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# Transcriptomic and physiological characterization of the *fefe* mutant of melon (*Cucumis melo*) reveals new aspects of iron-copper crosstalk

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## Abstract

Iron (Fe) and copper (Cu) homeostasis are tightly linked across biology. In previous work, Fe deficiency interacted with Cu-regulated genes and stimulated Cu accumulation. The C940-*fe* (*fefe*) Fe-uptake mutant of melon (*Cucumis melo*) was characterized, and the *fefe* mutant was used to test whether Cu deficiency could stimulate Fe uptake. Wild-type and *fefe* mutant transcriptomes were determined by RNA-seq under Fe and Cu deficiency. *FeFe*-regulated genes included core Fe uptake, metal homeostasis, and transcription factor genes. Numerous genes were regulated by both Fe and Cu. The *fefe* mutant was rescued by high Fe or by Cu deficiency, which stimulated ferric-chelate reductase activity, *FRO2* expression, and Fe accumulation. Accumulation of Fe in Cu-deficient plants was independent of the normal Fe-uptake system. One of the four *FRO* genes in the melon and cucumber (*Cucumis sativus*) genomes was Fe-regulated, and one was Cu-regulated. Simultaneous Fe and Cu deficiency synergistically up-regulated Fe-uptake gene expression. Overlap in Fe and Cu deficiency transcriptomes highlights the importance of Fe-Cu crosstalk in metal homeostasis. The *fefe* gene is not orthologous to *FIT*, and thus identification of this gene will provide clues to help understand regulation of Fe uptake in plants.

**Keywords:** copper (Cu), *fefe* mutant, ferrichelate reductase, iron (Fe), iron-copper crosstalk, melon (*Cucumis melo*), metal homeostasis

## Introduction

Iron (Fe) and copper (Cu) are trace metals that are required by plants for their roles in redox metabolism, such as mitochondrial respiration, photosynthesis, and nitrogen fixation (Puig et al., 2007; Burkhead et al., 2009; Hansch & Mendel, 2009; Pilon et al., 2011). Excess Fe or Cu leads to oxidative stress and damage from reactive oxygen species (Halliwell & Gutteridge, 1992). However, Fe and Cu are both involved in protection from reactive oxygen species (Hansch & Mendel, 2009) as components of peroxidases, catalase, and superoxide dismutases (SODs). Iron-containing SODs (FeSODs) and Cu-containing SODs (CuSODs) are functionally interchangeable, but are products of different genes (Kliebenstein et al., 1998; Alscher et al., 2002; Myouga et al., 2008; Pilon et al., 2011).

Iron deficiency responses include increased expression of certain genes to increase Fe uptake and to make cellular adjustments to maintain homeostasis. The basic helix-loop-helix (bHLH) transcription factor *FIT* is required for normal regulation of Fe-uptake genes in Arabidopsis (Colangelo & Guerinot, 2004; Jakoby et al., 2004), including the ferric-chelate reductase *FRO2*, the primary Fe transporter *IRT1*, and another Fe transporter, *NRAMP1*. The *FIT* protein interacts with other Fe-regulated bHLH proteins, such as bHLH100, bHLH101, bHLH038,

and bHLH039 (Yuan et al., 2008; Wang et al., 2013), and these proteins also have regulatory roles independent of *FIT* (Sivitz et al., 2012; Wang et al., 2013). Several metal homeostasis genes respond to both Fe and Cu, such as the metal transporters *COPT2* and *ZIP2*, and the ferric-chelate reductase *FRO3* (Sancenon et al., 2003; Wintz et al., 2003; Colangelo & Guerinot, 2004; Mukherjee et al., 2006; Buckhout et al., 2009; Garcia et al., 2010; del Pozo et al., 2010; Yang et al., 2010; Stein & Waters, 2012; Waters et al., 2012). Similarly, Cu deficiency results in up-regulated ferric-chelate reductase activity in roots (Norvell et al., 1993; Welch et al., 1993; Cohen et al., 1997; Romera et al., 2003; Chen et al., 2004). Arabidopsis *FRO4* and *FRO5* are up-regulated by Cu deficiency but not by Fe deficiency (Bernal et al., 2012), and provide low-level but significant ferrichelate reductase activity.

Changes in availability of one mineral nutrient often results in changes in homeostasis of other minerals. For example, Fe deficiency caused changes in the expression of genes related to potassium and phosphate (Wang et al., 2002) and sulfate (Paolacci et al., 2013) homeostasis. Fe homeostasis interacts with Zn tolerance (Pineau et al., 2012), and Cu deficiency interacts with phosphate signaling (Perea-García et al., 2013) and cadmium tolerance (Gayomba et al., 2013). Copper concentration was higher in Fe-deficient leaves (Welch et al., 1993; Chaignon

et al., 2002; Waters & Troupe, 2012; Waters et al., 2012). Several Cu-responsive genes and microRNAs had altered abundance under Fe deficiency in *Arabidopsis thaliana* (Stein & Waters, 2012; Waters et al., 2012). This suggested that a specific role for accumulation of Cu under Fe deficiency is the replacement of FeSOD, which decreases under Fe deficiency (Kurepa et al., 1997; Waters et al., 2012), with CuSOD, whose transcripts increase in Fe-deficient leaves (Waters et al., 2012). Supporting this hypothesis, counteraction of oxidative stress was impaired when formation of functional CuSOD protein was blocked under Fe deficiency (Waters et al., 2012). Increasing evidence points to the importance of Fe-Cu crosstalk in metal homeostasis (Bernal et al., 2012; Waters et al., 2012; Perea-García et al., 2013).

Mutant lines with altered metal homeostasis are valuable tools to study molecular and physiological responses to metal stress. The *fe fe* mutation originated spontaneously in the melon (*Cucumis melo*) variety Edisto, and was crossed into the variety Mainstream to generate the C940-fe germplasm (Nugent & Bhella, 1988; Nugent, 1994). The *fe fe* mutant lacks ferric-chelate reductase activity and rhizosphere acidification (Jolley et al., 1991), two of the important mechanisms of the reductive strategy of Fe uptake in dicots and nongrass monocots. The *fe fe* mutant has chlorotic leaves typical of Fe deficiency, which can be corrected by application of external Fe. These signs point to *fe fe* as a regulator of Fe uptake, but the mutant was not fully physiologically characterized to determine if the mutation is specific to root function. Additionally, gene expression levels in *fe fe* had not been characterized.

Our overall objective in this study was to use the *fe fe* mutant to increase understanding of Fe-uptake regulation and to explore Fe-Cu crosstalk through characterization of transcriptomes of Fe- and Cu-deficient plants. Our specific goals were to physiologically characterize the *fe fe* mutant; to use the *fe fe* mutant to test whether Cu deficiency can interact with the Fe regulatory pathway to stimulate Fe accumulation; and to determine transcriptomes in wild-type (WT) and *fe fe* plants in control and Fe- or Cu-deficient conditions to identify genes that are regulated by one or both metals. Here, we show that the *fe fe* defect caused loss of normal regulation of Fe accumulation, was specific to roots, and could be rescued by Cu deficiency, which stimulated Fe uptake. Furthermore, we uncovered new synergistic interactions between Fe and Cu deficiencies on Fe-uptake processes.

## Materials and Methods

### Plant growth and materials

Seeds were purchased for cucumber (*Cucumis sativus* L.) cv Ashley (Jung Seed Co., Randolph, WI, USA) and melon (*Cucumis melo* L.) cv Edisto (Victory Seed Company, Molalla, OR, USA). Seeds of "snake melon" (PI 435288) were obtained from the USDA National Plant Germplasm System. Seeds of C940-fe (*fe fe*) melon (Nugent, 1994) were a generous gift from Michael A. Grusak, USDA-ARS Children's Nutrition Research Center, Houston, TX, USA.

Plants were grown in a continuously aerated nutrient solution with the following composition: 0.8 mM KNO<sub>3</sub>, 0.4 mM Ca (NO<sub>3</sub>)<sub>2</sub>, 0.3 mM NH<sub>4</sub>H<sub>2</sub>PO<sub>4</sub>, 0.2 mM MgSO<sub>4</sub>, 20 μM Fe(III)-

EDDHA (Sprint 138, Becker-Underwood, Ames, IA, USA), 25 μM CaCl<sub>2</sub>, 25 μM H<sub>3</sub>BO<sub>3</sub>, 2 μM MnCl<sub>2</sub>, 2 μM ZnSO<sub>4</sub>, 0.5 μM CuSO<sub>4</sub>, 0.5 μM Na<sub>2</sub>MoO<sub>4</sub> and 1 mM MES buffer (pH 5.5) or, if indicated, HEPES buffer (pH 7.1). Fe was omitted or supplied as indicated for Fe-supply treatments, and Cu was omitted or supplied as indicated for Cu-supply treatments. For N source experiments, the same micronutrients were used, with a macronutrient solution as follows: 0.7 mM K<sub>2</sub>SO<sub>4</sub>, 0.1 mM KH<sub>2</sub>PO<sub>4</sub>, 0.1 mM KCl, 0.5 mM MgSO<sub>4</sub>, and 1 mM CaCl<sub>2</sub>. Nitrogen was added at a final concentration of 2.5 mM as (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> or KNO<sub>3</sub>.

Melon and cucumber seeds were sprouted on germination paper in a 30°C incubator until transplanting to hydroponics after 4 d. Seedlings were placed in sponge holders in lids of black plastic containers, four plants per 750 ml solution. Plants were grown in a growth chamber with a mix of incandescent and fluorescent light at 300 μmol m<sup>-2</sup>s<sup>-1</sup>. For cucumber, plants were pretreated in standard solution for 5 d before nutrient treatments for 3 d. For the -Cu *fe fe* mutant rescue and WT controls, seedlings were grown without Cu from initial planting for 9 d. Plants for the +/- Cu RNA-seq experiment (Edisto and *fe fe*) were collected at 9 d. For the +/- Fe RNA-seq experiment, WT (Edisto and snake melon) and *fe fe* mutants were pretreated for 9 d on -Cu solution, and only *fe fe* mutants that had green leaves were used for treatments of 3 d duration. The purpose of the -Cu pretreatment was to use only healthy *fe fe* plants so that the transcriptome would reflect the Fe-regulated genes in *fe fe* rather than secondary effects of severe Fe deficiency. To avoid potential variation resulting from the circadian clock, sampling for ferric-chelate reductase activity or RNA was always performed between 14:00 and 16:00 h.

For grafting experiments, melon seeds were germinated and planted as described earlier. After 2 d growth in the growth chamber in complete nutrient solution, seedlings were removed from sponge holders and stems were cut at an angle above the crown. Root stocks and scions were joined with a silicon grafting clip, plants were returned to hydroponic containers and placed in a high humidity chamber under dimmed lighting (150 μmol m<sup>-2</sup>s<sup>-1</sup>) for 7 d while the grafted tissues fused. Plants were then moved to a growth chamber for 3 d before Fe treatments were applied for 3 d.

### Ferric-chelate reductase activity

Root ferric reductase assays were performed for 30–60 min on individual roots, using 30 ml of an assay solution of 0.1 mM ferrozine (3-(2-pyridyl)-5,6-diphenyl-1,2,4-triazine-4',4'-disulfonic acid sodium salt; Sigma-Aldrich), 0.1 mM Fe(III)-EDTA and 1 mM MES buffer (pH 5.5) (Fisher Scientific, Fair Lawn, New Jersey, USA). Reduced Fe was calculated using absorbance at 562 nm with the extinction coefficient 28.6 mM<sup>-1</sup> cm<sup>-1</sup>.

### Mineral analysis

Iron and Cu concentrations were determined by inductively coupled plasma mass spectrometry (ICP-MS) as described previously (Waters & Troupe, 2012). To calculate total mineral quantity in each plant part and the sum of all parts, Fe and Cu contents were calculated by multiplying concentra-

tion by organ DW. Briefly, plant tissues were dried for at least 48 h at 60°C in a drying oven. Tissues were weighed and digested overnight at room temperature in 3 ml concentrated HNO<sub>3</sub>. Samples were then heated at 100°C for 2 h, followed by addition of 3 ml H<sub>2</sub>O<sub>2</sub>, then heated stepwise to 165°C until dry. Residues were resuspended in 5 ml 1% HNO<sub>3</sub> before ICP-MS.

### cDNA identification

Primers for full-length cucumber *IRT1* (Waters et al., 2007) were used with melon cDNA as a template to amplify a PCR product that was cloned and sequenced. The melon cDNA was 96% identical to cucumber *IRT1*. This transcript was Fe-regulated as expected and was designated *CmIRT1*. A full-length ferric reductase cDNA was identified from Fe-deficient roots by a degenerate primer rapid amplification of cDNA ends (RACE) PCR strategy as described previously (Waters et al., 2002) and designated *CmFRO1*. Following release of the cucumber genome, three additional *FRO* genes were identified by BLAST: *FRO2*, Cucsa.108040.1; *FRO4*, Cucsa.260380.1 (<http://www.phytozome.net>), and *FRO3*, Csa008439 (<http://www.icugi.org>). Of these melon *FRO* genes, *FRO1* is the ortholog of Arabidopsis *FRO2*. A *FIT* homolog (Csa015217) was identified by a BLAST search against the cucumber genome, version 1 (<http://www.icugi.org/cgi-bin/ICuGI/genome/home.cgi?ver=1&organism=cucumber>). Primers designed to amplify the full cDNA also amplified a single cDNA from melon, which was 97% identical at the nucleotide level and was Fe-regulated, and was designated *CmFIT*.

### Real-time reverse transcription polymerase chain reaction (RT-PCR)

Total RNA was extracted from roots using the Plant RNeasy kit (Qiagen). RNA quality and concentration were determined by UV spectrophotometry. One microgram of DNase-treated RNA (RNase-free DNase I; New England Biolabs, Ipswich, Massachusetts, USA) was used for cDNA synthesis, using the High Capacity cDNA Reverse Transcription kit (ABI, Foster City, California, USA) with random hexamers at 2.5 μM final concentration. cDNA corresponding to 1.5–2.5 ng of total RNA was used in a 15 μl real-time PCR reaction performed in a MyIQ (Bio-Rad) thermal cycler using GoTaq qPCR Master-Mix (Promega) and 0.2 μM gene-specific primers (see the supporting information, table S1). The following standard thermal profile was used for all PCRs: 50°C for 2 min, 95°C for 8 min; 40 cycles of 95°C for 15 s, 56°C or 65°C for 15 s, and 72°C for 15 s. The *Ct* values for all genes were calculated using Bio-Rad IQ5 System Software version 2.0. Gene expression was determined by normalizing to the *Ct* value of ubiquitin using the Livak method (Livak & Schmittgen, 2001), with the equation

$$\text{Relative Expression} = 2^{-\Delta\Delta C_t},$$

where  $\Delta\Delta C_t = (C_{t_{\text{target gene}}}(\text{treatment 1}) - C_{t_{\text{target gene}}}(\text{control treatment})) - (C_{t_{\text{UBQ}}}(\text{treatment 1}) - C_{t_{\text{UBQ}}}(\text{control treatment}))$ .

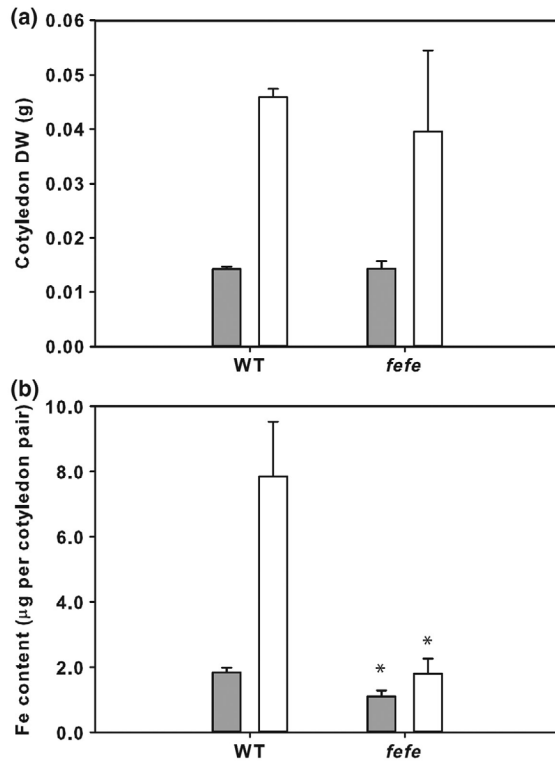
### Next-generation sequencing and bioinformatics

Sources of RNA samples were as described in the previous section. RNA-seq was performed using an Illumina HiSeq 2000 instrument. Barcoded libraries were constructed from 3 μg of root total RNA, with three biological replicate libraries per treatment. Replicates were run in separate lanes, with a total of six samples from different treatments in each lane. The reads are available as NCBI BioProject: PRJNA244361 (<http://www.ncbi.nlm.nih.gov/bioproject/244361>). Because there is high synteny between melon and cucumber, and orthologs of these species are highly collinear within large segments of chromosomes (Huang et al., 2009; González et al., 2010), the cucumber transcriptome was used as the reference for read mapping. The cucumber transcriptome sequence reference (cucumber\_v2.cds.gz) was obtained from the cucurbit genomics database (<ftp://www.icugi.org/pub/genome/cucumber/v2/>). Sequencing reads from each sample were mapped to the reference database using BOWTIE2 (Langmead & Salzberg, 2012) with -local -N 1 options and cleaving 15 bp from each end of the reads. The BOWTIE2 output bam files were converted to sam format using SAMtools (Li et al., 2009). Perl scripts were written to extract read counts from the sam files and to create a read count data matrix. The data matrix was imported into R and analyzed using the Bioconductor package edgeR (Robinson et al., 2010). Read counts in each library were normalized to account for the library size using the calcNormFactors function, and tag-wise dispersions were estimated by using an empirical Bayes estimate, which is dependent on the initial dispersion estimates, through the estimateGLMTagwiseDisp and estimateGLM-TrendedDisp functions, respectively. Differential expression was called for genes with an false discovery rate moderated *q*-value < 0.05 (Benjamini & Hochberg, 1995), and also showed a 1.0 log fold-change in expression and > 20 reads in at least one treatment.

## Results

### Physiological characterization the *fefe* mutant

When grown in standard nutrient solution, *fefe* cotyledons are green, but the first true leaf is chlorotic. We first corroborated previous reports (Nugent & Bhella, 1988; Nugent, 1994) that additional Fe supply could reverse leaf chlorosis. When three to five 2 μl droplets of 5 mM Fe(III)-EDDHA were applied to the second true leaf, that leaf and the emerging third true leaf had become green 36 h later (fig. S1). Other forms of Fe also led to re-greening of *fefe* leaves, including ferric-EDTA, ferric citrate, ferric ammonium sulfate, and ferric nitrate, demonstrating that additional Fe was sufficient for reversal of the phenotype. A second test was to increase Fe availability in hydroponics by manipulating the nutrient solution in two ways. First, we used MES or HEPES buffer to maintain the solution at pH 5.0 or 7.1, respectively, while supplying either 1 or 20 μM Fe. In the WT, these treatments had no discernible effect on leaf color (fig. S1). The first leaf of *fefe* was chlorotic in all treatments except the low pH and high Fe combination. A second manipulation of the nutrient solution was to grow plants

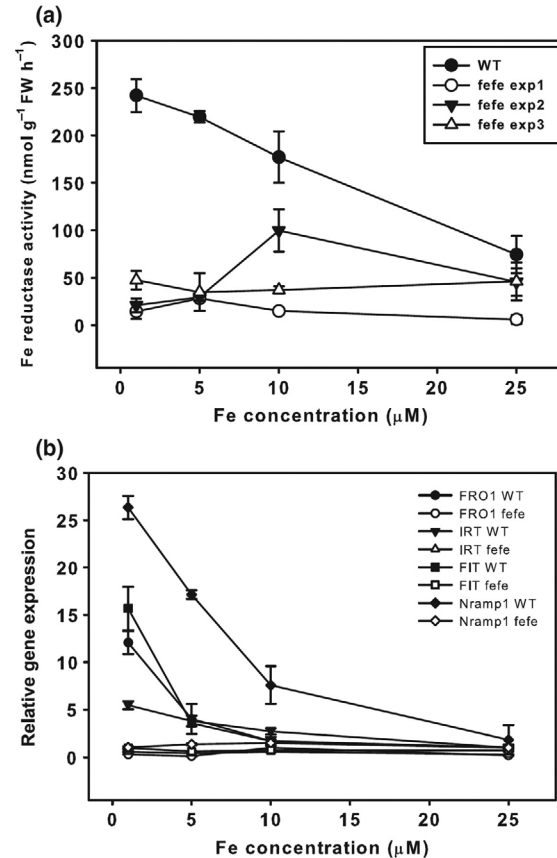


**Figure 1.** Accumulation of iron (Fe) during seedling early growth of *Cucumis melo*. (a) DW of wild-type (WT) and *fefe* mutant cotyledon pairs ( $\pm$  SD) at planting (d0, closed bars) and after 6 d of growth on complete nutrient solution (10  $\mu$ M Fe, 0.5  $\mu$ M Cu; open bars). (b) Fe content of cotyledon pairs ( $\pm$  SD) of WT and *fefe* mutant cotyledons at planting (d0; closed bars) and after 6 d growth (open bars) on complete solution. Significant difference between WT and *fefe*, \* $P < 0.05$ .

with either nitrate ( $\text{NO}_3^-$ ) or ammonium ( $\text{NH}_4^+$ ) as the sole N source. On  $\text{NO}_3^-$ , *fefe* plants had the usual chlorotic first leaf, whereas on  $\text{NH}_4^+$ , the first true leaf was green. Uptake of  $\text{NH}_4^+$  uses a  $\text{H}^+$  antiport mechanism (von Wieren et al., 2000), resulting in net efflux of  $\text{H}^+$  into the nutrient solution, which in this case lowered the pH to  $< 4.0$  and shifted Fe to the more readily available ferrous form. These manipulations support the idea that the defect in *fefe* is specific to Fe uptake.

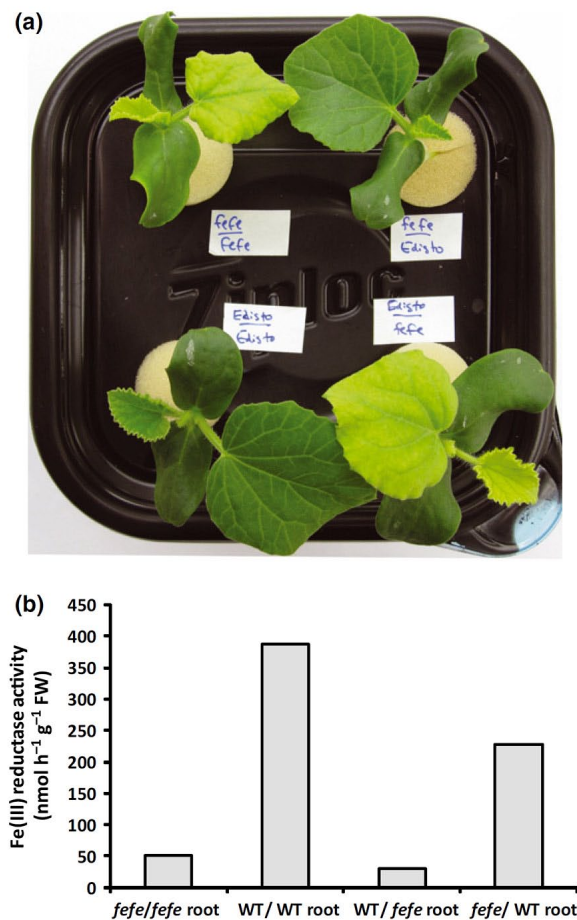
In previous work we showed that cucumber cotyledons grow (e.g., increase in DW) and accumulate Fe and certain other minerals over the first few days after germination (Waters & Troupe, 2012). To test whether *fefe* accumulated Fe or utilized Fe stored in cotyledons, we measured DW and Fe content of cotyledons in the WT and the *fefe* mutant (fig. 1). Cotyledons of *fefe* at germination were of a similar size to the WT (fig. 1a), and had slightly lower Fe content (fig. 1b). Cotyledons of *fefe* grew similarly to those of the WT, as evidenced by increased DW from germination to 6 d later. However, WT cotyledons gained over 5  $\mu$ g of Fe, while *fefe* cotyledons did not gain significant amounts of Fe, nor did they decrease in Fe, demonstrating that *fefe* seedlings did not accumulate Fe from the nutrient solution during early growth.

To corroborate previous reports that *fefe* roots do not induce ferric-chelate reductase activity, mutant and WT plants were grown on a range of Fe concentrations. WT roots had high ferric-chelate reductase activity at low Fe supply, but *fefe*



**Figure 2.** The *fefe* mutant of *Cucumis melo* does not up-regulate iron (Fe)-uptake genes. (a) Root ferric-chelate reductase activity ( $\pm$  SD) after 3 d of treatment. The figure shows a representative experiment of wild-type (WT) and three separate experiments of *fefe* roots over a range of Fe concentrations. (b) Quantitative real-time reverse transcription polymerase chain reaction (RT-PCR) for *FRO1*, *FIT*, *Nramp1*, and *IRT1* in WT and *fefe* mutant roots. Relative expression as normalized to ubiquitin and the WT at 25  $\mu$ M Fe.

had low activity at all Fe concentrations (fig. 2a), demonstrating that inducible ferric-chelate reductase activity is diminished in *fefe*. However, on some occasions, ferric-chelate reductase activity was somewhat elevated in *fefe* (e.g., Expt 2, 10  $\mu$ M), which indicated that the ferric-chelate reductase protein is functional, but not properly regulated. This led to the question of whether the *fefe* defect is specific to ferric reductase, or whether other Fe-uptake components are not expressed normally. To address this, we identified orthologs of Arabidopsis *FRO2*, *IRT1*, *Nramp1* and *FIT* in melon and designed primers to measure transcript abundance by real-time RT-PCR. These genes were up-regulated in low-Fe conditions in WT, but not in *fefe* (fig. 2b), suggesting that the *fefe* defect could be in the *FIT* gene, as melon *FIT* should regulate melon *FRO1* (the Arabidopsis *FRO2* ortholog) and *IRT1* as in Arabidopsis and tomato (Ling et al., 2002; Colangelo & Guerinot, 2004). Sequencing of *FRO1* and *IRT1* cDNAs, and genomic DNA of *FIT* in both WT and *fefe* mutants did not reveal any polymorphisms that would result in premature stop codons or frame shifts, or amino acid changes that would be expected to abolish protein function, suggesting that the *fefe* gene is a regulator of Fe uptake that acts upstream of the primary Fe-uptake genes and the *FIT* transcription factor.

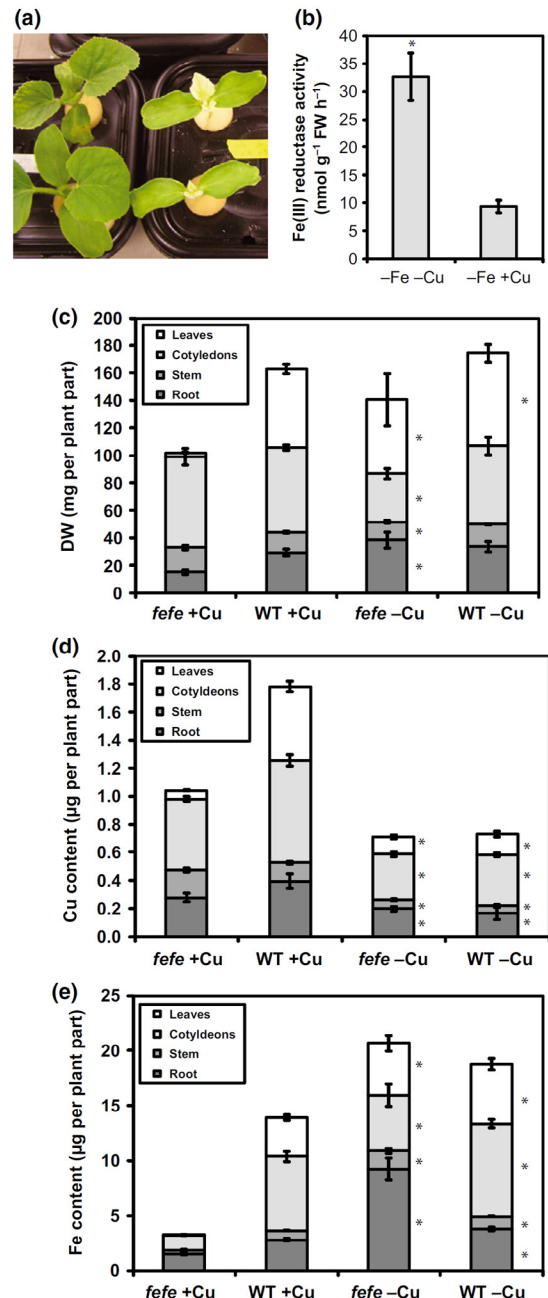


**Figure 3.** The *fefe* defect is localized to the roots of *Cucumis melo* as determined by grafting. (a) Shoot phenotype of grafted plants. Upper left, *fefe* scion grafted to *fefe* rootstock; upper right, *fefe* scion grafted to WT (Edisto) rootstock; lower left, wild-type (WT) scion grafted to WT rootstock; lower right, WT scion grafted to *fefe* rootstock. (b) Root ferric-chelate reductase activity after transferring individual plants shown in (a) to  $-Fe$  solution for 3 d. The x-axis indicates the scion first and the rootstock second.

As further characterization of the *fefe* mutant, we determined whether the defect was localized to roots or shoots. Reciprocal grafting was conducted with *fefe* and the parental WT Edisto roots or shoots, and as controls each genotype was grafted to itself. Grafted plants with *fefe* roots were chlorotic, with either *fefe* or Edisto shoots, whereas *fefe* shoots were of a normal green color if grafted to WT rootstock (fig. 3). Also, *fefe* roots of these plants did not induce ferric-chelate reductase activity regardless of shoot genotype. These results indicate that the *fefe* defect is in a regulatory component of the root system, and could result from an inability to receive a signal from the shoots, or from a signal transduction defect resulting in failure to respond and activate physiological and gene expression responses.

#### Can Cu deficiency stimulate Fe accumulation?

As low Fe supply caused plants to accumulate additional Cu in leaves (Welch et al., 1993; Chaignon et al., 2002; Waters & Troupe, 2012; Waters et al., 2012), we hypothesized that under low Cu supply there would be a higher demand for Fe, which

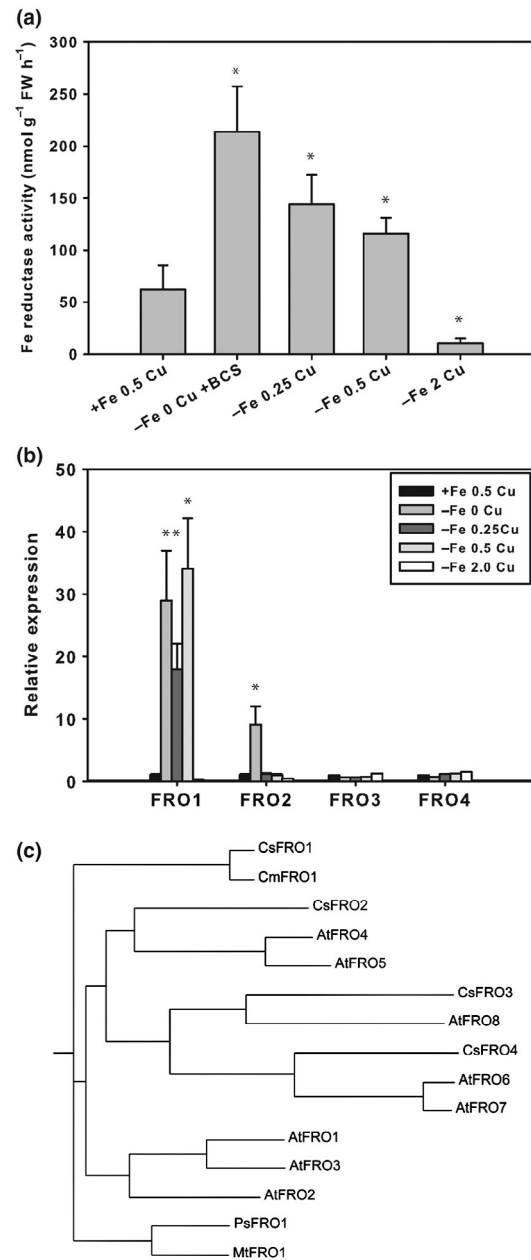


**Figure 4.** Copper (Cu) deficiency of *Cucumis melo* stimulates iron (Fe) uptake and rescues the *fefe* phenotype. (a) Photograph of *fefe* plants grown without Cu (left) and on complete nutrient solution (right). (b) Root ferric-chelate reductase activity ( $\pm$  SD) after transferring rescued *fefe* plants to  $-Fe-Cu$  or  $-Fe+Cu$  solution for 3 d. (c–e) Stacked bar graphs of DW (c), Cu content (d), and Fe content (e) of plant parts for *fefe* and wild-type (WT) plants ( $\pm$  SE) grown with or without Cu. Significant difference between +Cu and  $-Cu$  treatments: \*,  $P < 0.05$ .

should lead to increased Fe uptake and rescue the *fefe* phenotype. This hypothesis was correct, as *fefe* plants grown without Cu (+Fe,  $-Cu$ ) recovered within 9 d and had a green first leaf phenotype, while plants grown on complete solution (+Fe, +Cu) had the typical yellow first leaf (fig. 4a). We then asked whether ferric-chelate reductase activity was increased in the *fefe* plants under Cu deficiency. When rescued *fefe* plants

(green first leaf) were transferred to  $-Fe-Cu$  or  $-Fe+Cu$  treatments for 3 d, an approx. threefold increase in root ferric-chelate reductase activity was observed in the  $-Cu$  treatment (fig. 4b), although total activity was substantially lower than is typically seen in WT Fe-deficient roots. We also dissected *fefe* and WT plants grown with or without Cu for 12 d for mineral content analysis to determine the total quantity of Fe and Cu in the plants. The biomass of the plant parts showed that *fefe* primarily affected growth of the first leaf (fig. 4c). In  $-Cu$  treatments, Cu content (fig. 4d) was similar in both genotypes, and lower than plants in the  $+Cu$  treatment. In the control solution, the total plant Cu content was lower in *fefe* mutants than in the WT, primarily as a result of smaller leaves. There was no difference in Cu content between *fefe* and the WT in the  $-Cu$  treatment. The total Fe content was much lower in *fefe* plants grown in complete solution, and this was most pronounced in leaves (fig. 4e). The *fefe* and WT plants had a similar total quantity of Fe when Cu was withheld and *fefe* had recovered, demonstrating that Fe accumulation was stimulated by Cu deficiency. WT plants also accumulated more Fe under  $-Cu$  than under  $+Cu$  conditions (fig. 4e), even though DW was similar (fig. 4c). Thus, the stimulation of Fe accumulation by Cu deficiency in the whole plant, which by definition would require increased uptake, occurred in both WT and *fefe* mutant plants.

Because both WT and *fefe* plants accumulated additional Fe under Cu deficiency, and Cu-deficient *fefe* plants had increased ferric-chelate reductase activity (fig. 4), we determined which *FRO* gene(s) responded to each metal. We first addressed this question in cucumber, as the cucumber and melon genomes are highly homologous (Huang et al., 2009; González et al., 2010), and the cucumber genome has been sequenced (Huang et al., 2009) and annotated. Plants were treated with complete or  $-Fe$  solutions with a range of Cu concentrations, because ferric-chelate reductase activity is sensitive to Cu supply (Waters & Armbrust, 2013). Root reductase activity was highest in  $-Fe-Cu$  roots, and was slightly lower as Cu was supplied at 0.25 and 0.5  $\mu M$  (fig. 5a). Expression of *FRO1*, the primary ferric-chelate reductase (Waters et al., 2007), was elevated at 0, 0.25, and 0.5  $\mu M$  Cu (fig. 5b). Ferric-chelate reductase activity decreased as Cu supply increased, and did not tightly correspond to *FRO1* expression, which did not decrease at 0.5  $\mu M$  Cu. However, at 2.0  $\mu M$  Cu, both root ferric-chelate reductase activity and *FRO1* expression were abolished, and had lower values than those of control ( $+Fe$ , 0.5  $\mu M$  Cu) roots. The  $-Fe$  2.0  $\mu M$  Cu treated roots may have been suffering from Cu toxicity, as Cu is toxic at lower concentrations in Fe-deficient roots (Waters & Armbrust, 2013). The other three *FRO* genes in the cucumber genome have not been previously characterized. *FRO3* and *FRO4* were not elevated over control in any of the treatments, suggesting that they are not regulated by Fe or Cu status. However, *FRO2* was up-regulated in the  $-Fe-Cu$  treatment, but not in the  $-Fe+Cu$  treatments, demonstrating that *FRO2* is regulated by Cu status. This gene is also most closely related to Arabidopsis *FRO4* and *FRO5* (fig. 5c), which are Cu-regulated Cu(II) reductases involved in Cu uptake (Bernal et al., 2012).



**Figure 5.** Iron (Fe) and copper (Cu) regulation of cucumber (*Cucumis sativus*) *FRO* genes. (a) Root ferric-chelate reductase activity ( $\pm$  SD) after 3 d of treatment for control ( $+Fe$ , 0.5  $\mu M$  Cu) and  $-Fe$  with a range of Cu supplies. (b) Quantitative real-time reverse transcription polymerase chain reaction (RT-PCR) of expression ( $\pm$  SD) of four cucumber *FRO* genes from the plants in (a). Significant difference between control and treatments: \*,  $P < 0.05$ . (c) Phylogenetic tree drawn from ClustalW alignment of *FRO* protein sequences from cucumber (Cs), melon (Cm), Arabidopsis (At), *Pisum sativum* (Ps), and *Medicago truncatula* (Mt).

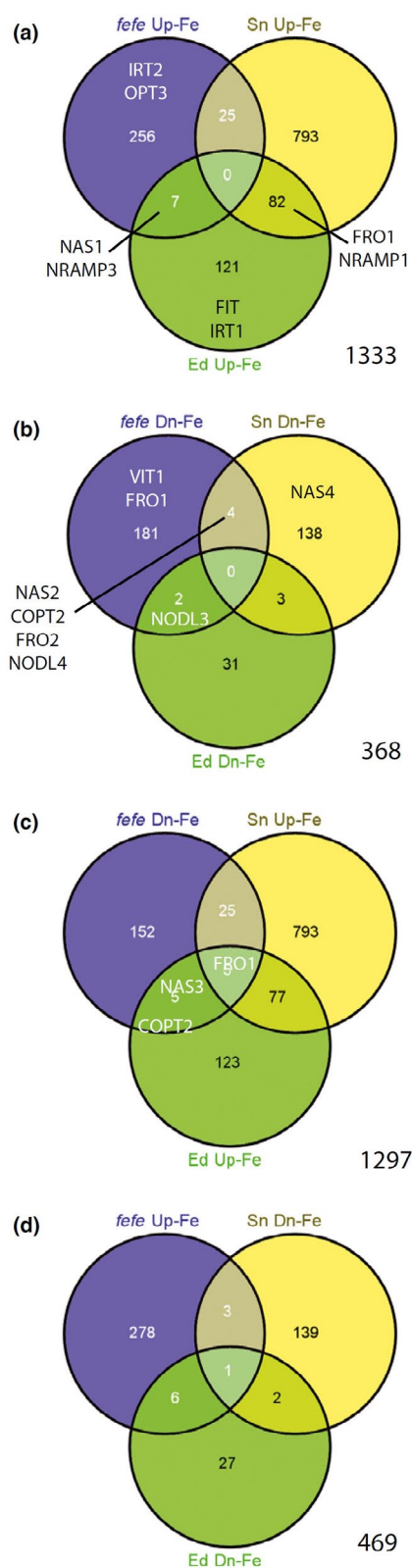
#### Transcriptomic characterization of Fe- and Cu-regulated genes

As Fe homeostasis is disrupted in the *fefe* mutant and the *fefe* phenotype is rescued by Cu deficiency, we next performed RNA-seq transcriptome analysis of *fefe* and WT roots under

control (+Fe, +Cu) conditions and Fe and Cu deficiency. To determine Fe-deficiency differentially expressed genes, we used the *fefe* mutant and two WT lines, Edisto and snake melon. The total number of Fe-deficiency up-regulated genes (1333) combined from all three genotypes (fig. 6) exceeded the number of downregulated genes (368); 91% of up-regulated genes and 98% of the Fe-deficiency down-regulated genes had differential expression in roots of only one genotype, similar to a previous microarray study with three accessions of Arabidopsis (Stein & Waters, 2012). Of Fe-deficiency up-regulated genes (fig. 6a), none were up-regulated in all three genotypes, and seven and 25 were up-regulated in *fefe* and Edisto, and *fefe* and snake melon roots, respectively (table S2). Eighty-two genes were up-regulated in the two WT plants but not in *fefe* (table S3). These genes reflect loss of regulation in *fefe* and probably include most or all of the *fefe*-regulated transcriptome. The genes that were up-regulated by Fe deficiency in only one genotype are shown in table S4. Of the Fe-deficiency down-regulated genes (fig. 6b), none were down-regulated in roots of all three genotypes, while two and four were down-regulated in *fefe* and Edisto, and *fefe* and snake melon, respectively, and three were down-regulated in both WT roots (table S5). Genes that were down-regulated in Fe-deficient roots in only one genotype are shown in table S6. We also noted that many genes that were up-regulated in one or both of the two WT roots were significantly down-regulated in *fefe* (fig. 6c). This opposite regulation pattern was present for five genes that were up-regulated in both WT roots, and for 25 and five genes that were up-regulated in snake melon and Edisto, respectively (table S7). For the other opposite expression pattern, genes up-regulated in *fefe* and downregulated in the WT roots (fig. 6d), one gene was down-regulated for both WT roots and up-regulated in *fefe*, and three and six genes were down-regulated in snake melon and Edisto, respectively (table S7).

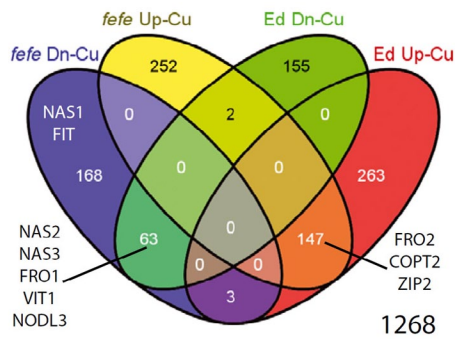
We also used RNA-seq to quantify changes in root transcript abundance in *fefe* and the WT Edisto in response to 9 d of Cu deficiency (fig. 7). In common to both WT and *fefe*, 147 genes were up-regulated and 63 were down-regulated (table S8). Of Cu-deficiency-regulated genes, 16.6% had the same expression pattern in both mutant and WT plants, which was substantially greater than the 1.5% of Fe-regulated genes that were in common between *fefe* and Edisto specifically (fig. 6), suggesting that the root Cu transcriptome is not as drastically affected by the *fefe* mutation as the root Fe transcriptome. Additionally, only five genes had opposite regulation patterns (e.g., up-regulated in one genotype and down-regulated in the other) under Cu deficiency (table S8). Supplementary table are presented for genes that were up-regulated (table S9) or down-regulated (table S10) in only one genotype.

We next compared the Fe- and Cu-deficiency differentially expressed genes to determine which genes were regulated by both metals in roots (fig. 8). We identified 83 genes of 1312 (6.3%) that were up-regulated by both Fe and Cu in various combinations (fig. 8a, table S11). Twenty-nine out of 677 genes (4.2%) were down-regulated by Fe and/or Cu deficiency in either or both *fefe* and Edisto (fig. 8b, table S12). To determine potential effects of Fe and Cu deficiencies on metal homeostasis, we focused on genes from known metal-related gene families. Cucumber coding sequence annotations from

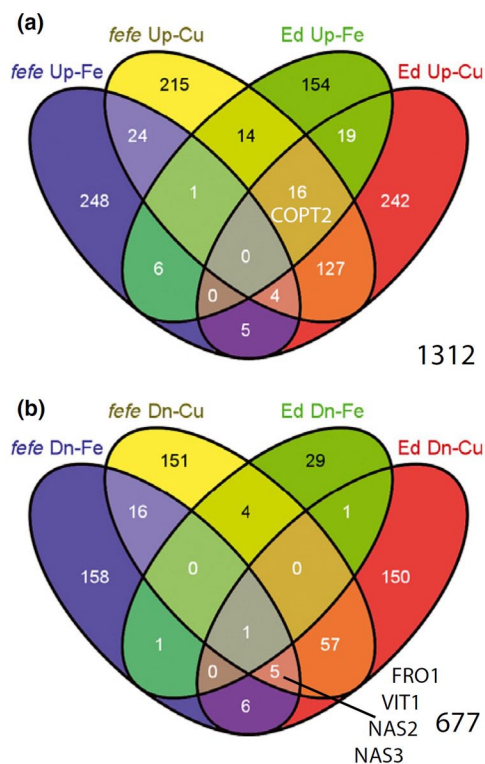


**Figure 6.** Venn diagrams for iron (Fe)-regulated genes in *fefe* and two wild-type (WT) *Cucumis melo* accessions, Edisto (Ed) and snake melon (sn). Genes of interest are shown in the appropriate set or overlap of sets. (a) Genes up-regulated (Up) under Fe deficiency; (b) genes down-regulated (Dn) under Fe deficiency; (c) genes down-regulated in *fefe* and up-regulated in WT plants; (d) genes up-regulated in *fefe* and down-regulated in WT plants.





**Figure 7.** Venn diagram of genes up-regulated (Up) or down-regulated (Dn) under copper (Cu) deficiency in *fefe* or wild-type (WT) Edisto (Ed) *Cucumis melo* roots. Genes of interest are shown in the appropriate set or overlap of sets.



**Figure 8.** Venn diagrams to identify number of overlapping genes in iron (Fe)- and copper (Cu)-regulated genes of *Cucumis melo* roots. (a) Genes up-regulated (Up) in *fefe* and Edisto (Ed) under Fe deficiency and/or Cu deficiency; (b) genes down-regulated (Dn) in *fefe* and Edisto (Ed) under Fe deficiency and/or Cu deficiency. Genes of interest are shown in the appropriate set or overlap of sets.

the ICuGI database, based on the closest *Arabidopsis thaliana* BLAST hit, were organized by gene family. Normalized read counts for each significantly up-regulated or down-regulated gene are presented in table 1. Notably, several genes of the classical strategy I Fe deficiency response (orthologs of *FRO2*, *IRT1*, *Nramp1* and *FIT*) were up-regulated in one or both WT, but were not up-regulated or were down-regulated in *fefe*. Notably, the *IRT* gene in melon that was most orthologous to *AtIRT1* function was most homologous to Arabidopsis *AtIRT2* sequence.

### Synergy between Fe and Cu regulation of Fe-uptake genes

We next examined Fe and Cu regulation of root ferric-chelate reductase activity and used real-time RT-PCR to measure expression of the melon *IRT1*, *FRO1*, *FRO2*, *FIT*, *Nramp1*, and *COPT2* genes to determine whether the combination of Fe and Cu deficiencies acted synergistically. WT and *fefe* plants grown on control (+Fe+Cu) solution had low ferric-chelate reductase activity (fig. 9a) and baseline gene expression (fig. 9b–g). As before, *fefe* roots did not increase ferric-chelate reductase activity under –Fe+Cu conditions, and did not have elevated *FRO1* expression, while WT roots had high ferric-chelate reductase activity and high expression of *FRO1*. Under the +Fe–Cu treatment, ferric-chelate reductase activity was elevated in both *fefe* and WT, and *FRO2* expression was increased in both *fefe* and WT roots, similar to the cucumber results (fig. 5). *FIT* expression increased in both genotypes under –Fe+Cu treatment but not in the +Fe–Cu treatment (fig. 9b), suggesting that *FRO2* expression was responsible for most of the ferric-chelate reductase activity in Cu-deficient roots in a *FIT*-independent manner. This also suggested that *fefe* roots can sometimes increase *FIT* expression, but this alone is not enough to induce *FRO1* (fig. 9c) or root ferric-chelate reductase activity. Ferric-chelate reductase activity was highly elevated under the simultaneous –Fe–Cu treatment in both WT and *fefe*, and *FIT* and *FRO1* expression were elevated in *fefe*. Both WT and *fefe* also had up-regulated *FRO2* expression in the –Fe–Cu treatment. These results show that *fefe* is unable to up-regulate *FRO1* normally, that is, under Fe deficiency, but can up-regulate *FRO1* under simultaneous Fe and Cu deficiency. Also, these results demonstrate that *FRO2* is a Cu-regulated gene that encodes a protein with ferric-chelate reductase activity and is regulated by Cu. *IRT1* was slightly (approx. twofold) up-regulated in the –Fe–Cu and –Fe+Cu treatments (fig. 9e), and more highly under simultaneous Fe and Cu deficiency, especially in *fefe*. *Nramp1* was up-regulated only in WT roots by Fe deficiency (fig. 9f), and only in *fefe* by simultaneous Fe and Cu deficiency. *COPT2* was up-regulated in both genotypes in response to Fe deficiency and responded strongly to simultaneous Fe and Cu deficiencies (fig. 9g).

### Discussion

The overall objective of this study was to use the *fefe* mutant as a tool to increase understanding of Fe-uptake regulation and how Fe–Cu crosstalk influences Fe-uptake regulation. Here, we showed that the *fefe* lesion is specific to roots and *FeFe* is required for normal expression of Fe-uptake genes, but is not homologous to *FIT*. Thus, *fefe* probably encodes a transcription factor or signaling molecule that functions upstream of *FIT* and Fe-uptake gene regulation. We also demonstrated Cu-regulated, *fefe*-independent Fe accumulation, by showing that Cu deficiency stimulates *FRO2* expression and plant Fe accumulation in quantities sufficient to reverse the *fefe* phenotype but not up-regulation of *FIT* or *FRO1*. Simultaneous Fe and Cu deficiencies acted synergistically in the *fefe* mutant to restore ferric-chelate reductase activity and allow expression of *FRO1*.

**Table 1.** Gene expression in wild-type (WT) melon (*Cucumis melo*) and *fefe* roots. RNA-seq reads were mapped to cucumber transcripts (Cucumber Locus ID)

Melon gene name	Cucumber locus ID	Top <i>Arabidopsis thaliana</i> hit	Normalized read counts														
			Log FC (-Fe/+Fe)		Log FC (-Cu/+Cu)		WT (Ed)		WT (sn)		WT (Edisto)		WT (snake)		WT (Edisto)		
			<i>fefe</i>	WT (Ed)	<i>fefe</i>	WT	+Fe	-Fe	+Fe	-Fe	+Fe	-Fe	+Fe	-Fe	+Cu	-Cu	+Cu
<b>Ferric reductase/oxidase family</b>																	
	Csa3M845500.1	AT5G47910.1 RBOHD (RESPIRATORY BURST OXIDASE HOMOLOGUE D); NAD(P)H oxidase	-1.7	4.3	1.1	1.2	1.7	1346	1976	3650	6671	7516	15847	6058	11256	1066	3005
FRO1	Csa5M175770.1	AT1G23020.1 FRO3; ferric-chelate reductase	-1.7	4.3	2.7	-5.0	-3.3	500	154	410	8058	291	1813	1737	44	1147	123
FRO2	Csa3M183380.1	AT5G23980.1 FRO4 (FERRIC REDUCTION OXIDASE 4); ferric-chelate reductase	-2.1		-2.6	3.8	2.6	2861	663	1004	1678	105	17	201	2424	1894	9337
	Csa1M423270.1	AT2G24520.1 AHA5 (Arabidopsis H(+)-ATPase 5); ATPase	1.1		1.1			6572	8012	5025	10303	4560	7387	4229	3279	6239	4469
<b>Metal transporters</b>																	
Nramp3	Csa2M423700.1	AT2G23150.1 NRAMP3 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 3); inorganic anion transmembrane transporter/manganese ion transmembrane transporter/metal ion transmembrane transporter	1.1	1.2				6111	13055	1241	2713	1609	2236	2468	1711	994	709
Nramp1	Csa6M382880.1	AT1G0830.1 NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inorganic anion transmembrane transporter/manganese ion transmembrane transporter/metal ion transmembrane transporter	3.7	1.7				174	84	775	9703	1688	5438	167	89	3078	1280
IRT1	Csa1M707110.1	AT4G19680.2 IRT2; iron ion transmembrane transporter/zinc ion transmembrane transporter	1.4			-2.5		386	248	428	1117	246	473	801	128	614	395
IRT2	Csa6M517980.1	AT4G19690.2 IRT1 (iron-regulated transporter 1); cadmium ion transmembrane transporter/copper uptake transmembrane transporter/iron ion transmembrane transporter/manganese ion transmembrane transporter/zinc ion transmembrane transporter	3.0					12	103	3	4	6	9	1	1	2	1

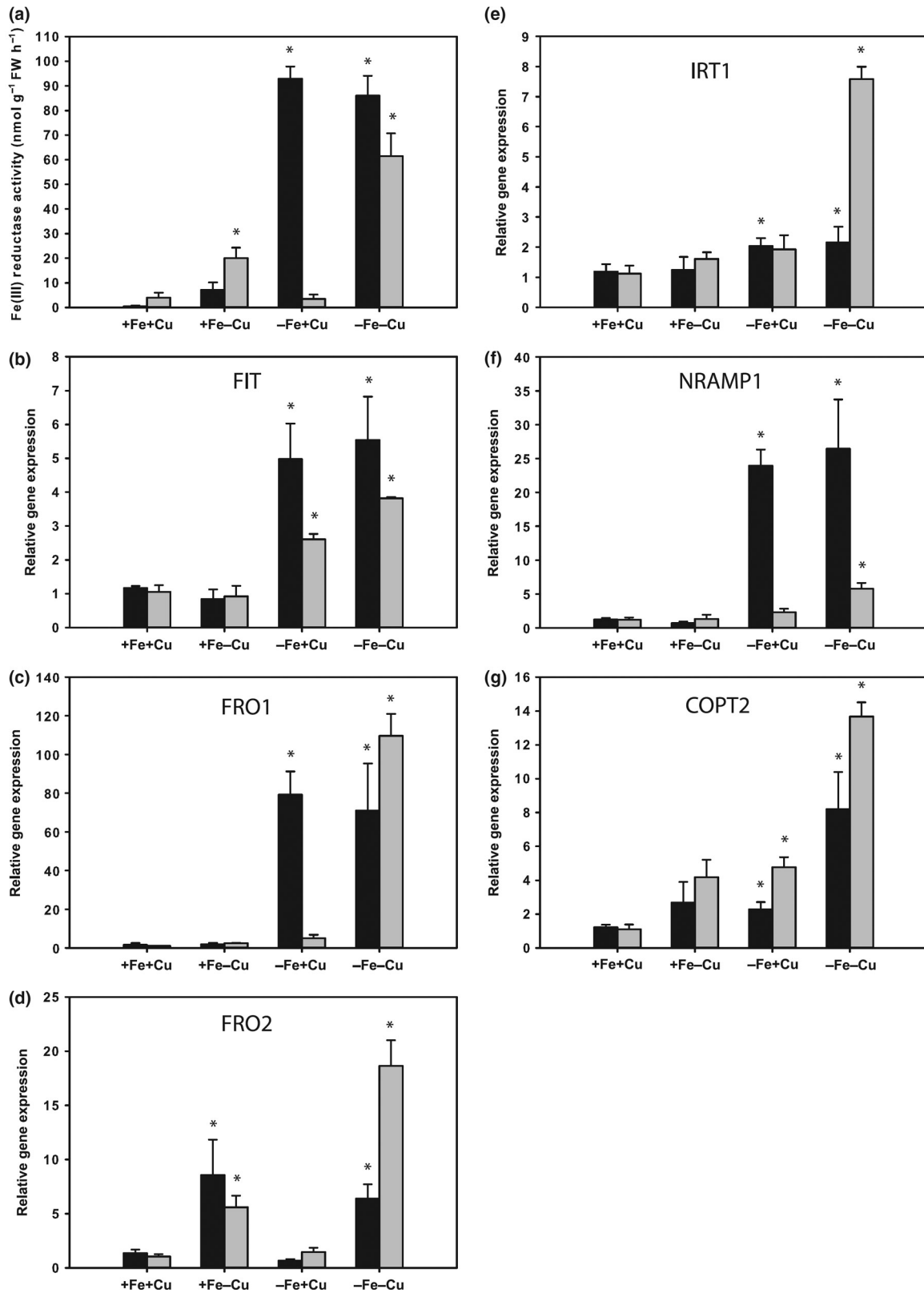
Table 1 (Continued)

Melon gene name	Cucumber locus ID	Top <i>Arabidopsis thaliana</i> hit	Normalized read counts													
			Log FC (-Fe/+Fe)		Log FC (-Cu/+Cu)		Log FC (Ed)		Log FC (sn)		Log FC (Edisto)		Log FC (snake)		Log FC (Edisto)	
			<i>fefe</i>	WT (Ed)	<i>fefe</i>	WT (Ed)	<i>fefe</i>	WT (Ed)	<i>fefe</i>	WT (sn)	<i>fefe</i>	WT (Edisto)	<i>fefe</i>	WT (snake)	<i>fefe</i>	WT (Edisto)
ZIP2	Csa7M162550.1	AT5G59520.1 ZIP2; copper ion transmembrane transporter/transferase, transferring glycosyl groups/zinc ion transmembrane transporter			1.3	2.2	140	72	54	46	78	81	42	43	170	
ZIP5	Csa4M618490.1	AT1G05300.1 ZIP5; cation transmembrane transporter/metal ion transmembrane transporter		-1.0		83	81	402	457	173	162	25	31	140	55	
COPT2	Csa1M526820.1	AT3G46900.1 COPT2; copper ion transmembrane transporter/high affinity copper ion transmembrane transporter	-2.5	1.8	1.4	1.7	278	49	57	194	47	15	87	179	515	
	Csa3M696860.1	AT3G08040.1 FRD3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter/transporter		-3.9	-2.4	65	50	3	19	179	12	20	3	6	14	
	Csa7M428170.1	AT3G08040.1 FRD3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter/transporter	1.3			1425	1322	792	1860	1269	1390	1543	774	2211	1417	
	Csa3M180310.1	AT4G23030.1 MATE efflux protein-related	1.0	1.1	1.3	74	70	158	316	304	620	741	1464	70	423	
	Csa2M404760.1	AT1G65730.1 YSL7 (YELLOW STRIPE LIKE 7); oligopeptide transporter	1.0			1129	633	1660	1335	2345	4611	332	333	602	436	
	Csa2M404780.1	AT1G48370.1 YSL8 (YELLOW STRIPE LIKE 8); oligopeptide transporter	1.0			71	44	124	108	183	366	27	31	47	43	
	Csa3M238100.1	AT5G53550.1 YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	-1.2	1.1	1.7	416	289	155	114	318	140	149	272	144	404	
	Csa1M329900.1	AT5G53550.1 YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	-1.5			103	37	19	14	37	44	8	14	16	25	
OPT3	Csa1M180750.1	AT4G16370.1 ATOPT3 (OLIGOPEPTIDE TRANSPORTER); oligopeptide transporter	2.1			3299	14592	457	872	484	742	1448	740	201	241	
Nicotianamine synthase family																
NAS1	Csa2M034520.1	AT5G04950.1 NAS1 (NICOTIANAMINE SYNTHASE 1); nicotianamine synthase	2.4	2.0	-2.7	501	2731	21	86	17	9	166	22	42	18	

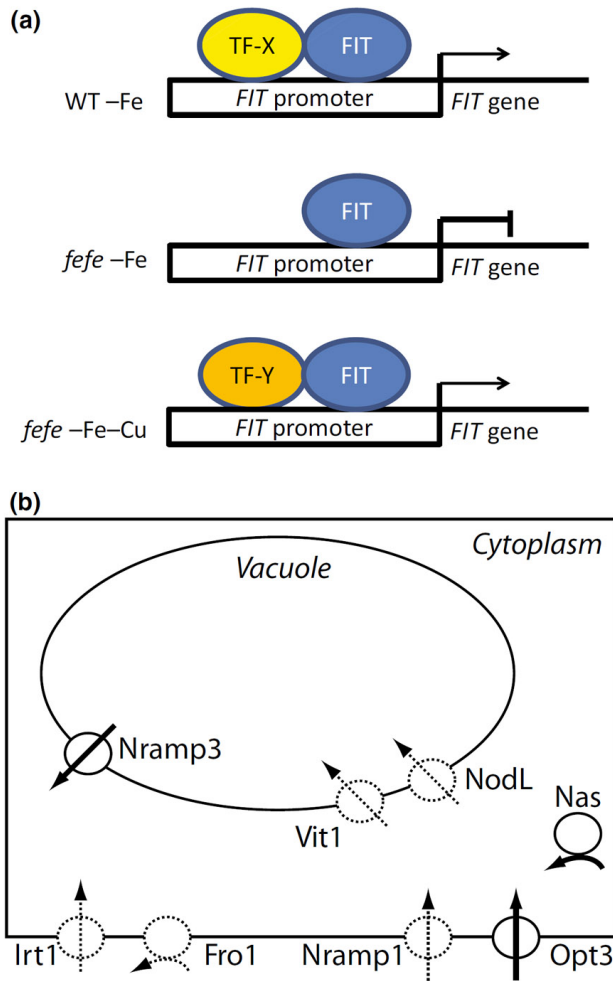
Table 1 (Continued)

Melon gene name	Cucumber locus ID	Top <i>Arabidopsis thaliana</i> hit	Normalized read counts													
			Log FC (-Fe/+Fe)		Log FC (-Cu/+Cu)		WT (sn)		WT (Edisto)		WT (snake)		WT (Edisto)			
			<i>fe</i>	<i>fe</i>	<i>fe</i>	<i>fe</i>	WT	WT	+Fe	-Fe	+Fe	-Fe	+Cu	-Cu		
NAS2	Csa1M423010.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase	-5.3	-1.4	-5.1	-4.4	3	522	210	57	21	80	2	1057	50	
NAS3	Csa2M034530.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase	-1.8	2.2	-3.5	-3.2	44	271	1215	602	469	324	23	520	54	
NAS4	Csa1M561410.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase	-2.2	-2.2	-3.3	-1.7	81	75	39	80	17	92	8	54	14	
VIT1 family																
VIT1	Csa5M550240.1	AT2G01770.1 VIT1 (vacuolar iron transporter 1); iron ion trans-membrane transporter	-3.4	-1.8	-1.8	-1.3	9	567	347	129	131	178	42	244	89	
NODL1	Csa1M288020.1	AT4G30420.1 nodulin MtN21 family protein	-1.8	1.1	-1.8	-1.3	98	1659	2205	1093	2324	104	118	65	36	
NODL2	Csa3M835770.1	AT5G40240.1 nodulin MtN21 family protein	-1.1	1.1	-1.1	-1.1	101	135	47	41	87	66	79	37	26	
NODL3	Csa6M411280.1	AT3G25190.1 nodulin, putative	-4.6	-1.8	-1.4	-1.0	62	295	80	124	68	153	48	928	392	
NODL4	Csa7M325150.1	AT3G43660.1 nodulin, putative	-2.7	-1.3	-2.7	-1.3	35	5	37	27	11	31	24	64	64	
Ferritin																
	Csa5M215130.1	AT2G40300.1 ATFER4 (ferritin 4); binding/ferric iron binding/oxido-reductase/transition metal ion binding	-1.2	-1.2	2.4	2.4	422	320	950	407	817	923	525	371	574	549
Transcription factors																
	Csa1M074400.1	AT4G20970.1 basic helix-loop-helix (bHLH) family protein	2.6	-1.2	2.4	2.4	69	442	95	186	150	201	65	272	144	243
	Csa1M589140.1	AT5G56960.1 basic helix-loop-helix (bHLH) family protein	1.3	1.2	1.3	1.2	94	227	212	178	518	1194	15	12	23	10
	Csa2M193320.1	AT5G43650.1 bHLH family protein	1.3	2.2	2.8	2.8	12	8	158	387	259	1140	25	148	5	15
	Csa2M354790.1	AT4G33880.1 bHLH family protein/RSL2	4.9	4.5	4.9	4.5	10	2	2	57	1	23	6	0	3	1
	Csa3M119500.1	AT1G01260.1 bHLH family protein	1.0	1.0	1.3	1.3	627	676	1342	2432	1569	3072	1573	2262	426	914
	Csa3M178580.1	AT5G51780.1 bHLH family protein	2.0	2.0	2.0	2.0	37	25	10	14	39	155	1	1	1	0
	Csa3M893390.1	AT5G65640.1 bHLH093 (beta HLH protein 93); DNA binding/transcription factor	-1.6	-1.0	-1.6	-1.0	594	762	1362	949	3043	2498	114	31	135	56





**Figure 9.** Regulation of melon (*Cucumis melo*) root ferric-chelate reductase activity and iron (Fe)-uptake gene expression by Fe and copper (Cu). (a) Ferric-chelate reductase activity ( $\pm$  SD) in roots after 3 d of treatment with 10  $\mu$ M Fe and 0.5  $\mu$ M Cu (+Fe+Cu), -Fe+Cu, +Fe-Cu, or -Fe-Cu solutions. Wild-type (WT), black bars; *fe* mutant, gray bars. Gene expression in roots of the plants in (a) for *FIT* (b), *FRO1* (c), *FRO2* (d), *IRT1* (e), *NRAMP1* (f), and *COPT2* (g). Significant difference between control (+Fe+Cu) and treatments: \*,  $P < 0.05$ .



**Figure 10.** Models of effects of the *fefe* mutation of *Cucumis melo*. (a) Model of potential *FIT* regulation under single iron (Fe) or copper (Cu) deficiencies, or simultaneous Fe and Cu deficiency. In the wild-type (WT), *FIT* up-regulates its own expression with a required partner basic helix-loop-helix (bHLH) protein, which is missing or mutated in *fefe*. A substitute partner protein is up-regulated by Cu deficiency, which allows the *fefe* mutant to transcribe *FIT* and activate *FIT* targets. (b) Model of metal homeostasis alterations in *fefe* roots based on transcript abundance. Dashed lines represent lower expression relative to the WT; solid lines represent higher expression relative to the WT. Transport of Fe into a generic cell is represented for *Fro1*, *Irt1*, *Nrap1* and *Opt3* proteins; transport of Fe into the vacuole is represented by *Vit1* and *NodL* proteins; transport out of a vacuole is represented by the *Nrap3* protein; and cytoplasmic synthesis of nicotianamine is represented by the *Nas* protein.

### The *fefe* gene is upstream of Fe-uptake genes

We showed that Fe applied to leaves, or increased Fe supply to roots, could rescue the *fefe* phenotype (fig. S1), which suggested that the *fefe* defect results in Fe deficiency specifically. Using grafting, it was clear that *fefe* shoots functioned normally, but the roots did not respond to Fe deficiency (fig. 3). This indicates that the *fefe* defect does not affect shoot-to-root communication processes (Vert et al., 2003; Garcia et al., 2013), at least at the shoot origin of such a signal, although it is pos-

sible that *fefe* roots receive a signal that they are unable to perceive or respond to. Another possibility was that lack of energy resulting from the low photosynthetic capacity of the chlorotic *fefe* leaves rendered the plant unable to produce or send a root-to-shoot signal. By growing *fefe* plants in conditions to allow green leaves before Fe-deficiency treatments, we ruled out this possibility.

The bHLH transcription factors *FER* in tomato (Ling et al., 2002) and *FIT* in Arabidopsis (Colangelo & Guerinot, 2004) are required for up-regulation of Fe-uptake genes under Fe deficiency. Here, we showed that, like *FER* and *FIT*, the *fefe* mutation also affected expression of Fe-uptake genes. In addition, *fefe* did not properly regulate the expression of melon *FIT* and a number of other genes that were Fe-regulated in one or both WT genotypes (table 1, figs. 2, 9). The up-regulation of *FIT* under Fe deficiency was abolished in the *fefe* mutant in fig. 2 and the RNA-seq experiments (table 1), but there was some up-regulation of *FIT* in fig. 9. This is similar to Arabidopsis *FIT* expression, where in some experiments *FIT* transcripts are increased under Fe deficiency (Colangelo & Guerinot, 2004; Buckhout et al., 2009; Garcia et al., 2010; Yang et al., 2010), and in others they are not (Dinnyen et al., 2008; Long et al., 2010; Ivanov et al., 2012; Stein & Waters, 2012). Regardless, the apparent increased *FIT* expression alone was insufficient to increase *FRO1* (orthologous to *FRO2* in A.t) and *IRT* expression (fig. 9 and Colangelo & Guerinot, 2004; Yuan et al., 2008). *FIT* protein activity is not entirely dependent on transcriptional control, as short-lived “active” forms of *FIT* protein have been described, and this post-translational control for the protein depends on Fe status (Meiser et al., 2011; Sivitz et al., 2011). Sequencing of the *fefe* *FIT* locus and RNA-seq sequences of WT and *fefe* *FIT* transcripts, as well as some level of *FIT* up-regulation in *fefe* in fig. 9, ruled out *FIT* as the mutant gene in *fefe*. Together, these results show that the *fefe* mutant has a defect in regulation of root Fe-uptake responses that is upstream of known -Fe uptake genes and potentially upstream of or in partnership with *FIT*, making this a valuable mutation for furthering our understanding of Fe-uptake regulation. So far, subgroup Ib bHLH transcription factors bHLH038, bHLH039 (Yuan et al., 2008), bHLH100 and bHLH101 (Wang et al., 2013) have been shown to interact physically with *FIT*, but single mutants of these genes have no discernible phenotype (Wang et al., 2007, 2013; Sivitz et al., 2012), while the *fefe* phenotype is severe. Thus, it is likely that the *fefe* gene is not homologous to these partner bHLHs, or there is less redundancy in the melon genome for subgroup Ib bHLH genes.

### Cu deficiency stimulates Fe uptake

Under Cu deficiency, FeSOD genes and miR398 transcripts are up-regulated, and CuSOD genes are down-regulated (Yamasaki et al., 2007; Abdel-Ghany & Pilon, 2008; Bernal et al., 2012). We showed an opposite regulatory pattern under Fe deficiency, which led to the Fe/Cu tradeoff hypothesis, that Fe deficiency up-regulates Cu accumulation to supply Cu for CuSOD proteins to replace down-regulated FeSOD proteins (Waters et al., 2012). Here, we hypothesized that Cu deficiency might stimulate Fe uptake, and the results supported this hypothesis (fig. 4). We showed that Cu deficiency stimulated the accumulation of Fe in WT and *fefe* plants and rescued the *fefe* phenotype, and also resulted in increased *FRO2*

expression and ferric-chelate reductase activity (figs. 5, 9). These results corroborate earlier work which showed that Cu deficiency induced ferric-chelate reductase activity (Norvell et al., 1993; Welch et al., 1993; Cohen et al., 1997; Romera et al., 2003), and expands that work by demonstrating Cu regulation of the *FRO2* genes of cucumber and melon (figs. 5, 9, table 1), which are most closely related to Cu-regulated Arabidopsis *FRO4* and *FRO5* genes (Bernal et al., 2012). This is in contrast to regulation of the *FRO1* gene, which was up-regulated by Fe deficiency but not by Cu deficiency. As the *fefe* mutant has a root localized defect (fig. 3) that prevented normal up-regulation of *FIT*, *FRO1* and *IRT1* (figs. 2, 9, table 1) and normal accumulation of Fe under standard conditions (figs. S1, 1, 4), rescue of this mutant by withholding Cu further supports the idea that Fe uptake is increased under Cu deficiency, consistent with the Fe/Cu tradeoff hypothesis. Cu-deficient WT melon plants also accumulated additional Fe (fig. 4), showing that this phenomenon is not limited to the *fefe* mutant.

#### *Cu- and Fe-deficiency effects on metal homeostasis genes*

As indicated by differential expression of key metal homeostasis genes (table 1) under Fe and Cu deficiency, it is clear that deficiency of either Fe or Cu affected overall metal homeostasis. One nicotianamine synthase (*NAS*) gene was down-regulated under Fe deficiency, and all three *NAS* genes were down-regulated under Cu deficiency. Nicotianamine is an intracellular metal chelator that has been implicated in homeostasis of Fe and Cu (Takahashi et al., 2003; Curie et al., 2009; Klatte et al., 2009). It is not clear if there is an overlap in the localization of expression of these three *NAS* genes, or if they are preferentially expressed in certain cell types or organelles. Yellow-stripe-like (*YSL*) and *MATE* genes (e.g., *FRD3*) are potentially involved in intraplant translocation (DiDonato et al., 2004; Green & Rogers, 2004; Waters et al., 2006), and changes in expression of *YSL3* and *MATE* orthologs could result in altered distribution of Fe and Cu under metal deficiency to help plant adaptation to stress. Such redistribution has been observed for Cu and Fe (Ravet et al., 2011; Bernal et al., 2012; Page et al., 2012). Under Cu deficiency, Cu-uptake genes *FRO2*, *COPT2*, and *ZIP2* were up-regulated, while Fe-uptake genes *FRO1* and *IRT1* had decreased expression. This suggests that Fe uptake by Cu-deficient melon does not use the primary Fe-uptake system, although it is not obvious from the root gene expression data which specific genes could play this role.

#### *Analysis of fefe provides new insights into Fe and Cu homeostasis*

Gene expression levels in the *fefe* mutant provide new insight into Fe and Cu homeostasis. First, *FRO2* can still be up-regulated by Cu deficiency in *fefe* (fig. 9). Regulation of *FIT* and *FRO1* was defective under Fe-deficient conditions (figs. 2, 9, table 1). Under simultaneous Fe and Cu deficiency, ferric-chelate reductase activity and expression of *FIT*, *FRO1*, *FRO2*, *IRT1* and *COPT2* were synergistically up-regulated in *fefe* (fig. 9). It

is not clear how this synergistic regulation occurs, but high expression of *FIT* in *fefe* suggests that the FIT protein could be involved. One possibility is that a bHLH protein that multimerizes with FIT under Fe deficiency is defective in *fefe*, but an alternative bHLH protein becomes present under Cu deficiency (fig. 10a) and allows *FIT* expression or activation of FIT and expression of FIT target genes. Several bHLH genes were up-regulated in Cu-deficient melon roots (table 1) and some bHLH transcripts were also Cu-regulated in Arabidopsis (Yamasaki et al., 2009; Bernal et al., 2012).

Altered transcript abundances (regardless of fold-changes) for metal homeostasis genes in *fefe* (table 1) indicate potential alterations in cellular metal metabolism. A model of these alterations is shown in fig. 10, where loss of expression of Fe-uptake genes (*FRO1*, *IRT1* and *Nramp1*) leads to higher expression of *OPT3*, potentially to increase Fe uptake, and higher *NAS1* expression to produce increased nicotianamine. This model also includes altered expression of vacuolar Fe transporters, with the efflux transporter *Nramp3* (Lanquar et al., 2005) being more highly expressed, and the influx transporters *VIT1* (Kim et al., 2006) and *NODL* (Gollhofer et al., 2011) at lower abundance, as Fe would be moved out of the vacuole in Fe-deficient plants, rather than into the vacuole for storage.

#### *Conclusions and future directions*

The Fe/Cu tradeoff hypothesis is that, when Fe or Cu is limiting, accumulation of the other metal is stimulated to compensate. This hypothesis was supported by increased Cu accumulation under Fe deficiency (Waters et al., 2012), and the results here show that a *fefe*-independent, Cu-regulated Fe-uptake system is present in melon plants. Thus, there are unidentified specific Fe- and Cu-uptake systems that fulfill this demand, rather than the normal uptake systems acting nonspecifically. The *fefe* mutant is a potential tool to identify the Cu-regulated Fe-uptake system. The *fefe* mutant could also further understanding of Fe-uptake regulation, as the *fefe* protein is likely to be upstream of FIT in the Fe signaling pathway, or works in partnership with the FIT protein. We are actively working to identify the *fefe* gene in melon by positional cloning. The specific mechanism of Fe sensing and signaling of Fe status is unknown, so discovery of the *fefe* gene will facilitate understanding of Fe signaling.

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### Supplemental materials (following)

Fig. S1 Rescue of the *fefe* phenotype by Fe supplementation.

Table S1 Primers used in this study

Table S2 Genes that were up-regulated under Fe deficiency in one WT plant and in the *fefe* mutant

Table S3 Genes that were up-regulated under Fe deficiency in two WT plants but not in the *fefe* mutant

Table S4 Genes that were up-regulated under Fe deficiency in one genotype

Table S5 Genes that were down-regulated by Fe deficiency in multiple genotypes

Table S6 Genes that were down-regulated under Fe deficiency in one genotype

Table S7 Genes with opposite regulatory patterns in WT and *fefe* under Fe deficiency

Table S8 Genes that were differentially expressed in Cu-deficient roots of *fefe* or WT Edisto

Table S9 Genes that were up-regulated under Cu deficiency in one genotype

Table S10 Genes that were down-regulated under Cu deficiency in one genotype

Table S11 Genes that were up-regulated by Fe and Cu deficiency in *fefe* and Edisto roots

Table S12 Genes that were down-regulated by Fe and Cu deficiency in *fefe* and Edisto roots

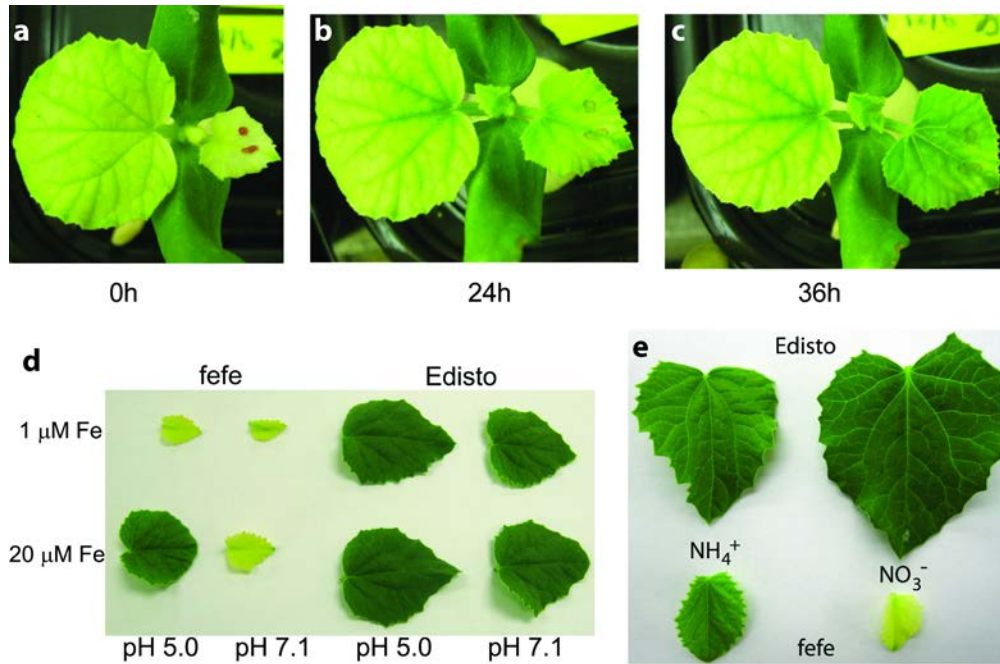


Figure S1. Rescue of the *fefe* phenotype by Fe supplementation. a-c): Time sequence of leaf re-greening after application of Fe-EDDHA to second leaf of *fefe* plant. a) Immediately after application, b) 24 h after application, c) 36 h after application. d) First leaf of *fefe* and WT Edisto plants grown for 7 d in solution buffered at pH 5.0 or 7.1, with 1 or 20 μM Fe. e) First leaf of *fefe* and WT Edisto plants grown for 5 d in hydroponic solution supplying nitrogen solely as  $\text{NH}_4^+$  or  $\text{NO}_3^-$ .

Table S1. Primers used in this study for real-time RT-PCR.

Target gene	Fw Primer	Rev Primer
FRO1	TCACAGCGATTTAGAACCAGA	GCCTTCGAGGGAAACTTGAA
FRO2	TCTATCTAATCCATGTGGGAGTAGC	AACAGCGCCAGAAGGAAGAT
FRO3	CGAAGGCTGAAGTATAAACCAAC	ACCTTGTCCATGACTCATCACA
FRO4	CACCGTCGAATTGGTCCT	TGGACTCGACGACACACTGAA
IRT1	ATCCCAATGTTGCACCCGGATAGA	AAACCGGTGGCGAGAATGATACCT
UBQ	TCTTTCTTGGCCTCGTGCTCTTCT	TTGCAGATGCGTGGAATCGACAAC
FIT	GACATCAACGATCAATTTGAG	CGATCCTCGATCAAGCAA
NRAMP1	CTGTAATAGCAGCCGATATTC	CTATCAACAGTTCAGCTTCC
COPT2	GCTGGTGTTCTCTTTTGC	CCGTTGAACGACATCAAAGC

**Table S2. Genes that were upregulated under Fe deficiency in one WT and in *fefe*.**

Common elements in "fefe Up-Fe" and "Ed Up-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa3M122660.1	AT2G45760.1 BAP2 (BON ASSOCIATION PROTEIN 2)				2.56	1.50	
Csa5M139760.1	AT5G24090.1 acidic endochitinase (CHIB1)				2.22	1.73	
Csa5M139770.1	AT5G24090.1 acidic endochitinase (CHIB1)				2.17	1.59	
Csa2M034520.1	AT5G04950.1 NAS1 (NICOTIANAMINE SYNTHASE 1); nicotianamine synthase				2.44	2.03	

AT5G42210.1 FUNCTIONS IN: molecular\_function unknown; INVOLVED IN: biological\_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Major facilitator superfamily MFS-1 (InterPro:IPR011701), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: tetracycline transporter (TAIR:AT2G16990.2); Has 985 Blast hits to 984 proteins in 348 species: Archae - 2; Bacteria - 541; Metazoa - 251; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 152 (source: NCBI BLink).

Csa6M045090.1	AT5G53450.1 ORG1 (OBP3-responsive gene 1); ATP binding / kinase/ protein kinase				1.28	2.66	
Csa3M603030.1	AT2G23150.1 NRAMP3 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 3); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter				1.63	1.05	
Csa2M423700.1					1.09	1.16	

Common elements in "fefe Up-Fe" and "Sn Up-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa6M000080.1	AT1G56600.1 AtGolS2 (Arabidopsis thaliana galactinol synthase 2); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups				3.39		2.09
Csa4M304750.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase				2.82		1.48
Csa4M303680.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase				2.63		1.57
Csa4M304760.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase				2.63		1.65
Csa7M419590.1	AT4G01870.1 tolB protein-related				2.58		1.37
Csa5M605060.1	No hits found				2.53		1.27
Csa5M613620.1	No hits found				2.27		1.22
Csa6M216410.1	AT5G05340.1 peroxidase, putative				2.27		2.57
Csa5M590160.1	AT3G13080.1 ATMRP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase				2.15		1.05
Csa1M032450.1	AT5G63160.1 BT1 (BTB AND TAZ DOMAIN PROTEIN 1); protein binding / transcription regulator				2.14		1.10
Csa7M432520.1	AT5G20230.1 ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier				1.99		1.19
Csa3M118040.1	AT3G60450.1 INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078), PRIB5 (InterPro:IPR012398); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G60440.1); Has 187 Blast hits to 185 proteins in 74 species: Archae - 0; Bacteria - 51; Metazoa - 14; Fungi - 36; Plants - 35; Viruses - 0; Other Eukaryotes - 51 (source: NCBI BLink).				1.97		1.04
Csa1M439830.1	AT1G30040.1 ATGA2OX2 (GIBBERELLIN 2-OXIDASE); gibberellin 2-beta-dioxygenase				1.85		1.26
Csa6M504470.1	AT2G18193.1 AAA-type ATPase family protein				1.75		1.31
Csa6M514860.1	AT1G61800.1 GPT2; antiporter/ glucose-6-phosphate transmembrane transporter				1.73		1.95
Csa6M094690.1	No hits found				1.65		1.34
Csa5M106010.1	AT2G02010.1 GAD4 (glutamate decarboxylase 4); calmodulin binding				1.44		1.41
Csa4M639960.1	AT5G42830.1 transferase family protein				1.42		1.02
Csa4M303690.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase				1.30		1.05

Csa1M589140.1	AT5G56960.1 basic helix-loop-helix (bHLH) family protein	1.28	1.24
Csa3M121730.1	AT2G22590.1 transferase, transferring glycosyl groups	1.25	1.15
Csa2M308370.2	AT1G22170.1 phosphoglycerate/bisphosphoglycerate mutase family protein	1.24	1.74
Csa4M304250.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	1.17	1.07
Csa3M000180.1	AT5G65980.1 auxin efflux carrier family protein	1.12	1.55
Csa6M504460.1	AT2G18193.1 AAA-type ATPase family protein	1.07	1.03

**Table S3. Genes that were upregulated under Fe deficiency in two WT's but not in *fe* mutant.**

<u>Cucumber Locus ID</u>	<u>Top <i>Arabidopsis thaliana</i> hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down <i>fe</i> -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up <i>fe</i> -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa2M354790.1	AT4G33880.1 basic helix-loop-helix (bHLH) family protein					4.93	4.47
Csa5M175770.1	AT1G23020.1 FRO3; ferric-chelate reductase	-1.70				4.33	2.67
Csa7M398170.1	AT2G47540.1 pollen Ole e 1 allergen and extensin family protein					4.13	10.61
Csa4M111580.1	AT5G64300.1 ATGCH; 3,4-dihydroxy-2-butanone-4-phosphate synthase/ GTP cyclohydrolase II					4.12	1.12
Csa7M398160.1	AT4G02270.1 pollen Ole e 1 allergen and extensin family protein					3.88	4.87
Csa1M059200.1	AT1G11920.1 pectate lyase family protein					3.83	5.37
Csa6M382880.1	AT1G80830.1 NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter					3.68	1.72
Csa5M156210.1	AT1G12560.1 ATEXPA7 (ARABIDOPSIS THALIANA EXPANSIN A7)					3.50	4.16
Csa4M111610.1	AT1G44191.1 Encodes a ECA1 gametogenesis related family protein					3.46	4.89
Csa7M072750.1	AT4G15480.1 UGT84A1; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase/ transferase, transferring glycosyl groups					3.33	1.47
Csa1M655920.1	AT3G47390.1 cytidine/deoxycytidylate deaminase family protein					3.27	1.38
Csa1M538170.1	AT3G10710.1 pectinesterase family protein					3.21	3.52
Csa3M910710.1	AT5G46940.1 invertase/pectin methylesterase inhibitor family protein					3.14	2.16
Csa6M134900.1	AT1G30870.1 cationic peroxidase, putative	-1.62				3.09	5.66
Csa7M420700.1	AT1G48930.1 AtGH9C1 ( <i>Arabidopsis thaliana</i> glycosyl hydrolase 9C1); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds					3.06	5.04
Csa1M051840.1	AT1G30870.1 cationic peroxidase, putative					3.05	1.33
Csa2M355010.1	No hits found					3.02	1.65
Csa1M654840.1	AT1G70170.1 MMP (MATRIX METALLOPROTEINASE); metalloendopeptidase/ metallopeptidase					2.94	1.61
Csa3M746570.1	AT3G09925.1 pollen Ole e 1 allergen and extensin family protein					2.89	2.73
Csa5M211030.1	AT5G05500.1 pollen Ole e 1 allergen and extensin family protein	-1.15				2.86	4.71
Csa6M298480.1	AT1G07890.3 APX1 (ascorbate peroxidase 1); L-ascorbate peroxidase					2.70	3.27
Csa1M655930.1	AT3G47390.1 cytidine/deoxycytidylate deaminase family protein					2.68	1.15
Csa1M654860.1	AT1G24140.1 matrixin family protein					2.65	1.20
Csa1M051830.1	AT4G20190.1 unknown protein					2.55	2.52
Csa3M218170.1	AT1G07750.1 cupin family protein					2.49	2.18
Csa3M078270.1	No hits found					2.29	2.62
Csa6M538760.1	AT1G30850.1 unknown protein					2.18	1.24
Csa5M577390.1	AT1G68765.1 IDA (INFLORESCENCE DEFICIENT IN ABSCISSION); receptor binding					2.01	1.49
Csa2M010160.1	AT3G56710.1 SIB1 (SIGMA FACTOR BINDING PROTEIN 1); binding / protein binding					1.91	1.36
Csa3M687760.1	AT2G34930.1 disease resistance family protein					1.89	1.33
Csa3M435010.3	AT4G26270.1 PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase					1.85	2.46
Csa7M447100.1	AT3G16240.1 DELTA-TIP; ammonia transporter/ methylammonium transmembrane transporter/ water channel					1.85	1.43
Csa5M517190.1	AT2G39690.2 unknown protein					1.85	1.41
Csa7M318970.1	AT3G21260.3 glycolipid transfer protein-related					1.81	1.96
Csa1M422980.1	AT4G25810.1 XTR6 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase					1.79	1.42
Csa3M435010.1	AT4G26270.1 PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase					1.76	2.23
Csa7M073520.1	AT4G34120.1 LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1)					1.71	1.45
Csa1M015670.1	AT3G03290.1 universal stress protein (USP) family protein					1.71	1.05
Csa3M435010.2	AT4G26270.1 PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase	-1.22				1.68	2.30



Csa2M010180.1	No hits found	1.68	2.29
Csa3M167380.1	AT5G49480.1 ATCP1 (Ca <sup>2+</sup> -binding protein 1); calcium ion binding	1.66	1.84
Csa3M126810.1	AT2G45220.1 pectinesterase family protein	1.64	1.07
Csa3M915140.1	AT4G25190.1 unknown protein	1.64	5.21
Csa3M101810.1	AT4G27410.2 RD26 (RESPONSIVE TO DESICCATION 26); transcription activator/ transcription factor	1.56	1.36
Csa6M523460.1	AT1G30135.1 JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8)	1.51	1.58
Csa6M016950.1	AT5G47850.1 CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase	1.51	1.78
Csa2M297760.1	AT5G50080.1 DNA binding / transcription factor	1.50	1.21
Csa6M505230.1	AT2G21320.1 zinc finger (B-box type) family protein	1.47	1.68
Csa3M857590.1	AT1G19715.1 jacalin lectin family protein	1.43	1.54
Csa6M526440.1	AT4G39720.1 VQ motif-containing protein	1.43	1.62
Csa1M534750.1	AT3G54420.1 ATEP3; chitinase	1.38	1.82
Csa7M073700.1	AT4G34410.1 RRTF1 ((REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor	1.38	2.12
Csa6M302190.1	AT5G59730.1 ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H7); protein binding	1.36	1.54
Csa3M141830.1	AT1G04330.1 unknown protein	1.35	2.92
Csa3M143510.1	AT1G04280.1 unknown protein	1.34	1.80
Csa2M193320.1	AT5G43650.1 basic helix-loop-helix (bHLH) family protein	1.33	2.17
Csa3M836500.1	AT5G14780.1 FDH (FORMATE DEHYDROGENASE); NAD or NADH binding / binding / catalytic/ cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	1.32	2.03
Csa1M063490.1	No hits found	1.31	1.33
Csa1M168910.1	AT2G36026.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF623, plant (InterPro:IPR006458); BEST Arabidopsis thaliana protein match is: OFP6 (OVATE FAMILY PROTEIN 6) (TAIR:AT3G52525.1); Has 230 Blast hits to 230 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 228; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	1.31	1.06
Csa3M405510.1	AT5G48150.1 PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor	1.30	1.51
Csa6M008740.1	AT5G02070.1 protein kinase-related	1.30	1.50
Csa4M279850.1	AT2G27180.1 unknown protein	1.30	1.06
Csa1M005770.1	AT3G48180.1 unknown protein	1.29	1.19
Csa4M192180.1	AT4G13180.1 short-chain dehydrogenase/reductase (SDR) family protein	1.27	1.18
Csa7M451920.1	AT1G17710.1 phosphatase	1.23	2.32
Csa5M146930.1	AT1G32928.1 unknown protein	1.23	2.10
Csa6M338100.1	AT3G21260.3 glycolipid transfer protein-related	1.21	1.90
Csa3M000690.1	AT5G65980.1 auxin efflux carrier family protein	1.21	2.35
Csa4M192100.1	AT5G58375.1 unknown protein	1.21	1.24
Csa4M665120.1	AT1G21010.1 unknown protein	1.16	1.20
Csa2M368260.1	AT1G75750.1 GASA1 (GAST1 PROTEIN HOMOLOG 1)	1.14	1.99
Csa6M109750.1	AT4G15550.1 IAGLU (INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE); UDP- glycosyltransferase/ transferase, transferring glycosyl groups	1.10	1.89
Csa2M360780.1	AT5G42650.1 AOS (ALLENE OXIDE SYNTHASE); allene oxide synthase/ hydro-lyase/ oxygen binding	1.10	1.76
Csa5M589920.1	AT1G13710.1 CYP78A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-2.27	1.07
Csa4M001810.1	AT3G62860.1 esterase/lipase/thioesterase family protein	1.07	1.04

Csa5M223070.1	AT2G40750.1 WRKY54; transcription factor	1.07	1.70
Csa1M025940.1	AT1G30220.1 INT2 (INOSITOL TRANSPORTER 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	1.05	1.02
Csa1M481200.1	AT5G59730.1 ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H7); protein binding	1.05	1.75
Csa3M180310.1	AT4G23030.1 MATE efflux protein-related	1.04	1.06
Csa3M598890.1	AT3G26760.1 short-chain dehydrogenase/reductase (SDR) family protein	1.03	1.80
Csa7M354520.1	AT4G13000.1 protein kinase family protein	1.02	1.14
Csa2M028460.1	AT1G55020.1 LOX1; lipoxygenase	1.01	1.56

**Table S4. Genes that were upregulated under Fe deficiency in one genotype.**

Elements only in "fefe Up-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa1M014460.1	No hits found				7.51		
Csa4M129030.1	AT3G29970.1 germination protein-related				7.13		
	AT3G22910.1 calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA13)						
Csa2M011490.1	AT1G18100.1 E12A11; phosphatidylethanolamine binding				6.63		
Csa3M807330.1	AT4G28500.1 ANAC073 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 73); transcription activator/ transcription factor				4.96		
Csa6M518170.1	AT5G45180.1 flavin-containing monooxygenase family protein / FMO family protein				4.42		
Csa1M264550.1	AT1G15780.1 unknown protein				4.31		
Csa3M819860.1	AT1G14790.1 RDR1 (RNA-DEPENDENT RNA POLYMERASE 1); RNA-directed RNA polymerase/ nucleic acid binding				4.28		
Csa5M564290.1	AT3G53040.1 late embryogenesis abundant protein, putative / LEA protein, putative				4.24		
Csa3M748200.1	AT5G54490.1 PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding / protein binding				4.14		
Csa1M071800.1	AT1G19250.1 FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase				3.87		
Csa1M264540.1	AT1G78780.2 pathogenesis-related family protein				3.81		
Csa7M318990.1	No hits found				3.80		
Csa2M351860.1	No hits found				3.76		
Csa3M120450.1	AT1G73325.1 trypsin and protease inhibitor family protein / Kunitz family protein				3.75		
Csa2M021500.1	AT3G11980.1 MS2 (MALE STERILITY 2); fatty acyl-CoA reductase (alcohol-forming)/ oxidoreductase, acting on the CH-CH group of donors, NAD or NADP as acceptor						
Csa4M551130.1	AT2G16050.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: DC1 (InterPro:IPR004146); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G20990.1); Has 719 Blast hits to 448 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 717; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).				3.62		
Csa5M515560.1	AT2G32530.1 ATCSLB03; cellulose synthase/ transferase/ transferase, transferring glycosyl groups				3.62		
Csa2M416170.2	AT4G25140.1 OLEO1 (OLEOSIN 1)				3.31		
Csa4M023040.1	AT2G26560.1 PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir				3.25		
Csa2M360560.1	AT1G12030.1 unknown protein				3.17		
Csa6M511780.1	No hits found				3.10		
Csa2M237730.1	No hits found				3.07		
Csa5M623920.1	No hits found				3.07		
Csa5M137410.1	No hits found				3.07		
Csa6M363020.1	AT4G10720.1 ankyrin repeat family protein				3.06		
	AT4G19690.2 IRT1 (iron-regulated transporter 1); cadmium ion transmembrane transporter/ copper uptake transmembrane transporter/ iron ion transmembrane transporter/ manganese ion transmembrane transporter/ zinc ion transmembrane transporter						
Csa6M517980.1	AT1G14790.1 RDR1 (RNA-DEPENDENT RNA POLYMERASE 1); RNA-directed RNA polymerase/ nucleic acid binding				2.96		
Csa5M544050.1	AT3G22240.1 unknown protein				2.89		
Csa7M237300.1	AT1G80810.1 binding				2.86		
Csa7M037490.1	AT3G48140.1 senescence-associated protein, putative	-1.41		-1.59	2.82		
Csa2M350420.1	AT4G31940.1 CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding				2.73		
Csa3M852630.1	AT3G43190.1 SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups				2.69		
Csa1M597800.1	AT4G37530.1 peroxidase, putative				2.68		
Csa7M414530.1		-3.11			2.65		

	AT5G59990.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot apex, stem, leaf whorl, flower; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: CCT domain (InterPro:IPR010402); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41380.1); Has 918 Blast hits to 918 proteins in 64 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 885; Viruses - 0; Other Eukaryotes - 32 (source: NCBI BLINK).		2.62
Csa6M301610.1			2.62
Csa1M074400.1	AT4G20970.1 basic helix-loop-helix (bHLH) family protein		2.56
Csa3M825010.1	AT5G39670.1 calcium-binding EF hand family protein		2.56
Csa2M068700.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase		2.50
Csa4M638520.1	AT5G42680.1 unknown protein		2.50
Csa4M047950.1	AT4G10550.1 subtilase family protein		2.49
Csa2M360680.1	AT1G47710.1 serpin, putative / serine protease inhibitor, putative		2.49
Csa5M137420.1	No hits found		2.47
Csa5M262770.1	AT1G14550.1 anionic peroxidase, putative		2.44
Csa7M419530.1	AT2G18150.1 peroxidase, putative	-3.08	2.41
	AT5G06760.1 late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein		2.41
Csa3M808370.1	AT5G10530.1 lectin protein kinase, putative		2.39
Csa2M439210.1	AT1G43800.1 acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative	-1.24	2.37
Csa6M338660.1	AT5G24090.1 acidic endochitinase (CHIB1)		2.37
Csa5M139740.1	AT3G53150.1 UGT73D1 (UDP-glucosyl transferase 73D1); UDP-glycosyltransferase/ transferase, transferring hexosyl groups		2.37
Csa6M448690.1	AT4G34131.1 UGT73B3 (UDP-glucosyl transferase 73B3); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring hexosyl groups		2.36
Csa7M073510.1	AT2G16050.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: DC1 (InterPro:IPR004146); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G20990.1); Has 719 Blast hits to 448 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 717; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).		2.34
Csa5M516560.1	AT5G35810.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Ankyrin (InterPro:IPR002110); BEST Arabidopsis thaliana protein match is: ankyrin repeat family protein (TAIR:AT3G54070.1); Has 446 Blast hits to 440 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 446; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).		2.33
Csa5M174620.1	AT3G05660.1 AtRLP33 (Receptor Like Protein 33); kinase/ protein binding		2.31
Csa6M080330.1	AT4G14640.1 CAM8 (CALMODULIN 8); calcium ion binding		2.31
Csa2M011480.1	No hits found		2.30
Csa5M606810.1	AT3G13080.1 ATMRP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase		2.28
Csa3M769610.1	AT3G50770.1 calmodulin-related protein, putative		2.24
Csa6M363560.1	AT5G26170.1 WRKY50; transcription factor		2.24
	AT3G11945.1 homogentisate farnesyltransferase/ homogentisate geranylgeranyltransferase/ homogentisate solanesyltransferase		2.23
Csa3M791510.1	AT4G14630.1 GLP9 (GERMIN-LIKE PROTEIN 9); manganese ion binding / nutrient reservoir	-1.21	2.21
Csa6M525590.1	AT4G31730.1 GDU1 (GLUTAMINE DUMPER 1)		2.20
Csa4M119770.1	AT2G38870.1 protease inhibitor, putative	-1.59	2.20
Csa3M142960.1	AT1G80840.1 WRKY40; transcription factor		2.19
Csa2M382650.1	AT3G28210.1 PMZ; zinc ion binding		2.15
Csa3M829160.1	AT4G39830.1 L-ascorbate oxidase, putative		2.15
Csa6M500640.2	AT1G06330.1 copper-binding family protein		2.14
Csa1M476010.1	AT5G36100.1 unknown protein		2.14
Csa1M555090.1	AT4G16370.1 ATOPT3 (OLIGOPEPTIDE TRANSPORTER); oligopeptide transporter		2.14
Csa1M180750.1	AT3G22060.1 receptor protein kinase-related		2.13
Csa7M044830.1	AT4G39830.1 L-ascorbate oxidase, putative		2.13
Csa6M500640.1			2.13

Csa2M406690.1	AT3G01910.1 SOX (SULFITE OXIDASE); sulfite oxidase	2.13
Csa1M660200.1	AT3G57240.1 BG3 (BETA-1,3-GLUCANASE 3); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	2.13
Csa2M238880.1	AT2G16060.1 AHB1 (ARABIDOPSIS HEMOGLOBIN 1); oxygen binding / oxygen transporter	2.12
Csa5M577370.1	AT1G68760.1 ATNUDX1 (ARABIDOPSIS THALIANA NUDIX HYDROLASE 1); dihydroneopterin triphosphate pyrophosphohydrolase/ hydrolase	2.12
Csa5M148520.1	AT1G64660.1 ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase	2.12
Csa2M357230.1	No hits found	2.11
Csa1M568480.1	No hits found	2.10
Csa3M105950.1	AT3G15353.1 MT3 (METALLOTHIONEIN 3); copper ion binding	2.09
Csa3M047750.1	AT5G55620.1 unknown protein	2.08
Csa2M416170.1	AT2G32540.1 ATCSLB04; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	2.08
Csa2M006090.1	AT5G25940.1 early nodulin-related	2.06
Csa3M035310.1	AT4G22620.1 auxin-responsive family protein	2.05
Csa4M188410.1	AT5G15120.1 unknown protein	2.05
Csa7M397010.1	AT2G47710.1 universal stress protein (USP) family protein	2.04
Csa1M043010.1	AT1G73480.1 hydrolase, alpha/beta fold family protein	2.04
Csa7M432490.1	AT5G20230.1 ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier	2.03
Csa7M419570.1	AT2G41480.1 electron carrier/ heme binding / peroxidase	2.02
Csa2M431070.1	AT5G17540.1 transferase family protein	2.00
Csa5M262240.1	AT5G37140.1 tRNA-splicing endonuclease positive effector-related	1.99
Csa6M020170.1	No hits found	1.99
Csa5M146870.1	AT4G10490.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.98
Csa2M406630.1	AT4G37530.1 peroxidase, putative	1.98
Csa3M651820.1	AT5G07990.1 TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	1.97
Csa5M182730.1	AT2G39730.1 RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	1.96
Csa6M012810.1	AT5G05410.1 DREB2A; DNA binding / transcription activator/ transcription factor	1.96
Csa1M614640.1	No hits found	1.96
Csa6M504480.1	AT2G18193.1 AAA-type ATPase family protein	1.95
Csa3M020090.1	AT4G25200.1 ATHSP23.6-MITO (MITOCHONDRION-LOCALIZED SMALL HEAT SHOCK PROTEIN 23.6)	1.93
Csa3M073790.1	AT4G33550.2 lipid binding	1.91
Csa3M744990.1	AT2G36790.1 UGT73C6 (UDP-glucosyl transferase 73C6); UDP-glucosyltransferase/ UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	1.88
Csa1M025150.1	AT4G02230.1 60S ribosomal protein L19 (RPL19C)	1.87
Csa6M401340.1	AT5G06570.1 hydrolase	1.87
Csa3M063110.1	AT1G50590.1 pirin, putative	1.85
Csa1M135270.1	No hits found	1.84
Csa6M518300.1	AT4G18450.1 ethylene-responsive factor, putative	1.82
Csa3M778380.1	AT5G42560.1 abscisic acid-responsive HVA22 family protein	1.82
Csa1M599480.1	AT4G04220.1 AtRLP46 (Receptor Like Protein 46); kinase/ protein binding	1.82
Csa1M574950.1	AT5G25930.1 leucine-rich repeat family protein / protein kinase family protein	1.82
Csa1M163150.1	No hits found	1.81
Csa1M348430.1	AT5G20230.1 ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier	1.81
Csa7M354530.1	AT3G07350.1 unknown protein	1.80
Csa1M065920.1	AT4G21410.1 protein kinase family protein	1.78
Csa4M377160.1	AT1G77760.1 NIA1 (NITRATE REDUCTASE 1); nitrate reductase	1.78
Csa3M820480.1	AT3G56710.1 SIB1 (SIGMA FACTOR BINDING PROTEIN 1); binding / protein binding	1.78
Csa3M017100.1	AT4G36230.1 unknown protein	1.78
Csa6M363520.1	No hits found	1.78

Csa3M151480.1	AT4G15610.1 integral membrane family protein		1.77
Csa3M816090.1	AT1G18410.1 kinesin motor protein-related		1.76
Csa3M651800.1	AT5G07990.1 TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding		1.76
Csa1M045660.1	AT5G40010.1 AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding		1.75
Csa5M155460.1	AT4G11650.1 ATOSM34 (osmotin 34)		1.75
Csa2M277630.1	AT5G67370.1 unknown protein		1.74
Csa3M592690.1	AT1G05680.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein		1.73
Csa1M595860.1	AT3G14690.1 CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		1.73
Csa6M517020.1	AT1G07180.1 NDA1 (ALTERNATIVE NAD(P)H DEHYDROGENASE 1); NADH dehydrogenase		1.72
Csa3M233980.1	AT3G23550.1 MATE efflux family protein		1.72
Csa3M142970.1	AT2G38870.1 protease inhibitor, putative		1.72
Csa1M573700.1	AT3G57940.1 unknown protein		1.70
Csa4M314390.1	AT5G05410.1 DREB2A; DNA binding / transcription activator/ transcription factor		1.69
Csa3M481240.1	No hits found		1.69
Csa4M443140.1	AT5G35790.1 G6PD1 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 1); glucose-6-phosphate dehydrogenase		1.68
Csa6M495830.1	AT5G65890.1 ACR1 (ACT Domain Repeat 1); amino acid binding		1.68
Csa7M432470.1	AT5G20230.1 ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier		1.68
Csa1M470460.1	AT5G05440.1 unknown protein		1.68
Csa2M033340.1	No hits found		1.68
Csa3M748240.1	AT3G10040.1 transcription factor		1.67
Csa2M033350.1	AT5G26920.1 CBP60G (CAM-BINDING PROTEIN 60-LIKE.G); calmodulin binding		1.67
Csa6M525450.1	AT4G05390.1 ATRFNR1 (ROOT FNR 1); FAD binding / NADP or NADPH binding / electron carrier/ ferredoxin-NADP+ reductase/ oxidoreductase		1.67
Csa6M525600.1	AT5G38910.1 germin-like protein, putative	-1.85	1.67
Csa1M062280.1	AT5G35830.1 ankyrin repeat family protein		1.64
Csa2M401340.1	AT1G07160.1 protein phosphatase 2C, putative / PP2C, putative		1.64
Csa3M643770.1	AT2G45570.1 CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		1.64
Csa1M590300.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase		1.63
Csa4M182290.1	AT5G15780.1 pollen Ole e 1 allergen and extensin family protein		1.63
Csa6M404180.1	AT2G02800.1 APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase		1.62
Csa2M070840.1	AT1G08860.1 BON3 (BONZAI 3); calcium-dependent phospholipid binding		1.62
Csa6M032470.1	AT1G13340.1 unknown protein		1.62
Csa3M730990.1	AT3G08970.1 ATERDJ3A; oxidoreductase		1.61
Csa3M133370.1	AT2G29420.1 ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase		1.60
Csa5M603950.1	AT1G59900.1 AT-E1 ALPHA; oxidoreductase, acting on the aldehyde or oxo group of donors, disulfide as acceptor / pyruvate dehydrogenase (acetyl-transferring)		1.56
Csa1M539350.1	AT5G44400.1 FAD-binding domain-containing protein		1.55
Csa5M262250.1	AT1G65810.1 tRNA-splicing endonuclease positive effector-related		1.54
Csa2M010200.1	AT1G03670.1 ankyrin repeat family protein		1.54
Csa7M019890.1	AT3G45970.1 ATEXLA1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A1)		1.53
Csa7M446780.1	AT5G18470.1 curculin-like (mannose-binding) lectin family protein		1.53
Csa4M193250.1	AT5G18270.2 ANAC087; transcription factor		1.52
Csa2M381800.1	AT5G04860.1 unknown protein		1.51
Csa2M000520.1	AT2G19590.1 ACO1 (ACC OXIDASE 1); 1-aminocyclopropane-1-carboxylate oxidase		1.51
Csa6M525580.1	AT5G39120.1 germin-like protein, putative	-1.13	1.51
Csa3M207890.1	AT2G15620.1 NIR1 (NITRITE REDUCTASE 1); ferredoxin-nitrate reductase/ nitrite reductase (NO-forming)		1.50
Csa2M069700.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase		1.50

Csa7M379090.1	No hits found	1.50
Csa4M285790.1	AT5G06720.1 peroxidase, putative	1.50
Csa1M024210.1	AT3G18290.1 EMB2454 (embryo defective 2454); protein binding / zinc ion binding	1.49
	AT2G27510.1 ATFD3 (ferredoxin 3); 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding	1.49
Csa1M163160.1	AT5G59190.1 subtilase family protein	1.48
Csa5M141040.1	AT3G23550.1 MATE efflux family protein	1.48
Csa3M233990.1	AT4G33550.2 lipid binding	1.48
Csa3M017110.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	1.48
Csa2M069200.1	AT5G39150.1 germin-like protein, putative	1.48
Csa1M662790.1	AT2G38250.1 DNA-binding protein-related	1.46
Csa3M731130.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	1.46
Csa2M070200.1	AT3G16770.1 ATEBP (ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN); DNA binding / protein binding / transcription activator/ transcription factor	1.45
Csa4M001970.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	1.45
Csa2M070210.1	AT5G11210.1 ATGLR2.5; intracellular ligand-gated ion channel	1.45
Csa2M357220.1	AT1G53620.1 unknown protein	1.45
Csa4M081280.1	No hits found	1.44
Csa1M042280.1	AT4G34630.1 unknown protein	1.43
Csa7M004150.1	AT1G19610.1 PDF1.4	1.43
Csa3M851940.1	AT2G29420.1 ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	1.43
Csa3M133380.1	AT3G13130.1 unknown protein	1.42
Csa7M032240.1	AT1G29670.1 GDSL-motif lipase/hydrolase family protein	1.42
Csa6M520420.1		
Csa1M528600.1	AT5G58860.1 CYP86A1 (CYTOCHROME P450 86 A1); fatty acid (omega-1)-hydroxylase/ oxygen binding	1.41
Csa5M593430.1	AT1G67800.1 copine-related	1.41
Csa3M912950.1	AT5G47120.1 ATBI1 (BAX INHIBITOR 1)	1.41
Csa1M042270.1	AT1G13360.1 unknown protein	1.41
Csa5M162590.1	AT4G17350.1 phosphoinositide binding	1.40
Csa2M406060.1	AT3G01970.1 WRKY45; transcription factor	1.39
Csa3M207340.1	AT4G34420.1 unknown protein	1.39
Csa7M322060.1	AT1G77120.1 ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase	1.38
Csa1M374520.1	AT5G19600.1 SULTR3;5 (SULFATE TRANSPORTER 3;5); sulfate transmembrane transporter	1.38
	AT1G71830.1 SERK1 (SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE 1); kinase/ transmembrane receptor protein serine/threonine kinase	1.38
Csa6M091960.1	AT1G16170.1 unknown protein	1.38
Csa7M431400.1	AT5G26340.1 MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter	1.37
Csa3M149310.1	AT3G26010.1 F-box family protein	1.36
Csa4M038740.1	AT5G14940.1 proton-dependent oligopeptide transport (POT) family protein	1.35
Csa3M829130.1	No hits found	1.34
Csa4M218340.1	AT5G44400.1 FAD-binding domain-containing protein	1.32
Csa1M539330.1	AT1G25550.1 myb family transcription factor	1.32
Csa6M031440.1	AT3G22910.1 calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA13)	1.32
Csa7M379080.1	AT1G23390.1 kelch repeat-containing F-box family protein	1.30
Csa5M600900.1	AT3G56400.1 WRKY70; transcription factor/ transcription repressor	1.30
Csa3M727990.1	AT5G25930.1 leucine-rich repeat family protein / protein kinase family protein	1.30
Csa1M574960.1	AT3G24310.1 MYB305 (myb domain protein 305); DNA binding / transcription factor	1.29
Csa2M169770.1	AT5G15490.1 UDP-glucose 6-dehydrogenase, putative	1.28
Csa1M012150.1		

	AT1G59710.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27100.1); Has 119 Blast hits to 107 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 119; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	1.28
Csa6M403600.1	AT1G44446.1 CH1 (CHLORINA 1); chlorophyllide a oxygenase	1.27
Csa6M385090.1	AT5G15490.1 UDP-glucose 6-dehydrogenase, putative	1.27
Csa1M012150.3	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	1.27
Csa4M288610.1	AT5G15490.1 UDP-glucose 6-dehydrogenase, putative	1.27
Csa1M012150.2	AT1G17860.1 trypsin and protease inhibitor family protein / Kunitz family protein	1.26
Csa1M043200.1	AT4G14640.1 CAM8 (CALMODULIN 8); calcium ion binding	1.25
Csa2M215510.1	AT3G47980.1 integral membrane HPP family protein	1.25
Csa1M045560.1	AT1G15000.1 scpl50 (serine carboxypeptidase-like 50); serine-type carboxypeptidase	1.24
Csa5M000020.1	AT2G44380.1 DC1 domain-containing protein	1.23
Csa3M806240.1	AT2G45360.1 unknown protein	1.23
Csa6M077420.1	AT5G64810.1 WRKY51; transcription factor	1.23
Csa2M297180.1	AT4G23130.1 CRK5 (CYSTEINE-RICH RLK5); kinase	1.22
Csa1M065420.1	AT4G04980.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: leaf whorl, male gametophyte, sepal, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis; BEST Arabidopsis thaliana protein match is: proline-rich family protein (TAIR:AT1G61080.1); Has 21967 Blast hits to 14118 proteins in 814 species: Archae - 74; Bacteria - 1795; Metazoa - 8707; Fungi - 2897; Plants - 2880; Viruses - 936; Other Eukaryotes - 4678 (source: NCBI BLink).	1.20
Csa1M073080.1	AT1G79160.1 unknown protein	1.18
Csa6M137580.1	AT1G44130.1 nucellin protein, putative	1.17
Csa4M361850.1	AT5G40850.1 UPM1 (UROPHORPHYRIN METHYLASE 1); uroporphyrin-III C-methyltransferase	1.15
Csa7M428980.1	AT3G51860.1 CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	1.15
Csa3M731720.1	AT2G47710.1 universal stress protein (USP) family protein	1.14
Csa7M396480.1	AT4G02390.1 APP (ARABIDOPSIS POLY(ADP-RIBOSE) POLYMERASE); NAD+ ADP-ribosyltransferase/ nucleic acid binding	1.14
Csa7M397590.1	AT4G37540.1 LBD39 (LOB DOMAIN-CONTAINING PROTEIN 39)	1.14
Csa4M642430.1	AT5G15120.1 unknown protein	1.13
Csa3M827270.1	No hits found	1.13
Csa6M500720.1	AT5G50200.3 WR3 (WOUND-RESPONSIVE 3); nitrate transmembrane transporter	1.12
Csa1M047430.1	AT3G52430.1 PAD4 (PHYTOALEXIN DEFICIENT 4); lipase/ protein binding / triacylglycerol lipase	1.12
Csa4M496760.1	AT4G37540.1 LBD39 (LOB DOMAIN-CONTAINING PROTEIN 39)	1.12
Csa6M495020.1	AT1G24430.1 transferase/ transferase, transferring acyl groups other than amino-acyl groups	1.12
Csa5M590220.1	AT5G14450.1 GDSL-motif lipase/hydrolase family protein	-1.00 1.11
Csa3M840430.1	AT4G31330.1 unknown protein	1.11
Csa2M376840.1	AT1G07040.1 unknown protein	1.11
Csa6M403620.1	AT3G02550.1 LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41)	1.11
Csa1M023060.1	AT1G47670.1 amino acid transporter family protein	1.10
Csa4M638420.1	AT5G07610.1 F-box family protein	1.09
Csa5M167090.1	AT5G46590.1 anac096 (Arabidopsis NAC domain containing protein 96); transcription factor	1.08
Csa4M639950.1	AT3G05030.1 NHX2 (SODIUM HYDROGEN EXCHANGER 2); sodium ion transmembrane transporter/ sodium:hydrogen antiporter	1.08
Csa7M393470.1	AT2G47680.1 zinc finger (CCCH type) helicase family protein	1.07
Csa4M001760.1	AT3G13080.1 ATMRP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase	1.07
Csa3M127200.1	AT5G52790.1 CBS domain-containing protein-related	1.07
Csa3M183990.1	AT4G02390.1 APP (ARABIDOPSIS POLY(ADP-RIBOSE) POLYMERASE); NAD+ ADP-ribosyltransferase/ nucleic acid binding	1.07
Csa7M397590.2		1.07



Csa1M007890.1	AT1G18980.1 germin-like protein, putative	-1.44	1.07
Csa4M580380.1	AT3G04440.1 unknown protein		1.06
Csa4M499310.1	AT5G06800.1 myb family transcription factor		1.04
Csa1M006320.1	AT3G48080.1 lipase class 3 family protein / disease resistance protein-related		1.04
Csa3M680630.1	No hits found		1.04
	AT5G25250.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Band 7 protein (InterPro:IPR001107); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25260.1); Has 4072 Blast hits to 3210 proteins in 656 species: Archae - 10; Bacteria - 1411; Metazoa - 994; Fungi - 195; Plants - 102; Viruses - 10; Other Eukaryotes - 1350 (source: NCBI BLink).		1.04
Csa2M382440.1	AT1G17290.1 AlaAT1 (ALANINE AMINOTRANSFERAS); ATP binding / L-alanine:2-oxoglutarate aminotransferase		1.03
Csa7M448000.2	AT3G14940.1 ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase		1.02
Csa7M048110.1	AT3G05500.1 rubber elongation factor (REF) family protein		1.02
Csa1M569430.1	AT4G09620.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Mitochondrial transcription termination factor-related (InterPro:IPR003690); Has 120 Blast hits to 97 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 103; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink).		1.02
Csa2M402090.1	AT1G17290.1 AlaAT1 (ALANINE AMINOTRANSFERAS); ATP binding / L-alanine:2-oxoglutarate aminotransferase		1.00
Csa7M448000.1	AT2G23200.1 protein kinase family protein		1.00
Csa2M425790.1	AT2G35980.1 YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)		1.00

Elements only in "Ed Up-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa7M169070.1	AT4G39250.1 ATRL1 (ARABIDOPSIS RAD-LIKE 1); DNA binding / transcription factor					4.96	
Csa2M006080.1	AT2G26695.1 binding / zinc ion binding					4.78	
Csa6M445150.1	AT3G53420.1 PIP2A (PLASMA MEMBRANE INTRINSIC PROTEIN 2A); water channel					4.67	
Csa2M010400.1	AT1G70330.1 ENT1,AT (EQUILIBRATIVE NUCLEOTIDE TRANSPORTER 1); nucleoside transmembrane transporter/ nucleoside transmembrane transporter, against a concentration gradient					4.52	
Csa2M010410.1	AT1G70330.1 ENT1,AT (EQUILIBRATIVE NUCLEOTIDE TRANSPORTER 1); nucleoside transmembrane transporter/ nucleoside transmembrane transporter, against a concentration gradient					4.52	
Csa3M038170.1	AT1G12560.1 ATEXPA7 (ARABIDOPSIS THALIANA EXPANSIN A7)					3.87	
Csa1M537450.1	AT5G44440.1 FAD-binding domain-containing protein					3.59	
Csa2M263850.1	AT2G45960.1 PIP1B (NAMED PLASMA MEMBRANE INTRINSIC PROTEIN 1B); water channel					2.84	
Csa1M202300.1	AT4G28850.1 xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative					2.81	
Csa1M502880.1	AT2G28780.1 unknown protein					2.65	
Csa2M420470.1	No hits found					2.65	
Csa1M039920.1	AT5G17390.1 universal stress protein (USP) family protein					2.65	
Csa1M051720.1	AT5G23660.1 MTN3 (Arabidopsis homolog of Medicago truncatula MTN3)					2.49	
Csa6M106810.1	AT4G00910.1 unknown protein		-2.13			2.43	
Csa2M000240.1	AT5G19530.1 ACL5 (ACAULIS 5); spermine synthase/ thermospermine synthase					2.36	
Csa5M168830.1	AT5G17165.1 unknown protein					2.24	
Csa2M034530.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase	-1.75				2.19	
Csa5M172830.1	AT4G25450.1 ATNAP8; ATPase, coupled to transmembrane movement of substances / transporter					2.18	
Csa4M083600.1	AT1G78710.1 unknown protein					2.11	
Csa4M268100.1	AT5G19790.1 RAP2.11 (related to AP2 11); DNA binding / transcription factor					2.09	
Csa1M589060.1	AT4G29740.2 CKX4 (CYTOKININ OXIDASE 4); amine oxidase/ cytokinin dehydrogenase					1.97	
Csa2M008720.1	AT2G24280.1 serine carboxypeptidase S28 family protein					1.97	
Csa6M213910.1	AT5G05340.1 peroxidase, putative					1.93	
Csa5M172830.2	AT4G25450.1 ATNAP8; ATPase, coupled to transmembrane movement of substances / transporter					1.93	

Csa6M148260.1	AT2G28160.1 FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor			1.93
Csa4M642470.1	AT2G14760.1 basic helix-loop-helix protein / bHLH protein			1.90
Csa1M046130.1	No hits found			1.90
Csa6M112500.1	AT3G07720.1 kelch repeat-containing protein			1.88
Csa1M574980.1	AT4G29140.1 MATE efflux protein-related			1.87
Csa6M148250.1	AT2G28160.1 FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor			1.83
Csa6M525610.1	AT4G14630.1 GLP9 (GERMIN-LIKE PROTEIN 9); manganese ion binding / nutrient reservoir			1.82
Csa7M388370.1	No hits found			1.81
Csa6M366300.1	AT2G44050.1 COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase			1.79
	AT3G46900.1 COPT2; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter	-2.55	-1.59	1.79
Csa1M526820.1	AT3G56360.1 unknown protein			1.79
Csa6M014570.1	AT1G49320.1 BURP domain-containing protein			1.78
Csa2M245470.1	AT1G15550.1 GA3OX1 (GIBBERELLIN 3-OXIDASE 1); gibberellin 3-beta-dioxygenase/ transcription factor binding			1.62
Csa7M434970.1	AT2G18540.1 cupin family protein			1.61
Csa4M031060.1	AT4G36010.1 pathogenesis-related thaumatin family protein			1.61
Csa6M506000.1	AT1G59870.1 PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter			1.58
Csa3M814320.1	AT1G79520.1 cation efflux family protein			1.57
Csa6M136000.1	AT3G63440.1 CKX6 (CYTOKININ OXIDASE/DEHYDROGENASE 6); cytokinin dehydrogenase			1.56
Csa1M589070.1	AT5G19750.1 peroxisomal membrane 22 kDa family protein			1.52
Csa3M816700.1	AT2G21320.1 zinc finger (B-box type) family protein			1.52
Csa6M505230.2	AT5G19790.1 RAP2.11 (related to AP2 11); DNA binding / transcription factor			1.48
Csa5M146300.1	AT1G48300.1 unknown protein			1.48
Csa3M171170.1	AT5G10530.1 lectin protein kinase, putative	-1.60		1.47
Csa2M439220.1	AT1G31930.1 XLG3 (extra-large GTP-binding protein 3); guanyl nucleotide binding / signal transducer			1.46
Csa1M026000.1	No hits found			1.46
Csa6M505880.1	AT1G79250.1 AGC1.7 (AGC KINASE 1.7); kinase			1.46
Csa4M561180.1	AT3G28910.1 MYB30 (MYB DOMAIN PROTEIN 30); DNA binding / transcription factor			1.44
Csa1M009700.1	AT5G63160.1 BT1 (BTB AND TAZ DOMAIN PROTEIN 1); protein binding / transcription regulator			1.43
Csa1M049460.1	AT3G23360.1 protein phosphatase 2C, putative / PP2C, putative			1.43
Csa2M173570.1	AT3G17850.1 protein kinase, putative			1.43
Csa5M171670.1	AT4G19680.2 IRT2; iron ion transmembrane transporter/ zinc ion transmembrane transporter			1.41
Csa1M707110.1	AT5G23950.1 C2 domain-containing protein			1.40
Csa3M183350.1	AT4G02280.1 SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups			1.37
Csa4M001950.1	AT4G13010.1 oxidoreductase, zinc-binding dehydrogenase family protein			1.35
Csa7M351890.3	AT1G11410.1 S-locus protein kinase, putative			1.34
Csa1M070620.1	AT4G26200.1 ACS7; 1-aminocyclopropane-1-carboxylate synthase			1.34
Csa1M580750.1				
Csa1M422480.1	AT5G57560.1 TCH4 (Touch 4); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase			1.33
Csa2M176170.1	No hits found			1.33
Csa6M519730.1	No hits found			1.31
Csa6M421790.1	AT1G07650.1 leucine-rich repeat transmembrane protein kinase, putative			1.30
Csa3M168410.1	AT5G49520.1 WRKY48; transcription factor			1.29
Csa5M150470.1	AT1G64340.1 unknown protein			1.28
Csa3M002400.1	AT1G20560.1 AAE1 (ACYL ACTIVATING ENZYME 1); AMP binding			1.28
Csa1M294020.1	AT5G57800.1 CER3 (ECERIFERUM 3); binding / catalytic/ iron ion binding / oxidoreductase			1.28
Csa3M743390.1	AT1G08080.1 ACA7 (ALPHA CARBONIC ANHYDRASE 7); carbonate dehydratase/ zinc ion binding			1.28
Csa1M008480.1	AT1G74770.1 protein binding / zinc ion binding			1.28
Csa2M418890.1	AT3G21680.1 unknown protein			1.27
Csa7M428170.1	AT3G08040.1 FRD3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter/ transporter			1.26
Csa6M521000.2	AT4G25310.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein			1.25
Csa3M816150.1	AT3G56930.1 zinc finger (DHHC type) family protein			1.24

Csa2M357340.1	AT1G18530.1 calmodulin, putative		1.24
Csa3M912920.1	AT4G17570.1 zinc finger (GATA type) family protein		1.24
Csa7M291190.1	AT1G71950.1 identical protein binding / serine-type endopeptidase		1.23
Csa5M571440.1	AT5G17350.1 unknown protein		1.22
Csa6M404290.1	No hits found		1.21
Csa1M039960.1	AT5G62940.1 Dof-type zinc finger domain-containing protein		1.21
Csa2M377370.1	AT5G26220.1 ChaC-like family protein		1.20
Csa6M087790.1	AT1G01320.1 tetratricopeptide repeat (TPR)-containing protein		1.20
Csa3M592130.1	AT5G14340.1 AtMYB40 (myb domain protein 40); DNA binding / transcription factor		1.19
Csa6M518000.1	AT1G28330.1 DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)		1.18
Csa1M569480.1	AT1G55110.1 AtIDD7 (Arabidopsis thaliana Indeterminate(ID)-Domain 7); nucleic acid binding / transcription factor/ zinc ion binding		1.18
Csa3M122650.1	AT2G45770.1 CPFTSY; 7S RNA binding / GTP binding / nucleoside-triphosphatase/ nucleotide binding		1.15
Csa5M647300.1	AT1G33480.1 protein binding / zinc ion binding		1.15
Csa6M487650.1	AT5G66650.1 unknown protein		1.15
Csa3M127170.1	AT1G32450.1 NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter		1.15
Csa4M641670.1	AT3G16150.1 L-asparaginase, putative / L-asparagine amidohydrolase, putative		1.14
Csa3M915160.1	AT4G27600.1 pfkB-type carbohydrate kinase family protein		1.14
Csa1M425940.1	AT5G57150.1 basic helix-loop-helix (bHLH) family protein		1.13
Csa5M139860.1	AT5G24030.1 SLAH3 (SLAC1 HOMOLOGUE 3); transporter		1.12
Csa6M518000.2	AT1G28330.1 DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)		1.12
Csa1M009870.1	AT5G61430.1 ANAC100 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 100); transcription factor		1.12
	AT4G15920.1 INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPR018169), RAG1-activating protein 1 homologue (InterPro:IPR018179), MtN3 and saliva related transmembrane protein (InterPro:IPR004316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	-2.27	1.11
Csa2M031160.1	AT3G26510.3 octicosapeptide/Phox/Bem1p (PB1) domain-containing protein		1.11
Csa2M349080.1	AT1G08280.1 glycosyl transferase family 29 protein / sialyltransferase family protein		1.10
Csa6M152940.1	AT4G25490.1 CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	-1.64	1.10
Csa3M180260.1	AT2G46240.1 BAG6 (BCL-2-ASSOCIATED ATHANOGENE 6); calmodulin binding / protein binding		1.09
Csa6M006890.1			
Csa3M015860.1	AT1G32450.1 NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	-1.45	1.09
Csa6M421780.1	AT1G07650.1 leucine-rich repeat transmembrane protein kinase, putative		1.09
Csa7M047970.1	AT4G28290.1 unknown protein		1.09
	AT1G17020.1 SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc		1.09
Csa6M521000.1	AT4G06534.1 unknown protein		1.08
Csa4M641570.1	AT1G28080.1 unknown protein		1.07
Csa6M091920.1	AT1G71100.1 RSW10 (RADIAL SWELLING 10); ribose-5-phosphate isomerase		1.07
Csa5M611700.1	AT2G24520.1 AHA5 (Arabidopsis H(+)-ATPase 5); ATPase		1.07
Csa1M423270.1			

Csa2M377350.1	AT2G24390.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Butirosin biosynthesis, BtrG-like (InterPro:IPR013024), AIG2-like (InterPro:IPR009288); BEST Arabidopsis thaliana protein match is: avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related (TAIR:AT4G31310.1); Has 204 Blast hits to 204 proteins in 63 species: Archae - 15; Bacteria - 49; Metazoa - 0; Fungi - 38; Plants - 61; Viruses - 0; Other Eukaryotes - 41 (source: NCBI BLink).		1.06
Csa6M303740.1	AT2G28710.1 zinc finger (C2H2 type) family protein		1.05
Csa4M295520.1	AT5G02430.1 WD-40 repeat family protein		1.05
Csa6M327430.1	AT5G49520.1 WRKY48; transcription factor		1.05
Csa1M338920.1	AT2G41480.1 electron carrier/ heme binding / peroxidase	-1.59	1.04
Csa4M290820.1	AT3G20870.1 metal transporter family protein		1.04

Csa3M849930.1	AT1G51745.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: PWWP (InterPro:IPR000313); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G21295.1); Has 414 Blast hits to 307 proteins in 88 species: Archae - 0; Bacteria - 106; Metazoa - 143; Fungi - 35; Plants - 61; Viruses - 3; Other Eukaryotes - 66 (source: NCBI BLink).		1.02
Csa6M502780.1	No hits found		1.02

Csa2M020850.1	AT1G54740.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: structural constituent of ribosome (TAIR:AT1G22110.1); Has 479 Blast hits to 317 proteins in 60 species: Archae - 0; Bacteria - 25; Metazoa - 81; Fungi - 16; Plants - 88; Viruses - 0; Other Eukaryotes - 269 (source: NCBI BLink).		1.01
Csa5M151000.1	AT1G64300.1 protein kinase family protein		1.01
Csa6M518190.1	AT1G28480.1 GRX480; electron carrier/ protein disulfide oxidoreductase		1.01
Csa1M039020.1	AT5G61210.1 SNAP33 (SOLUBLE N-ETHYLMALIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding		1.01
Csa5M155570.1	AT1G12610.1 DDF1 (DWARF AND DELAYED FLOWERING 1); DNA binding / sequence-specific DNA binding / transcription factor		1.01

Elements only in "Sn Up-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa3M076580.1	AT3G20390.1 endoribonuclease L-PSP family protein						5.28
Csa3M076560.1	AT4G21920.1 unknown protein						3.81
Csa4M075740.1	AT1G17147.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: VQ (InterPro:IPR008889); BEST Arabidopsis thaliana protein match is: VQ motif-containing protein (TAIR:AT1G78410.1); Has 18 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).						3.71
Csa6M485170.2	AT5G64700.1 nodulin MtN21 family protein						3.63
Csa1M166260.1	AT5G22410.1 peroxidase, putative	-2.92					3.36
Csa2M004690.1	AT3G24520.1 AT-HSFC1; DNA binding / transcription factor						3.34
Csa6M485170.1	AT5G64700.1 nodulin MtN21 family protein						3.34
Csa4M011720.1	No hits found						3.17
Csa7M419560.1	AT1G44970.1 peroxidase, putative						3.16
Csa3M895700.1	AT3G63520.1 CCD1 (CAROTENOID CLEAVAGE DIOXYGENASE 1); 9-cis-epoxycarotenoid dioxygenase	-3.40					3.16
Csa3M646530.1	AT5G40990.1 GLIP1 (GDSL LIPASE 1); carboxylesterase/ lipase						3.10
Csa7M419540.1	AT3G03670.1 peroxidase, putative						3.09
Csa6M169310.1	AT4G18880.1 AT-HSFA4A; DNA binding / transcription factor						3.07
Csa7M419550.1	AT3G03670.1 peroxidase, putative						3.05
Csa3M742880.1	AT1G08080.1 ACA7 (ALPHA CARBONIC ANHYDRASE 7); carbonate dehydratase/ zinc ion binding						3.00
Csa5M154800.1	AT1G63410.1 unknown protein						2.97
Csa1M002940.1	AT5G63130.1 octicosapeptide/Phox/Bem1p (PB1) domain-containing protein						2.94

Csa6M485670.1	AT5G64700.1 nodulin MtN21 family protein		2.94
Csa4M288090.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	-2.48	2.92
Csa4M637160.1	AT3G15350.1 glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein	-1.99	2.92
Csa6M519460.1	AT4G18540.1 unknown protein		2.91
Csa4M293330.1	AT2G37430.1 zinc finger (C2H2 type) family protein (ZAT11)		2.89
Csa6M147490.1	No hits found		2.84
Csa1M059710.1	AT1G11925.1 Encodes a Stigma-specific Stig1 family protein		2.82
Csa1M051690.1	AT5G50760.1 auxin-responsive family protein		2.80
Csa2M351540.1	AT5G43260.1 chaperone protein dnaJ-related		2.78
Csa2M354930.1	AT5G20480.1 EFR (EF-TU RECEPTOR); ATP binding / kinase/ protein serine/threonine kinase		2.76
Csa3M895690.1	AT3G14440.1 NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	-3.28	2.76
Csa4M280600.1	AT1G55230.1 unknown protein		2.74
Csa4M291920.1	AT5G19855.1 unknown protein		2.72
Csa6M216420.1	AT5G05340.1 peroxidase, putative		2.71
Csa2M420990.1	AT3G21720.1 ICL (ISOCITRATE LYASE); catalytic/ isocitrate lyase		2.70
Csa3M855350.1	AT1G75130.1 CYP721A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		2.70
Csa4M022220.1	No hits found		2.69
Csa2M373590.1	AT4G32810.1 CCD8 (CAROTENOID CLEAVAGE DIOXYGENASE 8); oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	-2.26	2.66
Csa6M509650.1	AT4G35590.1 RWP-RK domain-containing protein		2.66
Csa7M237830.1	AT3G12910.1 transcription factor		2.66
Csa7M127380.1	AT1G55850.1 ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups		2.64
Csa3M331330.1	AT1G70850.1 MLP34 (MLP-LIKE PROTEIN 34)		2.60
Csa7M237830.2	AT3G12910.1 transcription factor		2.60
Csa3M733910.1	No hits found		2.57
Csa6M139190.1	AT2G43000.1 anac042 (Arabidopsis NAC domain containing protein 42); transcription factor		2.57
Csa4M622240.1	AT1G17060.1 CYP72C1 (CYTOCHROME P450 72C1); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		2.55
Csa7M043050.1	AT1G62280.1 SLAH1 (SLAC1 HOMOLOGUE 1); transporter		2.55
Csa6M395130.1	AT1G21400.1 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative		2.53
Csa2M000420.1	AT5G56960.1 basic helix-loop-helix (bHLH) family protein		2.51
Csa3M855360.1	AT1G75130.1 CYP721A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		2.51
Csa3M146480.1	AT3G22620.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein		2.51
Csa6M006800.1	AT3G61510.1 ACS1 (ACC SYNTHASE 1); 1-aminocyclopropane-1-carboxylate synthase		2.48
Csa3M119720.1	AT4G01070.1 GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups		2.48
Csa1M627480.1	AT5G12340.1 unknown protein		2.47
Csa5M517170.1	AT3G55470.2 C2 domain-containing protein		2.45
Csa6M083030.1	No hits found		2.44
Csa4M288070.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase		2.44
Csa1M533650.1	AT5G05340.1 peroxidase, putative		2.42
Csa1M680120.1	AT1G08630.1 THA1 (Threonine Aldolase 1); aldehyde-lyase/ threonine aldolase		2.42
Csa2M298300.1	AT4G16730.1 lyase/ magnesium ion binding		2.39
Csa6M513600.1	AT4G04480.1 LOCATED IN: chloroplast; EXPRESSED IN: flower, pollen tube; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT4G22030.1); Has 51 Blast hits to 51 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).		2.39
Csa3M116720.1	AT2G44840.1 ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor		2.36
Csa2M055050.1	AT1G73050.1 (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative		2.36

Csa1M024160.1	AT1G48000.1 MYB112 (myb domain protein 112); DNA binding / transcription factor AT3G21510.1 AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 1); histidine phosphotransfer kinase	2.36
Csa1M572420.1		2.36
Csa3M600020.1	AT5G13930.1 TT4 (TRANSPARENT TESTA 4); naringenin-chalcone synthase	2.34
Csa3M535090.1	AT3G06490.1 MYB108 (myb domain protein 108); DNA binding / transcription factor	2.34
Csa6M486970.1	AT1G77280.1 protein kinase family protein	2.33
Csa6M519740.1	No hits found	2.32
Csa4M640960.1	AT5G42830.1 transferase family protein	2.32
Csa1M435720.1	AT2G34600.1 JAZ7 (JASMONATE-ZIM-DOMAIN PROTEIN 7)	2.31
Csa2M004710.1	AT5G53250.1 AGP22 (ARABINOGLACTAN PROTEIN 22)	2.30
Csa2M271490.1	No hits found	2.29
Csa3M271380.1	AT1G13340.1 unknown protein	2.29
Csa3M150740.1	AT4G15530.2 PPKDK (pyruvate orthophosphate dikinase); kinase/ pyruvate, phosphate dikinase	2.29
Csa6M513610.1	AT4G04480.1 LOCATED IN: chloroplast; EXPRESSED IN: flower, pollen tube; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT4G22030.1); Has 51 Blast hits to 51 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK). AT5G13720.1 LOCATED IN: chloroplast, chloroplast inner membrane, chloroplast envelope; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP022348 (InterPro:IPR016804), Uncharacterised protein family UPF0114 (InterPro:IPR005134); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G19390.1); Has 294 Blast hits to 294 proteins in 98 species: Archae - 18; Bacteria - 168; Metazoa - 0; Fungi - 0; Plants - 53; Viruses - 0; Other Eukaryotes - 55 (source: NCBI BLINK).	2.28
Csa2M360800.1	AT4G17500.1 ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	2.28
Csa5M165850.1		2.28
Csa6M018590.1	AT2G27035.1 plastocyanin-like domain-containing protein AT2G44840.1 ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	2.27
Csa3M116730.1		2.26
Csa1M071940.1	AT1G61260.1 unknown protein AT4G01070.1 GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	2.26
Csa3M119730.1	No hits found	2.25
Csa6M082530.1		2.25
Csa6M490950.1	AT4G36950.1 MAPKKK21; ATP binding / protein kinase/ protein serine/threonine kinase AT5G20230.1 ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier	2.25
Csa1M348950.1		2.24
Csa1M538280.1	AT4G21120.1 AAT1 (AMINO ACID TRANSPORTER 1); L-glutamate transmembrane transporter/ L-lysine transmembrane transporter/ arginine transmembrane transporter/ cationic amino acid transmembrane transporter	2.24
Csa4M617410.1	AT3G22250.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein	2.21
Csa4M285810.1	AT5G06730.1 peroxidase, putative	2.21
Csa3M142940.1	No hits found AT3G14680.1 CYP72A14; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	2.19
Csa4M621720.1		2.17
Csa3M567330.1	AT5G13080.1 WRKY75; transcription factor	2.17
Csa2M348140.1	No hits found	2.16
Csa6M139170.1	AT1G26870.1 FEZ (FEZ); transcription factor	2.16
Csa3M000170.1	AT5G65980.1 auxin efflux carrier family protein AT2G38940.1 ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter	2.13
Csa3M135080.1		2.12
Csa3M002690.1	AT1G19640.1 JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate O-methyltransferase	2.11
Csa4M658480.1	AT1G76240.1 unknown protein	2.10
Csa2M401240.1	AT1G22810.1 AP2 domain-containing transcription factor, putative	2.10

Csa1M326870.1	AT5G16990.1 NADP-dependent oxidoreductase, putative AT4G36810.1 GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltranstransferase	-2.77	2.09
Csa6M487640.1			2.09
Csa3M603600.1	AT2G25410.1 protein binding / zinc ion binding	-1.93	2.08
Csa6M520380.1	AT1G59740.1 proton-dependent oligopeptide transport (POT) family protein		2.08
Csa6M083530.1	No hits found		2.07
Csa4M640970.1	AT5G42830.1 transferase family protein		2.07
Csa3M910670.1	AT4G17030.1 ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1)		2.06
Csa6M011600.1	AT3G47570.1 leucine-rich repeat transmembrane protein kinase, putative	-1.40	2.04
Csa4M628880.1	AT5G48410.1 ATGLR1.3; intracellular ligand-gated ion channel		2.04
Csa3M257090.1	AT5G16170.1 unknown protein AT5G23320.1 ATSTE14A (ARABIDOPSIS HOMOLOG OF YEAST STE14 A); carboxyl-O- methyltransferase/ protein-S-isoprenylcysteine O-methyltransferase		2.04
Csa6M074600.1			2.03
Csa3M178580.1	AT5G51780.1 basix helix-loop-helix (bHLH) family protein		2.03
Csa2M406650.1	AT4G37530.1 peroxidase, putative	-2.28	2.02
Csa6M077360.1	AT3G60810.1 unknown protein		1.99
Csa3M077660.1	AT4G30580.1 ATS2; 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase		1.99
Csa2M070310.1	AT3G12580.1 HSP70 (heat shock protein 70); ATP binding		1.98
Csa5M609750.1	AT3G18360.1 VQ motif-containing protein		1.97
Csa1M589650.1	AT2G26190.1 calmodulin-binding family protein		1.96
Csa4M001850.1	AT4G02380.1 SAG21 (SENESCENCE-ASSOCIATED GENE 21)		1.96
Csa1M295170.1	AT4G31710.1 ATGLR2.4; intracellular ligand-gated ion channel AT3G23240.1 ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor		1.95
Csa7M375820.1			1.95
Csa5M623470.1	AT1G11310.1 MLO2 (MILDEW RESISTANCE LOCUS O 2); calmodulin binding		1.95
Csa7M394070.1	No hits found		1.95
Csa3M321300.1	AT1G70850.1 MLP34 (MLP-LIKE PROTEIN 34)		1.95
Csa6M350370.1	AT1G21270.1 WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase		1.95
Csa1M050210.1	AT1G24430.1 transferase/ transferase, transferring acyl groups other than amino-acyl groups AT2G29420.1 ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase		1.94
Csa3M133880.1			1.93
Csa4M269210.1	AT1G65690.1 harpin-induced protein-related / HIN1-related / harpin-responsive protein-related		1.93
Csa1M654920.1	AT4G12910.1 scpl20 (serine carboxypeptidase-like 20); serine-type carboxypeptidase		1.93
Csa5M172890.1	AT3G47420.1 glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative		1.93
Csa7M413890.1	AT5G49620.1 AtMYB78 (myb domain protein 78); DNA binding / transcription factor		1.93
Csa4M015100.1	AT1G60710.1 ATB2; oxidoreductase		1.92
Csa1M058140.1	AT2G39420.1 esterase/lipase/thioesterase family protein		1.92
Csa3M872740.1	AT1G20030.2 pathogenesis-related thaumatin family protein		1.91
Csa3M333840.1	AT1G70890.1 MLP43 (MLP-LIKE PROTEIN 43)		1.91
Csa3M303630.1	AT1G66230.1 MYB20 (myb domain protein 20); DNA binding / transcription factor		1.91
Csa4M361270.1	AT1G77330.1 1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative AT4G37330.1 CYP81D4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.37	1.91
Csa2M425750.1			1.91
Csa4M010410.1	AT5G67550.1 unknown protein		1.90
Csa6M497340.1	AT2G22620.1 lyase		1.90
Csa1M257870.1	AT2G24130.1 leucine-rich repeat transmembrane protein kinase, putative		1.89
Csa6M350360.1	AT1G21240.1 WAK3 (wall associated kinase 3); kinase/ protein serine/threonine kinase		1.89
Csa1M703580.1	AT1G31200.1 A1PP2-A9 (Phloem protein 2-A9); carbohydrate binding		1.89
Csa4M099750.1	AT5G65380.1 ripening-responsive protein, putative		1.88
Csa1M004920.1	AT5G62770.1 unknown protein		1.88
Csa4M652140.1	AT5G11000.1 unknown protein		1.88
Csa1M497810.1	AT5G02640.1 unknown protein		1.87
Csa6M085110.1	No hits found		1.87

Csa3M651750.1	AT1G73080.1 PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase		1.87
Csa5M571560.1	AT1G76650.1 calcium-binding EF hand family protein		1.86
Csa3M555690.1	AT1G52800.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	-2.02	1.86
Csa7M257340.1	AT3G18830.1 ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann		1.85
Csa3M778200.1	AT5G06250.2 transcription factor		1.85
Csa5M215140.1	AT2G30130.1 ASL5; DNA binding / protein binding		1.84
Csa4M000640.1	AT3G19660.1 unknown protein		1.84
Csa2M021560.1	AT2G35000.1 zinc finger (C3HC4-type RING finger) family protein		1.84
Csa3M779000.1	AT2G35980.1 YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)		1.84
Csa5M487690.1	AT4G16500.1 cysteine protease inhibitor family protein / cystatin family protein		1.84
Csa3M706170.1	AT2G31945.1 unknown protein		1.84
Csa4M411390.1	AT2G41640.1 transferase, transferring glycosyl groups		1.84
Csa2M177210.1	AT3G23240.1 ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor		1.83
Csa5M139780.1	AT1G64950.1 CYP89A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-2.48	1.83
Csa2M379900.1	AT5G11330.1 monooxygenase family protein		1.82
Csa3M416660.1	AT2G42850.1 CYP718; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		1.82
Csa5M641610.1	AT3G30210.1 MYB121 (MYB DOMAIN PROTEIN 121); DNA binding / transcription factor		1.82
Csa7M212670.1	No hits found		1.82
Csa4M015110.1	AT1G05894.1 unknown protein		1.81
Csa7M023970.1	AT2G17070.1 unknown protein		1.81
Csa4M631610.1	AT3G23560.1 ALF5 (ABERRANT LATERAL ROOT FORMATION 5); antiporter/ drug transporter/ transporter		1.81
Csa1M063510.1	AT1G11655.1 unknown protein		1.80
Csa3M126940.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase		1.80
Csa6M492310.1	AT2G14960.1 GH3.1		1.80
Csa1M306810.1	AT2G26695.1 binding / zinc ion binding		1.80
Csa3M875410.1	AT1G20310.1 unknown protein		1.80
Csa1M070610.1	AT1G11410.1 S-locus protein kinase, putative		1.80
Csa1M004920.2	AT5G62770.1 unknown protein		1.80
Csa2M020870.1	AT4G11170.1 disease resistance protein (TIR-NBS-LRR class), putative		1.78
Csa6M121970.1	AT2G16720.1 MYB7 (MYB DOMAIN PROTEIN 7); DNA binding / transcription factor		1.78
Csa4M314440.1	AT5G01650.1 macrophage migration inhibitory factor family protein / MIF family protein		1.78
Csa2M354820.1	AT1G27730.1 STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding		1.78
Csa6M421630.1	AT1G05010.1 EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase		1.77
Csa7M073780.1	AT2G26530.1 AR781		1.77
Csa1M324370.1	AT2G26690.1 nitrate transporter (NTP2)		1.77
Csa6M452040.1	AT5G03610.1 GDSDL-motif lipase/hydrolase family protein		1.76
Csa5M139810.1	No hits found		1.76
Csa3M120470.1	AT5G24090.1 acidic endochitinase (CHIB1)		1.76
Csa6M497110.1	AT4G37850.1 basic helix-loop-helix (bHLH) family protein		1.76
Csa7M023950.1	AT2G17080.1 unknown protein		1.75
Csa3M178500.1	AT1G68530.1 KCS6 (3-KETOACYL-COA SYNTHASE 6); catalytic/ transferase, transferring acyl groups other than amino-acyl groups		1.75
Csa2M371110.1	AT2G22500.1 UCP5 (UNCOUPLING PROTEIN 5); binding		1.75
Csa5M609110.1	No hits found		1.74
Csa4M288080.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase		1.74
Csa2M357190.1	AT5G67060.1 HEC1 (HECATE 1); transcription factor		1.73
Csa2M027460.1	AT1G55020.1 LOX1; lipoxygenase		1.73



Csa4M000840.1	AT3G19615.1 unknown protein		1.73
Csa3M852470.1	AT4G27410.2 RD26 (RESPONSIVE TO DESICCATION 26); transcription activator/ transcription factor		1.73
Csa5M209480.1	AT1G07160.1 protein phosphatase 2C, putative / PP2C, putative		1.72
Csa2M003060.1	AT4G28840.1 unknown protein	-2.07	1.72
Csa7M253810.1	AT3G18830.1 ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann		1.72
Csa4M110080.1	AT5G02070.1 protein kinase-related		1.72
Csa5M599860.1	AT1G12940.1 ATNRT2.5 (nitrate transporter2.5); nitrate transmembrane transporter	-2.93	1.71
Csa3M405520.1	No hits found		1.71
Csa5M146910.1	AT1G64720.1 CP5		1.71
Csa3M598370.1	AT5G14040.1 mitochondrial phosphate transporter		1.71
Csa1M420340.1	AT4G15560.1 CLA1 (CLOROPLASTOS ALTERADOS 1); 1-deoxy-D-xylulose-5-phosphate synthase		1.71
Csa4M109010.1	AT5G64210.1 AOX2; alternative oxidase		1.70
Csa1M039830.1	AT1G74110.1 CYP78A10; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		1.70
Csa4M290200.1	AT5G12890.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein		1.70
Csa4M246400.1	AT4G19380.1 alcohol oxidase-related		1.69
Csa7M229900.1	AT5G07170.1 unknown protein		1.69
Csa5M484630.1	AT1G70170.1 MMP (MATRIX METALLOPROTEINASE); metalloendopeptidase/ metallopeptidase		1.69
Csa1M569310.1	AT3G05540.1 INVOLVED IN: biological_process unknown; LOCATED IN: cytoplasm; CONTAINS InterPro DOMAIN/s: Translationally controlled tumour protein (InterPro:IPR018105), Translationally controlled tumour-associated TCTP (InterPro:IPR001983), Mss4/translationally controlled tumour-associated TCTP (InterPro:IPR011323), Translationally controlled tumour protein, conserved site (InterPro:IPR018103), Mss4 like (InterPro:IPR011057); BEST Arabidopsis thaliana protein match is: TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN) (TAIR:AT3G16640.1); Has 640 Blast hits to 640 proteins in 231 species: Archae - 0; Bacteria - 0; Metazoa - 343; Fungi - 110; Plants - 105; Viruses - 0; Other Eukaryotes - 82 (source: NCBI BLink).		1.69
Csa5M190550.1	AT5G59720.1 HSP18.2 (heat shock protein 18.2)		1.69
Csa5M027940.1	AT1G14870.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: plasma membrane; EXPRESSED IN: callus; CONTAINS InterPro DOMAIN/s: EGF-type aspartate/asparagine hydroxylation conserved site (InterPro:IPR000152), Protein of unknown function Cys-rich (InterPro:IPR006461); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35525.1); Has 492 Blast hits to 491 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 93; Fungi - 76; Plants - 297; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink).		1.69
Csa1M536320.1	No hits found		1.69
Csa4M050160.1	AT5G41590.1 unknown protein		1.68
Csa2M308370.1	AT1G22170.1 phosphoglycerate/bisphosphoglycerate mutase family protein		1.68
Csa4M280650.1	AT1G55210.1 disease resistance response		1.67
Csa5M606310.1	AT1G69490.1 NAP (NAC-like, activated by AP3/PI); transcription factor		1.66
Csa3M078260.1	AT5G54800.1 GPT1; antiporter/ glucose-6-phosphate transmembrane transporter		1.66
Csa5M622620.1	AT3G54850.1 PUB14; ubiquitin-protein ligase		1.65
Csa3M120480.1	AT5G24090.1 acidic endochitinase (CHIB1)		1.65
Csa4M000820.2	No hits found		1.65
Csa4M285740.1	AT5G06720.1 peroxidase, putative		1.64
Csa4M064040.1	AT1G16670.1 protein kinase family protein		1.64
Csa2M404730.1	AT4G33680.1 AGD2 (ABERRANT GROWTH AND DEATH 2); L,L-diaminopimelate aminotransferase/transaminase		1.64
Csa3M116790.1	AT3G60270.1 uclacyanin, putative		1.64
Csa4M012390.1	AT5G13080.1 WRKY75; transcription factor		1.63
Csa4M001900.1	AT4G02340.1 epoxide hydrolase, putative		1.63
Csa4M622230.1	AT3G14690.1 CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		1.63

Csa5M352630.1	AT3G19970.1 unknown protein	1.63
Csa7M211090.1	AT4G38460.1 GGR (geranylgeranyl reductase); farnesyltranstransferase	1.62
Csa7M396340.1	AT4G15800.1 RALFL33 (ralf-like 33); signal transducer	1.62
Csa2M371610.2	AT2G22500.1 UCP5 (UNCOUPLING PROTEIN 5); binding	1.62
Csa6M497100.1	AT2G22750.2 basic helix-loop-helix (bHLH) family protein	1.61
Csa3M135750.1	AT1G06620.1 2-oxoglutarate-dependent dioxygenase, putative	1.61
	AT2G16050.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: DC1 (InterPro:IPR004146); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G20990.1); Has 719 Blast hits to 448 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 717; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	
Csa2M239390.1	No hits found	1.61
Csa3M842740.1	AT5G53970.1 aminotransferase, putative	1.61
Csa4M629470.2	AT2G40080.1 ELF4 (EARLY FLOWERING 4)	1.60
Csa5M202370.1	No hits found	1.60
Csa2M000670.1	AT5G56550.1 OXS3 (OXIDATIVE STRESS 3)	1.60
Csa1M575060.1	No hits found	1.60
Csa3M827220.1	AT2G42760.1 unknown protein	1.60
Csa6M519700.1	AT5G10530.1 lectin protein kinase, putative	1.59
Csa7M066840.1	AT2G42760.1 unknown protein	1.59
Csa1M470240.1	AT4G14640.1 CAM8 (CALMODULIN 8); calcium ion binding	1.59
Csa2M228380.1	AT1G60940.1 SNRK2.10 (SNF1-RELATED PROTEIN KINASE 2.10); kinase	1.59
Csa4M457190.2	AT1G59590.1 ZCF37	1.59
Csa4M642550.1	AT4G24570.1 mitochondrial substrate carrier family protein	1.58
Csa6M499090.1	AT5G53970.1 aminotransferase, putative	1.58
Csa4M629470.1	AT3G45660.1 proton-dependent oligopeptide transport (POT) family protein	1.58
Csa1M479650.1	AT3G21550.1 unknown protein	1.58
Csa3M150790.1	No hits found	1.58
Csa4M017210.1	AT1G54120.1 unknown protein	1.58
Csa3M644780.1	AT1G10640.1 polygalacturonase	1.57
Csa5M601470.1	No hits found	1.57
Csa4M022250.1	AT1G61560.1 MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding	1.57
Csa6M292430.1	No hits found	1.57
Csa5M487700.1	AT2G22500.1 UCP5 (UNCOUPLING PROTEIN 5); binding	1.57
Csa2M371610.1	AT5G26340.1 MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter	1.57
Csa6M424540.1	AT3G29000.1 calcium-binding EF hand family protein	1.57
Csa5M636620.1	AT4G40020.1 unknown protein	1.57
Csa4M026890.1	AT2G12190.1 cytochrome P450, putative	1.57
Csa2M432220.1	AT1G08470.1 stricotosidine synthase family protein	1.56
Csa1M025790.1	AT2G46320.1 mitochondrial substrate carrier family protein	1.56
Csa3M120400.2	AT2G32510.1 MAPKKK17; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	1.56
Csa7M043040.1	AT1G09950.1 transcription factor-related	1.56
Csa3M731050.1	AT4G34135.1 UGT73B2 (UDP-GLUCOSYLTRANSFERASE 73B2); UDP-glucosyltransferase/ UDP-glycosyltransferase/ flavonol 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase	1.55
Csa7M073450.1	No hits found	1.55
Csa1M257330.1	AT3G51970.1 AtSAT1 (Arabidopsis thaliana sterol O-acyltransferase 1); acyltransferase	1.55
Csa3M684690.1	AT5G52390.1 photoassimilate-responsive protein, putative	1.55
Csa3M182150.1	No hits found	1.55
Csa4M000820.1	AT4G37370.1 CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	1.55
Csa6M492250.1	AT4G35390.1 AGF1 (AT-hook protein of GA feedback 1); transcription factor	1.55
Csa7M029400.1	AT5G49690.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein	1.55
Csa4M279800.1	AT1G55020.1 LOX1; lipoxygenase	1.55
Csa2M026940.1	AT3G08760.1 ATSIK; ATP binding / kinase/ protein kinase/ protein tyrosine kinase	1.55
Csa4M334120.1		1.55

Csa6M486960.1	AT5G64810.1 WRKY51; transcription factor	1.55
Csa4M009900.1	AT5G61760.1 ATIPK2BETA; inositol or phosphatidylinositol kinase/ inositol trisphosphate 6-kinase	1.54
Csa6M424530.1	AT5G26340.1 MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity	1.54
Csa5M591770.1	hydrogen:glucose symporter/ sugar:hydrogen symporter	1.54
Csa5M197120.1	AT3G48450.1 nitrate-responsive NOI protein, putative	1.53
Csa1M426980.1	No hits found	1.53
Csa2M336130.1	AT2G30590.1 WRKY21; calmodulin binding / transcription factor	1.53
Csa1M044320.1	AT2G02390.1 ATGSTZ1 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE ZETA 1); catalytic/ glutathione transferase	1.53
Csa6M502830.1	AT1G17830.1 unknown protein	1.53
Csa6M008710.1	AT4G36500.1 unknown protein	1.52
Csa6M522750.1	AT3G11420.1 fringe-related protein	1.52
Csa3M733870.1	AT5G46295.1 unknown protein	1.52
Csa6M519530.1	AT4G00340.1 RLK4 (RECEPTOR-LIKE PROTEIN KINASE 4); protein kinase/ sugar binding	1.51
Csa6M495810.1	AT2G27430.1 binding	1.51
Csa4M457190.1	AT2G22880.1 VQ motif-containing protein	1.50
Csa3M308190.1	AT1G60940.1 SNRK2.10 (SNF1-RELATED PROTEIN KINASE 2.10); kinase	1.50
Csa5M601620.1	AT5G37490.1 U-box domain-containing protein	1.50
Csa1M537320.1	AT1G60190.1 armadillo/beta-catenin repeat family protein / U-box domain-containing protein	1.49
Csa1M267230.1	AT1G30370.1 lipase class 3 family protein	1.49
Csa5M505170.1	AT4G19810.1 glycosyl hydrolase family 18 protein	1.49
Csa5M622590.1	AT3G55120.1 TT5 (TRANSPARENT TESTA 5); chalcone isomerase	1.49
Csa3M651870.1	AT3G54940.2 cysteine-type endopeptidase/ cysteine-type peptidase	1.49
Csa6M522650.1	No hits found	1.49
Csa6M454350.2	AT1G29860.1 WRKY71; transcription factor	1.49
Csa3M651880.1	AT3G02875.1 ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugate hydrolase/ IAA-Phe conjugate hydrolase/ metallopeptidase	1.49
Csa3M889690.1	AT3G22800.1 leucine-rich repeat family protein / extensin family protein	1.49
Csa4M279910.1	AT1G22280.2 protein phosphatase 2C, putative / PP2C, putative	1.48
Csa2M433930.1	AT3G13600.1 calmodulin-binding family protein	1.48
Csa6M497180.1	AT1G59870.1 PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances /	1.48
Csa6M490940.1	AT4G37870.1 PCK1 (PHOSPHOENOLPYRUVATE CARBOXYKINASE 1); ATP binding / phosphoenolpyruvate carboxykinase (ATP)/ phosphoenolpyruvate carboxykinase/ purine nucleotide binding	1.48
Csa7M041870.1	AT5G67050.1 lipase class 3 family protein	1.48
Csa6M507470.1	AT5G47530.1 auxin-responsive protein, putative	1.48
Csa2M292840.1	AT4G35720.1 unknown protein	1.48
Csa7M033410.1	AT2G26560.1 PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	1.48
Csa1M073880.1	AT5G35735.1 auxin-responsive family protein	1.48
Csa5M023870.1	No hits found	1.48
Csa3M179080.1	AT5G37490.1 U-box domain-containing protein	1.47
Csa3M852440.1	AT1G52540.1 protein kinase, putative	1.47
Csa1M060760.1	AT3G15518.1 unknown protein	1.47
Csa6M523440.1	No hits found	1.47
Csa5M205920.1	AT1G30100.1 NCED5 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 5); 9-cis-epoxycarotenoid dioxygenase	1.47
Csa6M014510.1	AT5G05600.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.47
Csa4M016470.1	No hits found	1.46
Csa3M730800.1	AT4G15390.1 transferase family protein	1.46
Csa3M168940.1	AT2G38470.1 WRKY33; transcription factor	1.46
Csa6M398210.1	AT3G06490.1 MYB108 (myb domain protein 108); DNA binding / transcription factor	1.46
Csa6M087190.2	AT1G31130.1 unknown protein	1.46
Csa4M022210.1	AT3G59680.1 unknown protein	1.46
	No hits found	1.46

-1.11

Csa2M000800.1	AT4G29140.1 MATE efflux protein-related		1.46
Csa1M499310.1	AT3G29590.1 AT5MAT; O-malonyltransferase/ transferase		1.46
Csa3M735030.1	AT3G09520.1 ATEXO70H4 (exocyst subunit EXO70 family protein H4); protein binding		1.45
Csa4M012430.1	No hits found		1.45
Csa5M524780.1	AT5G14700.1 cinnamoyl-CoA reductase-related		1.45
Csa3M146340.1	AT3G51895.1 SULTR3;1 (SULFATE TRANSPORTER 3;1); secondary active sulfate transmembrane transporter/ sulfate transmembrane transporter/ transporter		1.45
Csa4M624960.1	AT1G53440.1 leucine-rich repeat family protein / protein kinase family protein		1.45
Csa7M407810.1	No hits found		1.44
Csa3M207390.1	AT4G34410.1 RRTF1 ((REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor		1.44
Csa7M073500.1	AT4G34131.1 UGT73B3 (UDP-glucosyl transferase 73B3); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring hexosyl groups		1.44
Csa7M071700.1	AT4G34230.1 ATCAD5 (CINNAMYL ALCOHOL DEHYDROGENASE 5); cinnamyl-alcohol dehydrogenase		1.44
Csa6M046430.1	No hits found		1.44
CsaUNM003170.1	AT4G28890.1 protein binding / ubiquitin-protein ligase/ zinc ion binding		1.44
Csa3M146490.1	AT3G22600.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein		1.43
Csa6M160180.1	AT1G05010.1 EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase		1.43
CsaUNM024760.1	AT4G28890.1 protein binding / ubiquitin-protein ligase/ zinc ion binding		1.43
Csa2M171950.1	AT3G23530.1 cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative		1.43
Csa3M914060.1	AT4G16820.1 lipase class 3 family protein		1.43
Csa2M285340.1	AT4G37650.1 SHR (SHORT ROOT); protein binding / sequence-specific DNA binding / transcription factor		1.43
Csa5M610360.1	AT1G25390.1 protein kinase family protein		1.43
Csa1M555620.1	AT1G56580.1 unknown protein	-2.55	1.43
Csa3M516530.1	AT1G52830.1 IAA6 (INDOLE-3-ACETIC ACID 6); transcription factor		1.43
Csa1M569340.1	AT1G44750.2 ATPUP11; purine transmembrane transporter		1.42
Csa6M454350.1	AT3G02875.1 ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugate hydrolase/ IAA-Phe conjugate hydrolase/ metallopeptidase		1.42
Csa3M061000.1	AT4G26470.1 calcium ion binding		1.42
Csa4M607030.1	AT3G12955.1 auxin-responsive protein-related		1.42
Csa5M623670.1	AT2G38750.1 ANNAT4 (ANNEXIN ARABIDOPSIS 4); calcium ion binding / calcium-dependent phospholipid binding		1.42
Csa2M357260.1	AT4G35290.2 GLUR2 (GLUTAMATE RECEPTOR 2); intracellular ligand-gated ion channel		1.42
Csa3M812790.1	No hits found		1.41
Csa7M068600.1	AT1G58290.1 HEMA1; glutamyl-tRNA reductase		1.41
Csa3M800660.1	AT2G41970.1 protein kinase, putative	-1.08	1.41
Csa4M049610.2	AT4G11280.1 ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase		1.41
Csa2M336070.1	AT5G58890.1 AGL82 (AGAMOUS-LIKE 82); DNA binding / transcription factor		1.41
Csa4M608170.1	AT2G43000.1 anac042 (Arabidopsis NAC domain containing protein 42); transcription factor		1.41
Csa1M045480.1	AT1G18860.1 WRKY61; transcription factor		1.41
Csa2M373430.1	AT5G25880.1 ATNADP-ME3 (NADP-malic enzyme 3); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+); malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor		1.41
Csa2M369210.1	AT2G35000.1 zinc finger (C3HC4-type RING finger) family protein		1.41
Csa3M731160.1	AT3G11180.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein		1.41
Csa2M008110.1	AT5G20410.1 MGD2; 1,2-diaclyglycerol 3-beta-galactosyltransferase/ UDP-galactosyltransferase/ transferase, transferring glycosyl groups	-1.53	1.40
Csa1M589710.1	AT5G12010.1 unknown protein		1.40
Csa4M011070.1	No hits found		1.40
Csa6M056490.1	AT1G74450.1 unknown protein		1.40
Csa6M046420.1	AT5G04930.1 ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism		1.40

Csa5M577430.1	AT3G25690.1 CHUP1 (CHLOROPLAST UNUSUAL POSITIONING 1)	1.40
Csa1M011510.1	AT1G74360.1 leucine-rich repeat transmembrane protein kinase, putative	1.39
Csa1M479640.1	AT3G45680.1 proton-dependent oligopeptide transport (POT) family protein	1.39
Csa5M224130.1	AT5G24910.1 CYP714A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.44
Csa1M499320.1	AT3G29670.1 transferase family protein	1.39
Csa6M358680.1	AT4G35190.1 unknown protein	1.39
Csa2M010150.1	No hits found	1.39
Csa3M182790.1	No hits found	1.38
Csa5M387980.1	AT1G36940.1 unknown protein	1.38
Csa7M432180.1	AT3G02650.1 pentatricopeptide (PPR) repeat-containing protein	1.38
Csa6M425740.1	AT3G44326.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Cyclin-like F-box (InterPro:IPR001810); BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT2G27310.1); Has 56 Blast hits to 56 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	1.38
Csa3M778430.1	AT5G06300.1 carboxy-lyase	1.38
Csa2M373430.2	AT5G25880.1 ATNADP-ME3 (NADP-malic enzyme 3); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor	1.38
Csa1M015880.1	No hits found	1.38
Csa5M286040.1	AT2G38870.1 protease inhibitor, putative	1.38
Csa3M134610.1	AT4G21865.1 unknown protein	1.38
Csa6M081510.1	AT4G37650.1 SHR (SHORT ROOT); protein binding / sequence-specific DNA binding / transcription factor	1.38
Csa3M731870.1	AT5G01250.1 alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein	1.37
Csa5M285030.1	AT2G38870.1 protease inhibitor, putative	1.37
Csa4M420130.1	AT5G47580.1 unknown protein	1.37
Csa4M269770.1	AT2G02800.1 APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	1.37
Csa5M100000.1	AT2G02010.1 GAD4 (glutamate decarboxylase 4); calmodulin binding	1.37
Csa3M732610.1	AT2G37980.1 unknown protein	1.37
Csa4M022240.1	No hits found	1.37
Csa6M086130.1	No hits found	1.37
Csa6M495740.1	AT4G37670.2 GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein	1.36
Csa6M507370.2	AT4G35770.1 SEN1 (SENESCENCE 1)	1.36
Csa4M280630.1	AT1G55210.1 disease resistance response	1.36
Csa1M305750.1	AT5G20050.1 protein kinase family protein	1.36
Csa3M221730.1	AT4G22200.1 AKT2/3 (ARABIDOPSIS POTASSIUM TRANSPORT 2/3); cyclic nucleotide binding / inward rectifier potassium channel/ protein binding	1.35
Csa5M241640.1	AT1G68040.1 S-adenosyl-L-methionine:carboxyl methyltransferase family protein	1.35
Csa5M152160.1	AT1G64065.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G44000.1); Has 69 Blast hits to 69 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	1.35
Csa5M637750.1	AT5G19790.1 RAP2.11 (related to AP2 11); DNA binding / transcription factor	1.35
Csa2M437050.1	AT2G12190.1 cytochrome P450, putative	1.35
Csa3M123180.1	AT2G45760.1 BAP2 (BON ASSOCIATION PROTEIN 2)	1.35
Csa5M319910.1	AT1G66120.1 acyl-activating enzyme 11 (AAE11)	1.35
Csa6M507370.1	AT4G35770.1 SEN1 (SENESCENCE 1)	1.34
Csa3M710870.1	AT1G80840.1 WRKY40; transcription factor	1.34
Csa6M508520.1	AT3G12500.1 ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	1.34

	AT2G02220.1 PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein	
Csa6M518160.1	serine/threonine kinase	1.34
Csa2M250960.2	AT2G21340.1 antiporter/ drug transporter	1.34
Csa2M171940.1	AT3G23530.1 cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	1.34
Csa5M576730.1	AT3G62650.2 unknown protein	1.34
Csa5M152240.1	AT1G01490.1 heavy-metal-associated domain-containing protein	1.34
Csa6M508020.1	AT3G12500.1 ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	-1.21 1.34
Csa2M000280.1	AT4G29840.1 MTO2 (METHIONINE OVER-ACCUMULATOR 2); threonine synthase	1.33
Csa3M142410.1	AT2G38870.1 protease inhibitor, putative	1.33
Csa3M769110.1	AT3G13110.1 ATSERAT2;2 (SERINE ACETYLTRANSFERASE 2;2); serine O-acetyltransferase	1.33
Csa3M135050.1	AT3G23250.1 MYB15 (MYB DOMAIN PROTEIN 15); DNA binding / transcription factor	1.33
	AT3G50530.1 CRK (CDPK-related kinase); ATP binding / calcium ion binding / calcium-dependent protein	
Csa6M490240.1	serine/threonine phosphatase/ kinase/ protein kinase/ protein serine/threonine kinase	1.33
Csa3M881870.1	AT4G31550.1 WRKY11; calmodulin binding / transcription factor	1.33
Csa3M135720.1	AT1G06620.1 2-oxoglutarate-dependent dioxygenase, putative	1.33
Csa6M513670.1	AT4G04610.1 APR1 (APS REDUCTASE 1); adenylyl-sulfate reductase	1.32
	AT4G11280.1 ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase	
Csa4M049610.1		1.32
Csa6M216950.1	AT5G01720.1 F-box family protein (FBL3)	1.32
Csa5M613580.1	AT5G59190.1 subtilase family protein	1.32
	AT2G13650.1 GONST1 (Golgi Nucleotide Sugar Transporter 1); GDP-mannose transmembrane transporter/ nucleotide-sugar transmembrane transporter	
Csa2M302280.1		1.32
Csa1M480680.1	AT3G45680.1 proton-dependent oligopeptide transport (POT) family protein	1.31
Csa7M060690.1	AT1G78000.1 SULTR1;2 (SULFATE TRANSPORTER 1;2); sulfate transmembrane transporter	1.31
Csa2M023840.1	AT1G55020.1 LOX1; lipoxygenase	1.31
Csa5M241640.2	AT1G68040.1 S-adenosyl-L-methionine:carboxyl methyltransferase family protein	1.31
Csa3M141900.1	AT3G46860.1 serine protease inhibitor, potato inhibitor I-type family protein	1.31
Csa4M010990.1	AT5G13200.1 GRAM domain-containing protein / ABA-responsive protein-related	1.31
	AT2G38760.1 ANNAT3 (ANNEXIN ARABIDOPSIS 3); calcium ion binding / calcium-dependent phospholipid binding	
Csa5M623660.1		1.31
Csa1M042710.1	AT1G18140.1 LAC1 (Laccase 1); laccase	1.30
	AT2G27830.1 FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT4G22760.1); Has 68 Blast hits to 68 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	
Csa6M150560.1		1.30
Csa3M902190.1	AT4G17900.1 zinc-binding family protein	1.30
	AT2G26710.1 BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	
Csa2M006030.1		1.30
	AT4G14940.1 ATO1 (ARABIDOPSIS THALIANA AMINE OXIDASE 1); amine oxidase/ copper ion binding	
Csa6M423480.1		1.30
Csa3M829010.1	AT2G37440.1 endonuclease/exonuclease/phosphatase family protein	1.30
	AT4G16146.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Lg106-like (InterPro:IPR012482); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G69510.3); Has 94 Blast hits to 94 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 94; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	
Csa6M310500.1		1.30
Csa6M446280.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.30
Csa3M179090.1	AT4G29180.1 leucine-rich repeat protein kinase, putative	1.30
	AT4G40080.1 epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	
Csa2M369220.1		1.30
Csa2M334540.1	AT5G64660.1 U-box domain-containing protein	1.30
CsaUNM014640.1	AT1G68090.1 ANN5; calcium ion binding / calcium-dependent phospholipid binding	1.29
Csa7M072770.1	AT4G10250.1 ATHSP22.0	1.29

Csa3M135670.1	AT3G23200.1 unknown protein		1.29
Csa5M206420.1	AT5G05600.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein		1.29
Csa3M710870.2	AT1G80840.1 WRKY40; transcription factor		1.29
	AT5G23850.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Lipopolysaccharide-modifying protein (InterPro:IPR006598), Protein of unknown function DUF821, CAP10-like (InterPro:IPR008539); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48980.1); Has 588 Blast hits to 567 proteins in 103 species: Archae - 2; Bacteria - 34; Metazoa - 301; Fungi - 69; Plants - 115; Viruses - 3; Other Eukaryotes - 64 (source: NCBI BLINK).		
Csa3M182060.1	AT3G44260.1 CCR4-NOT transcription complex protein, putative		1.29
Csa6M425790.1	No hits found		1.29
Csa5M152180.1	AT5G01830.1 armadillo/beta-catenin repeat family protein / U-box domain-containing protein		1.29
Csa4M332090.1	AT3G21690.1 MATE efflux family protein		1.29
Csa7M043670.1	AT2G29120.1 ATGLR2.7; intracellular ligand-gated ion channel		1.29
Csa2M359920.1	AT1G73050.1 (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative		1.28
Csa2M057070.1	AT5G06900.1 CYP93D1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		1.28
Csa3M810500.1	AT4G14465.1 DNA-binding protein-related		1.28
Csa2M190760.1	AT5G13750.1 ZIFL1 (ZINC INDUCED FACILITATOR-like 1); tetracycline:hydrogen antiporter		1.28
Csa5M585390.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase		1.28
Csa4M304240.1	AT1G12060.1 ATBAG5 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 5); protein binding		1.28
Csa4M011820.1	AT5G57550.1 XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	-2.43	1.28
Csa1M423000.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase		1.27
Csa1M024860.1	AT4G13420.1 HAK5 (HIGH AFFINITY K+ TRANSPORTER 5); potassium ion transmembrane transporter/ potassium:sodium symporter		1.27
Csa4M007060.1	AT2G45850.1 DNA-binding family protein		1.27
Csa6M150520.1	AT5G64260.1 EXL2 (EXORDIUM LIKE 2)		1.27
Csa4M110050.1	No hits found		1.27
Csa4M639750.1	No hits found		1.27
Csa4M372070.1	AT5G65380.1 ripening-responsive protein, putative		1.27
Csa2M369230.1	No hits found		1.27
Csa3M019320.1	AT1G11330.1 S-locus lectin protein kinase family protein		1.27
Csa1M071270.1	AT4G33660.1 unknown protein		1.26
Csa7M069130.1	AT4G35210.1 unknown protein		1.26
Csa7M022920.1	No hits found		1.26
Csa1M479620.1	AT4G11070.1 WRKY41; transcription factor		1.26
Csa4M051470.1	AT5G14760.1 AO (L-ASPARTATE OXIDASE); L-aspartate oxidase/ electron carrier/ oxidoreductase		1.26
Csa5M524850.1	AT5G39050.1 transferase/ transferase, transferring acyl groups other than amino-acyl groups		1.26
Csa1M499330.1	AT1G16670.1 protein kinase family protein		1.26
Csa6M445070.1	AT4G17500.1 ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor		1.26
Csa3M017320.1	AT3G23000.1 CIPK7 (CBL-INTERACTING PROTEIN KINASE 7); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase		1.26
Csa2M205940.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase		1.25
Csa6M445780.1	AT4G32295.1 unknown protein		1.25
Csa2M381830.1	AT2G35930.1 PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase		1.25
Csa1M633420.1	AT4G27280.1 calcium-binding EF hand family protein		1.25
Csa3M081900.1	AT2G37040.1 pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase		1.25
Csa4M008260.1	AT3G21690.1 MATE efflux family protein		1.25
Csa1M071120.1	AT3G15760.1 unknown protein		1.25
Csa1M342430.1	AT2G47270.1 transcription factor/ transcription regulator		1.25
Csa3M536650.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase		1.25
Csa4M008770.1			1.25

Csa4M645920.1	AT5G26010.1 catalytic/ protein serine/threonine phosphatase	1.25
Csa1M070600.1	AT1G11340.1 S-locus lectin protein kinase family protein	1.25
	AT4G21380.1 ARK3 (A. THALIANA RECEPTOR KINASE 3); kinase/ transmembrane receptor protein	
Csa1M071220.1	serine/threonine kinase	1.25
Csa6M409360.1	No hits found	1.24
Csa1M042350.1	AT1G25340.1 MYB116 (myb domain protein 116); DNA binding / transcription factor	1.24
	AT1G79860.1 ROPGEF12 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 12); Rho guanyl-	
Csa3M483820.1	nucleotide exchange factor	1.24
Csa1M498810.1	AT5G39090.1 transferase family protein	1.24
Csa4M000850.1	No hits found	1.24
	AT4G34138.1 UGT73B1 (UDP-glucosyl transferase 73B1); UDP-glycosyltransferase/ abscisic acid	
Csa7M073470.1	glucosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase	1.24
Csa4M050280.1	AT5G41610.1 ATCHX18; monovalent cation:proton antiporter/ sodium:hydrogen antiporter	1.24
Csa5M154230.1	AT3G48990.1 AMP-dependent synthetase and ligase family protein	1.24
	AT2G01170.1 BAT1 (BIDIRECTIONAL AMINO ACID TRANSPORTER 1); amino acid transmembrane	
Csa5M610480.1	transporter	1.24
Csa6M007400.1	AT3G61600.1 ATPOB1; protein binding	1.24
	AT2G37210.1 Encodes a protein of unknown function. It has been crystallized and shown to be structurally	
Csa2M367210.1	almost identical to the protein encoded by At5g11950.	1.24
Csa3M734200.1	AT2G29050.1 ATRBL1 (Arabidopsis thaliana Rhomboid-like 1)	1.24
Csa6M421640.1	AT1G05000.2 tyrosine specific protein phosphatase family protein	1.23
Csa3M717370.1	AT1G15950.1 CCR1 (CINNAMOYL COA REDUCTASE 1); cinnamoyl-CoA reductase	1.23
Csa2M079120.1	AT1G64780.1 ATAMT1;2 (AMMONIUM TRANSPORTER 1;2); ammonium transmembrane transporter	1.23
Csa5M524850.2	AT5G14760.1 AO (L-ASPARTATE OXIDASE); L-aspartate oxidase/ electron carrier/ oxidoreductase	1.23
Csa2M006040.1	AT5G20030.1 agenet domain-containing protein	1.23
Csa4M377730.2	AT1G77810.1 galactosyltransferase family protein	1.23
Csa4M639070.1	AT2G26530.2 AR781	1.23
Csa3M850520.1	AT5G22730.1 F-box family protein	1.23
Csa1M597020.1	AT2G05940.1 protein kinase, putative	1.23
Csa5M585390.3	AT5G13750.1 ZIFL1 (ZINC INDUCED FACILITATOR-like 1); tetracycline:hydrogen antiporter	1.22
Csa2M277660.1	AT5G67385.1 protein binding / signal transducer	1.22
Csa1M532300.1	AT2G30020.1 protein phosphatase 2C, putative / PP2C, putative	1.22
Csa3M135740.1	AT1G06620.1 2-oxoglutarate-dependent dioxygenase, putative	1.22
	AT1G13210.1 ACA.I (autoinhibited Ca2+/ATPase II); ATPase, coupled to transmembrane movement of	
Csa1M041570.1	ions, phosphorylative mechanism / calmodulin binding	1.22
Csa2M423560.1	AT3G21890.1 zinc finger (B-box type) family protein	1.22
Csa3M708680.1	AT2G44260.1 unknown protein	1.22
Csa6M091930.1	AT5G13220.1 JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10)	1.22
	AT3G45650.1 NAXT1 (NITRATE EXCRETION TRANSPORTER1); nitrate efflux transmembrane	
Csa1M480160.1	transporter/ transporter	1.22
Csa4M022900.1	AT4G23340.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.22
Csa4M008250.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.22
Csa6M141420.1	AT2G28305.1 unknown protein	1.22
Csa6M008640.1	AT2G39710.1 aspartyl protease family protein	1.21
Csa1M073890.1	AT4G04960.1 lectin protein kinase, putative	1.21
Csa2M006860.1	AT4G27520.1 plastocyanin-like domain-containing protein	1.21
Csa4M008760.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.21
	AT4G22200.1 AKT2/3 (ARABIDOPSIS POTASSIUM TRANSPORT 2/3); cyclic nucleotide binding / inward	
Csa3M221730.2	rectifier potassium channel/ protein binding	1.21
Csa5M585390.2	AT5G13750.1 ZIFL1 (ZINC INDUCED FACILITATOR-like 1); tetracycline:hydrogen antiporter	1.21
Csa5M198120.1	AT1G53540.1 17.6 kDa class I small heat shock protein (HSP17.6C-CI) (AA 1-156)	1.21
Csa1M071270.2	AT1G11330.1 S-locus lectin protein kinase family protein	1.21
Csa3M782630.1	AT2G35930.1 PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase	1.21
Csa4M377730.1	AT1G77810.1 galactosyltransferase family protein	1.21
Csa6M290790.1	AT1G07900.1 LBD1 (LOB DOMAIN-CONTAINING PROTEIN 1)	1.21



Csa5M114650.1	No hits found	1.21
Csa2M023900.1	AT1G55020.1 LOX1; lipoxygenase	1.21
Csa7M432200.1	AT3G02650.1 pentatricopeptide (PPR) repeat-containing protein	1.21
Csa4M008780.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.21
Csa5M647320.1	AT5G23530.1 AtCXE18 (Arabidopsis thaliana carboxylesterase 18); carboxylesterase	1.21
Csa3M115060.1	AT5G10530.1 lectin protein kinase, putative	1.20
Csa6M446560.1	AT1G08080.1 ACA7 (ALPHA CARBONIC ANHYDRASE 7); carbonate dehydratase/ zinc ion binding	1.20
Csa1M025190.1	AT1G18290.1 unknown protein	1.20
Csa3M888550.1	AT2G25735.1 unknown protein	1.20
Csa1M207300.1	AT4G28840.1 unknown protein	1.20
Csa1M042070.1	AT1G68710.1 haloacid dehalogenase-like hydrolase family protein	1.20
Csa3M604620.1	AT5G53120.1 SPDS3 (SPERMIDINE SYNTHASE 3); spermidine synthase/ spermine synthase	1.20
Csa3M715370.1	AT1G80820.1 CCR2 (CINNAMOYL COA REDUCTASE); cinnamoyl-CoA reductase	1.20
Csa1M025240.1	AT2G27180.1 unknown protein	1.20
Csa5M002570.1	AT1G10310.1 short-chain dehydrogenase/reductase (SDR) family protein	1.20
	AT4G34135.1 UGT73B2 (UDP-GLUCOSYLTRANSFERASE 73B2); UDP-glucosyltransferase/ UDP-glycosyltransferase/ flavonol 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase	1.20
Csa7M073460.1	AT1G63410.1 unknown protein	1.20
Csa5M154790.1	AT3G51240.1 F3H (FLAVANONE 3-HYDROXYLASE); naringenin 3-dioxygenase	1.20
Csa6M108510.1		1.20
Csa4M622800.1	AT1G53670.1 MSRB1 (methionine sulfoxide reductase B 1); peptide-methionine-(S)-S-oxide reductase	1.19
Csa3M684680.1	AT3G51970.1 AtSAT1 (Arabidopsis thaliana sterol O-acyltransferase 1); acyltransferase	1.19
Csa6M516610.1	AT4G04500.1 protein kinase family protein	1.19
Csa1M042720.1	AT3G18040.1 MPK9 (MAP KINASE 9); MAP kinase	1.19
Csa5M139070.1	AT5G24660.1 LSU2 (RESPONSE TO LOW SULFUR 2)	1.19
	AT4G13420.1 HAK5 (HIGH AFFINITY K+ TRANSPORTER 5); potassium ion transmembrane transporter/ potassium:sodium symporter	1.19
Csa7M395260.1	AT4G21970.1 unknown protein	1.19
Csa7M211080.1	AT4G38540.1 monooxygenase, putative (MO2)	1.19
Csa7M014520.1	AT1G22750.4 unknown protein	1.19
Csa6M052750.1	AT4G02860.1 catalytic	1.19
Csa7M393450.1	AT1G12110.1 NRT1.1; nitrate transmembrane transporter/ transporter	1.19
Csa5M161290.1	AT1G68710.1 haloacid dehalogenase-like hydrolase family protein	1.19
Csa2M116250.1	AT1G07710.1 ankyrin repeat family protein	1.19
Csa6M302160.1	No hits found	1.18
Csa7M394060.1	AT3G10050.1 OMR1 (L-O-METHYLTHREONINE RESISTANT 1); L-threonine ammonia-lyase	1.18
Csa6M448730.1	AT5G61210.1 SNAP33 (SOLUBLE N-ETHYLMALIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding	1.18
Csa1M012100.1	AT3G03440.1 armadillo/beta-catenin repeat family protein	1.18
Csa5M418780.1	AT4G37340.1 CYP81D3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	1.18
Csa6M492220.1	No hits found	1.18
Csa1M005760.1	AT5G38280.1 PR5K; kinase/ transmembrane receptor protein serine/threonine kinase	1.18
Csa5M610370.1	AT5G59100.1 subtilase family protein	1.18
Csa5M613590.1	AT1G53050.1 protein kinase family protein	1.18
Csa6M127480.1	AT4G39330.1 CAD9 (CINNAMYL ALCOHOL DEHYDROGENASE 9); binding / catalytic/ oxidoreductase/ zinc ion binding	1.18
Csa3M874320.1	AT1G55020.1 LOX1; lipoxygenase	1.17
Csa2M023910.1	AT2G28260.1 ATCNGC15; calmodulin binding / cation channel/ cyclic nucleotide binding	1.17
Csa6M146420.1	AT2G21340.1 antiporter/ drug transporter	1.17
Csa2M250960.1	AT4G35240.1 unknown protein	1.17
Csa6M127350.1	AT1G77380.1 AAP3; amino acid transmembrane transporter	1.17
Csa4M361780.1	AT2G46320.1 mitochondrial substrate carrier family protein	1.17
Csa3M120400.3	AT1G47670.1 amino acid transporter family protein	1.17
Csa7M018800.1		1.17

Csa3M121750.1	AT3G61460.1 BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding		1.17
Csa3M142400.1	AT2G38870.1 protease inhibitor, putative		1.17
Csa6M079190.1	AT3G19380.1 PUB25 (PLANT U-BOX 25); binding / ubiquitin-protein ligase		1.17
Csa7M395810.1	AT1G02920.1 GSTF7; copper ion binding / glutathione binding / glutathione transferase		1.16
Csa6M419460.1	AT2G31090.1 unknown protein		1.16
Csa7M060160.1	AT4G33430.1 BAK1 (BR1-ASSOCIATED RECEPTOR KINASE); kinase/ protein binding / protein heterodimerization/ protein serine/threonine kinase		1.16
Csa3M716870.1	AT1G80820.1 CCR2 (CINNAMOYL COA REDUCTASE); cinnamoyl-CoA reductase		1.16
Csa4M308510.1	AT3G09032.1 unknown protein		1.16
Csa1M071840.1	AT4G21440.1 ATMYB102 (ARABIDOPSIS MYB-LIKE 102); DNA binding / transcription factor		1.16
Csa4M653480.1	AT4G35230.1 BSK1 (BR-SIGNALING KINASE 1); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase		1.16
Csa6M004600.2	AT3G61440.1 CYSC1 (CYSTEINE SYNTHASE C1); L-3-cyanoalanine synthase/ cysteine synthase		1.16
Csa3M038190.1	AT2G42010.1 PLDBETA1 (PHOSPHOLIPASE D BETA 1); phospholipase D		1.15
Csa7M014510.1	AT4G38540.1 monooxygenase, putative (MO2)		1.15
Csa2M000130.1	AT2G05940.1 protein kinase, putative		1.15
Csa7M070260.1	AT4G39230.1 isoflavone reductase, putative		1.15
Csa1M045860.1	AT5G65200.1 PUB38 (PLANT U-BOX 38); ubiquitin-protein ligase		1.15
Csa1M002130.1	AT4G24830.1 arginosuccinate synthase family		1.15
Csa6M510960.1	AT5G47740.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Rossmann-like alpha/beta/alpha sandwich fold (InterPro:IPR014729); BEST Arabidopsis thaliana protein match is: protein kinase family protein / U-box domain-containing protein (TAIR:AT2G45910.1); Has 196 Blast hits to 194 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 196; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).		1.15
Csa6M190450.1	AT1G07630.1 PLL5; catalytic/ protein serine/threonine phosphatase		1.15
Csa6M448720.1	AT3G10050.1 OMR1 (L-O-METHYLTHREONINE RESISTANT 1); L-threonine ammonia-lyase		1.15
Csa2M334530.1	No hits found		1.15
Csa2M277610.1	AT4G37470.1 hydrolase, alpha/beta fold family protein		1.15
Csa3M135730.1	AT1G06650.2 2-oxoglutarate-dependent dioxygenase, putative		1.14
Csa4M152280.1	AT3G12160.1 RABA4D (RAB GTPASE HOMOLOG A4D); GTP binding		1.14
Csa5M494420.1	No hits found		1.14
Csa6M439420.1	AT1G51410.1 cinnamyl-alcohol dehydrogenase, putative (CAD)		1.14
Csa2M324450.1	AT3G10420.2 sporulation protein-related		1.14
Csa3M760550.1	AT1G50590.1 pirin, putative		1.14
Csa2M367210.2	AT2G28305.1 unknown protein		1.14
Csa7M430220.1	AT2G31900.1 XIF; motor		1.14
Csa6M052130.1	AT1G34300.1 lectin protein kinase family protein		1.14
Csa6M040540.1	AT5G08640.1 FLS (FLAVONOL SYNTHASE); flavonol synthase		1.13
Csa6M526270.1	No hits found		1.13
Csa4M004870.1	AT5G20100.1 unknown protein		1.13
Csa2M404870.1	AT5G38200.1 hydrolase		1.13
Csa5M212090.1	AT1G09870.1 histidine acid phosphatase family protein		1.13
Csa1M611280.1	AT2G44450.1 BGLU15 (BETA GLUCOSIDASE 15); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	-1.70	1.13
Csa1M168870.1	AT2G27300.1 NTL8 (NTM1-LIKE 8); transcription factor		1.13
Csa2M354960.1	AT3G47110.1 leucine-rich repeat transmembrane protein kinase, putative		1.13
Csa4M454670.1	AT1G10940.1 SNRK2.4 (SNF1-RELATED PROTEIN KINASE 2.4); kinase		1.13
Csa2M024440.1	AT1G55020.1 LOX1; lipoxygenase		1.12
Csa1M288020.1	AT4G30420.1 nodulin MtN21 family protein	-1.83	1.12
Csa2M049900.1	No hits found		1.12
Csa1M042720.2	AT3G18040.1 MPK9 (MAP KINASE 9); MAP kinase		1.12
Csa1M575180.1	AT2G36890.1 RAX2 (REGULATOR OF AXILLARY MERISTEMS 2); DNA binding / transcription factor		1.12
Csa6M004600.1	AT3G61440.1 CYSC1 (CYSTEINE SYNTHASE C1); L-3-cyanoalanine synthase/ cysteine synthase		1.12

Csa6M499870.1	AT1G34370.2 STOP1 (sensitive to proton rhizotoxicity 1); nucleic acid binding / transcription factor/ zinc ion binding	1.12
Csa4M109030.1	AT5G64230.1 unknown protein	1.12
Csa3M175080.1	AT1G35710.1 leucine-rich repeat transmembrane protein kinase, putative	1.12
Csa3M734040.1	AT3G55550.1 lectin protein kinase, putative	1.11
Csa3M120400.1	AT2G46320.1 mitochondrial substrate carrier family protein	1.11
Csa2M023940.1	AT1G55020.1 LOX1; lipoxygenase	1.11
Csa6M004600.3	AT3G61440.1 CYSC1 (CYSTEINE SYNTHASE C1); L-3-cyanoalanine synthase/ cysteine synthase	1.11
Csa4M652810.1	AT5G11090.1 serine-rich protein-related	1.11
Csa3M845500.1	AT5G47910.1 RBOHD (RESPIRATORY BURST OXIDASE HOMOLOGUE D); NAD(P)H oxidase	1.11
Csa6M094700.1	AT4G27500.1 PPI1 (PROTON PUMP INTERACTOR 1); protein binding	1.11
Csa6M421640.2	AT1G05000.1 tyrosine specific protein phosphatase family protein	1.11
Csa3M118010.1	AT3G60490.1 AP2 domain-containing transcription factor TINY, putative	1.11
Csa4M647490.1	AT5G21482.1 CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase	1.11
Csa5M146210.1	AT1G33260.2 protein kinase family protein	1.11
Csa7M014510.2	AT4G38540.1 monooxygenase, putative (MO2)	1.11
Csa7M056470.1	AT5G09810.1 ACT7 (ACTIN 7); structural constituent of cytoskeleton	1.10
Csa3M179200.1	AT5G62150.1 peptidoglycan-binding LysM domain-containing protein	1.10
Csa1M629010.1	AT5G12300.1 C2 domain-containing protein	1.10
Csa3M716370.1	AT1G80820.1 CCR2 (CINNAMOYL COA REDUCTASE); cinnamoyl-CoA reductase	1.10
Csa6M496950.1	No hits found	1.10
Csa1M005750.1	AT5G13690.1 alpha-N-acetylglucosaminidase family / NAGLU family	1.10
Csa2M074200.1	AT2G47000.1 ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase	1.10
Csa6M087820.1	No hits found	1.10
Csa6M022370.1	AT1G14780.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24290.2); Has 119 Blast hits to 118 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 14; Fungi - 0; Plants - 105; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	1.09
Csa4M006310.1	AT1G15760.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Sterile alpha motif homology (InterPro:IPR010993); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80520.1); Has 30 Blast hits to 30 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	1.09
Csa3M835770.1	AT5G40240.1 nodulin MtN21 family protein	1.09
Csa2M360820.1	AT4G36860.1 zinc ion binding	1.09
Csa6M216960.1	AT2G38470.1 WRKY33; transcription factor	1.09
Csa3M912910.1	AT4G17030.1 ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1)	1.09
Csa4M194780.1	AT3G52450.1 PUB22 (PLANT U-BOX 22); ubiquitin-protein ligase	1.09
Csa1M231530.1	AT4G32280.1 IAA29 (INDOLE-3-ACETIC ACID INDUCIBLE 29); transcription factor	1.09
Csa3M733300.1	AT2G37900.1 proton-dependent oligopeptide transport (POT) family protein	1.09
Csa3M777680.1	AT2G36090.1 F-box family protein	1.09
Csa5M597510.1	AT3G55270.1 MKP1 (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 1); MAP kinase	1.09
Csa3M872170.1	tyrosine/serine/threonine phosphatase	1.09
Csa2M361610.1	AT1G75750.1 GASA1 (GAST1 PROTEIN HOMOLOG 1)	1.09
Csa2M360820.2	No hits found	1.09
Csa3M020060.1	AT4G36860.1 zinc ion binding	1.09
Csa5M420280.1	AT4G16563.1 aspartyl protease family protein	1.09
Csa6M483510.1	AT1G66470.1 basic helix-loop-helix (bHLH) family protein	1.09
Csa1M222880.1	No hits found	1.09

Csa3M135120.1	AT3G23240.1 ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	1.09
Csa1M005740.1	AT5G13690.1 alpha-N-acetylglucosaminidase family / NAGLU family	1.08
Csa4M308490.1	AT5G01210.1 transferase family protein	1.08
Csa7M071470.1	AT3G19553.1 amino acid permease family protein	1.08
Csa6M446290.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.08
Csa6M190430.1	AT5G02390.1 unknown protein	1.08
Csa5M139360.1	AT2G46550.1 unknown protein	1.08
Csa1M050360.1	AT5G03860.1 MLS (MALATE SYNTHASE); malate synthase	1.08
Csa6M519450.1	AT1G28570.1 GDSL-motif lipase, putative	1.08
Csa3M002860.1	AT4G17880.1 basic helix-loop-helix (bHLH) family protein	1.08
Csa5M167220.1	AT5G06730.1 peroxidase, putative	1.08
Csa2M074190.1	AT2G47000.1 ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase	1.08
Csa7M027830.1	No hits found	1.08
Csa5M207940.1	AT3G55980.1 SZF1 (SALT-INDUCIBLE ZINC FINGER 1); transcription factor	1.08
Csa1M071790.1	AT1G11350.1 SD1-13 (S-DOMAIN-1 13); kinase/ protein kinase/ protein serine/threonine kinase	1.08
Csa7M023920.1	AT2G17080.1 unknown protein	1.08
Csa1M002090.1	AT5G63450.1 CYP94B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	1.08
Csa7M049170.1	AT3G58710.1 WRKY69; transcription factor	1.07
Csa6M495000.1	AT5G67400.1 peroxidase 73 (PER73) (P73) (PRXR11)	1.07
Csa5M603310.1	No hits found	1.07
Csa3M901100.1	No hits found	1.07
Csa6M484580.1	AT1G49230.1 zinc finger (C3HC4-type RING finger) family protein	1.07
Csa4M653450.1	AT1G20510.1 OPCL1 (OPC-8:0 COA LIGASE1); 4-coumarate-CoA ligase	1.07
Csa2M369230.2	AT5G65380.1 ripening-responsive protein, putative	1.07
Csa1M701990.2	AT4G19880.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cadmium ion; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Glutathione S-transferase, predicted (InterPro:IPR016639), Glutathione S- transferase, C-terminal (InterPro:IPR004046), Glutathione S-transferase, C-terminal-like (InterPro:IPR010987), Glutathione S-transferase/chloride channel, C-terminal (InterPro:IPR017933), Thioredoxin-like fold (InterPro:IPR012336); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G45020.1); Has 1635 Blast hits to 1635 proteins in 489 species: Archae - 12; Bacteria - 905; Metazoa - 23; Fungi - 158; Plants - 57; Viruses - 0; Other Eukaryotes - 480 (source: NCBI BLink).	1.07
Csa1M265630.1	AT5G25240.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: NHL repeat-containing protein (TAIR:AT5G14890.1); Has 23 Blast hits to 23 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	1.06
Csa4M187820.1	AT1G58030.1 CAT2 (CATIONIC AMINO ACID TRANSPORTER 2); amino acid transmembrane transporter	1.06
Csa5M030450.1	AT2G01540.1 C2 domain-containing protein	1.06
Csa5M202350.1	AT2G40095.1 unknown protein	1.06
Csa7M043020.1	AT4G04450.1 WRKY42; transcription factor	1.06
Csa2M378000.1	AT5G10660.1 calmodulin-binding protein-related	1.06
Csa6M006900.1	No hits found	1.06
Csa3M164500.1	AT3G16720.1 ATL2; protein binding / zinc ion binding	1.06
Csa1M527880.1	No hits found	1.06
Csa2M435510.1	AT1G64950.1 CYP89A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	1.06
Csa1M056970.3	AT4G20070.1 ATAAH (Arabidopsis thaliana Allantoate Amidohydrolase); allantoate deiminase/ metallopeptidase	1.06

Csa4M001920.1	AT4G02340.1 epoxide hydrolase, putative	1.06
Csa4M622740.1	AT3G14690.1 CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	1.06
Csa3M354510.1	AT4G23810.1 WRKY53; DNA binding / protein binding / transcription activator/ transcription factor	1.06
Csa7M390060.1	AT4G02860.1 catalytic	1.06
Csa6M149400.1	AT5G22860.1 serine carboxypeptidase S28 family protein	1.05
Csa4M456680.1	AT1G78290.2 serine/threonine protein kinase, putative	1.05
Csa5M523190.1	AT5G40370.1 glutaredoxin, putative	1.05
Csa2M439140.1	No hits found	1.05
Csa7M029390.1	AT1G76490.1 HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	-1.37
Csa6M487750.1	AT2G23770.1 protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	1.05
Csa4M011820.2	AT1G12060.1 ATBAG5 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 5); protein binding	1.05
Csa5M622630.1	AT1G75950.1 SKP1 (S PHASE KINASE-ASSOCIATED PROTEIN 1); protein binding / ubiquitin-protein ligase	1.05
Csa5M033470.1	AT1G70740.1 protein kinase family protein	1.05
Csa2M234570.1	AT2G26530.1 AR781	1.05
Csa6M117710.1	AT2G17370.1 HMG2 (3-HYDROXY-3-METHYLGLUTARYL-COA REDUCTASE 2); hydroxymethylglutaryl-CoA reductase	1.05
Csa5M190530.1	AT3G46230.1 ATHSP17.4	1.05
Csa2M409500.1	No hits found	1.04
Csa3M133890.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	1.04
Csa5M175710.1	AT5G23240.1 DNAJ heat shock N-terminal domain-containing protein	1.04
Csa5M027950.1	AT2G38870.1 protease inhibitor, putative	1.04
Csa5M139270.1	AT2G46620.1 AAA-type ATPase family protein	1.04
Csa6M496960.1	AT5G57620.1 MYB36 (myb domain protein 36); DNA binding / transcription factor	1.04
Csa7M446980.1	AT1G52240.1 ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor	1.04
Csa5M139370.1	AT5G53050.2 hydrolase, alpha/beta fold family protein	1.04
Csa5M348050.1	AT5G17330.1 GAD; calmodulin binding / glutamate decarboxylase	1.04
Csa4M621220.1	AT3G14690.1 CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	1.04
Csa2M023850.1	AT1G55020.1 LOX1; lipoxygenase	1.04
Csa6M493310.1	AT4G37390.1 BRU6; indole-3-acetic acid amido synthetase	1.04
Csa4M303070.1	AT3G09280.1 unknown protein	1.03
Csa6M135970.1	AT1G54320.1 LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein	1.03
Csa3M135110.1	AT2G39840.1 TOPP4; protein serine/threonine phosphatase	1.03
Csa4M332110.1	AT5G58350.1 WNK4 (WITH NO K (=LYSINE) 4); kinase/ protein kinase	1.03
Csa2M369000.1	AT5G64260.1 EXL2 (EXORDIUM LIKE 2)	1.03
Csa2M191300.1	AT1G04280.1 unknown protein	1.03
Csa3M835270.1	AT5G40240.1 nodulin MtN21 family protein	1.03
CsaUNM026610.1	AT3G15790.1 MBD11; DNA binding / methyl-CpG binding	1.03
Csa1M267770.2	AT2G25180.1 ARR12 (ARABIDOPSIS RESPONSE REGULATOR 12); transcription factor/ two-component response regulator	1.03
Csa7M414440.2	AT3G62260.2 protein phosphatase 2C, putative / PP2C, putative	1.03
Csa3M119710.1	AT4G01070.1 GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	1.03
Csa3M640560.1	No hits found	1.03
Csa7M390070.1	AT4G02860.1 catalytic	1.03
Csa4M665110.1	AT1G20990.1 DC1 domain-containing protein	1.03
CsaUNM026600.1	AT2G26600.1 glycosyl hydrolase family 17 protein	1.03
Csa2M404780.1	AT1G48370.1 YSL8 (YELLOW STRIPE LIKE 8); oligopeptide transporter	1.03
Csa7M072810.1	AT2G15220.1 secretory protein, putative	1.03
Csa5M139090.1	AT3G49370.1 calcium-dependent protein kinase, putative / CDPK, putative	1.03

Csa2M027440.1	AT1G55020.1 LOX1; lipoxygenase		1.02
Csa6M010000.1	AT2G39980.1 transferase family protein	-1.37	1.02
Csa1M062880.1	AT1G11840.2 ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase/ metal ion binding		1.02
Csa4M628850.1	AT5G11210.1 ATGLR2.5; intracellular ligand-gated ion channel		1.02
Csa6M212860.1	AT5G58350.1 WNK4 (WITH NO K (=LYSINE) 4); kinase/ protein kinase		1.02
Csa3M733860.1	AT1G34300.1 lectin protein kinase family protein		1.02
Csa7M279240.2	AT5G55930.1 OPT1 (OLIGOPEPTIDE TRANSPORTER 1); oligopeptide transporter		1.02
Csa3M889760.1	AT1G22360.1 AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups		1.02
Csa3M842690.1	AT4G38040.1 exostosin family protein		1.02
Csa6M503370.1	AT3G21950.1 methyltransferase		1.02
Csa5M637680.1	AT1G69480.1 EXS family protein / ERD1/XPR1/SYG1 family protein		1.02
Csa4M638430.1	AT1G06870.1 signal peptidase, putative		1.02
Csa1M701990.1	AT4G19880.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cadmium ion; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Glutathione S-transferase, predicted (InterPro:IPR016639), Glutathione S-transferase, C-terminal (InterPro:IPR004046), Glutathione S-transferase, C-terminal-like (InterPro:IPR010987), Glutathione S-transferase/chloride channel, C-terminal (InterPro:IPR017933), Thioredoxin-like fold (InterPro:IPR012336); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G45020.1); Has 1635 Blast hits to 1635 proteins in 489 species: Archae - 12; Bacteria - 905; Metazoa - 23; Fungi - 158; Plants - 57; Viruses - 0; Other Eukaryotes - 480 (source: NCBI BLINK). AT1G15210.1 PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATPase, coupled to transmembrane movement of substances		1.02
Csa3M446120.1	AT1G08320.1 bZIP family transcription factor		1.02
Csa6M152350.1	AT1G60010.1 unknown protein		1.02
Csa5M603290.1	No hits found		1.02
Csa3M780540.1	AT3G25780.1 AOC3 (ALLENE OXIDE CYCLASE 3); allene-oxide cyclase		1.01
Csa5M366670.1	AT5G13550.1 SULTR4;1; sulfate transmembrane transporter		1.01
Csa5M505740.1	AT5G47635.1 unknown protein		1.01
Csa1M181380.1	AT1G34670.1 AtMYB93 (myb domain protein 93); DNA binding / transcription factor		1.01
Csa3M901090.1	AT4G31020.2 unknown protein		1.01
Csa1M267270.1	AT3G57120.1 protein kinase family protein		1.01
Csa6M147500.1	AT4G26850.1 VTC2 (vitamin c defective 2); GDP-D-glucose phosphorylase/ GDP-galactose:glucose-1-phosphate guanylyltransferase/ GDP-galactose:mannose-1-phosphate guanylyltransferase/ GDP-galactose:myoinositol-1-phosphate guanylyltransferase/ galactose-1-phosphate guanylyltra		1.01
Csa7M219200.1	AT1G07570.2 APK1A; kinase/ protein serine/threonine kinase		1.01
Csa6M190390.1	No hits found		1.01
Csa6M448080.1	AT1G55850.1 ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups		1.01
Csa7M200810.1	AT1G09250.1 transcription factor		1.01
Csa1M555600.2	AT3G45640.1 ATMPK3 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP kinase/ kinase/ protein binding / protein kinase		1.01
Csa1M479630.1	AT1G65730.1 YSL7 (YELLOW STRIPE LIKE 7); oligopeptide transporter		1.01
Csa2M404760.1	AT1G76390.1 armadillo/beta-catenin repeat family protein / U-box domain-containing protein		1.01
Csa5M034000.1	AT3G24503.1 ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase		1.01
Csa1M372010.1	AT4G28290.1 unknown protein		1.01
Csa5M146940.1	AT4G37340.1 CYP81D3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		1.01
Csa6M492230.1	AT1G59910.1 formin homology 2 domain-containing protein / FH2 domain-containing protein		1.01
Csa5M603920.1	AT1G69040.2 ACR4 (ACT REPEAT 4); amino acid binding		1.01
Csa6M367150.1	No hits found		1.01
Csa3M126950.1	AT4G04960.1 lectin protein kinase, putative		1.01
Csa7M048050.1	AT1G09970.1 LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase		1.00
Csa7M069690.1	AT4G08250.1 scarecrow transcription factor family protein		1.00
Csa6M040600.1			1.00

Csa3M119500.1	AT1G01260.1 basic helix-loop-helix (bHLH) family protein		1.00
Csa6M426370.1	AT2G35930.1 PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase	-1.04	1.00
Csa2M354750.1	AT5G43190.1 F-box family protein (FBX6)		1.00
	<p>AT4G15920.1 INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPR018169), RAG1-activating protein 1 homologue (InterPro:IPR018179), MtN3 and saliva related transmembrane protein (InterPro:IPR004316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).</p>		
Csa3M159450.1			1.00
Csa3M841490.1	No hits found		1.00

**Table S5. Genes that were downregulated by Fe deficiency in multiple genotypes.**

**Three genes downregulated in snake melon and Edisto**

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa6M525620.1	AT4G14630.1 GLP9 (GERMIN-LIKE PROTEIN 9); manganese ion binding / nutrient reservoir		-1.75	-2.40			
Csa7M037490.1	AT1G80810.1 binding		-1.41	-1.59	2.82		
Csa6M216930.1	AT5G05340.1 peroxidase, putative		-2.20	-1.14			

**Four genes downregulated in snake melon and fefe.**

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa1M423010.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase	-5.25		-1.40			
Csa7M325150.1	AT3G43660.1 nodulin, putative	-2.67		-1.27			
Csa1M526820.1	AT3G46900.1 COPT2; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter	-2.55		-1.59		1.79	
Csa3M183380.1	AT5G23980.1 FRO4 (FERRIC REDUCTION OXIDASE 4); ferric-chelate reductase	-2.12		-2.61			

**Two genes downregulated in Edisto and fefe.**

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa6M411280.1	AT3G25190.1 nodulin, putative	-4.58		-1.85			
Csa3M176250.1	AT4G25250.1 invertase/pectin methylesterase inhibitor family protein	-1.05		-1.06			



**Table S6. Genes that were downregulated under Fe deficiency in one genotype.**

Elements only in "fefe Dn-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa4M111600.1	No hits found	-7.22					
Csa2M423640.1	AT5G36220.1 CYP81D1 (CYTOCHROME P450 81D1); electron carrier/ heme binding / iron ion binding /						
Csa7M068570.1	monooxygenase/ oxygen binding	-4.70					
Csa4M006130.1	AT3G50170.1 unknown protein	-4.14					
Csa6M516910.1	AT3G15850.1 FAD5 (FATTY ACID DESATURASE 5); 16:0 monogalactosyldiacylglycerol desaturase/						
Csa5M161340.1	oxidoreductase	-3.62					
Csa3M895700.1	No hits found	-3.48					
Csa5M161350.1	AT4G12490.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-3.41					
Csa5M550240.1	AT3G63520.1 CCD1 (CAROTENOID CLEAVAGE DIOXYGENASE 1); 9-cis-epoxycarotenoid dioxygenase	-3.40					3.16
Csa5M161350.1	AT2G01770.1 VIT1 (vacuolar iron transporter 1); iron ion transmembrane transporter	-3.36					
Csa6M020140.1	AT4G12490.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-3.34					
Csa2M100530.1	AT2G36800.1 DOGT1 (DON-GLUCOSYLTRANSFERASE 1); UDP-glycosyltransferase/ cis-zeatin O-beta-						
Csa2M100530.1	D-glucosyltransferase/ glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-						
Csa3M895690.1	glucosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transf	-3.32					
Csa5M161850.1	AT2G03090.1 ATEXPA15 (ARABIDOPSIS THALIANA EXPANSIN A15)	-3.31					
Csa5M157280.1	AT3G14440.1 NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid						
Csa5M599860.1	dioxygenase	-3.28					2.76
Csa1M166260.1	AT4G12500.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-3.21					
Csa4M269730.1	AT5G22550.1 unknown protein	-2.97					
Csa2M226860.1	AT3G14067.1 subtilase family protein	-2.95					
Csa4M280510.1	AT1G12940.1 ATNRT2.5 (nitrate transporter2.5); nitrate transmembrane transporter	-2.93					1.71
Csa5M139780.1	AT4G12520.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-2.92					
Csa5M161310.1	AT5G22410.1 peroxidase, putative	-2.92					3.36
Csa4M288090.1	AT2G27080.1 harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	-2.84					
Csa1M326870.1	AT1G03055.1 unknown protein	-2.84					
Csa4M280510.1	AT5G16990.1 NADP-dependent oxidoreductase, putative	-2.77					2.09
Csa2M380070.1	AT5G17230.1 phytoene synthase (PSY) / geranylgeranyl-diphosphate geranylgeranyl transferase	-2.77					
Csa6M057130.1	AT3G50160.1 unknown protein	-2.76					
Csa2M381630.1	AT3G43660.1 nodulin, putative	-2.74					
Csa4M006120.1	AT3G50130.1 unknown protein	-2.68					
Csa1M555620.1	AT3G15850.1 FAD5 (FATTY ACID DESATURASE 5); 16:0 monogalactosyldiacylglycerol desaturase/						
Csa6M484540.1	oxidoreductase	-2.67					
Csa3M186690.1	AT1G56580.1 unknown protein	-2.55					1.43
Csa4M288090.1	AT4G08250.1 scarecrow transcription factor family protein	-2.49					
Csa5M139780.1	AT5G36110.1 CYP716A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen						
Csa5M472110.1	binding	-2.48					
Csa4M288090.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	-2.48					2.92
Csa5M139780.1	AT1G64950.1 CYP89A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen						
Csa5M472110.1	binding	-2.48					1.83
Csa4M001940.1	AT2G43890.1 polygalacturonase, putative / pectinase, putative	-2.45					
Csa1M423000.1	AT4G02290.1 AtGH9B13 (Arabidopsis thaliana glycosyl hydrolase 9B13); catalytic/ hydrolase, hydrolyzing						
Csa1M334910.1	O-glycosyl compounds	-2.44					
Csa1M154060.1	AT5G57550.1 XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3); hydrolase, acting on glycosyl						
Csa1M227450.1	bonds / xyloglucan:xyloglucosyl transferase	-2.43					1.28
Csa2M406650.1	AT2G41480.1 electron carrier/ heme binding / peroxidase	-2.39					
Csa5M589920.1	AT3G19430.1 late embryogenesis abundant protein-related / LEA protein-related	-2.31					
Csa2M406650.1	AT3G15850.1 FAD5 (FATTY ACID DESATURASE 5); 16:0 monogalactosyldiacylglycerol desaturase/						
Csa1M227450.1	oxidoreductase	-2.31					
Csa2M406650.1	AT4G37530.1 peroxidase, putative	-2.28					2.02
Csa5M589920.1	AT1G13710.1 CYP78A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen						
	binding	-2.27					1.09 1.07

	AT4G15920.1 INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPRO18169), RAG1-activating protein 1 homologue (InterPro:IPRO18179), MtN3 and saliva related transmembrane protein (InterPro:IPRO04316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLINK).	-2.27	1.11
Csa2M031160.1	AT4G32810.1 CCD8 (CAROTENOID CLEAVAGE DIOXYGENASE 8); oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	-2.26	2.66
Csa2M373590.1	AT1G59870.1 PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	-2.19	
Csa2M379370.1	AT3G15850.1 FAD5 (FATTY ACID DESATURASE 5); 16:0 monogalactosyldiacylglycerol desaturase/ oxidoreductase	-2.17	
Csa1M227460.1	AT3G19270.1 CYP707A4; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	-2.16	
Csa2M003060.1	AT4G28840.1 unknown protein	-2.07	1.72
Csa2M365120.1	AT2G21300.1 kinesin motor family protein	-2.06	
Csa3M857050.1	AT1G75220.1 integral membrane protein, putative	-2.05	
Csa5M157220.1	AT4G25410.1 DNA binding / transcription factor	-2.03	
Csa3M555690.1	AT1G52800.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	-2.02	1.86
Csa3M889750.1	AT1G78260.1 RNA recognition motif (RRM)-containing protein	-2.01	
Csa4M637170.1	AT4G27480.1 glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein	-2.01	
Csa3M133960.1	AT4G13510.1 AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter	-2.01	
Csa4M637160.1	AT3G15350.1 glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein	-1.99	2.92
Csa3M134700.1	AT1G04040.1 acid phosphatase class B family protein	-1.96	
Csa3M854770.1	AT5G42610.1 unknown protein	-1.96	
Csa5M352650.1	AT5G08350.1 GRAM domain-containing protein / ABA-responsive protein-related	-1.94	
Csa4M287010.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	-1.94	
Csa3M603600.1	AT2G25410.1 protein binding / zinc ion binding	-1.93	2.08
Csa4M287560.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	-1.92	
Csa3M857050.2	AT1G75220.1 integral membrane protein, putative	-1.91	
Csa3M153170.1	AT3G21420.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1.90	
Csa4M286990.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	-1.85	
Csa1M045430.1	AT1G74500.1 bHLH family protein	-1.84	
CsaUNM026590.1	AT5G20230.1 ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier	-1.84	
Csa1M662770.1	AT3G59850.1 polygalacturonase, putative / pectinase, putative	-1.83	
Csa1M288020.1	AT4G30420.1 nodulin MtN21 family protein	-1.83	1.12
Csa4M287550.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	-1.83	
Csa3M355060.1	AT5G24105.1 AGP41 (ARABINOGLACTAN-PROTEIN 41)	-1.82	
Csa6M418410.1	AT1G05680.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.81	
Csa6M358130.1	AT1G76240.1 unknown protein	-1.80	
Csa5M495960.1	AT1G09970.1 LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	-1.80	
Csa5M161870.1	AT1G12090.1 ELP (EXTENSIN-LIKE PROTEIN); lipid binding	-1.79	
Csa2M034530.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase	-1.75	2.19
Csa1M383520.1	AT4G13340.1 leucine-rich repeat family protein / extensin family protein	-1.73	
Csa4M111590.1	AT5G64300.1 ATGCH; 3,4-dihydroxy-2-butanone-4-phosphate synthase/ GTP cyclohydrolase II	-1.72	
Csa1M611280.1	AT2G44450.1 BGLU15 (BETA GLUCOSIDASE 15); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	-1.70	1.13
Csa5M175770.1	AT1G23020.1 FRO3; ferric-chelate reductase	-1.70	4.33
Csa1M042790.1	AT5G12250.1 TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton	-1.68	2.67
Csa1M059730.1	AT5G35830.1 ankyrin repeat family protein	-1.68	
Csa4M287000.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	-1.68	
Csa4M279820.1	AT5G49690.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.65	
Csa4M312240.1	AT5G01320.1 pyruvate decarboxylase, putative	-1.64	
Csa5M630970.1	AT3G28180.1 ATCSLC04 (CELLULOSE-SYNTHASE LIKE C4); cellulose synthase/ transferase, transferring glycosyl groups	-1.64	

Csa5M161320.1	No hits found	-1.64		
Csa3M180260.1	AT4G25490.1 CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	-1.64	1.10	
Csa5M161860.1	AT1G12090.1 ELP (EXTENSIN-LIKE PROTEIN); lipid binding	-1.63		
Csa5M161880.1	AT1G12090.1 ELP (EXTENSIN-LIKE PROTEIN); lipid binding	-1.63		
Csa5M161890.1	AT1G12090.1 ELP (EXTENSIN-LIKE PROTEIN); lipid binding	-1.63		
Csa6M134900.1	AT1G30870.1 cationic peroxidase, putative	-1.62	3.09	5.66
Csa4M571750.1	No hits found	-1.61		
Csa2M418940.1	AT1G05200.1 ATGLR3.4; intracellular ligand-gated ion channel	-1.60		
Csa2M439220.1	AT5G10530.1 lectin protein kinase, putative	-1.60	1.47	
Csa7M051380.1	AT1G05670.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.59		
Csa5M396000.1	AT1G78020.1 senescence-associated protein-related	-1.58		
Csa1M043060.1	AT3G17660.1 AGD15 (ARF-GAP domain 15); ARF GTPase activator/ DNA binding / zinc ion binding	-1.57		
Csa4M109540.1	AT2G39780.1 RNS2 (RIBONUCLEASE 2); RNA binding / endoribonuclease/ ribonuclease T2	-1.55		
Csa4M646170.1	AT2G26170.1 CYP711A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.55		
Csa1M044900.1	AT3G26040.1 transferase family protein	-1.53		
Csa2M008110.1	AT5G20410.1 MGD2; 1,2-diacylglycerol 3-beta-galactosyltransferase/ UDP-galactosyltransferase/ transferase, transferring glycosyl groups	-1.53		1.40
Csa4M003100.1	AT4G02100.1 DNAJ heat shock N-terminal domain-containing protein	-1.50		
Csa2M376820.1	AT5G44460.1 calcium-binding protein, putative	-1.49		
Csa7M058650.1	AT1G22340.1 AtUGT85A7 (UDP-glucosyl transferase 85A7); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups	-1.49		
Csa3M124900.1	AT2G45630.2 oxidoreductase family protein	-1.48		
Csa4M279810.1	AT5G49690.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.48		
Csa1M329900.1	AT5G53550.1 YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	-1.48		
Csa3M624020.1	AT5G48900.1 pectate lyase family protein	-1.47		
Csa3M094510.1	AT3G20660.1 AtOCT4 (Arabidopsis thaliana ORGANIC CATION/CARNITINE TRANSPORTER4); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	-1.46		
Csa4M358770.1	AT5G20240.1 PI (PISTILLATA); DNA binding / transcription factor	-1.45		
Csa6M504630.1	AT2G16430.2 PAP10 (PURPLE ACID PHOSPHATASE 10); acid phosphatase/ protein serine/threonine phosphatase	-1.44		
Csa5M224130.1	AT5G24910.1 CYP714A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.44		1.39
Csa7M420830.1	AT3G63470.1 scpl40 (serine carboxypeptidase-like 40); serine-type carboxypeptidase	-1.44		
Csa7M420780.1	AT5G08260.1 scpl35 (serine carboxypeptidase-like 35); serine-type carboxypeptidase	-1.42		
Csa4M361270.1	AT1G77330.1 1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative	-1.37		1.91
Csa6M010000.1	AT2G39980.1 transferase family protein	-1.37		1.02
Csa7M029390.1	AT1G76490.1 HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	-1.37		1.05
Csa5M175910.1	AT3G54770.1 RNA recognition motif (RRM)-containing protein	-1.35		
Csa6M338090.1	AT1G21340.1 Dof-type zinc finger domain-containing protein	-1.35		
Csa2M416070.1	AT2G42380.2 bZIP transcription factor family protein	-1.32		
Csa1M044870.1	AT4G25640.1 MATE efflux family protein	-1.31		
Csa6M493840.1	AT5G59845.1 gibberellin-regulated family protein	-1.31		
Csa6M088700.1	AT3G26040.1 transferase family protein	-1.31		
Csa5M175910.2	AT3G54770.1 RNA recognition motif (RRM)-containing protein	-1.30		
Csa5M621920.1	AT3G10520.1 AHB2 (ARABIDOPSIS HAEMOGLOBIN 2); oxygen transporter	-1.29		
Csa6M511710.1	AT1G12080.2 unknown protein	-1.29		
Csa7M059660.1	AT1G22370.2 AtUGT85A5 (UDP-glucosyl transferase 85A5); glucuronosyltransferase/ transferase, transferring glycosyl groups	-1.28		
Csa7M041360.1	AT3G58120.1 BZIP61; DNA binding / transcription activator/ transcription factor	-1.25		
Csa3M435010.2	AT4G26270.1 PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase	-1.22	1.68	2.30
Csa3M842070.1	AT5G20950.1 glycosyl hydrolase family 3 protein	-1.22		
Csa6M088180.1	AT4G37400.1 CYP81F3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.21		

Csa5M114570.1	AT2G02130.1 LCR68 (LOW-MOLECULAR-WEIGHT CYSTEINE-RICH 68); peptidase inhibitor	-1.21		
Csa7M063920.1	AT1G22360.1 AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups	-1.20		
Csa7M059150.1	AT1G22360.1 AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups	-1.20		
Csa2M234510.1	AT3G48690.1 CXE12; carboxylesterase	-1.20		
Csa6M088170.1	AT1G64950.1 CYP89A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.19		
Csa2M348270.1	AT1G60460.1 unknown protein	-1.19		
Csa7M041300.1	AT5G54010.1 glycosyltransferase family protein	-1.18		
Csa5M187840.1	AT5G59190.1 subtilase family protein	-1.18		
Csa6M107940.1	AT5G53560.1 CB5-E (CYTOCHROME B5 ISOFORM E); heme binding	-1.17		
	AT2G39518.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0497, trans-membrane plant (InterPro:IPR006702), Uncharacterised protein family UPF0497, trans- membrane plant subgroup (InterPro:IPR006459); BEST Arabidopsis thaliana protein match is: integral membrane protein, putative (TAIR:AT2G39530.1); Has 80 Blast hits to 80 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 80; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	-1.17		
Csa5M515010.1	AT1G73050.1 (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative	-1.16		
Csa2M055560.1	AT1G26945.1 KDR (KIDARI); transcription regulator	-1.16		
Csa6M404200.1	AT3G27890.1 NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN reductase	-1.16		
Csa5M435080.1	AT1G12740.1 CYP87A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.15		
Csa6M088710.1	AT4G37370.1 CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.15		
Csa6M088160.1	AT2G42250.1 CYP712A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.15		
Csa3M698490.1	AT5G05500.1 pollen Ole e 1 allergen and extensin family protein	-1.15	2.86	4.71
Csa5M211030.1	AT2G26710.1 BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	-1.14		
Csa1M305710.1	AT2G31790.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.12		
Csa6M366270.1	AT5G12380.1 annexin, putative	-1.11		
Csa3M842060.1	AT2G26560.1 PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	-1.11		1.48
Csa2M292840.1	AT4G21490.1 NDB3; NADH dehydrogenase	-1.10		
Csa1M071890.1	AT1G55740.1 AtSIP1 (Arabidopsis thaliana seed imbibition 1); hydrolase, hydrolyzing O-glycosyl compounds	-1.10		
Csa4M631570.1	AT3G24330.1 glycosyl hydrolase family 17 protein	-1.10		
Csa2M005360.1	AT2G44740.1 CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	-1.09		
Csa3M127030.1	AT3G15115.1 unknown protein	-1.09		
Csa3M236040.1	AT5G23870.2 pectinacetyltransferase family protein	-1.08		
Csa3M182200.1	AT2G47800.1 ATMTP4 (ARABIDOPSIS THALIANA MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 4); ATPase, coupled to transmembrane movement of substances / folic acid transporter	-1.08		
Csa7M396440.1	AT5G18840.1 sugar transporter, putative	-1.08		
Csa6M067380.1	AT5G10720.1 AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase	-1.08		
Csa4M650220.1	AT2G41970.1 protein kinase, putative	-1.08		1.41
Csa3M800660.1	AT3G03680.1 C2 domain-containing protein	-1.08		
Csa4M593900.1	AT2G16980.1 tetracycline transporter	-1.08		
Csa2M347100.1	AT1G52340.1 ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase	-1.07		
Csa1M044880.1	AT3G60130.1 BGLU16 (BETA GLUCOSIDASE 16); catalytic/ cation binding / hydrolase, hydrolyzing O- glycosyl compounds	-1.07		
Csa1M612830.1	AT3G19020.1 leucine-rich repeat family protein / extensin family protein	-1.06		
Csa6M485140.1	AT3G29590.1 AT5MAT; O-malonyltransferase/ transferase	-1.06		
Csa5M639480.1	AT1G78580.1 ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE); alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups	-1.06		
Csa1M467060.1	AT2G39210.1 nodulin family protein	-1.05		
Csa5M622530.1				

Csa2M055020.1	AT1G73050.1 (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative	-1.05	
Csa3M646550.1	AT1G53920.1 GLIP5; carboxylesterase/ lipase	-1.05	
Csa1M612860.1	AT1G02850.2 BGLU11 (BETA GLUCOSIDASE 11); hydrolase, hydrolyzing O-glycosyl compounds	-1.05	
Csa3M180430.1	AT3G61150.1 HDG1 (HOMEODOMAIN GLABROUS 1); DNA binding / transcription factor	-1.04	
Csa1M612850.1	AT5G25980.1 TGG2 (GLUCOSIDE GLUCOHYDROLASE 2); hydrolase, hydrolyzing O-glycosyl compounds / thioglucosidase	-1.04	
Csa6M426370.1	AT2G35930.1 PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase	-1.04	1.00
Csa6M366250.1	AT1G05680.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.03	
Csa6M507240.1	AT2G17760.1 aspartyl protease family protein	-1.02	
Csa2M374630.1	AT2G25810.1 TIP4;1 (tonoplast intrinsic protein 4;1); water channel	-1.02	
Csa4M650210.1	AT5G10720.1 AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase	-1.02	
Csa3M806800.1	AT3G12110.1 ACT11 (actin-11); structural constituent of cytoskeleton	-1.01	
Csa1M044890.1	AT1G12740.1 CYP87A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.01	
Csa3M836480.1	AT5G40270.1 metal-dependent phosphohydrolase HD domain-containing protein	-1.00	

Elements only in "Ed Dn-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa7M414530.1	AT4G37530.1 peroxidase, putative		-3.11		2.65		
Csa7M419530.1	AT2G18150.1 peroxidase, putative		-3.08		2.44		
Csa4M007620.1	AT4G30380.1 EXLB2 (EXPANSIN-LIKE B2 PRECURSOR)		-2.57				
Csa3M743950.1	AT1G20030.2 pathogenesis-related thaumatin family protein		-2.04				
Csa6M216940.1	AT5G05340.1 peroxidase, putative		-2.00				
Csa2M176180.1	AT1G44191.1 Encodes a ECA1 gametogenesis related family protein		-1.85				
Csa6M525600.1	AT5G38910.1 germin-like protein, putative		-1.85		1.67		
Csa6M352870.1	AT1G21270.1 WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase		-1.81				
Csa3M903510.1	AT1G05160.1 CYP88A3 (CYTOCHROME P450 88 A3); ent-kaurenoate oxidase/ oxygen binding		-1.68				
Csa7M044280.1	AT2G32350.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: protein modification process; LOCATED IN: cellular_component unknown; EXPRESSED IN: flower; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Ubiquitin (InterPro:IPR000626); BEST Arabidopsis thaliana protein match is: ubiquitin family protein (TAIR:AT4G05230.1); Has 132 Blast hits to 112 proteins in 46 species: Archae - 0; Bacteria - 0; Metazoa - 34; Fungi - 1; Plants - 50; Viruses - 12; Other Eukaryotes - 35 (source: NCBI BLink).		-1.68				
Csa5M272930.1	No hits found		-1.47				
Csa1M007890.1	AT1G18980.1 germin-like protein, putative		-1.44		1.07		
Csa4M285750.1	AT5G06730.1 peroxidase, putative		-1.41				
Csa6M011600.1	AT3G47570.1 leucine-rich repeat transmembrane protein kinase, putative		-1.40				2.04
Csa3M393910.1	AT1G04360.1 zinc finger (C3HC4-type RING finger) family protein		-1.40				
Csa6M351870.1	AT1G21240.1 WAK3 (wall associated kinase 3); kinase/ protein serine/threonine kinase		-1.39				
Csa6M354370.1	AT1G21270.1 WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase		-1.33				
Csa7M430230.1	AT3G21240.1 4CL2 (4-COUMARATE:COA LIGASE 2); 4-coumarate-CoA ligase		-1.31				
Csa4M129570.1	AT5G38990.1 protein kinase family protein		-1.29				
Csa1M097690.1	AT1G08090.1 ATNRT2:1 (NITRATE TRANSPORTER 2:1); nitrate transmembrane transporter		-1.25				
Csa4M285760.1	AT5G06720.1 peroxidase, putative		-1.23				
Csa6M508020.1	AT3G12500.1 ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase		-1.21				1.34
Csa6M405960.1	AT2G37040.1 pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase		-1.21				
Csa6M525590.1	AT4G14630.1 GLP9 (GERMIN-LIKE PROTEIN 9); manganese ion binding / nutrient reservoir		-1.21		2.21		
Csa5M215130.1	AT2G40300.1 ATERF4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal ion binding		-1.19				
Csa6M194680.1	No hits found		-1.17				
Csa6M525580.1	AT5G39120.1 germin-like protein, putative		-1.13		1.51		
Csa5M272920.1	AT1G60690.1 aldo/keto reductase family protein		-1.09				
Csa7M448650.1	AT3G14205.1 phosphoinositide phosphatase family protein		-1.09				
Csa5M636480.1	AT5G39785.1 structural constituent of ribosome		-1.09				
Csa5M648650.1	AT4G12020.1 WRKY19; transcription factor		-1.06				

Elements only in "Sn Dn-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-Fe vs +Fe)</u>					
		<u>down fefe -Fe</u>	<u>down Ed -Fe</u>	<u>down Sn -Fe</u>	<u>up fefe -Fe</u>	<u>up Ed -Fe</u>	<u>up Sn -Fe</u>
Csa6M235540.1	No hits found			-5.17			
Csa7M257320.1	AT3G18830.1 ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann					-4.47	
Csa3M696860.1	AT3G08040.1 FRD3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter/ transporter					-3.90	
Csa1M662810.1	AT3G05950.1 germin-like protein, putative					-3.81	
Csa4M639110.1	No hits found					-3.68	
Csa3M781620.1	AT3G11680.1 unknown protein					-3.25	
Csa3M782120.1	AT1G08430.1 ALMT1 (ALUMINUM-ACTIVATED MALATE TRANSPORTER 1); malate transmembrane transporter					-3.14	
Csa4M627800.1	AT1G73165.1 CLE1 (CLAVATA3/ESR-RELATED 1); protein binding / receptor binding					-2.86	
Csa5M190500.1	AT3G51030.1 ATTRX1; oxidoreductase, acting on sulfur group of donors, disulfide as acceptor					-2.64	
Csa4M244900.1	AT1G31670.1 copper amine oxidase, putative					-2.53	
CsaUNM013090.1	AT1G01900.1 SBT11.1; serine-type endopeptidase					-2.38	
Csa1M561410.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase					-2.24	
Csa7M209550.1	AT3G16720.1 ATL2; protein binding / zinc ion binding					-2.19	
Csa2M285370.1	No hits found					-2.14	
Csa6M106810.1	AT4G00910.1 unknown protein					-2.13	2.43
Csa1M533380.1	AT2G30090.1 GCN5-related N-acetyltransferase (GNAT) family protein					-2.08	
Csa3M776350.1	AT2G27550.1 ATC (ARABIDOPSIS THALIANA CENTRORADIALIS); phosphatidylethanolamine binding					-2.07	
Csa3M851930.1	No hits found					-2.04	
CsaUNM012590.1	AT1G01900.1 SBT11.1; serine-type endopeptidase					-2.04	
Csa4M043950.1	AT5G19730.1 pectinesterase family protein					-1.97	
Csa1M561420.1	AT2G24100.1 unknown protein					-1.90	
Csa2M062630.1	AT2G19330.1 leucine-rich repeat family protein					-1.87	
Csa7M044860.1	AT3G22060.1 receptor protein kinase-related					-1.77	
Csa2M340400.1	AT5G63660.1 PDF2.5					-1.72	
Csa1M689640.1	AT2G43890.1 polygalacturonase, putative / pectinase, putative					-1.69	
Csa7M446640.1	AT1G12660.1 Predicted to encode a PR (pathogenesis-related) protein. Belongs to the plant thionin (PR-13) family with the following members: At1g66100, At5g36910, At1g72260, At2g15010, At1g12663, At1g12660.					-1.64	
Csa1M422440.1	AT5G57560.1 TCH4 (Touch 4); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase					-1.63	
Csa1M008560.1	AT1G69850.1 ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter					-1.63	
Csa1M056980.1	AT1G31040.1 unknown protein					-1.63	
Csa1M434130.1	AT4G10310.1 HKT1 (HIGH-AFFINITY K+ TRANSPORTER 1); sodium ion transmembrane transporter					-1.63	
Csa1M338920.1	AT2G41480.1 electron carrier/ heme binding / peroxidase					-1.59	1.04
Csa3M142960.1	AT2G38870.1 protease inhibitor, putative					-1.59	2.20
Csa2M299890.1	AT4G16740.1 ATTPS03; (E)-beta-ocimene synthase/ myrcene synthase					-1.58	
Csa7M047960.1	AT5G56170.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: anchored to membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: LRE (LORELEI) (TAIR:AT4G26466.1); Has 71 Blast hits to 71 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 71; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).					-1.57	
Csa3M873800.2	AT1G20160.1 ATSBT5.2; identical protein binding / serine-type endopeptidase					-1.57	
Csa6M139130.1	AT1G31320.1 LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4)					-1.55	
Csa2M235600.1	AT1G49570.1 peroxidase, putative					-1.53	
Csa2M362450.1	AT1G75450.1 CKX5 (CYTOKININ OXIDASE 5); cytokinin dehydrogenase					-1.51	

	AT5G53750.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to wounding; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage; CONTAINS InterPro DOMAIN/s: Cystathionine beta-synthase, core (InterPro:IPR000644); BEST Arabidopsis thaliana protein match is: CBS domain-containing protein (TAIR:AT4G27460.1); Has 79 Blast hits to 78 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 79; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	-1.50	
Csa4M637820.1			
Csa6M504620.1	AT3G51030.1 ATTRX1; oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	-1.49	
Csa7M019860.1	AT4G38400.1 ATEXLA2 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A2)	-1.49	
Csa3M873800.1	AT1G20160.1 ATSBT5.2; identical protein binding / serine-type endopeptidase	-1.48	
Csa2M235100.1	AT1G49570.1 peroxidase, putative	-1.46	
Csa1M049960.1	AT5G63180.1 pectate lyase family protein	-1.46	
Csa3M178530.1	No hits found	-1.45	
Csa3M015860.1	AT1G32450.1 NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	-1.45	1.09
Csa3M629740.1	AT2G43870.1 polygalacturonase, putative / pectinase, putative	-1.41	
Csa7M044870.1	AT1G26250.1 proline-rich extensin, putative	-1.40	
Csa3M133940.1	No hits found	-1.39	
Csa1M001300.1	AT5G50790.1 nodulin MtN3 family protein	-1.38	
Csa1M051850.1	AT2G34930.1 disease resistance family protein	-1.38	
Csa1M418770.1	No hits found	-1.37	
Csa4M293210.1	AT2G39370.1 unknown protein	-1.35	
Csa3M009550.1	AT2G36120.1 DOT1 (DEFECTIVELY ORGANIZED TRIBUTARIES 1)	-1.34	
Csa2M139860.1	AT5G24910.1 CYP714A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.30	
	AT4G30200.3 Encodes a protein with similarity to VRN5 and VIN3. Contains both a fibronectin III and PHD finger domain. VEL1 is a part of a polycomb repressive complex (PRC2) that is involved in epigenetic silencing of the FLC flowering locus.		
Csa2M370440.2		-1.29	
Csa6M365140.1	AT5G43250.1 NF-YC13 (NUCLEAR FACTOR Y, SUBUNIT C13); DNA binding / transcription factor	-1.29	
Csa4M420190.1	No hits found	-1.28	
Csa6M454470.1	AT3G52500.1 aspartyl protease family protein	-1.28	
Csa2M234600.1	AT2G15790.1 SQN (SQUINT); peptidyl-prolyl cis-trans isomerase	-1.27	
Csa3M238100.2	AT5G53550.1 YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	-1.26	
Csa3M042390.1	AT1G12630.1 DNA binding / transcription activator/ transcription factor	-1.26	
Csa6M083540.1	AT5G24070.1 peroxidase family protein	-1.25	
Csa3M646540.1	AT5G40990.1 GLIP1 (GDSL LIPASE1); carboxylesterase/ lipase	-1.25	
Csa6M338660.1	AT1G43800.1 acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative	-1.24	2.39
Csa6M445010.1	AT2G37130.1 peroxidase 21 (PER21) (P21) (PRXR5)	-1.23	
Csa1M051880.1	AT2G34930.1 disease resistance family protein	-1.22	
Csa3M664600.1	AT1G02460.1 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	-1.22	
Csa1M257930.1	AT4G30845.1 unknown protein	-1.22	
Csa6M497240.1	AT5G65660.1 hydroxyproline-rich glycoprotein family protein	-1.21	
Csa1M062950.1	AT1G11710.1 pentatricopeptide (PPR) repeat-containing protein	-1.20	
Csa4M642510.1	AT4G37630.1 CYCD5;1 (cyclin d5;1); cyclin-dependent protein kinase	-1.19	
Csa6M517230.1	AT4G27460.1 CBS domain-containing protein	-1.19	
Csa7M392940.1	AT3G63110.1 ATIPT3 (ARABIDOPSIS THALIANA ISOPENTENYLTRANSFERASE 3); ATP binding / tRNA isopentenyltransferase/ transferase, transferring alkyl or aryl (other than methyl) groups	-1.18	
Csa3M094500.1	AT5G54585.1 unknown protein	-1.18	
Csa3M904070.1	AT1G32450.1 NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	-1.18	
Csa2M395190.1	AT1G35530.1 DEAD/DEAH box helicase, putative	-1.17	
Csa2M020880.1	No hits found	-1.16	
Csa3M238100.1	AT5G53550.1 YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	-1.16	
Csa1M153550.1	AT3G19430.1 late embryogenesis abundant protein-related / LEA protein-related	-1.15	
Csa5M266320.1	No hits found	-1.15	
Csa3M002410.1	No hits found	-1.14	
Csa3M099670.3	No hits found	-1.13	

Csa1M418780.1	AT2G24720.1 ATGLR2.2; intracellular ligand-gated ion channel	-1.12
Csa3M890080.1	AT2G47550.1 pectinesterase family protein	-1.12
Csa3M878930.2	AT5G25380.1 CYCA2;1 (cyclin a2;1); cyclin-dependent protein kinase regulator	-1.12
Csa1M074910.1	AT1G28290.2 AGP31 (arabinogalactan-protein 31)	-1.12
Csa7M031030.1	AT2G04235.1 unknown protein	-1.12
Csa7M019900.1	AT4G38400.1 ATEXLA2 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A2)	-1.11
Csa2M223160.1	AT3G22740.1 HMT3; homocysteine S-methyltransferase	-1.10
Csa5M151530.1	AT4G27950.1 CRF4 (CYTOKININ RESPONSE FACTOR 4); DNA binding / transcription factor	-1.10
Csa3M009540.1	AT5G46730.1 glycine-rich protein	-1.10
Csa5M077240.1	No hits found	-1.10
Csa3M148800.1	AT5G26340.1 MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter	-1.09
Csa1M005540.1	AT1G23820.1 SPDS1 (spermidine synthase 1); spermidine synthase	-1.09
Csa6M476630.1	AT5G06570.1 hydrolase	-1.08
Csa7M016600.1	AT2G16990.1 tetracycline transporter	-1.07
Csa6M199280.1	AT3G21460.1 electron carrier/ protein disulfide oxidoreductase	-1.07
Csa1M097650.1	AT5G22930.1 unknown protein	-1.07
Csa5M576630.1	AT5G38110.1 ASF1B (ANTI- SILENCING FUNCTION 1B)	-1.07
Csa6M013900.1	AT2G40435.1 EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: transcription regulator (TAIR:AT3G56220.1); Has 165 Blast hits to 165 proteins in 20 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 165; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	-1.07
Csa5M649880.1	AT1G15170.1 MATE efflux family protein	-1.06
Csa6M495090.1	AT5G67470.1 formin homology 2 domain-containing protein / FH2 domain-containing protein	-1.06
Csa2M287100.1	No hits found	-1.06
Csa6M358160.2	AT4G35240.1 unknown protein	-1.06
Csa4M310210.1	AT2G38250.1 DNA-binding protein-related	-1.06
Csa6M008770.1	AT3G55605.1 mitochondrial glycoprotein family protein / MAM33 family protein	-1.05
Csa3M782720.1	AT2G40210.1 AGL48 (AGAMOUS-LIKE 48); transcription factor	-1.05
Csa1M042550.1	AT1G18370.1 HIK (HINKEL); ATP binding / microtubule motor	-1.05
Csa2M033280.1	AT5G02070.1 protein kinase-related	-1.04
Csa6M421040.1	AT2G32990.1 AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	-1.04
Csa3M736730.1	AT3G53470.1 unknown protein	-1.04
Csa6M366580.1	AT1G69160.1 unknown protein	-1.04
Csa6M190340.1	AT2G39700.1 ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	-1.04
Csa4M000660.1	AT1G70210.1 CYCD1;1 (CYCLIN D1;1); cyclin-dependent protein kinase regulator	-1.04
Csa7M339140.1	AT5G48820.1 ICK6 (INHIBITOR/INTERACTOR WITH CYCLIN-DEPENDENT KINASE); cyclin binding / cyclin-dependent protein kinase inhibitor	-1.04
Csa3M730160.1	AT2G30400.1 OFP2 (OVATE FAMILY PROTEIN 2)	-1.03
Csa5M590170.1	AT3G25980.1 mitotic spindle checkpoint protein, putative (MAD2)	-1.03
Csa2M277090.1	AT5G27220.1 protein transport protein-related	-1.03
Csa4M219360.1	AT5G27000.1 ATK4 (ARABIDOPSIS THALIANA KINESIN 4); ATPase/ microtubule binding / microtubule motor	-1.02
Csa3M638510.2	AT4G19010.1 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	-1.02
Csa2M299920.1	AT3G25820.1 ATTPS-CIN (terpene synthase-like sequence-1,8-cineole); (E)-beta-ocimene synthase/ myrcene synthase	-1.02
Csa2M011570.1	No hits found	-1.02
Csa3M838140.1	AT3G26610.1 polygalacturonase, putative / pectinase, putative	-1.02
Csa7M407820.1	AT5G49520.1 WRKY48; transcription factor	-1.01
Csa7M047420.1	AT4G28250.1 ATEXPB3 (ARABIDOPSIS THALIANA EXPANSIN B3)	-1.01
Csa2M351570.1	AT1G67370.1 ASY1 (ASYNAPTIC 1); DNA binding	-1.01
Csa1M537610.1	AT5G44330.1 male sterility MS5 family protein	-1.01
Csa3M171060.1	AT3G17350.1 unknown protein	-1.01
Csa3M638510.1	AT4G19010.1 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	-1.01
Csa5M606590.1	AT5G61210.1 SNAP33 (SOLUBLE N-ETHYLMALIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding	-1.01



Csa6M111370.1	AT3G07770.1 ATP binding	-1.01	
	AT3G06030.1 ANP3 (ARABIDOPSIS NPK1-RELATED PROTEIN KINASE 3); ATP binding / kinase/ protein		
Csa6M425140.1	kinase/ protein serine/threonine kinase	-1.01	
Csa3M855280.1	AT1G75090.1 methyladenine glycosylase family protein	-1.01	
Csa6M190340.2	AT2G39700.1 ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	-1.01	
Csa4M002510.1	AT1G02730.1 ATCSLD5; 1,4-beta-D-xylan synthase/ cellulose synthase	-1.00	
Csa3M840430.1	AT5G14450.1 GDSL-motif lipase/hydrolase family protein	-1.00	1.11
Csa3M839810.1	AT3G27640.1 transducin family protein / WD-40 repeat family protein	-1.00	

<b>Table S7. Genes with opposite regulatory patterns in WT and <i>fe</i> under Fe deficiency.</b>							
<b>5 genes downregulated in <i>fe</i> by Fe deficiency and upregulated in both WT.</b>		<b>log fold change (-Fe vs +Fe)</b>					
<b>Cucumber Locus ID</b>	<b>Top <i>Arabidopsis thaliana</i> hit</b>	<b>down <i>fe</i> -Fe</b>	<b>down Ed -Fe</b>	<b>down Sn -Fe</b>	<b>up <i>fe</i> -Fe</b>	<b>up Ed -Fe</b>	<b>up Sn -Fe</b>
Csa5M589920.1	AT1G13710.1 CYP78A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-2.27				1.09	1.07
Csa5M175770.1	AT1G23020.1 FRO3; ferric-chelate reductase	-1.70				4.33	2.67
Csa6M134900.1	AT1G30870.1 cationic peroxidase, putative	-1.62				3.09	5.66
Csa3M435010.2	AT4G26270.1 PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase	-1.22				1.68	2.30
Csa5M211030.1	AT5G05500.1 pollen Ole e 1 allergen and extensin family protein	-1.15				2.86	4.71
<b>5 genes downregulated in <i>fe</i> by Fe deficiency and upregulated in Edisto.</b>		<b>log fold change (-Fe vs +Fe)</b>					
<b>Cucumber Locus ID</b>	<b>Top <i>Arabidopsis thaliana</i> hit</b>	<b>down <i>fe</i> -Fe</b>	<b>down Ed -Fe</b>	<b>down Sn -Fe</b>	<b>up <i>fe</i> -Fe</b>	<b>up Ed -Fe</b>	<b>up Sn -Fe</b>
Csa1M526820.1	AT3G46900.1 COPT2; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter	-2.55		-1.59		1.79	
Csa2M031160.1	AT4G15920.1 INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPR018169), RAG1-activating protein 1 homologue (InterPro:IPR018179), MtN3 and saliva related transmembrane protein (InterPro:IPR004316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	-2.27				1.11	
Csa2M034530.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase	-1.75				2.19	
Csa3M180260.1	AT4G25490.1 CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	-1.64				1.10	
Csa2M439220.1	AT5G10530.1 lectin protein kinase, putative	-1.60				1.47	
<b>25 genes downregulated in <i>fe</i> by Fe deficiency and upregulated in snake melon.</b>		<b>log fold change (-Fe vs +Fe)</b>					
<b>Cucumber Locus ID</b>	<b>Top <i>Arabidopsis thaliana</i> hit</b>	<b>down <i>fe</i> -Fe</b>	<b>down Ed -Fe</b>	<b>down Sn -Fe</b>	<b>up <i>fe</i> -Fe</b>	<b>up Ed -Fe</b>	<b>up Sn -Fe</b>
Csa4M637160.1	AT3G15350.1 glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	-1.99					2.92
Csa3M555690.1	AT1G52800.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	-2.02					1.86
Csa1M166260.1	AT5G22410.1 peroxidase, putative	-2.92					3.36
Csa4M288090.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	-2.48					2.92
Csa1M423000.1	AT5G57550.1 XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	-2.43					1.28
Csa3M895700.1	AT3G63520.1 CCD1 (CAROTENOID CLEAVAGE DIOXYGENASE 1); 9-cis-epoxycarotenoid dioxygenase	-3.40					3.16
Csa5M139780.1	AT1G64950.1 CYP89A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-2.48					1.83
Csa3M800660.1	AT2G41970.1 protein kinase, putative	-1.08					1.41
Csa2M292840.1	AT2G26560.1 PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	-1.11					1.48
Csa1M326870.1	AT5G16990.1 NADP-dependent oxidoreductase, putative	-2.77					2.09
Csa2M003060.1	AT4G28840.1 unknown protein	-2.07					1.72
Csa6M010000.1	AT2G39980.1 transferase family protein	-1.37					1.02
Csa1M288020.1	AT4G30420.1 nodulin MtN21 family protein	-1.83					1.12
Csa6M426370.1	AT2G35930.1 PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase	-1.04					1.00
Csa1M555620.1	AT1G56580.1 unknown protein	-2.55					1.43
Csa5M224130.1	AT5G24910.1 CYP714A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.44					1.39
Csa2M008110.1	AT5G20410.1 MGD2; 1,2-diacylglycerol 3-beta-galactosyltransferase/ UDP-galactosyltransferase/ transferase, transferring glycosyl groups	-1.53					1.40
Csa5M599860.1	AT1G12940.1 ATNRT2.5 (nitrate transporter2.5); nitrate transmembrane transporter	-2.93					1.71

Csa3M603600.1	AT2G25410.1 protein binding / zinc ion binding	-1.93					2.08
Csa2M373590.1	AT4G32810.1 CCD8 (CAROTENOID CLEAVAGE DIOXYGENASE 8); oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	-2.26					2.66
Csa3M895690.1	AT3G14440.1 NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	-3.28					2.76
Csa2M406650.1	AT4G37530.1 peroxidase, putative	-2.28					2.02
Csa7M029390.1	AT1G76490.1 HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	-1.37					1.05
Csa4M361270.1	AT1G77330.1 1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative	-1.37					1.91
Csa1M611280.1	AT2G44450.1 BGLU15 (BETA GLUCOSIDASE 15); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	-1.70					1.13
<b>3 genes upregulated in <i>fe</i> by Fe deficiency and downregulated in snake melon.</b>		<b>log fold change (-Fe vs +Fe)</b>					
<b>Cucumber Locus ID</b>	<b>Top <i>Arabidopsis thaliana</i> hit</b>	<b>down <i>fe</i> -Fe</b>	<b>down Ed -Fe</b>	<b>down Sn -Fe</b>	<b>up <i>fe</i> -Fe</b>	<b>up Ed -Fe</b>	<b>up Sn -Fe</b>
Csa6M338660.1	AT1G43800.1 acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative			-1.24	2.39		
Csa3M142960.1	AT2G38870.1 protease inhibitor, putative			-1.59	2.20		
Csa3M840430.1	AT5G14450.1 GDSL-motif lipase/hydrolase family protein			-1.00	1.11		
<b>6 genes upregulated in <i>fe</i> by Fe deficiency and downregulated in Edisto.</b>		<b>log fold change (-Fe vs +Fe)</b>					
<b>Cucumber Locus ID</b>	<b>Top <i>Arabidopsis thaliana</i> hit</b>	<b>down <i>fe</i> -Fe</b>	<b>down Ed -Fe</b>	<b>down Sn -Fe</b>	<b>up <i>fe</i> -Fe</b>	<b>up Ed -Fe</b>	<b>up Sn -Fe</b>
Csa6M525590.1	AT4G14630.1 GLP9 (GERMIN-LIKE PROTEIN 9); manganese ion binding / nutrient reservoir		-1.21		2.21		
Csa6M525600.1	AT5G38910.1 germin-like protein, putative		-1.85		1.67		
Csa7M419530.1	AT2G18150.1 peroxidase, putative		-3.08		2.44		
Csa7M414530.1	AT4G37530.1 peroxidase, putative		-3.11		2.65		
Csa6M525580.1	AT5G39120.1 germin-like protein, putative		-1.13		1.51		
Csa1M007890.1	AT1G18980.1 germin-like protein, putative		-1.44		1.07		
<b>One gene upregulated in <i>fe</i> by Fe deficiency and downregulated in both WT.</b>		<b>log fold change (-Fe vs +Fe)</b>					
<b>Cucumber Locus ID</b>	<b>Top <i>Arabidopsis thaliana</i> hit</b>	<b>down <i>fe</i> -Fe</b>	<b>down Ed -Fe</b>	<b>down Sn -Fe</b>	<b>up <i>fe</i> -Fe</b>	<b>up Ed -Fe</b>	<b>up Sn -Fe</b>
Csa7M037490.1	AT1G80810.1 binding		-1.41	-1.59	2.82		

**Table S8. Genes that were differentially expressed in Cu deficient roots of fefe or WT Edisto.**

**147 genes upregulated by Cu deficiency in both genotypes.**

Cucumber Locus ID	Top <i>Arabidopsis thaliana</i> hit	<u>log fold change (-Cu vs +Cu)</u>			
		up fefe -Cu	down fefe -Cu	up Ed -Cu	down Ed -Cu
Csa1M502880.1	AT2G28780.1 unknown protein	4.36		1.60	
Csa3M183380.1	AT5G23980.1 FRO4 (FERRIC REDUCTION OXIDASE 4); ferric-chelate reductase	3.83		2.64	
Csa6M497110.1	AT4G37850.1 basic helix-loop-helix (bHLH) family protein	3.13		2.22	
Csa5M366670.1	AT3G25780.1 AOC3 (ALLENE OXIDE CYCLASE 3); allene-oxide cyclase	2.71		2.77	
Csa4M001850.1	AT4G02380.1 SAG21 (SENESCENCE-ASSOCIATED GENE 21)	2.69		2.61	
Csa3M116720.1	AT2G44840.1 ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	2.65		3.80	
Csa6M525620.1	AT4G14630.1 GLP9 (GERMIN-LIKE PROTEIN 9); manganese ion binding / nutrient reservoir	2.51		1.37	
Csa6M350370.1	AT1G21270.1 WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase	2.41		2.03	
Csa2M351540.1	AT5G43260.1 chaperone protein dnaJ-related	2.38		1.15	
Csa6M350360.1	AT1G21240.1 WAK3 (wall associated kinase 3); kinase/ protein serine/threonine kinase	2.30		1.93	
Csa6M492310.1	AT2G14960.1 GH3.1	2.19		1.12	
Csa1M154090.1	AT2G27690.1 CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding	2.16		1.75	
Csa2M000280.1	AT4G29840.1 MTO2 (METHIONINE OVER-ACCUMULATOR 2); threonine synthase	2.06		1.01	
	AT1G12610.1 DDF1 (DWARF AND DELAYED FLOWERING 1); DNA binding / sequence-specific DNA binding / transcription factor	2.04		5.05	
Csa5M155570.1	AT2G26190.1 calmodulin-binding family protein	2.03		1.44	
Csa1M589650.1	AT1G19180.1 JAZ1 (JASMONATE-ZIM-DOMAIN PROTEIN 1); protein binding	2.00		2.07	
Csa7M448060.1	AT1G53885.1 senescence-associated protein-related	1.95		1.12	
Csa6M490950.1	AT4G36950.1 MAPKKK21; ATP binding / protein kinase/ protein serine/threonine kinase	1.92		2.86	
Csa5M591770.1	AT3G48450.1 nitrate-responsive NOI protein, putative	1.88		2.67	
Csa3M875940.1	AT4G38470.1 protein kinase family protein	1.78		1.27	
Csa5M205920.1	AT5G05600.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.76		1.47	
Csa4M296260.1	AT5G51670.1 unknown protein	1.74		2.25	
Csa4M111600.1	No hits found	1.73		3.05	
	AT4G17500.1 ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	1.73		1.66	
Csa5M165850.1	AT2G37430.1 zinc finger (C2H2 type) family protein (ZAT11)	1.72		1.95	
	AT1G64065.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G44000.1); Has 69 Blast hits to 69 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLINK).	1.67		1.81	
Csa5M152160.1	AT1G72520.1 lipoxygenase, putative	1.66		2.72	
Csa7M449420.1	AT3G44260.1 CCR4-NOT transcription complex protein, putative	1.64		2.96	
Csa6M425790.1	AT3G52450.1 PUB22 (PLANT U-BOX 22); ubiquitin-protein ligase	1.64		1.38	
Csa4M194780.1	AT3G21680.1 unknown protein	1.63		2.10	
Csa2M418890.1	AT5G47530.1 auxin-responsive protein, putative	1.63		3.52	
Csa7M041870.1	No hits found	1.61		1.79	
Csa4M000820.1	AT5G06300.1 carboxy-lyase	1.59		1.17	
Csa3M872060.1	AT4G34410.1 RRTF1 (REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor	1.58		4.08	
Csa7M073700.1	AT1G74930.1 ORA47; DNA binding / transcription factor	1.58		2.56	
Csa1M597730.1	AT2G31945.1 unknown protein	1.54		2.36	
Csa3M706170.1	AT5G35090.1 unknown protein	1.53		2.62	
Csa4M652740.1	AT1G17380.1 JAZ5 (JASMONATE-ZIM-DOMAIN PROTEIN 5)	1.52		2.02	
Csa3M645940.1	AT5G53250.1 AGP22 (ARABINOGALACTAN PROTEIN 22)	1.50		3.18	
Csa2M004710.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.48		1.81	
Csa6M445780.1	AT1G15170.1 MATE efflux family protein	1.46		1.16	
Csa5M649880.1	AT1G02630.1 equilibrative nucleoside transporter, putative (ENT8)	1.43		2.40	
CsaUNM026650.1	AT1G76650.1 calcium-binding EF hand family protein	1.42		2.33	
Csa2M406780.1					

Csa5M517150.1	AT2G28930.1 APK1B; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	1.42	3.06
Csa3M782630.1	AT2G35930.1 PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase	1.39	3.47
Csa1M257330.1	No hits found	1.37	1.87
Csa1M257320.1	No hits found	1.37	2.93
Csa3M207390.1	AT4G34410.1 RRTF1 ((REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor	1.37	3.33
Csa1M170520.1	No hits found	1.36	1.03
Csa1M063490.1	No hits found	1.35	1.10
Csa1M526820.1	AT3G46900.1 COPT2; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter	1.35	1.71
Csa5M152240.1	AT1G01490.1 heavy-metal-associated domain-containing protein	1.34	2.03
Csa1M145980.1	AT2G27820.1 PD1 (PREPHENATE DEHYDRATASE 1); arogenate dehydratase/ prephenate dehydratase	1.34	1.53
Csa6M302190.1	AT5G59730.1 ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H7); protein binding	1.33	2.20
Csa3M164500.1	AT3G16720.1 ATL2; protein binding / zinc ion binding	1.33	1.78
Csa4M008250.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.32	1.96
Csa4M008760.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.32	1.97
Csa2M348260.1	AT1G70480.2 unknown protein	1.31	1.03
Csa6M519700.1	AT2G42760.1 unknown protein	1.31	3.39
Csa3M185090.1	AT5G38060.1 unknown protein	1.30	2.44
Csa5M148570.1	AT4G24110.1 unknown protein	1.30	1.35
Csa7M162550.1	AT5G59520.1 ZIP2; copper ion transmembrane transporter/ transferase, transferring glycosyl groups / zinc ion transmembrane transporter	1.30	2.23
Csa2M360780.1	AT5G42650.1 AOS (ALLENE OXIDE SYNTHASE); allene oxide synthase/ hydro-lyase/ oxygen binding	1.29	2.97
Csa7M394060.1	No hits found	1.29	2.34
Csa3M135120.1	AT3G23240.1 ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	1.29	1.41
Csa3M180310.1	AT4G23030.1 MATE efflux protein-related	1.28	2.82
Csa1M470240.1	AT2G42760.1 unknown protein	1.28	1.41
Csa4M008780.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.27	1.88
Csa4M269210.1	AT1G65690.1 harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	1.26	1.49
Csa3M121750.1	AT3G61460.1 BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding	1.26	1.07
Csa1M573650.1	AT5G28770.1 BZO2H3; DNA binding / protein heterodimerization/ transcription factor	1.25	1.93
Csa2M351020.1	AT1G27910.1 PUB45 (PLANT U-BOX 45); ubiquitin-protein ligase	1.25	1.03
Csa1M287020.1	AT2G23810.1 TET8 (TETRASPANIN8)	1.25	2.29
Csa2M381800.1	AT5G04860.1 unknown protein	1.24	3.36
Csa2M270210.1	AT2G17840.1 ERD7 (EARLY-RESPONSIVE TO DEHYDRATION 7)	1.24	1.76
Csa3M852440.1	AT3G15518.1 unknown protein	1.21	2.20
Csa7M237300.1	AT3G22240.1 unknown protein	1.21	1.62
Csa6M495090.1	AT5G67470.1 formin homology 2 domain-containing protein / FH2 domain-containing protein	1.21	1.62
Csa2M032730.1	AT1G56240.1 AtPP2-B13 (Phloem protein 2-B13); carbohydrate binding	1.21	1.38
Csa4M008260.1	AT2G37040.1 pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase	1.20	1.53
Csa2M297180.1	AT5G64810.1 WRKY51; transcription factor	1.20	1.04
Csa3M872740.1	AT1G20030.2 pathogenesis-related thaumatin family protein	1.19	1.82
Csa3M710870.1	AT1G80840.1 WRKY40; transcription factor	1.19	3.40
Csa2M348950.1	AT1G70520.1 protein kinase family protein	1.19	1.06
Csa3M386830.1	AT2G31180.1 MYB14 (MYB DOMAIN PROTEIN 14); DNA binding / transcription factor	1.19	1.71
Csa3M845500.1	AT5G47910.1 RBOHD (RESPIRATORY BURST OXIDASE HOMOLOGUE D); NAD(P)H oxidase	1.18	1.68
Csa3M238100.2	AT5G53550.1 YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	1.18	1.83
Csa5M524780.1	AT5G14700.1 cinnamoyl-CoA reductase-related	1.18	1.37
Csa7M413380.1	AT1G78440.1 ATGA2OX1 (gibberellin 2-oxidase 1); gibberellin 2-beta-dioxygenase	1.17	1.81
Csa5M223070.1	AT2G40750.1 WRKY54; transcription factor	1.16	1.01
Csa6M495100.1	AT5G67480.1 BT4 (BTB AND TAZ DOMAIN PROTEIN 4); protein binding / transcription regulator	1.16	1.17
Csa2M371110.1	AT2G22500.1 UCP5 (UNCOUPLING PROTEIN 5); binding	1.16	3.06
Csa4M008770.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.15	2.04
Csa3M119700.1	AT4G23810.1 WRKY53; DNA binding / protein binding / transcription activator/ transcription factor	1.14	3.25
Csa2M032230.1	AT1G09155.1 AtPP2-B15 (Phloem protein 2-B15); carbohydrate binding	1.14	1.37

Csa6M523440.1	AT1G30100.1 NCED5 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 5); 9-cis-epoxycarotenoid dioxygenase	1.14	1.63
Csa2M338830.1	AT1G01720.1 ATAF1; transcription activator/ transcription factor	1.14	1.35
Csa2M409500.1	No hits found	1.14	1.85
Csa7M432520.1	AT5G20230.1 ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier	1.13	1.13
Csa6M519620.1	AT2G38300.1 DNA binding / transcription factor	1.13	1.51
Csa3M710870.2	AT1G80840.1 WRKY40; transcription factor	1.12	3.26
Csa6M363530.1	No hits found	1.12	1.69
Csa3M238100.1	AT5G53550.1 YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	1.12	1.74
Csa3M730800.1	AT2G38470.1 WRKY33; transcription factor	1.12	1.50
	AT1G17020.1 SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc	1.12	1.22
Csa6M521000.1	2-oxoglutarate as one donor, and inc	1.12	1.22
Csa2M371610.1	AT2G22500.1 UCP5 (UNCOUPLING PROTEIN 5); binding	1.12	2.57
Csa4M658570.1	AT2G30600.1 BTB/POZ domain-containing protein	1.11	1.13
Csa1M002110.1	AT1G76650.1 calcium-binding EF hand family protein	1.11	3.25
Csa7M420820.1	AT1G01550.1 BPS1 (BYPASS 1)	1.11	1.65
Csa7M049260.1	AT4G28400.1 protein phosphatase 2C, putative / PP2C, putative	1.10	1.94
Csa1M481200.1	AT5G59730.1 ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H7); protein binding	1.10	1.13
CsaUNM026660.1	AT5G20190.1 binding	1.10	1.94
Csa4M286310.1	AT5G19890.1 peroxidase, putative	1.10	1.14
	AT4G23180.1 CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	1.10	1.19
Csa1M064820.1	protein tyrosine kinase	1.10	1.19
Csa6M516580.1	AT4G23160.1 protein kinase family protein	1.10	1.16
Csa4M314510.1	AT2G38480.1 integral membrane protein, putative	1.09	1.25
Csa7M071510.1	AT1G49850.1 zinc finger (C3HC4-type RING finger) family protein	1.09	1.32
Csa4M056600.1	AT4G19230.1 CYP707A1; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	1.09	1.03
Csa7M407620.1	AT3G03280.1 unknown protein	1.09	1.88
Csa2M408940.1	AT2G20562.1 unknown protein	1.08	1.70
Csa1M537320.1	AT1G30370.1 lipase class 3 family protein	1.08	2.37
Csa1M042340.1	AT1G73830.1 BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor	1.07	1.24
Csa6M016950.1	AT5G47850.1 CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase	1.07	1.98
Csa6M483320.1	AT1G53570.2 MAP3KA; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	1.07	1.05
Csa5M155500.1	AT5G07250.1 ATRBL3 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 3)	1.07	2.61
Csa6M133830.1	AT1G57610.1 unknown protein	1.07	2.22
Csa6M521000.2	AT4G25310.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.06	1.33
Csa3M747620.1	AT2G36690.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.06	1.52
Csa2M234570.1	AT2G26530.1 AR781	1.06	1.34
Csa1M617380.1	AT1G78100.1 F-box family protein	1.05	2.63
Csa6M516500.1	AT4G21410.1 protein kinase family protein	1.05	1.30
Csa6M147620.1	AT5G60800.1 heavy-metal-associated domain-containing protein	1.05	2.60
Csa4M152270.1	No hits found	1.05	1.01
Csa3M009550.1	AT2G36120.1 DOT1 (DEFECTIVELY ORGANIZED TRIBUTARIES 1)	1.04	1.31
Csa1M033260.1	AT5G39670.1 calcium-binding EF hand family protein	1.04	2.22
Csa6M446290.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.04	1.36
Csa6M525670.1	AT4G20840.1 FAD-binding domain-containing protein	1.04	2.22
Csa1M004920.2	AT5G62770.1 unknown protein	1.04	1.04
Csa4M341560.1	AT3G10300.3 calcium-binding EF hand family protein	1.03	1.15
Csa1M005770.1	AT3G48180.1 unknown protein	1.02	2.19
	AT5G56170.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: anchored to membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: LRE (LORELEI) (TAIR:AT4G26466.1); Has 71 Blast hits to 71 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 71; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	1.02	1.65
Csa7M047960.1	Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 71; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	1.02	1.65
Csa5M484630.1	AT1G70170.1 MMP (MATRIX METALLOPROTEINASE); metalloendopeptidase/ metallopeptidase	1.01	2.11

Csa2M371610.2	AT2G22500.1 UCP5 (UNCOUPLING PROTEIN 5); binding	1.01	2.63
Csa6M525670.2	AT4G20840.1 FAD-binding domain-containing protein	1.01	2.16
Csa5M167110.1	AT5G07580.1 DNA binding / transcription factor	1.01	1.02
Csa3M180260.1	AT4G25490.1 CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	1.01	3.64
Csa7M071520.1	AT4G33920.1 protein phosphatase 2C family protein / PP2C family protein	1.01	2.82

**63 genes downregulated by Cu deficiency in both genotypes.**

Cucumber Locus ID	Top <i>Arabidopsis thaliana</i> hit	<u>log fold change (-Cu vs +Cu)</u>			
		fefe +Cu	fefe -Cu	Ed +Cu	Ed -Cu
Csa5M168830.1	AT5G17165.1 unknown protein		-9.03		-5.22
Csa1M423010.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase		-5.08		-4.36
Csa5M175770.1	AT1G23020.1 FRO3; ferric-chelate reductase		-5.02		-3.33
Csa1M537450.1	AT5G44440.1 FAD-binding domain-containing protein		-4.91		-4.08
Csa2M034530.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase		-3.50		-3.20
Csa4M303690.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase		-3.28		-4.13
Csa1M561410.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase		-3.26		-1.71
Csa4M304250.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase		-2.89		-5.22
Csa3M592690.1	AT1G05680.1 UDP-glucuronosyl/UDP-glucosyl transferase family protein		-2.82		-5.64
Csa7M037560.1	No hits found		-2.45		-1.78
Csa4M050240.1	AT1G64160.1 disease resistance-responsive family protein / dirigent family protein		-2.34		-1.80
Csa3M133380.1	AT2G29420.1 ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase		-2.27		-2.08
Csa6M504560.1	AT5G66390.1 peroxidase 72 (PER72) (P72) (PRXR8)		-2.23		-2.64
Csa5M139760.1	AT5G24090.1 acidic endochitinase (CHIB1)		-2.17		-1.80
Csa6M338110.1	AT1G78780.2 pathogenesis-related family protein		-2.17		-1.78
Csa5M152790.1	AT1G63910.1 AtMYB103 (myb domain protein 103); DNA binding / transcription activator/ transcription factor		-2.12		-1.92
Csa7M447190.1	AT2G24400.1 auxin-responsive protein, putative / small auxin up RNA (SAUR_D)		-2.05		-1.54
Csa6M013940.1	AT5G05340.1 peroxidase, putative		-1.95		-2.76
Csa6M213910.1	AT5G05340.1 peroxidase, putative		-1.87		-4.51
Csa5M550240.1	AT2G01770.1 VIT1 (vacuolar iron transporter 1); iron ion transmembrane transporter		-1.85		-1.25
Csa3M333840.1	AT1G70890.1 MLP43 (MLP-LIKE PROTEIN 43)		-1.79		-1.17
Csa4M050250.1	AT1G64160.1 disease resistance-responsive family protein / dirigent family protein		-1.76		-2.19
Csa7M049140.1	AT5G05340.1 peroxidase, putative		-1.74		-1.26
Csa4M294410.1	AT3G53720.1 ATCHX20 (CATION/H+ EXCHANGER 20); monovalent cation:proton antiporter/ sodium:hydrogen antiporter		-1.72		-1.40
Csa1M025190.1	AT1G18290.1 unknown protein		-1.69		-1.20
Csa1M498810.1	AT5G39090.1 transferase family protein		-1.66		-2.32
Csa3M893390.1	AT5G65640.1 bHLH093 (beta HLH protein 93); DNA binding / transcription factor		-1.62		-1.02
Csa5M139770.1	AT5G24090.1 acidic endochitinase (CHIB1)		-1.58		-1.90
Csa4M000850.1	No hits found		-1.56		-1.90
Csa3M736560.1	AT3G53510.1 ABC transporter family protein		-1.53		-1.69
Csa6M009490.1	AT2G38080.1 IRX12 (IRREGULAR XYLEM 12); laccase		-1.52		-2.03
Csa3M893390.2	AT5G65640.2 bHLH093 (beta HLH protein 93); DNA binding / transcription factor		-1.51		-1.25
Csa4M374620.1	No hits found		-1.51		-2.72
Csa6M410100.1	AT3G22600.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein		-1.50		-2.32
Csa3M904120.1	AT2G35380.1 peroxidase 20 (PER20) (P20)		-1.49		-1.75
Csa4M285730.1	AT5G06720.1 peroxidase, putative		-1.48		-2.60
Csa3M133370.1	AT2G29420.1 ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase		-1.48		-2.11
Csa5M606920.1	AT1G13635.1 methyladenine glycosylase family protein		-1.47		-1.41
Csa1M605670.1	AT2G05990.1 MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ enoyl-[acyl-carrier-protein] reductase/ oxidoreductase		-1.46		-1.47
Csa4M644740.1	AT4G37750.1 ANT (AINTEGUMENTA); DNA binding / transcription factor		-1.44		-1.08

Csa4M031010.1	AT5G10180.1 AST68; sulfate transmembrane transporter	-1.43	-1.41
Csa7M312940.1	AT1G23720.1 proline-rich extensin-like family protein	-1.42	-1.84
Csa1M042810.1	No hits found	-1.41	-1.75
Csa6M411280.1	AT3G25190.1 nodulin, putative	-1.41	-1.04
Csa6M094680.1	AT4G27500.1 PPI1 (PROTON PUMP INTERACTOR 1); protein binding	-1.40	-1.49
Csa3M303130.1	AT5G37690.1 GDSL-motif lipase/hydrolase family protein	-1.36	-1.61
Csa3M250900.1	AT5G13900.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-1.36	-2.23
Csa1M042800.2	AT3G18000.1 XPL1 (XIPOTL 1); methyltransferase/ phosphoethanolamine N-methyltransferase	-1.30	-1.39
Csa5M167140.1	AT5G07475.1 plastocyanin-like domain-containing protein	-1.27	-2.30
Csa6M182140.1	AT3G51780.1 ATBAG4 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 4); protein binding	-1.27	-1.04
Csa6M493860.1	AT5G43120.1 tetratricopeptide repeat (TPR)-containing protein	-1.21	-1.11
Csa1M042800.1	AT3G18000.1 XPL1 (XIPOTL 1); methyltransferase/ phosphoethanolamine N-methyltransferase	-1.16	-1.24
Csa1M383520.1	AT4G13340.1 leucine-rich repeat family protein / extensin family protein	-1.16	-1.13
Csa2M292780.1	AT2G23540.1 GDSL-motif lipase/hydrolase family protein	-1.14	-1.84
Csa5M505150.1	AT2G39350.1 ABC transporter family protein	-1.11	-1.09
Csa2M153580.1	AT1G31770.1 ABC transporter family protein	-1.10	-1.05
Csa5M590220.1	AT1G24430.1 transferase/ transferase, transferring acyl groups other than amino-acyl groups	-1.08	-1.20
Csa4M554680.1	AT2G03200.1 aspartyl protease family protein	-1.07	-1.55
Csa5M608020.1	AT1G68850.1 peroxidase, putative	-1.07	-1.67
Csa5M517820.1	AT3G27400.1 pectate lyase family protein	-1.04	-1.00
Csa4M051530.1	AT1G64390.1 AtGH9C2 (Arabidopsis thaliana glycosyl hydrolase 9C2); carbohydrate binding / catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	-1.04	-1.29
Csa2M245410.1	AT3G18830.1 ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann	-1.02	-1.32
Csa2M357330.1	AT4G33330.1 transferase, transferring glycosyl groups	-1.01	-1.00

**3 genes downregulated in *fe* and upregulated in *Edisto* by Cu deficiency.**

Cucumber Locus ID	Top <i>Arabidopsis thaliana</i> hit	<u>log fold change (-Cu vs +Cu)</u>			
		<i>fe</i> +Cu	<i>fe</i> -Cu	<i>Ed</i> +Cu	<i>Ed</i> -Cu
Csa1M024920.1	AT1G73680.1 pathogen-responsive alpha-dioxygenase, putative		-1.00	1.11	
Csa3M873800.2	AT1G20160.1 ATSBT5.2; identical protein binding / serine-type endopeptidase		-1.23	1.24	
Csa3M873800.1	AT1G20160.1 ATSBT5.2; identical protein binding / serine-type endopeptidase		-1.23	1.13	

**2 genes upregulated in *fe* and downregulated in *Edisto* by Cu deficiency.**

Cucumber Locus ID	Top <i>Arabidopsis thaliana</i> hit	<u>log fold change (-Cu vs +Cu)</u>			
		<i>fe</i> +Cu	<i>fe</i> -Cu	<i>Ed</i> +Cu	<i>Ed</i> -Cu
Csa1M534750.1	AT3G54420.1 ATEP3; chitinase	1.34			-1.36
Csa1M024860.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	1.32			-2.13



**Table S9. Genes that were upregulated under Cu deficiency in one genotype.**

<i>fefe</i> only		<b>log fold change (-Cu vs +Cu)</b>	
<u>Cucumber Locus ID</u>	<u>Top <i>Arabidopsis thaliana</i> hit</u>	<u>up <i>fefe</i> -Cu</u>	<u>up Ed -Cu</u>
Csa2M021520.1	AT5G11250.1 disease resistance protein (TIR-NBS-LRR class), putative	5.70	
Csa1M059710.1	AT1G11925.1 Encodes a Stigma-specific Stig1 family protein	3.87	
Csa2M023890.1	AT1G55020.1 LOX1; lipoxygenase	3.55	
Csa3M217140.1	No hits found	3.01	
Csa1M627480.1	AT5G12340.1 unknown protein	2.98	
Csa6M523460.1	AT1G30135.1 JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8)	2.95	
Csa2M379900.1	AT5G11330.1 monooxygenase family protein	2.91	
Csa2M193320.1	AT5G43650.1 basic helix-loop-helix (bHLH) family protein	2.83	
Csa2M171860.1	AT1G04500.1 zinc finger CONSTANS-related	2.81	
Csa6M361330.1	AT5G21960.1 AP2 domain-containing transcription factor, putative	2.74	
Csa3M217160.1	No hits found	2.58	
Csa4M000650.1	AT4G33800.1 unknown protein	2.57	
	AT1G14870.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: plasma membrane; EXPRESSED IN: callus; CONTAINS InterPro DOMAIN/s: EGF-type aspartate/asparagine hydroxylation conserved site (InterPro:IPR000152), Protein of unknown function Cys-rich (InterPro:IPR006461); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35525.1); Has 492 Blast hits to 491 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 93; Fungi - 76; Plants - 297; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink).	2.55	
Csa5M027940.1	No hits found	2.53	
Csa3M219180.1	No hits found	2.53	
Csa1M074400.1	AT4G20970.1 basic helix-loop-helix (bHLH) family protein	2.40	
Csa2M074170.1	AT5G16530.1 PIN5 (PIN-FORMED 5); auxin:hydrogen symporter/ transporter	2.31	
Csa2M020880.1	No hits found	2.27	
Csa3M340350.1	AT5G28010.1 Bet v I allergen family protein	2.24	
Csa1M420340.1	AT4G15560.1 CLA1 (CLOROPLASTOS ALTERADOS 1); 1-deoxy-D-xylulose-5-phosphate synthase	2.20	
Csa4M064690.1	AT3G14440.1 NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	2.17	
	AT5G07050.1 LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF6, transmembrane (InterPro:IPR000620); BEST Arabidopsis thaliana protein match is: nodulin MtN21 family protein (TAIR:AT2G40900.1); Has 2288 Blast hits to 2270 proteins in 280 species: Archae - 23; Bacteria - 774; Metazoa - 5; Fungi - 0; Plants - 641; Viruses - 0; Other Eukaryotes - 845 (source: NCBI BLink).	2.13	
Csa5M584380.1	Eukaryotes - 845 (source: NCBI BLink).	2.13	
Csa4M639870.1	AT1G45201.1 TLL1 (TRIACYLGLYCEROL LIPASE-LIKE 1); triacylglycerol lipase	2.12	
Csa3M116730.1	AT2G44840.1 ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	2.09	
Csa3M135750.1	AT1G06620.1 2-oxoglutarate-dependent dioxygenase, putative	2.09	
Csa1M435720.1	AT2G34600.1 JAZ7 (JASMONATE-ZIM-DOMAIN PROTEIN 7)	2.09	
Csa2M177210.1	AT3G23240.1 ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	2.05	
Csa7M073520.1	AT4G34120.1 LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1)	2.04	
Csa6M490230.1	AT1G49570.1 peroxidase, putative	2.03	
Csa7M388390.1	AT5G28150.1 unknown protein	2.02	
Csa3M535090.1	AT3G06490.1 MYB108 (myb domain protein 108); DNA binding / transcription factor	2.02	
Csa2M014830.1	AT1G61190.1 disease resistance protein (CC-NBS-LRR class), putative	2.01	
Csa4M025190.1	AT1G02170.1 AMC1 (METACASPASE 1); cysteine-type endopeptidase	2.00	
Csa2M010180.1	No hits found	1.99	
Csa3M416650.1	AT4G27020.1 unknown protein	1.96	
Csa3M779000.1	AT2G35980.1 YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	1.94	
Csa6M502000.1	AT5G66710.1 protein kinase, putative	1.93	

Csa6M486970.1	AT1G77280.1 protein kinase family protein	1.93
Csa3M875440.1	AT4G38470.1 protein kinase family protein	1.92
Csa2M433340.1	AT3G50950.2 disease resistance protein (CC-NBS-LRR class), putative	1.91
Csa1M503390.1	AT2G28780.1 unknown protein	1.90
Csa2M075330.1	AT5G41540.1 disease resistance protein (TIR-NBS-LRR class), putative	1.89
Csa3M127170.1	AT1G32450.1 NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	1.88
Csa3M076570.1	No hits found	1.88
Csa5M148520.1	AT1G64660.1 ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase	1.85
Csa6M495060.1	AT4G37580.1 HLS1 (HOOKLESS 1); N-acetyltransferase	1.85
Csa1M002900.1	AT3G57520.1 AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase, hydrolyzing O-glycosyl compounds	1.83
Csa1M642550.1	No hits found	1.81
	AT5G66170.2 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: aging; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G17850.1); Has 730 Blast hits to 728 proteins in 227 species: Archae - 18; Bacteria - 429; Metazoa - 13; Fungi - 9; Plants - 103; Viruses - 0; Other Eukaryotes - 158 (source: NCBI BLink).	
Csa6M507040.2		1.80
Csa2M369090.1	AT1G22440.1 alcohol dehydrogenase, putative	1.79
Csa5M603380.1	AT1G10480.1 ZFP5 (ZINC FINGER PROTEIN 5); nucleic acid binding / transcription factor/ zinc ion binding	1.76
Csa3M135070.1	AT1G08650.1 PPCK1 (PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE); kinase/ protein serine/threonine kinase	1.73
Csa4M000820.2	No hits found	1.72
Csa2M070840.1	AT1G08860.1 BON3 (BONZAI 3); calcium-dependent phospholipid binding	1.72
	AT4G04480.1 LOCATED IN: chloroplast; EXPRESSED IN: flower, pollen tube; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT4G22030.1); Has 51 Blast hits to 51 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	
Csa6M513600.1		1.72
Csa5M485690.1	No hits found	1.69
Csa3M150850.1	AT5G18840.1 sugar transporter, putative	1.67
Csa2M271490.1	No hits found	1.67
	AT5G66170.2 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: aging; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G17850.1); Has 730 Blast hits to 728 proteins in 227 species: Archae - 18; Bacteria - 429; Metazoa - 13; Fungi - 9; Plants - 103; Viruses - 0; Other Eukaryotes - 158 (source: NCBI BLink).	
Csa6M507040.1		1.67
	AT4G04480.1 LOCATED IN: chloroplast; EXPRESSED IN: flower, pollen tube; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT4G22030.1); Has 51 Blast hits to 51 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	
Csa6M513610.1		1.65
Csa2M069700.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	1.62
Csa5M206420.1	AT5G05600.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.62
Csa3M076020.1	AT1G11840.2 ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase/ metal ion binding	1.62
Csa3M119720.1	AT4G01070.1 GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	1.60
Csa4M011720.1	No hits found	1.59
Csa7M066840.1	AT5G10530.1 lectin protein kinase, putative	1.58
Csa6M106810.1	AT4G00910.1 unknown protein	1.58
Csa7M448810.1	AT1G74950.1 TIFY10B	1.56
Csa6M077360.1	AT3G60810.1 unknown protein	1.55
Csa3M875950.1	AT4G35780.1 protein kinase family protein	1.55
Csa3M002890.1	AT1G64660.1 ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase	1.55

Csa3M076000.1	AT1G11840.2 ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase/ metal ion binding	1.54
Csa7M375830.1	AT3G23230.1 ethylene-responsive factor, putative	1.54
Csa5M576840.1	AT1G68390.1 unknown protein	1.54
Csa3M135740.1	AT1G06620.1 2-oxoglutarate-dependent dioxygenase, putative	1.53
Csa6M190280.1	No hits found	1.50
Csa2M357260.1	AT4G35290.2 GLUR2 (GLUTAMATE RECEPTOR 2); intracellular ligand-gated ion channel	1.50
Csa1M257310.1	No hits found	1.49
Csa5M173520.1	AT5G52120.1 AtPP2-A14 (Phloem protein 2-A14); carbohydrate binding	1.49
Csa7M043050.1	AT1G62280.1 SLAH1 (SLAC1 HOMOLOGUE 1); transporter	1.49
Csa1M071800.1	AT5G54490.1 PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding / protein binding	1.48
Csa3M000690.1	AT5G65980.1 auxin efflux carrier family protein	1.48
Csa2M070210.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monoxygenase	1.48
Csa6M120420.1	AT1G19250.1 FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monoxygenase/ monoxygenase/ oxidoreductase	1.47
Csa3M017320.1	AT4G17500.1 ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	1.46
Csa6M511630.1	AT4G16460.1 unknown protein	1.44
Csa3M122660.1	AT2G45760.1 BAP2 (BON ASSOCIATION PROTEIN 2)	1.44
Csa4M031060.1	AT2G18540.1 cupin family protein	1.41
Csa6M292430.1	AT1G61560.1 MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding	1.40
Csa3M875410.1	AT1G20310.1 unknown protein	1.40
Csa3M842060.1	AT5G12380.1 annexin, putative	1.39
Csa3M664600.1	AT1G02460.1 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	1.39
Csa2M069200.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monoxygenase	1.37
Csa1M574880.2	AT4G26080.1 ABI1 (ABA INSENSITIVE 1); calcium ion binding / protein serine/threonine phosphatase	1.36
Csa4M377730.1	AT1G77810.1 galactosyltransferase family protein	1.36
Csa6M148230.1	AT5G22920.1 zinc finger (C3HC4-type RING finger) family protein	1.36
Csa2M403680.1	AT4G27220.1 disease resistance protein (NBS-LRR class), putative	1.35
Csa4M377730.2	AT1G77810.1 galactosyltransferase family protein	1.35
Csa4M051470.1	AT4G11070.1 WRKY41; transcription factor	1.35
Csa2M033340.1	No hits found	1.34
Csa6M425720.1	AT5G22380.1 anac090 (Arabidopsis NAC domain containing protein 90); transcription factor	1.34
Csa2M059700.1	AT5G36930.1 disease resistance protein (TIR-NBS-LRR class), putative	1.34
Csa1M007890.1	AT1G18980.1 germin-like protein, putative	1.34
Csa6M500640.1	AT4G39830.1 L-ascorbate oxidase, putative	1.34
Csa6M516810.1	AT4G05120.1 FUR1 (FUDR RESISTANT 1); nucleoside transmembrane transporter	1.34
Csa6M148230.2	AT5G25560.1 zinc finger (C3HC4-type RING finger) family protein	1.34
Csa4M003090.1	No hits found	1.33
Csa2M021540.1	AT4G11170.1 disease resistance protein (TIR-NBS-LRR class), putative	1.33
Csa6M502830.1	AT4G36500.1 unknown protein	1.32
Csa5M139600.1	AT5G53190.1 nodulin MtN3 family protein	1.32
Csa5M585990.1	AT3G19830.1 NTMC2T5.2	1.32
Csa3M716370.1	AT1G80820.1 CCR2 (CINNAMOYL COA REDUCTASE); cinnamoyl-CoA reductase	1.32
Csa2M359920.1	AT2G29120.1 ATGLR2.7; intracellular ligand-gated ion channel	1.32
Csa1M703060.1	AT2G02300.1 AtPP2-B5 (Phloem protein 2-B5); carbohydrate binding	1.32
Csa3M127770.1	AT1G02190.2 CER1 protein, putative	1.31
Csa3M797570.1	AT5G06610.1 unknown protein	1.30
Csa2M070200.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monoxygenase	1.30

Csa3M827930.1	AT5G40010.1 AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	1.30
Csa1M024160.1	AT1G48000.1 MYB112 (myb domain protein 112); DNA binding / transcription factor	1.29
Csa3M038190.1	AT2G42010.1 PLDBETA1 (PHOSPHOLIPASE D BETA 1); phospholipase D	1.29
Csa3M651820.1	AT5G07990.1 TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	1.29
Csa3M342350.1	AT1G70850.1 MLP34 (MLP-LIKE PROTEIN 34)	1.28
Csa2M021510.1	AT2G16870.1 disease resistance protein (TIR-NBS-LRR class), putative	1.28
Csa1M467120.1	AT4G18950.1 ankyrin protein kinase, putative	1.28
Csa3M135730.1	AT1G06650.2 2-oxoglutarate-dependent dioxygenase, putative	1.28
Csa3M175740.1	AT5G62360.1 invertase/pectin methylesterase inhibitor family protein	1.28
Csa7M060690.1	AT1G78000.1 SULTR1;2 (SULFATE TRANSPORTER 1;2); sulfate transmembrane transporter	1.27
Csa6M500640.2	AT4G39830.1 L-ascorbate oxidase, putative	1.27
Csa1M170510.1	AT1G03370.1 protein binding / zinc ion binding	1.27
Csa5M319910.1	AT1G66120.1 acyl-activating enzyme 11 (AAE11)	1.27
Csa3M271380.1	AT1G13340.1 unknown protein	1.26
Csa3M715370.1	AT1G80820.1 CCR2 (CINNAMOYL COA REDUCTASE); cinnamoyl-CoA reductase	1.26
Csa3M598380.1	No hits found	1.26
Csa1M064830.1	AT4G23180.1 CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	1.25
Csa6M446280.1	AT3G53260.1 PAL2; phenylalanine ammonia-lyase	1.25
Csa5M609750.1	AT3G18360.1 VQ motif-containing protein	1.25
Csa5M352630.1	AT3G19970.1 unknown protein	1.25
Csa3M119730.1	AT4G01070.1 GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	1.23
Csa6M445750.1	AT2G37040.1 pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase	1.23
Csa4M641670.1	AT3G16150.1 L-asparaginase, putative / L-asparagine amidohydrolase, putative	1.23
Csa5M613580.1	AT5G59190.1 subtilase family protein	1.23
Csa2M033350.1	AT5G26920.1 CBP60G (CAM-BINDING PROTEIN 60-LIKE.G); calmodulin binding	1.22
Csa3M828930.1	AT5G40010.1 AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	1.22
Csa6M519530.1	AT2G27430.1 binding	1.22
Csa3M446120.1	AT1G15210.1 PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATPase, coupled to transmembrane movement of substances	1.21
Csa3M143510.1	AT1G04280.1 unknown protein	1.20
Csa6M059230.1	AT1G12040.1 LRX1 (LEUCINE-RICH REPEAT/EXTENSIN 1); histidine phosphotransfer kinase/ protein binding / structural constituent of cell wall	1.20
Csa2M421020.1	AT4G11290.1 peroxidase, putative	1.20
Csa3M130880.1	AT4G13630.1 unknown protein	1.19
Csa2M297180.2	AT5G26170.1 WRKY50; transcription factor	1.19
Csa4M596000.1	No hits found	1.19
Csa6M169310.1	AT4G18880.1 AT-HSFA4A; DNA binding / transcription factor	1.19
Csa6M516820.1	AT4G05120.1 FUR1 (FUDR RESISTANT 1); nucleoside transmembrane transporter	1.19
Csa3M643770.1	AT2G45570.1 CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	1.19
Csa4M334120.1	AT3G08760.1 ATSIK; ATP binding / kinase/ protein kinase/ protein tyrosine kinase	1.17
Csa3M731720.1	AT3G51860.1 CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	1.17
Csa6M445140.2	AT2G37170.1 PIP2B (PLASMA MEMBRANE INTRINSIC PROTEIN 2); water channel	1.17
Csa6M091930.1	AT5G13220.1 JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10)	1.17
Csa1M542510.1	AT4G19840.1 ATPP2-A1; carbohydrate binding	1.17
Csa6M516820.3	AT4G05120.1 FUR1 (FUDR RESISTANT 1); nucleoside transmembrane transporter	1.17
Csa5M604960.1	No hits found	1.16

Csa3M874320.1	AT4G39330.1 CAD9 (CINNAMYL ALCOHOL DEHYDROGENASE 9); binding / catalytic/ oxidoreductase/ zinc ion binding	1.16
Csa3M828430.1	AT5G40010.1 AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	1.16
Csa6M517220.1	AT4G27450.1 unknown protein	1.16
Csa2M004720.1	AT3G24500.1 MBF1C (MULTIPROTEIN BRIDGING FACTOR 1C); DNA binding / transcription coactivator/ transcription factor	1.16
Csa3M778380.1	AT5G42560.1 abscisic acid-responsive HVA22 family protein	1.16
Csa5M158540.1	AT2G45360.1 unknown protein	1.16
Csa6M148230.3	AT5G22920.1 zinc finger (C3HC4-type RING finger) family protein	1.16
Csa5M158540.2	AT2G45360.1 unknown protein	1.16
Csa6M516820.2	AT4G05120.1 FUR1 (FUDR RESISTANT 1); nucleoside transmembrane transporter	1.16
Csa5M023870.1	AT5G37490.1 U-box domain-containing protein	1.15
Csa4M642520.1	AT1G27770.1 ACA1 (AUTO-INHIBITED CA2+-ATPASE 1); calcium channel/ calcium-transporting ATPase/ calmodulin binding	1.14
Csa6M445140.1	AT2G37170.1 PIP2B (PLASMA MEMBRANE INTRINSIC PROTEIN 2); water channel	1.14
Csa1M542500.1	AT4G19840.1 ATPP2-A1; carbohydrate binding	1.14
Csa3M651800.1	AT5G07990.1 TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	1.14
Csa7M011820.1	No hits found	1.14
Csa7M074920.1	AT2G23610.1 MES3 (METHYL ESTERASE 3); hydrolase, acting on ester bonds / methyl indole-3-acetate esterase/ methyl jasmonate esterase	1.14
Csa4M628850.1	AT5G11210.1 ATGLR2.5; intracellular ligand-gated ion channel	1.14
Csa7M073380.1	AT4G34150.1 C2 domain-containing protein	1.13
Csa3M175690.1	AT4G12430.1 trehalose-6-phosphate phosphatase, putative	1.13
Csa5M487700.1	No hits found	1.13
Csa2M055010.1	AT1G73050.1 (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative	1.13
Csa1M418250.1	AT1G52730.2 transducin family protein / WD-40 repeat family protein	1.13
Csa1M065410.1	AT4G21250.1 unknown protein	1.12
Csa3M002480.1	AT4G35780.1 protein kinase family protein	1.12
Csa6M124080.1	AT2G20830.2 folic acid binding / transferase	1.12
Csa3M732680.1	AT3G54040.1 photoassimilate-responsive protein-related	1.12
Csa5M033470.1	AT1G70740.1 protein kinase family protein	1.12
Csa6M445130.1	AT3G53420.1 PIP2A (PLASMA MEMBRANE INTRINSIC PROTEIN 2A); water channel	1.12
Csa2M004770.1	No hits found	1.12
Csa6M483320.3	AT1G53570.2 MAP3KA; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	1.11
Csa1M423150.1	AT4G30210.2 ATR2 (ARABIDOPSIS P450 REDUCTASE 2); NADPH-hemoprotein reductase	1.11
Csa1M181330.1	AT1G56600.1 AtGolS2 (Arabidopsis thaliana galactinol synthase 2); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	1.11
Csa4M001530.1	AT1G52820.1 2-oxoglutarate-dependent dioxygenase, putative	1.10
Csa1M031780.1	AT1G54400.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to heat; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: HSP20-like chaperone (InterPro:IPR008978); BEST Arabidopsis thaliana protein match is: heat shock family protein (TAIR:AT2G27140.1); Has 35 Blast hits to 35 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	1.10
Csa4M502330.1	No hits found	1.10
Csa5M635360.1	AT3G01310.1 acid phosphatase/ oxidoreductase/ transition metal ion binding	1.10
Csa5M613590.1	AT5G59100.1 subtilase family protein	1.10
Csa6M523410.1	AT1G30080.1 glycosyl hydrolase family 17 protein	1.10
Csa3M141830.1	AT1G04330.1 unknown protein	1.10
Csa1M062280.1	AT5G35830.1 ankyrin repeat family protein	1.09

Csa3M645980.1	AT3G14130.1 (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	1.09
Csa1M005690.1	AT5G57580.1 calmodulin-binding protein	1.09
Csa6M499800.1	AT4G39980.1 DHS1 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1); 3-deoxy-7-phosphoheptulonate synthase	1.09
Csa1M421890.1	AT2G02340.1 AtPP2-B8 (Phloem protein 2-B8); carbohydrate binding	1.09
Csa4M064040.1	AT1G16670.1 protein kinase family protein	1.09
Csa3M149300.1	AT5G26340.1 MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter	1.08
Csa6M516820.4	AT4G05120.1 FUR1 (FUDR RESISTANT 1); nucleoside transmembrane transporter	1.08
Csa6M362930.1	AT5G19530.1 ACL5 (ACAULIS 5); spermine synthase/ thermospermine synthase	1.08
Csa4M286980.1	AT3G45140.1 LOX2 (LIPOXYGENASE 2); lipoxygenase	1.08
Csa6M506000.1	AT4G36010.1 pathogenesis-related thaumatin family protein	1.08
Csa1M658010.1	AT3G02800.1 phosphatase/ phosphoprotein phosphatase/ protein tyrosine phosphatase	1.08
Csa3M778970.1	AT2G35980.1 YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	1.08
Csa6M517000.1	No hits found	1.08
Csa1M589090.1	AT5G56980.1 unknown protein	1.07
Csa6M538800.1	AT1G30820.1 CTP synthase, putative / UTP--ammonia ligase, putative	1.07
Csa1M066520.1	AT3G22104.1 phototropic-responsive NPH3 protein-related	1.07
Csa4M304840.1	AT2G37940.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: phosphatidic acid phosphatase-related / PAP2-related (TAIR:AT3G54020.1); Has 316 Blast hits to 316 proteins in 75 species: Archae - 0; Bacteria - 0; Metazoa - 213; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 55 (source: NCBI BLink).	1.07
Csa6M398210.1	AT1G31130.1 unknown protein	1.07
Csa6M445740.1	AT2G37040.1 pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase	1.06
Csa3M717370.1	AT1G15950.1 CCR1 (CINNAMOYL COA REDUCTASE 1); cinnamoyl-CoA reductase	1.05
Csa4M642500.1	AT1G27760.3 interferon-related developmental regulator family protein / IFRD protein family	1.05
Csa1M542490.1	AT4G19850.1 ATPP2-A2; carbohydrate binding	1.05
Csa3M727960.1	AT4G20780.1 calcium-binding protein, putative	1.05
Csa2M357220.1	AT5G11210.1 ATGLR2.5; intracellular ligand-gated ion channel	1.05
Csa1M267780.1	AT4G19850.1 ATPP2-A2; carbohydrate binding	1.05
Csa4M631570.1	AT1G55740.1 AtSIP1 (Arabidopsis thaliana seed imbibition 1); hydrolase, hydrolyzing O-glycosyl compounds	1.05
Csa6M445130.2	AT3G53420.1 PIP2A (PLASMA MEMBRANE INTRINSIC PROTEIN 2A); water channel	1.05
Csa6M483320.2	AT1G53570.1 MAP3KA; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	1.04
Csa2M116250.1	AT1G68710.1 haloacid dehalogenase-like hydrolase family protein	1.04
Csa2M348960.1	AT1G70520.1 protein kinase family protein	1.04
Csa1M004920.1	AT5G62770.1 unknown protein	1.04
Csa4M304840.2	AT2G37940.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: phosphatidic acid phosphatase-related / PAP2-related (TAIR:AT3G54020.1); Has 316 Blast hits to 316 proteins in 75 species: Archae - 0; Bacteria - 0; Metazoa - 213; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 55 (source: NCBI BLink).	1.03
Csa2M431070.1	AT5G17540.1 transferase family protein	1.03
Csa3M004500.1	AT5G45380.1 sodium:solute symporter family protein	1.03
Csa3M702070.1	AT2G44500.1 unknown protein	1.03
Csa5M606300.1	AT5G15290.1 integral membrane family protein	1.03
Csa6M216940.1	AT5G05340.1 peroxidase, putative	1.02

Csa7M448690.1	AT3G14200.1 DNAJ heat shock N-terminal domain-containing protein	1.02
Csa3M619930.1	AT4G28720.1 flavin-containing monooxygenase family protein / FMO family protein	1.02
Csa1M534720.1	AT4G21300.1 pentatricopeptide (PPR) repeat-containing protein	1.02
Csa4M500830.1	AT4G19840.1 ATPP2-A1; carbohydrate binding	1.02
Csa6M397190.1	AT5G25800.1 exonuclease family protein	1.02
Csa7M430250.1	AT3G21240.1 4CL2 (4-COUMARATE:COA LIGASE 2); 4-coumarate-CoA ligase	1.01
Csa5M610470.1	AT1G15080.1 LPP2 (LIPID PHOSPHATE PHOSPHATASE 2); acid phosphatase/ phosphatidate phosphatase	1.01
Csa1M334920.1	AT5G44510.1 TAO1 (TARGET OF AVR B OPERATION1); ATP binding / protein binding / transmembrane receptor	1.01
	AT5G66210.2 CPK28; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ protein kinase/ protein serine/threonine kinase	1.01
Csa6M505910.1	AT5G24520.1 TTG1 (TRANSPARENT TESTA GLABRA 1); DNA binding / nucleotide binding / protein binding	1.01
Csa4M097650.1	AT4G23020.1 unknown protein	1.01
Csa5M155580.1	AT4G23020.1 unknown protein	1.01
Csa6M363520.1	No hits found	1.01
Csa1M425940.1	AT5G57150.1 basic helix-loop-helix (bHLH) family protein	1.01
	AT5G54160.1 ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	1.00
Csa3M046220.1		1.00
Csa1M032450.1	AT5G63160.1 BT1 (BTB AND TAZ DOMAIN PROTEIN 1); protein binding / transcription regulator	1.00

**Edisto only**

**Cucumber Locus ID**

**Top Arabidopsis thaliana hit**

**log fold change (-Cu vs +Cu)**

**up fefe -Cu**

**up Ed -Cu**

Csa1M435790.1	No hits found	3.77
Csa3M405510.1	AT5G48150.1 PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor	3.64
Csa3M405520.1	No hits found	3.53
Csa5M174570.1	AT5G51990.1 CBF4 (C- REPEAT-BINDING FACTOR 4); DNA binding / transcription activator/ transcription factor	3.36
Csa4M429320.1	AT2G45760.1 BAP2 (BON ASSOCIATION PROTEIN 2)	3.36
Csa3M123180.1	AT2G45760.1 BAP2 (BON ASSOCIATION PROTEIN 2)	3.26
Csa1M075060.1	AT5G44210.1 ERF9 (ERF DOMAIN PROTEIN 9); DNA binding / transcription factor/ transcription repressor	3.06
Csa5M150470.1	AT1G64340.1 unknown protein	2.78
Csa1M532300.1	AT2G30020.1 protein phosphatase 2C, putative / PP2C, putative	2.75
	AT5G25240.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: NHL repeat-containing protein (TAIR:AT5G14890.1); Has 23 Blast hits to 23 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	
Csa1M265630.1		2.68
Csa5M571440.1	AT5G17350.1 unknown protein	2.67
Csa3M812790.1	No hits found	2.63
Csa3M011620.1	AT1G32640.1 MYC2; DNA binding / transcription activator/ transcription factor	2.63
Csa7M298820.1	AT1G74450.1 unknown protein	2.62
Csa1M589710.1	AT5G12010.1 unknown protein	2.60
Csa6M511770.1	AT4G22330.1 ATCES1; catalytic/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	2.58
Csa5M534980.1	No hits found	2.56
Csa7M414440.2	AT3G62260.2 protein phosphatase 2C, putative / PP2C, putative	2.55
Csa3M633290.1	AT3G07250.1 nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	2.52
Csa3M308190.1	AT5G37490.1 U-box domain-containing protein	2.49
Csa6M516960.1	AT1G61340.1 F-box family protein	2.49
Csa4M279850.1	AT2G27180.1 unknown protein	2.49
Csa7M414440.1	AT3G62260.1 protein phosphatase 2C, putative / PP2C, putative	2.48

	AT2G27830.1 FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT4G22760.1); Has 68 Blast hits to 68 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	
Csa6M150560.1		2.42
Csa6M010030.1	AT2G40000.1 HSPRO2 (ARABIDOPSIS ORTHOLOG OF SUGAR BEET HS1 PRO-1 2)	2.41
Csa5M146930.1	AT1G32928.1 unknown protein	2.37
Csa3M588520.1	AT3G50770.1 calmodulin-related protein, putative	2.29
Csa6M417860.1	No hits found	2.27
Csa3M041370.1	AT5G23960.1 TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	2.26
Csa5M155560.1	AT5G52020.1 AP2 domain-containing protein	2.26
Csa5M571560.1	AT1G76650.1 calcium-binding EF hand family protein	2.26
Csa1M045990.1	AT1G60190.1 armadillo/beta-catenin repeat family protein / U-box domain-containing protein	2.25
Csa4M638320.1	AT4G27450.1 unknown protein	2.25
Csa6M127980.1	AT4G03600.1 unknown protein	2.25
Csa6M518190.1	AT1G28480.1 GRX480; electron carrier/ protein disulfide oxidoreductase	2.23
Csa7M407500.1	AT5G38700.1 unknown protein	2.23
Csa1M000710.1	AT3G48800.1 sterile alpha motif (SAM) domain-containing protein	2.17
Csa5M494420.1	No hits found	2.17
Csa5M188890.1	No hits found	2.15
Csa7M068600.1	AT1G58290.1 HEMA1; glutamyl-tRNA reductase	2.15
Csa5M608080.1	AT1G13520.1 unknown protein	2.13
Csa2M174660.1	No hits found	2.13
Csa6M303740.1	AT2G28710.1 zinc finger (C2H2 type) family protein	2.12
Csa6M445770.1	AT2G37040.1 pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase	2.11
Csa5M598090.1	No hits found	2.11
Csa5M598080.1	AT1G12990.1 glycosyl transferase family 17 protein	2.09
Csa2M123610.1	AT2G44080.1 ARL (ARGOS-LIKE)	2.07
Csa6M454460.1	AT5G06320.1 NHL3	2.06
Csa1M422480.1	AT5G57560.1 TCH4 (Touch 4); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	2.04
Csa1M423060.1	AT5G57510.1 unknown protein	1.99
Csa5M601550.1	AT1G70420.1 unknown protein	1.98
Csa2M354820.1	AT1G27730.1 STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding	1.98
Csa5M613600.1	AT3G04640.1 glycine-rich protein	1.98
Csa5M207940.1	AT3G55980.1 SZF1 (SALT-INDUCIBLE ZINC FINGER 1); transcription factor	1.98
Csa7M328830.1	AT4G23810.1 WRKY53; DNA binding / protein binding / transcription activator/ transcription factor	1.98
Csa2M264570.1	AT4G36040.1 DNAJ heat shock N-terminal domain-containing protein (J11)	1.96
Csa3M081900.1	AT4G27280.1 calcium-binding EF hand family protein	1.96
Csa4M642430.1	AT4G37540.1 LBD39 (LOB DOMAIN-CONTAINING PROTEIN 39)	1.96
Csa7M049230.1	AT3G15210.1 ERF4 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4); DNA binding / protein binding / transcription factor/ transcription repressor	1.96
Csa4M637750.1	AT4G27470.1 zinc finger (C3HC4-type RING finger) family protein	1.95
Csa2M174670.1	AT3G23250.1 MYB15 (MYB DOMAIN PROTEIN 15); DNA binding / transcription factor	1.94
Csa5M636620.1	AT3G29000.1 calcium-binding EF hand family protein	1.91
Csa7M407550.1	AT1G02660.1 lipase class 3 family protein	1.89
Csa5M140450.1	AT1G01490.1 heavy-metal-associated domain-containing protein	1.88
Csa6M504440.1	AT3G50930.1 BCS1 (CYTOCHROME BC1 SYNTHESIS); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	1.88



Csa1M601000.1	AT2G27080.1 harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	1.87
Csa7M375780.1	AT1G06180.1 ATMYB13 (MYB DOMAIN PROTEIN 13); DNA binding / transcription factor	1.84
Csa7M451370.1	AT1G17665.1 unknown protein	1.84
Csa2M005340.1	AT4G13395.1 RTFL12 (ROTUNDIFOLIA LIKE 12)	1.83
Csa1M168920.1	AT5G22250.1 CCR4-NOT transcription complex protein, putative	1.83
Csa5M181480.1	AT3G55430.1 glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative	1.83
Csa6M014510.1	No hits found	1.83
Csa4M337890.2	AT4G32300.1 SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase	1.82
Csa4M214830.1	AT2G41430.3 ERD15 (EARLY RESPONSIVE TO DEHYDRATION 15); protein binding	1.82
Csa4M642460.1	AT1G27730.1 STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding	1.82
Csa1M039020.2	AT5G61210.1 SNAP33 (SOLUBLE N-ETHYLMALIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding	1.81
Csa4M630010.1	AT3G15210.1 ERF4 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4); DNA binding / protein binding / transcription factor/ transcription repressor	1.80
Csa6M426370.1	AT2G35930.1 PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase	1.78
Csa5M150420.1	AT1G64380.1 AP2 domain-containing transcription factor, putative	1.77
Csa1M422990.1	AT4G25810.1 XTR6 (XYLOGLUCAN ENDOTRANGLYCOSYLASE 6); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase	1.76
Csa3M782680.1	AT3G11820.1 SYP121 (SYNTAXIN OF PLANTS 121); SNAP receptor/ protein anchor	1.76
Csa3M855410.1	AT1G75160.1 unknown protein	1.75
Csa4M648560.1	AT2G05940.1 protein kinase, putative	1.75
Csa2M381670.1	AT2G18660.1 EXLB3 (EXPANSIN-LIKE B3 PRECURSOR)	1.74
Csa5M167120.1	AT5G61600.1 ethylene-responsive element-binding family protein	1.73
Csa4M293290.1	AT5G02580.1 unknown protein	1.73
Csa3M780540.1	No hits found	1.72
Csa5M604130.1	AT1G59710.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27100.1); Has 119 Blast hits to 107 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 119; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	1.71
Csa1M680120.1	AT1G08630.1 THA1 (Threonine Aldolase 1); aldehyde-lyase/ threonine aldolase	1.69
Csa1M025960.1	AT2G38470.1 WRKY33; transcription factor	1.68
Csa7M398090.1	AT4G02380.1 SAG21 (SENESCENCE-ASSOCIATED GENE 21)	1.68
Csa5M547610.1	AT2G01670.1 atnudt17 (Arabidopsis thaliana Nudix hydrolase homolog 17); hydrolase	1.68
Csa6M193600.1	No hits found	1.67
Csa4M303070.1	AT3G09280.1 unknown protein	1.67
Csa6M487750.1	AT2G23770.1 protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	1.66
Csa5M611700.1	AT1G71100.1 RSW10 (RADIAL SWELLING 10); ribose-5-phosphate isomerase	1.66
Csa7M446640.1	AT1G12660.1 Predicted to encode a PR (pathogenesis-related) protein. Belongs to the plant thionin (PR-13) family with the following members: At1g66100, At5g36910, At1g72260, At2g15010, At1g12663, At1g12660.	1.66
Csa6M403600.1	AT1G59710.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27100.1); Has 119 Blast hits to 107 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 119; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	1.66

Csa1M265650.1	AT2G46490.1 unknown protein	1.65
Csa5M609710.1	AT5G38410.1 ribulose biphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B)	1.64
Csa6M152950.1	AT2G27580.1 zinc finger (AN1-like) family protein	1.62
Csa4M046720.1	AT1G67530.1 armadillo/beta-catenin repeat family protein / U-box domain-containing family protein	1.62
Csa6M515500.1	AT4G38830.1 protein kinase family protein	1.62
Csa6M505230.1	AT2G21320.1 zinc finger (B-box type) family protein	1.62
Csa6M505230.2	AT2G21320.1 zinc finger (B-box type) family protein	1.62
Csa6M190250.1	AT3G46620.1 zinc finger (C3HC4-type RING finger) family protein	1.60
Csa3M730770.1	AT5G01710.1 LOCATED IN: endomembrane system; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; CONTAINS InterPro DOMAIN/s: Methyltransferase FkbM (InterPro:IPR006342); BEST Arabidopsis thaliana protein match is: methyltransferase (TAIR:AT4G24805.1); Has 224 Blast hits to 223 proteins in 16 species: Archae - 0; Bacteria - 7; Metazoa - 38; Fungi - 0; Plants - 137; Viruses - 0; Other Eukaryotes - 42 (source: NCBI BLink).	1.60
Csa6M502780.1	No hits found	1.59
Csa3M842740.1	No hits found	1.58
Csa1M039020.1	AT5G61210.1 SNAP33 (SOLUBLE N-ETHYLMALEIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding	1.58
Csa4M053250.1	AT4G23990.1 ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	1.58
Csa7M018780.1	AT2G47450.1 CAO (CHAOS); chromatin binding	1.58
Csa2M382470.1	No hits found	1.58
Csa4M003640.1	AT2G01275.1 zinc finger (C3HC4-type RING finger) family protein	1.57
Csa7M433340.1	AT4G21390.1 B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding	1.57
Csa5M487690.1	AT4G16500.1 cysteine protease inhibitor family protein / cystatin family protein	1.57
Csa7M044860.1	AT3G22060.1 receptor protein kinase-related	1.56
Csa4M641690.1	AT5G67300.1 MYBR1 (MYB DOMAIN PROTEIN R1); DNA binding / transcription factor	1.56
Csa2M030090.1	AT1G09070.1 SRC2 (SOYBEAN GENE REGULATED BY COLD-2); protein binding	1.56
Csa4M625060.1	AT2G05440.2 glycine-rich protein	1.56
Csa7M069140.3	AT1G06230.1 GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding	1.55
Csa3M779020.1	AT2G35980.1 YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	1.55
Csa5M593390.1	AT1G24530.1 transducin family protein / WD-40 repeat family protein	1.54
Csa2M401380.1	AT1G33590.1 disease resistance protein-related / LRR protein-related	1.54
Csa6M425740.1	AT3G44326.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Cyclin-like F-box (InterPro:IPR001810); BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT2G27310.1); Has 56 Blast hits to 56 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	1.53
Csa6M080930.1	AT2G15080.1 AtRLP19 (Receptor Like Protein 19); kinase/ protein binding	1.53
Csa6M499220.1	AT1G72220.1 zinc finger (C3HC4-type RING finger) family protein	1.51
Csa4M026920.1	No hits found	1.51
Csa7M432590.1	No hits found	1.50
Csa1M075030.1	AT1G28360.1 ERF12 (ERF DOMAIN PROTEIN 12); DNA binding / transcription factor/ transcription repressor	1.49
Csa4M049610.1	AT4G11280.1 ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase	1.49
Csa2M381820.1	AT4G32290.1 unknown protein	1.49
Csa1M002730.1	AT5G50300.1 xanthine/uracil/vitamin C permease family protein	1.49
Csa2M021690.1	AT3G05290.1 PNC1 (PEROXISOMAL ADENINE NUCLEOTIDE CARRIER 1); ADP transmembrane transporter/ ATP transmembrane transporter/ binding	1.48
Csa3M816710.1	AT3G56880.1 VQ motif-containing protein	1.46
Csa6M091870.1	AT3G26740.1 CCL (CCR-LIKE)	1.46

Csa1M045670.1	AT5G40010.1 AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	1.45
Csa7M071440.1	AT3G49930.1 zinc finger (C2H2 type) family protein	1.45
Csa3M781620.1	AT3G11680.1 unknown protein	1.44
Csa7M048060.1	AT4G32480.1 unknown protein	1.44
Csa4M642370.2	AT5G43150.1 unknown protein	1.44
Csa6M055410.1	AT5G42440.1 protein kinase family protein	1.44
Csa6M187390.1	AT2G29670.1 binding	1.43
Csa2M110250.1	AT1G14030.1 ribulose-1,5 bisphosphate carboxylase oxygenase large subunit N-methyltransferase, putative	1.42
Csa6M008680.1	AT2G39730.1 RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	1.42
Csa3M851910.1	AT3G15530.1 methyltransferase	1.42
Csa5M152250.1	AT1G01490.1 heavy-metal-associated domain-containing protein	1.41
Csa6M404290.1	No hits found	1.40
Csa3M730760.1	AT5G01670.1 aldose reductase, putative	1.40
Csa1M597020.1	AT2G05940.1 protein kinase, putative	1.40
Csa6M511620.1	AT4G17230.1 SCL13 (Scarecrow-like 13); transcription factor	1.39
Csa3M779010.1	AT2G35980.1 YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	1.39
Csa6M518040.1	AT3G15210.1 ERF4 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4); DNA binding / protein binding / transcription factor/ transcription repressor	1.38
Csa3M842100.1	AT1G56660.1 unknown protein	1.37
Csa7M069140.1	AT1G06230.1 GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding	1.36
Csa7M433330.1	AT1G67520.1 lectin protein kinase family protein	1.36
Csa4M052730.1	AT5G42050.1 FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27090.1); Has 5084 Blast hits to 2870 proteins in 85 species: Archae - 0; Bacteria - 24; Metazoa - 270; Fungi - 58; Plants - 157; Viruses - 8; Other Eukaryotes - 4567 (source: NCBI BLINK).	1.36
Csa6M518000.1	AT1G28330.1 DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)	1.35
Csa3M099590.1	AT4G27280.1 calcium-binding EF hand family protein	1.35
Csa1M422470.1	AT4G25810.1 XTR6 (XYLOGLUCAN ENDOTRANGLYCOSYLASE 6); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase	1.34
Csa3M181940.1	AT5G62020.1 AT-HSFB2A; DNA binding / transcription factor	1.34
Csa2M200440.2	AT5G43700.1 ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	1.33
Csa5M611020.1	AT4G13340.1 leucine-rich repeat family protein / extensin family protein	1.33
Csa3M119500.1	AT1G01260.1 basic helix-loop-helix (bHLH) family protein	1.31
CsaUNM031640.1	AT1G13260.1 RAV1; DNA binding / transcription factor/ transcription repressor	1.31
Csa6M490870.1	AT4G36990.1 HSF4 (HEAT SHOCK FACTOR 4); DNA binding / transcription factor/ transcription repressor	1.31
Csa3M124790.1	No hits found	1.31
Csa2M021560.1	AT2G35000.1 zinc finger (C3HC4-type RING finger) family protein	1.30
Csa4M624440.1	AT3G14840.1 leucine-rich repeat family protein / protein kinase family protein	1.29
Csa5M180920.1	AT2G28710.1 zinc finger (C2H2 type) family protein	1.29
Csa4M608080.1	AT2G42975.1 unknown protein	1.28
Csa6M511610.1	No hits found	1.28
Csa3M914060.1	AT4G16820.1 lipase class 3 family protein	1.27
Csa1M600790.1	AT5G19500.1 tryptophan/tyrosine permease family protein	1.27
Csa6M516870.1	AT4G10270.1 wound-responsive family protein	1.27
Csa2M200440.1	AT5G43700.1 ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	1.26
Csa6M358680.1	AT4G35190.1 unknown protein	1.26

Csa6M518000.2	AT1G28330.1 DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)	1.25
Csa2M034620.1	AT1G09250.1 transcription factor	1.25
Csa5M609630.1	AT1G68540.1 oxidoreductase family protein	1.24
Csa3M880040.1	No hits found	1.24
Csa5M030450.1	AT2G01540.1 C2 domain-containing protein	1.24
Csa1M025070.1	AT1G73590.1 PIN1 (PIN-FORMED 1); transporter	1.24
Csa2M009450.1	AT4G32060.1 calcium-binding EF hand family protein	1.23
	AT3G45640.1 ATMPK3 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP kinase/ kinase/ protein binding / protein kinase	1.23
Csa1M479630.1	AT2G15890.1 MEE14 (maternal effect embryo arrest 14)	1.23
Csa5M155480.2	AT4G11660.1 AT-HSFB2B; transcription factor/ transcription repressor	1.23
Csa2M239400.1	AT2G15980.1 pentatricopeptide (PPR) repeat-containing protein	1.22
Csa4M056540.1	No hits found	1.22
Csa6M516780.1	AT5G54470.1 zinc finger (B-box type) family protein	1.22
Csa1M023070.1	AT1G68490.1 unknown protein	1.21
Csa4M665120.1	AT1G21010.1 unknown protein	1.20
Csa2M366710.1	AT1G19830.1 auxin-responsive protein, putative	1.19
Csa2M360850.1	AT1G19310.1 zinc finger (C3HC4-type RING finger) family protein	1.19
Csa4M192100.1	AT5G58375.1 unknown protein	1.19
Csa3M124740.1	AT2G45740.1 PEX11D	1.19
	AT3G16770.1 ATEBP (ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN); DNA binding / protein binding / transcription activator/ transcription factor	1.18
Csa4M001970.1	No hits found	1.18
Csa4M645250.1	AT4G07960.1 ATCSLC12 (CELLULOSE-SYNTHASE LIKE C12); cellulose synthase/ transferase, transferring glycosyl groups	1.18
Csa5M636600.1	No hits found	1.18
Csa4M011840.1	AT1G69040.1 ACR4 (ACT REPEAT 4); amino acid binding	1.18
Csa3M889770.1	AT1G35140.1 PHI-1 (PHOSPHATE-INDUCED 1)	1.17
Csa7M069140.2	AT1G73150.1 GTE3 (GLOBAL TRANSCRIPTION FACTOR GROUP E 3); DNA binding / histone binding	1.17
Csa4M005540.1	AT1G80120.1 unknown protein	1.16
Csa5M614660.1	No hits found	1.16
Csa2M296090.2	AT2G18630.1 unknown protein	1.16
Csa6M095900.1	AT2G46820.1 PSI-P (PHOTOSYSTEM I P SUBUNIT); DNA binding	1.15
Csa3M000060.2	AT4G33220.1 enzyme inhibitor/ pectinesterase	1.15
Csa4M665100.1	AT1G21230.1 WAK5 (WALL ASSOCIATED KINASE 5); kinase/ protein serine/threonine kinase	1.15
	AT4G11280.1 ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase	1.14
Csa4M049610.2	AT1G70420.1 unknown protein	1.14
Csa3M483770.1	AT1G18530.1 calmodulin, putative	1.13
Csa2M357340.1	AT2G38040.1 CAC3; acetyl-CoA carboxylase	1.13
Csa3M122540.1	AT1G35830.1 VQ motif-containing protein	1.12
Csa3M895870.1	AT1G24170.1 LGT9; polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	1.12
Csa5M603940.1	AT5G18650.1 zinc finger (C3HC4-type RING finger) family protein	1.12
Csa3M151540.2	AT4G11660.1 AT-HSFB2B; transcription factor/ transcription repressor	1.12
Csa5M155480.1	AT1G35340.1 ATP-dependent protease La (LON) domain-containing protein	1.12
Csa5M652270.1	AT1G44830.1 AP2 domain-containing transcription factor TINY, putative	1.12
Csa4M370550.1	AT1G29340.1 PUB17 (PLANT U-BOX 17); ubiquitin-protein ligase	1.11
Csa1M467720.1		

Csa6M077420.1	AT2G45360.1 unknown protein	1.10
Csa3M009540.1	AT5G46730.1 glycine-rich protein	1.10
Csa2M223160.1	AT3G22740.1 HMT3; homocysteine S-methyltransferase	1.09
Csa3M402970.1	AT5G54570.1 BGLU41 (BETA GLUCOSIDASE 41); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	1.09
Csa6M361410.1	AT5G21940.1 unknown protein	1.09
Csa7M343340.1	AT5G39090.1 transferase family protein	1.09
Csa1M002810.1	AT5G61640.1 PMSR1 (PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 1); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor / peptide-methionine-(S)-S-oxide reductase	1.09
Csa6M423400.1	AT3G23730.1 xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	1.09
Csa6M445760.1	AT2G37040.1 pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase	1.08
Csa5M471600.1	AT1G14040.1 LOCATED IN: integral to membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03240.1); Has 732 Blast hits to 696 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 238; Fungi - 246; Plants - 151; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLINK).	1.08
Csa6M001760.1	AT1G73340.1 electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	1.07
Csa3M018320.1	AT4G17490.1 ATERF6 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 6); DNA binding / transcription factor	1.07
Csa2M355030.1	AT5G67300.1 MYBR1 (MYB DOMAIN PROTEIN R1); DNA binding / transcription factor	1.07
Csa6M087850.1	AT2G46500.1 phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	1.07
Csa2M296090.1	AT2G18630.1 unknown protein	1.06
Csa7M451390.1	AT3G13730.1 CYP90D1; oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding	1.06
Csa1M077190.1	No hits found	1.06
Csa6M504650.1	AT3G51060.1 STY1 (STYLISH 1); protein heterodimerization/ transcription factor	1.06
Csa7M074870.1	AT1G49560.1 myb family transcription factor	1.05
Csa4M642360.1	AT2G23090.1 unknown protein	1.04
Csa1M024150.1	AT1G73830.1 BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor	1.04
Csa5M636570.1	AT1G26800.1 zinc finger (C3HC4-type RING finger) family protein	1.04
Csa4M110050.1	AT5G64260.1 EXL2 (EXORDIUM LIKE 2)	1.04
Csa1M009810.1	AT3G47470.1 LHCA4 (LIGHT-HARVESTING CHLOROPHYLL-PROTEIN COMPLEX I SUBUNIT A4); chlorophyll binding	1.04
Csa3M017030.1	AT5G47070.1 protein kinase, putative	1.04
Csa7M004690.1	AT4G39070.1 zinc finger (B-box type) family protein	1.03
Csa2M239400.2	AT2G15980.1 pentatricopeptide (PPR) repeat-containing protein	1.03
Csa1M256780.1	AT5G57910.1 unknown protein	1.03
Csa4M124910.1	AT5G15850.1 COL1 (constans-like 1); transcription factor/ zinc ion binding	1.03
Csa6M517150.1	AT1G28310.2 Dof-type zinc finger domain-containing protein	1.02
Csa3M880030.1	AT5G25560.1 zinc finger (C3HC4-type RING finger) family protein	1.02
Csa7M432580.1	AT5G25360.1 unknown protein	1.02
Csa4M646370.1	AT4G12070.1 unknown protein	1.02
Csa6M496430.1	AT4G33700.1 CBS domain-containing protein	1.01
Csa3M859670.1	AT1G19530.1 unknown protein	1.01
Csa3M827310.1	AT3G54320.1 WRI1 (WRINKLED 1); DNA binding / transcription factor	1.01
Csa5M515060.1	No hits found	1.01
Csa6M032470.1	AT1G13340.1 unknown protein	1.01
Csa3M444620.1	AT1G79750.1 ATNADP-ME4 (NADP-malic enzyme 4); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor	1.01

Csa3M646620.1	AT1G53840.1 ATPME1; pectinesterase	1.00
Csa6M364120.1	AT5G26114.1 unknown protein	1.00
Csa2M379170.1	AT4G31115.1 unknown protein	1.00
Csa7M380130.1	AT3G22640.1 PAP85; nutrient reservoir	1.00

**Table S10. Genes that were downregulated under Cu deficiency in one genotype.**

<i>fe fe</i> only		<u>log fold change (-Cu vs +Cu)</u>	
Cucumber Locus ID	Top <i>Arabidopsis thaliana</i> hit	down <i>fe fe</i> -Cu	down Ed -Cu
Csa2M423640.1	AT5G36220.1 CYP81D1 (CYTOCHROME P450 81D1); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-5.76	
Csa4M182280.1	AT3G19430.1 late embryogenesis abundant protein-related / LEA protein-related	-3.22	
Csa4M182290.1	AT5G15780.1 pollen Ole e 1 allergen and extensin family protein	-3.07	
Csa3M222800.1	AT1G10960.1 ATFD1 (FERREDOXIN 1); 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding	-2.96	
Csa6M109750.1	AT4G15550.1 IAGLU (INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE); UDP-glycosyltransferase/ transferase, transferring glycosyl groups	-2.90	
Csa4M099750.1	AT5G65380.1 ripening-responsive protein, putative	-2.86	
Csa7M037530.1	No hits found	-2.82	
Csa2M034520.1	AT5G04950.1 NAS1 (NICOTIANAMINE SYNTHASE 1); nicotianamine synthase	-2.70	
Csa2M340400.1	AT5G63660.1 PDF2.5	-2.61	
Csa6M449250.1	AT5G03810.1 carboxylesterase/ hydrolase, acting on ester bonds / lipase	-2.56	
Csa1M707110.1	AT4G19680.2 IRT2; iron ion transmembrane transporter/ zinc ion transmembrane transporter	-2.48	
Csa3M696860.1	AT3G08040.1 FRD3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter/ transporter	-2.40	
Csa1M445860.1	AT2G34430.1 LHB1B1; chlorophyll binding	-2.37	
Csa6M511780.1	AT1G12030.1 unknown protein	-2.37	
Csa2M252020.2	AT2G21330.1 fructose-bisphosphate aldolase, putative	-2.35	
Csa2M418940.1	AT1G05200.1 ATGLR3.4; intracellular ligand-gated ion channel	-2.35	
Csa2M021000.1	AT1G73260.1 trypsin and protease inhibitor family protein / Kunitz family protein	-2.19	
Csa2M252020.1	AT4G38970.1 fructose-bisphosphate aldolase, putative	-2.16	
Csa5M571510.1	AT1G22990.1 heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	-2.13	
Csa5M577370.1	AT1G68760.1 ATNUDX1 (ARABIDOPSIS THALIANA NUDIX HYDROLASE 1); dihydroneopterin triphosphate pyrophosphohydrolase/ hydrolase	-2.12	
Csa6M011600.1	AT3G47570.1 leucine-rich repeat transmembrane protein kinase, putative	-2.09	
Csa7M351890.3	AT4G13010.1 oxidoreductase, zinc-binding dehydrogenase family protein	-2.04	
Csa2M049900.1	No hits found	-2.00	
Csa4M303700.1	AT1G53540.1 17.6 kDa class I small heat shock protein (HSP17.6C-CI) (AA 1-156)	-1.94	
Csa3M914600.1	AT3G48920.1 AtMYB45 (myb domain protein 45); DNA binding / transcription factor	-1.94	
Csa5M495960.1	AT1G09970.1 LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	-1.93	
Csa5M156210.1	AT1G12560.1 ATEXPA7 (ARABIDOPSIS THALIANA EXPANSIN A7)	-1.93	
Csa2M049890.1	AT3G49690.1 MYB84 (MYB DOMAIN PROTEIN 84); DNA binding / transcription factor	-1.92	
Csa7M414530.1	AT4G37530.1 peroxidase, putative	-1.88	
Csa6M085120.1	AT5G44280.1 RING1A (RING 1A); protein binding / zinc ion binding	-1.86	
Csa7M050800.1	AT4G28380.1 leucine-rich repeat family protein	-1.80	
Csa6M086130.1	No hits found	-1.79	
Csa6M428540.1	AT1G69940.1 PPME1; pectinesterase	-1.79	
Csa2M439180.1	AT5G10530.1 lectin protein kinase, putative	-1.75	
Csa1M595860.1	AT3G14690.1 CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.74	
Csa3M866440.1	AT1G19900.1 glyoxal oxidase-related	-1.73	
Csa6M085110.1	No hits found	-1.73	
Csa7M257340.1	AT3G18830.1 ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann	-1.72	

Csa6M318680.1	No hits found	-1.72
Csa6M152340.1	AT3G44450.1 unknown protein	-1.70
Csa2M008720.1	AT2G24280.1 serine carboxypeptidase S28 family protein	-1.70
Csa6M067410.1	AT2G39040.1 peroxidase, putative	-1.69
	AT2G36870.1 xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	-1.67
Csa1M109370.1		-1.67
Csa5M594450.1	AT3G26320.1 CYP71B36; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.66
Csa1M586250.1	AT5G05340.1 peroxidase, putative	-1.66
Csa1M132730.1	AT1G08160.1 harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	-1.65
Csa5M152170.1	AT1G64060.1 ATRBOH F (ARABIDOPSIS THALIANA RESPIRATORY BURST OXIDASE PROTEIN F); NAD(P)H oxidase	-1.64
Csa5M220390.1	AT3G56290.1 unknown protein	-1.64
	AT2G22430.1 ATHB6; DNA binding / protein binding / sequence-specific DNA binding / transcription activator/ transcription factor	-1.62
Csa3M889880.1		-1.62
	AT3G51895.1 SULTR3;1 (SULFATE TRANSPORTER 3;1); secondary active sulfate transmembrane transporter/ sulfate transmembrane transporter/ transporter	-1.61
Csa3M146340.1		-1.61
Csa1M662810.1	AT3G05950.1 germin-like protein, putative	-1.60
Csa2M006170.1	AT2G26690.1 nitrate transporter (NTP2)	-1.60
Csa6M127320.1	AT2G17040.1 anac036 (Arabidopsis NAC domain containing protein 36); transcription factor	-1.59
Csa1M588560.1	AT5G56970.1 CKX3 (CYTOKININ OXIDASE 3); amine oxidase/ cytokinin dehydrogenase	-1.59
Csa6M383530.2	AT2G41310.1 ATRR3 (RESPONSE REGULATOR 3); transcription regulator/ two-component response regulator	-1.59
Csa5M099500.1	AT2G37870.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-1.58
Csa7M351890.1	AT4G13010.1 oxidoreductase, zinc-binding dehydrogenase family protein	-1.58
Csa7M419530.1	AT2G18150.1 peroxidase, putative	-1.56
Csa5M211030.1	AT5G05500.1 pollen Ole e 1 allergen and extensin family protein	-1.55
Csa2M357280.1	AT3G19270.1 CYP707A4; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	-1.54
Csa2M401340.1	AT1G07160.1 protein phosphatase 2C, putative / PP2C, putative	-1.54
Csa5M322500.6	AT5G37180.1 SUS5; UDP-glycosyltransferase/ sucrose synthase	-1.53
Csa2M416780.1	AT5G42500.1 disease resistance-responsive family protein	-1.52
Csa1M539350.1	AT5G44400.1 FAD-binding domain-containing protein	-1.52
Csa6M421640.2	AT1G05000.1 tyrosine specific protein phosphatase family protein	-1.51
Csa1M537400.1	AT5G47750.1 D6PKL2 (D6 PROTEIN KINASE LIKE 2); kinase	-1.48
Csa3M536650.1	AT2G47270.1 transcription factor/ transcription regulator	-1.46
Csa3M684680.1	AT3G51970.1 AtSAT1 (Arabidopsis thaliana sterol O-acyltransferase 1); acyltransferase	-1.45
Csa5M322500.5	AT5G37180.1 SUS5; UDP-glycosyltransferase/ sucrose synthase	-1.44
Csa6M084580.1	AT1G55210.1 disease resistance response	-1.43
Csa6M149950.1	AT5G22810.1 GDSL-motif lipase, putative	-1.42
Csa3M171730.1	AT5G26620.1 unknown protein	-1.42
Csa1M071890.1	AT4G21490.1 NDB3; NADH dehydrogenase	-1.42
Csa3M746570.1	AT3G09925.1 pollen Ole e 1 allergen and extensin family protein	-1.41
Csa3M128920.1	ATCG01240.1 30S chloroplast ribosomal protein S7	-1.40
Csa6M148250.1	AT2G28160.1 FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor	-1.40
Csa3M895650.1	AT5G25830.1 zinc finger (GATA type) family protein	-1.39
	AT1G78580.1 ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE); alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups	-1.39
Csa1M467060.1		-1.39
	AT5G08370.1 AtAGAL2 (Arabidopsis thaliana ALPHA-GALACTOSIDASE 2); alpha-galactosidase/ catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	-1.39
Csa5M580630.2		-1.39



Csa5M322500.3	AT5G37180.1 SUS5; UDP-glycosyltransferase/ sucrose synthase	-1.38
Csa3M818250.1	AT1G68570.1 proton-dependent oligopeptide transport (POT) family protein	-1.38
Csa4M001640.1	AT4G15800.1 RALFL33 (ralf-like 33); signal transducer	-1.38
Csa2M350210.1	AT1G67750.1 pectate lyase family protein	-1.38
Csa2M013290.1	AT4G25050.1 ACP4 (acyl carrier protein 4); acyl carrier	-1.37
Csa5M606530.1	AT3G16520.3 UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.37
Csa7M420830.1	AT3G63470.1 scpl40 (serine carboxypeptidase-like 40); serine-type carboxypeptidase	-1.37
Csa5M146320.1	AT2G28100.1 ATFUC1 (alpha-L-fucosidase 1); alpha-L-fucosidase	-1.37
Csa4M639750.1	No hits found	-1.35
Csa4M285810.1	AT5G06730.1 peroxidase, putative	-1.34
Csa5M322500.4	AT5G37180.1 SUS5; UDP-glycosyltransferase/ sucrose synthase	-1.34
Csa3M730160.1	AT2G30400.1 OFP2 (OVATE FAMILY PROTEIN 2)	-1.33
Csa7M018820.1	AT3G45970.1 ATEXLA1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A1)	-1.33
Csa5M598640.1	AT3G26570.1 PHT2;1 (PHOSPHATE TRANSPORTER 2;1); low affinity phosphate transmembrane transporter	-1.31
Csa4M126430.1	AT5G15780.1 pollen Ole e 1 allergen and extensin family protein	-1.31
CsaUNM009930.1	AT5G25350.1 EBF2 (EIN3-BINDING F BOX PROTEIN 2); protein binding	-1.30
Csa4M625570.1	AT2G34250.1 protein transport protein sec61, putative	-1.29
Csa6M148170.1	AT3G44940.1 unknown protein	-1.29
	AT3G14880.2 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; BEST Arabidopsis thaliana protein match is: DOG1 (DELAY OF GERMINATION 1) (TAIR:AT5G45830.1); Has 368 Blast hits to 367 proteins in 28 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 366; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	-1.27
Csa4M463190.1	AT1G69530.1 ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1)	-1.26
Csa3M664560.1	AT2G34430.1 LHB1B1; chlorophyll binding	-1.25
Csa7M018830.1	No hits found	-1.22
Csa5M644580.1	AT5G38450.1 CYP735A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.22
Csa2M047780.1	AT2G47270.1 transcription factor/ transcription regulator	-1.22
	AT1G66840.1 INVOLVED IN: biological_process unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF827, plant (InterPro:IPR008545); BEST Arabidopsis thaliana protein match is: PMI15 (plastid movement impaired 15) (TAIR:AT5G38150.1); Has 66436 Blast hits to 37670 proteins in 1596 species: Archae - 890; Bacteria - 7464; Metazoa - 33216; Fungi - 4897; Plants - 2570; Viruses - 192; Other Eukaryotes - 17207 (source: NCBI BLink).	-1.22
Csa2M404900.1	AT3G24620.1 ROPGEF8; Rho guanyl-nucleotide exchange factor	-1.22
Csa2M004130.1	AT1G59910.1 formin homology 2 domain-containing protein / FH2 domain-containing protein	-1.21
Csa6M404250.1	AT2G24430.1 ANAC038 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 38); transcription factor	-1.20
Csa2M376790.1	AT2G34430.1 LHB1B1; chlorophyll binding	-1.20
Csa6M522690.1	AT2G34430.1 LHB1B1; chlorophyll binding	-1.20
Csa4M003100.1	AT4G02100.1 DNAJ heat shock N-terminal domain-containing protein	-1.19
Csa5M322500.1	AT5G37180.1 SUS5; UDP-glycosyltransferase/ sucrose synthase	-1.19
	AT5G01360.1 EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF231, plant (InterPro:IPR004253); BEST Arabidopsis thaliana protein match is: ESK1 (ESKIMO 1) (TAIR:AT3G55990.1); Has 710 Blast hits to 702 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 2; Plants - 705; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	-1.18
Csa6M419440.1	AT3G05470.1 formin homology 2 domain-containing protein / FH2 domain-containing protein	-1.17
Csa1M569460.1	AT3G58120.1 BZIP61; DNA binding / transcription activator/ transcription factor	-1.17
Csa4M628890.1	AT3G58120.1 BZIP61; DNA binding / transcription activator/ transcription factor	-1.17
Csa6M526250.1	AT3G23290.2 LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4)	-1.17
Csa3M002620.1	AT3G51325.1 zinc finger (C3HC4-type RING finger) family protein	-1.17

Csa1M039830.1	AT1G74110.1 CYP78A10; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.17
Csa3M743390.1	AT1G08080.1 ACA7 (ALPHA CARBONIC ANHYDRASE 7); carbonate dehydratase/ zinc ion binding	-1.17
Csa2M369740.1	AT1G28230.1 PUP1 (PURINE PERMEASE 1); purine nucleoside transmembrane transporter/ purine transmembrane transporter	-1.17
Csa5M322500.2	AT5G37180.1 SUS5; UDP-glycosyltransferase/ sucrose synthase	-1.16
Csa5M141160.1	AT4G39730.1 lipid-associated family protein	-1.16
Csa7M430200.1	AT2G18370.1 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-1.16
Csa6M110840.1	AT5G35740.1 glycosyl hydrolase family protein 17	-1.15
Csa3M732630.1	AT2G37970.1 SOUL-1; binding	-1.15
Csa6M421640.1	AT1G05000.2 tyrosine specific protein phosphatase family protein	-1.15
Csa5M630970.1	AT3G28180.1 ATCSLC04 (CELLULOSE-SYNTHASE LIKE C4); cellulose synthase/ transferase, transferring glycosyl groups	-1.14
Csa6M491070.1	AT5G67210.1 unknown protein	-1.14
Csa4M646410.1	AT1G54200.1 unknown protein	-1.14
Csa3M179150.1	AT5G62170.1 unknown protein	-1.13
Csa6M445010.1	AT2G37130.1 peroxidase 21 (PER21) (P21) (PRXR5)	-1.13
Csa5M635430.1	AT3G01220.1 ATHB20 (ARABIDOPSIS THALIANA HOMEBOX PROTEIN 20); DNA binding / transcription factor	-1.13
Csa7M354530.1	AT3G07350.1 unknown protein	-1.12
Csa5M272920.1	AT1G60690.1 aldo/keto reductase family protein	-1.12
Csa5M410730.1	AT1G66200.1 ATGSR2; copper ion binding / glutamate-ammonia ligase	-1.12
Csa1M049960.1	AT5G63180.1 pectate lyase family protein	-1.11
Csa2M379990.1	AT5G11420.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cell wall, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25460.1); Has 185 Blast hits to 157 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 185; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	-1.11
Csa7M059150.1	AT1G22360.1 AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups	-1.11
Csa3M037080.1	AT1G12460.1 leucine-rich repeat transmembrane protein kinase, putative	-1.11
Csa2M030040.1	AT3G05410.2 calcium ion binding	-1.11
Csa6M109730.1	AT1G05560.1 UGT75B1 (UDP-GLUCOSYLTRANSFERASE 75B1); UDP-glucose:4-aminobenzoate acylglucosyltransferase/ UDP-glucosyltransferase/ UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring glycosyl groups	-1.10
Csa3M731090.1	AT1G33970.1 avirulence-responsive protein, putative / avirulence induced gene protein, putative / AIG protein, putative	-1.10
Csa2M171950.1	AT3G23530.1 cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	-1.10
Csa2M360840.1	AT1G19300.1 PARVUS (PARVUS); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	-1.09
Csa6M404200.1	AT1G26945.1 KDR (KIDARI); transcription regulator	-1.09
Csa5M589390.1	AT3G61470.1 LHCA2; chlorophyll binding	-1.09
Csa3M150740.1	AT4G15530.2 PDK (pyruvate orthophosphate dikinase); kinase/ pyruvate, phosphate dikinase	-1.09
Csa2M427340.1	AT2G23300.1 leucine-rich repeat transmembrane protein kinase, putative	-1.08
Csa5M638350.2	AT5G15410.1 DND1 (DEFENSE NO DEATH 1); calcium channel/ calmodulin binding / cation channel/ cyclic nucleotide binding / intracellular cAMP activated cation channel/ intracellular cyclic nucleotide activated cation channel/ inward rectifier potassium channel	-1.08
Csa2M021550.1	AT1G22490.1 basic helix-loop-helix (bHLH) family protein	-1.08
Csa6M148260.1	AT2G28160.1 FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor	-1.07

Csa5M241140.1	AT1G68040.1 S-adenosyl-L-methionine:carboxyl methyltransferase family protein	-1.06
Csa2M234510.1	AT3G48690.1 CXE12; carboxylesterase	-1.05
Csa2M176700.1	AT1G44191.1 Encodes a ECA1 gametogenesis related family protein	-1.05
Csa5M633170.1	AT3G28345.1 ABC transporter family protein	-1.04
Csa2M171940.1	AT3G23530.1 cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	-1.04
Csa1M427510.1	AT2G19330.1 leucine-rich repeat family protein	-1.04
Csa2M348790.1	AT1G60590.1 polygalacturonase, putative / pectinase, putative	-1.04
Csa2M070320.1	AT5G17420.1 IRX3 (IRREGULAR XYLEM 3); cellulose synthase	-1.03
Csa6M088160.1	AT4G37370.1 CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.03
Csa5M577380.1	AT3G25640.1 unknown protein	-1.03
Csa7M041330.2	AT5G54060.1 UF3GT (udp-glucose:flavonoid 3-O-glucosyltransferase); transferase, transferring glycosyl groups	-1.03
Csa7M059660.1	AT1G22370.2 AtUGT85A5 (UDP-glucosyl transferase 85A5); glucuronosyltransferase/ transferase, transferring glycosyl groups	-1.03
Csa4M000660.1	AT1G70210.1 CYCD1;1 (CYCLIN D1;1); cyclin-dependent protein kinase regulator	-1.02
	AT3G11980.1 MS2 (MALE STERILITY 2); fatty acyl-CoA reductase (alcohol-forming)/ oxidoreductase, acting on the CH-CH group of donors, NAD or NADP as acceptor	-1.02
Csa6M151810.1		-1.02
Csa6M516850.1	AT4G21440.1 ATMYB102 (ARABIDOPSIS MYB-LIKE 102); DNA binding / transcription factor	-1.02
	AT3G18660.2 PGSIP1 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 1); transferase, transferring glycosyl groups	-1.02
Csa6M483470.1		-1.02
Csa3M127030.1	AT2G44740.1 CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	-1.00
Csa7M452960.1	AT5G25830.1 zinc finger (GATA type) family protein	-1.00
Csa1M532340.1	AT2G30070.1 ATKT1 (POTASSIUM TRANSPORTER 1); potassium ion transmembrane transporter	-1.00

#### Edisto only

Cucumber Locus ID	Top <i>Arabidopsis thaliana</i> hit	log fold change (-Cu vs +Cu) down efe -Cu    down Ed -Cu
Csa2M006080.1	AT2G26695.1 binding / zinc ion binding	-10.33
Csa7M169070.1	AT4G39250.1 ATRL1 (ARABIDOPSIS RAD-LIKE 1); DNA binding / transcription factor	-6.26
Csa7M318990.1	AT1G78780.2 pathogenesis-related family protein	-5.12
Csa4M374640.1	No hits found	-4.54
Csa4M304760.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	-4.51
	AT2G02390.1 ATGSTZ1 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE ZETA 1); catalytic/ glutathione transferase	-4.49
Csa2M336130.1		-4.49
Csa4M111580.1	AT5G64300.1 ATGCH; 3,4-dihydroxy-2-butanone-4-phosphate synthase/ GTP cyclohydrolase II	-4.40
Csa4M303680.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	-4.29
Csa4M304750.1	AT3G09270.1 ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	-3.88
	AT1G70330.1 ENT1,AT (EQUILIBRATIVE NUCLEOTIDE TRANSPORTER 1); nucleoside transmembrane transporter/ nucleoside transmembrane transporter, against a concentration gradient	-3.87
Csa2M010400.1		-3.87
	AT1G70330.1 ENT1,AT (EQUILIBRATIVE NUCLEOTIDE TRANSPORTER 1); nucleoside transmembrane transporter/ nucleoside transmembrane transporter, against a concentration gradient	-3.69
Csa2M010410.1		-3.69
Csa3M852630.1	AT4G31940.1 CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-3.46
Csa2M416170.1	AT2G32540.1 ATCSLB04; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	-3.31
Csa7M072870.1	AT1G26240.1 proline-rich extensin-like family protein	-3.15
Csa6M298480.1	AT1G07890.3 APX1 (ascorbate peroxidase 1); L-ascorbate peroxidase	-3.08
Csa4M640960.1	AT5G42830.1 transferase family protein	-3.08
Csa3M855350.1	AT1G75130.1 CYP721A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-3.01
Csa2M416170.2	AT2G32530.1 ATCSLB03; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	-2.99
Csa3M855360.1	AT1G75130.1 CYP721A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-2.79

	AT2G26250.1 KCS10 (3-KETOACYL-COA SYNTHASE 10); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	-2.47
Csa4M649640.1	AT1G47710.1 serpin, putative / serine protease inhibitor, putative	-2.35
Csa2M360680.1	AT2G21610.1 pectinesterase family protein	-2.30
Csa2M248110.1	AT3G19430.1 late embryogenesis abundant protein-related / LEA protein-related	-2.26
Csa1M154060.1	No hits found	-2.21
Csa4M375140.1	AT1G19610.1 PDF1.4	-2.19
Csa3M851940.1	AT2G42990.1 GDSL-motif lipase/hydrolase family protein	-2.15
Csa6M421680.1	AT2G34340.1 unknown protein	-2.11
Csa6M520440.1	AT1G75590.1 auxin-responsive family protein	-2.10
Csa7M007930.1	AT1G28110.1 SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase	-2.02
Csa3M823640.1	AT2G45970.1 CYP86A8; fatty acid (omega-1)-hydroxylase/ oxygen binding	-2.02
Csa6M004550.1	AT2G48140.1 EDA4 (embryo sac development arrest 4); lipid binding	-1.99
Csa6M410090.1	AT2G44050.1 COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase	-1.97
Csa6M366300.1	AT1G54540.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: hypocotyl, flower, root; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: harpin-induced protein-related / HIN1-related / harpin-responsive protein-related (TAIR:AT1G65690.1); Has 612 Blast hits to 611 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 612; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	-1.95
Csa5M182130.1	AT4G01870.1 toIB protein-related	-1.93
Csa7M419590.1	No hits found	-1.93
Csa2M420470.1	AT1G73050.1 (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative	-1.91
Csa2M050000.1	AT3G19430.1 late embryogenesis abundant protein-related / LEA protein-related	-1.87
Csa1M153550.1	AT5G42210.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Major facilitator superfamily MFS-1 (InterPro:IPR011701), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: tetracycline transporter (TAIR:AT2G16990.2); Has 985 Blast hits to 984 proteins in 348 species: Archae - 2; Bacteria - 541; Metazoa - 251; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 152 (source: NCBI BLink).	-1.84
Csa6M045090.1	AT4G29740.2 CKX4 (CYTOKININ OXIDASE 4); amine oxidase/ cytokinin dehydrogenase	-1.84
Csa1M589060.1	AT1G21550.1 calcium-binding protein, putative	-1.83
Csa6M376250.1	AT1G49430.1 LACS2 (LONG-CHAIN ACYL-COA SYNTHETASE 2); long-chain-fatty-acid-CoA ligase	-1.81
Csa2M238260.1	AT1G74460.1 GDSL-motif lipase/hydrolase family protein	-1.79
Csa1M009780.1	AT2G42360.1 zinc finger (C3HC4-type RING finger) family protein	-1.79
Csa6M420520.1	AT1G19840.1 auxin-responsive family protein	-1.78
Csa2M257100.1	AT2G25410.1 protein binding / zinc ion binding	-1.78
Csa3M603600.1	AT3G47390.1 cytidine/deoxycytidylate deaminase family protein	-1.78
Csa1M655920.1	AT5G23150.1 HUA2 (ENHANCER OF AG-4 2); transcription factor	-1.76
Csa6M499070.1	AT5G23950.1 C2 domain-containing protein	-1.75
Csa3M183350.1	AT5G49350.1 unknown protein	-1.75
Csa6M311000.1	AT5G23190.1 CYP86B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.71
Csa7M420770.1	AT5G41040.1 transferase family protein	-1.71
Csa1M001360.1	AT2G38110.1 GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase	-1.69
Csa3M732400.1	AT3G13600.1 calmodulin-binding family protein	-1.68
Csa4M279910.1	AT1G55230.1 unknown protein	-1.66
Csa4M280600.1	AT4G37330.1 CYP81D4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.64
Csa2M425750.1		

Csa4M081280.1	AT1G53620.1 unknown protein	-1.64
Csa1M716260.1	AT4G20390.1 integral membrane family protein	-1.64
Csa1M701960.1	AT2G35150.1 EXL1 (EXORDIUM LIKE 1)	-1.64
	AT4G14746.1 INVOLVED IN: biological_process unknown; LOCATED IN: anchored to membrane; CONTAINS InterPro DOMAIN/s: EGF (InterPro:IPR006210); Has 201 Blast hits to 179 proteins in 41 species: Archae - 0; Bacteria - 0; Metazoa - 168; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	
Csa2M011540.1		-1.62
Csa2M441240.1	AT2G23910.1 cinnamoyl-CoA reductase-related	-1.62
Csa3M127060.1	AT1G29000.1 heavy-metal-associated domain-containing protein	-1.61
Csa5M576690.1	No hits found	-1.60
Csa1M264010.1	AT2G12462.1 unknown protein	-1.59
Csa4M052070.1	No hits found	-1.57
Csa3M816090.1	AT1G18410.1 kinesin motor protein-related	-1.56
Csa3M180430.1	AT3G61150.1 HDG1 (HOMEODOMAIN GLABROUS 1); DNA binding / transcription factor	-1.56
Csa1M489250.1	AT2G28690.1 unknown protein	-1.56
	AT3G11430.1 GPAT5 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 5); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase/ organic anion transmembrane transporter	
Csa5M182690.1		-1.54
Csa7M069690.1	AT1G09970.1 LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	-1.52
Csa3M142970.1	AT2G38870.1 protease inhibitor, putative	-1.51
Csa1M015640.1	AT2G21100.1 disease resistance-responsive protein-related / dirigent protein-related	-1.51
Csa3M681140.1	AT5G23190.1 CYP86B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.50
Csa5M146870.1	AT4G10490.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1.48
Csa1M528600.1	AT5G58860.1 CYP86A1 (CYTOCHROME P450 86 A1); fatty acid (omega-1)-hydroxylase/ oxygen binding	-1.47
Csa2M286480.1	AT4G37160.1 sks15 (SKU5 Similar 15); copper ion binding / oxidoreductase	-1.46
Csa5M182670.1	AT2G39705.1 RTFL8 (ROTUNDIFOLIA LIKE 8)	-1.44
Csa6M094690.1	No hits found	-1.43
	AT5G25250.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Band 7 protein (InterPro:IPR001107); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25260.1); Has 4072 Blast hits to 3210 proteins in 656 species: Archae - 10; Bacteria - 1411; Metazoa - 994; Fungi - 195; Plants - 102; Viruses - 10; Other Eukaryotes - 1350 (source: NCBI BLink).	
Csa2M382440.1		-1.43
Csa6M514860.1	AT1G61800.1 GPT2; antiporter/ glucose-6-phosphate transmembrane transporter	-1.43
	AT5G26340.1 MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter	
Csa6M424530.1		-1.41
	AT5G12460.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF604 (InterPro:IPR006740); BEST Arabidopsis thaliana protein match is: fringe-related protein (TAIR:AT2G37730.1); Has 355 Blast hits to 351 proteins in 67 species: Archae - 0; Bacteria - 0; Metazoa - 96; Fungi - 121; Plants - 131; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	
Csa1M615150.1		-1.41
Csa6M499890.1	AT3G02940.1 MYB107 (myb domain protein 107); DNA binding / transcription factor	-1.40
Csa4M050130.1	AT1G64000.1 WRKY56; transcription factor	-1.39
Csa1M012150.2	AT5G15490.1 UDP-glucose 6-dehydrogenase, putative	-1.38
Csa5M139730.1	AT5G24090.1 acidic endochitinase (CHIB1)	-1.38
Csa2M005890.1	AT2G26910.1 PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances	-1.38
Csa4M064650.1	AT1G17180.1 ATGSTU25 (GLUTATHIONE S-TRANSFERASE TAU 25); glutathione transferase	-1.35
Csa3M180430.2	AT3G61150.1 HDG1 (HOMEODOMAIN GLABROUS 1); DNA binding / transcription factor	-1.34
Csa6M014540.1	AT2G40610.1 ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	-1.34

Csa3M816700.1	AT5G19750.1 peroxisomal membrane 22 kDa family protein	-1.34
Csa6M517100.1	AT4G28180.1 unknown protein	-1.32
Csa7M430230.1	AT3G21240.1 4CL2 (4-COUMARATE:COA LIGASE 2); 4-coumarate-CoA ligase	-1.30
Csa2M055560.1	AT1G73050.1 (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative	-1.30
Csa5M157220.1	AT4G25410.1 DNA binding / transcription factor	-1.30
Csa3M741330.1	AT2G36870.1 xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	-1.29
Csa5M162010.1	AT5G47500.1 pectinesterase family protein	-1.29
Csa5M180860.1	AT2G39490.1 F-box family protein	-1.28
Csa2M000930.1	AT2G44330.1 zinc finger (C3HC4-type RING finger) family protein	-1.27
Csa2M193350.1	AT3G01670.1 unknown protein	-1.26
Csa1M029570.1	AT1G17950.1 MYB52 (MYB DOMAIN PROTEIN 52); DNA binding / transcription factor	-1.24
Csa6M486900.1	AT5G64790.1 glycosyl hydrolase family 17 protein	-1.24
Csa3M883020.1	AT2G24400.1 auxin-responsive protein, putative / small auxin up RNA (SAUR_D)	-1.24
Csa1M051630.1	AT1G08510.1 FATB (fatty acyl-ACP thioesterases B); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase	-1.24
Csa5M604990.1	AT1G69700.1 ATHVA22C	-1.23
Csa1M294600.1	AT2G18650.1 MEE16 (maternal effect embryo arrest 16); protein binding / zinc ion binding	-1.22
Csa3M073920.1	AT5G55180.1 glycosyl hydrolase family 17 protein	-1.21
Csa6M012820.1	AT5G05390.1 LAC12 (laccase 12); laccase	-1.21
Csa3M144140.1	AT5G43760.1 KCS20 (3-KETOACYL-COA SYNTHASE 20); fatty acid elongase	-1.21
Csa3M258180.1	AT5G37478.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G15510.1); Has 39 Blast hits to 39 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	-1.21
Csa1M257950.1	AT4G30850.1 HHP2 (HEPTAHELICAL TRANSMEMBRANE PROTEIN2); receptor	-1.21
Csa6M000690.1	AT1G56720.1 protein kinase family protein	-1.20
Csa6M004540.1	AT4G00400.1 GPAT8 (glycerol-3-phosphate acyltransferase 8); acyltransferase/ glycerol-3-phosphate O-acyltransferase	-1.20
Csa4M361890.1	AT1G44170.1 ALDH3H1 (ALDEHYDE DEHYDROGENASE 3H1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	-1.18
Csa4M165900.1	AT2G41810.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41800.1); Has 161 Blast hits to 157 proteins in 12 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 159; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLINK).	-1.18
Csa5M056630.1	AT1G03940.1 transferase family protein	-1.17
Csa1M613500.1	No hits found	-1.17
Csa1M181380.1	AT5G47635.1 unknown protein	-1.16
Csa7M407810.1	No hits found	-1.16
Csa6M452040.1	AT5G03610.1 GDSL-motif lipase/hydrolase family protein	-1.15
Csa4M004780.1	AT3G15650.1 phospholipase/carboxylesterase family protein	-1.15
Csa1M533470.1	AT2G30210.1 LAC3 (laccase 3); laccase	-1.14
Csa1M012150.1	AT5G15490.1 UDP-glucose 6-dehydrogenase, putative	-1.14
Csa7M014510.1	AT4G38540.1 monooxygenase, putative (MO2)	-1.14
Csa6M424540.1	AT5G26340.1 MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter	-1.14
Csa4M652640.1	AT5G25190.1 ethylene-responsive element-binding protein, putative	-1.13

Csa6M497390.1	AT2G22590.1 transferase, transferring glycosyl groups	-1.13
Csa3M357110.1	AT4G27950.1 CRF4 (CYTOKININ RESPONSE FACTOR 4); DNA binding / transcription factor	-1.13
Csa3M129660.1	AT4G13940.1 MEE58 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding	-1.13
	AT2G36790.1 UGT73C6 (UDP-glucosyl transferase 73C6); UDP-glucosyltransferase/ UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	-1.11
Csa3M745000.1		-1.11
Csa1M589130.1	AT1G20300.1 pentatricopeptide (PPR) repeat-containing protein	-1.10
Csa1M614640.1	No hits found	-1.09
Csa6M312590.1	No hits found	-1.08
Csa5M622530.1	AT2G39210.1 nodulin family protein	-1.07
Csa3M646670.1	AT1G53820.1 zinc finger (C3HC4-type RING finger) family protein	-1.07
Csa7M047420.1	AT4G28250.1 ATEXPB3 (ARABIDOPSIS THALIANA EXPANSIN B3)	-1.06
Csa6M128550.1	AT2G20690.1 lumazine-binding family protein	-1.06
Csa1M015700.1	AT5G15630.1 IRX6	-1.05
Csa2M115750.1	AT3G19430.1 late embryogenesis abundant protein-related / LEA protein-related	-1.04
Csa6M128550.2	AT2G20690.1 lumazine-binding family protein	-1.04
Csa7M430240.1	AT3G21240.1 4CL2 (4-COUMARATE:COA LIGASE 2); 4-coumarate-CoA ligase	-1.04
Csa7M201850.1	No hits found	-1.04
Csa6M505950.1	AT4G36040.1 DNAJ heat shock N-terminal domain-containing protein (J11)	-1.03
	AT1G59870.1 PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	-1.03
Csa7M433950.1		-1.03
Csa1M044930.1	AT1G09610.1 unknown protein	-1.03
Csa3M912920.1	AT4G17570.1 zinc finger (GATA type) family protein	-1.03
Csa7M048110.1	AT3G14940.1 ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase	-1.03
Csa3M857600.1	AT4G13130.1 DC1 domain-containing protein	-1.02
Csa4M618490.1	AT1G05300.1 ZIP5; cation transmembrane transporter/ metal ion transmembrane transporter	-1.02
Csa3M915160.1	AT4G27600.1 pfkB-type carbohydrate kinase family protein	-1.02
Csa3M748240.1	AT3G10040.1 transcription factor	-1.01
Csa1M541390.1	AT1G30690.1 SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	-1.01
Csa4M038670.1	AT4G36640.1 SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	-1.01
Csa3M901690.1	AT5G46700.1 TRN2 (TORNADO 2)	-1.01
Csa3M151480.1	AT4G15610.1 integral membrane family protein	-1.01
Csa4M218340.1	No hits found	-1.01

**Table S11. Genes that were upregulated by Fe and Cu deficiency in *fefe* and *Edisto* roots.**

Common elements in "fefe Up-Fe" and "fefe Up-Cu":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>up fefe -Fe</u>	<u>up fefe -Cu</u>	<u>up Ed -Fe</u>	<u>up Ed -Cu</u>
Csa2M033340.1	No hits found	1.68	1.34		
Csa1M071800.1	AT5G54490.1 PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding / protein binding	3.88	1.48		
Csa2M070840.1	AT1G08860.1 BON3 (BONZAI 3); calcium-dependent phospholipid binding	1.62	1.72		
Csa3M651800.1	AT5G07990.1 TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	1.76	1.14		
Csa2M069700.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	1.50	1.62		
	AT3G51860.1 CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	1.15	1.17		
Csa2M070200.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	1.46	1.30		
Csa1M074400.1	AT4G20970.1 basic helix-loop-helix (bHLH) family protein	2.62	2.40		
Csa2M357220.1	AT5G11210.1 ATGLR2.5; intracellular ligand-gated ion channel	1.45	1.05		
Csa5M148520.1	AT1G64660.1 ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase	2.12	1.85		
Csa2M069200.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	1.48	1.37		
Csa3M651820.1	AT5G07990.1 TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	1.97	1.29		
Csa3M778970.1	AT2G35980.1 YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	1.00	1.08		
Csa2M070210.1	AT2G30490.1 C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	1.45	1.48		
Csa3M778380.1	AT5G42560.1 abscisic acid-responsive HVA22 family protein	1.82	1.16		
Csa1M007890.1	AT1G18980.1 germin-like protein, putative	1.07	1.34		
Csa2M033350.1	AT5G26920.1 CBP60G (CAM-BINDING PROTEIN 60-LIKE.G); calmodulin binding	1.67	1.22		
Csa6M500640.2	AT4G39830.1 L-ascorbate oxidase, putative	2.15	1.27		
Csa2M431070.1	AT5G17540.1 transferase family protein	2.00	1.03		
Csa1M062280.1	AT5G35830.1 ankyrin repeat family protein	1.64	1.09		
Csa6M500640.1	AT4G39830.1 L-ascorbate oxidase, putative	2.13	1.34		
Csa1M032450.1	AT5G63160.1 BT1 (BTB AND TAZ DOMAIN PROTEIN 1); protein binding / transcription regulator	2.14	1.00		
Csa3M643770.1	AT2G45570.1 CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	1.64	1.19		
Csa6M363520.1	No hits found	1.78	1.01		

Common elements in "Ed Up-Fe" and "Ed Up-Cu":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>up fefe -Fe</u>	<u>up fefe -Cu</u>	<u>up Ed -Fe</u>	<u>up Ed -Cu</u>
Csa6M404290.1	No hits found			1.21	1.40
Csa5M571440.1	AT5G17350.1 unknown protein			1.22	2.67
Csa4M279850.1	AT2G27180.1 unknown protein			1.30	2.49
Csa2M357340.1	AT1G18530.1 calmodulin, putative			1.24	1.13
Csa6M502780.1	No hits found			1.02	1.59
Csa6M505230.2	AT2G21320.1 zinc finger (B-box type) family protein			1.52	1.62
Csa6M505230.1	AT2G21320.1 zinc finger (B-box type) family protein			1.47	1.62
Csa5M146930.1	AT1G32928.1 unknown protein			1.23	2.37
Csa4M665120.1	AT1G21010.1 unknown protein			1.16	1.20
Csa6M518190.1	AT1G28480.1 GRX480; electron carrier/ protein disulfide oxidoreductase			1.01	2.23
Csa6M518000.2	AT1G28330.1 DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)			1.12	1.25
Csa5M150470.1	AT1G64340.1 unknown protein			1.28	2.78
Csa6M303740.1	AT2G28710.1 zinc finger (C2H2 type) family protein			1.05	2.12
Csa4M192100.1	AT5G58375.1 unknown protein			1.21	1.19
Csa6M518000.1	AT1G28330.1 DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)			1.18	1.35
Csa5M611700.1	AT1G71100.1 RSW10 (RADIAL SWELLING 10); ribose-5-phosphate isomerase			1.07	1.66
Csa1M422480.1	AT5G57560.1 TCH4 (Touch 4); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase			1.33	2.04



Csa1M039020.1	AT5G61210.1 SNAP33 (SOLUBLE N-ETHYLMALIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding	1.01	1.58
Csa3M405510.1	AT5G48150.1 PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor	1.30	3.64

Common elements in "fefe Up-Cu" and "Ed Up-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>up fefe -Fe</u>	<u>up fefe -Cu</u>	<u>up Ed -Fe</u>	<u>up Ed -Cu</u>
Csa6M506000.1	AT4G36010.1 pathogenesis-related thaumatin family protein		1.08	1.61	
Csa2M010180.1	No hits found		1.99	1.68	
Csa1M534750.1	AT3G54420.1 ATEP3; chitinase		1.34	1.38	
Csa6M523460.1	AT1G30135.1 JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8)		2.95	1.51	
Csa4M031060.1	AT2G18540.1 cupin family protein		1.41	1.61	
Csa7M073520.1	AT4G34120.1 LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1)		2.04	1.71	
Csa2M193320.1	AT5G43650.1 basic helix-loop-helix (bHLH) family protein		2.83	1.33	
Csa6M106810.1	AT4G00910.1 unknown protein		1.58	2.43	
Csa3M141830.1	AT1G04330.1 unknown protein		1.10	1.35	
Csa3M000690.1	AT5G65980.1 auxin efflux carrier family protein		1.48	1.21	
Csa1M425940.1	AT5G57150.1 basic helix-loop-helix (bHLH) family protein		1.01	1.13	
Csa3M143510.1	AT1G04280.1 unknown protein		1.20	1.34	
Csa4M641670.1	AT3G16150.1 L-asparaginase, putative / L-asparagine amidohydrolase, putative		1.23	1.14	
Csa3M127170.1	AT1G32450.1 NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter		1.88	1.15	

Common elements in "fefe Up-Fe", "fefe Up-Cu" and "Ed Up-Fe":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>up fefe -Fe</u>	<u>up fefe -Cu</u>	<u>up Ed -Fe</u>	<u>up Ed -Cu</u>
Csa3M122660.1	AT2G45760.1 BAP2 (BON ASSOCIATION PROTEIN 2)	2.56	1.44	1.50	

Common elements in "fefe Up-Cu", "Ed Up-Fe" and "Ed Up-Cu":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>up fefe -Fe</u>	<u>up fefe -Cu</u>	<u>up Ed -Fe</u>	<u>up Ed -Cu</u>
Csa1M502880.1	AT2G28780.1 unknown protein		4.36	2.65	1.60
Csa1M526820.1	AT3G46900.1 COPT2; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter		1.35	1.79	1.71
Csa1M063490.1	No hits found		1.35	1.31	1.10
Csa6M521000.2	AT4G25310.1 oxidoreductase, 2OG-Fe(II) oxygenase family protein		1.06	1.25	1.33
	AT1G17020.1 SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc		1.12	1.09	1.22
Csa6M521000.1	AT4G34410.1 RRTF1 (REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor		1.58	1.38	4.08
Csa7M073700.1	AT1G12610.1 DDF1 (DWARF AND DELAYED FLOWERING 1); DNA binding / sequence-specific DNA binding / transcription factor		2.04	1.01	5.05
Csa2M418890.1	AT3G21680.1 unknown protein		1.63	1.27	2.10
Csa5M223070.1	AT2G40750.1 WRKY54; transcription factor		1.16	1.07	1.01
Csa3M180310.1	AT4G23030.1 MATE efflux protein-related		1.28	1.04	2.82
Csa6M016950.1	AT5G47850.1 CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase		1.07	1.51	1.98
Csa1M481200.1	AT5G59730.1 ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H7); protein binding		1.10	1.05	1.13
Csa1M005770.1	AT3G48180.1 unknown protein		1.02	1.29	2.19
Csa6M302190.1	AT5G59730.1 ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H7); protein binding		1.33	1.36	2.20
Csa3M180260.1	AT4G25490.1 CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor		1.01	1.10	3.64
Csa2M360780.1	AT5G42650.1 AOS (ALLENE OXIDE SYNTHASE); allene oxide synthase/ hydro-lyase/ oxygen binding		1.29	1.10	2.97

Common elements in "fefe Up-Fe", "fefe Up-Cu" and "Ed Up-Cu":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>up fefe -Fe</u>	<u>up fefe -Cu</u>	<u>up Ed -Fe</u>	<u>up Ed -Cu</u>
Csa7M237300.1	AT3G22240.1 unknown protein	2.86	1.21		1.62

Csa2M381800.1	AT5G04860.1 unknown protein	1.51	1.24	3.36
Csa2M297180.1	AT5G64810.1 WRKY51; transcription factor	1.23	1.20	1.04
Csa7M432520.1	AT5G20230.1 ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier	1.99	1.13	1.13

Common elements in "fefe Up-Fe" and "Ed Up-Cu":

<u>Cucumber Locus ID</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>up fefe -Fe</u>	<u>up fefe -Cu</u>	<u>up Ed -Fe</u>	<u>up Ed -Cu</u>
Csa4M642430.1	AT4G37540.1 LBD39 (LOB DOMAIN-CONTAINING PROTEIN 39)	1.14			1.96
Csa6M077420.1	AT2G45360.1 unknown protein	1.23			1.10
Csa6M032470.1	AT1G13340.1 unknown protein	1.62			1.01
Csa4M001970.1	AT3G16770.1 ATEBP (ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN); DNA binding / protein binding / transcription activator/ transcription factor	1.45			1.18
Csa6M403600.1	AT1G59710.1 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27100.1); Has 119 Blast hits to 107 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 119; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	1.28			1.66

**Table S12. Genes that were downregulated by Fe and Cu deficiency in *fefe* and Edisto roots.**

Common elements in "fefe Dn-Fe" and "fefe Dn-Cu":

<u>Cucumber Locus I</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>down fefe -Fe</u>	<u>down fefe -Cu</u>	<u>down Ed -Fe</u>	<u>down Ed -Cu</u>
Csa2M357280.1	AT3G19270.1 CYP707A4; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	-2.16	-1.54		
Csa6M404200.1	AT1G26945.1 KDR (KIDARI); transcription regulator	-1.16	-1.09		
Csa5M495960.1	AT1G09970.1 LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	-1.80	-1.93		
Csa5M211030.1	AT5G05500.1 pollen Ole e 1 allergen and extensin family protein	-1.15	-1.55		
Csa1M467060.1	AT1G78580.1 ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE); alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups	-1.06	-1.39		
Csa2M418940.1	AT1G05200.1 ATGLR3.4; intracellular ligand-gated ion channel	-1.60	-2.35		
Csa4M003100.1	AT4G02100.1 DNAJ heat shock N-terminal domain-containing protein	-1.50	-1.19		
Csa7M059150.1	AT1G22360.1 AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups	-1.20	-1.11		
Csa2M423640.1	AT5G36220.1 CYP81D1 (CYTOCHROME P450 81D1); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-4.70	-5.76		
Csa5M630970.1	AT3G28180.1 ATCSLC04 (CELLULOSE-SYNTHASE LIKE C4); cellulose synthase/ transferase, transferring glycosyl groups	-1.64	-1.14		
Csa3M127030.1	AT2G44740.1 CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	-1.09	-1.00		
Csa7M420830.1	AT3G63470.1 scpl40 (serine carboxypeptidase-like 40); serine-type carboxypeptidase	-1.44	-1.37		
Csa2M234510.1	AT3G48690.1 CXE12; carboxylesterase	-1.20	-1.05		
Csa7M059660.1	AT1G22370.2 AtUGT85A5 (UDP-glucosyl transferase 85A5); glucuronosyltransferase/ transferase, transferring glycosyl groups	-1.28	-1.03		
Csa1M071890.1	AT4G21490.1 NDB3; NADH dehydrogenase	-1.10	-1.42		
Csa6M088160.1	AT4G37370.1 CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	-1.15	-1.03		

Common elements in "Ed Dn-Fe" and "Ed Dn-Cu":

<u>Cucumber Locus I</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>down fefe -Fe</u>	<u>down fefe -Cu</u>	<u>down Ed -Fe</u>	<u>down Ed -Cu</u>
Csa7M430230.1	AT3G21240.1 4CL2 (4-COUMARATE:COA LIGASE 2); 4-coumarate-CoA ligase			-1.31	-1.30

Common elements in "fefe Dn-Cu" and "Ed Dn-Fe":

<u>Cucumber Locus I</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>down fefe -Fe</u>	<u>down fefe -Cu</u>	<u>down Ed -Fe</u>	<u>down Ed -Cu</u>
Csa7M419530.1	AT2G18150.1 peroxidase, putative		-1.56	-3.08	
Csa6M011600.1	AT3G47570.1 leucine-rich repeat transmembrane protein kinase, putative		-2.09	-1.40	
Csa5M272920.1	AT1G60690.1 aldo/keto reductase family protein		-1.12	-1.09	
Csa7M414530.1	AT4G37530.1 peroxidase, putative		-1.88	-3.11	

Common elements in "fefe Dn-Fe", "fefe Dn-Cu", "Ed Dn-Fe" and "Ed Dn-Cu":

<u>Cucumber Locus I</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>down fefe -Fe</u>	<u>down fefe -Cu</u>	<u>down Ed -Fe</u>	<u>down Ed -Cu</u>
Csa6M411280.1	AT3G25190.1 nodulin, putative	-4.58	-1.41	-1.85	-1.04

Common elements in "fefe Dn-Fe", "fefe Dn-Cu" and "Ed Dn-Cu":

<u>Cucumber Locus I</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>down fefe -Fe</u>	<u>down fefe -Cu</u>	<u>down Ed -Fe</u>	<u>down Ed -Cu</u>
Csa5M550240.1	AT2G01770.1 VIT1 (vacuolar iron transporter 1); iron ion transmembrane transporter	-3.36	-1.85		-1.25
Csa1M423010.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase	-5.25	-5.08		-4.36
Csa2M034530.1	AT1G56430.1 NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase	-1.75	-3.50		-3.20
Csa5M175770.1	AT1G23020.1 FRO3; ferric-chelate reductase	-1.70	-5.02		-3.33
Csa1M383520.1	AT4G13340.1 leucine-rich repeat family protein / extensin family protein	-1.73	-1.16		-1.13

Common elements in "fefe Dn-Fe" and "Ed Dn-Cu":

<u>Cucumber Locus I</u>	<u>Top Arabidopsis thaliana hit</u>	<u>log fold change (-metal vs +metal)</u>			
		<u>down fefe -Fe</u>	<u>down fefe -Cu</u>	<u>down Ed -Fe</u>	<u>down Ed -Cu</u>
Csa3M180430.1	AT3G61150.1 HDG1 (HOMEODOMAIN GLABROUS 1); DNA binding / transcription factor	-1.04			-1.56
Csa5M622530.1	AT2G39210.1 nodulin family protein	-1.05			-1.07
Csa3M603600.1	AT2G25410.1 protein binding / zinc ion binding	-1.93			-1.78
Csa5M157220.1	AT4G25410.1 DNA binding / transcription factor	-2.03			-1.30
Csa2M055560.1	AT1G73050.1 (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative	-1.16			-1.30
Csa1M154060.1	AT3G19430.1 late embryogenesis abundant protein-related / LEA protein-related	-2.31			-2.26