AK324563	ATPDIL2-2 | ATPDIL2-2 (PDI-LIKE 2-2)	-1,022	0,010
30.2.99	signalling.receptor kinases.misc	SGN-U577087	AI776077	protein kinase, putative	-1,021	0,011
35.3	not assigned.disagreeing hits	SGN-U587075	BG713779	60S ribosomal protein L15 (RPL15A)	-1,021	0,012
30.2.17	signalling.receptor kinases.DUF 26	SGN-U566482	AI782826	B120 | B120; protein kinase/ sugar binding	-1,020	0,010
23.	nucleotide metabolism .phosphotransfer and pyrophosphatases.nucleoside diphosphate kinase	SGN-U569028	AI771616	NDPK3 | NDPK3 (NUCLEOSIDE DIPHOSPHATE KINASE 3)	-1,019	0,011
34.18	transport.unspecified cations	SGN-U580060	AK320352	bile acid:sodium symporter family protein	-1,016	0,015
34.19.4	transport.Major Intrinsic Proteins.PIP	SGN-U577606	AK323928	UBQ11 | UBQ11 (UBIQUITIN 11)	-1,015	0,015

17.	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U567495	NM_001247110	Unknown	-1,014	0,039
35.1	not assigned.no ontology	SGN-U583796	AK319425	hydrolase, alpha/beta fold family protein	-1,013	0,010
35.2	not assigned.unknown	SGN-U581901	AK319306	Unknown	-1,013	0,011
10.5.1	cell wall.cell wall proteins.RGP	SGN-U577150	ES896820	ATRGP1, ATRGP, RGP1 | RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1)	-1,011	0,010
31.4	cell.vesicle transport	SGN-U564688	AW221804	SEC8 | SEC8 (secretion 8)	-1,010	0,010
10.7	cell wall.modification	SGN-U585093	AJ560647	EXP15, ATEXP15, ATHEXP ALPHA 1.3, ATEXPA15 | ATEXPA15 (ARABIDOPSIS THALIANA EXPANSIN A15)	-1,009	0,029
35.2	not assigned.unknown	SGN-U569643	AK324533	Unknown	-1,007	0,010
35.2	not assigned.unknown	SGN-U568388	AK322282	Unknown	-1,006	0,019
33.99	development.unspecified	SGN-U563227	AK324295	MSI02, NFC02, NFC2, MSI2 | MSI2 (NUCLEOSOME/CHROMATIN ASSEMBLY FACTOR GROUP C 2)	-1,005	0,010
29.	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S4	SGN-U581547	BI921785	40S ribosomal protein S4 (RPS4D)	-1,004	0,016
34.2	transporter.sugars	SGN-U589401	GO374014	porin, putative	-1,004	0,014
35.3	not assigned.disagreeing hits	SGN-U564092	BT014571	ACR4 | ACR4 (ACT REPEAT 4)	-1,004	0,010
34.22	transport.cyclic nucleotide or calcium regulated channels	SGN-U565661	AW037755	CNGC4, HLM1, DND2, ATCNGC4 | ATCNGC4 (DEFENSE, NO DEATH 2)	-1,001	0,010
30.5	signalling.G-proteins	SGN-U582604	NM_001246952	ATARCA | ATARCA (Arabidopsis thaliana Homolog of the Tobacco ArcA)	-1,001	0,014

Table 3. List of genes whose expression level in the roots of the grafted ‘Kommeet’ plants onto ‘LA 1777’ (R/S: LA/KO) is significantly ($p < 0.05$) different from that in those grafted onto ‘Moneymaker’ (R/S: MM/KO) under sub-optimal root T stress.

Bin Code	BinName	SGN	NCBI	description	LA/KO LogFC	MM/KO Log FC	diff logFC
1.1.1.2	PS.lightreaction.photosystem II.PSII polypeptide subunits	SGN-U565346	TA39938_4081	PSBA | Encodes chlorophyll binding protein D1, a part of the photosystem II reaction center core	1,030	1,045	-0,015
1.2.2	PS.photorespiration.glycolate oxydase	SGN-U579320	BI925845	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative	-1,781	-1,245	-0,536
1.2.2	PS.photorespiration.glycolate oxydase	SGN-U579320	AW932681	glycolate oxidase	-1,812	-1,322	-0,490
1.2.2	PS.photorespiration.glycolate oxydase	SGN-U578941	TA36633_4081	glycolate oxidase X92888	-1,225	-1,687	0,462
1.2.2	PS.photorespiration.glycolate oxydase	SGN-U578941	X92888	glycolate oxidase X92888	-1,107	-1,825	0,718
1.3.7	PS.calvin cyle.FBPase	SGN-U579273	AK319637	fructose-1,6-bisphosphatase	-1,845	-2,463	0,618
2.1.1.1	major CHO metabolism.synthesis.sucrose.SPS	SGN-U574712	TA56892_4081	Sucrose phosphate synthase	-1,033	1,274	-2,306
2.2.1.3.2	major CHO metabolism.degradation.sucrose.invertases.cell wall	SGN-U584136	BI921788	ATCWINV2 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 2)	1,395	1,353	0,043
3.2.3	minor CHO metabolism.trehalose.potential TPS/TPP	SGN-U576715	GO376462	TPS9, ATTPS9 | ATTPS9 (Arabidopsis thaliana trehalose-phosphatase/synthase 9)	-1,120	-1,353	0,233
3.4.4	minor CHO metabolism.myo-inositol.myo inositol oxygenases	SGN-U565448	NM_001247664	MIOX4 | MIOX4 (MYO-INOSITOL OXYGENASE 4)	1,379	1,049	0,330
4.12	glycolysis.enolase	SGN-U578193	TA36709_4081	LOS2 | LOS2 (Low expression of osmotically responsive genes 1)	1,472	1,534	-0,062
4.12	glycolysis.enolase	SGN-U593305	TA36709_4081	LOS2 | LOS2 (Low expression of osmotically responsive genes 1)	1,653	1,605	0,048
4.13	glycolysis.PK	SGN-U577646	BT014317	PKP3 | PKP3 (PLASTIDIAL PYRUVATE KINASE 3)	1,236	1,345	-0,108

5.3	fermentation.ADH	SGN-U579420	AW224326	alcohol dehydrogenase-2	-2,529	-1,154	-1,375
5.3	fermentation.ADH	SGN-U579632	AW221691	ADH, ATADH, ADH1 | ADH1 (ALCOHOL DEHYDROGENASE 1)	-2,332	-1,212	-1,119
6.2	gluconeogenese/ glyoxylate cycle.malate synthase	SGN-U573204	TA37255_4081	MLS | MLS (MALATE SYNTHASE)	1,471	1,213	0,257
6.4	gluconeogenese/ glyoxylate cycle.PEPCK	SGN-U591990	NM_001247150	PCK2, PEPCK | PCK2/PEPCK (PHOSPHOENOLPYRUVATE CARBOXYKINASE 2)	-1,101	-1,057	-0,044
6.9	gluconeogenese/ glyoxylate cycle.isocitrate lyase	SGN-U572847	AW649647	isocitrate lyase, putative	-2,025	-2,181	0,156
6.9	gluconeogenese/ glyoxylate cycle.isocitrate lyase	SGN-U589721	NM_001246949	isocitrate lyase, putative	-1,532	-2,116	0,585
7.1.1	OPP.oxidative PP.G6PD	SGN-U570293	DB721420	G6PD1 | G6PD1 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 1)	-1,159	-1,857	0,697
10.1.2	cell wall.precursor synthesis.UGE	SGN-U564745		UGE1 | UGE1 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 1)	-1,280	-1,625	0,345
10.1.2	cell wall.precursor synthesis.UGE	SGN-U583214	AW649490	UGE2 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 2	1,634	1,270	0,364
10.1.2	cell wall.precursor synthesis.UGE	SGN-U564745	TA38185_4081	UDP-glucose 4-epimerase	-1,135	-1,614	0,479
10.2	cell wall.cellulose synthesis	SGN-U571201	AK320053	CSLA02, ATCSLA2, ATCSLA02 | ATCSLA02 (Cellulose synthase-like A2)	1,920	1,163	0,758
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U565184	AK320713	CSLG3, ATCSLG3 | ATCSLG3 (Cellulose synthase-like G3)	1,361	1,457	-0,096
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U565637	TA37439_4081	ATCSLD3, CSLD3 | CSLD3 (CELLULOSE SYNTHASE-LIKE 3)	1,228	1,288	-0,059
10.6.1	cell wall.degradation.cellulases and beta -1,4-glucanases	SGN-U583947	AK326061	glycosyl hydrolase family 3 protein	1,162	1,115	0,047
10.6.1	cell wall.degradation.cellulases and beta -1,4-glucanases	SGN-U582965	AK326061	glycosyl hydrolase family 3 protein	1,297	1,079	0,218
10.6.1	cell wall.degradation.cellulases and beta -1,4-glucanases	SGN-U582965	AW623119	glycosyl hydrolase family 3 protein	1,509	1,168	0,341
10.6.2	cell wall.degradation.mannan-xylose-arabinose-fucose	SGN-U567221	AK320902	(1-4)-beta-mannan endohydrolase, putative	-2,039	-2,217	0,179
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U572999	AW092292	polygalacturonase, putative / pectinase, putative	-1,710	-1,335	-0,375

10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U566288	NM_001247271	Sglycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	-1,186	-1,232	0,046
10.7	cell wall.modification	SGN-U563017	NM_001247430	EXP11, ATEXP11, ATHEXP ALPHA 1.14, ATEXPA11 | ATEXPA11 (ARABIDOPSIS THALIANA EXPANSIN A11)	1,420	1,181	0,238
10.7	cell wall.modification	SGN-U580110	NM_001247952	ATEXP4, ATHEXP ALPHA 1.6, ATEXPA4 | ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	-1,005	-1,439	0,434
10.8.1	cell wall.pectin*esterases.PME	SGN-U575256	NM_001246928	ATPME3 | ATPME3 (Arabidopsis thaliana pectin methylesterase 3)	1,278	1,595	-0,316
10.8.1	cell wall.pectin*esterases.PME	SGN-U601185	NP12919872	pectinesterase family protein	1,045	1,309	-0,264
11.1.15	lipid metabolism.FA synthesis and FA elongation.ACP desaturase	SGN-U578009	AW429094	Stearoyl-acyl carrier protein desaturase	-1,161	-1,613	0,451
11.1.3	lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase	SGN-U589665	AK322572	KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III)	1,076	1,189	-0,113
11.1.3	lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase	SGN-U591305	TA42387_4081	KAS I | KAS I	1,349	1,014	0,335
11.2.4	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U591148	ES896461	Omega-6 fatty acid desaturase	-1,874	-1,069	-0,804
11.2.4	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U574778	NM_001247313	FAD2 (FATTY ACID DESATURASE 2)	-2,212	-1,507	-0,705
11.8.3	lipid metabolism."exotics" (steroids, squalene etc).UDP-glucose:sterol glucosyltransferase	SGN-U571547	AK326178	UDP-glucose:sterol glucosyltransferase, putative	1,458	1,029	0,429
11.9.4.13	lipid metabolism.lipid degradation.beta-oxidation.acyl CoA reductase	SGN-U572683	AW649410	acyl CoA reductase, putative / male-sterility protein, putative	2,037	1,093	0,943
12.1.2	N-metabolism.nitrate metabolism.nitrite reductase	SGN-U585549	BT014587	NIR, ATHNIR, NIR1 | NIR1 (NITRITE REDUCTASE)	-1,290	-1,451	0,161
12.1.2	N-metabolism.nitrate metabolism.nitrite reductase	SGN-U585551	AW039265	nii1 nitrite reductase	-1,227	-1,569	0,342
12.2.2	N-metabolism.ammonia metabolism.glutamine synthase	SGN-U590191	AK319584	GLN2, ATGSL1, GS2 | GS2 (GLUTAMINE SYNTHETASE 2)	-1,136	-1,007	-0,130
13.1.3.4	amino acid metabolism.synthesis.aspartate family.methionine	SGN-U593132	BW688256	SAM-2, MAT2 | MAT2/SAM-2 (S-adenosylmethionine synthetase 2)	-1,748	-2,260	0,512

13.1.3.4	amino acid metabolism.synthesis.aspartate family.methionine	SGN-U591910	TA36644_4081	SAM1 (S-adenosylmethionine synthetase 1)	-1,461	-2,158	0,698
13.1.3.4	amino acid metabolism.synthesis.aspartate family.methionine	SGN-U591910	AW219361	SAM-1, MAT1, SAM1 | SAM1 (S-adenosylmethionine synthetase 1); methionine adenosyltransferase	-1,577	-2,449	0,872
13.1.4.1.4	amino acid metabolism.synthesis.branched chain group.common.branched-chain amino acid aminotransferase	SGN-U569828	DB712560	branched-chain amino acid aminotransferase SlBCAT1	-1,003	-2,843	1,840
13.2.6.2	amino acid metabolism.degradation.aromatic aa.tyrosine	SGN-U566281	AW034446	HGO (HOMOGENTISATE 1,2-DIOXYGENASE)	-1,017	-1,006	-0,011
14.3	S-assimilation.sulfite redox	SGN-U577417	JQ341913	SIR (sulfite reductase)	1,404	1,507	-0,103
15.1	metal handling.acquisition	SGN-U582218	TA37531_4081	ATFRO4, FRO4 | ATFRO4/FRO4 (FERRIC REDUCTION OXIDASE 4); ferric-chelate reductase	-2,471	-1,341	-1,131
15.2	metal handling.binding, chelation and storage	SGN-U573520	AW626369	Metal ion binding protein Heavy metal transport/detoxification protein	-1,499	1,034	-2,532
15.2	metal handling.binding, chelation and storage	SGN-U574969	AK325919	ATFER2 (FERRITIN 2)	-1,652	-1,370	-0,282
16.1.2.6	secondary metabolism.isoprenoids.mevalonate pathway.mevalonate diphosphate decarboxylase	SGN-U581971	NM_001247886	mevalonate diphosphate decarboxylase, putative	1,200	1,022	0,178
16.1.4.21	secondary metabolism.isoprenoids.carotenoids.violaxanthin de-epoxidase	SGN-U596022	AW944742	violaxanthin de-epoxidase-related	-1,034	-1,218	0,184
16.1.5	secondary metabolism.isoprenoids.terpenoids	SGN-U586113	BE459106	CAS1 (CYCLOARTENOL SYNTHASE 1)	-1,654	-1,008	-0,646
16.2	secondary metabolism.phenylpropanoids	SGN-U565929	AW738080	transferase family protein	-1,416	-1,651	0,235
16.2	secondary metabolism.phenylpropanoids	SGN-U564163	BI935350	transferase family protein	-1,031	-1,307	0,277
16.2	secondary metabolism.phenylpropanoids	SGN-U565929	TC216668	transferase family protein anthranilate N-hydroxycinnamoyl/benzoyltransferase	-1,310	-2,234	0,924

16.2.1.1	secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL	SGN-U578065	AK320002	PAL1 (PHE AMMONIA LYASE 1)	-1,130	-1,273	0,143
16.2.1.1	secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL	SGN-U577677	AJ831581	Phenylalanine ammonia-lyase	-1,096	-1,587	0,491
16.7	secondary metabolism.wax	SGN-U577635	TA38879_4081	CER1 Fatty acid hydroxylase	-1,021	1,094	-2,115
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U575063	AK224709	auxin-responsive family protein	-1,690	-1,513	-0,177
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U588103	BT013697	JAR1 (JASMONATE RESISTANT 1)	-1,121	-1,113	-0,008
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U568362	AK329809	auxin-responsive family protein	-1,038	-1,042	0,004
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U565271	TA56756_4081	GH3.6, DFL1 | DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase	1,819	1,133	0,686
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U581679	AK321659	oxidoreductase, 2OG-Fe(II) oxygenase family protein	-4,928	-4,483	-0,446
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U583842	NM_001247235	ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6)	-1,422	-1,013	-0,410
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U568205	BI933301	1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative	1,274	1,333	-0,059
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U567042	BE451579	1-aminocyclopropane-1-carboxylate oxidase 2	-1,052	-1,839	0,787
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U579250	AK247265	ethylene-forming enzyme	-1,228	-2,035	0,808
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U600915	BI209801	Flavonol synthase/flavanone 3-hydroxylase Oxoglutarate and iron-dependent oxygenase	-1,488	-2,941	1,453
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U581679	AW651011	1-aminocyclopropane-1-carboxylate oxidase 1 Oxoglutarate and iron-dependent oxygenase	-1,403	-3,013	1,610

17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U583504	AF204784	ripening regulated protein DDTFR10/A	-1,674	-1,069	-0,605
17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U583504	TA37488_4081	ATERF-5, ATERF5, ERF5 | ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5)	-1,620	-1,160	-0,459
17.5.3	hormone metabolism.ethylene.induced-regulated-responsive-activated	SGN-U584386	AI485291	ethylene-responsive protein -related	1,450	1,589	-0,139
17.6.3	hormone metabolism.gibberelin.induced-regulated-responsive-activated	SGN-U572163	AW649659	GASA4 | GASA4 (GAST1 PROTEIN HOMOLOG 4)	1,285	1,112	0,173
17.7.1.3	hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	SGN-U576466	NM_001247904	CYP74A, AOS | AOS (ALLENE OXIDE SYNTHASE)	1,994	1,331	0,663
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase	SGN-U590135	NM_001246939	12-oxophytodienoate reductase, putative	-1,776	-1,096	-0,680
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase	SGN-U579789	BF097290	12-oxophytodienoate reductase 2	-1,806	-1,336	-0,470
17.8.1	hormone metabolism.salicylic acid.synthesis-degradation	SGN-U572374	BI204548	Salicylic acid carboxyl methyltransferase	-2,231	2,098	-4,329
18	Co-factor and vitamine metabolism	SGN-U576672	AK320808	thiamine biosynthesis family protein / thiC family protein	-1,169	-1,264	0,096
19.10	tetrapyrrole synthesis.magnesium chelatase	SGN-U584294	TA37909_4081	CCH, CHLH, CCH1, GUN5 | GUN5 (GENOMES UNCOUPLED 5)	1,240	1,129	0,111
19.30	tetrapyrrole synthesis.urogen III methylase	SGN-U572308	AK247184	UPM1 (UROPHORPHYRIN METHYLASE 1)	-1,110	-1,306	0,196
20.1	stress.biotic	SGN-U584901	AK320732	PR3, PR-3, CHI-B, B-CHI, ATHCHIB | ATHCHIB (BASIC CHITINASE)	-2,187	-1,579	-0,608
20.1	stress.biotic	SGN-U582479	ES895666	ATLP-3 | ATLP-3 (Arabidopsis thaumatin-like protein 3)	1,519	1,245	0,273
20.1.3	stress.biotic.signalling	SGN-U596761	CN641307	ATMLO6, MLO6 | MLO6 (MILDEW RESISTANCE LOCUS O 6)	1,209	1,464	-0,254
20.2.1	stress.abiotic.heat	SGN-U579872	AF096251	ethylene-responsive heat shock protein	-3,403	-1,267	-2,136

				cognate 70			
20.2.1	stress.abiotic.heat	SGN-U578410	AI780273	heat shock protein 90	-3,257	-1,449	-1,809
20.2.1	stress.abiotic.heat	SGN-U581793	AW929113	15.7 kDa class I-related small heat shock protein-like (HSP15.7-CI)	-2,774	-1,941	-0,833
20.2.1	stress.abiotic.heat	SGN-U572726	AK326168	DNAJ heat shock N-terminal domain-containing protein	-2,073	-1,731	-0,341
20.2.1	stress.abiotic.heat	SGN-U566729	AK325271	17.8 kDa class I heat shock protein (HSP17.8-CI)	-1,578	-1,380	-0,198
20.2.1	stress.abiotic.heat	SGN-U581113	TA41965_4081	ATHSP17.4 (Arabidopsis thaliana heat shock protein 17.4)	-1,510	-1,368	-0,142
20.2.1	stress.abiotic.heat	SGN-U590313	NM_001247562	HSP70-1, AT-HSC70-1, HSC70, HSC70-1 | HSC70-1 (heat shock cognate 70 kDa protein 1)	-1,209	-1,099	-0,110
20.2.1	stress.abiotic.heat	SGN-U570963	AK327305	BIP1 | BIP1; ATP binding	1,159	1,178	-0,018
20.2.1	stress.abiotic.heat	SGN-U594100	AK327305	BIP2, BIP | BIP (LUMINAL BINDING PROTEIN)	1,041	1,013	0,028
20.2.1	stress.abiotic.heat	SGN-U591391	BP888362	ATJ2 | ATJ2 (Arabidopsis thaliana DnaJ homologue 2)	-1,979	-2,019	0,039
20.2.1	stress.abiotic.heat	SGN-U579872	BP884890	HSP70 | HSP70 (heat shock protein 70)	-1,442	-1,545	0,102
20.2.1	stress.abiotic.heat	SGN-U572726	TA54415_4081	DNAJ heat shock N-terminal domain-containing protein	-1,815	-1,964	0,150
20.2.1	stress.abiotic.heat	SGN-U585356	AK322398	26.5 kDa class P-related heat shock protein (HSP26.5-P)	-1,956	-2,234	0,278
20.2.1	stress.abiotic.heat	SGN-U591271	BP880052	ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3)	-1,108	-1,479	0,371
20.2.1	stress.abiotic.heat	SGN-U593108	EG553249	DNAJ chaperone	-1,555	-1,996	0,440
20.2.1	stress.abiotic.heat	SGN-U593428	BI926536	ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3)	-1,092	-1,597	0,505
20.2.1	stress.abiotic.heat	SGN-U572726	BT014144	haperone protein dnaJ Molecular chaperone, heat shock protein, Hsp40,	-1,352	-2,332	0,980
20.2.3	stress.abiotic.drought/salt	SGN-U588339	AW622602	Early-responsive to dehydration protein-like	-1,461	-1,012	-0,450
20.2.4	stress.abiotic.touch/wounding	SGN-U578406	EG554015	WI12, ATWI-12, SAG20 | SAG20 (WOUND-INDUCED PROTEIN 12)	-1,587	-1,902	0,316
20.2.99	stress.abiotic.unspecified	SGN-U563658	TA48280_4081	pollen Ole e 1 allergen and extensin family protein	1,258	1,819	-0,561
20.2.99	stress.abiotic.unspecified	SGN-U564604	TA54846_4081	MLP31 | MLP31 (MLP-LIKE PROTEIN 31)	-1,578	-1,996	0,419

20.2.99	stress.abiotic.unspecified	SGN-U579796	BG130581	Bet v I allergen family protein	-1,362	-2,051	0,689
20.2.99	stress.abiotic.unspecified	SGN-U579796	ES894925	MLP-like protein 28	-1,299	-2,223	0,924
21.1	redox.thioredoxin	SGN-U574477	AW930340	ATCXXS1 | ATCXXS1 (C-TERMINAL CYSTEINE RESIDUE IS CHANGED TO A SERINE 1)Thioredoxin-like	-2,199	-1,541	-0,658
21.2.1	redox.ascorbate and glutathione.ascorbate	SGN-U579887	AK246667	APX1B | APX2 (ASCORBATE PEROXIDASE 2)	-1,667	-1,118	-0,549
21.3	redox.heme	SGN-U567304	AW094344	ARATH GLB1, GLB1, NSHB1, ATGLB1, AHB1 | AHB1 (ARABIDOPSIS HEMOGLOBIN 1)	-1,740	-1,116	-0,624
21.4	redox.glutaredoxins	SGN-U575385	AW622091	glutaredoxin family protein GRX480; thiol-disulfide exchange intermediate	1,061	1,889	-0,828
21.4	redox.glutaredoxins	SGN-U574843	DB686084	glutaredoxin family protein	-1,552	-3,191	1,640
22.1.6	polyamine metabolism.synthesis.spermidine synthase	SGN-U566249	AM177607	putrescine N-methyltransferase	-1,721	-4,855	3,134
23.1.1.3	nucleotide metabolism.synthesis.pyrimidine.dihydroorotase	SGN-U582182	AK320064	ATALN (ARABIDOPSIS ALLANTOINASE)	2,041	1,868	0,172
23.2	nucleotide metabolism.degradation	SGN-U585151	BG127612	RNA binding / adenosine deaminase	-1,233	-1,793	0,560
23.3.1.1	nucleotide metabolism.salvage.phosphoribosyltransferases.aprt	SGN-U580961	BI927907	APT1, ATAPT1, APRT | APT1 adenine phosphoribosyltransferase-like	-1,163	-1,228	0,065
23.5	nucleotide metabolism.deoxynucleotide metabolism	SGN-U597719	BG132588	R1, RNR1 | R1/RNR1 (RIBONUCLEOTIDE REDUCTASE 1)	1,183	1,078	0,105
24.2	Biodegradation of Xenobiotics.lactoylglutathione lyase	SGN-U571540	AK319395	glyoxalase	-2,074	-3,183	1,110
26.1	misc.misc2	SGN-U582187	AK321215	CYP77A5P | CYP77A5P (cytochrome P450, family 77, subfamily A, polypeptide 5 pseudogene)	-1,654	-1,810	0,157
26.1	misc.misc2	SGN-U585197	BF051730	PDF1A | PDF1A (PEPTIDE DEFORMYLASE 1A)	-1,091	-1,299	0,208
26.10	misc.cytochrome P450	SGN-U580908	AW035889	CYP72A15 Cytochrome P450	-1,594	1,573	-3,167
26.10	misc.cytochrome P450	SGN-U588083	BI926887	CYP72A10 (cytochrome P450, family 72, subfamily A, polypeptide 10)	1,333	1,966	-0,632

26.10	misc.cytochrome P450	SGN-U583521	AK319823	CYP88A4, KAO2 | KAO2 (ENT-KAURENOIC ACID HYDROXYLASE 2)	1,193	1,453	-0,259
26.10	misc.cytochrome P450	SGN-U578058	NM_001247565	CYP72A15 | CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15)	1,142	1,317	-0,175
26.10	misc.cytochrome P450	SGN-U569016	TA54447_4081	CYP72A14 | CYP72A14 (cytochrome P450, family 72, subfamily A, polypeptide 14); oxygen&hellip	-1,420	-2,881	1,461
26.10	misc.cytochrome P450	SGN-U575254	BF114289	CYP71A22Cytochrome P450	-1,368	-3,613	2,245
26.13	misc.acid and other phosphatases	SGN-U571863	AK329218	LPP3, ATLPP3 | ATLPP3/LPP3 (LIPID PHOSPHATE PHOSPHATASE 3)	-1,069	-1,027	-0,042
26.19	misc.plastocyanin-like	SGN-U576554	AI485590	plastocyanin-like domain-containing protein	1,613	2,736	-1,124
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U576362	BG130041	UGT73C5, DOGT1 | DOGT1 (DON-GLUCOSYLTRANSFERASE); UDP-glycosyltransferase/ transferas&hellip	1,044	2,001	-0,957
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U586332	TA55690_4081	Glucosyltransferase	1,779	2,526	-0,746
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U565076	BT014484	UDP-glucose:glucosyltransferase	-1,955	-1,233	-0,722
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U577304	AK246973	UGT72E1 (UDP-glucosyl transferase 72E1)	1,145	1,833	-0,688
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U564478		UDP-GLUCOSYL TRANSFERASE 73B3	1,748	2,375	-0,626
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U576362	NM_001246924	UGT73C5, DOGT1 | DOGT1 (DON-GLUCOSYLTRANSFERASE)	1,574	1,863	-0,289
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U565331	EG553543	glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	1,027	1,095	-0,068
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U573227	AK325472	ATUGT85A3 | ATUGT85A3 (UDP-GLUCOSYL TRANSFERASE 85A3)	1,255	1,218	0,037
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U565076	TA41168_4081	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-1,227	-1,323	0,096
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U570731	AK321169	GATL9, LGT8 | GATL9/LGT8 (Galacturonosyltransferase-like 9)	1,619	1,076	0,543
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U581839	TA54427_4081	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-1,095	-1,749	0,654
26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP)	SGN-U579003	BG127115	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,145	1,219	-0,074

	family protein						
26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	SGN-U578475	BI924366	aspartic protease inhibitor 1 precursor	-1,126	-1,061	-0,064
26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	SGN-U579533	BI928461	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,259	1,080	0,179
26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	SGN-U582798	TA47685_4081	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	2,335	1,970	0,365
26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U571543	NM_001246927	short-chain dehydrogenase/reductase (SDR) family protein	1,136	1,711	-0,575
26.24	misc.GCN5-related N-acetyltransferase	SGN-U578909	TA37012_4081	GCN5-related N-acetyltransferase (GNAT) family protein	-1,509	-1,002	-0,507
26.3	misc.gluco-, galacto- and mannosidases	SGN-U570620	U13054	cell wall hydrolase LEU13054 endo-1,4-beta-glucanase precursor	-1,634	-2,719	1,085
26.4	misc.beta 1,3 glucan hydrolases	SGN-U599380	BI209487	glycosyl hydrolase family protein 17	-1,009	-2,478	1,469
26.7	misc.oxidases - copper, flavone etc.	SGN-U580450	TA52940_4081	Alcohol dehydrogenase zinc-containing	-2,574	-1,271	-1,303
26.7	misc.oxidases - copper, flavone etc.	SGN-U585073	AK326673	NADP-dependent oxidoreductase, putative	-1,297	-1,081	-0,215
26.7	misc.oxidases - copper, flavone etc.	SGN-U581586	BT013818	FMO1 | FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1)	-1,064	-1,293	0,230
26.7	misc.oxidases - copper, flavone etc.	SGN-U571186	BT013600	SKS5 | SKS5 (SKU5 Similar 5); copper ion binding / oxidoreductase	1,464	1,123	0,342
26.7	misc.oxidases - copper, flavone etc.	SGN-U581565	AK247107	partialpolyphenol oxidase A	1,673	1,089	0,584
26.7	misc.oxidases - copper, flavone etc.	SGN-U581332	TA56779_4081	allyl alcohol dehydrogenaseNADP-dependent oxidoreductase	-1,681	-2,905	1,225
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U575620	AK326781	FAD-binding domain-containing protein	1,472	1,088	0,383
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U575620	DB713269	FAD-binding domain-containing protein	1,971	1,189	0,782

27.1	RNA.processing	SGN-U566728	TA39696_4081	small nuclear ribonucleoprotein D1, putative	-1,770	1,198	-2,968
27.1.1	RNA.processing.splicing	SGN-U578946	AK321464	ATU2AF35A | ATU2AF35A	-1,029	-1,266	0,238
27.1.1	RNA.processing.splicing	SGN-U581665	BM535139	Arginine/serine-rich splicing factor	-1,629	-2,057	0,428
27.1.1	RNA.processing.splicing	SGN-U581665	AK324480	SRP34A | SRP34A (SER/ARG-RICH PROTEIN 34A)	-1,371	-1,910	0,539
27.1.19	RNA.processing.ribonucleases	SGN-U574525	AK321055	RTL2 | RTL2 (RNASE THREE-LIKE PROTEIN 2)	-1,150	-1,007	-0,143
27.2	RNA.transcription	SGN-U573801	AK323604	eukaryotic rpb5 RNA polymerase subunit family protein	1,111	1,003	0,107
27.3	RNA.regulation of transcription	SGN-U584337	AK325048	BPC6, BBR/BPC6, ATBPC6 | ATBPC6/BBR/BPC6/BPC6 (BASIC PENTACYSTEINE 6)	-1,274	-1,225	-0,050
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U580540	TA52639_4081	ZAT10, STZ | STZ (SALT TOLERANCE ZINC FINGER); nucleic acid binding / transcription factor/ zinc ion binding	-2,480	-1,706	-0,775
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U570501	EG553103	HAT22 | HAT22 (homeobox-leucine zipper protein 22)	-1,478	-1,879	0,402
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U571259	AK321993	AtMYB36, MYB36 | MYB36 (myb domain protein 36)	-1,004	-1,068	0,064
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U582039	AK326899	AtMYB70 | AtMYB70 (myb domain protein 70)	-1,173	-1,745	0,572
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U595316	EG364774	AtMYB48, MYB111 | MYB111 (myb domain protein 111)	-1,407	-2,371	0,964
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U581446	AK247148	DNA-binding family protein	-1,714	-1,343	-0,371
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U584090	AI488165	myb family transcription factor	-1,535	-2,174	0,639
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family	SGN-U580404	AK319741	WRKY family transcription factor	-1,099	-1,142	0,043
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U568565	BF051268	ATBZIP7 | ATBZIP7 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 7)	-1,759	-1,100	-0,659

27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U568565	BF051268	ATBZIP7 | ATBZIP7 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 7)	-1,585	-1,202	-0,383
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U566338	AK323598	TGA1 | TGA1	-1,234	-1,201	-0,033
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U570983	NM_001247685	TGA1 | TGA1	-1,050	-1,032	-0,018
27.3.37	RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family	SGN-U571488	AK329023	LBD37 | LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37)	-1,999	-1,252	-0,746
27.3.37	RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family	SGN-U566244	TA48654_4081	LBD37 | LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37)	-1,702	-1,395	-0,307
27.3.37	RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family	SGN-U566244	TA48654_4081	LBD37 | LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37)	-1,649	-1,406	-0,243
27.3.46	RNA.regulation of transcription.DNA methyltransferases	SGN-U575586	AK247916	DRM1 | DRM1 (DOMAINS REARRANGED METHYLASE 1)	1,426	1,189	0,237
27.3.50	RNA.regulation of transcription.General Transcription	SGN-U572682	BT013977	AtGRF3 | AtGRF3 (GROWTH-REGULATING FACTOR 3)	1,531	2,007	-0,476
27.3.50	RNA.regulation of transcription.General Transcription	SGN-U585663	BE463227	GIF, GIF1, AN3 | AN3 (ANGUSITFOLIA3)	1,357	1,514	-0,158
27.3.50	RNA.regulation of transcription.General Transcription	SGN-U580759	TA47633_4081	AtGRF1 | AtGRF1 (GROWTH-REGULATING FACTOR 1)	1,460	1,544	-0,084
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	SGN-U570747	AK322742	basic helix-loop-helix (bHLH) family protein	-1,225	-1,377	0,152
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U565490	AK323854	Unknown	1,136	1,057	0,079
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U575629	AK247914	DNA-binding family protein / AT-hook protein 1 (AHP1)	-1,087	-1,389	0,303

27.3.9	RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family	SGN-U571302	AK320499	zinc finger (GATA type) family protein	1,211	1,281	-0,070
27.3.99	RNA.regulation of transcription.unclassified	SGN-U584339	AK320956	zinc finger (AN1-like) family protein	-1,236	-1,135	-0,101
27.3.99	RNA.regulation of transcription.unclassified	SGN-U570561	AK324695	ATRBP45C | ATRBP45C	-1,237	-1,145	-0,091
27.3.99	RNA.regulation of transcription.unclassified	SGN-U570669	ES893737	aspartyl protease family protein	-1,011	-1,038	0,027
27.4	RNA.RNA binding	SGN-U570098	TA37663_4081	RNA recognition motif (RRM)-containing protein	-1,427	-1,423	-0,005
27.4	RNA.RNA binding	SGN-U581409	GO373033	GR-RBP2, GRP2, ATGRP2 | ATGRP2 (GLYCINE-RICH RNA-BINDING PROTEIN 2)	1,306	1,289	0,017
28.1	DNA.synthesis/chromatin structure	SGN-U574308	TA53447_4081	ORC6, ATORC6 | ATORC6/ORC6 (Origin recognition complex protein 6)	1,071	1,291	-0,220
28.1	DNA.synthesis/chromatin structure	SGN-U569920	TA42565_4081	replication protein, putative	1,307	1,139	0,168
28.1.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase.gypsy-like retrotransposon	SGN-U602375	AJ785333	PSBG | Encodes a protein which was originally thought to be part of photosystem II but its wheat homolog was later shown to encode for subunit K of NADH dehydrogenase	1,070	1,196	-0,126
28.1.3	DNA.synthesis/chromatin structure.histone	SGN-U578275	NM_001247460	HIS1-3 | HIS1-3 (HISTONE H1-3)	-1,512	-1,525	0,013
28.99	DNA.unspecified	SGN-U602656	BG132933	CAP 1, CAP1, ATCAP1 | ATCAP1 (CYCLASE ASSOCIATED PROTEIN 1)	1,262	1,102	0,160
29.2.1.1.1.1.16	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S16	SGN-U603793	DB715015	RPS16 | Homologous to the bacterial ribosomal protein S16	1,264	1,319	-0,055

29.2.1.2.2.535	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L35A	SGN-U578002	BG127312	60S ribosomal protein L35a (RPL35aC)	1,275	1,027	0,248
29.2.1.2.2.57	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L7A	SGN-U579366	TA48208_4081	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	1,312	1,602	-0,291
29.2.1.2.2.81	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.P1	SGN-U578632	BW691369	60s acidic ribosomal protein P1, putative	1,303	1,223	0,080
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U586021	TA36550_4081	RPL18 | RPL18 (RIBOSOMAL PROTEIN L18)	1,188	1,624	-0,436
29.2.4	protein.synthesis.elongation	SGN-U579112	TA36479_4081	elongation factor 1B-gamma, putative	1,050	1,323	-0,273
29.4	protein.postranslational modification	SGN-U563709	AK325194	SnRK3.3, CIPK4 | CIPK4 (CBL-INTERACTING PROTEIN KINASE 4)	-1,430	-1,133	-0,297
29.4	protein.postranslational modification	SGN-U571617	AW224544	lectin protein kinase, putative	-1,443	-1,191	-0,252
29.4	protein.postranslational modification	SGN-U563709	AK325194	SnRK3.3, CIPK4 | CIPK4 (CBL-INTERACTING PROTEIN KINASE 4)	-1,506	-1,551	0,045
29.4	protein.postranslational modification	SGN-U577609	AW031182	ATCKA1, CKA1 | CKA1 (CASEIN KINASE ALPHA 1)	-1,239	-1,285	0,046
29.4	protein.postranslational modification	SGN-U566705	AK319773	SIP3, SNRK3.14, CIPK6 | CIPK6 (CBL-INTERACTING PROTEIN KINASE 6)	1,124	1,003	0,122
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U564297	AK327844	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	1,062	1,030	0,032
29.5	protein.degradation	SGN-U585105	AW442278	ATMC9 | ATMC9 (METACASPASE 9)	-1,380	-1,535	0,155

29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U578489	GO376046	ubiquitin-protein ligase	-1,079	-1,292	0,213
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U565335:	TA56625_4081	UBC28 | UBC28; ubiquitin-protein ligase	1,549	1,107	0,442
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U590154	BE434965	BC13 | UBC13 (ubiquitin-conjugating enzyme 13); ubiquitin-protein ligase	-1,387	-2,242	0,855
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U593391	BE450375	UBC13 (ubiquitin-conjugating enzyme 13); ubiquitin-protein ligase |	-1,305	-2,271	0,966
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U601207	AK330036	zinc finger (C3HC4-type RING finger) family protein	-1,740	-1,355	-0,384
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U562848	AI490239	zinc finger (C3HC4-type RING finger) family protein	1,095	1,208	-0,113
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U582422	AW216567	zinc finger (C3HC4-type RING finger) family protein	-1,140	-1,137	-0,003
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U572569	AK324887	zinc finger (C3HC4-type RING finger) family protein	-1,070	-1,086	0,016
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U572569	AK324887	zinc finger (C3HC4-type RING finger) family protein	-1,203	-1,291	0,087
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U569718	BF097108	zinc finger (C3HC4-type RING finger) family protein	-1,055	-1,186	0,131
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U574794	AK325755	XERICO | XERICO	-1,088	-1,289	0,201
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U585614	DB683822	VIM1, ORTH2 | ORTH2/VIM1 (VARIANT IN METHYLATION 1)	1,474	1,200	0,274

29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U581531	NM_001247929	FBL6, EBF1 | EBF1 (EIN3-BINDING F BOX PROTEIN 1)	-1,428	-1,033	-0,395
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U578110	BI934624	FBL6, EBF1 | EBF1 (EIN3-BINDING F BOX PROTEIN 1)	-1,334	-1,314	-0,020
29.5.11.4.5.2	protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ	SGN-U583989	AK325824	BT1 | BT1 (BTB and TAZ domain protein 1)	-3,216	-4,058	0,842
29.5.4	protein.degradation.aspartate protease	SGN-U563114	AK323208	aspartyl protease family protein	-2,612	-3,024	0,412
29.5.9	protein.degradation.AAA type	SGN-U566579	DB720692	AATP1 (AAA-ATPASE 1); ATP binding / ATPase |	-1,211	1,250	-2,461
29.6	protein.folding	SGN-U579063	AW622808	immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related	1,202	1,066	0,136
30.1	signalling.in sugar and nutrient physiology	SGN-U575483	TA47144_4081	GLT1 | GLT1 (NADH-dependent glutamate synthase 1 gene)	-1,028	-1,698	0,670
30.11	signalling.light	SGN-U574291		Phototropic-responsive NPH3 family protein	-2,323	-1,414	-0,909
30.11	signalling.light	SGN-U581604	TA36441_4081	ELIP, ELIP1 | ELIP1 (EARLY LIGHT-INDUCABLE PROTEIN)	1,122	1,463	-0,340
30.11	signalling.light	SGN-U564423	BM411663	SPA3 | SPA3 (SPA1-RELATED 3)	1,587	1,346	0,242
30.2.17	signalling.receptor kinases.DUF 26	SGN-U585142	AW979578	protein kinase family protein	-1,018	-1,089	0,071
30.2.99	signalling.receptor kinases.misc	SGN-U586032	AI772843	leucine-rich repeat transmembrane protein kinase, putative	-1,463	-1,520	0,057
30.3	signalling.calcium	SGN-U600110	BI935842	ACA2 | ACA2 (CALCIUM ATPASE 2)	1,365	1,218	0,147

30.3	signalling.calcium	SGN-U598035	DB691251	CPK11, ATCDPK2 | ATCDPK2 (CALCIUM-DEPENDENT PROTEIN KINASE 2)	1,332	1,047	0,285
30.5	signalling.G-proteins	SGN-U582604	BT012967	ATARCA | ATARCA (Arabidopsis thaliana Homolog of the Tobacco ArcA)	1,035	1,127	-0,092
30.5	signalling.G-proteins	SGN-U569326	BT012784	AtRABA2b | AtRABA2b (Arabidopsis Rab GTPase homolog A2b)	-1,275	-1,502	0,227
31.1	cell.organisation	SGN-U578297	TA52406_4081	F-box protein At2g02240 MEE66 (maternal effect embryo arrest 66)	-2,284	1,714	-3,998
31.1	cell.organisation	SGN-U567874	BT014199	ATPP2-A15 | ATPP2-A15 (Phloem protein 2-A15)	-1,610	-1,468	-0,142
31.1	cell.organisation	SGN-U574717	BG135464	BOP2 | BOP2 (BLADE ON PETIOLE2)	-1,286	-1,322	0,035
31.1	cell.organisation	SGN-U577969	TA52108_4081	kinesin motor protein-related	1,330	1,140	0,190
31.1	cell.organisation	SGN-U584046	TA56746_4081	ADF7 (ACTIN DEPOLYMERIZING FACTOR 7)	2,157	1,823	0,334
31.2	cell.division	SGN-U573786	AK327122	regulator of chromosome condensation (RCC1) family protein	1,095	1,229	-0,134
31.2	cell.division	SGN-U586313	TA45765_4081	regulator of chromosome condensation (RCC1) family protein / UVB-resistance protein-related	1,142	1,223	-0,081
31.3	cell.cycle	SGN-U583476	NM_001246865	CYCD3;2 | CYCD3;2 (CYCLIN D3;2); cyclin-dependent protein kinase	1,067	1,151	-0,084
31.3	cell.cycle	SGN-U581874	FN794406	KRP3, ICK6 | ICK6/KRP3 (KIP-RELATED PROTEIN 3)	-1,336	-1,452	0,117

33.1	development.storage proteins	SGN-U581752	AI899710	PLP1, PLA IVA | PLA IVA/PLP1	1,256	1,523	-0,266
33.1	development.storage proteins	SGN-U591873	TA36939_4081	ATCRA1, CRU1, CRA1 | CRA1 (CRUCIFERINA)	1,525	1,381	0,144
33.1	development.storage proteins	SGN-U585072	AW218550	PLP1, PLA IVA | PLA IVA/PLP1	2,175	1,604	0,571
33.2	development.late embryogenesis abundant	SGN-U577990	NM_001247009	LEA14 (LATE EMBRYOGENESIS ABUNDANT 14)	1,538	2,452	-0,914
33.99	development.unspecified	SGN-U572159	AK328216	AIL6 | AIL6 (AINTEGUMENTA-LIKE 6)	1,066	1,756	-0,690
33.99	development.unspecified	SGN-U573640	BT014572	PAT1 | PAT1 (PHYTOCHROME A SIGNAL TRANSDUCTION 1)	-1,068	-1,169	0,101
33.99	development.unspecified	SGN-U583975	AK319691	integral membrane family protein / nodulin MtN21-related	-1,258	-1,429	0,171
33.99	development.unspecified	SGN-U581858	AI777160	senescence-associated protein-related	-1,257	-2,010	0,753
34.1.1	transport.p- and v-ATPases.H+-transporting two-sector ATPase	SGN-U578206	AY178911	V-type ATP synthase alpha chain	1,086	1,974	-0,888
34.13	transport.peptides and oligopeptides	SGN-U571941	BM410718	Yellow stripe-like protein 2.1	-1,363	-1,015	-0,348
34.13	transport.peptides and oligopeptides	SGN-U569974	AK323339	transporter	1,241	1,451	-0,210
34.13	transport.peptides and oligopeptides	SGN-U580977	AK323883	proton-dependent oligopeptide transport (POT) family protein	1,046	1,215	-0,169

34.15	transport.potassium	SGN-U575459	AK328285	ATKUP3, ATKT4, KUP3 | KUP3 (K+ uptake permease 3)	-1,147	-1,044	-0,103
34.15	transport.potassium	SGN-U585125	NM_001247329	AKT1 | AKT1 (ARABIDOPSIS K TRANSPORTER 1)	-1,219	-1,284	0,065
34.15	transport.potassium	SGN-U586041	BE449974	HAK5	2,857	1,807	1,051
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U564797	AK326928	ABC transporter family protein	1,295	1,212	0,083
34.18	transport.unspecified anions	SGN-U569048	TA41971_4081	anion exchange family protein	1,167	1,197	-0,030
34.2	transporter.sugars	SGN-U598419	DB722527	porin, putative	-1,915	-2,843	0,928
34.2	transporter.sugars	SGN-U600076	BP877934	Major facilitator superfamily transporter	-1,108	-2,121	1,013
34.21	transport.calcium	SGN-U564776	DB700370	ATHCX1, CAX1-LIKE, ATCAX3, CAX3 | CAX3 (cation exchanger 3)	-1,695	-1,202	-0,494
34.3	transport.amino acids	SGN-U585666	BT013629	amino acid transporter family protein	-1,201	-1,092	-0,109
34.6	transport.sulphate	SGN-U562840	AF347614	sulfate transporter 2	1,266	3,190	-1,923
34.6	transport.sulphate	SGN-U603236	BP881103	AST12, ATST1, SULTR3;1 | SULTR3;1 (SULFATE TRANSPORTER 1)	-1,012	-2,040	1,028
34.9	transport.metabolite transporters at the mitochondrial membrane	SGN-U568440	BT012718	mitochondrial substrate carrier family protein	1,242	1,611	-0,369

34.9	transport.metabolite transporters at the mitochondrial membrane	SGN-U596405	BT012709	mitochondrial substrate carrier family protein	-1,285	-1,127	-0,158
34.99	transport.misc	SGN-U577573	AK319777	MATE efflux family protein	1,537	1,795	-0,258
34.99	transport.misc	SGN-U572487	TA36730_4081	AtATG18a | AtATG18a (Arabidopsis thaliana homolog of yeast autophagy 18 (ATG18)	-1,173	-1,048	-0,125
34.99	transport.misc	SGN-U580116	GO376115	Unknown	-1,540	-1,941	0,402
35.1	not assigned.no ontology	SGN-U584983	AW220988	similar to Os01g0763300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001044334.1)	-2,742	-1,606	-1,137
35.1	not assigned.no ontology	SGN-U573384	TA39079_4081	mitochondrial glycoprotein family protein / MAM33 family protein	1,001	1,988	-0,987
35.1	not assigned.no ontology	SGN-U586347	AK327579	In2-1 protein, putative	-2,174	-1,365	-0,809
35.1	not assigned.no ontology	SGN-U573549	AK323935	extracellular dermal glycoprotein, putative	1,087	1,727	-0,640
35.1	not assigned.no ontology	SGN-U585430	BI928791	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-2,291	-1,698	-0,593
35.1	not assigned.no ontology	SGN-U574715	BM410715	T-complex protein 11	-1,516	-1,107	-0,409
35.1	not assigned.no ontology	SGN-U573485	AK319383	serine-rich protein-related	-1,373	-1,064	-0,309
35.1	not assigned.no ontology	SGN-U574885	AK246324	zinc-binding family protein	-1,584	-1,295	-0,289

35.1	not assigned.no ontology	SGN-U603049	BP888745	RXF12 | RXF12; hydrolase, hydrolyzing O-glycosyl compounds	-1,749	-1,496	-0,253
35.1	not assigned.no ontology	SGN-U573834	AK247709	YGGT family protein	-1,668	-1,443	-0,225
35.1	not assigned.no ontology	SGN-U580425	AK322829	CP5 | CP5	-1,498	-1,276	-0,222
35.1	not assigned.no ontology	SGN-U578084	AK321350	leucine-rich repeat family protein	-1,291	-1,092	-0,200
35.1	not assigned.no ontology	SGN-U574885	AK246324	zinc-binding family protein	-1,346	-1,164	-0,182
35.1	not assigned.no ontology	SGN-U596711	AK322582	ATGID1C, GID1C | ATGID1C/GID1C (GA INSENSITIVE DWARF1C)	-1,354	-1,192	-0,162
35.1	not assigned.no ontology	SGN-U578838	AK324667	Unknown	1,123	1,182	-0,059
35.1	not assigned.no ontology	SGN-U569661	AK320823	oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1,087	-1,097	0,010
35.1	not assigned.no ontology	SGN-U574884	GT166665	zinc-binding family protein	-1,274	-1,308	0,034
35.1	not assigned.no ontology	SGN-U601298	DB679120	Unknown	1,367	1,296	0,070
35.1	not assigned.no ontology	SGN-U565180	TA36707_4081	RALFL33 | RALFL33 (RALF-LIKE 33)	-1,073	-1,218	0,145
35.1	not assigned.no ontology	SGN-U563304	AK320109	transferase family protein	1,868	1,693	0,176

35.1	not assigned.no ontology	SGN-U573553	AK247398	Unknown	1,204	1,008	0,196
35.1	not assigned.no ontology	SGN-U569126	AJ850958	pathogen-responsive alpha-dioxygenase, putative	-1,362	-1,580	0,218
35.1	not assigned.no ontology	SGN-U575871	AK320534	molybdenum cofactor sulfurase family protein	-1,205	-1,499	0,294
35.1	not assigned.no ontology	SGN-U573176	BP903103	hydrolase, alpha/beta fold family protein	-1,812	-2,133	0,321
35.1	not assigned.no ontology	SGN-U565180	TA36707_4081	RALFL33 | RALFL33 (RALF-LIKE 33)	-1,115	-1,441	0,326
35.1	not assigned.no ontology	SGN-U572909	DV104692	transducin family protein / WD-40 repeat family protein	-1,050	-1,383	0,333
35.1	not assigned.no ontology	SGN-U575871	AK320534	molybdenum cofactor sulfurase family protein	-1,229	-1,579	0,350
35.1	not assigned.no ontology	SGN-U564941	AI491099	surfeit locus protein 2 family protein / SURF2 family protein	1,455	1,095	0,360
35.1	not assigned.no ontology	SGN-U572834	BM412114	unknown [Solanum lycopersicum] MSL2 | MSL2 (MSCS-LIKE 2)	-1,217	-1,649	0,432
35.1	not assigned.no ontology	SGN-U569126	AJ850958	pathogen-responsive alpha-dioxygenase, putative	-1,275	-1,731	0,456
35.1	not assigned.no ontology	SGN-U587047	BE459059	molybdenum cofactor sulfurase-like protein 1	-1,175	-1,644	0,468
35.1	not assigned.no ontology	SGN-U565180	TA36707_4081	RALFL33 | RALFL33 (RALF-LIKE 33)	-1,005	-1,514	0,509

35.1	not assigned.no ontology	SGN-U582833	AJ784441	translation release factor Immature colon carcinoma transcript 1 protein	-1,100	-1,687	0,587
35.1	not assigned.no ontology	SGN-U582832	TA42707_4081	translation release factor Immature colon carcinoma transcript 1 protein	-1,140	-1,960	0,820
35.1	not assigned.no ontology	SGN-U582833	TA42708_4081	translation release factor Immature colon carcinoma transcript 1 protein	-1,295	-2,178	0,883
35.1	not assigned.no ontology	SGN-U577745	BT014232	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42050.1); similar to hypothetical &hellip	-1,041	-1,966	0,925
35.1	not assigned.no ontology	SGN-U567239	BE449862	acyltransferase-like protein	-1,535	-2,725	1,190
35.1.19	not assigned.no ontology.C2 domain-containing protein	SGN-U604842	AW649285	C2 domain-containing protein	1,174	1,624	-0,450
35.1.40	not assigned.no ontology.glycine rich proteins	SGN-U575907	DB712184	ripening regulated protein DDTFR8	-1,911	-1,071	-0,840
35.1.40	not assigned.no ontology.glycine rich proteins	SGN-U571038	AK326564	similar to glycine-rich protein	-2,227	-2,117	-0,110
35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U574542	DB712421	pentatricopeptide (PPR) repeat-containing protein	1,229	1,074	0,156
35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U570619	AK320620	similar to pentatricopeptide (PPR) repeat-containing protein	-1,153	-1,370	0,217
35.2	not assigned.unknown	SGN-U565390	AK247844	Sigma factor binding protein 1	-1,051	2,068	-3,119
35.2	not assigned.unknown	SGN-U581061	TA53096_4081	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25460.1)	1,459	2,845	-1,385
35.2	not assigned.unknown	SGN-U571407	AW039879	Unknown Protein	-2,372	-1,581	-0,791
35.2	not assigned.unknown	SGN-U586374	DB698305	Plant-specific domain TIGR01615 family protein	1,171	1,928	-0,757

35.2	not assigned.unknown	SGN-U570726	TA55908_4081	Unknown	1,144	1,798	-0,654
35.2	not assigned.unknown	SGN-U576039	AK320732	chitinase	-1,993	-1,383	-0,610
35.2	not assigned.unknown	SGN-U599668	BG126526	Kelch domain-containing protein 3	1,012	1,614	-0,603
35.2	not assigned.unknown	SGN-U570708	BG125252	Unknown	1,164	1,612	-0,448
35.2	not assigned.unknown	SGN-U595703	AI775274	Unknown	1,250	1,662	-0,412
35.2	not assigned.unknown	SGN-U579035	AK328929	Unknown	-1,566	-1,164	-0,401
35.2	not assigned.unknown	SGN-U575504	BI208271	Unknown	1,099	1,493	-0,394
35.2	not assigned.unknown	SGN-U573448	TA42314_4081	Unknown	1,133	1,523	-0,390
35.2	not assigned.unknown	SGN-U565665	DB678738	Unknown	1,298	1,677	-0,379
35.2	not assigned.unknown	SGN-U578194	TA36493_4081	Unknown	-1,430	-1,109	-0,321
35.2	not assigned.unknown	SGN-U584912	TC233203	Unknown	1,067	1,383	-0,317
35.2	not assigned.unknown	SGN-U574247	AW038953	Unknown	-1,335	-1,045	-0,291
35.2	not assigned.unknown	SGN-U596163	TA39638_4081	Unknown	1,026	1,314	-0,288
35.2	not assigned.unknown	SGN-U603179	BP902924	Unknown	1,081	1,352	-0,271
35.2	not assigned.unknown	SGN-U600748	DB714372	Unknown	1,377	1,629	-0,251
35.2	not assigned.unknown	SGN-U565664	AK323528	Unknown	1,356	1,605	-0,249
35.2	not assigned.unknown	SGN-U568503	AI895694	Unknown	1,199	1,427	-0,228
35.2	not assigned.unknown	SGN-U588750	TC243804	Unknown	1,017	1,244	-0,227
35.2	not assigned.unknown	SGN-U599710	AJ785018	Unknown	-1,492	-1,267	-0,226
35.2	not assigned.unknown	SGN-U562678	BG643671	Unknown	1,092	1,294	-0,202
35.2	not assigned.unknown	SGN-U570317	BG123222	Unknown	-1,303	-1,103	-0,200
35.2	not assigned.unknown	SGN-U567341	BI927160	similar to transcription factor	1,131	1,320	-0,189
35.2	not assigned.unknown	SGN-U580332	BF051927	Unknown	-1,739	-1,562	-0,176
35.2	not assigned.unknown	SGN-U597612	DB693580	Unknown	-1,398	-1,229	-0,169
35.2	not assigned.unknown	SGN-U582114	BF112910	Unknown	1,147	1,310	-0,163
35.2	not assigned.unknown	SGN-U565816	TA37599_4081	Unknown	-1,677	-1,554	-0,123
35.2	not assigned.unknown	SGN-U575504	BI209956	Unknown	2,387	2,508	-0,120

35.2	not assigned.unknown	SGN-U586704	AW932894	Unknown	-1,442	-1,325	-0,118
35.2	not assigned.unknown	SGN-U564053	TA41825_4081	similar to TMAC2 (TWO OR MORE ABRES-CONTAINING GENE 2)	-1,420	-1,316	-0,104
35.2	not assigned.unknown	SGN-U580686	GO372321	Unknown	-1,229	-1,138	-0,091
35.2	not assigned.unknown	SGN-U587405	AK326406	Unknown	1,063	1,153	-0,090
35.2	not assigned.unknown	SGN-U576088	AI486910	Unknown	-1,340	-1,266	-0,074
35.2	not assigned.unknown	SGN-U603955	AK323241	Unknown	1,444	1,518	-0,073
35.2	not assigned.unknown	SGN-U589493	AW621238	Unknown	1,079	1,147	-0,069
35.2	not assigned.unknown	SGN-U579406	BP905721	Unknown	1,012	1,080	-0,068
35.2	not assigned.unknown	SGN-U566102	TA56783_4081	Unknown	-1,148	-1,088	-0,060
35.2	not assigned.unknown	SGN-U571985	BG127056	Unknown	1,506	1,561	-0,054
35.2	not assigned.unknown	SGN-U576690	AK319807	Unknown	-1,768	-1,720	-0,048
35.2	not assigned.unknown	SGN-U587779	NM_001246927	putative alcohol dehydrogenase	1,642	1,660	-0,018
35.2	not assigned.unknown	SGN-U583996	BI931250	nucleotidyltransferase	-1,246	-1,231	-0,015
35.2	not assigned.unknown	SGN-U577501		Unknown	1,162	1,176	-0,014
35.2	not assigned.unknown	SGN-U570610	AK247326	Unknown	-1,230	-1,219	-0,011
35.2	not assigned.unknown	SGN-U578657	AK320454	Unknown protein	1,971	1,978	-0,007
35.2	not assigned.unknown	SGN-U563460	EG364746	Unknown	-1,161	-1,173	0,012
35.2	not assigned.unknown	SGN-U583996	TA55291_4081	nucleotidyltransferase	-1,045	-1,074	0,029
35.2	not assigned.unknown	SGN-U579748	AK247584	Unknown	-1,030	-1,066	0,036
35.2	not assigned.unknown	SGN-U566853	CD002152	Unknown	-1,158	-1,220	0,062
35.2	not assigned.unknown	SGN-U585038	AK321200	Unknown	-1,120	-1,183	0,063
35.2	not assigned.unknown	SGN-U568201	TA42625_4081	Unknown	1,166	1,100	0,067
35.2	not assigned.unknown	SGN-U594548	AK325805	Unknown	-1,507	-1,599	0,092

35.2	not assigned.unknown	SGN-U586586	AK323461	GTP binding / RNA binding	1,105	1,013	0,092
35.2	not assigned.unknown	SGN-U582589	BG133592	Unknown	1,096	1,001	0,095
35.2	not assigned.unknown	SGN-U580686	GO372321	Unknown	-1,282	-1,379	0,097
35.2	not assigned.unknown	SGN-U562792	AK319366	Unknown	-1,292	-1,396	0,104
35.2	not assigned.unknown	SGN-U576294	AK321958	Unknown	-2,309	-2,415	0,107
35.2	not assigned.unknown	SGN-U602646	AK322107	integral membrane family protein	1,419	1,308	0,110
35.2	not assigned.unknown	SGN-U585405	TA42907_4081	Unknown	-1,324	-1,437	0,113
35.2	not assigned.unknown	SGN-U566116	AK328571	Unknown	-1,039	-1,177	0,138
35.2	not assigned.unknown	SGN-U582647	BW685294	Unknown	1,431	1,280	0,151
35.2	not assigned.unknown	SGN-U601313	AJ785396	Unknown	1,647	1,494	0,153
35.2	not assigned.unknown	SGN-U570610	AK247326	Unknown	-1,225	-1,384	0,159
35.2	not assigned.unknown	SGN-U598347	BI929467	Unknown	1,471	1,306	0,164
35.2	not assigned.unknown	SGN-U592678	BP892631	Unknown	-1,320	-1,489	0,169
35.2	not assigned.unknown	SGN-U571156	BP903262	hypothetical protein 154 - common tobacco chloroplast	2,221	2,048	0,173
35.2	not assigned.unknown	SGN-U600293	EG553575	Unknown	-1,850	-2,037	0,186
35.2	not assigned.unknown	SGN-U579574	AI772690	F-box family protein	1,522	1,332	0,190
35.2	not assigned.unknown	SGN-U582768	TC243102	Unknown	-1,163	-1,398	0,235
35.2	not assigned.unknown	SGN-U563948	AK323766	Unknown	-1,315	-1,554	0,239
35.2	not assigned.unknown	SGN-U578889	AK324633	Unknown	-1,026	-1,283	0,257
35.2	not assigned.unknown	SGN-U563247	AK328760	Unknown	-1,286	-1,622	0,336
35.2	not assigned.unknown	SGN-U603129	BI929750	Unknown	1,793	1,449	0,344
35.2	not assigned.unknown	SGN-U577753	AK328892	Unknown	-1,870	-2,230	0,359
35.2	not assigned.unknown	SGN-U585330	TA56053_4081	myb-like transcription factor 5	-1,489	-1,858	0,370
35.2	not assigned.unknown	SGN-U589196	AK247606	extensin-like protein ext1 precursor	1,876	1,478	0,399
35.2	not assigned.unknown	SGN-U579924	AK322852	similar to calmodulin-binding protein	1,675	1,271	0,404
35.2	not assigned.unknown	SGN-U572110	BP908751	Unknown	1,517	1,111	0,406
35.2	not assigned.unknown	SGN-U571304	AI488574	Unknown	1,428	1,009	0,419
35.2	not assigned.unknown	SGN-U572675	AK321033	Unknown	1,508	1,087	0,421

35.2	not assigned.unknown	SGN-U570550	TC217439	Unknown	1,709	1,285	0,424
35.2	not assigned.unknown	SGN-U594484	TA53909_4081	Unknown	1,662	1,217	0,445
35.2	not assigned.unknown	SGN-U581692	AK247251	Genomic DNA chromosome 5 TAC clone K1F13	-1,532	-2,008	0,476
35.2	not assigned.unknown	SGN-U603644	BW690011	Unknown	-1,082	-1,571	0,489
35.2	not assigned.unknown	SGN-U571021	TA41742_4081	Unknown	-1,095	-1,588	0,494
35.2	not assigned.unknown	SGN-U594480	BF098095	extensin-like protein dif10 precursor	1,818	1,294	0,524
35.2	not assigned.unknown	SGN-U574871	AI898739	Transcription factor Helix-loop-helix DNA-binding	-1,104	-1,694	0,590
35.2	not assigned.unknown	SGN-U590954	EG364927	serine-rich protein relared	-2,002	-2,594	0,592
35.2	not assigned.unknown	SGN-U573610	AK321211	Unknown	-1,548	-2,201	0,653
35.2	not assigned.unknown	SGN-U602912	BP892460	Unknown	-1,355	-2,061	0,706
35.2	not assigned.unknown	SGN-U596443	BF114030	Unknown Protein	-1,001	-1,740	0,739
35.2	not assigned.unknown	SGN-U569344	AK248036	similar to protein kinase family protein / U-box domain-containing protein	-1,139	-2,009	0,870
35.2	not assigned.unknown	SGN-U565596	AK321958	Unknown	-1,169	-2,175	1,006
35.2	not assigned.unknown	SGN-U586527	TA40353_4081	Unknown	-2,129	-3,143	1,014
35.2	not assigned.unknown	SGN-U574680	AK247236	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G33250.1); similar to Os01g0680600	-1,012	-2,028	1,015
35.2	not assigned.unknown	SGN-U581743	TC196867	heat shock protein homologue SSE1	-1,646	-2,746	1,100
35.2	not assigned.unknown	SGN-U572585	BI422106	Unknown	-1,164	-2,277	1,113
35.2	not assigned.unknown	SGN-U601068	BF114298	AMP-binding protein, putative	-1,416	-2,952	1,536
35.3	not assigned.disagreeing hits	SGN-U581131	U21800	2-oxoglutarate-dependent dioxygenase 2	-1,327	1,366	-2,693
35.3	not assigned.disagreeing hits	SGN-U570002	TA37682_4081	BAG6 (BCL-2-ASSOCIATED ATHANOGENE 6); calmodulin binding / protein binding	-2,385	-1,001	-1,384
35.3	not assigned.disagreeing hits	SGN-U586875	TA37681_4081	Unknown Protein	-2,613	-1,237	-1,376
35.3	not assigned.disagreeing hits	SGN-U580639	BG126930	Unknown	-2,574	-1,396	-1,178
35.3	not assigned.disagreeing hits	SGN-U579033	AJ831864	non-specific lipid transfer protein (ltpg2 gene)	-2,673	-1,963	-0,711
35.3	not assigned.disagreeing hits	SGN-U577827	BW685405	cytochrome c oxidase-related	-2,304	-1,816	-0,489
35.3	not assigned.disagreeing hits	SGN-U587779	NM_001246927	putative alcohol dehydrogenase	1,398	1,855	-0,457
35.3	not assigned.disagreeing hits	SGN-U578468	TA37430_4081	DIM, EVE1, DW1, DIM1, CBB1, DWF1 | DWF1 (DIMINUTO 1)	1,288	1,721	-0,433

35.3	not assigned.disagreeing hits	SGN-U580591		esterase, putative	-1,641	-1,212	-0,429
35.3	not assigned.disagreeing hits	SGN-U587778	AK322540	Short-chain dehydrogenase/reductase (SDR) family protein	1,592	1,936	-0,344
35.3	not assigned.disagreeing hits	SGN-U580100	AK246905	histone H3.2	-1,434	-1,118	-0,315
35.3	not assigned.disagreeing hits	SGN-U589370	AK323341	ATCLH2 | ATCLH2 (Chlorophyll-chlorophyllido hydrolase 2)	-1,932	-1,625	-0,307
35.3	not assigned.disagreeing hits	SGN-U582182	AK320064	ATALN | ATALN (ARABIDOPSIS ALLANTOINASE)	1,297	1,546	-0,250
35.3	not assigned.disagreeing hits	SGN-U579003	BG127115	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,156	1,394	-0,238
35.3	not assigned.disagreeing hits	SGN-U581719	BT013574	ERD3 | ERD3 (EARLY-RESPONSIVE TO DEHYDRATION 3)	1,117	1,299	-0,181
35.3	not assigned.disagreeing hits	SGN-U574969	AK325919	ATFER2 | ATFER2 (FERRITIN 2)	-1,583	-1,419	-0,164
35.3	not assigned.disagreeing hits	SGN-U577908	TA36388_4081	LTP1, ATLTP1, LP1 | LP1 (nonspecific lipid transfer protein 1)	1,001	1,155	-0,154
35.3	not assigned.disagreeing hits	SGN-U580896	BW687446	ATMAPR2 | ATMAPR2 (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED PROGESTERONE BINDING PROTEIN 2)	-1,295	-1,146	-0,149
35.3	not assigned.disagreeing hits	SGN-U569492	NM_001246953	sugar transporter, putative	1,016	1,153	-0,137
35.3	not assigned.disagreeing hits	SGN-U575508	BT014282	FAD3 | FAD3 (FATTY ACID DESATURASE 3)	1,191	1,324	-0,133
35.3	not assigned.disagreeing hits	SGN-U581131	NM_001246846	lipid-associated family protein	1,032	1,151	-0,119
35.3	not assigned.disagreeing hits	SGN-U592192	TA37507_4081	Unknown	-1,689	-1,588	-0,101
35.3	not assigned.disagreeing hits	SGN-U580149	TA40055_4081	LOL1 | LOL1 (LSD ONE LIKE 1)	-1,320	-1,241	-0,079
35.3	not assigned.disagreeing hits	SGN-U574358	AK322829	transformer serine/arginine-rich ribonucleoprotein, putative	-1,539	-1,469	-0,071
35.3	not assigned.disagreeing hits	SGN-U578577	TA39311_4081	ATPRP4, PRP4 | PRP4 (PROLINE-RICH PROTEIN 4)	-1,241	-1,189	-0,052
35.3	not assigned.disagreeing hits	SGN-U562651	NM_001247921	HCT | transferase family protein	1,438	1,486	-0,048
35.3	not assigned.disagreeing hits	SGN-U589558	AK320525	FLP1, YRE, CER3, WAX2 | CER3/FLP1/WAX2/YRE (ECERIFERUM 3)	1,097	1,122	-0,024
35.3	not assigned.disagreeing hits	SGN-U571293	AK326153	RAP2.4 | RAP2.4 (related to AP2 4)	-1,477	-1,464	-0,012
35.3	not assigned.disagreeing hits	SGN-U580189	NM_001246938	tudor domain-containing protein	-1,431	-1,446	0,015

35.3	not assigned.disagreeing hits	SGN-U573837	AW031075	DNAJ heat shock protein, putative	-1,279	-1,305	0,026
35.3	not assigned.disagreeing hits	SGN-U578110	BG643919	FBL6, EBF1 | EBF1 (EIN3-BINDING F BOX PROTEIN 1); ubiquitin-protein ligase	-1,238	-1,282	0,044
35.3	not assigned.disagreeing hits	SGN-U577748	GT167951	protein kinase family protein	-1,453	-1,555	0,102
35.3	not assigned.disagreeing hits	SGN-U581138	BG631302	CVP1, FRL1, SMT2 | SMT2 (STEROL METHYLTRANSFERASE 2)	1,119	1,011	0,108
35.3	not assigned.disagreeing hits	SGN-U567238	TA49668_4081	UGE2 | UGE2 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 2)	1,160	1,043	0,117
35.3	not assigned.disagreeing hits	SGN-U578489	TA36745_4081	UBC2, ATUBC2 | ATUBC2 (UBIQUITING-CONJUGATING ENZYME 2); ubiquitin-protein ligase	-1,343	-1,461	0,118
35.3	not assigned.disagreeing hits	SGN-U588895	AK319823	ent-kaurenoic acid hydroxylase, putative	1,552	1,424	0,127
35.3	not assigned.disagreeing hits	SGN-U579594	TA40228_4081	serine-rich protein-related	-1,281	-1,421	0,140
35.3	not assigned.disagreeing hits	SGN-U567229	AK326087	NOP56 | NOP56 (ARABIDOPSIS HOMOLOG OF NUCLEOLAR PROTEIN NOP56)	1,185	1,037	0,148
35.3	not assigned.disagreeing hits	SGN-U573837	AW031075	DNAJ heat shock protein, putative	-1,156	-1,323	0,167
35.3	not assigned.disagreeing hits	SGN-U589371	AK323341	chlorophyllase (CLH2)	-1,593	-1,775	0,182
35.3	not assigned.disagreeing hits	SGN-U577293	TA39739_4081	KAS I | KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I)	1,234	1,034	0,200
35.3	not assigned.disagreeing hits	SGN-U579222	NM_001247104	CHS, TT4, ATCHS | ATCHS/CHS/TT4 (CHALCONE SYNTHASE)	-1,515	-1,763	0,248
35.3	not assigned.disagreeing hits	SGN-U579003	AK324717	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,564	1,309	0,254
35.3	not assigned.disagreeing hits	SGN-U571293	AK326153	RAP2.4 | RAP2.4 (related to AP2 4)	-1,000	-1,280	0,280
35.3	not assigned.disagreeing hits	SGN-U592116	TA44511_4081	TCH1, ACAM-1, CAM1 | CAM1 (CALMODULIN 1)	-1,839	-2,165	0,326
35.3	not assigned.disagreeing hits	SGN-U578941	X92888	(S)-2-hydroxy-acid oxidase, peroxisomal, putative	-1,009	-1,371	0,362
35.3	not assigned.disagreeing hits	SGN-U584294	TA37909_4081	CCH, CHLH, CCH1, GUN5 | GUN5 (GENOMES UNCOUPLED 5)	1,404	1,030	0,374

35.3	not assigned.disagreeing hits	SGN-U564643	AI484723	AST12, ATST1, SULTR3;1 | SULTR3;1 (SULFATE TRANSPORTER 1)	1,444	1,011	0,433
35.3	not assigned.disagreeing hits	SGN-U577324	BT014046	ATRFNR2 | ATRFNR2 (ROOT FNR 2)	-1,120	-1,556	0,436
35.3	not assigned.disagreeing hits	SGN-U579055	AI780922	dormancy/auxin associated family protein	-1,415	-1,867	0,452
35.3	not assigned.disagreeing hits	SGN-U577275	TA38561_4081	binding / hydrogen ion transporting ATP synthase, rotational mechanism / hydrogen ion transpor	-1,072	-1,558	0,487
35.3	not assigned.disagreeing hits	SGN-U565448	DB720145	MIOX4 | MIOX4 (MYO-INOSITOL OXYGENASE 4)	1,518	1,012	0,506
35.3	not assigned.disagreeing hits	SGN-U578904	NM_001247570	eukaryotic translation initiation factor 5A, putative	-1,032	-1,571	0,538
35.3	not assigned.disagreeing hits	SGN-U574781	BT013035	lipid desaturase	-1,057	-1,624	0,566
35.3	not assigned.disagreeing hits	SGN-U574653	BG127730	ATHCX1, CAX1-LIKE, ATCAX3, CAX3 | CAX3 (cation exchanger 3)	-2,046	-2,619	0,573
35.3	not assigned.disagreeing hits	SGN-U564605	DB691711	MLP43 | MLP43 (MLP-LIKE PROTEIN 43)	-1,147	-1,778	0,632
35.3	not assigned.disagreeing hits	SGN-U579359	X55681	LRX2 | LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2)	1,817	1,125	0,693
35.3	not assigned.disagreeing hits	SGN-U577782	BT013281	unknown protein	1,802	1,086	0,716
35.3	not assigned.disagreeing hits	SGN-U579796	ES894925	Bet v I allergen family protein |MLP-like protein 28	-1,428	-2,185	0,758
35.3	not assigned.disagreeing hits	SGN-U587980	EG553907	1-aminocyclopropane-1-carboxylate oxidase 3	-1,315	-2,613	1,298

Table 4. List of up-regulated genes genes (log2 sub-/optimal T≥1 and q-value<0.05) deteced only in the roots of the grafted ‘Kommeet’ plants onto ‘LA 1777’ (R/S:LA/KO) under sub-optimal root T stress.

Bin Code	BinName	SGN	NCBI	description	LA/KO Log FC	adj.P.Val
34.99	transport.misc	SGN-U586539	BI209863	protein kinase family protein	3,490	0,018
29.5.3	protein.degradation.cysteine protease	SGN-U564978	BI928267	Wound-induced proteinase inhibitor serine-type endopeptidase inhibitor activity	3,296	0,014
35.2	not assigned.unknown	SGN-U591986	X55691	glycine rich protein X55690	3,177	0,014
34.99	transport.misc	SGN-U567069	BE463242	unknown	3,089	0,027
35.2	not assigned.unknown	SGN-U580449	AK224730	Abscicic acid stress ripening 4 Putative DNA-binding and chaperone-like protein	2,903	0,017
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U586661	BT012912	Late elongated hypocotyl and circadian clock associated-1-like protein 1	2,638	0,011
35.2	not assigned.unknown	SGN-U580787	AK224730	Abscicic acid stress ripening 4 Putative DNA-binding and chaperone-like protein	2,595	0,018
10.7	cell wall.modification	SGN-U562982	AW624841	xyloglucan endotransglucosylase-hydrolase 6	2,561	0,014
17.2.2	hormone metabolism.auxin.signal transduction	SGN-U576145	AW649068	Auxin Efflux FacilitatorBelongs to the PIN family of auxin efflux facilitators involved in polar auxin transport	2,518	0,011
35.3	not assigned.disagreeing hits	SGN-U591986	X55688	glycine-rich protein	2,460	0,013
35.2	not assigned.unknown	SGN-U578154	BI209189	Unknown	2,450	0,014
16.10	secondary metabolism.simple phenols	SGN-U567193	BT013137	laccase	2,412	0,011

26.3	misc.gluco-, galacto- and mannosidases	SGN-U571983	DB682135	glycosyl hydrolase family 1 protein	2,380	0,013
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U568404	AW218981	Tropinone reductase-like protein Glucose/ribitol dehydrogenase	2,379	0,022
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U593934	TA51297_4081	Cc-nbs-lrr resistance protein	2,368	0,030
35.1	not assigned.no ontology	SGN-U569285	TA53858_4081	PERQ Amino acid rich with GYF domain-containing protein	2,362	0,019
15.2	metal handling.binding, chelation and storage	SGN-U567922	BI925433	Metal ion binding protein Heavy metal transport/detoxification protein	2,277	0,011
35.2	not assigned.unknown	SGN-U579620	BF096394	Unknown	2,260	0,013
17.7.1.3	hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	SGN-U573672	AF461042	cytochrome P450 CYP74C4	2,120	0,014
28.1.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase. gypsy-like retrotransposon	SGN-U579150	AI896109	ORF158 | Identical to Hypothetical mitochondrial protein AtMg00860	2,115	0,011
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U579026	BT012911	Ring finger protein 12	2,018	0,034
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U574735	TA38509_4081	Late elongated hypocotyl and circadian clock associated-1-like protein 1	2,013	0,013
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U597792	DV103733	UDP-glucosyltransferase family 1 protein (UDP-glucuronosyl/UDP-glucosyltransferase	2,005	0,026
35.2	not assigned.unknown	SGN-U576446	TA55400_4081	JAZ8, TIFY5A | JAZ8/TIFY5A (JASMONATE-ZIM-DOMAIN PROTEIN 8)	1,973	0,046
35.2	not assigned.unknown	SGN-U574590	TA54348_4081	Unknown	1,913	0,032

26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U594150	AK321420	short-chain dehydrogenase/reductase (SDR) family protein	1,901	0,033
26.3	misc.gluco-, galacto- and mannosidases	SGN-U566569	NM_001247101	RSW3 | RSW3 (RADIAL SWELLING 3)	1,876	0,014
16.2.1.1	secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL	SGN-U580050	AW929506	PAL1 | PAL1 (PHE AMMONIA LYASE 1)	1,859	0,019
16.2.1.10	secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD	SGN-U569435	EG553769	mannitol dehydrogenase, putative	1,840	0,036
28.1.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase. gypsy-like retrotransposon	SGN-U595872	DB716302	polyprotein	1,829	0,013
35.3	not assigned.disagreeing hits	SGN-U584529	AK321410	CHL1-1, NRT1, B-1, ATNRT1, CHL1, NRT1.1 | NRT1.1 (NITRATE TRANSPORTER 1.1)	1,823	0,014
35.3	not assigned.disagreeing hits	SGN-U574760	BW687921	nodulin MtN3 family protein	1,821	0,049
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U574735	AK319264	CCA1 | CCA1 (CIRCADIAN CLOCK ASSOCIATED 1)	1,798	0,013
35.2	not assigned.unknown	SGN-U567070	BG133495	Unknown	1,779	0,015
16.10	secondary metabolism.simple phenols	SGN-U563099	AK324584	LAC12 | LAC12 (laccase 12)	1,776	0,035
28.2	DNA.repair	SGN-U576824	BE458334	UVR2, PHR1 | PHR1 (PHOTOLYASE 1)	1,773	0,013
35.3	not assigned.disagreeing hits	SGN-U584617	AK324031	ATHB13 | ATHB13; DNA binding / transcription factor	1,764	0,038
35.2	not assigned.unknown	SGN-U604349	BG125653	Unknown	1,753	0,013

35.1	not assigned.no ontology	SGN-U600175	AK327748	thioesterase family protein	1,727	0,048
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U584993	AW624998	UDP-glucoronosyl/UDP-glucosyl transferase family protein	1,726	0,014
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U573887	AI895826	FAD-binding domain-containing protein	1,723	0,013
16.10	secondary metabolism.simple phenols	SGN-U567193	NM_001246887	LAC7 | LAC7 (laccase 7)	1,720	0,014
29.4	protein.postranslational modification	SGN-U585018	TA41248_4081	ATPP2CA, AHG3 | AHG3/ATPP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA)	1,683	0,014
35.2	not assigned.unknown	SGN-U578022	AK327428	Unknown	1,681	0,013
35.2	not assigned.unknown	SGN-U569295	TA53069_4081	Unknown	1,673	0,013
35.2	not assigned.unknown	SGN-U586660	AK319264	Unknown	1,661	0,014
26.10	misc.cytochrome P450	SGN-U585133	AJ785145	CYP94C1 | CYP94C1 (cytochrome P450, family 94, subfamily C, polypeptide 1)	1,658	0,013
35.2	not assigned.unknown	SGN-U566189	TA55554_4081	Unknown	1,655	0,015
35.2	not assigned.unknown	SGN-U582290	TA56231_4081	Unknown	1,655	0,027
35.2	not assigned.unknown	SGN-U564677	TA51695_4081	Unknown	1,653	0,028
17.7.1.3	hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	SGN-U573672	NM_001247573	CYP74A, AOS | AOS (ALLENE OXIDE SYNTHASE)	1,650	0,043
35.3	not assigned.disagreeing hits	SGN-U574738	AK319264	CCA1 | CCA1 (CIRCADIAN CLOCK ASSOCIATED 1)	1,644	0,011

27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U585539	NM_001246962	RAP2.7, TOE1 | RAP2.7/TOE1 (TARGET OF EAT1 1)	1,637	0,021
10.8.1	cell wall.pectin*esterases.PME	SGN-U571810	TC244133	pectinesterase family protein	1,634	0,040
2.2.1.3.3	major CHO metabolism.degradation.sucrose.invertases.vacuolar	SGN-U578195	BI923413	beta-fructosidase (BFRUCT3)	1,630	0,014
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U568046	AK322397	protein kinase family protein	1,625	0,011
35.2	not assigned.unknown	SGN-U585123	AK247121	Unknown	1,593	0,013
20.2.3	stress.abiotic.drought/salt	SGN-U585087	BP886484	Dehydration-responsive protein-related	1,587	0,013
35.2	not assigned.unknown	SGN-U602148	BP907174	Unknown	1,586	0,013
26.3	misc.gluco-, galacto- and mannosidases	SGN-U571983	BG134728	glycosyl hydrolase family 1 protein	1,584	0,020
35.2	not assigned.unknown	SGN-U604565	X55682	tyrosine-rich hydroxyproline-rich glycoprotein	1,575	0,015
35.1	not assigned.no ontology	SGN-U602993	AK327114	LPAT4 | LPAT4; acyltransferase	1,561	0,013
35.2	not assigned.unknown	SGN-U584772	AW218360	Unknown	1,555	0,016
29.5.9	protein.degradation.AAA type	SGN-U569541	TA47551_4081	AAA-type ATPase family protein	1,552	0,029
27.3.4	RNA.regulation of transcription.ARF, Auxin Response Factor family	SGN-U567299	NM_001247673	ARF1 | ARF1 (AUXIN RESPONSE FACTOR 1)	1,548	0,013

20.1.7	stress.biotic.PR-proteins	SGN-U585506	AK247087	ATP binding / protein binding	1,547	0,036
28.1	DNA.synthesis/chromatin structure	SGN-U575096	AK322155	DEAD/DEAH box helicase, putative	1,542	0,011
35.3	not assigned.disagreeing hits	SGN-U566921	NM_001247489	2-dehydro-3-deoxyphosphoheptonate aldolase, putative	1,536	0,014
20.1.7	stress.biotic.PR-proteins	SGN-U584112	BF098197	disease resistance protein (CC-NBS-LRR class)	1,522	0,013
16.8.4.1	secondary metabolism.flavonoids.flavonols.dihydrokaempferol 4-reductase	SGN-U566207	AW932559	BEN1 | BEN1; oxidoreductase, acting on CH-OH group of donors	1,521	0,014
2.2.1.3.2	major CHO metabolism.degradation.sucrose.invertases.cell wall	SGN-U565004	BE449979	ATCWINV1, ATBFRUCT1 | ATBFRUCT1/ATCWINV1 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 1)	1,521	0,016
35.2	not assigned.unknown	SGN-U585623	AK319992	Unknown	1,516	0,016
26.3	misc.gluco-, galacto- and mannosidases	SGN-U569046	BE450960	ATGH9B8 | ATGH9B8 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9B8)	1,509	0,013
34.6	transport.sulphate	SGN-U565728	NM_001247636	SULTR1;3 | SULTR1;3 (sulfate transporter)	1,498	0,017
35.2	not assigned.unknown	SGN-U577584	Z29112	Unknown	1,495	0,040
34.2	transporter.sugars	SGN-U567438	TA55499_4081	TMT2 | TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2)	1,493	0,026
35.3	not assigned.disagreeing hits	SGN-U566667	BG625990	clathrin adaptor complexes medium subunit family protein	1,493	0,014
31.1	cell.organisation	SGN-U591651	AI777219	ATNAP57, CBF5, ATCBF5, NAP57 | NAP57 (ARABIDOPSIS THALIANA HOMOLOGUE OF NAP57)	1,490	0,017

34.3	transport.amino acids	SGN-U569872	AK246988	ser/thr protein phosphatase family protein	1,488	0,014
29.4	protein.postranslational modification	SGN-U566843	AK247485	ATPP2CA, AHG3 | AHG3/ATPP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA)	1,481	0,022
35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U567010	DB687130	GRP23 | GRP23 (GLUTAMINE-RICH PROTEIN23)	1,468	0,017
20.2.3	stress.abiotic.drought/salt	SGN-U573379	AK324967	Dehydration-responsive protein-related	1,460	0,015
10.5.5	cell wall.cell wall proteins.RGP	SGN-U583155	TA55240_4081	ATRGP1, ATRGP, RGP1 | RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1)	1,458	0,038
10.2	cell wall.cellulose synthesis	SGN-U576915	BG124425	CSLA09, ATCSLA9, CSLA9, RAT4, ATCSLA09 | ATCSLA09 (RESISTANT TO AGROBACTERIUM TRANSFORMATION 4)	1,457	0,033
35.1	not assigned.no ontology	SGN-U591569	AK323441	ATBAG1 | ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1)	1,456	0,011
26.19	misc.plastocyanin-like	SGN-U593812	AK319426	plastocyanin-like domain-containing protein	1,442	0,041
26.10	misc.cytochrome P450	SGN-U581343		COX3 | Encodes cytochrome c oxidase subunit 3	1,439	0,018
27.3.4	RNA.regulation of transcription.ARF, Auxin Response Factor family	SGN-U593847	BP894511	ARF6 | ARF6 (AUXIN RESPONSE FACTOR 6)	1,438	0,013
35.2	not assigned.unknown	SGN-U578752	AK320878	Unknown	1,438	0,017
10.5.1	cell wall.cell wall proteins.AGPs	SGN-U587978	AK324186	FLA1 | FLA1	1,436	0,015
35.2	not assigned.unknown	SGN-U564001	AK321218	hydroxyproline-rich systemin precursor (defense-signaling glycopeptide hormone)	1,430	0,023

29.5.9	protein.degradation.AAA type	SGN-U566579	TA51264_4081	AATP1 | AATP1 (AAA-ATPASE 1)	1,429	0,013
17.1.1	hormone metabolism.abscisic acid.synthesis-degradation	SGN-U577478	NM_001247526	ATNCED3, STO1, NCED3 | NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE3)	1,425	0,023
29.5.9	protein.degradation.AAA type	SGN-U604725	AW217422	AAA-type ATPase family protein	1,423	0,011
30.4	signalling.phosphinositides	SGN-U584505	AK324670	ATG5 | ATG5 (G5p-related protein)	1,423	0,013
35.2	not assigned.unknown	SGN-U581271	AW626189	Unknown	1,421	0,021
35.2	not assigned.unknown	SGN-U574549	AK246887	calcium-dependent protein kinase 2	1,420	0,020
35.2	not assigned.unknown	SGN-U603851	AK328731	Unknown	1,418	0,015
35.2	not assigned.unknown	SGN-U603669	AK322897	Unknown	1,418	0,013
34.18	transport.unspecified anions	SGN-U569047	DB725016	BOR1 | BOR1 (REQUIRES HIGH BORON 1)	1,408	0,025
35.3	not assigned.disagreeing hits	SGN-U593982	AK326695	protein kinase family protein	1,407	0,013
35.2	not assigned.unknown	SGN-U581982	BG133799	Unknown	1,405	0,016
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U602448	BG642529	UDP-glucoronosyl/UDP-glucosyl transferase family protein	1,400	0,033
35.2	not assigned.unknown	SGN-U587743	AK323025	Unknown	1,392	0,013
35.1	not assigned.no ontology	SGN-U568021	TA56642_4081	ATCXE12 | ATCXE12 (ARABIDOPSIS THALIANA CARBOXYESTERASE 12)	1,390	0,018

35.2	not assigned.unknown	SGN-U597833	BW692277	Unknown	1,390	0,013
35.2	not assigned.unknown	SGN-U568109	TA40057_4081	Unknown	1,381	0,016
35.2	not assigned.unknown	SGN-U579224	BG134548	Unknown	1,381	0,046
4.12	glycolysis.enolase	SGN-U579968	NP1427488	enolase,putative	1,380	0,013
30.3	signalling.calcium	SGN-U578018	BT013428	calreticulin 2 (CRT2)	1,378	0,015
29.5.5	protein.degradation.serine protease	SGN-U573675	AK320911	SCPL12 | SCPL12; serine carboxypeptidase	1,378	0,037
35.2	not assigned.unknown	SGN-U577656	AI899627	Unknown	1,377	0,013
35.1	not assigned.no ontology	SGN-U570129	AK319704	transferase family protein	1,376	0,034
27.3.9	RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family	SGN-U563049	BM411779	BME3-ZF, BME3 | BME3/BME3-ZF (BLUE MICROPYLAR END3)	1,376	0,014
35.2	not assigned.unknown	SGN-U582617	TA45158_4081	nbs-lrr type disease resistance protein	1,376	0,032
29.2.3	protein.synthesis.initiation	SGN-U575866	BI422275	EIF4B1 | EIF4B1 (eukaryotic translation initiation factor 4B1)	1,374	0,013
28.1.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase. gypsy-like retrotransposon	SGN-U595870	BI207577	polyprotein	1,371	0,016
26.10	misc.cytochrome P450	SGN-U573215	TA36310_4081	AR2, ATR2 | ATR2 (ARABIDOPSIS P450 REDUCTASE 2)	1,369	0,016
20.2.1	stress.abiotic.heat	SGN-U581845	BT014139	DNAJ heat shock N-terminal domain-containing protein	1,368	0,014

31.1	cell.organisation	SGN-U586122	AK323884	myosin heavy chain-related	1,368	0,013
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U585889	BT013754	ATH-A, CESA2 | CESA2 (CELLULOSE SYNTHASE 2)	1,367	0,013
34.99	transport.misc	SGN-U571260	BI925139	Unknown	1,366	0,044
26.7	misc.oxidases - copper, flavone etc.	SGN-U581285	BE451288	FMO1 | FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1)	1,361	0,020
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U599967	BG132953	MRP5, ATMRP5 | ATMRP5 (Arabidopsis thaliana multidrug resistance-associated protein 5)	1,361	0,014
30.2.24	signalling.receptor kinases.S-locus glycoprotein like	SGN-U577144	DB685663	ARK3 | ARK3 (Arabidopsis Receptor Kinase 3)	1,359	0,014
35.3	not assigned.disagreeing hits	SGN-U587509	BG630041	26S proteasome AAA-ATPase subunit (RPT1a)	1,357	0,014
35.3	not assigned.disagreeing hits	SGN-U581354	AW624957	delta-8 sphingolipid desaturase, putative	1,357	0,025
26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	SGN-U579003	TA49528_4081	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,354	0,038
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U581726	BP910310	CESA1, RSW1 | CESA1 (CELLULOSE SYNTHASE 1)	1,354	0,014
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	SGN-U578233	AK320636	HSFC1, AT-HSFC1 | AT-HSFC1 (Arabidopsis thaliana heat shock transcription factor C1)	1,350	0,014
35.1	not assigned.no ontology	SGN-U580259	AK322729	FLA17 | FLA17 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 17 PRECURSOR)	1,345	0,014
35.2	not assigned.unknown	SGN-U576015	BE460180	Unknown	1,344	0,013

29.4	protein.postranslational modification	SGN-U575470	DB720461	protein kinase family protein	1,343	0,014
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U585938	BG127854	TINY2 | TINY2 (TINY2)	1,342	0,016
33.99	development.unspecified	SGN-U603922	BI924203	VCS | VCS (VARICOSE)	1,342	0,014
10.2	cell wall.cellulose synthesis	SGN-U571201	AK320053	CSLA02, ATCSLA2, ATCSLA02 | ATCSLA02 (Cellulose synthase-like A2)	1,337	0,015
35.2	not assigned.unknown	SGN-U567279	AK325859	Unknown	1,334	0,015
29.4	protein.postranslational modification	SGN-U568532	NM_001247464	TSL | TSL (TOUSLED)	1,332	0,014
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U584759	BT013811	protein kinase family protein	1,332	0,013
35.2	not assigned.unknown	SGN-U581826	BF097466	Unknown	1,329	0,013
35.1	not assigned.no ontology	SGN-U563081	AK328035	transporter-related	1,327	0,013
35.2	not assigned.unknown	SGN-U567012	AK325632	Unknown	1,326	0,016
26.10	misc.cytochrome P450	SGN-U566498	NM_001247334	ATBR6OX, CYP85A1, BR6OX, BR6OX1 | BR6OX1 (BRASSINOSTEROID-6-OXIDASE)	1,325	0,018
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U573419	DB711782	CESA3, IXR1, ATCESA3, ATH-B, CEV1 | CESA3 (CELLULOSE SYNTHASE 3)	1,321	0,013
35.2	not assigned.unknown	SGN-U564787	BI932571	QRT3 | QRT3 (QUARTET 3)	1,314	0,017

35.3	not assigned.disagreeing hits	SGN-U578589	TA40170_4081	BGAL3 | BGAL3 (beta-galactosidase 3)	1,310	0,019
35.3	not assigned.disagreeing hits	SGN-U579591	NM_001247523	FLO2, FL1, AP2 | AP2 (APETALA 2)	1,305	0,013
29.4	protein.postranslational modification	SGN-U571570	BG131134	protein kinase family protein	1,303	0,013
27.3.4	RNA.regulation of transcription.ARF, Auxin Response Factor family	SGN-U601907	NM_001247867	ARF16 | ARF16 (AUXIN RESPONSE FACTOR 16)	1,301	0,027
35.2	not assigned.unknown	SGN-U596867	TC242094	glycinamide ribonucleotide transformylase	1,300	0,016
35.2	not assigned.unknown	SGN-U572103	AK324291	Unknown	1,297	0,013
35.2	not assigned.unknown	SGN-U564856	AK329878	Unknown	1,296	0,022
29.4	protein.postranslational modification	SGN-U572549	NM_001247217	calcium-dependent protein kinase, putative	1,296	0,015
35.2	not assigned.unknown	SGN-U571022	AK319405	Unknown	1,294	0,013
34.8	transport.metabolite transporters at the envelope membrane	SGN-U584826	TA43761_4081	phosphate translocator-related	1,294	0,018
27.3.7	RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family	SGN-U565146	NM_001247519	zinc finger (B-box type) family protein	1,293	0,034
26.17	misc.dynamin	SGN-U567269	DB718905	ADL1A, AG68, DRP1A | ADL1 (ARABIDOPSIS DYNAMIN-LIKE PROTEIN)	1,292	0,019
35.3	not assigned.disagreeing hits	SGN-U586659	AK319264	CCA1 | CCA1 (CIRCADIAN CLOCK ASSOCIATED 1)	1,289	0,013
2.2.1.3.2	major CHO metabolism.degradation.sucrose.inver	SGN-U587099	AK325200	ATCWINV2 | ATCWINV2 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 2)	1,289	0,013

	tases.cell wall					
35.1	not assigned.no ontology	SGN-U599878	BG126886	Unknown	1,288	0,015
29.3.3	protein.targeting.chloroplast	SGN-U571197	GO373858	TOC86, PPI2, TOC160, ATTOC159, TOC159 | TOC159 (PLASMID PROTEIN IMPORT 2)	1,288	0,019
26.24	misc.GCN5-related N-acetyltransferase	SGN-U583905	AK322227	GCN5-related N-acetyltransferase (GNAT) family protein	1,287	0,047
30.1	signalling.in sugar and nutrient physiology	SGN-U566807	BP909550	GLU1, GLS1, GLUS | GLS1/GLU1/GLUS (FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1)	1,287	0,014
35.2	not assigned.unknown	SGN-U574359	TA56262_4081	Unknown	1,283	0,016
30.5	signalling.G-proteins	SGN-U576904	BT013944	transducin family protein / WD-40 repeat family protein	1,283	0,014
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U583774	BP888197	ATMYB4, ATMYB86 | ATMYB4 (myb domain protein 4)	1,282	0,016
29.4	protein.postranslational modification	SGN-U576847	TA55935_4081	protein kinase family protein	1,280	0,014
8.1.8	TCA / org. transformation.TCA.fumarase	SGN-U595036	AK325138	FUM1 | FUM1 (FUMARASE 1)	1,279	0,014
28.1	DNA.synthesis/chromatin structure	SGN-U571933	AK327109	PMH2 | PMH2 (PUTATIVE MITOCHONDRIAL RNA HELICASE 2)	1,278	0,015
2.2.1.3.1	major CHO metabolism.degradation.sucrose.invertases.neutral	SGN-U575781	TA56589_4081	CINV1 | CINV1 (CYTOSOLIC INVERTASE 1)	1,276	0,028
35.1	not assigned.no ontology	SGN-U568037	BG631619	phosphorylase family protein	1,275	0,020

34.99	transport.misc	SGN-U581670	AK247859	putative gag polyprotein	1,273	0,014
29.5.9	protein.degradation.AAA type	SGN-U577393	GO374322	AAA-type ATPase family protein	1,272	0,015
28.1	DNA.synthesis/chromatin structure	SGN-U582888	DB720683	DEAD/DEAH box helicase, putative (RH18)	1,268	0,018
30.2.17	signalling.receptor kinases.DUF 26	SGN-U579557	TA53308_4081	protein kinase family protein	1,267	0,014
35.2	not assigned.unknown	SGN-U581847	TA55118_4081	Unknown	1,267	0,014
29.5.1	protein.degradation.subtilases	SGN-U586670	DB684636	subtilase family protein	1,266	0,016
35.2	not assigned.unknown	SGN-U597676	AW735938	Unknown	1,258	0,017
4.1	glycolysis.UGPase	SGN-U582001	AK325069	UGP | UGP (UDP-glucose pyrophosphorylase)	1,255	0,029
27.1.19	RNA.processing.ribonucleases	SGN-U580032	NM_001247266	RNS1 | RNS1 (RIBONUCLEASE 1)	1,251	0,014
10.5.1	cell wall.cell wall proteins.AGPs	SGN-U576059	AK324186	FLA2 | FLA2	1,251	0,035
35.2	not assigned.unknown	SGN-U578964	AK320269	Unknown	1,251	0,016
29.4	protein.postranslational modification	SGN-U573492	BT013516	kelch repeat-containing serine/threonine phosphoesterase family protein	1,250	0,014
22.1.2	polyamine metabolism.synthesis.SAM decarboxylase	SGN-U579425	TA36438_4081	adenosylmethionine decarboxylase family protein	1,250	0,029
35.2	not assigned.unknown	SGN-U583033	BI206277	Unknown	1,250	0,017

26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U568834	AK322442	ATUGT85A2 | ATUGT85A2 (UDP-GLUCOSYL TRANSFERASE 85A2)	1,248	0,014
29.5.1	protein.degradation.subtilases	SGN-U604298	AK319963	subtilase family protein	1,246	0,026
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U585884	DB719280	ATH-A, CESA2 | CESA2 (CELLULOSE SYNTHASE 2)	1,245	0,013
35.1	not assigned.no ontology	SGN-U586048	AK327250	transducin family protein / WD-40 repeat family protein \	1,241	0,016
23.4.99	nucleotide metabolism.phosphotransfer and pyrophosphatases.misc	SGN-U568784	AK321049	ATPPA4 | ATPPA4 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 4)	1,236	0,044
35.2	not assigned.unknown	SGN-U563383	AI778454	Unknown	1,236	0,018
27.4	RNA.RNA binding	SGN-U572257	BT013641	heterogeneous nuclear ribonucleoprotein, putative	1,235	0,013
27.3.46	RNA.regulation of transcription.DNA methyltransferases	SGN-U575586	AK247916	DRM1 | DRM1 (DOMAINS REARRANGED METHYLASE 1)	1,233	0,027
26.12	misc.peroxidases	SGN-U588272	TA39413_4081	peroxidase 12 (PER12) (P12) (PRXR6)	1,233	0,035
29.7	protein.glycosylation	SGN-U568972	AK247447	glycosyl transferase family 43 protein	1,232	0,014
35.2	not assigned.unknown	SGN-U596571	AK319992	Unknown	1,231	0,032
35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U600559	DB690373	NFD5 | NFD5 (NUCLEAR FUSION DEFECTIVE 5)	1,229	0,014
29.4	protein.postranslational modification	SGN-U583113	NM_001247303	PAPP5, PP5 | PAPP5/PP5 (PROTEIN PHOSPHATASE 5)	1,224	0,013
35.2	not assigned.unknown	SGN-U583088	AK320855	Unknown	1,223	0,014

35.1.1	not assigned.no ontology.ABC1 family protein	SGN-U594352	AK327570	ATATH10, ABC1At | ABC1At (ARABIDOPSIS THALIANA ABC TRANSPORTER 1)	1,222	0,014
35.3	not assigned.disagreeing hits	SGN-U585507	AK319250	disease resistance protein (CC-NBS-LRR class), putative	1,221	0,017
26.3	misc.gluco-, galacto- and mannosidases	SGN-U580766	NM_001247483	glycosyl hydrolase family 1 protein	1,220	0,020
35.2	not assigned.unknown	SGN-U583732	AK247321	Unknown	1,220	0,014
27.3.73	RNA.regulation of transcription.Zn-finger(CCHC)	SGN-U579182	TA40772_4081	tudor domain-containing protein / nuclease family protein	1,219	0,032
27.2	RNA.transcription	SGN-U585091	AK326467	RPOC2 | RNA polymerase beta' subunit-2	1,217	0,018
29.4	protein.postranslational modification	SGN-U569402	AK327767	SnRK3.15, CIPK14, ATSR1 | ATSR1 (SERINE/THREONINE PROTEIN KINASE 1)	1,217	0,040
29.4	protein.postranslational modification	SGN-U581223	AK320115	casein kinase II alpha chain, putative	1,217	0,014
20.2.3	stress.abiotic.drought/salt	SGN-U570254	AI778675	dehydration-responsive protein-related	1,216	0,025
35.2	not assigned.unknown	SGN-U601134	AI491002	Unknown	1,213	0,014
29.5.1	protein.degradation.subtilases	SGN-U578717	BG124520	ARA12 | ARA12; subtilase	1,212	0,015
31.1	cell.organisation	SGN-U564015		TUB1 | TUB1 (tubulin beta-1 chain)	1,212	0,021
29.5.1	protein.degradation.subtilases	SGN-U598216	DB683743	AIR3 | AIR3 (Auxin-Induced in Root cultures 3)	1,211	0,015
35.2	not assigned.unknown	SGN-U571696	AW737974	Unknown	1,211	0,039

35.2	not assigned.unknown	SGN-U601425	DB714360	UPF0202 protein	1,211	0,014
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U566926	AW218178	zinc finger (C3HC4-type RING finger) family protein	1,211	0,021
35.2	not assigned.unknown	SGN-U564377	BI422980	ESP4 | ESP4 (ENHANCED SILENCING PHENOTYPE 4)	1,208	0,017
26.3	misc.gluco-, galacto- and mannosidases	SGN-U581494	NM_001247388	Symbols: BGAL3 | BGAL3 (beta-galactosidase 3)	1,208	0,015
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U567944	DB702752	Polyvinylalcohol dehydrogenase	1,207	0,045
27.3.66	RNA.regulation of transcription.Psudo ARR transcription factor family	SGN-U585445	AW930845	PRR5, APRR5 | APRR5 (PSEUDO-RESPONSE REGULATOR 5)	1,206	0,014
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U570573	DB723477	malate oxidoreductase, putative	1,205	0,016
34.99	transport.misc	SGN-U586475	BI923833	SEC14 cytosolic factor family protein	1,204	0,014
27.3.99	RNA.regulation of transcription.unclassified	SGN-U575240	DB697465	MAK16 protein-related	1,204	0,013
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U597108	AK325274	UBC9 | UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin-protein ligase	1,202	0,022
35.2	not assigned.unknown	SGN-U567200	AK322178	Unknown	1,201	0,018
29.2.3	protein.synthesis.initiation	SGN-U584442	BG132234	eukaryotic translation initiation factor 4F, putative / eIF-4F, putative	1,201	0,014
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family	SGN-U575103	AW032956	trihelix DNA-binding protein, putative	1,201	0,032
34.1.1	transport.p- and v-ATPases.H+-transporting two-sector ATPase	SGN-U579398	AK323914	H+-transporting two-sector ATPase, putative	1,199	0,014

28.2	DNA.repair	SGN-U582993	GO372470	UVR2, PHR1 | PHR1 (PHOTOLYASE 1)	1,199	0,014
10.2	cell wall.cellulose synthesis	SGN-U575150	AK328307	CSLA09, ATCSLA9, CSLA9, RAT4, ATCSLA09 | ATCSLA09 (RESISTANT TO AGROBACTERIUM TRANSFORMATION 4)	1,199	0,013
13.1.1.3	amino acid metabolism.synthesis.central amino acid metabolism.alanine	SGN-U583520	BW685565	AGT2 | AGT2 (ALANINE:GLYOXYLATE AMINOTRANSFERASE 2)	1,199	0,014
35.2	not assigned.unknown	SGN-U603947	BP882967	Unknown	1,197	0,019
20.2.3	stress.abiotic.drought/salt	SGN-U583160	BT014452	Dehydration-responsive protein-related	1,197	0,016
35.2	not assigned.unknown	SGN-U585035	AK320300	PDE320 (PIGMENT DEFECTIVE 320)	1,195	0,017
35.1	not assigned.no ontology	SGN-U563985	AW626074	similar to fringe-related protein	1,193	0,050
35.2	not assigned.unknown	SGN-U566077	BP910815	RRP12-like protein	1,191	0,014
35.1.1	not assigned.no ontology.ABC1 family protein	SGN-U579429	BG130241	ATATH13 | ATATH13 (ABC2 homolog 13)	1,191	0,014
35.2	not assigned.unknown	SGN-U583222	TC237594	Unknown	1,190	0,018
30.5	signalling.G-proteins	SGN-U564057	BP910357	guanine nucleotide exchange family protein	1,189	0,014
35.2	not assigned.unknown	SGN-U598718	AW934616	Unknown	1,188	0,014
35.1	not assigned.no ontology	SGN-U568462	TA37392_4081	PEX11C | PEX11C	1,188	0,025

31.1	cell.organisation	SGN-U589343	BT013589	AAA-type ATPase family protein / ankyrin repeat family protein	1,187	0,019
16.8.3	secondary metabolism.flavonoids.dihydroflavonols	SGN-U565006	NM_001247368	IRX4, ATCCR1, CCR1 | CCR1 (CINNAMOYL COA REDUCTASE 1)	1,186	0,046
34.14	transport.unspecified cations	SGN-U568384	TA38084_4081	bile acid:sodium symporter family protein	1,183	0,016
30.3	signalling.calcium	SGN-U569480	BI926814	IQD17 | IQD17 (IQ-domain 17)	1,183	0,024
35.2	not assigned.unknown	SGN-U604750	BF050815	Unknown	1,182	0,014
34.99	transport.misc	SGN-U567457	AK320022	SEC14 cytosolic factor, putative	1,181	0,014
35.1	not assigned.no ontology	SGN-U600379	AK327901	hydrolase, alpha/beta fold family protein	1,180	0,027
35.3	not assigned.disagreeing hits	SGN-U578741	TA36665_4081	SPE2, ADC2 | ADC2 (ARGININE DECARBOXYLASE 2)	1,180	0,013
35.2	not assigned.unknown	SGN-U573045	BI935063	Unknown	1,179	0,017
26.10	misc.cytochrome P450	SGN-U585127	AW621409	CYP722A1 | CYP722A1 (cytochrome P450, family 722, subfamily A, polypeptide 1)	1,176	0,023
35.2	not assigned.unknown	SGN-U602966	DB684457	Unknown	1,175	0,024
35.2	not assigned.unknown	SGN-U600834	AI486004	Unknown	1,175	0,020
35.1	not assigned.no ontology	SGN-U604467	AW030270	Unknown	1,175	0,014
35.2	not assigned.unknown	SGN-U602366	DB720326	Unknown	1,175	0,013

35.3	not assigned.disagreeing hits	SGN-U579625	GO374731	25 kda protein dehydrin	1,173	0,013
35.2	not assigned.unknown	SGN-U580884	BG629752	Unknown	1,172	0,014
35.2	not assigned.unknown	SGN-U570093	AI485157	Unknown	1,171	0,019
35.2	not assigned.unknown	SGN-U599904	BE463142	Unknown	1,169	0,027
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U582391	AK320832	SAP domain-containing protein	1,166	0,018
25	C1-metabolism	SGN-U566475	TA39756_4081	SKB1, ATPRMT5, PRMT5 | ATPRMT5/PRMT5/SKB1 (SHK1 BINDING PROTEIN 1)	1,166	0,037
35.3	not assigned.disagreeing hits	SGN-U581582	GO373353	LHCB2.3, LHCB2, LHCB2:4 | LHCB2:4 (Photosystem II light harvesting complex gene 2.3)	1,165	0,021
35.2	not assigned.unknown	SGN-U576029	TC243937	Unknown	1,165	0,018
35.2	not assigned.unknown	SGN-U584712	AW934531	Unknown	1,163	0,019
35.2	not assigned.unknown	SGN-U569915	AK247805	Unknown	1,162	0,014
29.2.3	protein.synthesis.initiation	SGN-U579912	TA43416_4081	translation initiation factor IF-2, mitochondrial, putative	1,160	0,013
26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U564971	BW687973	short-chain dehydrogenase/reductase (SDR) family protein	1,160	0,014
29.2.4	protein.synthesis.elongation	SGN-U571049	TA56717_4081	elongation factor 1-alpha, putative	1,158	0,024
34.99	transport.misc	SGN-U584213	AK327689	SEC14 cytosolic factor, putative	1,158	0,020

30.3	signalling.calcium	SGN-U578326	AK326374	ATCDPK3, CPK6 | CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6)	1,158	0,017
29.5	protein.degradation	SGN-U583547	TA47207_4081	prolyl endopeptidase, putative	1,158	0,017
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U569558	BT014093	ATRLI2 | ATRLI2 (Arabidopsis thaliana RNase L inhibitor protein 2)	1,157	0,017
35.2	not assigned.unknown	SGN-U601347	AW933738	Unknown	1,157	0,015
35.3	not assigned.disagreeing hits	SGN-U595752	BT014087	secretory carrier membrane protein (SCAMP) family protein	1,157	0,030
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U581842	BI933653	TKI1 | TKI1 (TSL-KINASE INTERACTING PROTEIN 1)	1,157	0,014
25	C1-metabolism	SGN-U583127	TA38089_4081	THFS | THFS (10-FORMYLTETRAHYDROFOLATE SYNTHETASE)	1,154	0,014
35.2	not assigned.unknown	SGN-U578440	TA44897_4081	Unknown	1,152	0,014
26.3	misc.gluco-, galacto- and mannosidases	SGN-U574787	AK320706	SFR2 | SFR2 (SENSITIVE TO FREEZING 2)	1,152	0,015
35.3	not assigned.disagreeing hits	SGN-U573865	DB726037	Unknown	1,152	0,026
29.4	protein.postranslational modification	SGN-U565787	AK325478	protein kinase family protein	1,151	0,016
30.5	signalling.G-proteins	SGN-U568794	AK321343	transducin family protein / WD-40 repeat family protein	1,150	0,014
35.3	not assigned.disagreeing hits	SGN-U577438	TA35599_4081	PRH75 | PRH75 (plant RNA helicase 75)	1,149	0,016
34.1	transport.p- and v-ATPases	SGN-U584600	BT014617	ATAVP3, AVP-3, AVP1 | AVP1 (vacuolar-type H+-pumping pyrophosphatase 1)	1,148	0,019

35.3	not assigned.disagreeing hits	SGN-U578061	NM_001247914	ATBETAFRUCT4, VAC-INV | ATBETAFRUCT4/VAC-INV (VACUOLAR INVERTASE)	1,148	0,018
35.2	not assigned.unknown	SGN-U585275	AK247740	Unknown	1,148	0,016
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U581437	AK326294	Unknown	1,147	0,014
35.1	not assigned.no ontology	SGN-U563031	AW031785	CPL3 | CPL3 (C-TERMINAL DOMAIN PHOSPHATASE-LIKE 3)	1,147	0,014
35.2	not assigned.unknown	SGN-U603562		Unknown	1,144	0,024
35.1	not assigned.no ontology	SGN-U574200	AK327688	EMB2762 | EMB2762 (EMBRYO DEFECTIVE 2762)	1,144	0,013
34.13	transport.peptides and oligopeptides	SGN-U565615	X92853	CHL1-1, NRT1, B-1, ATNRT1, CHL1, NRT1.1 | NRT1.1 (NITRATE TRANSPORTER 1.1)	1,143	0,030
35.3	not assigned.disagreeing hits	SGN-U589068	DB726225	disease resistance protein (TIR class), putative	1,143	0,023
35.1	not assigned.no ontology	SGN-U604410	DB691078	ATP-binding region, ATPase-like domain-containing protein	1,142	0,016
28.99	DNA.unspecified	SGN-U565123	BW689867	endomembrane protein 70, putative	1,141	0,034
34.15	transport.potassium	SGN-U565469	BI926828	potassium channel tetramerisation domain-containing protein	1,140	0,016
34.99	transport.misc	SGN-U564667	AK322244	MATE efflux family protein	1,140	0,024
27.3.52	RNA.regulation of transcription.Global transcription factor group	SGN-U586533	TA53502_4081	GTE8 | GTE8 (GLOBAL TRANSCRIPTION FACTOR GROUP E8)	1,140	0,024
13.1.6.1.10	amino acid metabolism.synthesis.aromatic	SGN-U578253	AK326991	EMB3004, MEE32 | EMB3004/MEE32 (EMBRYO DEFECTIVE 3004)	1,139	0,017

	aa.chorismate.dehydroquinate/shikimate dehydrogenase					
29.4	protein.postranslational modification	SGN-U575581	AK246980	leucine-rich repeat family protein	1,138	0,023
35.3	not assigned.disagreeing hits	SGN-U568869	AK326827	ATBZIP53 | ATBZIP53 (BASIC REGION/LEUCINE ZIPPER MOTIF 53)	1,136	0,016
33.99	development.unspecified	SGN-U585161	AK326717	transducin family protein / WD-40 repeat family protein	1,135	0,017
35.2	not assigned.unknown	SGN-U582819	AK247224	Unknown	1,135	0,026
29.5.9	protein.degradation.AAA type	SGN-U585094	AK320982	PEX6 | PEX6 (PEROXIN6)	1,135	0,015
35.2	not assigned.unknown	SGN-U582265	AW735836	Unknown	1,135	0,030
35.2	not assigned.unknown	SGN-U580042	TA46601_4081	Unknown	1,135	0,027
35.3	not assigned.disagreeing hits	SGN-U595692	AW979389	Unknown	1,134	0,017
10.8.1	cell wall.pectin*esterases.PME	SGN-U576260	AK324780	ATPME1 | ATPME1 (Arabidopsis thaliana pectin methylesterase 1)	1,130	0,046
35.3	not assigned.disagreeing hits	SGN-U563303	AK320109	transferase-related	1,128	0,018
2.2.2.1	major CHO metabolism.degradation.starch.starch cleavage	SGN-U563342	AK247092	BMY4, BAM7 | BAM7/BMY4 (BETA-AMYLASE 7)	1,128	0,020
35.1	not assigned.no ontology	SGN-U574804	BI923668	similar to FF domain-containing protein / WW domain-containing protein	1,126	0,015
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U563256	AK320436	GAUT9 | GAUT9 (Galacturonosyltransferase 9)	1,125	0,018

34.14	transport.unspecified cations	SGN-U564655	AK247513	magnesium transporter CorA-like protein-related	1,125	0,014
35.2	not assigned.unknown	SGN-U595584	AW929513	Unknown	1,123	0,014
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U575018	AK320987	GAUT4 | GAUT4 (Galacturonosyltransferase 4)	1,122	0,018
10.7	cell wall.modification	SGN-U562981	BG128413	xyloglucan:xyloglucosyl transferase, putative	1,121	0,015
35.2	not assigned.unknown	SGN-U589507	AI781110	Unknown	1,118	0,013
34.1	transport.p- and v-ATPases	SGN-U577312	NM_001247548	AHA11 | AHA11 (ARABIDOPSIS H(+)-ATPASE 11)	1,118	0,013
17.5.3	hormone metabolism.ethylene.induced-regulated-responsive-activated	SGN-U589047	AK329666	ethylene-responsive family protein	1,117	0,020
29.2.4	protein.synthesis.elongation	SGN-U563538	DB712550	ATRNL, RNL | ATRNL/RNL (ARABIDOPSIS THALIANA RNA LIGASE)	1,117	0,014
35.1	not assigned.no ontology	SGN-U573549	AW033818	extracellular dermal glycoprotein, putative	1,117	0,017
35.2	not assigned.unknown	SGN-U599480	BI421818	Unknown	1,117	0,018
10.3	cell wall.hemicellulose synthesis	SGN-U565515	AK327565	KAM1, MUR3 | KAM1/MUR3 (MURUS 3)	1,116	0,013
19.10	tetrapyrrole synthesis.magnesium chelatase	SGN-U584293	TA37910_4081	CCH, CHLH, CCH1, GUN5 | GUN5 (GENOMES UNCOUPLED 5)	1,115	0,013
35.2	not assigned.unknown	SGN-U587562	BP909633	Unknown	1,113	0,014
29.5.5	protein.degradation.serine protease	SGN-U576878	AK323642	serine carboxypeptidase S10 family protein	1,113	0,017

35.2	not assigned.unknown	SGN-U564401	BG123179	Unknown	1,113	0,044
34.99	transport.misc	SGN-U598149	BI926185	armadillo repeat-containing protein	1,113	0,015
13.2.5.2	amino acid metabolism.degradation.serine-glycine-cysteine group.glycine	SGN-U580312	DB710078	ATGLDP1 | ATGLDP1 (ARABIDOPSIS THALIANA GLYCINE DECARBOXYLASE P-PROTEIN 1)	1,112	0,014
27.3.73	RNA.regulation of transcription.Zn-finger(CCHC)	SGN-U579301	BT013149	tudor domain-containing protein / nuclease family protein	1,112	0,025
29.7	protein.glycosylation	SGN-U598212	AK326376	galactosyltransferase family protein	1,112	0,020
35.2	not assigned.unknown	SGN-U569813	AW621608	Unknown	1,112	0,013
26.7	misc.oxidases - copper, flavone etc.	SGN-U573146	AK321718	SKS4 | SKS4 (SKU5 Similar 4); copper ion binding / oxidoreductase	1,111	0,020
31.2	cell.division	SGN-U580237	AK320692	cell division cycle protein 48, putative / CDC48, putative	1,110	0,030
35.2	not assigned.unknown	SGN-U597287	BP893827	Unknown	1,109	0,042
34.18	transport.unspecified anions	SGN-U574690	TA49718_4081	ATCCC1, CCC1 | CCC1	1,109	0,036
27.3.7	RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family	SGN-U580347	TA36469_4081	zinc finger (B-box type) family protein	1,108	0,018
35.3	not assigned.disagreeing hits	SGN-U592953	NM_001247139	FPS2 | FPS2 (FARNESYL DIPHOSPHATE SYNTHASE 2)	1,107	0,036
35.2	not assigned.unknown	SGN-U585660	AK247450	Unknown	1,106	0,014
11.8.10	lipid metabolism.'exotics' (steroids, squalene etc).phosphatidylcholinesterol O-	SGN-U582360	AW648854	ATPDAT | ATPDAT (Arabidopsis thaliana phospholipid:diacylglycerol acyltransferase)	1,102	0,016

	acyltransferase					
30.2.17	signalling.receptor kinases.DUF 26	SGN-U602814	AK320661	BRL2 | BRL2 (BRI1-LIKE 2)	1,101	0,023
30.2.5	signalling.receptor kinases.leucine rich repeat V	SGN-U571989	AK321807	SRF7 | SRF7 (STRUBBELIG-RECEPTOR FAMILY 7)	1,101	0,023
35.1	not assigned.no ontology	SGN-U583022	AK326020	conserved oligomeric Golgi complex component-related	1,101	0,032
15.2	metal handling.binding, chelation and storage	SGN-U567922		ATFP3 | ATFP3 (Arabidopsis thaliana farnesylated protein 3)	1,100	0,019
28.99	DNA.unspecified	SGN-U587959	AK326462	endomembrane protein 70, putative	1,100	0,014
35.1	not assigned.no ontology	SGN-U574398	BP880237	NUA | NUA (NUCLEAR PORE ANCHOR)	1,100	0,015
30.5	signalling.G-proteins	SGN-U599426	BG125906	AGD4 | AGD4 (ARF-GAP DOMAIN 4)	1,099	0,018
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U585731	AK322617	bZIP transcription factor family protein	1,098	0,024
35.3	not assigned.disagreeing hits	SGN-U580766	AI773607	glycosyl hydrolase family 1 protein	1,098	0,016
27.1	RNA.processing	SGN-U571310	AI895114	EMB2746 | EMB2746 (EMBRYO DEFECTIVE 2746)	1,097	0,017
11.8.1	lipid metabolism."exotics" (steroids, squalene etc).sphingolipids	SGN-U581354	BG642881	delta-8 sphingolipid desaturase, putative	1,097	0,027
26.10	misc.cytochrome P450	SGN-U585134	TA41318_4081	CYP94C1 | CYP94C1 (cytochrome P450, family 94, subfamily C, polypeptide 1)	1,097	0,030
35.3	not assigned.disagreeing hits	SGN-U580375	BI933909	Phytoene synthase 1	1,096	0,014

28.1	DNA.synthesis/chromatin structure	SGN-U584508	AK325143	similar to endonuclease/exonuclease	1,095	0,020
35.3	not assigned.disagreeing hits	SGN-U588966	BI925071	RNase H domain-containing protein	1,094	0,014
35.1	not assigned.no ontology	SGN-U574703	DB719701	catalytic	1,094	0,018
29.1	protein.aa activation	SGN-U583623	AK322339	pseudouridine synthase and archaeosine transglycosylase (PUA) domain-containing protein	1,093	0,013
28.1	DNA.synthesis/chromatin structure	SGN-U602692	DB725438	ATVT-1, HVT1 | HVT1 (HELICASE IN VASCULAR TISSUE AND TAPETUM)	1,093	0,017
35.3	not assigned.disagreeing hits	SGN-U581550	BG625977	PAD2 | PAD2 (20S proteasome alpha subunit D2)	1,092	0,015
27.1	RNA.processing	SGN-U575889	BP910096	CRM3, HCF152 | HCF152 (HIGH CHLOROPHYLL FLUORESCENCE 152)	1,091	0,031
29.4	protein.postranslational modification	SGN-U576726	AK325534	protein kinase-related	1,090	0,020
35.2	not assigned.unknown	SGN-U599150	BE463030	Unknown	1,090	0,013
29.1	protein.aa activation	SGN-U574106	AK327561	tRNA-binding region domain-containing protein	1,089	0,018
35.3	not assigned.disagreeing hits	SGN-U581138	TA36169_4081	CVP1, FRL1, SMT2 | SMT2 (STEROL METHYLTRANSFERASE 2)	1,089	0,034
35.3	not assigned.disagreeing hits	SGN-U590306	GO374731	25 kDa protein dehydrin	1,088	0,014
35.2	not assigned.unknown	SGN-U576911	AW029841	Unknown	1,088	0,019
35.2	not assigned.unknown	SGN-U576022	AK320395	serine-type endopeptidase	1,086	0,031

35.2	not assigned.unknown	SGN-U573313	BF098273	Unknown	1,085	0,025
35.2	not assigned.unknown	SGN-U574465	BT014138	carbohydrate binding	1,084	0,021
29.5	protein.degradation	SGN-U565226	DB715331	peptidase M3 family protein / thimet oligopeptidase family protein	1,084	0,014
35.1	not assigned.no ontology	SGN-U578271	AK246629	gamma interferon responsive lysosomal thiol reductase family protein	1,084	0,024
35.1	not assigned.no ontology	SGN-U572673	AK322057	Unknown	1,084	0,014
34.2	transporter.sugars	SGN-U571779	AK327074	UTR6, ATUTR6 | ATUTR6/UTR6 (UDP-GALACTOSE TRANSPORTER 6)	1,083	0,018
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U581244	BT014547	60S ribosomal protein L7A (RPL7aA)	1,083	0,014
21.1	redox.thioredoxin	SGN-U575297	AK326716	ATPDIL1-1 | ATPDIL1-1 (PDI-LIKE 1-1)	1,083	0,033
35.2	not assigned.unknown	SGN-U583464	BG627096	Unknown	1,083	0,020
13.1.6.1.5	amino acid metabolism.synthesis.aromatic aa.chorismate.shikimate kinase	SGN-U570855	NM_001247122	EMB3004, MEE32 | EMB3004/MEE32 (EMBRYO DEFECTIVE 3004)	1,082	0,024
30.5	signalling.G-proteins	SGN-U603516	BP899598	GTP binding / GTPase	1,082	0,017
35.2	not assigned.unknown	SGN-U582593	GO373734	Unknown	1,082	0,028
34.2	transporter.sugars	SGN-U571786	TC239905	integral membrane protein, putative	1,082	0,027
35.2	not assigned.unknown	SGN-U566503	TC243468	Unknown	1,081	0,020

29.4	protein.postranslational modification	SGN-U579855	TA43201_4081	tyrosine specific protein phosphatase family protein	1,081	0,032
16.2.1.9	secondary metabolism.phenylpropanoids.lignin biosynthesis.COMT	SGN-U572294	AK330130	OMT1, ATOMT1 | ATOMT1 (O-METHYLTRANSFERASE 1)	1,081	0,015
35.2	not assigned.unknown	SGN-U604334	AW931645	EMB2756 | EMB2756 (EMBRYO DEFECTIVE 2756)	1,080	0,017
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U563859	AK247744	F-box family protein (FBL15)	1,080	0,023
35.2	not assigned.unknown	SGN-U573642	BP884431	Unknown	1,080	0,016
35.2	not assigned.unknown	SGN-U576748	TC243415	Unknown	1,080	0,017
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U574664	AK325868	GAUT6 | GAUT6 (Galacturonosyltransferase 6)	1,080	0,018
30.2.11	signalling.receptor kinases.leucine rich repeat XI	SGN-U565314	AK320840	leucine-rich repeat transmembrane protein kinase, putative	1,079	0,028
19.10	tetrapyrrole synthesis.magnesium chelatase	SGN-U584294	TA37909_4081	CCH, CHLH, CCH1, GUN5 | GUN5 (GENOMES UNCOUPLED 5)	1,079	0,020
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U581111	NM_001247749	40S ribosomal protein S17 (RPS17D)	1,079	0,016
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U565135	AK326695	NCRK | protein kinase family protein	1,078	0,016
34.1	transport.p- and v-ATPases	SGN-U586352	DB714832	VHA-A1 | VHA-A1 (VACUOLAR PROTON ATPASE A 1)	1,078	0,016
35.1	not assigned.no ontology	SGN-U574481	AK329224	ChaC-like family protein	1,077	0,017
29.5.5	protein.degradation.serine protease	SGN-U583309	AK320911	SCPL18 | SCPL18 (serine carboxypeptidase-like 18)	1,077	0,015

35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U568826	BE463392	TTL1 | TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 1)	1,077	0,017
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U565042	BI421829	Unknown	1,077	0,018
23.1.2.31	nucleotide metabolism.synthesis.purine.GMP synthetase	SGN-U581676	BI928978	GMP synthase (glutamine-hydrolyzing)	1,076	0,018
29.6	protein.folding	SGN-U564192	BT012800	ATTCP-1 | ATTCP-1 (Arabidopsis thaliana T-complex protein 1 alpha subunit)	1,076	0,025
35.3	not assigned.disagreeing hits	SGN-U574622	TA45487_4081	Unknown	1,076	0,035
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U584655	AK328487	SRF8 | SRF8 (STRUBBELIG-RECEPTOR FAMILY 8)	1,076	0,020
33.99	development.unspecified	SGN-U586127	TA55963_4081	transducin family protein / WD-40 repeat family protein	1,074	0,016
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U591099	NM_001247022	ATNADP-ME2 | ATNADP-ME2 (NADP-MALIC ENZYME 2)	1,074	0,018
28.1.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase.gypsy-like retrotransposon	SGN-U578865	BI208826	polyprotein	1,074	0,042
35.2	not assigned.unknown	SGN-U601529	AK321701	Unknown	1,071	0,018
29.5.11.20	protein.degradation.ubiquitin.proteasom	SGN-U571876	AK326495	RPN6, ATS9 | ATS9 (19S PROTEOSOME SUBUNIT 9)	1,071	0,016
35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U584718	AK319804	tetratricopeptide repeat (TPR)-containing protein	1,071	0,016
35.2	not assigned.unknown	SGN-U568715	AK327933	Unknown	1,070	0,014

26.10	misc.cytochrome P450	SGN-U584419	AK327507	CYP721A1 | CYP721A1 (cytochrome P450, family 721, subfamily A, polypeptide 1)	1,069	0,014
15.2	metal handling.binding, chelation and storage	SGN-U568708	TA39691_4081	copper-binding family protein	1,067	0,014
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U593486	NM_001247068	EMB2207, RPL3A | ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1)	1,067	0,014
35.2	not assigned.unknown	SGN-U571394	TA49074_4081	Unknown	1,066	0,023
27.1.19	RNA.processing.ribonucleases	SGN-U563467	TA55598_4081	3' exoribonuclease family domain 1-containing protein	1,066	0,018
35.2	not assigned.unknown	SGN-U601306	BG133051	Unknown	1,066	0,018
35.1	not assigned.no ontology	SGN-U563131	BP908167	WD-40 repeat family protein	1,066	0,018
27.3.44	RNA.regulation of transcription.Chromatin Remodeling Factors	SGN-U571955	AW219669	ATBRM, CHR2, BRM | ATBRM/BRM/CHR2 (ARABIDOPSIS THALIANA BRAHMA)	1,065	0,016
29.7	protein.glycosylation	SGN-U572561	AK328417	galactosyltransferase family protein	1,064	0,017
28.1	DNA.synthesis/chromatin structure	SGN-U588684	AK322104	DEAD/DEAH box helicase, putative	1,064	0,023
11.1.3	lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase	SGN-U564580	TA39423_4081	KAS2, FAB1 | FAB1 (FATTY ACID BIOSYNTHESIS 1); fatty-acid synthase	1,064	0,014
35.2	not assigned.unknown	SGN-U574847	DB681288	peptidyl-prolyl cis-trans isomerase	1,063	0,020
29.8	protein assembly and cofactor ligation	SGN-U586752	TA56545_4081	YCF2.2 | hypothetical protein	1,063	0,016
13.1.5.1	amino acid metabolism.synthesis.serine-glycine-cysteine group.serine	SGN-U576885	DB720017	PSAT | PSAT (phosphoserine aminotransferase); phosphoserine transaminase	1,062	0,035

29.3.2	protein.targeting.mitochondria	SGN-U569105	AK326026	mitochondrial processing peptidase alpha subunit, putative	1,060	0,025
20.2.1	stress.abiotic.heat	SGN-U566621	TA53661_4081	heat shock family protein	1,060	0,015
35.3	not assigned.disagreeing hits	SGN-U581048	AK328025	SEC14 cytosolic factor, putative	1,059	0,018
28.1	DNA.synthesis/chromatin structure	SGN-U569920	BI207235	replication protein, putative	1,059	0,017
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U577031	TA54059_4081	glycosyltransferase family protein 1	1,058	0,016
11.1.1	lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	SGN-U574951	AK321685	CAC3 | CAC3 (acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit)	1,058	0,014
35.3	not assigned.disagreeing hits	SGN-U579317	DB679602	ATRZ-1A | ATRZ-1A	1,057	0,029
35.1	not assigned.no ontology	SGN-U585625	BF097548	transferase family protein	1,057	0,021
27.3.4	RNA.regulation of transcription.ARF, Auxin Response Factor family	SGN-U563944	JF911788	ARF10 | ARF10 (AUXIN RESPONSE FACTOR 10)	1,057	0,024
30.5	signalling.G-proteins	SGN-U569009	AK320649	transducin family protein / WD-40 repeat family protein	1,057	0,016
31.4	cell.vesicle transport	SGN-U575243	BT014065	clathrin heavy chain, putative	1,056	0,022
9.7	mitochondrial electron transport / ATP synthesis.cytochrome c oxidase	SGN-U562836	BG626470	cytochrome c oxidase family protein	1,056	0,027
35.2	not assigned.unknown	SGN-U604759	AK325137	Unknown	1,055	0,019
35.3	not assigned.disagreeing hits	SGN-U579275	AK319311	protein kinase family protein	1,055	0,031

3.4.5	minor CHO metabolism.myo-inositol.inositol phosphatase	SGN-U600217	NM_001246972	VTC4 | VTC4 |	1,054	0,024
35.1	not assigned.no ontology	SGN-U581851	BI933977	KH domain-containing protein	1,052	0,015
27.1	RNA.processing	SGN-U579030	BG132910	similar to small nuclear ribonucleoprotein D2, putative	1,051	0,017
20.2.3	stress.abiotic.drought/salt	SGN-U565822	TA39504_4081	QUA2, TSD2 | TSD2 (TUMOROUS SHOOT DEVELOPMENT 2)	1,051	0,019
35.3	not assigned.disagreeing hits	SGN-U589324	AK325069	UGP | Is thought to encodes a cytosolic UDP-glucose pyrophosphorylase with strong similarity to UTP--glucose-1-phosphate uridylyltransferase	1,051	0,014
35.2	not assigned.unknown	SGN-U562670	BE451616	Unknown	1,049	0,042
34.99	transport.misc	SGN-U563519	BE449940	antiporter/ drug transporter	1,049	0,016
23.3.1.1	nucleotide metabolism.salvage.phosphoribosyltransferases.aprt	SGN-U580093	TA36378_4081	APT1, ATAPT1, APRT | APT1	1,048	0,024
29.2.3	protein.synthesis.initiation	SGN-U569943	AK321795	EIF3B, ATEIF3B-1, EIF3B-1, ATTIF3B1, TIF3B1 | TIF3B1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 3B)	1,048	0,042
35.2	not assigned.unknown	SGN-U572950	AK321943	similar to mucin-related	1,048	0,028
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family	SGN-U575104	AK328268	trihelix DNA-binding protein, putative	1,048	0,024
27.3.69	RNA.regulation of transcription.SET-domain transcriptional regulator family	SGN-U576415	DB724330	SET domain-containing protein	1,048	0,014
30.3	signalling.calcium	SGN-U569248	GT167380	HhH-GPD base excision DNA repair family protein, similar to DEMETER protein (Arabidopsis thaliana)	1,048	0,014

20.2.3	stress.abiotic.drought/salt	SGN-U563766	BT013808	early-responsive to dehydration protein-related	1,047	0,016
13.2.4.1	amino acid metabolism.degradation.branched-chain group.shared	SGN-U568125	AK247473	2-oxoisovalerate dehydrogenase, putative	1,047	0,032
35.1	not assigned.no ontology	SGN-U584564	DB681969	FPA | FPA	1,047	0,015
35.1	not assigned.no ontology	SGN-U569459	FN556059	CDC20.1 | CDC20.1	1,046	0,025
29.5.11.20	protein.degradation.ubiquitin.proteasom	SGN-U570781	BG135721	RPT1A | RPT1A (regulatory particle triple-A 1A)	1,045	0,014
29.5.11.20	protein.degradation.ubiquitin.proteasom	SGN-U589320	BI935646	26S proteasome regulatory subunit, putative	1,045	0,018
27.3.46	RNA.regulation of transcription.DNA methyltransferases	SGN-U569088	NM_001247819	METI, DDM2, DMT01, MET2, DMT1, MET1 | MET1 (DECREASED METHYLATION 2DNA)	1,044	0,014
33.99	development.unspecified	SGN-U584554	DB720178	ANAC078, NAC2 | NAC2 (Arabidopsis NAC domain containing protein 78)	1,044	0,019
35.1	not assigned.no ontology	SGN-U592289	AK246629	gamma interferon responsive lysosomal thiol reductase family protein	1,044	0,022
3.4.4	minor CHO metabolism.myo-inositol.myo inositol oxygenases	SGN-U565448	NM_001247664	Symbols: MIOX4 | MIOX4 (MYO-INOSITOL OXYGENASE 4)	1,043	0,027
35.2	not assigned.unknown	SGN-U583892	TA55465_4081	Unknown	1,043	0,013
29.5	protein.degradation	SGN-U562601	GO374987	peptidase M1 family protein	1,042	0,031
27.1	RNA.processing	SGN-U598320	DB720040	polynucleotide adenylyltransferase family protein	1,042	0,018
35.2	not assigned.unknown	SGN-U580379		protein binding / protein transporter	1,042	0,015

35.2	not assigned.unknown	SGN-U568296	TC233940	Unknown	1,042	0,017
11.1.1	lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	SGN-U601457	AW928749	ATP binding / biotin binding / catalytic/ ligase	1,041	0,013
35.2	not assigned.unknown	SGN-U602497		Unknown	1,040	0,016
35.1	not assigned.no ontology	SGN-U564112	AK326994	transferase family protein	1,039	0,021
35.1	not assigned.no ontology	SGN-U575430	DB697932	LMBR1 integral membrane family protein	1,039	0,014
27.1	RNA.processing	SGN-U567991	AK320796	transducin family protein / WD-40 repeat family protein	1,039	0,017
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U575805	TA42606_4081	FER | FER (FERONIA)	1,038	0,036
29.4	protein.postranslational modification	SGN-U563668	TA54578_4081	protein kinase family protein	1,038	0,014
35.1	not assigned.no ontology	SGN-U567698	AK328940	metal-dependent phosphohydrolase HD domain-containing protein	1,038	0,015
31.4	cell.vesicle transport	SGN-U562686	AK246484	clathrin heavy chain, putative	1,037	0,014
13.1.3.4	amino acid metabolism.synthesis.aspartate family.methionine	SGN-U586307	AK322467	ATMETS, ATMS1, ATCIMS | ATCIMS (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)	1,037	0,019
35.2	not assigned.unknown	SGN-U599034	BP910500	Unknown	1,036	0,024
35.2	not assigned.unknown	SGN-U591251	DB714116	Unknown	1,035	0,025
9.2.2	mitochondrial electron transport / ATP synthesis.NADH-DH.type	SGN-U582810	AK319193	NDB2 | NDB2 (NAD(P)H DEHYDROGENASE B2)	1,034	0,023

	II.external					
35.1	not assigned.no ontology	SGN-U576585	AK319887	catalytic	1,033	0,026
34.99	transport.misc	SGN-U601546	TC243304	Unknown	1,033	0,020
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U568047	AK322397	protein kinase family protein	1,033	0,017
34.99	transport.misc	SGN-U564826	AK327950	calmodulin-binding protein	1,033	0,020
17.7.1.3	hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	SGN-U576466	NM_001247904	CYP74A, AOS | AOS (ALLENE OXIDE SYNTHASE)	1,032	0,028
31.3	cell.cycle	SGN-U593065	AK247372	CYCD4;2 | CYCD4;2 (CYCLIN D4;2); cyclin-dependent protein kinase	1,031	0,032
29.2.4	protein.synthesis.elongation	SGN-U569140	AK325579	elongation factor Tu, putative	1,030	0,018
33.99	development.unspecified	SGN-U570490	AW931215	AGO1 | AGO1 (ARGONAUTE 1)	1,030	0,016
27.3.99	RNA.regulation of transcription.unclassified	SGN-U574306	AK321625	ATLA1 | ATLA1 (ARABIDOPSIS THALIANA LA PROTEIN 1)	1,030	0,018
35.2	not assigned.unknown	SGN-U600607	EG553913	Unknown	1,029	0,014
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U569071		CSLG1, CSLG2, ATCSLG1 | ATCSLG1 (Cellulose synthase-like G1)	1,029	0,024
21.2.2	redox.ascorbate and glutathione.glutathione	SGN-U580790	AK320894	GGT3, GGT4 | GGT3/GGT4 (GAMMA-GLUTAMYL TRANSPEPTIDASE 3)	1,029	0,013

35.2	not assigned.unknown	SGN-U586930	BP910041	Unknown	1,028	0,028
28.1	DNA.synthesis/chromatin structure	SGN-U565609	AK325361	DEAD/DEAH box helicase, putative (RH22)	1,028	0,019
35.2	not assigned.unknown	SGN-U602317	DB717643	Unknown	1,027	0,018
30.3	signalling.calcium	SGN-U585337	TA41147_4081	ATBAG7 | ATBAG7 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 7)	1,026	0,030
35.2	not assigned.unknown	SGN-U568321	AW036282	Unknown	1,025	0,014
35.1	not assigned.no ontology	SGN-U570592	TA44737_4081	SART-1 family protein	1,025	0,015
35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U564997	BT013829	pentatricopeptide (PPR) repeat-containing protein	1,025	0,016
30.6	signalling.MAP kinases	SGN-U569855	BW687300	MPK7, ATMPK7 | ATMPK7 (MAP KINASE 7)	1,025	0,014
35.1	not assigned.no ontology	SGN-U600331	AK326973	hydrolase, alpha/beta fold family protein	1,024	0,022
35.2	not assigned.unknown	SGN-U601464	DB718443	Unknown	1,024	0,032
29.2.1.2.2.31	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L31	SGN-U580127	BG124508	60S ribosomal protein L31 (RPL31A)	1,024	0,015
35.1	not assigned.no ontology	SGN-U564396	AW032793	transducin family protein / WD-40 repeat family protein	1,022	0,019
34.99	transport.misc	SGN-U595514	AK320022	SEC14 cytosolic factor, putative	1,022	0,025

27.1.19	RNA.processing.ribonucleases	SGN-U565374	NP1427430	RNase H domain-containing protein	1,022	0,037
33.99	development.unspecified	SGN-U577343	AI490943	OCP11, AGO4 | AGO4 (ARGONAUTE 4)	1,021	0,032
30.1	signalling.in sugar and nutrient physiology	SGN-U565402	AK320123	glucose-inhibited division family A protein	1,021	0,022
25	C1-metabolism	SGN-U578810		SHM2 | SHM2 (SERINE HYDROXYMETHYLTRANSFERASE 2)	1,020	0,025
27.2	RNA.transcription	SGN-U572072	AK322543	similar to REV1 (Reversionless 1), damaged DNA binding	1,020	0,018
35.1	not assigned.no ontology	SGN-U574177	AW929412	EMB2773 | EMB2773 (EMBRYO DEFECTIVE 2773)	1,019	0,024
11.8.1	lipid metabolism."exotics" (steroids, squalene etc).sphingolipids	SGN-U577442	TC244886	delta-8 sphingolipid desaturase, putative	1,017	0,014
35.2	not assigned.unknown	SGN-U584685	AW979916	Unknown	1,017	0,017
35.2	not assigned.unknown	SGN-U569817	AK328106	Unknown	1,017	0,020
35.1	not assigned.no ontology	SGN-U580258	AK327292	D111/G-patch domain-containing protein	1,017	0,014
27.4	RNA.RNA binding	SGN-U568334	TC241353	RNA binding	1,016	0,016
29.2.1.1.1.1.7	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S7	SGN-U587845	AW650353	RPS7.1, RPS7 | encodes a chloroplast ribosomal protein S7, a constituent of the small subunit of the ribosomal complex	1,016	0,013
29.6	protein.folding	SGN-U571326	AK324824	EMB1241 | EMB1241 (EMBRYO DEFECTIVE 1241)	1,016	0,014
2.1.2.1	major CHO metabolism.synthesis.starch.AGPase	SGN-U569800	AK327489	APL3 | APL3 (large subunit of AGP 3)	1,015	0,018

33.99	development.unspecified	SGN-U585854	BP881483	VCS | VCS (VARICOSE)	1,015	0,014
35.1	not assigned.no ontology	SGN-U575094	BG126500	merozoite surface protein-related	1,015	0,015
35.2	not assigned.unknown	SGN-U566247	BG130280	Unknown	1,015	0,031
17.7.1.3	hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	SGN-U570004	NM_001247491	CYP74B2, HPL1 | HPL1 (HYDROPEROXIDE LYASE 1)	1,014	0,019
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U599802	BG126335	leucine-rich repeat family protein / protein kinase family protein	1,014	0,014
35.2	not assigned.unknown	SGN-U571662	AW219209	Unknown	1,014	0,015
35.2	not assigned.unknown	SGN-U573271	BP907652	Unknown	1,013	0,021
27.3.4	RNA.regulation of transcription.ARF, Auxin Response Factor family	SGN-U571612	NM_001247942	ARF1 | ARF1 (AUXIN RESPONSE FACTOR 1)	1,013	0,014
29.4	protein.postranslational modification	SGN-U566985	AK247067	Unknown	1,012	0,014
28.1	DNA.synthesis/chromatin structure	SGN-U599238		DNA topoisomerase, ATP-hydrolyzing, putative	1,012	0,019
27.3.52	RNA.regulation of transcription.Global transcription factor group	SGN-U572928	NM_001247445	GTE7 | GTE7 (GLOBAL TRANSCRIPTION FACTOR GROUP E 7)	1,012	0,016
13.1.5.1	amino acid metabolism.synthesis.serine-glycine-cysteine group.serine	SGN-U569119	BF097927	D-3-phosphoglycerate dehydrogenase, putative	1,011	0,032
31.1	cell.organisation	SGN-U570197	AK325490	myosin heavy chain-related	1,009	0,022

35.1.41	not assigned.no ontology.hydroxyproline rich proteins	SGN-U595364	BP910110	CHUP1 | CHUP1 (CHLOROPLAST UNUSUAL POSITIONING 1)	1,008	0,017
30.2.3	signalling.receptor kinases.leucine rich repeat III	SGN-U570451	DB721158	FAS3, FLO5, CLV1 | CLV1 (CLAVATA 1)	1,008	0,045
29.4	protein.postranslational modification	SGN-U570122	AK326278	protein kinase family protein	1,008	0,028
29.6	protein.folding	SGN-U570703	BT013503	HSP60 | HSP60 (Heat shock protein 60)	1,008	0,014
35.2	not assigned.unknown	SGN-U596305	AJ784685	Unknown	1,008	0,023
13.1.6.5	amino acid metabolism.synthesis.aromatic aa.tryptophan	SGN-U585350	AI487343	tryptophan synthase, beta subunit, putative	1,007	0,018
26.6	misc.O- methyl transferases	SGN-U584918	AK320784	protein arginine N-methyltransferase family protein	1,007	0,014
27.1.19	RNA.processing.ribonucleases	SGN-U574251	DB718787	XRN3 | XRN3 (5'-3' exoribonuclease 3); 5'-3' exoribonuclease	1,007	0,014
35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U575088	AK324163	tetratricopeptide repeat (TPR)-containing protein	1,006	0,019
27.2	RNA.transcription	SGN-U583812	AK321664	SIG5, SIGE | SIGE (RNA polymerase sigma subunit E)	1,006	0,018
23.1.2.5	nucleotide metabolism.synthesis.purine.AIR synthase	SGN-U564389	TA42486_4081	Catalytic	1,006	0,020
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U575476	TA53065_4081	WRI, ASML1, WRI1 | WRI1 (WRINKLED 1)	1,006	0,039
35.2	not assigned.unknown	SGN-U601369	BP878464	Unknown	1,006	0,017

30.3	signalling.calcium	SGN-U567628	BI934981	CPK9 | CPK9 (CALMODULIN-DOMAIN PROTEIN KINASE 9)	1,006	0,019
35.2	not assigned.unknown	SGN-U570276	TA53709_4081	Unknown	1,005	0,021
35.1	not assigned.no ontology	SGN-U565308	BP907082	GRL, NAP1, NAPP | GRL/NAP1/NAPP (NCK-ASSOCIATED PROTEIN)	1,005	0,026
1.1.4	PS.lightreaction.ATP synthase	SGN-U576640	BG625890	ATPE | ATPase epsilon subunit	1,005	0,017
29.4	protein.postranslational modification	SGN-U584542	AK247266	HAB1 | HAB1 (HOMOLOGY TO ABI1)	1,001	0,028
35.2	not assigned.unknown	SGN-U564177	DB683889	kinesin light chain-related	1,001	0,014
34.12	transport.metal	SGN-U570283	DB679965	CHX17, ATCHX17 | ATCHX17 (CATION/H+ EXCHANGER 17)	1,001	0,016

Table 5. List of down-regulated genes genes (log2 ratio sub-/optimal T≤−1 and q- value<0.05) deteced only in the roots of the grafted ‘Kommeet’ plants onto ‘LA 1777’ (R/S:LA/KO) under sub-optimal root T stress.

BinCode	BinName	SGN	NCBI	description	LA/KO Log FC	adj.P.Val
20.2.1	stress.abiotic.heat	SGN-U578410	AF123259	heat shock protein 90	-4,181	0,011
35.2	not assigned.unknown	SGN-U580955	BW692346	auxin and ethylene responsive GH3-like proteinProbable indole-3-acetic acid-amido synthetase	-3,573	0,036
35.2	not assigned.unknown	SGN-U565578	AI777810	Unknown	-3,530	0,014
31.1	cell.organisation	SGN-U582025	BT012689	kinesin light chain I2I isoform	-3,376	0,011
26.9	misc.glutathione S transferases	SGN-U578214	AI778098	Glutathione S-transferase-like protein	-3,118	0,019
29.2.3	protein.synthesis.initiation	SGN-U578546	AK246862	mitochondrial small heat shock protein	-3,094	0,018
20.2.1	stress.abiotic.heat	SGN-U580334	BM410601	HSP70 | HSP70 (heat shock protein 70); ATP binding	-2,960	0,014
20.2.1	stress.abiotic.heat	SGN-U593766	DV103891	HSP17.6II | 17.6 kDa class II heat shock protein	-2,628	0,016
35.1	not assigned.no ontology	SGN-U586347	AK246610	Glutathione S-transferase-like protein	-2,581	0,046
10.7	cell wall.modification	SGN-U577404	BT013002	Expansin-like protein Expansin 45, endoglucanase-like	-2,577	0,030
26.10	misc.cytochrome P450	SGN-U581088	AW625751	Cytochrome P450	-2,527	0,021
5.3	fermentation.ADH	SGN-U579191	M86724	alcohol dehydrogenase	-2,351	0,033
17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U568288	EG553451	Ethylene responsive transcription factor 1a	-2,349	0,013

35.2	not assigned.unknown	SGN-U567920	DB722922	Unknown	-2,276	0,020
35.3	not assigned.disagreeing hits	SGN-U579632	M86724	alcohol dehydrogenase	-2,207	0,014
20.1	stress.biotic	SGN-U575000	BI211052	PDF1.4 | plant defensin-fusion protein, putative (PDF1.4), plant defensin protein	-2,192	0,023
35.1	not assigned.no ontology	SGN-U563321	BT014218	Mpv17 protein	-2,189	0,013
35.1	not assigned.no ontology	SGN-U573548	DB704226	Xylanase inhibitor (Fragment) Peptidase A1	-2,136	0,011
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U584756	AY192368	ethylene response factor 2b transcription regulator activity	-2,114	0,014
35.3	not assigned.disagreeing hits	SGN-U582992	DB712015	SRC2 protein C2 calcium-dependent membrane targeting	-2,111	0,011
13.2.2.3	amino acid metabolism.degradation.glutamate family.arginine	SGN-U567875	AY656838	arginase 2	-2,101	0,014
35.2	not assigned.unknown	SGN-U578266	AK224823	Avr9/Cf-9 rapidly elicited protein 65 [Nicotiana tabacum]	-2,085	0,013
17.7.1.3	hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	SGN-U585215	AF317515	divinyl ether synthase	-2,074	0,014
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U570776	TA56107_4081	kelch repeat-containing F-box family protein	-2,069	0,030
29.1	protein.aa activation	SGN-U570742	X94451	lysyl-tRNA synthetase	-2,067	0,040
26.18	misc.invertase/pectin methylesterase inhibitor family protein	SGN-U579697	AJ010943	tomato invertase inhibitor	-2,063	0,014
35.2	not assigned.unknown	SGN-U591533	AK224683	AAA-type ATPase family protein	-2,040	0,011

30.3	signalling.calcium	SGN-U566130	DB719594	calcium-binding EF hand family protein	-2,014	0,011
20.2.1	stress.abiotic.heat	SGN-U580334	TA39592_4081	HSP70 | HSP70 (heat shock protein 70)	-1,993	0,013
35.2	not assigned.unknown	SGN-U572824	TA39658_4081	Unknown	-1,964	0,011
26.7	misc.oxidases - copper, flavone etc.	SGN-U570271	BI423084	monooxygenase, putative (MO1)	-1,963	0,013
20.2.1	stress.abiotic.heat	SGN-U581229	AK325130	ATHSP90.1, ATHS83, HSP81.1, HSP83, HSP81-1 | HSP81-1 (HEAT SHOCK PROTEIN 81-1)	-1,961	0,015
35.2	not assigned.unknown	SGN-U577872	NM_001247943	gamma-thionin precursor	-1,958	0,021
35.2	not assigned.unknown	SGN-U573706	TA56244_4081	Unknown	-1,920	0,023
29.4	protein.postranslational modification	SGN-U580895	AK326271	ATMTK | ATMTK; S-methyl-5-thioribose kinase	-1,916	0,026
13.2.2.3	amino acid metabolism.degradation.glutamate family.arginine	SGN-U567876	NM_001247649	arginase	-1,906	0,018
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U579714	AK322979	transcription factor jumonji (jmjC) domain-containing protein	-1,887	0,026
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U578883	AK322653	2-oxoglutarate-dependent dioxygenase, putative	-1,859	0,030
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U570342	AK320729	exostosin family protein	-1,823	0,013
35.3	not assigned.disagreeing hits	SGN-U595409	BF096608	ILR3 | ILR3 (IAA-LEUCINE RESISTANT3)	-1,814	0,015
35.2	not assigned.unknown	SGN-U588195	AK321978	Unknown	-1,813	0,016

20.2.1	stress.abiotic.heat	SGN-U580107	TA37064_4081	ATHSP90.1, ATHS83, HSP81.1, HSP83, HSP81-1 | HSP81-1 (HEAT SHOCK PROTEIN 81-1)	-1,778	0,011
34.3	transport.amino acids	SGN-U585666	DB698909	amino acid transporter family protein	-1,771	0,013
35.1	not assigned.no ontology	SGN-U563108	AI486533	DC1 domain-containing protein	-1,771	0,047
27.3.66	RNA.regulation of transcription.Psudo ARR transcription factor family	SGN-U564924	BM409758	APRR7, PRR7 | PRR7 (PSEUDO-RESPONSE REGULATOR 7)	-1,767	0,014
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U562994	AK319935	AP2 domain-containing transcription factor, putative	-1,762	0,035
35.3	not assigned.disagreeing hits	SGN-U593152	AK322979	transcription factor jumonji (jmjC) domain-containing protein	-1,759	0,023
35.2	not assigned.unknown	SGN-U589155	DB721908	Unknown	-1,759	0,016
26.7	misc.oxidases - copper, flavone etc.	SGN-U597056	BI422682	monooxygenase, putative (MO1)	-1,756	0,016
35.2	not assigned.unknown	SGN-U568025	BT013968	Unknown	-1,752	0,014
34.9	transport.metabolite transporters at the mitochondrial membrane	SGN-U585496	AK320448	mitochondrial substrate carrier family protein	-1,746	0,014
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U578910	NM_001247789	ZAT10, STZ | STZ (SALT TOLERANCE ZINC FINGER)	-1,743	0,013
20.2.1	stress.abiotic.heat	SGN-U578504	NM_001247562	HSP70-1, AT-HSC70-1, HSC70, HSC70-1 | HSC70-1 (heat shock cognate 70 kDa protein 1)	-1,742	0,014
35.1	not assigned.no ontology	SGN-U577321	TA44718_4081	nonsense-mediated mRNA decay NMD3 family protein	-1,733	0,014
30.3	signalling.calcium	SGN-U581708	TA41341_4081	calmodulin, putative	-1,719	0,013

27.3.12	RNA.regulation of transcription.C3H zinc finger family	SGN-U584538	AK319232	zinc finger (CCCH-type) family protein	-1,719	0,015
35.2	not assigned.unknown	SGN-U589870	DB694032	Unknown	-1,718	0,038
35.1.21	not assigned.no ontology.epsin N-terminal homology (ENTH) domain-containing protein	SGN-U578804	AK325279	epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	-1,715	0,017
35.2	not assigned.unknown	SGN-U564684	BT013183	Unknown	-1,710	0,014
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U573533	AK327684	GH3.1 | GH3.1	-1,707	0,014
23.5	nucleotide metabolism.deoxynucleotide metabolism	SGN-U574758	AK325523	deoxyuridine 5'-triphosphate nucleotidohydrolase family	-1,700	0,015
34.99	transport.misc	SGN-U566609	AK325064	alanine racemase family protein	-1,697	0,015
23.5	nucleotide metabolism.deoxynucleotide metabolism	SGN-U574842	DB690160	RNR2, RNR2A | RNR2/RNR2A (RIBONUCLEOTIDE REDUCTASE 2A); ribonucleoside-diphosphate reductase	-1,687	0,013
31.1	cell.organisation	SGN-U575853	AK319967	MEE66 | MEE66 (maternal effect embryo arrest 66)	-1,683	0,030
20.2.1	stress.abiotic.heat	SGN-U578772	AK322252	ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3)	-1,679	0,024
35.2	not assigned.unknown	SGN-U592246	DB714168	er lumen retaining receptor family-like protein	-1,675	0,016
35.3	not assigned.disagreeing hits	SGN-U581383	TA36621_4081	Unknown	-1,655	0,013
29.5	protein.degradation	SGN-U576671	BP906450	peptidase M28 family protein	-1,652	0,014
35.3	not assigned.disagreeing hits	SGN-U595215	AK319670	thylakoid lumenal protein-related	-1,651	0,022

5.10	fermentation.aldehyde dehydrogenase	SGN-U572014	BI422460	ALDH2, ALDH2B4 | ALDH2B4 (ALDEHYDE DEHYDROGENASE 2); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	-1,650	0,016
35.2	not assigned.unknown	SGN-U577824	TC217988	Unknown	-1,648	0,014
20.2.1	stress.abiotic.heat	SGN-U579266	TA36595_4081	HSP101, HOT1, ATHSP101 | ATHSP101 (HEAT SHOCK PROTEIN 101)	-1,632	0,017
35.2	not assigned.unknown	SGN-U570574	AK330018	Unknown	-1,625	0,036
20.2.99	stress.abiotic.unspecified	SGN-U564896	AK329642	germin-like protein, putative	-1,609	0,014
30.3	signalling.calcium	SGN-U584192	AK322468	calmodulin-binding protein	-1,605	0,023
9.1.2	mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear	SGN-U566850	GO376051	NADH-ubiquinone oxidoreductase 24 kDa subunit, putative	-1,598	0,033
35.1	not assigned.no ontology	SGN-U575187	AK323266	ORC2, ATORC2 | ATORC2/ORC2 (ORIGIN RECOGNITION COMPLEX SECOND LARGEST SUBUNIT)	-1,594	0,013
29.5.7	protein.degradation.metalloprotease	SGN-U573510	AK322919	Matrixin family protein	-1,585	0,034
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U578026	NM_001247012	BUM1, SHL, WAM1, BUM, WAM, STM | STM (SHOOT MERISTEMLESS)	-1,581	0,015
30.3	signalling.calcium	SGN-U582928	TA55900_4081	Calcium-binding EF hand family protein	-1,580	0,023
26.9	misc.glutathione S transferases	SGN-U582824	NM_001247293	ATGSTU8 | ATGSTU8 (Arabidopsis thaliana Glutathione S-transferase (class tau) 8)	-1,574	0,016
26.24	misc.GCN5-related N-acetyltransferase	SGN-U574896	AI774304	GCN5-related N-acetyltransferase (GNAT) family protein	-1,552	0,048
26.9	misc.glutathione S transferases	SGN-U581942	TA39120_4081	ATGSTU8 | ATGSTU8 (Arabidopsis thaliana Glutathione S-transferase (class tau) 8)	-1,548	0,032

35.3	not assigned.disagreeing hits	SGN-U570002	AK319191	BAG6, ATBAG6 | BAG6 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 6)	-1,546	0,014
21.1	redox.thioredoxin	SGN-U580753	AK319594	ATCDSP32, CDSP32 | ATCDSP32/CDSP32 (CHLOROPLASTIC DROUGHT-INDUCED STRESS PROTEIN OF 32 KD)	-1,540	0,017
35.2	not assigned.unknown	SGN-U578798	AK325905	Unknown	-1,538	0,014
11.9.3	lipid metabolism.lipid degradation.lysophospholipases	SGN-U573868	AI779886	transducin family protein / WD-40 repeat family protein	-1,537	0,023
35.3	not assigned.disagreeing hits	SGN-U592427	AK322252	DNAJ heat shock protein	-1,534	0,026
21.2.1	redox.ascorbate and glutathione.ascorbate	SGN-U579887	AK246667	APX1B | APX2 (ASCORBATE PEROXIDASE 2); L-ascorbate peroxidase	-1,529	0,016
35.1	not assigned.no ontology	SGN-U581038	BI933936	DC1 domain-containing protein	-1,526	0,016
20.2.1	stress.abiotic.heat	SGN-U580742	TA51875_4081	17.8 kDa class I heat shock protein (HSP17.8-CI)	-1,524	0,011
33.99	development.unspecified	SGN-U575389	AK320961	nodulin family protein	-1,523	0,024
35.3	not assigned.disagreeing hits	SGN-U579093	AK321445	SIP1;1, SIP1A | SIP1;1 (SMALL AND BASIC INTRINSIC PROTEIN 1A)	-1,523	0,013
20.1.7	stress.biotic.PR-proteins	SGN-U573229	NM_001247498	disease resistance family protein	-1,517	0,011
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U571171	AW032175	bZIP protein	-1,513	0,013
30.3	signalling.calcium	SGN-U580891	TA40531_4081	calcium-binding EF hand family protein	-1,512	0,013
27.1.19	RNA.processing.ribonucleases	SGN-U578982	TA39474_4081	CCR4-NOT transcription complex protein, putative	-1,509	0,014
1.1.5.3	PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase	SGN-U579448	BT013070	ATLFNR1 | ATLFNR1 (LEAF FNR 1); poly(U) binding	-1,505	0,018

26.28	misc.GDSL-motif lipase	SGN-U583252	GO376212	GDSL-motif lipase/hydrolase family protein	-1,503	0,032
34.99	transport.misc	SGN-U591906	AK319299	transport protein particle (TRAPP) component Bet3, putative	-1,498	0,032
27.1.19	RNA.processing.ribonucleases	SGN-U581727	ES893108	ATRTL1 | ribonuclease III family protein	-1,491	0,038
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U577538	TA40919_4081	zinc finger (C2H2 type) family protein (ZAT11)	-1,490	0,033
20.1	stress.biotic	SGN-U597839	AW933578	pathogenesis-related thaumatin family protein	-1,489	0,017
26.7	misc.oxidases - copper, flavone etc.	SGN-U581242	AW222567	oxidoreductase, zinc-binding dehydrogenase family protein	-1,487	0,023
35.2	not assigned.unknown	SGN-U576166	BF176502	Unknown	-1,486	0,011
30.5	signalling.G-proteins	SGN-U586065	AW036207	guanine nucleotide exchange family protein	-1,480	0,013
16.8.2	secondary metabolism.flavonoids.chalcones	SGN-U580856	NM_001247107	CHS, TT4, ATCHS | ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase	-1,478	0,014
29.5.4	protein.degradation.aspartate protease	SGN-U575434	TA54838_4081	Aspartyl protease family protein	-1,477	0,017
35.2	not assigned.unknown	SGN-U586548	AK329274	Unknown	-1,467	0,023
17.7.1.3	hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	SGN-U585217	NM_001247598	CYP74A, AOS | AOS (ALLENE OXIDE SYNTHASE); hydro-lyase/ oxygen binding	-1,456	0,016
35.1.19	not assigned.no ontology.C2 domain-containing protein	SGN-U567016	AW035188	C2 domain-containing protein	-1,453	0,011
35.2	not assigned.unknown	SGN-U569808	GO373235	Unknown	-1,453	0,017
35.2	not assigned.unknown	SGN-U572245	AK322746	Unknown	-1,451	0,014

10.7	cell wall.modification	SGN-U583203	BI921925	XET, XTH33 | XTH33 (xyloglucan:xyloglucosyl transferase 33)	-1,451	0,032
26.9	misc.glutathione S transferases	SGN-U577924	TA37423_4081	GST8, ATGSTU19 | ATGSTU19 (GLUTATHIONE TRANSFERASE 8)	-1,445	0,026
35.2	not assigned.unknown	SGN-U582095	AK325896	Unknown	-1,445	0,015
29.4	protein.postranslational modification	SGN-U579613	AK321489	peptide methionine sulfoxide reductase, putative	-1,441	0,014
2.2.1.5	major CHO metabolism.degradation.sucrose.Susy	SGN-U593624	NM_001247875	SUS1, ASUS1, ATSUS1 | SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase	-1,440	0,013
20.2.99	stress.abiotic.unspecified	SGN-U564895	AK330064	germin-like protein, putative	-1,438	0,027
26.9	misc.glutathione S transferases	SGN-U577816	NM_001247849	ATGSTU8 | ATGSTU8 (Arabidopsis thaliana Glutathione S-transferase (class tau) 8	-1,437	0,032
15.3	metal handling.regulation	SGN-U580506	GO375573	ATARD2 | ATARD2	-1,435	0,028
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U563455	TA42242_4081	IXR11, KNAT7 | KNAT7 (Knotted-like Arabidopsis thaliana)	-1,432	0,015
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U576324	AK321029	armadillo/beta-catenin repeat family protein	-1,430	0,015
35.3	not assigned.disagreeing hits	SGN-U578726	AI898286	exostosin family protein	-1,427	0,020
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U579164	AK322971	Unknown	-1,423	0,014
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U580551	AK327872	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-1,420	0,027
34.5	transport.ammonium	SGN-U577075	NM_001247324	ATAMT1;2 | ATAMT1;2 (AMMONIUM TRANSPORTER 1;2)	-1,420	0,016
20.1	stress.biotic	SGN-U564929	AK329225	pathogenesis-related family protein	-1,418	0,013

33.99	development.unspecified	SGN-U562912	TA45441_4081	senescence-associated protein-related	-1,412	0,021
20.2.4	stress.abiotic.touch/wounding	SGN-U579699	AK326221	Wound-responsive family protein	-1,409	0,011
35.2	not assigned.unknown	SGN-U581932	AK319947	Unknown	-1,408	0,014
35.2	not assigned.unknown	SGN-U597385	AK320866	Unknown	-1,405	0,014
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U578201	NM_001247321	ATHB1, HD-ZIP-1, HAT5, ATHB-1 | ATHB-1 (Homeobox-leucine zipper protein HAT5)	-1,401	0,017
20.2.1	stress.abiotic.heat	SGN-U580038	BW692560	J8 | J8; heat shock protein binding / unfolded protein binding	-1,401	0,026
35.3	not assigned.disagreeing hits	SGN-U578380	AK321205	Unknown	-1,397	0,024
30.3	signalling.calcium	SGN-U597836	BP904822	Calcium-binding EF hand family protein	-1,396	0,014
33.99	development.unspecified	SGN-U578908	TA35588_4081	ET8 | TET8 (TETRASPANIN8)	-1,391	0,011
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U589569	NM_001247235	ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6)	-1,389	0,017
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U576867	TA53701_4081	protein kinase, putative	-1,386	0,017
29.4	protein.postranslational modification	SGN-U575600	AK247509	SnRK3.16, CIPK1 | CIPK1 (CBL-INTERACTING PROTEIN KINASE 1)	-1,383	0,029
26.28	misc.GDSL-motif lipase	SGN-U583253	BI934958	GDSL-motif lipase/hydrolase family protein	-1,383	0,025
35.3	not assigned.disagreeing hits	SGN-U591510	NM_001247789	c2h2-type zinc finger protein	-1,371	0,018

26.10	misc.cytochrome P450	SGN-U565859	AW031132	CYP84A1, FAH1 | FAH1 (FERULATE-5-HYDROXYLASE 1); ferulate 5-hydroxylase	-1,370	0,021
35.2	not assigned.unknown	SGN-U573814	AK329756	Unknown	-1,369	0,037
35.2	not assigned.unknown	SGN-U579299	AK328355	Unknown	-1,367	0,019
26.10	misc.cytochrome P450	SGN-U573734	AK324374	CYP706A4 | CYP706A4 (cytochrome P450, family 706, subfamily A, polypeptide 4)	-1,364	0,014
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U563326	BW688854	F-box family protein	-1,364	0,037
18.2	Co-factor and vitamine metabolism.thiamine	SGN-U592837	AK319677	TZ, THI1 | THI1 (THIAZOLE REQUIRING)	-1,362	0,022
27.3.99	RNA.regulation of transcription.unclassified	SGN-U581473	NM_001247260	MIF2 | MIF2 (MINI ZINC FINGER 2)	-1,362	0,016
35.2	not assigned.unknown	SGN-U597654	AK329522	Unknown	-1,358	0,012
35.2	not assigned.unknown	SGN-U572399	AK322234	Unknown	-1,356	0,018
17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U577090	NM_001247919	ethylene-responsive element-binding protein, putative	-1,356	0,013
34.13	transport.peptides and oligopeptides	SGN-U603440	BI933762	nitrate transporter (NTP2)	-1,351	0,024
16.7	secondary metabolism.wax	SGN-U577635	AK319964	CER1 | CER1 (ECERIFERUM 1)	-1,350	0,030
2.2.2.1	major CHO metabolism.degradation.starch.starch cleavage	SGN-U577503	BI203568	ATAMY3, AMY3 | AMY3/ATAMY3 (ALPHA-AMYLASE-LIKE 3); alpha-amylase	-1,349	0,013
35.3	not assigned.disagreeing hits	SGN-U579815	AK325709	small nuclear ribonucleoprotein F, putative	-1,349	0,011
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U574471	AK247674	kelch repeat-containing F-box family protein	-1,338	0,023

13.2.4.1	amino acid metabolism.degradation.branched-chain group.shared	SGN-U585832	BG133708	DIN4 | DIN4 (DARK INDUCIBLE 4); 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)	-1,336	0,014
35.2	not assigned.unknown	SGN-U584346	AW037717	Unknown	-1,335	0,014
35.3	not assigned.disagreeing hits	SGN-U577571	GO374580	PGR1, PETC | PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C)	-1,329	0,014
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U572274	AK327073	zinc finger (C3HC4-type RING finger) family protein	-1,327	0,021
35.1.19	not assigned.no ontology.C2 domain-containing protein	SGN-U571659	BW687410	C2 domain-containing protein	-1,325	0,040
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U568678	AK321990	HAT22 | HAT22 (homeobox-leucine zipper protein 22)	-1,324	0,040
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U586119	DB715604	kelch repeat-containing F-box family protein	-1,322	0,014
26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U582802	AK323038	SIS4, GIN1, SDR1, ISI4, SRE1, ATABA2, ABA2 | ABA2 (ABA DEFICIENT 2)	-1,318	0,015
35.1	not assigned.no ontology	SGN-U577518	BW685814	BNR/Asp-box repeat family protein	-1,316	0,014
35.1	not assigned.no ontology	SGN-U600456	AW928726	NC domain-containing protein-related	-1,312	0,013
35.1	not assigned.no ontology	SGN-U571964	AK329506	lipid-associated family protein	-1,310	0,024
35.1	not assigned.no ontology	SGN-U566440	AK322874	phospholipid/glycerol acyltransferase family protein	-1,309	0,014
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U570987	BT014328	SKP2A | SKP2A	-1,309	0,050
35.2	not assigned.unknown	SGN-U578827	TA54304_4081	Unknown	-1,309	0,043
35.2	not assigned.unknown	SGN-U577844	AK325485	Unknown	-1,309	0,016

29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U568144	NM_001247480	APK1B | APK1B (Arabidopsis protein kinase 1B)	-1,307	0,014
34.8	transport.metabolite transporters at the envelope membrane	SGN-U581521	AK325683	GPT1 | GPT1 (glucose-6-phosphate transporter 1)	-1,303	0,013
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U580065	TA48542_4081	zinc finger protein-related	-1,303	0,042
35.1	not assigned.no ontology	SGN-U575272	AK322494	PQ-loop repeat family protein / transmembrane family protein	-1,302	0,037
35.2	not assigned.unknown	SGN-U598860	AK323171	Unknown	-1,300	0,013
35.3	not assigned.disagreeing hits	SGN-U591902	ES895330	PME1 | PME1; pectinesterase inhibitor	-1,297	0,021
30.5	signalling.G-proteins	SGN-U563414	AK323329	RAB GTPase activator	-1,296	0,014
20.2.1	stress.abiotic.heat	SGN-U572519	TA50993_4081	HSP70T-1, ERD2 | ERD2/HSP70T-1 (EARLY-RESPONSIVE TO DEHYDRATION 2)	-1,294	0,014
29.4	protein.postranslational modification	SGN-U574976	BG130800	protein phosphatase 2C family protein / PP2C family protein	-1,293	0,027
35.2	not assigned.unknown	SGN-U597893	DV105694	Unknown	-1,292	0,019
30.2.16	signalling.receptor kinases.Catharanthus roseus-like RLK1	SGN-U564180	BI422047	fringe-related protein	-1,288	0,013
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U604699	AK327872	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-1,288	0,017
1.2.2	PS.photorespiration.glycolate oxydase	SGN-U579320	AK325991	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	-1,285	0,018
26.10	misc.cytochrome P450	SGN-U601865	AK321968	CYP72A15 | CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15)	-1,283	0,049

35.2	not assigned.unknown	SGN-U569469	AK321376	Unknown	-1,279	0,018
16.2	secondary metabolism.phenylpropanoids	SGN-U570721	AK320662	ransferase family protein	-1,278	0,014
13.2.7	amino acid metabolism.degradation.histidine	SGN-U577168	NM_001246923	EMB1075 | EMB1075 (EMBRYO DEFECTIVE 1075); carboxy-lyase	-1,276	0,021
35.3	not assigned.disagreeing hits	SGN-U579433	AK325520	60S ribosomal protein L37 (RPL37B)	-1,275	0,013
35.2	not assigned.unknown	SGN-U603007	DV105192	DNA-binding storekeeper protein-related	-1,275	0,024
34.15	transport.potassium	SGN-U565469	AK319710	potassium channel tetramerisation domain-containing protein	-1,274	0,021
34.22	transport.cyclic nucleotide or calcium regulated channels	SGN-U583186	AK322829	ATCNGC1, CNGC1 | CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1)	-1,274	0,016
29.3.2	protein.targeting.mitochondria	SGN-U563007	ES895947	UNE3, PGA2, TATC, APG2 | APG2 (ALBINO AND PALE GREEN 2)	-1,268	0,014
35.2	not assigned.unknown	SGN-U578464	AK323787	Unknown	-1,265	0,016
35.2	not assigned.unknown	SGN-U595333	AK329386	Unknown	-1,260	0,020
35.1	not assigned.no ontology	SGN-U571043	NM_001246996	ARAF, ASD1 | ASD1 (ALPHA-L-ARABINOFURANOSIDASE)	-1,259	0,015
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U589210	AK320131	Protein kinase family protein	-1,258	0,016
35.2	not assigned.unknown	SGN-U565436	AK323666	Unknown	-1,258	0,033
29.4	protein.postranslational modification	SGN-U569235	AK324829	SnRK3.10, PKS7, ATSRPK1, ATSR2, CIPK7 | CIPK7 (CBL-INTERACTING PROTEIN KINASE 7)	-1,258	0,018
35.2	not assigned.unknown	SGN-U569130	BW692690	Unknown	-1,258	0,014

26.9	misc.glutathione S transferases	SGN-U587736	AK323839	GST18, ATGSTZ1 | ATGSTZ1 (GLUTATHIONE S-TRANSFERASE 18)	-1,258	0,014
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family	SGN-U585676	AI894956	transcription factor	-1,256	0,013
34.2.1	transporter.sugars.sucrose	SGN-U581233	AK322896	SUT1, ATSUC2, SUC2 | SUC2 (SUCROSE-PROTON SYMPORTER 2)	-1,251	0,014
35.2	not assigned.unknown	SGN-U567036	AK247592	Unknown	-1,248	0,028
35.2	not assigned.unknown	SGN-U563354	AK319348	Unknown	-1,245	0,019
26.9	misc.glutathione S transferases	SGN-U580000	NM_001247157	ATGSTU8 | ATGSTU8 (Arabidopsis thaliana Glutathione S-transferase (class tau) 8)	-1,244	0,022
26.7	misc.oxidases - copper, flavone etc.	SGN-U574333	AK327187	monooxygenase, putative (MO2)	-1,244	0,034
35.2	not assigned.unknown	SGN-U565893	AI777414	Unknown	-1,244	0,014
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U579343	AK321680	2-oxoglutarate-dependent dioxygenase, putative	-1,243	0,048
35.2	not assigned.unknown	SGN-U569130	BW692690	Unknown	-1,243	0,014
35.2	not assigned.unknown	SGN-U592141	TC243291	Unknown	-1,241	0,045
27.1.19	RNA.processing.ribonucleases	SGN-U592175	TA39474_4081	CCR4-NOT transcription complex protein, putative	-1,241	0,017
26.28	misc.GDSL-motif lipase	SGN-U597313	BP883249	GDSL-motif lipase/hydrolase family protein	-1,239	0,016
35.2	not assigned.unknown	SGN-U585103	AI778512	Unknown	-1,239	0,030
5.3	fermentation.ADH	SGN-U577949	BE458503	ADH, ATADH, ADH1 | ADH1 (ALCOHOL DEHYDROGENASE 1)	-1,239	0,041

29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U576266	AK321419	zinc finger (C3HC4-type RING finger) family protein	-1,239	0,021
35.2	not assigned.unknown	SGN-U578362	AK247103	Unknown	-1,236	0,028
35.3	not assigned.disagreeing hits	SGN-U573963	BI422058	ADT6 | ADT6 (AROGENATE DEHYDRATASE 6)	-1,233	0,013
35.2	not assigned.unknown	SGN-U572882	AK326323	Unknown	-1,232	0,016
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U586454	AK324716	GT, UGT74F2 | GT/UGT74F2 (UDP-GLUCOSYLTRANSFERASE 74F2)	-1,230	0,015
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U591099	AW030743	ATNADP-ME2 | ATNADP-ME2 (NADP-MALIC ENZYME 2); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor	-1,229	0,015
34.99	transport.misc	SGN-U575037	AK321305	flavin reductase-related	-1,229	0,014
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U581741	DB692542	auxin-responsive family protein	-1,228	0,018
29.5	protein.degradation	SGN-U578739	AK320049	peptidase M48 family protein	-1,228	0,014
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U579437	TA36862_4081	auxin/aluminum-responsive protein, putative	-1,227	0,029
30.3	signalling.calcium	SGN-U589560	AK321949	calmodulin binding	-1,225	0,027
35.2	not assigned.unknown	SGN-U563867	AK247726	Unknown	-1,224	0,014
35.2	not assigned.unknown	SGN-U604333	BW690754	Unknown	-1,222	0,016
35.2	not assigned.unknown	SGN-U566379	AK320501	Unknown	-1,222	0,013

2.1.1.1	major CHO metabolism.synthesis.sucrose.SPS	SGN-U601027	AW933045	ATSPS4F | ATSPS4F	-1,222	0,018
35.2	not assigned.unknown	SGN-U579187	TA35923_4081	Unknown	-1,220	0,023
26.12	misc.peroxidases	SGN-U564303	AK320190	peroxidase 72 (PER72) (P72) (PRXR8)	-1,216	0,016
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U586236	AK326989	RMA1 | RMA1 (Ring finger protein with Membrane Anchor 1)	-1,216	0,044
27.3.8	RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family	SGN-U577255	TA54195_4081	DAG1 | DAG1 (DOF AFFECTING GERMINATION 1)	-1,215	0,014
29.5.11.1	protein.degradation.ubiquitin.ubiquitin	SGN-U580697	BT012698	UBQ6 | UBQ6 (ubiquitin 6)	-1,214	0,013
34.8	transport.metabolite transporters at the envelope membrane	SGN-U577579	AK319565	TPT, APE2 | APE2 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT)	-1,213	0,014
34.99	transport.misc	SGN-U600947	JF518794	MATE efflux family protein	-1,211	0,014
10.7	cell wall.modification	SGN-U575872	AB036338	XTH27, ATXTH27, EXGT-A3 | EXGT-A3 (endo-xyloglucan transferase A3)	-1,210	0,038
35.2	not assigned.unknown	SGN-U564680	DB715291	Unknown	-1,208	0,018
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U563254	DB692593	Unknown	-1,205	0,048
35.2	not assigned.unknown	SGN-U571457	AK325542	Unknown	-1,204	0,030
27.3.14	RNA.regulation of transcription.CCAAT box binding factor family, HAP2	SGN-U580657	AK327097	CCAAT-binding transcription factor (CBF-B/NF-YA) family protein	-1,199	0,019
35.1	not assigned.no ontology	SGN-U563321	AK323156	peroxisomal membrane protein-related	-1,195	0,015
30.2.17	signalling.receptor kinases.DUF 26	SGN-U563765	AK320705	protein kinase family protein	-1,195	0,013

11.6	lipid metabolism.lipid transfer proteins etc	SGN-U571881	FS189318	LTP3 | LTP3 (LIPID TRANSFER PROTEIN 3); lipid binding	-1,189	0,039
10.2	cell wall.cellulose synthesis	SGN-U580265	AK326420	COB | COB (COBRA)	-1,188	0,014
35.3	not assigned.disagreeing hits	SGN-U586860	AW650060	CYP82C4 | CYP82C4 (cytochrome P450, family 82, subfamily C, polypeptide 4)	-1,187	0,027
35.2	not assigned.unknown	SGN-U593817	NM_001247321	homeobox	-1,186	0,014
35.1	not assigned.no ontology	SGN-U565434	AK321179	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-1,185	0,032
34.2	transporter.sugars	SGN-U604812	BF052115	ATOCT3 | ATOCT3 (ARABIDOPSIS THALIANA ORGANIC CATION/CARNITINE TRANSPORTER2)	-1,181	0,017
35.2	not assigned.unknown	SGN-U594717	AK246305	Unknown	-1,180	0,035
35.1	not assigned.no ontology	SGN-U589480	AK325612	GCR2, GPCR | GCR2/GPCR (G PROTEIN COUPLED RECEPTOR); abscisic acid binding/ catalytic	-1,180	0,013
31.1	cell.organisation	SGN-U577977	AI777842	OXY5, ATOXY5, ANNAT1 | ANNAT1 (ANNEXIN ARABIDOPSIS 1)	-1,178	0,017
20.2.99	stress.abiotic.unspecified	SGN-U567775	AK327264	RD2 | RD2 (RESPONSIVE TO DESSICATION 2)	-1,178	0,035
35.2	not assigned.unknown	SGN-U572721	AK319191	Unknown	-1,174	0,016
35.2	not assigned.unknown	SGN-U564446	NM_001247444	JAZ3, JAI3, TIFY6B | JAI3/JAZ3/TIFY6B (JASMONATE-ZIM-DOMAIN PROTEIN 3)	-1,174	0,014
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U571118	AK327747	GATL10 | GATL10 (Galacturonosyltransferase-like 10)	-1,174	0,014
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U573798	AK322246	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-1,173	0,021
29.4	protein.postranslational modification	SGN-U573512	AK321157	ATNRT3.1, NRT3.1, WR3 | WR3 (WOUND-RESPONSIVE 3); nitrate transmembrane	-1,173	0,018

				transporter		
29.5.4	protein.degradation.aspartate protease	SGN-U580642	NM_001247773	spartyl protease family protein	-1,172	0,020
11.2.4	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U590277	AK326063	FAD2 | FAD2 (FATTY ACID DESATURASE 2)	-1,171	0,014
26.7	misc.oxidases - copper, flavone etc.	SGN-U579609	BF113351	oxidoreductase, zinc-binding dehydrogenase family protein	-1,171	0,024
35.3	not assigned.disagreeing hits	SGN-U579965	GO375573	zinc finger (C3HC4-type RING finger) family protein	-1,169	0,028
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family	SGN-U564532	TA55041_4081	transcription factor	-1,168	0,017
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U586320	NM_001247632	protein kinase, putative	-1,168	0,016
35.3	not assigned.disagreeing hits	SGN-U580209	BT014166	APM2, PEX13 | APM2/PEX13 (ABERRANT PEROXISOME MORPHOLOGY 2)	-1,167	0,018
35.2	not assigned.unknown	SGN-U565188	AK319880	Unknown	-1,166	0,014
31.1	cell.organisation	SGN-U571972	AK319241	microtubule-associated protein	-1,164	0,019
34.12	transport.metal	SGN-U598134	BP891997	MHX1, ATMHX1, ATMHX | ATMHX (MAGNESIUM/PROTON EXCHANGER)	-1,164	0,014
35.2	not assigned.unknown	SGN-U580940	AK327947	MEE14 | MEE14 (maternal effect embryo arrest 14)	-1,163	0,046
35.2	not assigned.unknown	SGN-U564599	AK327171	similar to PBng143 [Vigna radiata]	-1,160	0,020
34.19.1	transport.Major Intrinsic Proteins.PIP	SGN-U578027	GO374090	PIP2;2, PIP2B | PIP2B (plasma membrane intrinsic protein 2;2)	-1,158	0,030
18	Co-factor and vitamine metabolism	SGN-U576673	BG132138	thiamine biosynthesis family protein / thiC family protein	-1,157	0,033

35.3	not assigned.disagreeing hits	SGN-U584943	NM_001247708	GF14 OMICRON, GRF11 | GRF11 (General regulatory factor 11)	-1,156	0,014
29.5.9	protein.degradation.AAA type	SGN-U581963	AW034581	AAA-type ATPase family protein	-1,155	0,029
8.3	TCA / org. transformation.carbonic anhydrases	SGN-U590031	NM_001246918	CA18, BETA CA2, CA2 | CA2 (BETA CARBONIC ANHYDRASE 2)	-1,154	0,038
33.99	development.unspecified	SGN-U570622	TA44200_4081	transducin family protein / WD-40 repeat family protein	-1,153	0,030
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U570665	AK247319	F-box family protein	-1,149	0,025
35.2	not assigned.unknown	SGN-U583576	TC240658	Unknown	-1,148	0,013
35.3	not assigned.disagreeing hits	SGN-U563637	AK319670	thylakoid lumenal protein-related	-1,146	0,023
35.2	not assigned.unknown	SGN-U574470	TA53116_4081	Unknown	-1,144	0,014
34.15	transport.potassium	SGN-U585125	NM_001247329	AKT1 | AKT1 (ARABIDOPSIS K TRANSPORTER 1)	-1,143	0,035
33.1	development.storage proteins	SGN-U601375	AK319188	SDP1 | SDP1 (SUGAR-DEPENDENT1); triacylglycerol lipase	-1,143	0,014
35.2	not assigned.unknown	SGN-U576005	AK327820	Unknown	-1,143	0,019
35.2	not assigned.unknown	SGN-U601183	AI898356	Unknown	-1,140	0,014
35.2	not assigned.unknown	SGN-U584217	BI206269	Unknown	-1,140	0,015
35.2	not assigned.unknown	SGN-U571963	NM_001247299	Unknown	-1,140	0,035
35.2	not assigned.unknown	SGN-U578108	TA37525_4081	Unknown	-1,138	0,016

35.2	not assigned.unknown	SGN-U583729	DB689823	Unknown	-1,137	0,016
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U585960	TA56030_4081	zinc finger (C3HC4-type RING finger) family protein	-1,137	0,028
34.2	transporter.sugars	SGN-U575116	AK322083	sugar transporter, putative	-1,136	0,014
35.3	not assigned.disagreeing hits	SGN-U579962	NM_001247691	glycosyl hydrolase family 1 protein	-1,132	0,014
35.2	not assigned.unknown	SGN-U575847	BG127600	Unknown	-1,130	0,019
30.3	signalling.calcium	SGN-U576592	BG127290	PBP1 | PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding	-1,130	0,013
19.99	tetrapyrrole synthesis.unspecified	SGN-U573737	AK324283	ATCLH2 | ATCLH2 (Chlorophyll-chlorophyllido hydrolase 2)	-1,129	0,017
35.2	not assigned.unknown	SGN-U574223	AK320947	Unknown	-1,129	0,013
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U591315	TC238383	Auxin-responsive protein, putative	-1,129	0,014
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	SGN-U568287	TA39946_4081	HSFA5, AT-HSFA5 | AT-HSFA5 (Arabidopsis thaliana heat shock transcription factor A5)	-1,129	0,013
35.2	not assigned.unknown	SGN-U582181	AK327784	Unknown	-1,127	0,039
29.5.11	protein.degradation.ubiquitin	SGN-U568822	BT014048	UBP3, ATUBP3 | ATUBP3 (UBIQUITIN-SPECIFIC PROTEASE 3); ubiquitin-specific protease	-1,127	0,014
26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	SGN-U580530	BG127002	60S ribosomal protein L12 (RPL12A)	-1,126	0,013
35.3	not assigned.disagreeing hits	SGN-U578237	AW221955	AXS2 | AXS2 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 2)	-1,126	0,013

35.1	not assigned.no ontology	SGN-U584548	AK324223	DJ-1 family protein / protease-related	-1,125	0,018
10.8.1	cell wall.pectin*esterases.PME	SGN-U590828	BI926194	pectinesterase family protein	-1,124	0,017
26.12	misc.peroxidases	SGN-U581530	AK320754	peroxidase, putative	-1,123	0,018
35.2	not assigned.unknown	SGN-U591581	AK324137	Unknown	-1,122	0,014
27.3.59	RNA.regulation of transcription.Methyl binding domain proteins	SGN-U583159	AK319725	MBD10 | MBD10 (methyl-CpG-binding domain 10)	-1,121	0,017
35.2	not assigned.unknown	SGN-U582835	TA55033_4081	Unknown	-1,120	0,041
1.1.1.1	PS.lightreaction.photosystem II.LHC-II	SGN-U579906	TA36231_4081	CAB4, LHCA4 | LHCA4 (Photosystem I light harvesting complex gene 4)	-1,120	0,047
2.1.1.3	major CHO metabolism.synthesis.sucrose.FBPase	SGN-U579019	AK327148	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	-1,117	0,026
35.2	not assigned.unknown	SGN-U582985	BG131803	Unknown	-1,117	0,025
35.3	not assigned.disagreeing hits	SGN-U599892	DV104684	leucine-rich repeat transmembrane protein kinase, putative	-1,114	0,015
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U569715	AW220490	protein kinase family protein	-1,113	0,022
29.5.4	protein.degradation.aspartate protease	SGN-U566608	AK328127	Aspartic-type endopeptidase/ pepsin A	-1,112	0,014
26.9	misc.glutathione S transferases	SGN-U565223	AK319411	GST18, ATGSTZ1 | ATGSTZ1 (GLUTATHIONE S-TRANSFERASE 18)	-1,109	0,016
29.2.3	protein.synthesis.initiation	SGN-U576828	AK326789	Eukaryotic translation initiation factor 2B family protein / eIF-2B family protein	-1,107	0,014

34.99	transport.misc	SGN-U565389	AK319737	alanine racemase family protein	-1,106	0,013
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U564795	AK327156	ATNAP8 | ATNAP8 (Arabidopsis thaliana non-intrinsic ABC protein 8)	-1,104	0,038
35.3	not assigned.disagreeing hits	SGN-U584460	TA37448_4081	LTP1, ATLTP1, LP1 | LP1 (nonspecific lipid transfer protein 1)	-1,104	0,034
27.3.55	RNA.regulation of transcription.HDA	SGN-U585360	TA45295_4081	HDA8, HDA08 | HDA08 (histone deacetylase 8)	-1,103	0,031
27.2	RNA.transcription	SGN-U573768	BF050158	RNA-dependent RNA polymerase family protein	-1,103	0,029
35.2	not assigned.unknown	SGN-U600561	BW689307	Unknown	-1,102	0,038
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U586490	TA55921_4081	elch repeat-containing F-box family protein	-1,101	0,017
35.3	not assigned.disagreeing hits	SGN-U581081	BT013070	ATLFNR1 | ATLFNR1 (LEAF FNR 1)	-1,100	0,015
35.3	not assigned.disagreeing hits	SGN-U579829	AK322115	aspartyl protease family protein	-1,099	0,014
34.13	transport.peptides and oligopeptides	SGN-U585724	BP893172	proton-dependent oligopeptide transport (POT) family protein	-1,098	0,023
29.5.1	protein.degradation.subtilases	SGN-U571112	AK323636	subtilase family protein	-1,098	0,014
35.3	not assigned.disagreeing hits	SGN-U579386	NM_001247637	TCTP | TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN)	-1,097	0,014
35.2	not assigned.unknown	SGN-U590091	BP905061	Unknown	-1,096	0,014
1.3.2	PS.calvin cyle.rubisco small subunit	SGN-U578438	TA39589_4081	ribulose bisphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B)	-1,095	0,016
34.10	transport.nucleotides	SGN-U576428	BT014013	ATPUP4 | ATPUP4 (Arabidopsis thaliana purine permease 4)	-1,095	0,030

26.13	misc.acid and other phosphatases	SGN-U568888	AK327948	ATPAP29, PAP29 | ATPAP29/PAP29 (purple acid phosphatase 29)	-1,092	0,027
31.1	cell.organisation	SGN-U579203	NM_001247172	ANNAT2 | ANNAT2 (ANNEXIN ARABIDOPSIS 2)	-1,092	0,040
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U583983	BP880101	JAR, FIN219, JAR1 | JAR1 (JASMONATE RESISTANT 1)	-1,091	0,024
12.2.2	N-metabolism.ammonia metabolism.glutamine synthase	SGN-U577964	AJ277561	ATGSR2 | ATGSR2 (Arabidopsis thaliana glutamine synthase clone R2); glutamate-ammonia ligase	-1,091	0,020
29.4	protein.postranslational modification	SGN-U580595	DB706671	protein kinase, putative	-1,091	0,013
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U580835	AK325516	DNA-binding protein-related	-1,091	0,014
26.9	misc.glutathione S transferases	SGN-U567445	AW621356	GST25, ATGSTU7 | ATGSTU7 (GLUTATHIONE S-TRANSFERASE 25)	-1,090	0,018
29.4	protein.postranslational modification	SGN-U571790	AK327349	PLL5 | PLL5 (POL-like 5); protein serine/threonine phosphatase	-1,090	0,014
11.9.4.2	lipid metabolism.lipid degradation.beta-oxidation.acyl CoA DH	SGN-U581236	BI931058	ATACX3, ACX3 | ACX3 (ACYL-COA OXIDASE 3); acyl-CoA oxidase	-1,089	0,023
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U573029	AW221294	kelch repeat-containing F-box family protein	-1,089	0,024
13.2.2.2	amino acid metabolism.degradation.glutamate family.proline	SGN-U578070	BT013418	proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative	-1,089	0,027
28.1	DNA.synthesis/chromatin structure	SGN-U604345	BP882905	endonuclease-related	-1,089	0,023
29.5.2	protein.degradation.autophagy	SGN-U580575	TA54492_4081	AtATG18f | AtATG18f (Arabidopsis thaliana homolog of yeast autophagy 18 (ATG18) f)	-1,088	0,016
33.99	development.unspecified	SGN-U565635	AK323233	nodulin MtN21 family protein	-1,088	0,027

13.1.6.2	amino acid metabolism.synthesis.aromatic aa.phenylalanine and tyrosine	SGN-U563165	NM_001247493	EMB1144 | EMB1144 (EMBRYO DEFECTIVE 1144); chorismate synthase	-1,088	0,015
35.2	not assigned.unknown	SGN-U563779	AK323338	Unknown	-1,087	0,017
26.7	misc.oxidases - copper, flavone etc.	SGN-U594512	AW934306	monooxygenase, putative (MO3)	-1,087	0,024
21.1	redox.thioredoxin	SGN-U577589	AK325466	ATAPRL4 | ATAPRL4 (APR-LIKE 4)	-1,086	0,017
26.1	misc.misc2	SGN-U563558	AK319706	Epoxide hydrolase, putative	-1,085	0,018
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U569960	BT013336	ZAT10, STZ | STZ (SALT TOLERANCE ZINC FINGER)	-1,084	0,014
13.2.3.2	amino acid metabolism.degradation.aspartate family.threonine	SGN-U578074	TA36079_4081	ATGLX1 | ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase	-1,084	0,017
20.2.1	stress.abiotic.heat	SGN-U592233	NM_001247201	HSP17.6II | HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN)	-1,083	0,014
35.1.3	not assigned.no ontology.armadillo/beta-catenin repeat family protein	SGN-U571207	AK324379	armadillo/beta-catenin repeat family protein	-1,082	0,016
33.99	development.unspecified	SGN-U566924	AK246316	SEN1, ATSEN1, DIN1 | SEN1 (DARK INDUCIBLE 1)	-1,081	0,019
27.3.37	RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family	SGN-U564260	AK326285	LBD41 | LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41)	-1,081	0,046
27.3.4	RNA.regulation of transcription.ARF, Auxin Response Factor family	SGN-U570279	NM_001247811	MSG1, IAA21, ARF7, TIR5, BIP, IAA23, IAA25, NPH4 | NPH4 (NON-PHOTOTROPHIC HYPOCOTYL)	-1,080	0,013
30.3	signalling.calcium	SGN-U601628	AK327043	calcium-dependent protein kinase, putative	-1,078	0,016
10.8.1	cell wall.pectin*esterases.PME	SGN-U581175	BI926194	pectinesterase family protein	-1,078	0,027

33.99	development.unspecified	SGN-U598683	AK320852	nodulin family protein	-1,078	0,018
35.2	not assigned.unknown	SGN-U572077	BI209839	Unknown	-1,077	0,040
17.5.3	hormone metabolism.ethylene.induced-regulated-responsive-activated	SGN-U575820	TA39809_4081	ethylene-responsive protein, putative	-1,077	0,021
35.3	not assigned.disagreeing hits	SGN-U564499	AK322231	UBX domain-containing protein	-1,076	0,018
34.3	transport.amino acids	SGN-U584049	AK320113	LTH1, LHT1 | LHT1 (LYSINE HISTIDINE TRANSPORTER 1)	-1,076	0,013
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U581951	BE354941	protein binding / zinc ion binding	-1,075	0,016
3.2.3	minor CHO metabolism.trehalose.potential TPS/TPP	SGN-U576716	CD002955	TPS11, ATTPSB, ATTPS11 | ATTPS11 (Arabidopsis thaliana trehalose phosphatase/synthase 11)	-1,075	0,013
26.7	misc.oxidases - copper, flavone etc.	SGN-U579941	TA35695_4081	polyphenol oxidase	-1,075	0,025
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U570676	NM_001247935	FBL6, EBF1 | EBF1 (EIN3-BINDING F BOX PROTEIN 1)	-1,074	0,018
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U580218	AK322971	Unknown	-1,072	0,017
35.3	not assigned.disagreeing hits	SGN-U574724	AK326273	Unknown	-1,072	0,017
35.2	not assigned.unknown	SGN-U581369	AK326352	Unknown	-1,070	0,016
34.99	transport.misc	SGN-U563442	AK247145	Unknown	-1,069	0,025
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U564520	TA41099_4081	2-oxoglutarate-dependent dioxygenase, putative	-1,068	0,033

35.2	not assigned.unknown	SGN-U565482	AK329290	Similar to hypothetical protein MtrDRAFT_AC150207g26v2	-1,068	0,021
35.2	not assigned.unknown	SGN-U585457	AK323150	Unknown	-1,067	0,019
35.2	not assigned.unknown	SGN-U581205	TA43398_4081	Unknown	-1,067	0,047
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U575342	AK327668	PUB17 | PUB17 (PLANT U-BOX17)	-1,067	0,017
20.1	stress.biotic	SGN-U585624	TA37200_4081	similar to pathogenesis-related protein sth-2	-1,067	0,042
35.2	not assigned.unknown	SGN-U563120	AK247886	Unknown	-1,067	0,045
35.2	not assigned.unknown	SGN-U582709	TA54839_4081	Unknown	-1,064	0,027
2.2.1.1	major CHO metabolism.degradation.sucrose.fructokinase	SGN-U586194	NM_001246959	pfkB-type carbohydrate kinase family protein	-1,064	0,032
35.1	not assigned.no ontology	SGN-U584377	AK326234	Glycogenin glucosyltransferase (glycogenin)-related	-1,064	0,013
35.1.19	not assigned.no ontology.C2 domain-containing protein	SGN-U579064	AK246682	C2 domain-containing protein	-1,063	0,021
26.7	misc.oxidases - copper, flavone etc.	SGN-U592601	BE435957	FMO1 | FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1)	-1,063	0,016
35.2	not assigned.unknown	SGN-U573139	AK323693	Unknown	-1,063	0,037
35.3	not assigned.disagreeing hits	SGN-U578420	GO374534	PSBW | PSBW (PHOTOSYSTEM II REACTION CENTER W)	-1,060	0,033
35.2	not assigned.unknown	SGN-U565192	AK325765	Unknown	-1,060	0,021
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U576439	AK326772	PEX2, TED3 | TED3 (REVERSAL OF THE DET PHENOTYPE)	-1,059	0,014

35.1	not assigned.no ontology	SGN-U571663	AK326304	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-1,059	0,045
4.9	glycolysis.glyceraldehyde 3-phosphate dehydrogenase	SGN-U577274	BG643089	GAPA-2 | GAPA-2 Glyceraldehyde-3-phosphate dehydrogenase	-1,058	0,018
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U578465	AK320853	auxin-responsive family protein	-1,057	0,023
2.2.2.2	major CHO metabolism.degradation.starch.starch phosphorylase	SGN-U594072	BE463090	glucan phosphorylase, putative	-1,057	0,014
20.1.7	stress.biotic.PR-proteins	SGN-U576485	AK247929	disease resistance protein (CC-NBS-LRR class)	-1,057	0,025
35.1	not assigned.no ontology	SGN-U576674	AK322385	ATPase, BadF/BadG/BcrA/BcrD-type family	-1,057	0,016
35.3	not assigned.disagreeing hits	SGN-U580659	ES893668	LP2, LTP2 | LTP2 (LIPID TRANSFER PROTEIN 2)	-1,056	0,024
34.12	transport.metal	SGN-U573437	NM_001251873	ZIP6 | ZIP6 (ZINC TRANSPORTER 6 PRECURSOR)	-1,055	0,013
35.1	not assigned.no ontology	SGN-U581528	AK321129	NC domain-containing protein	-1,053	0,018
35.1	not assigned.no ontology	SGN-U569352	BT014207	TMS membrane family protein / tumour differentially expressed (TDE) family protein	-1,053	0,016
35.2	not assigned.unknown	SGN-U571726	AK325662	Unknown	-1,052	0,014
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U594939	AK324851	F-box family protein	-1,052	0,015
33.99	development.unspecified	SGN-U577847	AK329344	TET8 | TET8 (TETRASPANIN8)	-1,051	0,023
35.1	not assigned.no ontology	SGN-U582131	AK322582	ATGID1C, GID1C | ATGID1C/GID1C (GA INSENSITIVE DWARF1C)	-1,051	0,023
29.4	protein.postranslational modification	SGN-U568975	AK327044	Protein phosphatase 2C family protein / PP2C family protein	-1,051	0,018

13.2.3.5	amino acid metabolism.degradation.aspartate family.lysine	SGN-U569509	AK322328	ATDCI1 | ATDCI1 (DELTA(3,5),DELTA(2,4)-DIENOYL-COA ISOMERASE 1)	-1,050	0,030
35.2	not assigned.unknown	SGN-U565150	TA38453_4081	Unknown	-1,049	0,014
15.1	metal handling.acquisition	SGN-U567779	AK322418	ATFRO8, FRO8 | ATFRO8/FRO8 (FERRIC REDUCTION OXIDASE 8); ferric-chelate reductase/ oxidoreductase	-1,049	0,030
30.3	signalling.calcium	SGN-U597811	AK324373	TCH1, ACAM-1, CAM1 | CAM1 (CALMODULIN 1)	-1,048	0,019
34.99	transport.misc	SGN-U577940	AK321729	secretory carrier membrane protein (SCAMP) family protein	-1,048	0,025
29.5	protein.degradation	SGN-U584121	EG553332	chloroplast thylakoidal processing peptidase	-1,047	0,016
26.4	misc.beta 1,3 glucan hydrolases	SGN-U571967	AK247276	Glucan 1 3-beta-glucosidase	-1,047	0,016
35.1	not assigned.no ontology	SGN-U582955	TA42029_4081	Similar to meprin and TRAF homology domain-containing protein / MATH domain-containing protein	-1,047	0,016
30.3	signalling.calcium	SGN-U569631	AK247102	IQD22 | IQD22 (IQ-domain 22); calmodulin binding	-1,047	0,014
35.3	not assigned.disagreeing hits	SGN-U578200	AK325215	alanine--glyoxylate aminotransferase, putative	-1,046	0,039
29.3.5	protein.targeting.peroxisomes	SGN-U567985	NM_001247370	PEX7 | PEX7 (peroxin 7)	-1,046	0,015
26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U580761	AK328694	short-chain dehydrogenase/reductase (SDR) family protein	-1,045	0,014
33.99	development.unspecified	SGN-U569518	AK328054	ANAC062 | ANAC062 (Arabidopsis NAC domain containing protein 62)	-1,045	0,014
2.2.1.5	major CHO metabolism.degradation.sucrose.Susy	SGN-U577970	NM_001247726	SUS4 | SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups	-1,044	0,019

29.4	protein.postranslational modification	SGN-U581656	BT013017	palmitoyl protein thioesterase family protein	-1,044	0,028
27.3.13	RNA.regulation of transcription.CCAAT box binding factor family, DR1	SGN-U589631	AK323516	TATA-binding protein-associated phosphoprotein Dr1 protein, putative	-1,043	0,018
26.10	misc.cytochrome P450	SGN-U565856	BG124625	CYP71B10 | CYP71B10 (cytochrome P450, family 71, subfamily B, polypeptide 10)	-1,043	0,022
35.2	not assigned.unknown	SGN-U566855	DB686620	Unknown	-1,042	0,016
35.2	not assigned.unknown	SGN-U573871	BP898262	Unknown	-1,040	0,022
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U574886	AK325559	kelch repeat-containing F-box family protein	-1,039	0,025
27.3.40	RNA.regulation of transcription.Aux/IAA family	SGN-U568849	AK320139	IAA9 | IAA9 (indoleacetic acid-induced protein 9)	-1,039	0,016
35.2	not assigned.unknown	SGN-U582852	TC239798	protein binding	-1,038	0,018
35.1	not assigned.no ontology	SGN-U582989	BT013800	esterase/lipase/thioesterase family protein	-1,038	0,017
35.2	not assigned.unknown	SGN-U567708	AK319995	Unknown	-1,037	0,014
35.2	not assigned.unknown	SGN-U582096	AI484388	Unknown	-1,036	0,014
29.5	protein.degradation	SGN-U584122	TA37902_4081	signal peptidase, putative	-1,036	0,014
35.3	not assigned.disagreeing hits	SGN-U576901	TA56864_4081	oxidoreductase family protein	-1,035	0,024
29.2.4	protein.synthesis.elongation	SGN-U570252	AK322741	PBS lyase HEAT-like repeat-containing protein	-1,035	0,016
21.6	redox.dismutases and catalases	SGN-U578479	NM_001247257	CAT2 | CAT2 (CATALASE 2); catalase	-1,033	0,019

23.3.1.1	nucleotide metabolism.salvage.phosphoribosyltransferases.aprt	SGN-U580961	AW622263	APT1, ATAPT1, APRT | APT1	-1,032	0,013
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U579902	BT014325	ATL2 | ATL2 (Arabidopsis T?xicos en Levadura 2)	-1,032	0,014
35.2	not assigned.unknown	SGN-U575183	AK324397	Unknown	-1,031	0,014
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U570082	AK327909	Unknown	-1,031	0,040
27.3.99	RNA.regulation of transcription.unclassified	SGN-U565881	AK327209	catalytic/ pyridoxal phosphate binding	-1,030	0,027
26.24	misc.GCN5-related N-acetyltransferase	SGN-U582389	AK322416	GCN5-related N-acetyltransferase (GNAT) family protein	-1,029	0,034
30.3	signalling.calcium	SGN-U583356	BE432606	ATCBL1, SCABP5 | CBL1 (CALCINEURIN B-LIKE PROTEIN 1)	-1,027	0,032
35.1	not assigned.no ontology	SGN-U574625	BW692022	phosphate-responsive 1 family protein	-1,027	0,044
16.1	secondary metabolism.isoprenoids	SGN-U589490	AK325074	ABC4 | ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4)	-1,027	0,016
30.5	signalling.G-proteins	SGN-U569009	NP9287470	Transducin family protein / WD-40 repeat family protein	-1,027	0,023
1.1.3	PS.lightreaction.cytochrome b6/f	SGN-U593129	TA36273_4081	PGR1, PETC | PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C)	-1,027	0,017
35.3	not assigned.disagreeing hits	SGN-U580949	TA36273_4081	ABC1 family protein	-1,026	0,025
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U564193	AK247211	Transducin-like	-1,026	0,032
31.2	cell.division	SGN-U586117	DB713139	regulator of chromosome condensation (RCC1) family protein	-1,026	0,018
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U564528	AK328452	RHC1A | RHC1A (RING-H2 finger C1A)	-1,026	0,016

35.2	not assigned.unknown	SGN-U577622	BE432742	Unknown	-1,026	0,016
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U588263	BG125179	TMK1 | TMK1 (TRANSMEMBRANE KINASE 1)	-1,025	0,019
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U568917	NM_001247818	ATGA2OX6, DTA1 | ATGA2OX6/DTA1 (GIBBERELLIN 2-OXIDASE 6); gibberellin 2-beta-dioxygenase	-1,025	0,033
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family	SGN-U566777		ATWRKY40, WRKY40 | WRKY40 (WRKY DNA-binding protein 40)	-1,024	0,016
35.1	not assigned.no ontology	SGN-U600541	AK319299	ACR8 | ACR8 (ACT Domain Repeat 8)	-1,024	0,049
35.3	not assigned.disagreeing hits	SGN-U583711	NM_001246903	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein,	-1,023	0,037
35.2	not assigned.unknown	SGN-U570333	TA49878_4081	hydrolase, acting on carbon-nitrogen (but not peptide) bonds	-1,023	0,014
35.1	not assigned.no ontology	SGN-U566455	AK320260	glycosyl hydrolase family protein 43	-1,022	0,049
29.5.9	protein.degradation.AAA type	SGN-U569442	AW442723	AAA-type ATPase family protein	-1,021	0,027
35.1	not assigned.no ontology	SGN-U568171	DB718923	aladin-related / adracalin-related	-1,019	0,035
27.3.55	RNA.regulation of transcription.HDA	SGN-U585359	AK324940	HDA8, HDA08 | HDA08 (histone deacetylase 8)	-1,019	0,045
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U580479	BG132683	UBC10 | UBC10 (UBIQUITIN-CONJUGATING ENZYME 10); ubiquitin-protein ligase	-1,017	0,017
30.3	signalling.calcium	SGN-U576944	AI487567	Calcium-binding EF hand family protein	-1,017	0,031
35.2	not assigned.unknown	SGN-U572228	AK247098	Unknown	-1,016	0,045

35.2	not assigned.unknown	SGN-U571948	AK322289	Unknown	-1,013	0,024
34.19.1	transport.Major Intrinsic Proteins.PIP	SGN-U578299	TA36259_4081	PIP1;3, PIP1C, TMP-B | PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1;3)	-1,012	0,020
7.1.2	OPP.oxidative PP.6-phosphogluconolactonase	SGN-U571897	BE451183	EMB2024 (EMBRYO DEFECTIVE 2024)	-1,012	0,016
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U594420	BP876895	RLK1 | RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); carbohydrate binding / kinase	-1,012	0,018
30.3	signalling.calcium	SGN-U568260	AK323680	CPK10, ATCDPK1 | ATCDPK1; calmodulin-dependent protein kinase	-1,011	0,018
35.2	not assigned.unknown	SGN-U589321	TA47736_4081	Unknown	-1,011	0,015
35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U580778	AK329949	tetratricopeptide repeat (TPR)-containing protein	-1,010	0,023
34.2	transporter.sugars	SGN-U565595	TA55494_4081	STP13, MSS1 | MSS1 (SUGAR TRANSPORT PROTEIN 13)	-1,010	0,025
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U565232	AI896450	glycosyltransferase family protein 28	-1,009	0,014
35.3	not assigned.disagreeing hits	SGN-U590221	BI926368	BNR/Asp-box repeat family protein	-1,008	0,017
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U576069	AK321849	oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1,008	0,015
35.2	not assigned.unknown	SGN-U575339	AK322437	Unknown	-1,006	0,017
27.3.20	RNA.regulation of transcription.G2-like transcription factor family, GARP	SGN-U582079	AI894696	myb family transcription factor	-1,006	0,020
35.3	not assigned.disagreeing hits	SGN-U581239	AK247307	CID11 | CID11	-1,005	0,022

11.3	lipid metabolism.Phospholipid synthesis	SGN-U569693	AK328204	PSD3 | PSD3 (PHOSPHATIDYLSERINE DECARBOXYLASE 3); calcium ion binding / phosphatidylserine decarboxylase	-1,004	0,014
35.2	not assigned.unknown	SGN-U565304	AK328151	Unknown	-1,004	0,017
35.2	not assigned.unknown	SGN-U584652	AW650672	Unknown	-1,003	0,019
29.4	protein.postranslational modification	SGN-U585750	AK247687	protein phosphatase 2C-related / PP2C-related	-1,001	0,013
35.2	not assigned.unknown	SGN-U565709	AK323228	Unknown	-1,001	0,035
5.2	fermentation.PDC	SGN-U575469	AK325545	pyruvate decarboxylase family protein	-1,001	0,048
30.3	signalling.calcium	SGN-U568257	AK328838	calcium-binding EF hand family protein	-1,000	0,037

Table 6. List of up-regulated genes genes (log2 ratio sub-/optimal T≥1 and q-value<0.05) deteced only in the roots of the grafted 'Kommeet' plants onto 'Moneymaker' (R/S:MM/KO) under sub-optimal root T stress.

BinCode	**BinName**	**SGN**	**NCBI**	**description**	**MM/KO Log FC**	**adj.P.Val**
35.3	not assigned.disagreeing hits	SGN-U579545	Y08804	PATHOGENESIS RELATED PROTEIN 1	7,059	0,000
29.5.11.1	protein.degradation.ubiquitin.ubiquitin	SGN-U580448	CK348294	ubiquitin extension protein UBQ6 | UBQ6 (ubiquitin 6); protein binding	5,291	0,001
20.1	stress.biotic	SGN-U580143	AI781976	PATHOGENESIS RELATED PROTEIN 1	4,760	0,002
35.2	not assigned.unknown	SGN-U592453	Y10149	Unknown	4,562	0,001
26.10	misc.cytochrome P450	SGN-U597824	BI422473	Cytochrome P450 E-class, group I	4,341	0,005
35.2	not assigned.unknown	SGN-U602563	CD579161	Fucosyltransferase 7 Xyloglucan fucosyltransferase	4,181	0,004
35.3	not assigned.disagreeing hits	SGN-U592334	X94946	VIROID-INDUCIBLE PROTEINASE INHIBITOR II	4,106	0,005
20.1	stress.biotic	SGN-U579068	TA37976_4081	PR3, PR-3, CHI-B, B-CHI, ATHCHIB | ATHCHIB (BASIC CHITINASE); chitinase Basic endochitinase	3,991	0,001
35.1	not assigned.no ontology	SGN-U584870	AK246411	Heme-binding protein 2	3,677	0,004
29.5.3	protein.degradation.cysteine protease	SGN-U580776	TA41652_4081	phytophthora-inhibited protease 1	3,668	0,002
20.1	stress.biotic	SGN-U579235	BT013355	pathogenesis-related protein P2	3,531	0,005
33.1	development.storage proteins	SGN-U569533	CK720570	PLP4, PLA V | PLA V/PLP4 (Patatin-like protein 4); nutrient reservoir	3,505	0,002

35.2	not assigned.unknown	SGN-U578863	BI421164	trypsin and protease inhibitor family protein / Kunitz family protein biotic cell death-associated protein	3,488	0,005
16.1.5	secondary metabolism.isoprenoids.terpenoids	SGN-U566179	BI421872	Alpha-humulene/(-)-(E)-beta-caryophyllene synthase	3,458	0,013
35.3	not assigned.disagreeing hits	SGN-U581430	Y10149	subtilisin	3,392	0,001
29.5.3	protein.degradation.cysteine protease	SGN-U591074	AW033950	VIROID-INDUCIBLE PROTEINASE INHIBITOR II	3,363	0,007
26.7	misc.oxidases - copper, flavone etc.	SGN-U577900	BT013158	Polyphenol oxidase	3,359	0,002
30.1	signalling.in sugar and nutrient physiology	SGN-U569162	DB699068	PAR-1c protein	3,359	0,002
26.10	misc.cytochrome P450	SGN-U573345	TA55550_4081	CYP71A25 | CYP71A25 (cytochrome P450, family 71, subfamily A, polypeptide 25)	3,358	0,006
29.5.1	protein.degradation.subtilases	SGN-U580556	TC191435	subtilisin	3,296	0,006
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U578607	BM412330	1-aminocyclopropane-1-carboxylate oxidase 1	3,133	0,006
16.1.2.3	secondary metabolism.isoprenoids.mevalonate pathway.HMG-CoA reductase	SGN-U578017	TC204775	HMGR1, HMG1 | HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)	3,054	0,009
20.1	stress.biotic	SGN-U580740	AK247106	LETSI1	3,049	0,003
26.10	misc.cytochrome P450	SGN-U573879	ES896905	Cytochrome P450	3,043	0,025
20.1	stress.biotic	SGN-U578815	TA36002_4081	TOMPRP4 PR (pathogenesis related) protein 4	3,042	0,003
35.1	not assigned.no ontology	SGN-U578033	AW216628	Probable gibberellin receptor GID1L2 similar to unknown protein [Arabidopsis	3,019	0,012

				thaliana] (TAIR:AT2G45600.1)		
16.2	secondary metabolism.phenylpropanoids	SGN-U565216	BT012835	transferase family protein	2,977	0,026
20.1	stress.biotic	SGN-U581507	AI895853	acidic extracellular 26 kD chitinase	2,905	0,006
35.3	not assigned.disagreeing hits	SGN-U579003	X94943	LECEVI16G peroxidase precursor	2,821	0,002
11.2.4	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U604418	BI205317	FAD2 | FAD2 (FATTY ACID DESATURASE 2); delta12-fatty acid dehydrogenase	2,802	0,003
29.5.3	protein.degradation.cysteine protease	SGN-U574954	TA56382_4081	Cathepsin B-like cysteine proteinase Peptidase, cysteine peptidase active site	2,798	0,008
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	SGN-U580800	TA36724_4081	HSFA6B, AT-HSFA6B | AT-HSFA6B (Arabidopsis thaliana heat shock transcription factor	2,734	0,001
13.1.2.3	amino acid metabolism.synthesis.glutamate family.arginine	SGN-U572542	AI487426	diaminopimelate decarboxylase, putative / DAP carboxylase, putative | orthinine decarboxylase	2,733	0,001
26.4	misc.beta 1,3 glucan hydrolases	SGN-U577505	DB694568	LEQB L.esculentum TomQ'b beta(1,3)glucanase	2,666	0,010
11.1.8	lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	SGN-U584932	TA54915_4081	Acyl-CoA synthetase/AMP-acid ligase II	2,665	0,004
35.3	not assigned.disagreeing hits	SGN-U577856	AB211525	pathogenesis-related protein STH-2	2,606	0,004
34.7	transport.phosphate	SGN-U593544	BI206370	PHT1;4, ATPT2 | ATPT2 (PHOSPHATE TRANSPORTER 2); carbohydrate transporter/ phosphate &hellip	2,557	0,001
35.2	not assigned.unknown	SGN-U604799	AW625109	Unknown	2,557	0,013

23.4.10	nucleotide metabolism.phosphotransfer and pyrophosphatases.nucleoside diphosphate kinase	SGN-U583106	EX149694	nucleoside diphosphate kinase	2,520	0,016
35.2	not assigned.unknown	SGN-U579404	Z21719	Tomato glycine rich protein 92	2,510	0,003
33.2	development.late embryogenesis abundant	SGN-U577990	EG553850	ethylene-responsive late embryogenesis	2,510	0,006
26.12	misc.peroxidases	SGN-U592829	AW216562	LECEVI16G peroxidase precursor	2,506	0,006
10.8.2	cell wall.pectin*esterases.acetyl esterase	SGN-U598156	BI204903	Pectinacetylesterase	2,490	0,008
10.7	cell wall.modification	SGN-U570132	AW218469	Xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / en&hellip carbohydrate metabolism	2,486	0,008
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U585283	AI782121	Tropinone reductase I Glucose/ribitol dehydrogenase	2,467	0,006
30.1	signalling.in sugar and nutrient physiology	SGN-U579798	TA35985_4081	photoassimilate-responsive protein-related	2,427	0,004
30.2.25	signalling.receptor kinases.wall associated kinase	SGN-U603134	DB679467	Receptor-like protein kinase Serine/threonine protein kinase	2,421	0,007
35.1	not assigned.no ontology	SGN-U580428	AK246699	phosphoglycerate/bisphosphoglycerate mutase family protein	2,410	0,004
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U564478	AI489089	UDP-glucoronosyl/UDP-glucosyl transferase family protein	2,405	0,001
11.1.8	lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	SGN-U601166	CK348342	Acyl-CoA synthetase/AMP-acid ligase II	2,404	0,004
26.10	misc.cytochrome P450	SGN-U569793	AW029862	jasmonic acid 1	2,401	0,019

26.12	misc.peroxidases	SGN-U591103	DB715819	LECEVI16G peroxidase precursor	2,401	0,003
26.13	misc.acid and other phosphatases	SGN-U571100	TA38596_4081	putative acid phosphatase	2,357	0,002
29.2.1.2.2.22	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L22	SGN-U579809	TA36000_4081	structural constituent of ribosome	2,344	0,002
35.2	not assigned.unknown	SGN-U575541	AK248063	Unknown	2,323	0,005
35.2	not assigned.unknown	SGN-U562737	TA54700_4081	NIMIN2c protein [Nicotiana tabacum]	2,317	0,004
35.3	not assigned.disagreeing hits	SGN-U590749	AK246433	photoassimilate-responsive protein-related	2,311	0,008
20.1	stress.biotic	SGN-U580857	Z15138	chitinase 2	2,293	0,007
29.5.1	protein.degradation.subtilases	SGN-U579833	BT013554	subtilisin-like protease [Solanum lycopersicum	2,292	0,004
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U575306	TA52190_4081	FAD-binding domain-containing protein	2,286	0,013
26.12	misc.peroxidases	SGN-U578562	X71593	LECEVI1A	2,273	0,005
35.2	not assigned.unknown	SGN-U584433	AK247049	NBS-LRR class disease resistance protein	2,269	0,002
35.2	not assigned.unknown	SGN-U589195	AJ417830	extensin-like protein Ext1	2,247	0,015
11.2.4	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U574775	BI421987	FAD2 | FAD2 (FATTY ACID DESATURASE 2) Omega-6 fatty acid desaturase,	2,243	0,006
29.5.9	protein.degradation.AAA type	SGN-U570898	ES897181	AAA-ATPase	2,224	0,004

11.1.8	lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	SGN-U598791	BI921508	Acyl-CoA synthetase/AMP-acid ligase II	2,215	0,007
35.2	not assigned.unknown	SGN-U585798	TA53412_4081	Phytosulfokines 3	2,195	0,011
35.2	not assigned.unknown	SGN-U572867	AW625265	ATGOS12, GOS12 | GOS12 (GOLGI SNARE 12); SNARE binding	2,193	0,007
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U568692	TA56994_4081	Myb-related transcription factor	2,188	0,004
35.2	not assigned.unknown	SGN-U562754	AK224692	Early tobacco anther 1	2,154	0,006
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U582635	BI204986	Small auxin up-regulated RNA36	2,154	0,040
29.5.9	protein.degradation.AAA type	SGN-U579496	EG553012	AAA-ATPase	2,146	0,004
35.3	not assigned.disagreeing hits	SGN-U587879	DB688404	WRKY transcription factor 45	2,138	0,009
35.2	not assigned.unknown	SGN-U594690	AW625823	Unknown	2,133	0,002
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U582348	BG631869	pectate lyase family protein	2,131	0,022
29.3	protein.targeting	SGN-U578830	BW689995	translocon-associated protein beta (TRAPB) family protein	2,114	0,002
35.2	not assigned.unknown	SGN-U569778	BG132489	Uridine kinase	2,112	0,002
20.2.99	stress.abiotic.unspecified	SGN-U564705	AW625548	Proline-rich protein Pollen Ole e 1 allergen and extensin	2,111	0,006
13.1.3.1	amino acid metabolism.synthesis.aspartate family.asparagine	SGN-U580427	AW625684	asparagine synthetase 1	2,091	0,018

13.2.7	amino acid metabolism.degradation.histidine	SGN-U578638	CK348340	aromatic amino acid decarboxylase 1A	2,053	0,009
35.1.41	not assigned.no ontology.hydroxyproline rich proteins	SGN-U582149	AK247606	hydroxyproline-rich glycoprotein family protein	2,047	0,031
35.3	not assigned.disagreeing hits	SGN-U578575	AI898755	gibberellin 2-oxidase 4	2,043	0,012
35.2	not assigned.unknown	SGN-U564035	TA53687_4081	QRP1, ER | ER (ERECTA, QUANTITATIVE RESISTANCE TO PLECTOSPHAERELLA 1)	2,041	0,002
34.99	transport.misc	SGN-U568892	BI208363	disease resistance-responsive protein-related / dirigent protein-related |	2,034	0,002
30.3	signalling.calcium	SGN-U576561	BI423269	calcium-binding EF hand family protein	2,032	0,009
26.18	misc.invertase/pectin methylesterase inhibitor family protein	SGN-U580995	ES893942	invertase/pectin methylesterase inhibitor family protein	2,031	0,005
35.3	not assigned.disagreeing hits	SGN-U583017	BW692889	WRKY transcription factor 46	2,028	0,004
30.2.17	signalling.receptor kinases.DUF 26	SGN-U574242	TA49109_4081	Receptor-like protein kinase Serine/threonine protein kinase	2,020	0,009
20.1	stress.biotic	SGN-U566861	BG132609	Acidic chitinase	2,017	0,003
26.7	misc.oxidases - copper, flavone etc.	SGN-U581220	BM410550	partialpolyphenol oxidase A	2,015	0,001
35.3	not assigned.disagreeing hits	SGN-U581154	ES896190	FRO1 | FRO1 (FROSTBITE1) Proteinase inhibitor	2,008	0,029
30.3	signalling.calcium	SGN-U563943	DB713735	Calmodulin-binding protein	2,005	0,003
26.10	misc.cytochrome P450	SGN-U578999	BI204128	Cytochrome P450 E-class, group I	2,005	0,018

26.28	misc.GDSL-motif lipase	SGN-U564645	AW622151	lipase, putative GDSL-like Lipase/Acylhydrolase family protein, expressed	2,004	0,002
35.2	not assigned.unknown	SGN-U562944	TA53162_4081	putative phytosulfokine peptide precursor	1,990	0,006
10.8.1	cell wall.pectin*esterases.PME	SGN-U585616	AI489536	pectinesterase family protein	1,978	0,005
35.3	not assigned.disagreeing hits	SGN-U583017	AK325041	TMV response-related gene product	1,978	0,006
16.1.2.3	secondary metabolism.isoprenoids.mevalonate pathway.HMG-CoA reductase	SGN-U578017	BI934195	HMGR1, HMG1 | HMG1 (3-HYDROXY-3-METHYLGLUTARYL COA REDUCTASE)	1,974	0,036
34.13	transport.peptides and oligopeptides	SGN-U577340	TA40120_4081	proton-dependent oligopeptide transport (POT) family protein	1,966	0,003
35.3	not assigned.disagreeing hits	SGN-U572575	AK328588	ATWRKY51, WRKY51 | WRKY51 (WRKY DNA-binding protein 51)	1,966	0,003
26.12	misc.peroxidases	SGN-U567591	AK329676	peroxidase, putative	1,963	0,002
30.3	signalling.calcium	SGN-U574034	AK320807	calmodulin-binding protein	1,961	0,006
35.2	not assigned.unknown	SGN-U572676	AW094229	Unknown	1,957	0,006
29.2.1.99.99	protein.synthesis.ribosomal protein.unknown.unknown	SGN-U576227	AK323381	Unknown	1,944	0,005
35.3	not assigned.disagreeing hits	SGN-U577578	TA36896_4081	inositol-3-phosphate synthase, putative	1,943	0,008
27.3.80	RNA.regulation of transcription.zf-HD	SGN-U568765	AW092295	ATHB22, MEE68 | ATHB22/MEE68 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 22)	1,938	0,028
35.3	not assigned.disagreeing hits	SGN-U581108	NM_001247130	eukaryotic translation initiation factor SUI1, putative	1,935	0,004

17.3.1.2.8	hormone metabolism.brassinosteroid.synthesis-degradation.sterols.DWF1	SGN-U578468	TA37429_4081	DIM, EVE1, DW1, DIM1, CBB1, DWF1 | DWF1 (DIMINUTO 1)	1,931	0,002
35.3	not assigned.disagreeing hits	SGN-U582150	BT013075	hydroxyproline-rich glycoprotein family protein	1,924	0,024
30.1	signalling.in sugar and nutrient physiology	SGN-U577576	AK328389	photoassimilate-responsive protein-related	1,921	0,005
13.1.3.1	amino acid metabolism.synthesis.aspartate family.asparagine	SGN-U580427	BI926449	DIN6, AT-ASN1, ASN1 | ASN1 (DARK INDUCIBLE 6)	1,920	0,017
11.2.4	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U574775	AK330134	FAD2 | FAD2 (FATTY ACID DESATURASE 2)	1,920	0,005
35.2	not assigned.unknown	SGN-U585591	BW686029	Unknown	1,916	0,005
35.2	not assigned.unknown	SGN-U573769	AI779338	Unknown	1,913	0,002
29.5.9	protein.degradation.AAA type	SGN-U571250	AI486498	AAA-type ATPase family protein	1,899	0,005
35.3	not assigned.disagreeing hits	SGN-U577605	AK326256	methionine sulfoxide reductase domain-containing protein	1,896	0,003
26.7	misc.oxidases - copper, flavone etc.	SGN-U581220	TA39971_4081	polyphenol oxidase	1,885	0,003
17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U571539	NM_001247058	ATERF1, ERF1 | ATERF1/ERF1 (ETHYLENE RESPONSE FACTOR 1)	1,873	0,011
35.1	not assigned.no ontology	SGN-U575764	AK325665	haloacid dehalogenase-like hydrolase family protein	1,869	0,002
26.12	misc.peroxidases	SGN-U583085	TA37168_4081	peroxidase 12 (PER12) (P12) (PRXR6)	1,867	0,004
35.3	not assigned.disagreeing hits	SGN-U578575	NM_001247823	ATGA2OX2 | ATGA2OX2	1,866	0,018

26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	SGN-U575179	AK320994	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,857	0,003
20.1	stress.biotic	SGN-U582384	EG553581	trypsin and protease inhibitor family protein	1,855	0,008
35.2	not assigned.unknown	SGN-U572083	AK329117	Unknown	1,844	0,011
35.2	not assigned.unknown	SGN-U602745	AW625905	Unknown	1,835	0,015
35.3	not assigned.disagreeing hits	SGN-U581546	NM_001247130	ferredoxin-1, chloroplast precursor	1,830	0,005
17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U569393	AW034080	ATERF2, ATERF-2, ERF2 | ATERF-2/ATERF2/ERF2 (ETHYLENE RESPONSE FACTOR 2)	1,827	0,018
34.2	transporter.sugars	SGN-U569492	TA53423_4081	sugar transporter, putative	1,803	0,007
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	SGN-U580800	AK326096	HSFA6B, AT-HSFA6B | AT-HSFA6B (Arabidopsis thaliana heat shock transcription factor A6B)	1,794	0,002
35.3	not assigned.disagreeing hits	SGN-U604744	BE432384	integral membrane family protein	1,785	0,003
35.2	not assigned.unknown	SGN-U563737	BG643749	Unknown	1,770	0,008
26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U587778	BP892917	short-chain dehydrogenase/reductase (SDR) family protein	1,765	0,010
26.4	misc.beta 1,3 glucan hydrolases	SGN-U590982	NM_001247876	AXR1 | AXR1 (AUXIN RESISTANT 1)	1,758	0,012
35.3	not assigned.disagreeing hits	SGN-U578830	TA51698_4081	translocon-associated protein beta (TRAPB) family protein	1,757	0,002
10.7	cell wall.modification	SGN-U578149	BF176393	xyloglucan:xyloglucosyl transferase, putative	1,755	0,006

30.2.17	signalling.receptor kinases.DUF 26	SGN-U563389	TA55468_4081	RLK4, CRK10 | CRK10 (CYSTEINE-RICH RLK10)	1,755	0,003
35.2	not assigned.unknown	SGN-U567758	AK323034	Unknown	1,755	0,016
35.3	not assigned.disagreeing hits	SGN-U592885	BI211002	phytophthora-inhibited protease 1	1,754	0,005
35.2	not assigned.unknown	SGN-U581493	NM_001247109	Unknown	1,753	0,031
35.1	not assigned.no ontology	SGN-U569417	CK714819	hydrolase, alpha/beta fold family protein	1,744	0,002
35.2	not assigned.unknown	SGN-U602544	BP893803	Unknown	1,742	0,005
30.3	signalling.calcium	SGN-U563943	AK320807	calmodulin-binding protein	1,740	0,005
35.2	not assigned.unknown	SGN-U600609	BI205665	Unknown	1,735	0,007
21.1	redox.thioredoxin	SGN-U574846	BT014226	ATPDIL1-2 | ATPDIL1-2 (PDI-LIKE 1-2)	1,725	0,015
16.2.1.10	secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD	SGN-U569434	AK324917	ELI3-1 | ELI3-1 (ELICITOR-ACTIVATED GENE 3)	1,724	0,031
35.3	not assigned.disagreeing hits	SGN-U564024	AK326325	TUB8 | TUB8 (tubulin beta-8)	1,721	0,014
26.10	misc.cytochrome P450	SGN-U567668	AK323868	CYP72A7 | CYP72A7 (cytochrome P450, family 72, subfamily A, polypeptide 7)	1,720	0,002
20.2.99	stress.abiotic.unspecified	SGN-U566316	AW626228	pollen Ole e 1 allergen and extensin family protein	1,713	0,038
29.4	protein.postranslational modification	SGN-U580845	BP891495	PMSR1 | PMSR1 (PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 1)	1,712	0,002

35.2	not assigned.unknown	SGN-U582651	ES897046	Unknown	1,712	0,004
25	C1-metabolism	SGN-U579280	BI422637	FDH | FDH (FORMATE DEHYDROGENASE)	1,711	0,011
17.3.1.2.7	hormone metabolism.brassinosteroid.synthesis-degradation.sterols.DWF5	SGN-U563525	AK322963	PA, LE, ST7R, 7RED, DWF5 | DWF5 (DWARF 5)	1,710	0,004
30.2.17	signalling.receptor kinases.DUF 26	SGN-U599162	AI894931	leucine-rich repeat family protein / protein kinase family protein	1,709	0,008
35.2	not assigned.unknown	SGN-U576445	EG553551	Unknown	1,707	0,029
26.12	misc.peroxidases	SGN-U563368	AW625997	cationic peroxidase, putative	1,707	0,018
35.2	not assigned.unknown	SGN-U580440	DV105097	Unknown	1,699	0,011
26.9	misc.glutathione S transferases	SGN-U582177	AK322433	ATGSTU25 | ATGSTU25 (Arabidopsis thaliana Glutathione S-transferase (class tau) 25)	1,698	0,017
35.2	not assigned.unknown	SGN-U602712	AK323773	Unknown	1,693	0,028
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U578672	AI778966	PRK | PRK (PHOSPHORIBULOKINASE)	1,692	0,005
35.2	not assigned.unknown	SGN-U575760	AW626343	Unknown	1,690	0,012
35.3	not assigned.disagreeing hits	SGN-U590707	AK321025	ADF4 | ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); actin binding	1,683	0,003
34.13	transport.peptides and oligopeptides	SGN-U569392	AW622916	proton-dependent oligopeptide transport (POT) family protein	1,677	0,011
26.7	misc.oxidases - copper, flavone etc.	SGN-U577633	BT013978	NADP-dependent oxidoreductase, putative	1,672	0,004

13.1.6.4.1	amino acid metabolism.synthesis.aromatic aa.tyrosine.arogenate dehydrogenase \& prephenate dehydrogenase	SGN-U570951	BI422114	prephenate dehydrogenase family protein	1,665	0,008
26.10	misc.cytochrome P450	SGN-U567669	AK323868	CYP72A7 | CYP72A7 (cytochrome P450, family 72, subfamily A, polypeptide 7)	1,661	0,003
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U579904	NM_001246911	oxidoreductase, 2OG-Fe(II) oxygenase family protein	1,659	0,012
11.1.1	lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	SGN-U588811	AK320937	acetyl-CoA C-acyltransferase, putative	1,655	0,005
34.6	transport.sulphate	SGN-U585383	AK322276	SULTR2;1, AST68 | AST68 (Sulfate transporter 2.1)	1,655	0,006
35.2	not assigned.unknown	SGN-U588215	DB693533	Unknown	1,653	0,013
35.2	not assigned.unknown	SGN-U568050	BI928475	Unknown	1,649	0,013
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	SGN-U590552	AK326096	HSFA7A, AT-HSFA7A | AT-HSFA7A (Arabidopsis thaliana heat shock transcription factor A7A)	1,648	0,009
16.7	secondary metabolism.wax	SGN-U577979	BM535116	CER1 | CER1 (ECERIFERUM 1)	1,645	0,003
35.3	not assigned.disagreeing hits	SGN-U577907	TA35664_4081	TET8 | TET8 (TETRASPANIN8)	1,642	0,004
17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U566374	TA54084_4081	ATERF1, ERF1 | ATERF1/ERF1 (ETHYLENE RESPONSE FACTOR 1)	1,640	0,016
35.1	not assigned.no ontology	SGN-U574371	TA55064_4081	MD-2-related lipid recognition domain-containing protein	1,633	0,008
29.5.3	protein.degradation.cysteine protease	SGN-U580776	NM_001247020	cysteine proteinase, putative	1,627	0,003

20.2.4	stress.abiotic.touch/wounding	SGN-U567804	DB707336	HEL, PR-4, PR4 | PR4 (PATHOGENESIS-RELATED 4)	1,622	0,006
27.1	RNA.processing	SGN-U576432	AI483324	ATFIB2, FIB2 | FIB2 (FIBRILLARIN 2)	1,620	0,003
35.2	not assigned.unknown	SGN-U594679	BF113541	Unknown	1,616	0,006
34.22	transport.cyclic nucleotide or calcium regulated channels	SGN-U584362	BI422205	ATCNGC1, CNGC1 | CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1)	1,611	0,007
35.1	not assigned.no ontology	SGN-U578748	ES896804	lipid-associated family protein	1,604	0,010
34.13	transport.peptides and oligopeptides	SGN-U585723	AI489986	proton-dependent oligopeptide transport (POT) family protein	1,603	0,002
34.99	transport.misc	SGN-U603728	BG126341	transcription factor	1,596	0,005
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U565055	BI206533	glycosyl transferase family 1 protein	1,595	0,006
26.13	misc.acid and other phosphatases	SGN-U576865	AK323548	PAP10, ATPAP10 | ATPAP10/PAP10	1,594	0,005
35.3	not assigned.disagreeing hits	SGN-U579592	BI205436	hsr201 protein	1,594	0,008
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U572473	AK324892	auxin-responsive family protein	1,590	0,025
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U579596	TA43518_4081	UDP-glucoronosyl/UDP-glucosyl transferase family protein	1,586	0,002
35.2	not assigned.unknown	SGN-U589195	AW218429	extensin-like protein ext1 precursor	1,580	0,015
10.7	cell wall.modification	SGN-U581358	NM_001247278	XTR7 | XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7)	1,580	0,003

35.2	not assigned.unknown	SGN-U574188	CK348350	Unknown	1,576	0,003
35.3	not assigned.disagreeing hits	SGN-U577771	AK319537	malate dehydrogenase, cytosolic, putative	1,571	0,005
29.5.9	protein.degradation.AAA type	SGN-U579496	TA37095_4081	AAA-type ATPase family protein	1,571	0,004
29.5.9	protein.degradation.AAA type	SGN-U581833	AW030818	AAA-type ATPase family protein	1,570	0,003
33.99	development.unspecified	SGN-U584751	TA46760_4081	TET3 | TET3 (TETRASPANIN3)	1,569	0,005
29.5.9	protein.degradation.AAA type	SGN-U566579	TA40785_4081	AATP1 | AATP1 (AAA-ATPASE 1)	1,562	0,002
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U576121	BT013271	oxidoreductase, 2OG-Fe(II) oxygenase family protein	1,559	0,009
35.2	not assigned.unknown	SGN-U566893	TA55945_4081	Unknown	1,554	0,006
26.4	misc.beta 1,3 glucan hydrolases	SGN-U581016	NM_001247876	BG1 | BG1 (BETA-1,3-GLUCANASE 1)	1,552	0,011
13.2.6.2	amino acid metabolism.degradation.aromatic aa.tyrosine	SGN-U577103	BT012990	aminotransferase, putative	1,550	0,006
26.12	misc.peroxidases	SGN-U572515	AW928514	peroxidase, putative	1,549	0,004
11.9.3.2	lipid metabolism.lipid degradation.lysophospholipases.carboxylesterase	SGN-U563298	TA49162_4081	phospholipase/carboxylesterase family protein	1,548	0,004
26.28	misc.GDSL-motif lipase	SGN-U568604	TA48008_4081	GDSL-motif lipase/hydrolase family protein	1,547	0,004
35.1	not assigned.no ontology	SGN-U570088	AW621313	extracellular dermal glycoprotein, putative	1,547	0,005

29.2.1.2.1.26	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S26	SGN-U580053	TA37097_4081	40S ribosomal protein S26 (RPS26C)	1,539	0,005
34.13	transport.peptides and oligopeptides	SGN-U577400	AK323172	proton-dependent oligopeptide transport (POT) family protein	1,537	0,006
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U567160	AK320407	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	1,536	0,003
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	SGN-U597589	AW223396	basic helix-loop-helix (bHLH) family protein	1,532	0,002
4.14	glycolysis.PEPCase	SGN-U576249	TA37863_4081	ATPPC3 | ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3)	1,532	0,010
2.1.2.2	major CHO metabolism.synthesis.starch.starch synthase	SGN-U567281	BT013430	starch synthase, putative	1,530	0,003
35.2	not assigned.unknown	SGN-U581688	BI922667	Unknown	1,529	0,042
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U583310	AJ784605	UDP-glucoronosyl/UDP-glucosyl transferase family protein	1,525	0,006
26.10	misc.cytochrome P450	SGN-U573345	TA54617_4081	CYP71A25 | CYP71A25 (cytochrome P450, family 71, subfamily A, polypeptide 25)	1,525	0,035
27.3.40	RNA.regulation of transcription.Aux/IAA family	SGN-U577993	AK323605	IAA4, ATAUX2-11 | ATAUX2-11 (indoleacetic acid-induced protein 4)	1,522	0,006
34.13	transport.peptides and oligopeptides	SGN-U575200	BT012913	ATPTR3, PTR3 | ATPTR3/PTR3 (PEPTIDE TRANSPORTER PROTEIN 3)	1,521	0,002
35.2	not assigned.unknown	SGN-U578506	NM_001247750	Unknown	1,517	0,005
35.2	not assigned.unknown	SGN-U594093	BG126749	Unknown	1,515	0,004
35.2	not assigned.unknown	SGN-U601835	BP889626	Unknown	1,514	0,006

20.2.4	stress.abiotic.touch/wounding	SGN-U567805	BT012973	HEL, PR-4, PR4 | PR4 (PATHOGENESIS-RELATED 4)	1,514	0,008
35.1	not assigned.no ontology	SGN-U573549	AK323935	extracellular dermal glycoprotein, putative	1,514	0,028
35.2	not assigned.unknown	SGN-U566419	AW218685	Unknown	1,512	0,006
30.5	signalling.G-proteins	SGN-U564361	AK248027	GTP binding	1,509	0,005
27.4	RNA.RNA binding	SGN-U594485	NM_001247049	Unknown	1,509	0,007
17.3.1.2.6	hormone metabolism.brassinosteroid.synthesis-degradation.sterols.DWF7	SGN-U582072	AK323765	DWF7, BUL1 | STE1 (STEROL 1)	1,506	0,002
30.11	signalling.light	SGN-U578072	TC223309	ELIP, ELIP1 | ELIP1 (EARLY LIGHT-INDUCABLE PROTEIN)	1,505	0,006
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U581877	EG553702	auxin-responsive protein, putative	1,505	0,016
23.1.1.10	nucleotide metabolism.synthesis.pyrimidine.CTP synthetase	SGN-U580475	BT013487	EMB2742 | EMB2742 (EMBRYO DEFECTIVE 2742)	1,503	0,005
33.99	development.unspecified	SGN-U581147	DB722895	senescence-associated protein-related	1,500	0,006
9.2.2	mitochondrial electron transport / ATP synthesis.NADH-DH.type II.external	SGN-U576144	AK319193	NDB3 | NDB3; NADH dehydrogenase	1,497	0,014
33.1	development.storage proteins	SGN-U578487	TA36972_4081	cupin family protein	1,494	0,036
11.8.1	lipid metabolism."exotics" (steroids, squalene etc).sphingolipids	SGN-U577442	AK321495	delta-8 sphingolipid desaturase	1,493	0,006
26.10	misc.cytochrome P450	SGN-U578818	AK320577	CYP72A15 | CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15)	1,493	0,003

35.3	not assigned.disagreeing hits	SGN-U582645	BI211069	senescence-associated protein-related	1,492	0,005
13.2.7	amino acid metabolism.degradation.histidine	SGN-U578638	NM_001246916	EMB1075 | EMB1075 (EMBRYO DEFECTIVE 1075)	1,487	0,042
35.2	not assigned.unknown	SGN-U591506	AK327683	jasmonate zim-domain protein 1	1,485	0,028
35.2	not assigned.unknown	SGN-U602653	BG135233	Unknown	1,483	0,017
35.2	not assigned.unknown	SGN-U596641	BF097249	cytochrome P450 family protein	1,480	0,005
26.4	misc.beta 1,3 glucan hydrolases	SGN-U577505	NM_001247229	BG1 | BG1 (BETA-1,3-GLUCANASE 1)	1,480	0,040
34.2	transporter.sugars	SGN-U579712	NM_001247856	STP13, MSS1 | MSS1 (SUGAR TRANSPORT PROTEIN 13)	1,478	0,006
10.8.1	cell wall.pectin*esterases.PME	SGN-U562676	BI209758	pectinesterase family protein	1,476	0,011
2.2.1.3.2	major CHO metabolism.degradation.sucrose.invertases.cell wall	SGN-U600157	NM_001247140	ATBETAFRUCT4, VAC-INV | ATBETAFRUCT4/VAC-INV (VACUOLAR INVERTASE)	1,473	0,017
35.1	not assigned.no ontology	SGN-U566885	AI782802	sterile alpha motif (SAM) domain-containing protein	1,471	0,007
35.3	not assigned.disagreeing hits	SGN-U574242	AW031816	leucine-rich repeat transmembrane protein kinase, putative	1,468	0,011
20.1.7	stress.biotic.PR-proteins	SGN-U564327	BF097728	disease resistance-responsive protein-related	1,466	0,004
35.1	not assigned.no ontology	SGN-U584518	AK326347	Unknown	1,462	0,006
13.1.1.1.1	amino acid metabolism.synthesis.central amino acid metabolism.GABA.Glutamate	SGN-U578934	NM_001246898	GAD4 | GAD4 (GLUTAMATE DECARBOXYLASE 4)	1,455	0,006

	decarboxylase					
35.2	not assigned.unknown	SGN-U570366	TC239414	Unknown	1,452	0,006
35.2	not assigned.unknown	SGN-U583342	NM_001247706	Unknown	1,451	0,007
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U600439	BI205687	ATL63 | ATL63; protein binding / zinc ion binding	1,450	0,014
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U576747	TA55423_4081	FAD-binding domain-containing protein	1,447	0,006
26.4	misc.beta 1,3 glucan hydrolases	SGN-U590649	AI895149	glycosyl hydrolase family 17 protein	1,445	0,008
34.99	transport.misc	SGN-U567687	AI774912	retrotransposon tto1 dna	1,442	0,016
29.5.9	protein.degradation.AAA type	SGN-U570898	AW040747	AAA-type ATPase family protein	1,436	0,020
35.2	not assigned.unknown	SGN-U583151		unknown	1,436	0,038
34.3	transport.amino acids	SGN-U574120	TA53875_4081	amino acid transporter family protein	1,435	0,013
26.10	misc.cytochrome P450	SGN-U591263	BI208057	CYP89A7 | CYP89A7 (cytochrome P450, family 87, subfamily A, polypeptide 7)	1,435	0,005
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U582180	TA55012_4081	glycoside hydrolase family 28 protein	1,434	0,003
20.2.1	stress.abiotic.heat	SGN-U565386	DV103971	17.6 kDa class I heat shock protein (HSP17.6A-CI)	1,431	0,025
35.2	not assigned.unknown	SGN-U584507	AK247286	Unknown	1,429	0,004

30.2.7	signalling.receptor kinases.leucine rich repeat VII	SGN-U599077	BG642964	leucine-rich repeat transmembrane protein kinase, putative	1,429	0,008
10.8.1	cell wall.pectin*esterases.PME	SGN-U599553	BI207671	pectinesterase family protein	1,428	0,007
35.2	not assigned.unknown	SGN-U572369	TA38951_4081	Unknown	1,425	0,005
35.2	not assigned.unknown	SGN-U572286	TA47398_4081	Unknown	1,424	0,009
35.3	not assigned.disagreeing hits	SGN-U583120	AK322333	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,422	0,006
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U583997	NM_001247728	AHDP, ANL2 | ANL2 (ANTHOCYANINLESS 2)	1,421	0,012
35.3	not assigned.disagreeing hits	SGN-U562651	NM_001247921	HCT | transferase family protein	1,421	0,004
35.3	not assigned.disagreeing hits	SGN-U564932	AK329507	pathogenesis-related family protein	1,417	0,005
34.19.1	transport.Major Intrinsic Proteins.PIP	SGN-U579836	BG626235	PIP2F, PIP2;4 | PIP2;4/PIP2F (plasma membrane intrinsic protein 2;4)	1,411	0,002
34.98	transporter.membrane system unknown	SGN-U587711	DV105226	glycerol-3-phosphate transporter, putative	1,410	0,003
35.2	not assigned.unknown	SGN-U594480	X99451	extensin-like protein dif10 precursor	1,409	0,012
29.2.1.2.2.82	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.P2	SGN-U580232	AK327999	60S acidic ribosomal protein P2 (RPP2D)	1,409	0,008
26.13	misc.acid and other phosphatases	SGN-U579724	NM_001247596	ATPAP17, PAP17, ATACP5 | ATACP5 (acid phosphatase 5)	1,407	0,016
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U566681	AK329158	RD22 | RD22 (RESPONSIVE TO DESSICATION 22)	1,402	0,015

28.1	DNA.synthesis/chromatin structure	SGN-U571525	AI897466	endonuclease/exonuclease/phosphatase family protein	1,399	0,002
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U574499	AW030833	AP2 domain-containing protein	1,398	0,029
2.2.2.2	major CHO metabolism.degradation.starch.starch phosphorylase	SGN-U568729	BT013295	ATPHS2, PHS2 | ATPHS2/PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2)	1,395	0,003
27.3.37	RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family	SGN-U574401	TA56163_4081	PCK1, LBD12, ASL5 | ASL5 (phosphoenolpyruvate carboxykinase1)	1,395	0,018
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U585818	BG735361	leucine-rich repeat transmembrane protein kinase, putative	1,394	0,006
35.2	not assigned.unknown	SGN-U570381	BP894400	Unknown	1,393	0,004
26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	SGN-U581146	BT013185	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,391	0,028
11.8.2	lipid metabolism."exotics" (steroids, squalene etc).methylsterol monooxygenase	SGN-U572947	AK247484	ATSMO1, ATSMO1-1, SMO1-1 | SMO1-1 (STEROL-4ALPHA-METHYL OXIDASE 1-1)	1,390	0,004
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U574112	AK328833	remorin family protein	1,387	0,012
18	Co-factor and vitamine metabolism	SGN-U578696	TA36042_4081	catalytic	1,387	0,021
17.2.1	hormone metabolism.auxin.synthesis-degradation	SGN-U575492	AW648744	JR3, IAR3 | IAR3 (IAA-ALANINE RESISTANT 3)	1,386	0,011
26.10	misc.cytochrome P450	SGN-U567361	AK321258	CYP94C1 | CYP94C1 (cytochrome P450, family 94, subfamily C, polypeptide 1)	1,384	0,016
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U583550	AJ832067	protein kinase, putative	1,383	0,016

35.2	not assigned.unknown	SGN-U598847	AK329310	Unknown	1,381	0,005
35.2	not assigned.unknown	SGN-U582018	AK321473	oxidoreductase, acting on the CH-CH group of donors	1,381	0,017
10.8.1	cell wall.pectin*esterases.PME	SGN-U603810		pectinesterase family protein	1,381	0,005
35.2	not assigned.unknown	SGN-U568324	AK320295	Unknown	1,380	0,006
29.5.5	protein.degradation.serine protease	SGN-U598503	AK325554	SCPL25 | SCPL25 (serine carboxypeptidase-like 25)	1,378	0,005
20	stress	SGN-U577338	BI206173	ozone-responsive stress-related protein, putative	1,378	0,012
35.2	not assigned.unknown	SGN-U598483	DB689447	Unknown	1,373	0,003
34.12	transport.metal	SGN-U583586	AW621284	ZIP5 | ZIP5 (ZINC TRANSPORTER 5 PRECURSOR)	1,373	0,004
4.14	glycolysis.PEPCase	SGN-U576254	AI897765	ATPPC3 | ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3)	1,372	0,006
26.3	misc.gluco-, galacto- and mannosidases	SGN-U565673	NM_001247161	ATGH9B13 | ATGH9B13 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9B13)	1,372	0,011
35.2	not assigned.unknown	SGN-U599411	AK324956	Unknown	1,371	0,003
30.2.17	signalling.receptor kinases.DUF 26	SGN-U574241	BI923074	leucine-rich repeat transmembrane protein kinase, putative	1,371	0,011
20.1	stress.biotic	SGN-U578836	NM_001247422	ATOSM34 | ATOSM34 (OSMOTIN 34)	1,370	0,010
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U569071	AK320713	CSLG1, CSLG2, ATCSLG1 | ATCSLG1 (Cellulose synthase-like G1)	1,368	0,012

11.9.3.4	lipid metabolism.lipid degradation.lysophospholipases.phospholipase A2	SGN-U569316	BG130237	ATSPLA2-ALPHA, PLA2-ALPHA | ATSPLA2-ALPHA/PLA2-ALPHA (PHOSPHOLIPASE A2-ALPHA)	1,368	0,008
35.2	not assigned.unknown	SGN-U578951	AK323970	CW14 | CW14	1,363	0,004
34.99	transport.misc	SGN-U595619	AK323125	auxin efflux carrier family protein	1,362	0,007
11.1.8	lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	SGN-U586544	AK321687	BZO1 | BZO1; benzoate-CoA ligase	1,361	0,018
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U578607	TA36692_4081	ACO4, EAT1, EFE | EFE (ETHYLENE FORMING ENZYME)	1,355	0,046
35.2	not assigned.unknown	SGN-U572004	AK321473	Unknown	1,354	0,013
22.1.6	polyamine metabolism.synthesis.spermidine synthase	SGN-U580117	TA36245_4081	SPDS1 | SPDS1 (SPERMIDINE SYNTHASE 1)	1,354	0,004
26.13	misc.acid and other phosphatases	SGN-U588082	DV105561	similar to phosphoric monoester hydrolase	1,354	0,006
35.3	not assigned.disagreeing hits	SGN-U567689	AI774692	Pleiotropic drug resistance protein 4	1,353	0,012
27.4	RNA.RNA binding	SGN-U581409	GO373033	GR-RBP2, GRP2, ATGRP2 | ATGRP2 (GLYCINE-RICH RNA-BINDING PROTEIN 2)	1,351	0,005
20.2.1	stress.abiotic.heat	SGN-U574337	TA39175_4081	PTAC4 | PTAC4 (PLASTID TRANSCRIPTIONALLY ACTIVE4)	1,350	0,007
29.4	protein.postranslational modification	SGN-U565103	NM_001247763	ATPP2CA, AHG3 | AHG3/ATPP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA)	1,349	0,005
27.2	RNA.transcription	SGN-U578940	GT166243	ATRPB15.9, RPB15.9.9, RPB15.9 | RPB15.9 (RNA polymerase II 15.9)	1,349	0,006

35.1	not assigned.no ontology	SGN-U576737	BT014408	membrane protein	1,347	0,003
35.2	not assigned.unknown	SGN-U572368	TA38950_4081	Unknown	1,345	0,007
35.3	not assigned.disagreeing hits	SGN-U580555	AK321589	RPS15 | RPS15 (CYTOSOLIC RIBOSOMAL PROTEIN S15)	1,345	0,005
35.2	not assigned.unknown	SGN-U581728	AK247363	Unknown	1,344	0,025
28.1.3	DNA.synthesis/chromatin structure.histone	SGN-U578512	AW621605	histone H4	1,343	0,009
11.2.3	lipid metabolism.FA desaturation.omega 3 desaturase	SGN-U575508	NM_001246862	FAD3 | FAD3 (FATTY ACID DESATURASE 3)	1,342	0,007
35.2	not assigned.unknown	SGN-U577093	AI488854	Unknown	1,340	0,023
29.2.1.2.1.30	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S30	SGN-U590834	BG125727	40S ribosomal protein S30 (RPS30C)	1,333	0,008
17.1.1	hormone metabolism.abscisic acid.synthesis-degradation	SGN-U577478	NM_001247526	ATNCED3, STO1, NCED3 | NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE3)	1,332	0,011
35.2	not assigned.unknown	SGN-U594155	AW029688	lipoxygenase	1,332	0,015
26.10	misc.cytochrome P450	SGN-U583521	AK319823	CYP88A4, KAO2 | KAO2 (ENT-KAURENOIC ACID HYDROXYLASE 2)	1,330	0,005
27.3.40	RNA.regulation of transcription.Aux/IAA family	SGN-U579607	AF022022	MSG2, IAA19 | IAA19 (indoleacetic acid-induced protein 19)	1,329	0,036
20.1	stress.biotic	SGN-U571781	AK323929	trypsin and protease inhibitor family protein	1,327	0,038
35.2	not assigned.unknown	SGN-U591840	AK319768	Unknown	1,322	0,006

20.1	stress.biotic	SGN-U577839	NM_001247199	pathogenesis-related protein, putative	1,319	0,011
20.1	stress.biotic	SGN-U578226	BI926952	ATLP-1 | ATLP-1 (Arabidopsis thaumatin-like protein 1)	1,319	0,004
20.1	stress.biotic	SGN-U585911	AK324689	glycosyl hydrolase family 18 protein	1,319	0,003
34.13	transport.peptides and oligopeptides	SGN-U577308	AK323172	proton-dependent oligopeptide transport (POT) family protein	1,316	0,004
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U577331	AW441207	MMZ4, UEV1D, UEV1D-4 | MMZ4/UEV1D/UEV1D-4 (MMS ZWEI HOMOLOGE 4, UBIQUITIN E2 VARIANT 1D-4)	1,316	0,008
35.2	not assigned.unknown	SGN-U581573	GO376336	JAZ1, TIFY10A | JAZ1/TIFY10A (JASMONATE-ZIM-DOMAIN PROTEIN 1)	1,316	0,010
35.3	not assigned.disagreeing hits	SGN-U578439	TC217573	RAP2.3, ATEBP, ERF72 | ATEBP/ERF72/RAP2.3 (RELATED TO AP2 3)	1,311	0,013
30.3	signalling.calcium	SGN-U566062	BP907910	ACA2 | ACA2 (CALCIUM ATPASE 2)	1,311	0,015
33.99	development.unspecified	SGN-U572541	AK326980	male sterility MS5 family protein	1,311	0,021
10.7	cell wall.modification	SGN-U586326	BI421662	EXPR, AT-EXPR, ATEXPR1, ATHEXP BETA 3.1, ATEXLB1 | ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1)	1,310	0,039
35.3	not assigned.disagreeing hits	SGN-U581131	NM_001246846	lipid-associated family protein	1,310	0,005
31.3	cell.cycle	SGN-U574298	BI925047	CYCB1;1, CYCB1, CYC1 | CYC1 (CYCLIN 1)	1,309	0,006
20.1	stress.biotic	SGN-U578851	GT167928	ATOSM34 | ATOSM34 (OSMOTIN 34)	1,304	0,004

26.10	misc.cytochrome P450	SGN-U573366	DB679675	CYP76C7 | CYP76C7 (cytochrome P450, family 76, subfamily C, polypeptide 7)	1,301	0,018
35.2	not assigned.unknown	SGN-U573448	TC237479	Unknown	1,301	0,007
35.1	not assigned.no ontology	SGN-U569186	AK325394	SOUL-1 | SOUL-1; binding	1,299	0,006
35.2	not assigned.unknown	SGN-U566999	TA37692_4081	Unknown	1,298	0,004
26.12	misc.peroxidases	SGN-U580841	AK320220	peroxidase, putative	1,297	0,004
27.3.20	RNA.regulation of transcription.G2-like transcription factor family, GARP	SGN-U604820	BE431711	transcription factor	1,296	0,011
30.3	signalling.calcium	SGN-U599723	BW686347	calmodulin, putative	1,296	0,004
35.2	not assigned.unknown	SGN-U575654	TA50315_4081	phosphoribulokinase/uridine kinase family protein	1,293	0,006
35.3	not assigned.disagreeing hits	SGN-U578210	BT013853	proton-dependent oligopeptide transport (POT) family protein	1,292	0,003
29.2.1.2.1.4	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S4	SGN-U579838	TA35753_4081	40S ribosomal protein S4 (RPS4D)	1,292	0,011
35.2	not assigned.unknown	SGN-U565813	TA54784_4081	unknown	1,291	0,003
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U577213	BW685608	PLP3B | PLP3B (PHOSDUCIN-LIKE PROTEIN 3 HOMOLOG)	1,290	0,006
35.3	not assigned.disagreeing hits	SGN-U589703	NM_001247921	HCT | transferase family protein	1,289	0,003
35.2	not assigned.unknown	SGN-U568614	BI210757	Unknown	1,289	0,008

27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U572337	DB710333	ZAT12, RHL41 | RHL41 (RESPONSIVE TO HIGH LIGHT 41)	1,288	0,003
34.99	transport.misc	SGN-U576098	AK323125	auxin efflux carrier family protein	1,287	0,010
14.1	S-assimilation.APS	SGN-U573423	AK320859	APS1 | APS1 (ATP sulfurylase 3)	1,286	0,005
34.6	transport.sulphate	SGN-U582421	AW040386	SULTR3;3, AST91 | AST91 (SULFATE TRANSPORTER 91)	1,285	0,018
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U563235	BI923348	ATMRP6 | ATMRP6 (Arabidopsis thaliana multidrug resistance-associated protein 6)	1,284	0,005
29.5.9	protein.degradation.AAA type	SGN-U568607	AK324797	AAA-type ATPase family protein	1,279	0,003
29.5.9	protein.degradation.AAA type	SGN-U575029	EG553404	AAA-type ATPase family protein	1,276	0,003
26.13	misc.acid and other phosphatases	SGN-U571100	NM_001247074	phosphoric monoester hydrolase	1,276	0,011
35.2	not assigned.unknown	SGN-U603511	DV935959	Unknown	1,275	0,040
30.1	signalling.in sugar and nutrient physiology	SGN-U568646	AW648872	phosphate-responsive protein, putative	1,274	0,021
35.2	not assigned.unknown	SGN-U574784	TA47606_4081	polyphenol oxidase	1,274	0,013
35.2	not assigned.unknown	SGN-U564962	TA54400_4081	pectinesterase family protein	1,273	0,021
30.11	signalling.light	SGN-U573472	BG130993	ELF4 | ELF4 (EARLY FLOWERING 4)	1,273	0,004
35.3	not assigned.disagreeing hits	SGN-U574445	TA38703_4081	CRT3 | CRT3 (CALRETICULIN 3)	1,272	0,005

35.2	not assigned.unknown	SGN-U583455	TA44067_4081	Unknown	1,270	0,005
29.4	protein.postranslational modification	SGN-U567234	NM_001247946	WEE1 | WEE1 (ARABIDOPSIS WEE1 KINASE HOMOLOG)	1,268	0,004
21.1	redox.thioredoxin	SGN-U576803	AK319465	ATM1, TRX-M1, ATHM1 | ATHM1 (Arabidopsis thioredoxin M-type 1)	1,268	0,004
20.2.99	stress.abiotic.unspecified	SGN-U592856	AK321589	Bet v I allergen family protein	1,266	0,010
34.99	transport.misc	SGN-U570358	AK327756	ripening-responsive protein, putative	1,265	0,009
35.2	not assigned.unknown	SGN-U604230	BI204004	Unknown	1,262	0,022
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family	SGN-U566778	AK326455	WRKY18 | WRKY18 (WRKY DNA-binding protein 18)	1,262	0,032
29.5.1	protein.degradation.subtilases	SGN-U578717	NM_001247328	ARA12 | ARA12	1,262	0,007
33.1	development.storage proteins	SGN-U581750	AW625062	PLP2, PLA2A, PLA IIA | PLP2 (PHOSPHOLIPASE A 2A)	1,255	0,007
17.6.3	hormone metabolism.gibberelin.induced-regulated-responsive-activated	SGN-U590997	AJ785329	GASA4 | GASA4 (GAST1 PROTEIN HOMOLOG 4)	1,253	0,044
35.2	not assigned.unknown	SGN-U573629	CN641308	Unknown	1,253	0,012
35.2	not assigned.unknown	SGN-U582193	TA50035_4081	Unknown	1,252	0,006
35.2	not assigned.unknown	SGN-U563121	AK247886	Unknown	1,251	0,006
35.2	not assigned.unknown	SGN-U598048	BI203679	unknown	1,248	0,005

29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U565968	AK320738	ADO3, FKF1 | FKF1 (FLAVIN-BINDING KELCH DOMAIN F BOX PROTEIN)	1,246	0,005
34.2	transporter.sugars	SGN-U589401	GO374014	porin, putative	1,245	0,013
3.1.2.2	minor CHO metabolism.raffinose family.raffinose synthases.putative	SGN-U577462	NM_001247834	ATSIP1 | ATSIP1 (ARABIDOPSIS THALIANA SEED IMBIBITION 1)	1,244	0,003
29.2.1.2.2.537	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L37A	SGN-U577334	AW034279	60S ribosomal protein L37a (RPL37aB)	1,242	0,008
35.3	not assigned.disagreeing hits	SGN-U586487	NM_001247105	SPX (SYG1/Pho81/XPR1) domain-containing protein	1,241	0,012
26.6	misc.O- methyl transferases	SGN-U578741	AW649598	SPE2, ADC2 | ADC2 (ARGININE DECARBOXYLASE 2)	1,240	0,009
26.9	misc.glutathione S transferases	SGN-U587908	AK323808	ATGSTU8 | ATGSTU8 (Arabidopsis thaliana Glutathione S-transferase (class tau) 8)	1,240	0,007
35.2	not assigned.unknown	SGN-U601643	BE354492	Unknown	1,238	0,005
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U581878	AK321469	auxin-responsive protein, putative	1,236	0,022
1.3.13	PS.calvin cyle.rubisco interacting	SGN-U566499	AK319595	ribulose-1,5 bisphosphate carboxylase oxygenase large subunit N-methyltransferase, putative	1,236	0,004
23.2	nucleotide metabolism.degradation	SGN-U565781	TA39294_4081	inosine-uridine preferring nucleoside hydrolase family protein	1,234	0,006
27.3.99	RNA.regulation of transcription.unclassified	SGN-U584308	BT012902	Symbols: ATRBP47C | ATRBP47C	1,233	0,006
35.3	not assigned.disagreeing hits	SGN-U578058	NM_001247565	CYP72A15 | CYP72A15 (cytochrome P450, family 72, subfamily A, polypeptide 15)	1,232	0,010
10.6.1	cell wall.degradation.cellulases and beta -1,4-glucanases	SGN-U583338		glycosyl hydrolase family 3 protein	1,231	0,007

35.2	not assigned.unknown	SGN-U598885	DB726788	Unknown	1,230	0,012
35.2	not assigned.unknown	SGN-U565287	AI487516	Unknown	1,230	0,006
35.2	not assigned.unknown	SGN-U577838	GO375294	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	1,229	0,013
35.3	not assigned.disagreeing hits	SGN-U591736	TA35884_4081	60S ribosomal protein L30 (RPL30B)	1,229	0,004
26.12	misc.peroxidases	SGN-U580621	AW928308	peroxidase, putative	1,228	0,004
30.5	signalling.G-proteins	SGN-U576730	NM_001247230	ATROPGEF12, ROPGEF12, MEE64 | ATROPGEF12/MEE64/ROPGEF12 (MATERNAL EFFECT EMBRYO ARREST 64)	1,227	0,043
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U604358	BG133762	auxin-responsive family protein	1,227	0,008
34.12	transport.metal	SGN-U565686	AK326383	metal transporter family protein	1,227	0,008
35.2	not assigned.unknown	SGN-U570454	BI208695	heavy-metal-associated domain-containing protein	1,225	0,027
10.5.5	cell wall.cell wall proteins.RGP	SGN-U577156	AK321777	ATRGP1, ATRGP, RGP1 | RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1)	1,225	0,003
31.1	cell.organisation	SGN-U564014	AK324246	TUB8 | TUB8 (tubulin beta-8)	1,225	0,007
35.1	not assigned.no ontology	SGN-U599248	AK328099	HEXO2, ATHEX3 | ATHEX3/HEXO2 (BETA-HEXOSAMINIDASE 2)	1,224	0,013
35.2	not assigned.unknown	SGN-U603779	DB685461	Unknown	1,224	0,005

20.2.1	stress.abiotic.heat	SGN-U584038	BG132741	ATP binding	1,223	0,004
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U598589	AJ320056	glycoside hydrolase family 28 protein	1,223	0,008
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U567978	AK323740	AT-ACC2, ACS2 | ACS2 (1-Amino-cyclopropane-1-carboxylate synthase 2)	1,222	0,026
29.5.9	protein.degradation.AAA type	SGN-U571301	AK327197	AAA-type ATPase family protein	1,222	0,005
29.4	protein.postranslational modification	SGN-U590037	TA35884_4081	PMSR1 | PMSR1 (PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 1)	1,220	0,007
35.2	not assigned.unknown	SGN-U599777	AW623311	myosin-related, low similarity to nonmuscle myosin heavy chain	1,219	0,019
35.2	not assigned.unknown	SGN-U570446	AK325642	Unknown	1,217	0,007
35.3	not assigned.disagreeing hits	SGN-U582968	TA53437_4081	aminotransferase, putative	1,215	0,018
35.2	not assigned.unknown	SGN-U574035	AW650005	Unknown	1,213	0,004
35.2	not assigned.unknown	SGN-U599068	AK320211	serine carboxypeptidase S28 family protein	1,211	0,010
10.8.1	cell wall.pectin*esterases.PME	SGN-U586246		pectinesterase family protein	1,210	0,006
35.1	not assigned.no ontology	SGN-U578838	AK324667	leucine-rich repeat family protein	1,210	0,014
35.1	not assigned.no ontology	SGN-U574895	AK324863	zinc knuckle (CCHC-type) family protein	1,210	0,004
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U582374	AK246984	UGT73B3 | UGT73B3 (UDP-GLUCOSYL TRANSFERASE 73B3)	1,205	0,017

35.3	not assigned.disagreeing hits	SGN-U592652	NM_001246846	2-oxoglutarate-dependent dioxygenase	1,204	0,008
29.2.1.2.1.10	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S10	SGN-U578330	AI487864	40S ribosomal protein S10 (RPS10C)	1,203	0,006
13.1.1.2	amino acid metabolism.synthesis.central amino acid metabolism.aspartate	SGN-U580738	AK319676	YLS4, ASP3 | ASP3 (ASPARTATE AMINOTRANSFERASE 3)	1,202	0,009
35.1	not assigned.no ontology	SGN-U566668	AK322423	NHL1 | NHL1 (NDR1/HIN1-like 1)	1,201	0,005
13.2.3.4.1	amino acid metabolism.degradation.aspartate family.methionine.methionine gamma-lyase	SGN-U569670	TA55162_4081	ATMGL | ATMGL; catalytic/ methionine gamma-lyase	1,201	0,005
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U570290	BP890451	esterase, putative	1,201	0,005
35.1	not assigned.no ontology	SGN-U571427	DB687120	harpin-induced protein-related	1,201	0,006
17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U573501	AK323177	ATERF1, ERF1 | ATERF1/ERF1 (ETHYLENE RESPONSE FACTOR 1)	1,201	0,026
27.3.99	RNA.regulation of transcription.unclassified	SGN-U579829	TA41140_4081	aspartyl protease family protein	1,200	0,006
26.28	misc.GDSL-motif lipase	SGN-U566206	AK319817	lipase, putative	1,200	0,004
10.8.2	cell wall.pectin*esterases.acetyl esterase	SGN-U602331	AI771198	pectinacetylesterase family protein	1,199	0,026
35.2	not assigned.unknown	SGN-U587682	DB725549	Unknown	1,198	0,008
17.3.1.1.1	hormone metabolism.brassinosteroid.synthesis-degradation.BRs.DET2	SGN-U575501	NM_001247111	DWF6, DET2 | DET2 (DE-ETIOLATED 2)	1,198	0,004

34.98	transporter.membrane system unknown	SGN-U574958	DV105574	glycerol-3-phosphate transporter, putative	1,197	0,010
35.2	not assigned.unknown	SGN-U574946	BP908157	Unknown	1,197	0,004
20.1.3	stress.biotic.signalling	SGN-U583686	BG127794	ATMLO6, MLO6 | MLO6 (MILDEW RESISTANCE LOCUS O 6)	1,197	0,019
9.4	mitochondrial electron transport / ATP synthesis.alternative oxidase	SGN-U576037	NM_001247188	ATAOX1A, AOX1A | AOX1A (alternative oxidase 1A)	1,196	0,005
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U579018	BT013761	SAR DNA-binding protein, putative	1,196	0,007
35.2	not assigned.unknown	SGN-U582258	TA51212_4081	Unknown	1,195	0,006
20.1.7	stress.biotic.PR-proteins	SGN-U585771	EG553627	disease resistance-responsive family protein	1,195	0,024
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U580194	BI208733	40S ribosomal protein S3 (RPS3C)	1,193	0,005
29.2.1.2.2.24	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L24	SGN-U577435	GO376363	RPL24B, RPL24, STV1 | STV1 (SHORT VALVE1)	1,193	0,009
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U573887	BI422350	FAD-binding domain-containing protein	1,193	0,008
17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U581695	NM_001247276	EIN4 | EIN4 (ETHYLENE INSENSITIVE 4)	1,193	0,013
35.2	not assigned.unknown	SGN-U571144	TA40927_4081	Unknown	1,191	0,008
16.1.2.2	secondary metabolism.isoprenoids.mevalonate pathway.HMG-CoA synthase	SGN-U578388	BI926044	HMGS, EMB2778, MVA1 | MVA1 (HYDROXYMETHYLGLUTARYL-COA SYNTHASE)	1,191	0,008
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U597416	AI782391	ATATH1 | ATATH1 (ABC2 homolog 1)	1,188	0,005

35.2	not assigned.unknown	SGN-U583755	AK322978	Unknown	1,187	0,016
29.6	protein.folding	SGN-U574475	TA45457_4081	chaperone protein dnaJ-related	1,186	0,008
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U563069	BT014506	RPL4 | RPL4 (ribosomal protein L4)	1,185	0,008
35.2	not assigned.unknown	SGN-U582943	AW930136	Unknown	1,185	0,006
20.2.1	stress.abiotic.heat	SGN-U569555	AK327661	J8 | J8; heat shock protein binding	1,184	0,007
35.2	not assigned.unknown	SGN-U583945	BE344440	Unknown	1,184	0,009
35.2	not assigned.unknown	SGN-U591308	AI773150	wound-induced basic protein	1,184	0,018
35.2	not assigned.unknown	SGN-U582381	AW443395	Unknown	1,184	0,020
10.7	cell wall.modification	SGN-U581597	NM_001247440	EXGT-A4 | EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4)	1,182	0,008
35.1	not assigned.no ontology	SGN-U563425	AK326749	hydrolase	1,182	0,004
35.2	not assigned.unknown	SGN-U583900	TA53970_4081	Unknown	1,182	0,045
35.3	not assigned.disagreeing hits	SGN-U593641	GO373807	pgps/nh21	1,180	0,007
11.1.15	lipid metabolism.FA synthesis and FA elongation.ACP desaturase	SGN-U571115	AK319571	FAB2, SSI2 | SSI2 (fatty acid biosynthesis 2)	1,179	0,004
29.4	protein.postranslational modification	SGN-U603987	BP907916	kinase	1,179	0,005

35.2	not assigned.unknown	SGN-U584972	NM_001247728	Unknown	1,178	0,004
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U580135	NM_001246979	FLO2, FL1, AP2 | AP2 (APETALA 2)	1,178	0,008
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U565756	AW032656	AtMYB78 | AtMYB78 (myb domain protein 78)	1,176	0,005
30.3	signalling.calcium	SGN-U581995	AK321297	calmodulin-related protein, putative	1,176	0,006
1.1.2.2	PS.lightreaction.photosystem I.PSI polypeptide subunits	SGN-U562929	AK322229	PSB28 | PSB28 (PHOTOSYSTEM II REACTION CENTER PSB28 PROTEIN)	1,175	0,005
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U578857	TA39146_4081	60S ribosomal protein L19 (RPL19B)	1,174	0,012
35.3	not assigned.disagreeing hits	SGN-U567631		dihydroneopterin aldolase, putative	1,173	0,008
31.4	cell.vesicle transport	SGN-U569494	TA56152_4081	Golgi transport complex protein-related	1,173	0,004
35.1	not assigned.no ontology	SGN-U566929	AJ832089	SWIB complex BAF60b domain-containing protein	1,173	0,013
34.9	transport.metabolite transporters at the mitochondrial membrane	SGN-U577891	TA39002_4081	BOU | BOU (A BOUT DE SOUFFLE)	1,171	0,012
27.4	RNA.RNA binding	SGN-U591153	DB713942	29 kDa ribonucleoprotein, chloroplast, putative	1,170	0,006
35.2	not assigned.unknown	SGN-U603527	BP903297	protein phosphatase 2C family protein	1,170	0,005
20.1	stress.biotic	SGN-U581103	AK322366	ATOSM34 | ATOSM34 (OSMOTIN 34)	1,170	0,023

29.2.1.2.2.537	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L37A	SGN-U581287	TA35772_4081	60S ribosomal protein L37a (RPL37aB)	1,170	0,008
27.3.99	RNA.regulation of transcription.unclassified	SGN-U583195	AK322123	aspartyl protease family protein	1,169	0,008
26.28	misc.GDSL-motif lipase	SGN-U581666	AK329631	GDSL-motif lipase/hydrolase family protein	1,168	0,012
33.99	development.unspecified	SGN-U574964	BW692388	senescence-associated protein-related	1,168	0,017
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U562647	TA54473_4081	Unknown	1,167	0,004
28.1	DNA.synthesis/chromatin structure	SGN-U599051	DB716099	ATNAP57, CBF5, ATCBF5, NAP57 | NAP57 (ARABIDOPSIS THALIANA HOMOLOGUE OF NAP57)	1,166	0,007
35.1	not assigned.no ontology	SGN-U567112	AI485775	rRNA processing protein-related	1,165	0,009
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U562848	AI490234	zinc finger (C3HC4-type RING finger) family protein	1,164	0,004
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U566266	NM_001246936	ATBZIP11, ATB2, BZIP11, GBF6 | GBF6 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 11)	1,163	0,008
29.2.1.2.1.7	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S7	SGN-U578651	AW626328	40S ribosomal protein S7 (RPS7A)	1,163	0,011
26.4	misc.beta 1,3 glucan hydrolases	SGN-U563505	BG123274	glycosyl hydrolase family 17 protein	1,163	0,008
26.10	misc.cytochrome P450	SGN-U579853	TA49451_4081	CYP81F3 | CYP81F3 (cytochrome P450, family 81, subfamily F, polypeptide 3)	1,162	0,006
35.2	not assigned.unknown	SGN-U598006	BP904698	Unknown	1,161	0,017
10.1.2	cell wall.precursor synthesis.UGE	SGN-U583215	TA42864_4081	UGE5 | UGE5 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 5)	1,161	0,032

34.22	transport.cyclic nucleotide or calcium regulated channels	SGN-U568271	AK325055	ATCNGC1, CNGC1 | CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1)	1,160	0,005
29.2.4	protein.synthesis.elongation	SGN-U575408	TA37782_4081	elongation factor 1-beta / EF-1-beta	1,158	0,009
31.4	cell.vesicle transport	SGN-U597104	AK322959	coatomer protein complex, subunit beta 2 (beta prime), putative	1,155	0,047
35.2	not assigned.unknown	SGN-U565478	DV104551	(ARABIDOPSIS THALIANA RAS ASSOCIATED WITH DIABETES PROTEIN 3)	1,154	0,049
4.13	glycolysis.PK	SGN-U571796	TA36048_4081	PDH-E1 ALPHA | PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA)	1,152	0,013
35.3	not assigned.disagreeing hits	SGN-U592447	NM_001247565	fructose-1,6-bisphosphatase, putative	1,152	0,008
35.2	not assigned.unknown	SGN-U580496	BG129184	2-oxoglutarate-dependent dioxygenase	1,152	0,042
35.3	not assigned.disagreeing hits	SGN-U579502	AK323974	AGL69, FCL4, MAF4 | MAF4 (MADS AFFECTING FLOWERING 4)	1,151	0,027
30.2.11	signalling.receptor kinases.leucine rich repeat XI	SGN-U572100	TA48836_4081	GSO1 | leucine-rich repeat transmembrane protein kinase, putative	1,151	0,016
35.1	not assigned.no ontology	SGN-U581598	GO373949	haloacid dehalogenase-like hydrolase family protein	1,149	0,025
18	Co-factor and vitamine metabolism	SGN-U584511	NM_001246885	TMT1, VTE4, G-TMT | G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERASE)	1,149	0,006
34.99	transport.misc	SGN-U569158	AI483799	Unknown	1,148	0,004
28.1	DNA.synthesis/chromatin structure	SGN-U580208		ATRAD21.3, SYN4 | ATRAD21.3/SYN4 (ARABIDOPSIS HOMOLOG OF RAD21 3)	1,147	0,007

33.99	development.unspecified	SGN-U567807	TA54783_4081	nodulin MtN21 family protein	1,147	0,009
35.1	not assigned.no ontology	SGN-U577362	GO373949	haloacid dehalogenase-like hydrolase family protein	1,147	0,012
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U567691	AK322767	UGT73B2 | UGT73B2; UDP-glycosyltransferase	1,146	0,046
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U599341	BI210410	galactosyl transferase GMA12/MNN10 family protein	1,146	0,004
26.13	misc.acid and other phosphatases	SGN-U568743	TA46208_4081	phosphoric monoester hydrolase	1,145	0,013
30.2.17	signalling.receptor kinases.DUF 26	SGN-U563388	AK324226	RLK4, CRK10 | CRK10 (CYSTEINE-RICH RLK10)	1,144	0,019
20.2.1	stress.abiotic.heat	SGN-U570963	AK327305	BIP1 | BIP1	1,143	0,004
28.1.1.5	DNA.synthesis/chromatin structure.retrotransposon/transposase. CACTA-like transposase	SGN-U564556	TC230974	Unknown	1,142	0,005
11.1.3	lipid metabolism.FA synthesis and FA elongation.ketoacyl ACP synthase	SGN-U570215	AK322572	KAS III | KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III)	1,141	0,004
29.5.11.5	protein.degradation.ubiquitin.ubiquitin protease	SGN-U569427	BI210821	UBP24 | UBP24 (UBIQUITIN-SPECIFIC PROTEASE 24)	1,139	0,004
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U567906	TA56085_4081	F-box family protein	1,139	0,010
35.1	not assigned.no ontology	SGN-U563214	TA52106_4081	SPX (SYG1/Pho81/XPR1) domain-containing protein	1,139	0,006
4.13	glycolysis.PK	SGN-U575372	AK326530	AT-E1 ALPHA | AT-E1 ALPHA (pyruvate dehydrogenase complex E1 alpha subunit)	1,139	0,005
35.2	not assigned.unknown	SGN-U603097	AW093537	Unknown	1,139	0,012

27.4	RNA.RNA binding	SGN-U579519	AK246918	GR-RBP7, GRP7, CCR2, ATGRP7 | ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2)	1,137	0,006
16.1.2.2	secondary metabolism.isoprenoids.mevalonate pathway.HMG-CoA synthase	SGN-U590860	AK321346	HMGS, EMB2778, MVA1 | MVA1 (HYDROXYMETHYLGLUTARYL-COA SYNTHASE)	1,136	0,006
35.2	not assigned.unknown	SGN-U601428	AK320223	catalytic	1,135	0,012
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U563618	AI490010	AtMYB62, BW62B, BW62C, MYB62 | MYB62 (myb domain protein 62)	1,134	0,029
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U578260	NM_001247550	60S ribosomal protein L29 (RPL29B)	1,134	0,006
35.3	not assigned.disagreeing hits	SGN-U582031	AK324494	Rho GDP-dissociation inhibitor family protein	1,134	0,010
5.10	fermentation.aldehyde dehydrogenase	SGN-U576701	BW687028	ALDH22a1 | ALDH22a1 (ALDEHYDE DEHYDROGENASE 22A1)	1,134	0,006
10.8.1	cell wall.pectin*esterases.PME	SGN-U575256	NM_001246928	ATPME3 | ATPME3 (Arabidopsis thaliana pectin methylesterase 3)	1,133	0,004
29.5.11.20	protein.degradation.ubiquitin.proteasom	SGN-U601274	AK246325	RPN1A, AtRPN1a | AtRPN1a/RPN1A (26S proteasome regulatory subunit S2 1A)	1,132	0,008
35.2	not assigned.unknown	SGN-U596676	AK325642	hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	1,132	0,004
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U587417	AK327208	tropinone reductase, putative	1,131	0,007
26.7	misc.oxidases - copper, flavone etc.	SGN-U568738	AK321718	SKS5 | SKS5 (SKU5 Similar 5)	1,131	0,049
27.3.55	RNA.regulation of transcription.HDA	SGN-U571822	BT013616	HDA19, ATHD1, HDA1, RPD3A | HD1 (HISTONE DEACETYLASE19)	1,131	0,005

35.2	not assigned.unknown	SGN-U581212	GO373375	Unknown	1,131	0,023
26.28	misc.GDSL-motif lipase	SGN-U563797	AK325329	GDSL-motif lipase/hydrolase family protein	1,130	0,027
35.2	not assigned.unknown	SGN-U602743	BG127276	Unknown	1,130	0,018
35.2	not assigned.unknown	SGN-U565561	TA56778_4081	Unknown	1,130	0,004
35.2	not assigned.unknown	SGN-U578131	BG124350	hydrolase	1,129	0,008
26.23	misc.rhodanese	SGN-U576844	AK323214	rhodanese-like domain-containing protein / PPIC-type PPIASE domain-containing protein	1,129	0,004
35.2	not assigned.unknown	SGN-U568034	AK323970	Unknown	1,129	0,005
29.8	protein assembly and cofactor ligation	SGN-U578041	AK319593	HCF136 | HCF136 (High chlorophyll fluorescence 136)	1,129	0,008
34.13	transport.peptides and oligopeptides	SGN-U597513	BP906995	NTL1, ATNRT1:2 | ATNRT1:2 (NITRATE TRANSPORTER 1:2)	1,128	0,006
35.2	not assigned.unknown	SGN-U568864	AK320187	binding	1,128	0,008
11.1.2	lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Transacylase	SGN-U572994	TA39671_4081	binding / catalytic/ transferase	1,126	0,017
35.1	not assigned.no ontology	SGN-U583929	AI778124	translocation protein-related	1,126	0,014
35.1	not assigned.no ontology	SGN-U578722	BT013105	lesion inducing protein-related	1,126	0,008
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U585040	BP894950	ATMRP10 | ATMRP10 (Arabidopsis thaliana multidrug resistance-associated protein 10)	1,126	0,008

34.16	transport.ABC transporters and multidrug resistance systems	SGN-U602005	BF097481	ATATH1 | ATATH1 (ABC2 homolog 1)	1,126	0,011
29.5.9	protein.degradation.AAA type	SGN-U580765	AK326125	AAA-type ATPase family protein	1,125	0,005
26.10	misc.cytochrome P450	SGN-U574105	AK322756	CYP86, CYP86A1 | CYP86A1 (cytochrome P450, family 86, subfamily A, polypeptide 1)	1,125	0,019
27.3.62	RNA.regulation of transcription.Nucleosome/chromatin assembly factor group	SGN-U566907	AW429152	high mobility group (HMG1/2) family protein	1,123	0,007
35.2	not assigned.unknown	SGN-U566050	BW685235	Unknown	1,121	0,011
30.2.17	signalling.receptor kinases.DUF 26	SGN-U563330	AK326711	RLK1 | RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1)	1,120	0,018
26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U580274	BI929170	short-chain dehydrogenase/reductase (SDR) family protein	1,119	0,006
35.3	not assigned.disagreeing hits	SGN-U587645	U21075	glycosyl hydrolase family 3 protein	1,119	0,010
35.3	not assigned.disagreeing hits	SGN-U580714	BF051302	ATPP2-B12 | F-box family protein / SKP1 interacting partner 3-related	1,118	0,044
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U581052	BG129530	UBC19 | UBC19 (UBIQUITIN-CONJUGATING ENZYME19)	1,117	0,007
31.2	cell.division	SGN-U573498	AK326373	mitotic checkpoint family protein	1,116	0,010
31.1	cell.organisation	SGN-U563743	AJ785223	TFC E, PFI | PFI (PFIFFERLING)	1,116	0,005
35.2	not assigned.unknown	SGN-U575520	AW031092	Unknown	1,115	0,023
33.99	development.unspecified	SGN-U564311	BI204861	ANAC008 | ANAC008 (Arabidopsis NAC domain containing protein 8)	1,115	0,005

35.2	not assigned.unknown	SGN-U586489	AK247237	Unknown	1,114	0,006
35.2	not assigned.unknown	SGN-U585022	TA55813_4081	Unknown	1,113	0,010
17.7.1.2	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase	SGN-U572041	BE451610	ATLOX2, LOX2 | LOX2 (LIPOXYGENASE 2)	1,112	0,014
19.10	tetrapyrrole synthesis.magnesium chelatase	SGN-U594672	TA37909_4081	CCH, CHLH, CCH1, GUN5 | GUN5 (GENOMES UNCOUPLED 5)	1,112	0,026
34.3	transport.amino acids	SGN-U590453	AK326509	amino acid permease family protein	1,112	0,007
29.2.1.1.1.1.17	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S17	SGN-U576007	DB722271	ORE4, CS17, PRPS17, RPS17 | RPS17 (ribosomal protein S17)	1,110	0,016
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U566267	BI204701	ATBZIP44 | ATBZIP44 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 44)	1,108	0,007
6.2	gluconeogenese/ glyoxylate cycle.malate synthase	SGN-U573204	AW648012	MLS | MLS (MALATE SYNTHASE)	1,107	0,032
35.2	not assigned.unknown	SGN-U583906	BT013593	Unknown	1,104	0,004
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U573638	AK321518	zinc finger protein-related	1,104	0,013
35.2	not assigned.unknown	SGN-U590370	AW934204	Unknown	1,102	0,021
3.5	minor CHO metabolism.others	SGN-U584325	AI487026	mannose 6-phosphate reductase (NADPH-dependent), putative	1,102	0,005
35.2	not assigned.unknown	SGN-U568124	AK324995	protein tyrosine phosphatase	1,102	0,006
35.1	not assigned.no ontology	SGN-U567673	AK329241	SRO2 | SRO2 (SIMILAR TO RCD ONE 2)	1,102	0,012

27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family	SGN-U578656	AK322575	ATWRKY70, WRKY70 | WRKY70 (WRKY DNA-binding protein 70)	1,098	0,012
34.2	transporter.sugars	SGN-U589402	AW623481	34 kda outer mitochondrial membrane protein porin	1,097	0,005
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U564710	BG134245	ankyrin repeat family protein	1,097	0,007
35.2	not assigned.unknown	SGN-U580809	TA51175_4081	Unknown	1,097	0,008
35.3	not assigned.disagreeing hits	SGN-U577961	AW649553	cold-stress inducible protein C17	1,096	0,031
35.2	not assigned.unknown	SGN-U597752	NM_001247513	stig1	1,095	0,006
35.1	not assigned.no ontology	SGN-U600340	AK323238	LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein	1,094	0,029
35.3	not assigned.disagreeing hits	SGN-U564092	BT014571	ACR4 | ACR4 (ACT REPEAT 4)	1,093	0,009
26.4	misc.beta 1,3 glucan hydrolases	SGN-U586345	AI778742	glycosyl hydrolase family protein 17	1,093	0,014
35.1	not assigned.no ontology	SGN-U569747	AK319948	ATGUS3 | ATGUS3 (ARABIDOPSIS THALIANA GLUCURONIDASE 3)	1,091	0,005
28.1.3	DNA.synthesis/chromatin structure.histone	SGN-U580517	TA53216_4081	histone H3	1,090	0,032
29.4	protein.postranslational modification	SGN-U566705	AK319773	SIP3, SNRK3.14, CIPK6 | CIPK6 (CBL-INTERACTING PROTEIN KINASE 6)	1,090	0,009
11.3.5	lipid metabolism.Phospholipid synthesis.diacylglycerol kinase	SGN-U604713	AJ784589	ATDGK2 | ATDGK2 (DIACYLGLYCEROL KINASE 2)	1,090	0,006
35.1	not assigned.no ontology	SGN-U567698	BI928699	metal-dependent phosphohydrolase HD domain-containing protein	1,090	0,006

10.6.2	cell wall.degradation.mannan-xylose-arabinose-fucose	SGN-U562631	AB612975	glycosyl hydrolase family 3 protein	1,089	0,006
30.2.3	signalling.receptor kinases.leucine rich repeat III	SGN-U597565	BP888947	leucine-rich repeat transmembrane protein kinase, putative	1,089	0,004
35.2	not assigned.unknown	SGN-U577652	AK323242	Unknown	1,087	0,036
11.9.3	lipid metabolism.lipid degradation.lysophospholipases	SGN-U590265	NM_001247934	PLD, PLDALPHA1 | PLDALPHA1 (PHOSPHOLIPASE D ALPHA 1)	1,087	0,013
34.99	transport.misc	SGN-U565034	DB711244	MATE efflux family protein	1,086	0,017
27.1	RNA.processing	SGN-U564219	FS195544	SAD1 | SAD1 (SUPERSENSITIVE TO ABA AND DROUGHT 1)	1,086	0,013
35.1.19	not assigned.no ontology.C2 domain-containing protein	SGN-U591334	AK323521	SRC2, (AT)SRC2 | (AT)SRC2/SRC2 (SOYBEAN GENE REGULATED BY COLD-2)	1,086	0,009
35.2	not assigned.unknown	SGN-U568974	TA37830_4081	Unknown	1,086	0,019
35.2	not assigned.unknown	SGN-U599004	AK324580	Unknown	1,085	0,010
14.3	S-assimilation.sulfite redox	SGN-U577417	JQ341913	SIR | SIR (sulfite reductase); sulfite reductase (ferredoxin)	1,084	0,006
35.2	not assigned.unknown	SGN-U579837	NM_001247954	JAZ1, TIFY10A | JAZ1/TIFY10A (JASMONATE-ZIM-DOMAIN PROTEIN 1)	1,084	0,048
30.3	signalling.calcium	SGN-U580728	AI490245	TCH1, ACAM-1, CAM1 | CAM1 (CALMODULIN 1)	1,084	0,012
20.1	stress.biotic	SGN-U570267	BI207419	avirulence-responsive protein-related	1,084	0,024
35.2	not assigned.unknown	SGN-U585156	DB709432	Unknown	1,083	0,006

17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U564627	BI422737	similar to auxin down-regulated protein ARG10	1,082	0,020
5.10	fermentation.aldehyde dehydrogenase	SGN-U584013	TA37853_4081	ALDH2, ALDH2B4 | ALDH2B4 (ALDEHYDE DEHYDROGENASE 2)	1,082	0,032
35.2	not assigned.unknown	SGN-U576761	AK247433	Unknown	1,082	0,047
35.2	not assigned.unknown	SGN-U584631	BI928208	Unknown	1,081	0,010
31.3	cell.cycle	SGN-U583476	TA48029_4081	CYCD3;2 | CYCD3;2 (CYCLIN D3;2)	1,081	0,005
35.2	not assigned.unknown	SGN-U604045	BI208128	nam-like protein 11	1,081	0,006
29.8	protein assembly and cofactor ligation	SGN-U571569	AK327831	YCF2.2 | hypothetical protein	1,081	0,010
35.2	not assigned.unknown	SGN-U585999	GO373145	Unknown	1,080	0,011
34.19.1	transport.Major Intrinsic Proteins.PIP	SGN-U593596	BG130774	PIP2E, PIP2;6 | PIP2;6/PIP2E (plasma membrane intrinsic protein 2;6)	1,080	0,021
35.3	not assigned.disagreeing hits	SGN-U591967	AI771162	oxidoreductase, 2OG-Fe(II) oxygenase family protein	1,078	0,022
35.3	not assigned.disagreeing hits	SGN-U581157	BI206028	S-locus protein kinase, putative	1,077	0,021
29.3.2	protein.targeting.mitochondria	SGN-U565738	BW687445	TOM9-2, ATTOM22-V, TOM22-V | TOM22-V (TRANSLOCASE OUTER MITOCHONDRIAL MEMBRANE 22-V)	1,076	0,024
23.4.99	nucleotide metabolism.phosphotransfer and pyrophosphatases.misc	SGN-U565218		ATPPA4 | ATPPA4 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 4)	1,076	0,018
3.2.1	minor CHO metabolism.trehalose.TPS	SGN-U580026	TA44724_4081	TPS1, ATTPS1 | ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE)	1,076	0,006

29.5.5	protein.degradation.serine protease	SGN-U576209	NM_001247762	SCPL20 | SCPL20 (serine carboxypeptidase-like 20)	1,076	0,005
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U579059	BT012841	PGIP1 | PGIP1 (POLYGALACTURONASE INHIBITING PROTEIN 1)	1,075	0,011
35.1	not assigned.no ontology	SGN-U572080	AK320751	DBP2, CYL2 | CYL2/DBP2 (DNA POLYMERASE EPSILON SUBUNIT B)	1,074	0,007
35.2	not assigned.unknown	SGN-U584101	BE459797	ATP binding / DNA binding	1,074	0,016
35.2	not assigned.unknown	SGN-U568905	AK322145	PTAC9, OSB2 | OSB2/PTAC9 (PLASTID TRANSCRIPTIONALLY ACTIVE9)	1,074	0,004
35.2	not assigned.unknown	SGN-U568454	AK324484	Unknown	1,073	0,005
27.4	RNA.RNA binding	SGN-U567488	AK247395	RNA recognition motif (RRM)-containing protein	1,071	0,008
29.3.4.2	protein.targeting.secretory pathway.golgi	SGN-U563732	AK324308	transport protein, putative	1,069	0,005
10.2	cell wall.cellulose synthesis	SGN-U566229	TA43171_4081	CSLC12, ATCSLC12 | ATCSLC12 (Cellulose synthase-like C12)	1,069	0,006
35.2	not assigned.unknown	SGN-U600739	BF096410	similar to exostosin family protein	1,068	0,017
30.2.3	signalling.receptor kinases.leucine rich repeat III	SGN-U604726	BG642611	leucine-rich repeat transmembrane protein kinase, putative	1,068	0,015
29.2.3	protein.synthesis.initiation	SGN-U572558	TC217682	EIF(ISO)4E, LSP, LSP1 | LSP1 (LOSS OF SUSCEPTIBILITY TO POTYVIRUSES)	1,067	0,014
35.2	not assigned.unknown	SGN-U577225	BG131976	Unknown	1,067	0,011
16.10	secondary metabolism.simple phenols	SGN-U577262	AW035109	LAC15, TT10 | TT10 (TRANSPARENT TESTA 10)	1,065	0,026

20.1	stress.biotic	SGN-U579414	TA36568_4081	ATOSM34 | ATOSM34 (OSMOTIN 34)	1,065	0,010
20.1	stress.biotic	SGN-U603545	BI422997	ATOSM34 | ATOSM34 (OSMOTIN 34)	1,064	0,023
13.2.4.1	amino acid metabolism.degradation.branched-chain group.shared	SGN-U568125	AK247473	2-oxoisovalerate dehydrogenase, putative	1,064	0,012
26.18	misc.invertase/pectin methylesterase inhibitor family protein	SGN-U584317	AI779401	invertase/pectin methylesterase inhibitor family protein	1,063	0,014
29.4	protein.postranslational modification	SGN-U602666	BM410966	IBS1 | IBS1 (IMPAIRED IN BABA-INDUCED STERILITY 1)	1,062	0,005
29.3	protein.targeting	SGN-U590317	BG124109	translocon-associated protein beta (TRAPB) family protein	1,062	0,005
20.1.7	stress.biotic.PR-proteins	SGN-U582531	AK324760	disease resistance-responsive family protein	1,062	0,011
33.99	development.unspecified	SGN-U563323	NM_001247043	ANAC072, RD26 | RD26 (RESPONSIVE TO DESSICATION 26)	1,062	0,016
34.99	transport.misc	SGN-U564504	TA47616_4081	permease, putative	1,060	0,007
35.3	not assigned.disagreeing hits	SGN-U571767	BT013743	cell division control protein CDC6b, putative (CDC6b)	1,059	0,007
10.2	cell wall.cellulose synthesis	SGN-U604442	AK323254	COBL4, IRX6 | COBL4/IRX6 (COBRA-LIKE4)	1,058	0,012
35.2	not assigned.unknown	SGN-U574985	AW218313	Unknown	1,057	0,011
30.3	signalling.calcium	SGN-U602929	BI925114	IQD6 | IQD6 (IQ-domain 6)	1,056	0,004
35.2	not assigned.unknown	SGN-U603661	AK327802	ATP binding / DNA binding	1,056	0,006

29.3.4.99	protein.targeting.secretory pathway.unspecified	SGN-U579118		protein transport protein sec61, putative	1,056	0,012
27.1	RNA.processing	SGN-U566728	TA39696_4081	small nuclear ribonucleoprotein D1, putative	1,056	0,014
35.1	not assigned.no ontology	SGN-U579144		DNA-binding protein-related	1,053	0,005
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U600010	AK321302	PHD finger family protein	1,053	0,018
35.2	not assigned.unknown	SGN-U590347	AK324500	binding	1,052	0,019
35.2	not assigned.unknown	SGN-U585009	TC224102	Unknown	1,052	0,010
35.2	not assigned.unknown	SGN-U578432	AK324597	nucleic acid binding	1,051	0,016
29.5.5	protein.degradation.serine protease	SGN-U569758	BP902483	SCPL48 | SCPL48 (serine carboxypeptidase-like 48)	1,050	0,049
28.1	DNA.synthesis/chromatin structure	SGN-U583123	AK327446	DNA primase, large subunit family	1,050	0,008
35.2	not assigned.unknown	SGN-U604677	AK319685	Unknown	1,049	0,033
29.5.5	protein.degradation.serine protease	SGN-U566079	AK325009	SCPL26 | SCPL26 (serine carboxypeptidase-like 26)	1,049	0,010
33.99	development.unspecified	SGN-U603486	AK330095	integral membrane family protein / nodulin MtN21-related	1,049	0,012
30.3	signalling.calcium	SGN-U566692	AI781905	calcium-binding EF hand family protein	1,048	0,007
18	Co-factor and vitamine metabolism	SGN-U584511	NM_001246885	TMT1, VTE4, G-TMT | G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERASE)	1,047	0,011

35.1	not assigned.no ontology	SGN-U569918	AI486269	similar to harpin-induced protein-related	1,047	0,035
30.3	signalling.calcium	SGN-U595376	BW690832	CRT3 | CRT3 (CALRETICULIN 3)	1,046	0,011
35.2	not assigned.unknown	SGN-U599571	AW651108	33 kDa secretory protein-related	1,046	0,005
34.22	transport.cyclic nucleotide or calcium regulated channels	SGN-U595415	AK325055	CNGC13, ATCNGC13 | ATCNGC13 (cyclic nucleotide gated channel 13)	1,045	0,008
35.2	not assigned.unknown	SGN-U563370	TA49761_4081	Unknown	1,045	0,007
30.5	signalling.G-proteins	SGN-U570512	AK325103	ARAC7, ATROP9, ATRAC7, RAC7, ROP9 | ARAC7/ATRAC7/ATROP9/RAC7/ROP9 (RHO-RELATED PROTEIN FROM PLANTS 9)	1,044	0,005
30.4	signalling.phosphinositides	SGN-U581869	AK321086	inositol 1,3,4-trisphosphate 5/6-kinase	1,044	0,005
23.4.99	nucleotide metabolism.phosphotransfer and pyrophosphatases.misc	SGN-U581120	BI206635	ATPPA3 | ATPPA3 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 3)	1,043	0,008
35.2	not assigned.unknown	SGN-U583364	AK329868	Unknown	1,043	0,004
28.1.3	DNA.synthesis/chromatin structure.histone	SGN-U580664	GO373047	LLS1, PAO, ACD1 | ACD1 (ACCELERATED CELL DEATH 1)	1,043	0,018
35.2	not assigned.unknown	SGN-U587710	DB716849	Unknown	1,042	0,035
29.2.1.1.1.2.2	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L2	SGN-U579087	TA36326_4081	60S ribosomal protein L8 (RPL8C)	1,042	0,007
11.2.4	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U564058	AK321995	FAD2 | FAD2 (FATTY ACID DESATURASE 2)	1,041	0,017

29.2.2.50	protein.synthesis.misc ribososomal protein.BRIX	SGN-U575177	AK319451	brix domain-containing protein	1,041	0,009
28.1	DNA.synthesis/chromatin structure	SGN-U573875	BT013038	MCM7, PRL | PRL (PROLIFERA)	1,041	0,009
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U577667	GO372499	UBC28 | UBC28; ubiquitin-protein ligase	1,040	0,005
2.2.1.3.2	major CHO metabolism.degradation.sucrose.invertases.cell wall	SGN-U584136	NM_001246913	ATCWINV2 | ATCWINV2 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 2)	1,040	0,035
35.1.5	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	SGN-U578461	TA54393_4081	pentatricopeptide (PPR) repeat-containing protein	1,040	0,027
35.2	not assigned.unknown	SGN-U576169	AK320703	Unknown	1,040	0,014
35.3	not assigned.disagreeing hits	SGN-U578997	TA37125_4081	HPD, PDS1 | PDS1 (PHYTOENE DESATURATION 1)	1,039	0,031
35.3	not assigned.disagreeing hits	SGN-U580351	TA37997_4081	60S ribosomal protein L4/L1 (RPL4A)	1,039	0,013
35.2	not assigned.unknown	SGN-U580648	AK319768	Unknown	1,038	0,017
30.2.11	signalling.receptor kinases.leucine rich repeat XI	SGN-U582787	TA54678_4081	leucine-rich repeat family protein / protein kinase family protein	1,038	0,006
34.99	transport.misc	SGN-U572132	AK246880	MATE efflux family protein	1,037	0,012
31.1	cell.organisation	SGN-U562938	TA45815_4081	MEE66 | MEE66 (maternal effect embryo arrest 66)	1,037	0,007
29.1	protein.aa activation	SGN-U583623	AK322339	pseudouridine synthase and archaeosine transglycosylase (PUA) domain-containing protein	1,037	0,009
27.1	RNA.processing	SGN-U584333	DB685759	small nuclear ribonucleoprotein, putative	1,036	0,007

26.13	misc.acid and other phosphatases	SGN-U600918	AK325263	ATPAP15, PAP15 | ATPAP15/PAP15 (purple acid phosphatase 15)	1,036	0,024
30.7	signalling.14-3-3 proteins	SGN-U579480	AW621809	GF14 OMEGA, GRF2 | GRF2 (GENERAL REGULATORY FACTOR 2)	1,036	0,013
28.1	DNA.synthesis/chromatin structure	SGN-U586357	BI922989	transducin family protein / WD-40 repeat family protein	1,035	0,037
34.99	transport.misc	SGN-U564863	AK324410	integral membrane transporter family protein	1,035	0,008
28.99	DNA.unspecified	SGN-U601089	AW934641	Unknown	1,035	0,008
29.2.1.1.3.1.5	protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30S subunit.S5	SGN-U574821	TA50738_4081	ribosomal protein S5 family protein	1,035	0,006
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U565891	NM_001247097	ACS9, ETO3 | ETO3 (ETHYLENE OVERPRODUCING 3)	1,034	0,008
27.3.44	RNA.regulation of transcription.Chromatin Remodeling Factors	SGN-U603668	AW160104	SNF2 domain-containing protein	1,034	0,012
35.2	not assigned.unknown	SGN-U584817	TA53516_4081	trehalose-6-phosphate phosphatase	1,034	0,015
35.2	not assigned.unknown	SGN-U573709	BI203564	Unknown	1,034	0,006
35.2	not assigned.unknown	SGN-U562953	AK320784	Unknown	1,033	0,007
21.5	redox.peroxiredoxin	SGN-U579709	BG130403	2-CYS PRX B | 2-cys peroxiredoxin, chloroplast, putative	1,033	0,007
20.1	stress.biotic	SGN-U578441	AK224718	pathogenesis-related protein 10	1,033	0,009
26.10	misc.cytochrome P450	SGN-U579686	TA36516_4081	CYP72A9 | CYP72A9 (cytochrome P450, family 72, subfamily A, polypeptide 9)	1,033	0,010

35.3	not assigned.disagreeing hits	SGN-U590925	AK323521	src2-like protein	1,032	0,005
26.7	misc.oxidases - copper, flavone etc.	SGN-U568742	AK321556	SKS17 | SKS17 (SKU5 Similar 17)	1,032	0,023
21.1	redox.thioredoxin	SGN-U579739	BW687555	ATTRX H1, ATTRX1 | ATTRX1 (Arabidopsis thaliana thioredoxin H-type 1)	1,032	0,009
35.2	not assigned.unknown	SGN-U575905	TA55898_4081	Unknown	1,031	0,008
35.3	not assigned.disagreeing hits	SGN-U575061	AK324018	similar to Rab5-interacting family protein	1,031	0,016
35.3	not assigned.disagreeing hits	SGN-U580759	AW032557	AtGRF1 | AtGRF1 (GROWTH-REGULATING FACTOR 1)	1,031	0,006
35.1	not assigned.no ontology	SGN-U583730	TA51252_4081	SH3 domain-containing protein 2 (SH3P2)	1,031	0,016
34.9	transport.metabolite transporters at the mitochondrial membrane	SGN-U564456	AK320575	mitochondrial substrate carrier family protein	1,031	0,012
35.3	not assigned.disagreeing hits	SGN-U583152	AK326000	L-asparaginase, putative	1,030	0,009
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U567225	TA53710_4081	GAUT3 | GAUT3 (Galacturonosyltransferase 3)	1,030	0,010
34.99	transport.misc	SGN-U601431	AW933158	SEC14 cytosolic factor, putative	1,030	0,007
34.2	transporter.sugars	SGN-U565600	AK320204	ATPLT5 | ATPLT5 (POLYOL TRANSPORTER 5)	1,029	0,040
35.1	not assigned.no ontology	SGN-U603556	BP890881	similar to Nrap protein	1,029	0,006
5.10	fermentation.aldehyde dehydrogenase	SGN-U587030	AK321263	ALDH7B4 | ALDH7B4 (ALDEHYDE DEHYDROGENASE 7B4)	1,028	0,019

29.5.3	protein.degradation.cysteine protease	SGN-U569507	AK326123	cysteine proteinase, putative / thiol protease, putative	1,028	0,005
28.1	DNA.synthesis/chromatin structure	SGN-U566679	BM535749	M protein repeat-containing protein	1,027	0,012
35.2	not assigned.unknown	SGN-U571512	AK319860	similar to transferase, transferring glycosyl groups	1,027	0,006
29.2.1.2.1.25	protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S25	SGN-U591470	TA39249_4081	40S ribosomal protein S25 (RPS25B)	1,026	0,008
29.4	protein.postranslational modification	SGN-U582812	AK326088	ATS6K2, S6K2, ATPK2, ATPK19 | ATPK19 (ARABIDOPSIS THALIANA PROTEIN KINASE 19)	1,026	0,007
35.2	not assigned.unknown	SGN-U593090	AJ784691	Unknown	1,026	0,005
35.3	not assigned.disagreeing hits	SGN-U583496	AK322816	biotin/lipoyl attachment domain-containing protein	1,026	0,020
27.3.62	RNA.regulation of transcription.Nucleosome/chromatin assembly factor group	SGN-U564375	AW154813	DDT domain-containing protein	1,025	0,005
35.3	not assigned.disagreeing hits	SGN-U585607	BW688729	ATPP2-B12 | ATPP2-B12 (Phloem protein 2-B12)	1,025	0,012
31.3	cell.cycle	SGN-U565450	NM_001246839	CYCA2;4 | CYCA2;4 (CYCLIN A2;4)	1,025	0,011
29.4	protein.postranslational modification	SGN-U579369	TA42693_4081	protein kinase family protein	1,025	0,005
35.2	not assigned.unknown	SGN-U567302	AW092697	PMR5 | PMR5 (POWDERY MILDEW RESISTANT 5)	1,025	0,009
26.13	misc.acid and other phosphatases	SGN-U585240	AK325263	ATPAP15, PAP15 | ATPAP15/PAP15 (purple acid phosphatase 15)	1,024	0,016
29.2.1.2.2.537	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L37A	SGN-U581034	TA36407_4081	60S ribosomal protein L37a (RPL37aB)	1,024	0,017

35.2	not assigned.unknown	SGN-U564821	AK247757	Unknown	1,024	0,006
28.1	DNA.synthesis/chromatin structure	SGN-U582081	AK322330	nucleolar protein, putative	1,023	0,013
35.2	not assigned.unknown	SGN-U564831	TA57026_4081	Unknown	1,023	0,024
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U580201	AK326004	FLO2, FL1, AP2 | AP2 (APETALA 2)	1,023	0,011
35.1	not assigned.no ontology	SGN-U594133	ES896896	ChaC-like family protein	1,023	0,029
23.3.2.2	nucleotide metabolism.salvage.nucleoside kinases.uridine kinase	SGN-U589436	DB701797	phosphoribulokinase/uridine kinase family protein	1,022	0,013
30.3	signalling.calcium	SGN-U582426	BT012792	CPK11, ATCDPK2 | ATCDPK2 (CALCIUM-DEPENDENT PROTEIN KINASE 2)	1,022	0,006
35.2	not assigned.unknown	SGN-U599298	BG129247	Unknown	1,021	0,013
11.2.1	lipid metabolism.FA desaturation.desaturase	SGN-U569117	AK319952	FADB, JB67, ADS3, FAD5 | FAD5 (FATTY ACID DESATURASE 5)	1,021	0,008
34.22	transport.cyclic nucleotide or calcium regulated channels	SGN-U598763	DB689254	ATCNGC1, CNGC1 | CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1)	1,020	0,024
35.2	not assigned.unknown	SGN-U567705	AK224872	Unknown	1,020	0,005
34.22	transport.cyclic nucleotide or calcium regulated channels	SGN-U582911	AK321302	CNGC18, ATCNGC18 | ATCNGC18/CNGC18 (CYCLIC NUCLEOTIDE-GATED CHANNEL 18)	1,020	0,039
34.99	transport.misc	SGN-U563072	BI206775	MATE efflux protein-related	1,018	0,022

21.3	redox.heme	SGN-U599417	BW690751	GLB3 | GLB3 (2-on-2 hemoglobin like gene 3)	1,018	0,021
11.1.6	lipid metabolism.FA synthesis and FA elongation.enoyl ACP reductase	SGN-U575779	TA39012_4081	ENR1, MOD1 | MOD1 (MOSAIC DEATH 1)	1,018	0,028
29.2.1.2.2.23	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L23	SGN-U593366	AK328602	EMB2171 | EMB2171 (EMBRYO DEFECTIVE 2171)	1,017	0,006
35.2	not assigned.unknown	SGN-U582826	AK328294	Unknown	1,016	0,012
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U588519	AK326997	Unknown	1,016	0,017
35.2	not assigned.unknown	SGN-U566061	AW624869	Unknown	1,016	0,020
29.4	protein.postranslational modification	SGN-U584777	TA39798_4081	calcium-binding EF hand family protein	1,016	0,008
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U574867	AK327372	ribosomal protein L4 family protein	1,015	0,008
13.1.1.2	amino acid metabolism.synthesis.central amino acid metabolism.aspartate	SGN-U567390	AK247511	aminotransferase class I and II family protein	1,015	0,008
34.9	transport.metabolite transporters at the mitochondrial membrane	SGN-U579511	AK324581	mitochondrial substrate carrier family protein	1,014	0,012
35.3	not assigned.disagreeing hits	SGN-U589847	AK322188	Unknown	1,014	0,007
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U586058	DB698684	CSLG3, ATCSLG3 | ATCSLG3 (Cellulose synthase-like G3)	1,013	0,012
35.2	not assigned.unknown	SGN-U579374	AJ785030	Unknown	1,012	0,012
9.4	mitochondrial electron transport / ATP synthesis.alternative oxidase	SGN-U589544	NM_001247191	ATAOX1A, AOX1A | AOX1A (alternative oxidase 1A)	1,012	0,010

9.9	mitochondrial electron transport / ATP synthesis.F1-ATPase	SGN-U580393	AW038405	ATP synthase epsilon chain, mitochondrial	1,012	0,027
26.10	misc.cytochrome P450	SGN-U573255	BT012820	CYP75B1, D501, TT7 | TT7 (TRANSPARENT TESTA 7)	1,011	0,028
35.2	not assigned.unknown	SGN-U562837	BI923373	Unknown	1,011	0,010
27.3.99	RNA.regulation of transcription.unclassified	SGN-U564367	AW648605	chloroplast nucleoid DNA-binding protein-related	1,011	0,024
35.2	not assigned.unknown	SGN-U573251	AK248060	Unknown	1,010	0,009
11.8.1	lipid metabolism."exotics" (steroids, squalene etc).sphingolipids	SGN-U579336	AK321495	delta-8 sphingolipid desaturase (SLD1)	1,009	0,009
1.1.4	PS.lightreaction.ATP synthase	SGN-U584963	BT013143	ATPA | Encodes the ATPase alpha subunit, which is a subunit of ATP synthase and part of the CF1 portion which catalyzes the conversion of ADP to ATP using the proton motive force.	1,009	0,006
23.3.2.1	nucleotide metabolism.salvage.nucleoside kinases.adenosine kinase	SGN-U586226	BT012983	ADK2 | ADK2 (ADENOSINE KINASE 2)	1,009	0,005
26.7	misc.oxidases - copper, flavone etc.	SGN-U581565	AK247107	polyphenol oxidase	1,009	0,012
29.5.11	protein.degradation.ubiquitin	SGN-U587700	AI898544	UBP24 | UBP24 (UBIQUITIN-SPECIFIC PROTEASE 24)	1,008	0,022
34.99	transport.misc	SGN-U599539	BF097431	MATE efflux family protein	1,008	0,008
26.4	misc.beta 1,3 glucan hydrolases	SGN-U568358	AK324687	glycosyl hydrolase family protein 17	1,008	0,017
34.11	transport.NDP-sugars at the ER	SGN-U583062		ATUTR3, UTR3 | ATUTR3/UTR3 (UDP-GALACTOSE TRANSPORTER 3)	1,008	0,006

26.7	misc.oxidases - copper, flavone etc.	SGN-U594163	TA53396_4081	amine oxidase-related	1,008	0,007
10.5.5	cell wall.cell wall proteins.RGP	SGN-U577151	NM_001247625	ATRGP1, ATRGP, RGP1 | RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1)	1,006	0,010
33.99	development.unspecified	SGN-U567572	NM_001247634	dem protein-related / defective embryo and meristems protein-related	1,006	0,009
17.3.1.2.4	hormone metabolism.brassinosteroid.synthesis-degradation.sterols.FACKEL	SGN-U582281	NM_001251870	HYD2, ELL1, FK | FK (FACKEL)	1,005	0,012
29.5.3	protein.degradation.cysteine protease	SGN-U577702	Z48736	AALP | AALP (ARABIDOPSIS ALEURAIN-LIKE PROTEASE)	1,005	0,006
21.1	redox.thioredoxin	SGN-U577811	AK323054	ATPDIL1-1 | ATPDIL1-1 (PDI-LIKE 1-1)	1,004	0,009
35.2	not assigned.unknown	SGN-U582981	DB701090	Unknown	1,004	0,014
35.1	not assigned.no ontology	SGN-U562677	AI486252	ryptophan/tyrosine permease family protein	1,004	0,019
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U567218	EG553904	CSLD2, ATCSLD2 | ATCSLD2 (Cellulose synthase-like D2)	1,004	0,009
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U585251	NM_001247100	pectate lyase family protein	1,004	0,013
29.2.1.1.3.2.36	protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S subunit.L36	SGN-U562868	AK328662	ribosomal protein L36 family protein	1,003	0,013
17.5.2	hormone metabolism.ethylene.signal transduction	SGN-U583503	NM_001247583	AP2 domain-containing transcription factor, putative	1,003	0,013
34.19.4	transport.Major Intrinsic Proteins.SIP	SGN-U591774	GO372236	SIP1;1, SIP1A | SIP1;1 (SMALL AND BASIC INTRINSIC PROTEIN 1A)	1,002	0,012
20.1	stress.biotic	SGN-U585479	NP000615	Unknown	1,001	0,013

35.2	not assigned.unknown	SGN-U585103	BT014245	Unknown	1,001	0,019
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U565717	GO374533	60S ribosomal protein L15 (RPL15A)	1,001	0,007
30.2.99	signalling.receptor kinases.misc	SGN-U575324	AK247169	serine/threonine protein kinase, putative	1,001	0,007
27.3.99	RNA.regulation of transcription.unclassified	SGN-U574306	AK321625	ATLA1 | ATLA1 (ARABIDOPSIS THALIANA LA PROTEIN 1)	1,000	0,031
35.2	not assigned.unknown	SGN-U585546	AK247404	Unknown	1,000	0,007
35.2	not assigned.unknown	SGN-U575201	AK320292	anion exchange family protein	1,000	0,010
29.2.2	protein.synthesis.misc ribososomal protein	SGN-U577863	GO375309	ribosomal protein L20 family protein	1,000	0,015

Table 7. List of down-regulated genes genes (log2 ratio sub-/optimal T≤−1 and q-value<0.05) deteced only in the roots of the grafted ‘Kommeet’ plants onto ‘Moneymaker’ (R/S:MM/KO) under sub-optimal root T stress.

Bin Code	**BinName**	**SGN**	**NCBI**	**description**	**MM/KO Log FC**	**adj.P.Val**
35.2	not assigned.unknown	SGN-U574979	AW219934	Unknown	-5,103	0,014
20.2.99	stress.abiotic.unspecified	SGN-U573221	TA56697_4081	Major latex-like protein Bet v I allergen	-3,772	0,050
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U589064	AW031582	Unknown Protein (AHRD V1)Dehydration-responsive protein RD22	-3,496	0,001
35.2	not assigned.unknown	SGN-U569998	TA44607_4081	Unknown	-3,450	0,024
26.10	misc.cytochrome P450	SGN-U565273	AW651341	CYP82C2 | CYP82C2 (cytochrome P450, family 82, subfamily C, polypeptide 2)	-3,224	0,003
16.2	secondary metabolism.phenylpropanoids	SGN-U575022	TA46410_4081	O-methyltransferase 3	-3,223	0,004
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U585266	DV103658	BURP domain-containing protein / polygalacturonase, putative	-3,096	0,002
27.3.20	RNA.regulation of transcription.G2-like transcription factor family, GARP	SGN-U583163	NP1427479	Myb family transcription factor SHAQKYF class	-3,073	0,002
35.2	not assigned.unknown	SGN-U576946	DV105201	Unknown	-3,003	0,015
13.1.4.1.4	amino acid metabolism.synthesis.branched chain group.common.branched-chain amino acid aminotransferase	SGN-U569828	AW223114	Branched-chain amino acid aminotransferase	-2,997	0,002

26.10	misc.cytochrome P450	SGN-U575254	TA49475_4081	Cytochrome P450 E-class, group I	-2,977	0,002
35.2	not assigned.unknown	SGN-U582549	DB693091	Unknown	-2,944	0,001
13.2.6.2	amino acid metabolism.degradation.aromatic aa.tyrosine	SGN-U585362	BM410725	Fumarylacetoacetase	-2,898	0,002
35.2	not assigned.unknown	SGN-U566341	BF114042	Unknown	-2,876	0,002
16.2.1.7	secondary metabolism.phenylpropanoids.lignin biosynthesis.CCR1	SGN-U572681	TA54590_4081	cinnamoyl-CoA reductase-related	-2,791	0,002
35.2	not assigned.unknown	SGN-U583883	TA54478_4081	Unknown	-2,737	0,001
12.1.1	N-metabolism.nitrate metabolism.NR	SGN-U579543	DY523708	B29, NIA2-1, CHL3, NR, NR2, NIA2 | NIA2 (NITRATE REDUCTASE 2)	-2,731	0,002
29.5.5	protein.degradation.serine protease	SGN-U585997	BI210344	Serine carboxypeptidase 1	-2,705	0,004
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U582289	EG553907	oxidoreductase, 2OG-Fe(II) oxygenase family protein	-2,704	0,001
35.2	not assigned.unknown	SGN-U594983	BG713830	Unknown	-2,703	0,025
35.1	not assigned.no ontology	SGN-U567240	TA56972_4081	Hydroxycinnamoyl CoA quinate transferase	-2,671	0,002
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U562848	AI483537	zinc finger (C3HC4-type RING finger) family protein	-2,667	0,002
35.2	not assigned.unknown	SGN-U585945	DB696245	Unknown Protein	-2,640	0,002

16.1.5	secondary metabolism.isoprenoids.terpenoids	SGN-U590970	AY840092	Monoterpenoid synthase 2	-2,583	0,002
21.4	redox.glutaredoxins	SGN-U597671	DB682649	glutaredoxin family protein	-2,558	0,001
35.2	not assigned.unknown	SGN-U584557	AI782257	Unknown	-2,521	0,002
35.2	not assigned.unknown	SGN-U586884	BF114177	Unknown	-2,520	0,006
35.2	not assigned.unknown	SGN-U599418	AW621279	Unknown Protein	-2,517	0,004
23.1.3	nucleotide metabolism.synthesis.PRS-PP	SGN-U581370	AK247885	Ribose-phosphate pyrophosphokinase 2 / phosphoribosyl diphosphate synthetase 2 (PRS2)	-2,496	0,003
11.9.2.1	lipid metabolism.lipid degradation.lipases.triacylglycerol lipase	SGN-U577332	BG131086	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase	-2,456	0,005
11.1.8	lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	SGN-U588040	BF096265	EST360314 tomato nutrient deficient	-2,455	0,002
23.2	nucleotide metabolism.degradation	SGN-U577747	BG131246	Ectonucleoside triphosphate diphosphohydrolase 6 Nucleoside phosphatase GDA1/CD39	-2,438	0,005
35.2	not assigned.unknown	SGN-U562812	AK247214	RNA helicase, putative	-2,411	0,005
27.3.24	RNA.regulation of transcription.MADS box transcription factor family	SGN-U569575	AK247462	MADS-box family protein | MADS-box transcription factor 50	-2,382	0,001
11.9.2.1	lipid metabolism.lipid degradation.lipases.triacylglycerol lipase	SGN-U577332	AW651229	Lipase-like class 3	-2,380	0,007
35.2	not assigned.unknown	SGN-U572585	BI422106	Unknown	-2,363	0,004

27.3.46	RNA.regulation of transcription.DNA methyltransferases	SGN-U581202	TA55071_4081	DNA (Cytosine-5-)-methyltransferase 3 C-5 cytosine-specific DNA methylase	-2,353	0,002
10.7	cell wall.modification	SGN-U578397	TA54505_4081	Xyloglucan endotransglucosylase/hydrolase 2	-2,324	0,003
26.10	misc.cytochrome P450	SGN-U567473	BF097967	Cytochrome P450 family protein E-class, group I	-2,303	0,004
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U572908	BE450859	ATBZIP42 | bZIP transcription factor family protein	-2,274	0,008
10.7	cell wall.modification	SGN-U577727	DQ234354	beta-expansin precursor	-2,254	0,011
35.2	not assigned.unknown	SGN-U570534	TA54117_4081	formamidase	-2,254	0,001
23.2	nucleotide metabolism.degradation	SGN-U600260	BG131498	Apyrase	-2,251	0,004
35.2	not assigned.unknown	SGN-U594881	AK247138	cyclin A1 [Solanum lycopersicum] similar to Os06g0163200 [Oryza sativa (japonica cultivar-group)]	-2,250	0,001
34.10	transport.nucleotides	SGN-U584176	BI205696	ATPUP11 | ATPUP11 (Arabidopsis thaliana purine permease 11); purine transporter	-2,221	0,001
35.1.40	not assigned.no ontology.glycine rich proteins	SGN-U571038	TA41190_4081	AT2G45380 protein	-2,216	0,002
26.9	misc.glutathione S transferases	SGN-U599987	DV105092	TGSTU25 | ATGSTU25 (Arabidopsis thaliana Glutathione S-transferase (class tau) 25)	-2,213	0,002
35.2	not assigned.unknown	SGN-U569320	TA55639_4081	zinc finger (C3HC4-type RING finger) family protein	-2,190	0,002
20.2.99	stress.abiotic.unspecified	SGN-U564429	BF113820	Major latex-like protein	-2,181	0,004

35.2	not assigned.unknown	SGN-U579741	TA48601_4081	similar to unknown protein	-2,145	0,002
16.1.5	secondary metabolism.isoprenoids.terpenoids	SGN-U579603	BG131411	Monoterpenoid synthase 2	-2,137	0,004
35.2	not assigned.unknown	SGN-U564553	BI934060	Coiled-coil domain-containing protein 109A	-2,129	0,005
35.2	not assigned.unknown	SGN-U596640	BI928771	SP1a /RYanodine receptor SPRY domain containing protein	-2,121	0,007
35.1	not assigned.no ontology	SGN-U587593	TA56935_4081	Leucine-rich repeat-like protein	-2,120	0,003
26.16	misc.myrosinases-lectin-jacalin	SGN-U577384	DB721794	jacalin lectin family protein	-2,094	0,002
26.3	misc.gluco-, galacto- and mannosidases	SGN-U591793	DB704940	Beta-glucosidase 47 Glycoside hydrolase, family 1	-2,087	0,002
27.4	RNA.RNA binding	SGN-U577339	BW687298	GR-RBP7, CCR2, ATGRP7 | ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2) Glycine-rich RNA-binding protein	-2,075	0,002
35.1	not assigned.no ontology	SGN-U577745	TA37617_4081	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42050.1)	-2,066	0,002
35.2	not assigned.unknown	SGN-U597367	BP890349	Unknown	-2,066	0,004
26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U580225	TA51929_4081	Tasselseed2-like short-chain dehydrogenase/reductase	-2,064	0,005
35.2	not assigned.unknown	SGN-U579247	BG628760	Unknown oxidoreductase activity	-2,063	0,014

35.2	not assigned.unknown	SGN-U585107	DB693901	Unknown	-2,061	0,005
35.2	not assigned.unknown	SGN-U603078	BG642864	CAM 9 Calmodulin 9 calcium binding calcium ion binding	-2,046	0,007
30.2.17	signalling.receptor kinases.DUF 26	SGN-U571180	AF230198	protein kinase LESK1	-2,043	0,002
21.4	redox.glutaredoxins	SGN-U564913	AW040108	glutaredoxin family protein	-2,028	0,002
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U595315	AW442364	AtMYB59, MYB59 | MYB59 (myb domain protein 59); DNA binding / transcription factor	-2,026	0,003
35.3	not assigned.disagreeing hits	SGN-U579605	TA39972_4081	partialpolyphenol oxidase A	-2,015	0,003
17.5.3	hormone metabolism.ethylene.induced-regulated-responsive-activated	SGN-U588289	CK715041	BHLH transcription factor-like protein	-2,014	0,005
35.2	not assigned.unknown	SGN-U570767	DB697345	Unknown	-2,011	0,002
3.5	minor CHO metabolism.others	SGN-U580238	BW691658	Reductase 2	-2,009	0,006
27.3.5	RNA.regulation of transcription.ARR	SGN-U566472	GO372605	ARR15 | ARR15 (RESPONSE REGULATOR 15)	-1,996	0,003
11.9.2.1	lipid metabolism.lipid degradation.lipases.triacylglycerol lipase	SGN-U575841	AK322920	triacylglycerol lipase	-1,977	0,004
35.2	not assigned.unknown	SGN-U568184	ES897358	Unknown	-1,973	0,011
35.2	not assigned.unknown	SGN-U603907	BP891479	Unknown	-1,963	0,003

1.1.2.2	PS.lightreaction.photosystem I.PSI polypeptide subunits	SGN-U581403	BF096921	PSAA | Encodes psaA protein comprising the reaction center for photosystem I along with psaB protein	-1,960	0,002
35.3	not assigned.disagreeing hits	SGN-U581326	CD003137	wound-responsive protein, putative	-1,952	0,006
26.10	misc.cytochrome P450	SGN-U566831	AK320874	CYP71A22 | CYP71A22 (cytochrome P450, family 71, subfamily A, polypeptide 22)	-1,927	0,002
35.2	not assigned.unknown	SGN-U602192	BW688716	Unknown	-1,926	0,002
13.1.4.1	amino acid metabolism.synthesis.branched chain group.common	SGN-U572742	GO373346	ALS, AHAS, TZP5, IMR1, CSR1 | CSR1 (CHLORSULFURON/IMIDAZOLINONE RESISTANT 1)	-1,922	0,002
26.3	misc.gluco-, galacto- and mannosidases	SGN-U600154	AK324830	BGLU46 | BGLU46; hydrolase, hydrolyzing O-glycosyl compounds	-1,908	0,002
34.99	transport.misc	SGN-U564625	BW685195	AWPM-19-like membrane family protein	-1,903	0,002
35.3	not assigned.disagreeing hits	SGN-U578946	AK321464	ATU2AF35A | ATU2AF35A	-1,896	0,002
23.2	nucleotide metabolism.degradation	SGN-U585151	AK322648	RNA binding / adenosine deaminase	-1,893	0,004
10.7	cell wall.modification	SGN-U582695	TA56542_4081	EXPR, AT-EXPR, ATEXPR1, ATHEXP BETA 3.1, ATEXLB1 | ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1)	-1,889	0,006
35.2	not assigned.unknown	SGN-U575606	BI928030	Unknown	-1,884	0,002
35.2	not assigned.unknown	SGN-U592552	GO373573	heat shock protein	-1,876	0,014

20.2.1	stress.abiotic.heat	SGN-U591410	AI771467	ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3)	-1,874	0,004
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U563523	AI772038	auxin-responsive protein, putative	-1,866	0,016
23.1.3	nucleotide metabolism.synthesis.PRS-PP	SGN-U581370	AK247885	ribose-phosphate pyrophosphokinase 2	-1,859	0,004
35.3	not assigned.disagreeing hits	SGN-U591988	BE462248	polyphenol oxidase b	-1,856	0,005
35.2	not assigned.unknown	SGN-U579741	AK247134	Unknown	-1,851	0,007
19.14	tetrapyrrole synthesis.protochlorophyllide reductase	SGN-U578669	AK319497	PORA | PORA (Protochlorophyllide reductase A)	-1,850	0,003
35.1	not assigned.no ontology	SGN-U582833	BF114308	translation release factor	-1,848	0,003
35.2	not assigned.unknown	SGN-U598048	BP902933	Unknown	-1,845	0,002
35.2	not assigned.unknown	SGN-U582464	TA57083_4081	Unknown	-1,819	0,005
20.2.1	stress.abiotic.heat	SGN-U593108	DB706064	ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3)	-1,816	0,002
26.16	misc.myrosinases-lectin-jacalin	SGN-U577384	AK327821	jacalin lectin family protein	-1,812	0,003
35.2	not assigned.unknown	SGN-U563310	AK320213	Unknown	-1,798	0,002
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	SGN-U576530	AK323121	basic helix-loop-helix (bHLH) family protein	-1,789	0,004

34.5	transport.ammonium	SGN-U577075	NM_001247324	ATAMT1;2 | ATAMT1;2 (AMMONIUM TRANSPORTER 1;2)	-1,788	0,042
27.3.24	RNA.regulation of transcription.MADS box transcription factor family	SGN-U577167	BT013384	SOC1, AGL20 | AGL20 (AGAMOUS-LIKE 20)	-1,784	0,002
16.2.1.1	secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL	SGN-U577677	AW624595	PAL1 | PAL1 (PHE AMMONIA LYASE 1)	-1,763	0,008
27.3.12	RNA.regulation of transcription.C3H zinc finger family	SGN-U563065	AK320618	zinc finger (CCCH-type) family protein	-1,762	0,003
35.2	not assigned.unknown	SGN-U576267	TC238985	Unknown	-1,759	0,003
35.2	not assigned.unknown	SGN-U569493	AW625623	Unknown	-1,742	0,006
27.3.24	RNA.regulation of transcription.MADS box transcription factor family	SGN-U569575	AK330015	AGL66; transcription factor	-1,742	0,002
10.7	cell wall.modification	SGN-U583026	NM_001247541	XTH30, XTR4 | XTR4 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 4)	-1,736	0,004
13.2.6.3	amino acid metabolism.degradation.aromatic aa.tryptophan	SGN-U573257	AK327673	enoyl-CoA hydratase/isomerase family protein	-1,732	0,003
30.11	signalling.light	SGN-U573685	AI484677	JK218, RPT3, NPH3 | NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3)	-1,730	0,006
1.1.5.2	PS.lightreaction.other electron carrier (ox/red).ferredoxin	SGN-U581108	TA35951_4081	eukaryotic translation initiation factor SUI1, putative	-1,730	0,002
35.2	not assigned.unknown	SGN-U584612	CK574991	Unknown	-1,722	0,010
35.2	not assigned.unknown	SGN-U583451	TA49855_4081	Unknown	-1,707	0,004

28.1	DNA.synthesis/chromatin structure	SGN-U582808	NM_001247860	IP5PII | IP5PII (INOSITOL POLYPHOSPHATE 5-PHOSPHATASE II)	-1,706	0,005
26.10	misc.cytochrome P450	SGN-U577243	AK320723	SUR2, RNT1, RED1, ATR4, CYP83B1 | CYP83B1 (CYTOCHROME P450 MONOOXYGENASE 83B1)	-1,698	0,003
35.2	not assigned.unknown	SGN-U592265	AI898525	Unknown	-1,697	0,005
16.8.3	secondary metabolism.flavonoids.dihydroflavonols	SGN-U578626	TA55055_4081	BEN1 | BEN1; oxidoreductase, acting on CH-OH group of donors	-1,691	0,004
35.2	not assigned.unknown	SGN-U575954	AK328961	Unknown	-1,689	0,004
35.1	not assigned.no ontology	SGN-U577745	BT014232	Unknown	-1,688	0,002
26.10	misc.cytochrome P450	SGN-U565636	AK322569	CYP82C4 | CYP82C4 (cytochrome P450, family 82, subfamily C, polypeptide 4)	-1,680	0,018
35.2	not assigned.unknown	SGN-U573563	BI204303	Unknown	-1,671	0,003
35.2	not assigned.unknown	SGN-U570266	AK325392	similar to hypothetical protein [Vitis vinifera]	-1,671	0,006
27.3.15	RNA.regulation of transcription.CCAAT box binding factor family, HAP3	SGN-U564651	AK325105	histone-like transcription factor (CBF/NF-Y) family protein	-1,671	0,006
26.9	misc.glutathione S transferases	SGN-U576366	BW690043	ATGSTU25 | ATGSTU25 (Arabidopsis thaliana Glutathione S-transferase (class tau) 25)	-1,664	0,003
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U575629	AK247914	DNA-binding family protein / AT-hook protein 1 (AHP1)	-1,663	0,002
35.3	not assigned.disagreeing hits	SGN-U575022		O-methyltransferase family 2 protein	-1,653	0,003

16.1.4	secondary metabolism.isoprenoids.carotenoids	SGN-U568606	NM_001247419	B1, CHY1, BETA-OHASE 1 | BETA-OHASE 1 (BETA-HYDROXYLASE 1)	-1,650	0,003
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U577938	AK324156	2-oxoglutarate-dependent dioxygenase, putative	-1,647	0,004
2.1.2.1	major CHO metabolism.synthesis.starch.AGPase	SGN-U563760	DB684886	DIN9 | DIN9 (DARK INDUCIBLE 9); mannose-6-phosphate isomerase	-1,644	0,040
20.2.99	stress.abiotic.unspecified	SGN-U580303	AK322851	MLP28 | MLP28 (MLP-LIKE PROTEIN 28)	-1,642	0,007
35.2	not assigned.unknown	SGN-U578892	GO374380	Unknown	-1,641	0,003
31.1	cell.organisation	SGN-U603490	AK328062	ATMAP70-5 | ATMAP70-5 (microtubule-associated proteins 70-5)	-1,641	0,002
35.2	not assigned.unknown	SGN-U565142	BG131339	Unknown	-1,634	0,009
35.2	not assigned.unknown	SGN-U578507	AI897490	Unknown	-1,633	0,007
35.2	not assigned.unknown	SGN-U582924	FS198575	Unknown	-1,626	0,003
35.2	not assigned.unknown	SGN-U599451	AW443662	Unknown	-1,624	0,041
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U574785	AI485163	armadillo/beta-catenin repeat family protein	-1,624	0,007
29.5.5	protein.degradation.serine protease	SGN-U586216	TA55552_4081	SCPL40 | SCPL40 (serine carboxypeptidase-like 40)	-1,623	0,018
1.2.2	PS.photorespiration.glycolate oxydase	SGN-U578941	AK327836	(S)-2-hydroxy-acid oxidase, peroxisomal, putative	-1,621	0,005

34.12	transport.metal	SGN-U582217	NM_001247323	ZIP10 | ZIP10 (ZINC TRANSPORTER 10 PRECURSOR)	-1,620	0,035
26.12	misc.peroxidases	SGN-U595916	AK328712	peroxidase 64 (PER64) (P64) (PRXR4)	-1,619	0,003
7.1.1	OPP.oxidative PP.G6PD	SGN-U576857	AK246881	G6PD2 | G6PD2 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 2)	-1,618	0,004
35.2	not assigned.unknown	SGN-U594425	DB715550	Unknown	-1,617	0,002
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U572527	DB696126	tropinone reductase, putative	-1,602	0,005
16.8.5	secondary metabolism.flavonoids.isoflavonols	SGN-U604493	AK322502	pinoresinol-lariciresinol reductase, putative	-1,598	0,002
16.1.5	secondary metabolism.isoprenoids.terpenoids	SGN-U572419	BF096704	terpene synthase/cyclase family protein	-1,598	0,009
16.1.5	secondary metabolism.isoprenoids.terpenoids	SGN-U565148	AW622483	myrcene/ocimene synthase, putative	-1,597	0,007
27.3.1	RNA.regulation of transcription.ABI3/VP1-related B3-domain-containing transcription factor family	SGN-U576077	BG131632	HSI2 | HSI2 (HIGH-LEVEL EXPRESSION OF SUGAR-INDUCIBLE GENE 2)	-1,596	0,003
35.2	not assigned.unknown	SGN-U584935	BF113757	Unknown	-1,596	0,005
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U589916	BG126253	2-oxoglutarate-dependent dioxygenase, putative	-1,594	0,002
27.4	RNA.RNA binding	SGN-U568906	BT013216	RNA recognition motif (RRM)-containing protein	-1,584	0,011
20.2.1	stress.abiotic.heat	SGN-U578090	AK325031	ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3)	-1,584	0,003

34.13	transport.peptides and oligopeptides	SGN-U586500	AK329203	proton-dependent oligopeptide transport (POT) family protein	-1,580	0,006
35.2	not assigned.unknown	SGN-U599472	AW219729	Unknown	-1,575	0,003
35.3	not assigned.disagreeing hits	SGN-U578204	TA35627_4081	RUB1-conjugating enzyme, putative	-1,574	0,005
13.1.4.1.4	amino acid metabolism.synthesis.branched chain group.common.branched-chain amino acid aminotransferase	SGN-U569828	BE460934	ATBCAT-2 | ATBCAT-2	-1,570	0,004
26.10	misc.cytochrome P450	SGN-U583027	AK326035	CYP707A1 | CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide 1)	-1,568	0,004
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U563574	BT012856	ATVPS11 | ATVPS11 (Arabidopsis thaliana vacuolar protein sorting 11)	-1,568	0,004
27.3.55	RNA.regulation of transcription.HDA	SGN-U588108	DB681247	HDA2 | HDA2 (histone deacetylase 2)	-1,565	0,004
35.2	not assigned.unknown	SGN-U576078	DB716276	Unknown	-1,563	0,016
27.3.4	RNA.regulation of transcription.ARF, Auxin Response Factor family	SGN-U579928	NM_001246836	ARF1-BP, HSS, ARF2 | ARF2 (AUXIN RESPONSE FACTOR 2)	-1,562	0,006
11.9.2	lipid metabolism.lipid degradation.lipases	SGN-U577466	AK329689	lipase class 3 family protein	-1,562	0,019
35.2	not assigned.unknown	SGN-U580084	TA54970_4081	Unknown	-1,558	0,011
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U587887	AK329700	ATHB7, ATHB-7 | ATHB-7 (ARABIDOPSIS THALIANA HOMEOBOX 7)	-1,554	0,006
12.1.2	N-metabolism.nitrate metabolism.nitrite reductase	SGN-U585551	AK324702	NIR, ATHNIR, NIR1 | NIR1 (NITRITE REDUCTASE); ferredoxin-nitrate reductase	-1,554	0,004

29.5.3	protein.degradation.cysteine protease	SGN-U584736	GO374811	OTU-like cysteine protease family protein	-1,552	0,004
35.3	not assigned.disagreeing hits	SGN-U595238	DB682164	basic helix-loop-helix (bHLH) family protein	-1,551	0,006
30.1	signalling.in sugar and nutrient physiology	SGN-U575483	DB678885	GLT1 | GLT1 (NADH-dependent glutamate synthase 1 gene)	-1,545	0,014
35.2	not assigned.unknown	SGN-U565227	AK247481	Unknown	-1,544	0,006
35.2	not assigned.unknown	SGN-U567303	BG126346	Unknown	-1,541	0,011
3.5	minor CHO metabolism.others	SGN-U562913	BT013379	aldose 1-epimerase family protein	-1,538	0,003
26.7	misc.oxidases - copper, flavone etc.	SGN-U584869	TA51530_4081	allyl alcohol dehydrogenase, putative	-1,534	0,002
15.1	metal handling.acquisition	SGN-U582231	AK322290	ATFRO4, FRO4 | ATFRO4/FRO4 (FERRIC REDUCTION OXIDASE 4)	-1,532	0,044
35.3	not assigned.disagreeing hits	SGN-U581586	BT013818	FMO1 | FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1)	-1,532	0,004
35.3	not assigned.disagreeing hits	SGN-U588398	BP902454	Unknown	-1,532	0,013
35.2	not assigned.unknown	SGN-U565443	BP893904	Unknown	-1,530	0,006
35.3	not assigned.disagreeing hits	SGN-U591542	ES895133	Bet v I allergen family protein	-1,529	0,015
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U585252		pectate lyase family protein	-1,528	0,002

29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U580887	BI207087	UBC13 | UBC13 (ubiquitin-conjugating enzyme 13)	-1,527	0,003
34.18	transport.unspecified anions	SGN-U598877	AI898832	CLC-A, CLCA, ATCLC-A | ATCLC-A (CHLORIDE CHANNEL A)	-1,525	0,004
27.3.8	RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family	SGN-U570634	AK247208	CDF2 | CDF2 (CYCLING DOF FACTOR 2)	-1,524	0,042
35.3	not assigned.disagreeing hits	SGN-U565857	TA52484_4081	CYP84A1, FAH1 | FAH1 (FERULATE-5-HYDROXYLASE 1)	-1,524	0,017
27.1.1	RNA.processing.splicing	SGN-U585588	BM410652	splicing factor, putative	-1,522	0,003
35.2	not assigned.unknown	SGN-U587434	TA50449_4081	Unknown	-1,521	0,003
35.2	not assigned.unknown	SGN-U569905	BG631096	ATNUDT2 | MutT/nudix family protein,	-1,519	0,004
20.2.99	stress.abiotic.unspecified	SGN-U579422	BE344506	MLP31 | MLP31 (MLP-LIKE PROTEIN 31)	-1,518	0,003
35.1	not assigned.no ontology	SGN-U577685	AK323488	esterase/lipase/thioesterase family protein	-1,514	0,011
35.2	not assigned.unknown	SGN-U594520	AW443153	Unknown	-1,513	0,002
35.2	not assigned.unknown	SGN-U597301	BI921867	Unknown	-1,512	0,006
35.2	not assigned.unknown	SGN-U586372	DB723178	Unknown	-1,508	0,003
35.2	not assigned.unknown	SGN-U565483	AI782210	Unknown	-1,508	0,031

10.5.2	cell wall.cell wall proteins.proline rich proteins	SGN-U578291	TA39311_4081	ATPRP4, PRP4 | PRP4 (PROLINE-RICH PROTEIN 4)	-1,503	0,016
29.5.7	protein.degradation.metalloprotease	SGN-U573510	AK322742	matrixin family protein	-1,501	0,005
29.5.3	protein.degradation.cysteine protease	SGN-U580463	TA38239_4081	wound-induced proteinase inhibitor 1 precursor	-1,499	0,034
28.1.1.3	DNA.synthesis/chromatin structure.retrotransposon/transposase.copia-like retrotransposon	SGN-U566912	AK325661	NADH-ubiquinone oxidoreductase-related	-1,491	0,015
34.99	transport.misc	SGN-U603863	CN641264	MATE efflux family protein	-1,491	0,005
26.7	misc.oxidases - copper, flavone etc.	SGN-U579941	AW626331	polyphenol oxidase	-1,488	0,007
35.2	not assigned.unknown	SGN-U600647	AK322179	Unknown	-1,478	0,003
35.1	not assigned.no ontology	SGN-U575871	AK320534	molybdenum cofactor sulfurase family protein	-1,477	0,003
35.2	not assigned.unknown	SGN-U602053	BF113208	Unknown	-1,472	0,004
34.19.1	transport.Major Intrinsic Proteins.PIP	SGN-U564966	BG134199	NIP1;2, NLM2 | NIP1;2/NLM2 (NOD26-like intrinsic protein 1;2)	-1,468	0,024
10.6.2	cell wall.degradation.mannan-xylose-arabinose-fucose	SGN-U576959	AB612973	ATBXL2, BXL2 | BXL2 (BETA-XYLOSIDASE 2)	-1,467	0,004
34.13	transport.peptides and oligopeptides	SGN-U562917	DB694352	proton-dependent oligopeptide transport (POT) family protein	-1,462	0,004
35.2	not assigned.unknown	SGN-U603713	DV105644	Unknown	-1,458	0,010

35.2	not assigned.unknown	SGN-U584513	BE344485	Unknown	-1,452	0,035
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U600408	BG133413	polygalacturonase, putative / pectinase, putative	-1,452	0,002
26.12	misc.peroxidases	SGN-U600978	BP898492	peroxidase	-1,450	0,003
13.1.3.4	amino acid metabolism.synthesis.aspartate family.methionine	SGN-U593578	NM_001247496	SAM-2, MAT2 | MAT2/SAM-2 (S-adenosylmethionine synthetase 2)	-1,450	0,007
3.7	minor CHO metabolism.sugar kinases	SGN-U601567	AW651461	xylulose kinase, putative	-1,446	0,004
34.13	transport.peptides and oligopeptides	SGN-U598906	DV105437	proton-dependent oligopeptide transport (POT) family protein	-1,443	0,003
35.2	not assigned.unknown	SGN-U579730	BF098003	heat shock protein	-1,443	0,019
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U576689	AK326074	ZFP2 | ZFP2 (ZINC FINGER PROTEIN 2)	-1,442	0,007
35.2	not assigned.unknown	SGN-U571329	AK329407	Unknown	-1,441	0,002
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U573609	AK319692	myb family transcription factor	-1,440	0,027
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U577496	AK319806	MMZ2, UEV1B | MMZ2/UEV1B (MMS ZWEI HOMOLOGE 2)	-1,440	0,005
21.6	redox.dismutases and catalases	SGN-U578839	NM_001247898	CAT2 | CAT2 (CATALASE 2)	-1,439	0,005
35.2	not assigned.unknown	SGN-U595296	AK247788	Unknown	-1,438	0,002

29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U568194	AI486655	protein binding / zinc ion binding	-1,437	0,005
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	SGN-U562747	AK247605	basic helix-loop-helix (bHLH) family protein	-1,436	0,016
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U572199	AK247624	AP2 domain-containing transcription factor, putative	-1,432	0,004
35.2	not assigned.unknown	SGN-U565433	TA56009_4081	Unknown	-1,430	0,007
35.3	not assigned.disagreeing hits	SGN-U591273	BG123747	photosystem I reaction center subunit IV, chloroplast, putative	-1,428	0,029
35.2	not assigned.unknown	SGN-U593975	AW091819	Unknown	-1,427	0,006
35.1	not assigned.no ontology	SGN-U572126	TA39717_4081	alcohol oxidase-related	-1,426	0,008
17.6.3	hormone metabolism.gibberelin.induced-regulated-responsive-activated	SGN-U566943	ES895415	gibberellin-regulated family protein	-1,426	0,021
35.2	not assigned.unknown	SGN-U586291	TA56121_4081	Unknown	-1,425	0,004
35.2	not assigned.unknown	SGN-U568080	AK329400	Unknown	-1,423	0,006
35.1	not assigned.no ontology	SGN-U588688	NM_001247132	pathogen-responsive alpha-dioxygenase, putative	-1,423	0,004
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U579436	AW455340	myb family transcription factor	-1,420	0,004
35.2	not assigned.unknown	SGN-U573525	AK327751	Unknown	-1,420	0,005

27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U586335	AK322126	AtMYB48, MYB111 | MYB111 (myb domain protein 111)	-1,420	0,005
30.2.17	signalling.receptor kinases.DUF 26	SGN-U571180	AF230198	leucine-rich repeat family protein	-1,417	0,005
29.4	protein.postranslational modification	SGN-U564868	AK322986	5'-AMP-activated protein kinase beta-2 subunit, putative	-1,416	0,004
35.2	not assigned.unknown	SGN-U578765	TA42075_4081	Unknown	-1,415	0,015
29.4	protein.postranslational modification	SGN-U568161	AK321643	protein kinase family protein	-1,413	0,003
33.99	development.unspecified	SGN-U581008	GO372423	DRM1 | DRM1 (DORMANCY-ASSOCIATED PROTEIN 1)	-1,413	0,006
35.1	not assigned.no ontology	SGN-U563582	AK324756	phosphate-responsive 1 family protein	-1,413	0,022
35.2	not assigned.unknown	SGN-U584459	BG128460	heat shock protein binding	-1,409	0,004
35.3	not assigned.disagreeing hits	SGN-U580543	AK329287	ATLEA5, SAG21 | SAG21 (SENESCENCE-ASSOCIATED GENE 21)	-1,408	0,004
35.1	not assigned.no ontology	SGN-U585430	TA56130_4081	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-1,404	0,005
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U578489	BG127230	UBC2, ATUBC2 | ATUBC2 (UBIQUITING-CONJUGATING ENZYME 2)	-1,403	0,013
35.2	not assigned.unknown	SGN-U580781	AK247834	Unknown	-1,399	0,003
35.2	not assigned.unknown	SGN-U580686	GO372321	Unknown	-1,399	0,014

17.4.2	hormone metabolism.cytokinin.signal transduction	SGN-U603568	BP910270	AHK1, ATHK1 | ATHK1 (HISTIDINE KINASE 1)	-1,399	0,008
35.2	not assigned.unknown	SGN-U601651	AK330039	Unknown	-1,398	0,004
35.2	not assigned.unknown	SGN-U586193	EG553149	Unknown	-1,398	0,006
35.2	not assigned.unknown	SGN-U580139	GO373573	heat shock protein	-1,395	0,016
26.7	misc.oxidases - copper, flavone etc.	SGN-U578738	BT013818	FMO1 | FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1)	-1,395	0,006
35.2	not assigned.unknown	SGN-U603455	AI483641	Unknown	-1,394	0,004
35.3	not assigned.disagreeing hits	SGN-U591716	BG123747	PSAE-2 | PSAE-2 (photosystem I subunit E-2)	-1,394	0,012
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U570984	AK319929	TGA1 | TGA1	-1,393	0,004
27.3.99	RNA.regulation of transcription.unclassified	SGN-U567696	AK327475	binding	-1,393	0,008
16.8.5	secondary metabolism.flavonoids.isoflavonols	SGN-U584727	BT014421	isoflavone reductase, putative	-1,392	0,005
31.1	cell.organisation	SGN-U566387	AI774539	kinesin light chain-related	-1,391	0,004
35.2	not assigned.unknown	SGN-U591606	BW690204	Unknown	-1,389	0,004
33.99	development.unspecified	SGN-U576708	AK326297	SPL3 | SPL3 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3)	-1,386	0,004

35.3	not assigned.disagreeing hits	SGN-U580565	AK319806	Symbols: ATPROT2, ProT2 | ProT2 (PROLINE TRANSPORTER 2)	-1,385	0,004
35.1	not assigned.no ontology	SGN-U565180	TA36707_4081	RALFL33 | RALFL33 (RALF-LIKE 33)	-1,382	0,021
35.3	not assigned.disagreeing hits	SGN-U594997	GO374421	Rho-GTPase-activating protein-related	-1,380	0,004
26.9	misc.glutathione S transferases	SGN-U594663	AK321041	GST6, ATGSTF5, GSTF8, ATGSTF8 | ATGSTF8 (GLUTATHIONE S-TRANSFERASE 8)	-1,379	0,007
35.3	not assigned.disagreeing hits	SGN-U578927	TA36971_4081	Unknown	-1,379	0,004
30.1	signalling.in sugar and nutrient physiology	SGN-U575484	CK468702	GLT1 | GLT1 (NADH-dependent glutamate synthase 1 gene)	-1,378	0,008
26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U585755	AK321754	similar to short-chain dehydrogenase	-1,376	0,004
35.2	not assigned.unknown	SGN-U573262	BT012940	Unknown	-1,375	0,014
26.19	misc.plastocyanin-like	SGN-U585780	BG131149	plastocyanin-like domain-containing protein	-1,374	0,010
34.99	transport.misc	SGN-U576596	BF096440	xanthine/uracil permease family protein	-1,374	0,042
35.2	not assigned.unknown	SGN-U584458	AK247032	Unknown	-1,373	0,004
29.5.5	protein.degradation.serine protease	SGN-U585997	TA37323_4081	SCPL17 | SCPL17 (serine carboxypeptidase-like 17)	-1,372	0,012
29.2.3	protein.synthesis.initiation	SGN-U578904	BE461873	eukaryotic translation initiation factor 5A, putative	-1,372	0,004

17.1.1	hormone metabolism.abscisic acid.synthesis-degradation	SGN-U570287	TA40730_4081	NCED4 | NCED4 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 4)	-1,372	0,007
13.1.2.3	amino acid metabolism.synthesis.glutamate family.arginine	SGN-U584902	NM_001247687	ornithine decarboxylase	-1,371	0,007
1.1.2.2	PS.lightreaction.photosystem I.PSI polypeptide subunits	SGN-U580420	BG123747	PSAE-2 | PSAE-2 (photosystem I subunit E-2)	-1,368	0,010
11.8.7	lipid metabolism."exotics" (steroids, squalene etc).trans-2-enoyl-CoA reductase (NADPH)	SGN-U562655	DV935725	oxidoreductase, zinc-binding dehydrogenase family protein	-1,368	0,040
35.2	not assigned.unknown	SGN-U587650	BI924120	Unknown	-1,368	0,004
13.2.3.5	amino acid metabolism.degradation.aspartate family.lysine	SGN-U581998	AK321039	3-hydroxybutyryl-CoA dehydrogenase, putative	-1,367	0,005
26.28	misc.GDSL-motif lipase	SGN-U569000	DB700274	GLIP1 | GLIP1 (GDSL LIPASE1)	-1,367	0,014
4.13	glycolysis.PK	SGN-U572677	BG134019	pyruvate kinase, putative	-1,367	0,006
27.2	RNA.transcription	SGN-U587900	TA45919_4081	transcription initiation factor IIB-2	-1,359	0,005
35.3	not assigned.disagreeing hits	SGN-U579982	NM_001247225	GCN5-related N-acetyltransferase (GNAT) family protein	-1,357	0,005
26.10	misc.cytochrome P450	SGN-U565859	AK324994	CYP84A1, FAH1 | FAH1 (FERULATE-5-HYDROXYLASE 1)	-1,354	0,017
35.2	not assigned.unknown	SGN-U601870	BM535938	Unknown	-1,351	0,005
26.9	misc.glutathione S transferases	SGN-U586601	AW218869	ATGSTU8 | ATGSTU8 (Arabidopsis thaliana Glutathione S-transferase (class tau) 8)	-1,350	0,003

26.9	misc.glutathione S transferases	SGN-U579363	TA35843_4081	ATGSTU8 | ATGSTU8 (Arabidopsis thaliana Glutathione S-transferase (class tau)8)	-1,349	0,034
8.3	TCA / org. transformation.carbonic anhydrases	SGN-U577363	AJ849375	carbonic anhydrase, putative	-1,347	0,004
34.19.1	transport.Major Intrinsic Proteins.PIP	SGN-U580848	AK246632	PIP1D, PIP1;5 | PIP1;5/PIP1D (plasma membrane intrinsic protein 1;5)	-1,347	0,018
34.99	transport.misc	SGN-U602351	AK324253	predicted protein - phaeosphaeria nodorum	-1,347	0,043
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	SGN-U570747	AK322742	basic helix-loop-helix (bHLH) family protein	-1,346	0,003
7.3	OPP.electron transfer	SGN-U577324	BT014046	ATRFNR2 | ATRFNR2 (ROOT FNR 2)	-1,345	0,009
2.2.1.5	major CHO metabolism.degradation.sucrose.Susy	SGN-U604329	EG553247	SUS1, ASUS1, ATSUS1 | SUS1 (SUCROSE SYNTHASE 1)	-1,344	0,007
27.3.55	RNA.regulation of transcription.HDA	SGN-U574537	AK247982	HDA2 | HDA2 (histone deacetylase 2)	-1,342	0,004
13.2.7	amino acid metabolism.degradation.histidine	SGN-U584469	BT012721	EMB1075 | EMB1075 (EMBRYO DEFECTIVE 1075)	-1,340	0,004
28.1.3	DNA.synthesis/chromatin structure.histone	SGN-U581474	TA39023_4081	HIS1-3 | HIS1-3 (HISTONE H1-3)	-1,338	0,005
35.2	not assigned.unknown	SGN-U578456	TA36495_4081	Unknown	-1,338	0,003
35.1	not assigned.no ontology	SGN-U569906	TA52095_4081	ATNUDT2 | ATNUDT2 (Arabidopsis thaliana Nudix hydrolase homolog 2)	-1,338	0,004
30.6	signalling.MAP kinases	SGN-U565359	NM_001247850	MAP3KE1, MAPKKK7 | MAPKKK7 (MAP3K EPSILON PROTEIN KINASE)	-1,337	0,005

26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	SGN-U578475	ES897217	aspartic protease inhibitor 1 precursor	-1,336	0,021
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U579555	AK322452	RAP2.4 | RAP2.4 (related to AP2 4)	-1,334	0,006
35.2	not assigned.unknown	SGN-U586767	BM410245	Unknown	-1,333	0,004
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U582039	AK326899	AtMYB70 | AtMYB70 (myb domain protein 70)	-1,333	0,003
20.2.1	stress.abiotic.heat	SGN-U578974	TA36583_4081	ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3)	-1,329	0,008
35.1	not assigned.no ontology	SGN-U576721	AK322879	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-1,327	0,005
35.2	not assigned.unknown	SGN-U577753		Unknown	-1,327	0,018
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	SGN-U580656	NM_001247925	HSFA3, AT-HSFA3 | AT-HSFA3 (Arabidopsis thaliana heat shock transcription factor A3)	-1,326	0,014
35.2	not assigned.unknown	SGN-U573825	TC242012	Unknown	-1,322	0,004
35.3	not assigned.disagreeing hits	SGN-U597045	AK224709	Unknown	-1,322	0,005
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U582530	TA53354_4081	leucine-rich repeat family protein	-1,321	0,005
35.1	not assigned.no ontology	SGN-U567852	AW626297	hydrolase	-1,320	0,005
35.3	not assigned.disagreeing hits	SGN-U579902	BG123747	ATL2 | ATL2 (Arabidopsis T?xicos en Levadura 2)	-1,319	0,024

35.2	not assigned.unknown	SGN-U604065	BT013960	amino acid transporter family protein	-1,316	0,022
35.2	not assigned.unknown	SGN-U567797	BM411358	Unknown	-1,311	0,015
34.13	transport.peptides and oligopeptides	SGN-U597249	BF050343	nitrate transporter (NTP2)	-1,311	0,016
34.99	transport.misc	SGN-U583607	BT014563	neurofilament protein-related	-1,309	0,016
35.3	not assigned.disagreeing hits	SGN-U571293	TC236312	RAP2.4 | RAP2.4 (related to AP2 4)	-1,308	0,006
13.2.3.5	amino acid metabolism.degradation.aspartate family.lysine	SGN-U591094	AK321339	LKR/SDH, LKR, SDH | LKR (SACCHAROPINE DEHYDROGENASE)	-1,308	0,009
20.2.1	stress.abiotic.heat	SGN-U579266	TA36595_4081	HSP101, HOT1, ATHSP101 | ATHSP101 (HEAT SHOCK PROTEIN 101)	-1,308	0,015
35.2	not assigned.unknown	SGN-U565439	AK247138	cyclin a1	-1,307	0,006
20.1	stress.biotic	SGN-U599301	BW692302	disease resistance-responsive family protein / dirigent family protein	-1,306	0,006
35.2	not assigned.unknown	SGN-U563741	AK325796	Unknown	-1,306	0,003
17.4.2	hormone metabolism.cytokinin.signal transduction	SGN-U576830	TA54219_4081	CRE1, WOL1, AHK4, WOL | WOL (WOODEN LEG)	-1,304	0,005
29.4	protein.postranslational modification	SGN-U567122	AW738237	SnRK3.16, CIPK1 | CIPK1 (CBL-INTERACTING PROTEIN KINASE 1)	-1,304	0,008
13.1.1.1.1	amino acid metabolism.synthesis.central amino acid metabolism.GABA.Glutamate decarboxylase	SGN-U578585	NM_001247112	GAD1, GAD | GAD (Glutamate decarboxylase 1)	-1,304	0,005

4.13	glycolysis.PK	SGN-U597111	BP903282	pyruvate kinase, putative	-1,303	0,003
35.2	not assigned.unknown	SGN-U574920	AI489331	Unknown	-1,302	0,007
35.2	not assigned.unknown	SGN-U600241	BW685785	Unknown	-1,302	0,004
34.15	transport.potassium	SGN-U599525	AK328159	ATKEA6, KEA6 | KEA6 (K+ efflux antiporter 6)	-1,300	0,031
13.1.4.1	amino acid metabolism.synthesis.branched chain group.common	SGN-U587249	BG134374	ALS, AHAS, TZP5, IMR1, CSR1 | CSR1 (CHLORSULFURON/IMIDAZOLINONE RESISTANT 1)	-1,299	0,006
35.2	not assigned.unknown	SGN-U572334	AK321519	Unknown	-1,299	0,013
35.2	not assigned.unknown	SGN-U582519	BW686484	Unknown	-1,299	0,014
35.2	not assigned.unknown	SGN-U590532	AI637336	Unknown	-1,298	0,049
35.3	not assigned.disagreeing hits	SGN-U575686	BI932108	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-1,298	0,025
35.2	not assigned.unknown	SGN-U574765	ES894377	sn-2 protein	-1,298	0,009
35.2	not assigned.unknown	SGN-U598868	AK320050	disease resistance protein, putative	-1,298	0,008
26.28	misc.GDSL-motif lipase	SGN-U570559	AK323178	lipase, putative	-1,297	0,003
35.2	not assigned.unknown	SGN-U582852	AI780791	protein binding	-1,297	0,008

17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reductase	SGN-U590135	NM_001246939	12-oxophytodienoate reductase, putative	-1,295	0,023
13.1.4.1	amino acid metabolism.synthesis.branched chain group.common	SGN-U572739	TA37274_4081	ALS, AHAS, TZP5, IMR1, CSR1 | CSR1 (CHLORSULFURON/IMIDAZOLINONE RESISTANT 1)	-1,293	0,005
29.4	protein.postranslational modification	SGN-U564206	GE468458	SRPK4 | SRPK4 (SER/ARG-RICH PROTEIN KINASE 4)	-1,292	0,005
35.2	not assigned.unknown	SGN-U590586	AK324020	similar to hypothetical protein	-1,287	0,014
35.2	not assigned.unknown	SGN-U588788	AK330032	Unknown	-1,286	0,006
35.2	not assigned.unknown	SGN-U571674	AK247987	Unknown	-1,286	0,005
35.2	not assigned.unknown	SGN-U567713	AK325805	Unknown	-1,286	0,005
35.2	not assigned.unknown	SGN-U578881	AK324961	Unknown	-1,286	0,008
35.2	not assigned.unknown	SGN-U573928	AK324773	Unknown	-1,285	0,007
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U567495	NM_001247110	Unknown	-1,284	0,015
35.1	not assigned.no ontology	SGN-U567217	TA55741_4081	Unknown	-1,283	0,013
29.4	protein.postranslational modification	SGN-U568978	TA37828_4081	PAC motif-containing protein	-1,281	0,023
27.3.99	RNA.regulation of transcription.unclassified	SGN-U586130	AK319949	remorin family protein	-1,281	0,004

35.2	not assigned.unknown	SGN-U588753	AK325824	Unknown	-1,281	0,006
35.2	not assigned.unknown	SGN-U582655		Unknown	-1,280	0,004
20.2.1	stress.abiotic.heat	SGN-U566729	AK325271	17.8 kDa class I heat shock protein (HSP17.8-CI)	-1,275	0,017
2.2.2.1	major CHO metabolism.degradation.starch.starch cleavage	SGN-U579298	NM_001247123	BAM9, BMY3 | BMY3 (BETA-AMYLASE 9)	-1,274	0,006
35.2	not assigned.unknown	SGN-U597844	AK321388	Unknown	-1,273	0,006
27.3.5	RNA.regulation of transcription.ARR	SGN-U572839	EG553392	ATRR4, ARR9 | ARR9 (RESPONSE REACTOR 4)	-1,272	0,004
16.2	secondary metabolism.phenylpropanoids	SGN-U565215	AW443470	transferase family protein	-1,272	0,022
35.2	not assigned.unknown	SGN-U569849	AI897590	Unknown	-1,271	0,014
35.2	not assigned.unknown	SGN-U573645	TC232099	Unknown	-1,270	0,019
26.28	misc.GDSL-motif lipase	SGN-U579520	BI925384	GDSL-motif lipase/hydrolase family protein	-1,267	0,004
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	SGN-U574720	TA55929_4081	BIM2 | BIM2 (BES1-INTERACTING MYC-LIKE PROTEIN 2)	-1,266	0,007
35.2	not assigned.unknown	SGN-U564001	AK247199	hydroxyproline-rich systemin precursor (defense-signaling glycopeptide hormone)	-1,265	0,006
35.2	not assigned.unknown	SGN-U575557	AK320655	ATAB2 | ATAB2	-1,263	0,015

34.99	transport.misc	SGN-U573100	FS182799	xanthine/uracil permease family protein	-1,262	0,014
35.2	not assigned.unknown	SGN-U590354	BI924449	Unknown	-1,260	0,040
27.3.24	RNA.regulation of transcription.MADS box transcription factor family	SGN-U578103	AK323934	AGL22, SVP | SVP (SHORT VEGETATIVE PHASE)	-1,259	0,005
8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U578521	TA38012_4081	S-locus lectin protein kinase family protein	-1,259	0,044
1.1.1.2	PS.lightreaction.photosystem II.PSII polypeptide subunits	SGN-U582566	FS201787	LPA2 | LPA2 (LOW PSII ACCUMULATION2)	-1,257	0,004
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	SGN-U565924	BF096555	basic helix-loop-helix (bHLH) family protein	-1,257	0,008
34.99	transport.misc	SGN-U575036	TA40539_4081	flavin reductase-related	-1,257	0,004
35.2	not assigned.unknown	SGN-U587974	AW933894	Unknown	-1,256	0,007
29.5.11.1	protein.degradation.ubiquitin.ubiquitin	SGN-U593421	AK326365	UBQ3 | UBQ3 (POLYUBIQUITIN 3)	-1,255	0,008
35.3	not assigned.disagreeing hits	SGN-U591183	DB714618	zinc finger (AN1-like) family protein	-1,255	0,005
29.4	protein.postranslational modification	SGN-U585951	NM_001247424	OST1, SNRK2-6, SRK2E, SNRK2.6, P44 | OST1/P44/SNRK2-6/SRK2E (OPEN STOMATA 1, SNF1-RELATED PROTEIN KINASE 2.6)	-1,253	0,006
17.4.1	hormone metabolism.cytokinin.synthesis-degradation	SGN-U585983	AK319371	ATCKX3, CKX3 | CKX3 (CYTOKININ OXIDASE 3)	-1,253	0,005

16.2.1.1	secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL	SGN-U591451	AK320002	PAL1 | PAL1 (PHE AMMONIA LYASE 1)	-1,252	0,007
35.3	not assigned.disagreeing hits	SGN-U581010	GO375260	YCF32, PSBY | PSBY (photosystem II BY)	-1,251	0,018
11.1.8	lipid metabolism.FA synthesis and FA elongation.acyl coa ligase	SGN-U572389	AK327858	AAE7, ACN1 | AAE7/ACN1 (ACYL-ACTIVATING ENZYME 7)	-1,251	0,009
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	SGN-U573319	BI935172	HSFB2A, AT-HSFB2A | AT-HSFB2A (Arabidopsis thaliana heat shock transcription factor B2A)	-1,250	0,009
35.2	not assigned.unknown	SGN-U571551	TC238160	Unknown	-1,247	0,006
30.2.25	signalling.receptor kinases.wall associated kinase	SGN-U583856	AI487264	WAK3 | WAK3 (WALL ASSOCIATED KINASE 3)	-1,247	0,026
35.2	not assigned.unknown	SGN-U595296	TC238042	Unknown	-1,247	0,005
33.99	development.unspecified	SGN-U576343	AK321163	nodulin MtN21 family protein	-1,247	0,046
35.2	not assigned.unknown	SGN-U599917	AK322846	Unknown	-1,246	0,005
35.2	not assigned.unknown	SGN-U565900	TA43947_4081	Thylakoid lumenal 19 kDa protein	-1,246	0,007
6.2	gluconeogenese/ glyoxylate cycle.malate synthase	SGN-U573203	AK320322	MLS | MLS (MALATE SYNTHASE); malate synthase	-1,245	0,017
28.1	DNA.synthesis/chromatin structure	SGN-U581126	AK320740	ATDRH1, DRH1 | DRH1 (DEAD box RNA helicase 1)	-1,244	0,009
35.3	not assigned.disagreeing hits	SGN-U595612	AI488811	IP5PII | IP5PII (INOSITOL POLYPHOSPHATE 5-PHOSPHATASE II)	-1,244	0,004

11.9.2.1	lipid metabolism.lipid degradation.lipases.triacylglycerol lipase	SGN-U592762	AK322821	lipase class 3 family protein	-1,242	0,029
29.5.11.1	protein.degradation.ubiquitin.ubiquitin	SGN-U578847	AK326365	UBQ10 | UBQ10 (POLYUBIQUITIN 10)	-1,242	0,011
35.2	not assigned.unknown	SGN-U569182	AK319353	SLT1 | SLT1 (SODIUM- AND LITHIUM-TOLERANT 1)	-1,242	0,005
29.2.4	protein.synthesis.elongation	SGN-U581517	AI779761	elongation factor 1-alpha	-1,241	0,029
11.9.2	lipid metabolism.lipid degradation.lipases	SGN-U579917	AK319975	lipase class 3 family protein	-1,241	0,042
35.3	not assigned.disagreeing hits	SGN-U575934	AK320331	DNAJ heat shock N-terminal domain-containing protein / cell division protein-related	-1,241	0,007
16.2.1.6	secondary metabolism.phenylpropanoids.lignin biosynthesis.CCoAOMT	SGN-U581378	TC238958	caffeoyl-CoA 3-O-methyltransferase, putative	-1,241	0,022
35.2	not assigned.unknown	SGN-U573174	BG123437	Unknown	-1,239	0,005
35.3	not assigned.disagreeing hits	SGN-U579071	NM_001247898	Catalase isozyme 1	-1,238	0,007
17.4.1	hormone metabolism.cytokinin.synthesis-degradation	SGN-U599440	NM_001257980	ATCKX1, CKX1 | ATCKX1/CKX1 (CYTOKININ OXIDASE/DEHYDROGENASE 1)	-1,237	0,017
27.1	RNA.processing	SGN-U566310	TA42278_4081	RNA polymerase I specific transcription initiation factor RRN3 family protein	-1,236	0,010
34.13	transport.peptides and oligopeptides	SGN-U566391	DY523780	proton-dependent oligopeptide transport (POT) family protein	-1,232	0,038
35.2	not assigned.unknown	SGN-U568587	AW220871	Unknown	-1,232	0,047

20.2.1	stress.abiotic.heat	SGN-U572726	TA39446_4081	DNAJ heat shock N-terminal domain-containing protein	-1,232	0,015
27.2	RNA.transcription	SGN-U567025	TA45919_4081	transcription initiation factor IIB-2 / general transcription factor TFIIB-2 (TFIIB2)	-1,231	0,004
34.10	transport.nucleotides	SGN-U584176	TA48443_4081	ATPUP11 | ATPUP11 (Arabidopsis thaliana purine permease 11)	-1,230	0,022
27.3.9	RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family	SGN-U574138	BP880167	TIFY2B, ZML1 | ZML1 (ZIM-LIKE 1)	-1,229	0,013
35.1	not assigned.no ontology	SGN-U569126	NM_001247132	pathogen-responsive alpha-dioxygenase, putative	-1,229	0,006
16.1.5	secondary metabolism.isoprenoids.terpenoids	SGN-U583641	TA44198_4081	dehydrodolichyl diphosphate synthase, putative	-1,229	0,027
20.2.1	stress.abiotic.heat	SGN-U593336	NM_001247510	ERD8, HSP81-2 | HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8)	-1,226	0,014
35.3	not assigned.disagreeing hits	SGN-U579106	TA39470_4081	TIF3H1 | TIF3H1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT H1)	-1,226	0,006
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U582862	DB702846	UGT84A1 | UGT84A1; UDP-glycosyltransferase	-1,225	0,006
30.3	signalling.calcium	SGN-U578921	AK325294	calcium-binding EF hand family protein	-1,223	0,050
30.11	signalling.light	SGN-U574292	TA39435_4081	signal transducer	-1,223	0,006
29.2.1.2.2.34	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L34	SGN-U575014	BE451290	structural constituent of ribosome	-1,223	0,004
34.10	transport.nucleotides	SGN-U573552	FS203530	ATPUP10 | ATPUP10 (Arabidopsis thaliana purine permease 10)	-1,219	0,009

16.8.4	secondary metabolism.flavonoids.flavonols	SGN-U587435	AW030105	ATSRG1, SRG1 | SRG1 (SENESCENCE-RELATED GENE 1)	-1,218	0,009
11.9.2.1	lipid metabolism.lipid degradation.lipases.triacylglycerol lipase	SGN-U600741	DB679544	triacylglycerol lipase	-1,218	0,003
35.2	not assigned.unknown	SGN-U589664	AK319692	Unknown	-1,218	0,018
21.6	redox.dismutases and catalases	SGN-U590926	AW930492	CAT2 | CAT2 (CATALASE 2)	-1,217	0,004
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U563057	AK323074	oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1,217	0,014
12.1.1	N-metabolism.nitrate metabolism.NR	SGN-U581608	NM_001247752	AT-SO, ATSO, SOX | SOX (SULFITE OXIDASE)	-1,217	0,012
20.2.99	stress.abiotic.unspecified	SGN-U582650	DV105669	Bet v I allergen family protein	-1,216	0,006
29.4	protein.postranslational modification	SGN-U572412	NM_001247305	OMR1 | OMR1 (L-O-METHYLTHREONINE RESISTANT 1)	-1,216	0,008
35.2	not assigned.unknown	SGN-U576950	AK321639	Unknown	-1,214	0,006
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U588636	BG126596	protein kinase family protein	-1,213	0,003
35.3	not assigned.disagreeing hits	SGN-U592193	TA35688_4081	RUB1-conjugating enzyme, putative	-1,212	0,007
35.1	not assigned.no ontology	SGN-U566864	AK322616	leucine-rich repeat family protein	-1,212	0,013
35.1	not assigned.no ontology	SGN-U574358	AK322829	transformer serine/arginine-rich ribonucleoprotein, putative	-1,211	0,007

35.2	not assigned.unknown	SGN-U565909	TA54283_4081	ant-like protein - nicotiana tabacum	-1,206	0,010
35.2	not assigned.unknown	SGN-U578462	AK321612	binding	-1,203	0,012
35.2	not assigned.unknown	SGN-U582095	AK325896	Unknown	-1,203	0,009
35.1	not assigned.no ontology	SGN-U568461	NM_001247534	PEX11C | PEX11C	-1,202	0,004
30.11	signalling.light	SGN-U574291	AK322551	signal transducer	-1,201	0,004
35.3	not assigned.disagreeing hits	SGN-U578747	BT013262	eukaryotic translation initiation factor SUI1, putative	-1,201	0,004
23.3.1.1	nucleotide metabolism.salvage.phosphoribosyltransferases.aprt	SGN-U590766	AK324960	APT3 | APT3 (ADENINE PHOSPHORIBOSYL TRANSFERASE 3)	-1,201	0,006
26.9	misc.glutathione S transferases	SGN-U584004	AK325577	drought-responsive family protein, similar to drought-induced mRNA	-1,200	0,012
26.21	misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	SGN-U576740	BI925360	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-1,199	0,006
35.3	not assigned.disagreeing hits	SGN-U573837	AW031075	DNAJ heat shock protein, putative	-1,199	0,008
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U570609	BP909137	similar to protein binding	-1,198	0,016
35.2	not assigned.unknown	SGN-U576407	BW689310	Unknown	-1,197	0,010
26.10	misc.cytochrome P450	SGN-U578296	AK329595	CYP71A25 | CYP71A25 (cytochrome P450, family 71, subfamily A, polypeptide 25)	-1,196	0,016

7.2.4	OPP.non-reductive PP.ribose 5-phosphate isomerase	SGN-U570785	TA43380_4081	ribose 5-phosphate isomerase-related	-1,195	0,004
1.1.5.3	PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase	SGN-U579448	BT013070	ATLFNR1 | ATLFNR1 (LEAF FNR 1)	-1,195	0,016
35.2	not assigned.unknown	SGN-U597904	AW034507	Unknown	-1,195	0,009
13.1.6.1.1	amino acid metabolism.synthesis.aromatic aa.chorismate.3-deoxy-D-arabino-heptulosonate 7-phosphate synthase	SGN-U581552	NM_001247486	DHS1 | DHS1 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1)	-1,194	0,009
35.3	not assigned.disagreeing hits	SGN-U592107	NM_001247584	UBC9 | UBC9 (UBIQUITIN CONJUGATING ENZYME 9)	-1,194	0,020
27.3.5	RNA.regulation of transcription.ARR	SGN-U577676	AK323990	ARR3 | ARR3 (RESPONSE REGULATOR 3)	-1,193	0,005
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U581159	NM_001246881	TCP family transcription factor, putative	-1,192	0,007
20.1	stress.biotic	SGN-U578995	TA36489_4081	PR3, PR-3, CHI-B, B-CHI, ATHCHIB | ATHCHIB (BASIC CHITINASE)	-1,191	0,028
35.2	not assigned.unknown	SGN-U566853	CD002152	Unknown	-1,191	0,006
35.2	not assigned.unknown	SGN-U596577	TA46914_4081	Unknown	-1,191	0,007
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U565075	AK322310	UGT75B2, UGT2 | UGT2/UGT75B2 (UDP-glucosyl transferase 75B2)	-1,190	0,011
35.3	not assigned.disagreeing hits	SGN-U593210	AF123256	17.8 kDa class I heat shock protein (HSP17.8-CI)	-1,189	0,038
35.2	not assigned.unknown	SGN-U574680	AK247236	Unknown	-1,188	0,023

30.3	signalling.calcium	SGN-U579814	CD003006	AK1, ATCPK1, CPK1 | CPK1 (calcium-dependent protein kinase isoform AK1)	-1,187	0,006
35.2	not assigned.unknown	SGN-U596712	BM409912	Unknown	-1,187	0,015
27.3.99	RNA.regulation of transcription.unclassified	SGN-U589023	AK327475	binding	-1,186	0,007
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U574792	ES891224	myb family transcription factor	-1,184	0,005
35.2	not assigned.unknown	SGN-U586604	BG127052	Unknown	-1,181	0,008
29.4	protein.postranslational modification	SGN-U584108	AK321714	SnRK3.13, PKS11, CIPK8 | CIPK8 (CBL-INTERACTING PROTEIN KINASE 8)	-1,181	0,006
33.99	development.unspecified	SGN-U568609	BM410928	ANAC056, ATNAC2 | ATNAC2 (Arabidopsis thaliana NAC domain containing protein 2)	-1,181	0,036
27.3.7	RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family	SGN-U581062	AK325127	zinc finger (B-box type) family protein	-1,180	0,008
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U584677	BG125915	auxin-responsive family protein	-1,179	0,015
35.1	not assigned.no ontology	SGN-U583122	TA54567_4081	transporter-related	-1,178	0,005
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U572630	NM_001246878	BP, BP1, KNAT1 | KNAT1 (BREVIPEDICELLUS 1)	-1,178	0,012
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U602073	DV104820	CESA7, ATCESA7, MUR10, IRX3 | IRX3 (IRREGULAR XYLEM 3, MURUS 10)	-1,175	0,008
27.3.66	RNA.regulation of transcription.Psudo ARR transcription factor family	SGN-U564924	TA42823_4081	APRR7, PRR7 | PRR7 (PSEUDO-RESPONSE REGULATOR 7)	-1,175	0,004

27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U575608	TA55364_4081	ATHB14, ATHB-14, PHB-1D, PHB | PHB (PHABULOSA)	-1,175	0,010
35.2	not assigned.unknown	SGN-U595722	AW932202	Unknown	-1,175	0,016
35.3	not assigned.disagreeing hits	SGN-U582350	BT013496	Encodes a protein with similarity to glycosyl transferase family 47 proteins that is involved in secondary cell wall biosynthesis.	-1,172	0,005
27.3.47	RNA.regulation of transcription.ELF3	SGN-U571949	AK321534	PYK20, ELF3 | ELF3 (EARLY FLOWERING 3)	-1,172	0,048
27.3.99	RNA.regulation of transcription.unclassified	SGN-U576026	AK321422	zinc finger (AN1-like) family protein	-1,172	0,010
10.5.1	cell wall.cell wall proteins.AGPs	SGN-U573243	AK329103	FLA11 | FLA11 (fasciclin-like arabinogalactan-protein 11)	-1,171	0,010
35.2	not assigned.unknown	SGN-U563251	AK330088	Unknown	-1,170	0,016
35.2	not assigned.unknown	SGN-U581834	BE435226	Unknown	-1,170	0,004
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U596115	BI204621	ATTAP2 | ATTAP2 (Arabidopsis thaliana transporter associated with antigen processing protein 2)	-1,169	0,007
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U567998	CD003356	Unknown	-1,168	0,047
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	SGN-U566338	AK323598	TGA1 | TGA1	-1,168	0,004
29.4	protein.postranslational modification	SGN-U577511	BG132057	CKB2 | CKB2 (casein kinase II beta chain 2)	-1,167	0,011

35.2	not assigned.unknown	SGN-U588367	TA54345_4081	Unknown	-1,167	0,004
10.7	cell wall.modification	SGN-U578473	NM_001247029	ATEXP4, ATHEXP ALPHA 1.6, ATEXPA4 | ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	-1,166	0,014
27.3.57	RNA.regulation of transcription.JUMONJI family	SGN-U601990	BG129795	ELF6 | ELF6 (EARLY FLOWERING 6)	-1,165	0,004
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U585886	BT013780	CESA7, ATCESA7, MUR10, IRX3 | IRX3 (IRREGULAR XYLEM 3, MURUS 10)	-1,164	0,009
34.10	transport.nucleotides	SGN-U568852	AW093671	ATPUP1, PUP1 | PUP1 (PURINE PERMEASE 1)	-1,164	0,008
27.2	RNA.transcription	SGN-U579100	AK319624	SIG1, SIG2, SIGB, RPOD1, SIGA | SIGA (SIGMA FACTOR A)	-1,161	0,007
11.1.1	lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	SGN-U568420	AK324475	CAC3 | CAC3 (acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit)	-1,161	0,015
31.1	cell.organisation	SGN-U576942	DB721548	ATMAP65-1 | ATMAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1)	-1,161	0,010
34.19.1	transport.Major Intrinsic Proteins.PIP	SGN-U590036	AK246632	PIP1;4, PIP1E, TMP-C | TMP-C (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4)	-1,160	0,010
9.1.2	mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not clear	SGN-U579403	AW035600	zinc finger (C3HC4-type RING finger) family protein	-1,160	0,006
26.1	misc.misc2	SGN-U581817	AK322928	dienelactone hydrolase family protein	-1,158	0,018
12.2.2	N-metabolism.ammonia metabolism.glutamine synthase	SGN-U578728	AK319584	GLN2, ATGSL1, GS2 | GS2 (GLUTAMINE SYNTHETASE 2)	-1,158	0,006
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U568744	AK247728	zinc finger (C3HC4-type RING finger) family protein	-1,157	0,011

35.2	not assigned.unknown	SGN-U603235	BE458658	Unknown	-1,156	0,010
28.1.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase.gypsy-like retrotransposon	SGN-U579218	TA40948_4081	putative polyprotein	-1,156	0,037
35.2	not assigned.unknown	SGN-U563091	DB696052	OSB1 | OSB1 (ORGANELLAR SINGLE-STRANDED)	-1,156	0,004
35.2	not assigned.unknown	SGN-U594883	AK326516	Unknown	-1,154	0,009
35.3	not assigned.disagreeing hits	SGN-U590679	TA35688_4081	RUB1-conjugating enzyme, putative	-1,153	0,007
35.2	not assigned.unknown	SGN-U601163	AW222294	Unknown	-1,152	0,014
20.1	stress.biotic	SGN-U585806	AK327757	pathogenesis-related family protein	-1,149	0,004
30.2.24	signalling.receptor kinases.S-locus glycoprotein like	SGN-U597176	AI777568	S-locus protein kinase, putative	-1,149	0,033
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	SGN-U572160	AW216678	basic helix-loop-helix (bHLH) family protein	-1,149	0,024
35.1	not assigned.no ontology	SGN-U563408	AW932923	esterase/lipase/thioesterase family protein	-1,148	0,004
35.2	not assigned.unknown	SGN-U577984	AK247631	Unknown	-1,147	0,014
35.2	not assigned.unknown	SGN-U575774	BF113819	Organ-specific protein S2	-1,147	0,030
35.2	not assigned.unknown	SGN-U584297	AK323920	non-specific lipid-transfer protein	-1,147	0,013

35.3	not assigned.disagreeing hits	SGN-U592492	AW623354	Unknown	-1,146	0,009
35.2	not assigned.unknown	SGN-U585504	AK323789	Unknown	-1,145	0,013
35.2	not assigned.unknown	SGN-U578350	AK325709	Unknown	-1,144	0,006
31.1	cell.organisation	SGN-U579866	AK319324	ATMAP65-6 | ATMAP65-6	-1,144	0,019
35.2	not assigned.unknown	SGN-U571748	TA48599_4081	Unknown	-1,142	0,013
20.2.1	stress.abiotic.heat	SGN-U577277	AK324395	HSP70 | HSP70 (heat shock protein 70)	-1,142	0,005
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family	SGN-U571279	BF098470	ATWRKY72, WRKY72 | WRKY72 (WRKY DNA-binding protein 72)	-1,142	0,010
34.99	transport.misc	SGN-U577378	AK247735	Unknown	-1,142	0,008
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U583296	AK322056	AtTLP1 | AtTLP1 (TUBBY LIKE PROTEIN 1)	-1,141	0,005
35.1	not assigned.no ontology	SGN-U583796	AK319425	hydrolase, alpha/beta fold family protein	-1,141	0,007
35.2	not assigned.unknown	SGN-U580637	TA36340_4081	Unknown	-1,138	0,009
35.2	not assigned.unknown	SGN-U604662	CD003293	Unknown	-1,138	0,014
11.2.4	lipid metabolism.FA desaturation.omega 6 desaturase	SGN-U574780	AK321037	FAD2 | FAD2 (FATTY ACID DESATURASE 2)	-1,138	0,007

16.1.5	secondary metabolism.isoprenoids.terpenoids	SGN-U578127	BI207683	lyase/ magnesium ion binding	-1,137	0,005
35.3	not assigned.disagreeing hits	SGN-U579823	AF083253	cysteine protease inhibitor, putative	-1,136	0,036
31.1	cell.organisation	SGN-U577552	AK325817	ANNAT5, ANN5 | ANN5/ANNAT5 (ANNEXIN ARABIDOPSIS 5)	-1,135	0,009
13.2.2.3	amino acid metabolism.degradation.glutamate family.arginine	SGN-U567848	AK322693	PSKF109, UREG | UREG (urease accessory protein G)	-1,134	0,009
35.2	not assigned.unknown	SGN-U566020		Unknown	-1,134	0,025
35.2	not assigned.unknown	SGN-U566147	AK324827	cysteine protease inhibitor, putative / cystatin, putative	-1,134	0,012
35.1	not assigned.no ontology	SGN-U573059	BM411337	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-1,133	0,037
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U566023	TA53397_4081	similar to F-box family protein-related	-1,133	0,010
35.2	not assigned.unknown	SGN-U567504	TA45397_4081	Unknown	-1,132	0,007
27.3.2	RNA.regulation of transcription.Alfin-like	SGN-U577885	AK327530	PHD finger family protein	-1,132	0,008
16.10	secondary metabolism.simple phenols	SGN-U599742	BF098375	IRX12, LAC4 | IRX12/LAC4 (laccase 4)	-1,131	0,006
31.4	cell.vesicle transport	SGN-U570934	AK329090	ATMAMI | ATMAMI (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED MANNITOL-INDUCED)	-1,131	0,008
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U566706	AK247557	zinc finger (DNL type) family protein	-1,130	0,010

35.2	not assigned.unknown	SGN-U592220	EG553690	FPF, FPF1 | FPF1 (FLOWERING PROMOTING FACTOR 1)	-1,130	0,015
34.99	transport.misc	SGN-U582851	AI487032	Unknown	-1,129	0,009
35.1	not assigned.no ontology	SGN-U572909	CK468690	transducin family protein / WD-40 repeat family protein	-1,129	0,010
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U602631	BP889238	AtMYB85, MYB85 | MYB85 (myb domain protein 85)	-1,129	0,009
27.3	RNA.regulation of transcription	SGN-U566321	AI486517	PTAC2 | PTAC2 (PLASTID TRANSCRIPTIONALLY ACTIVE2)	-1,129	0,004
35.2	not assigned.unknown	SGN-U565976	TA40532_4081	Unknown	-1,128	0,008
35.3	not assigned.disagreeing hits	SGN-U577431	TA36672_4081	proline-rich family protein	-1,128	0,006
35.1.3	not assigned.no ontology.armadillo/beta-catenin repeat family protein	SGN-U577120	AK328721	armadillo/beta-catenin repeat family protein / BTB/POZ domain-containing protein	-1,128	0,005
27.3.99	RNA.regulation of transcription.unclassified	SGN-U589024	AK327475	binding	-1,127	0,005
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U569785	AK329957	hydrolase, alpha/beta fold family protein	-1,127	0,008
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U566312	NM_001247690	UGT73B5 (UDP-GLUCOSYL TRANSFERASE 73B5)	-1,126	0,041
28.1	DNA.synthesis/chromatin structure	SGN-U600683	BM535873	phage-associated helicase	-1,126	0,018
26.7	misc.oxidases - copper, flavone etc.	SGN-U600669	AK325816	ATPPOX (A. THALIANA PYRIDOXIN (PYRODOXAMINE) 5'-PHOSPHATE OXIDASE)	-1,125	0,012

27.3.99	RNA.regulation of transcription.unclassified	SGN-U562903	AK325419	zinc finger (MYND type) family protein / F-box family protein	-1,125	0,020
35.2	not assigned.unknown	SGN-U568254	AK326862	Unknown	-1,125	0,004
35.1.41	not assigned.no ontology.hydroxyproline rich proteins	SGN-U581219		hydroxyproline-rich glycoprotein family protein	-1,125	0,004
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U564575	BI932154	tropinone reductase, putative / tropine dehydrogenase, putative	-1,125	0,023
35.1.19	not assigned.no ontology.C2 domain-containing protein	SGN-U598458	BP911006	C2 domain-containing protein	-1,124	0,007
33.99	development.unspecified	SGN-U586529	TA54866_4081	ANAC104, XND1 | ANAC104/XND1 (Arabidopsis NAC domain containing protein 104)	-1,123	0,016
33.99	development.unspecified	SGN-U571877	AK328772	nodulin MtN3 family protein	-1,123	0,019
35.2	not assigned.unknown	SGN-U563005	AK320341	Unknown	-1,123	0,009
29.5.1	protein.degradation.subtilases	SGN-U579302	TA37738_4081	subtilase family protein	-1,123	0,009
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U571347	AW223766	homeobox transcription factor, putative	-1,122	0,009
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U578448	AK328092	2-oxoglutarate-dependent dioxygenase, putative	-1,121	0,005
35.2	not assigned.unknown	SGN-U587081	CD003282	Unknown	-1,121	0,004
23.1.2.30	nucleotide metabolism.synthesis.purine.IMP dehydrogenase	SGN-U579386	AW934324	TCTP | TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN)	-1,120	0,022

26.22	misc.short chain dehydrogenase/reductase (SDR)	SGN-U586596	BI930115	YBR159 | YBR159; ketoreductase/ oxidoreductase	-1,119	0,013
27.3.8	RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family	SGN-U583873	AK323652	ADOF2 | ADOF2 (Arabidopsis dof zinc finger protein 2)	-1,119	0,013
35.2	not assigned.unknown	SGN-U565474	AK324669	UPF0406 protein C16orf57 homolog	-1,119	0,008
27.3.99	RNA.regulation of transcription.unclassified	SGN-U580149	GO376239	LOL1 | LOL1 (LSD ONE LIKE 1)	-1,118	0,034
33.99	development.unspecified	SGN-U580899	GO375239	senescence-associated protein, putative	-1,117	0,013
35.3	not assigned.disagreeing hits	SGN-U568662	BG626002	FMO1 | FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1)	-1,116	0,007
35.2	not assigned.unknown	SGN-U584153	AK246981	Unknown	-1,115	0,007
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U600359	AK322576	AtMYB71, MYB305 | MYB305 (myb domain protein 305)	-1,113	0,004
35.3	not assigned.disagreeing hits	SGN-U577260	NM_001247413	XTR3 | XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3); hydrolase, acting on glycosyl bonds	-1,112	0,007
35.2	not assigned.unknown	SGN-U566002	TC228435	Unknown	-1,112	0,004
35.2	not assigned.unknown	SGN-U593647	TA55498_4081	Unknown	-1,110	0,006
1.1.4	PS.lightreaction.ATP synthase	SGN-U570788	TA43379_4081	ATP synthase protein I -related	-1,110	0,016
35.2	not assigned.unknown	SGN-U573546	AK247094	Unknown	-1,110	0,008

31.2	cell.division	SGN-U586662	AK320331	DNAJ heat shock N-terminal domain-containing protein	-1,109	0,011
35.2	not assigned.unknown	SGN-U586515	AI780519	Unknown	-1,108	0,004
33.99	development.unspecified	SGN-U582839	AK323037	SGR7, SHR | SHR (SHORT ROOT)	-1,107	0,020
34.99	transport.misc	SGN-U570157	BF097588	cell wall-associated hydrolase	-1,107	0,022
13.2.7	amino acid metabolism.degradation.histidine	SGN-U578403	NM_001246930	EMB1075 | EMB1075 (EMBRYO DEFECTIVE 1075)	-1,106	0,023
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U580403	AW221440	2-oxoglutarate-dependent dioxygenase, putative	-1,105	0,010
20.2.4	stress.abiotic.touch/wounding	SGN-U578509	AK323477	wound-responsive protein-related	-1,105	0,006
35.2	not assigned.unknown	SGN-U576065	GO375587	Unknown	-1,105	0,016
20.2.2	stress.abiotic.cold	SGN-U583244	GT165145	C2 domain-containing protein	-1,104	0,005
35.3	not assigned.disagreeing hits	SGN-U575910	NM_001247375	PPCK1 | PPCK1 (PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE)	-1,104	0,011
35.2	not assigned.unknown	SGN-U563137	BI932074	ATGDU5 | ATGDU5 (ARABIDOPSIS THALIANA GLUTAMINE DUMPER 5)	-1,104	0,005
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U579238	NM_001247584	RAP2.12 | RAP2.12	-1,103	0,017
34.15	transport.potassium	SGN-U585125	NM_001247329	AKT1 | AKT1 (ARABIDOPSIS K TRANSPORTER 1)	-1,103	0,010

35.1	not assigned.no ontology	SGN-U562624	AK324366	integral membrane HPP family protein	-1,102	0,006
35.3	not assigned.disagreeing hits	SGN-U570422	TA51541_4081	trypsin and protease inhibitor family protein / Kunitz family protein	-1,102	0,008
35.1.2	not assigned.no ontology.agenet domain-containing protein	SGN-U597055		agenet domain-containing protein	-1,101	0,005
30.2.99	signalling.receptor kinases.misc	SGN-U582199	DV104633	receptor-like protein kinase-related	-1,101	0,007
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U585247	AW222974	pectate lyase family protein	-1,100	0,024
35.2	not assigned.unknown	SGN-U585146	AI778219	Unknown	-1,100	0,016
35.1	not assigned.no ontology	SGN-U564531	AK321308	leucine-rich repeat family protein	-1,099	0,013
31.1	cell.organisation	SGN-U603505	AW030035	kinesin motor family protein	-1,098	0,017
29.5.5	protein.degradation.serine protease	SGN-U583064	TA44398_4081	SCPL10 | SCPL10 (serine carboxypeptidase-like 10)	-1,098	0,005
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U570879	AK322391	zinc finger (C2H2 type) family protein	-1,097	0,011
30.3	signalling.calcium	SGN-U568260	AW032800	CPK10, ATCDPK1 | ATCDPK1	-1,097	0,022
10.1.5	cell wall.precursor synthesis.UXS	SGN-U569705	BG129868	GAE5 | GAE5 (UDP-D-GLUCURONATE 4-EPIMERASE 5)	-1,097	0,004
35.2	not assigned.unknown	SGN-U580344	BM413273	Unknown	-1,097	0,006

35.1	not assigned.no ontology	SGN-U562873	BG642804	hydrolase, alpha/beta fold family protein	-1,097	0,005
13.2.3.5	amino acid metabolism.degradation.aspartate family.lysine	SGN-U592415	TA37588_4081	LKR/SDH, LKR, SDH | LKR (SACCHAROPINE DEHYDROGENASE)	-1,097	0,012
27.4	RNA.RNA binding	SGN-U576832	AK319397	zinc finger (Ran-binding) family protein	-1,096	0,013
35.1	not assigned.no ontology	SGN-U571923	BI204487	Unknown	-1,096	0,004
35.2	not assigned.unknown	SGN-U586098	BF114182	Unknown	-1,096	0,013
6.4	gluconeogenese/ glyoxylate cycle.PEPCK	SGN-U579925	TA39438_4081	PCK1, PEPCK | PCK1/PEPCK (PHOSPHOENOLPYRUVATE CARBOXYKINASE 1)	-1,095	0,012
35.3	not assigned.disagreeing hits	SGN-U577781	AK324416	LHCA5 | LHCA5 (Photosystem I light harvesting complex gene 5)	-1,095	0,016
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases	SGN-U580563	DB686460	glycoside hydrolase family 28 protein	-1,095	0,015
26.19	misc.plastocyanin-like	SGN-U573041	TA56830_4081	plastocyanin-like domain-containing protein	-1,094	0,006
26.6	misc.O- methyl transferases	SGN-U588920	AW979867	Unknown	-1,091	0,010
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	SGN-U581047	TA36826_4081	myb family transcription factor	-1,089	0,005
35.2	not assigned.unknown	SGN-U569915	AK247805	Unknown	-1,089	0,006
35.2	not assigned.unknown	SGN-U574356	BM413270	Unknown	-1,089	0,006

27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U564617	AK328735	zinc finger protein-related	-1,088	0,013
35.1	not assigned.no ontology	SGN-U582883	EG553838	transaminase	-1,088	0,005
29.1	protein.aa activation	SGN-U567587	BE432458	pseudouridine synthase family protein	-1,087	0,007
33.99	development.unspecified	SGN-U571750	BI933542	nodulin, putative	-1,087	0,023
35.2	not assigned.unknown	SGN-U566116	AI896736	Unknown	-1,087	0,023
26.13	misc.acid and other phosphatases	SGN-U586186	AK327616	ATPAP27, PAP27 | ATPAP27/PAP27 (purple acid phosphatase 27)	-1,086	0,006
10.2.1	cell wall.cellulose synthesis.cellulose synthase	SGN-U595684	BW689978	CESA4, IRX5, NWS2 | CESA4 (CELLULOSE SYNTHASE 4)	-1,084	0,005
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U578617	AK320999	F-box family protein	-1,083	0,005
26.12	misc.peroxidases	SGN-U591329	TA35693_4081	PRXR1 | PRXR1 (peroxidase 42)	-1,081	0,024
35.2	not assigned.unknown	SGN-U566883	TA53779_4081	Unknown	-1,080	0,005
35.2	not assigned.unknown	SGN-U597269	TA55170_4081	Unknown	-1,079	0,022
34.2	transporter.sugars	SGN-U603018	AK323115	hexose transporter, putative	-1,078	0,004
35.2	not assigned.unknown	SGN-U581217	AK247983	Unknown	-1,078	0,006

35.1	not assigned.no ontology	SGN-U595411	BM410715	T-complex protein 11	-1,077	0,018
27.3.99	RNA.regulation of transcription.unclassified	SGN-U562897	NM_001247463	ATEXO70B1 | ATEXO70B1 (exocyst subunit EXO70 family protein B1)	-1,075	0,006
20.2.99	stress.abiotic.unspecified	SGN-U563782	AK330077	cupin family protein	-1,075	0,013
27.3.20	RNA.regulation of transcription.G2-like transcription factor family, GARP	SGN-U603639	AK323568	myb family transcription factor	-1,075	0,038
35.3	not assigned.disagreeing hits	SGN-U591309	CK715000	ubiquitin-conjugating enzyme 8	-1,073	0,018
27.4	RNA.RNA binding	SGN-U578467	AK247976	RNA recognition motif (RRM)-containing protein	-1,073	0,008
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U582076	DB718737	oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1,072	0,006
5.3	fermentation.ADH	SGN-U579632	NM_001247170	ADH, ATADH, ADH1 | ADH1 (ALCOHOL DEHYDROGENASE 1)	-1,071	0,019
29.4	protein.postranslational modification	SGN-U563240	NM_001247285	NPH1, JK224, RPT1, PHOT1 | PHOT1 (phototropin 1)	-1,071	0,024
35.2	not assigned.unknown	SGN-U600041	AW737603	Unknown	-1,070	0,016
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	SGN-U581520	TA41497_4081	ATIDD11 | ATIDD11 (ARABIDOPSIS THALIANA INDETERMINATE(ID)-DOMAIN 11)	-1,069	0,008
27.4	RNA.RNA binding	SGN-U564698	AK323564	similar to RNA-binding protein, putative	-1,069	0,004
4.13	glycolysis.PK	SGN-U586081	AW041832	pyruvate kinase, putative	-1,069	0,005

35.2	not assigned.unknown	SGN-U575377	TA54127_4081	Unknown	-1,068	0,011
34.21	transport.calcium	SGN-U581855	BM409047	RNA recognition motif (RRM)-containing protein	-1,067	0,005
35.2	not assigned.unknown	SGN-U571631	AK246413	Unknown	-1,067	0,017
35.1	not assigned.no ontology	SGN-U571363	AK322844	ACR4 | ACR4 (ACT REPEAT 4)	-1,066	0,008
26.8	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	SGN-U564811	AK319412	hydrolase	-1,065	0,010
30.8	signalling.misc	SGN-U576793	FS198511	nitrate-responsive NOI protein, putative	-1,065	0,008
35.2	not assigned.unknown	SGN-U577263	GO375243	Unknown	-1,064	0,008
35.3	not assigned.disagreeing hits	SGN-U571861	AK329218	LPP3, ATLPP3 | ATLPP3/LPP3 (LIPID PHOSPHATE PHOSPHATASE 3)	-1,064	0,006
35.1	not assigned.no ontology	SGN-U578753	TA36508_4081	translationally controlled tumor family protein	-1,063	0,033
31.2	cell.division	SGN-U567407	AK247144	asparagine synthase (glutamine-hydrolyzing)	-1,061	0,006
35.3	not assigned.disagreeing hits	SGN-U591834	TA39692_4081	PFN3, PRF3 | PFN3/PRF3 (PROFILIN 3)	-1,060	0,006
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	SGN-U578436	DV103959	HSFA6B, AT-HSFA6B | AT-HSFA6B (Arabidopsis thaliana heat shock transcription factor A6B)	-1,059	0,017
35.2	not assigned.unknown	SGN-U601467	AK329622	Unknown	-1,059	0,006

35.2	not assigned.unknown	SGN-U578870	TA40440_4081	CW14 | CW14	-1,059	0,005
27.3.99	RNA.regulation of transcription.unclassified	SGN-U578001	BT014337	zinc finger (AN1-like) family protein	-1,059	0,005
6.4	gluconeogenese/ glyoxylate cycle.PEPCK	SGN-U578470	NM_001247150	PCK1, PEPCK | PCK1/PEPCK (PHOSPHOENOLPYRUVATE CARBOXYKINASE 1)	-1,059	0,020
13.2.3.1	amino acid metabolism.degradation.aspartate family.asparagine	SGN-U564199	AK325562	L-asparaginase / L-asparagine amidohydrolase	-1,059	0,005
35.2	not assigned.unknown	SGN-U591664	AW621768	Unknown	-1,058	0,017
9.4	mitochondrial electron transport / ATP synthesis.alternative oxidase	SGN-U569026	AK329884	AOX2 | AOX2 (alternative oxidase 2)	-1,058	0,023
4.6	glycolysis.Fruc2,6BisPase	SGN-U563133	AW929583	fructose-1,6-bisphosphatase family protein	-1,057	0,021
35.1	not assigned.no ontology	SGN-U574818	AW621478	transmembrane protein, putative	-1,056	0,005
27.3.37	RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family	SGN-U587034	AI774397	LBD4 | LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4)	-1,056	0,010
35.2	not assigned.unknown	SGN-U563547	BI929472	Unknown	-1,055	0,006
35.3	not assigned.disagreeing hits	SGN-U578319	AK319584	zinc-binding protein, putative / protein kinase C inhibitor, putative	-1,055	0,012
16.2	secondary metabolism.phenylpropanoids	SGN-U564163	BI935350	transferase family protein	-1,054	0,009
35.2	not assigned.unknown	SGN-U571211	AK247040	Unknown	-1,054	0,027

1.1.2.1	PS.lightreaction.photosystem I.LHC-I	SGN-U581495	TA35894_4081	LHCA3 | LHCA3 (Photosystem I light harvesting complex gene 3)	-1,053	0,030
20.1.7	stress.biotic.PR-proteins	SGN-U572573	AK247069	protein binding	-1,053	0,007
17.5.1	hormone metabolism.ethylene.synthesis-degradation	SGN-U583842	NM_001247235	ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6)	-1,050	0,036
35.3	not assigned.disagreeing hits	SGN-U591548	NM_001247637	translationally controlled tumor family protein	-1,049	0,015
35.2	not assigned.unknown	SGN-U583490	TA42157_4081	Unknown	-1,049	0,006
35.3	not assigned.disagreeing hits	SGN-U585990	TC231827	KS, ATKS, GA2 | GA2 (GA REQUIRING 2)	-1,049	0,007
35.3	not assigned.disagreeing hits	SGN-U580772	AK319845	Protein binding / zinc ion binding	-1,048	0,008
29.4.1.57	protein.postranslational modification.kinase.receptor like cytoplasmatic kinase VII	SGN-U588635	DV105380	protein kinase family protein	-1,047	0,013
35.2	not assigned.unknown	SGN-U571627	AI894604	Unknown	-1,047	0,007
29.3.99	protein.targeting.unknown	SGN-U589543	AK325616	integral membrane protein, putative	-1,047	0,014
35.3	not assigned.disagreeing hits	SGN-U581548	AK323799	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	-1,046	0,008
35.2	not assigned.unknown	SGN-U565301	BI211139	Unknown	-1,046	0,007
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U562997	AI489641	HB-6, RPL, PNY, BLR, BLH9, VAN, LSN | LSN (LARSON)	-1,046	0,007

35.2	not assigned.unknown	SGN-U598267	BG134081	Unknown	-1,044	0,010
10.8.1	cell wall.pectin*esterases.PME	SGN-U585820	TA37079_4081	ATPMEPCRF | ATPMEPCRF	-1,042	0,018
35.3	not assigned.disagreeing hits	SGN-U578711	TA39895_4081	transformer serine/arginine-rich ribonucleoprotein, putative	-1,041	0,006
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U562646	EG553875	AP2 domain-containing transcription factor, putative	-1,041	0,008
16.2.1.3	secondary metabolism.phenylpropanoids.lignin biosynthesis.4CL	SGN-U577586	AI899107	AT4CL2, 4CL2 | 4CL2 (4-coumarate:CoA ligase 2)	-1,041	0,005
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX	SGN-U581531	NM_001247929	FBL6, EBF1 | EBF1 (EIN3-BINDING F BOX PROTEIN 1)	-1,041	0,004
16.2.1.1	secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL	SGN-U580612	AW035414	PAL2 | PAL2 (phenylalanine ammonia-lyase 2)	-1,040	0,022
35.1	not assigned.no ontology	SGN-U577921		transformer serine/arginine-rich ribonucleoprotein, putative	-1,039	0,009
17.1.2	hormone metabolism.abscisic acid.signal transduction	SGN-U585375	AK319227	HSL1, HSI2-L1 | HSI2-L1/HSL1 (HSI2-LIKE 1)	-1,039	0,008
35.3	not assigned.disagreeing hits	SGN-U590877	NM_001247312	ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3)	-1,039	0,005
35.2	not assigned.unknown	SGN-U572647	EG553709	ECT11 | ECT11 (evolutionarily conserved C-terminal region 11)	-1,037	0,008
20.2.1	stress.abiotic.heat	SGN-U579041	TA36602_4081	ERD8, HSP81-2 | HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8)	-1,037	0,009
35.3	not assigned.disagreeing hits	SGN-U585509	TA38865_4081	putative disease resistance protein	-1,037	0,013

35.2	not assigned.unknown	SGN-U587693	AK325896	Unknown	-1,036	0,010
16.2	secondary metabolism.phenylpropanoids	SGN-U574782	TA41295_4081	transferase family protein	-1,036	0,030
35.2	not assigned.unknown	SGN-U587870	AW031220	Unknown	-1,036	0,005
17.4.2	hormone metabolism.cytokinin.signal transduction	SGN-U583953	TA56986_4081	CRE1, WOL1, AHK4, WOL | WOL (WOODEN LEG)	-1,036	0,005
35.3	not assigned.disagreeing hits	SGN-U604769	BP893677	helicase domain-containing protein / IBR domain-containing protein	-1,034	0,011
12.4	N-metabolism.misc	SGN-U570124	AK322401	FAD binding / catalytic/ tRNA dihydrouridine synthase	-1,034	0,006
35.2	not assigned.unknown	SGN-U593919	AK247884	Unknown	-1,034	0,006
35.2	not assigned.unknown	SGN-U563141	GO372688	Unknown	-1,033	0,007
13.1.5.3.2	amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.SAT	SGN-U582407	AK328696	SAT-1, SAT-A, SAT3, AtSerat2;2 | AtSerat2;2 (SERINE ACETYLTRANSFERASE 1)	-1,033	0,011
20.1.7	stress.biotic.PR-proteins	SGN-U582534	BE450495	disease resistance protein (CC-NBS-LRR class), putative	-1,030	0,012
27.3.29	RNA.regulation of transcription.TCP transcription factor family	SGN-U563595	AK319300	TCP family transcription factor, putative	-1,030	0,008
35.1	not assigned.no ontology	SGN-U568488	TA49719_4081	DNA binding / hydrolase, acting on ester bonds / nuclease/ nucleic acid binding / recombinase	-1,030	0,007
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated	SGN-U588103	BT013697	JAR, FIN219, JAR1 | JAR1 (JASMONATE RESISTANT 1)	-1,029	0,022

35.2	not assigned.unknown	SGN-U573491	AK330014	Unknown	-1,028	0,010
35.2	not assigned.unknown	SGN-U582365	AK247621	Unknown	-1,028	0,013
35.2	not assigned.unknown	SGN-U569360	AK321862	Unknown	-1,028	0,008
21.3	redox.heme	SGN-U592616	NM_001247182	GLB2, ARATH GLB2, NSHB2, AHB2 | AHB2 (NON-SYMBIOTIC HAEMOGLOBIN 2)	-1,028	0,008
35.2	not assigned.unknown	SGN-U566855	BE436497	Unknown	-1,027	0,017
35.3	not assigned.disagreeing hits	SGN-U567511	BG128849	X-Pro dipeptidase	-1,027	0,009
35.2	not assigned.unknown	SGN-U562732	AK247027	Unknown	-1,027	0,024
31.4	cell.vesicle transport	SGN-U584171	BT013988	synaptobrevin-related family protein	-1,027	0,008
29.5.1	protein.degradation.subtilases	SGN-U579671	TA56265_4081	XSP1 | XSP1 (XYLEM SERINE PEPTIDASE 1)	-1,026	0,015
27.3.7	RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger family	SGN-U572381	BG130520	zinc finger (B-box type) family protein	-1,026	0,010
35.2	not assigned.unknown	SGN-U580186	AK323600	Unknown	-1,026	0,025
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U571691	TA53224_4081	ATUGT85A5 | ATUGT85A5 (UDP-GLUCOSYL TRANSFERASE 85A5)	-1,026	0,012
34.19.1	transport.Major Intrinsic Proteins.PIP	SGN-U569106	AK321561	NIP4;2, NLM5 | NIP4;2/NLM5 (NOD26-LIKE INTRINSIC PROTEIN 4;2)	-1,025	0,036

8.2.10	TCA / org. transformation.other organic acid transformaitons.malic	SGN-U567375	BF051038	O-methyltransferase family 2 protein	-1,025	0,048
35.2	not assigned.unknown	SGN-U573577	BF113531	Unknown	-1,024	0,008
31.4	cell.vesicle transport	SGN-U569317	BG643810	ATSYP132, SYP132 | SYP132 (syntaxin 132)	-1,024	0,006
35.2	not assigned.unknown	SGN-U580236	BP905929	Unknown	-1,024	0,017
35.3	not assigned.disagreeing hits	SGN-U577015	AK324835	basic helix-loop-helix (bHLH) family protein	-1,023	0,021
35.2	not assigned.unknown	SGN-U590599	TA36485_4081	Unknown	-1,022	0,011
16.2.1.9	secondary metabolism.phenylpropanoids.lignin biosynthesis.COMT	SGN-U570023	TA54543_4081	OMT1, ATOMT1 | ATOMT1 (O-METHYLTRANSFERASE 1)	-1,020	0,011
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U569120	AK325291	ABC transporter family protein	-1,020	0,008
35.2	not assigned.unknown	SGN-U562735	AW621633	Unknown	-1,020	0,013
10.5.1	cell wall.cell wall proteins.AGPs	SGN-U571051	TA53333_4081	FLA12 | FLA12 (fasciclin-like arabinogalactan-protein 12)	-1,019	0,038
35.2	not assigned.unknown	SGN-U566021	BT014060	Unknown	-1,019	0,005
35.3	not assigned.disagreeing hits	SGN-U581841	AK246674	GATA transcription factor 1 (GATA-1)	-1,019	0,012
34.16	transport.ABC transporters and multidrug resistance systems	SGN-U565426	BG124239	ABC transporter family protein	-1,018	0,049

19.30	tetrapyrrole synthesis.urogen III methylase	SGN-U572308	AK247184	UPM1 | UPM1 (UROPHORPHYRIN METHYLASE 1)	-1,018	0,008
35.2	not assigned.unknown	SGN-U598103	AW038563	Unknown	-1,017	0,008
29.4	protein.postranslational modification	SGN-U572104	AW621950	protein kinase family protein	-1,017	0,016
21.2.1	redox.ascorbate and glutathione.ascorbate	SGN-U584821	AK321929	APX3 | APX3 (ASCORBATE PEROXIDASE 3)	-1,017	0,005
11.1.1	lipid metabolism.FA synthesis and FA elongation.Acetyl CoA Carboxylation	SGN-U588443	BG124815	AT-ACC1, EMB22, GK, PAS3, ACC1 | ACC1 (ACETYL-COENZYME A CARBOXYLASE 1)	-1,017	0,008
35.2	not assigned.unknown	SGN-U564497	AW039031	Unknown	-1,016	0,005
35.2	not assigned.unknown	SGN-U584808	AW626365	phosphatase inhibitor/ protein phosphatase inhibitor	-1,016	0,014
35.2	not assigned.unknown	SGN-U591803	BM412657	Unknown	-1,015	0,008
27.4	RNA.RNA binding	SGN-U570098	AK322725	RNA recognition motif (RRM)-containing protein	-1,015	0,008
16.8.4	secondary metabolism.flavonoids.flavonols	SGN-U575810	BT013114	2-oxoacid-dependent oxidase, putative	-1,014	0,010
17.4.1	hormone metabolism.cytokinin.synthesis-degradation	SGN-U574427	NM_001257986	ATIPT3 | ATIPT3 (Arabidopsis thaliana isopentenyltransferase 3)	-1,013	0,022
26.2	misc.UDP glucosyl and glucoronyl transferases	SGN-U576136	AK319230	glycosyltransferase family protein 47	-1,013	0,013
35.1	not assigned.no ontology	SGN-U574715	BM410715	T-complex protein 11	-1,013	0,020

35.1	not assigned.no ontology	SGN-U572002	AW036354	NLI interacting factor (NIF) family protein	-1,012	0,008
13.1.4.1	amino acid metabolism.synthesis.branched chain group.common	SGN-U572728	TA36922_4081	ketol-acid reductoisomerase	-1,011	0,008
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	SGN-U586334	AK326919	AtMYB48, MYB111 | MYB111 (myb domain protein 111)	-1,011	0,028
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING	SGN-U586092	AK247957	zinc finger (C3HC4-type RING finger) family protein	-1,011	0,010
26.10	misc.cytochrome P450	SGN-U565856	DB721811	CYP71B10 | CYP71B10 (cytochrome P450, family 71, subfamily B, polypeptide 10)	-1,011	0,009
20.2.1	stress.abiotic.heat	SGN-U579954	TA37884_4081	HSP18.2 (HEAT SHOCK PROTEIN 18.2)	-1,010	0,010
30.6	signalling.MAP kinases	SGN-U571934	TA54650_4081	ZIK2, WNK4 | WNK4 (Arabidopsis WNK kinase 4)	-1,009	0,007
27.3.9	RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family	SGN-U581840	AK247401	GATA transcription factor 1 (GATA-1)	-1,009	0,010
29.5.11.3	protein.degradation.ubiquitin.E2	SGN-U578218	GO374120	UBC28 | UBC28; ubiquitin-protein ligase	-1,009	0,018
26.10	misc.cytochrome P450	SGN-U571791	AK320675	CYP84A1, FAH1 | FAH1 (FERULATE-5-HYDROXYLASE 1)	-1,008	0,026
16.10	secondary metabolism.simple phenols	SGN-U603045	AK321674	LAC17 | LAC17 (laccase 17)	-1,008	0,011
35.3	not assigned.disagreeing hits	SGN-U578118	TA39471_4081	histone H3	-1,008	0,007
35.2	not assigned.unknown	SGN-U581847	DB693623	Unknown	-1,007	0,027

29.2.1.2.2.80	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.P0	SGN-U566987	GO376128	acidic ribosomal protein P0-related	-1,007	0,011
35.3	not assigned.disagreeing hits	SGN-U593247	AK320740	ATP binding / ATP-dependent helicase	-1,007	0,008
35.2	not assigned.unknown	SGN-U597918	BG135688	Unknown	-1,006	0,008
33.99	development.unspecified	SGN-U588723		senescence-associated protein, putative	-1,006	0,016
27.3.67	RNA.regulation of transcription.putative transcription regulator	SGN-U580791	GO373329	MSRB1 | MSRB1 (METHIONINE SULFOXIDE REDUCTASE B 1)	-1,006	0,009
35.2	not assigned.unknown	SGN-U603533	AK323647	Unknown	-1,006	0,008
35.2	not assigned.unknown	SGN-U575230	AW221705	Unknown	-1,006	0,013
29.5.5	protein.degradation.serine protease	SGN-U583067	AK326113	SCPL10 | SCPL10 (serine carboxypeptidase-like 10)	-1,005	0,018
16.8.4	secondary metabolism.flavonoids.flavonols	SGN-U565165	AK320273	oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1,004	0,005
35.2	not assigned.unknown	SGN-U598549	BW692941	Unknown	-1,004	0,014
26.3	misc.gluco-, galacto- and mannosidases	SGN-U581248	NM_001247913	BGAL1 | BGAL1 (BETA GALACTOSIDASE 1)	-1,004	0,018
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	SGN-U575946	BG124295	GL2 | GL2 (GLABRA 2)	-1,004	0,008
16.1.5	secondary metabolism.isoprenoids.terpenoids	SGN-U572432	NM_001247126	terpene synthase/cyclase family protein	-1,004	0,018

35.2	not assigned.unknown	SGN-U590745	AK321612	binding	-1,004	0,031
30.2.3	signalling.receptor kinases.leucine rich repeat III	SGN-U563814	AW216540	leucine-rich repeat transmembrane protein kinase, putative	-1,003	0,017
35.2	not assigned.unknown	SGN-U574434	AK324860	Unknown	-1,003	0,007
35.3	not assigned.disagreeing hits	SGN-U574134	AK329527	basic helix-loop-helix (bHLH) family protein	-1,002	0,013
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	SGN-U579115	NM_001247584	RAP2.12 | RAP2.12	-1,002	0,034
34.99	transport.misc	SGN-U579258	ES893462	SEC14 cytosolic factor family protein	-1,001	0,008
20.2.1	stress.abiotic.heat	SGN-U578861	NM_001247312	ATJ, ATJ3 | ATJ3 (Arabidopsis thaliana DnaJ homologue 3)	-1,001	0,008
35.2	not assigned.unknown	SGN-U568069	TA53991_4081	Unknown	-1,001	0,009
35.2	not assigned.unknown	SGN-U584709	AK247720	Unknown	-1,000	0,016